## Supplemental information:

## SI Methods

### *Cell lines and reagents*

Human ovarian serous adenocarcinoma cell lines (A224, OVCA429, SKOV3 etc.) and human monocytic leukemia cell line THP-1 were grown in RPMI1640 supplemented with 10% FBS and penicillin/streptomycin (Invitrogen). HUVECs (Lonza) were grown in EBM supplemented with 2% FBS and EGM-2 SingleQuots (Lonza) as primary culture and used within 6 passages. All cells were maintained in exponential growth phase at 37°C in 5% $CO_2$.

To generate conditioned media from ovarian tumor cells, $1 \times 10^6$ cells were seeded in a T75 flask with RPMI1640 + 10% FBS overnight. The next day, culture medium was substituted by basal medium (EBM + 0.5% FBS for HUVECs experiments or RPMI1640 + 0.5% FBS for THP-1 experiments) for an additional 24 hours. The conditioned media were filtered through a low protein binding 0.45 μm PVDF filter (Millipore) and stored in a -80 °C freezer before use.

Antibodies were purchased from the following commercial sources: Sigma-Aldrich (FGF18), Santa Cruz Biotechnology (murine CD31), R&D Systems (FGFR4), AbD Serotec (F4/80), DAKO Cytomation (Ki-67 and human CD31), Thermo Scientific (CD163) and Cell Signaling Technology (all other antibodies).

Recombinant human FGF18 was purchased from Biovision. NF-κB pathway inhibitors QNZ (6-amino-4-(4-phenoxyphenylethylamino)quinazoline), SN-50 peptide (AAVALLPAVLLALLAPVQRKRQKLMP) and TPCA-1 (2-[(aminocarbonyl)amino]-5-(4-fluorophenyl)-3-thiophenecarboxamide) were purchased from Calbiochem. All the other chemicals including the pan-FGFR inhibitor PD173074 (1-t-butyl-3-(6-(3,5-dimethoxyphenyl)-

2-(4-diethylaminobutylamino)-pyrido[2,3-d]pyrimidin-7-yl)urea) were purchased from Sigma-Aldrich.

***In vitro assays for ovarian cancer cell lines and HUVECs***

In vitro adherent cell proliferation assay was performed in 96-well plates with RPMI1640 + 1% FBS. Cell number was determined by CellTiter-Blue® Cell Viability Assay kit (Promega).

Boyden chamber based migration assay was performed in a 24-well cell culture insert with 8.0 µm pore size PET membrane (BD Biosciences). Cells were resuspended at 10,000 per mL in basal medium (RPMI1640 + 0.1% FBS for ovarian cancer cells or EBM + 0.5% FBS for HUVECs) and plated in triplicate in 350 µL into the upper chamber. The bottom chamber contained 500 µL of basal media with chemoattractant (2% FBS for ovarian cancer cells; 100 ng/mL rhFGF18 or tumor cell-derived conditioned medium with / without 100 nM PD173074 for HUVECs). After cells were plated for 3 hours, the insert was removed and wiped with a cotton swab to dislodge the non-migrated cells. Migrated cells on the underside were fixed and stained with Diff-Quick Stain Set (Dade Behring) and quantified by counting under 40× magnification (field covers >80% of the membrane).

Cell invasion assays were performed in BD BioCoat™ Growth Factor Reduced Matrigel Invasion Chambers with 8.0 µm pore size PET membrane. The same protocol as above was used and cells were allowed to invade for 24 hours before staining.

In vitro angiogenesis assay was performed by assessing tube formation of HUVECs as previously described (1). HUVECs (15,000 cells in 100 µL EBM2 + 0.5% FBS) were seeded in triplicate into a 96-well plate coated with Growth Factor Reduced Matrigel (BD Biosciences, 60 µL per well). To induce tube formation, 100 ng/mL rhFGF18 with / without 100 nM PD173074 was added. After incubation for 2.5 hours, HUVECs were stained by 1 µM Calcein-AM and photographed under a fluorescent microscope (Ex/Em: 488/520 nm). Tube-like structures were quantified as total tube length by the skeleton plugin of ImageJ software (NCI).

### *In vitro assays for THP-1 cells*

Migration of THP-1 cells were performed in 24-well cell culture insert with 3.0 μm pore size, FluoroBlok®, PET membrane (BD Biosciences). THP-1 cells were pre-labeled with 1 μM Calcein-AM and seeded into the insert in triplicate at 250,000 cells per 350 μL of RPMI1640 + 0.5% FBS. The inserts were placed into the wells containing tumor cell conditioned medium and incubated for 6 hours at 37°C. Migrated THP-1 cells were visualized under fluorescent microscope and quantified by counting three randomized 100× fields.

Co-culture of THP-1 and ovarian cancer cells was done in RPMI1640 + 10% FBS on 6-well cell culture inserts with 0.4 μm pore size, permeable PET membrane (BD Biosciences). Tumor cells were seeded at a density of $2 \times 10^5$ cells per insert in 1.5 mL medium. THP-1 cells were seeded at a density of $2 \times 10^5$ cells in the lower well in 3 mL medium. After co-culture for indicated periods, THP-1 cells were harvested for RNA extraction and subjected to qRT-PCR analysis.

### *In vivo xenograft studies*

Five female SCID Hairless mice (aged 4-5 weeks, Charles River Laboratories) were randomly assigned to each experiment group. Xenografts were established in both subcutaneous (s.c.) and intraperitoneal (i.p.) models by injecting 5 million A224-derived cells or 2.5 million SKOV3-derived cells into the dorsal flank (s.c.) or abdominal right lower quadrant (i.p.) of the mouse. In the s.c. model, xenograft dimensions were measured by calipers twice a week and the tumor volume was calculated with the following formula: $V= 0.5 \times L \times W^2$ (L=larger diameter and W=smaller diameter). In the i.p. model, tumor burden was assessed by the total weight of the xenografts after sacrifice. Mice were sacrificed 4 weeks (for FGF18 overexpression studies, due to the reach of ethical limit of tumor size) or 8 weeks (for FGF18 knockdown study, due to the low tumor growth rate) after tumor cell inoculation. All xenografts were fixed in 10% neutral buffered formalin, embedded in paraffin and cut consecutively into 4 µm sections for further pathological examination (H&E staining) and IHC analysis.

### *Pharmacological treatment of PD173074 on in vivo xenografts*

PD173074 treatment on tumor-bearing SCID mice was performed as previously described (2). Intraperitoneal xenografts were established by i.p. injection of 5 million FGF18 overexpressing A224 cells for 2.5 weeks. Mice were then randomly assigned to two groups for treatment and control (n=5 for each group). PD173074 was administrated intraperitoneally at a dosage of 25 mg/kg/day everyday for 7 days until the termination of the experiment. Solvent vehicle (20% DMSO in 1× PBS) at the same volume (0.4 mL) was employed as control. The tumor burden was assessed by the total tumor weight at the time of sacrifice.

### *Quantitative PCR analysis*

Total RNA from cell culture was prepared by RNeasy mini kit (QIAGEN). Real-time quantitative PCR was performed on 50 ng of total RNA with SuperScript® III Platinum® One-Step qRT-PCR Kit (Invitrogen) in an iCycler iQ Real-Time PCR Detection System (Bio-Rad Laboratories). Relative expression of specific genes was calculated with the $2^{-\Delta\Delta CT}$ method. The expression levels of housekeeping genes GAPDH and PPIA (cyclophilin A) were used as internal controls in most of the cases except the THP-1 experiments, where ACTB (β-actin) was used instead of PPIA. The primer sequences are listed in Supplemental Table S5. Annealing temperature for all primer pairs was set at 59 °C.

Quantitative PCR for DNA copy number validation was performed on 10 ng of genomic DNA with iQ™ SYBR® Green Supermix (Bio-Rad). Three different primers sets were used for FGF18 and FGFR4. The paired primer sequences (F and R, 5' to 3') are list as follows. FGF18 gDNA F1, CAGGGCGGGTAAAGCGACCDNA; FGF18 gDNA R1, CCTCACCTGCCCACATTCGC; FGF18 gDNA F2, CGCTGGTGAGTGAGTGCGAG; FGF18 gDNA R2, CGATGCTCCCCAAGAACGCA; FGF18 gDNA F3, CTCCGCACTCCCTCGCCTAA; FGF18 gDNA R3, TTCACGGAGAGCGAGCGAAC; FGFR4 gDNA F1, CAGCAGGCAGAACCAAGTCTCC; FGFR4 gDNA R1, CCGCTGGAGGAGAGACGCA; FGFR4 gDNA F2, CAGGGTGCTTCTATGGGTGC; FGFR4 gDNA R2, GACGATGTGCTTCAGCCACT; FGFR4 gDNA F3, GGAAGGCAGTTGGTGGGAAG; FGFR4 gDNA R3, CTCTCCCACCTCAGAAGCCA; Line-1 F, AAAGCCGCTCAACTACATGG; Line-1 R, TGCTTTGAATGCGTCCCAGAG. Annealing temperature for all primer pairs was set at 59 °C. DNA content was normalized with the $2^{-\Delta\Delta CT}$ method to that of Line-1, a repetitive element for which copy numbers per haploid genome are similar among all normal and neoplastic cells (3). Relative DNA copy number was determined by normalizing to that of the average of three samples of normal human leukocyte DNA. Correlations between DNA copy numbers revealed from aCGH and qPCR were determined by Spearman's rho test.

### ***Western blot analysis and immunoprecipitation***

Total protein lysate was prepared from subconfluent cell culture by RIPA buffer with cocktail of protease and phosphatase inhibitors (Roche). For signal transduction analysis of pFRS2 and pErk1/2, subconfluent cells were first starved in RPMI + 0.1% FBS overnight before stimulation with 100 ng/mL rhFGF18 for 10 minutes. For compartmental protein extraction, cells were lysed in a hypotonic buffer with 0.5% IGEPAL CA-630 and centrifuged to get the intact nucleus and the cytoplasmic fraction (supernatant). Nuclei were then lysed in RPIA buffer to get the nuclear fraction.

Protein concentration was estimated with BCA Protein Assay kit (Thermo Scientific). 20 µg of protein was separated by 4-15% SDS-PAGE (Bio-Rad) and transferred to nitrocellulose membrane (Amersham Biosciences). Antibody detection was performed with horseradish peroxidase (HRP) conjugated antibodies and SuperSignal Chemiluminescence Substrate system (Thermo Scientific).

Immunoprecipitation (IP) was performed with Pierce® Classic IP kit (Thermo Scientific). rhFGF18 stimulated cells were lysed in IP buffer containing 1% NP-40. Proteins with phosphorylated tyrosine were precipitated from 1 mg total protein by 3 µg phospho-tyrosine antibody (4G10, Millipore), captured by Protein A/G Plus agarose beads, and reconstituted through boiling in 60 µL Laemmli sample buffer. An aliquot of 15 µL was subjected to Western blot to detect tyrosine phosphorylated FGFR4, Erk1/2 and p38.

### *Expression profiling and microarray pathway analysis*

Total genomic DNA free RNA was extracted by RNeasy Kit (QIAGEN) from three independent paired cultures of A224 cells overexpressing FGF18 or RFP. Synthesis of biotinylated cRNA was completed by one-round RNA amplification with GeneChip 3'-IVT Express Kit (Affymetrix) from 2.5 µg of total RNA. A 15 µg aliquot of cRNA was hybridized to an Affymetrix Human U133 Plus 2.0 GeneChip® array. Array data were collected with a laser confocal GeneChip® Scanner 3000 (Affymetrix).

JustRMA algorithm and median intensity of entire array were applied for data input and normalization by BRB ArrayTools version 4.1.0 (developed by Dr. Richard Simon et al, NCI, NIH). Differentially regulated genes were identified by a univariate paired t-test ($p<0.0001$, fold-change$>2.0$, random-variance model) from probe sets presenting in all arrays and displaying a variance in the top 50th percentile. Pathway enrichment analysis was performed by PathwayStudio 6.0 software (Ariadne Genomics). Potential FGF18-related pathways were identified by comparing the differential gene expression in response to ectopic FGF18 manipulation with a biological association network such as KEGG database (4).

## References

1. Arnaoutova I, Kleinman HK. In vitro angiogenesis: endothelial cell tube formation on gelled basement membrane extract. *Nat Protoc*. 2010;5(4):628-635.

2. Crose LE et al. FGFR4 blockade exerts distinct antitumorigenic effects in human embryonal versus alveolar rhabdomyosarcoma. *Clin Cancer Res*. 2012;18(14):3780-3790.

3. Wang TL et al. Digital karyotyping. *Proc Natl Acad Sci U S A*. 2002;99(25):16156-16161.

4. Kanehisa M et al. KEGG for integration and interpretation of large-scale molecular data sets. *Nucleic Acids Res*. 2012;40(Database issue):D109-D114.

## SI Figures:

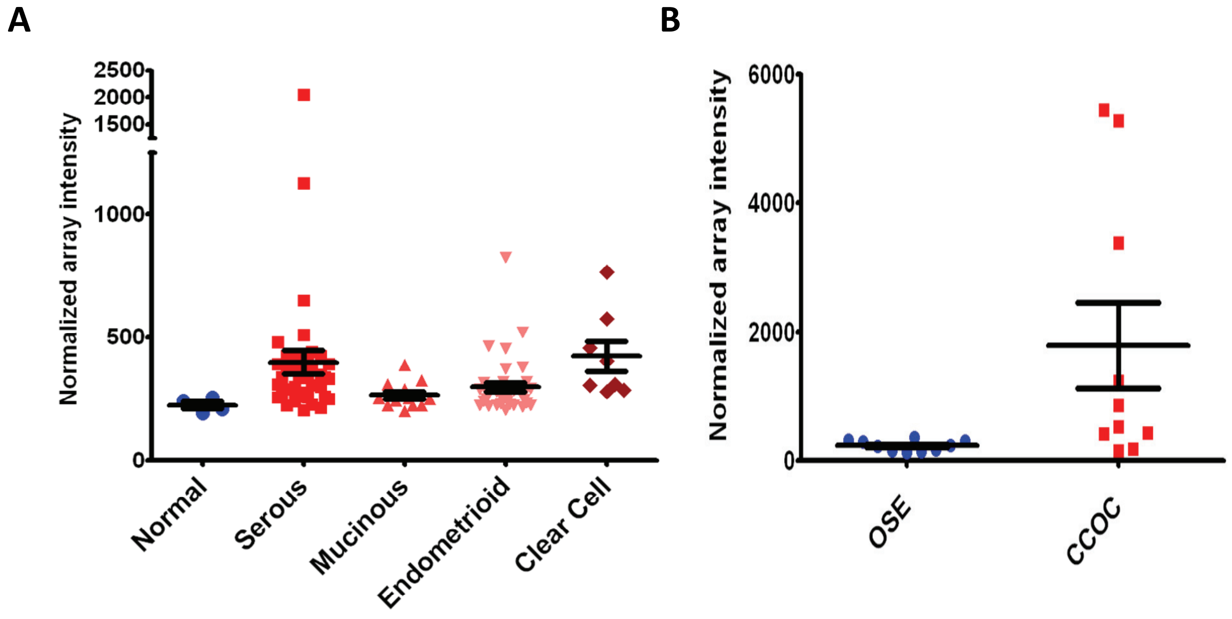

**Figure S1. The expression level of FGF18 in different histological subtypes of epithelial ovarian cancer. (A)** In dataset GSE6008 consisting of 41 serous, 13 mucinous, 37 endometrioid, 8 clear cell ovarian carcinomas and 4 individual normal ovary samples. **(B)** In dataset GSE29450 consisting of 10 clear cell ovarian carcinomas (CCOC) and 10 normal ovarian surface epithelium brushes (OSE). Array data import and normalization were performed by BRB array tools 4.1 with JustRMA algorism. Values on Y axis represent the cumulative intensity of all FGF18 probe sets. Mean±SEM is demonstrated for each group.

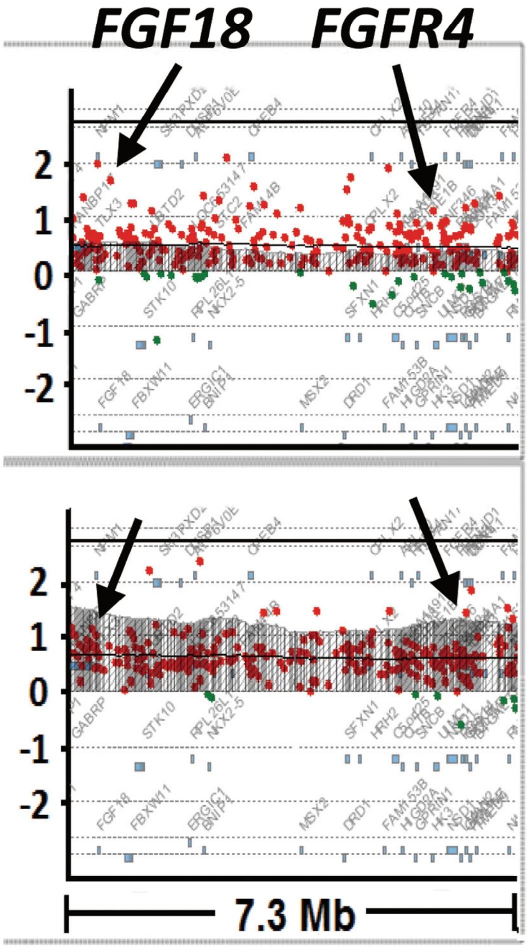

**Figure S2.** The detailed profile of the 7.3-Mb locus in chromosome 5 containing FGF18 and FGFR4 of the 2 representative tumors shown in Figure 1C (Upper panel: case 4595b; Lower panel: case 4963a). Copy number was presented by log2 minus 1 (value of 0 mean diploid, 1 mean 4 copies, 2 mean 8 copies).

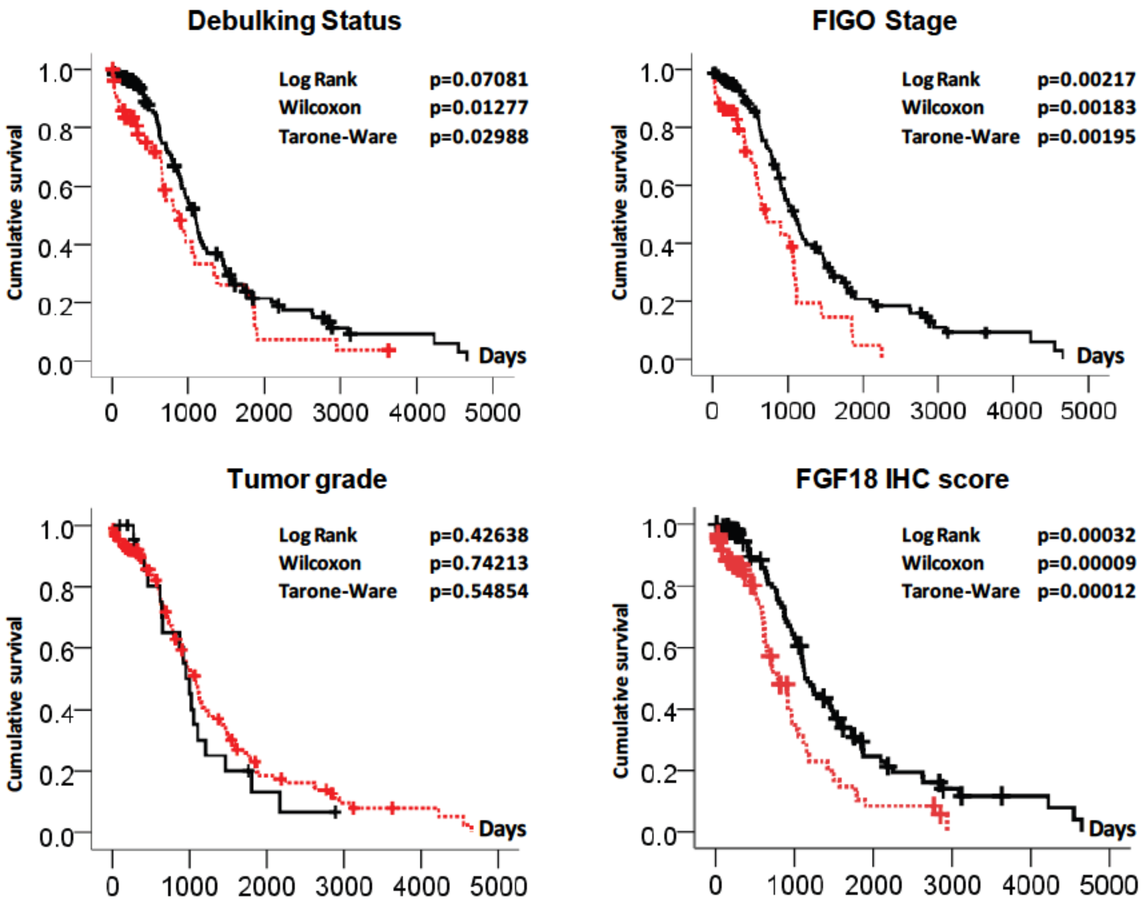

**Figure S3. Kaplan-Meier analyses of the prognostic effects of debulking status, FIGO stage, tumor grade and the FGF18 IHC score on the 192 tumor samples from the validation tissue microarray.** The cut-off of FGF18 IHC score was set at 6 (the highest score of FGF18 in benign ovarian cysts). Statistical significance was checked for each parameter. Detailed results were summarized in Table S1. Black lines: samples with optimal debulking / FIGO stage III / Grade 2 / Low FGF18; red broken lines: samples with suboptimal debulking / FIGO stage IV / Grade 3 / High FGF18; "+": censored samples.

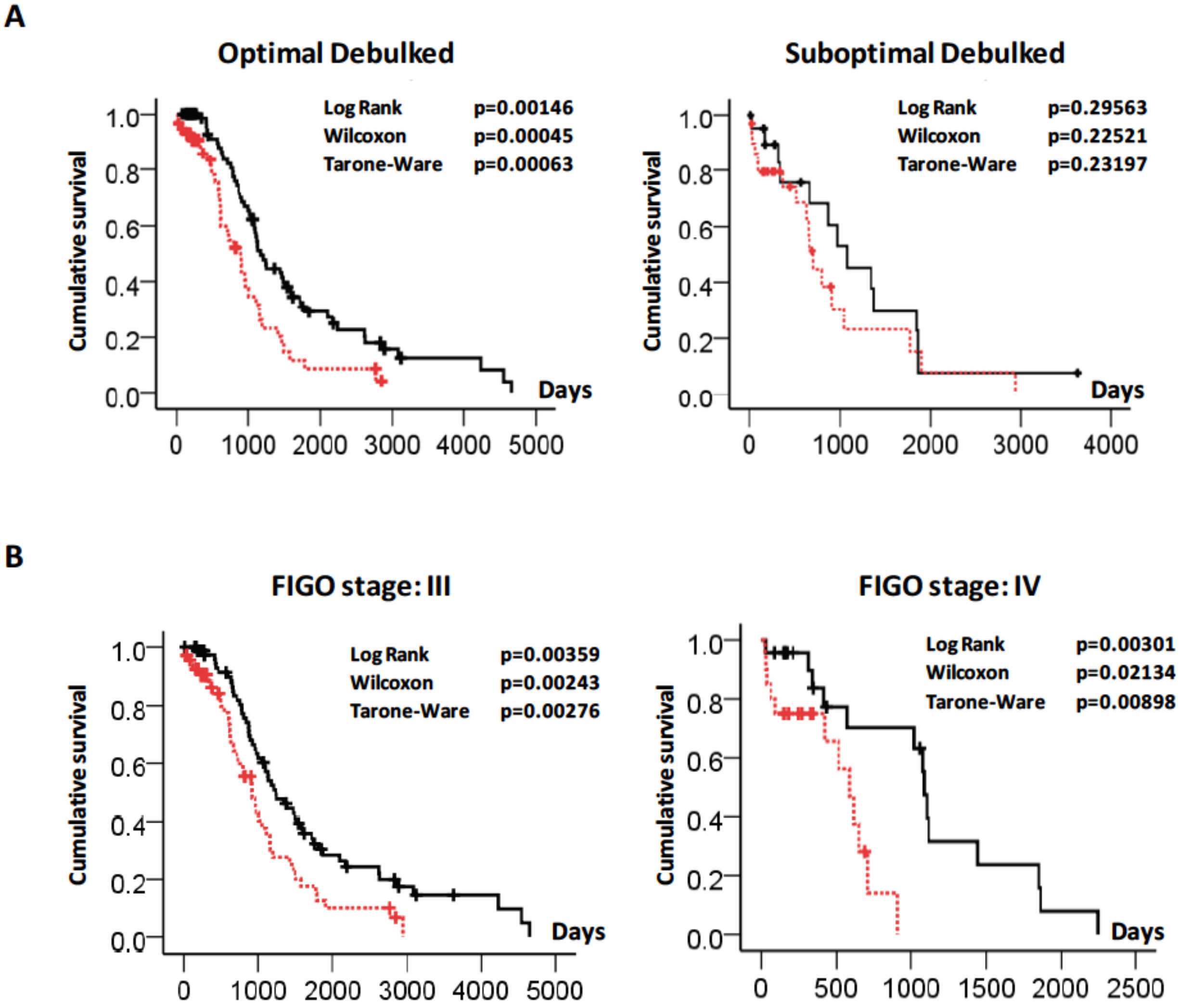

**Figure S4. Multivariate Kaplan-Meier analysis of the prognostic effects of FGF18 expression level adjusted for the debulking status (A) or FIGO stage (B) on the 192 tumor samples from the validation tissue array.** Statistical significance was checked for each parameter. The cut-off of FGF18 expression level was set at the IHC score of 6 (the highest score of FGF18 in benign ovarian cysts). Detailed results were summarized in Table S3. Black lines: samples with low FGF18; red broken lines: samples with high FGF18; “+”: censored samples.

