Supplement for

Gender Dependence for a Subset of the Low Abundance Signaling Proteome in Human Platelets

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S1. Supplemental Figure Legends:

Supplemental Figure 1. Light and electronmicroscopic images of platelets from male and female donors.

Supplemental Figure 1 shows representative optical and electron microscopy data for male and female platelets. At the light microscopy level, platelets from male donors (Supplemental Figure 1b) and female donors (Supplemental Figure 1d) appear as classically resting "face-on" flat discoids or "edge-on" fusiform structures. At the electron microscopic level both the platelets from male donors (Supplemental Figure 1a) and female donors (Supplemental Figure 1c) are shown in the "face-on" view as smoothly spherical bodies with uniformly distributed internal subcellular organelles. During the course of this study, platelet preparations are randomly checked by this direct measure of activation. Platelets prepared without added prostacyclin were often characterized by classical acanthocytic membrane protruberances, large scale aggregation, centralization of organelles, and massively dilated canalicular systems (not shown).

Supplemental Figure 2. 2D Gel Electrophoretic separation of platelet proteins from male and female donors. Proteins circled in green are significantly differentially expressed on the basis of gender. The statistical details are given in Supplemental Table 2.

Supplemental Figure 3. Distribution of SEM values for different proteins in platelets from male and female donors.
(a) Distribution of SEM values in the first group of eight donors. Individual data points are shown for all samples, males only, and females only.
(b) Distribution of SEM values for the aggregate of both first and second groups of eight each. Individual data points are shown as indicated for all samples, males only, and females only.

Supplemental Figure 4. ROC Curves for top gender-specific differences. The Figures represent a progression of area under the curve (AUC) values starting with near perfect discrimination (AUC = 1.0) and declining towards lesser values. The AUC is equal to the probability that one male or female protein expression level will rank higher (or lower) than a randomly chosen value from the opposite gender. The AUC is formally equivalent to the Mann-Whitney-Wilcoxon (MWW) non-parametric test or the Wilcoxon test of ranks.
S2. Supplemental Tables

Supplemental Table 1. Identification of protein features on 2DGE separations that distinguish platelets from male and female donors.

Supplemental Table 2. Mass spectrometry identification of proteins on 2DGE separations that distinguish platelets from male and female donors.

Supplemental Table 3. Most significant rank-order differences between platelets from female and male donors.

Supplemental Table 4. Male-specific gender differences in platelet protein expression.

Supplemental Table 5. Female-specific gender differences in platelet protein expression.

Supplemental Table 6. Female-specific platelet transcription factors.

Supplemental Table 7. Gender-dependent platelet membrane receptors

Supplemental Table 8. Gender-dependent platelet proteome gene ontology

Supplemental Table 9. Demographic description of normal control platelet donors.

Supplemental Table 10. Statistical properties of the differences between protein expression levels in male and female cohorts.
Supplemental Figure 1.

Light and electronmicroscopic images of platelets from male and female donors.

Details:

1. Platelets from a male donor are shown as electronmicrographs in Part A, and light micrographs of toluidine-stained thin sections in Part B.

2. Platelets from a female male donor are shown as electronmicrographs in Part C, and light micrographs of toluidine-stained thin sections in Part D.

3. Note that platelet profiles are smooth and non-acanthotic.

4. Note that two kinds of profiles are observable: flat-on "plate-like" platelet profiles, and edge-on fusiform profiles of plates.
Supplemental Figure 1. Light and electronmicroscopic images of platelets from male and female donors.
Supplemental Figure 2.

2D Gel Electrophoretic separation of male and female platelets

Details:

1. A typical 2DGE of 200 μg platelet protein from a male donor is shown.

2. A Progenesis® analysis of the protein in this sample is shown, based on studies of all 16 samples of platelets from male and female donors.

3. Spots that are circled in green are those predicted to be differentially expressed in male and female platelets.
Supplemental Figure 2. 2D Gel Electrophoretic separation of male and female platelets
Supplemental Figure 3.

Distribution of SEM values for different proteins in platelets from male and female donors.

Details: see text
Supplemental Figure 3. Distribution of SEM values for different proteins in platelets from male and female donors.
Supplemental Figure 4

ROC Curves for top gender-specific differences

DETAILS:

1. Each graph shows the ROC (Receiver Operating Characteristic) curve (red line) for the specified protein. The insets show the actual distributions of protein levels (in relative units) for females (magenta) and for males (cyan). Note that all the replicates for each individual are shown on the insets.

2. The ROC curves are plotted using the replicates - so that if the cutoff passes between the 3rd and 4th replicate out of 4 replicates it would count as 0.75 positive and 0.25 negative (or vice versa). This is slightly different than the way the AUC values were calculated in Supplemental Table 10, were the Averages and SDs of the replicates were used to calculate the chance of receiving a false positive of false negative measurement (see details in legend of Supplemental Table 10).

3. The graphs are ordered by the respective values of the AUC (Area Under the Curve). When the AUC is close to 1.0. this indicates complete separation of the distribution of protein levels between males and in female. The AUC is equal to the probability that one male or female protein expression level will rank higher (or lower) than a randomly chosen value from the opposite gender.

4. The AUC is formally equivalent to the Mann-Whitney-Wilcoxon (MWW) non-parametric test or the Wilcoxon test of ranks. For these proteins the ROC curves seem to hug the left and top axes. The values for AUC for each protein are given in Supplementary Table 10.
tumor protein p53 binding protein, 2
polymerase (DNA directed), epsilon
stathmin 1/oncoprotein 18 proteasome (prosome, macropain) 26S subunit, ATPase, 5
protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)

RAS p21 protein activator 2

thyroid autoantigen 70kDa (Ku antigen)

synapsin II

phospholipase C, beta 1 (phosphoinositide-specific)

synaptotagmin I

phosphatidylinositol 4-kinase, catalytic, beta polypeptide

annexin A11
general transcription factor II, i A kinase (PRKA) anchor protein (gravin) 12
multiple PDZ domain protein cyclin D-type binding-protein 1
G protein-coupled receptor kinase-interactor 1
neuronal Shc
chromogranin A (parathyroid secretory protein 1)
RAB5A, member RAS oncogene family
adaptor-related protein complex 2, alpha 1 subunit
antigen identified by monoclonal antibody Ki-67
caspase 14, apoptosis-related cysteine protease
FK506 binding protein 5
topo-isomerase (DNA) II beta 180kDa
colony stimulating factor 1 receptor
synuclein, alpha (non A4 component of amyloid precursor)
protein kinase, cAMP-dependent, catalytic, alpha
solute carrier family 9 (Na/H exchanger), isoform 3, RF 1
plectin 1, intermediate filament binding protein 500kDa
exportin 1 (CRM1 homolog, yeast)
A kinase (PRKA) anchor protein (yotiao) 9
caspase 7, apoptosis-related cysteine protease
dynamin 2
huntingtin-associated protein 1 (neuroan 1)
catechol-O-methyltransferase
pericentrin 2 (kendrin)
protein tyrosine phosphatase, non-receptor type 1
protein kinase C, epsilon
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent2
IQ motif containing GTPase activating protein 1
ras homolog gene family, member A
heme oxygenase (decycling) 1
peroxisomal D3,D2-enoyl-CoA isomerase
| Protein Name                                                                 | Protein Levels | ROC Curve |
|------------------------------------------------------------------------------|----------------|-----------|
| Tumor protein p53 (Li-Fraumeni syndrome)                                     |                | ![Diagram](image1) |
| Phosphoinositide-3-kinase, regulatory subunit, polypeptide 1                 |                | ![Diagram](image2) |
| L1 cell adhesion molecule                                                    |                | ![Diagram](image3) |
| Sortilin-related receptor, L(DLR class) A repeats-containing                 |                | ![Diagram](image4) |
| Mitogen-activated protein kinase kinase 5                                     |                | ![Diagram](image5) |
| Serine (or cysteine) proteinase inhibitor, member 5                          |                | ![Diagram](image6) |
| Ankyrin 2, neuronal                                                          |                | ![Diagram](image7) |
| Caveolin 1, caveolae protein, 22kDa                                         |                | ![Diagram](image8) |
SV40 Large T Antigen

catenin (cadherin-associated protein), beta 1, 88kDa

TGF β1 (Camurati-Engelmann disease)

GDNF family receptor alpha 1

chemokine (C-C motif) ligand 2

transcription factor Dp-1

Ras protein-specific guanine nucleotide-releasing factor 2

nitric oxide synthase 2A (inducible, hepatocytes)
contactin 1
5-hydroxytryptamine (serotonin) receptor 2C
leukocyte-associated Ig-like receptor 1
polymerase (DNA directed), delta 1, catalytic subunit 125kDa
Supplemental Table 1.

Identification of protein features on 2DGE separations that distinguish platelets from male and female donors.

Details:
1. Ratio’s are (+) Male/Female; (-) Female/Male
2. Normalized volumes are fractions of the total optical density of the synthetic Male and Female gels calculated from all the data.
3. The difference is the relative intensity of all male spots of a given number for all female spots with the same number.
4. The t-test (“T-Test”) is calculated from all available data.
Supplemental Table 1. Identification of protein features on 2DGE separations that distinguish between platelets from male and female donors.

| Match | Ave Male | Ave Female | Ratio | T-test (p) |
|-------|----------|------------|-------|------------|
| No.   | Volume   | Norm. Vol. | Volume | Norm. Vol. |       |       |
| 961   | 2506995  | 0.109      | 1900259 | 0.066      | 1.66 | 0.0128 |
| 1101  | 612632   | 0.027      | 482282  | 0.016      | 1.72 | 0.0043 |
| 1140  | 414782   | 0.017      | 866063  | 0.030      | -1.70 | 0.0033 |
| 1173  | 1156333  | 0.059      | 848497  | 0.028      | 2.12 | 0.0464 |
| 1391  | 805642   | 0.032      | 571860  | 0.018      | 1.77 | 0.0069 |
| 1448  | 1377509  | 0.048      | 3703655 | 0.121      | -2.52 | 0.0364 |
| 1476  | 666578   | 0.018      | 481603  | 0.009      | 2.02 | 0.0030 |
| 1552  | 2129233  | 0.086      | 1687266 | 0.055      | 1.55 | 0.0135 |
| 1557  | 1610807  | 0.065      | 1143428 | 0.037      | 1.75 | 0.0009 |
| 1583  | 3952415  | 0.156      | 1418827 | 0.051      | 3.08 | 0.0038 |
| 1596  | 2267172  | 0.092      | 1958031 | 0.064      | 1.45 | 0.0113 |
| 1602  | 808208   | 0.035      | 726655  | 0.024      | 1.42 | 0.0162 |
| 1609  | 1127978  | 0.046      | 740263  | 0.026      | 1.78 | 0.0077 |
| 1653  | 1281684  | 0.054      | 1007455 | 0.033      | 1.65 | 0.0005 |
| 1690  | 240931   | 0.010      | 177803  | 0.005      | 1.81 | 0.0243 |
| 1713  | 526356   | 0.021      | 320284  | 0.010      | 1.99 | 0.0007 |
| 1756  | 611122   | 0.024      | 399217  | 0.013      | 1.82 | 0.0077 |
| 1784  | 241020   | 0.010      | 495652  | 0.017      | -1.73 | 0.0269 |
| 1788  | 713193   | 0.029      | 545135  | 0.020      | 1.49 | 0.0404 |
| 1884  | 895146   | 0.037      | 752650  | 0.026      | 1.43 | 0.0027 |
| 2178  | 899503   | 0.036      | 651549  | 0.024      | 1.50 | 0.0139 |
| 2653  | 909278   | 0.038      | 805312  | 0.027      | 1.40 | 0.0442 |
Supplemental Table 2.

Mass spectrometry identification of proteins that significantly distinguish platelets from male and female donors.

Details:

1. In order to be certain about the identification, the molecular weight and the pI had to agree with the literature values.

2. In order to be secure in the identification by mass spectrometry, the protein needed to be identified by at least five peptides, covering at least 10% of the sequence (see Pollard et al, Proteomics.5: 2210-2226, 2005).

3. In the column marked "M/F", the (+) symbol indicates that [Male > Female]. The (-) symbol indicates that [Female > Male].

4. Methodological information is given in Methods (see Identification of proteins by 2D gel electrophoresis and mass spectrometry.)
Supplemental Table 2. Mass spectrometry identification of high abundance proteins that significantly distinguish platelets from male and female donors.

| platelet (#) | SWISS-PROT accession ( #) | Protein Name                              | HUGO  | Mr (Theor.) | pI (Theor.) | Matches (n) | Coverage (%) | Difference (M vs.F) | T test (P value) | Mowse score |
|--------------|---------------------------|-------------------------------------------|-------|-------------|-------------|--------------|---------------|---------------------|-----------------|-------------|
| 1101         | Q28294 Guanine nucleotide-binding protein G(q) alpha subunit | GNAQ  | 42   | 5.5         | 11          | 35           | 1.599        | 0.009               | 3.62E+03        |
| 1583         | Q9y4P1 Cysteine protease ATG4B | ATG4B | 42   | 5.2         | 6           | 17           | 1.599        | 0.009               | 3.18E+03        |
| 1140         | Q9ULV4 Coronin-1C          | KCTD13 | 36   | 6.3         | 7           | 19           | 3.246        | 0.003               | 1.31E+03        |
| 1476         | P30519 Heme oxygenase 2    | GSTO1 | 28   | 6.2         | 8           | 30           | 3.246        | 0.003               | 1.33E+03        |
| 1556         | P29992 Guanine nucleotide-binding protein G(Y), alpha subunit | CORD1C | 53   | 6.6         | 10          | 22           | -1.698       | 0.003               | 3.08E+03        |
| 2178         | P62487 DNA-directed RNA polymerase II 19 Kda polypeptide | POLR2G | 19   | 5.3         | 7           | 45           | -1.915       | 0.006               | 3.85E+04        |
Supplemental Table 3

Most Significant Rank-Order Differences between Female and Male Platelets.

Details:

1. Cohort: 8 males and 8 females.

2. Gender Code: [+1=M>F; -1=F>M]
**Supplemental Table 3: Most Significant Rank-Order Differences between Female and Male Platelets.** Cohort: 8 males and 8 females.

