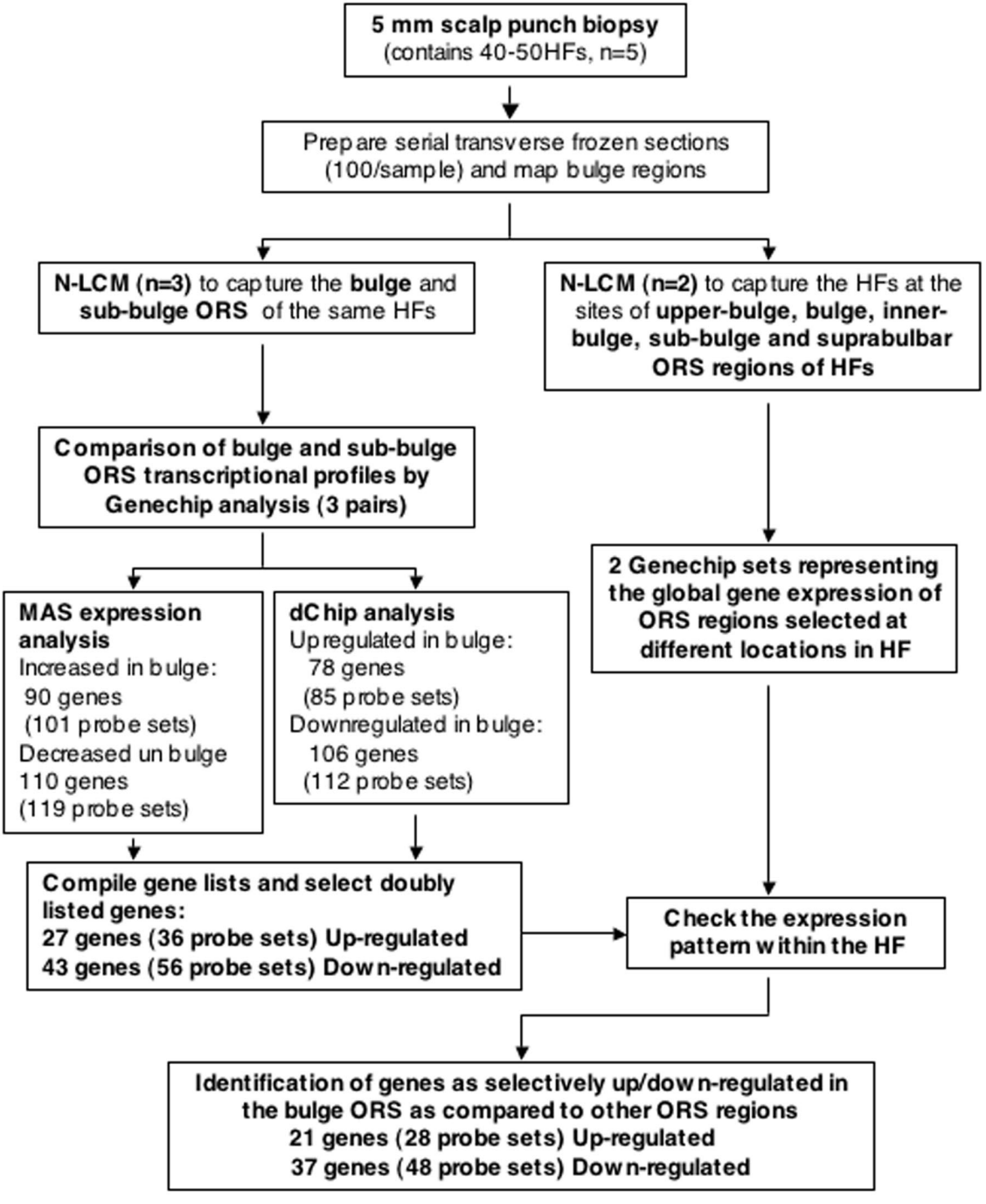
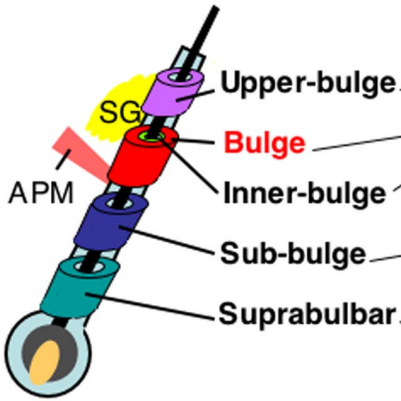
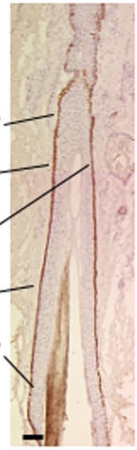
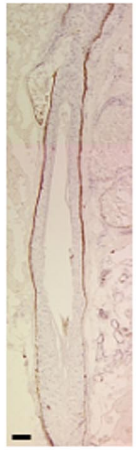
S Figure 1

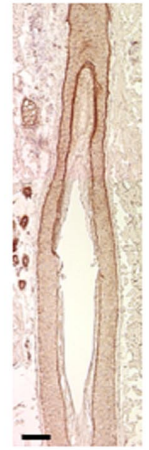

5 mm scalp punch biopsy
(contains 40-50HFs, n=5)
Prepare serial transverse frozen sections
(100/sample) and map bulge regions
N-LCM (n=3) to capture the bulge and sub-bulge ORS of the same HFs
N-LCM (n=2) to capture the HFs at the sites of upper-bulge, bulge, inner-bulge, sub-bulge and suprabulbar ORS regions of HFs
Comparison of bulge and sub-bulge ORS transcriptional profiles by Genechip analysis (3 pairs)
2 Genechip sets representing the global gene expression of ORS regions selected at different locations in HF
MAS expression analysis
Increased in bulge:
90 genes
(101 probe sets)
Decreased un bulge
110 genes
(119 probe sets)
dChip analysis
Upregulated in bulge:
78 genes
(85 probe sets)
Downregulated in bulge:
106 genes
(112 probe sets)
Compile gene lists and select doubly listed genes:
27 genes (36 probe sets) Up-regulated
43 genes (56 probe sets) Down-regulated
Check the expression pattern within the HF
Identification of genes as selectively up/down-regulated in the bulge ORS as compared to other ORS regions
21 genes (28 probe sets) Up-regulated
37 genes (48 probe sets) Down-regulated

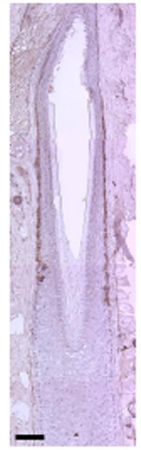
S Figure 2

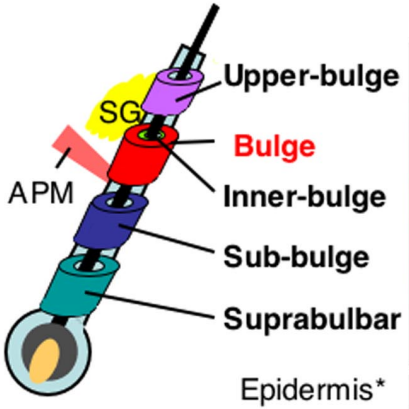






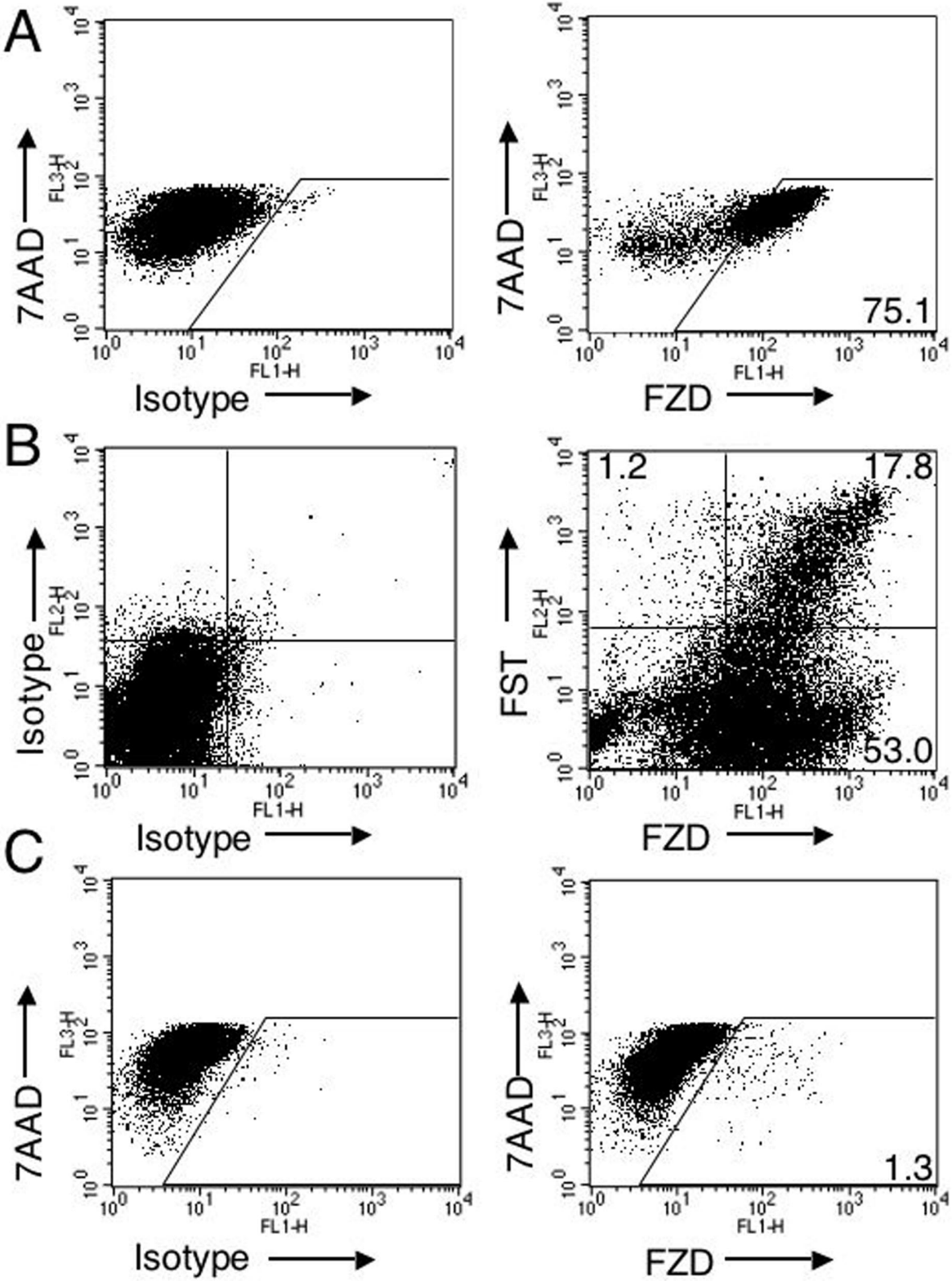




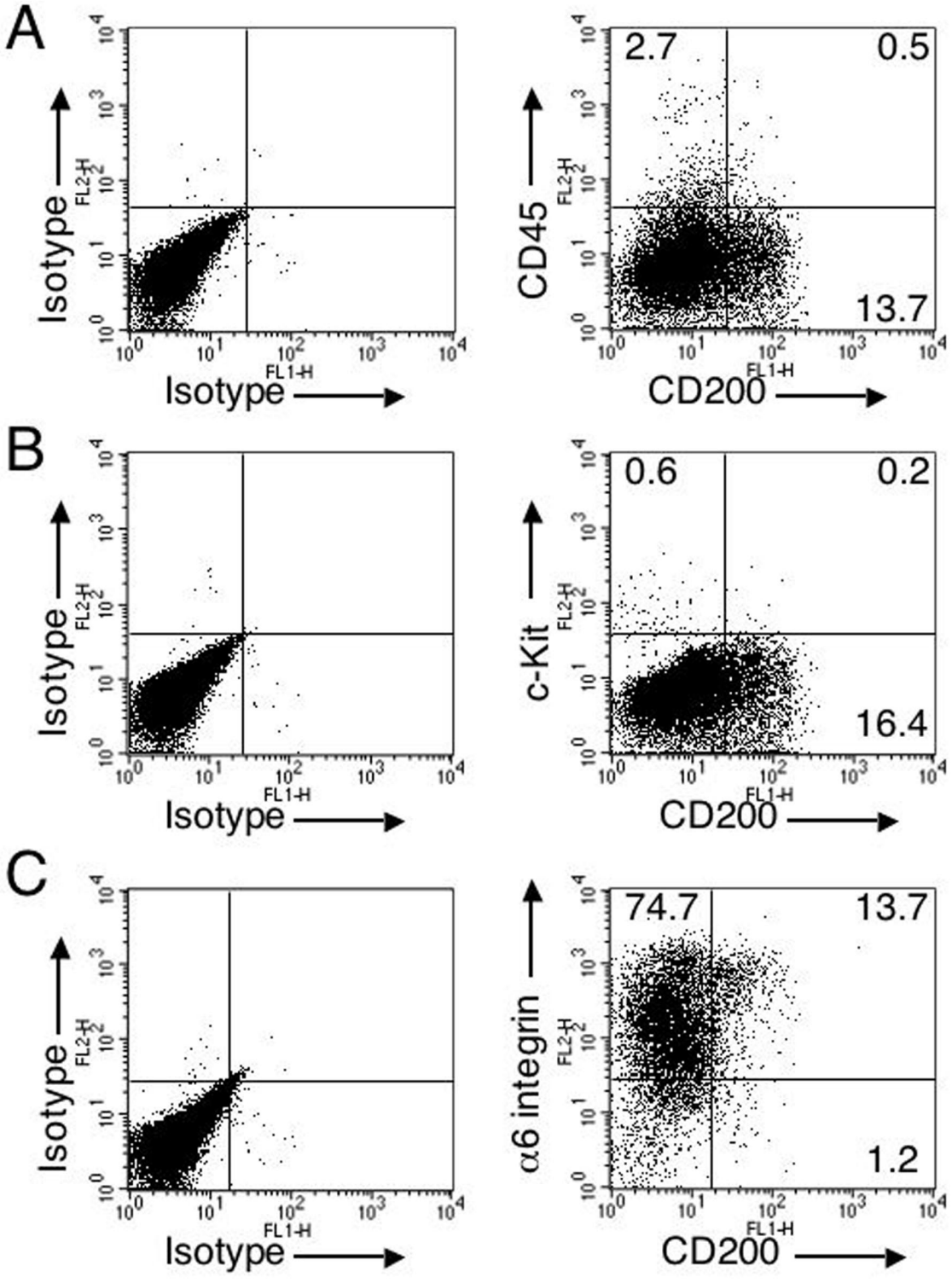


	KRT15 (204734_at)	FST (204948_s_at)	FZD1 (204451_at)	PHLDA1 (217996_at)
Upper-bulge	5776.5 P 5301.7 P	298.8 P 331.9 P	438.8 P 732.9 P	235.0 P 196.4 P
Bulge	5969.4 P 5013.0 P	252.4 A 179.8 P	385.1 P 692.6 P	210.2 P 120.0 P
Inner-bulge	149.5 A 301.0 P	391.4 A 163.9 A	219.6 A 224.2 P	67.3 P 73.4 P
Sub-bulge	5653.7 P 4846.8 P	163.9 A 122.6 A	394.3 P 435.9 P	67.5 P 61.2 P
Suprabulbar	3157.0 P 3524.6 P	115.2 A 103.2 A	280.0 P 258.3 A	46.0 P 84.0 P
Epidermis*	2633.6 P	107.7 A	284.9 P	189.9 P