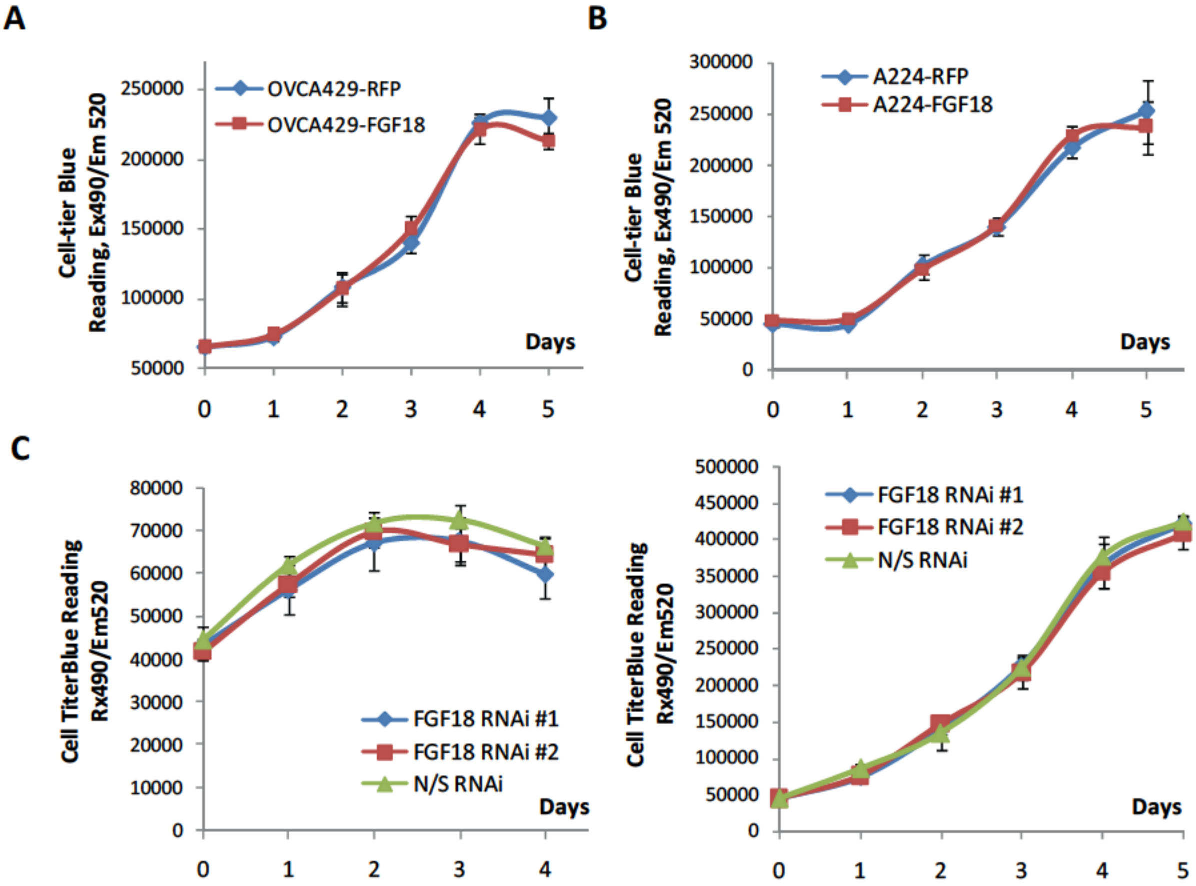

**Figure S5. Effect of FGF18 on the proliferation of OVCA429, A224 and SKOV3 cells**. **(A)** and **(B)** Minimal effect of FGF18 overexpression on the proliferation of OVCA429 (A) and A224 (B) cells. Cells were cultured in 1% FBS to minimize the effect from serum. **(C)** Minimal effect of FGF18 knockdown on the proliferation of SKOV3 cells. Cell growth was assayed in both 1% FBS (left panel) and 10% FBS (right panel, to get exponent growth curves). Typical results were shown from three independent experiments.

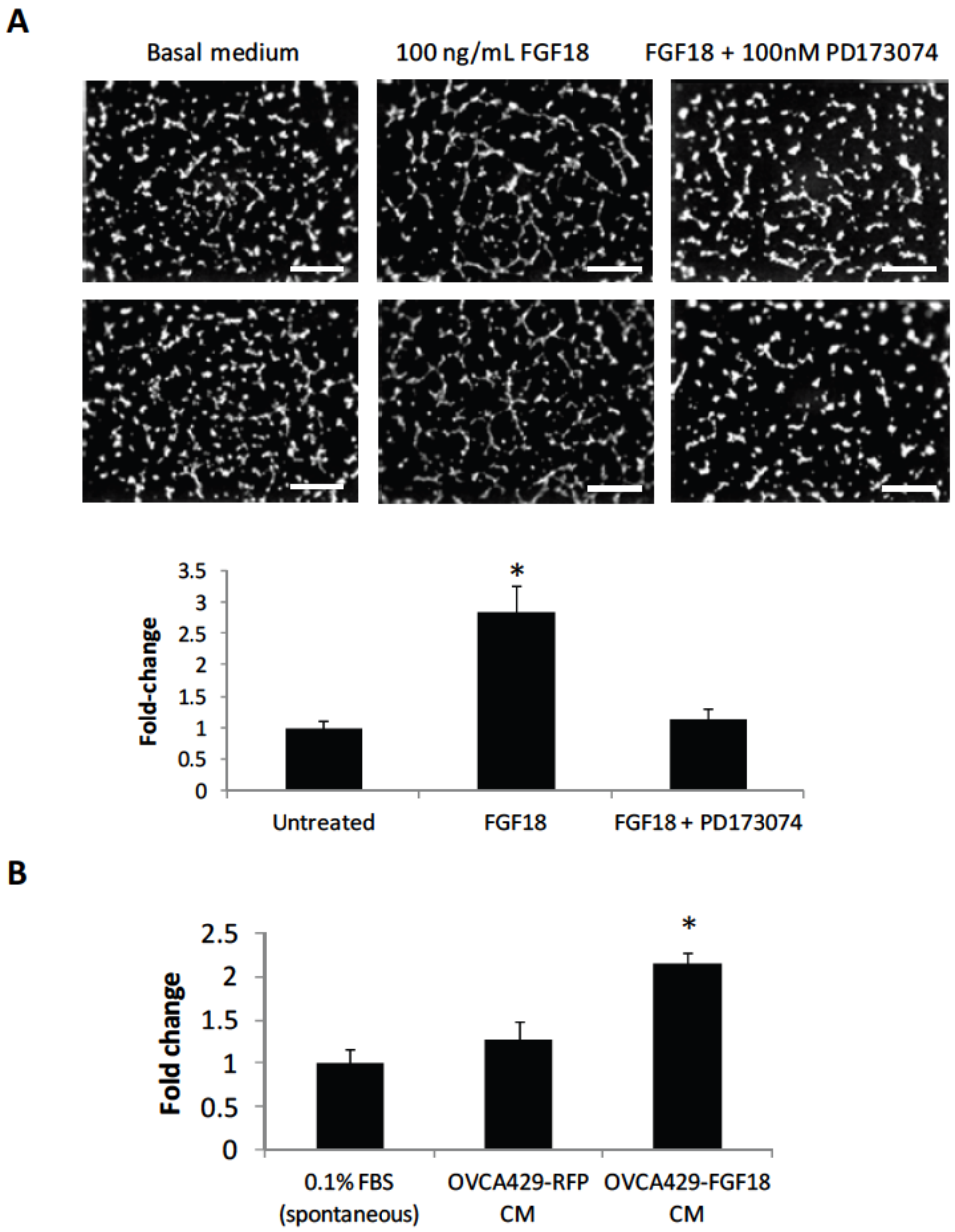

**Figure S6. Stimulatory effect of FGF18 on HUVEC cells**. **(A)** Stimulation of HUVEC tube formation by recombinant FGF18 (100 ng/mL), which can be ablated by the addition of 100 nM pan-FGFR inhibitor PD173074. Typical fluorescent microscopy images (bar: 500 µm) as well as the quantification were shown. **(B)** Conditioned medium from OVCA429 cells with ectopic FGF18 overexpression enhances HUVEC migration compared to conditioned medium from control RFP overexpressing cells. * $p<0.05$; mean±SD from three independent experiments.

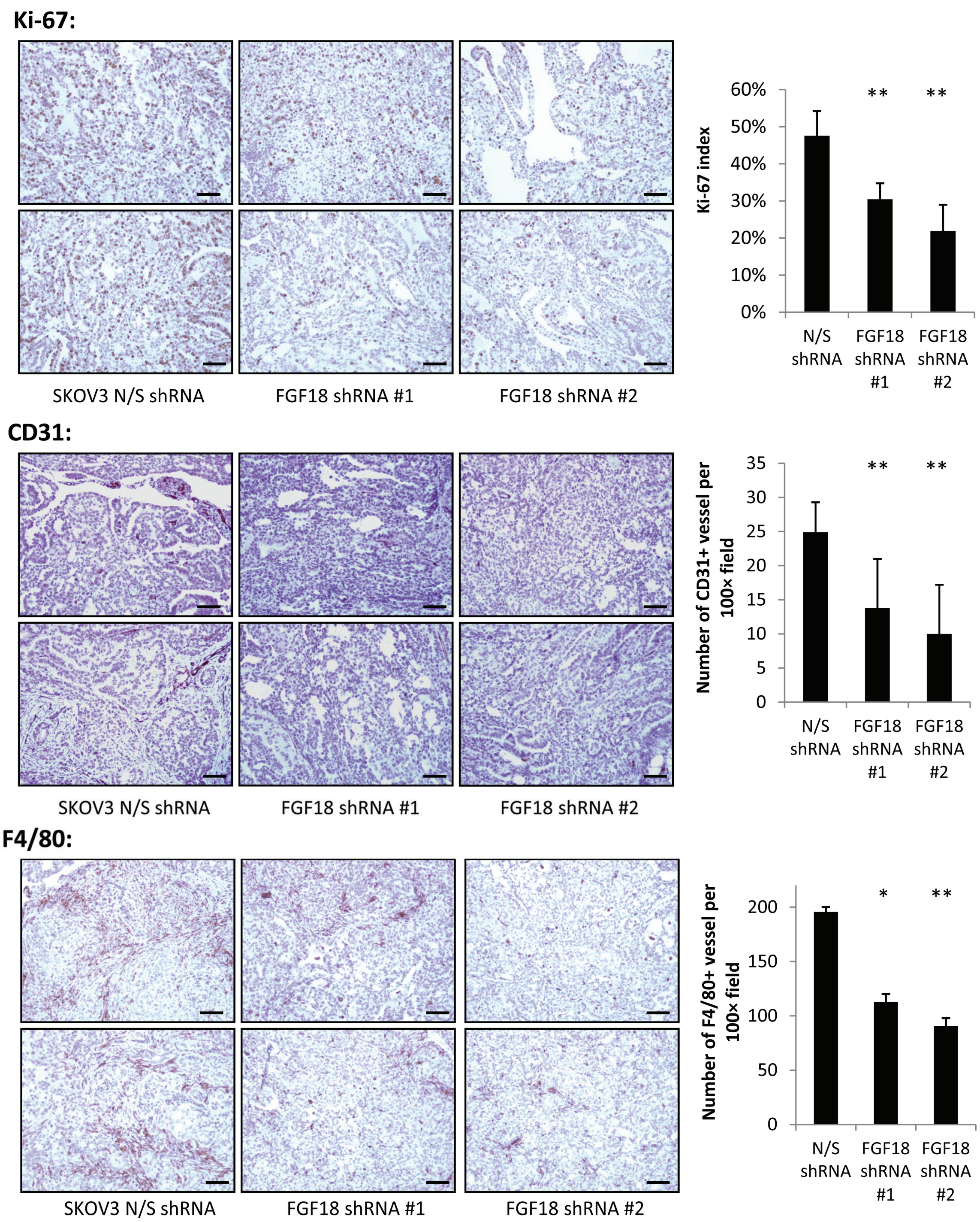

**Figure S7. Immunohistochemical staining of the intraperitoneal xenografts derived from SKOV3 cells with FGF18 knockdown.** Typical staining sections for human Ki-67, murine CD31 and murine F4/80 as well as the corresponding quantification are shown (bar: 100 μm). Comparison was performed with the control SKOV3 with N/S shRNA (* $p<0.05$, ** $p<0.001$).

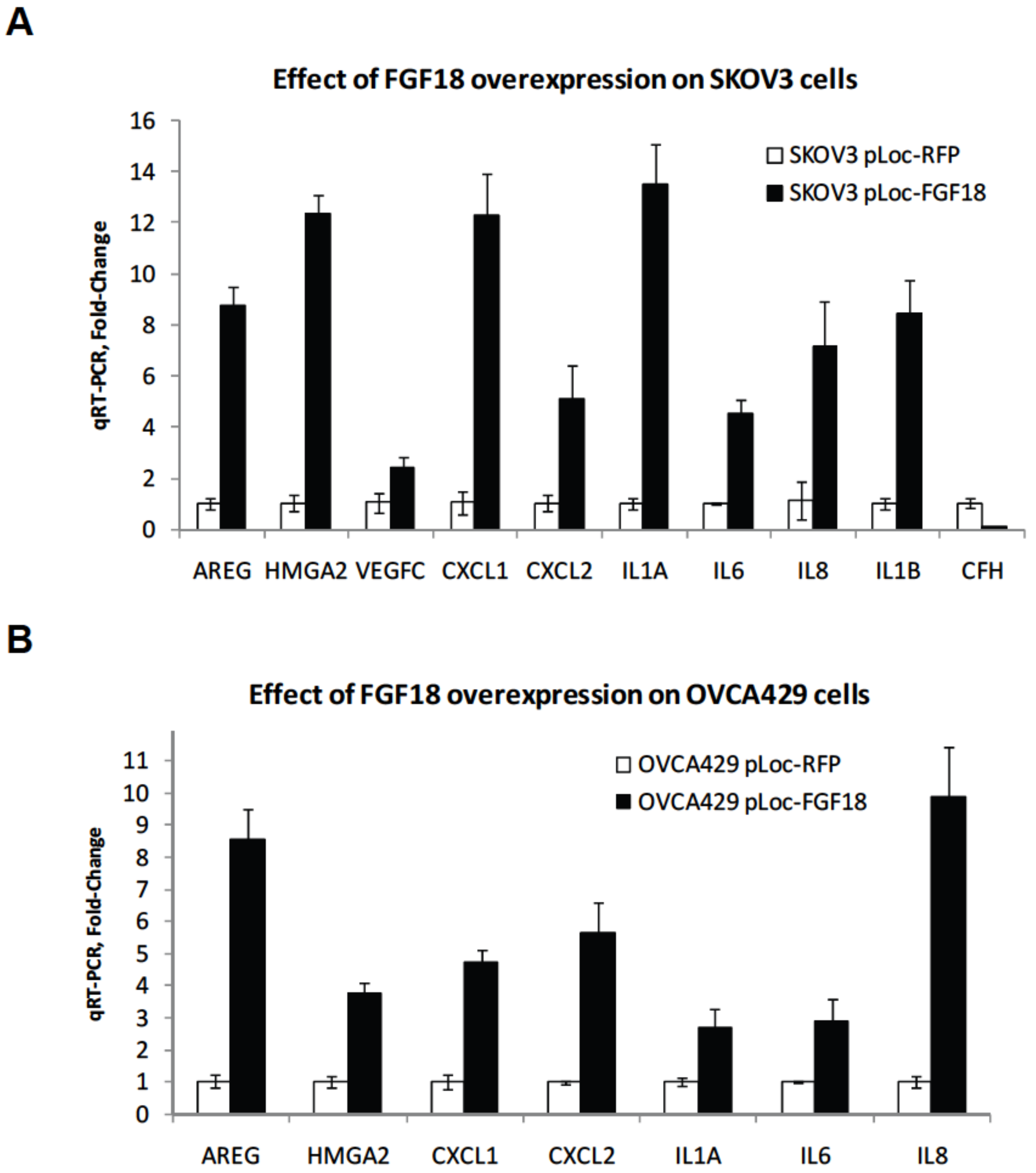

**Figure S8. qRT-PCR validation of expression changes in selected genes identified in the microarray analysis of A224 cells.** Validation was performed in SKOV3 **(A)** and OVCA429 **(B)** cells with ectopic overexpression of FGF18 or RFP (as control). qRT-PCR was performed on three independent RNA samples. Significant changes ($p<0.05$) were observed in all genes tested.

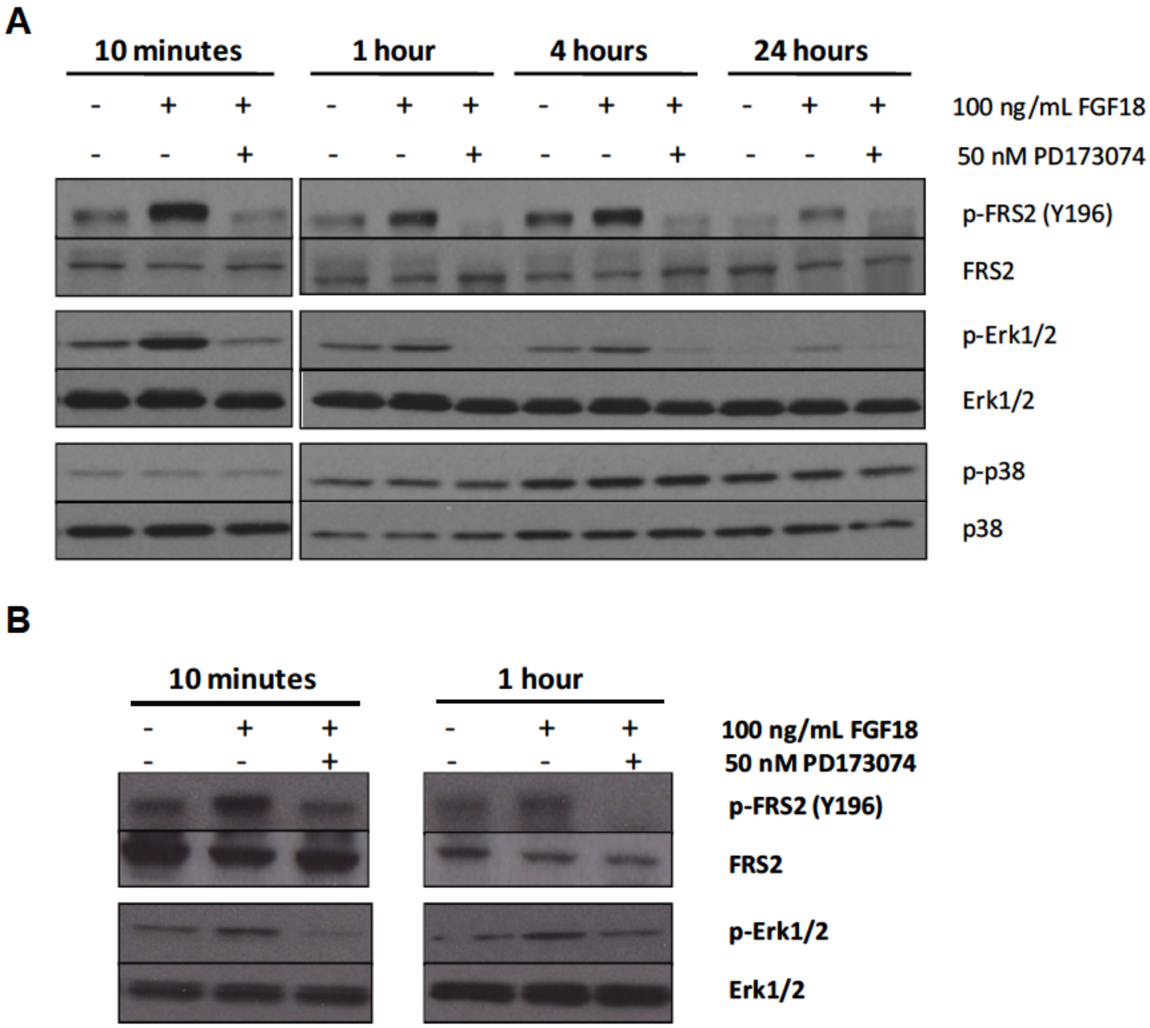

**Figure S9. Activation of FRS2 and MAPK/Erk signaling by FGF18 which is susceptible to pan-FGFR inhibitor PD173074.** The activation of FRS and Erk1/2 signals in A224 **(A)** and HUVEC **(B)** cells were detected by the increase of protein phosphorylation, as compared to untreated cells (FRS2 phosphorylation at Tyr-196, pErk1/2 phosphorylation at Thr202 and Tyr204). No effect on p38 activation was observed (detected by an antibody recognizing p38 only when phosphorylated at Thr180 and Tyr182). We therefore use the baseline p-p38 level as an internal control for the equal loading in Figure 6B.

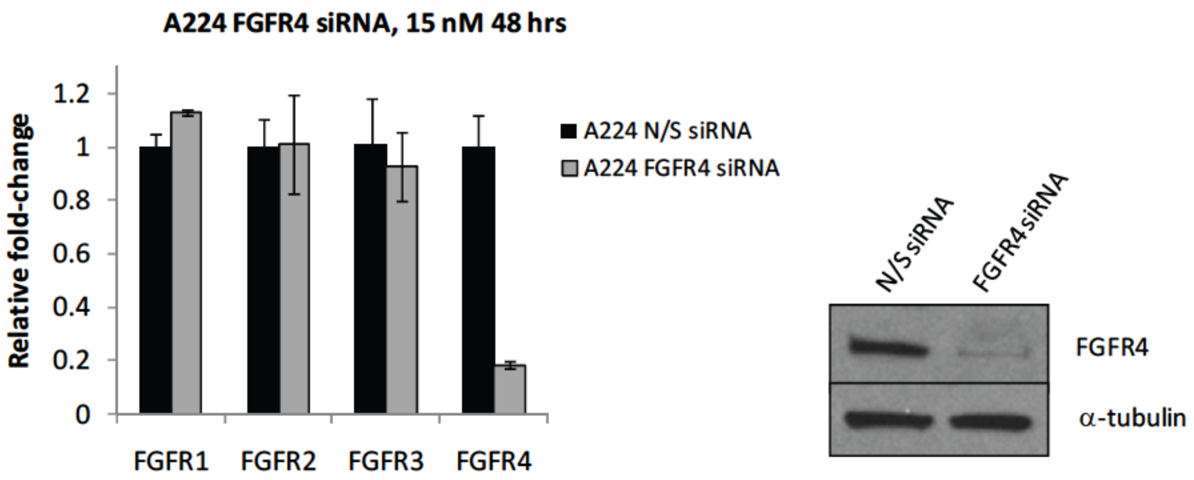

**Figure S10. Efficiency and specificity of siRNA mediated FGFR4 knockdown.** FGFR4 siRNA at a dosage of 15 nM was transfected into A224 cells for 48 hours before harvest for qRT-PCR (left panel) and immunoblot (right panel). A scrambled, non-targeting (N/S) siRNA at same concentration was used as control.

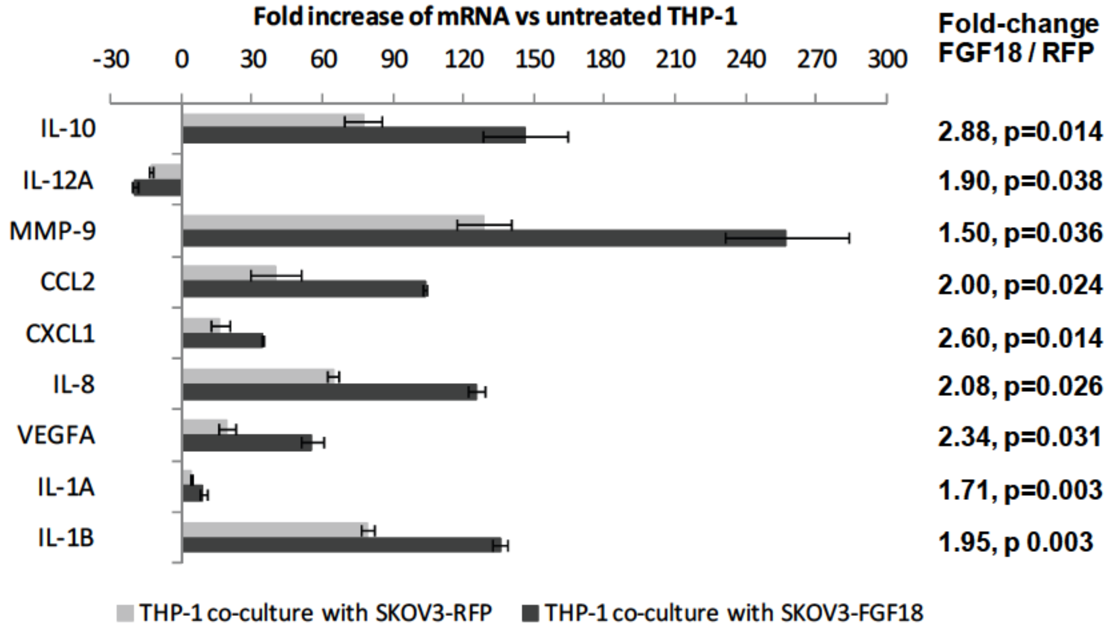

**Figure S11**. **M2 differentiation of THP-1 cells upon co-culture with RFP or FGF18-overexpressing SKOV3 cells.** THP-1 cells were co-cultured with SKOV3 cells overexpressing RFP or FGF18 for 4 days before RNA harvest. With untreated THP-1 cells serving as control, quantitative RT-PCR was performed to quantify the expression of tumor-associated macrophage differentiation markers (IL-10 for oncogenic M2 differentiation, IL-12A for tumor-suppressive M1 differentiation) and other trophic / angiogenic factors (VEGF-A, CCL-2, IL-1, IL-8, CXCL-1 and MMP9). To compare the polarizing effects on THP-1 from the co-culture with RFP or FGF18-overexpressing SKOV3 cells, the relative fold-change for each gene tested and the related p-value (by paired t-test) were calculated and listed on the right.

