Supplemental Methods

Database analysis and data mining

Analysis of copy number variation mutation rates in human cancer was done by using the TCGA liver cancer dataset (LIHC; https://tcga-data.nci.nih.gov/tcga/) with the ONCOMINE browser (https://www.oncomine.org/) and the COSMIC database (http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/) on 07-28-2015. The data for E2F7/8 developmental and tumor associated target expression was obtained from TCGA tumor data sets using cbioportal (http://www.cbioportal.org/). Patients from Liver Hepatocellular Carcinoma (TCGA, Provisional) project with RNA-seq v2 data were selected.

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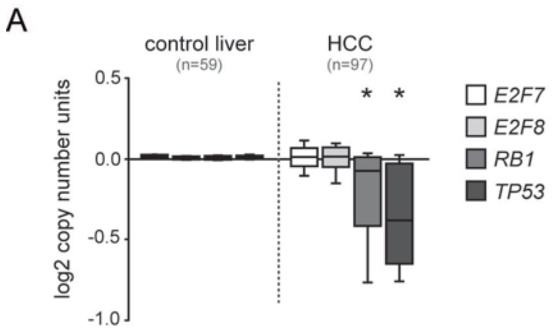
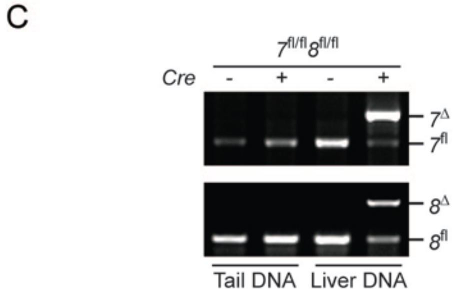
Supplemental Figure 1



B

COSMIC mutation rate analysis		
	Liver cancer	All cancers
E2F7	0.7% (10/1512)	0.8% (180/21329)
E2F8	0.5% (8/1512)	0.7% (151/21031)
RB1	2.3% (35/1534)	3.1% (856/27365)
TP53	27.6% (1219/4420)	27.7% (28253/101991)



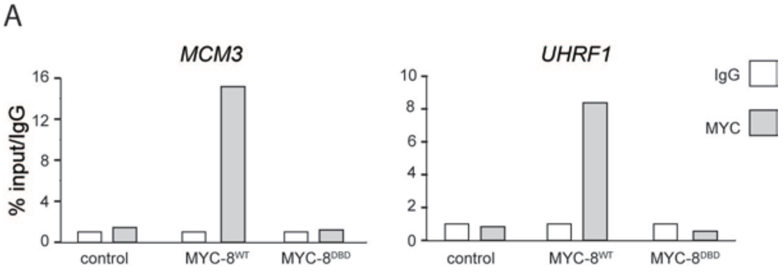
Supplemental Figure 1

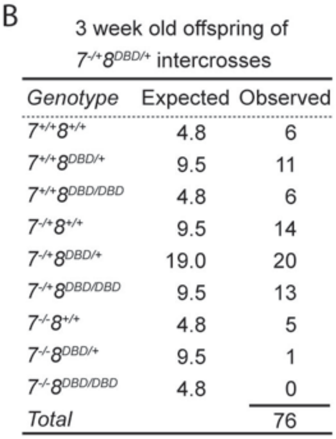
A. Box plots illustrating copy number variations in E2F pathway genes in normal and HCC liver samples using the TGCA database. The center lines in boxes represent the median. *, $P<0.001$; two-sided Student's *t*-test vs. control liver. n indicates the number of patients in each group.

B. Mutation frequency analysis of E2F pathway genes in liver cancer and all cancers using the COSMIC database. Percent of samples with mutation, number of samples with mutation and total sample number are displayed for each gene.

C. PCR genotyping showing deletion of *E2f7* and *E2f8* in the liver by *Albumin-cre*. DNA was isolated from the tail and liver of *cre-* $7^{fl/fl}8^{fl/fl}$ and *cre+* $7^{fl/fl}8^{fl/fl}$ mice and PCR was performed for *E2f7* (7^{fl}; 340bp and 7^{Δ}; 400bp) and *E2f8* (8^{fl}; 230bp and 8^{Δ}; 500bp).

Supplemental Figure 2





B

3 week old offspring of $7^{-/+}8^{DBD/+}$ intercrosses

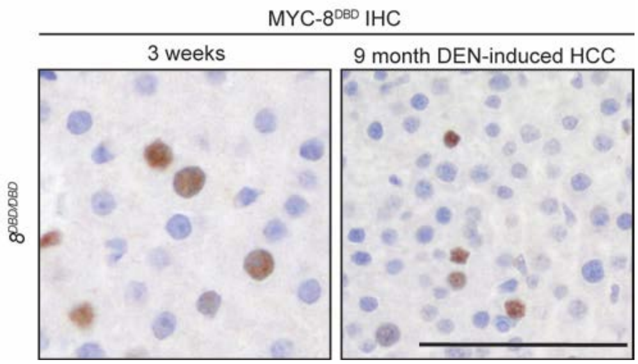
Genotype	Expected	Observed
$7^{+/+}8^{+/+}$	4.8	6
$7^{+/+}8^{DBD/+}$	9.5	11
$7^{+/+}8^{DBD/DBD}$	4.8	6
$7^{-/+}8^{+/+}$	9.5	14
$7^{-/+}8^{DBD/+}$	19.0	20
$7^{-/+}8^{DBD/DBD}$	9.5	13
$7^{-/-}8^{+/+}$	4.8	5
$7^{-/-}8^{DBD/+}$	9.5	1
$7^{-/-}8^{DBD/DBD}$	4.8	0
Total		76

Supplemental Figure 2

(A) ChIP-qPCR validation using IgG or MYC antibodies in HepG2 cells (control) or HepG2 cells expressing 5xMYC tagged wildtype E2F8 (MYC8^{wt}) or 5xMYC tagged DBD E2F8 (MYC8^{DBD}). *MCM3* and *UHRF1* are established E2F targets; *TUBA4A* is shown as a negative control. Percent of input values for MYC-tagged E2F8 were normalized to IgG.

(B) Table showing the ratios of expected and observed genotypes of mice surviving to 3 weeks of age. Ten litters from $7^{-/+}8^{DBD/+}$ x $7^{-/+-}8^{DBD/+}$ crosses were examined.

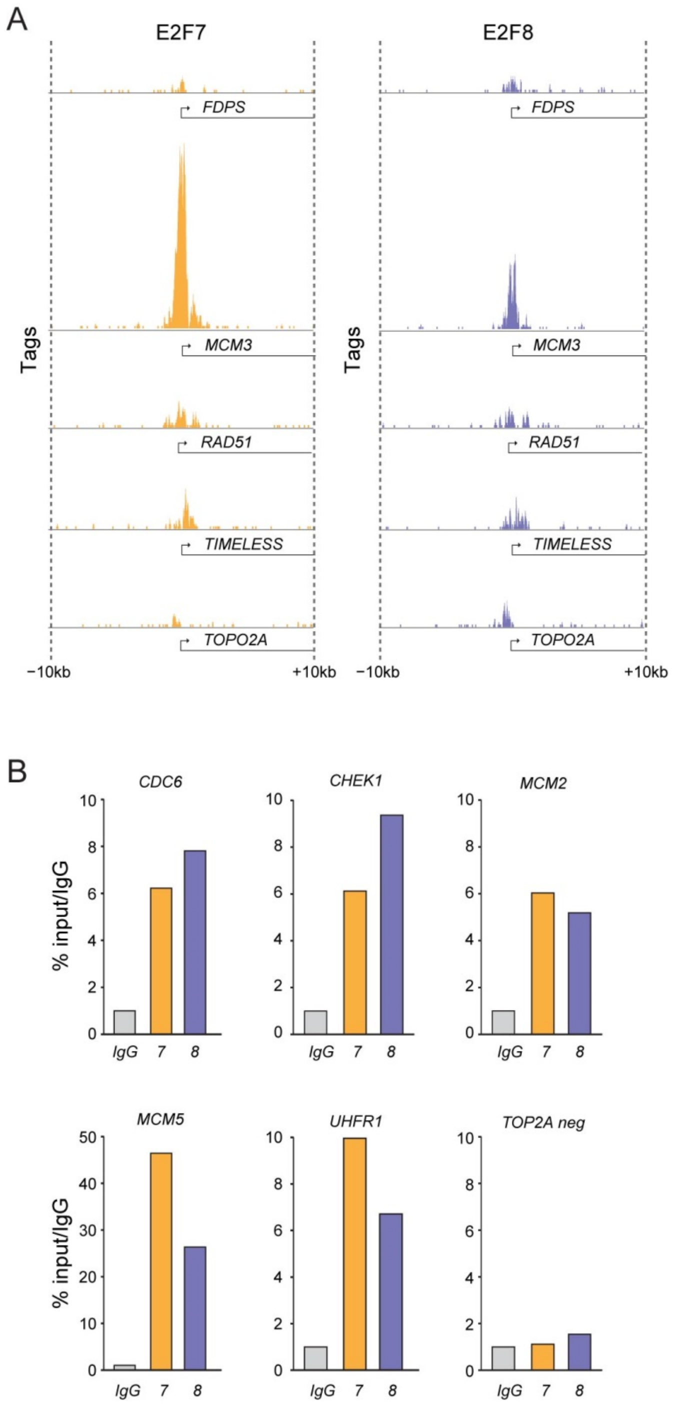
Supplemental Figure 3



Supplemental Figure 3

Immunohistochemistry for MYC recognizing the 5xMYC tagged E2F8^{DBD} protein (MYC-8^{DBD}) in livers from *E2f8*$^{DBD/DBD}$ mice showing the similar intensity of E2F8 staining in hepatocytes from 3 week old mice and HCC cells from 9 month old DEN-treated mice. Scale bar, 50 μm

Supplemental Figure 4

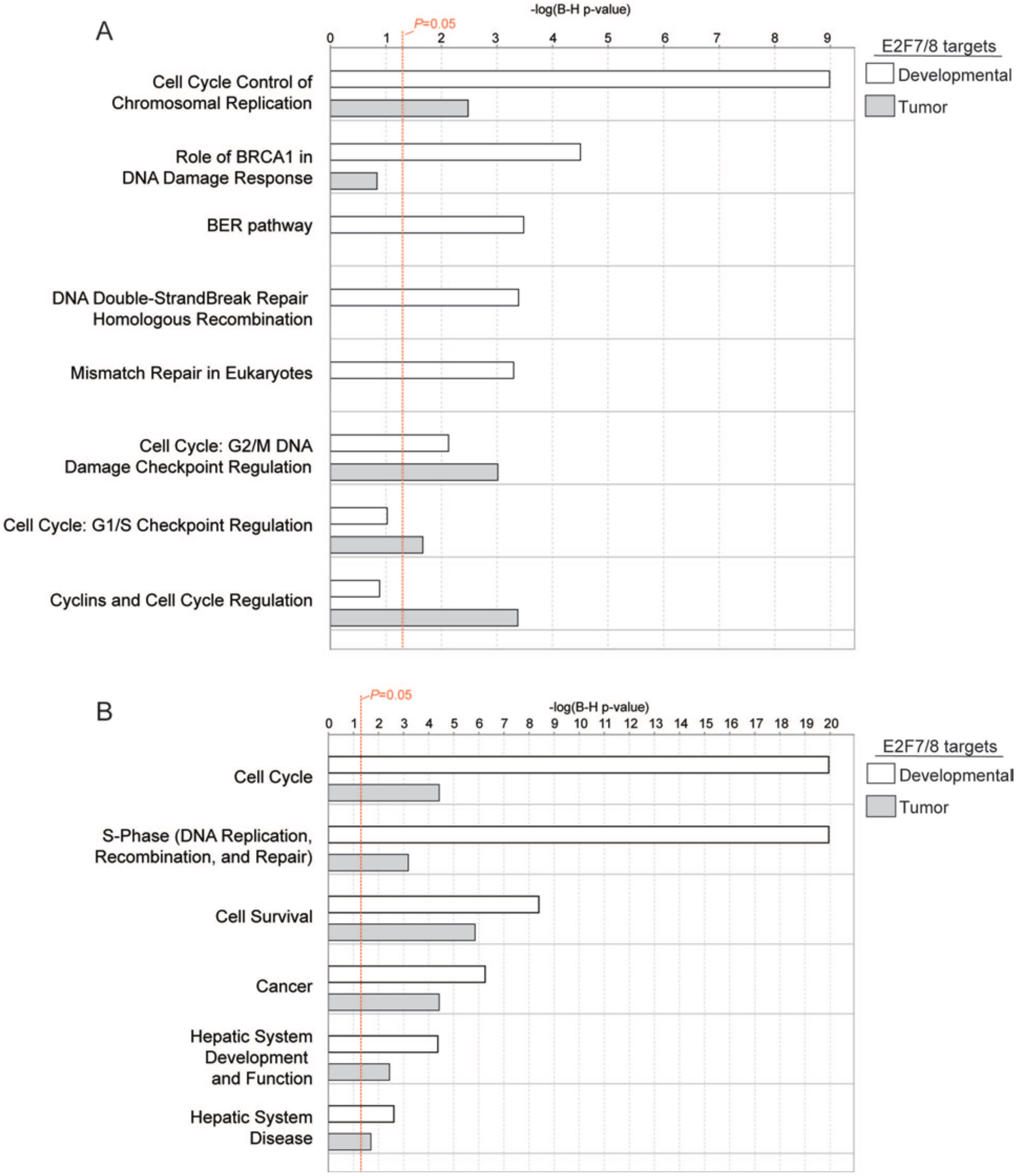


Supplemental Figure 4

(A) Examples of the promoter occupancy of E2Fs on selected gene promoters.

(B) ChIP-qPCR validation using IgG, E2F7 or E2F8 antibody's in THLE-2 cells to measure E2F7 and E2F8 on selected target promoters (*CDC6*, *CHEK1*, *MCM2*, *MCM5*, and *UHRF1*). A non-promoter region of *TOP2A* (*TOP2A neg*) was used as a negative control. % input values were normalized to IgG. Primers were designed to amplify ChIP-seq identified peak regions.

Supplemental Figure 5

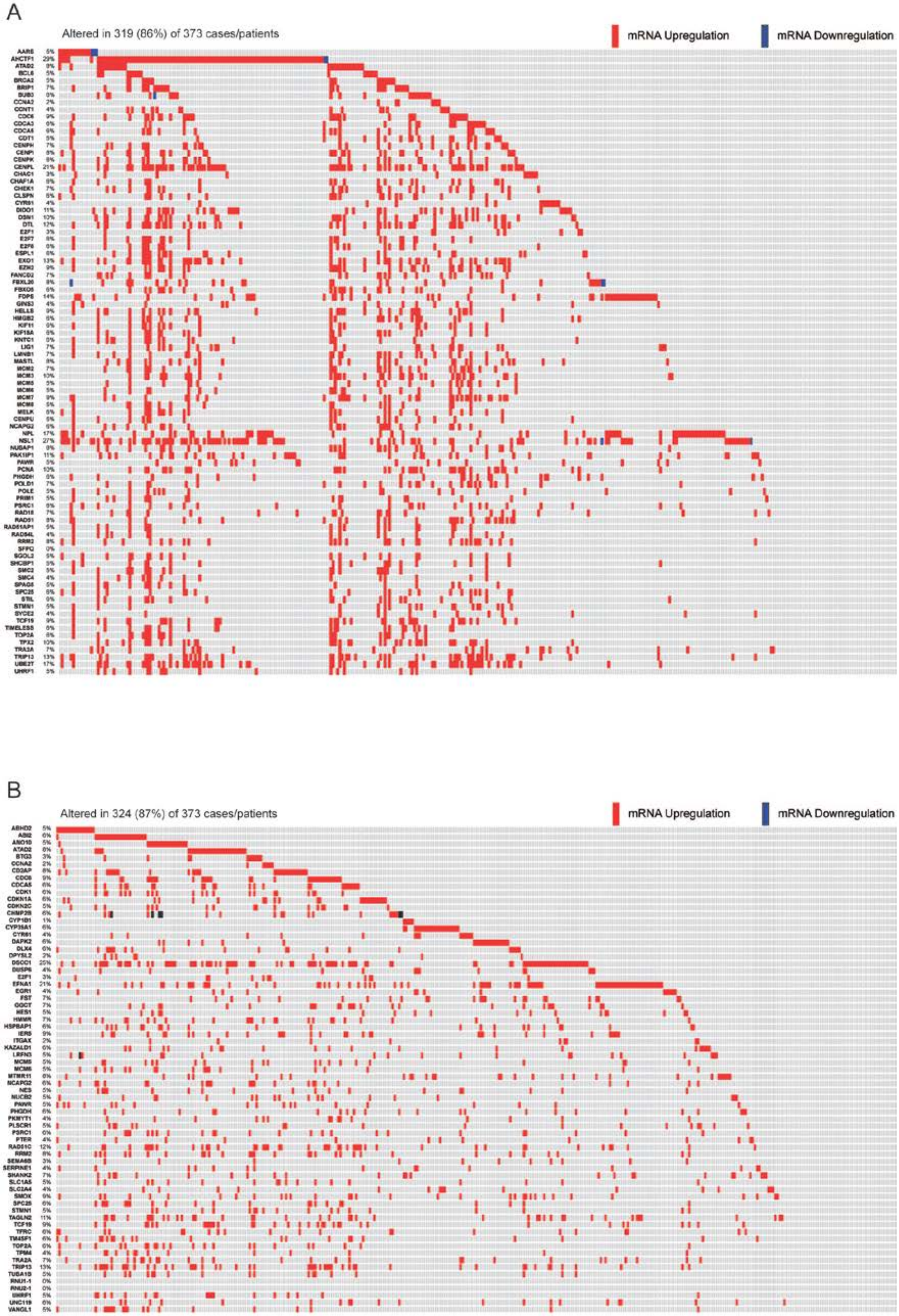


Supplemental Figure 5

A. Gene ontology using Ingenuity pathway analysis (IPA) software depicts the estimated contribution of E2F7/8 targets to functions related to canonical pathway involved in cell cycle, DNA repair and checkpoint control. Bars indicate the Benjamini-Hochberg adjusted *P*-value, the threshold of *P*=0.05 is shown.

B. Gene ontology using Ingenuity pathway analysis (IPA) software depicts the estimated contribution of E2F7/8 targets to functions related to cell cycle, cancer and liver disease. Bars indicate the Benjamini-Hochberg adjusted *P*-value, the threshold of *P*=0.05 is shown.

Supplemental Figure 6



Supplemental Figure 6

A. Map the expression of 88 E2F7/8 developmental associated targets in TCGA human HCC samples. Percent indicates the percent of tumors with upregulated (red boxes) or downregulated (blue boxes) mRNA expression of the indicated gene.
B. Map the expression of 69 E2F7/8 tumor associated targets in TCGA human HCC samples. Percent indicates the percent of tumors with upregulated (red boxes) or downregulated (blue boxes) mRNA expression of the indicated gene.

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CTC-276P9.3	ENST00000509530	chr5	134471889	134471890	-4952
GFI1B	ENST00000450530	chr9	135849283	135849284	-4814
EIF3FP1	ENST00000414503	chr21	11186617	11186618	-4804
CTBP2P1	ENST00000431853	chrY	58996746	58996747	-4644
RP11-774O3.2	ENST00000509453	chr4	8317512	8317513	-4390
AC136932.2	ENST00000583871	chr16	33950346	33950347	-4327
ROCK1P1	ENST00000576266	chr18	108226	108227	-4140
IGF2BP3	ENST00000258729	chr7	23514186	23514187	-4102
DUX4L16	ENST00000555130	chrY	13458630	13458631	-3963
RP11-241F15.3	ENST00000514077	chr4	49514765	49514766	-3944
BRCA1	ENST00000412061	chr17	41251805	41251806	-3924
UPP1	ENST00000416681	chr7	48124509	48124510	-3715
RP11-886I11.4	ENST00000557448	chrY	13484590	13484591	-3414
AC008132.1	ENST00000342888	chr22	18718162	18718163	-3264
RP11-886I11.3	ENST00000553347	chrY	13474066	13474067	-3166
7SK	ENST00000362961	chr1	55845657	55845658	-3134
AC073464.11	ENST00000429823	chr2	95475143	95475144	-2948
AL441988.1	ENST00000408392	chr20	29634568	29634569	-2593
RP11-886I11.4	ENST00000557448	chrY	13485432	13485433	-2572
C14orf164	ENST00000430154	chr14	23707174	23707175	-2380
RP11-886I11.2	ENST00000557360	chrY	13468248	13468249	-2348
RP11-886I11.3	ENST00000553347	chrY	13475061	13475062	-2171
Metazoa_SRP	ENST00000581926	chr19	11575920	11575921	-2170
RP11-886I11.3	ENST00000553347	chrY	13475289	13475290	-1943
LINC00273	ENST00000567668	chr16	33959031	33959032	-1918
CUX1	ENST00000437600	chr7	101457300	101457301	-1918
RRM2	ENST00000360566	chr2	10260546	10260547	-1908
CDC27P2	ENST00000425026	chrY	10031775	10031776	-1870
AC136932.1	ENST00000385251	chr16	33959879	33959880	-1772
ROCK1P1	ENST00000576266	chr18	110619	110620	-1747
PRDM7	ENST00000407825	chr16	90144039	90144040	-1703
RP11-241F15.3	ENST00000514077	chr4	49512355	49512356	-1534
DUX4L16	ENST00000555130	chrY	13461074	13461075	-1519
DND1P1	ENST00000580842	chr17	43661746	43661747	-1490
RP11-434D2.11	ENST00000583797	chr17	20460247	20460248	-1377
ANKRD30BL	ENST00000470729	chr2	133016886	133016887	-1346
SENP5	ENST00000489744	chr3	196625655	196625656	-1254
LTBP4	ENST00000595529	chr19	41111131	41111132	-1240
PPEF2	ENST00000513324	chr4	76807208	76807209	-1234
HCN3	ENST00000368358	chr1	155246150	155246151	-1223

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RP11-886I11.2	ENST00000557360	chrY	13469409	13469410	-1187
FOXK2	ENST00000575578	chr17	80542822	80542823	-1183
AC087491.2	ENST00000398554	chr17	37774739	37774740	-1126
PFKFB4	ENST00000412035	chr3	48595542	48595543	-1094
SCUBE2	ENST00000534295	chr11	9160738	9160739	-1079
POU2F1	ENST00000367866	chr1	167189039	167189040	-1026
CDC27P1	ENST00000445384	chr2	133018924	133018925	-976
PLEKHH3	ENST00000412503	chr17	40830008	40830009	-962
ATAD3A	ENST00000378756	chr1	1446598	1446599	-932
CR848007.2	ENST00000442354	chr9	44070759	44070760	-880
ANKRD30BL	ENST00000470729	chr2	133016419	133016420	-879
PRR24	ENST00000552360	chr19	47777267	47777268	-874
RP11-313F23.4	ENST00000545923	chr12	34372644	34372645	-858
UHRF1	ENST00000591733	chr19	4908598	4908599	-843
XXbac-BPG308K3.6	ENST00000440244	chr6	28831956	28831957	-831
CCNE1	ENST00000262643	chr19	30302008	30302009	-796
AL928970.1	ENST00000597269	chr9	10312	10313	-743
BAZ1B	ENST00000404251	chr7	72937338	72937339	-732
VEGFA	ENST00000476772	chr6	43737208	43737209	-712
RNU5E-6P	ENST00000365574	chr1	45286350	45286351	-683
LINC00273	ENST00000539813	chr16	33963142	33963143	-641
RP11-886I11.2	ENST00000557360	chrY	13469977	13469978	-619
FAM222A	ENST00000538780	chr12	110151435	110151436	-597
RP11-631N16.2	ENST00000550290	chr12	62995962	62995963	-569
RP11-423C15.3	ENST00000444800	chr9	128508573	128508574	-556
SIVA1	ENST00000329967	chr14	105218904	105218905	-532
SIK2	ENST00000304987	chr11	111472586	111472587	-528
RP1-85F18.5	ENST00000420537	chr22	41593981	41593982	-523
SPEN	ENST00000375759	chr1	16173844	16173845	-514
PIM1	ENST00000373509	chr6	37137469	37137470	-509
AP3D1	ENST00000591284	chr19	2164969	2164970	-507
CAMK2N2	ENST00000296238	chr3	183979750	183979751	-501
MSH6	ENST00000445503	chr2	48009736	48009737	-484
CXorf58	ENST00000379211	chrX	23925443	23925444	-474
PRR24	ENST00000552360	chr19	47777668	47777669	-473
AMIGO1	ENST00000369862	chr1	110052827	110052828	-469
ANXA4	ENST00000394295	chr2	69968640	69968641	-465
C6orf99	ENST00000367073	chr6	159290489	159290490	-464
ATOX1	ENST00000524142	chr5	151152541	151152542	-450
ZMYND19	ENST00000298585	chr9	140485389	140485390	-449

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RP11-386G11.10	ENST00000547712	chr12	49524505	49524506	-448
PPM1D	ENST00000305921	chr17	58677118	58677119	-425
SETX	ENST00000224140	chr9	135230792	135230793	-422
BRI3BP	ENST00000341446	chr12	125477828	125477829	-417
E2F7	ENST00000322886	chr12	77459766	77459767	-408
SERTAD4-AS1	ENST00000475406	chr1	210406718	210406719	-403
HCN3	ENST00000368358	chr1	155246973	155246974	-400
LINC00273	ENST00000567668	chr16	33957497	33957498	-384
FCHSD2	ENST00000409418	chr11	72853676	72853677	-372
SLC25A36	ENST00000446041	chr3	140660305	140660306	-366
STIL	ENST00000337817	chr1	47780182	47780183	-365
AGFG2	ENST00000430857	chr7	100136468	100136469	-365
CHAMP1	ENST00000361283	chr13	115079623	115079624	-364
FKBPL	ENST00000375156	chr6	32098429	32098430	-363
IGSF8	ENST00000448417	chr1	160069092	160069093	-361
DNAJC9-AS1	ENST00000440197	chr10	75006585	75006586	-360
KIF2A	ENST00000401507	chr5	61601631	61601632	-357
SUZ12P	ENST00000497969	chr17	29058376	29058377	-347
C3orf37	ENST00000509042	chr3	128997325	128997326	-345
ARHGEF40	ENST00000298694	chr14	21538085	21538086	-343
AEN	ENST00000332810	chr15	89164186	89164187	-340
E2F3	ENST00000346618	chr6	20402057	20402058	-340
HNRNPA0	ENST00000314940	chr5	137090372	137090373	-335
GBAP1	ENST00000313929	chr1	155197546	155197547	-334
RFX1	ENST00000589239	chr19	14117461	14117462	-329
RP11-59H1.3	ENST00000540583	chr12	12878522	12878523	-328
SCML1	ENST00000380045	chrX	17755261	17755262	-326
CD44	ENST00000263398	chr11	35160092	35160093	-324
ZBTB5	ENST00000307750	chr9	37465716	37465717	-322
RBFOX1	ENST00000570626	chr16	7559802	7559803	-321
PLEKHH3	ENST00000412503	chr17	40829365	40829366	-319
UXT	ENST00000333119	chrX	47518875	47518876	-317
XPO1	ENST00000443240	chr2	61766071	61766072	-312
PHF20	ENST00000461122	chr20	34359586	34359587	-309
FDXR	ENST00000442102	chr17	72869462	72869463	-308
EGR1	ENST00000239938	chr5	137800871	137800872	-307
BANP	ENST00000286122	chr16	87984733	87984734	-304
TRIM26	ENST00000453195	chr6	30181502	30181503	-300
PDE4DIP	ENST00000479408	chr1	144932849	144932850	-299
EEF1G	ENST00000532986	chr11	62341853	62341854	-297

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TCAM1P	ENST00000463377	chr17	61926355	61926356	-296
PMM1	ENST00000216259	chr22	41986188	41986189	-296
IRS2	ENST00000375856	chr13	110439208	110439209	-295
PDS5A	ENST00000303538	chr4	39979867	39979868	-293
CSTF2T	ENST00000331173	chr10	53459642	53459643	-289
SUZ12	ENST00000322652	chr17	30263752	30263753	-284
TTC33	ENST00000337702	chr5	40756355	40756356	-280
ARL15	ENST00000502271	chr5	53606689	53606690	-279
SMC3	ENST00000361804	chr10	112327170	112327171	-278
RIC8B	ENST00000392837	chr12	107168096	107168097	-276
SRSF1	ENST00000258962	chr17	56084981	56084982	-276
DEK	ENST00000397239	chr6	18265324	18265325	-272
SPOP	ENST00000504102	chr17	47755865	47755866	-271
AP1S2	ENST00000329235	chrX	15873323	15873324	-271
SLC1A5	ENST00000542575	chr19	47292117	47292118	-268
RBM14	ENST00000310137	chr11	66383786	66383787	-266
HLTF	ENST00000494055	chr3	148804604	148804605	-265
TMPO-AS1	ENST00000548760	chr12	98910462	98910463	-264
CD3EAP	ENST00000309424	chr19	45909208	45909209	-258
LEMD3	ENST00000308330	chr12	65563093	65563094	-257
TMX1	ENST00000555574	chr14	51706622	51706623	-257
FAM161A	ENST00000405894	chr2	62081531	62081532	-255
AC069277.2	ENST00000342990	chr3	6549216	6549217	-251
TBC1D1	ENST00000446803	chr4	37978682	37978683	-248
MCM4	ENST00000523944	chr8	48873213	48873214	-244
UHRF1	ENST00000591733	chr19	4909198	4909199	-243
RALGAPA2	ENST00000202677	chr20	20693505	20693506	-241
HIST1H4A	ENST00000359907	chr6	26021665	26021666	-241
EZH2	ENST00000536783	chr7	148581652	148581653	-241
ANP32E	ENST00000314136	chr1	150208737	150208738	-235
E2F8	ENST00000250024	chr11	19262726	19262727	-230
EBNA1BP2	ENST00000431635	chr1	43638468	43638469	-229
UBE2T	ENST00000367274	chr1	202311335	202311336	-229
CDK5RAP2	ENST00000491334	chr9	123342675	123342676	-229
CDCA7L	ENST00000406877	chr7	21985928	21985929	-228
STRADA	ENST00000392950	chr17	61819554	61819555	-226
SRSF10	ENST00000453840	chr1	24307176	24307177	-225
SUMO1	ENST00000392246	chr2	203103552	203103553	-223
MLF1IP	ENST00000281453	chr4	185655507	185655508	-222
FAM73B	ENST00000474534	chr9	131798679	131798680	-220

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
HNRNPUL1	ENST00000392006	chr19	41770018	41770019	-217
CYR61	ENST00000451137	chr1	86046229	86046230	-214
PRPS1	ENST00000372435	chrX	106871523	106871524	-213
RTTN	ENST00000255674	chr18	67873391	67873392	-212
ADAM15	ENST00000473905	chr1	155022831	155022832	-210
CHAF1A	ENST00000301280	chr19	4402449	4402450	-209
TRIM37	ENST00000393066	chr17	57184488	57184489	-208
FBXL20	ENST00000577399	chr17	37558977	37558978	-203
FLAD1	ENST00000492620	chr1	154955611	154955612	-202
ATP5G1	ENST00000355938	chr17	46969924	46969925	-202
U2	ENST00000411315	chr3	73159941	73159942	-201
U2AF2	ENST00000450554	chr19	56165312	56165313	-199
TXNRD1	ENST00000378070	chr12	104682300	104682301	-195
DHX40	ENST00000251241	chr17	57642690	57642691	-195
SNRPC	ENST00000244520	chr6	34724988	34724989	-194
RP11-544I20.2	ENST00000359491	chr14	64805508	64805509	-193
OIP5-AS1	ENST00000558945	chr15	41575994	41575995	-193
PHF14	ENST00000445996	chr7	11013306	11013307	-192
EBP	ENST00000276096	chrX	48379997	48379998	-189
COX8A	ENST00000314133	chr11	63741890	63741891	-188
CDKN2D	ENST00000335766	chr19	10679921	10679922	-188
MAK	ENST00000474039	chr6	10838950	10838951	-188
TTLL7	ENST00000474957	chr1	84465018	84465019	-187
SLC2A4	ENST00000317370	chr17	7184798	7184799	-187
MCM6	ENST00000264156	chr2	136634179	136634180	-185
SLBP	ENST00000489418	chr4	1714464	1714465	-184
FAM111B	ENST00000411426	chr11	58874475	58874476	-182
CDCA7	ENST00000347703	chr2	174219365	174219366	-182
MLF1IP	ENST00000514781	chr4	185654747	185654748	-181
TIPIN	ENST00000261881	chr15	66649230	66649231	-178
ATAD2	ENST00000287394	chr8	124408881	124408882	-178
MCM10	ENST00000378714	chr10	13203378	13203379	-175
ILF3-AS1	ENST00000591501	chr19	10764691	10764692	-173
CA5BP1	ENST00000380334	chrX	15693495	15693496	-173
MCFD2	ENST00000444761	chr2	47169162	47169163	-170
GABARAP	ENST00000302386	chr17	7146255	7146256	-168
CDT1	ENST00000562747	chr16	88870851	88870852	-167
AATF	ENST00000225402	chr17	35306008	35306009	-166
RP11-535A19.2	ENST00000531263	chr11	75526004	75526005	-164
GCDH	ENST00000222214	chr19	13001676	13001677	-163

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
AC093901.1	ENST00000414886	chr2	118944122	118944123	-162
7SK	ENST00000410327	chr9	34049801	34049802	-162
ZNF687	ENST00000443959	chr1	151253933	151253934	-160
CLCC1	ENST00000415331	chr1	109506268	109506269	-159
SYDE1	ENST00000342784	chr19	15218057	15218058	-156
CUEDC1	ENST00000581391	chr17	55945979	55945980	-155
CDC25A	ENST00000437972	chr3	48230045	48230046	-155
MLEC	ENST00000228506	chr12	121124518	121124519	-153
RAB11B	ENST00000600719	chr19	8454711	8454712	-153
TPD52L2	ENST00000369927	chr20	62496442	62496443	-153
METTL2B	ENST00000262432	chr7	128116629	128116630	-153
ABCB6	ENST00000265316	chr2	220083862	220083863	-152
SCO2	ENST00000395693	chr22	50964184	50964185	-151
ING3	ENST00000315870	chr7	120590651	120590652	-151
CREBZF	ENST00000490820	chr11	85376294	85376295	-150
ARL6IP6	ENST00000455875	chr2	153575282	153575283	-150
MYL6	ENST00000550697	chr12	56551795	56551796	-149
MIR17HG	ENST00000400282	chr13	91999926	91999927	-147
SLC12A4	ENST00000422611	chr16	68002742	68002743	-147
GPR180	ENST00000376958	chr13	95254011	95254012	-145
CDC23	ENST00000394886	chr5	137549174	137549175	-144
DHFR	ENST00000508282	chr5	79950061	79950062	-143
DERL3	ENST00000290730	chr22	24181455	24181456	-142
CEP85	ENST00000476272	chr1	26560550	26560551	-140
RFWD3	ENST00000361070	chr16	74700915	74700916	-138
CAMTA1	ENST00000303635	chr1	6845248	6845249	-135
RP5-1074L1.1	ENST00000449169	chr1	110881921	110881922	-130
RP5-1125A11.1	ENST00000432859	chr20	32581058	32581059	-130
FBXL3	ENST00000417323	chr13	77601456	77601457	-128
HNRNPL	ENST00000221419	chr19	39341099	39341100	-128
SUV420H2	ENST00000464185	chr19	55852856	55852857	-127
LTN1	ENST00000361371	chr21	30365402	30365403	-127
PM20D2	ENST00000275072	chr6	89855642	89855643	-126
RBM15	ENST00000369784	chr1	110881004	110881005	-123
GTPBP1	ENST00000216044	chr22	39101605	39101606	-122
WDYHV1	ENST00000287387	chr8	124428843	124428844	-121
RNU5E-6P	ENST00000365574	chr1	45285786	45285787	-119
TRA2B	ENST00000453386	chr3	185656041	185656042	-119
CASP8AP2	ENST00000552401	chr6	90539493	90539494	-119
GGCT	ENST00000275428	chr7	30544575	30544576	-117

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
WLS	ENST00000527864	chr1	68697620	68697621	-114
FANCG	ENST00000425676	chr9	35079802	35079803	-114
HNRNPF	ENST00000357065	chr10	43903378	43903379	-113
FAM82A2	ENST00000560905	chr15	41047645	41047646	-113
NOLC1	ENST00000405356	chr10	103911822	103911823	-110
MED17	ENST00000251871	chr11	93517282	93517283	-110
PRPF40A	ENST00000486100	chr2	153574619	153574620	-110
CTB-175E5.4	ENST00000592897	chr17	42264192	42264193	-109
NAP1L4	ENST00000380542	chr11	3013713	3013714	-108
SEC22C	ENST00000273156	chr3	42623626	42623627	-108
MBNL3	ENST00000370844	chrX	131624102	131624103	-108
PSENEN	ENST00000587708	chr19	36235907	36235908	-107
BAZ1B	ENST00000404251	chr7	72936713	72936714	-107
MCM5	ENST00000216122	chr22	35795949	35795950	-106
AP4B1	ENST00000369564	chr1	114447925	114447926	-104
HEATR6	ENST00000184956	chr17	58156392	58156393	-102
ASF1B	ENST00000263382	chr19	14247867	14247868	-101
RBL1	ENST00000373664	chr20	35724495	35724496	-99
RMI2	ENST00000312499	chr16	11439190	11439191	-97
MUM1	ENST00000592374	chr19	1354612	1354613	-97
PLCXD1	ENST00000415337	chrX	200034	200035	-97
RP11-806L2.5	ENST00000584679	chr18	657353	657354	-96
SLC25A42	ENST00000318596	chr19	19174711	19174712	-96
PAICS	ENST00000504188	chr4	57302109	57302110	-95
PSMA1	ENST00000533068	chr11	14542081	14542082	-92
E2F8	ENST00000527884	chr11	19263257	19263258	-92
MRPL11	ENST00000430466	chr11	66206408	66206409	-91
RP11-387D10.2	ENST00000559531	chr15	91260461	91260462	-91
RP11-452J21.2	ENST00000513586	chr4	16180472	16180473	-89
MUT	ENST00000274813	chr6	49430990	49430991	-88
ZNF219	ENST00000555697	chr14	21571821	21571822	-85
RP11-424C20.2	ENST00000540175	chr12	20704441	20704442	-82
GMNN	ENST00000378054	chr6	24775559	24775560	-81
CENPH	ENST00000283006	chr5	68485294	68485295	-80
E2F2	ENST00000361729	chr1	23857789	23857790	-79
GBA	ENST00000428024	chr1	155214730	155214731	-79
RBM23	ENST00000359890	chr14	23388469	23388470	-78
RP11-168G16.1	ENST00000340644	chr15	100890514	100890515	-78
TCF19	ENST00000376257	chr6	31126240	31126241	-78
DUT	ENST00000455976	chr15	48624224	48624225	-75

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
HIST1H4I	ENST00000354348	chr6	27107000	27107001	-75
TAF6	ENST00000453269	chr7	99717092	99717093	-73
OXSR1	ENST00000492714	chr3	38206509	38206510	-70
BSG	ENST00000346916	chr19	571228	571229	-68
SETMAR	ENST00000358065	chr3	4344919	4344920	-68
RPA2	ENST00000373909	chr1	28241320	28241321	-65
FANCL	ENST00000449070	chr2	58468570	58468571	-65
ZNFX1-AS1	ENST00000326677	chr20	47895113	47895114	-65
FDPS	ENST00000447866	chr1	155278475	155278476	-63
RP11-849H4.2	ENST00000531488	chr11	71639554	71639555	-63
UBC	ENST00000546120	chr12	125399257	125399258	-63
TICRR	ENST00000268138	chr15	90118651	90118652	-61
TOP2A	ENST00000423485	chr17	38574261	38574262	-61
MMAB	ENST00000537236	chr12	110011443	110011444	-60
PROSER1	ENST00000350125	chr13	39612310	39612311	-60
NUSAP1	ENST00000559046	chr15	41624993	41624994	-59
TGOLN2	ENST00000409232	chr2	85555204	85555205	-59
SPC25	ENST00000282074	chr2	169747011	169747012	-58
SYNGR4	ENST00000344846	chr19	48867595	48867596	-56
WEE1	ENST00000450114	chr11	9595172	9595173	-55
IER2	ENST00000588173	chr19	13262733	13262734	-55
CENPI	ENST00000218507	chrX	100353122	100353123	-55
CTC-453G23.8	ENST00000595201	chr19	48707285	48707286	-54
MSH2	ENST00000233146	chr2	47630053	47630054	-54
FICD	ENST00000552695	chr12	108908908	108908909	-53
GTF2A1	ENST00000434192	chr14	81687625	81687626	-52
DIAPH3	ENST00000400324	chr13	60738041	60738042	-51
CENPM	ENST00000402420	chr22	42342782	42342783	-51
MFAP1	ENST00000267812	chr15	44117048	44117049	-50
CDC7	ENST00000430031	chr1	91966358	91966359	-49
IMMT	ENST00000410111	chr2	86422940	86422941	-49
DIS3	ENST00000377767	chr13	73356117	73356118	-48
HIST1H2AM	ENST00000359611	chr6	27861009	27861010	-48
PRKCSH	ENST00000591462	chr19	11546061	11546062	-47
HDAC6	ENST00000423941	chrX	48659736	48659737	-47
EXO1	ENST00000366548	chr1	242011435	242011436	-46
LRR1	ENST00000540712	chr14	50065623	50065624	-46
CARHSP1	ENST00000570125	chr16	8962620	8962621	-46
AC004854.4	ENST00000443162	chr7	44887968	44887969	-46
CEP152	ENST00000560322	chr15	49103382	49103383	-41

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
PMAIP1	ENST00000316660	chr18	57567139	57567140	-40
WDPCP	ENST00000272321	chr2	63815970	63815971	-39
SNRPB	ENST00000438552	chr20	2451535	2451536	-38
RNF167	ENST00000575111	chr17	4843639	4843640	-36
ESYT1	ENST00000394048	chr12	56521804	56521805	-35
E2F1	ENST00000343380	chr20	32274243	32274244	-35
NFATC2IP	ENST00000320805	chr16	28962224	28962225	-33
TRIM56	ENST00000412507	chr7	100728769	100728770	-33
NUP205	ENST00000285968	chr7	135242634	135242635	-32
C18orf56	ENST00000323813	chr18	658369	658370	-31
MYC	ENST00000524013	chr8	128748434	128748435	-31
C11orf30	ENST00000427574	chr11	76155936	76155937	-30
UNG	ENST00000336865	chr12	109535893	109535894	-29
PLSCR1	ENST00000486631	chr3	146262455	146262456	-29
EEF1E1	ENST00000379715	chr6	8102838	8102839	-29
FAM212B	ENST00000444059	chr1	112298472	112298473	-28
AC079305.8	ENST00000455416	chr2	178077415	178077416	-27
SNHG1	ENST00000541416	chr11	62623308	62623309	-26
PAN2	ENST00000440411	chr12	56727861	56727862	-26
SIN3A	ENST00000565264	chr15	75744111	75744112	-26
ALDOA	ENST00000338110	chr16	30064384	30064385	-26
RP11-351A11.1	ENST00000518570	chr6	119255923	119255924	-26
DBR1	ENST00000505015	chr3	137893750	137893751	-25
ADAL	ENST00000428046	chr15	43622847	43622848	-24
HSPE1	ENST00000409729	chr2	198364839	198364840	-24
HNRNPD	ENST00000503822	chr4	83295336	83295337	-24
PPP1R7	ENST00000438799	chr2	242088967	242088968	-23
CDK5RAP3	ENST00000584168	chr17	46048706	46048707	-21
ORC2	ENST00000234296	chr2	201828422	201828423	-21
ZNF367	ENST00000375256	chr9	99180630	99180631	-21
DCLRE1A	ENST00000369305	chr10	115614160	115614161	-20
C3orf58	ENST00000315691	chr3	143690619	143690620	-20
ABHD11	ENST00000497897	chr7	73153129	73153130	-20
ITGB3BP	ENST00000271002	chr1	63988903	63988904	-19
POLE	ENST00000539357	chr12	133263967	133263968	-18
SHKBP1	ENST00000600552	chr19	41082970	41082971	-17
MSH5	ENST00000375755	chr6	31707708	31707709	-16
LHX2	ENST00000373615	chr9	126773873	126773874	-15
BIN1	ENST00000466111	chr2	127822515	127822516	-13
MCM2	ENST00000474964	chr3	127317239	127317240	-13

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RRM1	ENST00000533349	chr11	4116060	4116061	-12
RFC4	ENST00000418288	chr3	186524269	186524270	-11
PPOX	ENST00000352210	chr1	161136189	161136190	-10
RP11-580I16.2	ENST00000584391	chr17	45726794	45726795	-10
PPP1R13L	ENST00000593226	chr19	45909593	45909594	-10
RQCD1	ENST00000273064	chr2	219433292	219433293	-10
TFAP4	ENST00000573476	chr16	4322839	4322840	-9
ATAD5	ENST00000321990	chr17	29158978	29158979	-9
AC034193.5	ENST00000326237	chr3	10028585	10028586	-9
EAF2	ENST00000465664	chr3	121554046	121554047	-9
OGG1	ENST00000302036	chr3	9791619	9791620	-8
RAD54L	ENST00000463715	chr1	46713352	46713353	-7
DERA	ENST00000428559	chr12	16064098	16064099	-7
BTG1	ENST00000256015	chr12	92539678	92539679	-7
MTAP	ENST00000380172	chr9	21802534	21802535	-7
PSMC3IP	ENST00000587209	chr17	40729718	40729719	-5
RIF1	ENST00000453091	chr2	152266391	152266392	-5
RP3-410C9.1	ENST00000600225	chr20	26189996	26189997	-5
CLSPN	ENST00000318121	chr1	36235531	36235532	-4
GABPB2	ENST00000462520	chr1	151043049	151043050	-4
CDCA3	ENST00000545368	chr12	6960458	6960459	-4
RECQL	ENST00000396093	chr12	21654605	21654606	-4
CENPN	ENST00000569461	chr16	81040823	81040824	-4
DSN1	ENST00000438549	chr20	35402175	35402176	-4
PNPLA8	ENST00000436062	chr7	108166764	108166765	-4
XRCC3	ENST00000554974	chr14	104181797	104181798	-3
VPRBP	ENST00000504652	chr3	51534011	51534012	-3
RAD51AP1	ENST00000352618	chr12	4648053	4648054	-2
MTHFD1	ENST00000555709	chr14	64854756	64854757	-2
SLC25A3	ENST00000546766	chr12	98987431	98987432	-1
KNTC1	ENST00000535410	chr12	123011791	123011792	-1
PTK2B	ENST00000544172	chr8	27168997	27168998	-1
BRIP1	ENST00000259008	chr17	59940880	59940881	1
MLH1	ENST00000457004	chr3	37035006	37035007	1
PSMC3	ENST00000298852	chr11	47447985	47447986	2
ZNF384	ENST00000319770	chr12	6798524	6798525	2
LIN52	ENST00000553404	chr14	74551663	74551664	2
CNTRL	ENST00000373865	chr9	123837141	123837142	2
TMEM194A	ENST00000379391	chr12	57472542	57472543	3
ZNF524	ENST00000589521	chr19	56111389	56111390	3

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TUBB	ENST00000396384	chr6	30689477	30689478	3
TBC1D15	ENST00000550746	chr12	72233500	72233501	4
NOP58	ENST00000488403	chr2	203130461	203130462	4
RP11-159F24.1	ENST00000503484	chr5	43603034	43603035	4
DPYSL2	ENST00000311151	chr8	26435361	26435362	4
POLA1	ENST00000379059	chrX	24712066	24712067	4
CDK2	ENST00000554619	chr12	56360621	56360622	5
CTD-2339L15.1	ENST00000533146	chr15	40987288	40987289	5
RHEB	ENST00000496004	chr7	151217199	151217200	6
TK1	ENST00000301634	chr17	76183304	76183305	9
CDC6	ENST00000577249	chr17	38444167	38444168	10
AC005237.4	ENST00000458377	chr2	242003522	242003523	10
NADKD1	ENST00000506945	chr5	36242370	36242371	10
DEK	ENST00000505224	chr6	18264755	18264756	10
MMS22L	ENST00000275053	chr6	97731041	97731042	10
RFC2	ENST00000479105	chr7	73668656	73668657	10
CEP57	ENST00000537677	chr11	95523138	95523139	11
FANCD2	ENST00000383806	chr3	10068122	10068123	11
DTL	ENST00000542077	chr1	212209102	212209103	12
TFP1	ENST00000497521	chr3	133380853	133380854	12
MSH6	ENST00000456246	chr2	48010278	48010279	13
AP4M1	ENST00000359593	chr7	99699191	99699192	13
RAD51B	ENST00000487861	chr14	68286508	68286509	14
DCTPP1	ENST00000319285	chr16	30441380	30441381	15
POLD3	ENST00000530511	chr11	74303703	74303704	16
NUP155	ENST00000231498	chr5	37371266	37371267	16
POLA2	ENST00000541089	chr11	65029448	65029449	17
DDX39B	ENST00000431908	chr6	31509740	31509741	17
DDX11	ENST00000543756	chr12	31226859	31226860	18
CENPO	ENST00000498362	chr2	25016363	25016364	18
METTL2A	ENST00000333483	chr17	60501253	60501254	19
MCM3	ENST00000596983	chr6	52149659	52149660	19
FEN1	ENST00000305885	chr11	61560128	61560129	21
KIAA0101	ENST00000558008	chr15	64673615	64673616	21
HSD17B6	ENST00000555805	chr12	57145965	57145966	22
CASP2	ENST00000350623	chr7	142985564	142985565	22
HELLS	ENST00000348459	chr10	96305595	96305596	23
FAM60A	ENST00000337682	chr12	31479282	31479283	23
PRIM2	ENST00000419977	chr6	57182447	57182448	23
SOX6	ENST00000530378	chr11	16760165	16760166	24

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ABHD2	ENST00000352732	chr15	89631403	89631404	24
NUCB2	ENST00000533738	chr11	17297773	17297774	26
RP11-459F6.3	ENST00000569580	chr16	58163458	58163459	27
RAD51AP2	ENST00000399080	chr2	17699677	17699678	28
ZRANB3	ENST00000401392	chr2	136288270	136288271	30
ZBTB4	ENST00000311403	chr17	7387550	7387551	31
C17orf64	ENST00000461535	chr17	58469820	58469821	32
ZBTB8OS	ENST00000479075	chr1	33116469	33116470	34
AK2	ENST00000354858	chr1	33502558	33502559	34
SLC25A28	ENST00000496035	chr10	101380331	101380332	34
CHEK1	ENST00000534685	chr11	125495934	125495935	34
CTDSPL2	ENST00000260327	chr15	44719464	44719465	34
RFC3	ENST00000434425	chr13	34392241	34392242	37
CALM2	ENST00000272298	chr2	47403701	47403702	38
RNF219	ENST00000282003	chr13	79233274	79233275	39
STYK1	ENST00000075503	chr12	10826849	10826850	41
RP11-68I3.7	ENST00000584986	chr17	27919217	27919218	41
BTD	ENST00000449107	chr3	15643181	15643182	43
HAUS8	ENST00000598517	chr19	17186187	17186188	44
NR1H3	ENST00000419652	chr11	47279304	47279305	45
MIS12	ENST00000573759	chr17	5389762	5389763	48
MPDU1	ENST00000572936	chr17	7487033	7487034	51
CDC27	ENST00000571643	chr17	45214558	45214559	51
SLC46A1	ENST00000578217	chr17	26732712	26732713	52
CDC45	ENST00000438587	chr22	19467058	19467059	55
CCT5	ENST00000503026	chr5	10250094	10250095	55
YARS	ENST00000373477	chr1	33283694	33283695	59
TTI1	ENST00000373448	chr20	36661803	36661804	59
CPT2	ENST00000371486	chr1	53662159	53662160	60
RP11-348A11.4	ENST00000500025	chr11	33183292	33183293	60
CYP1B1-AS1	ENST00000589303	chr2	38303696	38303697	60
IGSF8	ENST00000314485	chr1	160068417	160068418	61
GPANK1	ENST00000456540	chr6	31632899	31632900	62
NR2C2AP	ENST00000537399	chr19	19314091	19314092	63
PIGW	ENST00000592983	chr17	34890933	34890934	66
CCNT2	ENST00000446247	chr2	135675875	135675876	66
PLAUR	ENST00000602141	chr19	44172328	44172329	67
DNMT1	ENST00000592054	chr19	10305226	10305227	75
RP11-418J17.1	ENST00000440150	chr1	119683123	119683124	77
XRCC2	ENST00000359321	chr7	152373171	152373172	78

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RNA5-8SP6	ENST00000515896	chrY	10037847	10037848	85
RP4-761J14.8	ENST00000407384	chr12	6772511	6772512	87
HMGB2	ENST00000296503	chr4	174256185	174256186	90
TMEM116	ENST00000437003	chr12	112450823	112450824	91
FANCI	ENST00000565522	chr15	89787570	89787571	91
GINS3	ENST00000318129	chr16	58426387	58426388	91
ZNF766	ENST00000599581	chr19	52772936	52772937	92
CBX3	ENST00000337620	chr7	26240873	26240874	93
HNRNPD	ENST00000509263	chr4	83294208	83294209	94
CISD2	ENST00000503643	chr4	103790589	103790590	98
EIF3B	ENST00000431643	chr7	2393817	2393818	98
MDC1	ENST00000376405	chr6	30685356	30685357	101
FANCC	ENST00000289081	chr9	98079880	98079881	103
CDKN2C	ENST00000396148	chr1	51434471	51434472	106
FBXO5	ENST00000367241	chr6	153304607	153304608	106
USP1	ENST00000371146	chr1	62902082	62902083	109
LAGE3	ENST00000357360	chrX	153707485	153707486	110
SLC25A25	ENST00000373064	chr9	130860694	130860695	113
9-Sep	ENST00000591198	chr17	75277646	75277647	115
SYPL1	ENST00000011473	chr7	105752905	105752906	116
UHRF1	ENST00000398240	chr19	4910681	4910682	117
RRM2	ENST00000474701	chr2	10263413	10263414	117
RBM15	ENST00000369784	chr1	110881245	110881246	119
hsa-mir-4259	ENST00000584466	chr1	159869744	159869745	124
NCAPH2	ENST00000520939	chr22	50946830	50946831	126
AL161626.1	ENST00000463508	chr9	79186856	79186857	127
C4orf21	ENST00000502805	chr4	113557885	113557886	132
HNRNPA1	ENST00000546500	chr12	54674111	54674112	136
RP4-564F22.2	ENST00000414142	chr20	37063779	37063780	136
SMC3	ENST00000462899	chr10	112328220	112328221	137
CCNE2	ENST00000517487	chr8	95906736	95906737	141
RPA3	ENST00000462723	chr7	7680063	7680064	144
CHRAC1	ENST00000519618	chr8	141522230	141522231	151
DDB2	ENST00000378601	chr11	47236646	47236647	155
AC079949.1	ENST00000488123	chr12	127650515	127650516	156
GINS2	ENST00000253462	chr16	85722442	85722443	162
WDR76	ENST00000452115	chr15	44119350	44119351	166
RP11-773H22.4	ENST00000588211	chr18	12991005	12991006	166
RFC1	ENST00000504849	chr4	39367788	39367789	166
OGT	ENST00000444774	chrX	70754316	70754317	167

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
MGST3	ENST00000367889	chr1	165600265	165600266	169
C1orf106	ENST00000367342	chr1	200860636	200860637	169
RP11-77H9.6	ENST00000570290	chr16	8963279	8963280	173
AP000974.1	ENST00000544076	chr11	85565790	85565791	195
PKMYT1	ENST00000572832	chr16	3018909	3018910	195
LIG1	ENST00000598938	chr19	48673266	48673267	198
U1	ENST00000364829	chr1	144534236	144534237	200
GPD2	ENST00000540309	chr2	157293195	157293196	200
ATL3	ENST00000398868	chr11	63438880	63438881	203
BCL2L12	ENST00000598306	chr19	50169472	50169473	204
ORC1	ENST00000371566	chr1	52869845	52869846	213
MB21D1	ENST00000370318	chr6	74161768	74161769	213
ZNF131	ENST00000504359	chr5	43121237	43121238	217
SUCO	ENST00000367723	chr1	172501705	172501706	218
ATP2A1	ENST00000536376	chr16	28891590	28891591	218
TREX1	ENST00000492235	chr3	48507888	48507889	221
RAVER1	ENST00000591969	chr19	10443937	10443938	229
GORAB	ENST00000464798	chr1	170501544	170501545	233
CNTRL	ENST00000373855	chr9	123837524	123837525	236
Z83844.1	ENST00000456099	chr22	38054145	38054146	238
TIMELESS	ENST00000554616	chr12	56842940	56842941	239
ZNF219	ENST00000451119	chr14	21572637	21572638	243
AC017099.3	ENST00000450072	chr2	98280925	98280926	247
C12orf57	ENST00000540506	chr12	7053536	7053537	249
DMC1	ENST00000439567	chr22	38965884	38965885	251
ARGLU1	ENST00000360629	chr13	107219709	107219710	261
SRSF7	ENST00000415527	chr2	38978018	38978019	261
DAXX	ENST00000446511	chr6	33290318	33290319	261
C4orf27	ENST00000506125	chr4	170678791	170678792	263
HAT1	ENST00000494601	chr2	172779379	172779380	264
HNRNPF	ENST00000498176	chr10	43891998	43891999	266
BRCA2	ENST00000530893	chr13	32889913	32889914	273
SCML1	ENST00000419185	chrX	17756119	17756120	276
C19orf57	ENST00000454313	chr19	14016630	14016631	278
NBR2	ENST00000467245	chr17	41277947	41277948	288
CCNE2	ENST00000520509	chr8	95908617	95908618	288
VRK2	ENST00000428021	chr2	58274307	58274308	299
SMC1A	ENST00000375340	chrX	53449303	53449304	299
ZCWPW1	ENST00000360951	chr7	100025979	100025980	307
WDR74	ENST00000525239	chr11	62608972	62608973	308

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
C15orf38	ENST00000460685	chr15	90455610	90455611	308
PHLPP2	ENST00000568954	chr16	71758288	71758289	315
CDC27	ENST00000576484	chr17	45234314	45234315	318
ZNF784	ENST00000591479	chr19	56135608	56135609	323
SKA2	ENST00000583380	chr17	57232194	57232195	340
USP1	ENST00000339950	chr1	62902665	62902666	341
CDT1	ENST00000301019	chr16	88869971	88869972	352
KLF11	ENST00000535335	chr2	10184727	10184728	357
CDC27P2	ENST00000425026	chrY	10029542	10029543	364
RNA28S5	ENST00000419932	chrX	108297425	108297426	366
TNFAIP8	ENST00000388882	chr5	118604818	118604819	371
RP11-413E6.7	ENST00000489078	chr3	75718461	75718462	381
IPO5	ENST00000475420	chr13	98628271	98628272	388
YEATS4	ENST00000552955	chr12	69753985	69753986	428
NUP160	ENST00000530326	chr11	47869431	47869432	433
CFDP1	ENST00000566254	chr16	75466835	75466836	453
CHAF1A	ENST00000585854	chr19	4403173	4403174	461
RP11-973N13.4	ENST00000554918	chr14	65006623	65006624	462
DEK	ENST00000515742	chr6	18263964	18263965	474
TTLL9	ENST00000375922	chr20	30468106	30468107	476
PARP1	ENST00000366790	chr1	226595204	226595205	478
DDX12P	ENST00000440299	chr12	9600329	9600330	479
NUP153	ENST00000262077	chr6	17706130	17706131	487
KHDC1	ENST00000484801	chr6	74019370	74019371	495
FBXO5	ENST00000229758	chr6	153303649	153303650	503
LINC00273	ENST00000567668	chr16	33956574	33956575	540
VAT1	ENST00000587173	chr17	41173798	41173799	574
PANK2	ENST00000336066	chr20	3870614	3870615	580
MYBL2	ENST00000217026	chr20	42296391	42296392	596
EIF1AX	ENST00000379593	chrX	20159343	20159344	600
MAK	ENST00000313243	chr6	10838121	10838122	606
LUC7L2	ENST00000456182	chr7	139045301	139045302	645
HIST1H2BK	ENST00000356950	chr6	27113930	27113931	646
CDC27	ENST00000571643	chr17	45213953	45213954	656
RP11-715J22.2	ENST00000563775	chr16	2517516	2517517	697
RP1-90J20.7	ENST00000597787	chr6	2989631	2989632	700
DHX15	ENST00000511553	chr4	24585195	24585196	709
PCNA	ENST00000379143	chr20	5099946	5099947	725
MB21D1	ENST00000370318	chr6	74161255	74161256	726
WDR76	ENST00000452115	chr15	44119929	44119930	745

Supplemental Table 1: Genes with significant occupancy of E2F7 at the promoter regions (-5kb to +2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
E2F1	ENST00000343380	chr20	32273453	32273454	756
SLC20A1	ENST00000272542	chr2	113404219	113404220	787
E2F3	ENST00000346618	chr6	20403186	20403187	790
RNA45S5	ENST00000445125	chrY	10035894	10035895	816
RNU1-5	ENST00000384010	chr1	149223402	149223403	818
KITLG	ENST00000228280	chr12	88973383	88973384	854
PPRC1	ENST00000413464	chr10	103893698	103893699	903
NASP	ENST00000351223	chr1	46050649	46050650	914
GMPS	ENST00000541628	chr3	155589425	155589426	927
E2F2	ENST00000361729	chr1	23856773	23856774	938
ELF2	ENST00000379549	chr4	140004365	140004366	978
AC002558.2	ENST00000599091	chr17	45213146	45213147	995
UCK2	ENST00000372212	chr1	165798092	165798093	1035
MIR3687	ENST00000577708	chr21	9827244	9827245	1043
ZNF367	ENST00000375256	chr9	99179555	99179556	1055
LMNB1	ENST00000463908	chr5	126114253	126114254	1184
ERVH48-1	ENST00000447535	chr21	44344342	44344343	1413
LINC00273	ENST00000567668	chr16	33955676	33955677	1438
KIF25	ENST00000496008	chr6	168436191	168436192	1515
MIR663B	ENST00000408361	chr2	133012951	133012952	1701
FSCN1	ENST00000405801	chr7	5636079	5636080	1764
AC007450.1	ENST00000408201	chr12	11693079	11693080	1899
CDKN1A	ENST00000462537	chr6	36648477	36648478	1931
SEMA6B	ENST00000586965	chr19	4556534	4556535	1934

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TTC32	ENST00000333610	chr2	20106670	20106671	-4925
SERPINE1	ENST00000223095	chr7	100765490	100765491	-4879
ERI3	ENST00000372259	chr1	44793588	44793589	-4875
CTC-276P9.3	ENST00000509530	chr5	134471798	134471799	-4861
KCNH3	ENST00000257981	chr12	49928083	49928084	-4856
SBF2-AS1	ENST00000525636	chr11	9792336	9792337	-4855
GFI1B	ENST00000450530	chr9	135849242	135849243	-4855
PRICKLE3	ENST00000376317	chrX	49047692	49047693	-4849
MRPL11	ENST00000430466	chr11	66211159	66211160	-4842
MALAT1	ENST00000534336	chr11	65260392	65260393	-4840
RP11-626K17.2	ENST00000569776	chr16	32476506	32476507	-4825
GABRQ	ENST00000370306	chrX	151801825	151801826	-4811
C5orf46	ENST00000515291	chr5	147290883	147290884	-4784
WDR25	ENST00000555865	chr14	100938043	100938044	-4767
PXN	ENST00000536957	chr12	120669411	120669412	-4766
AC131971.3	ENST00000439505	chr11	2960907	2960908	-4760
MEF2B	ENST00000409447	chr19	19285853	19285854	-4757
NFATC2IP	ENST00000564978	chr16	28957422	28957423	-4705
AC004383.3	ENST00000438135	chrX	133652030	133652031	-4701
RFX2	ENST00000592281	chr19	6061989	6061990	-4697
E2F2	ENST00000487237	chr1	23850580	23850581	-4694
FHL2	ENST00000409177	chr2	106020807	106020808	-4685
CTD-2277K2.1	ENST00000554436	chr14	62326947	62326948	-4650
TNS4	ENST00000394072	chr17	38641765	38641766	-4640
NCAN	ENST00000590187	chr19	19333019	19333020	-4632
ENPP6	ENST00000510054	chr4	185043576	185043577	-4604
SCGB1D2	ENST00000244926	chr11	62005093	62005094	-4588
F2RL1	ENST00000514165	chr5	76110189	76110190	-4568
U6	ENST00000459597	chr8	43153973	43153974	-4545
RP4-745E8.2	ENST00000444923	chr1	20654180	20654181	-4502
LINC00346	ENST00000538077	chr13	111526641	111526642	-4481
DNAJC6	ENST00000498720	chr1	65845307	65845308	-4461
MARVELD1	ENST00000451097	chr10	99468478	99468479	-4451
7SK	ENST00000410439	chr10	69913400	69913401	-4435
CCND1	ENST00000227507	chr11	69451433	69451434	-4421
Metazoa_SRP	ENST00000488637	chr7	72316702	72316703	-4399
RP11-803B1.3	ENST00000487255	chr3	75449072	75449073	-4387
CTD-3138B18.6	ENST00000595301	chr19	58773625	58773626	-4375
RP1-308E4.1	ENST00000438601	chr1	28775678	28775679	-4373
RP1-310O13.7	ENST00000449519	chr20	30623742	30623743	-4366

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
BTG3	ENST00000348354	chr21	18989627	18989628	-4364
SYS1	ENST00000372727	chr20	43986214	43986215	-4362
FTLP12	ENST00000578296	chr17	16290386	16290387	-4361
DUX4L16	ENST00000555130	chrY	13458260	13458261	-4333
SNORA40	ENST00000517238	chr1	150577433	150577434	-4300
RNF213	ENST00000508628	chr17	78230390	78230391	-4274
ARHGAP23	ENST00000548333	chr17	36621561	36621562	-4259
RP11-774O3.2	ENST00000509453	chr4	8317648	8317649	-4254
LEPROTL1	ENST00000321250	chr8	29948661	29948662	-4252
AL132671.1	ENST00000408507	chr6	117762306	117762307	-4246
AC009469.1	ENST00000546295	chr2	218670213	218670214	-4236
U6	ENST00000384019	chr18	60402792	60402793	-4229
PRR14	ENST00000563399	chr16	30657812	30657813	-4225
AC079780.3	ENST00000428259	chr7	23516151	23516152	-4220
BTC	ENST00000395743	chr4	75724112	75724113	-4218
MAP4	ENST00000477765	chr3	47903182	47903183	-4216
KCNN4	ENST00000262888	chr19	44289613	44289614	-4206
AC006967.1	ENST00000594086	chr7	156898501	156898502	-4172
FAM83A	ENST00000523819	chr8	124187041	124187042	-4158
KIAA0146	ENST00000517619	chr8	48635601	48635602	-4156
SLCO4A1	ENST00000370507	chr20	61283576	61283577	-4134
IGF2BP3	ENST00000258729	chr7	23514217	23514218	-4133
RP11-4O1.2	ENST00000563434	chr9	114804123	114804124	-4115
ROCK1P1	ENST00000576266	chr18	108287	108288	-4079
IGFL1	ENST00000437936	chr19	46728953	46728954	-4055
Y_RNA	ENST00000516627	chr2	62957916	62957917	-4043
AC073133.1	ENST00000436670	chr7	156242314	156242315	-4034
RP11-886I11.4	ENST00000557448	chrY	13483981	13483982	-4023
AC092687.4	ENST00000418835	chr2	10983682	10983683	-4020
CD99	ENST00000482293	chrX	2631406	2631407	-4008
RP11-145A3.4	ENST00000434499	chr1	225986874	225986875	-3975
RP5-940J5.8	ENST00000499202	chr12	6648703	6648704	-3966
LINC00489	ENST00000457816	chr20	36255476	36255477	-3957
FMNL1	ENST00000585852	chr17	43304097	43304098	-3938
RP11-241F15.3	ENST00000514077	chr4	49514754	49514755	-3933
MAP3K1	ENST00000469188	chr5	56177848	56177849	-3931
Y_RNA	ENST00000363413	chr2	29199313	29199314	-3928
ZNF275	ENST00000421401	chrX	152595696	152595697	-3916
RTEL1-TNFRSF6B	ENST00000480273	chr20	62313827	62313828	-3896
CTSZ	ENST00000217131	chr20	57586193	57586194	-3893