*Gender Code: [+1=M>F; -1=F>M]*

| ID | SAM |
|----|-----|
| ID | q-value | local-FDR | t-test | Swiss-Prot | Gen* code | HUGO | RANK |
|----|---------|-----------|-------|-----------|-----------|------|------|
| v-myc myelocytomatosis viral oncogene homolog avian | 0.00% | 0.00% | 3.5E-20 | P01106 | -1 | MYC | Females: 91 ± 2 %, Males: 25 ± 2 %, Delta: 66% |
| ras-related C3 botulinum toxin substrate 1 rho family, small GTP binding protein Rac1 | 0.00% | 0.00% | 8.9E-15 | P15154 | 1 | RAC1 | Females: 37 ± 2 %, Males: 83 ± 3 %, Delta: 46% |
| polymerase DNA directed, epsilon | 0.00% | 0.00% | 1.7E-14 | Q07864 | -1 | DPOE1 | Females: 60 ± 1 %, Males: 14 ± 1 %, Delta: 47% |
| proteasome prosome, macropain 26S subunit, ATPase, 5 | 0.00% | 0.00% | 2.2E-14 | P62195 | -1 | PSMC5 | Females: 90 ± 2 %, Males: 27 ± 1 %, Delta: 63% |
| synapsin II | 0.00% | 0.00% | 3.2E-14 | Q92777 | -1 | SYN2 | Females: 94 ± 1 %, Males: 34 ± 2 %, Delta: 60% |
| synaptopotamin I | 0.00% | 0.00% | 4.2E-14 | P21579 | -1 | SYT1 | Females: 88 ± 1 %, Males: 33 ± 2 %, Delta: 55% |
| A kinase PRKA anchor protein yotiao 9 | 0.00% | 0.00% | 2.6E-13 | Q99996 | 1 | AKAP9 | Females: 41 ± 3 %, Males: 86 ± 3 %, Delta: 45% |
| phosphatidylinositol 4-kinase, catalytic, beta polypeptide | 0.00% | 0.00% | 1.1E-12 | Q9UBF8 | -1 | PIK4CB | Females: 86 ± 1 %, Males: 38 ± 2 %, Delta: 48% |
| protein tyrosine phosphatase, non-receptor type 11 Noonan syndrome 1 | 0.00% | 0.00% | 3.6E-12 | Q06124 | -1 | PTPN11 | Females: 82 ± 3 %, Males: 28 ± 1 %, Delta: 55% |
| A kinase PRKA anchor protein gravin 12 | 0.00% | 0.00% | 5.2E-11 | Q02952 | 1 | AKAP12 | Females: 32 ± 1 %, Males: 83 ± 3 %, Delta: 52% |
| RAB5A, member RAS oncogene family | 0.00% | 0.00% | 1.3E-10 | P20339 | -1 | RAB5A | Females: 86 ± 2 %, Males: 59 ± 2 %, Delta: 27% |
| lymphocyte cytosolic protein 2 SH2 domain containing leukocyte protein of 76kDa | 0.00% | 0.00% | 1.3E-10 | Q13094 | -1 | LCP2 | Females: 79 ± 4 %, Males: 38 ± 4 %, Delta: 41% |
| amphiphysin Stiff-Man syndrome with breast cancer 128kDa autoantigen | 0.00% | 0.00% | 9.8E-10 | P49418 | -1 | AMPH | Females: 89 ± 4 %, Males: 48 ± 4 %, Delta: 41% |
| TRAF family member-associated NFKB activator | 0.00% | 0.00% | 1.6E-09 | Q92844 | -1 | TANK | Females: 55 ± 2 %, Males: 36 ± 2 %, Delta: 18% |
| solute carrier family 9 sodium/hydrogen exchanger, isoform 3 regulatory factor 1 | 0.00% | 0.00% | 4.1E-09 | Q9JJ19 | 1 | NHERF-1 | Females: 32 ± 2 %, Males: 75 ± 5 %, Delta: 43% |
| leukocyte-associated Ig-like receptor 1 | 0.00% | 0.00% | 4.9E-09 | n/d | -1 | LAIR1 | Females: 60 ± 2 %, Males: 40 ± 2 %, Delta: 20% |
| annexin A11 | 0.00% | 0.00% | 5.0E-09 | P50995 | -1 | ANXA11 | Females: 84 ± 5 %, Males: 19 ± 1 %, Delta: 65% |
| dynein, cytoplasmic, light polypeptide 1 | 0.00% | 0.00% | 7.5E-09 | Q15701 | 1 | DYNNL1 | Females: 49 ± 3 %, Males: 73 ± 2 %, Delta: 24% |
| retinol binding protein 4, plasma | 0.00% | 0.00% | 7.6E-09 | P02753 | 1 | RETBP | Females: 56 ± 3 %, Males: 81 ± 2 %, Delta: 25% |
| scavenger receptor class B, member 1 | 0.00% | 0.00% | 1.1E-08 | Q14016 | -1 | SCRB1 | Females: 93 ± 2 %, Males: 42 ± 7 %, Delta: 51% |
| ID                                                                 | SAM                  | local- FDR | t-test | Swiss-Protein code | Gen* code | HUGO | RANK          | Females | Males | Delta |
|-------------------------------------------------------------------|----------------------|------------|--------|--------------------|-----------|------|---------------|---------|-------|-------|
| origin recognition complex, subunit 5-like yeast                 | 0.00% 0.00%         | 1.1E-08    | O43913 | -1                 | ORC5L     | 53 ± 1% 37 ± 2% 15% |
| citron rho-interacting, serine/threonine kinase 21               | 0.00% 0.00%         | 1.2E-08    | O14578 | -1                 | CTRO      | 70 ± 4% 37 ± 3% 33% |
| SFRS protein kinase 1                                             | 0.00% 0.00%         | 3.1E-08    | Q12890 | -1                 | SRPK1     | 86 ± 2% 48 ± 5% 38% |
| sortilin-related receptor, LDLR class A repeats-containing      | 0.00% 0.00%         | 6.6E-08    | Q92673 | 1                  | SORL1     | 74 ± 2% 94 ± 2% 19% |
| BUB3 budding uninhibited by benzimidazoles 3 homolog yeast       | 0.00% 0.00%         | 9.2E-08    | O43684 | -1                 | BUB3      | 64 ± 4% 34 ± 2% 31% |
| DEAD Asp-Glu-Ala-Asp box polypeptide 1                           | 0.00% 0.00%         | 1.3E-07    | Q92499 | -1                 | DDX1      | 93 ± 2% 58 ± 5% 35% |
| aldehyde dehydrogenase 1 family, member A1                       | 0.00% 0.00%         | 1.8E-07    | P00352 | 1                  | ALDH1A1   | 44 ± 4% 83 ± 5% 39% |
| baculoviral IAP repeat-containing 6 apollon                      | 0.00% 0.00%         | 2.6E-07    | Q9NR09 | 1                  | BIRC6     | 12 ± 0% 17 ± 1% 5% |
| ras homolog gene family, member A                                | 0.00% 0.00%         | 4.6E-07    | P06749 | 1                  | RHOA      | 75 ± 3% 93 ± 1% 18% |
| FK506 binding protein 10, 65 kDa                               | 0.00% 0.00%         | 5.5E-07    | Q96AY3 | 1                  | FKB10     | 56 ± 5% 91 ± 2% 35% |
| lymphocyte-specific protein tyrosine kinase                      | 0.00% 0.00%         | 5.9E-07    | P06239 | -1                 | LCK       | 62 ± 5% 29 ± 2% 33% |
| KH domain containing, RNA binding, signal transduction associated | 0.00% 0.00%         | 6.0E-07    | Q07666 | -1                 | SAM68     | 35 ± 3% 17 ± 1% 18% |
| active BCR-related gene                                          | 0.00% 0.00%         | 7.9E-07    | Q12979 | 1                  | ABR       | 63 ± 4% 84 ± 2% 22% |
| signal-induced proliferation-associated gene 1                  | 0.00% 0.00%         | 1.2E-06    | Q06484 | 1                  | SIPA1     | 67 ± 3% 85 ± 2% 18% |
| neurexin 1                                                       | 0.00% 0.00%         | 1.4E-06    | Q9ULB1 | -1                 | NRXN1     | 87 ± 2% 46 ± 7% 40% |
| conserved helix-loop-helix ubiquitous kinase                     | 0.00% 0.00%         | 1.5E-06    | Q15111 | -1                 | CHUK      | 89 ± 2% 62 ± 4% 26% |
| non-metastatic cells 1, protein NM23A expressed in               | 0.00% 0.00%         | 2.2E-06    | P15531 | 1                  | NME1      | 23 ± 1% 51 ± 5% 28% |
| homer homolog 1 Drosophila                                       | 0.00% 0.00%         | 2.3E-06    | Q9Z2Y3 | 1                  | HOMER1    | 78 ± 2% 92 ± 1% 14% |
| general transcription factor IIB                                | 0.00% 0.00%         | 2.4E-06    | Q00403 | 1                  | GTF2B     | 63 ± 4% 87 ± 3% 25% |
| interleukin 1, beta                                              | 0.00% 0.00%         | 2.7E-06    | P01584 | -1                 | IL1B      | 80 ± 4% 38 ± 7% 43% |
| clathrin, heavy polypeptide Hc                                    | 0.00% 0.00%         | 3.0E-06    | Q00610 | 1                  | CLTC      | 61 ± 4% 83 ± 2% 22% |
| integrin-linked kinase                                           | 0.00% 0.00%         | 3.0E-06    | Q13418 | -1                 | ILK       | 10 ± 0% 6 ± 1% 4% |
| Ras protein-specific guanine nucleotide-releasing factor 2       | 0.00% 0.00%         | 3.3E-06    | Q9UK56 | 1                  | RASGRF2   | 48 ± 4% 75 ± 3% 27% |
| ID | SAM q-value | local-FDR | t-test | Swiss-Prot | Gen* code | HUGO | Females | Males | Delta |
|----|-------------|------------|--------|------------|-----------|-------|---------|-------|-------|
| neuropilin 2 | 0.00% | 0.00% | 3.4E-06 | O60462 | -1 | NRP2 | 92 ± 2 % | 59 ± 6 % | 32% |
| protein kinase, cAMP-dependent, regulatory, type II, alpha | 0.00% | 0.00% | 3.4E-06 | P13861 | -1 | PRKAR2A | 74 ± 3 % | 57 ± 2 % | 17% |
| centrosomal protein 2 | 0.00% | 0.00% | 3.5E-06 | O60588 | -1 | CEP2 | 92 ± 2 % | 63 ± 5 % | 29% |
| CrmA | 0.00% | 0.00% | 4.6E-06 | P07385 | 1 | CRMA | 22 ± 0 % | 36 ± 3 % | 14% |
| flap structure-specific endonuclease 1 | 0.00% | 0.00% | 5.1E-06 | P39748 | -1 | FEN1 | 8 ± 0 % | 5 ± 0 % | 2% |
| telomeric repeat binding factor 2 | 0.00% | 0.00% | 5.1E-06 | Q15554 | 1 | TERF2 | 70 ± 3 % | 86 ± 2 % | 17% |
| A kinase PRKA anchor protein 5 | 0.00% | 0.00% | 5.2E-06 | P24588 | -1 | AKAP5 | 71 ± 3 % | 51 ± 3 % | 20% |
| endothelin receptor type A | 0.00% | 0.00% | 6.4E-06 | P25101 | -1 | EDNRA | 52 ± 5 % | 25 ± 2 % | 27% |
| apolipoprotein E | 0.00% | 0.00% | 6.8E-06 | P02649 | -1 | APOE | 84 ± 2 % | 63 ± 4 % | 21% |
| protein phosphatase 1, regulatory inhibitor subunit 2 | 0.00% | 0.00% | 7.4E-06 | P41236 | 1 | PPP1R2 | 35 ± 3 % | 57 ± 4 % | 22% |
| docking protein 1, 62kDa downstream of tyrosine kinase 1 | 0.00% | 0.00% | 7.4E-06 | Q99704 | -1 | DOK1 | 75 ± 2 % | 52 ± 4 % | 23% |
| serine/threonine kinase 24 STE20 homolog, yeast | 0.00% | 0.00% | 7.7E-06 | Q9Y6E0 | 1 | STK24 | 37 ± 3 % | 71 ± 6 % | 34% |
| spleen focus forming virus proviral integration oncogene sp1 | 0.00% | 0.00% | 8.3E-06 | P17947 | 1 | SPI1 | 14 ± 1 % | 23 ± 2 % | 10% |
| DNA fragmentation factor, 45kDa, alpha polypeptide | 0.00% | 0.00% | 9.2E-06 | O00273 | 1 | DFFA | 39 ± 2 % | 55 ± 2 % | 15% |
| HPV-16 L1 | 0.00% | 0.00% | 9.7E-06 | P03101 | 1 | L1 | 59 ± 4 % | 84 ± 3 % | 25% |
| heat shock 90kDa protein 1, alpha | 0.00% | 0.00% | 9.8E-06 | P07900 | 1 | HSP90AA1 | 64 ± 2 % | 81 ± 3 % | 17% |
| colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral v-fms oncogene homolog | 0.00% | 0.00% | 1.0E-05 | P07333 | 1 | CSF1R | 52 ± 8 % | 93 ± 1 % | 41% |
| proliferating cell nuclear antigen | 0.00% | 0.00% | 1.0E-05 | P12004 | 1 | PCNA | 70 ± 3 % | 89 ± 2 % | 19% |
| MCM5 minichromosome maintenance deficient 5, cell division cycle 46 S. cerevisiae | 0.00% | 0.00% | 1.2E-05 | P33992 | -1 | MCM5 | 75 ± 3 % | 53 ± 3 % | 22% |
| cell division cycle 27 | 0.00% | 0.00% | 1.2E-05 | P03260 | -1 | CDC27 | 94 ± 1 % | 61 ± 7 % | 33% |
| neurogenin 1 | 0.00% | 0.00% | 1.4E-05 | Q92886 | -1 | NEUROG1 | 32 ± 3 % | 16 ± 1 % | 16% |
| cell division cycle 2, G1 to S and G2 to M | 0.00% | 0.00% | 1.6E-05 | P06493 | 1 | CDC2 | 66 ± 2 % | 79 ± 2 % | 13% |
| son of sevenless homolog 1 Drosophila | 0.00% | 0.00% | 2.1E-05 | Q07889 | 1 | SOS1 | 4 ± 0 % | 5 ± 0 % | 1% |
| ID | SAM | Swiss-Prot | Gen* code | HUGO | Females | Males | Delta |
|----|-----|------------|-----------|-------|---------|-------|-------|
| ID  | q-value | local-FDR | t-test | Swiss-Prot | Gen* code | HUGO | Females | Males | Delta |
| cytokine-inducible kinase | 0.00% | 0.00% | 2.2E-05 | Q9H4B4 | -1 | PLK3 | 77 ± 5 % | 42 ± 6 % | 35% |
| nuclear receptor coactivator 3 | 0.00% | 0.00% | 2.5E-05 | Q9UPG4 | 1 | NCOA3 | 41 ± 3 % | 56 ± 2 % | 15% |
| F11 receptor | 0.00% | 0.00% | 2.7E-05 | Q9Y624 | 1 | FT1R | 31 ± 4 % | 56 ± 4 % | 25% |
| growth associated protein 43 | 0.00% | 0.00% | 3.0E-05 | P17677 | 1 | GAP43 | 1 ± 0 % | 2 ± 0 % | 1% |
| cyclin D1 PRAD1: parathyroid adenomatosis 1 | 0.00% | 0.00% | 3.9E-05 | P24385 | 1 | CCND1 | 69 ± 2 % | 84 ± 2 % | 14% |
| Fas TNFRSF6 -associated via death domain | 0.00% | 0.00% | 4.4E-05 | Q13158 | -1 | FADD | 76 ± 3 % | 58 ± 3 % | 18% |
| adaptor-related protein complex 3, beta 2 subunit | 0.00% | 0.00% | 5.1E-05 | Q13367 | -1 | AP3B2 | 75 ± 2 % | 56 ± 4 % | 19% |
| CDC-like kinase 1 | 0.00% | 0.00% | 5.3E-05 | P21127 | 1 | CLK1 | 35 ± 4 % | 67 ± 6 % | 32% |
| gephyrin | 0.00% | 0.00% | 5.6E-05 | Q9NQX3 | -1 | GPHN | 62 ± 2 % | 47 ± 2 % | 14% |
| early endosome antigen 1, 162kD | 0.00% | 0.00% | 5.7E-05 | Q14221 | -1 | EEA1 | 71 ± 4 % | 50 ± 3 % | 22% |
| tight junction protein 1 zona occludens 1 | 0.00% | 0.00% | 6.1E-05 | Q07157 | -1 | TJP1 | 75 ± 4 % | 54 ± 3 % | 21% |
| optineurin | 0.00% | 0.00% | 7.6E-05 | Q9Y218 | -1 | OPTN | 61 ± 3 % | 43 ± 3 % | 18% |
| mutS homolog 2, colon cancer, nonpolyposis type 1 E. coli | 0.00% | 0.00% | 8.2E-05 | P43246 | -1 | MSH2 | 50 ± 3 % | 35 ± 1 % | 15% |
| doublecortin and CaM kinase-like 1 | 0.00% | 0.00% | 8.3E-05 | Q15075 | -1 | DCAMKL1 | 67 ± 2 % | 76 ± 1 % | 9% |
| golgi autoantigen, golgin subfamily a, 2 | 0.00% | 0.00% | 9.1E-05 | Q9NYF9 | 1 | - | 60 ± 3 % | 75 ± 2 % | 15% |
| cell division cycle 34 | 0.00% | 0.00% | 9.8E-05 | P49427 | -1 | CDC34 | 79 ± 5 % | 55 ± 3 % | 25% |
| 5-hydroxytryptamine serotonin receptor 2A | 0.00% | 0.00% | 1.1E-04 | P28223 | -1 | HTR2A | 78 ± 4 % | 52 ± 5 % | 27% |
| RAS p21 protein activator GTPase activating protein 1 | 0.00% | 0.00% | 1.1E-04 | P20936 | 1 | RASA1 | 48 ± 4 % | 70 ± 3 % | 22% |
| protein kinase, interferon-inducible double stranded RNA dependent | 0.00% | 0.00% | 1.2E-04 | P19525 | -1 | EIF2AK2 | 28 ± 2 % | 18 ± 1 % | 9% |