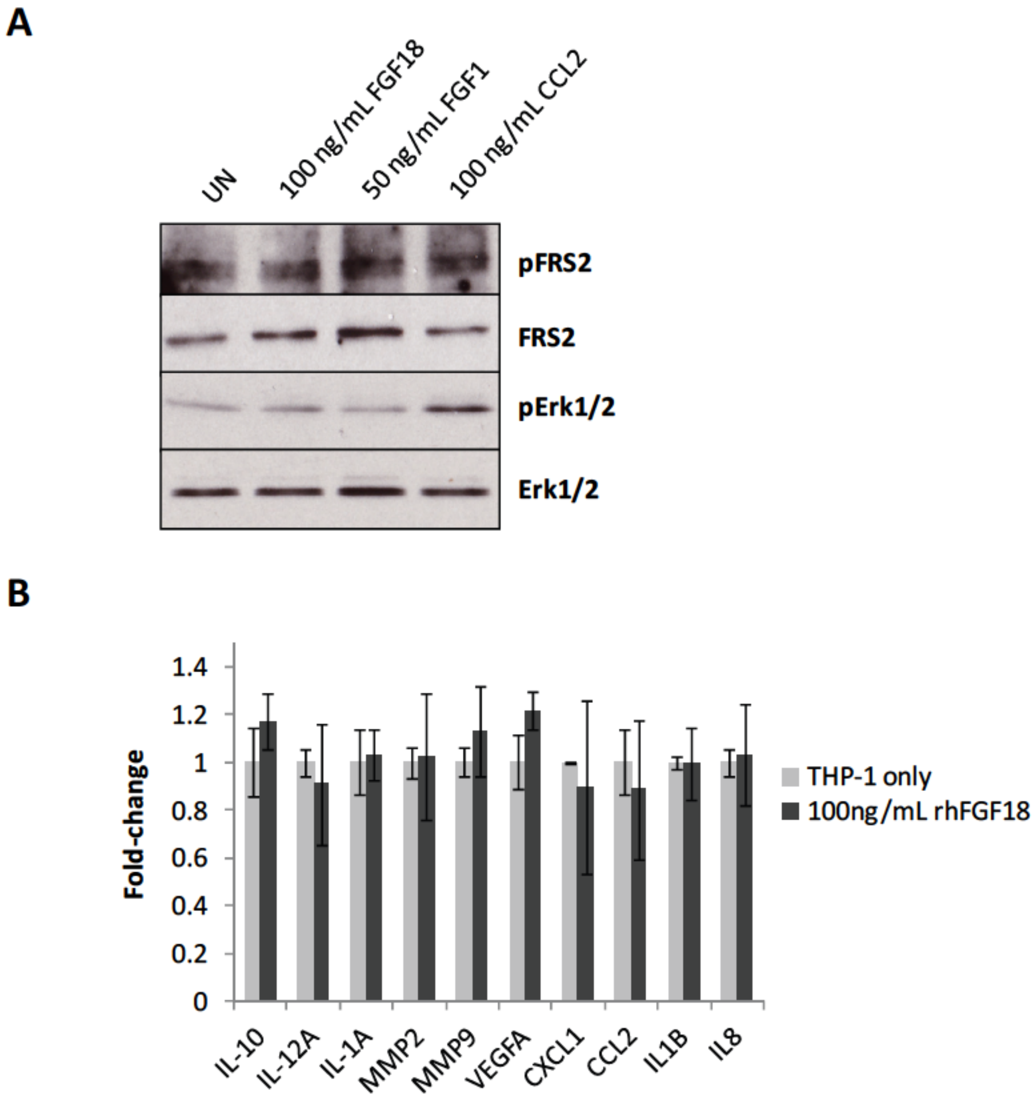

**Figure S12. Insignificant effect of direct human recombinant FGF18 treatment on THP-1 cells. (A)** THP-1 cells were starved in 0.5% FBS overnight before the treatment of rhFGF18, rhFGF1 or rhCCL2 at indicated concentrations for 10 minutes. FGF18 and FGF1 failed to induce phosphorylation of FRS2 and Erk1/2. In contrast, a significant activation of Erk1/2 was observed in response to CCL2. **(B)** Direct treatment of THP-1 cells with 100 ng/mL of rhFGF18 is insufficient for M2 polarization. Treatment was performed in RPMI + 2% FBS (to minimize the interference from growth factor in serum while keep the viability of THP-1 cells) for 4 days before RNA harvest for qRT-PCR analysis.

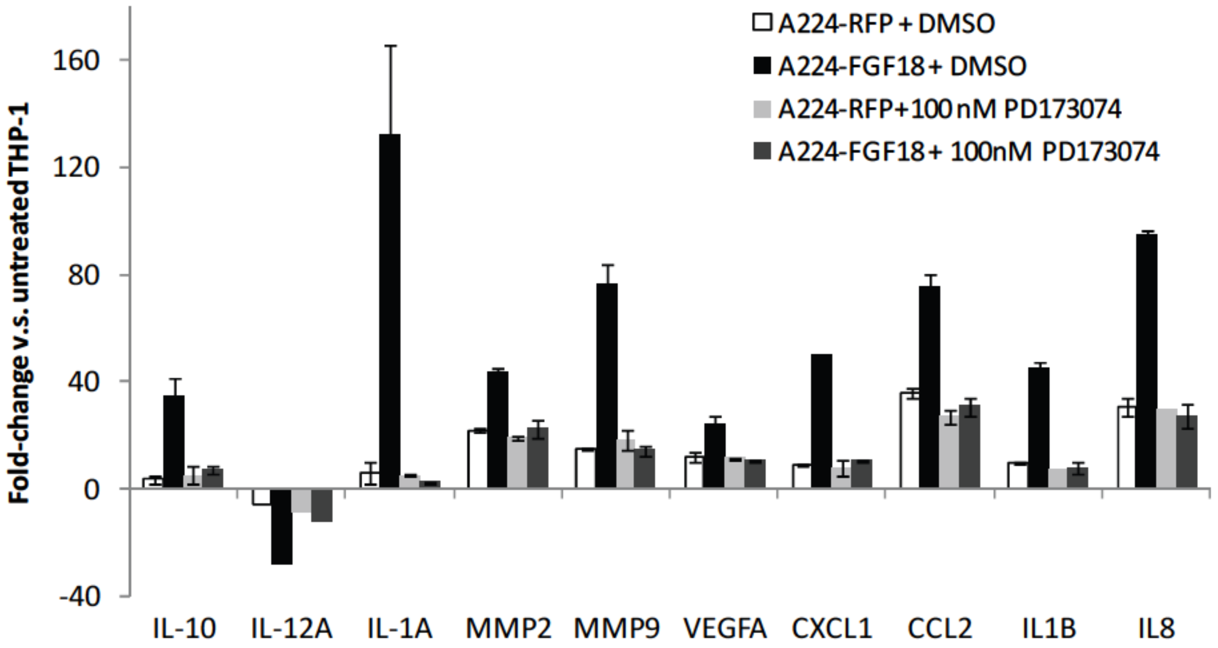

**Figure S13. Susceptibility of FGF18 overexpression induced M2 polarization potential to pan-FGFR inhibitor PD173074.** To make it comparable to Figure S11, co-culture of FGF18 or RFP overexpressing A224 cells and THP-1 cells was performed in RPMI + 2% FBS for 4 days before RNA harvest for qRT-PCR analysis. PD173074 (100 nM) or DMSO was added when co-culture was established until RNA harvest. Significant inhibitory effect of PD173074 on M2-polarizing potential ($p<0.05$) were observed in every marker checked in FGF18 overexpressing A224 cells but not RFP overexpressing A224 cells.

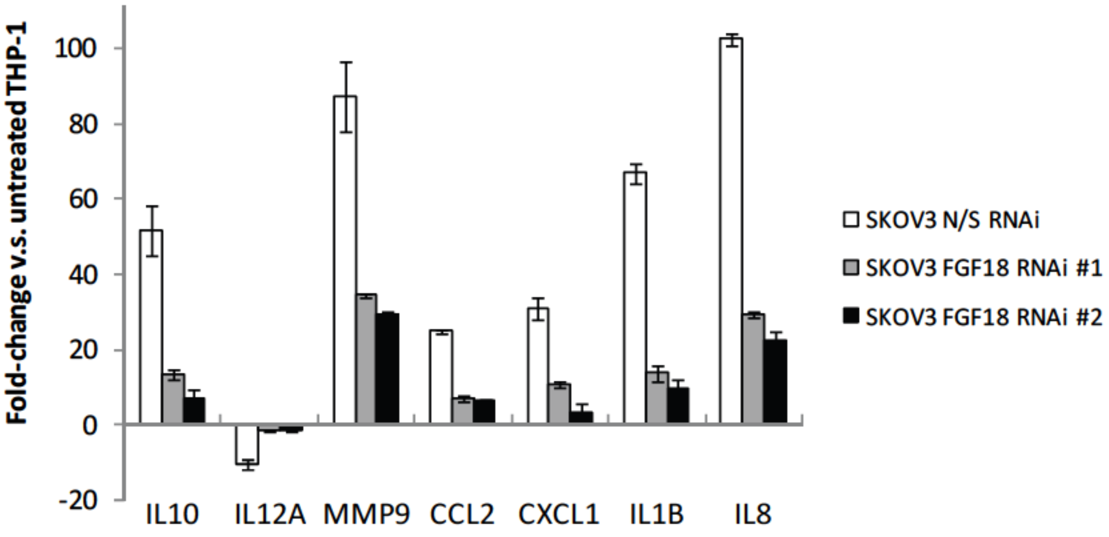

**Figure S14. Inhibitory effect of FGF18 knockdown on the M2 polarizing potential of SKOV3 cells.** THP-1 cells were co-cultured with SKOV3 cells with FGF18 shRNA and non-targeting scrambled (N/S) shRNA 4 days before RNA harvest. With untreated THP-1 cells serving as control, qRT-PCR was performed to quantify the expression of tumor-associated macrophage differentiation markers. Significant changes ($p<0.05$) were observed in every marker checked for both FGF18 shRNA #1 and FGF18 shRNA #2 in comparison to the control N/S shRNA.

## SI Tables

**Table S1. Details of each univariate Kaplan-Meier curve analyzed.** The information of sample description, estimated mean and median survival and comparative statistical tests were listed for **(A)** Mok et al (n=53); **(B)** Spentzos et al (n=70); **(C)** TAGA dataset (n=200); **(D)** FGF18 IHC staining of the tissue array (n=209); **(E)** The debulking status of the 192 tissue array samples (from the 209 samples on the same tissue array, for multivariate analysis); **(F)** The FIGO stage of the 192 tissue array samples; **(G)** The tumor grade of the 192 tissue array samples; and **(H)** The FGF18 expression level (IHC staining score) of the 192 tissue array samples.

| **(A) Mok et al (n=53)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Case Processing Summary** | | | | | **Overall Comparisons** | | | |
| FGF18 | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| High | 26 | 24 | 2 | 7.7% | Log Rank (Mantel-Cox) | 13.606 | 1.000 | 0.00023 |
| Low | 27 | 17 | 10 | 37.0% | Breslow (Generalized Wilcoxon) | 9.570 | 1.000 | 0.00198 |
| Overall | 53 | 41 | 12 | 22.6% | Tarone-Ware | 11.262 | 1.000 | 0.00079 |
| **Means and Medians for Survival Time** | | | | | | | | |
| FGF18 | Mean (Months) | | | | Median (Months) | | | |
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| High | 24.493 | 3.716 | 17.209 | 31.777 | 18.000 | 2.335 | 13.424 | 22.576 |
| Low | 73.822 | 11.545 | 51.195 | 96.450 | 45.000 | 30.808 | 0.000 | 105.383 |
| Overall | 48.695 | 7.081 | 34.816 | 62.573 | 25.000 | 5.349 | 14.516 | 35.484 |

| **(B) Spentzos et al (n=70)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Case Processing Summary** | | | | | **Overall Comparisons** | | | |
| FGF18 | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| High | 35 | 15 | 20 | 57.1% | Log Rank (Mantel-Cox) | 4.967 | 1.000 | 0.026 |
| Low | 35 | 25 | 10 | 28.6% | Breslow (Generalized Wilcoxon) | 4.053 | 1.000 | 0.044 |
| Overall | 70 | 40 | 30 | 42.9% | Tarone-Ware | 4.669 | 1.000 | 0.031 |
| **Means and Medians for Survival Time** | | | | | | | | |
| FGF18 | Mean (Months) | | | | Median (Months) | | | |
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| High | 65.802 | 8.958 | 48.244 | 83.361 | 54.000 | 8.567 | 37.209 | 70.791 |
| Low | 44.899 | 6.516 | 32.128 | 57.671 | 36.000 | 4.139 | 27.888 | 44.112 |
| Overall | 54.776 | 5.639 | 43.723 | 65.830 | 46.000 | 3.221 | 39.686 | 52.314 |

| **(C) TAGA dataset (n=200)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Case Processing Summary** | | | | | **Overall Comparisons** | | | |
| FGF18 | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| High | 100 | 55 | 45 | 45.0% | Log Rank (Mantel-Cox) | 5.470 | 1.000 | 0.019 |
| Low | 100 | 45 | 55 | 55.0% | Breslow (Generalized Wilcoxon) | 4.674 | 1.000 | 0.031 |
| Overall | 200 | 100 | 100 | 50.0% | Tarone-Ware | 4.889 | 1.000 | 0.027 |
| **Means and Medians for Survival Time** | | | | | | | | |
| FGF18 | Mean (Months) | | | | Median (Months) | | | |
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| High | 45.378 | 3.135 | 39.233 | 51.522 | 45.600 | 5.279 | 35.252 | 55.948 |
| Low | 72.804 | 8.086 | 56.956 | 88.652 | 52.600 | 5.376 | 42.064 | 63.136 |
| Overall | 61.712 | 5.272 | 51.380 | 72.045 | 49.000 | 2.822 | 43.470 | 54.530 |

| **(D) FGF18 IHC staining of the tissue array (n=209)** | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **Case Processing Summary** | | | | | **Overall Comparisons** | | | |
| FGF18 | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| High | 91 | 57 | 34 | 37.4% | Log Rank (Mantel-Cox) | 9.824 | 1.000 | 0.00172 |
| Low | 118 | 75 | 43 | 36.4% | Breslow (Generalized Wilcoxon) | 10.848 | 1.000 | 0.00099 |
| Overall | 209 | 132 | 77 | 36.8% | Tarone-Ware | 10.703 | 1.000 | 0.00107 |
| **Means and Medians for Survival Time** | | | | | | | | |
| FGF18 | Mean (Days) | | | | Median (Days) | | | |
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| High | 1037.053 | 110.363 | 820.741 | 1253.366 | 898.000 | 96.484 | 708.891 | 1087.109 |
| Low | 1570.738 | 138.110 | 1300.042 | 1841.435 | 1126.000 | 71.124 | 986.598 | 1265.402 |
| Overall | 1351.230 | 95.153 | 1164.729 | 1537.730 | 1047.000 | 72.038 | 905.806 | 1188.194 |

**(E) Debulking status of 192 tissue array samples**

| Case Processing Summary | | | | | Overall Comparisons | | | |
|---|---|---|---|---|---|---|---|---|
| Debulk | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| optimal | 141 | 91 | 50 | 35.5% | Log Rank (Mantel-Cox) | 3.264 | 1.000 | 0.071 |
| suboptimal | 51 | 31 | 20 | 39.2% | Breslow (Generalized Wilcoxon) | 6.201 | 1.000 | 0.013 |
| Overall | 192 | 122 | 70 | 36.5% | Tarone-Ware | 4.716 | 1.000 | 0.030 |

**Means and Medians for Survival Time**

| Debulk | Mean (Days) | | | | Median (Days) | | | |
|---|---|---|---|---|---|---|---|---|
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| optimal | 1463.980 | 123.518 | 1221.886 | 1706.074 | 1094.000 | 61.672 | 973.124 | 1214.876 |
| suboptimal | 1062.413 | 152.249 | 764.004 | 1360.821 | 870.000 | 162.775 | 550.962 | 1189.038 |
| Overall | 1364.482 | 102.464 | 1163.653 | 1565.311 | 1047.000 | 75.266 | 899.478 | 1194.522 |

**(F) FIGO stage of 192 tissue array samples**

| Case Processing Summary | | | | | Overall Comparisons | | | |
|---|---|---|---|---|---|---|---|---|
| FIGO Stage | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| III | 149 | 96 | 53 | 35.6% | Log Rank (Mantel-Cox) | 9.402 | 1.000 | 0.00217 |
| IV | 43 | 26 | 17 | 39.5% | Breslow (Generalized Wilcoxon) | 9.708 | 1.000 | 0.00183 |
| Overall | 192 | 122 | 70 | 36.5% | Tarone-Ware | 9.592 | 1.000 | 0.00195 |

**Means and Medians for Survival Time**

| FIGO Stage | Mean (Days) | | | | Median (Days) | | | |
|---|---|---|---|---|---|---|---|---|
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| III | 1487.063 | 120.627 | 1250.635 | 1723.492 | 1094.000 | 78.639 | 939.867 | 1248.133 |
| IV | 863.510 | 116.587 | 635.000 | 1092.020 | 711.000 | 222.052 | 275.779 | 1146.221 |
| Overall | 1364.482 | 102.464 | 1163.653 | 1565.311 | 1047.000 | 75.266 | 899.478 | 1194.522 |

**(G) Tumor grade of 192 tissue array samples**

| Case Processing Summary | | | | | Overall Comparisons | | | |
|---|---|---|---|---|---|---|---|---|
| Grade | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| 2 | 23 | 18 | 5 | 21.7% | Log Rank (Mantel-Cox) | .633 | 1.000 | 0.426 |
| 3 | 169 | 104 | 65 | 38.5% | Breslow (Generalized Wilcoxon) | .108 | 1.000 | 0.742 |
| Overall | 192 | 122 | 70 | 36.5% | Tarone-Ware | .360 | 1.000 | 0.549 |

**Means and Medians for Survival Time**

| Grade | Mean (Days) | | | | Median (Days) | | | |
|---|---|---|---|---|---|---|---|---|
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| 2 | 1106.188 | 156.732 | 798.994 | 1413.382 | 999.000 | 79.190 | 843.787 | 1154.213 |
| 3 | 1396.051 | 113.004 | 1174.563 | 1617.539 | 1085.000 | 90.208 | 908.192 | 1261.808 |
| Overall | 1364.482 | 102.464 | 1163.653 | 1565.311 | 1047.000 | 75.266 | 899.478 | 1194.522 |

**(H) FGF18 IHC staining of 192 tissue array samples**

| Case Processing Summary | | | | | Overall Comparisons | | | |
|---|---|---|---|---|---|---|---|---|
| FGF18 | Total N | N of Events | Censored | | | Chi-Square | df | Sig. |
| | | | N | Percent | | | | |
| High | 105 | 68 | 37 | 35.2% | Log Rank (Mantel-Cox) | 12.926 | 1.000 | 0.00032 |
| Low | 87 | 54 | 33 | 37.9% | Breslow (Generalized Wilcoxon) | 15.333 | 1.000 | 0.00009 |
| Overall | 192 | 122 | 70 | 36.5% | Tarone-Ware | 14.833 | 1.000 | 0.00012 |

**Means and Medians for Survival Time**

| FGF18 | Mean (Days) | | | | Median (Days) | | | |
|---|---|---|---|---|---|---|---|---|
| | Estimate | Std. Error | 95% Confidence Interval | | Estimate | Std. Error | 95% Confidence Interval | |
| High | 1623.305 | 146.902 | 1335.377 | 1911.232 | 1129.000 | 80.301 | 971.610 | 1286.390 |
| Low | 969.027 | 99.467 | 774.072 | 1163.981 | 795.000 | 112.204 | 575.080 | 1014.920 |
| Overall | 1364.482 | 102.464 | 1163.653 | 1565.311 | 1047.000 | 75.266 | 899.478 | 1194.522 |

**Table S2. Multivariate Cox regression analysis of the 192 samples on the validating tissue array.** The prognostic impacts of FGF18 expression level (IHC score of 6 as cut-off), debulking status, FIGO stage and tumor grade on overall patient survival were indicated by the hazard ratio [Exp(B) in the table] and the corresponding p-value.

| **Categorical Variable** | | Frequency | (1) |
|---|---|---|---|
| FGF18 | High | 87 | 1 |
| | Low | 105 | 0 |
| Debulking | Suboptimal | 51 | 1 |
| | Optimal | 141 | 0 |
| FIGO Stage | IV | 43 | 1 |
| | III | 149 | 0 |
| Grade | 3 | 169 | 1 |
| | 2 | 23 | 0 |

**Variables in the Equation**

| | p-value | Exp(B) | 95.0% CI for Exp(B) | |
|---|---|---|---|---|
| | | | Lower | Upper |
| FGF18 | 0.00004 | 2.332 | 1.558 | 3.491 |
| Debulking | 0.48851 | 1.170 | 0.751 | 1.822 |
| FIGO Stage | 0.00103 | 2.202 | 1.374 | 3.529 |
| Grade | 0.03707 | .560 | 0.324 | 0.966 |

**Table S3. Details of the multivariate Kaplan-Meier analyses of the prognostic effects of FGF18 expression level adjusted for the debulking status (A) or FIGO stage (B) on the 192 tumor samples from the validation tissue array.** The information of sample description, estimated mean and median survival and comparative statistical tests were listed.

**(A) Adjusted for Debulking status**

| Case Processing Summary | | | | | | Overall Comparisons | | | |
|---|---|---|---|---|---|---|---|---|---|
| Debulk | FGF18 | Total N | N of Events | Censored | | Debulk | | Chi-Square | Sig. |
| | | | | N | Percent | | | | |
| Optimal | FGF18- | 84 | 55 | 29 | 34.5% | Optimal | Log Rank | 10.129 | 0.00146 |
| | FGF18+ | 57 | 36 | 21 | 36.8% | | Wilcoxon | 12.309 | 0.00045 |
| | Overall | 141 | 91 | 50 | 35.5% | | Tarone-Ware | 11.683 | 0.00063 |
| Suboptimal | FGF18- | 21 | 13 | 8 | 38.1% | Suboptimal | Log Rank | 1.094 | 0.29563 |
| | FGF18+ | 30 | 18 | 12 | 40.0% | | Wilcoxon | 1.471 | 0.22521 |
| | Overall | 51 | 31 | 20 | 39.2% | | Tarone-Ware | 1.429 | 0.23198 |
| Pooled | | 192 | 122 | 70 | 36.5% | Pooled | Log Rank | 10.404 | 0.00126 |
| | | | | | | | Wilcoxon | 13.665 | 0.00022 |
| | | | | | | | Tarone-Ware | 13.097 | 0.00030 |

| Means and Medians for Survival Time | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Debulk | FGF18 | Mean (Days) | | | | Median (Days) | | | |
| | | Estimate | Std. Error | 95% Confidence | | Estimate | Std. Error | 95% Confidence | |
| | | | | Lower Bound | Upper Bound | | | Lower Bound | Upper Bound |
| Optimal | FGF18- | 1702.1 | 166.4 | 1376.1 | 2028.2 | 1168.0 | 77.4 | 1016.3 | 1319.7 |
| | FGF18+ | 992.2 | 112.9 | 771.0 | 1213.4 | 898.0 | 113.9 | 674.8 | 1121.2 |
| | Overall | 1464.0 | 123.5 | 1221.9 | 1706.1 | 1094.0 | 61.7 | 973.1 | 1214.9 |
| Suboptimal | FGF18- | 1229.5 | 239.3 | 760.5 | 1698.5 | 1085.0 | 278.4 | 539.4 | 1630.6 |
| | FGF18+ | 928.5 | 197.2 | 542.0 | 1314.9 | 709.0 | 56.1 | 599.1 | 818.9 |
| | Overall | 1062.4 | 152.2 | 764.0 | 1360.8 | 870.0 | 162.8 | 551.0 | 1189.0 |
| Overall | | 1364.5 | 102.5 | 1163.7 | 1565.3 | 1047.0 | 75.3 | 899.5 | 1194.5 |

**(B) Adjusted for FIGO stage**

| Case Processing Summary | | | | | | Overall Comparisons | | | |
|---|---|---|---|---|---|---|---|---|---|
| FIGO Stage | FGF18 | Total N | N of Events | Censored | | FIGO Stage | | Chi-Square | Sig. |
| | | | | N | Percent | | | | |
| III | FGF18- | 82 | 54 | 28 | 34.1% | III | Log Rank | 8.482 | 0.00359 |
| | FGF18+ | 67 | 42 | 25 | 37.3% | | Wilcoxon | 9.191 | 0.00243 |
| | Overall | 149 | 96 | 53 | 35.6% | | Tarone-Ware | 8.956 | 0.00277 |
| IV | FGF18- | 23 | 14 | 9 | 39.1% | IV | Log Rank | 8.800 | 0.00301 |
| | FGF18+ | 20 | 12 | 8 | 40.0% | | Wilcoxon | 5.298 | 0.02135 |
| | Overall | 43 | 26 | 17 | 39.5% | | Tarone-Ware | 6.827 | 0.00898 |
| Pooled | | 192 | 122 | 70 | 36.5% | Pooled | Log Rank | 14.902 | 0.00011 |
| | | | | | | | Wilcoxon | 11.338 | 0.00076 |
| | | | | | | | Tarone-Ware | 12.793 | 0.00035 |

| Means and Medians for Survival Time | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| FIGO Stage | FGF18 | Mean (Days) | | | | Median (Days) | | | |
| | | Estimate | Std. Error | 95% Confidence | | Estimate | Std. Error | 95% Confidence | |
| | | | | Lower Bound | Upper Bound | | | Lower Bound | Upper Bound |
| III | FGF18- | 1751.9 | 173.6 | 1411.5 | 2092.2 | 1236.0 | 141.3 | 959.0 | 1513.0 |
| | FGF18+ | 1077.0 | 115.1 | 851.4 | 1302.7 | 909.0 | 96.4 | 720.0 | 1098.0 |
| | Overall | 1487.1 | 120.6 | 1250.6 | 1723.5 | 1094.0 | 78.6 | 939.9 | 1248.1 |
| IV | FGF18- | 1110.4 | 163.0 | 790.9 | 1430.0 | 1085.0 | 25.3 | 1035.4 | 1134.6 |
| | FGF18+ | 502.0 | 74.7 | 355.5 | 648.4 | 589.0 | 75.7 | 440.6 | 737.4 |
| | Overall | 863.5 | 116.6 | 635.0 | 1092.0 | 711.0 | 222.1 | 275.8 | 1146.2 |
| Overall | | 1364.5 | 102.5 | 1163.7 | 1565.3 | 1047.0 | 75.3 | 899.5 | 1194.5 |

**Table S4. Identification of FGF18–responsive genes by transcriptional profiling.** Three paired RNA preparation of A224 cells overexpressing FGF18 or RFP (as control) were subjected to microarray analysis with Affymetrix Human U133 Plus 2.0 chips. Table sorted by fold-change between FGF18 and RFP-overexpressing A224 cells through paired comparison (class FGF18 and class RFP respectively). The first 704 probe sets are significant at the nominal 0.001 level of the univariate paired t-test.