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
PPP6R2	ENST00000359139	chr22	50777857	50777858	-3875
MAPK10	ENST00000514856	chr4	87285245	87285246	-3870
IL1R1	ENST00000409589	chr2	102717170	102717171	-3852
TNS4	ENST00000394072	chr17	38640966	38640967	-3841
MIR3159	ENST00000584572	chr11	18405533	18405534	-3800
LIPH	ENST00000452897	chr3	185255244	185255245	-3798
HRASLS2	ENST00000255695	chr11	63334619	63334620	-3766
IL12RB1	ENST00000322153	chr19	18201577	18201578	-3766
ZP3	ENST00000394857	chr7	76050477	76050478	-3746
SNORA77	ENST00000408156	chr1	8575710	8575711	-3734
TXNDC9	ENST00000409705	chr2	99960878	99960879	-3715
AC073133.1	ENST00000436670	chr7	156241981	156241982	-3701
RP11-960B9.2	ENST00000573698	chr17	6097555	6097556	-3696
EEF1A1P38	ENST00000567658	chr16	27150186	27150187	-3688
HOXD13	ENST00000392539	chr2	176953933	176953934	-3685
snoU13	ENST00000459157	chr2	178214365	178214366	-3678
MTND2P9	ENST00000422293	chr9	83184553	83184554	-3678
UPP1	ENST00000416681	chr7	48124585	48124586	-3639
SLC14A2	ENST00000586448	chr18	42789336	42789337	-3623
UNC13A	ENST00000517497	chr19	17733472	17733473	-3623
U4	ENST00000364351	chr20	34471966	34471967	-3614
PHKA2-AS1	ENST00000452900	chrX	18904803	18904804	-3610
ARHGAP23	ENST00000548333	chr17	36622224	36622225	-3596
RP11-234K19.1	ENST00000513155	chr4	80514126	80514127	-3569
LEPROTL1	ENST00000321250	chr8	29949356	29949357	-3557
SMS	ENST00000404933	chrX	21955144	21955145	-3546
MTND5P15	ENST00000434246	chr3	176732383	176732384	-3530
CXXC11	ENST00000419912	chr2	242808255	242808256	-3496
FAM204A	ENST00000487269	chr10	120105331	120105332	-3493
Y_RNA	ENST00000363435	chr15	40218571	40218572	-3486
7SK	ENST00000362813	chr20	36607364	36607365	-3483
DENND1A	ENST00000373618	chr9	126695901	126695902	-3472
HDGFRP2	ENST00000587016	chr19	4492868	4492869	-3461
GARNL3	ENST00000478702	chr9	130004217	130004218	-3398
AL590403.1	ENST00000408852	chr6	34040368	34040369	-3375
NID2	ENST00000541773	chr14	52539084	52539085	-3374
RP11-666A8.9	ENST00000588104	chr17	74562527	74562528	-3346
LINC00266-1	ENST00000279067	chr20	62918406	62918407	-3331
LINC00501	ENST00000425388	chr3	177008900	177008901	-3329
NCALD	ENST00000520690	chr8	102990881	102990882	-3326

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CCDC173	ENST00000419478	chr2	170541152	170541153	-3320
LSM4	ENST00000597776	chr19	18430382	18430383	-3315
TBL1X	ENST00000497555	chrX	9604545	9604546	-3314
RP3-391O22.2	ENST00000404151	chr6	34581010	34581011	-3304
FMNL1	ENST00000587489	chr17	43315166	43315167	-3275
CAPN2	ENST00000433674	chr1	223886028	223886029	-3266
CLCA2	ENST00000498802	chr1	86910565	86910566	-3251
MIR3646	ENST00000578301	chr20	43033511	43033512	-3248
SMCR7L	ENST00000464629	chr22	39892196	39892197	-3240
RP11-886I11.4	ENST00000557448	chrY	13484764	13484765	-3240
AC133041.1	ENST00000408675	chr3	75595712	75595713	-3235
IL17RE	ENST00000461534	chr3	9941062	9941063	-3233
AC068587.1	ENST00000459100	chr8	12490387	12490388	-3225
HPCAL1	ENST00000423674	chr2	10439797	10439798	-3217
RP11-705O24.4	ENST00000522049	chr8	62826567	62826568	-3208
GYG1P1	ENST00000460864	chr8	74830387	74830388	-3144
MIR3911	ENST00000577791	chr9	130456189	130456190	-3117
CHMP7	ENST00000397677	chr8	23098052	23098053	-3097
GLYCTK	ENST00000461183	chr3	52318018	52318019	-3086
ST13P3	ENST00000546640	chr12	106406606	106406607	-3068
HES7	ENST00000577735	chr17	8030451	8030452	-3043
AL121594.1	ENST00000578587	chr14	35757701	35757702	-2990
AC091435.1	ENST00000381778	chr5	38824568	38824569	-2989
RALGDS	ENST00000372047	chr9	135999543	135999544	-2982
IRF2BP2	ENST00000366609	chr1	234748231	234748232	-2962
PBX1	ENST00000558796	chr1	164618173	164618174	-2959
TNFRSF6B	ENST00000369996	chr20	62325070	62325071	-2950
ADAMTS12	ENST00000506952	chr5	33627404	33627405	-2950
WAS	ENST00000376701	chrX	48539221	48539222	-2946
RP11-388E23.3	ENST00000556165	chr14	24299548	24299549	-2945
ABR	ENST00000575770	chr17	964219	964220	-2934
UTP6	ENST00000261708	chr17	30231702	30231703	-2920
DUX4L16	ENST00000555130	chrY	13459677	13459678	-2916
RXRA	ENST00000356384	chr9	137260901	137260902	-2915
LRRK2	ENST00000416796	chr12	40587649	40587650	-2896
FAM3D	ENST00000358781	chr3	58655465	58655466	-2892
KLHL15	ENST00000328046	chrX	24048191	24048192	-2890
RP11-812D23.1	ENST00000548429	chr12	86406596	86406597	-2878
TRABD2A	ENST00000474298	chr2	85136997	85136998	-2867
AC097495.2	ENST00000415138	chr2	69056312	69056313	-2863

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
U6	ENST00000363650	chr4	140236683	140236684	-2848
ZNF592	ENST00000559607	chr15	85318647	85318648	-2843
SMOX	ENST00000305958	chr20	4126598	4126599	-2827
NFE2L2	ENST00000458603	chr2	178100022	178100023	-2809
CTD-2008L17.2	ENST00000382897	chr18	53861297	53861298	-2806
CEACAM3	ENST00000599662	chr19	42310050	42310051	-2800
RP1-24O22.3	ENST00000406017	chr6	147879	147880	-2798
PTPRE	ENST00000492479	chr10	129858394	129858395	-2788
CTB-133G6.1	ENST00000576789	chr19	7411066	7411067	-2781
ZFHX4	ENST00000521891	chr8	77590675	77590676	-2778
MYOZ3	ENST00000517768	chr5	150037663	150037664	-2772
DPEP1	ENST00000564645	chr16	89701215	89701216	-2768
SMAP2	ENST00000435168	chr1	40807759	40807760	-2762
TFEC	ENST00000320239	chr7	115673608	115673609	-2743
RP11-3M1.1	ENST00000563906	chr16	48203884	48203885	-2737
LYST	ENST00000462376	chr1	235878434	235878435	-2736
CENPM	ENST00000472374	chr22	42338953	42338954	-2732
RP11-141M1.3	ENST00000454681	chr13	34253612	34253613	-2709
MEF2D	ENST00000348159	chr1	156473324	156473325	-2706
ARF4P2	ENST00000430209	chr20	61507098	61507099	-2672
JPH2	ENST00000372980	chr20	42818879	42818880	-2663
IGLV3-30	ENST00000524362	chr22	22958380	22958381	-2661
WNT7B	ENST00000339464	chr22	46375641	46375642	-2634
DDX3X	ENST00000478993	chrX	41190022	41190023	-2628
CALCR	ENST00000394441	chr7	93191746	93191747	-2626
SSPO	ENST00000484709	chr7	149496287	149496288	-2595
FRAT1	ENST00000371021	chr10	99076446	99076447	-2575
RP11-779O18.2	ENST00000521069	chr5	172192828	172192829	-2569
RP11-886I11.4	ENST00000557448	chrY	13485435	13485436	-2569
XRCC1	ENST00000597811	chr19	44067651	44067652	-2552
ATP1A2	ENST00000463989	chr1	160103925	160103926	-2535
RALGDS	ENST00000372047	chr9	135999096	135999097	-2535
ZNF461	ENST00000540605	chr19	37137014	37137015	-2507
RXRA	ENST00000356384	chr9	137261317	137261318	-2499
RP11-886I11.2	ENST00000557360	chrY	13468100	13468101	-2496
RFX2	ENST00000592281	chr19	6059761	6059762	-2469
RP11-54O15.3	ENST00000439872	chr9	97699690	97699691	-2464
NAA60	ENST00000572584	chr16	3523718	3523719	-2457
RP11-290F20.1	ENST00000457853	chr20	48925060	48925061	-2450
SHANK2	ENST00000425049	chr11	70721652	70721653	-2427

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
DDX11L16	ENST00000445777	chrX	155260268	155260269	-2422
CDT1	ENST00000301019	chr16	88867221	88867222	-2399
RPL31P59	ENST00000486139	chr18	3380634	3380635	-2391
C14orf164	ENST00000430154	chr14	23707176	23707177	-2378
RBKS	ENST00000458185	chr2	28068396	28068397	-2370
CTD-2319I12.5	ENST00000592317	chr17	58219798	58219799	-2358
TNFRSF1A	ENST00000437813	chr12	6445762	6445763	-2354
TOP3B	ENST00000442653	chr22	22332693	22332694	-2354
ZNF385D	ENST00000281523	chr3	21795268	21795269	-2343
AL022315.1	ENST00000598460	chr22	37965866	37965867	-2339
GNAT1	ENST00000232461	chr3	50226710	50226711	-2334
HES1	ENST00000232424	chr3	193851599	193851600	-2334
SH2D3C	ENST00000429553	chr9	130527011	130527012	-2316
SLC27A3	ENST00000271857	chr1	153744514	153744515	-2315
FBXO46	ENST00000591686	chr19	46220844	46220845	-2310
LITAF	ENST00000576036	chr16	11725368	11725369	-2304
KRT42P	ENST00000458343	chr17	39789139	39789140	-2297
RP5-1087E8.2	ENST00000438895	chr1	227148246	227148247	-2280
TRIP13	ENST00000510412	chr5	912394	912395	-2279
CTD-2568A17.8	ENST00000594114	chr19	51299104	51299105	-2265
SERPINA12	ENST00000341228	chr14	94986433	94986434	-2254
APC2	ENST00000587869	chr19	1444069	1444070	-2230
RP11-886I11.3	ENST00000553347	chrY	13475011	13475012	-2221
RP11-438C19.1	ENST00000515822	chr5	114426384	114426385	-2214
FBXL20	ENST00000577399	chr17	37560984	37560985	-2210
CLPTM1L	ENST00000507195	chr5	1328758	1328759	-2209
RP11-301M17.1	ENST00000415381	chr1	147716245	147716246	-2194
RPL31P50	ENST00000471002	chr12	31752522	31752523	-2181
HM13-IT1	ENST00000421894	chr20	30148791	30148792	-2177
TRAPPC3	ENST00000373162	chr1	36617271	36617272	-2175
UCKL1	ENST00000492660	chr20	62580031	62580032	-2172
C19orf59	ENST00000333598	chr19	7739364	7739365	-2149
LRTOMT	ENST00000440313	chr11	71803896	71803897	-2139
RP11-255B23.4	ENST00000521815	chr8	128217594	128217595	-2129
BHLHE40	ENST00000256495	chr3	5018675	5018676	-2125
LTBP4	ENST00000595529	chr19	41110252	41110253	-2119
LIN28A	ENST00000326279	chr1	26735167	26735168	-2101
CTC-448F2.3	ENST00000585753	chr19	30409990	30409991	-2098
SREBF1	ENST00000338854	chr17	17742410	17742411	-2087
ARNTL2	ENST00000544915	chr12	27483707	27483708	-2079

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
AC099544.2	ENST00000399435	chr3	23173824	23173825	-2038
DDX11L8	ENST00000535849	chr12	95458	95459	-2030
SYS1	ENST00000372727	chr20	43988549	43988550	-2027
CTD-2073O6.1	ENST00000519121	chr5	78013927	78013928	-2024
DDX11L16	ENST00000445777	chrX	155259870	155259871	-2024
SPI1	ENST00000378538	chr11	47402127	47402128	-2002
ORAI2	ENST00000482237	chr7	102071560	102071561	-1992
SLC25A17	ENST00000478550	chr22	41178248	41178249	-1991
CDC27P2	ENST00000425026	chrY	10031888	10031889	-1983
RP5-1087E8.2	ENST00000438895	chr1	227147947	227147948	-1981
DHRS4-AS1	ENST00000354854	chr14	24405961	24405962	-1978
HMGCS1	ENST00000433297	chr5	43315582	43315583	-1970
KCTD10	ENST00000542954	chr12	109900167	109900168	-1969
TRIM25	ENST00000316881	chr17	54993364	54993365	-1967
IFI16	ENST00000448393	chr1	158982515	158982516	-1955
RP11-886I11.4	ENST00000557448	chrY	13486070	13486071	-1934
AE000662.93	ENST00000557232	chr14	23027887	23027888	-1933
RRM2	ENST00000360566	chr2	10260526	10260527	-1928
SOS1	ENST00000428721	chr2	39353406	39353407	-1922
RP11-909N17.2	ENST00000523002	chr8	144493000	144493001	-1918
FAM102A	ENST00000479828	chr9	130727934	130727935	-1912
PGAM1P2	ENST00000436071	chr9	35945840	35945841	-1911
AC091133.1	ENST00000435491	chr17	47007258	47007259	-1894
DDX11L2	ENST00000535848	chr2	114361008	114361009	-1866
MT2A	ENST00000245185	chr16	56640247	56640248	-1863
FBXO46	ENST00000591686	chr19	46220387	46220388	-1853
KRT36	ENST00000393986	chr17	39650648	39650649	-1852
MYO1F	ENST00000598005	chr19	8608687	8608688	-1849
IGFL1P1	ENST00000599950	chr19	46697654	46697655	-1840
CTB-43E15.4	ENST00000518675	chr5	173237876	173237877	-1836
CAMTA1	ENST00000467267	chr1	6932287	6932288	-1828
RP11-709A23.2	ENST00000538759	chr12	27748790	27748791	-1820
POLA2	ENST00000534785	chr11	65059832	65059833	-1816
BHLHE40	ENST00000256495	chr3	5018992	5018993	-1808
AC079325.6	ENST00000425002	chr17	72565285	72565286	-1805
CABLES2	ENST00000453274	chr20	60973158	60973159	-1773
LGMN	ENST00000555169	chr14	93185572	93185573	-1770
ASRGL1	ENST00000415229	chr11	62103150	62103151	-1769
CNOT3	ENST00000221232	chr19	54639677	54639678	-1766
PPP1R1C	ENST00000461410	chr2	182924439	182924440	-1750

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
LINC00659	ENST00000412500	chr20	61408508	61408509	-1746
RP3-522P13.1	ENST00000493462	chr6	25259724	25259725	-1742
RP11-535A19.2	ENST00000529719	chr11	75528184	75528185	-1735
AK2	ENST00000466029	chr1	33489015	33489016	-1713
DDX11L1	ENST00000456328	chr1	10161	10162	-1707
PRKCH	ENST00000555185	chr14	61652579	61652580	-1697
CD97	ENST00000591565	chr19	14513484	14513485	-1697
AFAP1	ENST00000513856	chr4	7865718	7865719	-1682
FBXL20	ENST00000577399	chr17	37560449	37560450	-1675
RP11-13L2.1	ENST00000510247	chr3	140340351	140340352	-1674
RP4-701O16.5	ENST00000520729	chr7	139185548	139185549	-1650
PCNXL2	ENST00000496510	chr1	233318493	233318494	-1647
CTTNBP2NL	ENST00000271277	chr1	112937157	112937158	-1645
CTD-2201E18.3	ENST00000499871	chr5	43020556	43020557	-1645
AC016831.6	ENST00000446451	chr7	130530122	130530123	-1640
ZNF219	ENST00000451119	chr14	21574507	21574508	-1628
DGKZ	ENST00000525242	chr11	46358520	46358521	-1627
Metazoa_SRP	ENST00000481521	chr1	19749252	19749253	-1625
CDK8	ENST00000477290	chr13	26910079	26910080	-1624
KDM4B	ENST00000592175	chr19	5045388	5045389	-1620
HCN3	ENST00000368358	chr1	155245778	155245779	-1595
U47924.27	ENST00000537269	chr12	7070833	7070834	-1575
SLC2A13	ENST00000380858	chr12	40501457	40501458	-1568
RP1-178F15.3	ENST00000446229	chr1	153619866	153619867	-1563
U6	ENST00000517223	chr5	55419937	55419938	-1560
DND1P1	ENST00000580842	chr17	43661682	43661683	-1554
NFIA	ENST00000479364	chr1	61545890	61545891	-1548
EBI3	ENST00000221847	chr19	4227947	4227948	-1547
RRM2	ENST00000360566	chr2	10260913	10260914	-1541
B3GNT5	ENST00000462559	chr3	183003726	183003727	-1541
DDX11L10	ENST00000545636	chr16	60015	60016	-1537
PPP1R12B	ENST00000464965	chr1	202405412	202405413	-1535
MIR4663	ENST00000582039	chr8	124229634	124229635	-1533
LINC00273	ENST00000567668	chr16	33958643	33958644	-1530
PAM	ENST00000510006	chr5	102341627	102341628	-1529
KB-173C10.2	ENST00000519844	chr8	101428194	101428195	-1509
RP4-604G5.1	ENST00000456499	chr7	99525509	99525510	-1505
ISY1	ENST00000393295	chr3	128881634	128881635	-1500
PRKCE	ENST00000421201	chr2	45876984	45876985	-1499
GAPDHP71	ENST00000511530	chr5	173938809	173938810	-1498

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TACC1	ENST00000521642	chr8	38613263	38613264	-1493
U6	ENST00000384663	chr2	219455517	219455518	-1476
PLB1	ENST00000481449	chr2	28806972	28806973	-1474
AL603766.1	ENST00000584589	chr6	149499398	149499399	-1470
BTN2A1	ENST00000480218	chr6	26463990	26463991	-1464
GPRIN1	ENST00000303991	chr5	176038590	176038591	-1458
ARFGEF2	ENST00000371917	chr20	47536969	47536970	-1457
ARL5C	ENST00000578912	chr17	37320431	37320432	-1446
PTPN2	ENST00000587703	chr18	12838261	12838262	-1440
ITGA5	ENST00000547744	chr12	54808637	54808638	-1427
HMGCS1	ENST00000433297	chr5	43315001	43315002	-1389
RNA5-8SP2	ENST00000363564	chr16	33964040	33964041	-1385
MT2A	ENST00000245185	chr16	56640746	56640747	-1364
PDE7A	ENST00000518667	chr8	66679265	66679266	-1360
C17orf74	ENST00000333870	chr17	7327576	7327577	-1357
KIAA0240	ENST00000314073	chr6	42748456	42748457	-1356
DUX4L16	ENST00000555130	chrY	13461240	13461241	-1353
LFNG	ENST00000493850	chr7	2561874	2561875	-1352
ABCA4	ENST00000460514	chr1	94492494	94492495	-1345
ACSL1	ENST00000515030	chr4	185749306	185749307	-1336
LINC00442	ENST00000456737	chr13	19581074	19581075	-1324
RP11-1055B8.6	ENST00000574717	chr17	79367954	79367955	-1320
KAZALD1	ENST00000370200	chr10	102820281	102820282	-1316
C16orf91	ENST00000442039	chr16	1472105	1472106	-1306
RP11-716H6.1	ENST00000527100	chr11	122173771	122173772	-1302
MARK3	ENST00000440884	chr14	103850444	103850445	-1284
CCR2	ENST00000445132	chr3	46393940	46393941	-1284
ANTXRL	ENST00000434908	chr10	47667364	47667365	-1277
N4BP2	ENST00000261435	chr4	40057169	40057170	-1276
RP11-886I11.2	ENST00000557360	chrY	13469327	13469328	-1269
FAM129B	ENST00000373312	chr9	130332630	130332631	-1265
POLG2	ENST00000539111	chr17	62494412	62494413	-1260
RP11-6N17.6	ENST00000582142	chr17	46026892	46026893	-1253
FOXP1	ENST00000318789	chr3	71634382	71634383	-1244
SENP5	ENST00000489744	chr3	196625666	196625667	-1243
GLB1L3	ENST00000467068	chr11	134178355	134178356	-1242
AC008265.2	ENST00000399037	chr7	138124192	138124193	-1242
U47924.27	ENST00000537269	chr12	7071172	7071173	-1236
PEG10	ENST00000465184	chr7	94292820	94292821	-1226
PCGF2	ENST00000580830	chr17	36907291	36907292	-1223

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CDCA7	ENST00000347703	chr2	174218333	174218334	-1214
NEAT1	ENST00000499732	chr11	65189031	65189032	-1213
KIAA1755	ENST00000435901	chr20	36856824	36856825	-1205
TMEM194A	ENST00000300128	chr12	57473734	57473735	-1184
snoU13	ENST00000516578	chr5	170709478	170709479	-1184
OSBPL5	ENST00000478260	chr11	3117287	3117288	-1180
PTK2	ENST00000430260	chr8	141730006	141730007	-1175
PFKFB4	ENST00000412035	chr3	48595622	48595623	-1174
AC087491.2	ENST00000398554	chr17	37774693	37774694	-1172
CCDC43	ENST00000457422	chr17	42768310	42768311	-1165
INADL	ENST00000371158	chr1	62206989	62206990	-1159
SCUBE2	ENST00000534295	chr11	9160815	9160816	-1156
RP11-1O10.1	ENST00000565136	chr15	62525246	62525247	-1154
RP11-104N10.1	ENST00000565623	chr16	89572020	89572021	-1154
TSC22D1	ENST00000486464	chr13	45148809	45148810	-1153
RP11-173M1.5	ENST00000582878	chr17	25680758	25680759	-1150
ZBTB20	ENST00000357258	chr3	114867264	114867265	-1148
RP4-781K5.8	ENST00000437601	chr1	234860000	234860001	-1147
CFLAR	ENST00000425030	chr2	201986056	201986057	-1143
TPM4	ENST00000590180	chr19	16189729	16189730	-1136
LINC00229	ENST00000443783	chr22	45022429	45022430	-1132
RP11-51O6.1	ENST00000591758	chr16	61090996	61090997	-1130
FKBP1A	ENST00000400137	chr20	1374934	1374935	-1130
LTBP4	ENST00000595529	chr19	41111246	41111247	-1125
CIZ1	ENST00000538431	chr9	130955496	130955497	-1122
RP11-109D24.1	ENST00000562568	chr16	61728762	61728763	-1110
PLAC8	ENST00000411416	chr4	84032104	84032105	-1110
PPIH	ENST00000304979	chr1	43122986	43122987	-1109
RP11-72K17.2	ENST00000509390	chr5	97015489	97015490	-1106
CASP8	ENST00000392266	chr2	202097066	202097067	-1099
COL8A1	ENST00000261037	chr3	99356219	99356220	-1099
KIAA0146	ENST00000517693	chr8	48571133	48571134	-1092
CAPS	ENST00000588776	chr19	5910630	5910631	-1087
HMGN2	ENST00000468388	chr1	26797856	26797857	-1084
RASSF4	ENST00000483709	chr10	45464528	45464529	-1084
CTD-2589M5.5	ENST00000530049	chr11	46258849	46258850	-1083
H3F3AP1	ENST00000404612	chr6	26323599	26323600	-1081
STT3B	ENST00000453168	chr3	31573050	31573051	-1079
AP005530.1	ENST00000575820	chr18	10024	10025	-1078
RP11-544I20.2	ENST00000359491	chr14	64806381	64806382	-1066

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ROBO2	ENST00000469233	chr3	77651828	77651829	-1066
AC025171.1	ENST00000451894	chr5	43040611	43040612	-1065
LINC00273	ENST00000539813	chr16	33963561	33963562	-1060
CHST12	ENST00000258711	chr7	2442163	2442164	-1059
C22orf39	ENST00000542103	chr22	19436809	19436810	-1056
RP1-152L7.5	ENST00000406724	chr6	52529016	52529017	-1055
RPL27A	ENST00000531102	chr11	8709624	8709625	-1052
AC093627.11	ENST00000497017	chr7	173868	173869	-1051
SMIM2-AS1	ENST00000444663	chr13	44715632	44715633	-1049
C16orf62	ENST00000566850	chr16	19709655	19709656	-1042
ICAM2	ENST00000418105	chr17	62099026	62099027	-1034
PRR24	ENST00000552360	chr19	47777108	47777109	-1033
FAIM3	ENST00000529560	chr1	207097622	207097623	-1032
ENOSF1	ENST00000583973	chr18	689039	689040	-1031
SSBP3	ENST00000371320	chr1	54873119	54873120	-1029
TMEM38B	ENST00000374692	chr9	108455797	108455798	-1027
GPR77	ENST00000600626	chr19	47839345	47839346	-1025
DTYMK	ENST00000305784	chr2	242627429	242627430	-1025
RP11-420G6.4	ENST00000420981	chr6	2877763	2877764	-1021
KCMF1	ENST00000409785	chr2	85197196	85197197	-1019
AC093620.5	ENST00000342963	chr7	5458441	5458442	-1016
ZMYND19	ENST00000298585	chr9	140485953	140485954	-1013
IGF2BP1	ENST00000290341	chr17	47073764	47073765	-1009
PLEKHH3	ENST00000412503	chr17	40830051	40830052	-1005
ATAD3A	ENST00000378756	chr1	1446535	1446536	-995
FBXL20	ENST00000577399	chr17	37559768	37559769	-994
RSPH10B2	ENST00000485920	chr7	6804350	6804351	-986
TPRA1	ENST00000490290	chr3	127310921	127310922	-985
PIM1	ENST00000373509	chr6	37136996	37136997	-982
NDE1	ENST00000574163	chr16	15765555	15765556	-964
ROCK1P1	ENST00000576266	chr18	111402	111403	-964
LRRC8A	ENST00000492784	chr9	131674064	131674065	-958
FOSL2	ENST00000460736	chr2	28614357	28614358	-957
AQP11	ENST00000528638	chr11	77299490	77299491	-945
SLC1A5	ENST00000542575	chr19	47292793	47292794	-944
XXbac-BPG308K3.6	ENST00000440244	chr6	28832063	28832064	-938
RP11-325P15.2	ENST00000438469	chr1	146556059	146556060	-934
RNA5SP60	ENST00000410620	chr1	159147330	159147331	-932
C18orf21	ENST00000592875	chr18	33551113	33551114	-932
TMPRSS5	ENST00000299882	chr11	113578020	113578021	-927

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ZC3H7A	ENST00000355758	chr16	11892045	11892046	-924
TMEM167B	ENST00000338272	chr1	109632436	109632437	-920
POU2F1	ENST00000367866	chr1	167189156	167189157	-909
CYP46A1	ENST00000554611	chr14	100149740	100149741	-900
LAMC1	ENST00000258341	chr1	182991700	182991701	-896
MAP3K12	ENST00000551511	chr12	53877264	53877265	-895
CTDSP2	ENST00000550144	chr12	58224221	58224222	-890
DLG4	ENST00000451807	chr17	7118111	7118112	-882
EHBP1L1	ENST00000309295	chr11	65342629	65342630	-879
CR848007.2	ENST00000442354	chr9	44070756	44070757	-877
U6	ENST00000516104	chr22	42966124	42966125	-870
FST	ENST00000256759	chr5	52775368	52775369	-870
RP11-313F23.4	ENST00000545923	chr12	34372654	34372655	-868
IL15RA	ENST00000532039	chr10	6009163	6009164	-863
RP11-536D16.2	ENST00000443838	chr9	16120281	16120282	-849
LSM14B	ENST00000253001	chr20	60696672	60696673	-844
CDC27P1	ENST00000445384	chr2	133019058	133019059	-842
KRI1	ENST00000312962	chr19	10677540	10677541	-829
RUSC2	ENST00000361226	chr9	35489299	35489300	-824
TNXB	ENST00000375244	chr6	32077969	32077970	-820
SHC1	ENST00000448116	chr1	154944040	154944041	-819
RP11-301M17.1	ENST00000415381	chr1	147717626	147717627	-813
EFNA1	ENST00000474413	chr1	155101228	155101229	-809
CCBL1	ENST00000416084	chr9	131609943	131609944	-809
RP11-386G11.10	ENST00000548149	chr12	49520762	49520763	-802
DLX4	ENST00000503410	chr17	48045534	48045535	-799
C18orf56	ENST00000323813	chr18	659133	659134	-795
HK2	ENST00000472302	chr2	75080667	75080668	-792
CDC42	ENST00000400259	chr1	22378330	22378331	-789
BANP	ENST00000393207	chr16	88002841	88002842	-782
RAP1B	ENST00000250559	chr12	69003837	69003838	-781
C15orf39	ENST00000562637	chr15	75490427	75490428	-779
AC006372.1	ENST00000444154	chr7	157317697	157317698	-779
RP11-981G7.2	ENST00000524047	chr8	10331299	10331300	-775
LMNA	ENST00000448611	chr1	156095178	156095179	-772
PARD6B	ENST00000371610	chr20	49347309	49347310	-771
AL132709.2	ENST00000579587	chr14	101504909	101504910	-770
FAM222A	ENST00000538780	chr12	110151269	110151270	-763
MIR4802	ENST00000581881	chr4	40504889	40504890	-755
SLBP	ENST00000489418	chr4	1715032	1715033	-752

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RP11-368P15.1	ENST00000554238	chr14	53477937	53477938	-751
CD300A	ENST00000360141	chr17	72461804	72461805	-750
CDKN1B	ENST00000228872	chr12	12869319	12869320	-738
FBXL19	ENST00000562798	chr16	30933637	30933638	-738
RXFP4	ENST00000368318	chr1	155910746	155910747	-733
JUNB	ENST00000302754	chr19	12901576	12901577	-733
C19orf10	ENST00000596031	chr19	4669438	4669439	-732
ATM	ENST00000527805	chr11	108092479	108092480	-731
TIGD3	ENST00000309880	chr11	65121516	65121517	-721
PSMB3	ENST00000225426	chr17	36908268	36908269	-720
DUSP7	ENST00000495880	chr3	52091283	52091284	-719
UHRF1	ENST00000591733	chr19	4908727	4908728	-714
BRI3BP	ENST00000341446	chr12	125477533	125477534	-712
STAT6	ENST00000300134	chr12	57505925	57505926	-711
MYC	ENST00000259523	chr8	128746968	128746969	-711
PRRC2A	ENST00000376007	chr6	31587787	31587788	-709
SLFNL1	ENST00000372611	chr1	41488115	41488116	-702
RP5-1065J22.4	ENST00000429752	chr1	109648088	109648089	-702
WAS	ENST00000376701	chrX	48541465	48541466	-702
DCAKD	ENST00000588295	chr17	43129728	43129729	-701
ARHGAP21	ENST00000396432	chr10	25013294	25013295	-699
CCNE1	ENST00000262643	chr19	30302107	30302108	-697
UBAP1	ENST00000543944	chr9	34178305	34178306	-697
RASGRP4	ENST00000587287	chr19	38902730	38902731	-696
RNase_MRP	ENST00000516656	chr2	161254173	161254174	-696
PARP3	ENST00000475782	chr3	51978106	51978107	-696
RP11-549L6.3	ENST00000451656	chr10	111969042	111969043	-695
RP1-85F18.5	ENST00000420537	chr22	41594152	41594153	-694
TESK1	ENST00000467424	chr9	35606282	35606283	-686
GATAD2A	ENST00000457895	chr19	19515919	19515920	-685
PLAC8	ENST00000411416	chr4	84031679	84031680	-685
AC005391.2	ENST00000585647	chr19	929493	929494	-678
APEH	ENST00000296456	chr3	49710756	49710757	-678
KAT5	ENST00000525600	chr11	65485144	65485145	-670
SPAG5	ENST00000321765	chr17	26926965	26926966	-670
TBX10	ENST00000335385	chr11	67407698	67407699	-669
FAM161A	ENST00000405894	chr2	62081943	62081944	-667
PIP5KL1	ENST00000388747	chr9	130693732	130693733	-658
ATM	ENST00000531957	chr11	108163455	108163456	-656
RP5-1033H22.2	ENST00000412628	chr1	94059294	94059295	-647

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RNF181	ENST00000441634	chr2	85822202	85822203	-645
NUP160	ENST00000526870	chr11	47870746	47870747	-641
FAM117B	ENST00000303116	chr2	203499261	203499262	-639
VEZF1	ENST00000583932	chr17	56066256	56066257	-638
MTHFD1	ENST00000545908	chr14	64854113	64854114	-635
PPP6R3	ENST00000393799	chr11	68227554	68227555	-631
MCFD2	ENST00000444761	chr2	47169622	47169623	-630
TFRC	ENST00000360110	chr3	195809688	195809689	-630
MNT	ENST00000174618	chr17	2305036	2305037	-626
LINC00273	ENST00000539813	chr16	33963125	33963126	-624
MYOCD	ENST00000579237	chr17	12568586	12568587	-620
U6	ENST00000362733	chr2	38373937	38373938	-619
CAMK2N2	ENST00000296238	chr3	183979868	183979869	-619
ELK3	ENST00000228741	chr12	96587541	96587542	-618
RPRD2	ENST00000401000	chr1	150336510	150336511	-615
LINC00273	ENST00000567668	chr16	33957728	33957729	-615
GCHFR	ENST00000260447	chr15	41055605	41055606	-612
ARL15	ENST00000502271	chr5	53607022	53607023	-612
HERPUD2	ENST00000396081	chr7	35735354	35735355	-611
TRIM26	ENST00000453195	chr6	30181811	30181812	-609
GDI2	ENST00000380191	chr10	5856113	5856114	-603
TRAPPC5	ENST00000596148	chr19	7745126	7745127	-602
SRRM2-AS1	ENST00000577055	chr16	2801409	2801410	-600
KIF11	ENST00000260731	chr10	94352444	94352445	-598
ZNF146	ENST00000456324	chr19	36704905	36704906	-598
DNAJB14	ENST00000442697	chr4	100868478	100868479	-597
AP3D1	ENST00000591284	chr19	2165057	2165058	-595
HIST1H4A	ENST00000359907	chr6	26021319	26021320	-587
SERBP1	ENST00000370994	chr1	67896675	67896676	-579
RBM14	ENST00000310137	chr11	66383473	66383474	-579
ZNF335	ENST00000426788	chr20	44601405	44601406	-574
UBE2QL1	ENST00000399816	chr5	6448162	6448163	-573
DTYMK	ENST00000305784	chr2	242626976	242626977	-572
COL7A1	ENST00000328333	chr3	48633269	48633270	-571
PCIF1	ENST00000372409	chr20	44562701	44562702	-565
HNRNPC	ENST00000336053	chr14	21738213	21738214	-562
SIK2	ENST00000304987	chr11	111472556	111472557	-558
ZBTB43	ENST00000449886	chr9	129566727	129566728	-557
MAD2L1BP	ENST00000372171	chr6	43602999	43603000	-556
KCTD21	ENST00000525447	chr11	77887900	77887901	-554

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
WNK1	ENST00000535572	chr12	861205	861206	-553
SPEN	ENST00000375759	chr1	16173806	16173807	-552
LRRC37A12P	ENST00000454917	chr1	32892939	32892940	-551
WARS	ENST00000355338	chr14	100843689	100843690	-549
GOLPH3	ENST00000265070	chr5	32175003	32175004	-549
EHMT1	ENST00000495657	chr9	140610997	140610998	-549
ABCF3	ENST00000429586	chr3	183903263	183903264	-547
ZNF131	ENST00000503599	chr5	43064730	43064731	-547
FAM9B	ENST00000327220	chrX	9002711	9002712	-545
DDX55	ENST00000542286	chr12	124086081	124086082	-542
SLC20A1	ENST00000423633	chr2	113404481	113404482	-542
ATP1B3	ENST00000475483	chr3	141594423	141594424	-542
MIR22HG	ENST00000577164	chr17	1621004	1621005	-538
AC006132.1	ENST00000591087	chr19	46144214	46144215	-537
CUL3	ENST00000344951	chr2	225450644	225450645	-536
UBE3C	ENST00000348165	chr7	156931070	156931071	-536
PPP2R5A	ENST00000542178	chr1	212458247	212458248	-534
RP11-333E13.4	ENST00000381811	chr4	40059351	40059352	-534
SIVA1	ENST00000329967	chr14	105218905	105218906	-531
COPS7B	ENST00000474042	chr2	232655785	232655786	-528
CXorf58	ENST00000379211	chrX	23925393	23925394	-524
SP1	ENST00000551969	chr12	53773436	53773437	-523
Metazoa_SRP	ENST00000577467	chr17	4268266	4268267	-520
NAA40	ENST00000338447	chr11	63705911	63705912	-519
ECE1	ENST00000415912	chr1	21672513	21672514	-518
STARD4	ENST00000502322	chr5	110848804	110848805	-518
C6orf99	ENST00000367073	chr6	159290436	159290437	-517
PHF19	ENST00000373896	chr9	123640120	123640121	-516
MST4	ENST00000394334	chrX	131156776	131156777	-516
C18orf56	ENST00000323813	chr18	658853	658854	-515
FOXN2	ENST00000413569	chr2	48541261	48541262	-514
ARRB1	ENST00000529741	chr11	74988466	74988467	-513
TRABD2A	ENST00000474298	chr2	85134642	85134643	-512
CNOT1	ENST00000317147	chr16	58664297	58664298	-509
RP11-423C15.3	ENST00000444800	chr9	128508523	128508524	-506
SEMA4B	ENST00000559300	chr15	90727646	90727647	-503
SENP3	ENST00000578868	chr17	7464688	7464689	-503
NEK8	ENST00000579671	chr17	27052416	27052417	-498
KHSRP	ENST00000398148	chr19	6425300	6425301	-497
ATOX1	ENST00000524142	chr5	151152588	151152589	-497

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ARFGEF2	ENST00000371917	chr20	47537939	47537940	-487
ZNF575	ENST00000598080	chr19	44036629	44036630	-486
SLFNL1	ENST00000359345	chr1	41489390	41489391	-483
AGFG2	ENST00000430857	chr7	100136350	100136351	-483
PAWR	ENST00000328827	chr12	80085356	80085357	-481
KATNAL1	ENST00000380615	chr13	30882099	30882100	-480
RP11-169L17.3	ENST00000416158	chrX	40621000	40621001	-479
SPSB1	ENST00000450402	chr1	9354113	9354114	-473
LA16c-325D7.2	ENST00000575693	chr16	2918090	2918091	-473
NBL1	ENST00000289749	chr1	19969256	19969257	-469
RP11-386G11.10	ENST00000547712	chr12	49524485	49524486	-468
FAM208A	ENST00000355628	chr3	56717731	56717732	-468
IGF2BP3	ENST00000468263	chr7	23508011	23508012	-468
AOAH	ENST00000471806	chr7	36554748	36554749	-468
OLFM1	ENST00000277415	chr9	137966801	137966802	-466
USP1	ENST00000452143	chr1	62901502	62901503	-465
RNA5SP346	ENST00000363541	chr11	96208319	96208320	-465
PPP1R12B	ENST00000406302	chr1	202317363	202317364	-463
TNRC6B	ENST00000454349	chr22	40573465	40573466	-463
BTBD10	ENST00000528120	chr11	13485301	13485302	-459
KRT86	ENST00000544024	chr12	52642624	52642625	-459
IWS1	ENST00000409725	chr2	128284919	128284920	-459
GNAZ	ENST00000248996	chr22	23412081	23412082	-458
RP11-446E9.1	ENST00000435260	chr8	56964222	56964223	-458
HIST1H2BD	ENST00000377777	chr6	26157891	26157892	-457
IGF2BP3	ENST00000258729	chr7	23510541	23510542	-457
AP1S2	ENST00000329235	chrX	15873509	15873510	-457
PPM1D	ENST00000305921	chr17	58677088	58677089	-455
RP1-85F18.5	ENST00000420537	chr22	41593912	41593913	-454
UBA7	ENST00000333486	chr3	49851829	49851830	-452
STRN	ENST00000263918	chr2	37194061	37194062	-448
TFB1M	ENST00000475849	chr6	155636073	155636074	-448
OCIAD1	ENST00000509122	chr4	48832572	48832573	-442
AGTRAP	ENST00000376637	chr1	11795700	11795701	-440
CLIP1	ENST00000537178	chr12	122907614	122907615	-437
GK	ENST00000378946	chrX	30671039	30671040	-436
CYP39A1	ENST00000480804	chr6	46606055	46606056	-435
UBE2N	ENST00000318066	chr12	93836469	93836470	-433
NEDD4	ENST00000435532	chr15	56286375	56286376	-433
HMGN4	ENST00000328219	chr6	26538138	26538139	-433

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CHAMP1	ENST00000361283	chr13	115079555	115079556	-432
KHDRBS1	ENST00000327300	chr1	32478999	32479000	-430
EIF4EBP2	ENST00000373218	chr10	72163705	72163706	-429
FLAD1	ENST00000492620	chr1	154955385	154955386	-428
RP11-59H1.3	ENST00000540583	chr12	12878423	12878424	-427
CREBRF	ENST00000540014	chr5	172482927	172482928	-427
E2F3	ENST00000346618	chr6	20401971	20401972	-426
N4BP2	ENST00000261435	chr4	40058020	40058021	-425
TXNIP	ENST00000369317	chr1	145438044	145438045	-424
HYAL3	ENST00000336307	chr3	50337318	50337319	-421
ABCD3	ENST00000394233	chr1	94883512	94883513	-420
HIST2H2AB	ENST00000331128	chr1	149859884	149859885	-420
HCN3	ENST00000368358	chr1	155246955	155246956	-418
SLC25A6	ENST00000447786	chrX	1512042	1512043	-418
SPRTN	ENST00000391858	chr1	231472432	231472433	-417
EPB41L5	ENST00000263713	chr2	120770164	120770165	-416
SLC29A1	ENST00000371740	chr6	44190886	44190887	-415
FAM168A	ENST00000064778	chr11	73309646	73309647	-414
ANO6	ENST00000426898	chr12	45609357	45609358	-412
KIF2A	ENST00000401507	chr5	61601576	61601577	-412
CNOT8	ENST00000521174	chr5	154236702	154236703	-410
PRPF6	ENST00000266079	chr20	62612079	62612080	-408
CANX	ENST00000514383	chr5	179105221	179105222	-407
HNRNPF	ENST00000337970	chr10	43905018	43905019	-406
APOA1BP	ENST00000488840	chr1	156562662	156562663	-404
RP11-631N16.2	ENST00000550290	chr12	62996127	62996128	-404
C12orf73	ENST00000547945	chr12	104351453	104351454	-404
ARHGAP39	ENST00000540274	chr8	145911594	145911595	-402
MRPS28	ENST00000521605	chr8	80942923	80942924	-401
PRR24	ENST00000552360	chr19	47777741	47777742	-400
XPO1	ENST00000443240	chr2	61766157	61766158	-398
TBCA	ENST00000380377	chr5	77072581	77072582	-398
SPAG5	ENST00000321765	chr17	26926691	26926692	-396
PRPS1	ENST00000372435	chrX	106871340	106871341	-396
7SK	ENST00000410327	chr9	34049569	34049570	-394
SLC25A14	ENST00000495156	chrX	129473479	129473480	-394
ANK3	ENST00000459732	chr10	61824441	61824442	-393
RBM3	ENST00000472897	chrX	48432443	48432444	-393
SUV420H2	ENST00000255613	chr19	55850830	55850831	-390
SP4	ENST00000222584	chr7	21467261	21467262	-390

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
STIL	ENST00000396221	chr1	47779193	47779194	-388
AHCYL2	ENST00000325006	chr7	128864475	128864476	-388
RP11-292F22.4	ENST00000453605	chr10	47555778	47555779	-386
PMAIP1	ENST00000316660	chr18	57566793	57566794	-386
MCAT	ENST00000290429	chr22	43539784	43539785	-386
PIM1	ENST00000373509	chr6	37137593	37137594	-385
SBF2	ENST00000256190	chr11	10316136	10316137	-384
EZH1	ENST00000435174	chr17	40897452	40897453	-383
SNX8	ENST00000222990	chr7	2354480	2354481	-383
ZFP62	ENST00000359141	chr5	180288666	180288667	-382
SLC35B2	ENST00000393810	chr6	44225670	44225671	-381
CDC14B	ENST00000474602	chr9	99382490	99382491	-380
AGPAT3	ENST00000479117	chr21	45379284	45379285	-379
GNAI3	ENST00000369851	chr1	110090855	110090856	-377
SNX24	ENST00000261369	chr5	122180767	122180768	-376
MPI	ENST00000569931	chr15	75181970	75181971	-375
BACE1	ENST00000528053	chr11	117187346	117187347	-373
MAP3K7	ENST00000369329	chr6	91297135	91297136	-373
UHRF1	ENST00000591733	chr19	4909069	4909070	-372
RAB8A	ENST00000300935	chr19	16222066	16222067	-372
PUM2	ENST00000420234	chr2	20550964	20550965	-371
TCP11L2	ENST00000553143	chr12	106695336	106695337	-370
STXBP5-AS1	ENST00000417502	chr6	147523968	147523969	-367
INTS4	ENST00000534064	chr11	77706088	77706089	-366
E2F1	ENST00000343380	chr20	32274574	32274575	-366
PHF14	ENST00000445996	chr7	11013132	11013133	-366
LMNA	ENST00000347559	chr1	156084095	156084096	-365
SEC24A	ENST00000398844	chr5	133984113	133984114	-365
ANXA4	ENST00000394295	chr2	69968742	69968743	-363
DGCR8	ENST00000383024	chr22	20067392	20067393	-362
TUBB	ENST00000330914	chr6	30688990	30688991	-360
PM20D2	ENST00000275072	chr6	89855408	89855409	-360
AP1S1	ENST00000337619	chr7	100797317	100797318	-360
THBS3	ENST00000460050	chr1	155173453	155173454	-359
RAB6A	ENST00000310653	chr11	73472539	73472540	-359
ZNF446	ENST00000599913	chr19	58985847	58985848	-359
P4HTM	ENST00000383729	chr3	49026960	49026961	-358
RASA2	ENST00000515549	chr3	141205530	141205531	-358
ACTR10	ENST00000545307	chr14	58666440	58666441	-357
PURA	ENST00000331327	chr5	139493351	139493352	-356

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CDC42SE2	ENST00000511432	chr5	130588364	130588365	-355
RIC8B	ENST00000392837	chr12	107168021	107168022	-351
RP11-380O24.1	ENST00000518331	chr3	9405336	9405337	-351
UNC119	ENST00000484980	chr17	26879168	26879169	-350
NUP214	ENST00000359428	chr9	134000598	134000599	-349
UBE2Q1	ENST00000497453	chr1	154531850	154531851	-348
PABPC4L	ENST00000421491	chr4	135123248	135123249	-347
TMEM56	ENST00000370203	chr1	95582547	95582548	-346
TEX10	ENST00000374902	chr9	103115565	103115566	-346
FDXR	ENST00000442102	chr17	72869497	72869498	-343
EPB41L2	ENST00000337057	chr6	131384802	131384803	-342
SGK3	ENST00000521960	chr8	67687107	67687108	-341
C3orf37	ENST00000509042	chr3	128997330	128997331	-340
PPP6R3	ENST00000393799	chr11	68227847	68227848	-338
TMEM120B	ENST00000342607	chr12	122150319	122150320	-338
CTD-2574D22.6	ENST00000562285	chr16	29828221	29828222	-338
SUZ12P	ENST00000497969	chr17	29058385	29058386	-338
TEC	ENST00000506752	chr4	48231013	48231014	-338
GLI3	ENST00000437480	chr7	42276994	42276995	-338
HDGFRP2	ENST00000301284	chr19	4471947	4471948	-336
LRPPRC	ENST00000260665	chr2	44223478	44223479	-336
CHMP2B	ENST00000471660	chr3	87276084	87276085	-336
PPP1CC	ENST00000340766	chr12	111181077	111181078	-335
MED6	ENST00000256379	chr14	71067717	71067718	-335
NDUFV2	ENST00000318388	chr18	9102292	9102293	-335
TRA2A	ENST00000297071	chr7	23571993	23571994	-335
PDHA1	ENST00000540249	chrX	19361676	19361677	-334
CCDC30	ENST00000475614	chr1	42928667	42928668	-333
RBBP7	ENST00000465042	chrX	16887546	16887547	-332
C2orf44	ENST00000406895	chr2	24270560	24270561	-331
RP11-145A3.1	ENST00000448264	chr1	225887975	225887976	-330
RFX1	ENST00000589239	chr19	14117462	14117463	-330
GBAP1	ENST00000313929	chr1	155197541	155197542	-329
ZMYND19	ENST00000298585	chr9	140485269	140485270	-329
TPX2	ENST00000300403	chr20	30326745	30326746	-328
SIN3A	ENST00000565264	chr15	75744412	75744413	-327
STAT2	ENST00000557417	chr12	56754262	56754263	-325
CTD-2035E11.3	ENST00000509036	chr5	43018205	43018206	-325
NEK4	ENST00000233027	chr3	52805285	52805286	-322
DDX23	ENST00000308025	chr12	49246265	49246266	-321

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
HMGB2	ENST00000511316	chr4	174255902	174255903	-321
CSTF2T	ENST00000331173	chr10	53459672	53459673	-319
KAT6B	ENST00000372724	chr10	76586038	76586039	-319
PNN	ENST00000553331	chr14	39644068	39644069	-318
TAOK2	ENST00000308893	chr16	29984643	29984644	-318
NUCKS1	ENST00000367142	chr1	205719719	205719720	-317
EFCAB12	ENST00000505956	chr3	129147809	129147810	-317
PIGM	ENST00000368090	chr1	160002096	160002097	-315
TMEM245	ENST00000374586	chr9	111882538	111882539	-315
C6orf62	ENST00000378119	chr6	24721375	24721376	-313
SLC1A5	ENST00000542575	chr19	47292161	47292162	-312
CTD-2616J11.14	ENST00000600765	chr19	51897429	51897430	-312
CYB5P4	ENST00000396692	chr20	22867015	22867016	-311
KIAA2018	ENST00000491165	chr3	113415802	113415803	-311
PGAP1	ENST00000374738	chr2	197791777	197791778	-310
TXNRD2	ENST00000491939	chr22	19921357	19921358	-310
PDS5A	ENST00000303538	chr4	39979884	39979885	-310
CALU	ENST00000535623	chr7	128379036	128379037	-309
BUB3	ENST00000368865	chr10	124913486	124913487	-306
LEMD3	ENST00000308330	chr12	65563044	65563045	-306
CTD-2319I12.4	ENST00000590744	chr17	58212663	58212664	-306
ARL6IP6	ENST00000455875	chr2	153575126	153575127	-306
TRIM37	ENST00000393066	chr17	57184585	57184586	-305
CDKN2D	ENST00000335766	chr19	10680038	10680039	-305
VANGL1	ENST00000355485	chr1	116184269	116184270	-304
TMEM55B	ENST00000250489	chr14	20930073	20930074	-304
SNRNP200	ENST00000349783	chr2	96971599	96971600	-304
U6	ENST00000517104	chr4	48935173	48935174	-304
PKN2	ENST00000495119	chr1	89298308	89298309	-303
CTD-2659N19.9	ENST00000590065	chr19	12896214	12896215	-301
ZNF613	ENST00000593395	chr19	52430098	52430099	-301
ARHGEF40	ENST00000298694	chr14	21538128	21538129	-300
HNRNPUL1	ENST00000392006	chr19	41769935	41769936	-300
CTC-250I14.6	ENST00000592882	chr19	13265304	13265305	-299
AEN	ENST00000332810	chr15	89164228	89164229	-298
MRPL53	ENST00000409710	chr2	74700110	74700111	-298
ERGIC3	ENST00000348547	chr20	34129472	34129473	-297
POM121	ENST00000434423	chr7	72395362	72395363	-297
MLF1IP	ENST00000514781	chr4	185654861	185654862	-295
SNORD118	ENST00000363593	chr17	8077197	8077198	-294

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
BANP	ENST00000286122	chr16	87984745	87984746	-292
TMEM57	ENST00000399763	chr1	25757096	25757097	-291
EIF4A1	ENST00000580888	chr17	7475732	7475733	-291
ZNF45	ENST00000588432	chr19	44439719	44439720	-291
FLCN	ENST00000389171	chr17	17140788	17140789	-288
PIAS3	ENST00000393045	chr1	145575701	145575702	-287
PRRC2A	ENST00000376007	chr6	31588209	31588210	-287
PHF20	ENST00000461122	chr20	34359609	34359610	-286
C3orf58	ENST00000315691	chr3	143690353	143690354	-286
HNRNPA0	ENST00000314940	chr5	137090322	137090323	-285
HLTF	ENST00000494055	chr3	148804623	148804624	-284
TRA2B	ENST00000471134	chr3	185654670	185654671	-284
SETX	ENST00000224140	chr9	135230654	135230655	-284
PSMA5	ENST00000538610	chr1	109969343	109969344	-283
WBP1L	ENST00000448841	chr10	104503443	104503444	-283
FCHSD2	ENST00000409418	chr11	72853586	72853587	-282
TMEM120B	ENST00000333310	chr12	122215398	122215399	-282
DAPK3	ENST00000596311	chr19	3971400	3971401	-281
CDCA7L	ENST00000406877	chr7	21985981	21985982	-281
KRT7	ENST00000548657	chr12	52638943	52638944	-279
RP11-544I20.2	ENST00000359491	chr14	64805594	64805595	-279
CASP2	ENST00000310447	chr7	142985029	142985030	-278
FH	ENST00000366560	chr1	241683336	241683337	-277
DHTKD1	ENST00000263035	chr10	12110693	12110694	-277
CTNND1	ENST00000530720	chr11	57573717	57573718	-277
SUZ12	ENST00000322652	chr17	30263760	30263761	-276
SRSF1	ENST00000258962	chr17	56084981	56084982	-276
PHF1	ENST00000427004	chr6	33377900	33377901	-275
AC090571.1	ENST00000544355	chr8	41820457	41820458	-275
CLTC	ENST00000269122	chr17	57696944	57696945	-274
ING3	ENST00000315870	chr7	120590528	120590529	-274
MIR3124	ENST00000582636	chr1	249120302	249120303	-273
ABHD6	ENST00000478253	chr3	58222959	58222960	-273
ZBTB5	ENST00000307750	chr9	37465667	37465668	-273
EBNA1BP2	ENST00000431635	chr1	43638511	43638512	-272
SLMAP	ENST00000295951	chr3	57741684	57741685	-272
FOXN2	ENST00000413569	chr2	48541504	48541505	-271
NCOA6	ENST00000359003	chr20	33413721	33413722	-271
MRPS18A	ENST00000372133	chr6	43655797	43655798	-271
PHLDB1	ENST00000530994	chr11	118478060	118478061	-269

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RP11-216B9.8	ENST00000427246	chr9	131448350	131448351	-269
PMM1	ENST00000216259	chr22	41986160	41986161	-268
DEDD	ENST00000392188	chr1	161102743	161102744	-267
SLC2A4	ENST00000317370	chr17	7184718	7184719	-267
RRM2	ENST00000360566	chr2	10262187	10262188	-267
GPR146	ENST00000444847	chr7	1083944	1083945	-267
CRTAP	ENST00000320954	chr3	33155204	33155205	-266
C9orf156	ENST00000375119	chr9	100685116	100685117	-266
PANX1	ENST00000227638	chr11	93861828	93861829	-265
HRH4	ENST00000256906	chr18	22040327	22040328	-265
GAS6	ENST00000357389	chr13	114567308	114567309	-264
ABCB6	ENST00000265316	chr2	220083973	220083974	-263
SLC25A36	ENST00000446041	chr3	140660408	140660409	-263
IMPG1	ENST00000369952	chr6	76645027	76645028	-263
KCNH4	ENST00000264661	chr17	40333556	40333557	-262
DCAF7	ENST00000310827	chr17	61627559	61627560	-262
TPM3	ENST00000509409	chr1	154155962	154155963	-261
HERC5	ENST00000264350	chr4	89378006	89378007	-261
TRIM26	ENST00000453195	chr6	30181463	30181464	-261
AMIGO1	ENST00000369862	chr1	110052618	110052619	-260
YWHAB	ENST00000353703	chr20	43514056	43514057	-260
HMGXB4	ENST00000420166	chr22	35653184	35653185	-260
RNU6ATAC	ENST00000408749	chr9	137029944	137029945	-260
RRP7A	ENST00000323013	chr22	42916065	42916066	-259
HMGCS1	ENST00000433297	chr5	43313871	43313872	-259
YIF1A	ENST00000376901	chr11	66056897	66056898	-258
TACO1	ENST00000258975	chr17	61677973	61677974	-257
POLR1E	ENST00000377798	chr9	37485676	37485677	-255
PFN1	ENST00000574872	chr17	4851016	4851017	-254
NCOA5	ENST00000290231	chr20	44718843	44718844	-254
G3BP1	ENST00000394123	chr5	151151216	151151217	-254
EGR3	ENST00000317216	chr8	22551067	22551068	-254
ARNTL2	ENST00000544915	chr12	27485533	27485534	-253
BRMS1L	ENST00000216807	chr14	36295270	36295271	-253
XPO1	ENST00000449444	chr2	61763974	61763975	-253
C6orf47	ENST00000375911	chr6	31628800	31628801	-253
CCNE2	ENST00000308108	chr8	95907735	95907736	-253
UFM1	ENST00000494372	chr13	38923733	38923734	-252
MYLPF	ENST00000563718	chr16	30382002	30382003	-252
KIAA0947	ENST00000296564	chr5	5422554	5422555	-252

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ERI3	ENST00000452396	chr1	44821181	44821182	-251
TMX1	ENST00000555574	chr14	51706628	51706629	-251
UXT	ENST00000333119	chrX	47518809	47518810	-251
ITPRIP	ENST00000337478	chr10	106098410	106098411	-250
GPR180	ENST00000376958	chr13	95253906	95253907	-250
U2AF2	ENST00000450554	chr19	56165261	56165262	-250
RP11-37N22.1	ENST00000523703	chr8	125259887	125259888	-250
RPL41	ENST00000546591	chr12	56510120	56510121	-249
CHAF1A	ENST00000301280	chr19	4402409	4402410	-249
NAIF1	ENST00000373078	chr9	130829847	130829848	-249
DLX6	ENST00000493273	chr7	96635556	96635557	-248
DSCC1	ENST00000313655	chr8	120868496	120868497	-248
VCP	ENST00000448530	chr9	35072870	35072871	-248
RP11-199F11.2	ENST00000571370	chr17	7589934	7589935	-247
AC069277.2	ENST00000342990	chr3	6549220	6549221	-247
SMUG1	ENST00000508394	chr12	54583022	54583023	-246
SYDE1	ENST00000342784	chr19	15217967	15217968	-246
FAM185A	ENST00000442873	chr7	102389172	102389173	-245
TMEM74	ENST00000297459	chr8	109800087	109800088	-245
MMD	ENST00000262065	chr17	53499595	53499596	-244
STRADA	ENST00000392950	chr17	61819572	61819573	-244
LGR4	ENST00000389858	chr11	27494563	27494564	-243
FKBP5	ENST00000357266	chr6	35656960	35656961	-243
STIL	ENST00000337817	chr1	47780059	47780060	-242
RNU6-1	ENST00000383898	chr15	68132623	68132624	-242
TESK2	ENST00000451835	chr1	45957111	45957112	-241
B3GAT3	ENST00000265471	chr11	62389886	62389887	-241
DLG4	ENST00000451807	chr17	7117469	7117470	-240
CYB5R4	ENST00000369681	chr6	84569122	84569123	-239
PDE4DIP	ENST00000479408	chr1	144932788	144932789	-238
DKFZP779L1853	ENST00000595310	chr12	48591931	48591932	-238
TSPAN3	ENST00000267970	chr15	77363806	77363807	-238
HSPBAP1	ENST00000306103	chr3	122512907	122512908	-238
CDK5RAP2	ENST00000491334	chr9	123342684	123342685	-238
DCAF15	ENST00000254337	chr19	14063066	14063067	-237
LRRCC1	ENST00000360375	chr8	86019145	86019146	-236
CA5BP1	ENST00000380334	chrX	15693432	15693433	-236
LRRC59	ENST00000225972	chr17	48475147	48475148	-235
ZNF580	ENST00000543039	chr19	56153182	56153183	-235
RP1-74B13.2	ENST00000551161	chr12	111269348	111269349	-234

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ARID3B	ENST00000346246	chr15	74833283	74833284	-234
FBXL20	ENST00000577399	chr17	37559008	37559009	-234
PTER	ENST00000343656	chr10	16478730	16478731	-233
EEF1G	ENST00000532986	chr11	62341789	62341790	-233
FANCC	ENST00000474949	chr9	98080222	98080223	-233
FANCL	ENST00000449070	chr2	58468737	58468738	-232
RPS6KC1	ENST00000543470	chr1	213224357	213224358	-231
PSMC3	ENST00000530912	chr11	47448222	47448223	-231
RAD52	ENST00000358495	chr12	1059117	1059118	-231
MFN2	ENST00000444836	chr1	12040007	12040008	-230
GABARAP	ENST00000302386	chr17	7146317	7146318	-230
RP4-669P10.18	ENST00000416037	chr22	42486706	42486707	-230
TNIP1	ENST00000521001	chr5	150473366	150473367	-230
ZNF687	ENST00000443959	chr1	151253864	151253865	-229
MTR	ENST00000366577	chr1	236958380	236958381	-229
AC019205.1	ENST00000584443	chr6	73972501	73972502	-229
RPS14	ENST00000407193	chr5	149829545	149829546	-228
USP4	ENST00000491791	chr3	49378370	49378371	-227
MBIP	ENST00000556427	chr14	36789300	36789301	-226
STAP2	ENST00000599736	chr19	4343007	4343008	-226
ZBTB7B	ENST00000535420	chr1	154974901	154974902	-225
SMS	ENST00000404933	chrX	21958465	21958466	-225
SLC38A1	ENST00000552197	chr12	46661705	46661706	-223
RNASEH2A	ENST00000221486	chr19	12917170	12917171	-223
PACSIN2	ENST00000263246	chr22	43411372	43411373	-223
BRD2	ENST00000395287	chr6	32940283	32940284	-223
NENF	ENST00000366988	chr1	212606006	212606007	-222
CCDC97	ENST00000596882	chr19	41816483	41816484	-222
FNBP4	ENST00000542975	chr11	47789214	47789215	-221
TAF15	ENST00000588240	chr17	34136237	34136238	-221
GTPBP1	ENST00000216044	chr22	39101506	39101507	-221
MCM4	ENST00000523944	chr8	48873236	48873237	-221
CASP8AP2	ENST00000552401	chr6	90539392	90539393	-220
NES	ENST00000368223	chr1	156647406	156647407	-219
RNU4-2	ENST00000365668	chr12	120729923	120729924	-219
DEK	ENST00000397239	chr6	18265271	18265272	-219
S100A13	ENST00000469931	chr1	153607089	153607090	-218
TTC33	ENST00000337702	chr5	40756293	40756294	-218
SLFN13	ENST00000285013	chr17	33776071	33776072	-217
TRIM56	ENST00000306085	chr7	100728502	100728503	-217

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TRIM44	ENST00000299413	chr11	35684136	35684137	-216
RTTN	ENST00000255674	chr18	67873395	67873396	-216
CCDC174	ENST00000303688	chr3	14693054	14693055	-216
DLAT	ENST00000533297	chr11	111895916	111895917	-215
PCNP	ENST00000265260	chr3	101292723	101292724	-215
DCTPP1	ENST00000568434	chr16	30440822	30440823	-214
CBX1	ENST00000444685	chr17	46178156	46178157	-214
EVI5L	ENST00000270530	chr19	7894905	7894906	-213
PWWP2A	ENST00000456329	chr5	159546641	159546642	-213
HIST1H4E	ENST00000360441	chr6	26204644	26204645	-213
BAZ1B	ENST00000404251	chr7	72936818	72936819	-212
RP11-312B8.1	ENST00000442889	chr1	6845112	6845113	-211
IRF2BP2	ENST00000491430	chr1	234744049	234744050	-211
PCGF2	ENST00000580830	chr17	36906279	36906280	-211
RPL19	ENST00000225430	chr17	37356324	37356325	-211
GTPBP3	ENST00000599429	chr19	17448114	17448115	-211
GORASP2	ENST00000444801	chr2	171785495	171785496	-211
RPIA	ENST00000283646	chr2	88990951	88990952	-210
TERF1	ENST00000276602	chr8	73920888	73920889	-210
NFIB	ENST00000397579	chr9	14314789	14314790	-210
MDM4	ENST00000367182	chr1	204485303	204485304	-207
NABP2	ENST00000267023	chr12	56617901	56617902	-207
PIGL	ENST00000581006	chr17	16120316	16120317	-206
TBP	ENST00000421512	chr6	170863183	170863184	-206
FAM220A	ENST00000533877	chr7	6388816	6388817	-206
BIRC3	ENST00000526421	chr11	102188009	102188010	-205
NQO2	ENST00000380472	chr6	2988674	2988675	-205
UCP2	ENST00000543714	chr11	73694090	73694091	-204
DCTN2	ENST00000552390	chr12	57929124	57929125	-204
FAM82A2	ENST00000560905	chr15	41047736	41047737	-204
COPS4	ENST00000264389	chr4	83956038	83956039	-204
SRSF6	ENST00000483871	chr20	42086364	42086365	-203
COL12A1	ENST00000322507	chr6	75915968	75915969	-203
ILF3	ENST00000318511	chr19	10764734	10764735	-202
CENPI	ENST00000218507	chrX	100352975	100352976	-202
CMPK1	ENST00000371873	chr1	47799267	47799268	-201
C20orf111	ENST00000372970	chr20	42838915	42838916	-201
TAF1	ENST00000373790	chrX	70585912	70585913	-201
U1	ENST00000363009	chr1	147735550	147735551	-200
SMC3	ENST00000361804	chr10	112327248	112327249	-200

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TMEM127	ENST00000435268	chr2	96926531	96926532	-200
ATF2	ENST00000437522	chr2	176033308	176033309	-200
LETM2	ENST00000527334	chr8	38243524	38243525	-200
CLCF1	ENST00000533438	chr11	67141845	67141846	-199
PDCD7	ENST00000204549	chr15	65426369	65426370	-197
AC093901.1	ENST00000414886	chr2	118944156	118944157	-196
KPNA1	ENST00000465882	chr3	122233985	122233986	-195
MALSU1	ENST00000466681	chr7	23338623	23338624	-195
FAM73B	ENST00000474534	chr9	131798704	131798705	-195
PEX16	ENST00000528674	chr11	45939822	45939823	-193
ANO10	ENST00000413397	chr3	43733276	43733277	-192
SLC2A8	ENST00000373371	chr9	130159228	130159229	-192
RNF181	ENST00000441634	chr2	85822656	85822657	-191
DCAF6	ENST00000450548	chr1	167904830	167904831	-190
GRB7	ENST00000445327	chr17	37894833	37894834	-190
SEC1P	ENST00000474419	chr19	49141137	49141138	-190
NR1D2	ENST00000312521	chr3	23986560	23986561	-190
DHX15	ENST00000336812	chr4	24586361	24586362	-190
MTMR4	ENST00000323456	chr17	56595453	56595454	-189
BLOC1S3	ENST00000433642	chr19	45681813	45681814	-189
CEP250	ENST00000446710	chr20	34042795	34042796	-189
RP11-699L21.1	ENST00000397645	chr3	193721635	193721636	-189
ARL15	ENST00000502271	chr5	53606599	53606600	-189
PHRF1	ENST00000264555	chr11	576297	576298	-188
MLEC	ENST00000228506	chr12	121124483	121124484	-188
CCNA2	ENST00000274026	chr4	122745273	122745274	-188
SNX8	ENST00000447136	chr7	2394139	2394140	-188
VCPIP1	ENST00000310421	chr8	67579638	67579639	-188
RP11-500G10.1	ENST00000456581	chr10	131909266	131909267	-187
ARL11	ENST00000282026	chr13	50202247	50202248	-187
GTF2A1	ENST00000556268	chr14	81687906	81687907	-187
ATP6V1A	ENST00000273398	chr3	113465678	113465679	-187
PPP1R3F	ENST00000438316	chrX	49126118	49126119	-187
UBE2T	ENST00000367274	chr1	202311292	202311293	-186
ARRB1	ENST00000393505	chr11	75063057	75063058	-186
NDUFB6	ENST00000379847	chr9	32573344	32573345	-186
RNF135	ENST00000443677	chr17	29297816	29297817	-185
CHCHD2	ENST00000395422	chr7	56174452	56174453	-185
ST7	ENST00000393446	chr7	116593106	116593107	-185
LAS1L	ENST00000484069	chrX	64754838	64754839	-185