| MAX protein | 0.00% | 0.00% | 1.3E-04 | P25912 | -1 | MAX | 70 ± 5 % | 42 ± 5 % | 28% |
| epidermal growth factor receptor erythroblastic leukemia viral v-erb-b oncogene homolog, avian | 0.00% | 0.00% | 1.3E-04 | P00533 | 1 | EGFR | 67 ± 4 % | 88 ± 2 % | 21% |
| ubiquitin-conjugating enzyme E2E 1 | 0.00% | 0.00% | 1.4E-04 | P51965 | 1 | UBE2E1 | 23 ± 2 % | 39 ± 3 % | 16% |
| G antigen 7 | 0.00% | 0.00% | 1.4E-04 | Q9UEU5 | 1 | GAGE7 | 36 ± 3 % | 58 ± 4 % | 22% |
| ID                                      | SAM        | t-test    | Swiss-Prot | Gen* code | HUGO | RANK Females | Males | Delta |
|-----------------------------------------|------------|-----------|------------|-----------|------|--------------|-------|-------|
| calnexin                                | 0.00%      | 1.5E-04   | P27824     | -1        | CANX | 69 ± 7 %     | 36 ± 3 % | 34 %  |
| interleukin 6 interferon, beta 2        | 0.00%      | 1.6E-04   | P05231     | 1         | IL6  | 40 ± 2 %     | 58 ± 4 % | 18 %  |
| sorting nexin 2                         | 0.00%      | 1.8E-04   | O06749     | -1        | SNX2 | 57 ± 3 %     | 40 ± 3 % | 17 %  |
| caspase 4, apoptosis-related cysteine protease | 0.00%  | 1.9E-04   | P49662     | -1        | CASP4 | 80 ± 4 %     | 47 ± 7 % | 33 %  |
| Mdm2, transformed 3T3 cell double minute 2, p53 binding protein mouse | 0.00% | 2.0E-04   | Q9UMT8     | 1         | MDM2 | 78 ± 4 %     | 95 ± 1 % | 17 %  |
| ribosomal protein S6 kinase, 70kDa, polypeptide 1 | 0.00% | 2.0E-04   | P23443     | 1         | RPS6KB1 | 59 ± 5 %     | 83 ± 3 % | 24 %  |
| thymopoietin                            | 0.00%      | 2.1E-04   | P42166     | 1         | TMPO | 41 ± 3 %     | 54 ± 2 % | 13 %  |
| deleted in colorectal carcinoma         | 0.00%      | 2.1E-04   | P43146     | -1        | DCC  | 70 ± 5 %     | 36 ± 6 % | 34 %  |
| density-regulated protein               | 0.00%      | 2.3E-04   | O43583     | 1         | DENR | 72 ± 3 %     | 84 ± 2 % | 12 %  |
| COP9 constitutive photomorphogenic homolog subunit 5 Arabidopsis | 0.00% | 2.3E-04   | Q92905     | 1         | COPS5 | 55 ± 4 %     | 75 ± 3 % | 20 %  |
| myogenin myogenic factor 4              | 0.00%      | 2.4E-04   | P15173     | 1         | MYOG | 72 ± 2 %     | 87 ± 2 % | 14 %  |
| likely ortholog of mouse raphilin 3A    | 0.00%      | 2.6E-04   | Q9Y2J0     | 1         | RPH3A | 21 ± 3 %     | 50 ± 7 % | 29 %  |
| cyclin D3                               | 0.00%      | 2.7E-04   | P30281     | -1        | CCND3| 79 ± 3 %     | 60 ± 4 % | 19 %  |
| protein kinase, cAMP-dependent, regulatory, type I, alpha tissue specific extinguisher 1 | 0.00% | 2.9E-04   | P10644     | -1        | PRKAR1A | 77 ± 2 %     | 66 ± 2 % | 11 %  |
| polyamine-modulated factor 1            | 0.00%      | 3.0E-04   | Q9UBQ3     | 1         | PMF1 | 64 ± 3 %     | 82 ± 3 % | 18 %  |
| ribosomal protein S6 kinase, 90kDa, polypeptide 1 | 0.00% | 3.1E-04   | Q15418     | 1         | RPS6KA1 | 50 ± 6 %     | 80 ± 5 % | 30 %  |
| tubulin, beta polypeptide               | 0.00%      | 3.2E-04   | Q13885     | 1         | TUBB2 | 64 ± 3 %     | 83 ± 4 % | 19 %  |
| nuclear receptor subfamily 3, group C, member 1 glucocorticoid receptor | 0.00% | 3.4E-04   | P04150     | -1        | NR3C1 | 88 ± 3 %     | 57 ± 7 % | 31 %  |
| Rho-associated, coiled-coil containing protein kinase 2 | 0.00% | 4.1E-04   | Q75116     | -1        | ROCK2 | 47 ± 3 %     | 34 ± 2 % | 12 %  |
| leucine zipper, putative tumor suppressor 1 | 0.00% | 4.1E-04   | Q9Y250     | 1         | LZTS1 | 62 ± 2 %     | 79 ± 3 % | 17 %  |
| elongation factor-2 kinase              | 0.00%      | 4.5E-04   | Q00418     | -1        | EEF2K | 59 ± 3 %     | 43 ± 3 % | 16 %  |
| topoisomerase DNA I                     | 0.00%      | 4.8E-04   | P11387     | 1         | TOP1  | 37 ± 5 %     | 63 ± 5 % | 26 %  |
| ubiquitin-conjugating enzyme E2L 3      | 0.00%      | 5.0E-04   | P51966     | 1         | UBE2L3| 79 ± 2 %     | 87 ± 1 % | 9 %   |
| ID | SAM gene | q-value | local-FDR | t-test | Swiss-Prot | Gen* code | HUGO | RANK |
|----|----------|---------|-----------|--------|------------|-----------|-------|------|
| v-crk sarcoma virus CT10 oncogene homolog avian | 0.00% | 0.00% | 6.9E-04 | P46108 | 1 | CRK | 58 ± 3% | 71 ± 2% | 13% |
| nuclear transport factor 2 | 0.00% | 0.00% | 7.4E-04 | P13662 | 1 | NUTF2 | 60 ± 4% | 81 ± 4% | 21% |
| transforming growth factor beta 1 induced transcript 1 | 0.00% | 0.00% | 8.2E-04 | O43294 | -1 | TGFBI1 | 41 ± 2% | 33 ± 1% | 8% |
| MCM4 minichromosome maintenance deficient 4 S. cerevisiae | 0.00% | 0.00% | 8.6E-04 | P33991 | -1 | MCM4 | 56 ± 3% | 41 ± 3% | 15% |
| LIM domain binding 3 | 0.00% | 0.00% | 9.0E-04 | O75112 | -1 | LDB3 | 75 ± 4% | 51 ± 5% | 24% |
| tumor protein p73 | 0.00% | 0.00% | 9.0E-04 | O15350 | -1 | TP73 | 80 ± 4% | 62 ± 4% | 18% |
| gelsolin amyloidosis, Finnish type | 0.00% | 0.00% | 1.0E-03 | P06396 | -1 | GSN | 71 ± 5% | 49 ± 4% | 22% |
| translocase of inner mitochondrial membrane 23 homolog yeast | 0.00% | 0.00% | 1.2E-03 | O14925 | 1 | TIMM23 | 50 ± 5% | 70 ± 4% | 20% |
| TNF receptor-associated factor 2 | 0.00% | 0.00% | 1.3E-03 | Q12933 | 1 | TRAF2 | 66 ± 4% | 84 ± 4% | 18% |
| lysosomal-associated membrane protein 1 | 0.00% | 0.00% | 1.6E-03 | P11279 | -1 | LAMP1 | 79 ± 2% | 56 ± 6% | 23% |
| kallikrein 10 | 0.00% | 0.00% | 1.7E-03 | O43240 | 1 | KLK10 | 64 ± 4% | 81 ± 4% | 17% |
| survival of motor neuron protein interacting protein 1 | 0.00% | 0.00% | 1.7E-03 | O14893 | -1 | SIP1 | 70 ± 7% | 43 ± 5% | 27% |
| epidermal growth factor receptor pathway substrate 8 | 0.00% | 0.00% | 2.4E-03 | Q12929 | -1 | EPS8 | 53 ± 3% | 39 ± 4% | 15% |
| protein kinase C-like 2 | 0.00% | 0.00% | 2.6E-03 | Q16513 | -1 | PKN2 | 3 ± 0% | 2 ± 0% | 1% |
| adaptor-related protein complex 3, mu 1 subunit | 0.00% | 0.00% | 3.3E-03 | Q9Y2T2 | 1 | AP3M1 | 63 ± 4% | 81 ± 5% | 18% |
| phospholipase C, gamma 1 formerly subtype 148 | 0.00% | 0.00% | 3.3E-03 | P19174 | 1 | PLCG1 | 51 ± 3% | 63 ± 2% | 12% |
| cytoplasmic linker 2 | 0.00% | 0.00% | 3.5E-03 | Q9UDT6 | 1 | CYLN2 | 69 ± 3% | 83 ± 3% | 13% |
| fatty acid synthase | 0.00% | 0.00% | 3.9E-03 | P49327 | 1 | FASN | 36 ± 4% | 53 ± 4% | 17% |
| von Hippel-Lindau syndrome | 0.00% | 0.00% | 4.3E-03 | P40337 | -1 | VHL | 79 ± 3% | 68 ± 2% | 11% |
| glutamate-ammonia ligase glutamine synthase | 0.00% | 0.00% | 5.4E-03 | P15104 | 1 | GLUL | 40 ± 5% | 66 ± 8% | 26% |
| protein tyrosine phosphatase, receptor-type, Z polypeptide 1 | 0.00% | 0.00% | 5.5E-03 | O76043 | 1 | HTPZP1 | 56 ± 6% | 78 ± 5% | 22% |
| adenomatosis polyposis coli | 0.00% | 0.00% | 5.8E-03 | P25054 | 1 | APC | 7 ± 1% | 15 ± 2% | 8% |
| ID | SAM | Swiss-Prot | Gen* code | HUGO | RANK |
|----|-----|------------|-----------|-------|------|
|    | q-value | local-FDR | t-test | Females | Males | Delta |
| myeloid/lymphoid or mixed-lineage leukemia trithorax homolog, Drosophila ; translocated to, 4 | 0.00% | 0.00% | 1.6E-02 | P55196 | -1 | MLLT4 | 82 ± 4 % | 64 ± 6 % | 18% |
| vesicle transport through interaction with t-SNAREs 1B homolog | 0.00% | 0.00% | 3.8E-02 | Q9UEU0 | -1 | VT11B | 62 ± 2 % | 54 ± 3 % | 8% |
| MCM2 minichromosome maintenance deficient 2, mitotin S. cerevisiae | 0.00% | 0.00% | 1.1E-01 | P49736 | 1 | MCM2 | 20 ± 4 % | 34 ± 8 % | 14% |
| BCL2-antagonist/killer 1 | 0.00% | 0.01% | 3.9E-10 | Q16611 | -1 | BAK1 | 53 ± 2 % | 36 ± 1 % | 17% |
| transforming growth factor, beta 1 Camurati-Engelmann disease | 0.00% | 0.01% | 4.2E-09 | P01137 | -1 | TGFB1 | 84 ± 2 % | 59 ± 3 % | 26% |
| diaphanous homolog 1 Drosophila | 0.00% | 0.01% | 5.9E-04 | O60610 | -1 | DIAF1 | 77 ± 6 % | 50 ± 5 % | 28% |
| serine or cysteine proteinase inhibitor, clade B ovalbumin , member 5 | 0.00% | 0.03% | 3.4E-10 | P36952 | -1 | SERPINB5 | 43 ± 2 % | 25 ± 1 % | 18% |
| 5-hydroxytryptamine serotonin receptor 2C | 0.00% | 0.03% | 1.6E-10 | P28335 | -1 | HTR2C | 79 ± 2 % | 45 ± 4 % | 34% |
| transcription factor Dp-1 | 0.00% | 0.04% | 5.4E-10 | Q14186 | -1 | TFDP1 | 46 ± 2 % | 29 ± 2 % | 18% |
| OLF-1/EBF associated zinc finger gene | 0.00% | 0.04% | 2.8E-06 | Q08961 | -1 | ROAZ | 76 ± 4 % | 42 ± 4 % | 33% |
| mitogen-activated protein kinase kinase 5 | 0.00% | 0.06% | 9.7E-12 | Q92961 | -1 | MAP2K5 | 87 ± 2 % | 40 ± 5 % | 47% |
| contactin 1 | 0.00% | 0.06% | 3.1E-08 | Q12860 | 1 | CNTN1 | 57 ± 3 % | 89 ± 3 % | 31% |
| mitogen-activated protein kinase 3 | 0.00% | 0.06% | 4.3E-04 | P27361 | 1 | MAPK3 | 71 ± 4 % | 88 ± 2 % | 16% |
| interferon-induced protein with tetratricopeptide repeats 4 | 0.00% | 0.07% | 8.8E-06 | O14879 | -1 | IFIT4 | 67 ± 4 % | 45 ± 1 % | 22% |
| glutamate receptor, ionotropic, N-methyl D-aspartate 2B | 0.00% | 0.07% | 5.7E-02 | Q13224 | 0 | GRIN2B | 7 ± 0 % | 7 ± 0 % | 0% |
| chemokine C-C motif ligand 2 | 0.00% | 0.08% | 8.2E-11 | P13500 | 1 | CCL2 | 38 ± 2 % | 73 ± 4 % | 36% |
| catenin cadherin-associated protein , beta 1, 88kDa | 0.00% | 0.08% | 5.2E-10 | P35222 | 1 | CTNNB1 | 28 ± 3 % | 57 ± 2 % | 29% |
| exportin 1 CRM1 homolog, yeast | 0.00% | 0.08% | 9.2E-14 | Q14980 | 1 | XPO1 | 27 ± 2 % | 66 ± 3 % | 39% |
| recombination activating gene 2 | 0.00% | 0.09% | 2.4E-08 | P55895 | 1 | RAG2 | 32 ± 3 % | 72 ± 5 % | 40% |
| chromogranin A parathyroid secretory protein 1 | 0.00% | 0.09% | 2.6E-11 | P10645 | -1 | CHGA | 88 ± 3 % | 41 ± 4 % | 46% |
| nitric oxide synthase 2A inducible, hepatocytes | 0.00% | 0.09% | 1.7E-11 | P35228 | 1 | NOS2A | 46 ± 5 % | 91 ± 2 % | 45% |
| tumor protein p53 binding protein, 2 | 0.00% | 0.10% | 4.5E-40 | Q13625 | -1 | TP53BP2 | 96 ± 0 % | 19 ± 1 % | 77% |
| ID | SAM | Swiss-Prot | Gen* code | HUGO | RANK |
|----|-----|-----------|-----------|------|------|
|     | q-value | local-FDR | t-test |      |      | Females | Males | Delta |
| ubiquitin fusion degradation 1-like | 0.00% | 0.10% | 2.4E-09 | Q92890 | 1 | UFD1L | 53 ± 4 % | 88 ± 2 % | 34% |
| huntingtin-associated protein 1 neuroan 1 | 0.00% | 0.11% | 1.4E-09 | P54257 | 1 | HAP1 | 36 ± 2 % | 77 ± 4 % | 41% |
| ankyrin 2, neuronal | 0.00% | 0.12% | 4.9E-14 | Q01484 | 1 | ANK2 | 57 ± 2 % | 86 ± 1 % | 28% |
| phosphoinositide-3-kinase, regulatory subunit, polyprotein 1 p85 alpha | 0.00% | 0.12% | 9.0E-16 | P27986 | 1 | PIK3R1 | 54 ± 2 % | 90 ± 2 % | 37% |
| caveolin 1, caveolae protein, 22kDa | 0.00% | 0.12% | 3.4E-08 | Q03135 | 1 | CAV1 | 60 ± 4 % | 89 ± 1 % | 29% |
| tripartite motif-containing 28 | 0.00% | 0.12% | 7.0E-14 | Q13263 | 1 | TRIM28 | 41 ± 2 % | 78 ± 3 % | 37% |
| plectin 1, intermediate filament binding protein 500kDa | 0.00% | 0.12% | 6.6E-13 | Q15149 | -1 | PLEC1 | 85 ± 2 % | 58 ± 2 % | 27% |
| SV40 Large T Antigen | 0.00% | 0.12% | 1.0E-09 | P03070 | -1 | - | 91 ± 1 % | 68 ± 3 % | 23% |
| general transcription factor II, i | 0.00% | 0.13% | 1.6E-14 | Q15359 | 1 | GTF2I | 45 ± 4 % | 96 ± 1 % | 52% |
| phospholipase C, beta 1 phosphoinositide-specific | 0.00% | 0.13% | 1.3E-24 | Q9NQ66 | 1 | PLCB1 | 26 ± 2 % | 94 ± 1 % | 68% |
| caspase 7, apoptosis-related cysteine protease | 0.00% | 0.13% | 3.0E-20 | P55210 | 1 | CASP7 | 18 ± 1 % | 80 ± 4 % | 62% |
| CDC37 cell division cycle 37 homolog S. cerevisiae | 0.00% | 0.13% | 1.4E-18 | Q16543 | 1 | CDC37 | 25 ± 1 % | 72 ± 3 % | 47% |
| heme oxygenase decycling 1 | 0.00% | 0.13% | 2.6E-14 | P09601 | -1 | HMOX1 | 65 ± 3 % | 31 ± 1 % | 34% |
| IQ motif containing GTPase activating protein 1 | 0.00% | 0.13% | 2.1E-14 | P46940 | -1 | IQGAP1 | 88 ± 1 % | 46 ± 4 % | 43% |
| antigen identified by monoclonal antibody Ki-67 | 0.00% | 0.14% | 1.2E-16 | P46013 | -1 | MKI67 | 73 ± 2 % | 33 ± 1 % | 40% |
| multiple PDZ domain protein | 0.00% | 0.15% | 3.7E-39 | Q75970 | -1 | MPDZ | 95 ± 1 % | 17 ± 2 % | 77% |
| tumor protein p53 Li-Fraumeni syndrome | 0.00% | 0.15% | 4.6E-26 | P04637 | -1 | TP53 | 91 ± 2 % | 24 ± 2 % | 67% |
| neuronal Shc | 0.00% | 0.15% | 1.8E-25 | Q92529 | -1 | SHC3 | 87 ± 2 % | 27 ± 2 % | 61% |
| protein kinase C, epsilon | 0.00% | 0.15% | 1.8E-18 | Q02156 | -1 | PKCE | 96 ± 1 % | 54 ± 3 % | 42% |
| protein tyrosine phosphatase, non-receptor type 1 | 0.00% | 0.15% | 2.1E-17 | P18031 | -1 | PTPN1 | 76 ± 2 % | 50 ± 1 % | 26% |
| nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 | 0.00% | 0.15% | 5.5E-17 | Q13469 | -1 | NFATC2 | 95 ± 1 % | 59 ± 3 % | 36% |
| myogenic factor 3 | 0.00% | 0.15% | 1.8E-12 | P15172 | -1 | MYOD1 | 49 ± 2 % | 26 ± 1 % | 23% |
| topoisomerase DNA II beta 180kDa | 0.00% | 0.15% | 2.8E-12 | Q02880 | -1 | TOP2B | 62 ± 5 % | 17 ± 1 % | 46% |
| pericentrin 2 kendrin | 0.00% | 0.15% | 6.9E-09 | O95613 | -1 | PCNT | 40 ± 4 % | 14 ± 1 % | 26% |
Supplemental Table 4:

Most Significant Rank-Order Differences in Male Platelets

Details:

1. Cohort: 8 males and 8 females.

2. Entries are listed in the order of rank in males.
Supplemental Table 4: Most Significant Rank-Order Differences between Female and Male Platelets. Cohort: 8 males and 8 females. Higher in Males, ordered by rank in males.

| ID                                      | Rank in Females | Rank in Males | Delta Rank | local FDR | Symbol     |
|-----------------------------------------|-----------------|---------------|------------|-----------|------------|
| general transcription factor II, i     | (44.8 ± 3.7)%   | (96.5 ± 1.0)% | ↓ 51.7%    | 13%       | GTF2I      |
| Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) | (78.2 ± 4.0)%   | (94.9 ± 1.3)% | ↓ 16.7%    | 0%        | MDM2       |
| phospholipase C, beta 1 (phosphoinositide-specific) | (26.0 ± 1.9)%   | (93.9 ± 1.1)% | ↓ 67.9%    | 13%       | PLCB1      |
| sortilin-related receptor, L(DLR class) A repeats-containing | (74.4 ± 2.3)%   | (93.6 ± 1.5)% | ↓ 19.3%    | 0%        | SORL1      |
| ras homolog gene family, member A      | (75.1 ± 2.6)%   | (93.5 ± 1.5)% | ↓ 18.4%    | 0%        | RHOA       |
| colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog | (52.1 ± 7.9)%   | (92.9 ± 1.0)% | ↓ 40.8%    | 0%        | CSF1R      |
| homer homolog 1 (Drosophila)           | (77.9 ± 2.4)%   | (92.2 ± 0.9)% | ↓ 14.3%    | 0%        | HOMER1     |
| FK506 binding protein 10, 65 kDa       | (56.2 ± 5.3)%   | (90.7 ± 2.0)% | ↓ 34.5%    | 0%        | FKBP10     |
| phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) | (53.9 ± 2.4)%   | (90.4 ± 2.0)% | ↓ 36.5%    | 12%       | PIK3R1     |
| caveolin 1, caveolae protein, 22kDa    | (59.6 ± 4.5)%   | (89.0 ± 0.9)% | ↓ 29.5%    | 12%       | CAV1       |
| proliferating cell nuclear antigen     | (69.6 ± 3.4)%   | (88.8 ± 2.1)% | ↓ 19.2%    | 0%        | PCNA       |
| contactin 1                            | (57.3 ± 3.5)%   | (88.6 ± 2.7)% | ↓ 31.4%    | 6%        | CNTN1      |
| mitogen-activated protein kinase 3     | (71.5 ± 3.9)%   | (87.7 ± 2.0)% | ↓ 16.2%    | 6%        | MAPK3      |
| ubiquitin fusion degradation 1-like     | (53.2 ± 4.4)%   | (87.6 ± 1.7)% | ↓ 34.4%    | 10%       | UFD1L      |
| ubiquitin-conjugating enzyme E2L 3     | (78.6 ± 2.2)%   | (87.4 ± 1.0)% | ↓ 8.9%     | 0%        | UBE2L3     |
| general transcription factor IIB       | (62.7 ± 3.5)%   | (87.3 ± 3.1)% | ↓ 24.6%    | 0%        | GTF2B      |
| myogenin (myogenic factor 4)           | (72.5 ± 3.3)%   | (86.7 ± 1.6)% | ↓ 14.3%    | 0%        | MYOG       |
| A kinase (PRKA) anchor protein (yotiao) 9 | (40.7 ± 2.7)%   | (86.1 ± 2.7)% | ↓ 45.4%    | 0%        | AKAP9      |
| telomeric repeat binding factor 2      | (69.5 ± 2.8)%   | (86.1 ± 1.7)% | ↓ 16.6%    | 0%        | TERF2      |
| ankyrin 2, neuronal                     | (57.3 ± 2.3)%   | (85.7 ± 1.5)% | ↓ 28.4%    | 12%       | ANK2       |
| signal-induced proliferation-associated gene 1 | (67.2 ± 2.9)%   | (85.2 ± 1.6)% | ↓ 18.0%    | 0%        | SIPA1      |
| active BCR-related gene                | (62.8 ± 3.5)%   | (84.4 ± 1.6)% | ↓ 21.6%    | 0%        | ABR        |
| HPV-16 L1                               | (59.1 ± 4.0)%   | (84.2 ± 3.3)% | ↓ 25.2%    | 0%        | HPV16L1    |
| density-regulated protein               | (71.7 ± 2.5)%   | (84.2 ± 1.9)% | ↓ 12.4%    | 0%        | DENR       |
| TNF receptor-associated factor 2        | (65.7 ± 4.0)%   | (84.0 ± 3.7)% | ↓ 18.3%    | 0%        | TRAF2      |
| ID | Rank in Females | Rank in Males | Delta Rank | local FDR | Symbol |
|----|----------------|---------------|------------|-----------|--------|
| aldehyde dehydrogenase 1 family, member A1 | (44.3 ± 3.8)% | (83.5 ± 4.7)% | ↓ 39.2% | 0% | ALDH1A1 |
| cyclin D1 (PRAD1: parathyroid adenomatosiS 1) | (69.5 ± 2.3)% | (83.5 ± 2.1)% | ↓ 14.1% | 0% | - |
| ribosomal protein S6 kinase, 70kDa, polypeptide 1 | (59.2 ± 5.2)% | (83.3 ± 3.2)% | ↓ 24.1% | 0% | RPS6KB1 |
| A kinase (PRKA) anchor protein (gravin) 12 | (31.6 ± 0.9)% | (83.2 ± 3.0)% | ↓ 51.6% | 0% | AKAP12 |
| ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | (37.5 ± 2.1)% | (83.1 ± 2.6)% | ↓ 45.6% | 0% | RAC1 |
| clathrin, heavy polypeptide (Hc) | (61.2 ± 3.8)% | (82.8 ± 1.7)% | ↓ 21.6% | 0% | CLTC |
| tubulin, beta polypeptide | (63.6 ± 3.5)% | (82.7 ± 3.6)% | ↓ 19.1% | 0% | TUB1 |
| cytoplasmic linker 2 | (69.3 ± 3.2)% | (82.6 ± 3.1)% | ↓ 13.4% | 0% | CYLN2 |
| polyamine-modulated factor 1 | (64.4 ± 3.2)% | (82.2 ± 3.4)% | ↓ 17.8% | 0% | PMF1 |
| nuclear transport factor 2 | (60.4 ± 3.9)% | (81.4 ± 4.5)% | ↓ 20.9% | 0% | NUTF2 |
| retinol binding protein 4, plasma | (56.2 ± 2.7)% | (81.4 ± 2.4)% | ↓ 25.2% | 0% | RBP4 |
| heat shock 90kDa protein 1, alpha | (64.2 ± 2.2)% | (81.1 ± 2.7)% | ↓ 16.9% | 0% | HSPA6 |
| adaptor-related protein complex 3, mu 1 subunit | (62.6 ± 4.0)% | (81.0 ± 4.5)% | ↓ 18.4% | 0% | AP3M1 |
| kallikrein 10 | (64.1 ± 3.5)% | (81.0 ± 3.8)% | ↓ 16.9% | 0% | KLK10 |
| ribosomal protein S6 kinase, 90kDa, polypeptide 1 | (50.4 ± 6.3)% | (80.0 ± 4.6)% | ↓ 29.6% | 0% | RPS6KA1 |
| caspase 7, apoptosis-related cysteine protease | (17.8 ± 1.3)% | (79.9 ± 3.8)% | ↓ 62.0% | 13% | CASP7 |
| leucine zipper, putative tumor suppressor 1 | (61.7 ± 3.7)% | (79.0 ± 2.8)% | ↓ 17.3% | 0% | LZTS1 |
| cell division cycle 2, G1 to S and G2 to M | (65.7 ± 2.2)% | (79.0 ± 1.8)% | ↓ 13.3% | 0% | CDC2 |
| protein tyrosine phosphatase, receptor-type, Z polypeptide 1 | (56.5 ± 5.5)% | (78.3 ± 5.3)% | ↓ 21.8% | 0% | PTPRZ1 |
| tripartite motif-containing 28 | (41.0 ± 2.0)% | (78.0 ± 3.0)% | ↓ 37.0% | 12% | TRIM28 |
| huntingtin-associated protein 1 (neuroan) | (35.9 ± 2.1)% | (76.7 ± 4.4)% | ↓ 41.0% | 11% | HAP1 |
| doublecortin and CaM kinase-like 1 | (66.8 ± 1.8)% | (75.6 ± 1.0)% | ↓ 8.7% | 0% | DCAMKL1 |
| Ras protein-specific guanine nucleotide-releasing factor 2 | (48.1 ± 3.7)% | (75.3 ± 3.2)% | ↓ 27.3% | 0% | RASGRF2 |
| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 | (32.1 ± 2.5)% | (75.2 ± 4.9)% | ↓ 43.1% | 0% | SLC9A3R1 |
| COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis) | (55.1 ± 3.8)% | (74.9 ± 3.4)% | ↓ 19.9% | 0% | COP5 |
| golgi autoantigen, golgin subfamily a, 2 | (59.9 ± 3.1)% | (74.9 ± 1.8)% | ↓ 15.1% | 0% | GOLGA2 |
| chemokine (C-C motif) ligand 2 | (37.7 ± 2.4)% | (73.4 ± 3.7)% | ↓ 35.7% | 8% | CCL2 |
| dynein, cytoplasmic, light polypeptide 1 | (49.3 ± 2.6)% | (73.3 ± 2.3)% | ↓ 24.0% | 0% | DNCL1 |
| recombination activating gene 2 | (32.0 ± 2.6)% | (72.4 ± 4.9)% | ↓ 40.4% | 9% | RAG2 |
| ID                                      | Rank in Females | Rank in Males | Delta Rank | local FDR | Symbol          |
|-----------------------------------------|-----------------|---------------|------------|-----------|-----------------|
| CDC37 cell division cycle 37 homolog (S. cerevisiae) | (24.5 ± 1.5)%   | (71.6 ± 3.0)% | ↓ 47.1%    | 13%       | CDC37           |
| v-crk sarcoma virus CT10 oncogene homolog (avian) | (58.0 ± 3.1)%   | (71.3 ± 2.1)% | ↓ 13.3%    | 0%        | CRK             |
| serine/threonine kinase 24 (STE20 homolog, yeast) | (36.8 ± 3.0)%   | (71.1 ± 6.3)% | ↓ 34.3%    | 0%        | STK24           |
| translocase of inner mitochondrial membrane 23 homolog (yeast) | (49.9 ± 4.5)%   | (69.9 ± 3.8)% | ↓ 20.0%    | 0%        | TIMM23          |
| RAS p21 protein activator (GTPase activating protein) 1 | (48.2 ± 4.1)%   | (69.7 ± 3.2)% | ↓ 21.6%    | 0%        | RASA1           |
| CDC-like kinase 1 | (35.1 ± 4.1)%   | (66.7 ± 5.6)% | ↓ 31.6%    | 0%        | CLK1            |
| exportin 1 (CRM1 homolog, yeast) | (27.4 ± 1.6)%   | (66.4 ± 2.7)% | ↓ 39.0%    | 8%        | XPO1            |
| glutamate-ammonia ligase (glutamine synthase) | (39.5 ± 4.6)%   | (66.0 ± 8.0)% | ↓ 26.5%    | 0%        | GLUL            |
| topoisomerase (DNA) I | (37.3 ± 4.7)%   | (63.3 ± 5.3)% | ↓ 26.0%    | 0%        | TOP1            |
| phospholipase C, gamma 1 (formerly subtype 148) | (50.8 ± 3.3)%   | (63.2 ± 2.4)% | ↓ 12.5%    | 0%        | PLCG1           |
| G antigen 7 | (36.4 ± 2.8)%   | (58.5 ± 4.4)% | ↓ 22.0%    | 0%        | GAGE7           |
| interleukin 6 (interferon, beta 2) | (40.0 ± 1.7)%   | (58.0 ± 3.9)% | ↓ 18.0%    | 0%        | IL6             |
| catenin (cadherin-associated protein), beta 1, 88kDa | (28.5 ± 2.8)%   | (57.2 ± 2.5)% | ↓ 28.7%    | 8%        | CTNNB1          |
| protein phosphatase 1, regulatory (inhibitor) subunit 2 | (34.8 ± 2.6)%   | (56.7 ± 3.6)% | ↓ 22.0%    | 0%        | PPP1R2          |
| nuclear receptor coactivator 3 | (40.8 ± 2.5)%   | (56.1 ± 2.2)% | ↓ 15.3%    | 0%        | NCOA3           |
| F11 receptor | (31.4 ± 3.6)%   | (55.9 ± 4.0)% | ↓ 24.5%    | 0%        | F11R            |
| DNA fragmentation factor, 45kDa, alpha polypeptide | (39.1 ± 2.4)%   | (54.5 ± 2.0)% | ↓ 15.4%    | 0%        | DFFA            |
| thymopoietin | (41.1 ± 2.9)%   | (54.4 ± 1.8)% | ↓ 13.3%    | 0%        | TMPO            |
| fatty acid synthase | (36.0 ± 3.6)%   | (52.5 ± 4.2)% | ↓ 16.6%    | 0%        | FASN            |
| non-metastatic cells 1, protein (NM23A) expressed in | (23.0 ± 1.2)%   | (51.3 ± 5.2)% | ↓ 28.3%    | 0%        | NME1            |
| likely ortholog of mouse raphphilin 3A | (21.0 ± 2.6)%   | (50.2 ± 7.1)% | ↓ 29.2%    | 0%        | RPH3A           |
| son of sevenless homolog 1 (Drosophila) | (4.0 ± 0.1)%    | (5.0 ± 0.2)%  | ↓ 1.0%     | 0%        | SOS1            |
| ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast) | (23.1 ± 2.3)%  | (39.0 ± 3.2)% | ↓ 16.0%    | 0%        | UBE2E1          |
| CrmA | (21.6 ± 0.4)%   | (35.9 ± 2.8)% | ↓ 14.3%    | 0%        | CRMA            |
| MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae) | (20.4 ± 4.1)%   | (34.3 ± 7.6)% | ↓ 13.9%    | 0%        | MCM2            |
| spleen focus forming virus (SFFV) proviral integration oncogene sp1 | (13.5 ± 0.8)% | (23.2 ± 1.8)% | ↓ 9.6%     | 0%        | SPI1            |
| growth associated protein 43 | (0.9 ± 0.2)%    | (2.3 ± 0.2)%  | ↓ 1.4%     | 0%        | GAP43           |
| baculoviral IAP repeat-containing 6 (apollon) | (12.0 ± 0.5)%  | (17.0 ± 0.7)% | ↓ 5.0%     | 0%        | BIRC6           |
| adenomatosis polyposis coli | (7.1 ± 1.0)%    | (14.7 ± 2.5)% | ↓ 7.6%     | 0%        | APC             |
Supplemental Table 5:

Most Significant Rank-Order Differences in Female Platelets

Details:
1. Cohort: 8 males and 8 females.
2. Entries are listed in the order of rank in females.
Supplemental Table 5: Most Significant Rank-Order Differences between Female and Male Platelets. Cohort: 8 males and 8 females. Higher in Females, ordered by rank in females.

| ID                                                   | Rank in Females | Rank in Males | Delta Rank | local FDR | Symbol     |
|------------------------------------------------------|-----------------|---------------|------------|-----------|------------|
| tumor protein p53 binding protein, 2                | (96.4 ± 0.5)%   | (19.0 ± 0.6)% | ↑ 77.4%    | 10%       | TP53BP2    |
| protein kinase C, epsilon                           | (96.3 ± 1.0)%   | (53.9 ± 2.9)% | ↑ 42.3%    | 15%       | PRKCE      |
| multiple PDZ domain protein                         | (94.8 ± 0.7)%   | (17.5 ± 1.6)% | ↑ 77.3%    | 15%       | MPDZ       |
| nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 | (94.7 ± 0.9)% | (58.5 ± 2.7)% | ↑ 36.2%    | 15%       | NFATC2     |
| synapsin II                                         | (94.0 ± 0.7)%   | (33.9 ± 2.0)% | ↑ 60.2%    | 0%        | SYN2       |
| cell division cycle 27                              | (93.8 ± 1.3)%   | (61.2 ± 6.7)% | ↑ 32.6%    | 0%        | CDC27      |
| DEAD (Asp-Glu-Ala-Asp) box polypeptide 1             | (93.4 ± 1.8)%   | (58.4 ± 5.4)% | ↑ 34.9%    | 0%        | DD1        |
| scavenger receptor class B, member 1                 | (93.0 ± 1.6)%   | (42.0 ± 7.3)% | ↑ 50.9%    | 0%        | SCARB1     |
| centrosomal protein 2                               | (92.1 ± 2.1)%   | (62.6 ± 5.0)% | ↑ 29.5%    | 0%        | CEP2       |
| neuropilin 2                                         | (91.9 ± 1.7)%   | (59.4 ± 5.6)% | ↑ 32.5%    | 0%        | NRP2       |
| tumor protein p53 (Li-Fraumeni syndrome)             | (91.2 ± 2.5)%   | (23.8 ± 1.9)% | ↑ 67.4%    | 15%       | TP53       |
| SV40 Large T Antigen                                | (91.0 ± 0.6)%   | (68.0 ± 3.0)% | ↑ 23.0%    | 12%       | -          |
| v-myc myelocytomatosis viral oncogene homolog (avian) | (90.6 ± 2.4)% | (24.9 ± 1.9)% | ↑ 65.7%    | 0%        | MYC        |
| proteasome (prosome, macropain) 26S subunit, ATPase, 5 | (89.8 ± 1.9)% | (26.8 ± 1.0)% | ↑ 63.0%    | 0%        | PSMC5      |
| amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen) | (89.3 ± 3.6)% | (48.2 ± 4.1)% | ↑ 41.1%    | 0%        | AMPH       |
| nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) | (88.5 ± 3.2)% | (57.3 ± 7.3)% | ↑ 31.1%    | 0%        | NR3C1      |
| conserved helix-loop-helix ubiquitous kinase         | (88.5 ± 2.1)%   | (62.2 ± 4.4)% | ↑ 26.4%    | 0%        | CHUK       |
| IQ motif containing GTPase activating protein 1       | (88.4 ± 1.2)%   | (45.5 ± 3.8)% | ↑ 42.9%    | 13%       | IQGAP1     |
| chromogranin A (parathyroid secretory protein 1)     | (87.5 ± 2.8)%   | (41.1 ± 3.7)% | ↑ 46.4%    | 9%        | CHGA       |
| synaptotagmin 1                                      | (87.5 ± 1.2)%   | (32.5 ± 1.5)% | ↑ 55.0%    | 0%        | SYT1       |
| neuronal Shc                                         | (97.2 ± 1.7)%   | (26.5 ± 2.3)% | ↑ 70.7%    | 15%       | SCC2       |
| neurexin 1                                           | (86.9 ± 2.4)%   | (46.5 ± 7.1)% | ↑ 40.4%    | 0%        | NRXN1      |
| mitogen-activated protein kinase kinase 5             | (86.6 ± 2.0)%   | (40.1 ± 4.9)% | ↑ 46.5%    | 6%        | MAP2K5     |
| RAB5A, member RAS oncogene family                    | (85.9 ± 2.3)%   | (58.7 ± 1.8)% | ↑ 27.2%    | 0%        | RAB5A      |
| SFRS protein kinase 1                                | (85.7 ± 2.4)%   | (48.0 ± 5.3)% | ↑ 37.6%    | 0%        | SRPK1      |
| ID                                                                 | Rank in Females       | Rank in Males       | Delta Rank | local FDR | Symbol      |
|-------------------------------------------------------------------|----------------------|---------------------|------------|-----------|-------------|
| phosphatidylinositol 4-kinase, catalytic, beta polypeptide       | (85.6 ± 1.4)%         | (37.6 ± 1.6)%       | ↑ 47.9%    | 0%        | PIK4CB      |
| plectin 1, intermediate filament binding protein 500kDa          | (84.9 ± 1.7)%         | (57.9 ± 2.2)%       | ↑ 27.0%    | 12%       | PLEC1       |
| transforming growth factor, beta 1 (Camurati-Engelmann disease)  | (84.4 ± 2.1)%         | (58.8 ± 2.5)%       | ↑ 25.6%    | 0%        | TGFBI       |
| annexin A11                                                       | (84.1 ± 5.4)%         | (19.1 ± 1.4)%       | ↑ 65.0%    | 0%        | ANXA11      |
| apolipoprotein E                                                  | (83.8 ± 2.0)%         | (62.8 ± 3.7)%       | ↑ 21.0%    | 0%        | APOE        |
| protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) | (82.4 ± 2.5)%         | (27.5 ± 0.9)%       | ↑ 54.9%    | 0%        | PTPN11      |
| myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila; translocated to, 4) | (81.9 ± 3.7)%         | (63.7 ± 6.4)%       | ↑ 18.2%    | 0%        | MLLT4       |
| interleukin 1, beta                                              | (80.3 ± 4.4)%         | (37.6 ± 6.8)%       | ↑ 42.8%    | 0%        | IL1B        |
| tumor protein p73                                                 | (80.2 ± 3.9)%         | (61.7 ± 3.6)%       | ↑ 18.5%    | 0%        | TP73        |
| caspase 4, apoptosis-related cysteine protease                    | (80.2 ± 3.8)%         | (47.2 ± 7.4)%       | ↑ 33.0%    | 0%        | CASP4       |
| cell division cycle 34                                            | (79.3 ± 4.9)%         | (54.6 ± 3.3)%       | ↑ 24.7%    | 0%        | CDC34       |
| lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) | (79.3 ± 3.5)%         | (38.3 ± 3.7)%       | ↑ 41.0%    | 0%        | LCP2        |
| cyclin D3                                                        | (79.0 ± 3.3)%         | (59.9 ± 3.6)%       | ↑ 19.1%    | 0%        | CCND3       |
| 5-hydroxytryptamine (serotonin) receptor 2C                       | (78.9 ± 1.7)%         | (45.0 ± 3.9)%       | ↑ 33.8%    | 3%        | HTR2C       |
| von Hippel-Lindau syndrome                                        | (78.7 ± 3.0)%         | (67.8 ± 2.2)%       | ↑ 10.9%    | 0%        | VHL         |
| lysosomal-associated membrane protein 1                           | (78.5 ± 2.4)%         | (55.7 ± 6.4)%       | ↑ 22.8%    | 0%        | LAMP1       |
| 5-hydroxytryptamine (serotonin) receptor 2A                       | (78.4 ± 4.1)%         | (51.6 ± 4.7)%       | ↑ 26.8%    | 0%        | HTR2A       |
| diaphanous homolog 1 (Drosophila)                                | (77.5 ± 6.0)%         | (50.0 ± 4.6)%       | ↑ 27.5%    | 1%        | DIAPH1      |
| protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) | (77.4 ± 1.8)%         | (66.4 ± 2.2)%       | ↑ 11.0%    | 0%        | PRKAR1A      |
| cytokine-inducible kinase                                         | (76.9 ± 4.5)%         | (42.0 ± 6.0)%       | ↑ 34.9%    | 0%        | PLK3        |
| protein tyrosine phosphatase, non-receptor type 1                 | (75.8 ± 1.6)%         | (50.1 ± 1.2)%       | ↑ 25.7%    | 15%       | PTPN1       |
| Fas (TNFRSF6)-associated via death domain                         | (75.7 ± 2.7)%         | (58.1 ± 2.9)%       | ↑ 17.6%    | 0%        | FADD        |
| OLF-1/EBF associated zinc finger gene                             | (75.6 ± 4.1)%         | (42.4 ± 4.3)%       | ↑ 33.2%    | 4%        | ZNF423       |
| tight junction protein 1 (zona occludens 1)                       | (75.3 ± 3.8)%         | (53.9 ± 3.2)%       | ↑ 21.4%    | 0%        | TJP1        |
| MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) | (75.1 ± 3.5)%         | (52.9 ± 3.0)%       | ↑ 22.2%    | 0%        | MCM5        |
| adaptor-related protein complex 3, beta 2 subunit                 | (75.0 ± 2.2)%         | (55.8 ± 3.8)%       | ↑ 19.2%    | 0%        | AP3B2       |
| ID                                           | Rank in Females       | Rank in Males       | Delta Rank | local FDR | Symbol  |
|----------------------------------------------|-----------------------|---------------------|------------|-----------|---------|
| LIM domain binding 3                         | (74.9 ± 4.5)%         | (50.9 ± 5.0)%       | ↑ 24.0%    | 0%        | LDB3    |
| docking protein 1, 62kDa (downstream of tyrosine kinase 1) | (74.9 ± 1.6)%         | (52.3 ± 4.0)%       | ↑ 22.6%    | 0%        | DOK1    |
| protein kinase, cAMP-dependent, regulatory, type II, alpha | (73.7 ± 2.8)%         | (56.9 ± 1.6)%       | ↑ 16.9%    | 0%        | PRKAR2A |
| antigen identified by monoclonal antibody Ki-67 | (73.3 ± 2.0)%         | (33.1 ± 1.5)%       | ↑ 40.1%    | 14%       | MKI67   |
| early endosome antigen 1, 162kD              | (71.3 ± 3.8)%         | (49.5 ± 3.2)%       | ↑ 21.8%    | 0%        | EEA1    |
| gelsolin (amyloidosis, Finnish type)         | (71.1 ± 4.6)%         | (49.0 ± 4.3)%       | ↑ 22.0%    | 0%        | GSN     |
| A kinase (PRKA) anchor protein 5             | (70.9 ± 2.5)%         | (51.4 ± 2.9)%       | ↑ 19.5%    | 0%        | AKAP5   |
| deleted in colorectal carcinoma              | (70.3 ± 5.1)%         | (36.4 ± 6.5)%       | ↑ 33.9%    | 0%        | DCC     |
| survival of motor neuron protein interacting protein 1 | (70.2 ± 6.5)%         | (43.2 ± 5.1)%       | ↑ 27.0%    | 0%        | SIP1    |
| MAX protein                                  | (70.1 ± 4.6)%         | (42.2 ± 5.0)%       | ↑ 27.9%    | 0%        | MAX     |
| flap structure-specific endonuclease 1       | (7.7 ± 0.3)%          | (5.4 ± 0.3)%        | ↑ 2.3%     | 0%        | FEN1    |
| citron (rho-interacting, serine/threonine kinase 21) | (69.7 ± 4.0)%         | (36.9 ± 2.8)%       | ↑ 32.8%    | 0%        | CIT     |
| calnexin                                     | (69.1 ± 7.2)%         | (35.6 ± 3.4)%       | ↑ 33.5%    | 0%        | CANX    |
| interferon-induced protein with tetratricopeptide repeats 4 | (67.1 ± 4.4)%         | (44.8 ± 1.1)%       | ↑ 22.3%    | 7%        | IFIT3   |
| heme oxygenase (decycling) 1                 | (65.0 ± 2.9)%         | (30.8 ± 1.3)%       | ↑ 34.2%    | 13%       | HMOX1   |
| BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) | (64.4 ± 4.3)%         | (33.9 ± 2.3)%       | ↑ 30.5%    | 0%        | BUB3    |
| topoisomerase (DNA) II beta 180kDa           | (62.4 ± 4.9)%         | (16.6 ± 0.8)%       | ↑ 45.8%    | 15%       | TOP2B   |
| gephrin                                      | (61.6 ± 2.4)%         | (47.1 ± 2.3)%       | ↑ 14.4%    | 0%        | GPHN    |
| vesicle transport through interaction with t-SNAREs 1B homolog | (61.6 ± 2.0)%         | (54.1 ± 3.0)%       | ↑ 7.6%     | 0%        | VTI1B   |
| lymphocyte-specific protein tyrosine kinase  | (61.5 ± 5.4)%         | (28.7 ± 2.0)%       | ↑ 32.9%    | 0%        | LCK     |
| optineurin                                   | (61.0 ± 2.5)%         | (42.9 ± 3.4)%       | ↑ 18.1%    | 0%        | OPTN    |
| polymerase (DNA directed), epsilon           | (60.5 ± 1.5)%         | (13.6 ± 0.5)%       | ↑ 46.8%    | 0%        | POLE    |
| leukocyte-associated Ig-like receptor 1      | (60.2 ± 2.1)%         | (40.2 ± 1.9)%       | ↑ 20.0%    | 0%        | LAIR1   |
| elongation factor-2 kinase                   | (58.6 ± 2.9)%         | (42.6 ± 3.2)%       | ↑ 16.0%    | 0%        | EEF2K   |
| sorting nexin 2                              | (57.4 ± 2.9)%         | (40.4 ± 3.1)%       | ↑ 17.0%    | 0%        | SNX2    |
| MCM4 minichromosome maintenance deficient 4 (S. cerevisiae) | (56.3 ± 2.7)%         | (41.5 ± 3.2)%       | ↑ 14.8%    | 0%        | MCM4    |
| TRAF family member-associated NFKB activator | (54.5 ± 2.0)%         | (36.1 ± 1.6)%       | ↑ 18.5%    | 0%        | TANK    |
| epidermal growth factor receptor pathway substrate 8 | (53.1 ± 2.7)%         | (38.6 ± 3.6)%       | ↑ 14.5%    | 0%        | EPS8    |
| BCL2-antagonist/killer 1                     | (52.7 ± 1.8)%         | (36.0 ± 1.2)%       | ↑ 16.7%    | 1%        | BAK1    |
| origin recognition complex, subunit 5-like (yeast) | (52.6 ± 1.2)%         | (37.2 ± 1.9)%       | ↑ 15.4%    | 0%        | ORC5L   |
| ID                                      | Rank in Females | Rank in Males | Delta Rank | local FDR | Symbol     |
|-----------------------------------------|-----------------|---------------|------------|-----------|------------|
| endothelin receptor type A              | (52.1 ± 5.0)%   | (24.9 ± 2.1)% | ↑ 27.2%    | 0%        | EDNRA      |
| mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) | (50.1 ± 3.2)% | (35.3 ± 1.5)% | ↑ 14.8%    | 0%        | MSH2       |
| myogenic factor 3                       | (49.4 ± 2.4)%   | (26.3 ± 0.7)% | ↑ 23.1%    | 15%       | MYOD1      |
| Rho-associated, coiled-coil containing protein kinase 2 | (46.6 ± 2.5)% | (34.4 ± 2.1)% | ↑ 12.2%    | 0%        | ROCK2      |
| transcription factor Dp-1               | (46.4 ± 1.8)%   | (28.5 ± 1.5)% | ↑ 17.8%    | 4%        | TFDP1      |
| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 | (43.4 ± 2.1)% | (25.1 ± 1.0)% | ↑ 18.3%    | 3%        | SERPINB5   |
| transforming growth factor beta 1 induced transcript 1 | (40.8 ± 1.9)% | (32.7 ± 1.3)% | ↑ 8.2%     | 0%        | TGFB1I1    |
| pericentrin 2 (kendrin)                 | (40.1 ± 3.7)%   | (14.5 ± 0.6)% | ↑ 25.7%    | 15%       | PCNT       |
| KH domain containing, RNA binding, signal transduction associated 1 | (35.0 ± 2.9)% | (16.7 ± 0.8)% | ↑ 18.3%    | 0%        | KHDRBS1    |
| neurogenin 1                           | (31.9 ± 3.0)%   | (16.4 ± 0.8)% | ↑ 15.5%    | 0%        | NEUROG1    |
| protein kinase, interferon-inducible double stranded RNA dependent | (27.6 ± 2.2)% | (18.2 ± 0.7)% | ↑ 9.4%     | 0%        | PRKRA      |
| protein kinase C-like 2                | (2.6 ± 0.2)%    | (1.8 ± 0.2)%  | ↑ 0.8%     | 0%        | PKN2       |
Supplemental Table 6:

Gender Dependent Platelet Transcription Factors

Details:
1. Cohort: 8 male and 8 female platelet donors.
2. Entries are listed in alphabetical order
a. Transcription Factor Enrichment in Male Platelets

| #  | Name               | Edges | Edges In | Edges Out |
|----|--------------------|-------|----------|-----------|
| 1  | ARNT               | 2     | 0        | 2         |
| 2  | c-Fos              | 15    | 7        | 7         |
| 3  | LZTS1              | 1     | 0        | 1         |
| 4  | Myo1               | 0     | 0        | 0         |
| 5  | MYOG               | 0     | 0        | 0         |
| 6  | PU.1               | 7     | 4        | 2         |
| 7  | SATB1              | 3     | 2        | 1         |
| 8  | STAT3              | 19    | 11       | 8         |
| 9  | TCERG1 (CA150)     | 0     | 0        | 0         |
| 10 | TFI-I              | 6     | 2        | 4         |
| 11 | TIF1-beta          | 1     | 0        | 1         |

b. Transcription Factor Enrichment in Female Platelets

| #  | Name               | Edges | Edges In | Edges Out |
|----|--------------------|-------|----------|-----------|
| 1  | ARNT               | 202   | 0        | 0         |
| 2  | c-Fos              | 15    | 7        | 7         |
| 3  | LZTS1              | 1     | 0        | 1         |
| 4  | Myo1               | 0     | 0        | 0         |
| 5  | MYOG               | 0     | 0        | 0         |
| 6  | PU.1               | 7     | 4        | 2         |
| 7  | SATB1              | 3     | 2        | 1         |
| 8  | STAT3              | 19    | 11       | 8         |
| 9  | TCERG1 (CA150)     | 0     | 0        | 0         |
| 10 | TFI-I              | 6     | 2        | 4         |
| 11 | TIF1-beta          | 1     | 0        | 1         |

* indicates that the core building block protein is present in the platelet proteome, but that none of the known interactants found in the defining literature are also present.
Supplemental Table 7:

Gender-Dependent Platelet Membrane Receptors

Details:
1. Cohort: 8 males and 8 females platelet donors
2. Entries are listed in alphabetical order
3. a = Female specific; b= male-specific

| Receptor | Female Specific | Male Specific |
|----------|----------------|--------------|
| GPIb-IX-V | a              | b            |
| GPVI      | a              | b            |
| GPRA      | a              | b            |
| CD36      | a              | b            |
| CD63      | a              | b            |
Gender Dependent Membrane Receptor Enrichment in Platelets

a. Enriched in Male Platelets

| # | Name                          | Edges | Edges In | Edges Out |
|---|-------------------------------|-------|----------|-----------|
| 1 | Dcc                           | 0     | 0        | 0         |
| 2 | HTR2A                         | 1     | 0        | 1         |
| 3 | HTR2C (HTR1C)                 | 2     | 0        | 1         |
| 4 | Neurexin 1-alpha              | 0     | 0        | 0         |
| 5 | Neuropilin-2                  | 1     | 1        | 0         |
| 6 | PTPRF (LAR)                   | 3     | 1        | 1         |
| 7 | Serotonin receptor *          | 0     | 0        | 0         |
| 8 | Serotonin receptor            | 2     | 2        | 0         |
| 9 | SR-BI                         | 2     | 2        | 0         |
|10 | Synaptotagmin I               | 0     | 0        | 0         |

b. Enriched in Female Platelets

| # | Name                  | Edges | Edges In | Edges Out |
|---|-----------------------|-------|----------|-----------|
| 1 | CSF1R                 | 3     | 2        | 1         |
| 2 | TGA3                  | 0     | 0        | 0         |
| 3 | M-CSF receptor        | 4     | 2        | 1         |
| 4 | M-CSF receptor *      | 0     | 0        | 0         |
| 5 | SORL1                 | 0     | 0        | 0         |
| 6 | Sortilin              | 0     | 0        | 0         |

* indicates that the core building block protein is present in the platelet proteome, but that none of the known interactants found in the defining literature are also present.
Supplemental Table 8

Gender-dependent Platelet Proteome Gene Ontogeny

Details:

1. "a" = increased expression in platelets from male donors.

2. "b" = increased expression in platelets from male donors.

3. "%" column is the percent of objects on the network that are linked to the process.

4. "p-value" is based on the probability that the association is random.
### Gender Dependent Platelet Proteome Gene Ontology

#### a. Increased Expression in Males

| #  | Process                                | %    | p-Value     |
|----|----------------------------------------|------|-------------|
| 1  | regulation of cellular process         | 81.93| 4.21E-18    |
| 2  | regulation of biological process       | 81.93| 1.49E-16    |
| 3  | cell communication                      | 73.49| 5.92E-16    |
| 4  | signal transduction                    | 69.88| 6.95E-16    |
| 5  | intracellular signaling cascade         | 49.4 | 1.46E-15    |
| 6  | biological regulation                  | 84.34| 2.79E-15    |
| 7  | regulation of developmental process    | 37.35| 3.13E-12    |
| 8  | negative regulation of developmental process | 25.3 | 9.54E-12 |
| 9  | negative regulation of apoptosis       | 20.48| 6.86E-11    |
| 10 | negative regulation of programmed cell death | 20.48| 7.98E-11 |
| 11 | cell development                       | 39.76| 1.05E-09    |
| 12 | cell differentiation                   | 46.99| 1.24E-09    |

#### b. Increased Expression in Females

| #  | Process                                | %    | p-Value     |
|----|----------------------------------------|------|-------------|
| 1  | positive regulation of cellular process | 43.53| 2.71E-13    |
| 2  | regulation of cellular process         | 74.12| 4.11E-13    |
| 3  | regulation of biological process       | 75.29| 1.74E-12    |
| 4  | death                                  | 35.29| 1.83E-12    |
| 5  | cell death                             | 35.29| 1.83E-12    |
| 6  | positive regulation of biological process | 43.53| 2.11E-12 |
| 7  | cell development                       | 43.53| 4.11E-12    |
| 8  | intracellular signaling cascade         | 43.53| 4.65E-12    |
| 9  | biological regulation                  | 78.82| 5.97E-12    |
| 10 | developmental process                  | 63.53| 1.84E-11    |
| 11 | programmed cell death                  | 32.94| 2.10E-11    |
| 12 | cell differentiation                   | 49.41| 3.79E-11    |
Supplemental Table 9

Demographic description of platelet donors

Details:

1. The “first set of donors” donated platelets which were used to generate the high abundance (2DGE) and low abundance (antibody Microarray) platelet proteomes.

2. The “second set of donors” were collected two months later, and used to test the tentative conclusions deduced from the first set.

3. The “third set of donors” was collected for the purpose of validating results using Western blot analyses.
### First set of donors

| Donor   | Age | Height (in) | Weight (lbs) |
|---------|-----|-------------|--------------|
| Male 1  | 61  | 68          | 180          |
| Male 2  | 23  | 73          | 170          |
| Male 3  | 25  | 67          | 165          |
| Male 4  | 26  | 67          | 247          |
| Female 5| 46  | 63.5        | 187          |
| Female 6| 30  | 64          | 140          |
| Female 7| 36  | 64          | 147          |
| Female 8| 29  | 65          | 140          |

### Second set of donors

| Donor   | Age | Height (in) | Weight (lbs) |
|---------|-----|-------------|--------------|
| Male 9  | 26  | 69          | 190          |
| Male 10 | 24  | 70          | 230          |
| Male 11 | 35  | 71          | 185          |
| Male 12 | 27  | 67          | 246          |
| Female 13| 46  | 63.5        | 187          |
| Female 14| 31  | 64          | 140          |
| Female 15| 36  | 64          | 147          |
| Female 16| 25  | 60          | 130          |

### Third set of donors (used for Westerns)

| Donor   | Age | Height (in) | Weight (lbs) |
|---------|-----|-------------|--------------|
| Male 17 | 35  | 67          | 183          |
| Male 18 | 25  | 70          | 185          |
| Male 19 | 27  | 69          | 186          |
| Male 20 | 28  | 75          | 225          |
| Female 21| 37  | 59          | 136          |
| Female 22| 24  | 61          | 120          |
| Female 23| 24  | 67          | 130          |
| Female 24| 25  | 64          | 124          |
Supplemental Table 10

Statistical properties of the differences between protein expression levels in male and female cohorts.

Details: Columns are labeled with both short names and lower case letters, as shown below:

- **a.** Name of the protein
- **b.** Sample size needed for 80% power with p<0.05
- **c.** Power for the current cohort of 10 male and 10 female subjects
- **d.** p-value (t-test) for the difference in normalized levels of fluorescent signal (relative to the median of 45 proteins common to all arrays)
- **e.** Local False Discovery Rate calculated by the SAM algorithm for the ranks of each protein.
- **f.** Area under the ROC Curve for the fluorescent levels of each protein in the two cohorts. AUC equal to 1 shows complete separation of the distributions in the two cohorts, i.e., all the values in one cohort are above the cutoff given in column i while all the values in the second cohort are below that cutoff. In order to plot the ROC curves we assumed that the measured replicates for each individual were normally distributed around the respective true level of the given protein, with a width estimated by the standard deviation of the measured replicas. Thus, for each cutoff level the % false Positives and % False Negatives were calculated by integrating the tail of the normal distribution in the respective direction. This approach actually estimates the chance of measuring a False Positive (or False Negative) given the, average, and SD of the measurement for that given cutoff. The AUC values were then calculated by integrating the ROC curve.

