

Supplement

for

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

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² National Institute for Mental Health, NIH, 9500 Rockville Pike, Bethesda, MD 20892

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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 Figure1b**) and female donors (**Supplemental Figure1d**) 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 Figure1a**) and female donors (**Supplemental Figure1c**) 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.

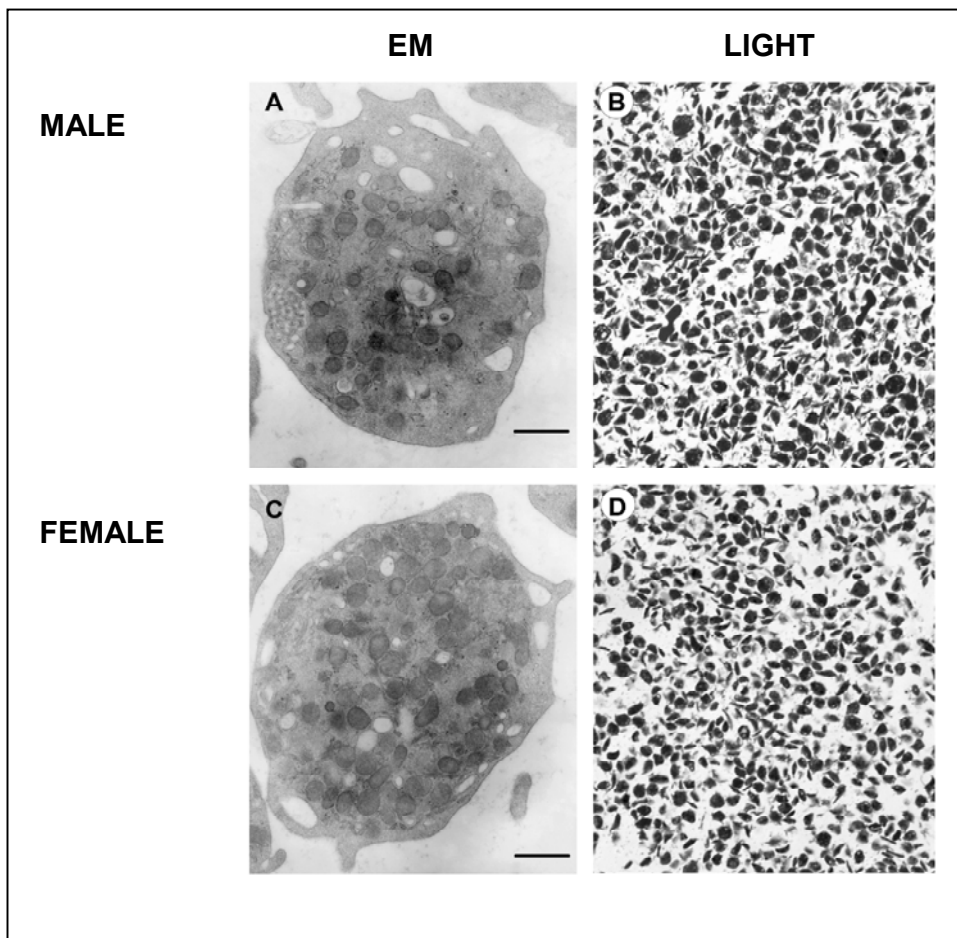
Supplemental Table 10. Statistical properties of the differences between protein expression levels in male and female cohorts.

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.