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
POLE4	ENST00000483063	chr2	75185435	75185436	-183
ARF4	ENST00000463880	chr3	57583416	57583417	-183
SMG7	ENST00000440812	chr1	183441168	183441169	-182
COX8A	ENST00000314133	chr11	63741896	63741897	-182
ZNF823	ENST00000440527	chr19	11850002	11850003	-180
PSENEN	ENST00000587708	chr19	36235834	36235835	-180
METTL2B	ENST00000462662	chr7	128095713	128095714	-180
GCA	ENST00000437150	chr2	163200418	163200419	-179
BRIX1	ENST00000336767	chr5	34915301	34915302	-179
HIVEP1	ENST00000491710	chr6	12008816	12008817	-178
SLBP	ENST00000489418	chr4	1714457	1714458	-177
ZNF131	ENST00000503599	chr5	43065100	43065101	-177
RP4-756H11.3	ENST00000448096	chr7	66119347	66119348	-177
ZC3HAV1	ENST00000471652	chr7	138794640	138794641	-177
AC008781.7	ENST00000422040	chr5	140997804	140997805	-176
BRPF1	ENST00000433861	chr3	9773237	9773238	-175
PDE12	ENST00000487257	chr3	57541827	57541828	-175
POLA1	ENST00000379068	chrX	24711860	24711861	-175
RBBP5	ENST00000264515	chr1	205091315	205091316	-174
ZNHIT3	ENST00000490126	chr17	34842298	34842299	-174
RAB28	ENST00000330852	chr4	13486161	13486162	-174
AATF	ENST00000225402	chr17	35306001	35306002	-173
FAM161A	ENST00000405894	chr2	62081449	62081450	-173
HIST1H3G	ENST00000305910	chr6	26271783	26271784	-173
SRSF10	ENST00000453840	chr1	24307123	24307124	-172
ZC3H10	ENST00000257940	chr12	56511770	56511771	-172
MAP3K2	ENST00000409947	chr2	128146211	128146212	-172
GMPR2	ENST00000560517	chr14	24706009	24706010	-171
NLRC5	ENST00000399221	chr16	57091805	57091806	-171
ZBTB45	ENST00000600990	chr19	59031287	59031288	-171
FKBPL	ENST00000375156	chr6	32098237	32098238	-171
AC093391.2	ENST00000419808	chr2	136742575	136742576	-170
BIN3	ENST00000522268	chr8	22526829	22526830	-170
WASF2	ENST00000430629	chr1	27816836	27816837	-169
HNRNPA3	ENST00000392524	chr2	178077121	178077122	-169
RP11-573D15.8	ENST00000354642	chr3	186464086	186464087	-169
HIST1H2AB	ENST00000259791	chr6	26033963	26033964	-169
ZNF782	ENST00000481138	chr9	99616936	99616937	-168
OIP5-AS1	ENST00000558945	chr15	41576020	41576021	-167
GMCL1	ENST00000282570	chr2	70056606	70056607	-167

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CDC23	ENST00000394886	chr5	137549197	137549198	-167
MAD2L1BP	ENST00000372171	chr6	43603388	43603389	-167
DDX50	ENST00000373585	chr10	70660867	70660868	-166
TAB1	ENST00000216160	chr22	39795579	39795580	-166
RPL32	ENST00000429711	chr3	12883251	12883252	-166
ZNF860	ENST00000489408	chr3	32023096	32023097	-166
PPIA	ENST00000468812	chr7	44836112	44836113	-166
NOL6	ENST00000353159	chr9	33474092	33474093	-166
CA5BP1	ENST00000380336	chrX	15692888	15692889	-166
GLO1	ENST00000373365	chr6	38671080	38671081	-165
BPGM	ENST00000344924	chr7	134331394	134331395	-165
SLC39A1	ENST00000356205	chr1	153936210	153936211	-164
LRIG1	ENST00000498287	chr3	66551849	66551850	-164
TCAM1P	ENST00000463377	chr17	61926488	61926489	-163
AC009005.2	ENST00000589457	chr19	571906	571907	-163
PRPF40A	ENST00000486100	chr2	153574672	153574673	-163
BAG6	ENST00000211379	chr6	31620643	31620644	-163
TOM1L2	ENST00000579586	chr17	17875896	17875897	-162
TOP2A	ENST00000423485	chr17	38574362	38574363	-162
GLI2	ENST00000438299	chr2	121549696	121549697	-162
FICD	ENST00000552695	chr12	108908800	108908801	-161
ATF4	ENST00000396680	chr22	39916408	39916409	-160
TMEM41B	ENST00000528080	chr11	9336484	9336485	-159
MUTYH	ENST00000372115	chr1	45806298	45806299	-158
RP11-222A11.1	ENST00000593568	chr10	67330474	67330475	-158
LINC00471	ENST00000313064	chr2	232379204	232379205	-156
AK2	ENST00000354858	chr1	33502746	33502747	-155
CREM	ENST00000469517	chr10	35485171	35485172	-155
PDCD4	ENST00000280154	chr10	112631409	112631410	-155
NEAT1	ENST00000499732	chr11	65190090	65190091	-154
GPRC5B	ENST00000569479	chr16	19897641	19897642	-154
SAMD13	ENST00000370671	chr1	84765087	84765088	-153
CENPA	ENST00000335756	chr2	27008712	27008713	-152
C20orf118	ENST00000436941	chr20	35515705	35515706	-152
DAXX	ENST00000490173	chr6	33288387	33288388	-152
ARHGEF19	ENST00000449495	chr1	16533187	16533188	-151
TMEM194A	ENST00000300128	chr12	57472701	57472702	-151
METTL2A	ENST00000311506	chr17	60501076	60501077	-151
HIST1H3B	ENST00000244661	chr6	26032437	26032438	-151
RP11-867G23.2	ENST00000533287	chr11	66035748	66035749	-150

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
XRCC5	ENST00000392132	chr2	216973869	216973870	-150
TUBA1B	ENST00000549870	chr12	49524043	49524044	-149
TRA2B	ENST00000453386	chr3	185656071	185656072	-149
GOLPH3	ENST00000265070	chr5	32174603	32174604	-149
TICRR	ENST00000268138	chr15	90118564	90118565	-148
RBL1	ENST00000373664	chr20	35724544	35724545	-148
SCML1	ENST00000380045	chrX	17755439	17755440	-148
MICU1	ENST00000398761	chr10	74386044	74386045	-147
MED17	ENST00000251871	chr11	93517245	93517246	-147
NPC2	ENST00000556009	chr14	74961025	74961026	-147
FHOD1	ENST00000258201	chr16	67281706	67281707	-147
HIST1H2BD	ENST00000377777	chr6	26158202	26158203	-146
ATAD2	ENST00000287394	chr8	124408849	124408850	-146
BMF	ENST00000558774	chr15	40401234	40401235	-143
SUCLG1	ENST00000393868	chr2	84686744	84686745	-142
DDX23	ENST00000552555	chr12	49246763	49246764	-140
CD320	ENST00000596246	chr19	8373378	8373379	-140
PDXP	ENST00000215904	chr22	38054593	38054594	-140
YIPF1	ENST00000412288	chr1	54355644	54355645	-139
TRMT112	ENST00000308774	chr11	64085167	64085168	-139
TMPO-AS1	ENST00000548760	chr12	98910337	98910338	-139
ATP5G1	ENST00000355938	chr17	46969988	46969989	-138
NR1H2	ENST00000595730	chr19	50879575	50879576	-138
PANK2	ENST00000336066	chr20	3869897	3869898	-138
AHCTF1	ENST00000478568	chr1	247095415	247095416	-137
MCM10	ENST00000378714	chr10	13203416	13203417	-137
TAF6L	ENST00000294168	chr11	62538637	62538638	-137
ZNF181	ENST00000599244	chr19	35224922	35224923	-137
GGCT	ENST00000275428	chr7	30544595	30544596	-137
USP24	ENST00000484447	chr1	55541306	55541307	-136
PER1	ENST00000581395	chr17	8059958	8059959	-136
LUC7L2	ENST00000545899	chr7	139044490	139044491	-136
POLQ	ENST00000264233	chr3	121264986	121264987	-135
KCNK1	ENST00000366621	chr1	233749615	233749616	-134
LINC00493	ENST00000411646	chr20	18547929	18547930	-134
DDX39B	ENST00000428098	chr6	31509927	31509928	-134
MMACHC	ENST00000474382	chr1	45974671	45974672	-133
NUCB1	ENST00000407032	chr19	49403443	49403444	-133
AMOTL2	ENST00000506107	chr3	134093891	134093892	-133
EIF3F	ENST00000309828	chr11	8008735	8008736	-131

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RP11-424C20.2	ENST00000540175	chr12	20704392	20704393	-131
ZNF219	ENST00000555697	chr14	21571867	21571868	-131
RANBP3	ENST00000587479	chr19	5978282	5978283	-131
HNRNPD	ENST00000509263	chr4	83294431	83294432	-130
TCF19	ENST00000376257	chr6	31126188	31126189	-130
COX7B	ENST00000481445	chrX	77154804	77154805	-130
PPP1R3E	ENST00000561178	chr14	23770276	23770277	-129
EIF2AK3	ENST00000303236	chr2	88927221	88927222	-129
BTG1	ENST00000256015	chr12	92539799	92539800	-128
COPS3	ENST00000268717	chr17	17184733	17184734	-128
CCT7	ENST00000540468	chr2	73461235	73461236	-128
LTN1	ENST00000361371	chr21	30365403	30365404	-128
KRR1	ENST00000550898	chr12	75905541	75905542	-127
UFM1	ENST00000494372	chr13	38923858	38923859	-127
EIF6	ENST00000374450	chr20	33872913	33872914	-127
KIAA0907	ENST00000491599	chr1	155904315	155904316	-126
HNRNPC	ENST00000336053	chr14	21737777	21737778	-126
TMEM102	ENST00000323206	chr17	7338635	7338636	-126
ANAPC5	ENST00000261819	chr12	121790388	121790389	-125
POLRMT	ENST00000215591	chr19	633691	633692	-125
PPP1R37	ENST00000421905	chr19	45596092	45596093	-125
HIST1H3F	ENST00000446824	chr6	26250958	26250959	-125
FBXO9	ENST00000370939	chr6	52929670	52929671	-125
RP11-316M1.11	ENST00000439374	chr1	151042923	151042924	-124
ACO2	ENST00000216254	chr22	41865004	41865005	-124
RP11-155G15.2	ENST00000504578	chr5	96519178	96519179	-124
ANP32E	ENST00000314136	chr1	150208625	150208626	-123
MRPL11	ENST00000430466	chr11	66206440	66206441	-123
DERL3	ENST00000290730	chr22	24181436	24181437	-123
PES1	ENST00000354694	chr22	30988048	30988049	-123
SOAT1	ENST00000426956	chr1	179263332	179263333	-122
TSG101	ENST00000536719	chr11	18548618	18548619	-122
KRT7	ENST00000552322	chr12	52638039	52638040	-122
CCNB1IP1	ENST00000398160	chr14	20801289	20801290	-122
RANGRF	ENST00000226105	chr17	8191692	8191693	-122
KLHDC3	ENST00000326974	chr6	42981828	42981829	-122
CTD-2319I12.4	ENST00000586143	chr17	58213124	58213125	-121
AP000351.10	ENST00000439866	chr22	24372995	24372996	-121
YBX1	ENST00000321358	chr1	43147977	43147978	-120
MED19	ENST00000534677	chr11	57479811	57479812	-120

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
HIST1H4A	ENST00000359907	chr6	26021786	26021787	-120
RP11-255B23.3	ENST00000500112	chr8	128231451	128231452	-120
SF3B4	ENST00000457312	chr1	149899600	149899601	-119
CIT	ENST00000392521	chr12	120315212	120315213	-119
RP11-407N17.4	ENST00000556537	chr14	39645201	39645202	-119
SH2B1	ENST00000359285	chr16	28875006	28875007	-119
MKRN2-AS1	ENST00000564146	chr3	12587138	12587139	-119
RPS3	ENST00000531188	chr11	75110411	75110412	-118
TRABD2A	ENST00000474298	chr2	85134248	85134249	-118
EEF1B2	ENST00000415904	chr2	207024532	207024533	-118
CNPY3	ENST00000372836	chr6	42896819	42896820	-118
TTI2	ENST00000523305	chr8	33370753	33370754	-118
INTS5	ENST00000330574	chr11	62420889	62420890	-117
OPA3	ENST00000323060	chr19	46088215	46088216	-117
UBXN4	ENST00000272638	chr2	136499071	136499072	-117
SFPQ	ENST00000357214	chr1	35658863	35658864	-116
ATG13	ENST00000580238	chr11	46638960	46638961	-116
FAM32A	ENST00000589852	chr19	16296074	16296075	-116
HIST1H2AG	ENST00000359193	chr6	27100715	27100716	-116
KTI12	ENST00000371614	chr1	52499601	52499602	-115
GBF1	ENST00000369983	chr10	104005173	104005174	-115
SNRPG	ENST00000438261	chr2	70520693	70520694	-115
CDCA7	ENST00000347703	chr2	174219432	174219433	-115
COPS7B	ENST00000410024	chr2	232646265	232646266	-115
PNISR	ENST00000438806	chr6	99873320	99873321	-115
NUDT2	ENST00000379158	chr9	34329388	34329389	-115
KLHL20	ENST00000493170	chr1	173684591	173684592	-114
HIST3H2A	ENST00000366695	chr1	228645672	228645673	-114
TUBB	ENST00000327892	chr6	30687864	30687865	-113
CNTLN	ENST00000380647	chr9	17134866	17134867	-113
SNAP23	ENST00000564153	chr15	42787719	42787720	-112
DDX39A	ENST00000590260	chr19	14530301	14530302	-111
IGFLR1	ENST00000587101	chr19	36231606	36231607	-111
PRMT5-AS1	ENST00000424245	chr14	23388554	23388555	-110
RP11-806L2.5	ENST00000584679	chr18	657367	657368	-110
TOMM40	ENST00000589253	chr19	45393715	45393716	-110
TARS2	ENST00000438568	chr1	150459777	150459778	-109
PTGS2	ENST00000367468	chr1	186649666	186649667	-109
CREBZF	ENST00000490820	chr11	85376253	85376254	-109
TPRA1	ENST00000355552	chr3	127309719	127309720	-109

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
PIN4	ENST00000423432	chrX	71401416	71401417	-109
HIST2H2AB	ENST00000331128	chr1	149859572	149859573	-108
VPS72	ENST00000463470	chr1	151167903	151167904	-108
DCTPP1	ENST00000319285	chr16	30441502	30441503	-108
CCT5	ENST00000515390	chr5	10250219	10250220	-108
PHF11	ENST00000482487	chr13	50069638	50069639	-107
SPC24	ENST00000592540	chr19	11266589	11266590	-107
C19orf53	ENST00000221576	chr19	13885185	13885186	-107
TMEM91	ENST00000392002	chr19	41882021	41882022	-107
RTN4	ENST00000394611	chr2	55277839	55277840	-107
TAX1BP1	ENST00000265393	chr7	27779606	27779607	-107
RP11-280G9.1	ENST00000505627	chr8	62678633	62678634	-107
RPS26	ENST00000548590	chr12	56435817	56435818	-106
HMGB1	ENST00000341423	chr13	31040206	31040207	-106
MFAP1	ENST00000267812	chr15	44117104	44117105	-106
RFWD3	ENST00000361070	chr16	74700883	74700884	-106
ADAT1	ENST00000307921	chr16	75657302	75657303	-106
CCDC115	ENST00000259229	chr2	131100026	131100027	-106
HIST1H4B	ENST00000377364	chr6	26027584	26027585	-106
FANCG	ENST00000378643	chr9	35080117	35080118	-106
WLS	ENST00000527864	chr1	68697611	68697612	-105
RHOV	ENST00000220507	chr15	41166590	41166591	-105
RBM14	ENST00000310137	chr11	66383949	66383950	-103
KRT7	ENST00000552183	chr12	52635208	52635209	-103
OSGEP	ENST00000553640	chr14	20923072	20923073	-103
C19orf45	ENST00000601292	chr19	7571577	7571578	-103
SLC25A25	ENST00000472769	chr9	130860712	130860713	-103
RIT1	ENST00000368323	chr1	155881295	155881296	-102
HNRNPF	ENST00000357065	chr10	43903367	43903368	-102
CRADD	ENST00000332896	chr12	94071048	94071049	-102
HAUS4	ENST00000555040	chr14	23426470	23426471	-102
TOP3A	ENST00000582981	chr17	18218421	18218422	-102
C19orf25	ENST00000592605	chr19	1479318	1479319	-102
BZW1	ENST00000464483	chr2	201676530	201676531	-102
ZNF335	ENST00000426788	chr20	44600933	44600934	-102
HECTD3	ENST00000372172	chr1	45477100	45477101	-101
CRYM-AS1	ENST00000338573	chr16	21312068	21312069	-101
PSMB3	ENST00000225426	chr17	36908887	36908888	-101
GTF2H1	ENST00000531757	chr11	18343993	18343994	-100
ALG3	ENST00000397676	chr3	183966857	183966858	-100

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CXCL2	ENST00000508487	chr4	74965108	74965109	-100
MB21D1	ENST00000370315	chr6	74162097	74162098	-100
UBXN11	ENST00000374221	chr1	26633233	26633234	-99
RP11-111M22.3	ENST00000571090	chr11	76155821	76155822	-99
RAD9B	ENST00000433301	chr12	110939360	110939361	-99
ONECUT1	ENST00000567155	chr15	53081690	53081691	-99
NGRN	ENST00000331497	chr15	90808791	90808792	-99
P4HB	ENST00000331483	chr17	79818667	79818668	-99
ZNF581	ENST00000270451	chr19	56154813	56154814	-99
LETMD1	ENST00000547318	chr12	51441985	51441986	-98
AHSA1	ENST00000555133	chr14	77924114	77924115	-98
MON1B	ENST00000569610	chr16	77224633	77224634	-98
EIF3D	ENST00000432675	chr22	36925327	36925328	-98
UBE2D3	ENST00000394803	chr4	103749412	103749413	-98
VTI1A	ENST00000489142	chr10	114206894	114206895	-97
ALDH3A1	ENST00000439102	chr17	19649088	19649089	-97
PAFAH1B3	ENST00000538771	chr19	42807024	42807025	-97
MOCS3	ENST00000244051	chr20	49575265	49575266	-97
KIAA1211	ENST00000264229	chr4	57036263	57036264	-97
HNRNPA2B1	ENST00000463181	chr7	26240499	26240500	-97
PNP	ENST00000554065	chr14	20938588	20938589	-96
YARS	ENST00000373477	chr1	33283847	33283848	-95
RPS11	ENST00000600027	chr19	49999526	49999527	-95
HIST1H4I	ENST00000354348	chr6	27106980	27106981	-95
NOLC1	ENST00000405356	chr10	103911838	103911839	-94
HAPLN3	ENST00000359595	chr15	89438948	89438949	-93
SYTL1	ENST00000490170	chr1	27673942	27673943	-92
METTL3	ENST00000298717	chr14	21979607	21979608	-92
PPCDC	ENST00000342932	chr15	75315803	75315804	-92
MEF2A	ENST00000338042	chr15	100106040	100106041	-92
PLEKHH3	ENST00000412503	chr17	40829138	40829139	-92
TTLL3	ENST00000419081	chr3	9851291	9851292	-92
RFC1	ENST00000381897	chr4	39368085	39368086	-92
COX6A1	ENST00000229379	chr12	120875801	120875802	-91
MCM6	ENST00000264156	chr2	136634085	136634086	-91
HOXB6	ENST00000490419	chr17	46681582	46681583	-90
ZFYVE19	ENST00000560078	chr15	41100229	41100230	-89
RP11-168G16.1	ENST00000340644	chr15	100890525	100890526	-89
AC002310.7	ENST00000486926	chr16	30583481	30583482	-89
MIR1181	ENST00000408639	chr19	10514301	10514302	-89

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CDC25A	ENST00000437972	chr3	48229979	48229980	-89
HIST1H2AM	ENST00000359611	chr6	27861050	27861051	-89
TMPO	ENST00000556029	chr12	98909201	98909202	-88
C12orf65	ENST00000425637	chr12	123717895	123717896	-88
TAF6	ENST00000487288	chr7	99716685	99716686	-88
SRRM1	ENST00000323848	chr1	24969415	24969416	-87
TRIM45	ENST00000485032	chr1	117664499	117664500	-87
ERCC5	ENST00000535557	chr13	103498086	103498087	-87
BRIP1	ENST00000577913	chr17	59940790	59940791	-87
GUCD1	ENST00000435822	chr22	24951369	24951370	-87
MORF4L2-AS1	ENST00000435306	chrX	102942124	102942125	-87
CDT1	ENST00000562747	chr16	88870932	88870933	-86
NUP155	ENST00000231498	chr5	37371367	37371368	-86
C6orf89	ENST00000480824	chr6	36853543	36853544	-86
CENPL	ENST00000479159	chr1	173793941	173793942	-85
TMEM138	ENST00000423772	chr11	61130055	61130056	-85
ZNF384	ENST00000538829	chr12	6798145	6798146	-85
SUPT5H	ENST00000599907	chr19	39948906	39948907	-85
CCNT2	ENST00000419781	chr2	135675719	135675720	-85
HIST1H2AH	ENST00000377459	chr6	27114775	27114776	-85
NONO	ENST00000276079	chrX	70503347	70503348	-85
GLA	ENST00000218516	chrX	100662996	100662997	-85
IMP3	ENST00000403490	chr15	75932634	75932635	-84
COPS7A	ENST00000442593	chr12	6833096	6833097	-83
B3GNTL1	ENST00000573629	chr17	81006741	81006742	-83
CTB-55O6.12	ENST00000588387	chr19	14247907	14247908	-83
SPC25	ENST00000282074	chr2	169747036	169747037	-83
RP11-306I1.2	ENST00000452618	chr1	165567617	165567618	-82
CD44	ENST00000263398	chr11	35160334	35160335	-82
MED24	ENST00000495586	chr17	38183482	38183483	-82
ZNF226	ENST00000590578	chr19	44669143	44669144	-82
SMU1	ENST00000536631	chr9	33076745	33076746	-82
FAM178A	ENST00000238961	chr10	102672638	102672639	-81
CCDC61	ENST00000595358	chr19	46498643	46498644	-81
CTC-329D1.2	ENST00000507521	chr5	139781031	139781032	-81
HDAC6	ENST00000423941	chrX	48659702	48659703	-81
CCDC9	ENST00000599398	chr19	47760708	47760709	-80
INO80B	ENST00000233331	chr2	74682069	74682070	-80
TMEM230	ENST00000202834	chr20	5093827	5093828	-80
POLR3A	ENST00000372371	chr10	79789380	79789381	-79

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
NCOA7	ENST00000444128	chr6	126240371	126240372	-79
DHX40	ENST00000251241	chr17	57642807	57642808	-78
MCFD2	ENST00000444761	chr2	47169070	47169071	-78
TMUB2	ENST00000446571	chr17	42264260	42264261	-77
ZSWIM3	ENST00000255152	chr20	44486178	44486179	-77
HIST1H4D	ENST00000340756	chr6	26189379	26189380	-77
UCHL5	ENST00000367452	chr1	193029311	193029312	-76
RAB5B	ENST00000553116	chr12	56367620	56367621	-76
AQR	ENST00000156471	chr15	35262114	35262115	-76
KAT7	ENST00000259021	chr17	47865840	47865841	-76
GRPEL2	ENST00000329271	chr5	148724916	148724917	-76
USP1	ENST00000339950	chr1	62902250	62902251	-75
RPS13	ENST00000525634	chr11	17099407	17099408	-75
SGTB	ENST00000506816	chr5	65018935	65018936	-75
RMND1	ENST00000367303	chr6	151773332	151773333	-75
GANAB	ENST00000534779	chr11	62414176	62414177	-74
CDK2	ENST00000556276	chr12	56360989	56360990	-74
CNOT2	ENST00000552231	chr12	70636699	70636700	-74
AC131097.3	ENST00000430555	chr2	242823439	242823440	-74
ATF6B	ENST00000375201	chr6	32096102	32096103	-74
DLEU1	ENST00000490577	chr13	50656233	50656234	-73
SPOP	ENST00000504102	chr17	47755667	47755668	-73
MRPS23	ENST00000313608	chr17	55927488	55927489	-73
GRWD1	ENST00000253237	chr19	48948956	48948957	-73
RRM2	ENST00000459969	chr2	10262765	10262766	-73
NOP16	ENST00000389158	chr5	175816047	175816048	-73
EEF1E1	ENST00000379715	chr6	8102882	8102883	-73
GBA	ENST00000427500	chr1	155211136	155211137	-72
HEATR6	ENST00000184956	chr17	58156362	58156363	-72
ZNF263	ENST00000572748	chr16	3333413	3333414	-71
ZNF430	ENST00000261560	chr19	21203354	21203355	-71
RP11-535A19.2	ENST00000531263	chr11	75525910	75525911	-70
USE1	ENST00000445667	chr19	17326084	17326085	-70
U2	ENST00000411315	chr3	73160072	73160073	-70
IPO11	ENST00000505902	chr5	61708417	61708418	-70
EBP	ENST00000276096	chrX	48380116	48380117	-70
C1orf35	ENST00000272139	chr1	228291230	228291231	-69
POLR2M	ENST00000299638	chr15	57998757	57998758	-69
SNIP1	ENST00000296215	chr1	38019969	38019970	-68
C12orf76	ENST00000551185	chr12	110486436	110486437	-68

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
THG1L	ENST00000521655	chr5	157158359	157158360	-68
MDC1	ENST00000425072	chr6	30685290	30685291	-68
ZNF684	ENST00000372699	chr1	40997165	40997166	-67
C1orf123	ENST00000483739	chr1	53685657	53685658	-67
ARID4B	ENST00000349213	chr1	235491599	235491600	-67
GPR113	ENST00000333478	chr2	26569750	26569751	-67
WEE1	ENST00000450114	chr11	9595161	9595162	-66
C19orf38	ENST00000592854	chr19	10947184	10947185	-66
MCM5	ENST00000216122	chr22	35795989	35795990	-66
PTP4A1	ENST00000370651	chr6	64281850	64281851	-66
ULBP2	ENST00000367351	chr6	150263070	150263071	-65
POLR2K	ENST00000353107	chr8	101162746	101162747	-65
E2F2	ENST00000361729	chr1	23857773	23857774	-63
RRNAD1	ENST00000519086	chr1	156698677	156698678	-63
LPXN	ENST00000528489	chr11	58345754	58345755	-63
ANKRD13A	ENST00000553025	chr12	110436927	110436928	-63
KCNN4	ENST00000262888	chr19	44285470	44285471	-63
NOP58	ENST00000264279	chr2	203130375	203130376	-63
NOL12	ENST00000359114	chr22	38082266	38082267	-63
SKIDA1	ENST00000449193	chr10	21814671	21814672	-62
TOPORS	ENST00000360538	chr9	32552611	32552612	-62
CCDC22	ENST00000376227	chrX	49091864	49091865	-62
RNASEH2C	ENST00000528220	chr11	65488348	65488349	-61
RP11-146F11.5	ENST00000563540	chr16	30597166	30597167	-61
BSG	ENST00000346916	chr19	571235	571236	-61
NDUFAF3	ENST00000451378	chr3	49058976	49058977	-61
CLCC1	ENST00000415331	chr1	109506169	109506170	-60
CDKL1	ENST00000216378	chr14	50864180	50864181	-60
RPL3	ENST00000216146	chr22	39715834	39715835	-60
OGT	ENST00000444774	chrX	70754090	70754091	-60
MKRN3	ENST00000570112	chr15	23810765	23810766	-59
MON1B	ENST00000439557	chr16	77225029	77225030	-59
WBP1	ENST00000492047	chr2	74685947	74685948	-59
DDX21	ENST00000354185	chr10	70715825	70715826	-58
UBR7	ENST00000554232	chr14	93673527	93673528	-58
SNHG11	ENST00000453698	chr20	37075162	37075163	-58
TFAP2A	ENST00000379613	chr6	10415537	10415538	-58
ALG10	ENST00000538927	chr12	34175345	34175346	-57
KLHL28	ENST00000556500	chr14	45431225	45431226	-57
TPD52L2	ENST00000369927	chr20	62496538	62496539	-57

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
KIAA1967	ENST00000308511	chr8	22462087	22462088	-57
FAM111A	ENST00000361723	chr11	58912195	58912196	-56
PUS7L	ENST00000344862	chr12	44152674	44152675	-56
TRIP10	ENST00000600428	chr19	6737879	6737880	-56
SLC35A3	ENST00000533028	chr1	100435936	100435937	-55
MPZL2	ENST00000527282	chr11	118135154	118135155	-55
HSP90AB1	ENST00000353801	chr6	44214768	44214769	-55
RP11-276H7.3	ENST00000426353	chr1	16485706	16485707	-54
NUCB2	ENST00000533738	chr11	17297694	17297695	-54
ZNF273	ENST00000476120	chr7	64363570	64363571	-54
XRCC3	ENST00000352127	chr14	104181892	104181893	-53
GANC	ENST00000561871	chr15	42565377	42565378	-53
C18orf56	ENST00000323813	chr18	658391	658392	-53
ERCC1	ENST00000423698	chr19	45982137	45982138	-53
DCAF16	ENST00000382247	chr4	17812432	17812433	-53
MUS81	ENST00000525768	chr11	65627963	65627964	-52
RP11-849H4.2	ENST00000531488	chr11	71639543	71639544	-52
HMGA2	ENST00000354636	chr12	66218187	66218188	-52
ZNF668	ENST00000564456	chr16	31085555	31085556	-52
MCM8	ENST00000378896	chr20	5931245	5931246	-52
VPS51	ENST00000530773	chr11	64863535	64863536	-51
ZNF384	ENST00000542605	chr12	6798787	6798788	-51
CDK4	ENST00000552254	chr12	58145709	58145710	-51
DAND5	ENST00000585548	chr19	13075921	13075922	-51
C19orf48	ENST00000391812	chr19	51308023	51308024	-51
SGOL2	ENST00000357799	chr2	201390828	201390829	-51
FGD5-AS1	ENST00000430166	chr3	14989980	14989981	-51
RP11-73M7.6	ENST00000585413	chr1	32110803	32110804	-50
AARS	ENST00000261772	chr16	70323494	70323495	-50
CENPM	ENST00000402420	chr22	42342781	42342782	-50
SNRPC	ENST00000244520	chr6	34725132	34725133	-50
PEX16	ENST00000532681	chr11	45940410	45940411	-49
LARP4	ENST00000293618	chr12	50794542	50794543	-49
SGTA	ENST00000221566	chr19	2783416	2783417	-49
MTMR9	ENST00000221086	chr8	11141875	11141876	-49
SAC3D1	ENST00000531072	chr11	64808324	64808325	-48
CTD-2370N5.3	ENST00000578021	chr17	29645704	29645705	-48
LSM4	ENST00000594828	chr19	18433968	18433969	-48
TAF11	ENST00000361288	chr6	34855912	34855913	-48
BUD31	ENST00000473447	chr7	99006659	99006660	-48

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
NCAPG2	ENST00000432615	chr7	158496441	158496442	-48
CHM	ENST00000467744	chrX	85302355	85302356	-48
RP11-152N13.5	ENST00000457147	chr10	75012501	75012502	-47
FARP1	ENST00000496052	chr13	99056277	99056278	-47
DUT	ENST00000455976	chr15	48624252	48624253	-47
SCAND2	ENST00000348993	chr15	85174634	85174635	-47
RP3-388M5.9	ENST00000563715	chr22	44208288	44208289	-47
AXDND1	ENST00000511157	chr1	179335060	179335061	-46
MMAB	ENST00000537236	chr12	110011429	110011430	-46
CEP95	ENST00000579860	chr17	62502936	62502937	-46
STAMBP	ENST00000339566	chr2	74056039	74056040	-46
EIF3H	ENST00000276682	chr8	117778538	117778539	-46
THOC2	ENST00000355725	chrX	122866950	122866951	-46
FAM111B	ENST00000411426	chr11	58874612	58874613	-45
RP3-416H24.1	ENST00000546686	chr12	52641275	52641276	-45
UNG	ENST00000336865	chr12	109535877	109535878	-45
SAP30BP	ENST00000355423	chr17	73663380	73663381	-45
KIF2C	ENST00000455186	chr1	45205580	45205581	-44
PCSK7	ENST00000524507	chr11	117102626	117102627	-44
C12orf45	ENST00000552951	chr12	105380043	105380044	-44
TXNDC16	ENST00000554399	chr14	53019282	53019283	-44
EMC7	ENST00000256545	chr15	34394191	34394192	-44
NUSAP1	ENST00000559046	chr15	41625008	41625009	-44
CTD-2521M24.8	ENST00000597028	chr19	17530625	17530626	-44
DDX18	ENST00000263239	chr2	118572181	118572182	-44
ASH2L	ENST00000343823	chr8	37962715	37962716	-44
TXNRD1	ENST00000378070	chr12	104682452	104682453	-43
NUBP1	ENST00000574334	chr16	10837599	10837600	-43
RP11-485G7.5	ENST00000572913	chr16	11439109	11439110	-43
TRIM28	ENST00000597136	chr19	59059617	59059618	-43
PTMA	ENST00000448874	chr2	232572296	232572297	-43
DLG1	ENST00000419354	chr3	197026212	197026213	-43
RP1-265C24.8	ENST00000565046	chr6	28104583	28104584	-43
BNIP3L	ENST00000523949	chr8	26240669	26240670	-43
RPS19	ENST00000598742	chr19	42363945	42363946	-42
CEP128	ENST00000555265	chr14	81408168	81408169	-41
TMEM101	ENST00000542039	chr17	42092456	42092457	-41
NDUFAF7	ENST00000455230	chr2	37458732	37458733	-41
RP4-694B14.5	ENST00000428254	chr20	25604751	25604752	-41
ZNFX1-AS1	ENST00000326677	chr20	47895137	47895138	-41

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CTA-211A9.5	ENST00000444388	chr22	27068688	27068689	-41
C3orf38	ENST00000486971	chr3	88199095	88199096	-41
TMEM18	ENST00000281017	chr2	677477	677478	-40
HIST1H4H	ENST00000289352	chr6	26285800	26285801	-40
AGPAT1	ENST00000395499	chr6	32144895	32144896	-40
RPS20	ENST00000520627	chr8	56987107	56987108	-40
DCTN5	ENST00000563998	chr16	23652752	23652753	-39
CD68	ENST00000584502	chr17	7482916	7482917	-39
CUEDC1	ENST00000581391	chr17	55945863	55945864	-39
TADA3	ENST00000439043	chr3	9834504	9834505	-39
TBCCD1	ENST00000446782	chr3	186288144	186288145	-39
UROD	ENST00000469548	chr1	45478324	45478325	-38
ARMC1	ENST00000276569	chr8	66546478	66546479	-38
CHTOP	ENST00000368694	chr1	153606487	153606488	-37
SPRTN	ENST00000295050	chr1	231473756	231473757	-37
KIAA0895L	ENST00000563831	chr16	67217524	67217525	-37
C16orf95	ENST00000253461	chr16	87351057	87351058	-37
PIK3R4	ENST00000356763	chr3	130465708	130465709	-37
RNF5	ENST00000375094	chr6	32146093	32146094	-37
ENO1	ENST00000463324	chr1	8935010	8935011	-36
CREB3L4	ENST00000405694	chr1	153940309	153940310	-36
ADAM15	ENST00000473905	chr1	155023005	155023006	-36
COG8	ENST00000562081	chr16	69373520	69373521	-36
RP11-773H22.4	ENST00000588211	chr18	12991206	12991207	-36
GOLGB1	ENST00000340645	chr3	121468636	121468637	-36
SART3	ENST00000546611	chr12	108955209	108955210	-35
AP2S1	ENST00000601498	chr19	47353606	47353607	-35
U2	ENST00000410792	chr2	88316099	88316100	-35
WWTR1-AS1	ENST00000479752	chr3	149375961	149375962	-35
TRMT13	ENST00000370143	chr1	100598671	100598672	-34
RP11-613D13.4	ENST00000528226	chr11	43942574	43942575	-34
RP11-6N17.4	ENST00000582787	chr17	45973210	45973211	-34
NME1	ENST00000393196	chr17	49230862	49230863	-34
RP5-1074L1.1	ENST00000449169	chr1	110881824	110881825	-33
RAD51AP1	ENST00000536886	chr12	4648001	4648002	-33
LCMT2	ENST00000305641	chr15	43622834	43622835	-33
SDF2	ENST00000585428	chr17	26988965	26988966	-33
MADD	ENST00000453571	chr11	47290679	47290680	-32
GMPR2	ENST00000355299	chr14	24701595	24701596	-32
GNG2	ENST00000553560	chr14	52313811	52313812	-32

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
SPG7	ENST00000563783	chr16	89557292	89557293	-32
LAMA3	ENST00000591749	chr18	21407335	21407336	-32
ARSK	ENST00000380009	chr5	94890745	94890746	-32
ZNF317	ENST00000247956	chr19	9251024	9251025	-31
DDX60	ENST00000393743	chr4	169239987	169239988	-31
MTAP	ENST00000380172	chr9	21802510	21802511	-31
RP11-326A19.3	ENST00000570120	chr15	89631526	89631527	-30
MIR3676	ENST00000579470	chr17	8090462	8090463	-30
CWC22	ENST00000295749	chr2	180871868	180871869	-30
CIDECP	ENST00000433871	chr3	10065459	10065460	-30
CYCS	ENST00000409764	chr7	25164907	25164908	-30
METTL2B	ENST00000262432	chr7	128116752	128116753	-30
YOD1	ENST00000315927	chr1	207224449	207224450	-29
HIST4H4	ENST00000537853	chr12	14923237	14923238	-29
RP5-1125A11.1	ENST00000432859	chr20	32580957	32580958	-29
DSCC1	ENST00000521795	chr8	120868125	120868126	-29
TPR	ENST00000367478	chr1	186344483	186344484	-28
BBS4	ENST00000395205	chr15	72978829	72978830	-28
GCA	ENST00000473240	chr2	163175321	163175322	-28
AP4M1	ENST00000422582	chr7	99699655	99699656	-28
MARS	ENST00000548674	chr12	57881779	57881780	-27
ORC2	ENST00000234296	chr2	201828428	201828429	-27
MAD2L1BP	ENST00000451025	chr6	43597249	43597250	-27
VPS45	ENST00000369130	chr1	150039342	150039343	-26
SMCR7	ENST00000323019	chr17	18163821	18163822	-26
RAB5C	ENST00000346213	chr17	40307059	40307060	-26
FAM117A	ENST00000514018	chr17	47866375	47866376	-26
MED26	ENST00000598608	chr19	16739897	16739898	-26
ZNF101	ENST00000444249	chr19	19779633	19779634	-26
CHCHD5	ENST00000324913	chr2	113341991	113341992	-26
SMARCA5	ENST00000283131	chr4	144434589	144434590	-26
MYC	ENST00000524013	chr8	128748439	128748440	-26
MED31	ENST00000574128	chr17	6554770	6554771	-25
SUMO1	ENST00000392246	chr2	203103354	203103355	-25
LEF1	ENST00000505297	chr4	108994075	108994076	-25
AGGF1	ENST00000312916	chr5	76326184	76326185	-25
KIAA0825	ENST00000312498	chr5	93954332	93954333	-25
MRPL18	ENST00000367034	chr6	160211472	160211473	-25
AKR1D1	ENST00000468877	chr7	137687044	137687045	-25
PLCXD1	ENST00000415337	chrX	200106	200107	-25

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
KLHL20	ENST00000479505	chr1	173684055	173684056	-24
ESPL1	ENST00000257934	chr12	53662058	53662059	-24
MCM3	ENST00000229854	chr6	52149604	52149605	-24
M6PR	ENST00000544245	chr12	9102352	9102353	-23
RPL41	ENST00000546654	chr12	56510528	56510529	-23
WDR24	ENST00000248142	chr16	740465	740466	-23
PPIL3	ENST00000497263	chr2	201753810	201753811	-23
EIF2B1	ENST00000534960	chr12	124118171	124118172	-22
N4BP2L2	ENST00000505213	chr13	33112990	33112991	-22
COASY	ENST00000585811	chr17	40714129	40714130	-22
NUP155	ENST00000381843	chr5	37370907	37370908	-22
PPOX	ENST00000352210	chr1	161136178	161136179	-21
ANAPC15	ENST00000545333	chr11	71823516	71823517	-21
ESYT1	ENST00000394048	chr12	56521818	56521819	-21
SNRPB	ENST00000339610	chr20	2451450	2451451	-21
COX17	ENST00000261070	chr3	119396269	119396270	-21
RPL9	ENST00000295955	chr4	39460587	39460588	-21
DCTN4	ENST00000521093	chr5	150138217	150138218	-21
PFDN6	ENST00000374606	chr6	33257350	33257351	-21
PHPT1	ENST00000463215	chr9	139744209	139744210	-21
HELLS	ENST00000419900	chr10	96305526	96305527	-20
EEF1G	ENST00000525340	chr11	62341350	62341351	-20
POLE	ENST00000539357	chr12	133263969	133263970	-20
KIAA0101	ENST00000380258	chr15	64673661	64673662	-20
SF3A2	ENST00000591121	chr19	2236819	2236820	-20
COPE	ENST00000262812	chr19	19030224	19030225	-20
PFKFB4	ENST00000412035	chr3	48594468	48594469	-20
LHFPL2	ENST00000510949	chr5	77886033	77886034	-20
PTK2B	ENST00000522338	chr8	27169125	27169126	-20
SHC1	ENST00000366442	chr1	154946888	154946889	-19
U4atac	ENST00000408512	chr12	890279	890280	-19
AC141586.5	ENST00000566272	chr16	2653401	2653402	-19
SUPT7L	ENST00000337768	chr2	27886693	27886694	-19
SNX5	ENST00000481323	chr20	17949471	17949472	-19
FANCD2	ENST00000287647	chr3	10068078	10068079	-19
SRP19	ENST00000503445	chr5	112196865	112196866	-19
CENPQ	ENST00000371200	chr6	49431120	49431121	-19
LRRC23	ENST00000428946	chr12	7013979	7013980	-18
WBP11	ENST00000537574	chr12	14956454	14956455	-18
RNFT2	ENST00000407967	chr12	117176077	117176078	-18

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
PNN	ENST00000554117	chr14	39644467	39644468	-18
PPP1R7	ENST00000438799	chr2	242088972	242088973	-18
ZNF678	ENST00000498759	chr1	227751218	227751219	-17
CDCA5	ENST00000404147	chr11	64851534	64851535	-17
KDM5A	ENST00000544760	chr12	498463	498464	-17
RP11-338E21.1	ENST00000546135	chr12	65003254	65003255	-17
RHEB	ENST00000262187	chr7	151217025	151217026	-17
RP11-195F19.5	ENST00000421828	chr9	34666061	34666062	-17
TMEM198B	ENST00000478241	chr12	56223512	56223513	-16
TMEM186	ENST00000333050	chr16	8891519	8891520	-16
TMEM159	ENST00000233047	chr16	21169681	21169682	-16
MPDU1	ENST00000571822	chr17	7487122	7487123	-16
C9orf84	ENST00000374287	chr9	114557226	114557227	-16
HINFP	ENST00000350777	chr11	118992281	118992282	-15
TTC23	ENST00000558613	chr15	99789828	99789829	-15
TMEM208	ENST00000564087	chr16	67261100	67261101	-15
WRAP53	ENST00000431639	chr17	7589373	7589374	-15
TK1	ENST00000586613	chr17	76183157	76183158	-15
RAD54L	ENST00000469835	chr1	46713426	46713427	-14
EXO1	ENST00000423131	chr1	242011512	242011513	-14
CCDC94	ENST00000262962	chr19	4247061	4247062	-14
SNRPD2	ENST00000588599	chr19	46195041	46195042	-14
RBM39	ENST00000361162	chr20	34330246	34330247	-14
CLSPN	ENST00000251195	chr1	36235579	36235580	-13
RRM1	ENST00000533349	chr11	4116059	4116060	-13
COX14	ENST00000550487	chr12	50505748	50505749	-13
PMEL	ENST00000548493	chr12	56360531	56360532	-13
FOXF1-AS1	ENST00000599749	chr16	86542716	86542717	-13
PET100	ENST00000594797	chr19	7694609	7694610	-13
ZNF584	ENST00000594993	chr19	58912924	58912925	-13
EXOC1	ENST00000346134	chr4	56719827	56719828	-13
RPA3	ENST00000462723	chr7	7680219	7680220	-13
MRPL37	ENST00000360840	chr1	54665827	54665828	-12
ST7L	ENST00000358039	chr1	113162050	113162051	-12
RIN1	ENST00000424433	chr11	66103887	66103888	-12
ITFG2	ENST00000228799	chr12	2921775	2921776	-12
RFC3	ENST00000380071	chr13	34392173	34392174	-12
PABPN1	ENST00000216727	chr14	23790485	23790486	-12
PIH1D1	ENST00000601053	chr19	49954797	49954798	-12
TBC1D17	ENST00000594996	chr19	50380946	50380947	-12

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RIF1	ENST00000453091	chr2	152266384	152266385	-12
CDK5RAP1	ENST00000339269	chr20	31989377	31989378	-12
RAD18	ENST00000469793	chr3	9005137	9005138	-12
AC025171.1	ENST00000505541	chr5	43041846	43041847	-12
DNAJC2	ENST00000379257	chr7	102985255	102985256	-12
RNASE4	ENST00000398001	chr14	21152360	21152361	-11
RP11-219B17.1	ENST00000558235	chr15	60771394	60771395	-11
TTC31	ENST00000489152	chr2	74710188	74710189	-11
RXRB	ENST00000544186	chr6	33168639	33168640	-11
ZNF451	ENST00000370708	chr6	56954862	56954863	-11
TUT1	ENST00000308436	chr11	62359117	62359118	-10
KIAA0753	ENST00000361413	chr17	6544255	6544256	-10
RMRP	ENST00000363046	chr9	35658022	35658023	-10
PRPF38A	ENST00000257181	chr1	52870226	52870227	-9
GPRC5A	ENST00000537783	chr12	13044483	13044484	-9
RECQL	ENST00000542432	chr12	21654536	21654537	-9
C16orf93	ENST00000544487	chr16	30773526	30773527	-9
MLH1	ENST00000456676	chr3	37035054	37035055	-9
H2AFZ	ENST00000511203	chr4	100871463	100871464	-9
TMEM39B	ENST00000336294	chr1	32538494	32538495	-8
PHB2	ENST00000535923	chr12	7079994	7079995	-8
TMEM116	ENST00000354825	chr12	112450941	112450942	-8
RNF168	ENST00000437070	chr3	196230554	196230555	-8
THAP5	ENST00000484452	chr7	108210138	108210139	-8
RP11-434I12.2	ENST00000514599	chr8	74268702	74268703	-8
COQ4	ENST00000300452	chr9	131084806	131084807	-8
FAM212B	ENST00000444059	chr1	112298451	112298452	-7
RPL23A	ENST00000582736	chr17	27047001	27047002	-7
RP11-318A15.2	ENST00000565271	chr17	74668016	74668017	-7
LDLR	ENST00000558013	chr19	11200146	11200147	-7
OSGEPL1	ENST00000522700	chr2	190627929	190627930	-7
TM9SF4	ENST00000398022	chr20	30697301	30697302	-7
CLIC1	ENST00000395892	chr6	31707545	31707546	-7
STK19	ENST00000463823	chr6	31940143	31940144	-7
VPS41	ENST00000265745	chr7	38948796	38948797	-7
POC1B-GALNT4	ENST00000548729	chr12	89919979	89919980	-6
MRPS31P5	ENST00000423686	chr13	52768517	52768518	-6
AP5M1	ENST00000431972	chr14	57735767	57735768	-6
FAM96A	ENST00000300030	chr15	64386221	64386222	-6
BRCA1	ENST00000309486	chr17	41277472	41277473	-6

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RAD1	ENST00000513914	chr5	34915724	34915725	-6
NFKBIL1	ENST00000376148	chr6	31515351	31515352	-6
MTBP	ENST00000523373	chr8	121457655	121457656	-6
OGT	ENST00000373701	chrX	70752966	70752967	-6
SCNM1	ENST00000368905	chr1	151138512	151138513	-5
DCLRE1A	ENST00000476112	chr10	115614102	115614103	-5
PRCP	ENST00000531801	chr11	82612703	82612704	-5
HSPA8	ENST00000532780	chr11	122933380	122933381	-5
NHLRC3	ENST00000473371	chr13	39612437	39612438	-5
C14orf80	ENST00000421892	chr14	105957396	105957397	-5
MED9	ENST00000268711	chr17	17380294	17380295	-5
AC006486.1	ENST00000378108	chr19	42746921	42746922	-5
MRPL30	ENST00000473743	chr2	99797609	99797610	-5
ROBO1	ENST00000436010	chr3	79068612	79068613	-5
MRPL22	ENST00000519059	chr5	154320731	154320732	-5
CUTA	ENST00000465956	chr6	33385669	33385670	-5
EEF1A1	ENST00000316292	chr6	74230744	74230745	-5
TAF6	ENST00000453269	chr7	99717024	99717025	-5
TCEA1	ENST00000521604	chr8	54935092	54935093	-5
ARID4A	ENST00000355431	chr14	58765098	58765099	-4
LRRC49	ENST00000559201	chr15	71184805	71184806	-4
CENPN	ENST00000569461	chr16	81040823	81040824	-4
C17orf76-AS1	ENST00000497774	chr17	16342320	16342321	-4
CNTD1	ENST00000591559	chr17	40950883	40950884	-4
RIOK3	ENST00000339486	chr18	21032782	21032783	-4
PPP1R13L	ENST00000593226	chr19	45909587	45909588	-4
IRF3	ENST00000600911	chr19	50168490	50168491	-4
CCDC12	ENST00000546280	chr3	47018272	47018273	-4
SKP2	ENST00000274254	chr5	36152086	36152087	-4
NCAPG2	ENST00000449727	chr7	158497459	158497460	-4
TXNIP	ENST00000369317	chr1	145438465	145438466	-3
IQGAP3	ENST00000361170	chr1	156542333	156542334	-3
ABI1	ENST00000376166	chr10	27149916	27149917	-3
KDM5A	ENST00000536014	chr12	497697	497698	-3
CTC-471J1.8	ENST00000598982	chr19	52674723	52674724	-3
DSN1	ENST00000447406	chr20	35402203	35402204	-3
DSCR3	ENST00000475009	chr21	38639705	38639706	-3
BPNT1	ENST00000498237	chr1	220263154	220263155	-2
DPP3	ENST00000544603	chr11	66247912	66247913	-2
C1RL	ENST00000545280	chr12	7261793	7261794	-2

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
DAZAP2	ENST00000549041	chr12	51632618	51632619	-2
SHMT2	ENST00000557740	chr12	57623441	57623442	-2
FAM192A	ENST00000309137	chr16	57219976	57219977	-2
PLAUR	ENST00000599546	chr19	44172456	44172457	-2
ZNF230	ENST00000585568	chr19	44507125	44507126	-2
SAE1	ENST00000540850	chr19	47634089	47634090	-2
BCL2L12	ENST00000594157	chr19	50169215	50169216	-2
HSPD1	ENST00000544407	chr2	198364812	198364813	-2
CDC45	ENST00000491520	chr22	19467258	19467259	-2
EAF2	ENST00000273668	chr3	121554059	121554060	-2
DBR1	ENST00000463982	chr3	137893708	137893709	-2
MYNN	ENST00000544106	chr3	169492050	169492051	-2
RFC4	ENST00000494047	chr3	186524257	186524258	-2
MRPS18B	ENST00000376508	chr6	30585634	30585635	-2
FAM54A	ENST00000420702	chr6	136571449	136571450	-2
CPT2	ENST00000371486	chr1	53662099	53662100	-1
TMBIM6	ENST00000549445	chr12	50135349	50135350	-1
CDK4	ENST00000257904	chr12	58146303	58146304	-1
ABCD4	ENST00000298816	chr14	74769671	74769672	-1
ARPP19	ENST00000567669	chr15	52861363	52861364	-1
MIR22HG	ENST00000577164	chr17	1620467	1620468	-1
HMGB2	ENST00000511316	chr4	174255582	174255583	-1
XRCC4	ENST00000396027	chr5	82373387	82373388	-1
RNGTT	ENST00000369475	chr6	89673279	89673280	-1
COA1	ENST00000448704	chr7	43769099	43769100	-1
NUP205	ENST00000417116	chr7	135242688	135242689	-1
NASP	ENST00000464190	chr1	46049712	46049713	1
SCP2	ENST00000533119	chr1	53480637	53480638	1
EFCAB7	ENST00000371088	chr1	63989060	63989061	1
TPCN1	ENST00000552985	chr12	113658884	113658885	1
EIF2S1	ENST00000557310	chr14	67827272	67827273	1
CDK5RAP3	ENST00000580670	chr17	46048516	46048517	1
ZNF580	ENST00000592881	chr19	56146381	56146382	1
UGGT1	ENST00000375990	chr2	128848781	128848782	1
GUSBP1	ENST00000509649	chr5	21459605	21459606	1
NNT	ENST00000505678	chr5	43602794	43602795	1
GNB2L1	ENST00000513060	chr5	180670945	180670946	1
PNPLA8	ENST00000453144	chr7	108166757	108166758	1
NOL8	ENST00000433029	chr9	95087650	95087651	1
TTF2	ENST00000464062	chr1	117602965	117602966	2

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
EFNA4	ENST00000359751	chr1	155036213	155036214	2
FDPS	ENST00000471117	chr1	155278654	155278655	2
TMEM79	ENST00000463670	chr1	156252726	156252727	2
TIMM10	ENST00000525587	chr11	57298273	57298274	2
MYL6	ENST00000550184	chr12	56552133	56552134	2
TBC1D15	ENST00000468049	chr12	72233543	72233544	2
POP5	ENST00000357500	chr12	121019198	121019199	2
ALDOA	ENST00000564521	chr16	30075755	30075756	2
ABCA10	ENST00000519732	chr17	67171919	67171920	2
TREX1	ENST00000492235	chr3	48507669	48507670	2
ACTL6A	ENST00000450518	chr3	179280674	179280675	2
EXOSC9	ENST00000511454	chr4	122722480	122722481	2
ZBED3-AS1	ENST00000514114	chr5	76383288	76383289	2
PPP1R11	ENST00000376772	chr6	30034865	30034866	2
GNL1	ENST00000376621	chr6	30524948	30524949	2
MRE11A	ENST00000536550	chr11	94226972	94226973	3
FAM60A	ENST00000337682	chr12	31479302	31479303	3
PSMC3IP	ENST00000586337	chr17	40729702	40729703	3
LENG8	ENST00000326764	chr19	54960066	54960067	3
OGG1	ENST00000302036	chr3	9791629	9791630	3
PRIM2	ENST00000419977	chr6	57182427	57182428	3
MRPS28	ENST00000522987	chr8	80942485	80942486	3
DTL	ENST00000475419	chr1	212209190	212209191	4
TFAM	ENST00000373895	chr10	60145196	60145197	4
MGEA5	ENST00000357797	chr10	103578170	103578171	4
NUMA1	ENST00000540843	chr11	71791535	71791536	4
POLD3	ENST00000527458	chr11	74303652	74303653	4
B2M	ENST00000559720	chr15	45003687	45003688	4
B9D1	ENST00000487415	chr17	19281198	19281199	4
PEX12	ENST00000225873	chr17	33905643	33905644	4
AC016683.6	ENST00000456685	chr2	113969101	113969102	4
QTRTD1	ENST00000460163	chr3	113775816	113775817	4
SMC4	ENST00000472282	chr3	160117433	160117434	4
DPH2	ENST00000495421	chr1	44435685	44435686	5
HIPK1	ENST00000369554	chr1	114471999	114472000	5
SCAMP3	ENST00000480219	chr1	155232114	155232115	5
FOXRED1	ENST00000534011	chr11	126139033	126139034	5
DIS3	ENST00000377780	chr13	73356057	73356058	5
MSH6	ENST00000493177	chr2	48010312	48010313	5
EIF6	ENST00000415116	chr20	33872583	33872584	5

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
NCAPH2	ENST00000420993	chr22	50946648	50946649	5
RP11-53O19.1	ENST00000505401	chr5	44808822	44808823	5
NREP	ENST00000453526	chr5	111093092	111093093	5
ORC3	ENST00000417380	chr6	88299866	88299867	5
MRPL18	ENST00000479638	chr6	160210921	160210922	5
RP11-863K10.7	ENST00000330539	chr8	37594938	37594939	5
MTF2	ENST00000370303	chr1	93544872	93544873	6
MTMR11	ENST00000482025	chr1	149908755	149908756	6
PRCC	ENST00000353233	chr1	156737350	156737351	6
SPCS2	ENST00000526883	chr11	74660573	74660574	6
OGFOD2	ENST00000536150	chr12	123459278	123459279	6
PPP5D1	ENST00000594701	chr19	47104175	47104176	6
FOXP1	ENST00000498154	chr3	71631097	71631098	6
PLSCR1	ENST00000448787	chr3	146262400	146262401	6
UBE2D3	ENST00000349311	chr4	103748999	103749000	6
ZCCHC9	ENST00000407610	chr5	80597435	80597436	6
OARD1	ENST00000467234	chr6	41040295	41040296	6
RRP12	ENST00000370992	chr10	99161092	99161093	7
SLC25A28	ENST00000496035	chr10	101380358	101380359	7
TMEM109	ENST00000227525	chr11	60681351	60681352	7
BANF1	ENST00000524663	chr11	65769792	65769793	7
RP4-761J14.8	ENST00000407384	chr12	6772431	6772432	7
TIPIN	ENST00000261881	chr15	66649046	66649047	7
RAB8A	ENST00000589697	chr19	16222730	16222731	7
C21orf49	ENST00000382375	chr21	34144416	34144417	7
L3MBTL2	ENST00000216237	chr22	41601214	41601215	7
ULK4	ENST00000459802	chr3	42003561	42003562	7
COX16	ENST00000389912	chr14	70826439	70826440	8
ZNF524	ENST00000589521	chr19	56111394	56111395	8
AC034193.5	ENST00000326237	chr3	10028601	10028602	8
ELP3	ENST00000521938	chr8	27950671	27950672	8
CDKN2C	ENST00000396148	chr1	51434374	51434375	9
LDHB	ENST00000396075	chr12	21810286	21810287	9
ALDOA	ENST00000562240	chr16	30064488	30064489	9
AC124789.1	ENST00000582919	chr17	36608180	36608181	9
SYCE2	ENST00000293695	chr19	13030080	13030081	9
CCNL1	ENST00000461804	chr3	156878539	156878540	9
LMAN2	ENST00000303127	chr5	176778843	176778844	9
ZKSCAN4	ENST00000377294	chr6	28219992	28219993	9
DBF4	ENST00000265728	chr7	87505551	87505552	9

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
MCM7	ENST00000465738	chr7	99698006	99698007	9
CDCA3	ENST00000545368	chr12	6960445	6960446	10
ARF3	ENST00000545855	chr12	49350212	49350213	10
AAAS	ENST00000552161	chr12	53715333	53715334	10
NUP107	ENST00000535718	chr12	69080794	69080795	10
SEC11A	ENST00000558134	chr15	85259309	85259310	10
SNRPA	ENST00000601545	chr19	41256550	41256551	10
AP2S1	ENST00000263270	chr19	47354238	47354239	10
AC023347.1	ENST00000435352	chr2	127066095	127066096	10
AC002467.7	ENST00000440971	chr7	107383415	107383416	10
GNL3L	ENST00000489691	chrX	54556754	54556755	10
RP11-515B12.1	ENST00000509114	chr12	14518425	14518426	11
RP11-347C12.10	ENST00000563252	chr16	30366771	30366772	11
RPL27	ENST00000589037	chr17	41150299	41150300	11
PRPF31	ENST00000445124	chr19	54619168	54619169	11
CYP1B1	ENST00000462864	chr2	38303284	38303285	11
HIST1H4C	ENST00000377803	chr6	26104113	26104114	11
DDX11	ENST00000535317	chr12	31227208	31227209	12
CCNT1	ENST00000417344	chr12	49110445	49110446	12
LEO1	ENST00000315141	chr15	52263960	52263961	12
COMMD4	ENST00000566843	chr15	75628372	75628373	12
EME1	ENST00000338165	chr17	48450591	48450592	12
CUL3	ENST00000497715	chr2	225344828	225344829	12
NSUN3	ENST00000461625	chr3	93781865	93781866	12
CDK1	ENST00000519078	chr10	62538100	62538101	13
ELP5	ENST00000573513	chr17	7155354	7155355	13
SIRT2	ENST00000392081	chr19	39390488	39390489	13
MTAP	ENST00000427788	chr9	21803288	21803289	13
RP11-348A11.4	ENST00000500025	chr11	33183246	33183247	14
TTC9C	ENST00000316461	chr11	62496023	62496024	14
TCEB1	ENST00000518127	chr8	74884507	74884508	14
SMC2	ENST00000374793	chr9	106856619	106856620	14
DNTTIP2	ENST00000496672	chr1	94344696	94344697	15
TROVE2	ENST00000432079	chr1	193028597	193028598	15
HNRNPL	ENST00000221419	chr19	39340957	39340958	15
CDKN2B-AS1	ENST00000584020	chr9	21994914	21994915	15
TMEM138	ENST00000278826	chr11	61129487	61129488	16
SLC25A45	ENST00000526432	chr11	65149405	65149406	16
SDSL	ENST00000403593	chr12	113860056	113860057	16
FAM174B	ENST00000555971	chr15	93353074	93353075	16

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RARA	ENST00000582914	chr17	38479257	38479258	16
C17orf53	ENST00000585683	chr17	42219290	42219291	16
SAE1	ENST00000594526	chr19	47616712	47616713	16
C11orf73	ENST00000528004	chr11	86013308	86013309	17
NUFIP1	ENST00000379161	chr13	45563600	45563601	17
RABEP2	ENST00000566762	chr16	28947829	28947830	17
PRKCSH	ENST00000591462	chr19	11546124	11546125	17
SNRPA	ENST00000601393	chr19	41257129	41257130	17
CENPO	ENST00000498362	chr2	25016362	25016363	17
C20orf196	ENST00000442185	chr20	5731114	5731115	17
DROSHA	ENST00000511367	chr5	31532150	31532151	17
RGL2	ENST00000497454	chr6	33267083	33267084	17
CHRAC1	ENST00000519618	chr8	141522096	141522097	17
PSRC1	ENST00000474126	chr1	109825639	109825640	18
LRTOMT	ENST00000544409	chr11	71791921	71791922	18
KNTC1	ENST00000333479	chr12	123011811	123011812	18
DCAF4	ENST00000353777	chr14	73393101	73393102	18
RPS9	ENST00000484121	chr19	54704693	54704694	18
CEP44	ENST00000503780	chr4	175204844	175204845	18
PAK1IP1	ENST00000379568	chr6	10694944	10694945	18
SNRPE	ENST00000469451	chr1	203830995	203830996	19
KIF18A	ENST00000526288	chr11	28129672	28129673	19
TRAPPC4	ENST00000533632	chr11	118889159	118889160	19
RP5-991G20.1	ENST00000563328	chr16	72699086	72699087	19
EDEM2	ENST00000542871	chr20	33735121	33735122	19
AIMP1	ENST00000394701	chr4	107237681	107237682	19
TRNAI2	ENST00000459170	chr6	26988131	26988132	19
DNTTIP2	ENST00000460191	chr1	94345453	94345454	20
CBX5	ENST00000550489	chr12	54673934	54673935	20
CEP152	ENST00000559630	chr15	49103252	49103253	20
USP37	ENST00000418019	chr2	219432993	219432994	20
SPATA5	ENST00000422835	chr4	123844274	123844275	20
DCLRE1B	ENST00000466480	chr1	114448050	114448051	21
LIN52	ENST00000554076	chr14	74551685	74551686	21
LSMD1	ENST00000333775	chr17	7761150	7761151	21
HAUS1	ENST00000593165	chr18	43684408	43684409	22
SLX4IP	ENST00000334534	chr20	10415971	10415972	22
RP3-406P24.3	ENST00000415144	chr6	4021426	4021427	22
VPS52	ENST00000436044	chr6	33239694	33239695	22
RP11-55L4.2	ENST00000584676	chr17	9548618	9548619	23

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RAB11B	ENST00000600719	chr19	8454886	8454887	23
AP4M1	ENST00000439416	chr7	99699235	99699236	23
NR1H3	ENST00000419652	chr11	47279283	47279284	24
CTD-2339L15.1	ENST00000533146	chr15	40987269	40987270	24
MSH2	ENST00000406134	chr2	47630291	47630292	24
U2SURP	ENST00000473835	chr3	142720203	142720204	24
RP11-315I20.1	ENST00000421764	chr1	145507464	145507465	25
C11orf10	ENST00000543510	chr11	61560248	61560249	25
CYB5B	ENST00000514123	chr16	69458545	69458546	25
IMMT	ENST00000410111	chr2	86422867	86422868	25
ISG20L2	ENST00000470713	chr1	156698194	156698195	26
RP11-251A15.4	ENST00000432246	chr10	93557926	93557927	26
ATM	ENST00000527805	chr11	108093235	108093236	26
WSB2	ENST00000537945	chr12	118500188	118500189	26
DHX8	ENST00000262415	chr17	41561358	41561359	26
ATP5SL	ENST00000595407	chr19	41945774	41945775	26
CACYBP	ENST00000461977	chr1	174968632	174968633	27
SLC43A3	ENST00000525474	chr11	57194865	57194866	27
POLA2	ENST00000541089	chr11	65029458	65029459	27
DDX12P	ENST00000440299	chr12	9600781	9600782	27
NFATC2IP	ENST00000564978	chr16	28962153	28962154	27
CHRNB1	ENST00000575379	chr17	7358938	7358939	27
DNMT1	ENST00000592054	chr19	10305274	10305275	27
ZNF224	ENST00000336976	chr19	44598570	44598571	27
SMC4	ENST00000344722	chr3	160118295	160118296	27
HNRNPD	ENST00000507010	chr4	83295269	83295270	27
RXRB	ENST00000374685	chr6	33168363	33168364	27
TNPO3	ENST00000482320	chr7	128695119	128695120	27
DUSP6	ENST00000308385	chr12	89746153	89746154	28
FOXL1	ENST00000593625	chr16	86610000	86610001	28
KHDC1	ENST00000370384	chr6	74019909	74019910	28
DPYSL2	ENST00000522745	chr8	26435482	26435483	28
E2F8	ENST00000531809	chr11	19262421	19262422	29
SRP54	ENST00000555746	chr14	35451934	35451935	29
SEC22C	ENST00000450981	chr3	42641986	42641987	29
VARS2	ENST00000477288	chr6	30876046	30876047	29
TIMM21	ENST00000577952	chr18	71815801	71815802	30
SERPINI1	ENST00000472747	chr3	167453541	167453542	30
HLA-E	ENST00000493699	chr6	30457317	30457318	30
WDR83	ENST00000547255	chr19	12780396	12780397	31

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
ZNF766	ENST00000599581	chr19	52772875	52772876	31
RANBP1	ENST00000402752	chr22	20104976	20104977	31
BTD	ENST00000449107	chr3	15643169	15643170	31
ATAD5	ENST00000321990	chr17	29159018	29159019	32
VMP1	ENST00000262291	chr17	57784856	57784857	32
SARNP	ENST00000552080	chr12	56211459	56211460	33
SETD8	ENST00000537270	chr12	123868751	123868752	33
MIS12	ENST00000573759	chr17	5389747	5389748	33
DHPS	ENST00000597152	chr19	12792112	12792113	33
NUPL2	ENST00000485250	chr7	23221491	23221492	33
PSMB2	ENST00000373237	chr1	36107410	36107411	34
RP11-77I22.3	ENST00000415632	chr12	30948009	30948010	34
TFAP4	ENST00000204517	chr16	4323041	4323042	34
XPC	ENST00000285021	chr3	14220248	14220249	34
ZNF443	ENST00000436821	chr19	12551799	12551800	35
ZRANB3	ENST00000492193	chr2	136288110	136288111	35
UTP3	ENST00000254803	chr4	71554229	71554230	35
PDLIM7	ENST00000504380	chr5	176911438	176911439	35
RUSC1	ENST00000473331	chr1	155295068	155295069	36
HIST1H2BC	ENST00000314332	chr6	26124117	26124118	36
PHGDH	ENST00000462324	chr1	120254564	120254565	37
AAAS	ENST00000547238	chr12	53714954	53714955	37
PTGES3	ENST00000456859	chr12	57082121	57082122	37
LINC00441	ENST00000436963	chr13	48877757	48877758	37
DHRS1	ENST00000561137	chr14	24763824	24763825	37
RTTN	ENST00000581161	chr18	67872898	67872899	37
ALKBH6	ENST00000490483	chr19	36505047	36505048	37
TM4SF1	ENST00000305366	chr3	149095614	149095615	37
COMMD10	ENST00000515539	chr5	115421206	115421207	37
TMEM60	ENST00000257663	chr7	77427859	77427860	37
MRPS21	ENST00000369084	chr1	150266376	150266377	38
PRIM1	ENST00000546761	chr12	57146014	57146015	38
RP11-1029J19.5	ENST00000557778	chr14	102197406	102197407	38
SIL1	ENST00000509400	chr5	138629184	138629185	38
SF3A3	ENST00000461869	chr1	38455707	38455708	39
NBR1	ENST00000589872	chr17	41323297	41323298	39
HAX1	ENST00000328703	chr1	154245025	154245026	40
CENPL	ENST00000495275	chr1	173793570	173793571	40
FLJ27352	ENST00000569691	chr15	55700784	55700785	40
IER2	ENST00000588173	chr19	13262827	13262828	40