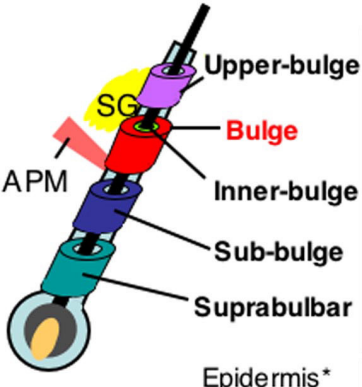
S Figure 3


A
7AAD
FL3-H
FL1-H
Isotype
FZD
75.1
B
Isotype
FL2-H
FST
1.2
17.8
53.0
C
1.3

S Figure 4

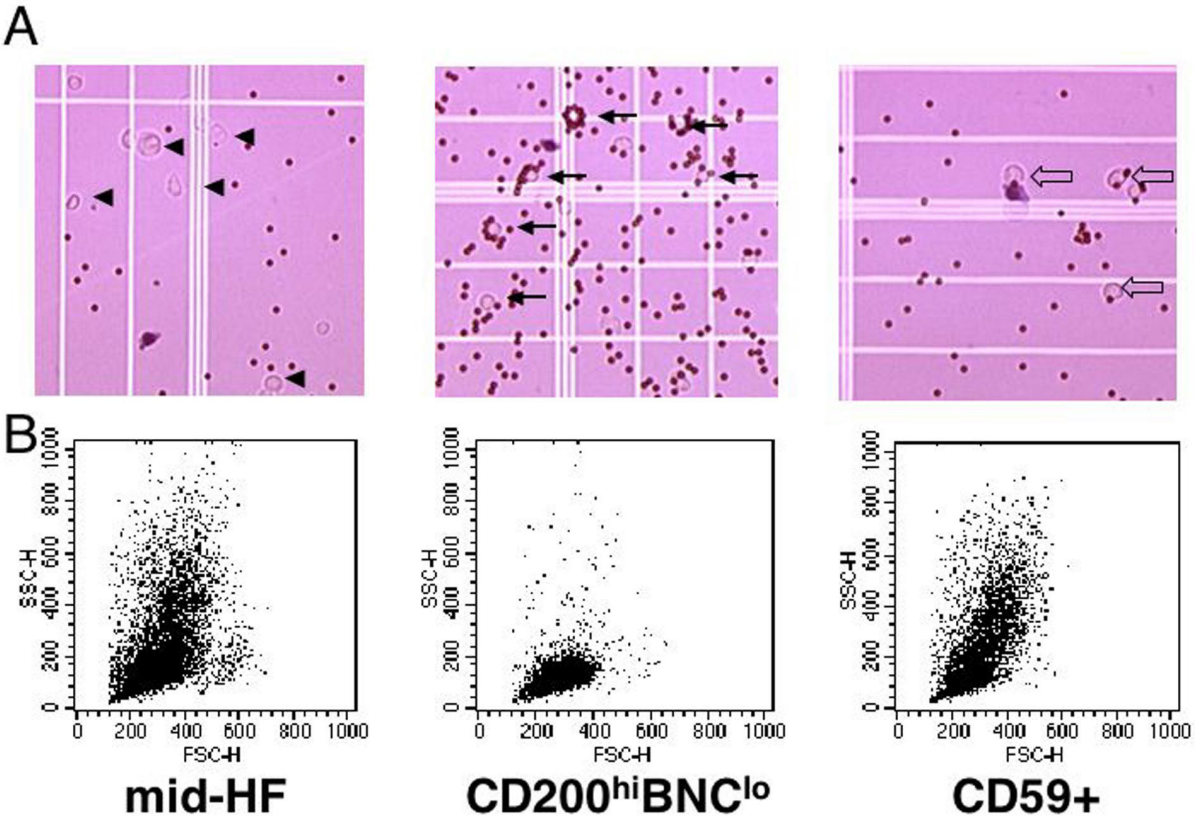

A
Isotype
Isotype
FL2-H
FL1-H
CD45
CD200
2.7
0.5
13.7
B
Isotype
Isotype
c-Kit
CD200
0.6
0.2
16.4
C
Isotype
Isotype
α6 integrin
CD200
74.7
13.7
1.2

S Figure 5



	CD59 (200985_s_at)	CD200 (209583_s_at)	CD24 (216379_x_at)	CD34 (209543_s_at)	CD71 (207332_s_at)	CD146 (209087_x_at)
Upper-bulge	867.7 P 909.9 P	285.4 P 395.8 P	732.1 P 1053.4 P	94.6 P 92.3 P	756.2 P 738.9 P	309.4 P 310.7 P
Bulge	990.9 P 979.4 P	278.9 P 230.3 P	509.9 P 993.4 P	109.3 P 77.2 P	666.1 P 735.7 P	436.8 P 504.0 P
Inner-bulge	468.0 P 643.2 P	47.8 A 110.9 P	6221.6 P 5051.5 P	117.9 P 76.1 A	729.1 P 638.3 P	181.4 P 279.4 P
Sub-bulge	768.0 P 751.3 P	84.2 P 135.0 P	415.9 P 635.0 P	157.7 P 185.6 P	772.9 P 911.1 P	719.4 P 720.9 P
Suprabulbar	831.4 P 624.6 P	107.6 P 102.7 P	373.6 P 773.5 P	268.4 P 151.5 P	982.2 P 1242.8 P	926.9 P 1162.0 P
Epidermis*	806.0 P	26.2 A	5743.6 P	68.5 A	713.7 P	82.5 P

S Figure 6



Supplemental Figure 1

Genechip data analysis. Three pairs of bulge and sub-bulge ORS Genechips were analyzed and compared by MASv5.0 and dChip 1.3 software algorithms in order to identify gene transcripts that were over-represented or under-represented in the bulge ORS by both algorithms. Two additional sets of Genechips were generated form the ORS regions of upper-bulge, bulge, inner-bulge, sub-bulge and suprabulbar ORS in order to precisely localize gene expression within the hair follicle. Genes that were not selectively and specifically over- or under-represented in the bulge ORS were excluded. Each Genechip pair or set was generated from an individual volunteer.

Supplemental Figure 2

The correlation between mRNA expression patterns and immunohistochemical findings for gene transcripts over-represented in bulge ORS. The upper panels demonstrate human hair follicle vertical sections stained with designated mAbs. Scale bars: 50μm.The lower boxes indicate the Genechip signal intensities (mRNA expression levels) detected for individual genes from corresponding ORS subsets. Genechips were normalized to the same parameters. The gene expression patterns correlated well with the immunohistochemical staining patterns of gene products in the ORS. Red and blue numbers indicate individual samples. P: detected as “expressed” or present according to MASv5.0 algorithm. A: detected as “not expressed” or absent according to MASv5.0 algorithm. Parenthesis; Probe set ID of Affymetrix U-133 Genechip sets. *Epidermis; Signal intensities in Genechips generated from human foreskin epidermis are shown.

Total RNA was isolated from epidermal sheet and RNA probes were generated by single-round amplification. Normalized to the same parameters as ORS Genechips.

Supplemental Figure 3

Anti-FZD1 monoclonal antibody could detect the bulge ORS cells in fixed mid-follicle cell suspension but not living mid-follicle cells. **(A)** Consistent with microarray and immunohistochemistry data, approximately 70% of fixed mid-follicle cells were variably FZD1 positive by FACS analysis. **(B)** The $FZD1^{hi}FST^{hi}$ cells in fixed mid-follicle suspension represented bulge ORS cells. **(C)** Anti-FZD1 antibody could only detect approximately 1% of living mid-follicle cells, suggesting that FZD1 detection by this mAb requires fixation.

Supplemental Figure 4

Mid-follicle $CD200^{hi}$ cells were $CD45^{lo}$ $c\text{-}Kit^{lo}$ and $\alpha 6$ integrin ^{hi}. **(A)** A mid-follicle cell suspension was stained for CD200 and CD45. Most of $CD200^{hi}$ cells were distinct form $CD45^{hi}$ bone marrow derived cells. **(B)** A mid-follicle cell suspension was stained for CD200 and c-Kit (CD117). Most of $CD200^{hi}$ cells were distinct from $c\text{-}Kit^{hi}$ melanocytes or mast cells. **(C)** A mid-follicle cell suspension was stained for CD200 and $\alpha 6$ integrin (CD49f). Most $CD200^{hi}$ cells were $\alpha 6$ $integrin^{hi}$. Gated to non-fixed living cells based on 7-AAD negative staining.

Supplemental Figure 5

Genechip data sets for the CD markers identified in human hair follicle. Numbers

in boxes indicate the signal intensities for each CD marker (mRNA expression levels) in the indicated ORS subsets. Red and blue numbers indicate individual experiments. P: detected as "expressed" or present according to MASv5.0 algorithm. A: detected as "not expressed" or absent according to MASv5.0 algorithm. Parenthesis; Probe set ID of Affymetrix U-133 Genechip sets. *Epidermis; signal intensities in Genechips generated from human foreskin epidermis. Total RNA was isolated from epidermal sheet and RNA probes were generated by single-round amplification. Normalized to the same parameters as ORS Genechips.

Supplemental Figure 6

Isolated $CD200^{hi}BNC^{lo}$ bulge cells were uniform, relatively compact and smooth when compared to mid-follicle cells or CD59+ hair follicle cells. $CD200^{hi}BNC^{lo}$ bulge cells were isolated from mid-follicle cell suspension by magnetic beads selection. **(A)** By light microscopy, isolated living bulge $CD200^{hi}$ cells (Arrows) possessed compact and smooth morphology compared to mid-follicle (arrowheads) cells or $CD59^{hi}$ cells (open arrows) isolated from mid-follicle suspension. Stained with trypan blue. Original magnification 400x. **(B)** FACS analysis confirmed the microscopic observation. Living 7-AAD negative cells were gated. Magnetic beads were also gated out.

Supplemental table 1. Genes detected as up-regulated in human bulge by MAS 5.0 software