- **g.** Average ± Standard Deviation for the normalized fluorescent signals in the female cohort
- **h.** Average ± Standard Deviation for the normalized fluorescent signals in the male cohort
- **i.** Cutoff separating the distribution of signals in the two cohorts
| Protein                                                                 | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC | Female cohort | Male cohort | cutoff |
|------------------------------------------------------------------------|----------------|-----------------|----------------|-------------------|-----|---------------|-------------|--------|
| tumor protein p53 binding protein, 2                                  | 4              | 100%            | 1.2E-27        | 0.1%              |     | 2.0 ± 0.1     | 0.4 ± 0.1   | 1.564  |
| polymerase (DNA directed), epsilon                                    | 5              | 100%            | 1.2E-15        | 0.0%              |     | 1.1 ± 0.1     | 0.3 ± 0.0   | 0.893  |
| stathmin 1/oncoprotein 18                                               | 5              | 100%            | 3.0E-11        | 2.1%              |     | 2.3 ± 0.2     | 1.0 ± 0.0   | 1.906  |
| proteasome (prosome, macropain) 26S subunit, ATPase, 5                | 9              | 90%             | 3.2E-11        | 0.0%              |     | 1.6 ± 0.1     | 0.6 ± 0.1   | 1.242  |
| protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) | 11             | 78%             | 6.8E-11        | 0.0%              |     | 1.4 ± 0.1     | 0.6 ± 0.0   | 1.118  |
| RAS p21 protein activator 2                                            | 12             | 68%             | 1.0E-10        | 10.1%             |     | 0.6 ± 0.1     | 1.8 ± 0.2   | 1.412  |
| thyroid autoantigen 70kDa (Ku antigen)                                 | 12             | 67%             | 6.0E-11        | 10.1%             |     | 0.6 ± 0.1     | 1.5 ± 0.1   | 1.290  |
| synapsin II                                                           | 13             | 60%             | 3.9E-10        | 0.0%              |     | 1.7 ± 0.2     | 0.8 ± 0.1   | 1.427  |
| phospholipase C, beta 1 (phosphoinositide-specific)                    | 14             | 58%             | 1.4E-19        | 0.1%              |     | 0.6 ± 0.2     | 1.8 ± 0.2   | 1.427  |
| synaptotagmin I                                                       | 14             | 54%             | 1.9E-12        | 0.0%              |     | 1.5 ± 0.1     | 0.7 ± 0.1   | 1.275  |
| phosphatidylinositol 4-kinase, catalytic, beta polypeptide             | 17             | 40%             | 3.4E-12        | 0.0%              |     | 1.4 ± 0.1     | 0.8 ± 0.1   | 1.269  |
| annexin A11                                                            | 21             | 26%             | 4.1E-06        | 0.0%              |     | 1.8 ± 0.5     | 0.5 ± 0.1   | 1.142  |
| general transcription factor II, i                                     | 22             | 22%             | 2.4E-15        | 0.1%              |     | 0.9 ± 0.2     | 2.0 ± 0.2   | 1.608  |
| A kinase (PRKA) anchor protein (gravin) 12                             | 22             | 22%             | 6.3E-10        | 0.0%              |     | 0.7 ± 0.1     | 1.6 ± 0.2   | 1.280  |
| multiple PDZ domain protein                                            | 23             | 20%             | 5.3E-16        | 0.1%              |     | 2.1 ± 0.6     | 0.4 ± 0.2   | 1.396  |
| cyclin D-type binding-protein 1                                        | 25             | 17%             | 7.3E-08        | 1.4%              |     | 1.1 ± 0.1     | 0.7 ± 0.0   | 0.940  |
| G protein-coupled receptor kinase-interactor 1                         | 32             | 9%              | 3.4E-08        | 75.7%             |     | 1.9 ± 0.1     | 1.2 ± 0.1   | 1.684  |
| neuronal Shc                                                           | 35             | 7%              | 5.8E-15        | 0.1%              |     | 1.7 ± 0.4     | 0.6 ± 0.2   | 1.284  |
| chromogranin A (parathyroid secretory protein 1)                      | 46             | 3%              | 1.3E-10        | 0.1%              |     | 1.6 ± 0.2     | 0.9 ± 0.2   | 1.288  |
| RAB5A, member RAS oncogene family                                      | 68             | 1%              | 4.6E-07        | 0.0%              |     | 1.6 ± 0.3     | 1.1 ± 0.1   | 1.300  |
| adaptor-related protein complex 2, alpha 1 subunit                     | 77             | 1%              | 4.7E-08        | 26.3%             |     | 0.9 ± 0.0     | 1.2 ± 0.1   | 1.141  |
| antigen identified by monoclonal antibody Ki-67                        | 39             | 5%              | 9.3E-14        | 0.1%              |     | 1.3 ± 0.1     | 0.8 ± 0.1   | 1.100  |
| caspase 14, apoptosis-related cysteine protease                        | 135            | 0%              | 1.6E-05        | 0.9%              |     | 1.2 ± 0.1     | 0.9 ± 0.1   | 1.072  |
| FK506 binding protein 5                                                | 158            | 0%              | 1.6E-04        | 97.4%             |     | 1.2 ± 0.1     | 1.5 ± 0.2   | 1.321  |
| topoisomerase (DNA) II beta 180kDa                                     | 41             | 5%              | 1.3E-12        | 0.1%              |     | 1.2 ± 0.4     | 0.4 ± 0.1   | 0.636  |
| colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog | 52             | 2%              | 4.2E-08        | 0.0%              |     | 0.9 ± 0.4     | 1.8 ± 0.2   | 1.552  |
| synuclein, alpha (non A4 component of amyloid precursor)              | 145            | 0%              | 5.3E-05        | 9.8%              |     | 0.7 ± 0.1     | 0.966      | 0.915  |
| Protein                                                                 | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC | Female cohort | Male cohort | cutoff |
|------------------------------------------------------------------------|-----------------|------------------|-----------------|-------------------|-----|---------------|-------------|--------|
| protein kinase, cAMP-dependent, catalytic, alpha                       | 52              | 3%               | 2.8E-13         | 13.5%             | 0.996 | 1.4 ± 0.1     | 0.8 ± 0.1   | 1.217  |
| neuropilin 2                                                           | 69              | 1%               | 3.5E-08         | 0.0%              | 0.995 | 1.8 ± 0.3     | 1.1 ± 0.3   | 1.508  |
| katanin p80 (WD repeat containing) subunit B 1                         | 66              | 1%               | 6.6E-07         | 2.3%              | 0.994 | 1.3 ± 0.1     | 0.9 ± 0.1   | 1.178  |
| HIV TAT specific factor 1                                               | 137             | 0%               | 1.5E-12         | 7.9%              | 0.994 | 0.9 ± 0.0     | 1.1 ± 0.1   | 0.973  |
| v-myc myelocytomatosis viral oncogene homolog (avian)                  | 23              | 20%              | 2.9E-12         | 0.0%              | 0.994 | 1.8 ± 0.4     | 0.6 ± 0.2   | 1.396  |
| KH domain containing, RNA binding, signal transduction associated 1    | 58              | 2%               | 2.6E-11         | 0.0%              | 0.992 | 0.8 ± 0.1     | 0.4 ± 0.1   | 0.651  |
| myogenic factor 3                                                       | 71              | 1%               | 7.4E-17         | 0.1%              | 0.992 | 1.0 ± 0.1     | 0.6 ± 0.1   | 0.860  |
| CDC37 cell division cycle 37 homolog (S. cerevisiae)                   | 62              | 2%               | 7.1E-14         | 0.1%              | 0.991 | 0.6 ± 0.1     | 1.3 ± 0.3   | 0.988  |
| ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | 48              | 3%               | 1.9E-12         | 0.0%              | 0.990 | 0.9 ± 0.1     | 1.6 ± 0.2   | 1.323  |
| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 | 86              | 1%               | 2.9E-06         | 0.0%              | 0.990 | 0.7 ± 0.2     | 1.5 ± 0.5   | 1.003  |
| plectin 1, intermediate filament binding protein 500kDa                | 93              | 1%               | 7.7E-11         | 0.1%              | 0.990 | 1.5 ± 0.2     | 1.1 ± 0.1   | 1.314  |
| exportin 1 (CRM1 homolog, yeast)                                       | 61              | 2%               | 3.8E-11         | 0.1%              | 0.989 | 0.7 ± 0.1     | 1.2 ± 0.2   | 1.028  |
| A kinase (PRKA) anchor protein (yotiao) 9                               | 51              | 3%               | 8.4E-11         | 0.0%              | 0.988 | 0.9 ± 0.1     | 1.7 ± 0.3   | 1.423  |
| caspase 7, apoptosis-related cysteine protease                          | 42              | 4%               | 1.5E-14         | 0.1%              | 0.988 | 0.5 ± 0.2     | 1.5 ± 0.4   | 1.214  |
| dynamin 2                                                              | 180             | 0%               | 1.2E-04         | 78.4%             | 0.988 | 1.5 ± 0.1     | 1.2 ± 0.1   | 1.386  |
| huntingtin-associated protein 1 (neuroan 1)                            | 84              | 1%               | 4.7E-09         | 0.1%              | 0.988 | 0.8 ± 0.1     | 1.4 ± 0.3   | 1.021  |
| growth associated protein 43                                            | 1590            | 0%               | 2.2E-11         | 0.0%              | 0.987 | 0.0 ± 0.0     | 0.0 ± 0.0   | 0.024  |
| catechol-O-methyltransferase                                            | 439             | 0%               | 1.5E-10         | 83.4%             | 0.986 | 0.1 ± 0.0     | 0.2 ± 0.0   | 0.113  |
| pericentrin 2 (kendrin)                                                 | 61              | 2%               | 2.3E-12         | 0.1%              | 0.986 | 0.8 ± 0.2     | 0.4 ± 0.1   | 0.510  |
| protein tyrosine phosphatase, non-receptor type 1                       | 80              | 1%               | 2.5E-16         | 0.1%              | 0.986 | 1.3 ± 0.1     | 1.0 ± 0.1   | 1.201  |
| protein kinase C, epsilon                                               | 67              | 1%               | 8.1E-08         | 0.1%              | 0.985 | 2.6 ± 1.2     | 1.0 ± 0.2   | 1.743  |
| nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 | 41              | 5%               | 5.9E-15         | 0.1%              | 0.984 | 1.9 ± 0.3     | 1.1 ± 0.2   | 1.586  |
| IQ motif containing GTPase activating protein 1                         | 60              | 2%               | 3.9E-13         | 0.1%              | 0.983 | 1.6 ± 0.3     | 0.9 ± 0.2   | 1.390  |
| ras homolog gene family, member A                                       | 66              | 1%               | 2.6E-10         | 0.0%              | 0.982 | 1.3 ± 0.2     | 1.9 ± 0.2   | 1.682  |
| heme oxygenase (decycling) 1                                             | 70              | 1%               | 1.5E-13         | 0.1%              | 0.982 | 1.2 ± 0.2     | 0.7 ± 0.1   | 0.988  |
| peroxisomal D3,D2-enoyl-CoA isomerase                                   | 201             | 0%               | 1.9E-04         | 70.2%             | 0.981 | 1.1 ± 0.1     | 1.3 ± 0.1   | 1.173  |
| tumor protein p53 (Li-Fraumeni syndrome)                                | 43              | 4%               | 4.0E-10         | 0.1%              | 0.976 | 2.6 ± 1.3     | 0.6 ± 0.2   | 1.667  |
| Protein                                                                 | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC   | Female cohort | Male cohort | cutoff |
|------------------------------------------------------------------------|-----------------|------------------|-----------------|-------------------|-------|---------------|-------------|--------|
| phosphoinositol-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)| 60              | 2%               | 4.5E-14         | 0.1%              | 0.975 | 1.0 ± 0.1     | 1.8 ± 0.3   | 1.439  |
| L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1) | 179             | 0%               | 2.1E-03         | 5.1%              | 0.975 | 0.8 ± 0.1     | 1.2 ± 0.3   | 1.017  |
| sortilin-related receptor, L(DLR class) A repeats-containing           | 73              | 1%               | 6.2E-09         | 0.0%              | 0.971 | 1.3 ± 0.1     | 2.0 ± 0.3   | 1.687  |
| mitogen-activated protein kinase kinase 5                               | 60              | 2%               | 4.1E-12         | 0.1%              | 0.971 | 1.6 ± 0.3     | 0.8 ± 0.3   | 1.330  |
| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5 | 134             | 0%               | 1.7E-12         | 0.0%              | 0.970 | 0.9 ± 0.1     | 0.6 ± 0.1   | 0.823  |
| ankyrin 2, neuronal                                                     | 96              | 1%               | 2.1E-12         | 0.1%              | 0.967 | 1.1 ± 0.1     | 1.6 ± 0.2   | 1.278  |
| caveolin 1, caveolae protein, 22kDa                                    | 92              | 1%               | 6.5E-10         | 0.1%              | 0.961 | 1.1 ± 0.3     | 1.7 ± 0.2   | 1.375  |
| SV40 Large T Antigen                                                   | 135             | 0%               | 1.2E-09         | 0.1%              | 0.958 | 1.7 ± 0.2     | 1.3 ± 0.2   | 1.502  |
| catenin (cadherin-associated protein), beta 1, 88kDa                   | 137             | 0%               | 8.8E-08         | 0.1%              | 0.955 | 0.7           | 1.1         | 0.920  |
| transforming growth factor, beta 1 (Camurati-Engelmann disease)        | 118             | 0%               | 6.4E-08         | 0.0%              | 0.954 | 1.5 ± 0.2     | 1.1 ± 0.1   | 1.352  |
| GDNF family receptor alpha 1                                           | 284             | 0%               | 1.4E-03         | 85.1%             | 0.953 | 0.6 ± 0.1     | 0.8 ± 0.2   | 0.709  |
| chemokine (C-C motif) ligand 2                                         | 113             | 0%               | 1.0E-09         | 0.1%              | 0.953 | 0.8 ± 0.2     | 1.4 ± 0.3   | 1.060  |
| Cy3/5 Alb:10                                                           | 259             | 0%               | 1.6E-03         | 96.4%             | 0.951 | 0.3 ± 0.1     | 0.6 ± 0.2   | 0.424  |
| transcription factor Dp-1                                              | 198             | 0%               | 3.2E-10         | 0.0%              | 0.949 | 1.0 ± 0.1     | 0.7 ± 0.1   | 0.795  |
| Ras protein-specific guanine nucleotide-releasing factor 2             | 152             | 0%               | 1.1E-06         | 0.0%              | 0.948 | 1.0 ± 0.2     | 1.3 ± 0.2   | 1.206  |
| nitric oxide synthase 2A (inducible, hepatocytes)                      | 63              | 2%               | 4.5E-09         | 0.1%              | 0.942 | 0.9 ± 0.3     | 2.1 ± 0.7   | 1.214  |
| contactin 1                                                             | 96              | 1%               | 1.3E-05         | 0.1%              | 0.942 | 1.1 ± 0.2     | 1.9 ± 0.6   | 1.507  |
| 5-hydroxytryptamine (serotonin) receptor 2C                            | 152             | 0%               | 2.7E-09         | 0.0%              | 0.942 | 1.4 ± 0.1     | 0.9 ± 0.3   | 1.269  |
| leukocyte-associated Ig-like receptor 1                                 | 215             | 0%               | 2.1E-09         | 0.0%              | 0.937 | 1.1 ± 0.1     | 0.9 ± 0.1   | 1.038  |
| polymerase (DNA directed), delta 1, catalytic subunit 125kDa           | 91              | 1%               | 2.5E-04         | 48.0%             | 0.935 | 0.8 ± 0.2     | 1.2 ± 0.1   | 1.099  |
| tripartite motif-containing 28                                          | 108             | 0%               | 2.4E-10         | 0.1%              | 0.935 | 0.9 ± 0.1     | 1.5 ± 0.3   | 1.184  |
| aldehyde dehydrogenase 1 family, member A1                             | 80              | 1%               | 3.4E-07         | 0.0%              | 0.935 | 0.9 ± 0.2     | 1.7 ± 0.4   | 1.353  |
| period homolog 2 (Drosophila)                                          | 173             | 0%               | 8.0E-04         | 100.0%            | 0.935 | 1.3 ± 0.1     | 1.7 ± 0.2   | 1.463  |
| ubiquitin fusion degradation 1-like                                    | 96              | 1%               | 8.7E-09         | 0.1%              | 0.935 | 1.0 ± 0.3     | 1.7 ± 0.4   | 1.360  |
| BCL2-antagonist/killer 1                                               | 218             | 0%               | 5.6E-10         | 0.0%              | 0.934 | 1.0 ± 0.1     | 0.8 ± 0.1   | 0.946  |
| Protein                                                                 | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC       | Female cohort | Male cohort | Male cohort cutoff |
|------------------------------------------------------------------------|-----------------|------------------|-----------------|-------------------|-----------|---------------|-------------|-------------------|
| proliferating cell nuclear antigen                                      | 146             | 0%               | 5.3E-08         | 0.0%              | 0.933     | 1.2           | 1.7         | 1.469             |
| scavenger receptor class B, member 1                                    | 52              | 3%               | 1.1E-10         | 0.0%              | 0.932     | 2.1 ± 0.5     | 0.8 ± 0.6   | 1.739             |
| recombination activating gene 2                                          | 106             | 0%               | 1.0E-06         | 0.1%              | 0.929     | 0.8 ± 0.2     | 1.4 ± 0.4   | 1.158             |
| v-fos FBJ murine osteosarcoma viral oncogene homolog                    | 378             | 0%               | 2.5E-06         | 0.2%              | 0.927     | 0.2 ± 0.1     | 0.3 ± 0.1   | 0.253             |
| protein tyrosine phosphatase, receptor type, F                           | 174             | 0%               | 9.2E-04         | 19.9%             | 0.926     | 1.4 ± 0.2     | 1.1 ± 0.1   | 1.202             |
| neurogenin 3                                                             | 142             | 0%               | 3.2E-03         | 41.4%             | 0.915     | 1.1           | 0.7         | 0.902             |
| OLF-1/EBF associated zinc finger gene                                    | 128             | 0%               | 2.3E-06         | 0.0%              | 0.915     | 1.3 ± 0.2     | 0.9 ± 0.2   | 1.128             |
| lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) | 87              | 1%               | 1.2E-10         | 0.0%              | 0.914     | 1.4 ± 0.3     | 0.8 ± 0.3   | 1.155             |
| docking protein 1, 62kDa (downstream of tyrosine kinase 1)              | 229             | 0%               | 6.9E-06         | 0.0%              | 0.912     | 1.3           | 1.0         | 1.177             |
| TRAF family member-associated NFKB activator                            | 220             | 0%               | 2.3E-09         | 0.0%              | 0.911     | 1.0 ± 0.1     | 0.8 ± 0.1   | 0.898             |