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
MMS22L	ENST00000275053	chr6	97731011	97731012	40
LRRC46	ENST00000584809	chr17	45909576	45909577	41
TFP1	ENST00000497521	chr3	133380884	133380885	43
ACE2	ENST00000471548	chrX	15584366	15584367	43
RP11-727A23.5	ENST00000529607	chr11	82904566	82904567	44
CSDA	ENST00000540747	chr12	10874950	10874951	44
CEP97	ENST00000465011	chr3	101443544	101443545	44
KBTBD4	ENST00000529499	chr11	47600445	47600446	45
SYNGR4	ENST00000344846	chr19	48867695	48867696	45
CTB-131B5.4	ENST00000520928	chr5	139486021	139486022	45
TFAP2A	ENST00000474952	chr6	10412233	10412234	45
PAN2	ENST00000547994	chr12	56727674	56727675	46
HAUS8	ENST00000598517	chr19	17186185	17186186	46
SEC31A	ENST00000503210	chr4	83822272	83822273	46
WDPCP	ENST00000272321	chr2	63815885	63815886	47
STK11IP	ENST00000468584	chr2	220462961	220462962	47
CCDC167	ENST00000373408	chr6	37467650	37467651	47
CD274	ENST00000492923	chr9	5462980	5462981	47
CAP1	ENST00000449311	chr1	40506041	40506042	48
GBA	ENST00000428024	chr1	155214604	155214605	48
U3	ENST00000390893	chr17	56709148	56709149	48
HSPB6	ENST00000592984	chr19	36248931	36248932	48
PUS10	ENST00000407787	chr2	61244279	61244280	48
ING2	ENST00000434682	chr4	184427406	184427407	48
APITD1-CORT	ENST00000465026	chr1	10491362	10491363	49
TTC9C	ENST00000294161	chr11	62495631	62495632	49
MAP3K11	ENST00000524856	chr11	65382803	65382804	49
DIAPH3	ENST00000400330	chr13	60738069	60738070	49
RNF167	ENST00000262482	chr17	4843470	4843471	49
UBB	ENST00000302182	chr17	16284160	16284161	49
C4orf21	ENST00000502805	chr4	113557968	113557969	49
RP1-151F17.1	ENST00000423260	chr6	16761416	16761417	49
C11orf58	ENST00000228136	chr11	16759996	16759997	50
PFKM	ENST00000549003	chr12	48499313	48499314	50
RP11-141J13.3	ENST00000574133	chr17	4469095	4469096	50
MRPS25	ENST00000449354	chr3	15106716	15106717	50
ZNF367	ENST00000375256	chr9	99180560	99180561	50
KIAA1279	ENST00000361983	chr10	70748536	70748537	51
XPO1	ENST00000443240	chr2	61765709	61765710	51
TSHZ2	ENST00000371497	chr20	51588996	51588997	52

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
EIF4A2	ENST00000445596	chr3	186501144	186501145	52
SRSF3	ENST00000477442	chr6	36562218	36562219	52
CDC123	ENST00000281141	chr10	12238016	12238017	53
ITFG3	ENST00000399932	chr16	284596	284597	53
ZBTB4	ENST00000311403	chr17	7387528	7387529	53
RP11-68I3.7	ENST00000584986	chr17	27919205	27919206	53
FHL2	ENST00000409177	chr2	106016070	106016071	53
ELL3	ENST00000433927	chr15	44069458	44069459	54
ZNF142	ENST00000450765	chr2	219524323	219524324	54
SYF2	ENST00000474160	chr1	25558867	25558868	55
CDC20B	ENST00000513180	chr5	54468787	54468788	55
STMN1	ENST00000446334	chr1	26231923	26231924	56
ENSA	ENST00000513281	chr1	150601535	150601536	56
RP11-810P12.5	ENST00000524942	chr11	61849599	61849600	56
MTHFD1	ENST00000555709	chr14	64854813	64854814	56
CLN3	ENST00000360019	chr16	28503566	28503567	56
GGCX	ENST00000473665	chr2	85781590	85781591	56
TTI1	ENST00000373448	chr20	36661806	36661807	56
ISY1	ENST00000393295	chr3	128880079	128880080	56
RP11-293M10.2	ENST00000555909	chr14	75726169	75726170	57
RPL32P3	ENST00000506593	chr3	129118440	129118441	57
MCM4	ENST00000519170	chr8	48874112	48874113	57
U6	ENST00000411377	chrX	48816485	48816486	57
AC004854.4	ENST00000443162	chr7	44888071	44888072	58
GINS3	ENST00000318129	chr16	58426355	58426356	59
TJAP1	ENST00000372449	chr6	43445369	43445370	60
RP11-351A11.1	ENST00000518570	chr6	119256008	119256009	60
TROAP	ENST00000551567	chr12	49717216	49717217	61
ZWILCH	ENST00000307897	chr15	66797356	66797357	61
MBNL1	ENST00000355460	chr3	151986316	151986317	61
NAF1	ENST00000502973	chr4	164087842	164087843	61
TUSC1	ENST00000358022	chr9	25678794	25678795	61
EIF2S3	ENST00000253039	chrX	24072892	24072893	61
POC1A	ENST00000394970	chr3	52188643	52188644	62
NOC3L	ENST00000371361	chr10	96122632	96122633	63
PNKP	ENST00000594661	chr19	50370194	50370195	63
CCDC51	ENST00000395694	chr3	48481411	48481412	63
LMNB1	ENST00000395354	chr5	126112942	126112943	63
HRH1	ENST00000413416	chr3	11267779	11267780	64
CCNL1	ENST00000467081	chr3	156877165	156877166	64

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
DHFR	ENST00000513314	chr5	79949789	79949790	64
RP11-231D20.2	ENST00000518213	chr8	42128650	42128651	64
RCC1	ENST00000419074	chr1	28836652	28836653	65
ERBB2	ENST00000406381	chr17	37844456	37844457	65
ZNF503-AS2	ENST00000425916	chr10	77162876	77162877	66
CHEK1	ENST00000534685	chr11	125495967	125495968	67
RAD51B	ENST00000488612	chr14	68286611	68286612	67
PSMC5	ENST00000310144	chr17	61904608	61904609	67
SUPT4H1	ENST00000577396	chr17	56429715	56429716	68
KHK	ENST00000429697	chr2	27309728	27309729	68
OXSR1	ENST00000492714	chr3	38206646	38206647	68
DPM2	ENST00000473360	chr9	130699989	130699990	68
KIFC1	ENST00000428849	chr6	33359380	33359381	69
ATL3	ENST00000538786	chr11	63439310	63439311	70
SLC1A3	ENST00000505202	chr5	36607060	36607061	70
CASP2	ENST00000350623	chr7	142985612	142985613	70
PARP1	ENST00000366790	chr1	226595611	226595612	71
DCLRE1C	ENST00000378289	chr10	14996359	14996360	71
MIR4500	ENST00000579472	chr13	88270923	88270924	71
RPA2	ENST00000373912	chr1	28241181	28241182	72
EAF1	ENST00000396842	chr3	15468933	15468934	73
RFC2	ENST00000470266	chr7	73668565	73668566	73
TMEM69	ENST00000372025	chr1	46152958	46152959	74
NCAPD3	ENST00000525964	chr11	134094035	134094036	74
DNAJC14	ENST00000357606	chr12	56224489	56224490	75
COG4	ENST00000534772	chr16	70557027	70557028	75
LAGE3	ENST00000357360	chrX	153707520	153707521	75
LRRC41	ENST00000343304	chr1	46769203	46769204	76
BYSL	ENST00000230340	chr6	41889000	41889001	76
MYL6B	ENST00000549380	chr12	56551474	56551475	77
CCDC159	ENST00000589477	chr19	11457332	11457333	77
VPRBP	ENST00000504652	chr3	51533932	51533933	77
CEP57	ENST00000537677	chr11	95523205	95523206	78
CCDC82	ENST00000538597	chr11	96122497	96122498	78
CTD-3014M21.4	ENST00000592135	chr17	41465601	41465602	78
ETV1	ENST00000403685	chr7	14030795	14030796	78
NDUFS2	ENST00000392179	chr1	161172015	161172016	80
TSSK6	ENST00000585580	chr19	19626923	19626924	80
DARS	ENST00000441323	chr2	136743373	136743374	80
FAM104B	ENST00000478918	chrX	55187293	55187294	80

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
LONP1	ENST00000540670	chr19	5720500	5720501	82
RBM34	ENST00000468751	chr1	235324402	235324403	83
LINC00669	ENST00000591629	chr18	37380198	37380199	83
MRPS18C	ENST00000505719	chr4	84377324	84377325	83
CDC6	ENST00000577249	chr17	38444241	38444242	84
TGOLN2	ENST00000282120	chr2	85555289	85555290	84
ZMYND8	ENST00000311275	chr20	45984316	45984317	84
POLR2H	ENST00000460083	chr3	184080313	184080314	84
SLFNL1	ENST00000359345	chr1	41488823	41488824	85
TMEM59	ENST00000452421	chr1	54518992	54518993	85
AHCYL1	ENST00000393614	chr1	110546838	110546839	85
METTL20	ENST00000395763	chr12	31812204	31812205	85
WDR81	ENST00000446363	chr17	1619979	1619980	86
LINC00473	ENST00000581850	chr6	166401315	166401316	86
ZBTB8OS	ENST00000479075	chr1	33116416	33116417	87
ERH	ENST00000557016	chr14	69865256	69865257	87
GART	ENST00000426819	chr21	34915011	34915012	87
SF3B5	ENST00000367569	chr6	144416666	144416667	87
NDUFAF6	ENST00000519136	chr8	95908150	95908151	87
MYL12A	ENST00000217652	chr18	3247614	3247615	88
ASTE1	ENST00000514044	chr3	130745547	130745548	88
TUBB	ENST00000396384	chr6	30689562	30689563	88
OTUD5	ENST00000428668	chrX	48815559	48815560	88
PSMA1	ENST00000396394	chr11	14542152	14542153	89
PPP2R3C	ENST00000553273	chr14	35591377	35591378	89
PAGR1	ENST00000320330	chr16	29827372	29827373	89
EIF2S1	ENST00000256383	chr14	67826802	67826803	90
ZCCHC8	ENST00000536663	chr12	122984703	122984704	91
RP11-10O17.2	ENST00000568853	chr15	74753774	74753775	91
UBXN8	ENST00000518239	chr8	30601796	30601797	91
CDC7	ENST00000234626	chr1	91966540	91966541	92
CDCA5	ENST00000462902	chr11	64851275	64851276	92
RNF121	ENST00000530137	chr11	71640218	71640219	92
LRMP	ENST00000361433	chr12	25205296	25205297	92
SREK1IP1	ENST00000495198	chr5	64064353	64064354	92
C11orf65	ENST00000525729	chr11	108338164	108338165	93
RNF219	ENST00000282003	chr13	79233220	79233221	93
C19orf60	ENST00000595077	chr19	18700773	18700774	93
KRT17	ENST00000463128	chr17	39780999	39781000	94
POLD1	ENST00000593887	chr19	50887722	50887723	94

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TLK1	ENST00000486857	chr2	171948224	171948225	95
PRSS16	ENST00000478690	chr6	27219194	27219195	95
RP5-890E16.2	ENST00000578660	chr17	46125315	46125316	96
PARP4	ENST00000381989	chr13	25086850	25086851	97
ALDH3A2	ENST00000580550	chr17	19551582	19551583	97
RP11-516C1.1	ENST00000558047	chr15	44719243	44719244	98
LAPTM4A	ENST00000175091	chr2	20251690	20251691	98
IWS1	ENST00000409725	chr2	128284363	128284364	98
RFC4	ENST00000411792	chr3	186524748	186524749	98
RP4-616B8.4	ENST00000570096	chr20	37590653	37590654	100
MAFA	ENST00000528185	chr8	144511967	144511968	100
RIBC2	ENST00000538017	chr22	45809673	45809674	101
RP1-197B17.3	ENST00000547799	chr12	48099968	48099969	102
WDR76	ENST00000452115	chr15	44119286	44119287	102
UBE4B	ENST00000377153	chr1	10093433	10093434	103
RP11-408H20.2	ENST00000581836	chr18	28681653	28681654	104
BLZF1	ENST00000426663	chr1	169337578	169337579	105
SLC39A8	ENST00000514000	chr4	103266488	103266489	105
RPL37	ENST00000504562	chr5	40835182	40835183	105
RP11-418J17.1	ENST00000440150	chr1	119683152	119683153	106
RP11-466F5.8	ENST00000423121	chr1	165738270	165738271	106
TOE1	ENST00000372090	chr1	45805448	45805449	108
ARHGEF12	ENST00000528681	chr11	120347815	120347816	108
NR2C2AP	ENST00000537399	chr19	19314046	19314047	108
CBLB	ENST00000545639	chr3	105588134	105588135	108
NUP214	ENST00000451030	chr9	134001087	134001088	108
FCF1	ENST00000553673	chr14	75180014	75180015	109
WDR53	ENST00000425888	chr3	196295283	196295284	109
ZCWPW1	ENST00000360951	chr7	100026176	100026177	110
XRCC2	ENST00000359321	chr7	152373139	152373140	110
GPR137	ENST00000546139	chr11	64037643	64037644	111
SHQ1	ENST00000444040	chr3	72897454	72897455	111
AC005076.5	ENST00000433446	chr7	86781486	86781487	111
HDLBP	ENST00000413241	chr2	242254974	242254975	112
LEKR1	ENST00000485017	chr3	156544581	156544582	112
ZRANB2	ENST00000370920	chr1	71546866	71546867	113
CSTF1	ENST00000428552	chr20	54967578	54967579	113
SNRPD1	ENST00000582475	chr18	19192404	19192405	114
TM2D1	ENST00000371180	chr1	62190979	62190980	115
LIG1	ENST00000263274	chr19	48673743	48673744	116

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
MSH6	ENST00000455383	chr2	48010839	48010840	117
SLC1A5	ENST00000412532	chr19	47290480	47290481	118
RBAK	ENST00000407184	chr7	5023465	5023466	118
CTD-2047H16.2	ENST00000576808	chr17	78289568	78289569	119
MPV17	ENST00000492879	chr2	27545809	27545810	119
MCM2	ENST00000480910	chr3	127317822	127317823	119
RP5-1073O3.2	ENST00000418238	chr1	114355348	114355349	120
RP11-24M17.4	ENST00000569596	chr15	76051025	76051026	120
GPANK1	ENST00000456540	chr6	31632841	31632842	120
U1	ENST00000364829	chr1	144534157	144534158	121
SEC22B	ENST00000453618	chr1	145096340	145096341	122
C1orf106	ENST00000367342	chr1	200860590	200860591	123
RP11-31F15.1	ENST00000420168	chr1	113499264	113499265	124
Y_RNA	ENST00000364918	chr12	45274626	45274627	125
UBC	ENST00000541046	chr12	125399352	125399353	125
ADPRHL1	ENST00000413169	chr13	114103730	114103731	125
MGST3	ENST00000367889	chr1	165600222	165600223	126
TIMM8A	ENST00000372902	chrX	100604056	100604057	127
ACYP1	ENST00000555135	chr14	75530581	75530582	128
PTN	ENST00000393083	chr7	137028391	137028392	128
ITGA7	ENST00000553893	chr12	56109684	56109685	129
CCNE2	ENST00000521809	chr8	95907296	95907297	129
U1	ENST00000363009	chr1	147735879	147735880	130
RRM2	ENST00000474701	chr2	10263426	10263427	130
PSMD13	ENST00000532097	chr11	236675	236676	131
BAZ2A	ENST00000550730	chr12	57030468	57030469	131
CCDC111	ENST00000515152	chr4	185571064	185571065	131
DDB2	ENST00000378601	chr11	47236623	47236624	132
AC017099.3	ENST00000450072	chr2	98280810	98280811	132
PAICS	ENST00000505164	chr4	57302048	57302049	132
RFX3	ENST00000382004	chr9	3525850	3525851	132
MLF1IP	ENST00000514781	chr4	185654434	185654435	133
C1orf216	ENST00000270815	chr1	36184938	36184939	134
CALM2	ENST00000484408	chr2	47403457	47403458	134
HINT2	ENST00000474908	chr9	35815214	35815215	134
RP11-973N13.4	ENST00000554918	chr14	65006950	65006951	135
RP11-361D15.2	ENST00000560199	chr15	59980849	59980850	135
MCL1	ENST00000464132	chr1	150551116	150551117	136
MASTL	ENST00000375940	chr10	27444433	27444434	136
Z83844.1	ENST00000456099	chr22	38054246	38054247	137

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CTD-2527I21.7	ENST00000600959	chr19	35490934	35490935	139
EED	ENST00000528180	chr11	85955933	85955934	140
ARHGAP5-AS1	ENST00000553596	chr14	32545858	32545859	140
SNRPA1	ENST00000560496	chr15	101834969	101834970	140
ERGIC2	ENST00000546839	chr12	29533940	29533941	142
ATF7IP	ENST00000536444	chr12	14518804	14518805	143
GINS2	ENST00000253462	chr16	85722461	85722462	143
SUGP2	ENST00000456085	chr19	19141694	19141695	144
PPWD1	ENST00000511908	chr5	64859268	64859269	144
DUSP11	ENST00000480948	chr2	74006859	74006860	145
SYNCRIP	ENST00000369622	chr6	86352856	86352857	146
LETM2	ENST00000518121	chr8	38244207	38244208	146
SCYL3	ENST00000423670	chr1	169863260	169863261	147
USP54	ENST00000339859	chr10	75385260	75385261	147
RP11-580I16.2	ENST00000582389	chr17	45726620	45726621	147
DGKA	ENST00000548407	chr12	56325402	56325403	148
RP11-756H6.1	ENST00000547552	chr12	57825045	57825046	148
SNX15	ENST00000525648	chr11	64795168	64795169	150
TRIM56	ENST00000412507	chr7	100728951	100728952	150
CTD-2083E4.6	ENST00000512642	chr5	271479	271480	151
CYP1B1-AS1	ENST00000589303	chr2	38303788	38303789	152
C1orf112	ENST00000459772	chr1	169764372	169764373	154
ZNF184	ENST00000211936	chr6	27440742	27440743	154
THAP9-AS1	ENST00000504718	chr4	83821498	83821499	156
PPIL1	ENST00000373699	chr6	36842643	36842644	156
AIDA	ENST00000541237	chr1	222886368	222886369	157
FSTL3	ENST00000591573	chr19	680908	680909	159
PER1	ENST00000584202	chr17	8059512	8059513	160
TRIM37	ENST00000583945	chr17	57089605	57089606	162
DAXX	ENST00000446511	chr6	33290417	33290418	162
RP11-284F21.7	ENST00000448869	chr1	156631052	156631053	163
C17orf64	ENST00000428000	chr17	58470088	58470089	163
U1	ENST00000365538	chr1	147806721	147806722	164
EXOSC5	ENST00000602129	chr19	41902995	41902996	165
ZNF143	ENST00000396604	chr11	9482233	9482234	166
XRCC5	ENST00000417391	chr2	216974238	216974239	166
RP11-387D10.2	ENST00000558105	chr15	91260111	91260112	168
EHBP1	ENST00000467436	chr2	62933614	62933615	168
SECISBP2	ENST00000534113	chr9	91933932	91933933	168
UQCRH	ENST00000496387	chr1	46769549	46769550	170

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TAF1A	ENST00000391883	chr1	222762930	222762931	170
KRTAP21-4P	ENST00000454921	chr21	32114739	32114740	173
FDFT1	ENST00000525551	chr8	11660777	11660778	175
SGK494	ENST00000461399	chr17	26940449	26940450	177
CTD-3014M21.4	ENST00000586231	chr17	41466388	41466389	178
RP11-455G16.1	ENST00000326780	chr4	120133487	120133488	179
MIS12	ENST00000381165	chr17	5390425	5390426	180
TNFAIP1	ENST00000582302	chr17	26663671	26663672	180
PCNA	ENST00000379160	chr20	5107091	5107092	180
PHF17	ENST00000514740	chr4	129731364	129731365	180
PRPF40B	ENST00000551063	chr12	49962334	49962335	181
RAD51	ENST00000526763	chr15	40987840	40987841	181
RP11-739L10.1	ENST00000578831	chr18	20513545	20513546	181
DMC1	ENST00000439567	chr22	38965954	38965955	181
BLM	ENST00000559724	chr15	91260815	91260816	182
CDK5RAP3	ENST00000584168	chr17	46048909	46048910	183
AC092573.3	ENST00000437243	chr2	174220752	174220753	183
ANAPC5	ENST00000536837	chr12	121837514	121837515	184
LCN12	ENST00000484304	chr9	139844185	139844186	184
FAF1	ENST00000487898	chr1	51425224	51425225	185
GPD2	ENST00000540309	chr2	157293180	157293181	185
LIAS	ENST00000515061	chr4	39460923	39460924	185
BRD4	ENST00000602230	chr19	15375023	15375024	187
ACTR6	ENST00000551652	chr12	100593086	100593087	188
EXOSC2	ENST00000463488	chr9	133569379	133569380	188
LEPREL4	ENST00000355468	chr17	39968665	39968666	189
CTC-453G23.8	ENST00000595201	chr19	48707527	48707528	189
WRN	ENST00000298139	chr8	30891504	30891505	189
TATDN2	ENST00000448281	chr3	10290787	10290788	193
TARS	ENST00000513066	chr5	33441293	33441294	193
CDK17	ENST00000552262	chr12	96792947	96792948	194
CLASP2	ENST00000464961	chr3	33546745	33546746	197
RP11-110I1.12	ENST00000526453	chr11	118868515	118868516	198
RPS21	ENST00000370592	chr20	60962577	60962578	198
ESYT2	ENST00000483958	chr7	158620133	158620134	198
RCOR3	ENST00000533469	chr1	211431947	211431948	199
ACAT2	ENST00000367048	chr6	160181558	160181559	200
HAUS5	ENST00000428854	chr19	36103903	36103904	203
ARL6IP6	ENST00000425034	chr2	153575674	153575675	203
CHAC1	ENST00000446533	chr15	41245549	41245550	204

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
UBE2D3	ENST00000508238	chr4	103789813	103789814	204
FANCG	ENST00000462124	chr9	35079459	35079460	206
TAF2	ENST00000521007	chr8	120844866	120844867	207
NUP160	ENST00000530326	chr11	47869654	47869655	210
AC115115.4	ENST00000449927	chr2	113103796	113103797	210
U6	ENST00000363690	chr17	61650493	61650494	212
PPM1B	ENST00000419807	chr2	44395318	44395319	212
NME1-NME2	ENST00000513177	chr17	49243387	49243388	213
EZH2	ENST00000476773	chr7	148580387	148580388	213
NDUFC1	ENST00000394223	chr4	140223417	140223418	215
C2	ENST00000497706	chr6	31865778	31865779	216
GORAB	ENST00000464798	chr1	170501528	170501529	217
CCBL1	ENST00000320665	chr9	131643989	131643990	218
ZC3H18	ENST00000567085	chr16	88653242	88653243	219
MRPL24	ENST00000434558	chr1	156711161	156711162	220
ZCRB1	ENST00000551102	chr12	42719578	42719579	220
SKP2	ENST00000513263	chr5	36152489	36152490	220
RP11-459F6.3	ENST00000569580	chr16	58163652	58163653	221
LRCH4	ENST00000467201	chr7	100178274	100178275	221
KANSL3	ENST00000487070	chr2	97303534	97303535	222
RP11-159F24.2	ENST00000511991	chr5	43336486	43336487	222
RPS20	ENST00000523936	chr8	56986692	56986693	222
PHF3	ENST00000509330	chr6	64346607	64346608	223
UBE2N	ENST00000549833	chr12	93834807	93834808	224
LIMCH1	ENST00000513024	chr4	41361846	41361847	224
GMNN	ENST00000476555	chr6	24775919	24775920	226
ZMAT2	ENST00000274712	chr5	140080144	140080145	227
CTDSPL2	ENST00000558968	chr15	44720238	44720239	228
EHD2	ENST00000540884	chr19	48233100	48233101	228
SUCO	ENST00000367723	chr1	172501716	172501717	229
ACTN1-AS1	ENST00000553944	chr14	69446986	69446987	230
TMEM237	ENST00000463205	chr2	202507144	202507145	231
MYO19	ENST00000586886	chr17	34890384	34890385	232
SGK3	ENST00000518388	chr8	67688032	67688033	233
CCNE2	ENST00000520509	chr8	95908672	95908673	233
BX470102.3	ENST00000420695	chr1	153506312	153506313	235
TMEM97	ENST00000336687	chr17	26646714	26646715	235
UMPS	ENST00000460034	chr3	124449532	124449533	235
MATR3	ENST00000504023	chr5	138630562	138630563	237
ARHGAP1	ENST00000311956	chr11	46721909	46721910	239

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
HYDIN	ENST00000538382	chr16	71209299	71209300	241
SRP9	ENST00000366838	chr1	225965877	225965878	242
TMEM123	ENST00000526676	chr11	102322843	102322844	242
RP11-331F9.4	ENST00000428948	chr9	35646507	35646508	242
IPO5	ENST00000475420	chr13	98628126	98628127	243
GAPDH	ENST00000229239	chr12	6643335	6643336	244
RP11-524O1.4	ENST00000565098	chr14	21852693	21852694	244
NUDT1	ENST00000454650	chr7	2282154	2282155	244
TAF12	ENST00000263974	chr1	28969271	28969272	245
RGS2	ENST00000487236	chr1	192778516	192778517	245
C2orf81	ENST00000518863	chr2	74648472	74648473	245
MECOM	ENST00000464456	chr3	168865276	168865277	245
RP11-390B4.5	ENST00000563601	chr10	17685630	17685631	246
TIMELESS	ENST00000554616	chr12	56842931	56842932	248
C2CD3	ENST00000544293	chr11	73881663	73881664	249
ATP2A1	ENST00000536376	chr16	28891621	28891622	249
KIF24	ENST00000345050	chr9	34328948	34328949	249
C14orf159	ENST00000522837	chr14	91527424	91527425	250
WDHD1	ENST00000455555	chr14	55493517	55493518	251
RP11-342M1.2	ENST00000416809	chr1	43311780	43311781	252
METTL13	ENST00000361735	chr1	171751092	171751093	252
DERL2	ENST00000571476	chr17	5389214	5389215	253
CAMLG	ENST00000514518	chr5	134074524	134074525	253
AP001462.6	ENST00000594089	chr11	64546678	64546679	254
ALDH7A1	ENST00000509459	chr5	125930508	125930509	254
LIPT2	ENST00000527115	chr11	74204103	74204104	256
CNGA4	ENST00000533426	chr11	6256250	6256251	257
RSBN1L-AS1	ENST00000447009	chr7	77325312	77325313	257
NSL1	ENST00000366978	chr1	212964664	212964665	258
WDR74	ENST00000525239	chr11	62609020	62609021	260
RP11-150C16.1	ENST00000547590	chr12	59314678	59314679	260
TRIM37	ENST00000580122	chr17	57183559	57183560	260
POC5	ENST00000507421	chr5	75012908	75012909	260
RPP30	ENST00000277882	chr10	92632002	92632003	264
PFN1	ENST00000225655	chr17	4852042	4852043	266
POLR3C	ENST00000466003	chr1	145610462	145610463	267
MRRF	ENST00000470366	chr9	125027472	125027473	269
U1	ENST00000365207	chr17	56736394	56736395	271
XXbac-BPG249D20.9	ENST00000415195	chr6	30484313	30484314	272
MIR3193	ENST00000578262	chr20	30195260	30195261	273

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
SUPT5H	ENST00000594990	chr19	39927068	39927069	274
SMC1A	ENST00000375340	chrX	53449327	53449328	275
METTL21B	ENST00000548256	chr12	58165550	58165551	277
CENPH	ENST00000502689	chr5	68485844	68485845	277
AC092865.1	ENST00000408177	chr12	8519558	8519559	278
AC116562.1	ENST00000408374	chr4	4086337	4086338	278
KBTBD2	ENST00000424468	chr7	32932066	32932067	278
ZNF562	ENST00000453372	chr19	9785440	9785441	279
FANCI	ENST00000565522	chr15	89787759	89787760	280
FAM173B	ENST00000504390	chr5	10249716	10249717	280
TMEM209	ENST00000462753	chr7	129844906	129844907	281
AP000974.1	ENST00000544076	chr11	85565703	85565704	282
PRPF3	ENST00000414970	chr1	150294283	150294284	283
AL603831.1	ENST00000579524	chr10	323407	323408	285
TCHP	ENST00000536408	chr12	110338697	110338698	285
HMMR	ENST00000517936	chr5	162887949	162887950	285
SHKBP1	ENST00000597649	chr19	41091764	41091765	287
RP4-798C17.6	ENST00000476560	chr7	144051943	144051944	287
PNP	ENST00000553591	chr14	20937987	20937988	289
GOSR2	ENST00000570879	chr17	45000850	45000851	289
NFKBIB	ENST00000313582	chr19	39390926	39390927	289
MORF4L1	ENST00000559258	chr15	79165673	79165674	290
TAGLN2	ENST00000368096	chr1	159893215	159893216	291
AC004924.1	ENST00000408626	chr11	67700974	67700975	291
HAT1	ENST00000494601	chr2	172779406	172779407	291
TRANK1	ENST00000463764	chr3	36949717	36949718	291
HIGD2B	ENST00000311755	chr15	72978197	72978198	292
S100A10	ENST00000368809	chr1	151964759	151964760	294
PHKG2	ENST00000569762	chr16	30760457	30760458	294
CBX3	ENST00000497498	chr7	26242375	26242376	294
CDC27P2	ENST00000425026	chrY	10029612	10029613	294
10-Sep	ENST00000411469	chr2	110370785	110370786	295
OMG	ENST00000584094	chr17	29600342	29600343	297
JRKL	ENST00000458427	chr11	96123454	96123455	298
APEX2	ENST00000471758	chrX	55027123	55027124	299
AC009120.4	ENST00000569389	chr16	74330348	74330349	300
ARMC5	ENST00000268314	chr16	31470618	31470619	303
PP13439	ENST00000331659	chr3	171527410	171527411	303
ATP6AP1	ENST00000484908	chrX	153660369	153660370	303
C19orf57	ENST00000454313	chr19	14016604	14016605	304

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
CENPK	ENST00000508311	chr5	64858645	64858646	304
C4orf27	ENST00000506125	chr4	170678747	170678748	307
TMEM241	ENST00000542162	chr18	21017506	21017507	310
SLC25A25	ENST00000433501	chr9	130861144	130861145	310
NOC3L	ENST00000371361	chr10	96122384	96122385	311
C5orf22	ENST00000504464	chr5	31532732	31532733	311
RAD51C	ENST00000584617	chr17	56770335	56770336	313
RPSAP52	ENST00000489520	chr12	66220436	66220437	317
RP1-117B12.4	ENST00000511627	chr17	48474114	48474115	317
RFC1	ENST00000504849	chr4	39367634	39367635	320
BCL6	ENST00000480458	chr3	187462903	187462904	321
SFR1	ENST00000336358	chr10	105882325	105882326	322
RP11-49C24.1	ENST00000562874	chr16	70610527	70610528	325
NOD1	ENST00000413433	chr7	30517926	30517927	325
KRT7	ENST00000552322	chr12	52638486	52638487	326
KRT7	ENST00000548657	chr12	52639547	52639548	326
MBD1	ENST00000585595	chr18	47807350	47807351	326
CTD-2203K17.1	ENST00000507251	chr5	33440398	33440399	326
SPATS2	ENST00000552171	chr12	49761655	49761656	327
MIR7-3HG	ENST00000588758	chr19	4769618	4769619	327
CTD-2571L23.8	ENST00000599924	chr19	48111106	48111107	327
RP11-65I12.1	ENST00000553319	chr2	113998632	113998633	327
RBMS1	ENST00000475103	chr2	161132866	161132867	329
TIPIN	ENST00000367709	chr15	66648692	66648693	330
LUC7L3	ENST00000507200	chr17	48797491	48797492	330
CLK1	ENST00000481641	chr2	201728643	201728644	331
ARGLU1	ENST00000360629	chr13	107219638	107219639	332
CTB-157D17.1	ENST00000524264	chr5	153825039	153825040	333
FADS2	ENST00000574708	chr11	61560784	61560785	334
DLGAP1-AS1	ENST00000573355	chr18	3594787	3594788	336
TOR3A	ENST00000367627	chr1	179050847	179050848	337
WSB2	ENST00000441406	chr12	118499636	118499637	342
WIBG	ENST00000302533	chr12	56320551	56320552	343
NUP188	ENST00000550219	chr9	131710637	131710638	343
PHLPP2	ENST00000568954	chr16	71758258	71758259	345
SNRPD1	ENST00000582475	chr18	19192636	19192637	346
DENND6A	ENST00000464875	chr3	57678224	57678225	346
STK4	ENST00000487587	chr20	43595539	43595540	347
SIGMAR1	ENST00000478146	chr9	34637061	34637062	347
FOXG1	ENST00000313071	chr14	29236633	29236634	348

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
PTP4A2	ENST00000475464	chr1	32403033	32403034	349
HKR1	ENST00000587570	chr19	37804127	37804128	349
SAE1	ENST00000392776	chr19	47634499	47634500	349
ATAD2	ENST00000519124	chr8	124408269	124408270	349
MIR3678	ENST00000578455	chr17	73402499	73402500	351
RP11-112J3.15	ENST00000425499	chr9	35757585	35757586	351
PLEKHA6	ENST00000564627	chr1	204346440	204346441	352
HIPK3	ENST00000525975	chr11	33278568	33278569	352
STK24	ENST00000481288	chr13	99228105	99228106	352
MIR3188	ENST00000583494	chr19	18393237	18393238	352
MIR487B	ENST00000385021	chr14	101513144	101513145	354
CDC45	ENST00000487669	chr22	19468025	19468026	354
VRK2	ENST00000428021	chr2	58274363	58274364	355
WDR33	ENST00000408998	chr2	128568171	128568172	355
XRN2	ENST00000539513	chr20	21284785	21284786	355
CYB5R4	ENST00000369679	chr6	84569729	84569730	356
MYPOP	ENST00000322217	chr19	46405504	46405505	357
SPRED2	ENST00000443619	chr2	65593425	65593426	358
SUPT16H	ENST00000556309	chr14	21851744	21851745	360
LCMT2	ENST00000544735	chr15	43622409	43622410	363
CIC	ENST00000575839	chr19	42784505	42784506	365
KRT1	ENST00000252244	chr12	53073824	53073825	366
YEATS4	ENST00000552955	chr12	69753925	69753926	368
ZBTB9	ENST00000487326	chr6	33422726	33422727	368
CHTF8	ENST00000398235	chr16	69165679	69165680	369
USP1	ENST00000339950	chr1	62902696	62902697	372
RP11-313D6.3	ENST00000416249	chr10	112629871	112629872	372
COX5A	ENST00000568517	chr15	75229744	75229745	372
GIN1	ENST00000513747	chr5	102455420	102455421	372
CTD-2527I21.7	ENST00000600959	chr19	35490699	35490700	374
DHX9	ENST00000483416	chr1	182809242	182809243	375
DERA	ENST00000532964	chr12	16064670	16064671	375
CTD-2296D1.4	ENST00000513219	chr5	7372811	7372812	375
PFN1	ENST00000574872	chr17	4850386	4850387	377
E2F6	ENST00000455198	chr2	11605623	11605624	381
TCF19	ENST00000376255	chr6	31126703	31126704	381
TP53	ENST00000514944	chr17	7590362	7590363	382
AC023797.1	ENST00000441644	chr3	196359072	196359073	385
SCML1	ENST00000419185	chrX	17756229	17756230	386
SLC35C2	ENST00000484188	chr20	44992609	44992610	390

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
EMBP1	ENST00000458200	chr1	121261533	121261534	392
RNU4-1	ENST00000363925	chr12	120730647	120730648	392
AAGAB	ENST00000558725	chr15	67546599	67546600	392
DDX23	ENST00000551098	chr12	49245527	49245528	393
CRCP	ENST00000486848	chr7	65580237	65580238	393
SKA2	ENST00000583380	chr17	57232139	57232140	395
TM9SF4	ENST00000417389	chr20	30697963	30697964	395
CIDECP	ENST00000445082	chr3	10067614	10067615	395
NRAS	ENST00000369535	chr1	115259118	115259119	396
SLC25A25	ENST00000373069	chr9	130830966	130830967	396
PHGDH	ENST00000462324	chr1	120254924	120254925	397
HIST1H2BD	ENST00000289316	chr6	26158769	26158770	397
CHAF1A	ENST00000585854	chr19	4403110	4403111	398
KLHDC3	ENST00000244670	chr6	42982384	42982385	399
HSPB11	ENST00000488884	chr1	54410872	54410873	402
ZMYM4	ENST00000441447	chr1	35735035	35735036	403
EED	ENST00000525244	chr11	85956711	85956712	403
GPS2	ENST00000574458	chr17	7216185	7216186	403
TTLL9	ENST00000375922	chr20	30468033	30468034	403
TOR1B	ENST00000427860	chr9	132565951	132565952	406
RPL23AP79	ENST00000595439	chr19	59098057	59098058	407
CAB39L	ENST00000410043	chr13	50017780	50017781	408
COA1	ENST00000459713	chr7	43687944	43687945	408
ADAM17	ENST00000478059	chr2	9695493	9695494	409
WHSC1L1	ENST00000529223	chr8	38238839	38238840	409
SRSF7	ENST00000415527	chr2	38977869	38977870	410
SOCS6	ENST00000578377	chr18	67964246	67964247	413
NUBP2	ENST00000564227	chr16	1833438	1833439	416
MCM10	ENST00000484800	chr10	13203994	13203995	417
IGSF11	ENST00000494802	chr3	118864422	118864423	417
RP11-86H7.7	ENST00000435559	chr1	95089320	95089321	419
MRPL11	ENST00000534488	chr11	66205877	66205878	419
BRCA2	ENST00000530893	chr13	32890060	32890061	420
TNFRSF1A	ENST00000366159	chr12	6450592	6450593	421
MELK	ENST00000487398	chr9	36573340	36573341	421
RRAGB	ENST00000262850	chrX	55744739	55744740	423
AP2A1	ENST00000597774	chr19	50270815	50270816	424
HDDC3	ENST00000561036	chr15	91475279	91475280	426
RING1	ENST00000374656	chr6	33176696	33176697	426
NUMBL	ENST00000598773	chr19	41195069	41195070	427

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
HIST1H4A	ENST00000359907	chr6	26022332	26022333	427
NCAPD3	ENST00000533155	chr11	134093406	134093407	428
ZNHIT3	ENST00000588357	chr17	34842999	34843000	429
PALD1	ENST00000426268	chr10	72299902	72299903	434
AC090340.1	ENST00000581316	chr18	55103485	55103486	434
C16orf95	ENST00000567970	chr16	87350548	87350549	437
TNFAIP8	ENST00000388882	chr5	118604884	118604885	437
SZRD1	ENST00000475078	chr1	16679507	16679508	439
SETD5-AS1	ENST00000521267	chr3	9437848	9437849	440
SLC29A1	ENST00000371713	chr6	44191998	44191999	440
RBM14	ENST00000461478	chr11	66385054	66385055	442
PARP11	ENST00000453942	chr12	3982073	3982074	442
NCAPH2	ENST00000520939	chr22	50947149	50947150	445
RP11-793H13.4	ENST00000546894	chr12	53902491	53902492	446
IQCD	ENST00000546692	chr12	113658384	113658385	447
LRFN3	ENST00000587257	chr19	36427041	36427042	448
CLK2	ENST00000361168	chr1	155242628	155242629	449
CAV2	ENST00000495841	chr7	116140550	116140551	454
FGD5-AS1	ENST00000440079	chr3	14988555	14988556	456
CTD-2201E18.3	ENST00000503152	chr5	43067064	43067065	456
MCM3	ENST00000419835	chr6	52149046	52149047	458
TCTEX1D2	ENST00000426563	chr3	196044622	196044623	462
ID3	ENST00000463312	chr1	23885100	23885101	465
LTN1	ENST00000389194	chr21	30364804	30364805	465
HIST1H2BC	ENST00000314332	chr6	26123688	26123689	465
DIAPH3	ENST00000400319	chr13	60737432	60737433	467
FBL	ENST00000599134	chr19	40336501	40336502	467
SKA3	ENST00000475251	chr13	21750143	21750144	468
CASP8AP2	ENST00000548224	chr6	90540131	90540132	473
SMAD9-AS1	ENST00000437983	chr13	37423975	37423976	474
SNORA43	ENST00000516652	chr16	28892453	28892454	474
ZNF180	ENST00000592095	chr19	45004072	45004073	474
PMVK	ENST00000368467	chr1	154908991	154908992	475
FBXO4	ENST00000506496	chr5	41925897	41925898	476
IDO2	ENST00000502986	chr8	39792951	39792952	479
FANCI	ENST00000566895	chr15	89822391	89822392	482
SUGP1	ENST00000588731	chr19	19430816	19430817	484
RP4-564F22.2	ENST00000414142	chr20	37063429	37063430	486
RP11-96D1.6	ENST00000564147	chr16	68271080	68271081	489
G3BP2	ENST00000507745	chr4	76597375	76597376	489

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
MTCH1	ENST00000373550	chr6	36953267	36953268	489
PLXDC1	ENST00000579190	chr17	37310156	37310157	490
PHF8	ENST00000448003	chrX	54028612	54028613	490
MASTL	ENST00000375940	chr10	27444788	27444789	491
CNTRL	ENST00000373855	chr9	123837779	123837780	491
FOXK2	ENST00000570585	chr17	80478660	80478661	492
MRPL53	ENST00000467349	chr2	74699181	74699182	492
BUD13	ENST00000375445	chr11	116643209	116643210	493
C12orf57	ENST00000540506	chr12	7053780	7053781	493
OPA3	ENST00000263275	chr19	46087583	46087584	493
IMPA2	ENST00000588927	chr18	11982161	11982162	494
C1ORF220	ENST00000367636	chr1	178512447	178512448	499
PALLD	ENST00000512127	chr4	169553266	169553267	500
KHDC1	ENST00000484801	chr6	74019365	74019366	500
DLGAP3	ENST00000495979	chr1	35390593	35390594	501
B3GAT3	ENST00000532585	chr11	62388951	62388952	504
UNC13A	ENST00000523229	chr19	17722464	17722465	504
RP13-507I23.1	ENST00000444489	chrX	149108876	149108877	504
STK35	ENST00000246032	chr20	2083031	2083032	505
BIN3	ENST00000519335	chr8	22526086	22526087	505
UNG	ENST00000446767	chr12	109536460	109536461	506
TCOF1	ENST00000515516	chr5	149737850	149737851	506
SUV39H1	ENST00000453214	chrX	48555653	48555654	506
REL	ENST00000394479	chr2	61109296	61109297	507
SHCBP1	ENST00000564272	chr16	46654750	46654751	512
SPPL2A	ENST00000560288	chr15	51057392	51057393	513
PAN3	ENST00000399613	chr13	28713683	28713684	515
CLDN7	ENST00000574070	chr17	7163948	7163949	515
CLCC1	ENST00000369976	chr1	109505555	109505556	516
FASTK	ENST00000483953	chr7	150775480	150775481	517
TOP3A	ENST00000580095	chr17	18217495	18217496	521
MYNN	ENST00000356716	chr3	169491374	169491375	523
ST13P12	ENST00000508958	chr5	82265228	82265229	523
FAM105B	ENST00000284274	chr5	14665379	14665380	524
PARP1	ENST00000366790	chr1	226595157	226595158	525
POLD3	ENST00000530511	chr11	74304212	74304213	525
DBR1	ENST00000477557	chr3	137893174	137893175	526
ZNF791	ENST00000498389	chr19	12722297	12722298	527
RAP1A	ENST00000545460	chr1	112163296	112163297	529
RAVER1	ENST00000591969	chr19	10443637	10443638	529

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
NUP35	ENST00000452137	chr2	183989714	183989715	530
AGPAT4	ENST00000437165	chr6	161569790	161569791	530
LINC00473	ENST00000581850	chr6	166400871	166400872	530
CAD	ENST00000403525	chr2	27440805	27440806	531
RTN3	ENST00000354497	chr11	63449575	63449576	532
ITM2B	ENST00000378549	chr13	48807869	48807870	532
UGGT2	ENST00000376747	chr13	96705104	96705105	532
ENAH	ENST00000284563	chr1	225839882	225839883	535
RFC5	ENST00000535092	chr12	118455068	118455069	536
ACIN1	ENST00000473758	chr14	23538197	23538198	536
NFKB1	ENST00000505458	chr4	103423589	103423590	536
FAIM	ENST00000393034	chr3	138328450	138328451	538
MLLT11	ENST00000368921	chr1	151030771	151030772	539
KRCC1	ENST00000347055	chr2	88354708	88354709	539
LINC00441	ENST00000436963	chr13	48877254	48877255	540
KIAA0240	ENST00000394167	chr6	42715234	42715235	540
MALSU1	ENST00000481564	chr7	23339499	23339500	541
RPA3	ENST00000401447	chr7	7679112	7679113	544
IGBP1	ENST00000356413	chrX	69353855	69353856	544
POLR1D	ENST00000302979	chr13	28195447	28195448	546
RMI2	ENST00000576027	chr16	11439853	11439854	548
CEP57	ENST00000538658	chr11	95524371	95524372	550
DNMT1	ENST00000592054	chr19	10304747	10304748	554
PPM1G	ENST00000472077	chr2	27631866	27631867	555
FICD	ENST00000361549	chr12	108909648	108909649	557
FUCA2	ENST00000438118	chr6	143832241	143832242	557
PATL1	ENST00000300146	chr11	59435893	59435894	559
FLII	ENST00000579294	chr17	18161310	18161311	559
PRR5L	ENST00000530627	chr11	36477397	36477398	560
NAMPT	ENST00000484527	chr7	105924517	105924518	560
RP4-675G8.4	ENST00000423265	chr1	44620411	44620412	561
DENND5A	ENST00000530044	chr11	9286072	9286073	561
RP11-796E2.4	ENST00000499685	chr12	92540517	92540518	562
PARP14	ENST00000494811	chr3	122400266	122400267	562
C17orf64	ENST00000428000	chr17	58470488	58470489	563
CAND1	ENST00000540525	chr12	67664243	67664244	564
VAT1	ENST00000587173	chr17	41173807	41173808	565
TRPV4	ENST00000537083	chr12	110252033	110252034	567
ARL8B	ENST00000419534	chr3	5164547	5164548	568
UCHL3	ENST00000377595	chr13	76124494	76124495	569

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
TADA3	ENST00000492635	chr3	9833522	9833523	569
SART3	ENST00000431469	chr12	108954364	108954365	570
UQCC	ENST00000496812	chr20	33894287	33894288	570
NUP153	ENST00000262077	chr6	17706045	17706046	572
JTB	ENST00000428469	chr1	153949296	153949297	573
USP21	ENST00000487163	chr1	161131724	161131725	573
EFHC1	ENST00000433625	chr6	52285738	52285739	575
QTRTD1	ENST00000462966	chr3	113802194	113802195	580
GALNT1	ENST00000590654	chr18	33235199	33235200	581
COMMD4	ENST00000568301	chr15	75629029	75629030	585
OXR1	ENST00000438229	chr8	107670702	107670703	585
NDUFA8	ENST00000537618	chr9	124921480	124921481	585
SUMO1	ENST00000409205	chr2	203102594	203102595	590
SST	ENST00000287641	chr3	187387596	187387597	590
HEXIM1	ENST00000332499	chr17	43225273	43225274	591
DAPK2	ENST00000559306	chr15	64363638	64363639	593
RELT	ENST00000393580	chr11	73088309	73088310	598
CBX5	ENST00000209875	chr12	54673285	54673286	600
CTD-3252C9.2	ENST00000591242	chr19	13907146	13907147	600
AEN	ENST00000558327	chr15	89165215	89165216	605
IER2	ENST00000588173	chr19	13263394	13263395	607
UBA52P9	ENST00000483523	chr18	24935116	24935117	611
SESTD1	ENST00000435047	chr2	180128316	180128317	613
POLR2A	ENST00000572844	chr17	7388551	7388552	614
DSN1	ENST00000373740	chr20	35401501	35401502	621
PANK2	ENST00000336066	chr20	3870660	3870661	626
SNX8	ENST00000494722	chr7	2353448	2353449	627
MSH2	ENST00000406134	chr2	47630899	47630900	632
SNRPB	ENST00000474384	chr20	2450742	2450743	635
HIST1H4I	ENST00000354348	chr6	27107709	27107710	635
CHRAC1	ENST00000519618	chr8	141522718	141522719	639
PEA15	ENST00000368076	chr1	160175851	160175852	642
HYDIN	ENST00000543639	chr16	71113643	71113644	645
PHF12	ENST00000582853	chr17	27276229	27276230	645
DHX15	ENST00000511553	chr4	24585258	24585259	646
MUL1	ENST00000264198	chr1	20834004	20834005	649
RIF1	ENST00000430328	chr2	152267254	152267255	652
HNRNPA2B1	ENST00000354667	chr7	26239712	26239713	653
SRSF10	ENST00000495785	chr1	24306106	24306107	654
RP11-736I10.2	ENST00000528891	chr11	59845475	59845476	654

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
SAMD9	ENST00000446617	chr7	92746620	92746621	654
HIST1H2BK	ENST00000356950	chr6	27113921	27113922	655
ISCU	ENST00000535405	chr12	108957047	108957048	656
CCDC19	ENST00000475911	chr1	159849828	159849829	661
ANKRD11	ENST00000562275	chr16	89382820	89382821	662
MCM6	ENST00000264156	chr2	136633329	136633330	666
NEK4	ENST00000535191	chr3	52804205	52804206	666
RP11-715J22.2	ENST00000563775	chr16	2517544	2517545	669
ZNF263	ENST00000575823	chr16	3334622	3334623	669
POLD1	ENST00000593887	chr19	50888298	50888299	670
E2F1	ENST00000343380	chr20	32273538	32273539	671
PSMC1	ENST00000543772	chr14	90723595	90723596	675
CFDP1	ENST00000566254	chr16	75466610	75466611	678
CTD-2616J11.14	ENST00000600765	chr19	51898421	51898422	681
CELF4	ENST00000586009	chr18	34850196	34850197	686
KITLG	ENST00000228280	chr12	88973548	88973549	689
CC2D1B	ENST00000491136	chr1	52831136	52831137	691
INPP4A	ENST00000409540	chr2	99062102	99062103	691
SRD5A1	ENST00000538824	chr5	6634275	6634276	696
NPAS4	ENST00000525148	chr11	66189258	66189259	698
PREB	ENST00000406567	chr2	27356780	27356781	699
HIATL1	ENST00000375344	chr9	97137536	97137537	705
CHIC2	ENST00000510894	chr4	54929757	54929758	707
ZFYVE16	ENST00000512442	chr5	79704640	79704641	708
RP11-443B7.3	ENST00000549744	chr1	235115841	235115842	709
USP37	ENST00000418019	chr2	219432303	219432304	710
EIF1AX	ENST00000379593	chrX	20159230	20159231	713
IRF9	ENST00000560852	chr14	24631238	24631239	714
FBXO11	ENST00000424163	chr2	48131634	48131635	714
NIM1	ENST00000512796	chr5	43193667	43193668	715
HIST1H2BG	ENST00000244601	chr6	26216156	26216157	715
RP11-651L5.2	ENST00000552486	chr12	106640016	106640017	717
SIRT5	ENST00000379250	chr6	13575590	13575591	717
TAF3	ENST00000344293	chr10	7861184	7861185	719
IKBIP	ENST00000420861	chr12	99038012	99038013	719
SLC16A6	ENST00000327268	chr17	66286533	66286534	723
HIST1H4B	ENST00000377364	chr6	26026755	26026756	724
ASGR2	ENST00000446679	chr17	7016832	7016833	726
PPRC1	ENST00000413464	chr10	103893526	103893527	731
DIDO1	ENST00000266070	chr20	61568541	61568542	732

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
FANCE	ENST00000229769	chr6	35420868	35420869	732
RNU1-1	ENST00000383925	chr1	16840046	16840047	733
WDR82	ENST00000469000	chr3	52311603	52311604	733
SGPL1	ENST00000373202	chr10	72576463	72576464	739
PHLDB2	ENST00000393925	chr3	111579380	111579381	739
SNORA76	ENST00000408535	chr17	62224437	62224438	740
POGZ	ENST00000358476	chr1	151430908	151430909	745
RFX3	ENST00000382004	chr9	3525237	3525238	745
RP4-724E13.2	ENST00000582616	chr7	51085908	51085909	750
HIST1H1PS1	ENST00000404269	chr6	26196545	26196546	753
1-Mar	ENST00000366910	chr1	220960853	220960854	754
RP11-65J3.1	ENST00000436710	chr9	132096937	132096938	754
AC009948.5	ENST00000415236	chr2	179279503	179279504	755
HNRNPA1	ENST00000551803	chr12	54680491	54680492	762
PTPN12	ENST00000435495	chr7	77168149	77168150	765
HMBS	ENST00000539045	chr11	118964087	118964088	768
RP5-1021I20.4	ENST00000556551	chr14	74319442	74319443	770
RABIF	ENST00000367262	chr1	202857487	202857488	775
MAP3K4	ENST00000490904	chr6	161413650	161413651	776
RNF138	ENST00000580499	chr18	29673441	29673442	778
ZCCHC11	ENST00000257177	chr1	53017874	53017875	779
NCAPD3	ENST00000533155	chr11	134093055	134093056	779
ELF2	ENST00000379549	chr4	140004560	140004561	783
TFAP2A	ENST00000461628	chr6	10404033	10404034	793
CENPM	ENST00000404067	chr22	42341896	42341897	795
GCA	ENST00000233612	chr2	163201642	163201643	796
RP1-90J20.7	ENST00000597787	chr6	2989728	2989729	797
CD2AP	ENST00000359314	chr6	47446321	47446322	798
RP11-191N8.2	ENST00000431729	chr1	222013204	222013205	803
FBXL20	ENST00000394294	chr17	37557067	37557068	808
DDX39A	ENST00000590239	chr19	14529064	14529065	809
NFIA	ENST00000407417	chr1	61543758	61543759	814
RNU1-5	ENST00000384010	chr1	149223403	149223404	817
IDH3B	ENST00000466999	chr20	2639742	2639743	819
CPEB3	ENST00000394210	chr10	94050016	94050017	827
AC016700.5	ENST00000414141	chr2	70351620	70351621	828
RNU1-2	ENST00000384278	chr1	17223302	17223303	829
RP11-323I15.2	ENST00000558778	chr15	35385513	35385514	833
BX470102.3	ENST00000420695	chr1	153506911	153506912	834
CDC25A	ENST00000443342	chr3	48228619	48228620	836

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
AC093887.1	ENST00000584185	chr4	147561247	147561248	836
FADD	ENST00000301838	chr11	70050105	70050106	838
U2AF2	ENST00000587196	chr19	56167311	56167312	838
LUC7L2	ENST00000456182	chr7	139045497	139045498	841
RP11-773H22.4	ENST00000588211	chr18	12990329	12990330	842
MAPRE1	ENST00000375571	chr20	31408539	31408540	842
U8	ENST00000459095	chr10	5003914	5003915	845
AC009892.2	ENST00000433549	chr19	55064099	55064100	848
CSRNP1	ENST00000273153	chr3	39194214	39194215	851
SERP1	ENST00000491660	chr3	150263434	150263435	851
MB21D1	ENST00000370318	chr6	74161130	74161131	851
TMEM38B	ENST00000374692	chr9	108457675	108457676	852
CTD-2296D1.4	ENST00000513219	chr5	7372332	7372333	854
MAP4	ENST00000439356	chr3	48129458	48129459	855
B4GALT5	ENST00000371711	chr20	48329553	48329554	861
PDZD2	ENST00000502489	chr5	31855902	31855903	861
RNF169	ENST00000299563	chr11	74460777	74460778	866
RP11-973N13.4	ENST00000554918	chr14	65006217	65006218	868
EIF4A3	ENST00000576547	chr17	78120065	78120066	872
ALMS1	ENST00000264448	chr2	73613760	73613761	876
CNBP	ENST00000502372	chr3	128901829	128901830	877
STAT5B	ENST00000293328	chr17	40427545	40427546	878
CDC37	ENST00000588869	chr19	10513307	10513308	879
PCNA	ENST00000379143	chr20	5099791	5099792	880
NPL	ENST00000367554	chr1	182759797	182759798	888
RSPH3	ENST00000449822	chr6	159419924	159419925	888
SMURF1	ENST00000361368	chr7	98740749	98740750	892
FBXO5	ENST00000229758	chr6	153303251	153303252	901
KPNA6	ENST00000537234	chr1	32574793	32574794	906
CENPV	ENST00000584214	chr17	16255850	16255851	908
HSBP1L1	ENST00000589516	chr18	77725536	77725537	908
TRIP12	ENST00000487178	chr2	230669951	230669952	913
CLDN3	ENST00000395145	chr7	73183684	73183685	915
PAN3	ENST00000399613	chr13	28714087	28714088	919
SGCA	ENST00000504073	chr17	48246803	48246804	922
FOXF2	ENST00000259806	chr6	1390989	1390990	922
MIR5000	ENST00000577717	chr2	75318860	75318861	923
ADAM17	ENST00000478059	chr2	9694973	9694974	929
CRYGB	ENST00000260988	chr2	209009960	209009961	931
MIR3687	ENST00000577708	chr21	9827143	9827144	942

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
NPM1	ENST00000518587	chr5	170815830	170815831	943
PHLDA3	ENST00000485436	chr1	201436761	201436762	947
GORASP2	ENST00000497928	chr2	171786916	171786917	975
E2F2	ENST00000361729	chr1	23856734	23856735	977
MIR181A2HG	ENST00000429139	chr9	127421724	127421725	980
GREB1L	ENST00000269218	chr18	18823299	18823300	982
Metazoa_SRP	ENST00000581811	chr1	150540759	150540760	985
RNU5A-8P	ENST00000364102	chr1	210546625	210546626	985
AL732363.1	ENST00000581702	chr1	149035389	149035390	987
GNAI2	ENST00000446079	chr3	50265156	50265157	989
NASP	ENST00000351223	chr1	46050733	46050734	998
IMP3	ENST00000403490	chr15	75931547	75931548	1004
UCK2	ENST00000372212	chr1	165798067	165798068	1010
ZNF837	ENST00000427624	chr19	58891377	58891378	1011
GTF2A1	ENST00000553612	chr14	81686250	81686251	1015
DNAAF1	ENST00000564928	chr16	84210763	84210764	1018
ASB3	ENST00000470916	chr2	54012961	54012962	1024
RP11-7C6.1	ENST00000443282	chr10	14695765	14695766	1026
ARHGAP42	ENST00000531183	chr11	100785259	100785260	1030
FRG2C	ENST00000464571	chr3	75714509	75714510	1030
HMBS	ENST00000539045	chr11	118964353	118964354	1034
QSER1	ENST00000527250	chr11	32915845	32915846	1041
CTD-2587H24.1	ENST00000587647	chr19	55630708	55630709	1042
TNFRSF1A	ENST00000366159	chr12	6449962	6449963	1051
BMF	ENST00000220446	chr15	40397232	40397233	1054
NEAT1	ENST00000601801	chr11	65191345	65191346	1061
RGMA	ENST00000555584	chr15	93605236	93605237	1061
RNF167	ENST00000574548	chr17	4848737	4848738	1064
LMNB1	ENST00000463908	chr5	126114145	126114146	1076
POU4F1	ENST00000377208	chr13	79176594	79176595	1078
ZNF263	ENST00000538765	chr16	3314877	3314878	1079
SNORA76	ENST00000408535	chr17	62224780	62224781	1083
7SK	ENST00000410325	chr4	45998234	45998235	1100
TMOD3	ENST00000560549	chr15	52168325	52168326	1104
HIST1H2BO	ENST00000303806	chr6	27862310	27862311	1109
CMIP	ENST00000537098	chr16	81479883	81479884	1110
WNT2B	ENST00000478360	chr1	113058487	113058488	1115
IGFL1P1	ENST00000599950	chr19	46700615	46700616	1122
JUND	ENST00000600972	chr19	18390614	18390615	1124
SKIDA1	ENST00000444772	chr10	21805715	21805716	1132

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
EME1	ENST00000507616	chr17	48458252	48458253	1134
CTD-2049J23.3	ENST00000471921	chr3	159745581	159745582	1135
LUC7L2	ENST00000456182	chr7	139045803	139045804	1147
NLRC5	ENST00000543402	chr16	57094262	57094263	1152
UBE2D3	ENST00000508238	chr4	103788863	103788864	1154
MAP3K19	ENST00000486077	chr2	135803852	135803853	1160
ELF2	ENST00000379549	chr4	140004177	140004178	1166
HMGN5	ENST00000373250	chrX	80375970	80375971	1166
RPL7A	ENST00000492798	chr9	136218871	136218872	1168
GATA6	ENST00000581694	chr18	19752072	19752073	1180
EIF2S2	ENST00000374980	chr20	32698957	32698958	1180
KCTD2	ENST00000581589	chr17	73029888	73029889	1183
USP1	ENST00000339950	chr1	62903509	62903510	1185
HSD17B12	ENST00000533090	chr11	43852799	43852800	1188
SYNCRIP	ENST00000355238	chr6	86351516	86351517	1192
HES1	ENST00000476918	chr3	193855130	193855131	1195
RP5-1157M23.2	ENST00000464958	chr3	52274514	52274515	1200
GMPS	ENST00000541628	chr3	155589700	155589701	1202
HIST2H2BE	ENST00000369155	chr1	149857025	149857026	1206
WHSC1	ENST00000514045	chr4	1874393	1874394	1207
BBC3	ENST00000439096	chr19	47733237	47733238	1213
FLG-AS1	ENST00000420707	chr1	152163051	152163052	1226
AGGF1P3	ENST00000493675	chr3	75702697	75702698	1226
ABI2	ENST00000454023	chr2	204256993	204256994	1228
DUS2L	ENST00000575677	chr16	68029925	68029926	1238
TRIM24	ENST00000494040	chr7	138190277	138190278	1244
NAPA	ENST00000597271	chr19	47993486	47993487	1245
RNA45S5	ENST00000445125	chrY	10035465	10035466	1245
TRIM33	ENST00000358465	chr1	115052520	115052521	1260
TTC25	ENST00000591658	chr17	40088167	40088168	1260
ZCCHC11	ENST00000257177	chr1	53017388	53017389	1265
THNSL1	ENST00000524413	chr10	25306856	25306857	1271
LEPREL4	ENST00000587455	chr17	39966127	39966128	1284
CTC-344H19.4	ENST00000601033	chr19	46532410	46532411	1285
CD160	ENST00000369288	chr1	145714274	145714275	1290
RP4-535B20.1	ENST00000448344	chr1	65532128	65532129	1291
ZC3HAV1	ENST00000464606	chr7	138792801	138792802	1298
MSI2	ENST00000584476	chr17	55335784	55335785	1301
LINC00092	ENST00000583864	chr9	98788933	98788934	1308
SCARB2	ENST00000502908	chr4	77115685	77115686	1312

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RP5-1103G7.4	ENST00000414676	chr20	304545	304546	1332
PRR9	ENST00000368744	chr1	153191401	153191402	1343
U6	ENST00000516731	chr20	48412691	48412692	1345
RP11-151G14.1	ENST00000557286	chr14	89576220	89576221	1346
DIEXF	ENST00000457820	chr1	210013506	210013507	1358
LRP8	ENST00000465675	chr1	53791708	53791709	1362
CTD-2659N19.9	ENST00000590065	chr19	12894545	12894546	1369
RNA5SP42	ENST00000364278	chr1	34579922	34579923	1374
ZNF367	ENST00000375256	chr9	99179235	99179236	1375
HIST1H2AG	ENST00000359193	chr6	27102210	27102211	1380
RHOF	ENST00000537265	chr12	122229873	122229874	1392
GADD45GIP1	ENST00000316939	chr19	13066657	13066658	1392
TNFSF9	ENST00000245817	chr19	6532415	6532416	1407
MRPL41	ENST00000371443	chr9	140447065	140447066	1416
TRIM41	ENST00000510072	chr5	180662122	180662123	1418
LRCH1	ENST00000389797	chr13	47128814	47128815	1421
SIPA1L3	ENST00000595384	chr19	38592044	38592045	1424
LINC00273	ENST00000567668	chr16	33955684	33955685	1430
TPM4	ENST00000588410	chr19	16189262	16189263	1433
IDE	ENST00000478361	chr10	94332380	94332381	1443
C3AR1	ENST00000546241	chr12	8217483	8217484	1449
CDKN1A	ENST00000462537	chr6	36647997	36647998	1451
ITGAX	ENST00000562138	chr16	31384253	31384254	1460
SURF1	ENST00000495952	chr9	136219642	136219643	1465
FAM24A	ENST00000368894	chr10	124671689	124671690	1474
NLGN3	ENST00000358741	chrX	70366185	70366186	1475
GDPD4	ENST00000527489	chr11	77011213	77011214	1480
RGPD1	ENST00000398193	chr2	87142417	87142418	1484
DLGAP1	ENST00000485480	chr18	3741028	3741029	1486
7-Sep	ENST00000537785	chr7	35842317	35842318	1490
RP11-540O11.7	ENST00000558101	chr15	41305284	41305285	1491
ERVH48-1	ENST00000447535	chr21	44344264	44344265	1491
CTD-2296D1.4	ENST00000513219	chr5	7371678	7371679	1508
MOCOS	ENST00000261326	chr18	33769008	33769009	1528
UNC13A	ENST00000519716	chr19	17797478	17797479	1529
UBE2G2	ENST00000496395	chr21	46220123	46220124	1535
TMEM14A	ENST00000211314	chr6	52537449	52537450	1544
USP1	ENST00000339950	chr1	62903871	62903872	1547
VCAN	ENST00000502527	chr5	82769298	82769299	1556
JHDM1D	ENST00000006967	chr7	139875181	139875182	1559

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
RGCC	ENST00000379359	chr13	42033254	42033255	1561
NKD2	ENST00000382730	chr5	1038455	1038456	1562
PCNA	ENST00000379143	chr20	5099101	5099102	1570
MIR554	ENST00000384874	chr1	151519848	151519849	1578
ACTB	ENST00000464611	chr7	5566129	5566130	1599
CNN2P9	ENST00000417134	chr6	111181042	111181043	1602
ZNF697	ENST00000421812	chr1	120188777	120188778	1618
NR4A3	ENST00000330847	chr9	102590628	102590629	1621
SHC1	ENST00000412170	chr1	154945176	154945177	1635
PSMC3IP	ENST00000587268	chr17	40728051	40728052	1638
BAZ2A	ENST00000549506	chr12	57028460	57028461	1641
KIF25	ENST00000496008	chr6	168436317	168436318	1641
snoU13	ENST00000459231	chr2	70184417	70184418	1642
SEMA6A	ENST00000513137	chr5	115803589	115803590	1650
SNORD65	ENST00000391079	chr17	16346201	16346202	1663
RPS21P4	ENST00000487122	chr4	16256487	16256488	1690
STIM1	ENST00000524822	chr11	3911006	3911007	1691
IER5	ENST00000367577	chr1	181059329	181059330	1693
U6	ENST00000384376	chrX	54371690	54371691	1713
RP11-44F14.2	ENST00000565189	chr16	53414087	53414088	1721
C1orf174	ENST00000486765	chr1	3815087	3815088	1723
FURIN	ENST00000268171	chr15	91413545	91413546	1725
RP11-443B7.3	ENST00000549744	chr1	235114801	235114802	1749
RP4-814E15.1	ENST00000428811	chr1	52716691	52716692	1753
RP5-968P14.2	ENST00000569378	chr1	27018860	27018861	1761
SKA3	ENST00000475251	chr13	21748845	21748846	1766
MIR5689	ENST00000581998	chr6	10441724	10441725	1776
LMNB1	ENST00000463908	chr5	126114854	126114855	1785
RP4-761J14.8	ENST00000407384	chr12	6774232	6774233	1808
BASP1	ENST00000322611	chr5	17219479	17219480	1812
PROB1	ENST00000434752	chr5	138729071	138729072	1813
LINC00265	ENST00000340510	chr7	39775042	39775043	1813
SNORA65	ENST00000364432	chr9	130209095	130209096	1813
TMEM173	ENST00000502825	chr5	138858856	138858857	1815
SFN	ENST00000339276	chr1	27191459	27191460	1828
U6	ENST00000517277	chr1	11214243	11214244	1838
SLC7A10	ENST00000590036	chr19	33714862	33714863	1841
GALNT9	ENST00000328957	chr12	132903941	132903942	1847
AC010886.2	ENST00000437380	chr2	218560481	218560482	1865
AC006486.1	ENST00000378108	chr19	42748804	42748805	1879

Supplemental Table 2: Genes with significant occupancy of E2F8 at the promoter regions (-5kb to+2kb)

Gene Symbol	Ensembl ID	Chromosome	Start	End	distance from TSS
OSBPL9	ENST00000533825	chr1	52239631	52239632	1885
BBC3	ENST00000439096	chr19	47732558	47732559	1892
FSCN1	ENST00000405801	chr7	5636208	5636209	1893
HYDIN	ENST00000546257	chr16	70895177	70895178	1895
RP11-168O16.1	ENST00000458003	chr1	200994983	200994984	1896
AL022344.2	ENST00000435210	chr10	43158076	43158077	1902
SNORD35A	ENST00000363389	chr19	49996333	49996334	1903
MUC4	ENST00000486425	chr3	195494651	195494652	1907
COQ5	ENST00000546838	chr12	120952569	120952570	1917
U7	ENST00000516597	chr9	34016401	34016402	1917
DHRS7B	ENST00000579303	chr17	21032193	21032194	1918
CAPN3	ENST00000397163	chr15	42653702	42653703	1919
MPDZ	ENST00000542806	chr9	13138122	13138123	1921
SLC22A4	ENST00000491257	chr5	131633043	131633044	1927
ASB3	ENST00000470916	chr2	54012046	54012047	1939
AC016700.3	ENST00000457870	chr2	70320174	70320175	1951
PERP	ENST00000421351	chr6	138426688	138426689	1959
KDM6B	ENST00000570632	chr17	7750191	7750192	1960
ANKRD44	ENST00000473081	chr2	197973593	197973594	1960
CTC-524C5.2	ENST00000575890	chr17	5334227	5334228	1968
AUTS2	ENST00000403018	chr7	69066563	69066564	1968
SKOR2	ENST00000425639	chr18	44773568	44773569	1985
ATP11C	ENST00000370557	chrX	139013239	139013240	1989
TRAPPC9	ENST00000521700	chr8	140816481	140816482	1994
FOXK1	ENST00000328914	chr7	4723936	4723937	1998