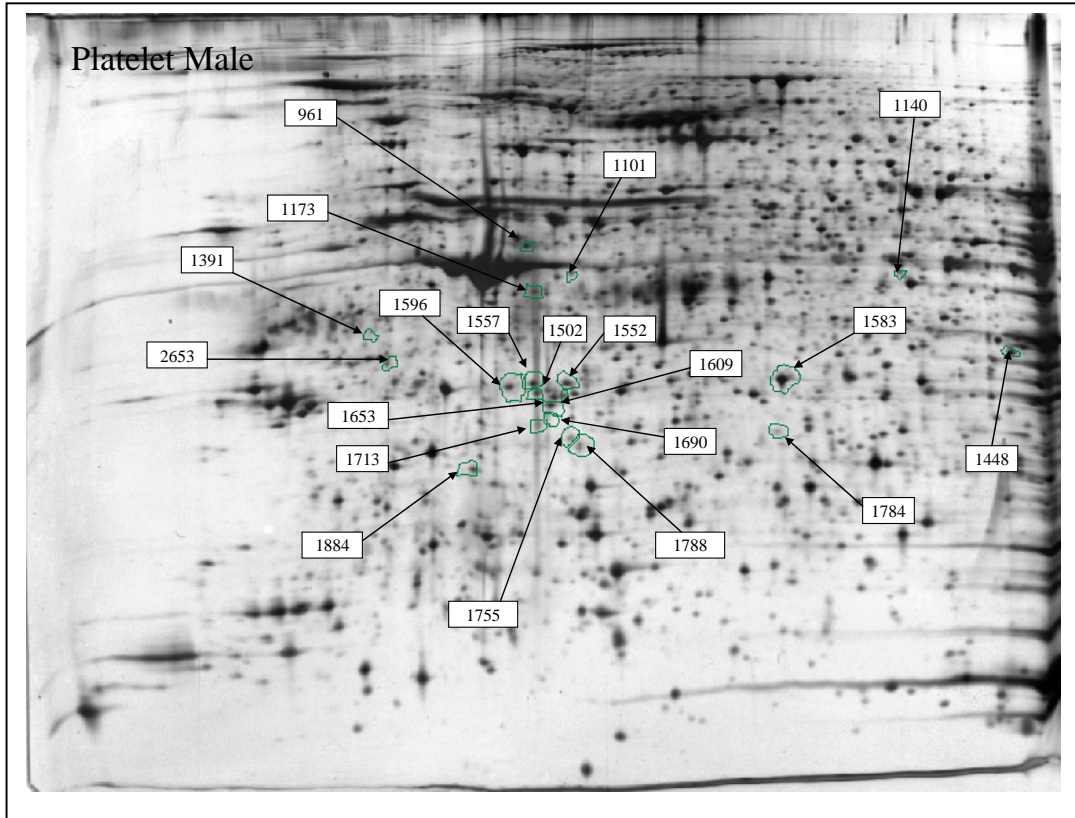
Supplemental Figure 1. Light and electronmicroscopic images of platelets from male and female donors.

Supplemental Figure 2.

2D Gel Electrophoretic separation of male and female platelets

Details:

1. A typical 2DGE of 200 μ g 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.

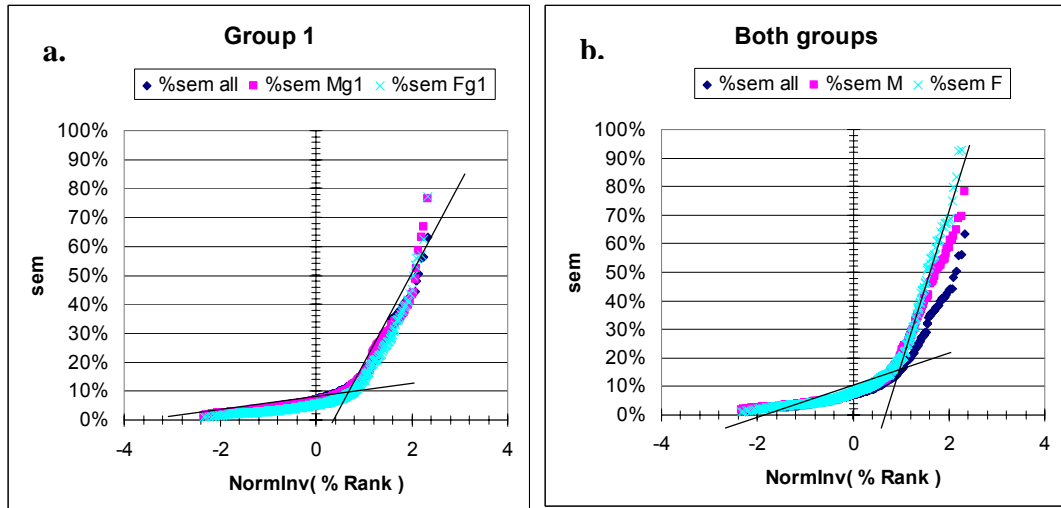


Supplemental Figure 2. 2D Gel Electrophoretic separation of male and female platelets

Supplemental Figure 3.

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

Details: see text



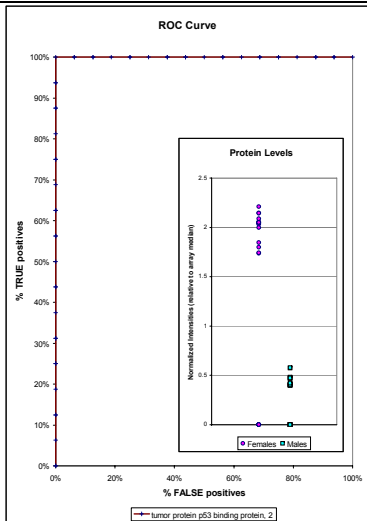
Supplemental Figure 3. Distribution of SEM values for different proteins in platelets from male and female donors.