Gene	Probe set	Mouse bulge	Bulge 1		Sub-bulge 1		Fold change 1	Bulge 2		Sub-bulge 2		Fold change 2	Bulge 3		Sub-bulge 3		Fold change 3	Average Fold change
trinucleotide repeat containing 9 (TNRC9)	216623_x_at		110.6	P	38.3	P	2.89	112.3	P	1.6	A	70.19	145.1	P	12.9	A	11.25	28.11
trinucleotide repeat containing 9 (TNRC9)	214774_x_at		188.7	P	33.8	P	5.58	132.5	P	2.2	A	60.23	191.3	P	32.5	A	5.89	23.90
deiodinase, iodothyronine, type II (DIO2)	203699_s_at		964.3	P	140.3	P	6.87	685.5	P	27.5	A	24.20	3173.7	P	171.8	P	18.47	16.52
Small proline-rich protein SPRK human, odontogenic keratocysts (SPRR1A)	213796_at		720.4	P	354.9	P	2.03	1473.1	P	86.8	A	16.97	302	P	33.9	A	8.91	9.30
adenylate cyclase 2 (brain) (ADCY2)	213217_at		339.1	A	168.6	A	2.01	162.2	A	8.9	A	18.22	198.7	A	89.6	A	2.22	7.48
cystatin EM (CST6)	206595_at		2407.2	P	1310	P	1.84	2468.3	P	201	P	12.28	1526.9	P	222.6	P	6.86	6.99
DBCCR1-like (DCCR1L)	217562_at		82.3	P	33.2	P	2.48	72.4	P	10.6	A	6.83	225.5	P	20.4	A	11.05	6.79
Wnt inhibitory factor-1 (WIF1)	204712_at	***	1359.3	P	746.1	P	1.82	1205.3	P	105.8	P	11.39	1407	P	356.1	P	3.95	5.72
deiodinase, iodothyronine, type II (DIO2), transcript variant 1	203700_s_at		937.2	P	197	P	4.76	359.9	P	91.6	P	3.93	1811.3	P	214.6	P	8.44	5.71
aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3)	209160_at		162.7	P	66.9	P	2.43	83.7	P	53.5	P	1.56	195.6	P	15	A	13.04	5.68
trinucleotide repeat containing 9 (TNRC9)	215108_x_at		131.2	P	26.6	P	4.93	108.1	P	15.8	A	6.84	92.8	P	22.8	A	4.07	5.28
dickkopf (Xenopus laevis) homolog 3 (DKK3)	202196_s_at	*,**	324.8	P	129.6	P	2.51	132	P	40.1	A	3.29	338.8	P	41.6	P	8.14	4.65
aquaporin 3 (AQP3)	39248_at		2143.7	P	1108.3	P	1.93	1530.2	P	312	P	4.90	1474.3	P	215.7	P	6.83	4.56
pleckstrin homology-like domain, family A, member 1(PHLDA1)	217996_at		214.2	P	63.2	P	3.39	104.2	P	27.5	A	3.79	255.7	P	60.4	P	4.23	3.80
calcium/calmodulin-dependent protein kinaseII (CaMKIINalpha)	218309_at		559	P	253.8	P	2.20	325.4	P	55.6	P	5.85	563.4	P	177.2	P	3.18	3.74
dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT)	205337_at		209	P	144.6	P	1.45	142.6	P	21.8	A	6.54	426.4	P	148.9	P	2.86	3.62
monooxygenase, DBH-like 1 (MOXD1)	209708_at		308.1	P	71.7	P	4.30	139.4	P	69.3	P	2.01	334	P	76.4	A	4.37	3.56
estrogen receptor 1 (ESR1)	205225_at		470.2	P	110.6	P	4.25	149	P	82.8	A	1.80	389.1	P	84.2	M	4.62	3.56
mRNA; cDNA DKFZp779H233 (from clone DKFZp779H233)	206652_at		29.4	P	27.3	A	1.08	42.5	P	6.9	A	6.16	28.8	P	8.9	A	3.24	3.49
creatine kinase, mitochondrial 1 (ubiquitous) (CKMT1), nuclear gene encoding mitochondrial protein	202712_s_at		205.1	P	89.5	P	2.29	141.7	P	61	A	2.32	405.1	P	70.3	P	5.76	3.46
dickkopf (Xenopus laevis) homolog 3 (DKK3)	214247_s_at	*,**	3238.3	P	1711.8	P	1.89	2221.9	P	669	P	3.32	3113.5	P	695.5	P	4.48	3.23
RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1)	205590_at		143.6	P	37.3	P	3.85	48.7	P	33.1	A	1.47	152.1	P	36.2	P	4.20	3.17
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin6A) (SEMA6A)	215028_at		118.4	P	68.5	P	1.73	108.5	P	28.2	M	3.85	157.5	P	40.7	A	3.87	3.15
angiopoietin-like 2 (ANGPTL2)	213004_at		242.8	P	126.4	P	1.92	143.7	P	65	P	2.21	203.4	P	43.1	P	4.72	2.95
protein tyrosine phosphate, receptor type, D (PTPRD)	213362_at		117	P	55.4	M	2.11	27.6	A	7.6	A	3.63	158.8	P	51.2	A	3.10	2.95
family with sequence similarity 13, memberA1 (FAM13A1)	202972_s_at		643.8	P	347.1	P	1.85	470.1	P	154	P	3.05	1280.3	P	356.2	P	3.59	2.83
Ral guanine nucleotide exchange factor RalGPS1A (RalGPS1A)	204199_at		144.7	P	60	P	2.41	93.8	P	49.8	A	1.88	125	P	30.3	A	4.13	2.81
Forkhead box C1 (FOXC1)	**213260_at**		**618**	**P**	**338.4**	**P**	**1.83**	**455.2**	**P**	**99.3**	**P**	**4.58**	**443.7**	**P**	**222.1**	**P**	**2.00**	**2.80**
zinc finger, BED domain containing 1 (ZBED1)	203043_at		353.3	P	204.1	P	1.73	268.4	P	53.9	A	4.98	555.9	P	342	P	1.63	2.78
nebulette (NEBL)	**203962_s_at**		**258.8**	**P**	**136**	**P**	**1.90**	**229.5**	**P**	**60.9**	**P**	**3.77**	**170.7**	**P**	**70.8**	**P**	**2.41**	**2.69**
pleiomorphic adenoma gene 1 (PLAG1)	205372_at		117.6	P	156.2	P	0.75	145.5	P	32.7	P	4.45	205.1	P	77.1	P	2.66	2.62
phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) (PIK3R1)	212239_at		617.1	P	408.2	P	1.51	680.5	P	148.3	P	4.59	787	P	480.8	P	1.64	2.58
angiopoietin-like 2 (ANGPTL2)	213001_at		747.5	P	314.1	P	2.38	340.1	P	176.8	P	1.92	738.5	P	221.2	P	3.34	2.55
fibroblast growth factor 13 (FGF13)	205110_s_at		101.1	P	44.7	A	2.26	133.5	P	36	A	3.71	69.8	P	42.2	A	1.65	2.54
signal peptide, CUB domain, EGF-like 2	219197_s_at		217.6	P	94.3	P	2.31	235.8	P	140.3	P	1.68	728.1	P	200.4	P	3.63	2.54
dihydropyrimidinase-like 2 (DPYSL2)	200762_at		1930.8	P	1196.5	P	1.61	1306	P	395.3	P	3.30	1571	P	589.8	P	2.66	2.53
seizure related 6 homolog (mouse)-like (SEZ6L)	213609_s_at		186.6	P	74	A	2.52	110.9	P	42.2	A	2.63	259.2	P	107.5	A	2.41	2.52
decorin (DCN)	211896_s_at		544.4	P	417.7	P	1.30	367	P	111.2	P	3.30	507.6	P	171.9	P	2.95	2.52
nebulette (NEBL)	203961_at		971.7	P	314.7	P	3.09	434.7	P	184.8	P	2.35	602.3	P	289.2	P	2.08	2.51
LERK-5 (EPLG5, ephrin-B2, EFNB2)	202669_s_at	*	152.2	P	110.9	P	1.37	154.8	P	38.2	A	4.05	382.6	P	192.5	P	1.99	2.47
hypothetical protein FLJ10847 (FLJ10847)	219525_at		296.4	P	170.7	P	1.74	174	P	90.2	A	1.93	427	P	114.5	P	3.73	2.46
hypothetical protein FLJ11795 (FLJ11795)	220112_at		74.4	P	34.1	A	2.18	65.7	P	55.6	A	1.18	45.5	P	11.9	A	3.82	2.40
SCLAC2-B	214734_at		569.6	P	294.3	P	1.94	995.6	P	350.6	P	2.84	1456.5	P	623.6	P	2.34	2.37
serine (or cysteine) proteinase inhibitor, clade), member 1 (SERPINF1)	202283_at		504.7	P	286.2	P	1.76	261.2	P	85.8	A	3.04	1054.1	P	458.6	P	2.30	2.37
dihydropyrimidinase-like 3 (DPYSL3)	201431_s_at		575.4	P	296.7	P	1.94	210.5	P	87.2	M	2.41	424.6	P	154.4	P	2.75	2.37
protein tyrosine phosphate, receptor type, D (PTPRD)	214043_at		392.2	P	260.4	P	1.51	179.4	P	93.1	P	1.93	421.4	P	115	P	3.66	2.37
very long-chain acyl-CoA synthetase; lipidosin (BG1)	209465_at		218.4	P	106.5	P	2.05	142	P	50.2	A	2.83	167.8	M	80.3	A	2.09	2.32
major histocompatibility complex, classII, DQ beta2 (HLA-DQB2)	215536_at		122.6	P	48.3	P	2.54	75.3	P	89.4	P	0.84	202	P	56.3	M	3.59	2.32
transforming growth factor-beta-2 (TGFB2)	209909_s_at	*	173.5	P	107.3	P	1.62	108.3	P	33.2	P	3.26	169.2	P	91.9	P	1.84	2.24
golgi phosphoprotein 4 (GOLPH4)	204324_s_at		382.2	P	223.6	P	1.71	351.7	P	116.3	P	3.02	484.2	P	271.4	P	1.78	2.17
phospholipase C-beta-1 (PLCB1, PLC-I)	213222_at		351.1	P	151.7	P	2.31	312.9	P	169.8	P	1.84	546.1	P	235.7	P	2.32	2.16
decorin (DCN)	201893_x_at		2344.3	P	1447	P	1.62	1506.8	P	581.9	P	2.59	1961.7	P	877.9	P	2.23	2.15
latrophilin 3 (LPHN3)	209866_s_at		853.2	P	693.7	P	1.23	1083	P	368.8	P	2.94	1478.1	P	652.7	P	2.26	2.14
abhydrolase domain containing 6 (ABDH6)	45288_at		104.4	P	72.1	P	1.45	93.8	P	42.2	P	2.22	143.9	P	53.3	P	2.70	2.12
Ca2+-dependent activator protein for secretion 2 (CADPS2)	219572_at		369	P	209.1	P	1.76	417.9	P	179.6	P	2.33	395.8	P	175.6	P	2.25	2.12
aldo-keto reductase family1, member C2 (AKR1C2)	211653_x_at		153.9	P	59.1	P	2.60	66.6	P	37	A	1.80	167.2	A	89.6	P	1.87	2.09
met proto-oncogene (hepatocyte growth factor receptor) (MET)	203510_at		248.1	P	130.7	P	1.90	123.8	P	67.1	P	1.85	200.5	P	80.6	P	2.49	2.08
KIAA1036 protein	203940_s_at		559.8	P	293.8	P	1.91	327.4	P	141.5	P	2.31	1870.1	P	933.8	P	2.00	2.07
Keratin15 (KRT15)	204734_at	**	5305.8	P	2529.3	P	2.10	3439.1	P	1727.1	P	1.99	8583.3	P	4038.1	P	2.13	2.07
bromodomain containing 2 (BRD2)	214911_s_at		782.4	P	631.7	P	1.24	900.6	P	283.1	P	3.18	1746.9	P	1038.3	P	1.68	2.03
growth-arrest-specific 6 (Gas6)	1598_g_at	*,**(Gas1)	995	P	499.9	P	1.99	754.6	P	306	P	2.47	1546.4	P	944.9	P	1.64	2.03
C-terminal binding protein 2 (CTBP2)	210835_s_at	*	1904.8	P	1112.1	P	1.71	1490.3	P	861.2	P	1.73	2319.4	P	890.9	P	2.60	2.02
dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT)	205338_s_at		285.4	P	116.7	P	2.45	145.5	P	95	A	1.53	386.5	P	195.7	P	1.97	1.98
CD200 antigen (CD200)	209583_s_at	**	261.7	P	171.4	P	1.53	107	P	86	P	1.24	390.7	P	123.2	P	3.17	1.98
60S Ribosomal Protein L21 pseudogene and an HNRNP A3 pseudogene	217322_x_at		36.4	P	24.6	A	1.48	45.5	P	14.1	A	3.23	51.8	P	42.5	A	1.22	1.98
glycoprotein M6B (GPM6B)	209167_at		377.5	P	231.1	A	1.63	277.2	P	108.3	A	2.56	315.7	M	191.2	A	1.65	1.95
latrophilin 3 (LPHN3)	209867_s_at		828.8	P	569.8	P	1.45	1031.7	P	587.2	P	1.76	1011.9	P	391.8	P	2.58	1.93
chromogranin A (parathyroid secretory protein 1) (CHGA)	204697_s_at		76.8	P	62.3	A	1.23	97.1	P	41.1	A	2.36	144.2	P	65.7	A	2.19	1.93
collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive) (COL7A1)	204136_at		405.9	P	218.6	P	1.86	304.7	P	185.8	P	1.64	1139.6	P	511.9	P	2.23	1.91
solute carrier family 43, member 3 (SLC43A3)	213113_s_at		367.5	P	186.2	P	1.97	342.8	P	188.8	P	1.82	710.4	P	375.9	P	1.89	1.89
inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2)	201565_s_at	*,**	275.7	A	173.2	A	1.59	339.5	M	136.8	A	2.48	420.1	A	265.1	A	1.58	1.89
Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10)	216620_s_at		819.2	P	430.2	P	1.90	583.3	P	421.4	P	1.38	967	P	418.1	P	2.31	1.87
glycoprotein M6B (GPM6B)	209170_s_at		234	P	115.3	P	2.03	117.8	P	51.9	A	2.27	130.1	P	101.2	P	1.29	1.86
nuclear factor (erythroid-derived 2)-like 1	200758_s_at		279.3	P	158.1	P	1.77	217.6	P	99.6	A	2.18	464.8	P	305.5	P	1.52	1.82
pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 1 (PLEKHA1)	219024_at		273	P	218.9	P	1.25	332.3	P	156.1	P	2.13	472.8	P	227.4	P	2.08	1.82
Hypothetical LOC389177	217016_x_at		41.8	P	35.9	A	1.16	51.3	P	28.5	A	1.80	33.5	P	13.7	A	2.45	1.80
Follistatin (FST)	204948_s_at	*(Fstl)	200.1	P	102.7	A	1.95	199.4	P	109.4	A	1.82	189.9	P	117.5	A	1.62	1.80
zinc finger protein (ZFD25)	205739_x_at		122	P	79.3	P	1.54	98.5	P	60.2	M	1.64	81.7	P	37.9	P	2.16	1.78
C-terminal binding protein 2 (CTBP2), transcript variant 1	201220_x_at	*(CTBP2)	1395.6	P	937.2	P	1.49	1266.4	P	824.1	P	1.54	2290.2	P	1063.5	P	2.15	1.73
regulated in glioma (RIG)	221127_s_at		218.9	P	128.3	P	1.71	89.2	P	57.5	A	1.55	160.3	P	83.8	P	1.91	1.72
dual specificity phosphatase 1 (DUSP1)	201041_s_at		295.3	P	158.8	P	1.86	311.1	P	203.4	P	1.53	1184.5	P	768.6	P	1.54	1.64
natural killer-tumor recognition sequence (NKTR)	202379_s_at		562.3	P	375.5	P	1.50	503.1	P	332.1	P	1.51	1065.2	P	581.8	P	1.83	1.61
TDP-glucose 4,6-dehydratase (TGDS)	208249_s_at		224.4	P	181.5	P	1.24	267.6	P	160.5	P	1.67	321.8	P	172.8	P	1.86	1.59
A kinase (PRKA) anchor protein 1 (AKAP1)	201674_s_at		256.5	A	176.6	A	1.45	162.7	A	194.4	A	0.84	653.7	P	269.5	A	2.43	1.57
ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	215577_at		90.7	P	46.8	A	1.94	63.1	P	48.4	A	1.30	79.4	P	56.4	A	1.41	1.55
chromosome 14 open reading frame 78 (C14orf78)	212992_at		1942	P	1301.3	P	1.49	1297.3	P	808.2	P	1.61	1829.6	P	1192.6	P	1.53	1.54
Homo sapiens frizzled (Drosophila) homolog 1 (FZD1)	204451_at	*,**(FZD2)	514.8	P	376.3	P	1.37	585.7	P	298.3	P	1.96	535.7	P	412.6	P	1.30	1.54
FXYD domain-containing ion transport regulator 6 (FXYD6)	217897_at		247.1	P	238.7	P	1.04	252.8	P	115.2	P	2.19	753.4	P	538.6	P	1.40	1.54
parvin, alpha (PARVA)	215418_at		113.6	P	74.7	A	1.52	82.8	P	76.7	A	1.08	109.3	P	59.7	A	1.83	1.48
dystonin (DST)	212254_s_at		2952.4	P	2076.2	P	1.42	2125.7	P	1484.5	P	1.43	2952.3	P	1905.2	P	1.55	1.47
hypothetical protein LOC283445	49452_at		173.8	P	125.6	P	1.38	155.5	P	113.2	A	1.37	193.7	P	118.7	P	1.63	1.46
nuclear factor of activated T-cells 5, tonicity-resonsive (NFAT5)	208003_s_at		297.9	P	230.9	P	1.29	296.5	P	140.4	P	2.11	287.7	P	314.4	P	0.92	1.44
recombining binding protein supressor of hairless (Drosophila) (RBPSUH)	211974_x_at		1002.7	P	751	P	1.34	1023	P	638.8	P	1.60	1711.3	P	1349.1	P	1.27	1.40
immunoglobulin superfamily, member 4 (IGSF4)	209031_at	*,**	395.3	P	249.1	P	1.59	236.6	P	184.6	P	1.28	490.7	P	377	P	1.30	1.39
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1)	211105_s_at	*	439	P	275.1	P	1.60	377.3	P	297	P	1.27	538.4	P	413.5	P	1.30	1.39
POU domain, class 2, transcription factor 1 (POU2F1)	206789_s_at		115.2	P	101.2	A	1.14	104.6	P	119	A	0.88	169.4	P	80.2	A	2.11	1.38
transient receptor potential cation channel, subfamily V, member 2)	219282_s_at		55.1	P	22.3	A	2.47	21.1	P	30.4	A	0.69	30.9	P	32.5	A	0.95	1.37
calmodulin 1(phosphorylase kinase, delta) (CALM1)	211984_at		413.3	P	287	P	1.44	244.1	P	213.4	P	1.14	360.5	P	239.4	P	1.51	1.36
plexin A1 (PLXNA1)	221537_at	**(Plxn2)	92.9	P	108.8	A	0.85	88.1	P	54.6	A	1.61	128	P	83.2	A	1.54	1.34
zinc fingers ans homeoboxes 3 (ZHX3)	217367_s_at		87.5	P	70	A	1.25	110.7	P	77.2	A	1.43	84.4	P	69.7	A	1.21	1.30
nebulette protein (NEBL)	216882_s_at		83.5	P	53	A	1.58	54.5	P	63.8	A	0.85	84	P	57.9	A	1.45	1.29