**Table S4:**

## Genes which are differentially expressed between FGF18 overexpressing A224 cells (class FGF18) and RFP overexpressing A224 cells (class RFP):

Number of genes significant at 0.001 level of the univariate test: 704
Sorted by p-value of the univariate test.

| | Parametric p-value | FDR | Geometric mean of intensities (class FGF18 /class RFP) | Probe set | Gene symbol | Description | DefinedGenelist |
|---|---|---|---|---|---|---|---|
| 1 | < 1e-07 | < 1e-07 | 93.95 | 211485_s_at | FGF18 | fibroblast growth factor 18 | membrane & extracellular protein,<br>MAPK signaling pathway,<br>Regulation of actin cytoskeleton |
| 3 | < 1e-07 | < 1e-07 | 90.76 | 206987_x_at | FGF18 | fibroblast growth factor 18 | |
| 2 | < 1e-07 | < 1e-07 | 79.38 | 211029_x_at | FGF18 | fibroblast growth factor 18 | |
| 101 | 2.7E-06 | 2.8E-05 | 16.28 | 205767_at | EREG | epiregulin | membrane & extracellular protein |
| 35 | 6.0E-07 | 1.7E-05 | 12.41 | 201324_at | EMP1 | epithelial membrane protein 1 | membrane & extracellular protein,<br>tsonc |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 4 | < 1e-07 | < 1e-07 | 11.45 | 201860_s_at | PLAT | plasminogen activator, tissue | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Acute Myocardial Infarction, Fibrinolysis Pathway, Platelet Amyloid Precursor Protein Pathway, Complement and coagulation cascades, immunology |
| 9 | < 1e-07 | < 1e-07 | 9.98 | 203889_at | SCG5 | secretogranin V (7B2 protein) | membrane & extracellular protein |
| 119 | 3.3E-06 | 2.9E-05 | 8.68 | 223484_at | C15orf48 | chromosome 15 open reading frame 48 | Nuclear protein |
| 65 | 1.4E-06 | 2.1E-05 | 7.95 | 205239_at | AREG | amphiregulin | membrane & extracellular protein, immunology, misc |
| 164 | 5.6E-06 | 3.6E-05 | 7.73 | 211506_s_at | IL8 | interleukin 8 | membrane & extracellular protein, Adhesion and Diapedesis of Granulocytes, Adhesion and Diapedesis of Lymphocytes, Cells and Molecules involved in local acute inflammatory response, Cytokine Network, Cytokines and Inflammatory Response, Free Radical Induced Apoptosis, IL 17 Signaling Pathway, NFkB activation by Nontypeable Hemophilus influenzae, Proepithelin Conversion to Epithelin and Wound Repair Control, Regulation of hematopoiesis by cytokines, Cytokine-cytokine |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | | | | | | receptor interaction, Epithelial cell signaling in Helicobacter pylori infection, Leukocyte transendothelial migration, Toll-like receptor signaling pathway, immunology |
| 6 | < 1e-07 | < 1e-07 | 7.49 | 206074_s_at | HMGA1 | high mobility group AT-hook 1 | Nuclear protein |
| 43 | 8.0E-07 | 1.9E-05 | 7.26 | 215856_at | SIGLEC15 | sialic acid binding Ig-like lectin 15 | membrane & extracellular protein |
| 168 | 5.9E-06 | 3.7E-05 | 7.17 | 222934_s_at | CLEC4E | C-type lectin domain family 4, member E | membrane & extracellular protein |
| 443 | 1.1E-04 | 2.5E-04 | 7.01 | 232504_at | LOC285628 | hypothetical protein LOC285628 | |
| 170 | 5.9E-06 | 3.7E-05 | 7 | 208025_s_at | HMGA2 | high mobility group AT-hook 2 | Nuclear protein |
| 21 | 2.0E-07 | 8.8E-06 | 6.98 | 203939_at | NT5E | 5'-nucleotidase, ecto (CD73) | membrane & extracellular protein, Nicotinate and nicotinamide metabolism, Purine metabolism, Pyrimidine metabolism |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 166 | 5.7E-06 | 3.6E-05 | 6.4 | 204470_at | CXCL1 | chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Cytokine-cytokine receptor interaction, Epithelial cell signaling in Helicobacter pylori infection |
| 45 | 9.0E-07 | 1.9E-05 | 6.3 | 205952_at | KCNK3 | potassium channel, subfamily K, member 3 | membrane & extracellular protein |
| 36 | 6.0E-07 | 1.7E-05 | 6.14 | 205207_at | IL6 | interleukin 6 (interferon, beta 2) | membrane & extracellular protein, Cells and Molecules involved in local acute inflammatory response, Cytokine Network, Cytokines and Inflammatory Response, Erythrocyte Differentiation Pathway, IL 17 Signaling Pathway, IL 5 Signaling Pathway, IL 6 signaling pathway, IL-10 Anti-inflammatory Signaling Pathway, Low-density lipoprotein (LDL) pathway during atherogenesis, Regulation of hematopoiesis by cytokines, Role of ERBB2 in Signal Transduction and Oncology, Signal transduction through IL1R, Cytokine-cytokine receptor interaction, Hematopoietic cell lineage, Jak-STAT signaling pathway, Toll-like receptor signaling pathway, immunology |
| 277 | 2.4E-05 | 9.1E-05 | 5.91 | 202859_x_at | IL8 | interleukin 8 | |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| 10 | < 1e-07 | < 1e-07 | 5.88 | 201438_at | COL6A3 | collagen, type VI, alpha 3 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 312 | 3.2E-05 | 1.1E-04 | 5.37 | 209774_x_at | CXCL2 | chemokine (C-X-C motif) ligand 2 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 113 | 3.1E-06 | 2.9E-05 | 5.17 | 210229_s_at | CSF2 | colony stimulating factor 2 (granulocyte-macrophage) | membrane & extracellular protein, Cytokines and Inflammatory Response, Dendritic cells in regulating TH1 and TH2 Development, Erythrocyte Differentiation Pathway, Regulation of hematopoiesis by cytokines, Selective expression of chemokine receptors during T-cell polarization, The Role of Eosinophils in the Chemokine Network of Allergy, Cytokine-cytokine receptor interaction, Fc epsilon RI signaling pathway, Hematopoietic cell lineage, Jak-STAT signaling pathway, Natural killer cell mediated cytotoxicity, T cell receptor signaling pathway, immunology |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 358 | 4.4E-05 | 1.3E-04 | 5.13 | 210118_s_at | IL1A | interleukin 1, alpha | membrane & extracellular protein, Adhesion and Diapedesis of Granulocytes, Adhesion and Diapedesis of Lymphocytes, Cells and Molecules involved in local acute inflammatory response, Cytokine Network, Cytokines and Inflammatory Response, Erythrocyte Differentiation Pathway, IL-10 Anti-inflammatory Signaling Pathway, NF-kB Signaling Pathway, Signal transduction through IL1R, Stress Induction of HSP Regulation, Apoptosis, Cytokine-cytokine receptor interaction, Hematopoietic cell lineage, MAPK signaling pathway, Type I diabetes mellitus, immunology |
| 210 | 1.1E-05 | 5.7E-05 | 4.94 | 215101_s_at | CXCL5 | chemokine (C-X-C motif) ligand 5 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 59 | 1.2E-06 | 2.1E-05 | 4.85 | 201325_s_at | EMP1 | epithelial membrane protein 1 | membrane & extracellular protein, tsonc |
| 85 | 1.8E-06 | 2.2E-05 | 4.49 | 203037_s_at | MTSS1 | metastasis suppressor 1 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes |
| 49 | 9.0E-07 | 1.9E-05 | 4.47 | 227566_at | NTM | neurotrimin | membrane & extracellular protein |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 23 | 2.0E-07 | 8.8E-06 | 4.45 | 1553995_a_at | NT5E | 5'-nucleotidase, ecto (CD73) | membrane & extracellular protein, Nicotinate and nicotinamide metabolism, Purine metabolism, Pyrimidine metabolism |
| 24 | 2.0E-07 | 8.8E-06 | 4.44 | 206157_at | PTX3 | pentraxin-related gene, rapidly induced by IL-1 beta | membrane & extracellular protein, cell_cycle, cell_signaling, immunology |
| 336 | 3.8E-05 | 1.2E-04 | 4.28 | 219859_at | CLEC4E | C-type lectin domain family 4, member E | membrane & extracellular protein |
| 397 | 6.5E-05 | 1.7E-04 | 4.16 | 219764_at | FZD10 | frizzled homolog 10 (Drosophila) | membrane & extracellular protein, Colorectal cancer, Wnt signaling pathway |
| 251 | 1.8E-05 | 7.4E-05 | 4.13 | 219911_s_at | SLCO4A1 | solute carrier organic anion transporter family, member 4A1 | membrane & extracellular protein |
| 204 | 1.1E-05 | 5.5E-05 | 4.1 | 204726_at | CDH13 | cadherin 13, H-cadherin (heart) | membrane & extracellular protein, cell_signaling, metastasis |
| 5 | < 1e-07 | < 1e-07 | 4.02 | 1554624_a_at | SIRPB1 | signal-regulatory protein beta 1 | membrane & extracellular protein |
| 209 | 1.1E-05 | 5.7E-05 | 4.01 | 210119_at | KCNJ15 | potassium inwardly-rectifying channel, subfamily J, member 15 | membrane & extracellular protein |
| 142 | 4.2E-06 | 3.1E-05 | 3.99 | 242649_x_at | C15orf21 | Dresden prostate cancer 2 | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 153 | 5.1E-06 | 3.5E-05 | 3.92 | 205780_at | BIK | BCL2-interacting killer (apoptosis-inducing) | membrane & extracellular protein, Role of Mitochondria in Apoptotic Signaling |
| 169 | 5.9E-06 | 3.7E-05 | 3.89 | 239201_at | CDK15 | cyclin-dependent kinase 15 | |
| 93 | 2.3E-06 | 2.6E-05 | 3.84 | 222878_s_at | OTUB2 | OTU domain, ubiquitin aldehyde binding 2 | Biotin metabolism, Lysine degradation |
| 22 | 2.0E-07 | 8.8E-06 | 3.77 | 206934_at | SIRPB1 | signal-regulatory protein beta 1 | membrane & extracellular protein |
| 275 | 2.3E-05 | 9.0E-05 | 3.77 | 218182_s_at | CLDN1 | claudin 1 | membrane & extracellular protein, Cell adhesion molecules (CAMs), Leukocyte transendothelial migration, Tight junction |
| 511 | 1.9E-04 | 4.0E-04 | 3.74 | 225381_at | LOC399959 | hypothetical LOC399959 | |
| 77 | 1.6E-06 | 2.2E-05 | 3.69 | 235146_at | TMCC3 | transmembrane and coiled-coil domain family 3 | membrane & extracellular protein |
| 7 | < 1e-07 | < 1e-07 | 3.55 | 204734_at | KRT15 | keratin 15 | Cell Communication |
| 381 | 5.4E-05 | 1.5E-04 | 3.55 | 214974_x_at | CXCL5 | chemokine (C-X-C motif) ligand 5 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 62 | 1.3E-06 | 2.1E-05 | 3.53 | 201042_at | TGM2 | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) | membrane & extracellular protein, Phospholipase C d1 in phospholipid associated cell signaling, Huntington\'s disease, immunology |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 308 | 3.1E-05 | 1.1E-04 | 3.53 | 210511_s_at | INHBA | inhibin, beta A | membrane & extracellular protein, Cytokine-cytokine receptor interaction, TGF-beta signaling pathway, development |
| 309 | 3.2E-05 | 1.1E-04 | 3.52 | 213711_at | KRT81 | keratin 81 | Cell Communication |
| 383 | 5.7E-05 | 1.6E-04 | 3.48 | 221019_s_at | COLEC12 | collectin sub-family member 12 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes |
| 375 | 5.0E-05 | 1.4E-04 | 3.46 | 202409_at | NA | NA | membrane & extracellular protein |
| 63 | 1.3E-06 | 2.1E-05 | 3.4 | 227486_at | NT5E | 5'-nucleotidase, ecto (CD73) | membrane & extracellular protein, Nicotinate and nicotinamide metabolism, Purine metabolism, Pyrimidine metabolism |
| 160 | 5.3E-06 | 3.5E-05 | 3.39 | 224480_s_at | AGPAT9 | 1-acylglycerol-3-phosphate O-acyltransferase 9 | membrane & extracellular protein |
| 487 | 1.5E-04 | 3.3E-04 | 3.39 | 210538_s_at | BIRC3 | baculoviral IAP repeat-containing 3 | Nuclear protein, Caspase Cascade in Apoptosis, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors , Role of Mitochondria in Apoptotic Signaling, SODD/TNFR1 Signaling Pathway, Apoptosis, Focal adhesion |
| 70 | 1.5E-06 | 2.2E-05 | 3.37 | 1553994_at | NT5E | 5'-nucleotidase, ecto (CD73) | membrane & extracellular protein, Nicotinate and nicotinamide metabolism, Purine metabolism, Pyrimidine metabolism |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 190 | 8.3E-06 | 4.6E-05 | 3.37 | 208892_s_at | DUSP6 | dual specificity phosphatase 6 | Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases, MAPK signaling pathway |
| 53 | 1.0E-06 | 2.0E-05 | 3.35 | 219369_s_at | OTUB2 | OTU domain, ubiquitin aldehyde binding 2 | Biotin metabolism, Lysine degradation |
| 442 | 1.0E-04 | 2.5E-04 | 3.31 | 222549_at | CLDN1 | claudin 1 | membrane & extracellular protein, Cell adhesion molecules (CAMs), Leukocyte transendothelial migration, Tight junction |
| 335 | 3.8E-05 | 1.2E-04 | 3.26 | 204420_at | FOSL1 | FOS-like antigen 1 | membrane & extracellular protein, Nuclear protein, Bone Remodelling, Wnt signaling pathway, tsonc |
| 11 | < 1e-07 | < 1e-07 | 3.23 | 214702_at | FN1 | fibronectin 1 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion, Regulation of actin cytoskeleton, angiogenesis, cell_signaling, immunology, metastasis |
| 83 | 1.8E-06 | 2.2E-05 | 3.23 | 229461_x_at | NEGR1 | neuronal growth regulator 1 | membrane & extracellular protein, Cell adhesion molecules (CAMs) |
| 99 | 2.6E-06 | 2.8E-05 | 3.22 | 221577_x_at | NA | NA | membrane & extracellular protein |
| 265 | 2.0E-05 | 8.1E-05 | 3.21 | 225626_at | PAG1 | phosphoprotein associated with glycosphingolipid microdomains 1 | membrane & extracellular protein |
| 148 | 4.6E-06 | 3.3E-05 | 3.17 | 211343_s_at | COL13A1 | collagen, type XIII, alpha 1 | membrane & extracellular protein |

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|---|---|---|---|---|---|---|---|
| 80 | 1.8E-06 | 2.2E-05 | 3.15 | 208607_s_at | NA | NA | membrane & extracellular protein |
| 635 | 5.5E-04 | 9.1E-04 | 3.14 | 221911_at | ETV1 | ets variant 1 | Nuclear protein, transcription, tsonc |
| 50 | 9.0E-07 | 1.9E-05 | 3.11 | 211003_x_at | TGM2 | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase ) | membrane & extracellular protein, Phospholipase C d1 in phospholipid associated cell signaling, Huntington\'s disease, immunology |
| 145 | 4.3E-06 | 3.1E-05 | 3.1 | 211573_x_at | TGM2 | transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase ) | membrane & extracellular protein, Phospholipase C d1 in phospholipid associated cell signaling, Huntington\'s disease, immunology |
| 69 | 1.4E-06 | 2.1E-05 | 3.07 | 1552793_at | C8orf31 | chromosome 8 open reading frame 31 |  |
| 38 | 7.0E-07 | 1.8E-05 | 3.04 | 1558683_a_at | HMGA2 | high mobility group AT-hook 2 | Nuclear protein |
| 691 | 8.9E-04 | 1.4E-03 | 3.04 | 207850_at | CXCL3 | chemokine (C-X-C motif) ligand 3 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 31 | 4.0E-07 | 1.4E-05 | 2.99 | 209946_at | VEGFC | vascular endothelial growth factor C | membrane & extracellular protein, Cytokine-cytokine receptor interaction, Focal adhesion, mTOR signaling pathway, angiogenesis |
| 208 | 1.1E-05 | 5.7E-05 | 2.99 | 225842_at | PHLDA1 | pleckstrin homology-like domain, family A, | membrane & extracellular protein, Nuclear protein |

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|---|---|---|---|---|---|---|---|
|  |  |  |  |  |  | member 1 |  |
| 385 | 5.8E-05 | 1.6E-04 | 2.94 | 223782_s_at | TINAG | tubulointerstitial nephritis antigen | membrane & extracellular protein |
| 248 | 1.7E-05 | 7.2E-05 | 2.93 | 231779_at | IRAK2 | interleukin-1 receptor-associated kinase 2 | Signal transduction through IL1R, Apoptosis, immunology, signal_transduction |
| 278 | 2.4E-05 | 9.1E-05 | 2.93 | 227354_at | PAG1 | phosphoprotein associated with glycosphingolipid microdomains 1 | membrane & extracellular protein |
| 74 | 1.6E-06 | 2.2E-05 | 2.92 | 217999_s_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | membrane & extracellular protein, Nuclear protein |
| 52 | 1.0E-06 | 2.0E-05 | 2.86 | 225166_at | ARHGAP18 | Rho GTPase activating protein 18 |  |
| 17 | 2.0E-07 | 8.8E-06 | 2.83 | 230494_at | SLC20A1 | solute carrier family 20 (phosphate transporter), member 1 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, immunology |
| 304 | 3.0E-05 | 1.1E-04 | 2.83 | 225622_at | PAG1 | phosphoprotein associated with glycosphingolipid microdomains 1 | membrane & extracellular protein |

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|---|---|---|---|---|---|---|---|
| 34 | 6.0E-07 | 1.7E-05 | 2.8 | 203180_at | ALDH1A3 | aldehyde dehydrogenase 1 family, member A3 | Nuclear protein, Arginine and proline metabolism, Ascorbate and aldarate metabolism, beta-Alanine metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Limonene and pinene degradation, Lysine degradation, Metabolism of xenobiotics by cytochrome P450, Phenylalanine metabolism, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Tyrosine metabolism, Valine, leucine and isoleucine degradation |
| 250 | 1.7E-05 | 7.2E-05 | 2.74 | 227478_at | SETBP1 | SET binding protein 1 | Nuclear protein |
| 26 | 3.0E-07 | 1.1E-05 | 2.73 | 211668_s_at | PLAU | plasminogen activator, urokinase | membrane & extracellular protein, Fibrinolysis Pathway, Platelet Amyloid Precursor Protein Pathway, Complement and coagulation cascades, angiogenesis |
| 293 | 2.7E-05 | 9.6E-05 | 2.72 | 227342_s_at | MYEOV | myeloma overexpressed (in a subset of t(11;14) positive multiple myelomas) | |

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| 183 | 7.6E-06 | 4.4E-05 | 2.71 | 209016_s_at | KRT7 | keratin 7 | Perou's- Intrinsic- Breast-Cancer-Genes, Cell Communication |
| 384 | 5.8E-05 | 1.6E-04 | 2.7 | 211806_s_at | KCNJ15 | potassium inwardly-rectifying channel, subfamily J, member 15 | membrane & extracellular protein |
| 477 | 1.4E-04 | 3.1E-04 | 2.69 | 223541_at | HAS3 | hyaluronan synthase 3 | membrane & extracellular protein |
| 297 | 2.7E-05 | 9.6E-05 | 2.65 | 203030_s_at | PTPRN2 | protein tyrosine phosphatase, receptor type, N polypeptide 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Type I diabetes mellitus, cell_cycle, cell_signaling |
| 674 | 7.8E-04 | 1.2E-03 | 2.63 | 209277_at | TFPI2 | tissue factor pathway inhibitor 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, immunology |
| 41 | 7.0E-07 | 1.8E-05 | 2.61 | 225847_at | NCEH1 | neutral cholesterol ester hydrolase 1 | membrane & extracellular protein |
| 318 | 3.4E-05 | 1.1E-04 | 2.6 | 201721_s_at | LAPTM5 | lysosomal protein transmembrane 5 | membrane & extracellular protein |
| 90 | 2.1E-06 | 2.5E-05 | 2.59 | 205479_s_at | PLAU | plasminogen activator, urokinase | membrane & extracellular protein, Fibrinolysis Pathway, Platelet Amyloid Precursor Protein Pathway, Complement and coagulation cascades, angiogenesis |
| 642 | 5.7E-04 | 9.3E-04 | 2.57 | 209278_s_at | TFPI2 | tissue factor pathway inhibitor 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, immunology |

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| 641 | 5.6E-04 | 9.3E-04 | 2.51 | 205552_s_at | OAS1 | 2',5'-oligoadenylate synthetase 1, 40/46kDa | Nuclear protein, cell_cycle, cell_signaling, immunology |
| 263 | 2.0E-05 | 7.9E-05 | 2.48 | 217997_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | membrane & extracellular protein, Nuclear protein |
| 56 | 1.1E-06 | 2.1E-05 | 2.47 | 205003_at | DOCK4 | dedicator of cytokinesis 4 | membrane & extracellular protein |
| 404 | 7.1E-05 | 1.9E-04 | 2.47 | 201720_s_at | LAPTM5 | lysosomal protein transmembrane 5 | membrane & extracellular protein |
| 558 | 2.8E-04 | 5.3E-04 | 2.47 | 215189_at | KRT86 | keratin 86 | Cell Communication |
| 276 | 2.4E-05 | 9.1E-05 | 2.46 | 202267_at | LAMC2 | laminin, gamma 2 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 653 | 6.3E-04 | 1.0E-03 | 2.45 | 214841_at | CNIH3 | cornichon homolog 3 (Drosophila) | membrane & extracellular protein |
| 29 | 3.0E-07 | 1.1E-05 | 2.42 | 208891_at | DUSP6 | dual specificity phosphatase 6 | Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases, MAPK signaling pathway |
| 413 | 7.8E-05 | 2.0E-04 | 2.41 | 235318_at | FBN1 | fibrillin 1 | membrane & extracellular protein, immunology |
| 227 | 1.4E-05 | 6.6E-05 | 2.39 | 217998_at | NA | NA | membrane & extracellular protein, Nuclear protein |

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|---|---|---|---|---|---|---|---|
| 324 | 3.6E-05 | 1.2E-04 | 2.39 | 203788_s_at | SEMA3C | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Axon guidance |
| 544 | 2.5E-04 | 4.8E-04 | 2.39 | 208712_at | CCND1 | cyclin D1 | Nuclear protein, Perou's- Intrinsic-Breast-Cancer-Genes, BTG family proteins and cell cycle regulation, CARM1 and Regulation of the Estrogen Receptor, Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S Transition, p53 Signaling Pathway, WNT Signaling Pathway, Cell cycle, Colorectal cancer, Focal adhesion, Jak-STAT signaling pathway, Wnt signaling pathway, cell_cycle, tsonc |

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| 490 | 1.6E-04 | 3.4E-04 | 2.36 | 208711_s_at | CCND1 | cyclin D1 | Nuclear protein, Perou's- Intrinsic-Breast-Cancer-Genes, BTG family proteins and cell cycle regulation, CARM1 and Regulation of the Estrogen Receptor, Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S Transition, p53 Signaling Pathway, WNT Signaling Pathway, Cell cycle, Colorectal cancer, Focal adhesion, Jak-STAT signaling pathway, Wnt signaling pathway, cell_cycle, tsonc |
| 196 | 9.7E-06 | 5.2E-05 | 2.35 | 214701_s_at | FN1 | fibronectin 1 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion, Regulation of actin cytoskeleton, angiogenesis, cell_signaling, immunology, metastasis |
| 134 | 3.9E-06 | 3.1E-05 | 2.32 | 225171_at | ARHGAP18 | Rho GTPase activating protein 18 | |
| 137 | 4.1E-06 | 3.1E-05 | 2.32 | 209457_at | DUSP5 | dual specificity phosphatase 5 | Nuclear protein, MAPK signaling pathway |
| 647 | 5.8E-04 | 9.5E-04 | 2.32 | 207517_at | LAMC2 | laminin, gamma 2 | membrane & extracellular protein, Cell Communication, ECM-receptor |

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| | | | | | | | interaction, Focal adhesion |
| 206 | 1.1E-05 | 5.6E-05 | 2.31 | 201645_at | TNC | tenascin C | membrane & extracellular protein, Nuclear protein, Perou's- Intrinsic- Breast-Cancer-Genes, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 120 | 3.3E-06 | 2.9E-05 | 2.3 | 225566_at | NRP2 | neuropilin 2 | membrane & extracellular protein, angiogenesis |
| 194 | 9.5E-06 | 5.1E-05 | 2.3 | 203029_s_at | PTPRN2 | protein tyrosine phosphatase, receptor type, N polypeptide 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Type I diabetes mellitus, cell_cycle, cell_signaling |
| 290 | 2.6E-05 | 9.5E-05 | 2.3 | 36711_at | MAFF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | Nuclear protein, Oxidative Stress Induced Gene Expression Via Nrf2 |
| 180 | 6.9E-06 | 4.1E-05 | 2.29 | 226489_at | TMCC3 | transmembrane and coiled-coil domain family 3 | membrane & extracellular protein |
| 205 | 1.1E-05 | 5.6E-05 | 2.29 | 218000_s_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | membrane & extracellular protein |
| 579 | 3.3E-04 | 6.1E-04 | 2.29 | 217388_s_at | KYNU | kynureninase (L-kynurenine hydrolase) | Tryptophan metabolism |