Supplemental Figure 4

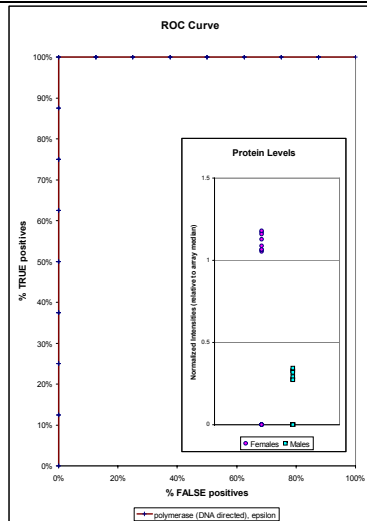
ROC Curves for top gender-specific differences

DETAILS:

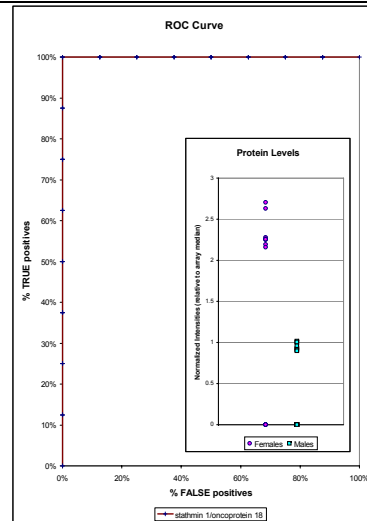
1. Each graph shows the ROC (Receiver Operating Characteristic) curve (red line) for the specified protein. The insets show the actual distributions of protein levels (in relative units) for females (magenta) and for males (cyan). Note that all the replicates for each individual are shown on the insets.
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, where the Averages and SDs of the replicates were used to calculate the chance of receiving a false positive or 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**.



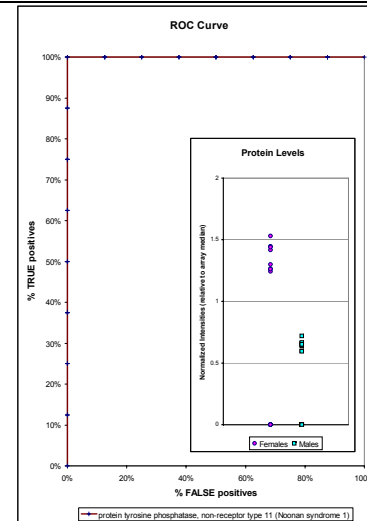
tumor protein p53 binding protein, 2



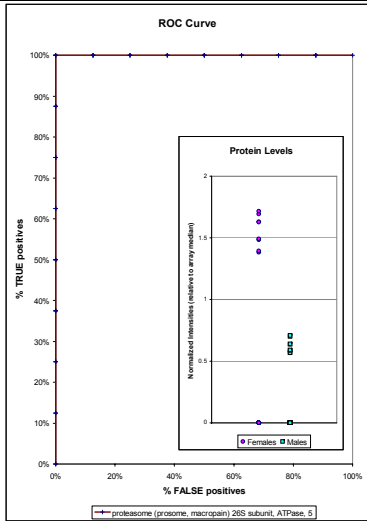
polymerase (DNA directed), epsilon



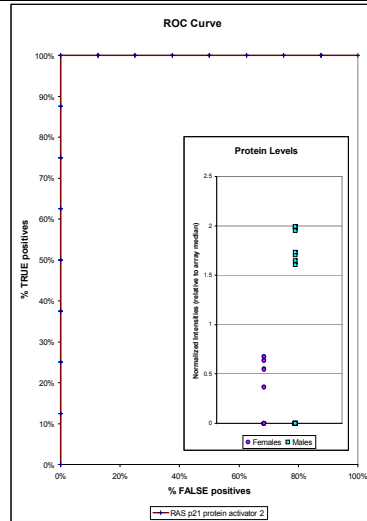
stathmin 1/oncoprotein 18



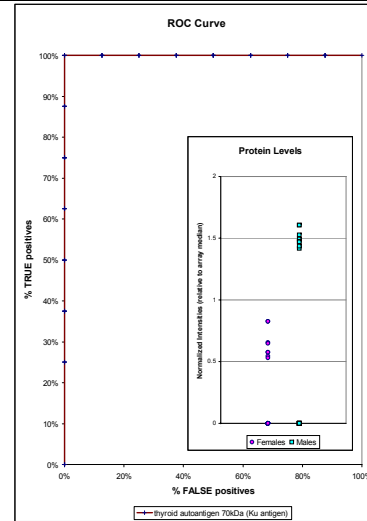
proteasome (prosome, macropain) 26S subunit, ATPase, 5



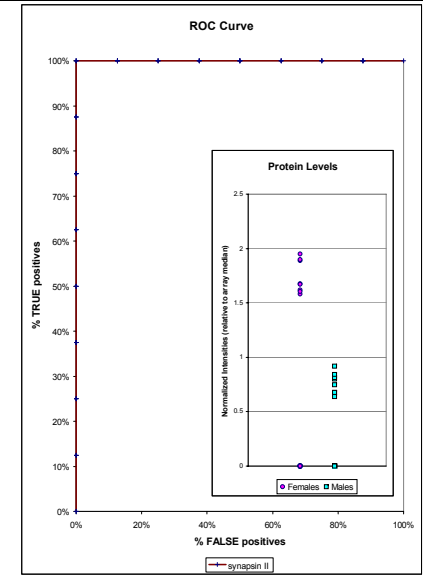
protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)