Numbers indicate signal intensities detected for each probe sets
P: "present" call, detected as expressed, A: "Absent" call, detected as not expressed.

Bold: Up-regulated in both MAS 5.0 and dChip analysis

Underline: "membrane" protein annotated by GOA analysis

Mouse bulge column: asterisks indicate the up-regulation of same or similar genes in mouse bulge transcription profiling data
* Tumbar et al. Science, 303 359-363, 2004.
**Morris et al. Nat Biotechnol, 22 411-417, 2004.
*** Fuchs et al. Cell 116 769-778, 2004.
parenthesis: gene of similar function was detected as upregulated.

Supplemental table 2. Genes detected as down-regulated in human bulge by MAS 5.0 software

Gene	Probe set	Bulge 1	Sub-bulge 1	Fold change 1	Bulge 2	Sub-bulge 2	Fold change 2	Bulge 3	Sub-bulge 3	fold change 3	Average fold change
microfibrillar associated protein 5 (MFAP5)	213764_s_at	72.2P	648.8P	8.99	70.7P	471.3P	6.67	1.2A	108.1P	90.08	35.25
cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP)	205713_s_at	113.9P	1175.2P	10.32	412.6P	992.1P	2.40	50.9A	1723.2P	33.85	15.53
angiopoietin-like 7 (ANGPTL7)	206423_at	628.5P	4165.6P	6.63	2422.9P	5226P	2.16	111.5P	2068.6P	18.55	9.11
endothelin receptor type B (EDNRB)	204273_at	82.5P	264.1P	3.20	69.4P	187.6P	2.70	2.7A	44.5P	16.48	7.46
aldehyde oxidase 1 (AOX1)	205083_at	119.3A	163.8P	1.37	68.7M	149.1P	2.17	3.3A	48.9A	14.82	6.12
wingless-type MMTV integration site family, member 5A (WNT5A)	213425_at	48.2P	652.6P	13.54	313.4P	467.7P	1.49	43.4P	143.9P	3.32	6.12
topoisomerase (DNA) II alpha (170kD) (TOP2A)	201292_at	80.5P	198.4P	2.46	207.7P	469.2P	2.26	15.3A	207.7P	13.58	6.10
protocadherin 8 (PCDH8)	206935_at	39.5P	225.4P	5.71	180.1P	314.6P	1.75	31.8P	187.9P	5.91	4.45
aminolevulinate, delta-, dehydratase (ALAD)	218487_at	180.5P	1034.8P	5.73	312P	1176.6P	3.77	180.4A	638.7P	3.54	4.35
calcium channel voltage-dependent alpha2/delta3 subunit (CACNA2D3)	219714_s_at	10.2A	57.6A	5.65	52.8A	120.9A	2.29	9.5A	48.1A	5.06	4.33
microfibrillar associated protein 5 (MFAP5)	213765_at	66.7P	291.5P	4.37	38.5P	117.3P	3.05	11.3A	60P	5.31	4.24
tripartite motif protein TRIM9 isoform alpha (TRIM9)	209859_at	142.3P	429P	3.01	178.7P	658.6P	3.69	69.7P	361.6P	5.19	3.96
wingless-type MMTV integration site family, member 5A (WNT5A)	205990_s_at	248.2P	1329.4P	5.36	647.9P	1095.9P	1.69	94.2A	412.3P	4.38	3.81
fibroblast growth factor 18 (FGF18)	211029_x_at	63.3P	214.6P	3.39	155.4P	407P	2.62	61.2A	316P	5.16	3.72
prostaglandin E receptor 4 (subtype EP4) (PTGER4)	204897_at	141.3P	272.7P	1.93	243.4P	794.6P	3.26	20.9A	115.8P	5.54	3.58
tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)	201147_s_at	167.3P	421.1P	2.52	240.1P	652.8P	2.72	87A	472.3P	5.43	3.55
keratin associated protein 1-3 (KRTAP1-3)	220978_at	37.5A	97.7P	2.61	59.6A	292.6P	4.91	37A	97.7P	2.64	3.39
fibroblast growth factor 18 (FGF18)	206987_x_at	77.8A	234.8P	3.02	155.7P	482.1P	3.10	85.8A	318.5P	3.71	3.28
matrix Gla protein (MGP)	202291_s_at	1321.4P	2617P	1.98	1430P	3909.4P	2.73	473P	2384.6P	5.04	3.25
platelet derived growth factor C (PDGFC)	218718_at	398.9P	1106.4P	2.77	830.8P	1647.9P	1.98	227.5P	832.6P	3.66	2.81
cell division cycle 2, G1 to S and G2 to M (CDC2)	203213_at	69.8P	192.2P	2.75	167P	429.5P	2.57	59.3P	170.6P	2.88	2.73
isochorismatase domain containing 1 (ISOC1)	218170_at	299.4P	1137.7P	3.80	823.3P	1299.3P	1.58	228.8P	635.9P	2.78	2.72
tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)	201150_s_at	621P	1840.3P	2.96	1353.4P	1893.5P	1.40	515.7P	1772.8P	3.44	2.60
syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated) (SDC2)	212158_at	396.3P	1221.5P	3.08	766.7P	1649.8P	2.15	281.2P	717P	2.55	2.59
ets variant gene 5 (ets-related molecule) (ETV5)	203349_s_at	158.8P	379.7P	2.39	209.8P	384.1P	1.83	161.9P	575.2P	3.55	2.59
proprotein convertase subtilisinkexin type 5 (PCSK5)	205559_s_at	57P	112.5P	1.97	83.5P	330.3P	3.96	36.6A	58.2P	1.59	2.51
hyaluronan-mediated motility receptor (RHAMM) (HMMR)	207165_at	78.2P	173.2P	2.21	167.1P	347.3P	2.08	58.4A	188.3P	3.22	2.51
EH-domain containing 3 (EHD3)	218935_at	221.9M	484.4P	2.18	310P	923P	2.98	178.9P	417.6P	2.33	2.50
laminin, beta 1 (LAMB1)	201505_at	108P	261.9P	2.43	207.6P	383.3P	1.85	37.1P	116.2P	3.13	2.47
growth hormone receptor (GHR)	205498_at	103.6P	168P	1.62	127.2P	329.3P	2.59	35.4M	111.1P	3.14	2.45
KIAA0101 gene product (KIAA0101)	202503_s_at	353.7P	548.1P	1.55	580.2P	1679.2P	2.89	216.7P	626.5P	2.89	2.44
nucleolar and spindle associated protein 1 (NUSAP1)	218039_at	282.7P	668.1P	2.36	729.4P	1617.8P	2.22	265.9P	725P	2.73	2.44
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13)	217272_s_at	134.9P	249.7P	1.85	210.5P	416.8P	1.98	57.5A	189P	3.29	2.37
solute carrier family 30 (zinc transporter), member1 (SLC30A1)	212907_at	233.3P	400.5P	1.72	428.5P	1292.6P	3.02	218.7P	479.9P	2.19	2.31
collagen, type XI, alpha 1 (COL11A1)	37892_at	1042P	1825.1P	1.75	1324P	2778.1P	2.10	409.3P	1227.3P	3.00	2.28
solute carrier family 1 (glutamateneutral amino acid transporter), member 4 (SLC1A4)	212810_s_at	242.7P	491.9P	2.03	478.5P	1026.2P	2.14	199.7P	533P	2.67	2.28
response gene to complement 32 (RGC32)	218723_s_at	219.3P	435.1P	1.98	160.1P	214.2P	1.34	39A	132.7P	3.40	2.24
lipoma HMGIC fusion partner (LHFP)	218656_s_at	255.4P	377.5P	1.48	427.6P	727.1P	1.70	58A	205.5P	3.54	2.24
phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL)	202990_at	278.9P	627.4P	2.25	456.7P	681.9P	1.49	197.5P	564.6P	2.86	2.20
protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C)	204284_at	397.9P	798.6P	2.01	517.2P	791.5P	1.53	259.3P	756.5P	2.92	2.15
basic helix-loop-helix domain containing, class B, 3 (BHLHB3)	221530_s_at	355.5P	497.8P	1.40	244.5P	647.8P	2.65	194.7A	467.8P	2.40	2.15
glypican 4 (GPC4)	204984_at	183.8P	278P	1.51	260.1P	397.4P	1.53	122.9P	411.5P	3.35	2.13
KIAA0186 gene product (KIAA0186)	206102_at	59A	110.7P	1.88	116.7P	178.1P	1.53	63.1A	183P	2.90	2.10
MAD2 (mitotic arrest deficient, yeast, homolog)-like 1 (MAD2L1)	203362_s_at	39.9P	135P	3.38	166.6P	245.3P	1.47	54.2P	77.6P	1.43	2.10
solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7)	209884_s_at	58.2P	165.6P	2.85	105.9P	167.5P	1.58	22.6A	40.8P	1.81	2.08
Rac GTPase activating protein 1 (RACGAP1)	222077_s_at	128.3P	295.3P	2.30	269P	476.9P	1.77	90.7P	193.1P	2.13	2.07
carbonic anhydrase II (CA2)	209301_at	75.5P	174.6P	2.31	177P	250.4P	1.41	37.8A	90.2P	2.39	2.04
phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A)	210145_at	98.9P	214.2P	2.17	173.3P	297.6P	1.72	151.3P	326.3P	2.16	2.01
RAD51-interacting protein (RAD51AP)	204146_at	39.9P	105.4P	2.64	101.9P	237.9P	2.33	54P	55.3P	1.02	2.00
adenosine A2b receptor (ADORA2B)	205891_at	111.1A	149.4A	1.34	154.9P	255.9P	1.65	88.7A	264.4P	2.98	1.99
karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2)	211762_s_at	71.6P	146.4P	2.04	197.4P	341.3P	1.73	104.9P	223.3P	2.13	1.97
ZW10 interactor (ZWINT)	204026_s_at	227.3P	487.8P	2.15	420.1P	821.6P	1.96	227.6P	407.3P	1.79	1.96
endothelin receptor typeB (EDNRB)	204271_s_at	189P	275.2P	1.46	130.6P	258.5P	1.98	62.5P	149.5P	2.39	1.94
ribonucleotide reductase M2 polypeptide (RRM2)	201890_at	95.8A	242P	2.53	260.4P	429.2P	1.65	124.6P	192.6P	1.55	1.91
melanoma adhesion molecule (MCAM, CD146)	209087_x_at	439P	832.8P	1.90	723.4P	1139.8P	1.58	306.9P	683.5P	2.23	1.90
phosphoglycerate dehydrogenase (PHGDH)	201397_at	435.5P	686.8P	1.58	446.1P	552.5P	1.24	432.9P	1239P	2.86	1.89
PRP4 pre-mRNA processing factor 4 homolog (PRPF4)	209161_at	148.7M	209.9P	1.41	198.2P	392.1P	1.98	120.2A	271.6P	2.26	1.88