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| 594 | 3.7E-04 | 6.6E-04 | 2.28 | 205476_at | CCL20 | chemokine (C-C motif) ligand 20 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 115 | 3.2E-06 | 2.9E-05 | 2.26 | 202765_s_at | FBN1 | fibrillin 1 | membrane & extracellular protein, immunology |
| 273 | 2.3E-05 | 8.9E-05 | 2.26 | 225173_at | ARHGAP18 | Rho GTPase activating protein 18 | |
| 112 | 3.1E-06 | 2.9E-05 | 2.25 | 202766_s_at | FBN1 | fibrillin 1 | membrane & extracellular protein, immunology |
| 260 | 1.9E-05 | 7.6E-05 | 2.25 | 227529_s_at | AKAP12 | A kinase (PRKA) anchor protein 12 | membrane & extracellular protein, Nuclear protein |
| 211 | 1.2E-05 | 6.0E-05 | 2.23 | 231154_x_at | TINAG | tubulointerstitial nephritis antigen | membrane & extracellular protein |
| 464 | 1.2E-04 | 2.7E-04 | 2.22 | 204011_at | SPRY2 | sprouty homolog 2 (Drosophila) | membrane & extracellular protein, Sprouty regulation of tyrosine kinase signals, Jak-STAT signaling pathway |
| 537 | 2.4E-04 | 4.6E-04 | 2.21 | 230966_at | NA | NA | membrane & extracellular protein, Nuclear protein |
| 71 | 1.5E-06 | 2.2E-05 | 2.19 | 226028_at | ROBO4 | roundabout homolog 4, magic roundabout (Drosophila) | membrane & extracellular protein |
| 193 | 9.0E-06 | 4.9E-05 | 2.19 | 214453_s_at | IFI44 | interferon-induced protein 44 | |
| 239 | 1.6E-05 | 7.0E-05 | 2.19 | 206298_at | ARHGAP22 | Rho GTPase activating protein 22 | Nuclear protein |

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| 589 | 3.6E-04 | 6.4E-04 | 2.19 | 205923_at | RELN | reelin | membrane & extracellular protein, Lissencephaly gene (LIS1) in neuronal migration and development, Reelin Signaling Pathway, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 692 | 9.0E-04 | 1.4E-03 | 2.19 | 1553313_s_at | SLC5A3 | solute carrier family 5 (sodium/myo-inositol cotransporter), member 3 | membrane & extracellular protein |
| 32 | 5.0E-07 | 1.7E-05 | 2.18 | 210675_s_at | PTPRR | protein tyrosine phosphatase, receptor type, R | membrane & extracellular protein, Erk1/Erk2 Mapk Signaling pathway, MAPK signaling pathway |
| 614 | 4.5E-04 | 7.8E-04 | 2.18 | 219922_s_at | LTBP3 | latent transforming growth factor beta binding protein 3 | membrane & extracellular protein |
| 175 | 6.5E-06 | 3.9E-05 | 2.17 | 201830_s_at | NET1 | neuroepithelial cell transforming 1 | Nuclear protein |
| 245 | 1.6E-05 | 7.1E-05 | 2.17 | 237737_at | LOC100289026 | similar to hCG1744891 | |
| 247 | 1.7E-05 | 7.1E-05 | 2.17 | 203789_s_at | SEMA3C | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Axon guidance |

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| 386 | 5.8E-05 | 1.6E-04 | 2.15 | 213797_at | RSAD2 | radical S-adenosyl methionine domain containing 2 | membrane & extracellular protein |
| 173 | 6.4E-06 | 3.9E-05 | 2.14 | 210517_s_at | AKAP12 | A kinase (PRKA) anchor protein 12 | membrane & extracellular protein, Nuclear protein |
| 202 | 1.0E-05 | 5.4E-05 | 2.12 | 203725_at | GADD45A | growth arrest and DNA-damage-inducible, alpha | Nuclear protein, ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway, Cell cycle, MAPK signaling pathway |
| 518 | 2.0E-04 | 4.0E-04 | 2.12 | 209199_s_at | MEF2C | myocyte enhancer factor 2C | Nuclear protein, ALK in cardiac myocytes, CARM1 and Regulation of the Estrogen Receptor, NFAT and Hypertrophy of the heart (Transcription in the broken heart), MAPK signaling pathway |
| 125 | 3.5E-06 | 2.9E-05 | 2.11 | 229437_at | MIR155HG | MIR155 host gene (non-protein coding) | |
| 334 | 3.8E-05 | 1.2E-04 | 2.11 | 229225_at | NRP2 | neuropilin 2 | membrane & extracellular protein, angiogenesis |
| 533 | 2.3E-04 | 4.6E-04 | 2.11 | 230493_at | SHISA2 | shisa homolog 2 (Xenopus laevis) | membrane & extracellular protein |
| 151 | 4.8E-06 | 3.4E-05 | 2.1 | 202566_s_at | SVIL | supervillin | membrane & extracellular protein, Nuclear protein |
| 149 | 4.8E-06 | 3.4E-05 | 2.08 | 1567224_at | HMGA2 | high mobility group AT-hook 2 | Nuclear protein |

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| 186 | 8.1E-06 | 4.6E-05 | 2.08 | 218986_s_at | DDX60 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 | |
| 416 | 7.8E-05 | 2.0E-04 | 2.08 | 210663_s_at | KYNU | kynureninase (L-kynurenine hydrolase) | Tryptophan metabolism |
| 89 | 2.1E-06 | 2.5E-05 | 2.07 | 211844_s_at | NRP2 | neuropilin 2 | membrane & extracellular protein, angiogenesis |
| 133 | 3.8E-06 | 3.0E-05 | 2.07 | 202565_s_at | SVIL | supervillin | membrane & extracellular protein, Nuclear protein |
| 323 | 3.6E-05 | 1.2E-04 | 2.07 | 228033_at | E2F7 | E2F transcription factor 7 | Nuclear protein |
| 359 | 4.4E-05 | 1.3E-04 | 2.07 | 229610_at | CKAP2L | cytoskeleton associated protein 2-like | |
| 506 | 1.9E-04 | 3.9E-04 | 2.07 | 218810_at | ZC3H12A | zinc finger CCCH-type containing 12A | Nuclear protein |
| 574 | 3.2E-04 | 6.0E-04 | 2.07 | 203439_s_at | STC2 | stanniocalcin 2 | membrane & extracellular protein |
| 576 | 3.3E-04 | 6.0E-04 | 2.07 | 204439_at | IFI44L | interferon-induced protein 44-like | |
| 351 | 4.2E-05 | 1.3E-04 | 2.06 | 224826_at | GPCPD1 | glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae) | |
| 584 | 3.5E-04 | 6.3E-04 | 2.06 | 219161_s_at | CKLF | chemokine-like factor | membrane & extracellular protein |

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| 159 | 5.3E-06 | 3.5E-05 | 2.05 | 204523_at | ZNF140 | zinc finger protein 140 | Nuclear protein, transcription |
| 333 | 3.8E-05 | 1.2E-04 | 2.05 | 206632_s_at | APOBEC3B | apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B | Atrazine degradation |
| 361 | 4.5E-05 | 1.3E-04 | 2.05 | 206376_at | SLC6A15 | solute carrier family 6 (neutral amino acid transporter), member 15 | membrane & extracellular protein |
| 432 | 9.2E-05 | 2.2E-04 | 2.04 | 204401_at | KCNN4 | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4 | membrane & extracellular protein |
| 271 | 2.2E-05 | 8.5E-05 | 2.02 | 243409_at | FOXL1 | forkhead box L1 | |
| 302 | 2.9E-05 | 1.0E-04 | 2.02 | 222895_s_at | BCL11B | B-cell CLL/lymphoma 11B (zinc finger protein) | Nuclear protein |
| 539 | 2.4E-04 | 4.7E-04 | 2.02 | 219010_at | C1orf106 | chromosome 1 open reading frame 106 | |
| 572 | 3.2E-04 | 6.0E-04 | 2.02 | 1552546_a_at | LETM2 | leucine zipper-EF-hand containing transmembrane protein 2 | membrane & extracellular protein |

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| 106 | 2.9E-06 | 2.9E-05 | 2.01 | 202888_s_at | ANPEP | alanyl (membrane) aminopeptidase | membrane & extracellular protein, Dendritic cells in regulating TH1 and TH2 Development, SARS Coronavirus Protease, Glutathione metabolism, Hematopoietic cell lineage, angiogenesis, immunology, metastasis |
| 217 | 1.3E-05 | 6.3E-05 | 2.01 | 221530_s_at | BHLHE41 | basic helix-loop-helix family, member e41 | Circadian rhythm |
| 226 | 1.4E-05 | 6.6E-05 | 2.01 | 215177_s_at | ITGA6 | integrin, alpha 6 | membrane & extracellular protein, Cell adhesion molecules (CAMs), Cell Communication, ECM-receptor interaction, Focal adhesion, Hematopoietic cell lineage, Regulation of actin cytoskeleton, cell_signaling, immunology, metastasis |
| 497 | 1.8E-04 | 3.8E-04 | 2.01 | 218663_at | NCAPG | non-SMC condensin I complex, subunit G | Nuclear protein |
| 631 | 5.3E-04 | 8.9E-04 | 2.01 | 218400_at | OAS3 | 2'-5'-oligoadenylate synthetase 3, 100kDa | |
| 138 | 4.1E-06 | 3.1E-05 | 2 | 219528_s_at | BCL11B | B-cell CLL/lymphoma 11B (zinc finger protein) | Nuclear protein |

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| 255 | 1.8E-05 | 7.4E-05 | 2 | 223503_at | TMEM163 | transmembrane protein 163 | membrane & extracellular protein |
| 564 | 2.9E-04 | 5.5E-04 | 2 | 204729_s_at | STX1A | syntaxin 1A (brain) | membrane & extracellular protein, Blockade of Neurotransmitter Relase by Botulinum Toxin |
| 285 | 2.6E-05 | 9.5E-05 | 1.99 | 202862_at | FAH | fumarylacetoacetate hydrolase (fumarylacetoacetase) | Styrene degradation, Tyrosine metabolism, immunology |
| 352 | 4.2E-05 | 1.3E-04 | 1.99 | 202644_s_at | TNFAIP3 | tumor necrosis factor, alpha-induced protein 3 | Nuclear protein, CD40L Signaling Pathway, NF-kB Signaling Pathway, TNFR2 Signaling Pathway |
| 436 | 9.9E-05 | 2.4E-04 | 1.99 | 201829_at | NET1 | neuroepithelial cell transforming 1 | Nuclear protein |
| 612 | 4.5E-04 | 7.8E-04 | 1.99 | 208608_s_at | SNTB1 | syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) | membrane & extracellular protein |
| 339 | 4.0E-05 | 1.2E-04 | 1.98 | 216252_x_at | FAS | Fas (TNF receptor superfamily, member 6) | membrane & extracellular protein, Antigen Dependent B Cell Activation, Bystander B Cell Activation, CTL mediated immune response against target cells , FAS signaling pathway ( CD95 ), HIV Induced T Cell Apoptosis, HIV-I Nef: negative effector of Fas and TNF, IL-2 Receptor Beta Chain in T |

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| | | | | | | | cell Activation, Keratinocyte Differentiation, Regulation of transcriptional activity by PML, Stress Induction of HSP Regulation, Apoptosis, Cytokine-cytokine receptor interaction, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, Type I diabetes mellitus |
| 409 | 7.3E-05 | 1.9E-04 | 1.97 | 218943_s_at | DDX58 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 | |
| 560 | 2.8E-04 | 5.3E-04 | 1.97 | 243357_at | NEGR1 | neuronal growth regulator 1 | membrane & extracellular protein, Cell adhesion molecules (CAMs) |
| 68 | 1.4E-06 | 2.1E-05 | 1.96 | 222835_at | THSD4 | thrombospondin, type I, domain containing 4 | membrane & extracellular protein |
| 689 | 8.6E-04 | 1.3E-03 | 1.96 | 202869_at | OAS1 | 2',5'-oligoadenylate synthetase 1, 40/46kDa | Nuclear protein, cell_cycle, cell_signaling, immunology |
| 700 | 9.6E-04 | 1.5E-03 | 1.96 | 213927_at | MAP3K9 | mitogen-activated protein kinase kinase kinase 9 | MAPKinase Signaling Pathway, p38 MAPK Signaling Pathway |
| 369 | 4.7E-05 | 1.3E-04 | 1.95 | 219209_at | IFIH1 | interferon induced with helicase C domain 1 | Nuclear protein, Folate biosynthesis, Starch and sucrose metabolism |
| 435 | 9.7E-05 | 2.4E-04 | 1.95 | 227530_at | AKAP12 | A kinase (PRKA) anchor protein 12 | membrane & extracellular protein, Nuclear protein |

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| 96 | 2.5E-06 | 2.7E-05 | 1.94 | 232024_at | GIMAP2 | GTPase, IMAP family member 2 | membrane & extracellular protein |
| 354 | 4.3E-05 | 1.3E-04 | 1.94 | 218084_x_at | FXYD5 | FXYD domain containing ion transport regulator 5 | membrane & extracellular protein |
| 580 | 3.4E-04 | 6.1E-04 | 1.94 | 221058_s_at | CKLF | chemokine-like factor | membrane & extracellular protein |
| 144 | 4.3E-06 | 3.1E-05 | 1.93 | 206084_at | PTPRR | protein tyrosine phosphatase, receptor type, R | membrane & extracellular protein, Erk1/Erk2 Mapk Signaling pathway, MAPK signaling pathway |
| 461 | 1.2E-04 | 2.7E-04 | 1.93 | 218211_s_at | MLPH | melanophilin | |
| 131 | 3.8E-06 | 3.0E-05 | 1.92 | 243296_at | NAMPT | nicotinamide phosphoribosyltransferase | Nicotinate and nicotinamide metabolism |
| 326 | 3.6E-05 | 1.2E-04 | 1.92 | 224252_s_at | FXYD5 | FXYD domain containing ion transport regulator 5 | membrane & extracellular protein |
| 509 | 1.9E-04 | 4.0E-04 | 1.92 | 215719_x_at | FAS | Fas (TNF receptor superfamily, member 6) | membrane & extracellular protein, Antigen Dependent B Cell Activation, Bystander B Cell Activation, CTL mediated immune response against target cells , FAS signaling pathway ( CD95 ), HIV Induced T Cell Apoptosis, HIV-I Nef: negative effector of Fas and TNF, IL-2 Receptor Beta Chain in T cell Activation, Keratinocyte |

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| | | | | | | | Differentiation, Regulation of transcriptional activity by PML, Stress Induction of HSP Regulation, Apoptosis, Cytokine-cytokine receptor interaction, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, Type I diabetes mellitus |
| 643 | 5.7E-04 | 9.4E-04 | 1.92 | 228353_x_at | UBASH3B | ubiquitin associated and SH3 domain containing, B | Nuclear protein |
| 665 | 7.0E-04 | 1.1E-03 | 1.92 | 202477_s_at | TUBGCP2 | tubulin, gamma complex associated protein 2 | |
| 368 | 4.7E-05 | 1.3E-04 | 1.91 | 228083_at | CACNA2D4 | calcium channel, voltage-dependent, alpha 2/delta subunit 4 | membrane & extracellular protein, MAPK signaling pathway |
| 476 | 1.4E-04 | 3.1E-04 | 1.91 | 217996_at | PHLDA1 | pleckstrin homology-like domain, family A, member 1 | membrane & extracellular protein, Nuclear protein |

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| 535 | 2.3E-04 | 4.6E-04 | 1.91 | 201502_s_at | NFKBIA | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha | Nuclear protein, Acetylation and Deacetylation of RelA in The Nucleus, Activation of PKC through G protein coupled receptor, AKT Signaling Pathway, ATM Signaling Pathway, Cadmium induces DNA synthesis and proliferation in macrophages, CD40L Signaling Pathway, Chaperones modulate interferon Signaling Pathway, Double Stranded RNA Induced Gene Expression, Erythropoietin mediated neuroprotection through NF-kB, fMLP induced chemokine gene expression in HMC-1 cells, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors , Influence of Ras and Rho proteins on G1 to S Transition, Keratinocyte Differentiation, MAPKinase Signaling Pathway, Mechanism of Gene Regulation by Peroxisome Proliferators via PPARa(alpha), Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, NFkB activation by Nontypeable Hemophilus influenzae, NF-kB Signaling Pathway, Signal |

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| | | | | | | | transduction through IL1R, T Cell Receptor Signaling Pathway, The 4-1BB-depend ... |
| 109 | 3.0E-06 | 2.9E-05 | 1.9 | 206693_at | IL7 | interleukin 7 | membrane & extracellular protein, Cytokines and Inflammatory Response, IL-7 Signal Transduction, Regulation of hematopoiesis by cytokines, Cytokine-cytokine receptor interaction, Hematopoietic cell lineage, Jak-STAT signaling pathway, immunology |
| 157 | 5.2E-06 | 3.5E-05 | 1.9 | 209806_at | HIST1H2BK | histone cluster 1, H2bk | Nuclear protein |

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| 625 | 5.0E-04 | 8.5E-04 | 1.9 | 218662_s_at | NCAPG | non-SMC condensin I complex, subunit G | Nuclear protein |
| 299 | 2.8E-05 | 9.9E-05 | 1.89 | 233857_s_at | ASB2 | ankyrin repeat and SOCS box-containing 2 | |
| 365 | 4.6E-05 | 1.3E-04 | 1.89 | 240572_s_at | LOC374443 | CLR pseudogene | |
| 516 | 2.0E-04 | 4.0E-04 | 1.89 | 226614_s_at | FAM167A | family with sequence similarity 167, member A | |
| 657 | 6.6E-04 | 1.1E-03 | 1.89 | 213164_at | NA | NA | membrane & extracellular protein |
| 556 | 2.8E-04 | 5.3E-04 | 1.88 | 1558750_a_at | LOC100288693 | hypothetical protein LOC100288693 | |
| 234 | 1.5E-05 | 6.7E-05 | 1.87 | 205193_at | MAFF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | Nuclear protein, Oxidative Stress Induced Gene Expression Via Nrf2 |
| 317 | 3.4E-05 | 1.1E-04 | 1.87 | 227609_at | EPSTI1 | epithelial stromal interaction 1 (breast) | |
| 427 | 8.7E-05 | 2.1E-04 | 1.87 | 210286_s_at | SLC4A7 | solute carrier family 4, sodium bicarbonate cotransporter, member 7 | membrane & extracellular protein |

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| 534 | 2.3E-04 | 4.6E-04 | 1.86 | 209270_at | LAMB3 | laminin, beta 3 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 626 | 5.1E-04 | 8.6E-04 | 1.86 | 203349_s_at | ETV5 | ets variant 5 | Nuclear protein, IL12 and Stat4 Dependent Signaling Pathway in Th1 Development, gene_regulation, transcription |
| 418 | 7.9E-05 | 2.0E-04 | 1.85 | 217967_s_at | FAM129A | family with sequence similarity 129, member A | |
| 605 | 4.1E-04 | 7.2E-04 | 1.85 | 223279_s_at | UACA | uveal autoantigen with coiled-coil domains and ankyrin repeats | membrane & extracellular protein, Nuclear protein |
| 155 | 5.2E-06 | 3.5E-05 | 1.84 | 203836_s_at | MAP3K5 | mitogen-activated protein kinase kinase kinase 5 | membrane & extracellular protein, HIV-I Nef: negative effector of Fas and TNF, Keratinocyte Differentiation, MAPKinase Signaling Pathway, p38 MAPK Signaling Pathway , The 4-1BB-dependent immune response, MAPK signaling pathway |
| 268 | 2.1E-05 | 8.3E-05 | 1.84 | 214456_x_at | NA | NA | membrane & extracellular protein |
| 345 | 4.1E-05 | 1.3E-04 | 1.84 | 214012_at | ERAP1 | endoplasmic reticulum aminopeptidase 1 | membrane & extracellular protein |
| 468 | 1.3E-04 | 2.9E-04 | 1.84 | 217966_s_at | FAM129A | family with sequence similarity 129, member A | |

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| 554 | 2.7E-04 | 5.2E-04 | 1.84 | 214059_at | IFI44 | interferon-induced protein 44 | |
| 651 | 6.1E-04 | 9.9E-04 | 1.84 | 223451_s_at | CKLF | chemokine-like factor | membrane & extracellular protein |
| 195 | 9.5E-06 | 5.1E-05 | 1.83 | 203837_at | MAP3K5 | mitogen-activated protein kinase kinase kinase 5 | membrane & extracellular protein, HIV-I Nef: negative effector of Fas and TNF, Keratinocyte Differentiation, MAPKinase Signaling Pathway, p38 MAPK Signaling Pathway , The 4-1BB-dependent immune response, MAPK signaling pathway |
| 422 | 8.1E-05 | 2.0E-04 | 1.83 | 215726_s_at | CYB5A | cytochrome b5 type A (microsomal) | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes |
| 640 | 5.6E-04 | 9.3E-04 | 1.83 | 204014_at | DUSP4 | dual specificity phosphatase 4 | Nuclear protein, Perou's- Intrinsic-Breast-Cancer-Genes, Regulation of MAP Kinase Pathways Through Dual Specificity Phosphatases, MAPK signaling pathway, cell_cycle, cell_signaling |
| 393 | 6.3E-05 | 1.7E-04 | 1.82 | 236207_at | SSFA2 | sperm specific antigen 2 | membrane & extracellular protein |
| 515 | 2.0E-04 | 4.0E-04 | 1.82 | 212944_at | SLC5A3 | solute carrier family 5 (sodium/myo-inositol cotransporter), | membrane & extracellular protein |

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|  |  |  |  |  |  | member 3 |  |
| 703 | 9.8E-04 | 1.5E-03 | 1.82 | 223513_at | CENPJ | centromere protein J |  |
| 230 | 1.4E-05 | 6.6E-05 | 1.81 | 1554067_at | C12orf66 | chromosome 12 open reading frame 66 |  |
| 600 | 4.0E-04 | 7.1E-04 | 1.81 | 204780_s_at | FAS | Fas (TNF receptor superfamily, member 6) | membrane & extracellular protein, Antigen Dependent B Cell Activation, Bystander B Cell Activation, CTL mediated immune response against target cells , FAS signaling pathway ( CD95 ), HIV Induced T Cell Apoptosis, HIV-I Nef: negative effector of Fas and TNF, IL-2 Receptor Beta Chain in T cell Activation, Keratinocyte Differentiation, Regulation of transcriptional activity by PML, Stress Induction of HSP Regulation, Apoptosis, Cytokine-cytokine receptor interaction, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, Type I diabetes mellitus |

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| 623 | 4.9E-04 | 8.3E-04 | 1.81 | 226907_at | PPP1R14C | protein phosphatase 1, regulatory (inhibitor) subunit 14C | membrane & extracellular protein |
| 329 | 3.7E-05 | 1.2E-04 | 1.8 | 205659_at | HDAC9 | histone deacetylase 9 | NA, Signal Dependent Regulation of Myogenesis by Corepressor MITR, Sumoylation by RanBP2 Regulates Transcriptional Repression |
| 171 | 6.0E-06 | 3.7E-05 | 1.79 | 223423_at | GPR160 | G protein-coupled receptor 160 | membrane & extracellular protein |
| 340 | 4.0E-05 | 1.2E-04 | 1.79 | 211080_s_at | NEK2 | NIMA (never in mitosis gene a)-related kinase 2 | Nuclear protein |
| 652 | 6.2E-04 | 1.0E-03 | 1.79 | 202481_at | DHRS3 | dehydrogenase/reductase (SDR family) member 3 | membrane & extracellular protein, 1- and 2-Methylnaphthalene degradation, Benzoate degradation via CoA ligation, Bisphenol A degradation, Ethylbenzene degradation, gamma-Hexachlorocyclohexane degradation, Limonene and pinene degradation |
| 288 | 2.6E-05 | 9.5E-05 | 1.78 | 231899_at | ZC3H12C | zinc finger CCCH-type containing 12C | |
| 347 | 4.1E-05 | 1.3E-04 | 1.78 | 202902_s_at | CTSS | cathepsin S | membrane & extracellular protein, Antigen processing and presentation, immunology |

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| 355 | 4.3E-05 | 1.3E-04 | 1.78 | 207375_s_at | IL15RA | interleukin 15 receptor, alpha | membrane & extracellular protein, Nuclear protein, Cytokine-cytokine receptor interaction, Jak-STAT signaling pathway, immunology |
| 484 | 1.5E-04 | 3.2E-04 | 1.78 | 211924_s_at | PLAUR | plasminogen activator, urokinase receptor | membrane & extracellular protein, Complement and coagulation cascades, angiogenesis |
| 172 | 6.3E-06 | 3.9E-05 | 1.77 | 219073_s_at | OSBPL10 | oxysterol binding protein-like 10 | Nuclear protein |
| 650 | 6.0E-04 | 9.8E-04 | 1.77 | 226438_at | SNTB1 | syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) | membrane & extracellular protein |
| 469 | 1.3E-04 | 2.9E-04 | 1.76 | 223381_at | NUF2 | NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae) | Nuclear protein |
| 242 | 1.6E-05 | 7.0E-05 | 1.75 | 210845_s_at | PLAUR | plasminogen activator, urokinase receptor | membrane & extracellular protein, Complement and coagulation cascades, angiogenesis |
| 553 | 2.7E-04 | 5.1E-04 | 1.75 | 224919_at | MRPS6 | mitochondrial ribosomal protein S6 | |
| 634 | 5.4E-04 | 8.9E-04 | 1.75 | 204886_at | PLK4 | polo-like kinase 4 (Drosophila) | |