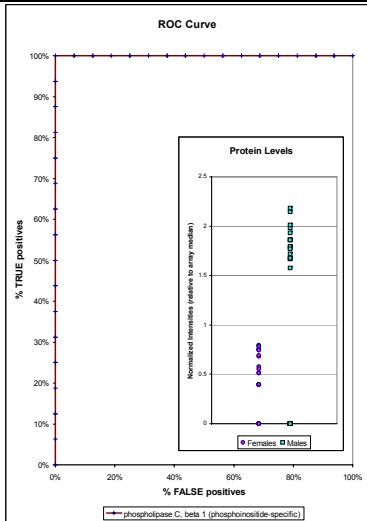
RAS p21 protein activator 2



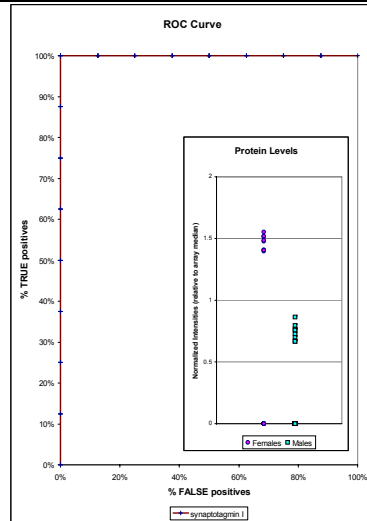
thyroid autoantigen 70kDa (Ku antigen)



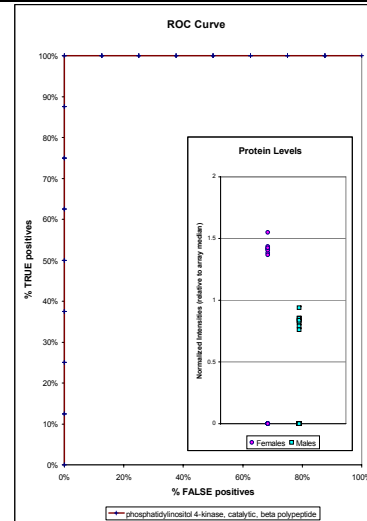
synapsin II



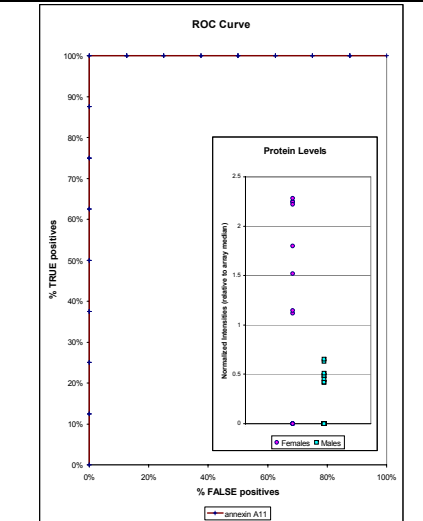
phospholipase C, beta 1 (phosphoinositide-specific)



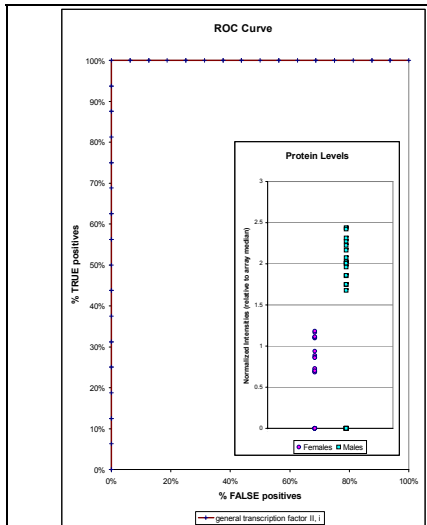
synaptotagmin I



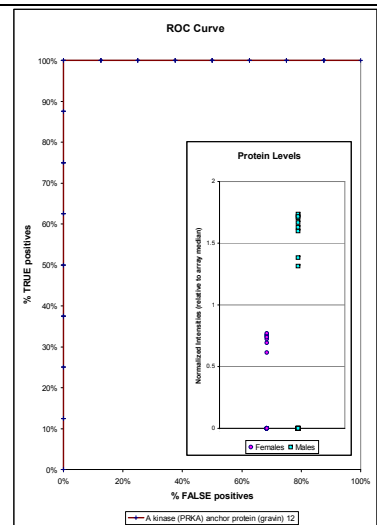
phosphatidylinositol 4-kinase, catalytic, beta polypeptide