hypothetical protein MAC30 (MAC30)	212281_s_at	251.1P	435.8P	1.74	341.7P	748.6P	2.19	351.9P	599.2P	1.70	1.88
similar to CG9996-PA	222288_at	193.5P	339.4P	1.75	244.4P	523.4P	2.14	113.6A	194.1P	1.71	1.87
syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2)	212154_at	126.9P	228.6P	1.80	171.4P	297.9P	1.74	84.9M	171.8P	2.02	1.85
amylo-1,6-glucosidase, 4-alpha-glucanotransferase (AGL)	203566_s_at	472.1P	799.9P	1.69	661.1P	1483.9P	2.24	235.9P	380.3P	1.61	1.85
retinoic acid induced 14 (RAI14)	202052_s_at	230P	469.5P	2.04	387.8P	358.3P	0.92	101P	258P	2.55	1.84
influenza virus NS1A binding protein (IVNS1ABP)	201362_at	382.1P	715.8P	1.87	492P	894.9P	1.82	248.8P	441.7P	1.78	1.82
DNA segment on chromosome 4 (unique) 234 expressed sequence (D4S234E)	209570_s_at	306P	354P	1.16	363.8P	1109.2P	3.05	372.9P	466.3P	1.25	1.82
chromosome 20 open reading frame 42 (C20orf42)	218796_at	474P	943.2P	1.99	960.3P	1664P	1.73	536.7P	885.1P	1.65	1.79
solute carrier family 39 (zinc transporter), member6 (SLC39A6)	202088_at	1834.6P	3116.9P	1.70	3424P	5386.2P	1.57	1275.2P	2638.2P	2.07	1.78
solute carrier family 1 (glutamateneutral amino acid transporter), member 4 (SLC1A4)	209610_s_at	182.3P	332.3P	1.82	392.4P	543.9P	1.39	146P	302.5P	2.07	1.76
adenylyl cyclase-associated protein1 (CAP1)	200625_s_at	934.9P	1242.2P	1.33	1087.9P	2386.5P	2.19	705.3P	1217.3P	1.73	1.75
mesoderm specific transcript (mouse) homolog (MEST)	202016_at	287.1P	460.5P	1.60	359.8P	750.1P	2.08	207.5P	320.2P	1.54	1.74
metastasis suppressor 1 (MTSS1)	203037_s_at	1227P	2197.9P	1.79	1781.8P	3366.3P	1.89	1125.7P	1744.3P	1.55	1.74
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13)	211361_s_at	113.8P	172.5P	1.52	113.6P	236P	2.08	38.8P	63.1P	1.63	1.74
chloride channel, calcium activated, family member 2 (CLCA2)	206165_s_at	819P	1097.1P	1.34	918.8P	1668.4P	1.82	358P	725.6P	2.03	1.73
homeodomain-only protein (HOP)	211597_s_at	631.3P	848.5P	1.34	852.6P	1382.9P	1.62	405.9P	898.8P	2.21	1.73
glutamate-cysteine ligase, catalytic subunit (GCLC)	202923_s_at	325.3P	743.2P	2.28	680.6P	987P	1.45	252.4P	363.2P	1.44	1.72
latent transforming growth factor beta binding protein 2 (LTBP2)	204682_at	2048.6P	2614.6P	1.28	1706.5P	3362.8P	1.97	1445.7P	2718.9P	1.88	1.71
SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 (SMC4L1)	201664_at	177P	317.7P	1.79	363.7P	586.8P	1.61	166.2P	285.2P	1.72	1.71
vav 3 oncogene (VAV3)	218807_at	658P	1343.3P	2.04	778.8P	1071.2P	1.38	436.4P	741.2P	1.70	1.71
tumor rejection antigen (gp96) 1 (TRA1)	200599_s_at	885P	1379.6P	1.56	796.8P	1943.9P	2.44	728.9P	800.9P	1.10	1.70
L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC)	201036_s_at	398.6P	514.7P	1.29	419.6P	1074.2P	2.56	279.1P	339.4P	1.22	1.69
defender against cell death 1 (DAD1)	200046_at	366.9P	685.1P	1.87	670.2P	892.6P	1.33	536.2P	987.1P	1.84	1.68
solute carrier family 7(cationic amino acid transporter, y+ system), member 1 (SLC7A1)	212295_s_at	1470.2P	2589.9P	1.76	2825.7P	4696.3P	1.66	1929.6P	3051P	1.58	1.67
tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10)	202688_at	757.4P	1102.7P	1.46	670.2P	935.9P	1.40	434.8P	922.4P	2.12	1.66
fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3)	204379_s_at	1780.8P	2710.1P	1.52	2103P	3286.5P	1.56	1792.1P	3378.7P	1.89	1.66
solute carrier family 31 (copper transporters), member 2 (SLC31A2)	204204_at	245.3P	468.2P	1.91	343.8P	535.2P	1.56	234.5P	345.4P	1.47	1.65
regulator of cytokinesis 1 (PRC1)	218009_s_at	182.5P	262.6P	1.44	254.7P	413.6P	1.62	202P	377P	1.87	1.64
hypothetical protein MAC30 (MAC30)	212282_at	315.2P	400.1P	1.27	346.8P	584.2P	1.68	296P	584.4P	1.97	1.64
MLF1 interacting protein (MLF1IP)	218883_s_at	217.3P	292.8P	1.35	463.4P	857.1P	1.85	165.1P	285.3P	1.73	1.64
N-myc downstream regulated (NDRG1)	200632_s_at	723.2P	1393.5P	1.93	1497.8P	1700.5P	1.14	1070.4P	1993P	1.86	1.64
procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2)	202620_s_at	166.3P	227.9P	1.37	158.1P	294.5P	1.86	63.4P	107P	1.69	1.64
histone acetyltransferase 1 (HAT1)	203138_at	159.7P	273.7P	1.71	299.9P	385.8P	1.29	138.2P	252P	1.82	1.61
chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1)	209396_s_at	193P	325.1P	1.68	186.6P	386.9P	2.07	315.9P	331.4P	1.05	1.60
activated RNA polymerase II transcription cofactor 4 (PC4)	221727_at	208.1P	332.7P	1.60	202.7P	329.1P	1.62	157.8P	247.5P	1.57	1.60
chromosome 3 open reading frame 14 (C3orf14)	219288_at	451.1P	771.5P	1.71	724.9P	976.7P	1.35	552.6P	935.7P	1.69	1.58
Ras homolog enriched in brain (RHEB)	213404_s_at	517.7P	749P	1.45	548P	811.1P	1.48	229.2P	403.1P	1.76	1.56
lipase A, lysosomal acid, cholesterol esterase (Wolman disease) (LIPA)	201847_at	432.6P	742.4P	1.72	523.7P	836.2P	1.60	382.8P	514.1P	1.34	1.55
FN5 protein (FN5)	219806_s_at	427.5P	534.5P	1.25	512.1P	773.6P	1.51	260.9P	490.2P	1.88	1.55
flap structure-specific endonuclease 1 (FEN1)	204767_s_at	176P	282.5P	1.61	266.7P	453P	1.70	192P	252.6P	1.32	1.54
leukotriene A-4 hydrolase (LTA4H)	208771_s_at	747.1P	1206.5P	1.61	1073.8P	1392.9P	1.30	649.3P	1047P	1.61	1.51
myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L) (MACS)	201669_s_at	395.2P	638.2P	1.61	457P	743.1P	1.63	257.2P	329.5P	1.28	1.51
transmembrane 4 superfamily member 1 (TM4SF1)	215034_s_at	211P	349.8P	1.66	363.1P	531P	1.46	231.4P	319.1P	1.38	1.50
PTPL1-associated RhoGAP 1 (PARG1)	203910_at	407.2P	617.7P	1.52	427.5P	637.3P	1.49	203.8P	300.9P	1.48	1.49
thymidylate synthetase (TYMS)	202589_at	245.9P	359.2P	1.46	539.1P	648.5P	1.20	258.6P	465.9P	1.80	1.49
CDC28 protein kinase 2 (CKS2)	204170_s_at	120.4P	191.3P	1.59	289.1P	311.4P	1.08	104.4P	187.4P	1.80	1.49
similar to lysosome-associated membrane glycoprotein (TSC403)	205569_at	530.6P	838.6P	1.58	529.8P	771.2P	1.46	409.9P	559.9P	1.37	1.47
nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1)	221923_s_at	2179.2P	3009.1P	1.38	2827.6P	4370.5P	1.55	1804.5P	2595.6P	1.44	1.45
influenza virus NS1A binding protein (IVNS1ABP)	206245_s_at	144.3P	209.7P	1.45	196.9P	268.9P	1.37	159.7P	245.6P	1.54	1.45
high-mobility group nucleosome binding domain 1 (HMGN1)	200944_s_at	2582.8P	3412.4P	1.32	2810.4P	4303.8P	1.53	2223.8P	3295.2P	1.48	1.44
proliferating cell nuclear antigen (PCNA)	201202_at	415.1P	601.3P	1.45	617.8P	852.5P	1.38	258.2P	383.6P	1.49	1.44
glyoxalase I (GLO1)	200681_at	624.6P	945.3P	1.51	869.4P	1175.9P	1.35	743P	1000.4P	1.35	1.40
von Hippel-Lindau binding protein 1 (VBP1)	201472_at	668.3P	1022.6P	1.53	1078.4P	1430.7P	1.33	562.5P	753.9P	1.34	1.40
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1)	211755_s_at	1021.4P	1473.9P	1.44	1448.8P	1859.2P	1.28	1072.4P	1497.7P	1.40	1.37
tumor necrosis factor, alpha-induced protein 1 (endothelial) (TNFAIP1)	201207_at	411P	474.8P	1.16	512P	752.1P	1.47	458.4P	670.7P	1.46	1.36
profilin 2 (PFN2)	204992_s_at	1169.7P	1559.7P	1.33	1155.8P	1792.3P	1.55	753.5P	899.9P	1.19	1.36
chromosome 7 open reading frame 24 (C7orf24)	215380_s_at	763.9P	1114.6P	1.46	1057.5P	1512.4P	1.43	859P	1007.2P	1.17	1.35
thymopoietin (TMPO)	203432_at	72.2P	83.2P	1.15	95.9P	183.6P	1.91	88.2P	86.8P	0.98	1.35
basic transcription factor (BTF3)	211939_x_at	2325.2P	3061.1P	1.32	3215.3P	4074.9P	1.27	2694.1P	3900.2P	1.45	1.34
syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2)	212157_at	225P	312.8P	1.39	255.9P	359P	1.40	233.6P	279.1P	1.19	1.33
tubulin, alpha3 tubrin, alpha, ubiquitous (TUBA3 K-ALPHA-1)	212639_x_at	2906.6P	3722.8P	1.28	2814.9P	3846.1P	1.37	4411.5P	5696.1P	1.29	1.31
brain acid-soluble protein 1 (BASP1)	202391_at	1815.6P	2171.6P	1.20	1950.7P	2958.3P	1.52	2079.4P	2536.4P	1.22	1.31