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| 201 | 1.0E-05 | 5.4E-05 | 1.74 | 209200_at | MEF2C | myocyte enhancer factor 2C | Nuclear protein, ALK in cardiac myocytes, CARM1 and Regulation of the Estrogen Receptor, NFAT and Hypertrophy of the heart (Transcription in the broken heart), MAPK signaling pathway |
| 430 | 8.8E-05 | 2.2E-04 | 1.74 | 202506_at | SSFA2 | sperm specific antigen 2 | membrane & extracellular protein |
| 474 | 1.4E-04 | 3.1E-04 | 1.74 | 204641_at | NEK2 | NIMA (never in mitosis gene a)-related kinase 2 | Nuclear protein |
| 673 | 7.8E-04 | 1.2E-03 | 1.74 | 234725_s_at | SEMA4B | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B | membrane & extracellular protein, Axon guidance |
| 444 | 1.1E-04 | 2.5E-04 | 1.73 | 240407_at | LOC100126784 | hypothetical LOC100126784 | |
| 536 | 2.3E-04 | 4.6E-04 | 1.73 | 223974_at | MGC11082 | hypothetical LOC84777 | |
| 648 | 5.9E-04 | 9.6E-04 | 1.73 | 220346_at | MTHFD2L | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like | |

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| 677 | 7.9E-04 | 1.2E-03 | 1.73 | 227198_at | AFF3 | AF4/FMR2 family, member 3 | Nuclear protein |
| 446 | 1.1E-04 | 2.5E-04 | 1.72 | 235122_at | HIVEP3 | human immunodeficiency virus type I enhancer binding protein 3 | Nuclear protein |
| 488 | 1.5E-04 | 3.3E-04 | 1.72 | 204781_s_at | FAS | Fas (TNF receptor superfamily, member 6) | membrane & extracellular protein, Antigen Dependent B Cell Activation, Bystander B Cell Activation, CTL mediated immune response against target cells , FAS signaling pathway ( CD95 ), HIV Induced T Cell Apoptosis, HIV-I Nef: negative effector of Fas and TNF, IL-2 Receptor Beta Chain in T cell Activation, Keratinocyte Differentiation, Regulation of transcriptional activity by PML, Stress Induction of HSP Regulation, Apoptosis, Cytokine-cytokine receptor interaction, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, Type I diabetes mellitus |
| 494 | 1.7E-04 | 3.6E-04 | 1.72 | 235927_at | XPO1 | exportin 1 (CRM1 homolog, yeast) | Nuclear protein, Regulation of Spermatogenesis by CREM, Sonic Hedgehog (SHH) Receptor Ptc1 Regulates cell cycle, gene_regulation, transcription |

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| 658 | 6.6E-04 | 1.1E-03 | 1.72 | 228359_at | UBASH3B | ubiquitin associated and SH3 domain containing, B | |
| 663 | 7.0E-04 | 1.1E-03 | 1.72 | 217010_s_at | CDC25C | cell division cycle 25 homolog C (S. pombe) | Nuclear protein, Activation of Src by Protein-tyrosine phosphatase alpha, cdc25 and chk1 Regulatory Pathway in response to DNA damage, Cell Cycle: G2/M Checkpoint, How Progesterone Initiates the Oocyte Maturation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, Regulation of cell cycle progression by Plk3, Sonic Hedgehog (SHH) Receptor Ptc1 Regulates cell cycle, Cell cycle, cell_cycle, cell_signaling |
| 439 | 1.0E-04 | 2.4E-04 | 1.71 | 203504_s_at | ABCA1 | ATP-binding cassette, sub-family A (ABC1), member 1 | membrane & extracellular protein, FXR and LXR Regulation of Cholesterol Metabolism, Nuclear Receptors in Lipid Metabolism and Toxicity |
| 472 | 1.4E-04 | 3.0E-04 | 1.71 | 223774_at | SNHG12 | small nucleolar RNA host gene 12 (non-protein coding) | |
| 696 | 9.4E-04 | 1.4E-03 | 1.71 | 204887_s_at | PLK4 | polo-like kinase 4 (Drosophila) | |

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| 259 | 1.9E-05 | 7.6E-05 | 1.7 | 207535_s_at | NFKB2 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) | membrane & extracellular protein, Nuclear protein, Adipocytokine signaling pathway, Apoptosis, B cell receptor signaling pathway, Epithelial cell signaling in Helicobacter pylori infection, MAPK signaling pathway, T cell receptor signaling pathway, Toll-like receptor signaling pathway, gene_regulation, immunology, transcription, tsonc |
| 342 | 4.1E-05 | 1.3E-04 | 1.7 | 213589_s_at | B3GNTL1 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 | |
| 471 | 1.3E-04 | 3.0E-04 | 1.7 | 225524_at | ANTXR2 | anthrax toxin receptor 2 | membrane & extracellular protein |
| 507 | 1.9E-04 | 3.9E-04 | 1.7 | 209642_at | BUB1 | budding uninhibited by benzimidazoles 1 homolog (yeast) | Nuclear protein, Cell cycle, immunology |
| 590 | 3.6E-04 | 6.5E-04 | 1.7 | 205379_at | CBR3 | carbonyl reductase 3 | Arachidonic acid metabolism |
| 598 | 4.0E-04 | 7.0E-04 | 1.7 | 239058_at | FOXC2 | forkhead box C2 (MFH-1, mesenchyme forkhead 1) | |
| 267 | 2.1E-05 | 8.3E-05 | 1.69 | 234023_s_at | CENPJ | centromere protein J | |

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| 563 | 2.9E-04 | 5.4E-04 | 1.69 | 203234_at | UPP1 | uridine phosphorylase 1 | Pyrimidine metabolism |
| 654 | 6.3E-04 | 1.0E-03 | 1.69 | 235020_at | TAF4B | TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa | Basal transcription factors |
| 221 | 1.4E-05 | 6.5E-05 | 1.68 | 205076_s_at | MTMR11 | myotubularin related protein 11 |  |
| 223 | 1.4E-05 | 6.5E-05 | 1.68 | 201920_at | SLC20A1 | solute carrier family 20 (phosphate transporter), member 1 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, immunology |
| 281 | 2.5E-05 | 9.4E-05 | 1.68 | 1555137_a_at | FGD6 | FYVE, RhoGEF and PH domain containing 6 |  |
| 316 | 3.3E-05 | 1.1E-04 | 1.67 | 228617_at | XAF1 | XIAP associated factor 1 | Nuclear protein |
| 699 | 9.6E-04 | 1.5E-03 | 1.67 | 219544_at | C13orf34 | chromosome 13 open reading frame 34 |  |
| 619 | 4.7E-04 | 8.0E-04 | 1.66 | 203395_s_at | HES1 | hairy and enhancer of split 1, (Drosophila) | Nuclear protein, Segmentation Clock, Maturity onset diabetes of the young, Notch signaling pathway |
| 306 | 3.1E-05 | 1.1E-04 | 1.65 | 243541_at | IL31RA | interleukin 31 receptor A | membrane & extracellular protein |

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| 414 | 7.8E-05 | 2.0E-04 | 1.65 | 206364_at | KIF14 | kinesin family member 14 | Nuclear protein |
| 455 | 1.1E-04 | 2.6E-04 | 1.65 | 201925_s_at | CD55 | CD55 molecule, decay accelerating factor for complement (Cromer blood group) | membrane & extracellular protein, Complement and coagulation cascades, Hematopoietic cell lineage |
| 541 | 2.4E-04 | 4.8E-04 | 1.65 | 215509_s_at | BUB1 | budding uninhibited by benzimidazoles 1 homolog (yeast) | Cell cycle, immunology |
| 668 | 7.3E-04 | 1.2E-03 | 1.65 | 231219_at | CMTM1 | CKLF-like MARVEL transmembrane domain containing 1 | membrane & extracellular protein |
| 676 | 7.8E-04 | 1.2E-03 | 1.65 | 202388_at | RGS2 | regulator of G-protein signaling 2, 24kDa | immunology |
| 690 | 8.9E-04 | 1.4E-03 | 1.65 | 205933_at | SETBP1 | SET binding protein 1 | Nuclear protein |
| 597 | 3.9E-04 | 6.9E-04 | 1.64 | 211519_s_at | KIF2C | kinesin family member 2C | Nuclear protein |
| 262 | 1.9E-05 | 7.7E-05 | 1.63 | 202363_at | SPOCK1 | sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1 | membrane & extracellular protein |

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| 366 | 4.6E-05 | 1.3E-04 | 1.63 | 226603_at | SAMD9L | sterile alpha motif domain containing 9-like | |
| 447 | 1.1E-04 | 2.5E-04 | 1.62 | 202863_at | SP100 | SP100 nuclear antigen | Nuclear protein, Regulation of transcriptional activity by PML, gene_regulation, transcription |
| 520 | 2.0E-04 | 4.1E-04 | 1.61 | 212543_at | AIM1 | absent in melanoma 1 | |
| 636 | 5.5E-04 | 9.1E-04 | 1.61 | 201802_at | SLC29A1 | solute carrier family 29 (nucleoside transporters), member 1 | membrane & extracellular protein |
| 270 | 2.2E-05 | 8.5E-05 | 1.6 | 224917_at | NA | NA | membrane & extracellular protein |
| 508 | 1.9E-04 | 4.0E-04 | 1.6 | 205874_at | ITPKA | inositol 1,4,5-trisphosphate 3-kinase A | Calcium signaling pathway, Inositol phosphate metabolism, Phosphatidylinositol signaling system |
| 401 | 6.7E-05 | 1.8E-04 | 1.59 | 205184_at | GNG4 | guanine nucleotide binding protein (G protein), gamma 4 | membrane & extracellular protein |
| 573 | 3.2E-04 | 6.0E-04 | 1.59 | 232263_at | SLC6A15 | solute carrier family 6 (neutral amino acid transporter), member 15 | membrane & extracellular protein |
| 617 | 4.7E-04 | 8.0E-04 | 1.59 | 204492_at | ARHGAP11A | Rho GTPase activating protein 11A | |

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| 659 | 6.8E-04 | 1.1E-03 | 1.59 | 227080_at | ZNF697 | zinc finger protein 697 | Nuclear protein |
| 420 | 7.9E-05 | 2.0E-04 | 1.56 | 1569003_at | TMEM49 | transmembrane protein 49 | membrane & extracellular protein |
| 524 | 2.1E-04 | 4.2E-04 | 1.56 | 214179_s_at | NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | Nuclear protein |
| 394 | 6.4E-05 | 1.7E-04 | 1.55 | 1555765_a_at | GNG4 | guanine nucleotide binding protein (G protein), gamma 4 | membrane & extracellular protein |
| 513 | 1.9E-04 | 4.0E-04 | 1.55 | 237400_at | ATP5S | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B) | |
| 529 | 2.2E-04 | 4.4E-04 | 1.55 | 228323_at | CASC5 | cancer susceptibility candidate 5 | Nuclear protein |
| 610 | 4.3E-04 | 7.5E-04 | 1.55 | 223773_s_at | SNHG12 | small nucleolar RNA host gene 12 (non-protein coding) | |
| 629 | 5.2E-04 | 8.7E-04 | 1.55 | 219918_s_at | ASPM | asp (abnormal spindle) homolog, microcephaly associated (Drosophila) | Nuclear protein |

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| 542 | 2.4E-04 | 4.8E-04 | 1.54 | 242625_at | RSAD2 | radical S-adenosyl methionine domain containing 2 | membrane & extracellular protein |
| 704 | 9.9E-04 | 1.5E-03 | 1.54 | 201926_s_at | CD55 | CD55 molecule, decay accelerating factor for complement (Cromer blood group) | membrane & extracellular protein, Complement and coagulation cascades, Hematopoietic cell lineage |
| 664 | 7.0E-04 | 1.1E-03 | 1.53 | 202935_s_at | SOX9 | SRY (sex determining region Y)-box 9 | Nuclear protein, development |
| 679 | 7.9E-04 | 1.2E-03 | 1.53 | 220241_at | TMCO3 | transmembrane and coiled-coil domains 3 | membrane & extracellular protein |
| 445 | 1.1E-04 | 2.5E-04 | 1.52 | 1557116_at | APOL6 | apolipoprotein L, 6 | membrane & extracellular protein |
| 451 | 1.1E-04 | 2.6E-04 | 1.52 | 202864_s_at | SP100 | SP100 nuclear antigen | Nuclear protein, Regulation of transcriptional activity by PML, gene_regulation, transcription |
| 662 | 7.0E-04 | 1.1E-03 | 1.52 | 236957_at | CDCA2 | cell division cycle associated 2 | Nuclear protein |
| 685 | 8.1E-04 | 1.2E-03 | 1.52 | 230036_at | SAMD9L | sterile alpha motif domain containing 9-like | |
| 603 | 4.1E-04 | 7.2E-04 | 1.51 | 200759_x_at | NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | Nuclear protein |

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| 551 | 2.7E-04 | 5.1E-04 | 1.5 | 213338_at | TMEM158 | transmembrane protein 158 | membrane & extracellular protein |
| 583 | 3.5E-04 | 6.3E-04 | 1.5 | 216268_s_at | JAG1 | jagged 1 (Alagille syndrome) | membrane & extracellular protein, Phosphoinositides and their downstream targets., Notch signaling pathway, angiogenesis, development, metastasis |
| 501 | 1.8E-04 | 3.9E-04 | 1.49 | 219863_at | HERC5 | hect domain and RLD 5 | |
| 568 | 3.0E-04 | 5.6E-04 | 1.49 | 202411_at | IFI27 | interferon, alpha-inducible protein 27 | membrane & extracellular protein |
| 697 | 9.4E-04 | 1.4E-03 | 1.49 | 200758_s_at | NFE2L1 | nuclear factor (erythroid-derived 2)-like 1 | Nuclear protein |
| 504 | 1.9E-04 | 3.9E-04 | 1.47 | 239697_x_at | C3orf67 | chromosome 3 open reading frame 67 | |
| 644 | 5.7E-04 | 9.4E-04 | 1.47 | 213359_at | HNRNPD | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) | Nuclear protein |
| 661 | 6.9E-04 | 1.1E-03 | 1.47 | 1552619_a_at | ANLN | anillin, actin binding protein | Nuclear protein |
| 613 | 4.5E-04 | 7.8E-04 | 1.46 | 205122_at | TMEFF1 | transmembrane protein with EGF-like and two | membrane & extracellular protein |

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| | | | | | | follistatin-like domains 1 | |
| 500 | 1.8E-04 | 3.9E-04 | 1.44 | 226997_at | ADAMTS12 | ADAM metallopeptidase with thrombospondin type 1 motif, 12 | membrane & extracellular protein |
| 596 | 3.8E-04 | 6.8E-04 | 1.44 | 222608_s_at | ANLN | anillin, actin binding protein | Nuclear protein |
| 682 | 8.0E-04 | 1.2E-03 | 1.44 | 230097_at | GART | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase | Nuclear protein, One carbon pool by folate, Purine metabolism, gene_regulation, transcription |
| 599 | 4.0E-04 | 7.0E-04 | 1.42 | 204612_at | PKIA | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | Nuclear protein |
| 557 | 2.8E-04 | 5.3E-04 | 1.41 | 218543_s_at | PARP12 | poly (ADP-ribose) polymerase family, member 12 | Nuclear protein |
| 602 | 4.1E-04 | 7.2E-04 | 1.37 | 243999_at | SLFN5 | schlafen family member 5 | Nuclear protein |

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| 637 | 5.5E-04 | 9.1E-04 | 1.36 | 238430_x_at | SLFN5 | schlafen family member 5 | Nuclear protein |
| 694 | 9.1E-04 | 1.4E-03 | 1.32 | 1557078_at | SLFN5 | schlafen family member 5 | Nuclear protein |
| 681 | 8.0E-04 | 1.2E-03 | 0.71 | 219225_at | PGBD5 | piggyBac transposable element derived 5 | membrane & extracellular protein |
| 532 | 2.3E-04 | 4.6E-04 | 0.7 | 219935_at | ADAMTS5 | ADAM metallopeptidase with thrombospondin type 1 motif, 5 | membrane & extracellular protein, Nuclear protein |
| 546 | 2.5E-04 | 4.8E-04 | 0.69 | 205306_x_at | KMO | kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) | membrane & extracellular protein, Tryptophan metabolism |
| 622 | 4.8E-04 | 8.2E-04 | 0.69 | 215046_at | C2orf67 | chromosome 2 open reading frame 67 | |
| 666 | 7.2E-04 | 1.1E-03 | 0.68 | 208483_x_at | KRT33A | keratin 33A | Cell Communication |
| 698 | 9.5E-04 | 1.4E-03 | 0.67 | 227481_at | CNKSR3 | CNKSR family member 3 | membrane & extracellular protein |
| 423 | 8.2E-05 | 2.0E-04 | 0.66 | 229357_at | ADAMTS5 | ADAM metallopeptidase with thrombospondin type 1 motif, 5 | membrane & extracellular protein, Nuclear protein |

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| 485 | 1.5E-04 | 3.2E-04 | 0.66 | 227614_at | HKDC1 | hexokinase domain containing 1 | |
| 399 | 6.6E-05 | 1.7E-04 | 0.65 | 201243_s_at | ATP1B1 | ATPase, Na+/K+ transporting, beta 1 polypeptide | membrane & extracellular protein |
| 633 | 5.3E-04 | 8.9E-04 | 0.65 | 210589_s_at | GBAP1 | glucosidase, beta, acid pseudogene 1 | |
| 688 | 8.5E-04 | 1.3E-03 | 0.65 | 209064_x_at | PAIP1 | poly(A) binding protein interacting protein 1 | |
| 503 | 1.8E-04 | 3.9E-04 | 0.64 | 212928_at | TSPYL4 | TSPY-like 4 | Nuclear protein |
| 586 | 3.5E-04 | 6.4E-04 | 0.64 | 217908_s_at | DCAF6 | DDB1 and CUL4 associated factor 6 | Nuclear protein |
| 678 | 7.9E-04 | 1.2E-03 | 0.64 | 229566_at | LOC645638 | WDNM1-like pseudogene | |
| 702 | 9.7E-04 | 1.5E-03 | 0.64 | 227919_at | UCA1 | urothelial cancer associated 1 (non-protein coding) | |
| 402 | 6.9E-05 | 1.8E-04 | 0.63 | 227556_at | NME7 | non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase) | membrane & extracellular protein, Purine metabolism, Pyrimidine metabolism |
| 552 | 2.7E-04 | 5.1E-04 | 0.63 | 229199_at | SCN9A | sodium channel, voltage-gated, type IX, alpha subunit | membrane & extracellular protein |
| 611 | 4.4E-04 | 7.7E-04 | 0.63 | 209087_x_at | MCAM | melanoma cell adhesion molecule | membrane & extracellular protein, Nuclear protein |

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| 649 | 5.9E-04 | 9.6E-04 | 0.63 | 231863_at | ING3 | inhibitor of growth family, member 3 | Nuclear protein |
| 348 | 4.2E-05 | 1.3E-04 | 0.62 | 235085_at | PRAGMIN | homolog of rat pragma of Rnd2 | membrane & extracellular protein |
| 417 | 7.8E-05 | 2.0E-04 | 0.62 | 228948_at | EPHA4 | EPH receptor A4 | membrane & extracellular protein, Eph Kinases and ephrins support platelet aggregation, Axon guidance, cell_cycle, cell_signaling, signal_transduction |
| 438 | 1.0E-04 | 2.4E-04 | 0.62 | 211214_s_at | DAPK1 | death-associated protein kinase 1 | membrane & extracellular protein, cell_signaling, immunology |
| 456 | 1.1E-04 | 2.6E-04 | 0.62 | 228494_at | PPP1R9A | protein phosphatase 1, regulatory (inhibitor) subunit 9A | |
| 491 | 1.6E-04 | 3.4E-04 | 0.62 | 226360_at | ZNRF3 | zinc and ring finger 3 | membrane & extracellular protein |
| 550 | 2.6E-04 | 4.9E-04 | 0.62 | 209120_at | NR2F2 | nuclear receptor subfamily 2, group F, member 2 | Nuclear protein |
| 349 | 4.2E-05 | 1.3E-04 | 0.61 | 220244_at | LOH3CR2A | loss of heterozygosity, 3, chromosomal region 2, gene A | |
| 357 | 4.4E-05 | 1.3E-04 | 0.61 | 205407_at | RECK | reversion-inducing-cysteine-rich protein with kazal motifs | membrane & extracellular protein, Inhibition of Matrix Metalloproteinases |

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|---|---|---|---|---|---|---|---|
| 433 | 9.2E-05 | 2.2E-04 | 0.61 | 210869_s_at | MCAM | melanoma cell adhesion molecule | membrane & extracellular protein, Nuclear protein |
| 527 | 2.2E-04 | 4.3E-04 | 0.61 | 1561396_at | EPHA6 | EPH receptor A6 | membrane & extracellular protein |
| 555 | 2.8E-04 | 5.3E-04 | 0.61 | 202427_s_at | BRP44 | brain protein 44 | |
| 559 | 2.8E-04 | 5.3E-04 | 0.61 | 211555_s_at | GUCY1B3 | guanylate cyclase 1, soluble, beta 3 | Ion Channels and Their Functional Role in Vascular Endothelium, Gap junction, Long-term depression, Purine metabolism, signal_transduction |
| 570 | 3.2E-04 | 5.9E-04 | 0.61 | 211237_s_at | FGFR4 | fibroblast growth factor receptor 4 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, MAPK signaling pathway, Regulation of actin cytoskeleton, development, misc |
| 638 | 5.6E-04 | 9.2E-04 | 0.61 | 233555_s_at | SULF2 | sulfatase 2 | membrane & extracellular protein |
| 645 | 5.8E-04 | 9.4E-04 | 0.61 | 226776_at | ENY2 | enhancer of yellow 2 homolog (Drosophila) | Nuclear protein |
| 687 | 8.4E-04 | 1.3E-03 | 0.61 | 203060_s_at | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | Perou's- Intrinsic- Breast-Cancer-Genes, Purine metabolism, Selenoamino acid metabolism, Sulfur metabolism |
| 236 | 1.5E-05 | 6.8E-05 | 0.6 | 207177_at | PTGFR | prostaglandin F receptor (FP) | membrane & extracellular protein, Eicosanoid Metabolism, Calcium signaling pathway, Neuroactive ligand-receptor interaction |
| 241 | 1.6E-05 | 7.0E-05 | 0.6 | 205347_s_at | TMSB15A | thymosin beta 15a | |

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|---|---|---|---|---|---|---|---|
| 282 | 2.5E-05 | 9.4E-05 | 0.6 | 227752_at | SPTLC3 | serine palmitoyltransferase, long chain base subunit 3 | membrane & extracellular protein |
| 291 | 2.6E-05 | 9.5E-05 | 0.6 | 221942_s_at | GUCY1A3 | guanylate cyclase 1, soluble, alpha 3 | Ion Channels and Their Functional Role in Vascular Endothelium, Gap junction, Long-term depression, Purine metabolism, immunology |
| 356 | 4.4E-05 | 1.3E-04 | 0.6 | 202796_at | SYNPO | synaptopodin | membrane & extracellular protein |
| 481 | 1.4E-04 | 3.2E-04 | 0.6 | 202607_at | NDST1 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 | membrane & extracellular protein, Glycan structures - biosynthesis 1, Heparan sulfate biosynthesis |
| 496 | 1.7E-04 | 3.7E-04 | 0.6 | 233078_at | API5 | apoptosis inhibitor 5 | Nuclear protein |
| 530 | 2.2E-04 | 4.4E-04 | 0.6 | 208134_x_at | PSG2 | pregnancy specific beta-1-glycoprotein 2 | membrane & extracellular protein |
| 531 | 2.3E-04 | 4.5E-04 | 0.6 | 203817_at | GUCY1B3 | guanylate cyclase 1, soluble, beta 3 | Ion Channels and Their Functional Role in Vascular Endothelium, Gap junction, Long-term depression, Purine metabolism, signal_transduction |
| 587 | 3.6E-04 | 6.4E-04 | 0.6 | 209298_s_at | ITSN1 | intersectin 1 (SH3 domain protein) | membrane & extracellular protein |
| 200 | 1.0E-05 | 5.3E-05 | 0.59 | 218031_s_at | FOXN3 | forkhead box N3 | Nuclear protein |
| 218 | 1.3E-05 | 6.3E-05 | 0.59 | 221886_at | DENND2A | DENN/MADD domain containing 2A | |

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|---|---|---|---|---|---|---|---|
| 370 | 4.7E-05 | 1.4E-04 | 0.59 | 219093_at | PID1 | phosphotyrosine interaction domain containing 1 | |
| 400 | 6.6E-05 | 1.8E-04 | 0.59 | 205440_s_at | NPY1R | neuropeptide Y receptor Y1 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Neuroactive ligand-receptor interaction, immunology |
| 428 | 8.7E-05 | 2.1E-04 | 0.59 | 244461_at | CYTSB | cytospin B | Nuclear protein |
| 452 | 1.1E-04 | 2.6E-04 | 0.59 | 233255_s_at | BIVM | basic, immunoglobulin-like variable motif containing | Nuclear protein |
| 482 | 1.4E-04 | 3.2E-04 | 0.59 | 226775_at | ENY2 | enhancer of yellow 2 homolog (Drosophila) | Nuclear protein |
| 486 | 1.5E-04 | 3.2E-04 | 0.59 | 224836_at | TP53INP2 | tumor protein p53 inducible nuclear protein 2 | Nuclear protein |
| 521 | 2.0E-04 | 4.1E-04 | 0.59 | 239761_at | GCNT1 | glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase) | membrane & extracellular protein, Glycan structures - biosynthesis 1, O-Glycan biosynthesis |
| 660 | 6.9E-04 | 1.1E-03 | 0.59 | 231879_at | COL12A1 | collagen, type XII, alpha 1 | membrane & extracellular protein |
| 222 | 1.4E-05 | 6.5E-05 | 0.58 | 201242_s_at | ATP1B1 | ATPase, Na+/K+ transporting, beta 1 polypeptide | membrane & extracellular protein |