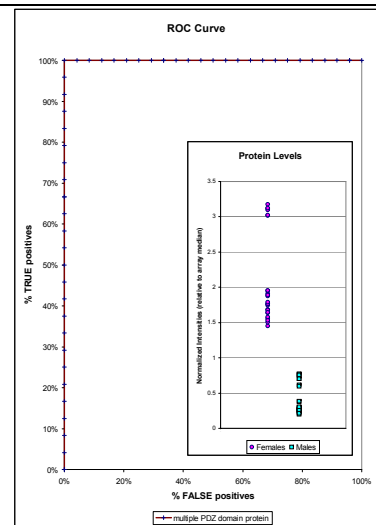
annexin A11



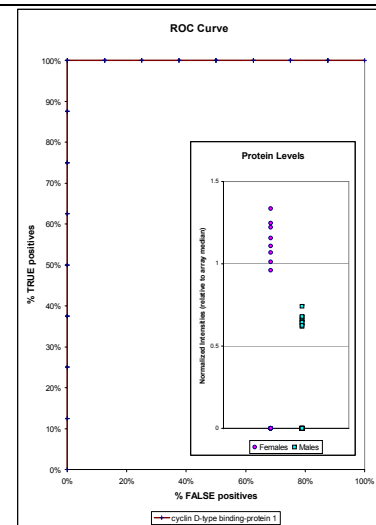
general transcription factor II, i



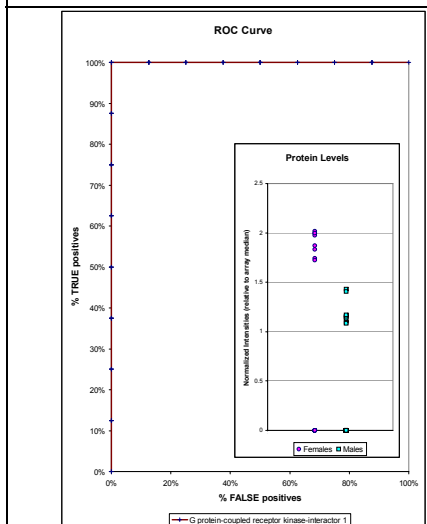
A kinase (PRKA) anchor protein (gravin) 12



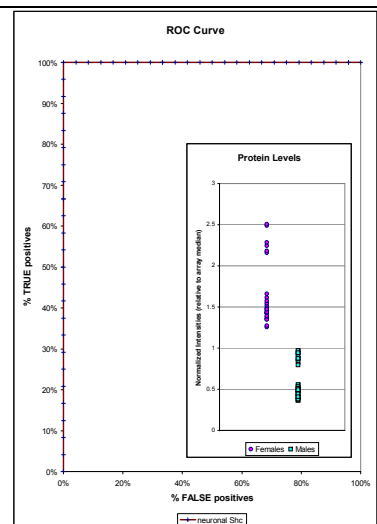
multiple PDZ domain protein



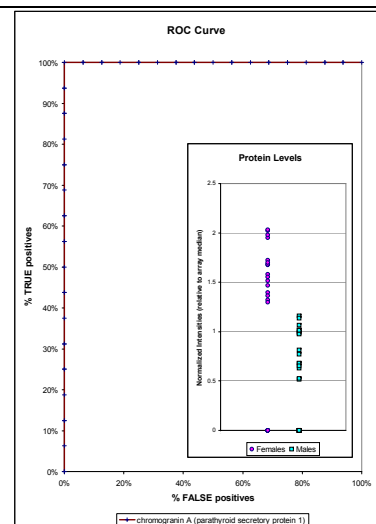
cyclin D-type binding-protein 1



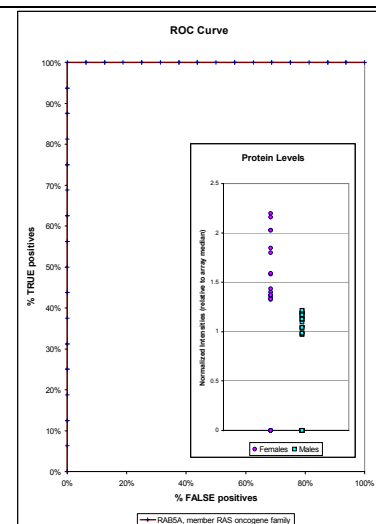
G protein-coupled receptor kinase-interactor 1