Numbers indicate signal intensities detected for each probe sets
P: "present" call, detected as expressed, A: "Absent" call, detected as not expressed.

Bold: Up-regulated in both MAS 5.0 and dChip analysis

Underline: "membrane" protein annotated by GOA analysis

Supplemental table 3. Genes detected as up-regulated in human bulge by dChip1.3 software

Gene	Probe set	Mouse bulge	Sub-bulge 1	Sub-bulge 2	Sub-bulge 3	Baseline mean	Bulge 1	Bulge 2	Bulge 3	Experiment mean	Fold change	Paired p-value
vasoactive intestinal peptide (VIP)	206577_at		5.56	5.42	3.1	4.78	23	30.83	26.67	26.51	5.55	0.025413
trinucleotide repeat containing 9 (TNRC9)	214774_x_at		57.68	17.37	48.29	41.07	211.76	193.08	209.98	205.92	5.01	0.002865
trinucleotide repeat containing 9 (TNRC9)	215108_x_at		54.77	22.92	39.64	39.32	193.35	184.38	188.33	189.75	4.83	0.005001
deiodinase, iodothyronine, type II	203700_s_at		623.45	378.53	417.71	475.97	2360.15	1504.88	2872.54	2243.96	4.71	0.044693
trinucleotide repeat containing 9 (TNRC9)	216623_x_at		49.87	28.99	48.24	43.12	139.93	125.33	213.31	159.3	3.69	0.042241
pleckstrin homology-like domain, family A, member 1 (PHLDA1)	217997_at		86.13	52.54	67.79	70.19	286.96	193.19	269.94	250.06	3.56	0.016539
Forkhead box C1 (FOXC1)	213260_at		684	381.35	456.46	507.84	1543.52	1049.33	1709.6	1434.27	2.82	0.033348
angiopoietin-like 2 (ANGPTL2)	213001_at		666.02	230.9	309.97	403.02	1594.63	667.93	1099.19	1121.61	2.78	0.042792
WNT inhibitory factor 1 (WIF1)	204712_at	***	1562.12	124.1	681.88	788.93	2397.44	2035.25	2107.31	2185.3	2.77	0.047338
nebulette (NEBL)	203961_at		532.88	308.21	298.14	379.65	1322.37	738.6	998.58	1020.64	2.69	0.030551
regulated in glioma (RIG)	221127_s_at		335.72	136.87	135.79	202.74	668.9	397.53	443.81	503.6	2.48	0.006284
dickkopf homolog 3 (Xenopus laevis) (DKK3)	214247_s_at	*,**	2236.41	1029.26	1623.64	1628.98	4600.71	2573.15	4811.42	3997.38	2.45	0.038471
hypothetical protein FLJ10134	219410_at		1468.6	516.5	237.4	739.17	2179.29	1751.4	1300.5	1744.13	2.36	0.022927
aquaporin 3(AQP3)	39248_at		3116.22	1235.82	1226.17	1860.13	4911.36	3800.5	4067.24	4262.32	2.29	0.017042
calcium/calmodulin-dependent protein kinase II (CaMKIINalpha)	218309_at		259.88	138.04	188.04	196.65	483.58	346.26	508.14	446.7	2.27	0.022261
dihydropyrimidinase-like 2 (DPYSL2)	200762_at		1524.21	585.98	550.11	884.61	2229.1	1892.36	1871.18	1999.8	2.26	0.032716
pleckstrin homology-like domain, family A, member 1 (PHLDA1)	217996_at		92.74	72.43	87.47	84.99	201.98	149.56	222.34	191.61	2.25	0.037251
glycoprotein M6B (GPM6B)	209167_at		362.9	152.46	211.71	242.66	657.85	443.19	442.04	514.19	2.12	0.011893
dihydropyrimidinase-like 3 (DPYSL3)	201431_s_at		674.18	301.14	376.07	450.59	1327.12	638.1	846.54	937.1	2.08	0.035933
decorin (DCN)	201893_x_at		2540.15	1088.42	1241.63	1615.51	3679.78	2608.67	3256.74	3181.56	1.97	0.029408
serine (or cysteine) proteinase inhibitor, clade F, member 1 (SERPINF1)	202283_at		933.02	520.8	1347.6	932.06	1642.42	1227.69	2483.67	1783.87	1.91	0.028594
transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila) (TLE4)	204872_at		251.08	159.27	86.47	166.05	344.52	316.96	279.6	313.92	1.89	0.041789
Ca2+-dependent activator protein for secretion 2 (CADPS2)	219572_at		228.18	197.89	178.37	202.16	359.97	412.93	369.79	377.99	1.87	0.026818
transforming growth factor, beta 2 (TGFB2)	209909_s_at	*	154.34	67	136.68	119.38	214.71	166.45	259.54	213.98	1.79	0.038516
nebulette (NEBL)	203962_s_at		195.71	120.62	139.6	152.37	308.05	267.74	230.44	269.2	1.77	0.03446
keratin 15 (KRT15)	204734_at	**	3875.12	1881.46	4516.96	3416.63	5734.26	4298.23	7899.47	5973.03	1.75	0.041042
adrenergic, alpha-2A-, receptor (ADRA2A)	209869_at		438.2	387.58	355.45	395.59	719.8	676.8	666.69	688.98	1.74	0.005552
chromosome 14 open reading frame 78 (C14orf78)	212992_at		1635.79	878.86	1253.19	1255.49	2655.87	1488.73	2415.31	2184.07	1.74	0.035434
PTPRF interacting protein, binding protein 1 (liprin beta 1)	214375_at		142.59	102.77	169.85	138.19	211.34	191.73	310.01	237.39	1.72	0.04908
dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD)	207660_at	**	294.76	137.9	388.45	274.99	450.84	382.38	583.23	471.49	1.71	0.025787
coagulation factor II (thrombin) receptor-like 1 (F2RL1)	213506_at		737.59	898.09	353.46	661.32	1166.52	1463.66	699.34	1110.9	1.68	0.027426
iduronate 2-sulfatase (Hunter syndrome) (IDS)	210666_at		309.04	208.22	180.68	235.25	506.8	321.74	351.19	392.01	1.67	0.04103
catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2)	209617_s_at		779.13	350.42	1018.46	714.85	1067.8	944.97	1538.43	1185.55	1.66	0.039348
fibulin 1 (FBLN1)	202994_s_at	*	631.72	452.77	716.59	599.37	1135.41	701.07	1134.48	989.54	1.65	0.044114
peptidylglycine alpha-amidating monooxygenase (PAM)	212958_x_at		827.24	444.38	629.68	633.16	1072.64	887.44	1119.47	1026.77	1.62	0.042043
microphthalmia-associated transcription factor (MITF)	207233_s_at		1475.65	919.99	1311.2	1235.65	2054.64	1665.25	2218.87	1980.59	1.6	0.016932
glycoprotein M6B (GPM6B)	209170_s_at		158.27	100.77	113.52	124.54	247.74	166.7	178.65	197.64	1.59	0.028373
frizzled homolog 1 (Drosophila) (FZD1)	204451_at	*,**(FZD2)	953.14	633.17	807.38	799.48	1348.27	1282.97	1143.18	1260.82	1.58	0.049557
cDNA clone IMAGE:5265581, partial cds	216527_at		40.65	36.17	53.86	43.94	67.29	57.89	81.87	68.98	1.57	0.02112
dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) (DUSP3)	201536_at		1116.3	810.15	855.22	927.61	1521.49	1412.67	1397.26	1446.41	1.56	0.018613
pyridoxal (pyridoxine, vitamin B6) kinase (PDXK)	218019_s_at		846.65	537.1	709.56	700	1108.55	893.05	1265.77	1089.16	1.56	0.047197
SH3 domain binding glutamic acid-rich protein like 3 (SH3BGRL3)	221269_s_at		641.02	333.08	514.25	496.86	859.98	539.09	884.97	760.64	1.53	0.044015
neuroblastoma, suppression of tumorigenicity 1 (NBL1)	37005_at		998.21	730.73	1063.02	931.02	1547.64	1029.89	1673.39	1416.61	1.52	0.03884
bone morphogenetic protein 5 (BMP5)	205430_at		62.95	57.74	35.43	52.14	94.13	84.23	56.13	78.65	1.51	0.043172
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1)	211105_s_at	*,**	1246.47	952.22	1073.28	1089.62	1667.37	1490.63	1792.15	1645.8	1.51	0.024906
inositol 1,4,5-triphosphate receptor, type 3 (ITPR3)	201188_s_at		460.99	303.55	604.93	459.19	748.72	472.04	830.32	683.5	1.49	0.03404
follistatin (FST)	204948_s_at	*,**(Fstl)	258.65	219.03	248.58	240.36	364.4	348.45	360.1	357.38	1.49	0.027832
erythrocyte membrane protein band 4.1-like 2 (EPB41L2)	201718_s_at		257.99	187.16	241.86	229.72	362.32	316.48	342.35	339.84	1.48	0.014605
chromosome 15 open reading frame 25 (C15orf25)	220071_x_at		1027.73	808.01	1215.59	1016.91	1390.63	1235.74	1886.78	1504.19	1.48	0.036405
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3)	204917_s_at		232.97	197.18	224.85	219.32	320.22	308.32	342.95	322.82	1.47	0.032075
glycoprotein M6B (GPM6B)	209168_at		391.91	270.5	308.48	324.34	514.94	389.76	525.08	476.38	1.47	0.045799
hypothetical protein FLJ21075 (FLJ21075)	221172_at		494	462.47	320.74	427.01	729.51	643.12	507.97	626.89	1.47	0.016593
angiopoietin-like 2 (ANGPTL2)	213004_at		270.62	184.75	186.64	214.85	383.14	266.06	289.69	313.31	1.46	0.029257
rap2 interacting protein X (RIPX)	213939_s_at		591.4	460.22	363.67	473.26	833.51	598.78	631.8	689.23	1.46	0.048406
KH-type splicing regulatory protein (FUSE binding protein 2) (KHSRP)	204372_s_at		945.64	895.97	1221.92	1034.79	1386.84	1328.82	1805.01	1498.14	1.45	0.030925
interferon regulatory factor 4 (IRF4)	216987_at		22.82	29.99	18.73	23.96	31.34	42.47	30.27	34.71	1.45	0.044146
solute carrier family 12 (potassium/chloride transporters), member 4 (SLC12A4)	211112_at	**(Scl29al)	512.13	445.92	496.82	486.11	650.22	695.22	756.69	700.22	1.44	0.033863
collagen, type V, alpha 1 (COL5A1)	212489_at		420.35	336.7	480.14	413.22	575.35	483.19	710.56	589.22	1.43	0.026542
cytochrome b-5 (CYB5)	217021_at		87.43	67.73	67.89	74.38	122.91	105.53	90.12	106.35	1.43	0.038124
zinc finger protein (ZFD25)	205739_x_at		232.45	178.67	90.75	167.18	306.99	243.51	161.19	237.38	1.42	0.009638
neuregulin 1 (NRG1)	208230_s_at		235.37	208.81	346.54	263.72	356.07	283.71	484.06	374.42	1.42	0.039857
calmodulin 1 (phosphorylase kinase, delta) (CALM1)	211984_at		484.48	352.47	488.45	442.03	702.82	491.31	665.85	618.67	1.4	0.043798
solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 (SLC11A1)	217473_x_at		298.35	253.2	530.07	361.12	487.87	371.86	649.64	503.04	1.39	0.033019
hexokinase 1 (HK1)	200697_at		1372.2	1270.05	1237.06	1301.97	1779.86	1719.67	1898.67	1799.02	1.38	0.039661
CD59 antigen p18-20 (CD59)	200985_s_at		2460.34	2084.3	1463.3	2013.25	3009.08	2789.52	2515.62	2770.05	1.38	0.048048
KIAA0924 protein	205594_at		240.19	297.32	141.19	226.19	343.46	349.1	242.17	311.53	1.38	0.041858
carcinoembryonic antigen gene (CEA)	217291_at		415.56	395.82	327.08	379.77	611.54	529.53	433.73	524.82	1.38	0.042904
WW domain containing oxidoreductase (WWOX)	221147_x_at	*,**(Wwp2)	113.65	113.65	83.26	103.59	151.41	142.24	137.71	143.08	1.38	0.046091
transportin (importin 3, karyopherin beta 2b) (TNPO2)	221506_s_at		692.94	317.93	970.29	660.44	934.74	536.71	1260.98	911.41	1.38	0.014984
KIAA1128 protein (KIAA1128)	209379_s_at		503.17	522.55	310.51	445.35	628.78	709.34	487.83	609.32	1.37	0.018517
interferon induced transmembrane protein 1(9-27) (IFITM1)	214022_s_at		1237.15	550.27	697.14	828.29	1623.99	781.87	987.03	1131.04	1.37	0.036385
forkhead box O3A	204131_s_at		1547.9	1470.81	1142.41	1390.54	2143.11	1810.51	1720.87	1890	1.36	0.038975
chemokine (C-X-C motif) ligand 11 (CXCL11)	211122_s_at	*(Cxcl14)	54.74	58.61	87.61	67.13	84.37	85.02	104.94	91.41	1.36	0.034197
transcription elongation factor A (SII)-like (TCEAL2)	211276_at		1403.05	1021.9	1550.96	1326.54	1746.88	1413.43	2177.84	1777.82	1.34	0.049615
dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT)	216513_at		90.41	97.66	105.8	99.19	134.16	123.19	142.86	133.21	1.34	0.044342
immunoglobulin superfamily, member 4 (IGSF4)	209030_s_at	*,**	277.05	258.92	508.6	347.83	398.29	369.7	627.09	463.71	1.33	0.039843
serine (or cysteine) proteinase inhibitor, clade E), member 2 (SERPINE2)	212190_at		2704.13	1544.02	1770.96	1997.23	3249.96	2251.7	2410.21	2644.98	1.32	0.033421
AE binding protein 1 (AEBP1)	201792_at		196.09	116.18	216.21	175.12	246.13	171.12	270.34	228.62	1.31	0.042068
lethal giant larvae homolog 2 (Drosophila) (LLGL2)	203713_s_at		392.91	284.19	360.34	345.79	461.03	421.35	480.96	453.71	1.31	0.039112
Glycine-, glutamate-thienylcyclohexylpiperidine binding protein (KIAA0562)	204074_s_at		234.79	201.2	325.67	253.99	299.52	290.96	411.79	333.16	1.31	0.045634
adrenergic, beta-1-, receptor (ADRB1)	208214_at		145.86	125.61	140.17	137.39	187.69	178.38	174.21	179.68	1.31	0.03003
CD1A antigen, a polypeptide (CD1A)	210325_at		593.38	622.17	571.28	592.45	726.04	805.42	806.21	778.15	1.31	0.033867
cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	214353_at		163.62	120.04	173.4	152.93	195.56	175.28	230.93	200.87	1.31	0.048004
apoptosis inhibitor 5 (API5)	214959_s_at		312.09	312.09	312.09	312.09	370.59	462.85	396.97	409.94	1.31	0.016095
peptide YY, 2 (seminalplasmin) (PYY2)	220209_at		351.05	501.49	377.62	409.55	500.35	600.85	498.93	533.08	1.3	0.034828

Numbers indicate Model Based Expression Indexes (MBEIs) detected for each probe sets

Bold: Up-regulated in both MAS 5.0 and dChip analysis

Underline: "membrane" protein annotated by GOA analysis

Mouse bulge column: asterisks indicate the up-regulation of same or similar genes in mouse bulge transcription profiling data
* Tumbar et al. Science, 303 359-363, 2004.
**Morris et al. Nat Biotechnol, 22 411-417, 2004.
*** Fuchs et al. Cell 116 769-778, 2004.
parenthesis; gene of similar function was detected as upregulated.

Supplemental table 4. Genes detected as down-regulated in human bulge by dChip1.3 software