Supplemental Table 3: Functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
Cancer	E2F7	2.99E-10	VRK2,RNF219,RALGAPA2,ELF2,ALDOA,HNRNPL,CCNT2,ARGLU1,FAM212B,CDC6,CBX3,KHDC1,TOP2A,C1orf106,PMM1,FKBPL,SENP5,LEMD3,CDK5RAP2,SYDE1,DERL3,GBA,ANP32E,HAT1,MTAP,SETMAR,FBXO5,ZNF219,PMAIP1,RECQL,CYR61,PRIM2,EIF3B,SIK2,ORC1,RFC2,SIN3A,DSN1,EIF1AX,NASP,SNRPC,EGR1,GPR180,TRIM56,PARP1,DAXX,LUC7L2,RHEB,CDC23,TK1,C12orf57,RRM2,GINS3,CDKN2D,CDCA7,UNG,SLC25A25,GGCT,IGF2BP3,ADAM15,BRIP1,SUCO,GMPS,mir663,FBXL20,SMC1A,LIG1,FAM111B,FAM60A,SETX,ZNF524,MSH6,METTL2A,CEP85,E2F8,E2F2,HCN3,PNPLA8,SOX6,FCHSD2,SEMA6B,RNA45S5,CUEDC1,SRSF7,CD44,WEE1,FBXL3,SYNGR4,MMS22L,UCK2,NAP1L4,DUT,RPA3,FOXK2,POU2F1,FEN1,PANK2,ABCB6,CLSPN,RAD51AP2,E2F3,TFAP4,LAGE3,RAB11B,CXorf58,CFDP1,RAD54L,MCM10,ATAD5,PSMC3IP,LTN1,SLC12A4,RFC1,C19orf57,BRCA2,YEATS4,EXO1,STRADA,HEATR6,E2F1,CEP152,PCNA,ARL15,STIL,CCNE1,WLS,NR1H3,CDC45,SLC1A5,FANCG,CENPU,BRI3BP,CCT5,PLAUR,TXNRD1,GABARAP,VAT1,SLC46A1,E2F7,CENPI,ATL3,CAMTA1,BTG1,BAZ1B,CEP57,PAICS,PLEKHH3,KIAA0101,METTL2B,EEF1G,XRCC2,GINS2,AP3D1,PPRC1,SEC22C,CCNE2,RAVER1,CASP8AP2,BIN1,CDC25A,RIF1,DCLRE1A,RBM15,GTF2A1,C4orf27,ZBTB5,CREBZF,XPO1,ZNF784,UHRF1,DHX40,MCM3,CSTF2T,MSH2,ABHD2,TBC1D1,IER2,RPA2,FAM161A,HNRNPF,ATAD2,AP1S2,UPP1,TRIM37,TPD52L2,IGSF8,TTLL9,HNRNPA0,LINC00273,SYPL1,TBC1D15,OGG1,CDK2,SLC25A3,ZNF367,PRKCSH,MUT,PRDM7,SLC25A42,RIC8B,RFC3,POLA1,FANCC,FDPS,MMAB,ATP2A1,PDE4DIP,MDC1,MFAP1,DNAJC9AS1,ZBTB8OS,UXT,MSH5,KITLG,UBE2T,NBR2,RFC4,CENPO,NUP155,PSMA1,PROSER1,CDC27,MIR17HG,KMT5C,CD3EAP,CDKN2C,PLCXD1,DPYSL2,HELLS,NOLC1,CDK5RAP3,HNRNPA1,HNRNPUL1,PFKFB4,CNTRL,DIAPH3,MCM4,AMIGO1,EBP,ARL6IP6,PHF20,ATAD3A,EEF1E1,RFWD3,AK2,STYK1,IMMT,PDS5A,RTTN,SRSF1,POLD3,TGOLN2,WDR74,DTL,DEK,HMGB2,PRPF40A,ZGRF1,HAUS8,DERA,BCL2L12,FDXR,YARS,RBM14,PPM1D,MUM1,LHX2,NUP153,WDPCP,RQCD1,MLEC,ZRANB3,CA5BP1,HIST1H2BK,MGST3,PPOX,ZCWPW1,VEGFA,TICRR,C3orf58,RNF167,HIST1H4I,MYC,EZH2,KLF11,WDYHV1,TRIM26,KIF25,DCTPP1,FAM222A,WDR76,MCM2,TMX1,HSD17B6,HIST1H2AM,BSG,RAD51B,CASP2,TTI1,UBC,NR2C2AP,CUX1,IRS2,FANCL,LMNB1,TUBB,ORC2,CDC7,ADAL,SHKBP1,ARHGEF40,CHEK1,PHF14,GTPBP1,VPRBP,ZNF131,SMC3,CTDSPL2,ABHD11,TCF19,RBL1,CDT1,XRCC3,SCUBE2,NFATC2IP,MLH1,DBR1,ATP5G1,SLC25A36,FANCD2,RRM1,PTK2B,BANP,AP4M1,CALM1 ncludesothers),MTHFD1,DNMT1,SLC20A1,MB21D1,NUSAP1,GFI1B,PPP1R13L,CAMK2N2,FANCI,OXSR1,CISD2,ZNF766,CPT2,MCM6,MAK,CENPN,DMC1,ZNF384,CHRAC1,SPOP,KNTC1,OGT,AP4B1,MYL6,HDAC6,SUZ12,PIM1,SPC25,FAM73B,MYBL2,ANXA4,NOP58,CHAF1A,ZNF687,EAF2,PPEF2,MBNL3,CDCA3,ASF1B,RAD51AP1,USP1,BTD,CDCA7L,TAF6,PHLPP2,TTLL7,AEN,TIMELESS,HLTF,NUP160,SPEN,EMSY,GCDH,AGFG2,DIS3,POLE,CLCC1,MCM5,NCAPH2,ESYT1,ZMYND19,DHX15,PLSCR1,PPP1R7,IPO5,LRR1,GMNN,HSPE1,ZBTB4,DHFR,RFX1,DDX11,DDX39B,NUP205,CDKN1A,RBM23,TMEM116,SLBP,FSCN1,LTBP4,DDB2,BRCA1,NUCB2,MIS12,PSMC3,TREX1,CENPH,GORAB,MED17,ANKRD30BL,TIPIN,PRPS1,RBFOX1,PAN2,TRA2B,SNRPB,C17orf64,GPD2

Supplemental Table 3: Functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
Cancer	E2F8	7.95E-24	RNF219,CLDN3,ELF2,FADD,NDE1,FAM104B,AAGAB,PPP2R5A,YOD1,DPP3,CDC6,CHST12,YIPF1,ZNF180,TATDN2,SST,TOP2A,C10orf106,RING1,LEMD3,WDR25,COL8A1,EFCAB12,ANO10,GBA,SLF2,RIN1,GBF1,WRAP53,ENPP6,PTPN12,MTAP,SUPT5H,PMAIP1,ZMYND8,ZNF219,NUDT1,SF3A2,TPM4,PRIM2,TMUB2,RFX3,CLIP1,FARP1,CNTLN,CUTA,ENO1,EIF1AX,SPCS2,FCF1,SNRPC,SEC22B,SH2B1,SKIDA1,TM9SF4,TRIM56,TPM3,PTP4A1,LEO1,RHEB,FURIN,TK1,NUP188,SKA3,TRIM24,HAUS1,TMEM127,PALLD,MCAT,GINS3,KANSL3,ANO6,CDCA7,CBLB,POLQ,SLX4IP,TMEM237,AHCTF1,SMOX,ALDH7A1,WNK1,TOP3B,SUCO,UBB,XPC,DLEU1,MINOS1-NBL1/NBL1,COASY,HRH1,FAM117A,FAM60A,NREP,SETX,ZNF524,ACSL1,CCDC159,MSH6,CALCR,TESK2,HCN3,USP24,PNPLA8,PLEKHA6,HNRNPA3,SMS,NAIF1,RNA45S5,CBX1,TRIM25,SRSF7,UTP6,FAM102A,TPR,KCNN4,RCOR3,ZBTB9,MMS22L,IER5,ARSK,CCDC167,SBF2,NAMPT,CAMLG,MRPL22,GUCD1,SHC1,CC2D1B,EFHC1,POU2F1,PANK2,AP1S1,ABCB6,CLSPN,LHFPL2,C3AR1,ATP11C,HIST3H2A,ZNF275,FAM117B,TFAP4,PHF8,C1orf216,CXorf58,DNAJC6,PEG10,PABPC4L,PATL1,SERBP1,MED9,ZMAT2,HMGXB4,CREB3L4,PPP6R2,NR1D2,RBKS,B3GNTL1,HES1,MYOCD,ATF2,HEATR6,DNAAF1,ALG10,KDM4B,ARHGEF12,ENOSF1,HINFP,HDLBP,TP53,STARD4,ARL15,ZNF782,G3BP2,CLN3,CDC45,TRABD2A,WLS,RUSC1,BRI3BP,RTN3,TCOF1,ABCD4,RXRB,KHSRP,SIL1,VAT1,CPEB3,CENPI,ATL3,KIAA0907,FHOD1,BRD4,SLC25A6,IRF2BP2,KAT6B,NUP214,BAZ1B,MARVELD1,PAICS,C2orf44,JPH2,PABPN1,CCDC22,PPWD1,IQGAP3,ABCA10,MRPS28,SPIDR,KRT1,FAM220A,VPS72,CDC25A,PFDN6,GTF2A1,GRB7,CREBZF,PSMC5,ARHGAP42,DHX40,SARNP,EIF3F,KCNH4,IER2,DIDO1,HNRNPF,ATAD2,ORAI2,TMEM123,COL12A1,IL1R1,ARMC1,EBI3,CAPN2,C19orf53,HMGCS1,MAP3K11,SNX5,GLI3,SMC4,PRKCSH,EIF3D,DLX4,DDX55,TAB1,ARNTL2,RIC8B,GAS6,POLA1,ZKSCAN4,CNGA4,EHBP1L1,ACAT2,ZBTB8OS,PWWP2A,BRMS1L,WAS,EXOC1,UXT,UGGT1,NCOA6,KITLG,HOXB6,KMT5C,SRD5A1,EZH1,FBL,PLCXD1,EVI5L,PPP1R12B,HIST1H2AB,PDLIM7,FANCE,CNTRL,CRYGB,HIST1H2BD,BUD31,GTF2H1,ARL6IP6,ANKRD11,PHF20,ELP5,FOXP1,NUFIP1,ATAD3A,NLRC5,BAG6,NEAT1,RBBP7,CNPY3,ERGIC2,CD68,NES,EME1,UCP2,PACSIN2,TGOLN2,TTF2,MYL12A,CDCA5,C19orf45,TSPAN3,HMGB2,PRPF40A,CEP250,TFB1M,CRTAP,EMC7,FDXR,EFNA4,PPM1D,ATF7IP,B9D1,YBX3,AGPAT3,ZNF860,AAAS,DLGAP3,MPI,TFEC,CAD,UBXN8,CYP39A1,HIST1H2BK,WARS,LRRC46,PGAP1,ATP1B3,HIST4H4,ROBO2,PDCD4,HIST1H4D,ZCWPW1,PTER,POGZ,IRF3,HIST1H3B,HERPUD2,HIST1H3F,HIST1H4E,HIST1H4H,HIST1H3G,CSTF1,TMEM38B,HIST1H4I,HIST1H4B,BLM,HIST1H2BC,HIST2H2BE,STT3B,VCP,TRIM26,GMPR2,RNF121,TBP,RBBP5,TMEM74,STK11IP,CDC37,LITAF,TMX1,RNF5,HIST1H2AG,HIST1H2AM,HIST1H2BG,WDR33,ZNF385D,TERF1,METTL3,INPP4A,CASP2,DENND5A,CAB39L,PPP6R3,CSRNP1,FANCL,LMNB1,TUBB,PXN,ORC2,PMEL,GNL3L,RIT1,GOLGB1,KBTBD4,TNIP1,UBE2Q1,SHKBP1,APC2,LGMN,CD2AP,VPRBP,NR4A3,MRPL37,SUGP2,ZNF230,TMEM69,CD274,SPRED2,LENG8,SNIP1,MTBP,NOP16,PUS7L,RPS11,RBL1,KIF1BP,RXFP4,SRP19,MUC4,SCUBE2,UBE2G2,SF3B5,ARHGAP1,TMEM60,RTN4,DNAJC14,PHKG2,POU4F1,TNXB,PHF12,AP2S1,SLC27A3,SYTL1,ITGA5,LIAS,JUNB,DCAKD,DCLRE1B,TCP11L2,PURA,TJAP1,C22orf39,MYOZ3,BTG3,BYSL,PARP14,SLC1A3,XRN2,XRCC4,SMURF1,EAF1,CCR2,ZNF384,QTRTD1,LRRC8A,SREBF1,CHRAC1,BBS4,BMF,CAP1,MBNL1,RPS14,TM4SF1,SUZ12,KHK,MYLPF,SPC25,C17orf53,ANXA4,PROB1,GREB1L,B4GALT5,CDK1,IL17RE,TMPRSS5,LIN28A,CDCA3,COX5A,TRPV4,NOD1,SGCA,MTMR11,UCKL1,VPS41,DGCR8,STRN,AEN,REL,GATAD2A,MTF2,MTR,LRPPRC,LEF1,STAT2,RGPD4 (includesothers),CABLES2,TIMELESS,TMEM258,CNOT1,DDX50,UBXN11,TTC23,ADGRE5,COPE,CLCC1,NCAN,ADPRHL1,RABEP2,NUBP1,LETMD1,CDK5RAP1,MCM5,NPL,C6orf89,P4HB,THBS3,WSB2,PHGDH,DHX15,PLSCR1,IQCD,IPO5,BLZF1,GMNN,NUP205,WDHD1,KCNK1,COPS4,PSMB3,TMEM116,YWHAB,NUCB2,RBMS1,MRPS18A,FNBP4,TOPORS,SKOR2,PSMC3,NUCKS1,CENPH,RNF181,FDFT1,SIRT2,NR1H2,POC5,PERP,SGTA,BPGM,RFC5,DLX6,ILF3,WDR53,ST7L,GPRC5A,DCTN5,SNRPB,TRA2B,IL12RB1,XRCC1,PPP1R1C,ALDOA,HNRNPL,ITGA7,CCNT2,ARGLU1,TCHP,PHRF1,NFKBIL1,UQCRH,OSGEP,NFKBIB,SCARB2,MRPS23,FAM212B,KHDC1,NCOA7,OTUD5,DERL3,SMAP2,GPR146,ANP32E,C19orf48,CDC123,THNSL1,CWC22,TRIM45,SFPQ,ZSWIM3,FCMR,MAP3K4,CCDC30,NHLRC3,RECQL,MALSU1,FKBP1A,FBXO46,PEA15,FKBP5,RFC2,SIN3A,PHPT1,EFNA1,HK2,TSG101,CEP128,ARID4A,PTGS2,LUC7L2,SLC43A3,CCDC82,CDC23,C1orf35,PARP11,MRPS25,AKR1D1,TMEM209,CLTC,PAWR,KIAA0825,CDK8,TIMM21,EHBP1,NENF,GMPS,TOR3A,RRP12,HAPLN3,SMARCA5,METTL2A,CENPL,TROVE2,MRPL30,QSER1,TMEM120B,RCC1,CUEDC1,PRICKLE3,MYO1F,LRRC49,AIMP1,LIPT2,MRPL24,ZNF273,ABCA4,TMEM55B,ACTR10,CCDC115,KIFC1,FOXK2,DPH2,SART3,LAMC1,RAP1A,CRADD,MFN2,BTBD10,LCMT2,RGS2,PRKCE,STAP2,MCM10,ZWILCH,PRCC,ZNF446,TFAP2A,COG8,RFC1,VCAN,STAT6,RAP1B,C6orf62,GPRIN1,RHOV,KRT17,YEATS4,EXO1,STRADA,SCGB1D2,MED31,E2F1,CDK17,STIM1,BAZ2A,PCNA,ARRB1,DDX18,ADAM17,RAD52,LRMP,PDE7A,CCNE1,SNRPA1,NR1H3,DHRS1,SLC1A5,FANCG,MOCOS,TOE1,SFN,USP37,UNC119,COPS7B,CD99,ABR,GABARAP,SAP30BP,ACIN1,IWS1,KBTBD2,PDZD2,CAMTA1,SOAT1,KPNA6,PSMD13,LPXN,C16orf95,COG4,LAPTM4A,BTG1,E2F6,CEP97,TCEA1,IRF9,CEP57,TBL1X,C14orf159,SNRPD1,RNFT2,FLII,ING2,DDX23,GINS2,AP3D1,RGCC,ISY1,RMND1,SLC14A2,SRSF6,N4BP2L2,MARK3,C1orf123,PIK3R4,RSPH3,CCDC12,XPO1,POLR2M,MUS81,SIRT5,LIPH,RPA2,HSPD1,AP1S2,UPP1,GATA6,KRT86,BPNT1,NCAPG2,TRIM37,KCTD21,ZP3,LINC00273,HMGN5,NFKB1,FOXL1,ITGAX,UBE2N,MED24,ZNF451,CXCL2,BRPF1,TPCN1,ZNF367,POM121/POM121C,ABCF3,ARID4B,WBP1,CEP95,ZRANB2,MEF2A,FANCC,SLC35C2,AQR,LRIG1,PSMB2,RFC4,RIOK3,KPNA1,C9orf84,CDKN2C,KCNH3,DSCR3,ANKRD44,HNRNPUL1,RAD9B,BUD13,POLR3A,TTC9C,CIZ1,KIAA0753,POLD1,EEF1E1,ZCCHC9,HOXD13,ASH2L,HRH4,TMEM57,PSMC1,USP4,SERPINA12,KRI1,WDR74,TMEM230,DHTKD1,FAM111A,C12orf73,TADA3,HAUS8,INTS4,FMNL1,RANBP1,PHF3,LMNA,TRAPPC9,PEX12,CA5BP1,TMPO,PPOX,KRT7,SLC7A10,TICRR,PLXDC1,TUSC1,TRAPPC5,PMVK,EZH2,WDR81,HECTD3,FAM222A,RNF168,WDR76,VPS52,GPR137,OCIAD1,GNAI2,CDC20B,RPIA,SPRTN,TTI1,UBC,MAP3K7,SGPL1,TAX1BP1,SSBP3,GANAB,POLR2H,THG1L,ZFP62,CHTOP,CIT,UCHL3,LRFN3,HSPBAP1,RHOF,ST7,TSSK6,PIP5KL1,SAMD9,NCAPD3,CDT1,MCEMP1,DBR1,SLC25A17,NFIA,COPS3,TMEM91,RRM1,METTL13,PHF1,PRPF38A,BANP,EIF3H,DCLRE1C,AMOTL2,AP4M1,MCL1,SGOL2,DNMT1,PPIL1,HIPK1,MRPL18,RNF213,LIMCH1,MB21D1,KRCC1,MPDZ,GLO1,RPRD2,SIGMAR1,ZNF766,MTFR2,PFKM,MCM6,CCAR2,HYAL3,CENPN,ULBP2,SIPA1L3,LRCH1,MAP3K12,SPOP,OGT,SOS1,CREBRF,ZCCHC8,AP2A1,NOP58,CHIC2,HNRNPA2B1,TRA2A,PTMA,KIAA1211,LYST,MKRN3,POLR2A,NQO2,HNRNPC,ATP6AP1,FSTL3,DENND6A,TTC25,LETM2,MRE11A,BACE1,TCTEX1D2,C16orf62,UBA7,FAF1,HLTF,DAPK3,CRCP,SLC35B2,ARF4,DUSP7,ESYT1,ZNF224,MYNN,RPS26,PPP1R7,ZBTB4,RFX1,ZNF837,KLHL15,FOXN2,MUL1,ZFHX4,ARFGEF2,UGGT2,CANX,ICAM2,C20orf196,FRG2C,GORAB,RPS3,EGR3,PHLDB1,PCIF1,ICE1,ZCRB1,WHSC1,KDM6B,VRK2,AUTS2,C11orf58,SPSB1,BIN3,STK24,DBF4,DCAF16,DDX39A,MRPS18B,PIAS3,FKBPL,KTI12,LRRC59,SENP5,SYDE1,SEMA4B,C8orf44SGK3/SGK3,FAM96A,RPS6KC1,FOXG1,TMEM102,NRAS,GTPBP3,ZC3H10,HAT1,ZC3HAV1,MAP3K1,PARP3,PHLDA3,ERGIC3,TMEM97,DLAT,SLCO4A1,ERCC5,FAIM,PET100,ZNF791,VTI1A,GIN1,ARHGEF19,PFN1,PPP1R37,PER1,LSM14B,CELF4,OLFM1,VPS51,NASP,APOA1BP,CEP44,ARMC5,DCTN4,PTPRE,DENND1A,ZNF697,ZMYM4,HAX1,IPO11,RRM2,GGCX,ZC3H7A,SKP2,UCHL5,CCDC9,FBXO9,PLB1,BTN2A1,UBE2QL1,UNG,GGCT,IGF2BP3,CACYBP,BRIP1,IMPG1,PUS10,CCND1,MASTL,OSGEPL1,ATP1A2,TRIP13,NDUFAF3,E2F8,PPP2R3C,KIF18A,SLC39A8,PRR5L,FCHSD2,CDK4,TTLL3,GABRQ,COQ5,UCK2,LRRCC1,TOMM40,E2F3,MYPOP,PHLDB2,ZNF335,HRASLS2,FAM129B,HSPB6,VARS2,CFDP1,PSRC1,MED26,PSMC3IP,LTN1,G3BP1,MALAT1,C19orf57,ZCCHC11,GRWD1,BRCA2,RNF138,IKBIP,MTMR4,MAFA,CEP152,STIL,CENPU,CCT5,UBAP1,POLE4,TXNRD1,ZNF181,ANKRD13A,DIEXF,SF3B4,JTB,PLEKHH3,SLC2A8,METTL2B,SUCLG1,PNKP,TEX10,AXDND1,CCDC189,MMACHC,KAT5,RIF1,KHDRBS1,FAM185A,CLPTM1L,ARL11,MCM3,MSH2,PPCDC,CHRNB1,EFCAB7,WDR82,TPD52L2,TTLL9,TBC1D15,NLGN3,SP4,OGG1,IDH3B,PCNXL2,IGFLR1,ITPRIP,DLGAP1,TM2D1,STK19,ERI3,PPM1B,FDPS,MMAB,RASGRP4,SLC22A4,MDC1,KATNAL1,CMIP,WNT2B,ANAPC5,VANGL1,CFLAR,AARS,HIPK3,LUC7L3,CD160,COX17,ABCD3,UBE2T,PSMA1,SCP2,ZBTB45,NSUN3,NKD2,UROD,DPYSL2,OGFOD2,FAM3D,NOLC1,SUGP1,PFKFB4,RBAK,MCM4,PRPF31,AMIGO1,EBP,ERCC1,C2orf81,CCNT1,SRSF3,ASRGL1,RFWD3,KIF11,POLR1D,LCN12,AK2,IMMT,PYM1,EIF4A1,MEF2D,TPX2,NUMBL,SLMAP,SRSF1,NCOA5,POLD3,WNT7B,NME1,RAD51C,RALGDS,DEK,SLC25A45,HERC5,HSP90AB1,IGBP1,MAP4,GADD45GIP1,RBM14,C6orf47,FLCN,BNIP3L,CD320,NUP153,TMEM245,GNAI3,SMUG1,TMOD3,PRKCH,MGST3,ZNF668,NSL1,HEXIM1,MLLT11,MYC,COX6A1,DUSP6,ZNF143,POLR3C,KIF25,AOAH,L3MBTL2,KDM5A,USP54,INTS5,ULK4,BSG,TXNDC9,KAT7,PAFAH1B3,AHCYL2,ZBTB43,NBR1,ATM,PEX16,MCM8,CDC7,IDE,SPPL2A,GAPDH,AHCYL1,ARHGEF40,FAM208A,RTP5,CLASP2,ZNF131,EDEM2,HIST1H2BO,BIRC3,ALDH3A2,NEK8,SMG7,S100A10,PHF11,C12orf45,GDPD4,XRCC3,RPL19,GPRC5B,DLG1,CENPK,NOL12,MLH1,EPB41L2,ACYP1,B3GNT5,FANCD2,RAB28,CCDC97,LONP1,STAT5B,KRR1,ARHGAP39,EHD2,LFNG,RNASEH2A,SPATA5,SLFNL1,CALM1 (includes others),UBE4B,TNS4,DNAJC2,RPS20,KIAA1755,GFI1B,PPP1R13L,TFAM,ALG3,NAA60,OXSR1,ZC3H18,PNP,CPT2,TXNRD2,MON1B,GNB2L1,GMCL1,KNTC1,CENPQ,EIF2S3,HDAC6,PIM1,GARNL3,FAM73B,C1RL,CEACAM3,ASTE1,EIF2AK3,C11orf65,ZBTB7B,INADL,RAD51AP1,CCT7,UBXN4,CDCA7L,ABI1,RUSC2,MED19,GNL1,SPAG5,ZNF317,UNC13A,SEMA6A,NAF1,PRPF3,ISG20L2,NUP160,USE1,SPEN,TRIM33,ANK3,KIF2C,NUDT2,AGFG2,DIS3,TNPO3,LRRC23,TMEM39B,AP5M1,ZMYND19,LGR4,TRAPPC3,MOCS3,TNFSF9,ZFYVE16,NEK4,IDO2,DHFR,XRCC5,GLYCTK,SUPT16H,FSCN1,CLK2,LTBP4,DDB2,DHRS7B,FBXL19,FBXO4,MIS12,CENPV,FH,TREX1,FAM83A,GLI2,DLG4,ATF4,TIPIN,MAP3K2,KIF24,RNGTT,ZNF263,PRPS1,FHL2,PKN2,PAN2,C17orf64,GPD2,ZNF592,DAPK2,HMGN2,MTCH1,HYDIN,CD300A,CALU,PRRC2A,ELL3,CBX3,KRT36,FAM173B,EEF1A1,PMM1,APEH,TXNIP,POLG2,CDK5RAP2,MYL6B,LRRC41,SMC2,ENAH,OSBPL9,TARS,NOL6,FST,FBXO5,CCDC61,DUSP11,C17orf74,EIF4A2,CNOT3,POLRMT,SIK2,SECISBP2,CREM,SEC24A,RNF135,LRTOMT,ZNF823,TLDC2,TMEM41B,GANC,DSN1,EXOSC9,KCTD2,PAN3,FOXRED1,HIVEP1,RAD1,GPR180,PARP1,DAXX,GART,CHMP2B,DUS2,ADAMTS12,TACO1,TMEM59,SPG7,TAOK2,AFAP1,RPL7A,C12orf57,TNRC6B,USP21,CCDC173,ENSA,CYB5R4,CDKN2D,ERBB2,ZNF146,UMPS,C2CD3,SLC25A25,U2SURP,ADAM15,ATP6V1A,PREB,SLC38A1,NAA40,NPAS4,CDKN1B,SHANK2,CIC,RPL27,PRIM1,SESTD1,TMEM167B,GALNT9,MT2A,DNTTIP2,F2RL1,FBXL20,SMC1A,TAF1A,EED,LIG1,IL15RA,FAM111B,PTN,PPIL3,E2F2,RPL37,DDX60,EPB41L5,SNRPG,NOC3L,PPIA,SNRPE,VPS45,RBM3,KMT5A,C1orf174,CD44,WEE1,MSI2,SYNGR4,BZW1,TRIM28,DUT,ELK3,RPA3,CAND1,MPV17,ARHGAP21,TBCCD1,ETV1,CLDN7,CBX5,CCDC94,PUM2,LRCH4,TROAP,TOP3A,PR14,KLHL20,P4HTM,JUND,LAGE3,ZNF443,RAB11B,PCNP,MATR3,TAF15,GNAZ,RAD54L,SREK1IP1,GLB1L3,ATAD5,NUMA1,CHAC1,LARP4,ZNF101,EIF2S1,HPCAL1,CHMP7,RARA,MTMR9,ZFYVE19,OSBPL5,GALNT1,PPP1R3F,ATP5SL,TESK1,C3orf38,KCMF1,SUPT7L,FAM234A,SUV39H1,ECE1,YBX1,RPS21,NPM1,CUL3,PPM1G,DHX8,SURF1,PLAUR,WDR24,C12orf76,SHQ1,CLK1,AHSA1,TSC22D1,C15orf39,TAF6L,RSPH10B/RSPH10B2,THOC2,EHMT1,WHSC1L1,SAC3D1,TRIP12,KIAA0101,TRAPPC4,BASP1,ZNF461,CHM,EEF1G,XRCC2,SYNCRIP,SYCE2,PPRC1,GORASP2,SRRM1,TTI2,HKR1,SEC22C,PRPF40B,NGRN,BRD2,RELT,RAVER1,CCNE2,CASP8AP2,PRPF6,NFIB,NUP107,RANBP3,DCLRE1A,SPATS2,C4orf27,ZBTB5,CYP46A1,RRAGB,THAP5,UHRF1,TUBA1B,CSTF2T,RAD18,DGKA,EXOSC2,VEZF1,FAM161A,ZNF613,HNRNPA0,TBX10,UBE3C,WASF2,POLR1E,PRSS16,RFX2,BUB3,CDK2,TLK1,ID3,RASSF4,GOLPH3,KLHDC3,TACC1,RFC3,COL7A1,TAGLN2,TNFRSF1A,LAMA3,MAPK10,ATP2A1,PDE4DIP,GDI2,MFAP1,PNISR,PES1,RPS13,DERL2,NDUFA8,MARS,HMGB1,PCSK7,HMGA2,SRP54,GPS2,mir-154,CENPO,NUP155,MBIP,ARID3B,GOSR2,DARS,PTK2,HELLS,COQ4,BCL6,CDK5RAP3,ZNF684,GK,HNRNPA1,RPS9,SOCS6,AGPAT4,DIAPH3,IFI16,CNTD1,PAK1IP1,SERPINI1,SHMT2,MRRF,MCM7,KAZALD1,CLIC1,PDS5A,RTTN,HSPA8,SLFN13,RPL41,MBD1,SENP3,NCALD,TAF2,DTL,STK35,SP1,NUPL2,ZGRF1,POP5,DERA,BCL2L12,ITM2B,BHLHE40,YARS,DPM2,KLHL28,FOXK1,ZNF678,LRP8,RGL2,DDX3X,HAUS4,WDPCP,MLEC,ZRANB3,HIST2H2AB,ORC3,ZNF430,PARP4,DROSHA,MECOM,C3orf58,MELK,RNF167,RBM39,TRANK1,FBXO11,CTDSP2,SAMD13,DCTPP1,CENPA,MCM2,TOM1L2,CTNND1,SCAMP3,WBP11,RAD51B,C1orf112,LAS1L,NR2C2AP,SGTB,DHPS,RGMA,CMPK1,TNFRSF6B,FAM174B,ATF6B,CHEK1,PHF14,GTPBP1,MUTYH,PNN,CYCS,SMC3,GLA,RPS19,CAPN3,C2,SRP9,CTDSPL2,ACTB,NUCB1,TCF19,ARF3,VMP1,CYP1B1,CTTNBP2NL,TAF1,MDM4,PALD1,NFATC2IP,NDUFAF6,TSHZ2,CNOT2,ACO2,NUP35,OXR1,PLAC8,ATP5G1,SLC25A36,NID2,PANX1,PTK2B,TUT1,ACE2,ZNF142,RNASE4,GNAT1,SAE1,TMEM79,STK4,CTSZ,PPP1CC,FOSL2,MTHFD1,ZBTB20,PPIH,SLC20A1,AIDA,NUSAP1,DPEP1,TARS2,ELP3,SNRNP200,CAMK2N2,FANCI,SEC11A,FUCA2,TEC,MEF2B,PHF19,NDUFV2,IGSF11,CCDC51,DMC1,CCNB1IP1,RASA2,HLA-E,IGF2BP1,ROBO1,TRIM41,VCPIP1,NOL8,B2M,FOXF2,ABI2,MYL6,PCGF2,NEDD4,NDUFS2,AGGF1,CCNA2,CHAF1A,GNG2,RAD51,ZNF687,EAF2,AQP11,MGEA5,PAM,USF3,ESPL1,DCTN2,ONECUT1,USP1,N4BP2,BTD,RXRA,SLC16A6,TIMM8A,TAF6,PHLPP2,FADS2,CCNL1,COPS7A,TFRC,HMMR,NNT,DSCC1,C14orf80,ZNF184,SEC31A,SPI1,RAB5B,KIAA0895L,SNX8,MADD,POLE,CLCA2,SERPINE1,ALDH3A1,LRRK2,NCAPH2,CCDC43,BBC3,OSER1,MAPRE1,CCBL1,TAF3,HSD17B12,DEDD,RRP7A,SLC29A1,C5orf22,TXNDC16,STAMBP,C16orf91,RPL9,LDLR,EIF2S2,DDX11,DDX39B,ERH,CCDC174,CDKN1A,TCEB1,TBC1D17,EIF2B1,RPL3,SLC25A14,EIF6,SLBP,NONO,ASGR2,M6PR,ESYT2,TIGD3,ABHD6,BRCA1,MNT,TRIP10,TNFAIP1,PTPN2,MED17,EEF1B2,PDHA1,STMN1,WRN,SCYL3

Supplemental Table 3: Functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
DNA Replication, Recombination, and Repair	E2F7	1.38E-21	POU2F1,FEN1,RFC3,POLA1,FANCC,ABCB6,VPRBP,CLSPN,MDC1,E2F3,SMC3,MSH5,KITLG,TFAP4,UBE2T,RBL1,CDT1,XRCC3,CDC6,CBX3,KMT5C,TOP2A,RAD54L,MCM10,CDKN2C,CDK5RAP2,SYDE1,MLH1,PSMC3IP,HELLS,EBNA1BP2,RFC1,CDK5RAP3,HNRNPA1,FANCD2,RRM1,HAT1,PTK2B,BRCA2,MCM4,SETMAR,ZNF219,RECQL,EXO1,CYR61,RMI2,DNMT1,E2F1,RFWD3,NUSAP1,CEP152,PCNA,SUMO1,ORC1,PDS5A,FANCI,STIL,CCNE1,CDC45,RFC2,FANCG,SIN3A,MCM6,DMC1,DSN1,POLD3,NASP,DTL,KNTC1,DEK,PARP1,DAXX,HMGB2,PIM1,SPC25,MYBL2,CHAF1A,BAZ1B,CEP57,PPM1D,ASF1B,MUM1,SKA2,KIAA0101,XRCC2,USP1,RAD51AP1,RRM2,POLA2,CDKN2D,ZRANB3,AEN,CCNE2,UNG,VEGFA,CDC25A,HIST1H4A,BIN1,TIMELESS,HLTF,RIF1,DCLRE1A,HIST1H4I,BRIP1,MYC,EZH2,XPO1,POLE,UHRF1,MCM3,NCAPH2,MSH2,TNFAIP8,KIF25,RPA2,SMC1A,PPP1R7,MCM2,IPO5,LIG1,GMNN,BSG,SETX,ZBTB4,MSH6,E2F2,CDKN1A,RAD51B,CASP2,TTI1,DDB2,BRCA1,OGG1,IRS2,MIS12,FANCL,TREX1,CENPH,CDK2,ORC2,WEE1,CDC7,UCK2,MMS22L,TIPIN,DUT,RPA3,SNRPB,CHEK1
	E2F8	5.70E-20	XRCC1,HMGN2,STK24,FADD,DBF4,NDE1,MTCH1,PPP2R5A,AAGAB,ELL3,CDC6,CBX3,TOP2A,POLG2,RING1,CDK5RAP2,SYDE1,SMC2,NRAS,SLF2,HAT1,PARP3,PHLDA3,SFPQ,SUPT5H,ZMYND8,ZNF219,RECQL,NUDT1,BTC,ERCC5,MORF4L1,SUMO1,PEA15,CREM,PFN1,RFC2,SIN3A,ENO1,DSN1,TSG101,SUPT4H1,NASP,RAD1,SH2B1,ARID4A,PARP1,DAXX,CHMP2B,PTGS2,PTPRE,TAOK2,FURIN,SKA2,SKA3,RRM2,CDKN2D,SKP2,ERBB2,POLQ,UNG,SMOX,CLTC,CACYBP,PAWR,BRIP1,TOP3B,CDKN1B,CCND1,XPC,SMC1A,LIG1,SMARCA5,SETX,PTN,TRIP13,MSH6,E2F2,KIF18A,RCC1,CBX1,CDK4,PPIA,AIMP1,KMT5A,SF3A3,WEE1,MMS22L,TRIM28,ABCA4,DUT,RPA3,KIFC1,SHC1,POU2F1,CBX5,ABCB6,SART3,CLSPN,RAP1A,E2F3,TOP3A,TFAP4,RAD54L,MCM10,ZWILCH,PRCC,PSMC3IP,RFC1,STAT6,RAP1B,BRCA2,EXO1,ATF2,RARA,KDM4B,E2F1,HINFP,CEP152,BAZ2A,TP53,PCNA,ARRB1,RAD52,STIL,SUV39H1,CCNE1,SNRPA1,FANCG,YBX1,NPM1,CCT5,P3H4,PPM1G,SFN,ACIN1,BRD4,TAF6L,SF3B4,TCEA1,E2F6,BAZ1B,CEP57,EHMT1,SAC3D1,TRIP12,KIAA0101,ING2,PNKP,XRCC2,SYCE2,SPIDR,BRD2,CCNE2,PRPF6,CDC25A,KAT5,RIF1,DCLRE1A,XPO1,MUS81,UHRF1,RAD18,MCM3,MSH2,CDC14B,RPA2,HSPD1,ARL8B,ATAD2,NCAPG2,CAPN2,OGG1,NFKB1,BUB3,CDK2,UBE2N,TLK1,ID3,SMC4,ARID4B,RFC3,POLA1,FANCC,TNFRSF1A,MDC1,HMGB1,ABCD3,NCOA6,KITLG,UBE2T,HMGA2,RIOK3,KPNA1,KMT5C,CDKN2C,FBL,PTK2,HELLS,BCL6,HNRNPA1,RPS9,FANCE,RBAK,MCM4,IFI16,CIZ1,ERCC1,MCM7,POLD1,BAG6,RFWD3,RBBP7,KIF11,PDS5A,ASH2L,HSPA8,DGKZ,MEF2D,TPX2,EME1,POLD3,DTL,RAD51C,SP1,NME1,FAM111A,DEK,CDCA5,HMGB2,BANF1,ACTL6A,CDC42,ATF7IP,FLCN,DDX3X,LMNA,GNAI3,SMUG1,ZRANB3,TMPO,PRKCH,ORC3,HIST4H4,HIST1H4D,POGZ,IRF3,HIST1H4C,HIST1H3B,HIST1H4A,MELK,HIST1H3F,HIST1H4E,HIST1H4H,HIST1H3G,HIST1H4I,HIST1H4B,BLM,MYC,EZH2,VCP,KIF25,TBP,RBBP5,RNF168,CENPA,RNF169,MCM2,CTNND1,BSG,GNAI2,TERF1,RAD51B,KAT7,CASP2,SPRTN,TTI1,MAD2L1BP,FANCL,ATM,ORC2,PXN,MCM8,CDC7,CIT,CHEK1,MUTYH,VPRBP,NR4A3,CYCS,SMC3,MTBP,PRIMPOL,PUS7L,VMP1,NCAPD3,RBL1,CDT1,XRCC3,CYP1B1,MDM4,SF3B5,MLH1,ARHGAP1,ACO2,EBNA1BP2,FANCD2,RRM1,PTK2B,PHF1,BANP,LONP1,SYTL1,STAT5B,DCLRE1C,ITGA5,RNASEH2A,PPP1CC,MCL1,DNMT1,DCLRE1B,ZBTB20,HIPK1,NUSAP1,DNAJC2,PURA,ELP3,SNRNP200,TFAM,FANCI,NAA60,PNP,MCM6,XRN2,XRCC4,DMC1,NOL8,MAP3K12,KNTC1,LSM4,SNRPD2,PCGF2,PIM1,SPC25,CCNA2,CHAF1A,RAD51,CDK1,MGEA5,ESPL1,DCTN2,HNRNPC,USP1,RAD51AP1,N4BP2,POLA2,SYF2,GNL1,MRE11A,COPS7A,APITD1/APITD1-CORT,AEN,SPAG5,GATAD2A,REL,DSCC1,LEF1,TIMELESS,HLTF,SPI1,TRIM33,KIF2C,TNPO3,POLE,RNASEH2C,NUBP1,ALDH3A1,NCAPH2,TNFAIP8,BBC3,PPP1R7,IPO5,DEDD,GMNN,SLC29A1,NEK4,STAMBP,ZBTB4,LDLR,XRCC5,CDKN1A,WDHD1,SUPT16H,DDB2,BRCA1,TOPORS,MIS12,CENPV,TREX1,CENPH,TNFAIP1,GLI2,SIRT2,WRN,STMN1,RPS3,TIPIN,NABP2,PKN2,WHSC1,SNRPB,DHX9,CASP8
Cell Cycle	E2F7	3.44E-17	RFC3,FEN1,POLA1,FANCC,VPRBP,CLSPN,MDC1,HNRNPD,E2F3,SMC3,CCNT2,PKMYT1,MSH5,KITLG,TFAP4,RBL1,CDT1,XRCC3,CDC6,CDC27,MIR17HG,KMT5C,TOP2A,RAD54L,MCM10,CDKN2C,LEMD3,CDK5RAP2,MLH1,PSMC3IP,HELLS,EBNA1BP2,NOLC1,RFC1,CDK5RAP3,FANCD2,RRM1,HAT1,PTK2B,BANP,BRCA2,DIAPH3,MCM4,SETMAR,FBXO5,ZNF219,RECQL,YEATS4,EXO1,CYR61,STRADA,RMI2,CALM1 (includes others),DNMT1,E2F1,RFWD3,NUSAP1,CEP152,PCNA,GFI1B,PPP1R13L,PDS5A,CAMK2N2,STIL,CCNE1,RFC2,CDC45,FANCG,DMC1,DSN1,SRSF1,NASP,PLAUR,DTL,KNTC1,EGR1,E2F7,CENPI,DEK,DAXX,PARP1,HMGB2,PIM1,SPC25,PRPF40A,MYBL2,CHAF1A,RHEB,HAUS8,BCL2L12,CDC23,BTG1,RBM14,PPM1D,CEP57,ING3,SKA2,KIAA0101,NUP153,XRCC2,USP1,RAD51AP1,CDKN2D,ZRANB3,TAF6,CCNE2,CASP8AP2,VEGFA,CDC25A,AATF,RNF167,DCLRE1A,KIF2A,ZBTB5,MYC,XPO1,EZH2,POLE,UHRF1,MCM3,NCAPH2,MSH2,KIF25,RPA2,PLSCR1,SMC1A,PPP1R7,MCM2,IPO5,LIG1,GMNN,DHFR,DDX11,E2F8,MSH6,E2F2,CDKN1A,RAD51B,CASP2,UBC,TTI1,DDB2,BRCA1,CUX1,IRS2,MIS12,FANCL,LMNB1,TUBB,CENPH,CDK2,ORC2,CD44,WEE1,CDC7,MMS22L,TIPIN,RPA3,SNRPB,CHEK1
Cell Cycle	E2F8	1.04E-18	HMGN2,XRCC1,FADD,DBF4,NDE1,CCNT2,PPP2R5A,CDC6,SST,TOP2A,TXNIP,SENP5,LEMD3,CDK5RAP2,SMC2,OSBPL9,FOXG1,NRAS,GBF1,CDC123,HAT1,MAP3K1,SFPQ,SUPT5H,FBXO5,ZMYND8,ZNF219,RECQL,NUDT1,BTC,FKBP1A,MORF4L1,PEA15,CREM,PFN1,CLIP1,PER1,RFC2,DSN1,TSG101,SUPT4H1,NASP,RAD1,SH2B1,PARP1,DAXX,CHMP2B,PTP4A1,PTGS2,RHEB,TAOK2,CDC23,RPL7A,SKA2,SKA3,TRIM24,HAUS1,SKP2,CDKN2D,ERBB2,AHCTF1,CLTC,WNK1,CDK8,PAWR,HAUS5,TOP3B,CDKN1B,CCND1,XPC,MASTL,F2RL1,SMC1A,LIG1,SMARCA5,PTN,TRIP13,E2F8,CALCR,MSH6,E2F2,KIF18A,ARPP19,RCC1,CDK4,CBX1,TRIM25,RBM3,TPR,KMT5A,AIMP1,SF3A3,WEE1,CD44,MMS22L,NAMPT,RPA3,KIFC1,SHC1,POU2F1,EFHC1,CLSPN,E2F3,MFN2,JUND,TFAP4,PHF8,PRKCE,MYO19,RAD54L,MCM10,ZWILCH,PRCC,PSMC3IP,NUMA1,RFC1,VCAN,STAT6,BRCA2,HES1,EIF2S1,MYOCD,YEATS4,EXO1,ATF2,STRADA,RARA,KDM4B,E2F1,HINFP,CEP152,BAZ2A,TP53,PCNA,ARRB1,RAD52,STIL,SUV39H1,CCNE1,SNRPA1,FANCG,YBX1,NPM1,CUL3,PPM1G,SFN,USP37,PLAUR,ACIN1,CENPI,CLK1,BRD4,TSC22D1,TAF6L,NUP214,SF3B4,E2F6,JTB,BTG1,BAZ1B,IRF9,CEP57,EHMT1,THOC2,SAC3D1,KIAA0101,ING2,XRCC2,IQGAP3,SYCE2,GORASP2,RGCC,SPIDR,CCNE2,CASP8AP2,PRPF6,PIK3R4,CDC25A,KAT5,DCLRE1A,KIF2A,ZBTB5,KHDRBS1,XPO1,PDXP,THAP5,MUS81,PSMC5,TUBA1B,UHRF1,RAD18,MCM3,MSH2,CDC14B,RPA2,ARL8B,GATA6,NCAPG2,CAPN2,NFKB1,MAP3K11,BUB3,CDK2,ID3,SMC4,DTYMK,TAB1,ARNTL2,GAS6,RFC3,POLA1,FANCC,TNFRSF1A,MDC1,HNRNPD,PES1,WAS,LRIG1,HMGB1,KITLG,HMGA2,GPS2,mir-154,RIOK3,KPNA1,KMT5C,CDKN2C,DARS,PTK2,HELLS,BCL6,NOLC1,CDK5RAP3,RPS9,PDLIM7,RAD9B,PTGES3,DIAPH3,IFI16,MCM4,GTF2H1,CIZ1,ERCC1,KIAA0753,CCNT1,SRSF3,RMI2,MCM7,POLD1,RFWD3,RBBP7,KIF11,PDS5A,HSPA8,NES,DGKZ,TPX2,EME1,SRSF1,TAF2,DTL,NME1,RAD51C,SP1,CDCA5,DEK,HMGB2,PRPF40A,BANF1,HERC5,CEP250,TADA3,HAUS8,ACTL6A,MAP4,BCL2L12,BHLHE40,CDC42,RBM14,PPM1D,FLCN,ING3,CD320,FOXK1,NUP153,RANBP1,DDX3X,LMNA,GNAI3,RGL2,HAUS4,CDKL1,ZRANB3,TMOD3,PRKCH,TMPO,ORC3,HEXIM1,MECOM,MELK,RNF167,BLM,MYC,EZH2,VCP,KIF25,CENPA,KDM5A,MCM2,CDC37,CTNND1,GNAI2,TERF1,RAD51B,CASP2,LAS1L,UBC,TTI1,MAP3K7,MAD2L1BP,LMNB1,TUBB,ATM,ORC2,MCM8,UBE2D3,CDC7,CIT,CHEK1,CD2AP,VPRBP,NR4A3,PNN,SMC3,CD274,MTBP,PRIMPOL,NCAPD3,RBL1,CDT1,XRCC3,CYP1B1,OMG,TAF1,MDM4,DLG1,SF3B5,MLH1,ARHGAP1,PLAC8,EBNA1BP2,FANCD2,RRM1,PTK2B,BANP,STAT5B,DCLRE1C,ITGA5,JUNB,PPP1CC,FOSL2,CALM1 (includes others),MCL1,DCLRE1B,ZBTB20,DNMT1,NUSAP1,PURA,SNRNP200,GFI1B,PPP1R13L,CAMK2N2,BTG3,XRCC4,DMC1,CCNB1IP1,SREBF1,GNB2L1,BBS4,CAP1,VCPIP1,MAP3K12,KNTC1,LSM4,TM4SF1,SNRPD2,PCGF2,PIM1,SPC25,CCNA2,CHAF1A,RAD51,PTMA,EIF2AK3,CDK1,MGEA5,LIN28A,POLR2A,ESPL1,DCTN2,HNRNPC,USP1,RAD51AP1,SYF2,RXRA,TAF6,MRE11A,COPS7A,TFRC,SPAG5,REL,MTF2,UBA7,LEF1,RGPD4 (includes others),SPI1,AATF,TRIM33,KIF2C,DAPK3,TNPO3,MADD,POLE,NUBP1,ALDH3A1,CDK5RAP1,NCAPH2,C6orf89,PLSCR1,PPP1R7,MAPRE1,IPO5,GMNN,NEK4,DHFR,DDX11,XRCC5,CDKN1A,WDHD1,TCEB1,EIF6,YWHAB,SUPT16H,DDB2,BRCA1,MIS12,FBXO4,CENPV,MNT,NUCKS1,CENPH,PTPN2,GLI2,SIRT2,NR1H2,STMN1,WRN,RPS3,TIPIN,NABP2,PBX1,FHL2,PHB2,PKN2,WHSC1,DHX9,SNRPB,CASP8,NFE2L2
Cellular Growth and Proliferation	E2F7	7.15E-08	FEN1,RFC3,GTPBP1,POLA1,ABCB6,VPRBP,FANCC,ZNF131,CLSPN,ALDOA,HNRNPL,HNRNPD,E2F3,SMC3,UXT,KITLG,TFAP4,TCF19,RBL1,RFC4,CDT1,CDC6,CDC27,MIR17HG,KMT5C,CFDP1,TOP2A,MCM10,CDKN2C,LEMD3,MLH1,DPYSL2,SLC12A4,HELLS,EBNA1BP2,ATP5G1,RFC1,NOLC1,CDK5RAP3,FANCD2,HNRNPA1,RRM1,HAT1,PTK2B,BRCA2,MTAP,MCM4,SETMAR,PMAIP1,RECQL,YEATS4,CYR61,CALM1 (includes others),MTHFD1,DNMT1,ATAD3A,EEF1E1,E2F1,SLC20A1,EIF3B,PCNA,SUMO1,AK2,ORC1,GFI1B,PPP1R13L,IMMT,CAMK2N2,STIL,CCNE1,NR1H3,CISD2,CDC45,WLS,SIN3A,CCT5,SRSF1,NASP,PLAUR,DTL,GABARAP,TXNRD1,EGR1,OGT,E2F7,PARP1,DAXX,HDAC6,HMGB2,SUZ12,SLC2A4,PIM1,MYBL2,MCFD2,RHEB,NOP58,EAF2,BTG1,FDXR,YARS,PPM1D,GABPB2,KIAA0101,XRCC2,RRM2,USP1,CDKN2D,PPRC1,CDCA7L,CDCA7,TAF6,CA5BP1,PHLPP2,TTLL7,CCNE2,VEGFA,BIN1,CDC25A,IGF2BP3,TIMELESS,HLTF,ADAM15,AATF,DCLRE1A,RBM15,ZBTB5,KIF2A,BRIP1,MYC,EZH2,UHRF1,MCM3,KLF11,MCM5,TNFAIP8,MSH2,mir-663,DHX15,HNRNPF,PLSCR1,SMC1A,MCM2,LIG1,ATAD2,UPP1,GMNN,BSG,TPD52L2,HNRNPA0,RFX1,DHFR,E2F8,E2F2,CDKN1A,RAD51B,CASP2,FSCN1,UBC,LTBP4,DDB2,BRCA1,SOX6,NUCB2,OGG1,CUX1,SEMA6B,IRS2,LMNB1,FANCL,TUBB,PSMC3,CDK2,CD44,WEE1,CDC7,PRKCSH,TIPIN,RPA3,SLC25A42,PHF14,CHEK1

Supplemental Table 3: Functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
Cellular Growth and Proliferation	E2F8	2.68E-15	DAPK2,BIN3,XRCC1,STK24,ALDOA,HNRNPL,FADD,DBF4,ITGA7,MTCH1,POLR2K,NDE1,TCHP,AAGAB,CD300A,NFKBIB,CDC6,SST,PIAS3,TOP2A,EEF1A1,TXNIP,RING1,LEMD3,COL8A1,ENAH,C8orf44-SGK3/SGK3,FOXG1,NRAS,GTPBP3,GBF1,HAT1,CDC123,PTPN12,MAP3K1,SFPQ,FST,MTAP,MAP3K4,PMAIP1,RECQL,NUDT1,SF3A2,BTC,INO80B,PTP4A2,FKBP1A,MORF4L1,SUMO1,FAIM,PEA15,CREM,FKBP5,VTI1A,PFN1,CLIP1,PER1,SIN3A,EFNA1,HK2,ENO1,TSG101,EXOSC9,NASP,SH2B1,ARID4A,TPM3,PARP1,DAXX,PTP4A1,DUS2,PTGS2,PTPRE,MCFD2,RHEB,AFAP1,FURIN,HAX1,MICU1,TRIM24,USP21,TMEM127,RRM2,PALLD,SKP2,CDKN2D,ERBB2,CDCA7,FBXO9,CBLB,SMOX,CLTC,IGF2BP3,WNK1,CACYBP,ADAM15,CDK8,PAWR,PREB,BRIP1,NPAS4,TOP3B,CDKN1B,CCND1,XPC,MT2A,F2RL1,SMC1A,LIG1,EED,HRH1,IL15RA,SMARCA5,NREP,PTN,NDUFAF3,E2F8,CALCR,E2F2,KIF18A,EPB41L5,NAIF1,NOC3L,CDK4,CBX1,TRIM25,PPIA,UTP6,RBM3,TPR,AIMP1,KMT5A,KCNN4,SF3A3,CD44,WEE1,MSI2,TRIM28,NAMPT,CCDC115,RPA3,SHC1,ETV1,CLDN7,ABCB6,SART3,LAMC1,CLSPN,E2F3,CRADD,C3AR1,TOP3A,ZNF335,MFN2,JUND,TFAP4,RGS2,HSPB6,PRKCE,PSRC1,CFDP1,PEG10,STAP2,MCM10,PRCC,CFAP45,TFAP2A,NUMA1,G3BP1,MALAT1,RFC1,CAV2,VCAN,STAT6,RAP1B,BRCA2,HES1,GPRIN1,KRT17,YEATS4,MYOCD,ATF2,RARA,MED31,ARHGEF12,E2F1,MAFA,STIM1,TESK1,TP53,PCNA,ARRB1,ADAM17,RAD52,CLN3,SUV39H1,STIL,CCNE1,NR1H3,WLS,CDC45,RUSC1,YBX1,NPM1,CCT5,CUL3,PPM1G,SFN,TOE1,TCOF1,USP37,SURF1,CD99,UNC119,PLAUR,TXNRD1,S100A13,GABARAP,RXRB,ACIN1,CLK1,AHSA1,SLC25A6,BRD4,TSC22D1,KAT6B,NUP214,E2F6,BTG1,JTB,SAC3D1,KIAA0101,SLC2A8,BASP1,FLII,ING2,PNKP,XRCC2,PPRC1,RGCC,RELT,SRSF6,CCNE2,PRPF6,CDC25A,NFIB,DCLRE1A,GRB7,ZBTB5,KHDRBS1,KIF2A,RRAGB,RAB8A,MUS81,PSMC5,UHRF1,ARL11,MCM3,DGKA,EXOSC2,EIF3F,MSH2,CDC14B,DIDO1,HNRNPF,HSPD1,ATAD2,UPP1,GATA6,BPNT1,TPD52L2,ZP3,HNRNPA0,IL1R1,EBI3,WASF2,HMGN5,CAPN2,OGG1,NFKB1,FOXL1,MAP3K11,BUB3,CDK2,ITGAX,UBE2N,GLI3,ID3,ZNF451,CXCL2,BRPF1,RASSF4,DTYMK,ZNF580,PRKCSH,GOLPH3,ARID4B,DLX4,ARNTL2,GAS6,TACC1,CNBP,RFC3,TAGLN2,POLA1,TNFRSF1A,FANCC,MAPK10,LAMA3,RASGRP4,SLC22A4,HNRNPD,CMIP,PES1,VANGL1,DERL2,ANAPC5,CFLAR,WAS,AARS,LRIG1,HMGB1,UXT,CD160,COX17,KITLG,HMGA2,PSMB2,GPS2,RFC4,mir-154,ARID3B,KMT5C,CDKN2C,DPYSL2,PTK2,HELLS,APEX2,BCL6,NOLC1,CDK5RAP3,HNRNPA1,HIST1H2AB,RPS9,PTGES3,SOCS6,IFI16,PAK1IP1,MCM4,PRPF31,CIZ1,ERCC1,SRSF3,SHMT2,FOXP1,MCM7,ATAD3A,BAG6,EEF1E1,RBBP7,KIF11,HOXD13,CLIC1,AK2,IMMT,HSPA8,ASH2L,PSMC1,EIF4A1,NES,DGKZ,MEF2D,TPX2,USP4,NUMBL,MBD1,UCP2,SRSF1,NCOA5,PACSIN2,WNT7B,DTL,NME1,SP1,RALGDS,CDCA5,TSPAN3,HMGB2,TADA3,IGBP1,HSP90AB1,GADD45GIP1,ACTL6A,SH2D3C,FDXR,BHLHE40,EFNA4,CDC42,YARS,PPM1D,FLCN,YBX3,CD320,FOXK1,RANBP1,LMNA,RGL2,DDX3X,PRKCH,CA5BP1,TMPO,WARS,ZNF668,KRT7,ROBO2,PDCD4,DROSHA,HEXIM1,IRF3,MECOM,MELK,BLM,MYC,EZH2,NAA38,DUSP6,STT3B,FBXO11,ZNF143,VCP,PRCP,TBP,CENPA,KDM5A,MCM2,DDX21,CDC37,LITAF,RNF5,CTNND1,BSG,SCAMP3,GNAI2,TERF1,RAD51B,HDGFRP2,METTL3,INPP4A,CASP2,LAS1L,UBC,MAP3K7,DHPS,LMNB1,FANCL,SGPL1,TUBB,ATM,PXN,PMEL,SSBP3,MCM8,TNFRSF6B,RIT1,UBE2D3,RPL23A,CDC7,POLR2H,IDE,THG1L,UCHL3,GAPDH,PHF14,CHEK1,GTPBP1,CLASP2,VPRBP,CD2AP,ZNF131,NR4A3,PNN,CD274,SMC3,BIRC3,GLA,SNIP1,RPS19,MTBP,H2AFZ,ACTB,PUS7L,TCF19,VMP1,S100A10,RBL1,CDT1,KIF1BP,CYP1B1,OMG,MDM4,MUC4,DLG1,ARHGAP1,MLH1,CNOT2,B3GNT5,NFIA,RTN4,PLAC8,EBNA1BP2,ATP5G1,COPS3,POU4F1,FANCD2,RRM1,RAB28,PTK2B,PHF1,ACE2,TNXB,EIF3H,LONP1,STAT5B,GNAT1,SAE1,ITGA5,DCLRE1C,STK4,JUNB,CTSZ,PPP1CC,FOSL2,MCL1,CALM1 (includes others),MYDGF,UBE4B,CNOT8,MTHFD1,PPIL1,ZBTB20,DNMT1,TNS4,HIPK1,SLC20A1,LEPROTL1,DNAJC2,DPEP1,PURA,SNRNP200,GFI1B,PPP1R13L,TFAM,CAMK2N2,TJAP1,NAA60,BTG3,BYSL,PNP,TEC,SLC1A3,XRN2,TXNRD2,XRCC4,CCAR2,ULBP2,CCR2,HLA-E,CAPS,LRRC8A,IGF2BP1,SREBF1,GNB2L1,BMF,ROBO1,MAP3K12,NOL8,B2M,FOXF2,OGT,ABI2,SOS1,RPS14,PCGF2,HDAC6,SUZ12,SLC2A4,PIM1,AGGF1,CCNA2,GNG2,NOP58,RAD51,PTMA,HNRNPA2B1,TRA2A,EIF2AK3,EAF2,CDK1,AQP11,MGEA5,LIN28A,ESPL1,NQO2,ZBTB7B,HNRNPC,DCTN2,FSTL3,USP1,CCT7,CDCA7L,RXRA,SYF2,ABI1,TIMM8A,TAF6,MED19,PHLPP2,FADS2,DGCR8,TFRC,STRN,MRE11A,REL,HMMR,MTF2,LEF1,STAT2,RGPD4 (includes others),TIMELESS,SEMA6A,HLTF,SPI1,PRPF3,AATF,TRIM33,ANK3,AGTRAP,KIF2C,DAPK3,MADD,CRCP,COPE,NCAN,CLCA2,SERPINE1,NUBP1,LRRK2,ALDH3A1,MCM5,C6orf89,TNFAIP8,CLCF1,ALMS1,LGR4,BBC3,DHX15,PLSCR1,MAPRE1,BLZF1,TNFSF9,GMNN,SLC29A1,STAMBP,RFX1,DHFR,XRCC5,CDKN1A,EIF2B1,MUL1,ARFGEF2,SLC25A14,COPS4,EIF6,FSCN1,CLK2,LTBP4,DDB2,BRCA1,NUCB2,TOPORS,FBXO4,MNT,PSMC3,PTPN2,GLI2,FAM83A,FDFT1,SIRT2,EEF1B2,NR1H2,STMN1,WRN,ATF4,DLG4,TIPIN,EGR3,PBX1,DLX6,MAP3K2,ILF3,FHL2,ST7L,WHSC1,DHX9,CASP8,NFE2L2,IL12RB1
Cell Death and Survival	E2F7	2.47E-08	POU2F1,FEN1,FANCC,VPRBP,ABCB6,FDPS,ATP2A1,CLSPN,MDC1,ALDOA,E2F3,SMC3,UXT,PKMYT1,MSH5,KITLG,TFAP4,RBL1,CDT1,XRCC3,PSMA1,CDC6,MIR17HG,TOP2A,FKBPL,MCM10,RAD54L,CDKN2C,MLH1,GBA,HELLS,RFC1,NOLC1,CDK5RAP3,FANCD2,RRM1,HNRNPA1,HAT1,PTK2B,HNRNPUL1,PSENEN,BRCA2,SETMAR,PMAIP1,FBXO5,RECQL,YEATS4,EXO1,CYR61,CALM1 (includes others),DNMT1,ATAD3A,EEF1E1,E2F1,SLC20A1,NUSAP1,EIF3B,SUMO1,PCNA,GFI1B,IMMT,PPP1R13L,CAMK2N2,STIL,CCNE1,NR1H3,CDC45,CISD2,FANCG,SIN3A,CCT5,DMC1,SRSF1,SIVA1,DTL,PLAUR,TXNRD1,GABARAP,EGR1,OGT,SLC46A1,E2F7,CENPI,DEK,GPR180,PARP1,DAXX,HMGB2,HDAC6,SUZ12,SLC2A4,PIM1,SPC25,MYBL2,ANXA4,MCFD2,RHEB,NOP58,COX8A,HAUS8,EAF2,BCL2L12,PPEF2,BTG1,TK1,FDXR,YARS,PPM1D,ING3,LHX2,KIAA0101,RRM2,XRCC2,CDKN2D,CDCA7L,TAF6,PHLPP2,AEN,CASP8AP2,UNG,VEGFA,BIN1,CDC25A,IGF2BP3,HLTF,ADAM15,AATF,DCLRE1A,BRIP1,MYC,EZH2,XPO1,DIS3,ITGB3BP,UHRF1,KLF11,MSH2,TNFAIP8,PLSCR1,SMC1A,MCM2,LIG1,ATAD2,TMX1,GMNN,HSPE1,BSG,SETX,DHFR,DDX11,E2F8,MSH6,E2F2,NUP205,CDKN1A,TBC1D15,PNPLA8,CASP2,UBC,DDB2,BRCA1,OGG1,SOX6,CUX1,IRS2,LMNB1,FANCL,TREX1,TUBB,PSMC3,CDK2,ORC2,WEE1,CD44,CDC7,MMS22L,DUT,PRPS1,FOXK2,CHEK1

Supplemental Table 3: Functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
Cell Death and Survival	E2F8	1.73E-13	DAPK2,XRCC1,CLDN3,PPP1R1C,STK24,ALDOA,FADD,MTCH1,ITGA7,TCHP,PPP2R5A,CD300A,NFKBIB,SCARB2,DPP3,CDC6,SST,TOP2A,PIAS3,EEF1A1,FKBPL,TXNIP,DCAF7,GBA,C8orf44-SGK3/SGK3,FOXG1,NRAS,HAT1,MAP3K1,PHLDA3,SFPQ,FCMR,FST,MAP3K4,SUPT5H,PMAIP1,FBXO5,RECQL,NUDT1,BTC,PTP4A2,FKBP1A,ERCC5,TMEM109,SUMO1,FAIM,PEA15,CREM,FKBP5,VTI1A,PFN1,PER1,SIN3A,EFNA1,ENO1,HK2,OLFM1,TSG101,RAD1,GPR180,TPM3,DAXX,PARP1,DUS2,ADAMTS12,PTGS2,PTPRE,LEO1,MCFD2,RHEB,TAOK2,SPG7,AFAP1,FURIN,TK1,HAX1,FRAT1,SKA3,TRIM24,HAUS1,RRM2,PALLD,SKP2,CDKN2D,ERBB2,ANO6,CBLB,FBXO9,RPL27A,SMOX,UNG,AHCTF1,MRPL41,IGF2BP3,ADAM15,CACYBP,PAWR,CDK8,BRIP1,NPAS4,CDKN1B,PUS10,CCND1,UBB,XPC,RPL27,MT2A,F2RL1,SMC1A,LIG1,IL15RA,ATP1A2,SMARCA5,PTN,SETX,MSH6,CALCR,E2F8,E2F2,RPL37,TESK2,KIF18A,PNPLA8,CDK4,PPIA,SNRPE,RBM3,TPR,AIMP1,KMT5A,KCNN4,WEE1,CD44,MSI2,TRIM28,MMS22L,NAMPT,DUT,CAMLG,FOXK2,KIFC1,SHC1,TBCCD1,EFHC1,POU2F1,CLDN7,CBX5,ABCB6,CLSPN,E2F3,CRADD,RAP1A,C3AR1,ATP11C,MFN2,TMEM173,KLHL20,JUND,TFAP4,FAM129B,ZNF443,HSPB6,PRKCE,PEG10,STAP2,MCM10,RAD54L,PRCC,TFAP2A,NUMA1,MALAT1,RFC1,VCAN,STAT6,RAP1B,BRCA2,HES1,EIF2S1,KRT17,YEATS4,MYOCD,ATF2,EXO1,RARA,MTMR9,KDM4B,E2F1,PPP1R3F,STIM1,TP53,PCNA,ARRB1,ADAM17,RAD52,CLN3,STIL,SUV39H1,CCNE1,SNRPA1,NR1H3,ECE1,CDC45,FANCG,YBX1,NPM1,CCT5,CUL3,PPM1G,SFN,TCOF1,SURF1,CD99,UNC119,PLAUR,TXNRD1,GABARAP,RXRB,SAP30BP,ACIN1,SHQ1,CENPI,AHSA1,BRD4,SLC25A6,SOAT1,TSC22D1,IRF2BP2,COX8A,BTG1,E2F6,IRF9,EHMT1,THOC2,KIAA0101,SNRPD1,BASP1,FLII,ING2,PNKP,XRCC2,TEX10,BRD2,SPIDR,SRSF6,CASP8AP2,CDC25A,KAT5,NFIB,PFDN6,DCLRE1A,KHDRBS1,GRB7,XPO1,MUS81,PSMC5,UHRF1,RAD18,ARL11,DGKA,EIF3F,MSH2,DIDO1,HSPD1,ATAD2,ARL8B,GATA6,NCAPG2,TMEM123,IL1R1,TBC1D15,HMGN5,CAPN2,OGG1,NFKB1,MAP3K11,CDK2,GLI3,UBE2N,ID3,CXCL2,DTYMK,ITPRIP,RASSF4,GOLPH3,TM2D1,WBP1,DLX4,C5AR2,MEF2A,GAS6,TACC1,FASTK,TAGLN2,PPM1B,TNFRSF1A,FANCC,MAPK10,LAMA3,FDPS,ATP2A1,MDC1,CMIP,CFLAR,WAS,AARS,LRIG1,HIPK3,UXT,HMGB1,CD160,NCOA6,KITLG,HMGA2,GPS2,SCP2,mir-154,PSMA1,ARID3B,CDKN2C,FBL,PTK2,HELLS,PPP1R12B,BCL6,NOLC1,CDK5RAP3,HNRNPA1,FANCE,PDLIM7,HNRNPUL1,PTGES3,RAD9B,IFI16,SERPINI1,ERCC1,CCNT1,SHMT2,MCM7,FOXP1,ATAD3A,BAG6,EEF1E1,KIF11,POLR1D,IMMT,HSPA8,TMEM57,PSMC1,EIF4A1,MEF2D,TPX2,NUMBL,MBD1,UCP2,EME1,NCOA5,SRSF1,SIVA1,DTL,NME1,SP1,RAD51C,TMBIM6,DEK,HMGB2,BANF1,HSP90AB1,TADA3,HAUS8,MAP4,ACTL6A,GADD45GIP1,BCL2L12,TFB1M,ITM2B,FDXR,BHLHE40,EFNA4,CDC42,YARS,PPM1D,FLCN,ING3,BNIP3L,YBX3,LRP8,RANBP1,DDX3X,LMNA,GNAI3,SMUG1,TFEC,TMOD3,PRKCH,PDCD4,PARP4,DROSHA,IRF3,HEXIM1,MECOM,MELK,MLLT11,BLM,MYC,NAA38,EZH2,DUSP6,VCP,WDR81,PRCP,TBP,CENPA,MCM2,CDC37,TMX1,RNF5,CTNND1,BSG,GNAI2,TERF1,KAT7,PAFAH1B3,INPP4A,EIF4A3,CASP2,UBC,MAP3K7,CSRNP1,FANCL,LMNB1,TAX1BP1,SGPL1,TUBB,ATM,PXN,ORC2,PMEL,TNFRSF6B,RIT1,MCM8,CDC7,IDE,THG1L,CIT,UCHL3,CHTOP,TNIP1,HSPBAP1,UBE2Q1,GAPDH,SERP1,CHEK1,LGMN,MUTYH,VPRBP,CD2AP,NR4A3,TSSK6,TMEM69,HIST1H2BO,CYCS,CD274,SMC3,BIRC3,RPS19,NEK8,MTBP,CAPN3,ACTB,SFR1,S100A10,RBL1,CDT1,XRCC3,CYP1B1,MDM4,MUC4,MLH1,ARHGAP1,CNOT2,ACO2,RTN4,PLAC8,OXR1,POU4F1,FANCD2,RRM1,PANX1,RAB28,PTK2B,PHF1,PSENEN,EIF3H,LONP1,STAT5B,GNAT1,ITGA5,DCLRE1C,STK4,RNASEH2A,JUNB,PPP1CC,FOSL2,MCL1,CALM1 (includes others),MYDGF,UBE4B,DNMT1,DCLRE1B,ZBTB20,NAPA,HIPK1,TNS4,SLC20A1,NUSAP1,DPEP1,PURA,GFI1B,PPP1R13L,TFAM,CAMK2N2,GLO1,BTG3,SIGMAR1,PNP,TEC,SLC1A3,PARP14,PFKM,XRCC4,TXNRD2,SMURF1,CCAR2,NDUFV2,PPP1R11,DMC1,ULBP2,CCR2,HLA-E,LRRC8A,IGF2BP1,SREBF1,GNB2L1,BBS4,BMF,GMCL1,MAP3K12,B2M,FOXF2,OGT,PCGF2,HDAC6,SUZ12,SLC2A4,KHK,PIM1,SPC25,AGGF1,ANXA4,GNG2,CEACAM3,CCNA2,NOP58,RAD51,PTMA,EIF2AK3,B4GALT5,EAF2,CDK1,AQP11,MGEA5,COX5A,POLR2A,ESPL1,NQO2,NOD1,HNRNPC,DCTN2,ATP6AP1,FSTL3,SGCA,CCT7,COMMD4,MED6,CDCA7L,RXRA,SYF2,VPS41,TAF6,TMEM14A,PHLPP2,MRE11A,TFRC,BACE1,DGCR8,AEN,REL,SPAG5,GATAD2A,HMMR,UBA7,FAF1,LEF1,STAT2,ZNF184,RGPD4 (includes others),CABLES2,SEMA6A,HLTF,SPI1,AATF,USE1,TRIM33,ANK3,AGTRAP,NUDT2,DAPK3,DIS3,MADD,ARF4,CLCA2,SERPINE1,LRRK2,ALDH3A1,DUSP7,TNFAIP8,P4HB,CLCF1,ALMS1,LGR4,BBC3,PLSCR1,TNFSF9,CCBL1,ZFYVE16,DEDD,SLC29A1,GMNN,ATG13,NEK4,STAMBP,LDLR,DHFR,DDX11,NUP205,XRCC5,CDKN1A,TCEB1,EIF2B1,CANX,EIF6,YWHAB,M6PR,CLK2,DDB2,ICAM2,BRCA1,HSPB11,TOPORS,MNT,TREX1,PSMC3,FH,TRIP10,TNFAIP1,PTPN2,GLI2,FDFT1,NR1H2,SIRT2,PDHA1,STMN1,WRN,RPS3,SCYL3,PERP,ATF4,DLG4,EGR3,PBX1,MAP3K2,ILF3,PRPS1,PHB2,FHL2,PKN2,WHSC1,KDM6B,DHX9,CASP8,NFE2L2