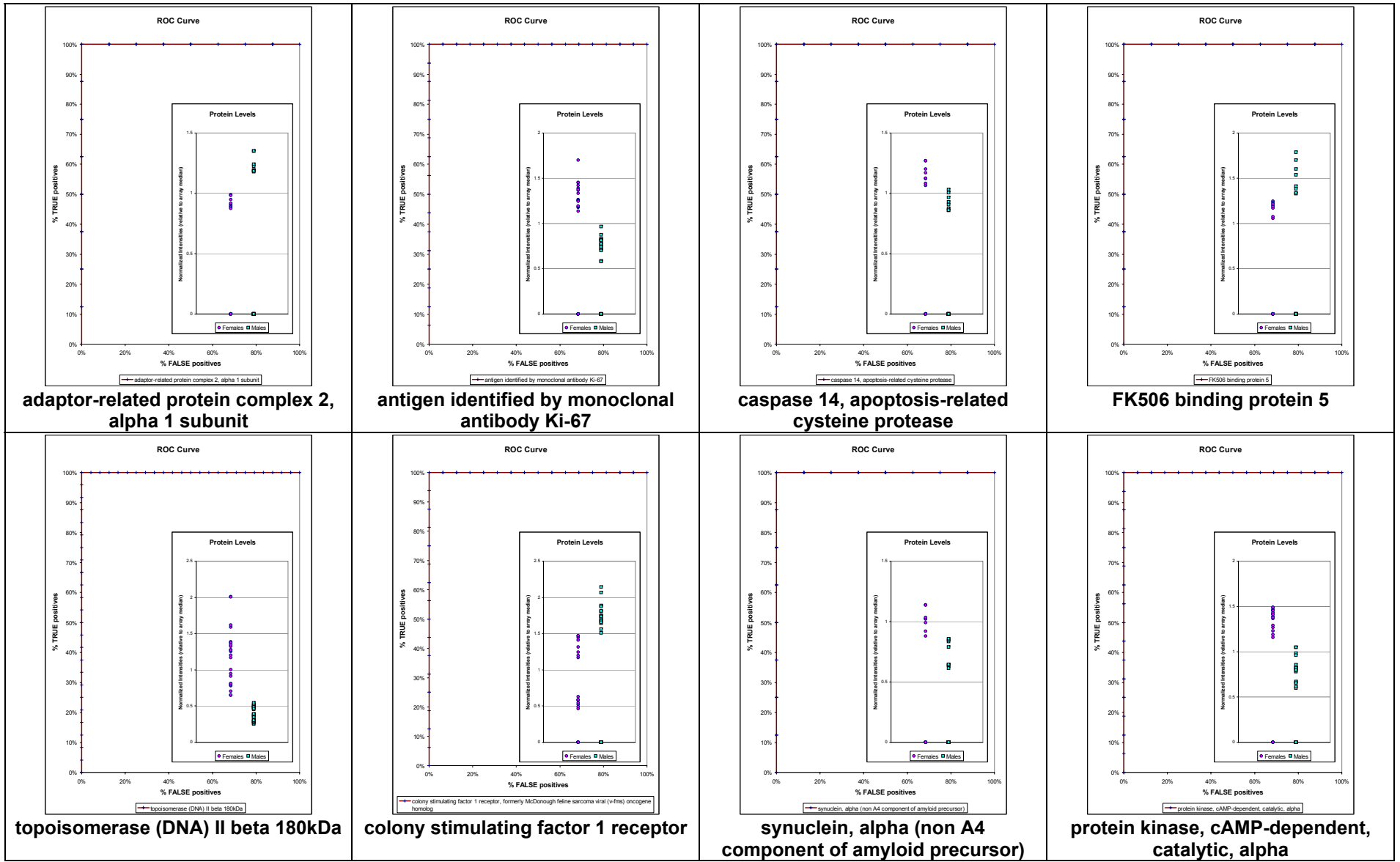
neuronal Shc

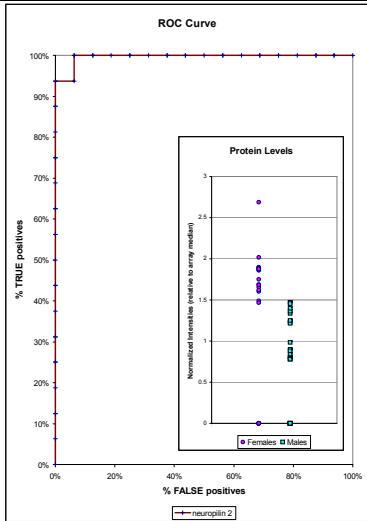


chromogranin A (parathyroid secretory protein 1)