Gene	Probe set	Sub-bulge1	Sub-bulge2	Sub-bulge3	Baseline mean	Bulge 1	Bulge 2	Bulge 3	Experiment mean	Fold change	Paired p- value
cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP)	205713_s_at	1716.38	1593.3	1956.04	1751.99	184.19	785.75	114.04	359.42	-4.87	0.047178
cytokine receptor-like factor 1 (CRLF1)	206315_at	929.31	675.12	764.7	789.57	144.63	329.03	95.62	191.02	-4.13	0.045728
angiopoietin-like 7 (ANGPTL7)	206423_at	6061.65	6340.22	3907.42	5433	1361.32	3802.65	232.33	1794.01	-3.03	0.029137
tripartite motif-containing 9 (TRIM9)	209859_at	807.32	882.01	756.42	817.26	250.12	421.11	230.94	300.4	-2.72	0.005148
aminolevulinate, delta-, dehydratase (ALAD)	218487_at	2133.76	3151.65	2117.44	2472.04	972.55	1153.39	715.72	944.77	-2.62	0.028474
protocadherin 8 (PCDH8)	206935_at	404.67	518.61	226.85	383.72	86.24	305.33	51.18	147.35	-2.6	0.031851
collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1)	217428_s_at	54.91	63.94	35.24	51.47	20.71	27.41	13.57	21.12	-2.44	0.0396
solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6)	219932_at	525.87	659.06	326.51	503.99	111.23	459.1	58.35	209.52	-2.41	0.044084
tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)	201147_s_at	724.77	994.49	724.73	814.35	322.57	475.75	222.12	341.36	-2.39	0.011716
nucleolar and spindle associated protein 1 (NUSAP1)	218039_at	844.29	1727.49	734.84	1102.81	308	835.58	269.39	472.66	-2.33	0.044673
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13)	217272_s_at	434.38	570.24	255.15	419.9	202.22	248.61	89.15	180	-2.33	0.035614
platelet derived growth factor C (PDGFC)	218718_at	2010.81	2838.21	1559.27	2137.11	878.02	1430.65	482.08	928.9	-2.3	0.008504
solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7)	207604_s_at	683.93	1026.59	550.17	754.29	251.76	571.79	211.37	345.17	-2.19	0.01117
tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)	201150_s_at	2562.63	3089.02	2579.27	2749.03	1011.24	1909.86	842.74	1253.78	-2.19	0.015102
chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1)	209395_at	754.16	745.21	788.55	762.47	288.11	381.54	387.56	351.65	-2.17	0.010826
chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1)	209396_s_at	671.56	767.26	599.83	679.14	256.3	316.93	385.18	318.53	-2.13	0.039638
laminin, beta 1 (LAMB1)	201505_at	439.91	632.15	396.36	490.61	227.15	286.89	181.83	232.46	-2.11	0.0334
ets variant gene 5 (ets-related molecule) (ETV5)	203349_s_at	1417.79	1663.85	1154.81	1410.53	751.11	889.98	426.65	690.93	-2.04	0.005374
cell division cycle 2, G1 to S and G2 to M (CDC2)	203213_at	479.57	945.53	472.96	632.74	205.12	516.54	210.72	310.42	-2.04	0.027974
phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A)	210145_at	371.01	428.05	292.26	365.55	127.99	294.67	121.88	181.03	-2.02	0.034494
kinesin family member 20A (KIF20A)	218755_at	314.91	634.17	227.76	392.24	129.06	371.6	99.33	201.18	-1.95	0.047333
GRB2-associated binding protein 2 (GAB2)	203853_s_at	580.43	718.21	519.91	601.78	318.08	433.6	189.28	313.65	-1.92	0.024622
protein regulator of cytokinesis 1 (PRC1)	218009_s_at	342.79	582.67	436.87	454.08	171.2	311.85	239.31	241.5	-1.88	0.030253
glypican 4 (GPC4)	204984_at	375.2	465	350.27	395.41	154.63	280.45	193.69	210.23	-1.88	0.016245
ribonucleotide reductase M2 polypeptide (RRM2)	201890_at	283.68	504.78	329.62	371.11	141	272.72	177.29	198.57	-1.87	0.045817
insulin-like 3 (Leydig cell) (INSL3)	214400_at	130.34	107.57	121.37	119.47	61.3	74.44	53.85	64.12	-1.86	0.049578
vav 3 oncogene (VAV3)	218807_at	2016.21	2009.47	969.62	1665.97	1010.33	1210.67	513.38	912.83	-1.83	0.045876
ZW10 interactor (ZWINT)	204026_s_at	746.55	1151.75	554.58	819.33	351.14	674.27	314.9	446.78	-1.83	0.042375
phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL)	202990_at	845.26	1033.32	689.5	855.92	395.27	679.52	334.32	469.4	-1.82	0.011002
syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2)	212157_at	601.04	791.08	574.23	657.16	298.93	439.63	353.98	362.58	-1.81	0.025263
syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2)	212158_at	2144.06	2916.78	1886.83	2316.22	1311.3	1488.55	1072.97	1289.44	-1.8	0.040781
karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2)	211762_s_at	258.63	471.8	310.55	346.89	134.16	278.84	171.45	194.22	-1.79	0.023885
protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C)	204284_at	2033.09	3027.84	1516.94	2191.23	1296.44	1778.75	596.46	1221.27	-1.79	0.028321
MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (MCM6)	201930_at	915.18	1121.14	808.33	948.54	482.18	633.11	486.25	529.18	-1.79	0.016524
flap structure-specific endonuclease 1 (FEN1)	204767_s_at	324.92	557.74	329.92	404.05	170.56	319	198.37	229.91	-1.76	0.045059
retinoic acid induced 14 (RAI14)	202052_s_at	832.98	1054.46	383.25	757.14	401.45	722.34	166.67	430.24	-1.76	0.037846
topoisomerase (DNA) II alpha 170kDa (TOP2A)	201292_at	277.46	499.9	272.1	349.84	146.18	297.41	145.19	198.89	-1.76	0.041424
CS box-containing WD protein	213734_at	179.45	189.52	127.1	165.9	97.35	115.58	68.99	94.58	-1.75	0.026457
solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4)	209610_s_at	566.89	908.81	579.15	683.54	328.6	508.58	332.77	389.66	-1.75	0.045452
WAP four-disulfide core domain 1 (WFDC1)	219478_at	236.26	311.6	261.65	268.57	150.51	162.09	148.07	154.45	-1.74	0.039546
a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMTS5)	219935_at	518.81	836.89	224.73	526.74	235.05	597.65	94.16	308.65	-1.71	0.047076
homeodomain-only protein (HOP)	211597_s_at	1423.37	1940.25	1178.07	1514.29	879.68	1227.89	556.15	886.65	-1.71	0.010569
chromosome 22 open reading frame 18 (C22orf18)	218741_at	199.02	350.15	212.2	253.14	93.35	211.76	142.92	149.9	-1.69	0.04837
thymidine kinase 1, soluble (TK1)	202338_at	274.76	453.16	374.32	367.14	150.31	249.81	251.31	217.37	-1.69	0.034024
fibroblast growth factor 18 (FGF18)	211485_s_at	187.48	225.68	196.86	203.58	103.2	156.75	104.76	121.3	-1.68	0.016685
topoisomerase (DNA) II alpha 170kDa (TOP2A)	201291_s_at	172.97	268.21	146.66	195.7	67.72	206.33	75.39	116.51	-1.68	0.03485
ribosomal protein L39-like (RPL39L)	210115_at	745.17	1123.27	769.85	878.89	420.21	695.05	480.71	532.08	-1.65	0.017415
thymidylate synthetase (TYMS)	202589_at	489.13	671.92	453.65	540.74	216.58	519.63	250.09	327.85	-1.65	0.040977
Rac GTPase activating protein 1 (RACGAP1)	222077_s_at	694.91	1191.12	613.75	833.7	324.93	847.36	348.25	507.07	-1.64	0.013201
putative lymphocyte G0/G1 switch gene (GOS2)	213524_s_at	524.46	403.45	338.36	421.66	361.83	207.14	201.65	258.79	-1.63	0.027072
collagen, type XI, alpha 1 (COL11A1)	37892_at	2586.75	2995.72	1859.26	2479.75	1469.19	2378.62	712.72	1517.41	-1.63	0.035433
lactamase, beta 2 (LACTB2)	218701_at	217.12	270.14	125.06	204.29	118.24	182.24	79.66	126.48	-1.62	0.045786
melanoma cell adhesion molecule (MCAM, CD146)	209087_x_at	1328.83	1533.78	1210.16	1363.11	734.68	1094.83	738.38	857.18	-1.59	0.028843
chloride channel, calcium activated, family member 2 (CLCA2)	206165_s_at	1072.6	1414.62	670.36	1052.82	659.18	942.65	393.47	663.78	-1.59	0.027252
latent transforming growth factor beta binding protein 2 (LTBP2)	204682_at	2521.61	2547.37	2704	2593.62	1851.58	1606.74	1416.69	1631.55	-1.59	0.045789
fibroblast growth factor 18 (FGF18)	214284_s_at	243.38	270.21	187.51	233.31	139.61	183.43	114.52	148.11	-1.58	0.046143
MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)(MCM2)	202107_s_at	505.13	703.39	553.01	586.1	299.62	429.89	396.56	375	-1.56	0.033763
phosphodiesterase 4D interacting protein (myomegalin) (PDE4DIP)	210305_at	90.02	103.52	61.3	85.11	55.41	67.87	38.83	54.77	-1.55	0.039946
down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1)	216652_s_at	228.61	280.02	203.35	237.65	128.06	226.06	110.09	154.88	-1.53	0.044
ADP-ribosylation factor-like 6 interacting protein (ARL6IP)	211935_at	1384.94	1750.61	979.54	1371.58	775.81	1329.82	584.06	896.22	-1.53	0.025904
sorting nexin 7 (SNX7)	205573_s_at	1242.16	1272.87	790.34	1102.48	708.61	988.38	467.51	720.18	-1.53	0.041973
G protein-coupled receptor 87 (GPR87)	219936_s_at	1042.63	1416.72	861.19	1107.23	605.11	1011.49	578.44	729.73	-1.52	0.023033
jagged 1 (Alagille syndrome) (JAG1)	216268_s_at	4069.09	4561.49	3250.7	3965.66	2736.54	2767.71	2356.82	2608.06	-1.52	0.044568
N-myc downstream regulated gene 1(NDRG1)	200632_s_at	1406.51	2109.07	1806.71	1773.48	833.12	1296.31	1375.11	1167.49	-1.52	0.049508
adaptor-related protein complex 1, sigma 2 subunit (AP1S2)	203299_s_at	647.27	586.63	438.96	557.67	408.54	469.36	231.49	369.54	-1.51	0.042486
similar to Transcription factor BTF3 homolog 3 (LOC132556)	217467_at	260.29	301.9	219.38	260.68	157.47	214.94	147.18	173.51	-1.5	0.012418
thymosin, beta, identified in neuroblastoma cells (TMSNB)	205347_s_at	372.87	567.4	421.65	452.29	257.54	403.52	242.37	301.75	-1.5	0.035674
polo-like kinase (Drosophila) (PLK2)	201939_at	281.23	385.21	227.61	298.04	154.92	291.77	149.02	198.7	-1.5	0.033635
hairy and enhancer of split 1, (Drosophila) (HES1)	203395_s_at	1061.27	1449.94	965.73	1159.3	618.19	1111.05	605.43	779.18	-1.49	0.011991
neuromedin U (NMU)	206023_at	309.42	563.59	295.85	389.09	210.65	394.39	181.35	262.56	-1.48	0.04232
H2A histone family, member V (H2AFV)	202487_s_at	449.16	585.69	601.15	543.78	320.55	398.25	397.5	368.2	-1.48	0.0376
ubiquitin specific protease 4 (proto-oncogene) (USP4)	211800_s_at	753.81	665.49	1205.36	871.55	448.09	439.67	890.92	595.52	-1.46	0.038215
carbonic anhydrase II (CA2)	209301_at	343.83	399.63	227.33	323.58	217.54	305.67	144.94	222.15	-1.46	0.032248
Hypothetical protein LOC339692 (LOC339692)	215247_at	231.34	242.81	188.8	219.3	165.17	165.78	126.09	152.81	-1.44	0.043702
F-box protein 28 (FBXO28)	202272_s_at	606.68	508.74	373.71	497.34	418.13	391.12	226.78	345.42	-1.44	0.035624
core-binding factor, beta subunit (CBFB)	202370_s_at	835.1	847.26	674.42	786.2	532.67	699.12	428.88	553.09	-1.42	0.047462
von Hippel-Lindau binding protein 1 (VBP1)	201472_at	1120.98	1392.23	848.12	1120.18	848.31	1017.24	494.77	786.23	-1.42	0.035078
DEK oncogene (DNA binding) (DEK)	200934_at	1898.03	2017.28	1622.97	1849.01	1140.5	1563.76	1220.59	1304.64	-1.42	0.048881
squamous cell carcinoma antigen recognized by T cell (SART2)	218854_at	368.02	378.55	239.62	329.45	250.23	293.36	155.39	233.69	-1.41	0.047962
ubiquitin-conjugating enzyme E2A (RAD6 homolog) (UBE2A)	201899_s_at	931.71	1089.28	804.29	946.81	643.62	827.98	550.94	672.79	-1.41	0.022641
karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2)	201088_at	1153.34	1779.5	872.12	1267.45	752.41	1404.84	544.94	899.81	-1.41	0.022454
endothelin receptor type B (EDNRB)	204271_s_at	355.41	303.66	242.08	300.59	274.37	234.84	134.13	214.61	-1.4	0.04104
FN5 protein (FN5)	219806_s_at	775.25	959.89	410.17	716.65	509.07	749.59	279.75	513.89	-1.39	0.04909
Ras homolog enriched in brain (RHEB)	213404_s_at	820.28	881.47	672.08	796.53	554.92	685.36	472.61	574.01	-1.39	0.038488
neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1)	210631_at	92.45	87.95	66.45	82.33	64.77	64.64	48.46	59.28	-1.39	0.035175
B-cell CLL/lymphoma 10 (BCL10)	205263_at	1052.07	1111.08	702.1	954.84	720.48	888.39	457.37	688.43	-1.39	0.024639
nuclear receptor subfamily 4, group A, member 2 (NR4A2)	204622_x_at	201.15	209.58	186.88	199.27	145.46	144.05	138.48	143.19	-1.39	0.03275
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa (NDUFB6)	203613_s_at	941.1	1041.79	783.96	924.2	650.78	726.79	623.72	662.95	-1.39	0.043511
Ras and Rab interactor 3 (RIN3)	220439_at	322.6	248.95	240.37	269.72	216.55	192.07	174.3	194.97	-1.38	0.044542
solute carrier family 7(cationic amino acid transporter, y+ system), member 1 (SLC7A1)	212295_s_at	3401.72	4447.92	3666.19	3832.24	2295.91	3304.34	2819.87	2803.32	-1.37	0.030742
down-regulator of transcription 1, TBP-binding (negative cofactor 2) (DR1)	209188_x_at	458.69	567.27	437.12	486.68	292.64	477.29	290.1	354.27	-1.37	0.038036
SH3-domain GRB2-like endophilin B1 (SH3GLB1)	209091_s_at	320.49	451.88	321.83	363.15	238.07	324.77	226.81	264.48	-1.37	0.040344
annexin A2 pseudogene 2 (ANXA2P2)	208816_x_at	3360.49	3733.48	3881.15	3652.92	2596.51	2810.96	2636.19	2683.92	-1.36	0.031004
microfibrillar-associated protein 2 (MFAP2)	203417_at	477.63	625.03	739.31	613.73	352.94	452.18	543.47	451.62	-1.36	0.033685
myeloid cell leukemia sequence 1 (BCL2-related) (MCL1)	200798_x_at	396.11	524.61	329.13	417.94	269.43	412.34	242.48	308.05	-1.36	0.026962
diacylglycerol kinase, theta 110kDa	207562_at	302.11	282.79	306.06	297.59	223.6	216.16	230.06	222.04	-1.34	0.028525
chromosome 9 open reading frame 76 (C9orf76)	218979_at	413.44	420.33	347.1	394.48	301.45	360.23	226.09	295.94	-1.33	0.046553
tripartite motif-containing 2 (TRIM2)	214248_s_at	78.6	67.35	61.22	69.14	61.74	48.49	45.59	51.97	-1.33	0.048147
adenosine kinase (ADK)	204119_s_at	757.27	924.27	1032.49	903.92	586.02	693.71	769.6	682.12	-1.33	0.030026
CDC28 protein kinase regulatory subunit 1B (CKS1B)	201897_s_at	451.32	492.1	536.73	491.5	318.46	389.53	406.17	369.78	-1.33	0.041785
glycogenin 2 (GYG2)	210964_s_at	165.48	159.89	150.65	158.85	132.89	116.59	109.97	120.33	-1.32	0.027782
dual specificity phosphatase 6 (DuSP6)	208891_at	690.02	664.22	292.67	549.02	581.41	483.28	179.34	414.47	-1.32	0.036613
isopentenyl-diphosphate delta isomerase (IDI1)	208881_x_at	465.15	465.67	641.14	523.61	360.04	345.05	485.94	397.05	-1.32	0.040551
Rho GTPase activating protein 22 (ARHGAP22)	206298_at	284.69	275.64	250.4	271.22	201.23	209.52	201.11	205.1	-1.32	0.041794
mitogen-activated protein kinase 10 (MAPK10)	204813_at	439.19	386.92	527.61	450.85	328.81	275.46	416.01	341.31	-1.32	0.015745
ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3)	204616_at	834.49	1002.13	801.58	879.72	616.11	832.67	549.89	665.29	-1.32	0.022698
peptidylprolyl isomerase D (cyclophilin D) (PPID)	204185_x_at	468.76	366.69	398.03	410.77	354.32	249.13	327.82	311.57	-1.32	0.049833
myotubularin related protein 2 (MTMR2)	203211_s_at	320.04	338.68	305.98	322.31	248.84	259.63	223.1	243.45	-1.32	0.032846
thioredoxin domain containing 9 (TXNDC9)	203008_x_at	993.18	1283.49	972.17	1082.53	727.95	977.96	755.85	819.38	-1.32	0.029952
ESTs, Moderately similar to RL39_HUMAN 60S ribosomal protein L39 [H.sapiens]	217665_at	298.58	371.89	140.33	270.3	231.21	298.78	90.51	206.85	-1.31	0.025499
gamma-glutamyl carboxylase (GGCX)	214005_at	518.13	703.37	403.72	542.37	402.18	535.2	305.15	414.07	-1.31	0.038912
DC13 protein	218447_at	572.74	747.02	536.82	620.02	451.67	561.42	413.48	475.81	-1.3	0.037633