| origin recognition complex, subunit 5-like (yeast)                      | 331             | 0%               | 6.7E-08         | 0.0%              | 0.911     | 1.0           | 0.8         | 0.987             |
| SFRS protein kinase 1                                                   | 85              | 1%               | 7.8E-09         | 0.0%              | 0.906     | 1.7 ± 0.4     | 0.9 ± 0.4   | 1.519             |
| Rho GDP dissociation inhibitor (GDI) beta                               | 226             | 0%               | 2.8E-09         | 0.2%              | 0.904     | 0.5 ± 0.1     | 0.4 ± 0.0   | 0.421             |
| Fk506 binding protein 1A, 12kDa                                        | 108             | 0%               | 1.4E-05         | 3.8%              | 0.902     | 1.3           | 2.0         | 1.760             |
| telomeric repeat binding factor 2                                       | 195             | 0%               | 1.2E-07         | 0.0%              | 0.902     | 1.2           | 1.6         | 1.527             |
| farnesyl-diphosphate farnesyltransferase 1                              | 177             | 0%               | 9.7E-04         | 31.1%             | 0.900     | 1.5           | 1.0         | 1.177             |
| Fk506 binding protein 10, 65 kDa                                       | 130             | 0%               | 3.6E-05         | 0.0%              | 0.897     | 1.1           | 1.8         | 1.398             |
| BTAFl RNA polymerase II, B-TFID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae) | 589             | 0%               | 2.4E-03         | 62.4%             | 0.894     | 1.3           | 1.2         | 1.266             |
| linker for activation of T cells                                        | 171             | 0%               | 1.9E-05         | 36.6%             | 0.893     | 1.4           | 1.9         | 1.634             |
| tumor necrosis factor (TNF superfamily, member 2)                       | 130             | 0%               | 1.0E-05         | 0.3%              | 0.889     | 1.5           | 0.7         | 1.042             |
| nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) | 128             | 0%               | 2.1E-05         | 0.0%              | 0.887     | 1.7           | 1.1         | 1.511             |
| interferon-induced protein with tetratricopeptide repeats 4            | 170             | 0%               | 5.3E-05         | 0.1%              | 0.883     | 1.3           | 0.9         | 1.009             |
| tyrosine 3-monoxygenase/fryptophan 5-monoxygenase activation protein, epsilon polypeptide | 490             | 0%               | 4.3E-03         | 91.3%             | 0.883     | 1.0           | 1.2         | 1.110             |
| integrin-linked kinase                                                  | 1174            | 0%               | 5.1E-05         | 0.0%              | 0.883     | 0.2           | 0.1         | 0.151             |
| retinol binding protein 4, plasma                                       | 143             | 0%               | 3.2E-09         | 0.0%              | 0.880     | 1.1 ± 0.1     | 1.5 ± 0.3   | 1.182             |
| CDC-like kinase 1                                                       | 151             | 0%               | 1.1E-04         | 0.0%              | 0.879     | 0.8           | 1.4         | 1.121             |
| cell division cycle 34                                                  | 169             | 0%               | 2.1E-05         | 0.0%              | 0.877     | 1.6           | 1.1         | 1.363             |
| Protein                                                                 | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC | Female cohort | Male cohort | cutoff  |
|------------------------------------------------------------------------|-----------------|-----------------|-----------------|------------------|-----|---------------|-------------|--------|
| G antigen 7                                                            | 236             | 0%              | 9.0E-05         | 0.0%             | 0.872 | 0.8           | 1.2        | 0.920  |
| spleen focus forming virus (SFFV) proviral integration oncogene spi1  | 298             | 0%              | 5.2E-07         | 0.0%             | 0.872 | 0.3           | 0.6        | 0.445  |
| Protein                                                                | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC | Females       | Males       | cutoff  |
| tumor protein p53 binding protein, 2                                   | 4               | 100%            | 1.2E-27         | 0.1%             | 1.000 | 2.0 ± 0.1     | 0.4 ± 0.1   | 1.448  |
| stathmin 1/oncoprotein 18                                               | 5               | 100%            | 3.0E-11         | 2.1%             | 1.000 | 2.3 ± 0.2     | 1.0 ± 0.0   | 1.884  |
| polymerase (DNA directed), epsilon                                      | 5               | 100%            | 1.2E-15         | 0.0%             | 1.000 | 1.1 ± 0.1     | 0.3 ± 0.0   | 0.879  |
| proteasome (prosome, macropain) 26S subunit, ATPase, 5                 | 9               | 89%             | 3.2E-11         | 0.0%             | 1.000 | 1.6 ± 0.1     | 0.6 ± 0.1   | 1.216  |
| protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1) | 11              | 78%             | 6.8E-11         | 0.0%             | 1.000 | 1.4 ± 0.1     | 0.6 ± 0.0   | 1.117  |
| RAS p21 protein activator 2                                             | 12              | 68%             | 1.0E-10         | 10.1%            | 1.000 | 0.6 ± 0.1     | 1.8 ± 0.2   | 1.383  |
| thyroid autoantigen 70kDa (Ku antigen)                                  | 12              | 67%             | 6.0E-11         | 10.1%            | 1.000 | 0.6 ± 0.1     | 1.5 ± 0.1   | 1.274  |
| synaptotagmin I                                                        | 14              | 58%             | 1.4E-19         | 0.1%             | 1.000 | 0.6 ± 0.2     | 1.8 ± 0.2   | 1.404  |
| synaptotagmin I                                                        | 14              | 54%             | 1.9E-12         | 0.0%             | 1.000 | 1.5 ± 0.1     | 0.7 ± 0.1   | 1.266  |
| phosphatidylinositol 4-kinase, catalytic, beta polypeptide             | 17              | 40%             | 3.4E-12         | 0.0%             | 1.000 | 1.4 ± 0.1     | 0.8 ± 0.1   | 1.265  |
| annexin A11                                                            | 21              | 26%             | 4.1E-06         | 0.0%             | 1.000 | 1.8 ± 0.5     | 0.5 ± 0.1   | 1.008  |
| general transcription factor II, i                                     | 22              | 22%             | 2.4E-15         | 0.1%             | 1.000 | 0.9 ± 0.2     | 2.0 ± 0.2   | 1.569  |
| A kinase (PRKA) anchor protein (gravin) 12                             | 22              | 22%             | 6.3E-10         | 0.0%             | 1.000 | 0.7 ± 0.1     | 1.6 ± 0.2   | 1.196  |
| v-myc myelocytomatosis viral oncogene homolog (avian)                  | 23              | 20%             | 2.9E-12         | 0.0%             | 1.000 | 1.8 ± 0.4     | 0.6 ± 0.2   | 1.106  |
| multiple PDZ domain protein                                            | 23              | 20%             | 5.3E-16         | 0.1%             | 1.000 | 2.1 ± 0.6     | 0.4 ± 0.2   | 1.292  |
| cyclin D-type binding-protein 1                                         | 25              | 17%             | 7.3E-08         | 1.4%             | 1.000 | 1.1 ± 0.1     | 0.7 ± 0.0   | 0.918  |
| G protein-coupled receptor kinase-interactor 1                          | 32              | 8%              | 3.4E-08         | 75.7%            | 1.000 | 1.9 ± 0.1     | 1.2 ± 0.1   | 1.655  |
| neuronal Shc                                                            | 35              | 7%              | 5.8E-15         | 0.1%             | 1.000 | 1.7 ± 0.4     | 0.6 ± 0.2   | 1.189  |
| antigen identified by monoclonal antibody Ki-67                        | 39              | 5%              | 9.3E-14         | 0.1%             | 1.000 | 1.3 ± 0.1     | 0.8 ± 0.1   | 1.104  |
| nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 | 41              | 5%              | 5.9E-15         | 0.1%             | 1.000 | 1.9 ± 0.3     | 1.1 ± 0.2   | 1.489  |
| topoisomerase (DNA) II beta 180kDa                                     | 41              | 5%              | 1.3E-12         | 0.1%             | 1.000 | 1.2 ± 0.4     | 0.4 ± 0.1   | 0.625  |
| Protein                                                                 | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC    | Female cohort | Male cohort | cutoff |
|------------------------------------------------------------------------|-----------------|------------------|-----------------|-------------------|--------|---------------|-------------|--------|
| caspase 7, apoptosis-related cysteine protease                          | 42              | 4%               | 1.5E-14         | 0.1%              | 1.000  | 0.5 ± 0.2     | 1.5 ± 0.4   | 0.918  |
| tumor protein p53 (Li-Fraumeni syndrome)                               | 43              | 4%               | 4.0E-10         | 0.1%              | 1.000  | 2.6 ± 1.3     | 0.6 ± 0.2   | 1.149  |
| chromogranin A (parathyroid secretory protein 1)                       | 46              | 3%               | 1.3E-10         | 0.1%              | 1.000  | 1.6 ± 0.2     | 0.9 ± 0.2   | 1.270  |
| ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) | 48              | 3%               | 1.9E-12         | 0.0%              | 1.000  | 0.9 ± 0.1     | 1.6 ± 0.2   | 1.140  |
| A kinase (PRKA) anchor protein (yotiao) 9                              | 51              | 2%               | 8.4E-11         | 0.0%              | 1.000  | 0.9 ± 0.1     | 1.7 ± 0.3   | 1.163  |
| protein kinase, cAMP-dependent, catalytic, alpha                       | 52              | 2%               | 2.8E-13         | 13.5%             | 1.000  | 1.4 ± 0.1     | 0.8 ± 0.1   | 1.139  |
| colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog | 52              | 2%               | 4.2E-08         | 0.0%              | 1.000  | 0.9 ± 0.1     | 1.8 ± 0.2   | 1.513  |
| KH domain containing, RNA binding, signal transduction associated 1    | 58              | 2%               | 2.6E-11         | 0.0%              | 1.000  | 0.8 ± 0.1     | 0.4 ± 0.1   | 0.638  |
| exportin 1 (CRM1 homolog, yeast)                                        | 61              | 2%               | 3.8E-11         | 0.1%              | 1.000  | 0.7 ± 0.1     | 1.2 ± 0.2   | 0.983  |
| CDC37 cell division cycle 37 homolog (S. cerevisiae)                   | 62              | 2%               | 7.1E-14         | 0.1%              | 1.000  | 0.6 ± 0.1     | 1.3 ± 0.3   | 0.931  |
| katanin p80 (WD repeat containing) subunit B 1                          | 66              | 1%               | 6.6E-07         | 2.3%              | 1.000  | 1.3 ± 0.1     | 0.9 ± 0.1   | 1.186  |
| ras homolog gene family, member A                                       | 66              | 1%               | 2.6E-10         | 0.0%              | 1.000  | 1.3 ± 0.2     | 1.9 ± 0.2   | 1.553  |
| protein kinase C, epsilon                                               | 67              | 1%               | 8.1E-08         | 0.1%              | 1.000  | 2.6 ± 1.2     | 1.0 ± 0.2   | 1.398  |
| RAB5A, member RAS oncogene family                                       | 68              | 1%               | 4.6E-07         | 0.0%              | 1.000  | 1.6 ± 0.3     | 1.1 ± 0.1   | 1.299  |
| myogenic factor 3                                                       | 71              | 1%               | 7.4E-17         | 0.1%              | 1.000  | 1.0 ± 0.1     | 0.6 ± 0.1   | 0.804  |
| adaptor-related protein complex 2, alpha 1 subunit                     | 77              | 1%               | 4.7E-08         | 26.3%             | 1.000  | 0.9 ± 0.0     | 1.2 ± 0.1   | 1.133  |
| caspase 14, apoptosis-related cysteine protease                         | 135             | 0%               | 1.6E-05         | 0.9%              | 1.000  | 1.2 ± 0.1     | 0.9 ± 0.1   | 1.060  |
| HIV TAT specific factor 1                                               | 137             | 0%               | 1.5E-12         | 7.9%              | 1.000  | 0.9 ± 0.0     | 1.1 ± 0.1   | 0.948  |
| synuclein, alpha (non A4 component of amyloid precursor)               | 145             | 0%               | 5.3E-05         | 9.8%              | 1.000  | 1.0 ± 0.1     | 0.7 ± 0.1   | 0.886  |
| FK506 binding protein 5                                                 | 158             | 0%               | 1.6E-04         | 97.4%             | 1.000  | 1.2 ± 0.1     | 1.5 ± 0.2   | 1.310  |
| dynamin 2                                                              | 180             | 0%               | 1.2E-04         | 78.4%             | 1.000  | 1.5 ± 0.1     | 1.2 ± 0.1   | 1.377  |
| peroxisomal D3,D2-enoyl-CoA isomerase                                   | 201             | 0%               | 1.9E-04         | 70.2%             | 1.000  | 1.1 ± 0.1     | 1.3 ± 0.1   | 1.142  |
| growth associated protein 43                                            | 1590            | 0%               | 2.2E-11         | 0.0%              | 1.000  | 0.0 ± 0.0     | 0.0 ± 0.0   | 0.022  |
| pericentrin 2 (kendrin)                                                | 61              | 2%               | 2.3E-12         | 0.1%              | 0.997  | 0.8 ± 0.2     | 0.4 ± 0.1   | 0.507  |
| protein tyrosine phosphatase, non-receptor type 1                      | 80              | 1%               | 2.5E-16         | 0.1%              | 0.997  | 1.3 ± 0.1     | 1.0 ± 0.1   | 1.124  |
| neuropilin 2                                                           | 69              | 1%               | 3.5E-08         | 0.0%              | 0.996  | 1.8 ± 0.3     | 1.1 ± 0.3   | 1.475  |
| plectin 1, intermediate filament binding protein 500kDa                | 93              | 1%               | 7.7E-11         | 0.1%              | 0.995  | 1.5 ± 0.2     | 1.1 ± 0.1   | 1.290  |
| phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) | 60              | 2%               | 4.5E-14         | 0.1%              | 0.993  | 1.0 ± 0.1     | 1.8 ± 0.3   | 1.331  |
| Protein                                                                 | a   | b   | c   | d   | e   | f   | g   | h   | i   |
|------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| heme oxygenase (decycling) 1                                           | 70  | 1%  | 1.5E-13 | 0.1% | 0.993 | 1.2 ± 0.2 | 0.7 ± 0.1 | 0.888 |
| IQ motif containing GTPase activating protein 1                        | 60  | 2%  | 3.9E-13 | 0.1% | 0.993 | 1.6 ± 0.3 | 0.9 ± 0.2 | 1.318 |
| sortilin-related receptor, L(DLR class) A repeats-containing           | 73  | 1%  | 6.2E-09 | 0.0% | 0.992 | 1.3 ± 0.1 | 2.0 ± 0.3 | 1.485 |
| huntingtin-associated protein 1 (neuron 1)                            | 84  | 1%  | 4.7E-09 | 0.1% | 0.988 | 0.8 ± 0.1 | 1.4 ± 0.3 | 1.015 |
| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3         | 86  | 1%  | 2.9E-06 | 0.0% | 0.988 | 0.7 ± 0.2 | 1.5 ± 0.5 | 0.968 |
| huntingtin-associated protein 1 (neuron 1)                            | 113 | 1%  | 2.7E-09 | 0.0% | 0.979 | 1.0 ± 0.1 | 1.5 ± 0.2 | 0.980 |
| ubiquitin fusion degradation 1-like                                    | 118 | 0%  | 3.2E-09 | 0.0% | 0.968 | 0.9 ± 0.2 | 1.4 ± 0.3 | 1.145 |
| mitogen-activated protein kinase kinase 5                              | 179 | 0%  | 2.1E-03 | 5.1% | 0.969 | 0.8 ± 0.1 | 1.2 ± 0.3 | 1.006 |
| L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of     | 179 | 0%  | 2.1E-03 | 5.1% | 0.969 | 0.8 ± 0.1 | 1.2 ± 0.3 | 1.006 |
| aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling    | 179 | 0%  | 2.1E-03 | 5.1% | 0.969 | 0.8 ± 0.1 | 1.2 ± 0.3 | 1.006 |
| gait and adducted thumbs) syndrome, spastic paraplegia 1)             | 179 | 0%  | 2.1E-03 | 5.1% | 0.969 | 0.8 ± 0.1 | 1.2 ± 0.3 | 1.006 |
| caveolin 1, caveolae protein, 22kDa                                    | 92  | 1%  | 6.5E-10 | 0.1% | 0.967 | 1.1 ± 0.3 | 1.7 ± 0.2 | 1.428 |
| transcription factor Dp-1                                              | 198 | 0%  | 3.2E-10 | 0.0% | 0.967 | 1.0 ± 0.1 | 0.7 ± 0.1 | 0.852 |
| tripartite motif-containing 28                                         | 108 | 0%  | 2.4E-10 | 0.1% | 0.965 | 0.9 ± 0.1 | 1.5 ± 0.3 | 1.145 |
| SV40 Large T Antigen                                                   | 135 | 0%  | 1.2E-09 | 0.1% | 0.964 | 1.7 ± 0.2 | 1.3 ± 0.2 | 1.512 |
| contactin 1                                                             | 96  | 1%  | 1.3E-05 | 0.1% | 0.961 | 1.1 ± 0.2 | 1.9 ± 0.6 | 1.324 |
| lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein| 87  | 1%  | 1.2E-10 | 0.0% | 0.957 | 1.4 ± 0.3 | 0.8 ± 0.3 | 1.145 |
| recombinating activating gene 2                                        | 106 | 0%  | 1.0E-06 | 0.1% | 0.953 | 0.8 ± 0.2 | 1.4 ± 0.4 | 0.906 |
| chemokine (C-C motif) ligand 2                                         | 113 | 0%  | 1.0E-09 | 0.1% | 0.953 | 0.8 ± 0.2 | 1.4 ± 0.3 | 1.018 |
| period homolog 2 (Drosophila)                                          | 173 | 0%  | 8.0E-04 | 100.0%| 0.953 | 1.3 ± 0.1 | 1.7 ± 0.2 | 1.440 |
| Cy3/5 Alb:10                                                           | 259 | 0%  | 1.6E-03 | 96.4%| 0.953 | 0.3 ± 0.1 | 0.6 ± 0.2 | 0.420 |
| v-fos FBJ murine osteosarcoma viral oncogene homolog                    | 378 | 0%  | 2.5E-06 | 0.2% | 0.953 | 0.2 ± 0.1 | 0.3 ± 0.1 | 0.223 |
| leukocyte-associated Ig-like receptor 1                                 | 215 | 0%  | 2.1E-09 | 0.0% | 0.950 | 1.1 ± 0.1 | 0.9 ± 0.1 | 0.999 |
| Protein                                      | n for 80% power | Power for n = 10 | t-test (values) | local FDR (ranks) | AUC | Female cohort | Male cohort | cutoff  |
|----------------------------------------------|-----------------|------------------|-----------------|-------------------|-----|---------------|------------|--------|
| BCL2-antagonist/killer 1                     | 218             | 0%               | 5.6E-10         | 0.0%              | 0.950 | 1.0 ± 0.1    | 0.8 ± 0.1 | 0.912   |
| Ras protein-specific guanine nucleotide-releasing factor 2 | 152             | 0%               | 1.1E-06         | 0.0%              | 0.949 | 1.0 ± 0.2    | 1.3 ± 0.2 | 1.196   |
| Rho GDP dissociation inhibitor (GDI) beta    | 226             | 0%               | 2.8E-09         | 0.2%              | 0.948 | 0.5 ± 0.1    | 0.4 ± 0.0 | 0.425   |
| retinol binding protein 4, plasma            | 143             | 0%               | 3.2E-09         | 0.0%              | 0.939 | 1.1 ± 0.1    | 1.5 ± 0.3 | 1.221   |