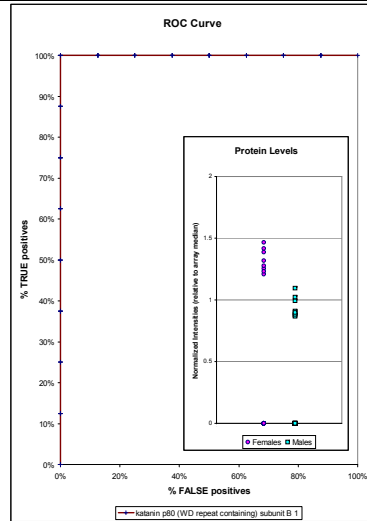


RAB5A, member RAS oncogene family

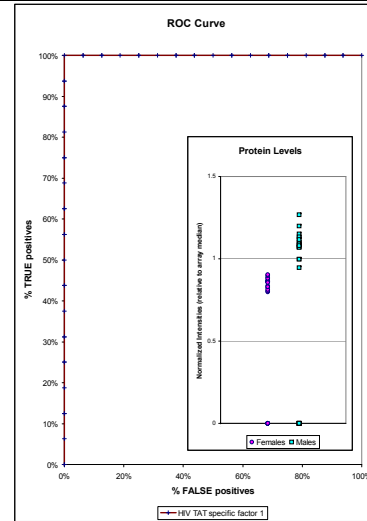




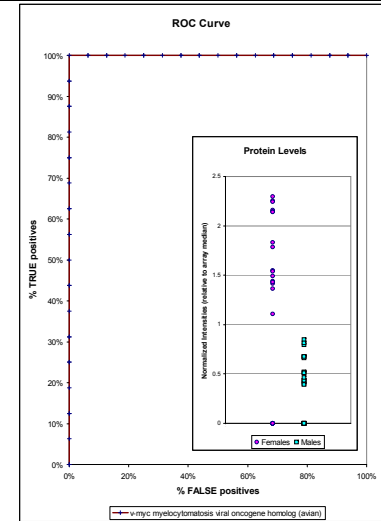
neuropilin 2



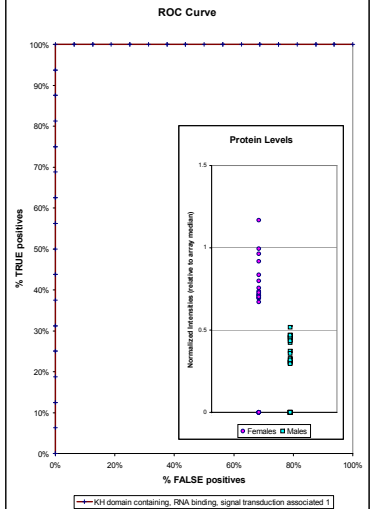
katanin p80 (WD repeat containing) subunit B 1



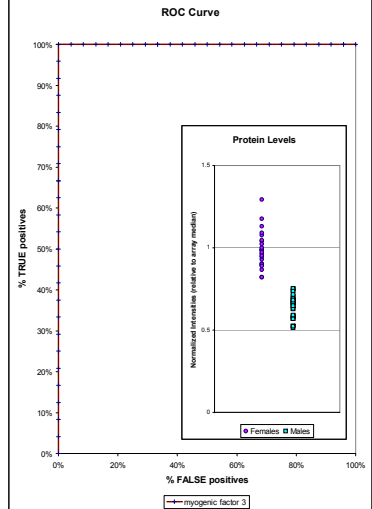
HIV TAT specific factor 1



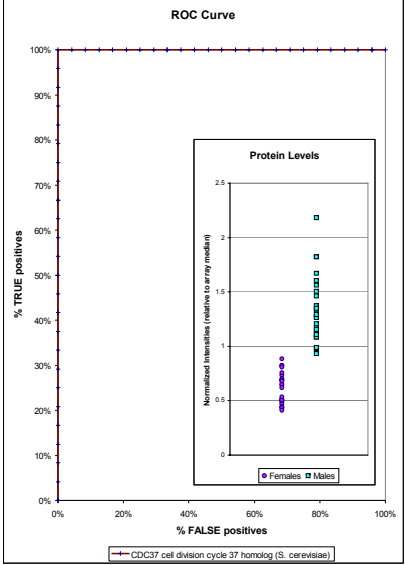
v-myc myelocytomatosis viral oncogene homolog (avian)



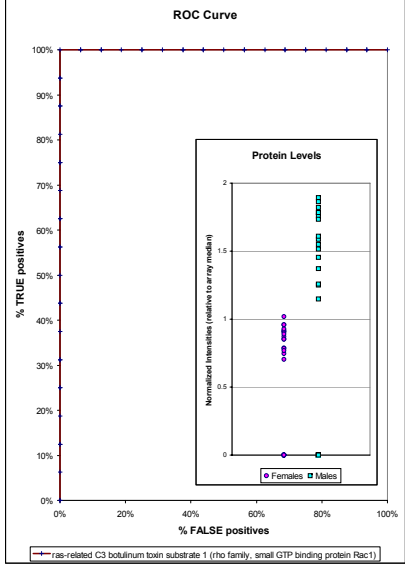
KH domain containing, RNA binding, signal transduction associated 1