Numbers indicate Model Based Expression Indexes (MBEIs) detected for each probe sets

Bold: Up-regulated in both MAS 5.0 and dChip analysis

Underline: "membrane" protein annotated by GOA analysis

Supplemental table 5. mRNA expression patterns of genes on table 1 and 2 in different ORS locations

gene	probe set	Upper-bulge 1	Bulge 1	Inner-bulge 1	Sub-bulge 1	Suprabulbar 1	Upper-bulge 2	Bulge 2	Inner-bulge 2	Sub-bulge 2	Suprabulbar 2
trinucleotide repeat containing 9 (TNRC9)	214774_x_at	237.7P	124.8P	0.9A	40.3A	15.4A	313.6P	176.6P	1A	57.1P	7.2A
deiodinase, iodothyronine, type II (DIO2)	203700_s_at	1216.9P	1169P	94.6A	374P	253.4P	672.3P	773.7P	111.5A	228.2P	162.1P
pleckstrin homology-like domain, family A, member 1 (PHLDA1)	217996_at	235P	210.2P	67.3P	67.5P	46P	196.4P	120P	73.4P	61.2P	84P
angiopoietin-like 2 (ANGPTL2)	213001_at	782.2P	831.1P	464.9P	318.8P	263.2P	807.6P	551.3P	324.5P	246.1P	176.8P
WNT inhibitory factor 1 (WIF1)	204712_at	1307.5P	987.1P	15.4A	1365.6P	480.8P	1112.4P	1169P	54.4P	370.4P	31.5P
regulated in glioma (RIG)	221127_s_at	163.7P	100.6P	4.5A	106.7P	45.5P	152.7P	90.9P	3.2A	59.2P	21.4M
dickkopf homolog 3 (Xenopus laevis) (DKK3)	214247_s_at	2468.5P	2708.9P	169.5P	1795.7P	746P	3713.5P	2385.4P	234.7P	1033.7P	493.4P
calcium/calmodulin-dependent protein kinase II (CaMKIINalpha)	218309_at	514.2P	675.7P	42A	405.3P	138.8P	471P	324.8P	76.6A	104.6P	100.3P
dihydropyrimidinase-like 2 (DPYSL2)	200762_at	1668.2P	1406.4P	418.5P	1246.6P	424P	1885.3P	1341.7P	469.4P	827.5P	471.1P
glycoprotein M6B (GPM6B)	209167_at	290M	291.4A	72.8A	217.4A	151.4A	415.5M	329M	124.2A	207.9A	80.8A
dihydropyrimidinase-like 3 (DPYSL3)	201431_s_at	724.1P	486.3P	166.4A	263.8P	135.4P	558.1P	438.1P	151.8P	450P	181P
decorin	201893_x_at	2024.6P	2172.1P	613P	1279.7P	784.4P	1591P	2258.3P	178.4P	1682.4P	790.7P
serine (or cysteine) proteinase inhibitor, clade F, member 1 (SERPINF1)	202283_at	564.8P	681.7P	29.3A	572.2P	160.9A	406.9P	681.4P	92A	448.3P	150.4A
Ca2+-dependent activator protein for secretion 2 (CADPS2)	219572_at	227.5P	216.2P	105P	161.3P	169.3P	515.2P	322.8P	143.4P	177.7P	152.8P
transforming growth factor, beta 2 (TGFB2)	209909_s_at	97.2P	82.9P	19.4A	262.6P	83.5P	119.1P	158.3P	14.2A	97.2P	30.1P
keratin 15 (KRT15)	204734_at	5776.5P	5969.4P	149.5A	5653.7P	3157P	5301.7P	5013P	301P	4846.8P	3524.6P
frizzled homolog 1 (Drosophila) (FZD1)	204451_at	438.8P	385.1P	219.6A	394.3P	280P	732.9P	692.6P	224.2P	435.9P	258.3P
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (NFATC1)	211105_s_at	534.8P	507.8P	485.8A	337.7P	342.6P	557.3P	431.9P	321.1P	308.5P	307.3P
follistatin (FST)	204948_s_at	298.8P	252.4A	391.4A	163.9A	115.2A	331.9P	179.8P	163.8A	122.6A	103.2A
calmodulin 1 (phosphorylase kinase, delta) (CALM1)	211984_at	338.5P	320P	312P	219.1P	196.2P	470.6P	444.4P	273.3P	275.2P	244.9P
dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT)	205337_at	211.4P	158.8P	30.7A	86.5P	107.6P	264.9P	259.8P	6.9A	128.2P	30.8P
solute carrier family 7(cationic amino acid transporter, y+ system), member 1 (SLC7A1)	212295_s_at	1368P	1280P	210.6P	2337.7P	2983.9P	1228P	806.6P	203.1P	1350.6P	2857.1P
Ras homolog enriched in brain (RHEB)	213404_s_at	385.3P	325.2P	335.7P	528.4P	544.5P	692.7P	584.1P	498.7P	640.3P	635.4P
endothelin receptor type B (EDNRB)	204271_s_at	77.3P	129.1P	54.3A	99.6P	127.1P	62.7P	129.4P	20.2A	337.6P	265.5P
von Hippel-Lindau binding protein 1 (VBP1)	201472_at	583.2P	510.8P	385.7P	585.1P	891.9P	886.5P	747.1P	483.1P	910.3P	927.4P
N-myc downstream regulated gene 1(NDRG1)	200632_s_at	925.4P	774.1P	1154.2P	1149.7P	1412.5P	1302.2P	1724.3P	1315.3P	2823.1P	2786.8P
latent transforming growth factor beta binding protein 2 (LTBP2)	204682_at	836.7P	1731.9P	383.1P	3191.8P	2712.3P	1188.9P	1892.9P	365.7P	2498.6P	2425.9P
melanoma cell adhesion molecule (MCAM, CD146)	209087_x_at	309.4P	436.8P	181.4P	719.4P	926.9P	310.7P	504P	279.4P	720.9P	1162P
collagen, type XI, alpha 1 (COL11A1)	37892_at	827.1P	722.1P	11.9A	1069.7P	1529.3P	698.3P	1142.9P	43.4A	1843.6P	2241.6P
Rac GTPase activating protein 1 (RACGAP1)	222077_s_at	193.1P	128.5P	72.1P	138.2P	242.2P	344.8P	187P	115.4P	322.6P	475.1P
thymidylate synthetase (TYMS)	202589_at	502.2P	323.3P	127P	397.9P	610.2P	425.5P	291.9P	76.7P	391P	452.1P
fibroblast growth factor 18 (FGF18)	211029_x_at	25.9A	25.7A	15.2A	157.6P	443.2P	33.1A	58.9A	22.7A	347.7P	466.5P
solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4)	209610_s_at	205.7P	118.5P	10.2A	241.7P	387.4P	167.7P	131.4P	26.1A	482.8P	856.7P
topoisomerase (DNA) II alpha 170kDa (TOP2A)	201292_at	265P	140.7P	12.8A	122P	271.2P	199.9P	179.1P	6.7A	221.1P	387.7P
retinoic acid induced 14 (RAI14)	202052_s_at	128M	146.9P	105.4A	178.8P	407P	151P	203.2P	182P	687.2P	702.3P
flap structure-specific endonuclease 1 (FEN1)	204767_s_at	305.4P	213.9P	114.8A	282.5P	421.8P	358.2P	223.5P	84.6P	443.7P	596.3P
protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C)	204284_at	343.7P	468.8P	229.1P	778.7P	1338.1P	225.3P	326.1P	147.3P	1064.9P	1399P
karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2)	211762_s_at	445.6P	139P	182.2P	180P	215.3P	294.3P	205.7P	148.4P	263P	423.2P
syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2)	212157_at	205.1P	286.9P	226.4P	316.3P	399.2P	160.2P	209P	220.5P	405.3P	507.5P
phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL)	202990_at	150P	196.7P	172.4P	577.8P	728.8P	273.9P	306.8P	211.1P	600.8P	1135.2P
ZW10 interactor (ZWINT)	204026_s_at	467.6P	344.1P	262.7P	322.7P	555.6P	461.1P	269.2P	155.7P	499P	763.2P
vav 3 oncogene (VAV3)	218807_at	699.3P	658.1P	394.2P	1078.1P	1291.8P	520.2P	393.7P	326.4P	547.8P	806.3P
ribonucleotide reductase M2 polypeptide (RRM2)	201890_at	208.5P	117.1P	30.3A	216.7P	239.4P	368.8P	176P	18.1A	258.6P	613.4P
glypican 4 (GPC4)	204984_at	72.2A	166.4A	28A	233.5P	265.3P	96.9P	128.8P	77.8A	273.8P	284.1P
protein regulator of cytokinesis 1 (PRC1)	218009_s_at	407P	219.1P	80.3A	174.3P	396.1P	343.3P	293.6P	63A	382.4P	548.6P
phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A)	210145_at	104.6P	103.3P	95.1P	162.5P	276.7P	154.9P	195.2P	175.4P	391.5P	272P
cell division cycle 2, G1 to S and G2 to M (CDC2)	203213_at	162.6P	83.1P	44.5A	140.9P	157.8P	164.5P	65.9P	49.9A	161.2P	274.1P
ets variant gene 5 (ets-related molecule) (ETV5)	203349_s_at	221.4P	180.1P	106.6A	428.5P	241.1P	111P	195.3P	73.9A	328.2P	207.5P
laminin, beta 1 (LAMB1)	201505_at	43.2P	97.4P	23.6A	121.4P	206.8P	96P	118.1P	15.8A	238.3P	312.4P
solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7)	209884_s_at	40.3P	32A	47.7A	68.4P	147.6P	40.6P	32.2P	55.3M	74.6P	88.4P
platelet derived growth factor C (PDGFC)	218718_at	187.5P	458.8P	180.9P	847.4P	878.3P	189.9P	269.3P	199P	573.4P	1397.7P
nucleolar and spindle associated protein 1 (NUSAP1)	218039_at	657P	669P	158.8P	648.5P	841.8P	751.2P	368.1P	122.4P	658P	1196.6P
tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3)	201147_s_at	93.2A	74.5A	49.2A	599.8P	452.6P	69.8A	145.9P	143.5A	388.7P	599.3P
protocadherin 8 (PCDH8)	206935_at	17.9A	21.1A	13.6A	117.1P	105.4P	13.9A	68.2P	22.7P	150.8P	299.8P
aminolevulinate, delta-, dehydratase (ALAD)	218487_at	170.4A	184.3P	115.7A	563P	1281.9P	120.2A	193.3P	112.3A	821.9P	1690.3P
tripartite motif-containing 9 (TRIM9)	209859_at	86.2P	100.5P	153.4P	253.9P	616.8P	122.3P	140.7P	254.3P	391.3P	817.3P
angiopoietin-like 7 (ANGPTL7)	206423_at	21.6A	408.1P	41.9A	2997.4P	5260.3P	32.4A	219.1P	3A	2019.3P	3471.8P
cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP)	205713_s_at	155.9P	197.5P	3.4A	959.9P	1566.3P	48A	169.5P	2A	1154.6P	3605.8P

The Results from 2 experiments are shown. In each experiment , Genechips representing the global gene expressions in upper-bulge, bulge, inner-bulge, sub-bulge and suprabulbar ORS were generated.
BOLD probe sets are detected as up-regulated in the bulge ORS, while plain probe sets are detected as down-regulated.
The numbers in columns are signal intensities (RNA expression level) detected by MAS 5.0. Genechips were normalized accoridng to the same parameters.
"P" means detected as "expressed", while "A" means detected as "Not expressed" by MAS 5.0 software.
Underlined genes are "membrane" protein annotated by GOA analysis.