Supplemental Table 4: Liver specific functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
Hepatocellular Carcinoma	E2F7	9.12E-02	VRK2,POU2F1,RFC3,POLA1,PANK2,FANCC,ABCB6,MMAB,RALGAPA2,PDE4DIP,MDC1,DNAJC9-AS1,ZBTB8OS,CCNT2,ARGLU1,UBE2T,PSMA1,CBX3,PROSER1,CDC27,TOP2A,CFDP1,SCUBE2,LEMD3,MLH1,ATAD5,PSMC3IP,DERL3,LTN1,SLC25A36,CDK5RAP3,ANP32E,RRM1,HNRNPA1,FANCD2,HNRNPUL1,CNTRL,BANP,DIAPH3,MCM4,PMAIP1,RECQL,AP4M1,CYR61,PHF20,HEATR6,MTHFD1,EEF1E1,E2F1,PRIM2,NUSAP1,CEP152,SIK2,AK2,PDS5A,RTTN,FANCI,STIL,RFC2,CDC45,SLC1A5,SIN3A,CENPU,MCM6,MAK,DSN1,SRSF1,POLD3,NASP,PLAUR,TXNRD1,KNTC1,OGT,ATL3,CENPI,CAMTA1,DAXX,PARP1,LUC7L2,NOP58,ZNF687,HAUS8,EAF2,BCL2L12,BAZ1B,YARS,RBM14,MBNL3,ASF1B,CDCA3,PAICS,METTL2B,RRM2,USP1,AP3D1,PPRC1,RQCD1,ZRANB3,CA5BP1,TTLL7,PPOX,CASP8AP2,ZCWPW1,TICRR,BIN1,C3orf58,IGF2BP3,HLTF,ADAM15,NUP160,RNF167,ZBTB5,EMSY,MYC,EZH2,AGFG2,DIS3,SUCO,CLCC1,POLE,GMPS,MCM3,TRIM26,KIF25,TBC1D1,DCTPP1,IPO5,ATAD2,AP1S2,HSD17B6,BSG,IGSF8,TTLL9,SETX,RFX1,DDX39B,LINC00273,METTL2A,E2F8,MSH6,NUP205,E2F2,CDKN1A,RAD51B,RBM23,TBC1D15,TMEM116,CASP2,TTI1,LTBP4,OGG1,SOX6,BRCA1,CUX1,FCHSD2,NUCB2,IRS2,CENPH,CDK2,CD44,WEE1,MMS22L,PRKCSH,ADAL,MUT,NAP1L4,PRDM7,PAN2,SLC25A42,TRA2B,RIC8B,ARHGEF40,GPD2
	E2F8	1.53E-03	VRK2,AUTS2,STK24,ITGA7,CCNT2,ARGLU1,HYDIN,TCHP,PHRF1,NFKBIL1,YOD1,ELL3,DPP3,CBX3,PIAS3,TOP2A,EEF1A1,NCOA7,LRRC59,LEMD3,OTUD5,WDR25,DERL3,ENAH,SEMA4B,FOXG1,NRAS,ANP32E,GTPBP3,ZC3H10,WRAP53,NOL6,MAP3K1,SFPQ,ZSWIM3,MAP3K4,SUPT5H,PMAIP1,ZMYND8,RECQL,DLAT,DUSP11,FKBP1A,PRIM2,ERCC5,CNOT3,POLRMT,SIK2,FAIM,PET100,SEC24A,PFN1,FARP1,CLIP1,PPP1R37,CUTA,PER1,RFC2,SIN3A,HK2,DSN1,EXOSC9,NASP,KCTD2,CEP44,PAN3,HIVEP1,FOXRED1,ARMC5,SKIDA1,TM9SF4,ARID4A,DAXX,PARP1,PTGS2,DCTN4,PTPRE,LUC7L2,DENND1A,CCDC82,ZMYM4,NUP188,RPL7A,TNRC6B,SKA3,TRIM24,TMEM127,RRM2,PALLD,KANSL3,SKP2,ERBB2,ANO6,FBXO9,CBLB,POLQ,PLB1,UMPS,AKR1D1,TMEM237,AHCTF1,SMOX,TMEM209,CLTC,ALDH7A1,IGF2BP3,WNK1,U2SURP,ADAM15,CACYBP,KIAA0825,CDK8,EHBP1,IMPG1,CDKN1B,SUCO,CCND1,NENF,GMPS,TOR3A,CIC,TMEM167B,GALNT9,MT2A,DNTTIP2,TAF1A,OSGEPL1,MINOS1-NBL1/NBL1,COASY,ATP1A2,SMARCA5,SETX,ACSL1,METTL2A,MSH6,E2F8,E2F2,RPL37,TROVE2,USP24,QSER1,SLC39A8,PRR5L,FCHSD2,CDK4,TRIM25,VPS45,TTLL3,MYO1F,LRRC49,TPR,GABRQ,KMT5A,WEE1,CD44,MSI2,MRPL24,RCOR3,ZBTB9,MMS22L,IER5,ABCA4,TMEM55B,CCDC115,ACTR10,KIFC1,MPV17,ARHGAP21,SHC1,EFHC1,POU2F1,ETV1,PANK2,ABCB6,SART3,LAMC1,TROAP,LHFPL2,MYPOP,C3AR1,ZNF335,ATP11C,MFN2,FAM129B,PHF8,VARS2,CFDP1,SREK1IP1,STAP2,ATAD5,PRCC,PSMC3IP,LTN1,TFAP2A,NUMA1,MALAT1,PPP6R2,VCAN,ZCCHC11,GPRIN1,MYOCD,ATF2,CHMP7,HEATR6,MTMR9,RARA,ZFYVE19,KDM4B,OSBPL5,MED31,ARHGEF12,E2F1,MAFA,CDK17,PPP1R3F,CEP152,HDLBP,BAZ2A,TP53,ARRB1,C3orf38,ADAM17,LRMP,STIL,CDC45,SLC1A5,RUSC1,CENPU,RTN3,NPM1,PPM1G,TOE1,TCOF1,USP37,DHX8,PLAUR,TXNRD1,WDR24,KHSRP,RXRB,SIL1,CPEB3,CENPI,ZNF181,KBTBD2,ATL3,PDZD2,CLK1,KIAA0907,CAMTA1,FHOD1,BRD4,KPNA6,KAT6B,NUP214,SF3B4,BAZ1B,THOC2,WHSC1L1,TBL1X,C14orf159,PAICS,C2orf44,TRAPPC4,JPH2,METTL2B,PABPN1,CCDC22,IQGAP3,TEX10,AP3D1,GORASP2,PPRC1,SRRM1,ABCA10,MRPS28,SPIDR,BRD2,RELT,CASP8AP2,N4BP2L2,MMACHC,PRPF6,PIK3R4,KAT5,NFIB,VPS72,ZBTB5,CCDC12,POLR2M,RRAGB,PSMC5,MCM3,DGKA,VEZF1,KCNH4,DIDO1,HSPD1,ATAD2,AP1S2,BPNT1,NCAPG2,TTLL9,COL12A1,LINC00273,TBC1D15,UBE3C,SP4,OGG1,HMGCS1,NFKB1,PRSS16,MAP3K11,IDH3B,PCNXL2,CDK2,UBE2N,TLK1,GLI3,ID3,MED24,IGFLR1,ZNF451,TPCN1,DLGAP1,PRKCSH,GOLPH3,ABCF3,TM2D1,ARID4B,ARNTL2,MEF2A,RIC8B,GAS6,STK19,RFC3,COL7A1,POLA1,FANCC,MMAB,EHBP1L1,LAMA3,PDE4DIP,GDI2,MDC1,ZBTB8OS,PNISR,WNT2B,ANAPC5,BRMS1L,CFLAR,EXOC1,MARS,HIPK3,HMGB1,NCOA6,UBE2T,HMGA2,PSMA1,ZBTB45,MBIP,HOXB6,RIOK3,KPNA1,C9orf84,DARS,NKD2,EVI5L,ANKRD44,CDK5RAP3,HNRNPA1,HNRNPUL1,CNTRL,RBAK,SOCS6,HIST1H2BD,AGPAT4,DIAPH3,IFI16,MCM4,CIZ1,C2orf81,KIAA0753,ANKRD11,CCNT1,PHF20,FOXP1,NUFIP1,MCM7,BAG6,EEF1E1,ASRGL1,ZCCHC9,CLIC1,AK2,PDS5A,RTTN,HSPA8,PSMC1,NES,EIF4A1,TPX2,UCP2,SENP3,NCOA5,SRSF1,POLD3,NCALD,TTF2,KRI1,TMEM230,DHTKD1,NME1,RAD51C,SP1,C12orf73,CEP250,HAUS8,POP5,INTS4,BCL2L12,TFB1M,ITM2B,BHLHE40,YARS,RBM14,FLCN,KLHL28,FOXK1,LRP8,AAAS,RGL2,PHF3,LMNA,DLGAP3,TRAPPC9,MPI,SMUG1,CAD,ZRANB3,CA5BP1,PRKCH,WARS,LRRC46,PGAP1,ATP1B3,PPOX,KRT7,ROBO2,SLC7A10,ZCWPW1,DROSHA,TICRR,PTER,POGZ,MECOM,HIST1H3B,C3orf58,HIST1H3F,HIST1H3G,RNF167,CSTF1,TMEM38B,TRAPPC5,PMVK,BLM,MYC,EZH2,TRANK1,FBXO11,VCP,WDR81,TRIM26,KIF25,AOAH,DCTPP1,RBBP5,TBP,STK11IP,RNF168,L3MBTL2,CENPA,USP54,INTS5,RNF5,HIST1H2BG,BSG,WDR33,CDC20B,RAD51B,C1orf112,INPP4A,DENND5A,CASP2,TTI1,ZBTB43,MAP3K7,SGTB,NBR1,SGPL1,TAX1BP1,ATM,PMEL,PEX16,GNL3L,TNFRSF6B,GOLGB1,GANAB,IDE,CHTOP,CIT,TNIP1,APC2,ARHGEF40,FAM208A,CLASP2,LGMN,NR4A3,HIST1H2BO,CD274,NEK8,MTBP,SMG7,NOP16,ACTB,PUS7L,VMP1,NCAPD3,GDPD4,TAF1,PALD1,MUC4,DLG1,SCUBE2,MLH1,ACO2,NUP35,RTN4,DNAJC14,OXR1,SLC25A36,POU4F1,RRM1,FANCD2,NID2,METTL13,TUT1,RNASE4,TNXB,BANP,EIF3H,LONP1,GNAT1,STAT5B,TMEM79,ITGA5,DCLRE1C,AP4M1,DCAKD,SPATA5,MTHFD1,PPIL1,TNS4,RNF213,LIMCH1,MPDZ,DNAJC2,NUSAP1,SNRNP200,FANCI,TJAP1,ALG3,RPRD2,TEC,SLC1A3,PARP14,MEF2B,MCM6,XRN2,TXNRD2,PHF19,NDUFV2,EAF1,ULBP2,CCNB1IP1,RASA2,QTRTD1,LRRC8A,SREBF1,IGF2BP1,GNB2L1,ROBO1,TRIM41,VCPIP1,NOL8,KNTC1,B2M,OGT,NEDD4,ZCCHC8,MYLPF,GARNL3,C17orf53,AGGF1,CCNA2,NOP58,GREB1L,ZNF687,HNRNPA2B1,EAF2,B4GALT5,KIAA1211,MGEA5,LYST,PAM,LIN28A,USF3,CDCA3,ESPL1,TRPV4,ONECUT1,INADL,FSTL3,USP1,SGCA,UBXN4,MTMR11,TTC25,SLC16A6,RUSC2,VPS41,MED19,GNL1,BACE1,DGCR8,CCNL1,COPS7A,TCTEX1D2,REL,HMMR,UNC13A,MTR,C16orf62,FAF1,LRPPRC,STAT2,LEF1,C14orf80,SEMA6A,SEC31A,CABLES2,HLTF,CNOT1,PRPF3,NUP160,TRIM33,ANK3,AGFG2,DAPK3,DIS3,KIAA0895L,CLCC1,POLE,SLC35B2,NCAN,CLCA2,SERPINE1,CDK5RAP1,LRRK2,DUSP7,NPL,P4HB,BLZF1,IPO5,MAPRE1,TNFSF9,CCBL1,SLC29A1,C5orf22,TXNDC16,LDLR,RFX1,ZNF837,DDX39B,NUP205,CDKN1A,WDHD1,ZFHX4,ARFGEF2,UGGT2,GLYCTK,TMEM116,CLK2,LTBP4,DHRS7B,NUCB2,C20orf196,BRCA1,MRPS18A,FRG2C,FNBP4,FBXO4,SKOR2,CENPV,CENPH,TRIP10,PTPN2,FAM83A,GLI2,SIRT2,PDHA1,PHLDB1,PCIF1,KIF24,RNGTT,ILF3,PKN2,ICE1,PAN2,TRA2B,KDM6B,WHSC1,CASP8,GPD2,NFE2L2,IL12RB1

Supplemental Table 4: Liver specific functional annotation of genes bound by E2F7/8 in the promoter region

IPA Category	ChIP-seq	B-H *P*-value	Molecules
Liver Hyperplasia/Hyperproliferation	E2F7	9.12E-02	VRK2,POU2F1,RFC3,POLA1,PANK2,FANCC,ABCB6,MMAB,RALGAPA2,PDE4DIP,MDC1,DNAJC9-AS1,ZBTB8OS,CCNT2,ARGLU1,KITLG,UBE2T,PSMA1,CBX3,PROSER1,CDC27,CFDP1,TOP2A,SCUBE2,LEMD3,MLH1,ATAD5,PSMC3IP,DERL3,LTN1,SLC25A36,ANP32E,CDK5RAP3,RRM1,HNRNPA1,FANCD2,HNRNPUL1,CNTRL,BANP,DIAPH3,MCM4,PMAIP1,RECQL,AP4M1,CYR61,PHF20,HEATR6,MTHFD1,EEF1E1,E2F1,PRIM2,NUSAP1,CEP152,SIK2,AK2,PDS5A,RTTN,FANCI,STIL,CCNE1,RFC2,CDC45,SLC1A5,SIN3A,CENPU,MCM6,MAK,DSN1,SRSF1,EIF1AX,POLD3,NASP,PLAUR,TXNRD1,KNTC1,OGT,ATL3,CENPI,CAMTA1,DAXX,PARP1,LUC7L2,NOP58,ZNF687,HAUS8,EAF2,BCL2L12,BAZ1B,YARS,RBM14,MBNL3,ASF1B,CDCA3,PAICS,METTL2B,RRM2,USP1,AP3D1,PPRC1,RQCD1,ZRANB3,CA5BP1,TTLL7,PPOX,CASP8AP2,ZCWPW1,VEGFA,TICRR,BIN1,C3orf58,IGF2BP3,HLTF,ADAM15,NUP160,RNF167,ZBTB5,EMSY,MYC,EZH2,AGFG2,DIS3,SUCO,CLCC1,POLE,GMPS,MCM3,MSH2,TRIM26,KIF25,TBC1D1,DCTPP1,IPO5,ATAD2,AP1S2,HSD17B6,BSG,IGSF8,TTLL9,SETX,RFX1,DDX39B,LINC00273,METTL2A,E2F8,MSH6,NUP205,E2F2,CDKN1A,RAD51B,RBM23,TBC1D15,TMEM116,CASP2,TTI1,LTBP4,OGG1,SOX6,BRCA1,CUX1,FCHSD2,NUCB2,IRS2,CENPH,CDK2,CD44,WEE1,MMS22L,PRKCSH,ADAL,MUT,NAP1L4,PRDM7,PAN2,SLC25A42,TRA2B,RIC8B,ARHGEF40,GPD2
	E2F8	1.53E-03	VRK2,AUTS2,STK24,ITGA7,CCNT2,ARGLU1,HYDIN,TCHP,PHRF1,NFKBIL1,YOD1,ELL3,DPP3,CBX3,PIAS3,TOP2A,EEF1A1,TXNIP,NCOA7,LRRC59,LEMD3,OTUD5,WDR25,DERL3,ENAH,SEMA4B,FOXG1,NRAS,ANP32E,GTPBP3,ZC3H10,WRAP53,NOL6,MAP3K1,SFPQ,ZSWIM3,MAP3K4,SUPT5H,PMAIP1,ZMYND8,RECQL,NUDT1,DLAT,DUSP11,FKBP1A,PRIM2,ERCC5,CNOT3,POLRMT,SIK2,FAIM,PET100,SEC24A,PFN1,FARP1,CLIP1,PPP1R37,CUTA,PER1,RFC2,SIN3A,HK2,DSN1,EIF1AX,EXOSC9,NASP,KCTD2,CEP44,PAN3,HIVEP1,FOXRED1,ARMC5,SKIDA1,TM9SF4,ARID4A,DAXX,PARP1,PTGS2,DCTN4,PTPRE,LUC7L2,DENND1A,CCDC82,ZMYM4,NUP188,RPL7A,TNRC6B,SKA3,TRIM24,TMEM127,RRM2,PALLD,KANSL3,SKP2,ERBB2,ANO6,FBXO9,CBLB,POLQ,PLB1,UMPS,AKR1D1,TMEM237,AHCTF1,SMOX,TMEM209,CLTC,ALDH7A1,IGF2BP3,WNK1,U2SURP,ADAM15,CACYBP,PAWR,KIAA0825,CDK8,EHBP1,IMPG1,CDKN1B,SUCO,CCND1,NENF,GMPS,TOR3A,CIC,XPC,TMEM167B,GALNT9,MT2A,F2RL1,DNTTIP2,TAF1A,OSGEPL1,MINOS1-NBL1/NBL1,COASY,IL15RA,ATP1A2,SMARCA5,SETX,ACSL1,METTL2A,MSH6,E2F8,E2F2,RPL37,TROVE2,USP24,QSER1,SLC39A8,PRR5L,FCHSD2,CDK4,TRIM25,VPS45,TTLL3,MYO1F,LRRC49,TPR,GABRQ,KMT5A,WEE1,CD44,MSI2,MRPL24,BZW1,RCOR3,TRIM28,ZBTB9,MMS22L,IER5,ABCA4,TMEM55B,CCDC115,ACTR10,KIFC1,MPV17,ARHGAP21,SHC1,EFHC1,POU2F1,ETV1,PANK2,ABCB6,SART3,LAMC1,TROAP,LHFPL2,MYPOP,C3AR1,ZNF335,ATP11C,MFN2,FAM129B,PHF8,VARS2,CFDP1,PEG10,SREK1IP1,STAP2,ATAD5,PRCC,PSMC3IP,LTN1,TFAP2A,NUMA1,MALAT1,PPP6R2,VCAN,ZCCHC11,GPRIN1,MYOCD,ATF2,CHMP7,HEATR6,MTMR9,RARA,ZFYVE19,KDM4B,OSBPL5,MED31,ARHGEF12,E2F1,MAFA,CDK17,PPP1R3F,CEP152,HDLBP,BAZ2A,TP53,ARRB1,C3orf38,ADAM17,LRMP,STIL,CCNE1,CDC45,SLC1A5,RUSC1,CENPU,RTN3,NPM1,PPM1G,TOE1,TCOF1,USP37,DHX8,PLAUR,TXNRD1,WDR24,KHSRP,RXRB,SIL1,CPEB3,CENPI,ZNF181,KBTBD2,ATL3,PDZD2,CLK1,KIAA0907,CAMTA1,FHOD1,BRD4,KPNA6,KAT6B,NUP214,SF3B4,BAZ1B,THOC2,WHSC1L1,TBL1X,C14orf159,PAICS,C2orf44,TRAPPC4,JPH2,METTL2B,PABPN1,CCDC22,IQGAP3,TEX10,AP3D1,GORASP2,PPRC1,SRRM1,ABCA10,MRPS28,SPIDR,BRD2,RELT,CASP8AP2,N4BP2L2,MMACHC,PRPF6,PIK3R4,KAT5,NFIB,VPS72,ZBTB5,CCDC12,POLR2M,RRAGB,PSMC5,MCM3,DGKA,MSH2,VEZF1,KCNH4,DIDO1,HSPD1,ATAD2,AP1S2,BPNT1,NCAPG2,TTLL9,COL12A1,LINC00273,TBC1D15,UBE3C,SP4,OGG1,HMGCS1,NFKB1,PRSS16,MAP3K11,IDH3B,PCNXL2,CDK2,UBE2N,TLK1,GLI3,ID3,MED24,IGFLR1,ZNF451,TPCN1,DLGAP1,PRKCSH,GOLPH3,ABCF3,TM2D1,ARID4B,ARNTL2,MEF2A,RIC8B,GAS6,STK19,RFC3,COL7A1,POLA1,FANCC,MMAB,EHBP1L1,LAMA3,PDE4DIP,GDI2,MDC1,ZBTB8OS,PNISR,WNT2B,ANAPC5,BRMS1L,CFLAR,EXOC1,MARS,HIPK3,HMGB1,NCOA6,KITLG,UBE2T,HMGA2,mir-154,SCP2,PSMA1,ZBTB45,MBIP,HOXB6,RIOK3,KPNA1,C9orf84,DARS,NKD2,EVI5L,ANKRD44,CDK5RAP3,HNRNPA1,HNRNPUL1,CNTRL,RBAK,SOCS6,HIST1H2BD,AGPAT4,DIAPH3,IFI16,MCM4,CIZ1,C2orf81,KIAA0753,ANKRD11,CCNT1,PHF20,FOXP1,NUFIP1,MCM7,BAG6,EEF1E1,ASRGL1,ZCCHC9,CLIC1,AK2,PDS5A,RTTN,HSPA8,PSMC1,NES,EIF4A1,TPX2,UCP2,SENP3,NCOA5,SRSF1,POLD3,NCALD,TTF2,KRI1,TMEM230,DHTKD1,NME1,RAD51C,SP1,C12orf73,CEP250,HAUS8,POP5,INTS4,BCL2L12,TFB1M,ITM2B,BHLHE40,YARS,RBM14,FLCN,KLHL28,FOXK1,LRP8,DDX3X,AAAS,RGL2,PHF3,LMNA,DLGAP3,TRAPPC9,MPI,SMUG1,CAD,ZRANB3,CA5BP1,PRKCH,WARS,LRRC46,PGAP1,ATP1B3,PPOX,KRT7,ROBO2,SLC7A10,ZCWPW1,DROSHA,TICRR,PTER,POGZ,MECOM,HIST1H3B,C3orf58,HIST1H3F,HIST1H3G,RNF167,CSTF1,TMEM38B,TRAPPC5,PMVK,BLM,MYC,EZH2,TRANK1,FBXO11,VCP,WDR81,TRIM26,KIF25,AOAH,DCTPP1,TBP,RBBP5,STK11IP,RNF168,L3MBTL2,CENPA,USP54,INTS5,RNF5,HIST1H2BG,BSG,WDR33,CDC20B,RAD51B,C1orf112,INPP4A,DENND5A,CASP2,TTI1,ZBTB43,MAP3K7,SGTB,NBR1,SGPL1,TAX1BP1,ATM,PMEL,PEX16,GNL3L,TNFRSF6B,GOLGB1,GANAB,IDE,CHTOP,CIT,TNIP1,APC2,ARHGEF40,FAM208A,CLASP2,LGMN,NR4A3,HIST1H2BO,CD274,NEK8,MTBP,SMG7,NOP16,ACTB,PUS7L,VMP1,NCAPD3,GDPD4,CYP1B1,TAF1,PALD1,MUC4,DLG1,SCUBE2,MLH1,ACO2,NUP35,RTN4,DNAJC14,OXR1,SLC25A36,POU4F1,RRM1,FANCD2,NID2,METTL13,TUT1,RNASE4,TNXB,BANP,EIF3H,LONP1,GNAT1,STAT5B,TMEM79,ITGA5,DCLRE1C,AP4M1,DCAKD,SPATA5,MTHFD1,PPIL1,TNS4,RNF213,LIMCH1,MPDZ,DNAJC2,NUSAP1,SNRNP200,FANCI,TJAP1,ALG3,RPRD2,TEC,SLC1A3,PARP14,MEF2B,MCM6,XRN2,TXNRD2,PHF19,NDUFV2,EAF1,ULBP2,CCNB1IP1,HLA-E,RASA2,QTRTD1,LRRC8A,SREBF1,IGF2BP1,GNB2L1,ROBO1,TRIM41,VCPIP1,NOL8,KNTC1,B2M,OGT,NEDD4,ZCCHC8,MYLPF,GARNL3,C17orf53,AGGF1,CCNA2,NOP58,GREB1L,ZNF687,HNRNPA2B1,B4GALT5,EAF2,KIAA1211,MGEA5,LYST,PAM,LIN28A,USF3,CDCA3,ESPL1,NQO2,TRPV4,ONECUT1,INADL,FSTL3,USP1,SGCA,UBXN4,MTMR11,TTC25,SLC16A6,RUSC2,VPS41,MED19,GNL1,MRE11A,BACE1,DGCR8,CCNL1,COPS7A,TCTEX1D2,REL,HMMR,UNC13A,MTR,C16orf62,FAF1,LRPPRC,STAT2,LEF1,C14orf80,SEMA6A,SEC31A,CABLES2,HLTF,CNOT1,PRPF3,SPI1,NUP160,TRIM33,ANK3,AGFG2,DAPK3,DIS3,KIAA0895L,CLCC1,POLE,SLC35B2,NCAN,CLCA2,SERPINE1,CDK5RAP1,LRRK2,DUSP7,NPL,P4HB,PHGDH,BLZF1,IPO5,MAPRE1,TNFSF9,CCBL1,SLC29A1,C5orf22,TXNDC16,LDLR,RFX1,ZNF837,DDX39B,NUP205,WDHD1,CDKN1A,ZFHX4,ARFGEF2,UGGT2,GLYCTK,TMEM116,CLK2,LTBP4,DHRS7B,NUCB2,C20orf196,BRCA1,MRPS18A,FRG2C,FNBP4,FBXO4,SKOR2,CENPV,CENPH,TRIP10,PTPN2,FAM83A,GLI2,SIRT2,PDHA1,PHLDB1,PCIF1,KIF24,RNGTT,ILF3,PKN2,ICE1,PAN2,TRA2B,KDM6B,WHSC1,CASP8,GPD2,NFE2L2,IL12RB1
Liver Necrosis/Cell Death	E2F7	2.17E-01	MYC,DAXX,TREX1,CDKN1A,ATP2A1,SLC20A1,E2F1
	E2F8	2.68E-03	ERCC1,ATF2,BBC3,MCL1,TNFRSF1A,ATP2A1,HSPD1,FKBP1A,SLC20A1,E2F1,FADD,CD274,TP53,BIRC3,FAIM,CFLAR,JUND,LDLR,HMGB1,NFKBIB,CDKN1A,RXRA,SST,REL,CCR2,NCOA5,NFKB1,MNT,TREX1,IRF3,BMF,TNFRSF6B,TMBIM6,MYC,DAXX,CDKN1B,CCND1,PTGS2,CIT,STAT6,TNIP1,SERPINE1,STK4,SHC1,CASP8,NFE2L2

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*-value
Galp	ENSMUSG00000034660.7	0.0	1.4	**94.3**	0.0003	0.0072
Prom2	ENSMUSG00000027376.9	0.5	23.1	**42.7**	0.0001	0.0016
Gm4794	ENSMUSG00000090298.1	1.2	44.5	**37.7**	0.0001	0.0016
Sult2a6	ENSMUSG00000070810.3	2.0	65.2	**32.3**	0.0002	0.0041
Adcy1	ENSMUSG00000020431.5	0.1	3.2	**31.7**	0.0001	0.0016
Sult3a1	ENSMUSG00000069668.2	3.5	106.6	**30.1**	0.0001	0.0016
Cyp17a1	ENSMUSG00000003555.7	2.2	61.6	**27.9**	0.0001	0.0016
Gm14936	ENSMUSG00000084963.1	0.0	0.9	**27.4**	0.0001	0.0016
Akr1b7	ENSMUSG00000052131.7	1.2	28.7	**23.2**	0.0001	0.0016
Ighv12-3	ENSMUSG00000076676.1	4.6	101.8	**22.1**	0.0001	0.0016
Gldn	ENSMUSG00000046167.5	0.6	11.8	**19.7**	0.0001	0.0016
Gm11728	ENSMUSG00000086902.1	0.1	1.0	**19.7**	0.0006	0.0125
Esm1	ENSMUSG00000042379.8	0.6	11.3	**19.4**	0.0001	0.0016
Sult2a4	ENSMUSG00000074377.4	0.2	3.4	**17.7**	0.0013	0.0224
Nfe2l3	ENSMUSG00000029832.9	0.1	1.9	**15.7**	0.0001	0.0016
Lcn13	ENSMUSG00000062061.3	0.5	7.3	**14.8**	0.0001	0.0016
Tuba8	ENSMUSG00000030137.7	0.5	7.5	**14.5**	0.0001	0.0016
Wfdc3	ENSMUSG00000076434.3	0.2	3.0	**14.1**	0.0006	0.0118
Prom1	ENSMUSG00000029086.8	0.8	10.7	**14.0**	0.0001	0.0016
Afp	ENSMUSG00000054932.3	1.4	19.5	**13.7**	0.0001	0.0016
Pde6c	ENSMUSG00000024992.6	0.2	2.9	**13.1**	0.0001	0.0016
Psg18	ENSMUSG00000003505.8	0.2	2.1	**13.1**	0.0001	0.0016
Igkv4-91	ENSMUSG00000076532.2	5.1	64.7	**12.8**	0.0001	0.0016
Zfp618	ENSMUSG00000028358.9	0.1	1.5	**12.7**	0.0005	0.0110
Chrna4	ENSMUSG00000027577.8	0.4	5.1	**12.6**	0.0001	0.0016
Kif5c	ENSMUSG00000026764.9	0.7	8.3	**12.5**	0.0003	0.0072
Sult2a2	ENSMUSG00000070811.4	0.7	8.6	**12.3**	0.0020	0.0312
Boll	ENSMUSG00000025977.9	0.1	1.1	**12.1**	0.0001	0.0016
Mab21l3	ENSMUSG00000044313.7	0.1	1.7	**11.5**	0.0001	0.0016
Igfbp1	ENSMUSG00000020429.7	17.5	196.9	**11.2**	0.0001	0.0016
Akr1c18	ENSMUSG00000021214.7	1.6	17.3	**11.0**	0.0001	0.0016
Usp43	ENSMUSG00000020905.5	0.1	0.8	**10.9**	0.0012	0.0210
Tlr1	ENSMUSG00000044827.6	0.7	7.1	**10.9**	0.0001	0.0016
Stc1	ENSMUSG00000014813.7	0.1	1.4	**10.8**	0.0001	0.0016
Ipcef1	ENSMUSG00000064065.8	0.2	2.0	**10.8**	0.0001	0.0016
Cdhr2	ENSMUSG00000034918.8	0.3	3.5	**10.7**	0.0001	0.0016
Tinag	ENSMUSG00000032357.5	0.2	1.9	**10.7**	0.0018	0.0293

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* - value
Lpl	ENSMUSG00000015568.8	8.9	87.8	**9.8**	0.0001	0.0016
Nid1	ENSMUSG00000005397.7	3.6	35.8	**9.8**	0.0001	0.0016
Sult2a5	ENSMUSG00000078799.2	0.3	3.2	**9.8**	0.0032	0.0450
Atp10a	ENSMUSG00000025324.6	0.2	2.2	**9.7**	0.0001	0.0029
Mtmr11	ENSMUSG00000045934.9	2.0	18.3	**9.3**	0.0001	0.0016
Cpe	ENSMUSG00000037852.7	3.0	27.8	**9.3**	0.0001	0.0016
Cldnd2	ENSMUSG00000038973.1	0.1	1.3	**9.1**	0.0002	0.0051
Tff3	ENSMUSG00000024029.4	22.4	202.9	**9.1**	0.0001	0.0016
Nupr1	ENSMUSG00000030717.3	1.1	10.3	**9.1**	0.0001	0.0016
1700055N04Rik	ENSMUSG00000037263.6	0.2	1.7	**8.9**	0.0017	0.0276
Sparcl1	ENSMUSG00000029309.3	0.5	4.8	**8.9**	0.0001	0.0016
Col4a3	ENSMUSG00000079465.2	0.1	1.0	**8.9**	0.0014	0.0237
Pnpla5	ENSMUSG00000018868.3	0.2	1.5	**8.8**	0.0002	0.0041
Klrb1c	ENSMUSG00000030325.9	0.2	1.5	**8.8**	0.0001	0.0016
Igdcc4	ENSMUSG00000032816.8	0.4	3.4	**8.6**	0.0001	0.0016
Pls1	ENSMUSG00000049493.7	0.7	6.4	**8.6**	0.0001	0.0016
Pnpla3	ENSMUSG00000041653.4	0.9	7.4	**8.6**	0.0001	0.0016
Itih5	ENSMUSG00000025780.7	0.5	4.0	**8.6**	0.0001	0.0016
Dhrs9	ENSMUSG00000027068.6	0.3	2.9	**8.5**	0.0001	0.0016
Nt5e	ENSMUSG00000032420.6	1.7	14.2	**8.4**	0.0001	0.0016
Hr	ENSMUSG00000022096.8	0.1	0.8	**8.4**	0.0002	0.0041
Atf3	ENSMUSG00000026628.8	1.3	10.9	**8.2**	0.0001	0.0016
Prss8	ENSMUSG00000030800.8	2.1	17.1	**8.1**	0.0001	0.0029
C87414	ENSMUSG00000070686.4	0.2	1.5	**8.0**	0.0001	0.0016
Gm5648	ENSMUSG00000083668.1	0.3	2.4	**8.0**	0.0001	0.0016
Fabp4	ENSMUSG00000062515.2	5.9	45.3	**7.7**	0.0001	0.0016
Kcne3	ENSMUSG00000035165.6	0.2	1.6	**7.6**	0.0004	0.0091
Pygb	ENSMUSG00000033059.7	2.6	19.9	**7.6**	0.0001	0.0016
Chka	ENSMUSG00000024843.9	8.3	62.8	**7.6**	0.0001	0.0016
Ccdc120	ENSMUSG00000031150.6	1.4	10.5	**7.6**	0.0008	0.0149
Gm2399	ENSMUSG00000078141.2	8.2	60.6	**7.4**	0.0001	0.0016
Grhl1	ENSMUSG00000020656.9	0.4	3.0	**7.4**	0.0001	0.0016
Klrb1b	ENSMUSG00000079298.3	0.8	5.6	**7.4**	0.0031	0.0439
Apoa4	ENSMUSG00000032080.6	228.5	1685.2	**7.4**	0.0006	0.0125
Mki67	ENSMUSG00000031004.7	0.1	1.0	**7.4**	0.0001	0.0016
Angpt2	ENSMUSG00000031465.6	0.3	1.9	**7.3**	0.0030	0.0434
Rhbg	ENSMUSG00000001417.4	4.7	34.3	**7.3**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Phlda2	ENSMUSG00000010760.4	0.5	3.3	**7.2**	0.0001	0.0029
Plxna3	ENSMUSG00000031398.6	0.4	2.7	**7.1**	0.0003	0.0072
Cdh1	ENSMUSG00000000303.6	4.8	33.9	**7.1**	0.0001	0.0016
Nptx1	ENSMUSG00000025582.4	0.1	0.9	**7.1**	0.0001	0.0016
Gm12387	ENSMUSG00000084220.1	0.2	1.3	**7.0**	0.0022	0.0343
Arntl	ENSMUSG00000055116.6	0.9	6.0	**7.0**	0.0002	0.0041
Hao2	ENSMUSG00000027870.7	1.3	8.9	**6.9**	0.0001	0.0016
Tubb2a	ENSMUSG00000058672.6	14.0	95.5	**6.8**	0.0001	0.0016
Ifi27l2b	ENSMUSG00000021208.8	6.4	43.8	**6.8**	0.0001	0.0016
Dusp5	ENSMUSG00000034765.6	0.7	4.9	**6.8**	0.0001	0.0016
Wfdc15b	ENSMUSG00000018211.6	2.7	18.2	**6.8**	0.0001	0.0016
Cib3	ENSMUSG00000074240.3	1.1	7.6	**6.8**	0.0001	0.0016
Pkmyt1	ENSMUSG00000023908.7	0.2	1.5	**6.8**	0.0011	0.0203
Esco2	ENSMUSG00000022034.9	0.4	2.5	**6.7**	0.0001	0.0016
Btg2	ENSMUSG00000020423.6	3.2	21.4	**6.7**	0.0001	0.0016
Asb11	ENSMUSG00000031382.8	0.2	1.1	**6.7**	0.0028	0.0411
Scd2	ENSMUSG00000025203.5	9.4	63.2	**6.7**	0.0001	0.0016
Scn8a	ENSMUSG00000023033.7	0.3	2.1	**6.5**	0.0001	0.0016
Hcn2	ENSMUSG00000020331.3	0.2	1.0	**6.5**	0.0001	0.0016
9330182L06Rik	ENSMUSG00000056004.9	0.2	1.3	**6.5**	0.0026	0.0389
Abcc4	ENSMUSG00000032849.7	0.8	5.2	**6.4**	0.0001	0.0016
Tnfsf13	ENSMUSG00000089669.1	2.9	18.4	**6.4**	0.0024	0.0362
Ccdc164	ENSMUSG00000073102.2	0.4	2.3	**6.3**	0.0001	0.0016
Sult1e1	ENSMUSG00000029272.7	2.2	13.6	**6.2**	0.0001	0.0016
Inpp5j	ENSMUSG00000034570.5	0.1	0.7	**6.1**	0.0001	0.0016
Ly6d	ENSMUSG00000034634.6	3.7	22.4	**6.1**	0.0001	0.0016
Sult2a1	ENSMUSG00000078798.2	0.7	4.0	**6.1**	0.0015	0.0255
Anxa5	ENSMUSG00000027712.8	20.0	121.0	**6.0**	0.0001	0.0016
Galnt6	ENSMUSG00000037280.6	0.9	5.3	**6.0**	0.0001	0.0016
Ngp	ENSMUSG00000032484.6	0.3	2.1	**6.0**	0.0001	0.0016
Pkp1	ENSMUSG00000026413.6	0.2	1.1	**6.0**	0.0024	0.0362
Hmmr	ENSMUSG00000020330.8	0.2	1.4	**5.9**	0.0001	0.0016
Ccna2	ENSMUSG00000027715.3	1.0	6.2	**5.9**	0.0017	0.0282
Phgdh	ENSMUSG00000053398.5	0.6	3.3	**5.8**	0.0001	0.0016
Car2	ENSMUSG00000027562.7	2.4	13.9	**5.7**	0.0001	0.0016
Serpine1	ENSMUSG00000037411.4	2.7	15.5	**5.7**	0.0001	0.0016
Kif19a	ENSMUSG00000010021.7	0.3	1.9	**5.6**	0.0005	0.0110

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Tc2n	ENSMUSG00000021187.8	0.3	1.7	**5.6**	0.0007	0.0141
Aebp1	ENSMUSG00000020473.7	0.9	4.8	**5.6**	0.0001	0.0016
Uap1l1	ENSMUSG00000026956.9	9.2	50.3	**5.4**	0.0001	0.0016
Sprr1a	ENSMUSG00000050359.6	2.1	11.1	**5.4**	0.0001	0.0016
Gm10567	ENSMUSG00000073738.2	0.6	3.5	**5.4**	0.0001	0.0016
Rims4	ENSMUSG00000035226.5	1.3	7.2	**5.4**	0.0001	0.0016
Nuf2	ENSMUSG00000026683.7	0.2	1.2	**5.3**	0.0004	0.0082
Lysmd2	ENSMUSG00000032184.4	0.3	1.5	**5.3**	0.0005	0.0100
Pdk4	ENSMUSG00000019577.4	0.9	4.9	**5.3**	0.0001	0.0016
Slc1a4	ENSMUSG00000020142.6	1.7	8.8	**5.3**	0.0001	0.0016
Tspan8	ENSMUSG00000034127.7	5.3	28.2	**5.3**	0.0001	0.0016
Cd36	ENSMUSG00000002944.8	7.0	37.3	**5.3**	0.0001	0.0016
Ptgfrn	ENSMUSG00000027864.7	0.8	4.1	**5.3**	0.0001	0.0016
Klk1b1	ENSMUSG00000063133.2	0.3	1.8	**5.3**	0.0004	0.0082
Tnfrsf10b	ENSMUSG00000022074.5	0.3	1.6	**5.3**	0.0004	0.0082
Tubb2b	ENSMUSG00000045136.5	2.9	15.2	**5.3**	0.0001	0.0016
Ccdc69	ENSMUSG00000049588.7	0.2	1.2	**5.2**	0.0004	0.0082
Tfrc	ENSMUSG00000022797.9	4.3	22.5	**5.2**	0.0001	0.0016
Apln	ENSMUSG00000037010.7	0.6	3.1	**5.2**	0.0001	0.0016
Klk1b4	ENSMUSG00000066513.4	1.3	6.5	**5.1**	0.0001	0.0016
Slc34a2	ENSMUSG00000029188.8	0.4	2.2	**5.1**	0.0001	0.0016
Vill	ENSMUSG00000038775.8	0.7	3.5	**5.1**	0.0006	0.0118
Birc5	ENSMUSG00000017716.8	1.0	5.2	**5.1**	0.0001	0.0016
Rbp1	ENSMUSG00000046402.9	6.0	30.0	**5.0**	0.0001	0.0016
Ppl	ENSMUSG00000039457.3	1.4	6.9	**5.0**	0.0001	0.0016
1700009P17Rik	ENSMUSG00000026649.8	0.3	1.6	**5.0**	0.0009	0.0165
Plk1	ENSMUSG00000030867.6	0.3	1.4	**5.0**	0.0001	0.0016
Ly6c1	ENSMUSG00000079018.3	2.8	13.8	**4.9**	0.0001	0.0016
Pycr1	ENSMUSG00000025140.9	0.5	2.2	**4.8**	0.0002	0.0041
Cdkn1a	ENSMUSG00000023067.7	3.9	18.6	**4.7**	0.0001	0.0016
Sh3bp4	ENSMUSG00000036206.6	0.4	1.8	**4.7**	0.0001	0.0016
Cd63	ENSMUSG00000025351.7	13.7	64.5	**4.7**	0.0001	0.0016
Golm1	ENSMUSG00000021556.5	1.3	6.2	**4.7**	0.0001	0.0016
Fam110c	ENSMUSG00000036136.8	0.2	1.0	**4.7**	0.0001	0.0016
Slc39a4	ENSMUSG00000063354.5	13.4	62.8	**4.7**	0.0001	0.0016
Meox1	ENSMUSG00000001493.9	0.2	1.0	**4.7**	0.0003	0.0072
Hist2h3c2	ENSMUSG00000081058.2	0.4	2.0	**4.6**	0.0002	0.0051

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Gm13998	ENSMUSG00000081056.1	2.2	10.2	**4.6**	0.0007	0.0141
Lyve1	ENSMUSG00000030787.3	0.8	3.6	**4.6**	0.0001	0.0016
Mcam	ENSMUSG00000032135.8	1.4	6.4	**4.6**	0.0001	0.0016
Cdca5	ENSMUSG00000024791.4	0.4	1.7	**4.6**	0.0001	0.0016
Slc22a26	ENSMUSG00000053303.8	4.5	20.6	**4.5**	0.0001	0.0016
U1	ENSMUSG00000075736.1	20.5	92.9	**4.5**	0.0003	0.0062
Gm7334	ENSMUSG00000044645.6	2.2	10.1	**4.5**	0.0001	0.0016
Slc5a1	ENSMUSG00000011034.3	1.0	4.4	**4.5**	0.0001	0.0016
Cdca2	ENSMUSG00000048922.10	0.3	1.3	**4.5**	0.0008	0.0149
Anxa2	ENSMUSG00000032231.8	28.2	125.8	**4.5**	0.0001	0.0016
U2	ENSMUSG00000065820.1	63.1	281.6	**4.5**	0.0001	0.0016
Gm14328	ENSMUSG00000082401.1	19.9	88.2	**4.4**	0.0014	0.0237
Fam198a	ENSMUSG00000038233.7	0.7	3.1	**4.4**	0.0001	0.0016
Sybu	ENSMUSG00000022340.7	0.3	1.2	**4.4**	0.0018	0.0293
Cd200	ENSMUSG00000022661.8	2.6	11.5	**4.4**	0.0025	0.0378
U2	ENSMUSG00000065944.1	59.1	257.7	**4.4**	0.0001	0.0016
Neu3	ENSMUSG00000035239.6	0.6	2.7	**4.3**	0.0001	0.0016
Dlx4	ENSMUSG00000020871.7	0.2	1.1	**4.3**	0.0015	0.0255
Rcan2	ENSMUSG00000039601.8	3.7	15.8	**4.3**	0.0001	0.0016
Plat	ENSMUSG00000031538.5	0.8	3.4	**4.3**	0.0001	0.0016
Fst	ENSMUSG00000021765.6	1.6	6.8	**4.3**	0.0001	0.0016
Ces2c	ENSMUSG00000061825.3	21.8	92.3	**4.2**	0.0001	0.0016
Fabp5	ENSMUSG00000027533.9	14.3	60.3	**4.2**	0.0001	0.0016
Chrm3	ENSMUSG00000046159.8	0.7	2.8	**4.2**	0.0001	0.0016
Rhoc	ENSMUSG00000002233.6	14.7	61.8	**4.2**	0.0001	0.0016
Mpzl1	ENSMUSG00000026566.9	1.0	4.3	**4.2**	0.0001	0.0016
Prc1	ENSMUSG00000038943.9	1.3	5.4	**4.2**	0.0001	0.0016
Loxl4	ENSMUSG00000025185.7	0.3	1.1	**4.2**	0.0027	0.0400
Glns-ps1	ENSMUSG00000082100.1	151.1	631.5	**4.2**	0.0002	0.0041
Slc1a5	ENSMUSG00000001918.10	2.4	9.9	**4.2**	0.0001	0.0016
Gm447	ENSMUSG00000045790.4	0.4	1.6	**4.2**	0.0011	0.0203
Kazald1	ENSMUSG00000025213.5	0.5	1.9	**4.1**	0.0001	0.0029
Cdkn2c	ENSMUSG00000028551.8	2.7	11.0	**4.1**	0.0001	0.0016
Shc2	ENSMUSG00000020312.5	0.3	1.1	**4.1**	0.0001	0.0016
Icosl	ENSMUSG00000000732.7	0.3	1.1	**4.1**	0.0006	0.0125
Mmp13	ENSMUSG00000050578.9	0.4	1.4	**4.1**	0.0004	0.0082
Ccdc88c	ENSMUSG00000021182.7	0.2	0.8	**4.1**	0.0002	0.0041

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Uhrf1	ENSMUSG00000001228.8	3.2	12.8	**4.0**	0.0003	0.0062
U2	ENSMUSG00000064682.1	18.4	74.4	**4.0**	0.0001	0.0029
Pak6	ENSMUSG00000074923.4	0.4	1.5	**4.0**	0.0023	0.0357
Ier3	ENSMUSG00000003541.6	0.3	1.4	**4.0**	0.0002	0.0041
Nfe2	ENSMUSG00000058794.6	2.4	9.7	**4.0**	0.0001	0.0016
Cyp2a4	ENSMUSG00000074254.3	170.0	682.6	**4.0**	0.0001	0.0016
Emcn	ENSMUSG00000054690.10	1.3	5.1	**4.0**	0.0001	0.0016
Galntl2	ENSMUSG00000021903.5	0.4	1.5	**4.0**	0.0001	0.0016
Dntt	ENSMUSG00000025014.6	0.8	3.3	**4.0**	0.0005	0.0100
Acacb	ENSMUSG00000042010.10	2.4	9.4	**3.9**	0.0001	0.0016
Tnfrsf12a	ENSMUSG00000023905.8	4.4	17.4	**3.9**	0.0010	0.0189
Arhgef2	ENSMUSG00000028059.7	1.3	5.0	**3.9**	0.0001	0.0016
Psrc1	ENSMUSG00000068744.6	0.5	1.8	**3.9**	0.0001	0.0016
Cd34	ENSMUSG00000016494.3	1.7	6.7	**3.9**	0.0003	0.0072
Fam83f	ENSMUSG00000022408.5	0.5	2.1	**3.9**	0.0001	0.0016
Tmem71	ENSMUSG00000036944.5	1.6	6.1	**3.8**	0.0001	0.0016
Dll4	ENSMUSG00000027314.6	0.6	2.3	**3.8**	0.0001	0.0016
Mrgpre	ENSMUSG00000048965.8	0.4	1.5	**3.8**	0.0001	0.0016
Slc41a3	ENSMUSG00000030089.9	1.5	5.8	**3.8**	0.0001	0.0016
Rrm2	ENSMUSG00000020649.5	6.6	24.9	**3.8**	0.0001	0.0016
AC110211.1	ENSMUSG00000092920.1	3.3	12.5	**3.8**	0.0018	0.0293
U2	ENSMUSG00000064856.1	71.0	266.6	**3.8**	0.0001	0.0016
Bex1	ENSMUSG00000050071.8	0.7	2.5	**3.8**	0.0006	0.0125
Gm15428	ENSMUSG00000046057.4	2.5	9.4	**3.7**	0.0015	0.0255
Cyp2b23	ENSMUSG00000040650.8	0.2	0.7	**3.7**	0.0012	0.0210
Atp6v0d2	ENSMUSG00000028238.6	3.8	14.1	**3.7**	0.0001	0.0016
Gdpd1	ENSMUSG00000061666.6	1.4	5.2	**3.7**	0.0001	0.0016
Cd93	ENSMUSG00000027435.8	1.1	4.2	**3.7**	0.0001	0.0016
Smoc2	ENSMUSG00000023886.8	3.6	13.4	**3.7**	0.0001	0.0016
Cep55	ENSMUSG00000024989.8	0.3	1.0	**3.7**	0.0005	0.0100
Kcnj2	ENSMUSG00000041695.2	0.3	1.3	**3.7**	0.0001	0.0016
Spon2	ENSMUSG00000037379.4	2.8	10.3	**3.7**	0.0001	0.0016
Slfn9	ENSMUSG00000069793.5	1.3	4.7	**3.7**	0.0001	0.0016
Bcmo1	ENSMUSG00000031845.8	5.6	20.6	**3.7**	0.0001	0.0016
Igfbp3	ENSMUSG00000020427.5	12.0	44.1	**3.7**	0.0001	0.0016
Gm11223	ENSMUSG00000046341.4	6.2	22.6	**3.7**	0.0001	0.0016
Lhx6	ENSMUSG00000026890.11	1.7	6.2	**3.7**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
U2	ENSMUSG00000064702.1	73.1	267.8	**3.7**	0.0001	0.0016
Ddr1	ENSMUSG00000003534.10	1.1	3.9	**3.6**	0.0013	0.0230
Hexa	ENSMUSG00000025232.6	11.1	40.2	**3.6**	0.0001	0.0016
Ankrd13b	ENSMUSG00000037907.9	0.5	1.9	**3.6**	0.0008	0.0157
Cdk1	ENSMUSG00000019942.6	5.3	19.1	**3.6**	0.0001	0.0029
U2	ENSMUSG00000065251.1	76.0	270.2	**3.6**	0.0001	0.0016
Fmo3	ENSMUSG00000026691.8	10.2	36.2	**3.6**	0.0001	0.0016
Unc13b	ENSMUSG00000028456.10	1.8	6.5	**3.5**	0.0001	0.0016
Dscc1	ENSMUSG00000022422.7	0.2	0.7	**3.5**	0.0023	0.0357
Aurkb	ENSMUSG00000020897.6	0.6	2.1	**3.5**	0.0006	0.0118
Lrfn3	ENSMUSG00000036957.7	0.8	2.8	**3.5**	0.0001	0.0016
Nrarp	ENSMUSG00000078202.2	0.2	0.8	**3.5**	0.0002	0.0051
Top2a	ENSMUSG00000020914.10	0.9	3.0	**3.5**	0.0001	0.0029
Pdzk1ip1	ENSMUSG00000028716.8	3.7	13.0	**3.5**	0.0002	0.0041
Fam81a	ENSMUSG00000032224.8	0.8	2.9	**3.5**	0.0014	0.0243
Tes	ENSMUSG00000029552.12	2.7	9.5	**3.5**	0.0001	0.0029
Dlgap5	ENSMUSG00000037544.5	0.2	0.7	**3.5**	0.0019	0.0305
Nek2	ENSMUSG00000026622.8	1.3	4.6	**3.5**	0.0001	0.0016
Ckap2l	ENSMUSG00000048327.6	0.3	1.1	**3.5**	0.0001	0.0029
Inhbb	ENSMUSG00000037035.5	0.3	1.2	**3.5**	0.0001	0.0016
Chst1	ENSMUSG00000027221.5	0.3	0.9	**3.5**	0.0005	0.0100
Gm5593	ENSMUSG00000048574.8	0.3	1.2	**3.4**	0.0012	0.0216
Slc13a3	ENSMUSG00000018459.9	9.7	33.4	**3.4**	0.0002	0.0051
Tnfrsf23	ENSMUSG00000037613.9	0.4	1.4	**3.4**	0.0013	0.0230
Ecscr	ENSMUSG00000073599.3	2.7	9.1	**3.4**	0.0005	0.0110
Slc16a11	ENSMUSG00000040938.9	1.7	5.7	**3.4**	0.0001	0.0016
Il1rn	ENSMUSG00000026981.9	6.4	21.9	**3.4**	0.0001	0.0016
Gale	ENSMUSG00000028671.10	3.6	12.3	**3.4**	0.0001	0.0016
Cry1	ENSMUSG00000020038.9	3.1	10.5	**3.4**	0.0001	0.0016
Paqr4	ENSMUSG00000023909.3	0.8	2.6	**3.4**	0.0001	0.0016
Gstm3	ENSMUSG00000004038.7	120.5	405.5	**3.4**	0.0006	0.0125
Gpr55	ENSMUSG00000049608.7	0.2	0.7	**3.4**	0.0020	0.0319
Ccnb2	ENSMUSG00000032218.6	0.7	2.3	**3.3**	0.0002	0.0041
Pbk	ENSMUSG00000022033.3	1.0	3.4	**3.3**	0.0022	0.0338
Cxcr4	ENSMUSG00000045382.6	1.9	6.3	**3.3**	0.0001	0.0016
Abi2	ENSMUSG00000026782.8	0.7	2.2	**3.3**	0.0001	0.0016
Cyp2c55	ENSMUSG00000025002.5	1.3	4.2	**3.3**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Ccnb1	ENSMUSG00000041431.10	0.6	2.1	**3.3**	0.0010	0.0182
Tgfbr2	ENSMUSG00000032440.5	2.8	9.2	**3.3**	0.0001	0.0016
Ttc39a	ENSMUSG00000028555.9	3.6	11.6	**3.3**	0.0016	0.0262
Tnfrsf19	ENSMUSG00000060548.5	2.0	6.6	**3.3**	0.0001	0.0016
Gm6166	ENSMUSG00000074280.4	23.7	77.1	**3.3**	0.0001	0.0016
Mthfd2	ENSMUSG00000005667.6	4.7	15.3	**3.3**	0.0024	0.0362
Lrrc8b	ENSMUSG00000070639.3	0.7	2.1	**3.3**	0.0029	0.0423
Fos	ENSMUSG00000021250.7	0.6	1.8	**3.2**	0.0025	0.0378
Itpr3	ENSMUSG00000042644.8	0.3	0.9	**3.2**	0.0001	0.0016
Chmp4c	ENSMUSG00000027536.5	1.1	3.6	**3.2**	0.0001	0.0016
Pcyox1l	ENSMUSG00000024579.2	0.3	1.1	**3.2**	0.0009	0.0165
Gpr56	ENSMUSG00000031785.8	0.9	2.8	**3.2**	0.0001	0.0016
Cyp2b13	ENSMUSG00000040583.6	9.9	31.7	**3.2**	0.0001	0.0016
Prss23	ENSMUSG00000039405.6	0.8	2.5	**3.2**	0.0001	0.0016
Smox	ENSMUSG00000027333.9	2.3	7.2	**3.2**	0.0004	0.0091
Cyb561	ENSMUSG00000019590.9	1.9	5.9	**3.2**	0.0001	0.0016
9430020K01Rik	ENSMUSG00000033960.5	1.0	3.2	**3.1**	0.0001	0.0016
Rad51c	ENSMUSG00000007646.7	0.6	1.8	**3.1**	0.0008	0.0157
Fam101b	ENSMUSG00000020846.6	0.6	1.9	**3.1**	0.0001	0.0016
Pdp1	ENSMUSG00000049225.8	0.8	2.5	**3.1**	0.0001	0.0016
Tmem229a	ENSMUSG00000048022.9	0.4	1.1	**3.1**	0.0001	0.0016
C630004H02Rik	ENSMUSG00000034586.8	1.6	4.9	**3.1**	0.0008	0.0149
Fam55b	ENSMUSG00000032028.8	10.0	31.3	**3.1**	0.0001	0.0016
Cxcr7	ENSMUSG00000044337.5	0.3	1.0	**3.1**	0.0004	0.0082
Gm12856	ENSMUSG00000084133.1	0.4	1.1	**3.1**	0.0008	0.0157
Clip2	ENSMUSG00000063146.5	0.4	1.4	**3.1**	0.0001	0.0016
Trp53i11	ENSMUSG00000068735.7	1.9	5.9	**3.1**	0.0001	0.0016
Jub	ENSMUSG00000022178.9	0.8	2.5	**3.1**	0.0001	0.0016
Ptpn9	ENSMUSG00000032290.6	4.8	14.7	**3.1**	0.0001	0.0016
Btg3	ENSMUSG00000022863.8	3.5	10.9	**3.1**	0.0006	0.0125
Cyp39a1	ENSMUSG00000023963.8	9.1	28.0	**3.1**	0.0001	0.0016
Ncaph	ENSMUSG00000034906.7	0.5	1.5	**3.1**	0.0028	0.0411
Tspan15	ENSMUSG00000037031.8	1.3	4.1	**3.1**	0.0001	0.0016
Ckap2	ENSMUSG00000037725.7	0.6	1.7	**3.1**	0.0001	0.0016
Tlr6	ENSMUSG00000051498.4	0.9	2.8	**3.0**	0.0001	0.0016
Ncapg2	ENSMUSG00000042029.6	0.5	1.4	**3.0**	0.0006	0.0118
St5	ENSMUSG00000031024.6	3.3	10.1	**3.0**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*-value
Col4a1	ENSMUSG00000031502.9	2.7	8.1	**3.0**	0.0002	0.0051
Anln	ENSMUSG00000036777.7	0.2	0.7	**3.0**	0.0027	0.0400
Tceal8	ENSMUSG00000051579.4	6.5	19.6	**3.0**	0.0001	0.0016
Ifit2	ENSMUSG00000045932.6	1.2	3.7	**3.0**	0.0001	0.0016
Stmn1	ENSMUSG00000028832.5	4.7	14.3	**3.0**	0.0001	0.0016
Nxn	ENSMUSG00000020844.6	0.6	1.7	**3.0**	0.0025	0.0378
Incenp	ENSMUSG00000024660.7	0.6	1.9	**3.0**	0.0001	0.0016
Hist2h3c1	ENSMUSG00000070392.2	1.4	4.3	**3.0**	0.0001	0.0016
Tmprss2	ENSMUSG00000000385.7	3.2	9.5	**3.0**	0.0001	0.0016
Sh2d4a	ENSMUSG00000053886.3	0.6	1.8	**3.0**	0.0002	0.0051
Isyna1	ENSMUSG00000019139.9	4.5	13.3	**3.0**	0.0001	0.0016
n-R5s156	ENSMUSG00000065311.1	4246.7	12559.6	**3.0**	0.0001	0.0016
Cldn15	ENSMUSG00000001739.7	0.5	1.3	**3.0**	0.0013	0.0230
Gm20419	ENSMUSG00000092215.1	1.8	5.3	**2.9**	0.0004	0.0082
Endod1	ENSMUSG00000037419.7	2.2	6.5	**2.9**	0.0001	0.0016
Ect2	ENSMUSG00000027699.9	1.6	4.6	**2.9**	0.0007	0.0133
Slc30a2	ENSMUSG00000028836.8	0.6	1.7	**2.9**	0.0032	0.0454
0610010O12Rik	ENSMUSG00000046727.6	5.4	15.8	**2.9**	0.0001	0.0016
Tmem45b	ENSMUSG00000041737.7	1.3	3.7	**2.9**	0.0026	0.0383
Vangl1	ENSMUSG00000027860.9	3.5	10.3	**2.9**	0.0014	0.0243
Blnk	ENSMUSG00000061132.7	2.4	6.9	**2.9**	0.0001	0.0016
Vash1	ENSMUSG00000021256.4	0.6	1.7	**2.9**	0.0002	0.0041
Synpo	ENSMUSG00000043079.10	1.8	5.2	**2.9**	0.0012	0.0216
Hunk	ENSMUSG00000053414.6	1.3	3.7	**2.9**	0.0003	0.0062
Aurka	ENSMUSG00000027496.9	0.8	2.3	**2.9**	0.0001	0.0029
Tjp2	ENSMUSG00000024812.8	2.1	6.1	**2.9**	0.0001	0.0016
Gm6788	ENSMUSG00000090737.1	5.5	15.8	**2.9**	0.0026	0.0383
Rcan3	ENSMUSG00000059713.6	0.8	2.3	**2.8**	0.0029	0.0423
Slc44a3	ENSMUSG00000039865.7	2.8	7.9	**2.8**	0.0001	0.0016
Arhgap11a	ENSMUSG00000041219.7	0.6	1.7	**2.8**	0.0001	0.0016
Ces2d-ps	ENSMUSG00000031884.8	3.7	10.5	**2.8**	0.0001	0.0016
Gm11912	ENSMUSG00000083214.1	9.1	25.8	**2.8**	0.0012	0.0216
Fmo2	ENSMUSG00000040170.7	9.1	25.5	**2.8**	0.0001	0.0016
Efna1	ENSMUSG00000027954.3	15.3	42.6	**2.8**	0.0001	0.0016
Hspbap1	ENSMUSG00000022849.4	0.3	0.9	**2.8**	0.0016	0.0269
Aqp8	ENSMUSG00000030762.5	48.0	133.5	**2.8**	0.0001	0.0016
Casp12	ENSMUSG00000025887.3	1.2	3.3	**2.8**	0.0006	0.0118