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|---|---|---|---|---|---|---|---|
| 305 | 3.1E-05 | 1.1E-04 | 0.58 | 201818_at | LPCAT1 | lysophosphatidylcholine acyltransferase 1 | membrane & extracellular protein |
| 322 | 3.6E-05 | 1.2E-04 | 0.58 | 205670_at | GAL3ST1 | galactose-3-O-sulfotransferase 1 | membrane & extracellular protein, Sphingolipid metabolism |
| 441 | 1.0E-04 | 2.5E-04 | 0.58 | 209699_x_at | AKR1C2 | aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) | Perou's- Intrinsic- Breast-Cancer-Genes, Metabolism of xenobiotics by cytochrome P450 |
| 457 | 1.1E-04 | 2.6E-04 | 0.58 | 226705_at | FGFR1 | fibroblast growth factor receptor 1 | membrane & extracellular protein, Adherens junction, MAPK signaling pathway, Regulation of actin cytoskeleton, angiogenesis, cell_cycle, cell_signaling, development, immunology, misc, signal_transduction |
| 609 | 4.3E-04 | 7.5E-04 | 0.58 | 204105_s_at | NRCAM | neuronal cell adhesion molecule | membrane & extracellular protein, Cell adhesion molecules (CAMs) |
| 670 | 7.5E-04 | 1.2E-03 | 0.58 | 223079_s_at | GLS | glutaminase | D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, immunology |
| 680 | 8.0E-04 | 1.2E-03 | 0.58 | 226649_at | PANK1 | pantothenate kinase 1 | Pantothenate and CoA biosynthesis |

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|---|---|---|---|---|---|---|---|
| 253 | 1.8E-05 | 7.4E-05 | 0.57 | 202555_s_at | MYLK | myosin light chain kinase | Calcium signaling pathway, Focal adhesion, Regulation of actin cytoskeleton |
| 341 | 4.0E-05 | 1.2E-04 | 0.57 | 226188_at | HSPC159 | galectin-related protein |  |
| 498 | 1.8E-04 | 3.8E-04 | 0.57 | 219872_at | FAM198B | family with sequence similarity 198, member B | membrane & extracellular protein |
| 601 | 4.0E-04 | 7.1E-04 | 0.57 | 218458_at | GMCL1 | germ cell-less homolog 1 (Drosophila) | Nuclear protein |
| 165 | 5.7E-06 | 3.6E-05 | 0.56 | 220441_at | DNAJC22 | DnaJ (Hsp40) homolog, subfamily C, member 22 | membrane & extracellular protein |
| 320 | 3.5E-05 | 1.2E-04 | 0.56 | 1555097_a_at | PTGFR | prostaglandin F receptor (FP) | membrane & extracellular protein, Eicosanoid Metabolism, Calcium signaling pathway, Neuroactive ligand-receptor interaction |
| 434 | 9.5E-05 | 2.3E-04 | 0.56 | 201487_at | CTSC | cathepsin C | immunology |
| 463 | 1.2E-04 | 2.7E-04 | 0.56 | 227449_at | EPHA4 | EPH receptor A4 | membrane & extracellular protein, Eph Kinases and ephrins support platelet aggregation, Axon guidance, cell_cycle, cell_signaling, signal_transduction |
| 538 | 2.4E-04 | 4.7E-04 | 0.56 | 230875_s_at | ATP11A | ATPase, class VI, type 11A | membrane & extracellular protein |
| 621 | 4.8E-04 | 8.1E-04 | 0.56 | 235228_at | CCDC85A | coiled-coil domain containing 85A |  |

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| 684 | 8.1E-04 | 1.2E-03 | 0.56 | 234488_s_at | NA | NA | Nuclear protein |
| 215 | 1.3E-05 | 6.1E-05 | 0.55 | 221305_s_at | NA | NA | membrane & extracellular protein |
| 338 | 4.0E-05 | 1.2E-04 | 0.55 | 202237_at | NNMT | nicotinamide N-methyltransferase | Nicotinate and nicotinamide metabolism, immunology |
| 449 | 1.1E-04 | 2.5E-04 | 0.55 | 208753_s_at | NAP1L1 | nucleosome assembly protein 1-like 1 | Nuclear protein |
| 450 | 1.1E-04 | 2.6E-04 | 0.55 | 225646_at | CTSC | cathepsin C | immunology |
| 646 | 5.8E-04 | 9.4E-04 | 0.55 | 223721_s_at | DNAJC12 | DnaJ (Hsp40) homolog, subfamily C, member 12 | |
| 292 | 2.6E-05 | 9.6E-05 | 0.54 | 225136_at | PLEKHA2 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2 | membrane & extracellular protein, Nuclear protein |
| 392 | 6.3E-05 | 1.7E-04 | 0.54 | 206953_s_at | LPHN2 | latrophilin 2 | membrane & extracellular protein |
| 540 | 2.4E-04 | 4.7E-04 | 0.54 | 223827_at | TNFRSF19 | tumor necrosis factor receptor superfamily, member 19 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 549 | 2.5E-04 | 4.9E-04 | 0.54 | 206026_s_at | TNFAIP6 | tumor necrosis factor, alpha-induced protein 6 | immunology |
| 595 | 3.8E-04 | 6.8E-04 | 0.54 | 239443_at | PCDHB6 | protocadherin beta 6 | membrane & extracellular protein |

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| 620 | 4.7E-04 | 8.1E-04 | 0.54 | 241703_at | RUNDC3B | RUN domain containing 3B | |
| 683 | 8.1E-04 | 1.2E-03 | 0.54 | 205206_at | KAL1 | Kallmann syndrome 1 sequence | membrane & extracellular protein, immunology |
| 102 | 2.7E-06 | 2.8E-05 | 0.53 | 209772_s_at | CD24 | CD24 molecule | membrane & extracellular protein |
| 103 | 2.7E-06 | 2.8E-05 | 0.53 | 210026_s_at | CARD10 | caspase recruitment domain family, member 10 | |
| 141 | 4.1E-06 | 3.1E-05 | 0.53 | 203399_x_at | PSG3 | pregnancy specific beta-1-glycoprotein 3 | membrane & extracellular protein |
| 337 | 4.0E-05 | 1.2E-04 | 0.53 | 213199_at | C2CD3 | C2 calcium-dependent domain containing 3 | |
| 371 | 4.7E-05 | 1.4E-04 | 0.53 | 227812_at | TNFRSF19 | tumor necrosis factor receptor superfamily, member 19 | membrane & extracellular protein, Cytokine-cytokine receptor interaction |
| 374 | 4.9E-05 | 1.4E-04 | 0.53 | 235343_at | VASH2 | vasohibin 2 | |
| 378 | 5.3E-05 | 1.5E-04 | 0.53 | 230930_at | LOC338620 | hypothetical protein LOC338620 | |
| 389 | 6.0E-05 | 1.6E-04 | 0.53 | 226794_at | STXBP5 | syntaxin binding protein 5 (tomosyn) | membrane & extracellular protein |
| 458 | 1.1E-04 | 2.6E-04 | 0.53 | 222714_s_at | LACTB2 | lactamase, beta 2 | |
| 483 | 1.5E-04 | 3.2E-04 | 0.53 | 243818_at | SFTA1P | surfactant associated 1 (pseudogene) | |

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| 514 | 1.9E-04 | 4.0E-04 | 0.53 | 225647_s_at | CTSC | cathepsin C | immunology |
| 522 | 2.1E-04 | 4.2E-04 | 0.53 | 209815_at | PTCH1 | patched homolog 1 (Drosophila) | membrane & extracellular protein, Sonic Hedgehog (Shh) Pathway, Sonic Hedgehog (SHH) Receptor Ptc1 Regulates cell cycle, Hedgehog signaling pathway |
| 569 | 3.1E-04 | 5.8E-04 | 0.53 | 227669_at | BRP44 | brain protein 44 | |
| 571 | 3.2E-04 | 6.0E-04 | 0.53 | 228397_at | TUG1 | taurine upregulated 1 (non-protein coding) | |
| 624 | 4.9E-04 | 8.3E-04 | 0.53 | 206025_s_at | TNFAIP6 | tumor necrosis factor, alpha-induced protein 6 | immunology |
| 328 | 3.7E-05 | 1.2E-04 | 0.52 | 242301_at | CBLN2 | cerebellin 2 precursor | membrane & extracellular protein |
| 462 | 1.2E-04 | 2.7E-04 | 0.52 | 209377_s_at | HMGN3 | high mobility group nucleosomal binding domain 3 | |
| 467 | 1.3E-04 | 2.9E-04 | 0.52 | 205795_at | NRXN3 | neurexin 3 | membrane & extracellular protein, Synaptic Proteins at the Synaptic Junction, Cell adhesion molecules (CAMs) |
| 517 | 2.0E-04 | 4.0E-04 | 0.52 | 225664_at | COL12A1 | collagen, type XII, alpha 1 | membrane & extracellular protein |
| 229 | 1.4E-05 | 6.6E-05 | 0.51 | 225602_at | GLIPR2 | GLI pathogenesis-related 2 | membrane & extracellular protein |

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| 266 | 2.1E-05 | 8.2E-05 | 0.51 | 221697_at | MAP1LC3C | microtubule-associated protein 1 light chain 3 gamma | membrane & extracellular protein |
| 296 | 2.7E-05 | 9.6E-05 | 0.51 | 231882_at | FLJ39632 | hypothetical LOC642477 | |
| 332 | 3.7E-05 | 1.2E-04 | 0.51 | 215821_x_at | PSG3 | pregnancy specific beta-1-glycoprotein 3 | membrane & extracellular protein |
| 346 | 4.1E-05 | 1.3E-04 | 0.51 | 211828_s_at | TNIK | TRAF2 and NCK interacting kinase | |
| 380 | 5.4E-05 | 1.5E-04 | 0.51 | 225627_s_at | CACHD1 | cache domain containing 1 | membrane & extracellular protein |
| 403 | 6.9E-05 | 1.8E-04 | 0.51 | 218261_at | AP1M2 | adaptor-related protein complex 1, mu 2 subunit | membrane & extracellular protein |
| 426 | 8.6E-05 | 2.1E-04 | 0.51 | 201279_s_at | DAB2 | disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) | membrane & extracellular protein |
| 431 | 9.0E-05 | 2.2E-04 | 0.51 | 225241_at | CCDC80 | coiled-coil domain containing 80 | membrane & extracellular protein |
| 489 | 1.6E-04 | 3.4E-04 | 0.51 | 215321_at | RUNDC3B | RUN domain containing 3B | |
| 502 | 1.8E-04 | 3.9E-04 | 0.51 | 203158_s_at | GLS | glutaminase | D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, immunology |

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|---|---|---|---|---|---|---|---|
| 100 | 2.6E-06 | 2.8E-05 | 0.5 | 227550_at | GFRA1 | GDNF family receptor alpha 1 | membrane & extracellular protein |
| 105 | 2.8E-06 | 2.8E-05 | 0.5 | 212093_s_at | MTUS1 | microtubule associated tumor suppressor 1 | membrane & extracellular protein, Nuclear protein |
| 156 | 5.2E-06 | 3.5E-05 | 0.5 | 204984_at | GPC4 | glypican 4 | membrane & extracellular protein |
| 279 | 2.5E-05 | 9.3E-05 | 0.5 | 213882_at | TM2D1 | TM2 domain containing 1 | membrane & extracellular protein |
| 421 | 8.0E-05 | 2.0E-04 | 0.5 | 201309_x_at | C5orf13 | chromosome 5 open reading frame 13 | |
| 562 | 2.9E-04 | 5.4E-04 | 0.5 | 213183_s_at | CDKN1C | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | Nuclear protein, Cell cycle, cell_cycle, immunology, tsonc |
| 567 | 3.0E-04 | 5.6E-04 | 0.5 | 244183_x_at | PCDHB3 | protocadherin beta 3 | membrane & extracellular protein |
| 628 | 5.1E-04 | 8.6E-04 | 0.5 | 231726_at | PCDHB14 | protocadherin beta 14 | membrane & extracellular protein |
| 55 | 1.1E-06 | 2.1E-05 | 0.49 | 218574_s_at | LMCD1 | LIM and cysteine-rich domains 1 | Nuclear protein |
| 146 | 4.4E-06 | 3.2E-05 | 0.49 | 213307_at | SHANK2 | SH3 and multiple ankyrin repeat domains 2 | membrane & extracellular protein |
| 197 | 9.7E-06 | 5.2E-05 | 0.49 | 202017_at | EPHX1 | epoxide hydrolase 1, microsomal (xenobiotic) | membrane & extracellular protein, Eicosanoid Metabolism, Metabolism of xenobiotics by cytochrome P450, immunology, metabolism, pharmacology |

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|---|---|---|---|---|---|---|---|
| 228 | 1.4E-05 | 6.6E-05 | 0.49 | 218995_s_at | EDN1 | endothelin 1 | membrane & extracellular protein, Hypoxia-Inducible Factor in the Cardiovascular System, NFAT and Hypertrophy of the heart (Transcription in the broken heart), Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy, Neuroactive ligand-receptor interaction, development, immunology, misc |
| 238 | 1.6E-05 | 6.9E-05 | 0.49 | 236344_at | PDE1C | phosphodiesterase 1C, calmodulin-dependent 70kDa | Calcium signaling pathway, Olfactory transduction, Purine metabolism |
| 261 | 1.9E-05 | 7.6E-05 | 0.49 | 242546_at | FLJ39632 | hypothetical LOC642477 | |
| 364 | 4.6E-05 | 1.3E-04 | 0.49 | 206363_at | MAF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | Nuclear protein, tsonc |
| 390 | 6.0E-05 | 1.6E-04 | 0.49 | 201301_s_at | ANXA4 | annexin A4 | |
| 466 | 1.3E-04 | 2.9E-04 | 0.49 | 209426_s_at | AMACR | alpha-methylacyl-CoA racemase | membrane & extracellular protein |
| 505 | 1.9E-04 | 3.9E-04 | 0.49 | 204720_s_at | DNAJC6 | DnaJ (Hsp40) homolog, subfamily C, member 6 | |
| 591 | 3.7E-04 | 6.5E-04 | 0.49 | 218976_at | DNAJC12 | DnaJ (Hsp40) homolog, subfamily C, member 12 | |

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|---|---|---|---|---|---|---|---|
| 630 | 5.2E-04 | 8.8E-04 | 0.49 | 229327_s_at | MAF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | Nuclear protein, tsonc |
| 655 | 6.4E-04 | 1.0E-03 | 0.49 | 1554966_a_at | FILIP1L | filamin A interacting protein 1-like | membrane & extracellular protein |
| 671 | 7.6E-04 | 1.2E-03 | 0.49 | 229800_at | DCLK1 | doublecortin-like kinase 1 | membrane & extracellular protein |
| 54 | 1.0E-06 | 2.0E-05 | 0.48 | 228754_at | SLC6A6 | solute carrier family 6 (neurotransmitter transporter, taurine), member 6 | membrane & extracellular protein |
| 81 | 1.8E-06 | 2.2E-05 | 0.48 | 218660_at | DYSF | dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) | membrane & extracellular protein |
| 269 | 2.1E-05 | 8.3E-05 | 0.48 | 216627_s_at | B4GALT1 | UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer- Genes, Galactose metabolism, Glycan structures - biosynthesis 1, Glycan structures - biosynthesis 2, Glycosphingolipid biosynthesis - neo-lactoseries, Keratan sulfate biosynthesis, N-Glycan biosynthesis |

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|---|---|---|---|---|---|---|---|
| 300 | 2.8E-05 | 9.9E-05 | 0.48 | 227404_s_at | EGR1 | early growth response 1 | Nuclear protein, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, cell_cycle, cell_signaling, gene_regulation, immunology, transcription |
| 313 | 3.3E-05 | 1.1E-04 | 0.48 | 207808_s_at | PROS1 | protein S (alpha) | membrane & extracellular protein, Nuclear protein, Acute Myocardial Infarction, Extrinsic Prothrombin Activation Pathway, Intrinsic Prothrombin Activation Pathway, Complement and coagulation cascades, immunology |
| 398 | 6.5E-05 | 1.7E-04 | 0.48 | 201280_s_at | DAB2 | disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) | membrane & extracellular protein |
| 425 | 8.5E-05 | 2.1E-04 | 0.48 | 226225_at | MCC | mutated in colorectal cancers | immunology, tsonc |
| 437 | 9.9E-05 | 2.4E-04 | 0.48 | 223854_at | PCDHB10 | protocadherin beta 10 | membrane & extracellular protein |
| 547 | 2.5E-04 | 4.8E-04 | 0.48 | 221207_s_at | NBEA | neurobeachin | membrane & extracellular protein |
| 627 | 5.1E-04 | 8.6E-04 | 0.48 | 243864_at | CCDC80 | coiled-coil domain containing 80 | membrane & extracellular protein |
| 57 | 1.2E-06 | 2.1E-05 | 0.47 | 226071_at | ADAMTSL4 | ADAMTS-like 4 | membrane & extracellular protein |
| 104 | 2.8E-06 | 2.8E-05 | 0.47 | 219304_s_at | PDGFD | platelet derived growth factor D | membrane & extracellular protein, Focal adhesion, Gap junction |

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| 108 | 3.0E-06 | 2.9E-05 | 0.47 | 209994_s_at | NA | NA | membrane & extracellular protein |
| 158 | 5.3E-06 | 3.5E-05 | 0.47 | 206517_at | CDH16 | cadherin 16, KSP-cadherin | membrane & extracellular protein |
| 295 | 2.7E-05 | 9.6E-05 | 0.47 | 229978_at | SHISA9 | shisa homolog 9 (Xenopus laevis) | |
| 419 | 7.9E-05 | 2.0E-04 | 0.47 | 226439_s_at | NBEA | neurobeachin | membrane & extracellular protein |
| 578 | 3.3E-04 | 6.0E-04 | 0.47 | 221747_at | TNS1 | tensin 1 | Integrin Signaling Pathway |
| 695 | 9.3E-04 | 1.4E-03 | 0.47 | 218162_at | OLFML3 | olfactomedin-like 3 | membrane & extracellular protein |
| 67 | 1.4E-06 | 2.1E-05 | 0.46 | 213974_at | ADAMTSL3 | ADAMTS-like 3 | membrane & extracellular protein |
| 127 | 3.6E-06 | 3.0E-05 | 0.46 | 225817_at | CGNL1 | cingulin-like 1 | |
| 128 | 3.6E-06 | 3.0E-05 | 0.46 | 223737_x_at | CHST9 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 | membrane & extracellular protein, Cysteine metabolism |
| 136 | 4.0E-06 | 3.1E-05 | 0.46 | 215425_at | BTG3 | BTG family, member 3 | Perou's- Intrinsic- Breast-Cancer-Genes |
| 212 | 1.2E-05 | 6.1E-05 | 0.46 | 207020_at | HSF2BP | heat shock transcription factor 2 binding protein | |
| 289 | 2.6E-05 | 9.5E-05 | 0.46 | 225968_at | PRICKLE2 | prickle homolog 2 (Drosophila) | membrane & extracellular protein, Nuclear protein, Wnt signaling pathway |
| 314 | 3.3E-05 | 1.1E-04 | 0.46 | 204579_at | FGFR4 | fibroblast growth factor receptor 4 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, MAPK signaling pathway, Regulation of actin cytoskeleton, development, misc |

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| 395 | 6.4E-05 | 1.7E-04 | 0.46 | 201278_at | DAB2 | disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) | membrane & extracellular protein |
| 616 | 4.6E-04 | 7.9E-04 | 0.46 | 202746_at | ITM2A | integral membrane protein 2A | membrane & extracellular protein |
| 33 | 6.0E-07 | 1.7E-05 | 0.45 | 203126_at | IMPA2 | inositol(myo)-1(or 4)-monophosphatase 2 | Inositol phosphate metabolism, Phosphatidylinositol signaling system, Streptomycin biosynthesis |
| 46 | 9.0E-07 | 1.9E-05 | 0.45 | 213171_s_at | MMP24 | matrix metallopeptidase 24 (membrane-inserted) | membrane & extracellular protein |
| 51 | 9.0E-07 | 1.9E-05 | 0.45 | 209993_at | ABCB1 | ATP-binding cassette, sub-family B (MDR/TAP), member 1 | membrane & extracellular protein, Hypoxia and p53 in the Cardiovascular system, Multi-Drug Resistance Factors, Nuclear Receptors in Lipid Metabolism and Toxicity |
| 214 | 1.2E-05 | 6.1E-05 | 0.45 | 225604_s_at | GLIPR2 | GLI pathogenesis-related 2 | membrane & extracellular protein |
| 232 | 1.4E-05 | 6.6E-05 | 0.45 | 223449_at | SEMA6A | sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A | membrane & extracellular protein, Axon guidance |

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| 235 | 1.5E-05 | 6.7E-05 | 0.45 | 222802_at | EDN1 | endothelin 1 | membrane & extracellular protein, Hypoxia-Inducible Factor in the Cardiovascular System, NFAT and Hypertrophy of the heart (Transcription in the broken heart), Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy, Neuroactive ligand-receptor interaction, development, immunology, misc |
| 237 | 1.5E-05 | 6.9E-05 | 0.45 | 218807_at | VAV3 | vav 3 guanine nucleotide exchange factor | B cell receptor signaling pathway, Fc epsilon RI signaling pathway, Focal adhesion, Leukocyte transendothelial migration, Natural killer cell mediated cytotoxicity, Regulation of actin cytoskeleton, T cell receptor signaling pathway |
| 479 | 1.4E-04 | 3.1E-04 | 0.45 | 219619_at | DIRAS2 | DIRAS family, GTP-binding RAS-like 2 | membrane & extracellular protein |
| 543 | 2.4E-04 | 4.8E-04 | 0.45 | 212192_at | KCTD12 | potassium channel tetramerisation domain containing 12 | membrane & extracellular protein |
| 582 | 3.5E-04 | 6.3E-04 | 0.45 | 209425_at | AMACR | alpha-methylacyl-CoA racemase | membrane & extracellular protein |
| 60 | 1.2E-06 | 2.1E-05 | 0.44 | 239093_at | DHDPSL | dihydrodipicolinate synthase-like, mitochondrial | |

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| 139 | 4.1E-06 | 3.1E-05 | 0.44 | 213227_at | PGRMC2 | progesterone receptor membrane component 2 | membrane & extracellular protein |
| 143 | 4.2E-06 | 3.1E-05 | 0.44 | 203157_s_at | GLS | glutaminase | D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, immunology |
| 213 | 1.2E-05 | 6.1E-05 | 0.44 | 217677_at | PLEKHA2 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2 | membrane & extracellular protein, Nuclear protein |
| 327 | 3.6E-05 | 1.2E-04 | 0.44 | 238013_at | PLEKHA2 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2 | membrane & extracellular protein, Nuclear protein |
| 575 | 3.3E-04 | 6.0E-04 | 0.44 | 205499_at | SRPX2 | sushi-repeat-containing protein, X-linked 2 | membrane & extracellular protein |
| 693 | 9.0E-04 | 1.4E-03 | 0.44 | 230432_at | LOC553137 | hypothetical LOC553137 | |
| 124 | 3.5E-06 | 2.9E-05 | 0.43 | 243951_at | ABCB1 | ATP-binding cassette, sub-family B (MDR/TAP), member 1 | membrane & extracellular protein, Hypoxia and p53 in the Cardiovascular system, Multi-Drug Resistance Factors, Nuclear |

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|  |  |  |  |  |  |  | Receptors in Lipid Metabolism and Toxicity |
| 167 | 5.9E-06 | 3.7E-05 | 0.43 | 224400_s_at | CHST9 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 | membrane & extracellular protein, Cysteine metabolism |
| 192 | 8.6E-06 | 4.7E-05 | 0.43 | 201302_at | ANXA4 | annexin A4 |  |
| 220 | 1.3E-05 | 6.3E-05 | 0.43 | 207052_at | HAVCR1 | hepatitis A virus cellular receptor 1 | membrane & extracellular protein |
| 298 | 2.8E-05 | 9.9E-05 | 0.43 | 205602_x_at | PSG7 | pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene) | membrane & extracellular protein |
| 373 | 4.9E-05 | 1.4E-04 | 0.43 | 220014_at | PRR16 | proline rich 16 |  |
| 499 | 1.8E-04 | 3.8E-04 | 0.43 | 219534_x_at | CDKN1C | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | Nuclear protein, Cell cycle, cell_cycle, immunology, tsonc |
| 526 | 2.1E-04 | 4.3E-04 | 0.43 | 221916_at | NEFL | neurofilament, light polypeptide | Amyotrophic lateral sclerosis (ALS) |
| 581 | 3.4E-04 | 6.3E-04 | 0.43 | 209866_s_at | LPHN3 | latrophilin 3 | membrane & extracellular protein |
| 593 | 3.7E-04 | 6.6E-04 | 0.43 | 232099_at | PCDHB16 | protocadherin beta 16 | membrane & extracellular protein |
| 86 | 1.9E-06 | 2.3E-05 | 0.42 | 205920_at | SLC6A6 | solute carrier family 6 (neurotransmitter transporter, taurine), member 6 | membrane & extracellular protein |

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| 122 | 3.4E-06 | 2.9E-05 | 0.42 | 235670_at | STX11 | syntaxin 11 | membrane & extracellular protein, SNARE interactions in vesicular transport |
| 178 | 6.7E-06 | 4.0E-05 | 0.42 | 212614_at | ARID5B | AT rich interactive domain 5B (MRF1-like) | Nuclear protein |
| 188 | 8.3E-06 | 4.6E-05 | 0.42 | 224221_s_at | VAV3 | vav 3 guanine nucleotide exchange factor | B cell receptor signaling pathway, Fc epsilon RI signaling pathway, Focal adhesion, Leukocyte transendothelial migration, Natural killer cell mediated cytotoxicity, Regulation of actin cytoskeleton, T cell receptor signaling pathway |
| 303 | 2.9E-05 | 1.0E-04 | 0.42 | 212099_at | RHOB | ras homolog gene family, member B | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes |
| 319 | 3.5E-05 | 1.2E-04 | 0.42 | 210195_s_at | PSG1 | pregnancy specific beta-1-glycoprotein 1 | membrane & extracellular protein |
| 372 | 4.8E-05 | 1.4E-04 | 0.42 | 235836_at | MXRA7 | matrix-remodelling associated 7 | membrane & extracellular protein |
| 387 | 5.9E-05 | 1.6E-04 | 0.42 | 212148_at | PBX1 | pre-B-cell leukemia homeobox 1 | Nuclear protein, development, gene_regulation, transcription |
| 424 | 8.4E-05 | 2.1E-04 | 0.42 | 204475_at | MMP1 | matrix metallopeptidase 1 (interstitial collagenase) | membrane & extracellular protein, PPAR signaling pathway, angiogenesis |