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Pck2	ENSMUSG00000040618.5	1.7	4.8	**2.8**	0.0001	0.0016
B4galt6	ENSMUSG00000056124.5	0.5	1.4	**2.8**	0.0001	0.0016
Abhd2	ENSMUSG00000039202.6	19.8	54.6	**2.8**	0.0001	0.0016
Adrb2	ENSMUSG00000045730.3	1.4	3.8	**2.8**	0.0001	0.0016
Fndc3b	ENSMUSG00000039286.6	5.0	13.8	**2.7**	0.0001	0.0016
Gspt2	ENSMUSG00000071723.6	1.3	3.5	**2.7**	0.0001	0.0016
Slc39a10	ENSMUSG00000025986.5	0.7	2.0	**2.7**	0.0012	0.0210
Maff	ENSMUSG00000042622.7	3.5	9.6	**2.7**	0.0001	0.0016
Gpr110	ENSMUSG00000041293.5	1.0	2.6	**2.7**	0.0001	0.0029
Gm12499	ENSMUSG00000081688.1	9.0	24.3	**2.7**	0.0001	0.0016
Twf2	ENSMUSG00000023277.5	1.6	4.3	**2.7**	0.0001	0.0016
Dusp6	ENSMUSG00000019960.6	11.7	31.7	**2.7**	0.0001	0.0016
Cdc6	ENSMUSG00000017499.9	0.7	1.8	**2.7**	0.0002	0.0051
Ptgr1	ENSMUSG00000028378.6	1.3	3.4	**2.7**	0.0001	0.0016
Gm7665	ENSMUSG00000063628.2	9.8	26.3	**2.7**	0.0002	0.0051
Slc10a2	ENSMUSG00000023073.1	16.4	43.9	**2.7**	0.0001	0.0016
Pparg	ENSMUSG00000000440.6	3.4	9.2	**2.7**	0.0001	0.0016
Klhl13	ENSMUSG00000036782.6	4.6	12.2	**2.7**	0.0006	0.0125
Nedd9	ENSMUSG00000021365.7	1.8	4.8	**2.7**	0.0002	0.0041
Ier5	ENSMUSG00000056708.4	1.5	3.9	**2.7**	0.0001	0.0016
Tmed6	ENSMUSG00000031919.5	1.9	4.9	**2.7**	0.0005	0.0100
Slc6a8	ENSMUSG00000019558.8	3.3	8.7	**2.6**	0.0024	0.0366
Fkbp11	ENSMUSG00000003355.6	9.3	24.5	**2.6**	0.0001	0.0016
Cldn4	ENSMUSG00000047501.2	0.4	1.2	**2.6**	0.0024	0.0362
Itgax	ENSMUSG00000030789.7	0.4	1.0	**2.6**	0.0001	0.0029
Abcd2	ENSMUSG00000055782.7	9.2	24.4	**2.6**	0.0002	0.0041
Fam84b	ENSMUSG00000072568.3	2.0	5.3	**2.6**	0.0001	0.0016
Lamb2	ENSMUSG00000052911.4	0.9	2.3	**2.6**	0.0001	0.0016
Usp18	ENSMUSG00000030107.9	5.5	14.5	**2.6**	0.0001	0.0029
Fhl3	ENSMUSG00000032643.6	0.8	2.1	**2.6**	0.0005	0.0100
Myadm	ENSMUSG00000068566.6	13.1	33.9	**2.6**	0.0001	0.0016
Cldn1	ENSMUSG00000022512.2	26.5	68.8	**2.6**	0.0001	0.0016
Trip13	ENSMUSG00000021569.8	0.5	1.4	**2.6**	0.0012	0.0210
Enpp2	ENSMUSG00000022425.9	29.2	75.1	**2.6**	0.0001	0.0016
Sox18	ENSMUSG00000046470.5	1.0	2.5	**2.6**	0.0001	0.0016
Prkcdbp	ENSMUSG00000037060.2	1.3	3.2	**2.6**	0.0010	0.0182
Scamp5	ENSMUSG00000040722.6	4.8	12.4	**2.6**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* - value
Afap1l1	ENSMUSG00000033032.9	0.7	1.8	**2.6**	0.0002	0.0041
Dyrk3	ENSMUSG00000016526.7	1.2	3.0	**2.5**	0.0002	0.0051
Pecam1	ENSMUSG00000020717.11	7.6	19.4	**2.5**	0.0014	0.0237
Dcbld1	ENSMUSG00000019891.7	0.8	2.0	**2.5**	0.0005	0.0100
Ggct	ENSMUSG00000002797.7	4.5	11.4	**2.5**	0.0002	0.0051
Sox4	ENSMUSG00000076431.3	0.7	1.8	**2.5**	0.0001	0.0016
Specc1	ENSMUSG00000042331.7	0.4	1.1	**2.5**	0.0012	0.0210
Nes	ENSMUSG00000004891.10	0.3	0.9	**2.5**	0.0002	0.0041
Sox9	ENSMUSG00000000567.4	1.4	3.6	**2.5**	0.0028	0.0411
Dynll1	ENSMUSG00000009013.4	37.7	94.7	**2.5**	0.0001	0.0016
Kctd12b	ENSMUSG00000041633.8	0.6	1.4	**2.5**	0.0001	0.0016
Tdrkh	ENSMUSG00000041912.6	1.1	2.6	**2.5**	0.0004	0.0091
Zfp251	ENSMUSG00000022526.7	0.3	0.8	**2.5**	0.0015	0.0250
Akr1b10	ENSMUSG00000061758.6	0.9	2.3	**2.5**	0.0019	0.0299
Mfge8	ENSMUSG00000030605.9	11.0	27.4	**2.5**	0.0001	0.0016
2010003K11Rik	ENSMUSG00000042041.6	10.5	26.1	**2.5**	0.0001	0.0016
Dem1	ENSMUSG00000028629.2	2.8	7.0	**2.5**	0.0032	0.0454
Syne1	ENSMUSG00000019769.9	0.9	2.3	**2.5**	0.0014	0.0237
Epha2	ENSMUSG00000006445.3	1.5	3.8	**2.5**	0.0002	0.0051
Kif22	ENSMUSG00000030677.7	0.5	1.2	**2.5**	0.0032	0.0454
Gpc1	ENSMUSG00000034220.6	1.7	4.2	**2.5**	0.0001	0.0016
Fmnl3	ENSMUSG00000023008.11	1.2	2.9	**2.5**	0.0003	0.0062
Slc1a2	ENSMUSG00000005089.8	52.2	129.3	**2.5**	0.0027	0.0400
Rarg	ENSMUSG00000001288.8	1.6	3.9	**2.5**	0.0007	0.0141
Fmnl2	ENSMUSG00000036053.9	1.2	2.9	**2.5**	0.0005	0.0100
Map4k4	ENSMUSG00000026074.7	2.1	5.2	**2.5**	0.0001	0.0016
Fam115a	ENSMUSG00000036667.8	2.4	6.0	**2.5**	0.0001	0.0029
Rtkn	ENSMUSG00000034930.9	2.2	5.3	**2.5**	0.0004	0.0082
Tubb6	ENSMUSG00000001473.6	4.5	11.1	**2.5**	0.0001	0.0016
Mlkl	ENSMUSG00000012519.8	4.0	9.7	**2.5**	0.0032	0.0454
Pppde1	ENSMUSG00000026502.7	4.8	11.8	**2.4**	0.0001	0.0016
Gm15611	ENSMUSG00000084923.1	4.2	10.2	**2.4**	0.0021	0.0324
Fgf21	ENSMUSG00000030827.4	2.5	6.2	**2.4**	0.0003	0.0072
Abhd5	ENSMUSG00000032540.8	28.8	70.3	**2.4**	0.0001	0.0016
Pawr	ENSMUSG00000035873.6	4.0	9.8	**2.4**	0.0001	0.0016
Ets2	ENSMUSG00000022895.8	10.2	24.8	**2.4**	0.0002	0.0051
Abcg1	ENSMUSG00000024030.6	2.9	6.9	**2.4**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
S100a11	ENSMUSG00000027907.4	8.9	21.6	**2.4**	0.0001	0.0016
Plek2	ENSMUSG00000021118.7	0.7	1.8	**2.4**	0.0023	0.0351
Itga6	ENSMUSG00000027111.8	2.4	5.7	**2.4**	0.0001	0.0016
Ly96	ENSMUSG00000025779.4	6.9	16.7	**2.4**	0.0007	0.0141
Trim2	ENSMUSG00000027993.10	4.8	11.5	**2.4**	0.0016	0.0269
Acot9	ENSMUSG00000025287.9	2.6	6.4	**2.4**	0.0001	0.0029
Ptgds	ENSMUSG00000015090.7	2.5	6.0	**2.4**	0.0014	0.0243
Pdgfb	ENSMUSG00000000489.6	0.7	1.7	**2.4**	0.0003	0.0072
Ccl20	ENSMUSG00000026166.8	4.1	9.9	**2.4**	0.0010	0.0189
Gstm2	ENSMUSG00000040562.6	89.5	214.6	**2.4**	0.0001	0.0016
Scn1b	ENSMUSG00000019194.8	4.7	11.3	**2.4**	0.0001	0.0016
Kcnc3	ENSMUSG00000062785.6	0.3	0.7	**2.4**	0.0008	0.0157
Klf6	ENSMUSG00000000078.6	4.9	11.6	**2.4**	0.0001	0.0016
Chic1	ENSMUSG00000031327.9	1.3	3.0	**2.4**	0.0036	0.0493
B930041F14Rik	ENSMUSG00000074738.2	0.6	1.4	**2.4**	0.0011	0.0196
Acsl4	ENSMUSG00000031278.6	18.7	44.1	**2.4**	0.0001	0.0016
Shank2	ENSMUSG00000037541.12	1.2	2.8	**2.4**	0.0007	0.0133
2010002N04Rik	ENSMUSG00000038059.6	0.7	1.7	**2.3**	0.0020	0.0312
Entpd2	ENSMUSG00000015085.7	4.9	11.5	**2.3**	0.0027	0.0400
Rnf145	ENSMUSG00000019189.7	17.0	39.6	**2.3**	0.0004	0.0082
Cxadr	ENSMUSG00000022865.7	22.0	51.3	**2.3**	0.0001	0.0016
Sema6b	ENSMUSG00000001227.5	0.7	1.5	**2.3**	0.0005	0.0100
Plscr1	ENSMUSG00000032369.7	8.6	20.1	**2.3**	0.0001	0.0016
N4bp3	ENSMUSG00000001053.9	1.2	2.8	**2.3**	0.0025	0.0373
Acmsd	ENSMUSG00000026348.6	7.7	17.9	**2.3**	0.0001	0.0016
E2f1	ENSMUSG00000027490.10	2.0	4.7	**2.3**	0.0001	0.0016
Unc5b	ENSMUSG00000020099.6	1.4	3.2	**2.3**	0.0001	0.0016
Gm6484	ENSMUSG00000047822.7	16.2	37.5	**2.3**	0.0021	0.0324
Gm5844	ENSMUSG00000082896.1	23.2	53.3	**2.3**	0.0001	0.0016
Amot	ENSMUSG00000041688.10	2.5	5.8	**2.3**	0.0007	0.0141
Sel1l3	ENSMUSG00000029189.6	1.7	3.9	**2.3**	0.0001	0.0016
9030619P08Rik	ENSMUSG00000053168.4	15.6	35.9	**2.3**	0.0001	0.0016
Cyp4f16	ENSMUSG00000048440.9	5.5	12.6	**2.3**	0.0015	0.0255
Pcp4l1	ENSMUSG00000038370.6	12.1	27.7	**2.3**	0.0001	0.0016
Ywhah	ENSMUSG00000018965.9	95.1	218.2	**2.3**	0.0001	0.0016
Fam46a	ENSMUSG00000032265.8	1.4	3.1	**2.3**	0.0001	0.0016
Fam84a	ENSMUSG00000020607.6	0.4	0.9	**2.3**	0.0010	0.0189

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*- value
Efha1	ENSMUSG00000021973.8	7.3	16.7	**2.3**	0.0001	0.0016
Unc119	ENSMUSG00000002058.7	4.0	9.2	**2.3**	0.0001	0.0029
Dtx4	ENSMUSG00000039982.7	1.8	4.1	**2.3**	0.0001	0.0016
Nkd1	ENSMUSG00000031661.5	1.1	2.6	**2.3**	0.0002	0.0041
5-Sep	ENSMUSG00000072214.5	1.1	2.5	**2.3**	0.0007	0.0141
Trib2	ENSMUSG00000020601.7	0.5	1.1	**2.3**	0.0011	0.0196
Osmr	ENSMUSG00000022146.5	0.7	1.5	**2.3**	0.0033	0.0466
Zfp704	ENSMUSG00000040209.7	0.6	1.4	**2.3**	0.0002	0.0051
Slc2a4	ENSMUSG00000018566.7	2.4	5.3	**2.3**	0.0013	0.0230
Dpysl2	ENSMUSG00000022048.8	1.7	3.9	**2.3**	0.0001	0.0016
Tagln2	ENSMUSG00000026547.9	23.1	51.9	**2.2**	0.0001	0.0016
Robo4	ENSMUSG00000032125.12	1.2	2.7	**2.2**	0.0001	0.0016
Gm12346	ENSMUSG00000083899.1	31.1	69.6	**2.2**	0.0001	0.0016
Dab2ip	ENSMUSG00000026883.10	1.8	4.0	**2.2**	0.0003	0.0062
Nucb2	ENSMUSG00000030659.7	1.3	3.0	**2.2**	0.0016	0.0262
Zfp295	ENSMUSG00000046962.8	1.1	2.4	**2.2**	0.0001	0.0016
Slc16a1	ENSMUSG00000032902.1	14.8	32.6	**2.2**	0.0001	0.0016
Kifc3	ENSMUSG00000031788.7	2.0	4.4	**2.2**	0.0004	0.0091
Il17rb	ENSMUSG00000015966.9	5.6	12.4	**2.2**	0.0001	0.0016
Hes1	ENSMUSG00000022528.7	4.8	10.5	**2.2**	0.0001	0.0016
Rdh11	ENSMUSG00000066441.7	33.9	74.5	**2.2**	0.0001	0.0016
Mmrn2	ENSMUSG00000041445.8	1.8	3.9	**2.2**	0.0001	0.0016
Ptrf	ENSMUSG00000004044.8	2.7	6.0	**2.2**	0.0001	0.0029
Fubp1	ENSMUSG00000028034.8	4.0	8.9	**2.2**	0.0001	0.0016
Ypel2	ENSMUSG00000018427.7	2.3	5.1	**2.2**	0.0001	0.0016
Ifngr1	ENSMUSG00000020009.6	18.0	39.5	**2.2**	0.0001	0.0016
Timp3	ENSMUSG00000020044.7	6.0	13.0	**2.2**	0.0018	0.0288
Tcf19	ENSMUSG00000050410.9	1.9	4.0	**2.2**	0.0010	0.0189
Atad2	ENSMUSG00000022360.6	1.0	2.2	**2.2**	0.0010	0.0189
Fam43a	ENSMUSG00000046546.3	0.7	1.6	**2.2**	0.0007	0.0141
App	ENSMUSG00000022892.9	54.1	117.3	**2.2**	0.0001	0.0029
Ces2e	ENSMUSG00000031886.7	61.9	133.8	**2.2**	0.0002	0.0041
Dcaf12l1	ENSMUSG00000045284.3	0.8	1.7	**2.2**	0.0004	0.0091
Ppard	ENSMUSG00000002250.9	2.1	4.4	**2.2**	0.0013	0.0224
Nr0b2	ENSMUSG00000037583.2	9.5	20.6	**2.2**	0.0001	0.0029
Plau	ENSMUSG00000021822.2	1.0	2.2	**2.2**	0.0013	0.0230
Apold1	ENSMUSG00000090698.1	0.5	1.0	**2.1**	0.0024	0.0366

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Mcm6	ENSMUSG00000026355.4	4.6	9.9	**2.1**	0.0001	0.0016
Acnat2	ENSMUSG00000060317.3	68.4	146.4	**2.1**	0.0001	0.0016
Gm9372	ENSMUSG00000090474.1	6.0	12.9	**2.1**	0.0030	0.0434
Cmpk2	ENSMUSG00000020638.7	1.1	2.4	**2.1**	0.0003	0.0062
Srxn1	ENSMUSG00000032802.7	23.8	50.5	**2.1**	0.0022	0.0338
Gm5530	ENSMUSG00000087008.2	7.2	15.2	**2.1**	0.0001	0.0016
Gm16854	ENSMUSG00000085607.1	2.6	5.5	**2.1**	0.0001	0.0016
Ctps2	ENSMUSG00000031360.8	9.9	20.9	**2.1**	0.0018	0.0293
Ddit4	ENSMUSG00000020108.3	2.1	4.5	**2.1**	0.0002	0.0051
Emp2	ENSMUSG00000022505.7	18.9	39.9	**2.1**	0.0020	0.0312
Gm11694	ENSMUSG00000081376.1	1216.6	2550.9	**2.1**	0.0001	0.0016
Net1	ENSMUSG00000021215.8	18.1	37.9	**2.1**	0.0001	0.0016
Tm4sf1	ENSMUSG00000027800.8	4.4	9.2	**2.1**	0.0001	0.0016
S1pr3	ENSMUSG00000067586.3	1.3	2.6	**2.1**	0.0001	0.0029
Dapk2	ENSMUSG00000032380.2	9.0	18.7	**2.1**	0.0003	0.0072
Tspyl2	ENSMUSG00000041096.6	1.0	2.1	**2.1**	0.0008	0.0149
Plxna2	ENSMUSG00000026640.6	1.4	3.0	**2.1**	0.0001	0.0016
Spc25	ENSMUSG00000005233.9	3.8	7.9	**2.1**	0.0026	0.0383
Gm14107	ENSMUSG00000080844.1	81.0	168.0	**2.1**	0.0001	0.0016
Gyg	ENSMUSG00000019528.9	2.4	5.0	**2.1**	0.0003	0.0062
Enc1	ENSMUSG00000041773.7	1.2	2.4	**2.1**	0.0002	0.0041
Hapln4	ENSMUSG00000007594.9	2.0	4.1	**2.1**	0.0001	0.0029
Cyp1b1	ENSMUSG00000024087.2	0.7	1.4	**2.0**	0.0026	0.0389
Nipal1	ENSMUSG00000067219.5	3.5	7.1	**2.0**	0.0001	0.0016
Vcam1	ENSMUSG00000027962.9	6.1	12.5	**2.0**	0.0001	0.0016
Pkp2	ENSMUSG00000041957.8	11.5	23.5	**2.0**	0.0001	0.0016
Cyb5r1	ENSMUSG00000026456.11	4.0	8.2	**2.0**	0.0001	0.0016
Cd24a	ENSMUSG00000047139.8	4.3	8.8	**2.0**	0.0001	0.0029
Slc16a5	ENSMUSG00000045775.9	7.4	14.9	**2.0**	0.0002	0.0051
Tubb2c	ENSMUSG00000036752.4	31.7	64.1	**2.0**	0.0001	0.0016
Gpihbp1	ENSMUSG00000022579.4	7.2	14.6	**2.0**	0.0005	0.0110
Cys1	ENSMUSG00000062563.8	3.2	6.5	**2.0**	0.0031	0.0439
Itpripl2	ENSMUSG00000073859.2	1.2	2.5	**2.0**	0.0035	0.0488
Pea15a	ENSMUSG00000013698.6	7.2	14.6	**2.0**	0.0001	0.0016
Capn10	ENSMUSG00000026270.5	8.1	16.4	**2.0**	0.0021	0.0324
Nlrp4e	ENSMUSG00000045693.7	1.5	2.9	**2.0**	0.0001	0.0016
2310014L17Rik	ENSMUSG00000033967.4	2.3	4.7	**2.0**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Cdk6	ENSMUSG00000040274.5	3.7	7.4	**2.0**	0.0031	0.0443
1700017B05Rik	ENSMUSG00000032300.5	2.3	4.7	**2.0**	0.0009	0.0165
Spib	ENSMUSG00000008193.6	5.1	10.1	**2.0**	0.0007	0.0141
Epcam	ENSMUSG00000045394.8	2.2	4.4	**2.0**	0.0033	0.0466
Gimap8	ENSMUSG00000064262.4	1.2	2.4	**2.0**	0.0009	0.0165
Kctd3	ENSMUSG00000026608.6	2.7	5.4	**2.0**	0.0001	0.0029
Rrbp1	ENSMUSG00000027422.9	65.0	128.6	**2.0**	0.0005	0.0110
Acot10	ENSMUSG00000047565.4	2.0	4.0	**2.0**	0.0016	0.0262
Pold4	ENSMUSG00000024854.3	10.8	21.3	**2.0**	0.0002	0.0051
2310016C08Rik	ENSMUSG00000043421.8	2.8	5.5	**2.0**	0.0019	0.0305
Egr1	ENSMUSG00000038418.6	12.7	25.0	**2.0**	0.0003	0.0062
Nudt18	ENSMUSG00000045211.4	2.5	4.9	**2.0**	0.0001	0.0016
Sparc	ENSMUSG00000018593.6	37.9	74.5	**2.0**	0.0001	0.0016
Gramd4	ENSMUSG00000035900.12	1.5	2.8	**2.0**	0.0029	0.0417
Gm17383	ENSMUSG00000058625.5	19.1	37.3	**2.0**	0.0001	0.0016
Ppap2c	ENSMUSG00000052151.5	12.6	24.5	**2.0**	0.0001	0.0016
Psph	ENSMUSG00000029446.7	7.3	14.2	**1.9**	0.0017	0.0276
Il22ra1	ENSMUSG00000037157.8	1.6	3.0	**1.9**	0.0011	0.0203
Abhd8	ENSMUSG00000007950.8	1.9	3.7	**1.9**	0.0015	0.0255
Pvr	ENSMUSG00000040511.7	3.8	7.4	**1.9**	0.0004	0.0082
Wwtr1	ENSMUSG00000027803.8	3.8	7.4	**1.9**	0.0005	0.0100
Gm12013	ENSMUSG00000082099.1	1511.4	2920.1	**1.9**	0.0001	0.0029
Krt8	ENSMUSG00000049382.9	72.2	139.0	**1.9**	0.0004	0.0091
Tuba1c	ENSMUSG00000043091.8	22.3	42.9	**1.9**	0.0001	0.0016
Wdr67	ENSMUSG00000022364.7	1.9	3.6	**1.9**	0.0019	0.0305
Hist1h1c	ENSMUSG00000036181.1	7.6	14.6	**1.9**	0.0002	0.0051
Tbc1d25	ENSMUSG00000039201.3	1.8	3.4	**1.9**	0.0024	0.0366
Ptplb	ENSMUSG00000035376.9	10.0	19.1	**1.9**	0.0002	0.0041
F2r	ENSMUSG00000048376.5	3.9	7.5	**1.9**	0.0001	0.0029
B3galt1	ENSMUSG00000034780.4	8.7	16.5	**1.9**	0.0002	0.0051
Vegfb	ENSMUSG00000024962.7	4.6	8.8	**1.9**	0.0017	0.0276
Gng11	ENSMUSG00000032766.8	6.0	11.5	**1.9**	0.0022	0.0338
Gm5620	ENSMUSG00000056904.2	15.5	29.5	**1.9**	0.0001	0.0029
Tgm1	ENSMUSG00000022218.8	7.1	13.5	**1.9**	0.0007	0.0133
Kcnj8	ENSMUSG00000030247.7	2.4	4.6	**1.9**	0.0006	0.0125
Fam46c	ENSMUSG00000044468.8	2.9	5.4	**1.9**	0.0002	0.0051
Ifit3	ENSMUSG00000074896.3	3.8	7.1	**1.9**	0.0024	0.0362

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Ctla2a	ENSMUSG00000044258.9	3.9	7.3	**1.9**	0.0021	0.0332
Jun	ENSMUSG00000052684.3	4.5	8.5	**1.9**	0.0017	0.0276
Ccdc85b	ENSMUSG00000042878.5	1.0	1.8	**1.9**	0.0031	0.0443
Tuba1a	ENSMUSG00000072235.5	13.0	24.1	**1.9**	0.0012	0.0210
Ripk4	ENSMUSG00000005251.8	2.2	4.1	**1.9**	0.0007	0.0133
Gm12715	ENSMUSG00000059195.8	38.9	72.1	**1.9**	0.0002	0.0051
Acer2	ENSMUSG00000038007.8	3.2	5.9	**1.9**	0.0027	0.0396
Mcm5	ENSMUSG00000005410.4	3.5	6.4	**1.9**	0.0033	0.0460
Chmp6	ENSMUSG00000025371.6	8.3	15.3	**1.8**	0.0003	0.0072
Frrs1	ENSMUSG00000033386.6	12.6	23.3	**1.8**	0.0001	0.0016
Slc35c1	ENSMUSG00000049922.7	5.7	10.5	**1.8**	0.0007	0.0141
Abcc9	ENSMUSG00000030249.8	3.1	5.8	**1.8**	0.0015	0.0250
Ifrd1	ENSMUSG00000001627.5	24.4	45.0	**1.8**	0.0036	0.0499
Trim68	ENSMUSG00000073968.3	1.5	2.7	**1.8**	0.0031	0.0439
Mdfic	ENSMUSG00000041390.11	9.6	17.8	**1.8**	0.0002	0.0051
As3mt	ENSMUSG00000003559.7	11.2	20.6	**1.8**	0.0005	0.0110
Lsr	ENSMUSG00000001247.9	61.9	113.9	**1.8**	0.0036	0.0493
Gm11401	ENSMUSG00000081153.1	38.8	71.3	**1.8**	0.0018	0.0293
Rock2	ENSMUSG00000020580.8	2.0	3.7	**1.8**	0.0004	0.0091
Myo1c	ENSMUSG00000017774.12	10.1	18.5	**1.8**	0.0004	0.0082
Ctsf	ENSMUSG00000083282.2	3.7	6.7	**1.8**	0.0010	0.0189
Tra2a	ENSMUSG00000029817.8	5.9	10.7	**1.8**	0.0011	0.0196
Tpm4	ENSMUSG00000031799.9	10.3	18.8	**1.8**	0.0002	0.0041
Cd276	ENSMUSG00000035914.4	2.0	3.6	**1.8**	0.0016	0.0262
Ptpn21	ENSMUSG00000021009.7	4.7	8.6	**1.8**	0.0028	0.0411
Nfil3	ENSMUSG00000056749.7	6.5	11.7	**1.8**	0.0007	0.0141
Arhgef5	ENSMUSG00000033542.6	4.0	7.3	**1.8**	0.0003	0.0062
Avpr1a	ENSMUSG00000020123.5	14.3	25.9	**1.8**	0.0012	0.0216
Ano10	ENSMUSG00000037949.6	7.5	13.6	**1.8**	0.0002	0.0051
Mat2a	ENSMUSG00000053907.8	29.7	53.5	**1.8**	0.0008	0.0149
Pnrc1	ENSMUSG00000040128.9	29.4	52.9	**1.8**	0.0024	0.0366
Lnx2	ENSMUSG00000016520.7	1.9	3.4	**1.8**	0.0022	0.0343
Atp6v0e2	ENSMUSG00000039347.5	2.5	4.4	**1.8**	0.0034	0.0477
Tuba1b	ENSMUSG00000023004.8	24.4	43.7	**1.8**	0.0001	0.0029
Tpm1	ENSMUSG00000032366.9	31.4	56.0	**1.8**	0.0001	0.0016
Cd2ap	ENSMUSG00000061665.6	7.0	12.4	**1.8**	0.0002	0.0051
Abca8b	ENSMUSG00000020620.8	10.6	18.8	**1.8**	0.0008	0.0149

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Lrp5	ENSMUSG00000024913.9	10.4	18.5	**1.8**	0.0003	0.0062
Prkx	ENSMUSG00000035725.7	1.9	3.3	**1.8**	0.0019	0.0299
Hn1	ENSMUSG00000020737.6	8.0	14.2	**1.8**	0.0005	0.0110
Atpif1	ENSMUSG00000054428.6	36.3	64.0	**1.8**	0.0013	0.0230
Slc45a3	ENSMUSG00000026435.8	5.3	9.4	**1.8**	0.0006	0.0125
Dgkd	ENSMUSG00000070738.4	3.4	6.0	**1.8**	0.0006	0.0118
Fat1	ENSMUSG00000070047.5	1.7	3.0	**1.8**	0.0007	0.0133
Chmp2b	ENSMUSG00000004843.6	18.3	32.2	**1.8**	0.0001	0.0029
Gm11295	ENSMUSG00000084038.1	11.3	19.8	**1.7**	0.0030	0.0428
Pter	ENSMUSG00000026730.6	80.8	141.1	**1.7**	0.0030	0.0434
Emp1	ENSMUSG00000030208.9	3.3	5.8	**1.7**	0.0019	0.0305
Scd3	ENSMUSG00000025202.6	38.7	67.2	**1.7**	0.0009	0.0174
Elovl6	ENSMUSG00000041220.6	12.9	22.4	**1.7**	0.0015	0.0250
Agfg1	ENSMUSG00000026159.6	5.4	9.3	**1.7**	0.0028	0.0406
Cd14	ENSMUSG00000051439.6	7.6	13.1	**1.7**	0.0016	0.0269
Itm2c	ENSMUSG00000026223.9	17.0	29.3	**1.7**	0.0003	0.0062
Obfc2a	ENSMUSG00000026107.5	4.1	7.1	**1.7**	0.0015	0.0255
H2afx	ENSMUSG00000049932.2	4.9	8.3	**1.7**	0.0034	0.0472
Impact	ENSMUSG00000024423.5	4.2	7.2	**1.7**	0.0015	0.0250
Cyr61	ENSMUSG00000028195.3	4.6	7.8	**1.7**	0.0026	0.0383
Ces2g	ENSMUSG00000031877.8	24.3	41.4	**1.7**	0.0006	0.0125
Ermp1	ENSMUSG00000046324.6	10.7	18.3	**1.7**	0.0014	0.0243
Ankrd56	ENSMUSG00000045314.5	3.1	5.3	**1.7**	0.0014	0.0243
Gusb	ENSMUSG00000025534.10	8.4	14.2	**1.7**	0.0024	0.0362
Mfsd6	ENSMUSG00000041439.8	2.9	4.9	**1.7**	0.0027	0.0400
Anpep	ENSMUSG00000039062.8	44.6	74.8	**1.7**	0.0026	0.0383
Sdf2l1	ENSMUSG00000022769.7	15.0	25.1	**1.7**	0.0013	0.0230
Tubb5	ENSMUSG00000001525.9	30.8	51.5	**1.7**	0.0019	0.0299
Slc48a1	ENSMUSG00000081534.2	23.9	39.8	**1.7**	0.0019	0.0299
Megf9	ENSMUSG00000039270.3	4.4	7.3	**1.7**	0.0010	0.0182
Creld2	ENSMUSG00000023272.3	18.6	30.8	**1.7**	0.0014	0.0243
Ly6a	ENSMUSG00000075602.4	24.4	40.1	**1.6**	0.0034	0.0477
Wdr1	ENSMUSG00000005103.9	19.1	31.2	**1.6**	0.0012	0.0216
Ostc	ENSMUSG00000041084.7	58.8	94.7	**1.6**	0.0017	0.0276
Gars	ENSMUSG00000029777.9	27.6	44.3	**1.6**	0.0021	0.0324
Gm1840	ENSMUSG00000043192.3	35.7	56.8	**1.6**	0.0015	0.0255
Arhgdia	ENSMUSG00000025132.7	49.1	77.7	**1.6**	0.0028	0.0411

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Cyp2j6	ENSMUSG00000052914.4	15.2	23.8	**1.6**	0.0035	0.0488
Gm10080	ENSMUSG00000060467.2	115.1	178.8	**1.6**	0.0033	0.0466
Hn1l	ENSMUSG00000024165.8	8.7	13.4	**1.5**	0.0035	0.0483
5730437N04Rik	ENSMUSG00000004945.8	34.9	22.3	**-1.6**	0.0033	0.0466
Abhd3	ENSMUSG00000002475.9	39.9	25.4	**-1.6**	0.0036	0.0499
Gm9846	ENSMUSG00000050621.4	173.4	110.1	**-1.6**	0.0031	0.0443
Cox7a2	ENSMUSG00000032330.6	187.0	117.6	**-1.6**	0.0036	0.0493
Sod2	ENSMUSG00000006818.4	47.2	29.7	**-1.6**	0.0027	0.0400
Rps2-ps13	ENSMUSG00000081684.2	45.6	28.5	**-1.6**	0.0018	0.0288
Slc25a16	ENSMUSG00000071253.2	37.1	23.0	**-1.6**	0.0022	0.0343
Scarb2	ENSMUSG00000029426.7	55.3	34.3	**-1.6**	0.0025	0.0373
Gm13436	ENSMUSG00000083716.2	65.3	40.4	**-1.6**	0.0031	0.0443
Ccdc107	ENSMUSG00000028461.6	45.9	28.4	**-1.6**	0.0027	0.0400
0910001L09Rik	ENSMUSG00000050552.7	39.8	24.5	**-1.6**	0.0026	0.0383
S100a1	ENSMUSG00000044080.9	190.7	117.5	**-1.6**	0.0016	0.0262
Rps25-ps1	ENSMUSG00000067344.5	158.8	97.2	**-1.6**	0.0011	0.0203
Gm7536	ENSMUSG00000057036.5	73.7	45.1	**-1.6**	0.0017	0.0282
AW112010	ENSMUSG00000075010.3	187.0	114.0	**-1.6**	0.0013	0.0230
Cyp2d40	ENSMUSG00000068083.1	54.5	33.2	**-1.6**	0.0017	0.0276
Gm8226	ENSMUSG00000066452.4	26.0	15.8	**-1.6**	0.0024	0.0366
Ndufa6	ENSMUSG00000022450.5	348.7	211.9	**-1.6**	0.0020	0.0312
Enpp3	ENSMUSG00000019989.7	29.3	17.8	**-1.6**	0.0022	0.0343
Pts	ENSMUSG00000032067.5	24.7	14.9	**-1.7**	0.0035	0.0488
Gm11273	ENSMUSG00000079941.1	130.9	78.9	**-1.7**	0.0010	0.0182
Fcgrt	ENSMUSG00000003420.7	94.9	57.2	**-1.7**	0.0013	0.0224
Fam125a	ENSMUSG00000031813.7	26.6	15.9	**-1.7**	0.0018	0.0293
Hint3	ENSMUSG00000019791.5	76.5	45.9	**-1.7**	0.0030	0.0434
Higd2a	ENSMUSG00000025868.6	66.9	40.0	**-1.7**	0.0009	0.0165
Sepw1	ENSMUSG00000041571.7	74.6	44.6	**-1.7**	0.0011	0.0196
Gm6265	ENSMUSG00000066491.4	407.7	243.1	**-1.7**	0.0017	0.0276
Tgds	ENSMUSG00000022130.9	12.2	7.2	**-1.7**	0.0019	0.0299
Acy3	ENSMUSG00000024866.9	41.5	24.6	**-1.7**	0.0007	0.0141
Dhrs4	ENSMUSG00000022210.6	83.5	49.4	**-1.7**	0.0012	0.0216
Slc25a48	ENSMUSG00000021509.5	8.1	4.8	**-1.7**	0.0018	0.0288
Rpl37a	ENSMUSG00000046330.9	47.6	28.1	**-1.7**	0.0019	0.0305
Phf17	ENSMUSG00000025764.8	11.0	6.5	**-1.7**	0.0008	0.0149
Rps17	ENSMUSG00000061787.8	89.2	52.7	**-1.7**	0.0017	0.0282

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Klf13	ENSMUSG00000052040.7	12.8	7.6	**-1.7**	0.0034	0.0477
Rps10-ps1	ENSMUSG00000060438.3	143.6	84.7	**-1.7**	0.0006	0.0125
Gm10294	ENSMUSG00000081895.2	40.0	23.6	**-1.7**	0.0026	0.0383
Naprt1	ENSMUSG00000022574.6	36.4	21.4	**-1.7**	0.0006	0.0125
C030044B11Rik	ENSMUSG00000086252.1	3.5	2.0	**-1.7**	0.0027	0.0396
Rpsa-ps12	ENSMUSG00000080746.2	30.5	17.9	**-1.7**	0.0008	0.0149
Gm12166	ENSMUSG00000069899.3	20.9	12.3	**-1.7**	0.0017	0.0282
Gm10768	ENSMUSG00000074828.2	23.5	13.8	**-1.7**	0.0005	0.0110
Slc25a10	ENSMUSG00000025792.3	53.3	31.2	**-1.7**	0.0006	0.0118
Gm11687	ENSMUSG00000082480.1	17.5	10.3	**-1.7**	0.0028	0.0411
Gm5638	ENSMUSG00000081084.1	106.2	62.1	**-1.7**	0.0004	0.0091
Klf9	ENSMUSG00000033863.1	37.0	21.6	**-1.7**	0.0014	0.0243
Bckdha	ENSMUSG00000060376.6	87.7	51.1	**-1.7**	0.0011	0.0196
Klhl21	ENSMUSG00000073700.3	7.4	4.3	**-1.7**	0.0006	0.0118
Rp9	ENSMUSG00000032239.8	30.1	17.6	**-1.7**	0.0013	0.0230
Gm11249	ENSMUSG00000083087.1	19.8	11.5	**-1.7**	0.0021	0.0324
Gm5436	ENSMUSG00000042962.4	133.9	77.4	**-1.7**	0.0006	0.0118
Coq10b	ENSMUSG00000025981.7	34.8	20.1	**-1.7**	0.0003	0.0062
Lpin1	ENSMUSG00000020593.7	34.3	19.8	**-1.7**	0.0022	0.0338
Wdr45	ENSMUSG00000039382.5	22.0	12.7	**-1.7**	0.0005	0.0100
Lonp2	ENSMUSG00000047866.11	89.1	51.2	**-1.7**	0.0018	0.0293
1300018J18Rik	ENSMUSG00000035757.9	71.3	40.9	**-1.7**	0.0014	0.0237
Slc22a28	ENSMUSG00000063590.3	35.2	20.2	**-1.7**	0.0014	0.0243
Haus4	ENSMUSG00000022177.8	10.3	5.9	**-1.7**	0.0022	0.0343
Gm10269	ENSMUSG00000091449.1	44.6	25.6	**-1.7**	0.0026	0.0383
Shpk	ENSMUSG00000005951.6	27.8	16.0	**-1.7**	0.0003	0.0072
Mast3	ENSMUSG00000031833.8	4.1	2.4	**-1.7**	0.0026	0.0389
Hibadh	ENSMUSG00000029776.9	191.5	109.6	**-1.7**	0.0016	0.0269
Uqcr10	ENSMUSG00000059534.8	160.2	91.6	**-1.7**	0.0006	0.0125
Gm17150	ENSMUSG00000091410.1	55.9	32.0	**-1.7**	0.0031	0.0439
Rpl35a-ps5	ENSMUSG00000067558.6	70.6	40.4	**-1.7**	0.0034	0.0472
L2hgdh	ENSMUSG00000020988.8	21.9	12.5	**-1.7**	0.0002	0.0041
Serpina3l-ps	ENSMUSG00000091157.1	158.6	90.6	**-1.8**	0.0005	0.0100
Inhbe	ENSMUSG00000047492.4	17.3	9.9	**-1.8**	0.0006	0.0125
Rpl13-ps3	ENSMUSG00000059835.1	39.7	22.7	**-1.8**	0.0011	0.0203
Dmgdh	ENSMUSG00000042102.6	125.8	71.6	**-1.8**	0.0023	0.0357
Atp5k	ENSMUSG00000050856.10	188.9	107.5	**-1.8**	0.0005	0.0100

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Eci1	ENSMUSG00000024132.5	78.2	44.5	**-1.8**	0.0002	0.0051
2310011J03Rik	ENSMUSG00000020133.8	7.2	4.1	**-1.8**	0.0030	0.0428
Suox	ENSMUSG00000049858.7	74.2	42.1	**-1.8**	0.0002	0.0051
Dedd2	ENSMUSG00000054499.8	7.0	4.0	**-1.8**	0.0032	0.0454
Ndufa4	ENSMUSG00000029632.5	381.7	216.3	**-1.8**	0.0002	0.0051
Trip4	ENSMUSG00000032386.8	25.5	14.4	**-1.8**	0.0017	0.0282
BC031353	ENSMUSG00000034858.8	12.2	6.9	**-1.8**	0.0007	0.0133
Sdhb	ENSMUSG00000009863.8	171.5	96.9	**-1.8**	0.0007	0.0141
Extl1	ENSMUSG00000028838.5	3.9	2.2	**-1.8**	0.0024	0.0366
Gm10713	ENSMUSG00000074553.3	90.9	51.3	**-1.8**	0.0011	0.0196
Ndufs6	ENSMUSG00000021606.6	53.2	30.0	**-1.8**	0.0011	0.0203
Slc25a42	ENSMUSG00000002346.9	21.0	11.8	**-1.8**	0.0004	0.0091
Scp2-ps2	ENSMUSG00000058492.4	2470.3	1389.8	**-1.8**	0.0032	0.0454
Aes	ENSMUSG00000054452.8	228.4	128.3	**-1.8**	0.0015	0.0255
Csrnp1	ENSMUSG00000032515.7	3.8	2.1	**-1.8**	0.0025	0.0378
Zfp185	ENSMUSG00000031351.8	1.5	0.9	**-1.8**	0.0020	0.0319
Ido2	ENSMUSG00000031549.9	56.0	31.3	**-1.8**	0.0005	0.0110
Pebp1	ENSMUSG00000032959.6	84.7	47.4	**-1.8**	0.0002	0.0041
2610528J11Rik	ENSMUSG00000028536.6	14.5	8.1	**-1.8**	0.0024	0.0362
Gm11225	ENSMUSG00000082368.1	32.5	18.1	**-1.8**	0.0004	0.0091
Clec4g	ENSMUSG00000074491.3	32.5	18.1	**-1.8**	0.0020	0.0319
Rpl18-ps2	ENSMUSG00000053173.8	44.7	24.9	**-1.8**	0.0011	0.0203
Ndufa5	ENSMUSG00000023089.6	135.5	75.4	**-1.8**	0.0010	0.0189
Rpl34-ps1	ENSMUSG00000068396.7	220.3	122.6	**-1.8**	0.0002	0.0041
Apol7a	ENSMUSG00000010601.5	66.1	36.7	**-1.8**	0.0003	0.0072
Gm10362	ENSMUSG00000072489.2	31.7	17.6	**-1.8**	0.0010	0.0189
Gabarapl1	ENSMUSG00000030161.6	232.2	128.7	**-1.8**	0.0031	0.0439
F630206G17Rik	ENSMUSG00000086686.1	4.6	2.6	**-1.8**	0.0018	0.0288
Nxt2	ENSMUSG00000042271.7	16.8	9.3	**-1.8**	0.0002	0.0041
2810405K02Rik	ENSMUSG00000029059.3	35.5	19.7	**-1.8**	0.0008	0.0157
Slc2a9	ENSMUSG00000005107.7	29.4	16.3	**-1.8**	0.0027	0.0400
Gm8017	ENSMUSG00000063427.6	177.6	98.0	**-1.8**	0.0001	0.0029
Casp7	ENSMUSG00000025076.9	16.3	9.0	**-1.8**	0.0004	0.0091
Gm12034	ENSMUSG00000083878.3	75.8	41.7	**-1.8**	0.0006	0.0125
Mosc1	ENSMUSG00000026621.6	206.4	113.5	**-1.8**	0.0017	0.0282
Serpina3a	ENSMUSG00000041536.7	73.5	40.4	**-1.8**	0.0003	0.0062
Gm9786	ENSMUSG00000043801.6	357.3	196.4	**-1.8**	0.0001	0.0029

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*- value
Gm14450	ENSMUSG00000081661.1	586.8	322.1	**-1.8**	0.0001	0.0016
Nr1h4	ENSMUSG00000047638.9	63.7	34.9	**-1.8**	0.0012	0.0216
Slc35e3	ENSMUSG00000060181.5	4.6	2.5	**-1.8**	0.0006	0.0118
Nfkbia	ENSMUSG00000021025.7	36.3	19.8	**-1.8**	0.0001	0.0016
Gm4913	ENSMUSG00000083151.1	32.6	17.8	**-1.8**	0.0001	0.0029
Gm13611	ENSMUSG00000066068.4	41.6	22.7	**-1.8**	0.0026	0.0389
Cisd1	ENSMUSG00000037710.8	139.8	76.1	**-1.8**	0.0001	0.0029
Akr7a5	ENSMUSG00000028743.7	83.7	45.6	**-1.8**	0.0002	0.0041
Acadm	ENSMUSG00000062908.6	175.8	95.6	**-1.8**	0.0007	0.0133
Fau	ENSMUSG00000038274.4	153.4	83.3	**-1.8**	0.0001	0.0016
Glo1	ENSMUSG00000024026.6	146.7	79.6	**-1.8**	0.0004	0.0091
Ttc36	ENSMUSG00000039438.6	449.5	243.8	**-1.8**	0.0002	0.0041
Rgs16	ENSMUSG00000026475.7	29.6	16.0	**-1.8**	0.0035	0.0483
Gbp11	ENSMUSG00000092021.1	20.2	11.0	**-1.8**	0.0006	0.0125
Cyp2j5	ENSMUSG00000052520.7	292.7	158.6	**-1.8**	0.0034	0.0477
Nfu1	ENSMUSG00000029993.10	23.4	12.6	**-1.8**	0.0014	0.0237
Gm10925	ENSMUSG00000090378.1	102.1	55.1	**-1.9**	0.0001	0.0016
Slc25a15	ENSMUSG00000031482.8	127.4	68.7	**-1.9**	0.0008	0.0157
Gm9843	ENSMUSG00000050299.7	309.7	167.0	**-1.9**	0.0001	0.0016
Gchfr	ENSMUSG00000046814.3	93.8	50.5	**-1.9**	0.0002	0.0051
Ppdpf	ENSMUSG00000016344.8	37.5	20.2	**-1.9**	0.0022	0.0343
Cyp3a59	ENSMUSG00000061292.6	108.9	58.6	**-1.9**	0.0015	0.0255
Ripk2	ENSMUSG00000041135.6	6.5	3.5	**-1.9**	0.0015	0.0250
Gm10319	ENSMUSG00000071204.4	228.0	122.5	**-1.9**	0.0003	0.0072
Decr2	ENSMUSG00000036775.6	128.6	69.1	**-1.9**	0.0019	0.0299
Rpl36	ENSMUSG00000057863.5	31.5	16.9	**-1.9**	0.0025	0.0373
Slc22a30	ENSMUSG00000052562.8	62.3	33.4	**-1.9**	0.0007	0.0141
Tmem86b	ENSMUSG00000045282.6	119.2	63.8	**-1.9**	0.0001	0.0029
Gm8731	ENSMUSG00000080779.1	35.4	18.9	**-1.9**	0.0021	0.0324
C8b	ENSMUSG00000029656.7	180.9	96.6	**-1.9**	0.0012	0.0216
Ethe1	ENSMUSG00000064254.6	23.2	12.4	**-1.9**	0.0006	0.0125
Gm8225	ENSMUSG00000068604.4	9.1	4.8	**-1.9**	0.0028	0.0411
Cebpa	ENSMUSG00000034957.9	110.5	58.9	**-1.9**	0.0003	0.0062
Gm14337	ENSMUSG00000081700.1	226.6	120.1	**-1.9**	0.0016	0.0262
Deb1	ENSMUSG00000032526.9	67.0	35.5	**-1.9**	0.0001	0.0029
Uqcr11	ENSMUSG00000020163.6	84.6	44.8	**-1.9**	0.0002	0.0041
Ugt2b5	ENSMUSG00000054630.6	403.1	212.9	**-1.9**	0.0027	0.0400

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Gstk1	ENSMUSG00000029864.5	225.2	118.8	**-1.9**	0.0001	0.0029
Ephx2	ENSMUSG00000022040.6	334.2	176.2	**-1.9**	0.0036	0.0493
Tmem205	ENSMUSG00000040883.8	206.1	108.6	**-1.9**	0.0002	0.0051
Gm11428	ENSMUSG00000069792.5	36.9	19.4	**-1.9**	0.0006	0.0125
Apon	ENSMUSG00000051716.5	359.0	189.1	**-1.9**	0.0015	0.0255
Klf15	ENSMUSG00000030087.5	57.5	30.2	**-1.9**	0.0001	0.0016
Rps18-ps1	ENSMUSG00000083914.2	33.5	17.6	**-1.9**	0.0005	0.0110
Cd5l	ENSMUSG00000015854.6	44.5	23.4	**-1.9**	0.0003	0.0072
Bag4	ENSMUSG00000037316.8	8.7	4.6	**-1.9**	0.0023	0.0357
Hoga1	ENSMUSG00000025176.8	138.8	72.8	**-1.9**	0.0024	0.0362
Haao	ENSMUSG00000000673.8	267.7	140.4	**-1.9**	0.0006	0.0125
C1qa	ENSMUSG00000036887.5	30.7	16.1	**-1.9**	0.0001	0.0016
Pbld2	ENSMUSG00000020068.4	71.9	37.7	**-1.9**	0.0001	0.0016
1700019G17Rik	ENSMUSG00000068299.5	92.4	48.3	**-1.9**	0.0008	0.0149
Dact2	ENSMUSG00000048826.6	5.1	2.6	**-1.9**	0.0004	0.0082
Gm15118	ENSMUSG00000083854.1	95.6	49.7	**-1.9**	0.0001	0.0029
Timm9	ENSMUSG00000021079.8	19.1	9.9	**-1.9**	0.0031	0.0443
Bmp2	ENSMUSG00000027358.6	3.9	2.0	**-1.9**	0.0013	0.0230
Gm12247	ENSMUSG00000081223.1	12.4	6.4	**-1.9**	0.0018	0.0288
Ypel3	ENSMUSG00000042675.9	30.3	15.7	**-1.9**	0.0031	0.0443
Cyp2d34	ENSMUSG00000062185.5	24.6	12.7	**-1.9**	0.0001	0.0016
Cox6b1	ENSMUSG00000036751.6	181.1	93.3	**-1.9**	0.0002	0.0041
Cxcl12	ENSMUSG00000061353.5	141.6	72.9	**-1.9**	0.0006	0.0125
Fam13a	ENSMUSG00000037709.7	7.7	4.0	**-1.9**	0.0014	0.0237
Hyi	ENSMUSG00000006395.9	25.1	12.8	**-2.0**	0.0030	0.0428
Olfml1	ENSMUSG00000051041.7	13.6	7.0	**-2.0**	0.0001	0.0016
Gm16437	ENSMUSG00000024761.2	35.5	18.1	**-2.0**	0.0006	0.0125
Ugt2b38	ENSMUSG00000061906.5	158.5	80.9	**-2.0**	0.0001	0.0016
BC026585	ENSMUSG00000033488.5	8.0	4.1	**-2.0**	0.0012	0.0216
Per3	ENSMUSG00000028957.6	6.8	3.5	**-2.0**	0.0028	0.0406
Cd300e	ENSMUSG00000048498.7	2.8	1.4	**-2.0**	0.0034	0.0477
Gm5403	ENSMUSG00000083250.1	1.7	0.9	**-2.0**	0.0030	0.0428
Gm10063	ENSMUSG00000059333.1	31.1	15.8	**-2.0**	0.0011	0.0203
Timd4	ENSMUSG00000055546.6	4.4	2.2	**-2.0**	0.0025	0.0378
Hint2	ENSMUSG00000028470.4	123.7	62.8	**-2.0**	0.0001	0.0029
Cyp26b1	ENSMUSG00000063415.5	1.4	0.7	**-2.0**	0.0022	0.0338
Dera	ENSMUSG00000030225.8	30.2	15.3	**-2.0**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Prdx5	ENSMUSG00000024953.9	126.1	63.7	**-2.0**	0.0004	0.0082
Rpl28	ENSMUSG00000030432.6	87.3	43.9	**-2.0**	0.0006	0.0118
Pank1	ENSMUSG00000033610.8	130.9	65.8	**-2.0**	0.0001	0.0016
Atoh8	ENSMUSG00000037621.7	6.1	3.1	**-2.0**	0.0029	0.0417
Agphd1	ENSMUSG00000035878.7	19.2	9.6	**-2.0**	0.0001	0.0016
Tlr2	ENSMUSG00000027995.9	2.6	1.3	**-2.0**	0.0012	0.0210
Fbp1	ENSMUSG00000069805.4	577.3	289.0	**-2.0**	0.0019	0.0305
Plekhb1	ENSMUSG00000030701.10	40.5	20.3	**-2.0**	0.0001	0.0016
Gstt2	ENSMUSG00000033318.6	62.0	31.0	**-2.0**	0.0001	0.0016
Gcdh	ENSMUSG00000003809.7	243.9	121.5	**-2.0**	0.0007	0.0141
Gm13443	ENSMUSG00000075391.4	519.8	258.6	**-2.0**	0.0001	0.0016
Ech1	ENSMUSG00000053898.6	407.4	202.5	**-2.0**	0.0001	0.0016
Clec4f	ENSMUSG00000014542.2	53.9	26.7	**-2.0**	0.0009	0.0165
Gm11361	ENSMUSG00000061330.6	41.9	20.8	**-2.0**	0.0002	0.0051
1190003J15Rik	ENSMUSG00000025481.5	212.1	105.0	**-2.0**	0.0001	0.0029
Zkscan14	ENSMUSG00000029627.10	4.0	2.0	**-2.0**	0.0012	0.0210
Clec2d	ENSMUSG00000030157.5	13.6	6.7	**-2.0**	0.0003	0.0072
9530008L14Rik	ENSMUSG00000058022.6	145.8	72.1	**-2.0**	0.0002	0.0051
Mbl2	ENSMUSG00000024863.5	430.7	212.1	**-2.0**	0.0004	0.0082
Aadat	ENSMUSG00000057228.4	62.8	30.9	**-2.0**	0.0001	0.0016
Gm11686	ENSMUSG00000080711.3	47.4	23.3	**-2.0**	0.0011	0.0196
Gm4459	ENSMUSG00000083626.1	79.4	39.0	**-2.0**	0.0001	0.0016
Lipc	ENSMUSG00000032207.8	132.7	65.0	**-2.0**	0.0002	0.0041
Gm11808	ENSMUSG00000068240.3	156.6	76.7	**-2.0**	0.0001	0.0016
Cmbl	ENSMUSG00000022235.8	140.1	68.6	**-2.0**	0.0006	0.0125
Nr1i3	ENSMUSG00000005677.7	78.1	38.1	**-2.1**	0.0007	0.0133
Oaz1	ENSMUSG00000035242.8	228.0	111.1	**-2.1**	0.0001	0.0016
AI317395	ENSMUSG00000038522.4	22.4	10.9	**-2.1**	0.0001	0.0016
Ugt2b37	ENSMUSG00000057425.3	67.2	32.7	**-2.1**	0.0001	0.0016
Ndufb11	ENSMUSG00000031059.9	91.9	44.7	**-2.1**	0.0001	0.0016
Gypc	ENSMUSG00000090523.2	6.5	3.1	**-2.1**	0.0005	0.0100
Fzd8	ENSMUSG00000036904.5	5.7	2.8	**-2.1**	0.0001	0.0016
Igfals	ENSMUSG00000046070.7	53.8	26.0	**-2.1**	0.0001	0.0016
Saa4	ENSMUSG00000040017.7	257.0	124.1	**-2.1**	0.0012	0.0216
Creb3l3	ENSMUSG00000035041.8	106.3	51.2	**-2.1**	0.0009	0.0165
Kynu	ENSMUSG00000026866.9	66.9	32.2	**-2.1**	0.0002	0.0041
Kcnk5	ENSMUSG00000023243.8	7.4	3.6	**-2.1**	0.0018	0.0288

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*-value
Aspg	ENSMUSG00000037686.5	27.2	13.1	**-2.1**	0.0003	0.0062
Gch1	ENSMUSG00000037580.9	49.4	23.7	**-2.1**	0.0001	0.0016
Gnat1	ENSMUSG00000034837.7	8.7	4.2	**-2.1**	0.0001	0.0016
Bglap-rs1	ENSMUSG00000074489.3	1.7	0.8	**-2.1**	0.0024	0.0366
Mt2	ENSMUSG00000031762.6	177.2	84.4	**-2.1**	0.0002	0.0051
Raet1d	ENSMUSG00000078452.2	8.0	3.8	**-2.1**	0.0004	0.0082
Gm4285	ENSMUSG00000085829.1	4.1	2.0	**-2.1**	0.0033	0.0460
Gm14303	ENSMUSG00000081344.3	1173.8	557.7	**-2.1**	0.0001	0.0016
Hsd3b4	ENSMUSG00000056351.5	5.0	2.4	**-2.1**	0.0012	0.0210
D10Jhu81e	ENSMUSG00000053329.6	57.0	27.0	**-2.1**	0.0001	0.0016
Gm10681	ENSMUSG00000074380.2	4.8	2.3	**-2.1**	0.0014	0.0243
Macrod1	ENSMUSG00000036278.6	16.1	7.6	**-2.1**	0.0029	0.0423
Cox7c	ENSMUSG00000017778.8	267.5	126.3	**-2.1**	0.0001	0.0016
Ldhd	ENSMUSG00000031958.9	55.4	26.0	**-2.1**	0.0001	0.0016
Pim3	ENSMUSG00000035828.9	9.3	4.3	**-2.1**	0.0001	0.0016
Mn1	ENSMUSG00000070576.4	1.5	0.7	**-2.1**	0.0014	0.0243
Cyp2d12	ENSMUSG00000057138.5	85.7	40.1	**-2.1**	0.0001	0.0016
Ces2a	ENSMUSG00000055730.8	201.7	93.8	**-2.2**	0.0001	0.0016
Sult1b1	ENSMUSG00000029269.5	41.1	19.1	**-2.2**	0.0001	0.0016
Sepx1	ENSMUSG00000075705.6	389.1	180.7	**-2.2**	0.0001	0.0016
Cyp2d11	ENSMUSG00000068085.5	185.2	86.0	**-2.2**	0.0001	0.0016
Serpine2	ENSMUSG00000026249.4	12.4	5.8	**-2.2**	0.0001	0.0029
Pecr	ENSMUSG00000026189.7	141.1	65.4	**-2.2**	0.0003	0.0062
Mrps36	ENSMUSG00000061474.5	7.9	3.6	**-2.2**	0.0022	0.0338
Gm8835	ENSMUSG00000092457.1	3.8	1.8	**-2.2**	0.0015	0.0255
Saa2	ENSMUSG00000057465.4	49.5	22.8	**-2.2**	0.0003	0.0062
Fxyd1	ENSMUSG00000036570.7	317.8	146.7	**-2.2**	0.0001	0.0016
Rps29	ENSMUSG00000034892.8	131.4	60.6	**-2.2**	0.0001	0.0016
Ndufs7	ENSMUSG00000020153.8	50.6	23.3	**-2.2**	0.0001	0.0016
Orm2	ENSMUSG00000061540.3	132.1	60.6	**-2.2**	0.0001	0.0016
Fbxo21	ENSMUSG00000032898.6	45.2	20.7	**-2.2**	0.0002	0.0051
Slc25a34	ENSMUSG00000040740.7	1.1	0.5	**-2.2**	0.0023	0.0357
Ces1g	ENSMUSG00000057074.6	82.1	37.5	**-2.2**	0.0001	0.0016
Id3	ENSMUSG00000007872.3	34.9	15.9	**-2.2**	0.0002	0.0051
Pex16	ENSMUSG00000027222.8	52.5	23.9	**-2.2**	0.0001	0.0016
Gm10222	ENSMUSG00000067736.1	56.7	25.8	**-2.2**	0.0003	0.0062
Hebp1	ENSMUSG00000042770.6	278.7	126.8	**-2.2**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*-value
Rasgef1b	ENSMUSG00000029333.8	12.5	5.7	**-2.2**	0.0004	0.0091
1810027O10Rik	ENSMUSG00000070394.4	96.5	43.9	**-2.2**	0.0001	0.0016
Orm3	ENSMUSG00000028359.4	42.5	19.3	**-2.2**	0.0001	0.0016
Cyp2j9	ENSMUSG00000015224.9	2.3	1.1	**-2.2**	0.0035	0.0488
Cyp3a57	ENSMUSG00000070419.5	36.1	16.4	**-2.2**	0.0001	0.0016
Pbld1	ENSMUSG00000020072.7	82.6	37.3	**-2.2**	0.0001	0.0016
Mzt2	ENSMUSG00000022671.6	12.4	5.6	**-2.2**	0.0001	0.0016
Uqcrq	ENSMUSG00000044894.8	626.5	281.7	**-2.2**	0.0001	0.0016
Timm13	ENSMUSG00000020219.6	18.3	8.2	**-2.2**	0.0001	0.0016
Ces1h	ENSMUSG00000074156.3	5.3	2.4	**-2.2**	0.0002	0.0051
Col6a2	ENSMUSG00000020241.7	2.0	0.9	**-2.2**	0.0009	0.0165
Plxnc1	ENSMUSG00000074785.3	2.4	1.1	**-2.2**	0.0008	0.0157
Slc7a2	ENSMUSG00000031596.9	124.4	55.1	**-2.3**	0.0002	0.0051
Hand2	ENSMUSG00000038193.3	1.9	0.8	**-2.3**	0.0010	0.0182
Aqp11	ENSMUSG00000042797.7	51.5	22.7	**-2.3**	0.0001	0.0016
P2ry1	ENSMUSG00000027765.1	6.5	2.8	**-2.3**	0.0001	0.0016
2310010J17Rik	ENSMUSG00000085650.2	10.8	4.8	**-2.3**	0.0024	0.0366
Nudt16	ENSMUSG00000032565.7	8.2	3.6	**-2.3**	0.0001	0.0016
BC024139	ENSMUSG00000044361.8	3.2	1.4	**-2.3**	0.0002	0.0051
Mmd	ENSMUSG00000003948.9	71.6	31.4	**-2.3**	0.0001	0.0016
Gm13392	ENSMUSG00000083373.1	201.4	88.0	**-2.3**	0.0018	0.0293
Kcnn2	ENSMUSG00000054477.7	24.2	10.5	**-2.3**	0.0010	0.0182
Inca1	ENSMUSG00000057054.4	16.4	7.1	**-2.3**	0.0002	0.0051
Dpyd	ENSMUSG00000033308.9	153.3	66.3	**-2.3**	0.0001	0.0016
Ces3b	ENSMUSG00000062181.7	466.4	201.3	**-2.3**	0.0012	0.0216
Thrsp	ENSMUSG00000035686.7	678.2	292.6	**-2.3**	0.0007	0.0141
Rnf152	ENSMUSG00000047496.5	3.0	1.3	**-2.3**	0.0001	0.0016
BC021614	ENSMUSG00000058216.6	1313.9	562.9	**-2.3**	0.0007	0.0133
Nat8b	ENSMUSG00000089634.1	73.1	31.3	**-2.3**	0.0001	0.0016
Chchd10	ENSMUSG00000049422.6	184.9	79.1	**-2.3**	0.0001	0.0016
Ndufb7	ENSMUSG00000033938.5	44.1	18.9	**-2.3**	0.0001	0.0016
Gm7866	ENSMUSG00000061390.3	108.5	46.4	**-2.3**	0.0001	0.0016
Gm11507	ENSMUSG00000044639.3	10.0	4.3	**-2.3**	0.0029	0.0423
Gm11407	ENSMUSG00000082179.1	4.5	1.9	**-2.3**	0.0006	0.0118
Gm13340	ENSMUSG00000083563.1	79.7	33.9	**-2.4**	0.0001	0.0016
Gm5054	ENSMUSG00000083812.2	8.6	3.7	**-2.4**	0.0014	0.0237
Pdgfra	ENSMUSG00000029231.9	1.4	0.6	**-2.4**	0.0028	0.0411

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P* value
Tymp	ENSMUSG00000022615.6	39.5	16.6	**-2.4**	0.0001	0.0016
Dnajc12	ENSMUSG00000036764.5	34.5	14.5	**-2.4**	0.0002	0.0041
Ugt2b1	ENSMUSG00000035836.2	366.7	153.9	**-2.4**	0.0014	0.0243
Prdx6-ps2	ENSMUSG00000083737.1	10.9	4.6	**-2.4**	0.0001	0.0029
Eci3	ENSMUSG00000021416.5	17.3	7.2	**-2.4**	0.0001	0.0029
Angptl4	ENSMUSG00000002289.9	34.9	14.6	**-2.4**	0.0001	0.0016
Csrp3	ENSMUSG00000030470.7	25.5	10.6	**-2.4**	0.0001	0.0029
Gm5612	ENSMUSG00000074501.4	12.1	5.0	**-2.4**	0.0010	0.0189
Aspdh	ENSMUSG00000038704.4	49.5	20.5	**-2.4**	0.0001	0.0016
Polg2	ENSMUSG00000020718.6	4.3	1.8	**-2.4**	0.0031	0.0443
Gm13131	ENSMUSG00000081772.1	107.2	44.2	**-2.4**	0.0001	0.0016
Foxq1	ENSMUSG00000038415.8	12.0	4.9	**-2.4**	0.0001	0.0016
Apoa5	ENSMUSG00000032079.5	571.3	234.1	**-2.4**	0.0013	0.0224
Gm4952	ENSMUSG00000071633.4	41.9	17.1	**-2.5**	0.0001	0.0016
Ppm1k	ENSMUSG00000037826.3	13.8	5.6	**-2.5**	0.0001	0.0016
Pllp	ENSMUSG00000031775.4	4.1	1.7	**-2.5**	0.0001	0.0029
Arid5b	ENSMUSG00000019947.8	12.1	4.9	**-2.5**	0.0001	0.0016
Cyp7b1	ENSMUSG00000039519.6	254.1	102.3	**-2.5**	0.0001	0.0016
Mug2	ENSMUSG00000030131.7	126.9	50.7	**-2.5**	0.0001	0.0016
4930528F23Rik	ENSMUSG00000024155.7	23.4	9.3	**-2.5**	0.0001	0.0016
Gm6684	ENSMUSG00000047168.5	11.1	4.4	**-2.5**	0.0003	0.0072
Agmat	ENSMUSG00000040706.4	111.5	44.2	**-2.5**	0.0001	0.0016
Gm14719	ENSMUSG00000082192.1	34.0	13.4	**-2.5**	0.0020	0.0319
Zap70	ENSMUSG00000026117.7	4.2	1.7	**-2.5**	0.0009	0.0174
Sox12	ENSMUSG00000051817.7	1.1	0.4	**-2.5**	0.0004	0.0091
Slc25a47	ENSMUSG00000048856.8	223.2	87.9	**-2.5**	0.0001	0.0016
Abcc6	ENSMUSG00000030834.5	10.0	3.9	**-2.5**	0.0001	0.0016
Ccrn4l	ENSMUSG00000023087.9	8.3	3.3	**-2.5**	0.0001	0.0016
Kdm5d	ENSMUSG00000056673.7	2.7	1.1	**-2.6**	0.0006	0.0118
Cd163	ENSMUSG00000008845.3	2.4	0.9	**-2.6**	0.0018	0.0288
Sucnr1	ENSMUSG00000027762.5	24.5	9.5	**-2.6**	0.0001	0.0016
Dcxr	ENSMUSG00000039450.5	50.3	19.5	**-2.6**	0.0001	0.0016
Nat1	ENSMUSG00000025588.3	2.6	1.0	**-2.6**	0.0003	0.0072
Gm5239	ENSMUSG00000062742.3	58.2	22.3	**-2.6**	0.0001	0.0016
Pdilt	ENSMUSG00000030968.2	3.7	1.4	**-2.6**	0.0005	0.0100
Rpl36-ps3	ENSMUSG00000066629.1	35.5	13.4	**-2.6**	0.0001	0.0016
Cyp2d9	ENSMUSG00000068086.5	677.0	255.7	**-2.6**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*-value
Mup20	ENSMUSG00000078672.2	862.4	325.6	**-2.6**	0.0010	0.0182
Adh4	ENSMUSG00000037797.8	336.2	126.7	**-2.7**	0.0011	0.0196
Necab1	ENSMUSG00000040536.9	16.0	6.0	**-2.7**	0.0002	0.0041
Khdrbs3	ENSMUSG00000022332.7	9.4	3.5	**-2.7**	0.0006	0.0125
Gm14630	ENSMUSG00000081100.1	51.7	19.4	**-2.7**	0.0003	0.0062
Ubd	ENSMUSG00000035186.6	22.6	8.5	**-2.7**	0.0001	0.0016
Amdhd1	ENSMUSG00000015890.2	67.2	24.5	**-2.7**	0.0001	0.0016
Adra1a	ENSMUSG00000045875.5	1.4	0.5	**-2.7**	0.0016	0.0269
Cyp2c50	ENSMUSG00000054827.6	357.9	129.8	**-2.8**	0.0001	0.0016
Colec10	ENSMUSG00000038591.3	7.6	2.8	**-2.8**	0.0001	0.0016
AY036118	ENSMUSG00000045999.8	30.0	10.9	**-2.8**	0.0001	0.0016
Fabp7	ENSMUSG00000019874.5	6.3	2.3	**-2.8**	0.0005	0.0110
Fbln2	ENSMUSG00000064080.6	3.4	1.2	**-2.8**	0.0010	0.0182
Gm8290	ENSMUSG00000074854.3	4.6	1.6	**-2.8**	0.0032	0.0454
Agxt	ENSMUSG00000026272.5	171.2	60.8	**-2.8**	0.0001	0.0016
Pck1	ENSMUSG00000027513.5	568.5	201.4	**-2.8**	0.0004	0.0091
Fam131c	ENSMUSG00000006218.4	2.1	0.7	**-2.8**	0.0007	0.0133
Saa1	ENSMUSG00000074115.3	182.1	64.0	**-2.8**	0.0001	0.0016
Bdh2	ENSMUSG00000028167.9	11.0	3.9	**-2.8**	0.0005	0.0100
Gm7079	ENSMUSG00000068243.6	164.3	57.6	**-2.9**	0.0002	0.0041
Igfbp2	ENSMUSG00000039323.11	225.1	78.8	**-2.9**	0.0001	0.0016
Gm6571	ENSMUSG00000092253.1	2.2	0.8	**-2.9**	0.0006	0.0118
Cyp2g1	ENSMUSG00000049685.7	2.8	1.0	**-2.9**	0.0001	0.0029
1110001J03Rik	ENSMUSG00000019689.4	36.0	12.4	**-2.9**	0.0001	0.0016
Fn3k	ENSMUSG00000025175.6	14.7	5.1	**-2.9**	0.0001	0.0016
Nox4	ENSMUSG00000030562.9	20.2	6.9	**-2.9**	0.0001	0.0016
Lrit1	ENSMUSG00000041044.8	2.5	0.9	**-2.9**	0.0001	0.0016
Ugt3a1	ENSMUSG00000072664.3	88.1	29.4	**-3.0**	0.0001	0.0016
Syt3	ENSMUSG00000030731.7	2.4	0.8	**-3.0**	0.0003	0.0062
Retsat	ENSMUSG00000056666.6	212.5	69.5	**-3.1**	0.0021	0.0324
9130409I23Rik	ENSMUSG00000038768.7	8.5	2.8	**-3.1**	0.0001	0.0016
Marco	ENSMUSG00000026390.1	3.4	1.1	**-3.1**	0.0024	0.0366
Folr2	ENSMUSG00000032725.8	10.5	3.4	**-3.1**	0.0002	0.0041
Spsb4	ENSMUSG00000046997.5	6.5	2.1	**-3.1**	0.0011	0.0196
Gnmt	ENSMUSG00000002769.8	973.3	312.3	**-3.1**	0.0036	0.0493
Sntg2	ENSMUSG00000020672.7	7.0	2.2	**-3.2**	0.0001	0.0029
Chpt1	ENSMUSG00000060002.8	131.3	41.4	**-3.2**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*- value
Tlr5	ENSMUSG00000079164.2	2.2	0.7	**-3.2**	0.0011	0.0203
Gm8215	ENSMUSG00000081409.1	2.2	0.7	**-3.2**	0.0004	0.0091
Gsn	ENSMUSG00000026879.7	12.1	3.7	**-3.2**	0.0001	0.0016
Dpm3	ENSMUSG00000042737.3	22.9	7.1	**-3.2**	0.0001	0.0016
Gpcpd1	ENSMUSG00000027346.9	55.5	17.2	**-3.2**	0.0001	0.0016
Gm11410	ENSMUSG00000083219.1	1.2	0.4	**-3.3**	0.0014	0.0237
Cadm4	ENSMUSG00000054793.7	6.3	1.9	**-3.3**	0.0001	0.0016
2310001H17Rik	ENSMUSG00000085930.1	34.6	10.5	**-3.3**	0.0001	0.0016
Cd207	ENSMUSG00000034783.6	8.9	2.7	**-3.3**	0.0001	0.0016
Serpina3b	ENSMUSG00000066364.2	14.7	4.4	**-3.3**	0.0001	0.0016
Phlda1	ENSMUSG00000020205.6	53.0	15.9	**-3.3**	0.0001	0.0016
Mmp2	ENSMUSG00000031740.7	1.8	0.5	**-3.4**	0.0001	0.0016
Cyp4a12b	ENSMUSG00000078597.2	117.3	34.5	**-3.4**	0.0001	0.0016
AI324046	ENSMUSG00000076615.2	1.5	0.5	**-3.4**	0.0010	0.0189
Cpsf4l	ENSMUSG00000018727.12	8.6	2.5	**-3.4**	0.0031	0.0443
Cyp4a14	ENSMUSG00000028715.2	14.0	4.1	**-3.4**	0.0006	0.0118
Dio1	ENSMUSG00000034785.8	60.7	17.6	**-3.5**	0.0001	0.0016
Upp2	ENSMUSG00000026839.10	364.2	105.1	**-3.5**	0.0001	0.0016
Gm17041	ENSMUSG00000090570.1	25.7	7.4	**-3.5**	0.0002	0.0051
Ndufa3	ENSMUSG00000035674.7	115.1	33.1	**-3.5**	0.0001	0.0016
Mafb	ENSMUSG00000074622.3	9.7	2.8	**-3.5**	0.0001	0.0016
Cyp4a12a	ENSMUSG00000066071.5	301.7	86.3	**-3.5**	0.0003	0.0062
Cyp8b1	ENSMUSG00000050445.4	162.4	45.5	**-3.6**	0.0002	0.0041
Gpx1	ENSMUSG00000063856.5	1139.6	316.8	**-3.6**	0.0001	0.0016
Car1	ENSMUSG00000027556.8	9.1	2.5	**-3.6**	0.0001	0.0016
2610507I01Rik	ENSMUSG00000085882.1	0.7	0.2	**-3.6**	0.0012	0.0216
AI606181	ENSMUSG00000074873.3	0.7	0.2	**-3.8**	0.0001	0.0016
Slc22a7	ENSMUSG00000067144.5	36.8	9.8	**-3.8**	0.0001	0.0016
Cyp2c29	ENSMUSG00000003053.9	890.4	232.7	**-3.8**	0.0002	0.0041
Bmf	ENSMUSG00000040093.9	6.3	1.6	**-3.8**	0.0004	0.0091
Gna14	ENSMUSG00000024697.3	2.9	0.7	**-3.8**	0.0007	0.0133
Slc2a5	ENSMUSG00000028976.4	11.5	3.0	**-3.9**	0.0002	0.0051
Mup-ps21	ENSMUSG00000083524.1	541.1	139.1	**-3.9**	0.0001	0.0016
Dpy19l3	ENSMUSG00000043671.8	34.7	8.8	**-3.9**	0.0018	0.0293
Gm5617	ENSMUSG00000042293.7	6.1	1.5	**-3.9**	0.0001	0.0016
Mcm10	ENSMUSG00000026669.8	87.5	22.1	**-4.0**	0.0001	0.0016
Igkv12-41	ENSMUSG00000076568.1	8.6	2.1	**-4.0**	0.0010	0.0182

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P*-value	adjusted *P*-value
Gm7808	ENSMUSG00000091460.1	227.6	56.5	**-4.0**	0.0001	0.0016
Cxcl13	ENSMUSG00000023078.4	2.5	0.6	**-4.0**	0.0002	0.0041
Gm13203	ENSMUSG00000087273.1	2.7	0.7	**-4.0**	0.0036	0.0499
Nudt7	ENSMUSG00000031767.7	496.3	122.9	**-4.0**	0.0001	0.0016
Hspa1b	ENSMUSG00000090877.2	2.8	0.7	**-4.1**	0.0001	0.0016
Cyp2c54	ENSMUSG00000067225.1	271.7	66.2	**-4.1**	0.0001	0.0016
4930480G23Rik	ENSMUSG00000086332.1	2.3	0.6	**-4.1**	0.0018	0.0293
Hamp	ENSMUSG00000050440.7	6344.3	1492.1	**-4.3**	0.0001	0.0016
Ppargc1b	ENSMUSG00000033871.8	3.8	0.9	**-4.3**	0.0001	0.0016
Ankrd55	ENSMUSG00000049985.7	17.9	4.1	**-4.3**	0.0001	0.0029
Scnn1a	ENSMUSG00000030340.8	4.1	0.9	**-4.3**	0.0001	0.0016
Hamp2	ENSMUSG00000056978.6	646.0	148.7	**-4.3**	0.0001	0.0016
Igkv1-135	ENSMUSG00000076502.1	13.0	3.0	**-4.4**	0.0001	0.0016
Dbp	ENSMUSG00000059824.4	102.1	23.3	**-4.4**	0.0025	0.0378
Klf1	ENSMUSG00000054191.7	2.7	0.6	**-4.4**	0.0001	0.0016
Mup-ps22	ENSMUSG00000080738.1	267.5	60.0	**-4.5**	0.0001	0.0016
Gm13152	ENSMUSG00000078496.3	3.3	0.7	**-4.5**	0.0001	0.0016
1810019J16Rik	ENSMUSG00000037600.10	0.7	0.2	**-4.5**	0.0015	0.0250
Mup-ps3	ENSMUSG00000084242.1	8.9	1.9	**-4.6**	0.0009	0.0165
Zfp458	ENSMUSG00000055480.6	1.9	0.4	**-4.6**	0.0001	0.0016
Gm129	ENSMUSG00000038550.4	14.3	3.1	**-4.7**	0.0002	0.0051
Nr1d1	ENSMUSG00000020889.10	42.0	8.8	**-4.7**	0.0006	0.0118
Gas1	ENSMUSG00000052957.6	4.3	0.9	**-4.8**	0.0001	0.0016
Ces1e	ENSMUSG00000061959.6	142.7	28.8	**-5.0**	0.0001	0.0016
Syde2	ENSMUSG00000036863.6	1.5	0.3	**-5.1**	0.0001	0.0016
Mup-ps19	ENSMUSG00000082644.1	1301.9	251.0	**-5.2**	0.0001	0.0016
1700095J07Rik	ENSMUSG00000084861.1	0.7	0.1	**-5.2**	0.0001	0.0016
Gm13775	ENSMUSG00000081207.3	21.6	4.0	**-5.4**	0.0001	0.0016
Mmd2	ENSMUSG00000039533.7	1.8	0.3	**-5.6**	0.0001	0.0016
Gm13773	ENSMUSG00000086253.1	19.7	3.4	**-5.9**	0.0001	0.0016
1100001G20Rik	ENSMUSG00000051748.2	1194.9	200.0	**-6.0**	0.0001	0.0016
Lect1	ENSMUSG00000022025.7	13.0	2.1	**-6.1**	0.0001	0.0016
Tex12	ENSMUSG00000032065.5	3.4	0.5	**-6.2**	0.0009	0.0165
Cyp2u1	ENSMUSG00000027983.8	33.7	5.3	**-6.4**	0.0001	0.0016
1810046K07Rik	ENSMUSG00000036027.4	4.6	0.7	**-6.4**	0.0001	0.0029
Mup-ps10	ENSMUSG00000082173.1	22.3	3.3	**-6.8**	0.0001	0.0016
2810007J24Rik	ENSMUSG00000030378.7	634.7	93.3	**-6.8**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Saa3	ENSMUSG00000040026.7	88.6	13.0	**-6.8**	0.0001	0.0016
Mitf	ENSMUSG00000035158.8	5.6	0.8	**-6.9**	0.0004	0.0091
Mup-ps14	ENSMUSG00000082065.1	22.7	3.3	**-6.9**	0.0001	0.0016
A2m	ENSMUSG00000030111.8	1.2	0.2	**-6.9**	0.0011	0.0203
Mup4	ENSMUSG00000041333.6	193.3	27.2	**-7.1**	0.0001	0.0016
Gm16002	ENSMUSG00000073835.5	22.4	3.1	**-7.1**	0.0001	0.0016
Igkv16-104	ENSMUSG00000076522.1	11.4	1.6	**-7.2**	0.0002	0.0041
AI428936	ENSMUSG00000019737.7	2.0	0.3	**-7.3**	0.0001	0.0016
2210415F13Rik	ENSMUSG00000013643.7	1.6	0.2	**-7.3**	0.0002	0.0051
Xlr3a	ENSMUSG00000057836.6	3.4	0.5	**-7.3**	0.0001	0.0029
Gm14432	ENSMUSG00000078885.3	3.2	0.4	**-7.4**	0.0031	0.0439
Hsd3b5	ENSMUSG00000038092.5	68.3	9.1	**-7.5**	0.0001	0.0016
Mup-ps13	ENSMUSG00000082425.1	203.6	27.0	**-7.5**	0.0001	0.0016
Mup21	ENSMUSG00000066153.2	1984.0	263.3	**-7.5**	0.0001	0.0016
Pcsk4	ENSMUSG00000020131.8	5.9	0.8	**-7.6**	0.0001	0.0016
AC111115.1	ENSMUSG00000080412.1	460.9	60.0	**-7.7**	0.0001	0.0016
Capn8	ENSMUSG00000038599.8	3.9	0.5	**-7.8**	0.0001	0.0016
Igf2	ENSMUSG00000048583.9	17.2	2.2	**-7.8**	0.0001	0.0029
Aqp4	ENSMUSG00000024411.8	2.0	0.2	**-7.9**	0.0001	0.0016
Mfsd2a	ENSMUSG00000028655.5	25.2	3.2	**-8.0**	0.0001	0.0016
Susd4	ENSMUSG00000038576.8	21.5	2.7	**-8.1**	0.0001	0.0016
Mup-ps4	ENSMUSG00000078685.4	8.7	1.0	**-8.3**	0.0001	0.0016
Clec2h	ENSMUSG00000030364.3	1.5	0.2	**-8.4**	0.0001	0.0016
Rd3	ENSMUSG00000049353.8	1.6	0.2	**-8.7**	0.0003	0.0062
Elovl3	ENSMUSG00000038754.3	20.9	2.3	**-8.9**	0.0001	0.0016
Igkv12-44	ENSMUSG00000076566.1	17.4	1.9	**-9.0**	0.0001	0.0016
Mup-ps7	ENSMUSG00000078679.4	6.5	0.7	**-9.2**	0.0001	0.0029
Mup10	ENSMUSG00000078680.3	6536.7	663.2	**-9.9**	0.0004	0.0091
Slc15a5	ENSMUSG00000044378.5	5.8	0.6	**-10.1**	0.0001	0.0016
Xlr3b	ENSMUSG00000073125.4	1.3	0.1	**-10.2**	0.0002	0.0051
Mup-ps20	ENSMUSG00000084309.1	22.6	2.2	**-10.2**	0.0001	0.0016
Xlr3c	ENSMUSG00000058147.1	1.0	0.1	**-10.6**	0.0008	0.0149
Mup19	ENSMUSG00000078673.3	6046.3	566.9	**-10.7**	0.0001	0.0016
Mup-ps16	ENSMUSG00000090090.1	15.2	1.4	**-10.7**	0.0018	0.0293
Mup11	ENSMUSG00000073834.4	6613.9	615.6	**-10.7**	0.0001	0.0016
Mup18	ENSMUSG00000078674.2	5436.5	504.9	**-10.8**	0.0008	0.0149
Mup17	ENSMUSG00000089681.2	5550.9	506.8	**-11.0**	0.0001	0.0016

Supplemental Table 5: Significantly altered transcripts in E2F7/8 deleted liver tumors vs. wildtype liver identified by RNA sequencing.

Gene Symbol	Ensembl ID	WT mean (n=4)	78DKO tumor mean (n=4)	Fold change (WT vs. 78DKO tumor)	*P* -value	adjusted *P* value
Mup16	ENSMUSG00000078675.3	4673.9	425.1	**-11.0**	0.0001	0.0029
Mup-ps18	ENSMUSG00000082363.1	2743.2	248.1	**-11.1**	0.0001	0.0016
Mup12	ENSMUSG00000073839.6	6968.1	625.1	**-11.1**	0.0001	0.0016
Mup7	ENSMUSG00000073842.4	6025.8	537.0	**-11.2**	0.0029	0.0417
Mup2	ENSMUSG00000078688.4	6757.2	599.4	**-11.3**	0.0005	0.0100
Mup1	ENSMUSG00000078683.2	6514.3	577.1	**-11.3**	0.0002	0.0041
Mup8	ENSMUSG00000078687.3	5370.8	474.2	**-11.3**	0.0001	0.0016
Mup13	ENSMUSG00000089873.2	5255.3	463.4	**-11.3**	0.0008	0.0149
Mup-ps9	ENSMUSG00000081521.1	17.1	1.5	**-11.5**	0.0001	0.0016
Mup-ps2	ENSMUSG00000073840.4	20.0	1.7	**-11.5**	0.0001	0.0016
Dct	ENSMUSG00000022129.2	1.6	0.1	**-11.6**	0.0001	0.0016
Nnmt	ENSMUSG00000032271.7	50.4	4.3	**-11.8**	0.0001	0.0016
Mup-ps6	ENSMUSG00000082813.1	72.9	6.1	**-12.0**	0.0001	0.0016
Mup6	ENSMUSG00000078689.2	392.7	31.7	**-12.4**	0.0001	0.0016
Mup5	ENSMUSG00000058523.2	570.1	45.7	**-12.5**	0.0001	0.0016
Igkv1-133	ENSMUSG00000076503.1	28.7	2.3	**-12.7**	0.0001	0.0016
Mup-ps15	ENSMUSG00000083304.1	12.1	0.9	**-13.5**	0.0001	0.0016
Mup-ps5	ENSMUSG00000082868.1	1166.1	83.8	**-13.9**	0.0001	0.0029
1500017E21Rik	ENSMUSG00000087579.1	34.8	2.1	**-16.3**	0.0001	0.0016
Mup-ps8	ENSMUSG00000078678.4	37.7	2.1	**-18.1**	0.0001	0.0016
Mup-ps17	ENSMUSG00000081053.1	16335.3	895.7	**-18.2**	0.0001	0.0016
C330002G04Rik	ENSMUSG00000087169.2	12.6	0.6	**-19.9**	0.0001	0.0016
Thbs4	ENSMUSG00000021702.7	0.9	0.0	**-26.3**	0.0008	0.0149
Gm2788	ENSMUSG00000085995.1	27.0	0.8	**-32.1**	0.0017	0.0282
Fgf13	ENSMUSG00000031137.11	2.5	0.1	**-33.5**	0.0001	0.0016
Ccdc38	ENSMUSG00000036168.8	1.2	0.0	**-58.4**	0.0003	0.0072
Crabp1	ENSMUSG00000032291.8	2.4	0.0	**-114.8**	0.0001	0.0016

Supplemental Table 6: Putative direct E2F7/8 target genes (developmental)

Gene ID	Expression during development in 78dko livers (4 wks)	regulated by
ATAD2	upregulated	E2F7/8
BRCA2	upregulated	E2F7/8
BRIP1	upregulated	E2F7/8
CDC6	upregulated	E2F7/8
CDCA3	upregulated	E2F7/8
CDT1	upregulated	E2F7/8
CENPH	upregulated	E2F7/8
CENPI	upregulated	E2F7/8
CHAF1A	upregulated	E2F7/8
CHEK1	upregulated	E2F7/8
CLSPN	upregulated	E2F7/8
DSN1	upregulated	E2F7/8
DTL	upregulated	E2F7/8
E2F1	upregulated	E2F7/8
E2F8	upregulated	E2F7/8
EXO1	upregulated	E2F7/8
EZH2	upregulated	E2F7/8
FANCD2	upregulated	E2F7/8
FBXL20	upregulated	E2F7/8
FBXO5	upregulated	E2F7/8
FDPS	upregulated	E2F7/8
GINS3	upregulated	E2F7/8
HELLS	upregulated	E2F7/8
HMGB2	upregulated	E2F7/8
KNTC1	upregulated	E2F7/8
LIG1	upregulated	E2F7/8
LMNB1	upregulated	E2F7/8
MCM2	upregulated	E2F7/8
MCM3	upregulated	E2F7/8
MCM5	upregulated	E2F7/8
MCM6	upregulated	E2F7/8
MLF1IP	upregulated	E2F7/8
NUSAP1	upregulated	E2F7/8
PCNA	upregulated	E2F7/8
POLE	upregulated	E2F7/8
RAD51AP1	upregulated	E2F7/8
RAD54L	upregulated	E2F7/8
RRM2	upregulated	E2F7/8
SPC25	upregulated	E2F7/8
STIL	upregulated	E2F7/8

Supplemental Table 6: Putative direct E2F7/8 target genes (developmental)

Gene ID	Expression during development in 78dko livers (4 wks)	regulated by
TCF19	upregulated	E2F7/8
TIMELESS	upregulated	E2F7/8
TOP2A	upregulated	E2F7/8
UBE2T	upregulated	E2F7/8
UHRF1	upregulated	E2F7/8
CYR61	upregulated	E2F7
E2F7	upregulated	E2F7
PKMYT1	upregulated	E2F7
AARS	upregulated	E2F8
AHCTF1	upregulated	E2F8
BCL6	upregulated	E2F8
BUB3	upregulated	E2F8
CCNA2	upregulated	E2F8
CCNT1	upregulated	E2F8
CDCA5	upregulated	E2F8
CENPK	upregulated	E2F8
CENPL	upregulated	E2F8
CHAC1	upregulated	E2F8
DIDO1	upregulated	E2F8
ESPL1	upregulated	E2F8
KIF11	upregulated	E2F8
KIF18A	upregulated	E2F8
MASTL	upregulated	E2F8
MCM7	upregulated	E2F8
MCM8	upregulated	E2F8
MELK	upregulated	E2F8
NCAPG2	upregulated	E2F8
NPL	upregulated	E2F8
NSL1	upregulated	E2F8
PAK1IP1	upregulated	E2F8
PAWR	upregulated	E2F8
PHGDH	upregulated	E2F8
POLD1	upregulated	E2F8
PRIM1	upregulated	E2F8
PSRC1	upregulated	E2F8
RAD18	upregulated	E2F8
RAD51	upregulated	E2F8
SFPQ	upregulated	E2F8
SGOL2	upregulated	E2F8
SHCBP1	upregulated	E2F8

Supplemental Table 6: Putative direct E2F7/8 target genes (developmental)

Gene ID	Expression during development in 78dko livers (4 wks)	regulated by
SMC2	upregulated	E2F8
SMC4	upregulated	E2F8
SPAG5	upregulated	E2F8
STMN1	upregulated	E2F8
SYCE2	upregulated	E2F8
TPX2	upregulated	E2F8
TRA2A	upregulated	E2F8
TRIP13	upregulated	E2F8
MYC	downregulated	E2F7/8
PHF14	downregulated	E2F7/8
UBC	downregulated	E2F7/8
FST	downregulated	E2F8
GNAT1	downregulated	E2F8
PHLDA3	downregulated	E2F8
TRIM24	downregulated	E2F8
WNK1	downregulated	E2F8

Supplemental Table 7: Putative direct E2F7/8 target genes (tumor)

Gene ID	Expression in 7/8dko liver tumors (12 months)	regulated by
ATAD2	upregulated	E2F7/8
CDC6	upregulated	E2F7/8
CDKN1A	upregulated	E2F7/8
CDKN2C	upregulated	E2F7/8
DPYSL2	upregulated	E2F7/8
E2F1	upregulated	E2F7/8
GGCT	upregulated	E2F7/8
MCM5	upregulated	E2F7/8
MCM6	upregulated	E2F7/8
NUCB2	upregulated	E2F7/8
PLSCR1	upregulated	E2F7/8
RRM2	upregulated	E2F7/8
SLC1A5	upregulated	E2F7/8
SLC2A4	upregulated	E2F7/8
SPC25	upregulated	E2F7/8
TCF19	upregulated	E2F7/8
TOP2A	upregulated	E2F7/8
U1	upregulated	E2F7/8
U2	upregulated	E2F7/8
UHRF1	upregulated	E2F7/8
ABHD2	upregulated	E2F7
CYR61	upregulated	E2F7
EGR1	upregulated	E2F7
PKMYT1	upregulated	E2F7
SEMA6B	upregulated	E2F7
ABI2	upregulated	E2F8
ANO10	upregulated	E2F8
BTG3	upregulated	E2F8
CCNA2	upregulated	E2F8
CD2AP	upregulated	E2F8
CDCA5	upregulated	E2F8
CDK1	upregulated	E2F8
CHMP2B	upregulated	E2F8
CYP1B1	upregulated	E2F8
CYP39A1	upregulated	E2F8
DAPK2	upregulated	E2F8
DLX4	upregulated	E2F8
DSCC1	upregulated	E2F8
DUSP6	upregulated	E2F8
EFNA1	upregulated	E2F8

Supplemental Table 7: Putative direct E2F7/8 target genes (tumor)

Gene ID	Expression in 7/8dko liver tumors (12 months)	regulated by
FST	upregulated	E2F8
HES1	upregulated	E2F8
HMMR	upregulated	E2F8
HSPBAP1	upregulated	E2F8
IER5	upregulated	E2F8
ITGAX	upregulated	E2F8
KAZALD1	upregulated	E2F8
LRFN3	upregulated	E2F8
MTMR11	upregulated	E2F8
NCAPG2	upregulated	E2F8
NES	upregulated	E2F8
PAWR	upregulated	E2F8
PHGDH	upregulated	E2F8
PSRC1	upregulated	E2F8
PTER	upregulated	E2F8
RAD51C	upregulated	E2F8
SERPINE1	upregulated	E2F8
SHANK2	upregulated	E2F8
SMOX	upregulated	E2F8
STMN1	upregulated	E2F8
TAGLN2	upregulated	E2F8
TFRC	upregulated	E2F8
TM4SF1	upregulated	E2F8
TPM4	upregulated	E2F8
TRA2A	upregulated	E2F8
TRIP13	upregulated	E2F8
TUBA1B	upregulated	E2F8
UNC119	upregulated	E2F8
VANGL1	upregulated	E2F8
DERA	downregulated	E2F7/8
MCM10	downregulated	E2F7/8
GCDH	downregulated	E2F7
SLC25A42	downregulated	E2F7
AQP11	downregulated	E2F8
BMF	downregulated	E2F8
CSRNP1	downregulated	E2F8
GCHFR	downregulated	E2F8
GLO1	downregulated	E2F8
GNAT1	downregulated	E2F8

Supplemental Table 7: Putative direct E2F7/8 target genes (tumor)

Gene ID	Expression in 7/8dko liver tumors (12 months)	regulated by
HAUS4	downregulated	E2F8
HINT2	downregulated	E2F8
ID3	downregulated	E2F8
IDO2	downregulated	E2F8
MMD	downregulated	E2F8
PEX16	downregulated	E2F8
PHF17	downregulated	E2F8
POLG2	downregulated	E2F8
SCARB2	downregulated	E2F8

Supplemental Table 8: Contribution of E2F7/8 target genes to canonical pathways

Ingenuity Canonical Pathways	E2F7/8 targets	-log(B-H p-value)	Ratio	Molecules
Cell Cycle Control of Chromosomal Replication	developmental	8.98E00	2.59E-01	MCM5,MCM3,MCM6,MCM2,CDT1,CDC6,MCM7
	tumor	2.48E00	1.11E-01	MCM5,MCM6,CDC6
Role of BRCA1 in DNA Damage Response	developmental	4.5E00	7.69E-02	RAD51,FANCD2,E2F1,BRCA2,BRIP1,CHEK1
	tumor	8.39E-01	2.56E-02	E2F1,CDKN1A
BER pathway	developmental	3.48E00	2.5E-01	LIG1,PCNA,POLE
DNA Double-Strand Break Repair by Homologous Recombination	developmental	3.39E00	2.14E-01	RAD51,LIG1,BRCA2
Mismatch Repair in Eukaryotes	developmental	3.3E00	1.88E-01	PCNA,POLD1,EXO1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	developmental	2.13E00	6.12E-02	TOP2A,PKMYT1,CHEK1
	tumor	3.01E00	8.16E-02	CDKN1A,TOP2A,PKMYT1,CDK1
Cell Cycle: G1/S Checkpoint Regulation	developmental	1.02E00	3.12E-02	PAK1IP1,E2F1
	tumor	1.67E00	4.69E-02	E2F1,CDKN1A,CDKN2C
Cyclins and Cell Cycle Regulation	developmental	8.88E-01	2.56E-02	CCNA2,E2F1
	tumor	3.37E00	6.41E-02	CCNA2,E2F1,CDKN1A,CDKN2C,CDK1

Supplemental Table 9: Functional annotation of E2F7/8 target genes

IPA Category	E2F7/8 targets	B-H *P*-value	Molecules
Cell Cycle	developmental	1.12E-20	LIG1,MCM8,SMC4,DSN1,SFPQ,MELK,KNTC1,BCL6,LMNB1,CHAF1A,STMN1,EZH2,STIL,ESPL1,RAD54L,HELLS,PAWR,MASTL,TPX2,CCNT1,PCNA,SMC2,E2F1,RAD18,AHCTF1,PKMYT1,CLSPN,CYR61,KIF11,BUB3,CDT1,HMGB2,SPAG5,CHEK1,RAD51,CCNA2,FANCD2,TOP2A,SGOL2,CDCA5,EXO1,E2F8,DTL,SYCE2,TRIP13,NUSAP1,UHRF1,POLE,CDC6,SPC25,POLD1,NCAPG2,MCM3,MCM2,CENPI,E2F7,BRCA2,FBXO5,RAD51AP1,KIF18A,CENPH,MCM7
	tumor	3.81E-05	TUBA1B,BTG3,CDKN2C,HES1,STMN1,CCNA2,CD2AP,CHMP2B,TOP2A,CDCA5,RAD51C,PLSCR1,NES,TRIP13,UHRF1,EGR1,CDC6,SPC25,PAWR,CYP1B1,CDK1,NCAPG2,CDKN1A,E2F1,TFRC,PKMYT1,CYR61,TM4SF1
DNA Replication, Recombination, and Repair	developmental	1.12E-20	LIG1,MCM6,MCM8,SMC4,DSN1,SFPQ,MELK,KNTC1,BCL6,CHAF1A,STMN1,EZH2,BRIP1,ESPL1,RRM2,RAD54L,PAWR,HELLS,ATAD2,MASTL,TPX2,PCNA,SMC2,TIMELESS,E2F1,RAD18,CLSPN,CYR61,KIF11,BUB3,CDT1,HMGB2,SPAG5,CHEK1,RAD51,CCNA2,FANCD2,TOP2A,SGOL2,CDCA5,EXO1,DTL,SYCE2,TRIP13,NUSAP1,UHRF1,CDC6,SPC25,POLE,POLD1,UBE2T,NCAPG2,MCM3,CENPI,MCM2,BRCA2,FBXO5,RAD51AP1,KIF18A,CENPH,MCM7
	tumor	6.44E-04	TRIP13,FST,SPC25,CDC6,RRM2,PAWR,ATAD2,CYP1B1,NCAPG2,CDK1,STMN1,CCNA2,CHMP2B,SMOX,CDKN1A,DSCC1,E2F1,TOP2A,CDCA5,RAD51C
Cell Death and Survival	developmental	4.05E-09	LIG1,MCM8,SFPQ,MELK,BCL6,LMNB1,STMN1,EZH2,BRIP1,STIL,ESPL1,DIDO1,RRM2,RAD54L,HELLS,PAWR,ATAD2,TPX2,CCNT1,PCNA,E2F1,AHCTF1,RAD18,PKMYT1,CLSPN,AARS,CYR61,KIF11,CDT1,HMGB2,CHEK1,SPAG5,RAD51,CCNA2,FANCD2,TOP2A,EXO1,E2F8,DTL,NUSAP1,UHRF1,SPC25,CDC6,NCAPG2,FDPS,CENPI,MCM2,E2F7,BRCA2,FBXO5,KIF18A,MCM7
	tumor	1.42E-06	BTG3,DAPK2,HMMR,DUSP6,CDKN2C,DLX4,HES1,UNC119,STMN1,CCNA2,CD2AP,TOP2A,HSPBAP1,RAD51C,SERPINE1,PLSCR1,FST,UHRF1,EGR1,SPC25,CDC6,RRM2,PAWR,SLC2A4,ATAD2,CDK1,CYP1B1,NCAPG2,EFNA1,SMOX,CDKN1A,E2F1,PKMYT1,TFRC,CYR61,TAGLN2
Cancer	developmental	5.57E-07	LIG1,MCM6,MCM8,PAK1IP1,SMC4,SFPQ,DSN1,MELK,KNTC1,BCL6,LMNB1,CHAF1A,NPL,STMN1,EZH2,CDCA3,BRIP1,MCM5,STIL,ESPL1,CENPL,DIDO1,RRM2,FBXL20,RAD54L,HELLS,PAWR,GINS3,ATAD2,TPX2,MASTL,CCNT1,PCNA,SMC2,TIMELESS,E2F1,RAD18,AHCTF1,CLSPN,AARS,CYR61,KIF11,BUB3,CDT1,NSL1,HMGB2,CHEK1,SPAG5,RAD51,TRA2A,CCNA2,PRIM1,FANCD2,PHGDH,TOP2A,SGOL2,CDCA5,E2F8,EXO1,DTL,SYCE2,TRIP13,NUSAP1,PSRC1,UHRF1,SPC25,CDC6,POLE,CENPU,POLD1,UBE2T,NCAPG2,CENPK,FDPS,MCM3,CENPI,MCM2,E2F7,CHAC1,FBXO5,TCF19,BRCA2,KIF18A,RAD51AP1,CENPH,MCM7
Cancer	tumor	3.81E-05	DPYSL2,TUBA1B,MCM6,HMMR,CDKN2C,SEMA6B,HES1,STMN1,CD2AP,CHMP2B,RAD51C,SERPINE1,TPM4,MCM5,ANO10,FST,MTMR11,RRM2,KAZALD1,PAWR,ATAD2,SLC2A4,SMOX,E2F1,TFRC,CYR61,TAGLN2,ABI2,CYP39A1,SLC1A5,DAPK2,BTG3,DUSP6,DLX4,UNC119,LRFN3,TRA2A,CCNA2,PHGDH,ABHD2,TOP2A,HSPBAP1,CDCA5,SHANK2,IER5,PLSCR1,NES,TRIP13,PSRC1,UHRF1,EGR1,VANGL1,CDC6,SPC25,GGCT,CDK1,CYP1B1,NCAPG2,EFNA1,CDKN1A,DSCC1,TCF19,NUCB2,PTER,TM4SF1,ITGAX

Supplemental Table 9: Functional annotation of E2F7/8 target genes

IPA Category	E2F7/8 targets	B-H *P*-value	Molecules
Hepatic System Development and Function	developmental	4.31E-05	E2F1,E2F7,E2F8
	tumor	3.65E-03	EGR1,CDKN1A,E2F1,HES1
Hepatic System Disease	developmental	2.42E-03	CCNA2,POLE,RRM2,TPX2
	tumor	2.00E-02	CCNA2,TOP2A,RRM2,HES1,TM4SF1

Supplemental Table 10: Expression of E2F7/8 regulated targets (developmental) in human liver disease

Gene Symbol	Median expression value					Fold Change (Cirrhotic/Normal)	Cirrhotic *P* -value‡	Fold Change (Adv HCC/Normal)	Adv HCC *P* -value‡
	Normal	Cirrhotic	dysplastic	Early HCC	Advanced HCC				
TOP2A	3.78	3.98	3.95	5.60	8.28	1.05	0.051	2.19	0.000 *
RRM2	5.30	6.15	5.75	7.23	8.97	1.16	0.006 *	1.69	0.000 *
CENPK	2.96	3.40	3.10	3.53	5.00	1.15	0.033 *	1.69	0.000 *
MLF1IP	4.40	4.58	4.84	5.81	7.40	1.04	0.392	1.68	0.000 *
HELLS	3.44	3.91	3.73	4.39	5.75	1.14	0.004 *	1.67	0.000 *
DTL	4.31	4.53	4.45	5.56	7.17	1.05	0.369	1.66	0.000 *
KIF11	3.14	3.35	3.23	3.54	5.21	1.06	0.044 *	1.66	0.000 *
UBE2T	4.55	4.77	4.64	5.60	7.48	1.05	0.188	1.64	0.000 *
SGOL2	3.60	3.78	3.61	4.39	5.86	1.05	0.116	1.63	0.000 *
E2F8	3.33	3.43	3.45	3.78	5.28	1.03	0.051	1.59	0.000 *
EZH2	4.27	4.46	4.50	5.29	6.57	1.04	0.033 *	1.54	0.000 *
UHRF1	4.07	4.46	4.27	4.99	6.13	1.10	0.029 *	1.51	0.000 *
CCNA2	4.08	4.12	3.96	4.49	6.14	1.01	0.512	1.51	0.000 *
CDC6	3.31	3.41	3.47	3.59	4.97	1.03	0.053	1.50	0.000 *
RAD51AP1	4.38	4.51	4.39	5.05	6.38	1.03	0.156	1.46	0.000 *
KIF18A	3.14	3.09	3.12	3.31	4.56	0.98	0.440	1.45	0.000 *
NUSAP1	6.05	6.17	6.02	7.23	8.69	1.02	0.302	1.44	0.000 *
TPX2	5.68	5.84	5.86	6.19	8.10	1.03	0.302	1.42	0.000 *
SPC25	3.33	3.36	3.26	3.47	4.67	1.01	0.128	1.40	0.000 *
SHCBP1	3.06	3.20	3.15	3.47	4.28	1.05	0.011 *	1.40	0.000 *
MELK	5.21	5.37	5.11	6.03	7.17	1.03	0.172	1.38	0.000 *
KNTC1	4.72	4.95	4.84	5.15	6.40	1.05	0.065	1.36	0.000 *
ATAD2	6.54	6.38	6.70	7.79	8.72	0.97	0.917	1.33	0.000 *
TRIP13	4.57	4.60	4.47	5.01	6.02	1.01	0.608	1.32	0.000 *
CENPL	3.93	4.12	4.10	4.42	5.06	1.05	0.006 *	1.29	0.000 *
STMN1	5.90	6.16	5.84	6.61	7.46	1.04	0.015 *	1.26	0.000 *
MCM2	6.14	6.08	6.04	6.28	7.75	0.99	0.739	1.26	0.000 *
CDCA5	5.31	5.24	5.28	5.59	6.71	0.99	0.812	1.26	0.000 *
MCM5	6.39	6.95	6.81	6.81	8.04	1.09	0.033 *	1.26	0.000 *
STIL	4.70	4.82	4.67	5.20	5.89	1.03	0.156	1.25	0.000 *
MASTL	4.49	4.87	4.95	4.88	5.62	1.08	0.083	1.25	0.000 *
HMGB2	7.37	8.17	7.45	8.10	9.17	1.11	0.029 *	1.24	0.000 *
MCM6	7.38	7.73	7.47	7.92	9.02	1.05	0.051	1.22	0.000 *
MCM3	7.04	7.12	7.06	7.18	8.59	1.01	0.223	1.22	0.000 *
NCAPG2	4.78	4.72	4.65	4.99	5.81	0.99	0.896	1.22	0.000 *
PRIM1	6.18	5.64	5.48	6.21	7.49	0.91	0.998	1.21	0.000 *
LMNB1	5.90	5.65	5.62	6.15	7.14	0.96	0.962	1.21	0.000 *
SMC2	5.51	5.40	5.40	5.67	6.61	0.98	0.858	1.20	0.000 *
MCM7	6.97	7.07	7.00	7.35	8.35	1.01	0.416	1.20	0.000 *
PSRC1	4.38	4.55	4.84	4.70	5.19	1.04	0.104	1.18	0.000 *
PAK1IP1	6.66	6.81	7.09	7.73	7.83	1.02	0.281	1.17	0.002 *
SPAG5	6.56	6.68	6.65	6.72	7.69	1.02	0.369	1.17	0.000 *
EXO1	4.87	4.65	4.73	4.95	5.70	0.95	0.979	1.17	0.000 *
SMC4	7.42	7.41	7.53	8.06	8.66	1.00	0.795	1.17	0.000 *
PCNA	8.27	8.67	8.73	8.92	9.63	1.05	0.015 *	1.16	0.000 *
TCF19	5.51	5.46	5.24	5.75	6.38	0.99	0.676	1.16	0.000 *
CDCA3	5.84	5.78	5.73	5.98	6.74	0.99	0.739	1.15	0.000 *

Supplemental Table 10: Expression of E2F7/8 regulated targets (developmental) in human liver disease

Gene Symbol	Median expression value					Fold Change (Cirrhotic/Normal)	Cirrhotic *P*-value‡	Fold Change (Adv HCC/Normal)	Adv HCC *P*-value‡
	Normal	Cirrhotic	dysplastic	Early HCC	Advanced HCC				
DSN1	4.91	4.90	4.77	5.06	5.63	1.00	0.536	1.15	0.000 *
CENPH	4.64	4.55	4.57	4.56	5.32	0.98	0.896	1.15	0.000 *
BUB3	8.31	8.73	8.76	9.20	9.42	1.05	0.001 *	1.13	0.000 *
TIMELESS	6.27	6.13	6.10	6.40	7.10	0.98	0.975	1.13	0.000 *
BRIP1	5.32	4.90	4.91	5.34	6.01	0.92	0.926	1.13	0.005 *
LIG1	6.01	6.04	6.07	6.35	6.74	1.01	0.369	1.12	0.000 *
FBXO5	5.57	5.52	5.55	5.64	6.19	0.99	0.828	1.11	0.001 *
CDT1	5.33	5.24	5.33	5.48	5.90	0.98	0.858	1.11	0.002 *
RAD18	4.83	4.62	4.90	5.02	5.32	0.96	0.758	1.10	0.016 *
NSL1	8.38	8.31	8.48	9.00	9.08	0.99	0.512	1.08	0.000 *
GINS3	4.79	4.78	4.54	4.78	5.19	1.00	0.772	1.08	0.005 *
CLSPN	3.77	3.78	3.84	3.72	4.07	1.00	0.512	1.08	0.003 *
BRCA2	3.24	3.16	3.29	3.21	3.47	0.98	0.884	1.07	0.015 *
FDPS	9.84	9.13	9.16	9.77	10.52	0.93	0.987	1.07	0.003 *
CENPI	3.94	3.79	3.82	3.86	4.21	0.96	0.935	1.07	0.023 *
CHAF1A	6.22	6.10	6.24	6.30	6.63	0.98	0.858	1.07	0.000 *
FANCD2	4.73	4.74	4.76	4.76	5.03	1.00	0.392	1.06	0.023 *
RAD51	4.50	4.36	4.27	4.41	4.78	0.97	0.982	1.06	0.006 *
POLD1	5.91	5.64	5.66	6.04	6.24	0.96	0.967	1.06	0.001 *
CCNT1	7.82	7.95	7.99	8.20	8.22	1.02	0.093	1.05	0.001 *
TRA2A	7.95	8.15	7.92	8.06	8.34	1.02	0.104	1.05	0.004 *
DIDO1	6.63	6.68	6.64	6.74	6.94	1.01	0.142	1.05	0.020 *
NPL	7.62	7.74	7.62	7.65	7.92	1.02	0.044 *	1.04	0.093
AARS	8.99	8.68	8.86	8.85	9.28	0.97	0.917	1.03	0.026 *
SFPQ	4.07	4.12	4.18	4.09	4.20	1.01	0.281	1.03	0.167
RAD54L	4.73	4.58	4.63	4.61	4.84	0.97	0.904	1.02	0.077
ESPL1	5.97	5.73	5.75	5.66	6.10	0.96	0.926	1.02	0.268
E2F1	6.10	5.88	5.92	6.02	6.14	0.96	0.896	1.01	0.193
AHCTF1	6.64	6.55	6.42	7.56	7.43	0.99	0.758	1.12	0.000 *
BCL6	9.06	8.98	9.60	9.64	8.98	0.99	0.464	0.99	0.748
PAWR	7.85	7.74	7.75	8.14	8.10	0.99	0.488	1.03	0.207
FBXL20	7.29	7.11	7.06	7.35	7.31	0.98	0.893	1.00	0.451
PHGDH	8.61	7.40	7.77	6.80	6.93	0.86	0.997	0.81	1.000
POLE	7.11	6.84	6.88	6.82	6.91	0.96	0.907	0.97	0.778
CHAC1	6.04	5.82	5.99	5.56	5.46	0.96	0.758	0.90	0.998
CHEK1	4.98	4.61	4.76	4.78	4.91	0.92	0.999	0.99	0.549
MCM8	4.47	4.40	4.47	4.29	4.40	0.98	0.631	0.98	0.936
SYCE2	4.41	4.21	4.38	4.22	4.26	0.96	0.956	0.96	0.954
E2F7	5.06	4.94	5.14	4.93	4.99	0.98	0.816	0.99	0.763
CYR61	9.86	10.41	9.99	8.66	7.79	1.06	0.025 *	0.79	1.000
PKMYT1	6.45	6.34	6.23	6.22	6.44	0.98	0.942	1.00	0.626

‡ *P*-value vs. normal Wilcoxon method with Benjamini–Hochberg (BH) correction.

*P≤0.05 vs. normal

Supplemental Table 11: Expression of E2F7/8 regulated targets (tumor) in human liver disease

	Median expression value								
Gene Symbol	Normal	Cirrhotic	dysplastic	Early HCC	Advanced HCC	Fold Change (Cirrhotic/Normal)	Cirrhotic *P* -value‡	Fold Change (Adv HCC/Normal)	Adv HCC *P* -value‡
TOP2A	3.78	3.98	3.95	5.60	8.28	1.05	0.051	2.19	0.000 *
HMMR	4.34	4.42	4.53	6.10	7.63	1.02	0.058	1.76	0.000 *
RRM2	5.30	6.15	5.75	7.23	8.97	1.16	0.006 *	1.69	0.000 *
CDK1	4.55	4.95	4.86	5.71	7.54	1.09	0.065	1.66	0.000 *
UHRF1	4.07	4.46	4.27	4.99	6.13	1.10	0.029 *	1.51	0.000 *
CCNA2	4.08	4.12	3.96	4.49	6.14	1.01	0.512	1.51	0.000 *
CDC6	3.31	3.41	3.47	3.59	4.97	1.03	0.053	1.50	0.000 *
SPC25	3.33	3.36	3.26	3.47	4.67	1.01	0.128	1.40	0.000 *
ATAD2	6.54	6.38	6.70	7.79	8.72	0.97	0.917	1.33	0.000 *
TRIP13	4.57	4.60	4.47	5.01	6.02	1.01	0.608	1.32	0.000 *
STMN1	5.90	6.16	5.84	6.61	7.46	1.04	0.015 *	1.26	0.000 *
CDCA5	5.31	5.24	5.28	5.59	6.71	0.99	0.812	1.26	0.000 *
MCM5	6.39	6.95	6.81	6.81	8.04	1.09	0.033 *	1.26	0.000 *
MCM6	7.38	7.73	7.47	7.92	9.02	1.05	0.051	1.22	0.000 *
NCAPG2	4.78	4.72	4.65	4.99	5.81	0.99	0.896	1.22	0.000 *
PSRC1	4.38	4.55	4.84	4.70	5.19	1.04	0.104	1.18	0.000 *
IER5	6.92	7.75	7.52	7.77	8.19	1.12	0.000 *	1.18	0.002 *
TCF19	5.51	5.46	5.24	5.75	6.38	0.99	0.676	1.16	0.000 *
TAGLN2	9.08	9.65	9.62	10.06	10.24	1.06	0.013 *	1.13	0.010 *
MTMR11	5.92	6.20	6.04	6.29	6.50	1.05	0.128	1.10	0.029 *
BTG3	7.46	7.95	7.83	7.95	8.12	1.07	0.093	1.09	0.005 *
CD2AP	7.80	7.73	7.89	8.00	8.48	0.99	0.608	1.09	0.000 *
ABI2	7.02	7.52	7.27	7.35	7.60	1.07	0.000 *	1.08	0.000 *
RAD51C	6.86	6.67	6.59	6.91	7.42	0.97	0.942	1.08	0.029 *
TUBA1B	11.00	11.26	11.14	11.62	11.87	1.02	0.156	1.08	0.001 *
GGCT	8.89	8.88	8.90	9.20	9.49	1.00	0.346	1.07	0.000 *
CDKN2C	6.37	6.23	6.35	6.54	6.76	0.98	0.858	1.06	0.001 *
EFNA1	10.09	10.12	10.52	10.50	10.65	1.00	0.654	1.06	0.014 *
TRA2A	7.95	8.15	7.92	8.06	8.34	1.02	0.104	1.05	0.004 *
SLC1A5	6.11	6.14	6.08	6.04	6.23	1.01	0.242	1.02	0.132
FST	9.86	9.56	9.64	10.00	10.06	0.97	0.758	1.02	0.222
U2	2.94	2.93	2.90	2.94	2.96	1.00	0.512	1.01	0.119
E2F1	6.10	5.88	5.92	6.02	6.14	0.96	0.896	1.01	0.193
SHANK2	7.16	7.46	7.41	8.24	7.79	1.04	0.058	1.09	0.014 *
HSPBAP1	5.46	5.72	5.94	6.27	5.65	1.05	0.038 *	1.03	0.042 *
ANO10	6.52	6.77	6.88	7.15	6.95	1.04	0.011 *	1.07	0.001 *
CYP1B1	6.34	6.89	6.63	6.90	6.45	1.09	0.011 *	1.02	0.356
DAPK2	6.02	5.94	5.92	6.38	6.10	0.99	0.369	1.01	0.077
VANGL1	5.80	6.00	6.01	6.06	6.03	1.03	0.044 *	1.04	0.029 *
PAWR	7.85	7.74	7.75	8.14	8.10	0.99	0.488	1.03	0.207
LRFN3	4.60	4.67	4.60	4.73	4.70	1.02	0.223	1.02	0.252
NUCB2	8.61	8.15	8.34	8.61	8.61	0.95	0.967	1.00	0.549
TFRC	10.08	9.64	11.19	10.32	10.79	0.96	0.631	1.07	0.121
PTER	7.59	7.59	8.12	7.61	7.63	1.00	0.654	1.01	0.510
SMOX	6.33	6.18	6.39	6.18	6.22	0.98	0.962	0.98	0.999
CDKN1A	8.51	9.55	9.31	8.82	7.94	1.12	0.001 *	0.93	0.984
TPM4	6.41	7.18	6.47	6.23	7.14	1.12	0.009 *	1.11	0.033 *

Supplemental Table 11: Expression of E2F7/8 regulated targets (tumor) in human liver disease

	Median expression value								
Gene Symbol	**Normal**	**Cirrhotic**	**dysplastic**	**Early HCC**	**Advanced HCC**	**Fold Change (Cirrhotic/Normal)**	**Cirrhotic *P* -value‡**	**Fold Change (Adv HCC/Normal)**	**Adv HCC *P* -value‡**
DPYSL2	8.93	9.73	8.83	9.07	8.65	1.09	0.001 *	0.97	0.888
TM4SF1	9.58	10.43	10.18	10.00	10.08	1.09	0.001 *	1.05	0.023 *
PLSCR1	9.77	10.45	10.23	9.61	9.05	1.07	0.018 *	0.93	0.977
DUSP6	10.21	10.74	10.21	9.86	9.64	1.05	0.001 *	0.94	0.997
HES1	8.14	8.48	8.47	7.82	7.69	1.04	0.346	0.95	0.984
NES	6.39	6.59	6.17	6.40	6.57	1.03	0.242	1.03	0.102
ITGAX	5.46	5.62	5.42	5.50	5.51	1.03	0.051	1.01	0.252
UNC119	6.88	6.99	6.87	6.93	6.91	1.02	0.142	1.00	0.285
DSCC1	6.07	6.09	6.03	5.93	6.02	1.00	0.654	0.99	0.915
SERPINE1	9.79	8.85	9.20	7.94	7.05	0.90	0.967	0.72	0.999
CYP39A1	9.24	8.41	9.17	7.01	6.23	0.91	0.975	0.67	1.000
PHGDH	8.61	7.40	7.77	6.80	6.93	0.86	0.997	0.81	1.000
CHMP2B	8.28	8.24	8.25	8.21	8.24	1.00	0.719	1.00	0.763
KAZALD1	5.29	5.25	5.19	5.10	5.21	0.99	0.654	0.98	0.833
SLC2A4	4.47	4.26	4.41	4.21	4.21	0.95	0.987	0.94	0.999
DLX4	4.37	4.24	4.27	4.27	4.27	0.97	0.795	0.98	0.943
CYR61	9.86	10.41	9.99	8.66	7.79	1.06	0.025 *	0.79	1.000
PKMYT1	6.45	6.34	6.23	6.22	6.44	0.98	0.942	1.00	0.626
ABHD2	9.61	9.36	9.66	8.84	8.47	0.97	0.631	0.88	0.999
EGR1	12.38	11.73	11.26	10.12	9.41	0.95	0.907	0.76	1.000
SEMA6B	6.89	6.78	6.82	6.70	6.68	0.98	0.982	0.97	0.995

‡ *P* -value vs. normal Wilcoxon method with Benjamini–Hochberg (BH) correction.
*P≤0.05 vs. normal

Supplemental Table 12: Overview of E2F7/8 targets

Developmental targets

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F8	AARS	alanyl-tRNA synthetase	tRNA synthase	--	--
E2F8	AHCTF1	AT hook containing transcription factor 1	cell cycle/ nuclear pore assembly/cell division	--	--
E2F8	BCL6	B-cell CLL/lymphoma 6	gene expression/ zinc finger transcription factor	--	--
E2F7/8	BRCA2	breast cancer 2, early onset	DNA repair	Highly expressed	43
E2F7/8	BRIP1	BRCA1 interacting protein C-terminal helicase 1	cell cycle/ DNA replication	--	--
E2F8	BUB3	BUB3 mitotic checkpoint protein	cell cycle/ spindle checkpoint	--	--
E2F8	CCNT1	cyclin T1	cell cycle/ CDK9 cyclin	--	--
E2F7/8	CDCA3	cell division cycle associated 3	cell cycle/ ubiquitin pathway	Highly expressed, poor prognosis	44
E2F7/8	CDT1	chromatin licensing and DNA replication factor 1	cell cycle/ pre-replication complex	--	--
E2F7/8	CENPH	centromere protein H	cell cycle/ centromere-kinetochore complex	Highly expressed, poor prognosis	45
E2F7/8	CENPI	centromere protein I	cell cycle/ centromere-kinetochore complex	--	--
E2F8	CENPK	centromere protein K	cell cycle/ centromere-kinetochore complex	--	--
E2F8	CENPL	centromere protein L	cell cycle/ centromere-kinetochore complex	--	--
E2F8	CHAC1	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	endoplasmic reticulum stress pathway	--	--
E2F7/8	CHAF1A	chromatin assembly factor 1, subunit A (p150)	cell cycle/ DNA replication	--	--
E2F7/8	CHEK1	checkpoint kinase 1	cell cycle/ Cell cycle arrest	Highly expressed, poor prognosis	46
E2F7/8	CLSPN	claspin	cell cycle/ DNA replication/Cell cycle arrest	--	--
E2F8	DIDO1	death inducer-obliterator 1	apoptosis	--	--
E2F7/8	DSN1	DSN1 homolog, MIS12 kinetochore complex component	cell cycle/ kinetochore assembly	--	--
E2F7/8	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	cell cycle/ ubiquitin pathway	Highly expressed, poor prognosis	47
E2F7	E2F7	E2F transcription factor 7	cell cycle/ transcription factor	--	--
E2F7/8	E2F8	E2F transcription factor 8	cell cycle/ transcription factor	Highly expressed	20
E2F8	ESPL1	extra spindle pole bodies like 1, separase	cell cycle/ separation of sister chromatids	--	--
E2F7/8	EXO1	exonuclease 1	DNA repair	--	--
E2F7/8	EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit	gene expression/ methyltransferase, transcriptional repression	Highly expressed, poor prognosis	48
E2F7/8	FANCD2	Fanconi anemia, complementation group D2	DNA repair	--	--
E2F7/8	FBXL20	F-box and leucine-rich repeat protein 20	ubiquitin pathway	--	--
E2F7/8	FBXO5	F-box protein 5	cell cycle/ ubiquitin pathway	Highly expressed, poor prognosis	49
E2F7/8	FDPS	farnesyl diphosphate synthase	metabolism/ cholesterol and sterol biosynthesis	--	--

Supplemental Table 12: Overview of E2F7/8 targets
Developmental targets (cont)

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F7/8	GINS3	GINS complex subunit 3 (Psf3 homolog)	cell cycle/ DNA replication	--	--
E2F7/8	HELLS	helicase, lymphoid-specific	cell cycle/ DNA repair/DNA methylation	--	--
E2F7/8	HMGB2	high mobility group box 2	DNA repair	Highly expressed, poor prognosis	50
E2F8	KIF11	kinesin family member 11	cell cycle/ spindle dynamics	--	--
E2F8	KIF18A	kinesin family member 18A	microtubule-associated molecular motor	Highly expressed, poor prognosis	51
E2F7/8	KNTC1	kinetochore associated 1	cell cycle/ chromosome segregation	--	--
E2F7/8	LIG1	ligase I, DNA, ATP-dependent	cell cycle/ DNA replication, recombination, and repair	--	--
E2F7/8	LMNB1	lamin B1	nuclear stability, chromatin structure and gene expression	--	--
E2F8	MASTL	microtubule associated serine/threonine kinase-like	microtubule-associated serine/threonine kinase	--	--
E2F7/8	MCM2	minichromosome maintenance complex component 2	cell cycle/ initiation of DNA replication	Highly expressed, poor prognosis	52
E2F7/8	MCM3	minichromosome maintenance complex component 3	cell cycle/ initiation of DNA replication	--	--
E2F8	MCM7	minichromosome maintenance complex component 7	cell cycle/ initiation of DNA replication	Highly expressed, poor prognosis	53
E2F8	MCM8	minichromosome maintenance 8 homologous recombination repair factor	cell cycle/ initiation of DNA replication	--	--
E2F8	MELK	maternal embryonic leucine zipper kinase	cell cycle/ kinase	--	--
E2F7/8	MLF1IP	centromere protein U	cell cycle/ centromere-kinetochore complex	--	--
E2F8	NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	metabolism/ sialic acid	--	--
E2F7/8	NSL1	NSL1, MIS12 kinetochore complex component	cell cycle/ chromosome movements	--	--
E2F8	NUSAP1	nucleolar and spindle associated protein 1	cell cycle/ mitosis	Highly expressed, poor prognosis	54
E2F8	PAK1IP1	PAK1 interacting protein 1	cell-cycle/ ribosomal stress-induced nucleolar protein	--	--
E2F7/8	PCNA	proliferating cell nuclear antigen	cell cycle/ DNA synthesis	Highly expressed, poor prognosis	55
E2F7/8	POLD1	polymerase (DNA directed), delta 1, catalytic subunit	cell cycle/ DNA replication, and repair	Highly expressed	56
E2F8	POLE	polymerase (DNA directed), epsilon, catalytic subunit	cell cycle/ DNA replication, recombination, and repair	--	--
E2F8	PRIM1	primase, DNA, polypeptide 1 (49kDa)	cell cycle/ Okazaki fragments	--	--
E2F8	RAD18	RAD18 E3 ubiquitin protein ligase	cell cycle/ replication fork-stalling	--	--
E2F8	RAD51	RAD51 recombinase	DNA repair	--	--
E2F7/8	RAD51AP1	RAD51 associated protein 1	cell cycle	--	--
E2F7/8	RAD54L	RAD54-like (S. cerevisiae)	DNA repair	--	--

Supplemental Table 12: Overview of E2F7/8 targets

Developmental targets (cont)

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F8	SFPQ	splicing factor proline/glutamine-rich	mRNA trafficking	--	--
E2F8	SGOL2	shugoshin-like 2 (S. pombe)	meiosis	--	--
E2F8	SHCBP1	SHC SH2-domain binding protein 1	cell cycle/ cytokinesis	Highly expressed	57
E2F8	SMC2	structural maintenance of chromosomes 2	cell cycle/ chromosome condensation /DNA repair	--	--
E2F8	SMC4	structural maintenance of chromosomes 4	cell cycle/ chromosome condensation /DNA repair	Highly expressed, poor prognosis	58, 59
E2F8	SPAG5	sperm associated antigen 5	cell cycle/ regulation of mitotic spindles	--	--
E2F7/8	STIL	SCL/TAL1 interrupting locus	cell cycle/ mitotic spindle checkpoint	--	--
E2F8	SYCE2	synaptonemal complex central element protein 2	meiosis	--	--
E2F7/8	TIMELESS	timeless circadian clock	cell survival after damage or stress/ circadian rhythm	Reduced expression, poor prognosis	60
E2F8	TPX2	TPX2, microtubule-associated	cell cycle/ spindle assembly	Highly expressed, poor prognosis	61, 62
E2F7/8	UBE2T	ubiquitin-conjugating enzyme E2T	ubiquitin pathway	--	--

Developmental and tumor targets

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F7/8	ATAD2	ATPase family, AAA domain containing 2	ATPase	Highly expressed, poor prognosis	63-65
E2F8	CCNA2	cyclin A2	cell cycle/ S/M phase cyclin	Highly expressed, poor prognosis	66
E2F7/8	CDC6	cell division cycle 6	cell cycle/ initiation of DNA replication	Highly expressed	67
E2F8	CDCA5	cell division cycle associated 5	cell cycle/ chromatid cohesion	--	--
E2F7	CYR61	cysteine rich angiogenic inducer 61	secreted; interacts with itegrins/heperan sulfate proteoglycan	Highly expressed in primary tumor and metastatic tumors, DNA damage response	68-70
E2F7/8	E2F1	E2F transcription factor 1	cell cycle/ G1/S transcription factor	Highly expressed, poor prognosis	71, 72
E2F7/8	MCM5	minichromosome maintenance complex component 5	cell cycle/ initiation of DNA replication	--	--
E2F7/8	MCM6	minichromosome maintenance complex component 6	cell cycle/ initiation of DNA replication	Highly expressed, poor prognosis	73
E2F8	NCAPG2	non-SMC condensin II complex subunit G2	cell cycle/ chromosome assembly and segregation during mitosis	--	--
E2F8	PAWR	PRKC, apoptosis, WT1, regulator	gene expression/ transcription factor	--	--
E2F8	PHGDH	phosphoglycerate dehydrogenase	metabolism/ enzyme, L-serine synthesis	--	--
E2F7	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	cell cycle/ negatively regulates the G2/M transition	--	--

E2F8	PSRC1	proline/serine-rich coiled-coil 1	cell cycle/ mitosis, microtubule destabilization	Highly expressed	74

Developmental and tumor targets (cont)

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F7/8	RRM2	ribonucleotide reductase regulatory subunit M2	ribonucleotide reductase	Highly expressed	75
E2F7/8	SPC25	SPC25, NDC80 kinetochore complex component	cell cycle/ kinetochore-microtubule interaction and spindle checkpoint activity		
E2F8	STMN1	stathmin 1	destabilizing microtubules	Highly expressed, poor prognosis, regulated by E2F1 in hcc	72, 76
E2F7/8	TCF19	transcription factor 19	PHD-type zinc finger transcription factor	--	--
E2F7/8	TOP2A	topoisomerase (DNA) II alpha	cell cycle/ controls topologic states of DNA during transcription and replication	Highly expressed, poor prognosis	77, 78
E2F8	TRA2A	transformer 2 alpha homolog	regulation of pre-mRNA splicing	Highly expressed	79
E2F8	TRIP13	thyroid hormone receptor interactor 13	gene expression/ hormone-dependent transcription factor/thyroid hormone receptors	--	--
E2F7/8	UHRF1	ubiquitin-like with PHD and ring finger domains 1	E3 ubiquitin ligase	Highly expressed, poor prognosis, induces hypomethylation	80, 81

Tumor targets

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F7	ABHD2	abhydrolase domain containing 2	hydratase	--	--
E2F8	ABI2	abl-interactor 2	tumor suppressor	--	--
E2F8	ANO10	anoctamin 10	calcium-activated chloride channel	--	--
E2F8	BTG3	BTG family, member 3	cell cycle/ anti-proliferative	Reduced expression, poor prognosis	82
E2F8	CD2AP	CD2-associated protein	actin remodeling/membrane trafficking during endocytosis and cytokinesis	--	--
E2F8	CDK1	cyclin-dependent kinase 1	cell cycle/ kinase, G1/S and G2/M transitions	Highly expressed	83
E2F7/8	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	cell cycle/ G1 progression	Highly expressed	84-86
E2F7/8	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	cell cycle/ inhibits Cdk4 and Cdk6	Reduced expression, poor prognosis	87
E2F8	CHMP2B	charged multivesicular body protein 2B	signaling/ recycling and degradation of cell surface receptors	--	--
E2F8	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	metabolism/ procarcinogens to carcinogens, estrogen	--	--
E2F8	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	metabolism/ cholesterol to bile acids	--	--
E2F8	DAPK2	death-associated protein kinase 2	serine/threonine kinase/ pro-apoptotic	--	--

Supplemental Table 12: Overview of E2F7/8 targets

E2F8	DLX4	distal-less homeobox 4	gene expression/ transcription factor, differentiation	Highly expressed, poor prognosis	88
E2F7/8	DPYSL2	dihydropyrimidinase-like 2	Collapsin response mediator proteins/ regulation of neurons	--	--

Tumor targets (cont)

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F8	DSCC1	DNA replication and sister chromatid cohesion 1	cell cycle/ S phase; replication factor C complex	--	--
E2F8	DUSP6	dual specificity phosphatase 6	signaling/ phosphatase, negatively regulates MAPK	Highly expressed, indicates recurrence	89
E2F8	EFNA1	ephrin-A1	signaling/ receptor protein-tyrosine kinase/ development (nervous system/ erythropoiesis)	Highly expressed, indicates recurrence	90, 91
E2F7	EGR1	early growth response 1	gene expression/ transcriptional regulator, MAPK signaling	No expression	92
E2F8	FST	follistatin	signaling/ inhibits follicle-stimulating hormone release	Highly expressed	93
E2F7/8	GGCT	gamma-glutamylcyclotransferase	metabolism/ glutathione catabolism; cell proliferation	--	--
E2F8	HES1	hes family bHLH transcription factor 1	signaling/ Notch, bHLH transcription factor	High expression corrliates with good prognosis	94
E2F8	HMMR	hyaluronan-mediated motility receptor (RHAMM)	cell motility	Highly expressed, poor prognosis	95
E2F8	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	binds heat shock proteins, involved with cell growth and differentiation	Highly expressed	96
E2F8	IER5	immediate early response 5	signaling/ cellular response to mitogenic signals	--	--
E2F8	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	Integrins/ adherence/ neuron marker	--	--
E2F8	KAZALD1	Kazal-type serine peptidase inhibitor domain 1	signaling/ secreted member of the insulin growth factor-binding protein (IGFBP) superfamily	--	--
E2F8	LRFN3	leucine rich repeat and fibronectin type III domain containing 3	development/ neuronal	--	--
E2F8	MTMR11	myotubularin related protein 11	protein phosphatase	--	--
E2F8	NES	nestin	intermediate filament protein	Highly expressed, poor prognosis	97
E2F7/8	NUCB2	nucleobindin 2	metabolism/ energy and insulin resistance	--	--
E2F7/8	PLSCR1	phospholipid scramblase 1	antiviral activity against DNA and RNA viruses including HBV	--	--
E2F8	PTER	phosphotriesterase related		--	--
E2F8	RAD51C	RAD51 paralog C	DNA repair	--	--
E2F7	SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	nervous system development	--	--
E2F8	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	serine proteinase inhibitor inhibitor of tissue plasminogen activator (tPA) and urokinase (uPA)	--	--
E2F8	SHANK2	SH3 and multiple ankyrin repeat domains 2	molecular scaffolds	--	--

Supplemental Table 12: Overview of E2F7/8 targets

E2F7/8	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	transporter/ sodium-dependent neutral amino acid transporter that can act as a receptor for RD114/type D retrovirus	Highly expressed	98

Tumor targets (cont)

Promoter occupied by	Gene	Name	Function	in HCC (human tumors) by qPCR, IHC, IB	ref
E2F7/8	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4	transporter/ insulin-regulated facilitative glucose transporter	--	--
E2F8	SMOX	spermine oxidase	metabolism/ catalyzes the oxidation of spermine to spermadine and secondarily produces hydrogen peroxide	--	--
E2F8	TAGLN2	transgelin 2	actin regulation	--	--
E2F8	TFRC	transferrin receptor	signaling/ cell surface receptor necessary for cellular iron uptake	Highly expressed	99
E2F8	TM4SF1	transmembrane 4 L six family member 1	signaling/ cell development, activation, growth and motility	Highly expressed	100
E2F8	TPM4	tropomyosin 4	actin-binding, contraction	--	--
E2F8	TUBA1B	tubulin, alpha 1b	cell cycle/ cytoskeleton component	Highly expressed, poor prognosis	101
E2F7/8	U1	RNA, U1 small nuclear 1	splicing of pre-mRNAs	--	--
E2F7/8	U2	RNA, U2 small nuclear 1	splicing of pre-mRNAs	--	--
E2F8	UNC119	unc-119 lipid binding chaperone	signaling/ G protein trafficking, SRC-type tyrosine kinases	Highly expressed, poor prognosis	102
E2F8	VANGL1	VANGL planar cell polarity protein 1	signaling/ WNT, cell polarity	Highly expressed	103

Supplemental Table S13: Oligonucleotide sequences used for genotyping

Allele(s)	Primer 1	Primer 2	Primer 3
Cre	CCTGTTTTGCACGTTCACCG	ATGCTTCTGTCCGTTTGCCG	
$E2f7^{+}$, $E2f7^{fl}$, $E2f7^{\Delta}$,	AGGCAGCACACTTGACACG	ACTTTTGGGACAGAGGTAGGA	CCAAGATGAAGGCCGAGATGCTAC
$E2f8^{+}$, $E2f8^{fl}$, $E2f8^{\Delta}$, $E2f8^{-}$	TAAAAAGCTTTGCGGTCGTT	AAGCCAACCTCGATGAATTG	CTCGCATCATCGTCTGCTAA
$E2f8^{+}$, $E2f8^{fl}$, $E2f8^{\Delta}$, $E2f8^{-}$	CTCGCATCATCGTCTGCTAA	CCTGAGTTTGATCCACAGCA	GGGAATTCAAAGCCTCACAA
$E2f8^{+}$, $E2f8^{DBD}$	TTTTTAAATCGAAGGCGGAAGGTC	CAGGTACAGTCCCCAGCAGT	

Supplemental Table S14: Oligonucleotide sequences used for quantitative PCR

Gene symbol	**Forward (5’ -> 3’)**	**Reverse (5’ -> 3’)**
E2f7	GATGCGTTCGTGAACTCCCTG	AGAAACTTCTGGCACAGCAGCC
E2f8	GAGAAATCCCAGCCGAGTC	CATAAATCCGCCGACGTT
Gapdh	GAAGGTCGGTGTGAACGG	TGAAGGGGTCGTTGATGG

Supplemental Table S15: Oligonucleotide sequences used for ChIP-qPCR

Gene symbol	**Forward (5’ -> 3’)**	**Reverse (5’ -> 3’)**
CDC6	AAAGGCTCTGTGACTACAGCCA	GATCCTTCTCACGTCTCTCACA
MCM3	AGGGGAGGAACAGAGAATCC	CGCTGCCAAAGAACTACCTC
MCM5	ATTGTTCCGCACACAAAATG	ACCAGGGGAGACAAGAACCT
TUBA4A	ATGGAGGGATGAATGGTTATGC	CTTTTTGGGTCTGGCTTCTTTCAC
UHFR1	AGAGTTCAGGGGGTCTGTACC	ACTCGGCATTTGGGAGTTG
CHEK1	GCTGTCTTGCTTTACGGCG	ACTGTCCTTTGCCCACCAC
FDPS	GGGCACATTGGGAGTTGTAG	CTTGTTGGCGGGTACTCCTA
MCM2	GTTCCGTAGGGCTCTTCCCG	CAGTACCACGATCCTCTCCGC
PRIM1	CGCCAATTCCTGTGGTAATC	CCATCACCTCCACCGTAGTT
RAD51	GCTCAGACGATACTCTCGCCTC	CGCTAACCCAAGACGGGAG
TIMELESS	GAGTGAGTGTGTGGCGAGAG	CGGGAGACTAAGGAGCAGAG
TOP2A	CGGGCTAAAGGAAGGTTCA	AAGCGACTAAACAGGCAGGA
TOP2Aneg	TCAGGATTCCCATCTTCCTG	GAAAGGGTGGAGTGGTGCTA