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| 548 | 2.5E-04 | 4.8E-04 | 0.42 | 206290_s_at | RGS7 | regulator of G-protein signaling 7 | Nuclear protein, cell_signaling, signal_transduction |
| 608 | 4.2E-04 | 7.4E-04 | 0.42 | 225660_at | SEMA6A | sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A | membrane & extracellular protein, Axon guidance |
| 76 | 1.6E-06 | 2.2E-05 | 0.41 | 203159_at | GLS | glutaminase | D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, immunology |
| 97 | 2.5E-06 | 2.7E-05 | 0.41 | 225606_at | BCL2L11 | BCL2-like 11 (apoptosis facilitator) | membrane & extracellular protein |
| 199 | 9.9E-06 | 5.3E-05 | 0.41 | 209365_s_at | ECM1 | extracellular matrix protein 1 | membrane & extracellular protein |
| 315 | 3.3E-05 | 1.1E-04 | 0.41 | 218701_at | LACTB2 | lactamase, beta 2 | |
| 379 | 5.3E-05 | 1.5E-04 | 0.41 | 229649_at | NRXN3 | neurexin 3 | membrane & extracellular protein, Synaptic Proteins at the Synaptic Junction, Cell adhesion molecules (CAMs) |
| 460 | 1.2E-04 | 2.7E-04 | 0.41 | 1553962_s_at | RHOB | ras homolog gene family, member B | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes |
| 528 | 2.2E-04 | 4.4E-04 | 0.41 | 203951_at | CNN1 | calponin 1, basic, smooth muscle | |
| 607 | 4.2E-04 | 7.3E-04 | 0.41 | 209230_s_at | NUPR1 | nuclear protein, transcriptional | Nuclear protein |

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|  |  |  |  |  |  | regulator, 1 |  |
| 130 | 3.7E-06 | 3.0E-05 | 0.4 | 243681_at | SHANK2 | SH3 and multiple ankyrin repeat domains 2 | membrane & extracellular protein |
| 179 | 6.8E-06 | 4.0E-05 | 0.4 | 208106_x_at | PSG6 | pregnancy specific beta-1-glycoprotein 6 | membrane & extracellular protein |
| 396 | 6.5E-05 | 1.7E-04 | 0.4 | 212188_at | KCTD12 | potassium channel tetramerisation domain containing 12 | membrane & extracellular protein |
| 577 | 3.3E-04 | 6.0E-04 | 0.4 | 244852_at | DSEL | dermatan sulfate epimerase-like | membrane & extracellular protein |
| 15 | 1.0E-07 | 6.6E-06 | 0.39 | 208998_at | UCP2 | uncoupling protein 2 (mitochondrial, proton carrier) | membrane & extracellular protein, immunology, misc |
| 30 | 3.0E-07 | 1.1E-05 | 0.39 | 218806_s_at | VAV3 | vav 3 guanine nucleotide exchange factor | B cell receptor signaling pathway, Fc epsilon RI signaling pathway, Focal adhesion, Leukocyte transendothelial migration, Natural killer cell mediated cytotoxicity, Regulation of actin cytoskeleton, T cell receptor signaling pathway |
| 163 | 5.5E-06 | 3.6E-05 | 0.39 | 212157_at | SDC2 | syndecan 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer- Genes, Cell adhesion molecules (CAMs), ECM-receptor interaction, |

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| | | | | | | | angiogenesis, metastasis |
| 216 | 1.3E-05 | 6.3E-05 | 0.39 | 205405_at | SEMA5A | sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A | membrane & extracellular protein, Axon guidance |
| 249 | 1.7E-05 | 7.2E-05 | 0.39 | 213169_at | SEMA5A | sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A | membrane & extracellular protein, Axon guidance |
| 415 | 7.8E-05 | 2.0E-04 | 0.39 | 203786_s_at | TPD52L1 | tumor protein D52-like 1 | |
| 632 | 5.3E-04 | 8.9E-04 | 0.39 | 225242_s_at | CCDC80 | coiled-coil domain containing 80 | membrane & extracellular protein |
| 225 | 1.4E-05 | 6.6E-05 | 0.38 | 231738_at | PCDHB7 | protocadherin beta 7 | membrane & extracellular protein |

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| 240 | 1.6E-05 | 7.0E-05 | 0.38 | 227095_at | LEPR | leptin receptor | Reversal of Insulin Resistance by Leptin, Adipocytokine signaling pathway, Cytokine-cytokine receptor interaction, Jak-STAT signaling pathway, Neuroactive ligand-receptor interaction, immunology |
| 287 | 2.6E-05 | 9.5E-05 | 0.38 | 209348_s_at | MAF | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | Nuclear protein, tsonc |
| 480 | 1.4E-04 | 3.1E-04 | 0.38 | 213182_x_at | CDKN1C | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | Nuclear protein, Cell cycle, cell_cycle, immunology, tsonc |
| 14 | 1.0E-07 | 6.6E-06 | 0.37 | 49077_at | PPME1 | protein phosphatase methylesterase 1 | 2,4-Dichlorobenzoate degradation, Alkaloid biosynthesis II, Butanoate metabolism |
| 95 | 2.5E-06 | 2.7E-05 | 0.37 | 205533_s_at | CDH6 | cadherin 6, type 2, K-cadherin (fetal kidney) | membrane & extracellular protein, Nuclear protein |
| 140 | 4.1E-06 | 3.1E-05 | 0.37 | 213624_at | SMPDL3A | sphingomyelin phosphodiesterase, acid-like 3A | membrane & extracellular protein |
| 203 | 1.1E-05 | 5.5E-05 | 0.37 | 210372_s_at | TPD52L1 | tumor protein D52-like 1 | |
| 272 | 2.3E-05 | 8.7E-05 | 0.37 | 213348_at | CDKN1C | cyclin-dependent kinase inhibitor 1C (p57, Kip2) | Nuclear protein, Cell cycle, cell_cycle, immunology, tsonc |

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| 274 | 2.3E-05 | 8.9E-05 | 0.37 | 230163_at | GFRA1 | GDNF family receptor alpha 1 | membrane & extracellular protein |
| 311 | 3.2E-05 | 1.1E-04 | 0.37 | 229427_at | SEMA5A | sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A | membrane & extracellular protein, Axon guidance |
| 675 | 7.8E-04 | 1.2E-03 | 0.37 | 206167_s_at | ARHGAP6 | Rho GTPase activating protein 6 | Rho cell motility signaling pathway |
| 28 | 3.0E-07 | 1.1E-05 | 0.36 | 1555716_a_at | CXADR | coxsackie virus and adenovirus receptor | membrane & extracellular protein |
| 47 | 9.0E-07 | 1.9E-05 | 0.36 | 205921_s_at | SLC6A6 | solute carrier family 6 (neurotransmitter transporter, taurine), member 6 | membrane & extracellular protein |
| 181 | 7.1E-06 | 4.1E-05 | 0.36 | 202458_at | PRSS23 | protease, serine, 23 | membrane & extracellular protein, Nuclear protein, Perou's- Intrinsic-Breast-Cancer-Genes |
| 184 | 7.6E-06 | 4.4E-05 | 0.36 | 208257_x_at | PSG1 | pregnancy specific beta-1-glycoprotein 1 | membrane & extracellular protein |

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| 307 | 3.1E-05 | 1.1E-04 | 0.36 | 207298_at | SLC17A3 | solute carrier family 17 (sodium phosphate), member 3 | membrane & extracellular protein |
| 363 | 4.5E-05 | 1.3E-04 | 0.36 | 228821_at | ST6GAL2 | ST6 beta-galactosamide alpha-2,6-sialyltranferase 2 | membrane & extracellular protein |
| 391 | 6.1E-05 | 1.7E-04 | 0.36 | 232654_s_at | NA | NA | membrane & extracellular protein |
| 448 | 1.1E-04 | 2.5E-04 | 0.36 | 227190_at | TMEM37 | transmembrane protein 37 | membrane & extracellular protein |
| 618 | 4.7E-04 | 8.0E-04 | 0.36 | 204259_at | MMP7 | matrix metallopeptidase 7 (matrilysin, uterine) | membrane & extracellular protein, Wnt signaling pathway, immunology |
| 107 | 2.9E-06 | 2.9E-05 | 0.35 | 228602_at | SGCD | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) | membrane & extracellular protein, immunology |
| 114 | 3.1E-06 | 2.9E-05 | 0.35 | 225671_at | SPNS2 | spinster homolog 2 (Drosophila) | membrane & extracellular protein |
| 283 | 2.5E-05 | 9.5E-05 | 0.35 | 225496_s_at | SYTL2 | synaptotagmin-like 2 | membrane & extracellular protein |
| 465 | 1.3E-04 | 2.9E-04 | 0.35 | 232914_s_at | SYTL2 | synaptotagmin-like 2 | membrane & extracellular protein |
| 495 | 1.7E-04 | 3.6E-04 | 0.35 | 228221_at | SLC44A3 | solute carrier family 44, member 3 | membrane & extracellular protein |

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| 64 | 1.3E-06 | 2.1E-05 | 0.34 | 223732_at | SLC23A1 | solute carrier family 23 (nucleobase transporters), member 1 | membrane & extracellular protein, Vitamin C in the Brain |
| 40 | 7.0E-07 | 1.8E-05 | 0.33 | 229441_at | PRSS23 | protease, serine, 23 | membrane & extracellular protein, Nuclear protein, Perou's- Intrinsic-Breast-Cancer-Genes |
| 82 | 1.8E-06 | 2.2E-05 | 0.33 | 227276_at | PLXDC2 | plexin domain containing 2 | membrane & extracellular protein |
| 94 | 2.3E-06 | 2.6E-05 | 0.33 | 203917_at | CXADR | coxsackie virus and adenovirus receptor | membrane & extracellular protein |
| 118 | 3.3E-06 | 2.9E-05 | 0.33 | 201212_at | LGMN | legumain | membrane & extracellular protein, Antigen processing and presentation |
| 126 | 3.5E-06 | 2.9E-05 | 0.33 | 203570_at | LOXL1 | lysyl oxidase-like 1 | membrane & extracellular protein, Arginine and proline metabolism |
| 254 | 1.8E-05 | 7.4E-05 | 0.33 | 229271_x_at | COL11A1 | collagen, type XI, alpha 1 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 343 | 4.1E-05 | 1.3E-04 | 0.33 | 223204_at | FAM198B | family with sequence similarity 198, member B | membrane & extracellular protein |
| 350 | 4.2E-05 | 1.3E-04 | 0.33 | 221748_s_at | TNS1 | tensin 1 | Integrin Signaling Pathway |
| 408 | 7.3E-05 | 1.9E-04 | 0.33 | 227598_at | C7orf29 | chromosome 7 open reading frame 29 | |
| 454 | 1.1E-04 | 2.6E-04 | 0.33 | 214587_at | COL8A1 | collagen, type VIII, alpha 1 | membrane & extracellular protein |

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| 512 | 1.9E-04 | 4.0E-04 | 0.33 | 221805_at | NEFL | neurofilament, light polypeptide | Amyotrophic lateral sclerosis (ALS) |
| 294 | 2.7E-05 | 9.6E-05 | 0.32 | 205696_s_at | GFRA1 | GDNF family receptor alpha 1 | membrane & extracellular protein |
| 18 | 2.0E-07 | 8.8E-06 | 0.31 | 217841_s_at | PPME1 | protein phosphatase methylesterase 1 | 2,4-Dichlorobenzoate degradation, Alkaloid biosynthesis II, Butanoate metabolism |
| 88 | 2.1E-06 | 2.5E-05 | 0.31 | 1556499_s_at | COL1A1 | collagen, type I, alpha 1 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion, immunology |
| 111 | 3.0E-06 | 2.9E-05 | 0.31 | 235774_at | LOC553137 | hypothetical LOC553137 | |
| 191 | 8.3E-06 | 4.6E-05 | 0.31 | 214606_at | TSPAN2 | tetraspanin 2 | membrane & extracellular protein |
| 440 | 1.0E-04 | 2.5E-04 | 0.31 | 206969_at | KRT34 | keratin 34 | Cell Communication |
| 110 | 3.0E-06 | 2.9E-05 | 0.3 | 229657_at | THRB | thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) | Nuclear protein, Map Kinase Inactivation of SMRT Corepressor, Neuroactive ligand-receptor interaction, immunology, tsonc |
| 174 | 6.4E-06 | 3.9E-05 | 0.3 | 219250_s_at | FLRT3 | fibronectin leucine rich transmembrane protein 3 | membrane & extracellular protein |
| 233 | 1.5E-05 | 6.7E-05 | 0.3 | 209738_x_at | PSG6 | pregnancy specific beta-1-glycoprotein 6 | membrane & extracellular protein |

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| 310 | 3.2E-05 | 1.1E-04 | 0.3 | 222071_s_at | SLCO4C1 | solute carrier organic anion transporter family, member 4C1 | membrane & extracellular protein |
| 344 | 4.1E-05 | 1.3E-04 | 0.3 | 1559459_at | LOC613266 | hypothetical LOC613266 | |
| 13 | 1.0E-07 | 6.6E-06 | 0.29 | 204437_s_at | FOLR1 | folate receptor 1 (adult) | membrane & extracellular protein, immunology |
| 78 | 1.7E-06 | 2.2E-05 | 0.29 | 226279_at | PRSS23 | protease, serine, 23 | membrane & extracellular protein, Nuclear protein, Perou's- Intrinsic-Breast-Cancer-Genes |
| 669 | 7.5E-04 | 1.2E-03 | 0.29 | 204988_at | FGB | fibrinogen beta chain | membrane & extracellular protein, Nuclear protein, Acute Myocardial Infarction, Extrinsic Prothrombin Activation Pathway, Fibrinolysis Pathway, Intrinsic Prothrombin Activation Pathway, Complement and coagulation cascades, immunology |
| 8 | < 1e-07 | < 1e-07 | 0.28 | 205380_at | PDZK1 | PDZ domain containing 1 | membrane & extracellular protein, Downregulated of MTA-3 in ER-negative Breast Tumors |
| 73 | 1.6E-06 | 2.2E-05 | 0.28 | 228716_at | THRB | thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) | Nuclear protein, Map Kinase Inactivation of SMRT Corepressor, Neuroactive ligand-receptor interaction, immunology, tsonc |

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| 98 | 2.6E-06 | 2.8E-05 | 0.28 | 219479_at | KDELC1 | KDEL (Lys-Asp-Glu-Leu) containing 1 | |
| 353 | 4.2E-05 | 1.3E-04 | 0.28 | 217478_s_at | NA | NA | membrane & extracellular protein |
| 44 | 9.0E-07 | 1.9E-05 | 0.27 | 212154_at | SDC2 | syndecan 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Cell adhesion molecules (CAMs), ECM-receptor interaction, angiogenesis, metastasis |
| 280 | 2.5E-05 | 9.4E-05 | 0.27 | 209594_x_at | PSG9 | pregnancy specific beta-1-glycoprotein 9 | membrane & extracellular protein |
| 510 | 1.9E-04 | 4.0E-04 | 0.27 | 232235_at | DSEL | dermatan sulfate epimerase-like | membrane & extracellular protein |
| 545 | 2.5E-04 | 4.8E-04 | 0.27 | 216238_s_at | FGB | fibrinogen beta chain | membrane & extracellular protein, Acute Myocardial Infarction, Extrinsic Prothrombin Activation Pathway, Fibrinolysis Pathway, Intrinsic Prothrombin Activation Pathway, Complement and coagulation cascades, immunology |
| 48 | 9.0E-07 | 1.9E-05 | 0.26 | 227236_at | TSPAN2 | tetraspanin 2 | membrane & extracellular protein |
| 91 | 2.2E-06 | 2.5E-05 | 0.26 | 212158_at | SDC2 | syndecan 2 | membrane & extracellular protein, Perou's- Intrinsic- Breast-Cancer-Genes, Cell adhesion molecules (CAMs), ECM-receptor interaction, angiogenesis, metastasis |

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| 176 | 6.6E-06 | 4.0E-05 | 0.26 | 212094_at | PEG10 | paternally expressed 10 | Nuclear protein |
| 258 | 1.9E-05 | 7.6E-05 | 0.26 | 204320_at | COL11A1 | collagen, type XI, alpha 1 | membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 264 | 2.0E-05 | 8.0E-05 | 0.26 | 221541_at | CRISPLD2 | cysteine-rich secretory protein LCCL domain containing 2 | membrane & extracellular protein |
| 367 | 4.6E-05 | 1.3E-04 | 0.26 | 1569777_a_at | ZPLD1 | zona pellucida-like domain containing 1 | membrane & extracellular protein |
| 412 | 7.6E-05 | 2.0E-04 | 0.26 | 227195_at | ZNF503 | zinc finger protein 503 | Nuclear protein |
| 19 | 2.0E-07 | 8.8E-06 | 0.25 | 232206_at | ULK4 | unc-51-like kinase 4 (C. elegans) | |
| 147 | 4.5E-06 | 3.2E-05 | 0.25 | 222853_at | FLRT3 | fibronectin leucine rich transmembrane protein 3 | membrane & extracellular protein |
| 182 | 7.2E-06 | 4.2E-05 | 0.25 | 208191_x_at | PSG4 | pregnancy specific beta-1-glycoprotein 4 | membrane & extracellular protein |
| 72 | 1.6E-06 | 2.2E-05 | 0.24 | 209493_at | PDZD2 | PDZ domain containing 2 | membrane & extracellular protein, Nuclear protein |
| 376 | 5.2E-05 | 1.5E-04 | 0.24 | 202435_s_at | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | membrane & extracellular protein, Metabolism of xenobiotics by cytochrome P450, Tryptophan metabolism, immunology, |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | | | | | | pharmacology |
| 58 | 1.2E-06 | 2.1E-05 | 0.23 | 227233_at | TSPAN2 | tetraspanin 2 | membrane & extracellular protein |
| 257 | 1.9E-05 | 7.6E-05 | 0.23 | 202436_s_at | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | membrane & extracellular protein, Metabolism of xenobiotics by cytochrome P450, Tryptophan metabolism, immunology, pharmacology |
| 470 | 1.3E-04 | 3.0E-04 | 0.23 | 230217_at | CLVS1 | clavesin 1 | |
| 493 | 1.7E-04 | 3.6E-04 | 0.23 | 1561969_at | ZPLD1 | zona pellucida-like domain containing 1 | membrane & extracellular protein |
| 61 | 1.3E-06 | 2.1E-05 | 0.22 | 206070_s_at | EPHA3 | EPH receptor A3 | membrane & extracellular protein, Axon guidance, immunology, tsonc |
| 150 | 4.8E-06 | 3.4E-05 | 0.22 | 212651_at | RHOBTB1 | Rho-related BTB domain containing 1 | |
| 116 | 3.2E-06 | 2.9E-05 | 0.21 | 232752_at | LOC100287616 | hypothetical protein LOC100287616 | |
| 129 | 3.6E-06 | 3.0E-05 | 0.21 | 223928_s_at | GUCA1C | guanylate cyclase activator 1C | Olfactory transduction |
| 25 | 3.0E-07 | 1.1E-05 | 0.2 | 223075_s_at | AIF1L | allograft inflammatory factor 1-like | |
| 87 | 2.1E-06 | 2.5E-05 | 0.2 | 212092_at | PEG10 | paternally expressed 10 | Nuclear protein |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 256 | 1.8E-05 | 7.6E-05 | 0.2 | 37892_at | COL11A1 | collagen, type XI, alpha 1 | FGF18, membrane & extracellular protein, Cell Communication, ECM-receptor interaction, Focal adhesion |
| 224 | 1.4E-05 | 6.5E-05 | 0.19 | 205818_at | DBC1 | deleted in bladder cancer 1 | |
| 429 | 8.7E-05 | 2.2E-04 | 0.19 | 202437_s_at | CYP1B1 | cytochrome P450, family 1, subfamily B, polypeptide 1 | membrane & extracellular protein, Metabolism of xenobiotics by cytochrome P450, Tryptophan metabolism, immunology, pharmacology |
| 123 | 3.4E-06 | 2.9E-05 | 0.18 | 202350_s_at | MATN2 | matrilin 2 | membrane & extracellular protein |
| 75 | 1.6E-06 | 2.2E-05 | 0.16 | 213800_at | CFH | complement factor H | membrane & extracellular protein, Complement and coagulation cascades |
| 79 | 1.7E-06 | 2.2E-05 | 0.16 | 215388_s_at | NA | NA | membrane & extracellular protein |
| 20 | 2.0E-07 | 8.8E-06 | 0.15 | 204830_x_at | PSG5 | pregnancy specific beta-1-glycoprotein 5 | membrane & extracellular protein |
| 330 | 3.7E-05 | 1.2E-04 | 0.15 | 214930_at | SLITRK5 | SLIT and NTRK-like family, member 5 | membrane & extracellular protein |
| 39 | 7.0E-07 | 1.8E-05 | 0.12 | 231867_at | ODZ2 | odz, odd Oz/ten-m homolog 2 (Drosophila) | membrane & extracellular protein |
| 12 | 1.0E-07 | 6.6E-06 | 0.07 | 1555564_a_at | CFI | complement factor I | membrane & extracellular protein, Nuclear protein, Complement and coagulation cascades |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 27 | 3.0E-07 | 1.1E-05 | 0.06 | 203854_at | CFI | complement factor I | membrane & extracellular protein, Nuclear protein, Complement and coagulation cascades |
| 362 | 4.5E-05 | 1.3E-04 | 0.058 | 1560851_at | C10orf136 | chromosome 10 open reading frame 136 | |

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**Filtering parameters:**

Name of the project file: A224 FGF18 -Project -JustRMA.xls
Time of the analysis: Sat Dec 25 13:11:54 2010
BRB-ArrayTools Version: 4.1.0 - Beta_3 Release (October 2010)
Project annotated by Bioconductor (www.bioconductor.org) Dec 23 14:07:46 2010
annotation package hgu133plus2.db(Version:2.4.1) on Thu

**Spot Filters: OFF**

**Normalization: OFF**

**Exclude a gene under any of the following conditions:**
Less than 20 % of expression data have at least a 1.5 -fold change in either direction from gene's median value
Percent of data missing or filtered out exceeds 50 %

**Gene Subsets: OFF**

**Table S5. Primers for quantitative RT-PCR (5’-3’).**

| | Forward | Reverse |
|---|---|---|
| FGF18[#] | GACCTCCCGACGACAGAC | GATAGCAGCATCCTCCAGAACT |
| GAPDH[#] | ACCCACTCCTCCACCTTTG | CACCACCCTGTTGCTGTAG |
| PPIA3[#] | GCTTGCTGGCAGTTAGATGTC | AAATCCGCCACCTCTAGGATA |
| FGF18 | TGCTTCCAGGTACAGGTGCT | GCTGCTTACGGCTCACATCG |
| AREG | ACGAACCACAAATACCTGGC | TTTCACTTTCCGTCTTGTTTTG |
| PLAT | CTGGAGAGAAAACCTCTGCG | GCAGAGCCCTCTCTTCATTG |
| PLAU | TGACCCACAGTGGAAAACAG | CCAGCTCACAATTCCAGTCA |
| HMGA2 | AAAGCAGAAGCCACTGGAGA | TCTTCGGCAGACTCTTGTGA |
| CXCL1 | GAAAGCTTGCCTCAATCCTG | CTTCCTCCTCCCTTCTGGTC |
| CXCL2 | GGGCAGAAAGCTTGTCTCAA | GCTTCCTCCTTCCTTCTGGT |
| IL1A | TGTGACTGCCCAAGATGAAG | CTTAGTGCCGTGAGTTTCCC |
| IL6 | GCCACTCACCTCTTCAGAAC | TGCCTCTTTGCTGCTTTCA |
| IL8 | TCCTGATTTCTGCAGCTCTGT | AAATTTGGGGTGGAAAGGTT |
| VEGFC | TGTGTCCGTCTACAGATGT | GGCAGGAAGTGTGATTGG |
| TGM2 | TCAGCTACAATGGGATCTTGG | CCGTAAGGCAGTCACGGTAT |
| CD73 | ACTTCATGAACGCCCTGC | TTGGAAATTTGGCCTCTTTG |
| CFH | GCTGGTCTCCTACTCCCAGA | TTCGCTTTTTCTTTTAAGGCA |
| CFI | GTGCTTCCACTTAAGGTTTTGC | TGGCAGAAGACTTTATCGCA |
| MMP2 | ATGCCGCCTTTAACTGGAG | GGGAAGCCAGGATCCATTTT |
| MMP9 | GGGACGCAGACATCGTCATC | TCGTCATCGTCGAAATGGGC |
| VEGFA | CACGAAGTGGTGAAGTTC | AGGATGGCTTGAAGATGT |
| IL10 | GCTGTCATCGATTTCTTCCC | CTCATGGCTTTGTAGATGCCT |
| IL12A | TCAGCAACATGCTCCAGAAG | CCTCCACTGTGCTGGTTTTAT |
| IL1B | GAAGCTGATGGCCCTAAACA | AAGCCCTTGCTGTAGTGGTG |
| CCL2 | GTCTCTGCCGCCCTTCTGTG | AGGTGACTGGGGCATTGATTG |
| FGFR1 | GTCACAGCCACACTCTGCAC | GGAAGGACTCCACTTCCACA |
| FGFR2 | CGGCCCTCCTTCAGTTTAGT | CGCAGCCACGTACACTTCT |
| FGFR3 | GTCCTTGGGGACGGAGC | TCAGCTCCACAGCATCCC |
| FGFR4 | CTGACCAAGCCAGCACTGT | CTTCATCACCTCCATCTCCG |
| GAPDH | GAAGGTGAAGGTCGGAGTC | CATGTAGTTGAGGTCAATGAAGG |
| PPIA | CACCGTGTTCTTCGACATTG | TCCTTTCTCTCCAGTGCTCAG |
| ACTB | GCACAGAGCCTCGCCTT | GTTGTCGACGACGAGCG |

# Primers used for microarray validation (the 53-tumor panel).