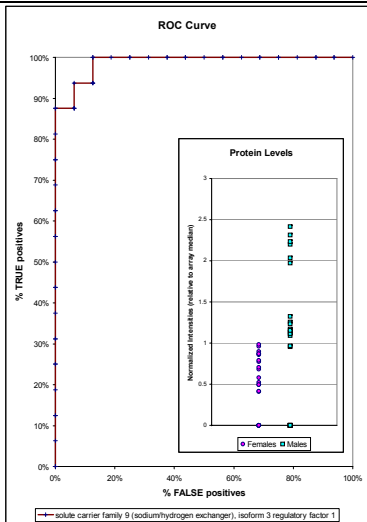
myogenic factor 3



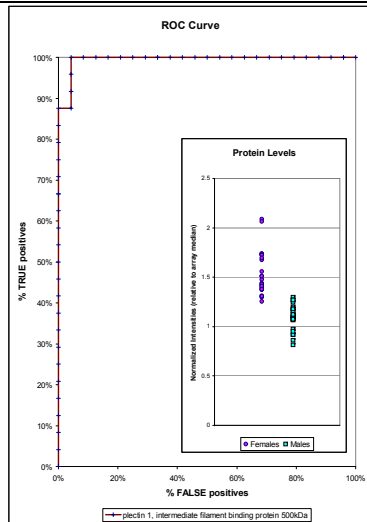
CDC37 cell division cycle 37 homolog (S. cerevisiae)



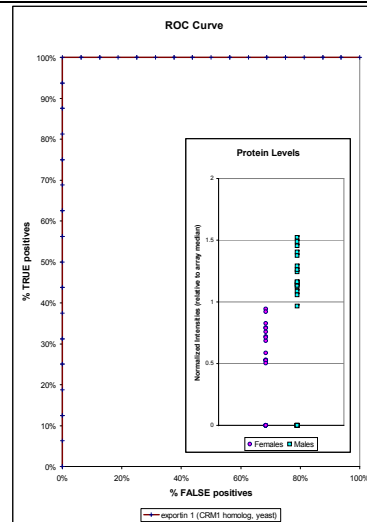
ras-related C3 botulinum toxin substrate 1



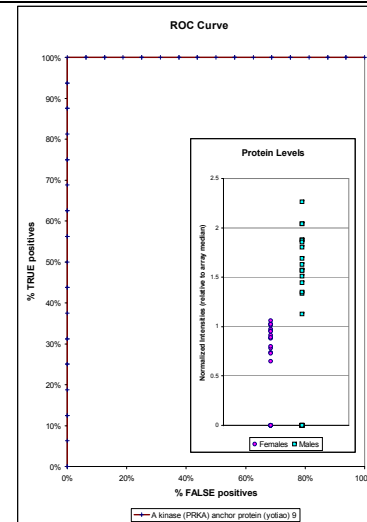
solute carrier family 9 (Na/H exchanger), isoform 3, RF 1



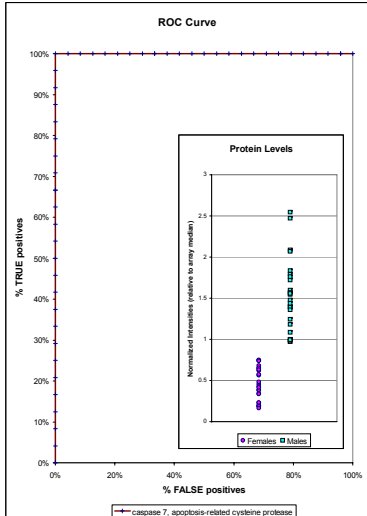
plectin 1, intermediate filament binding protein 500kDa



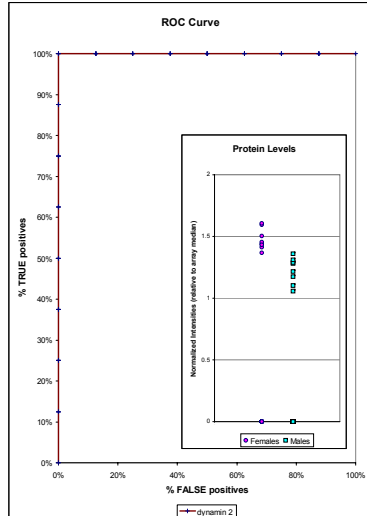
exportin 1 (CRM1 homolog, yeast)



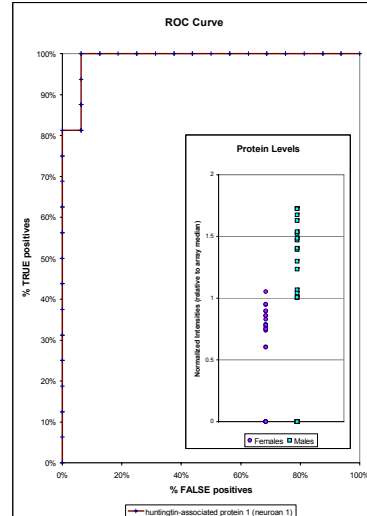
A kinase (PRKA) anchor protein (yotiao) 9



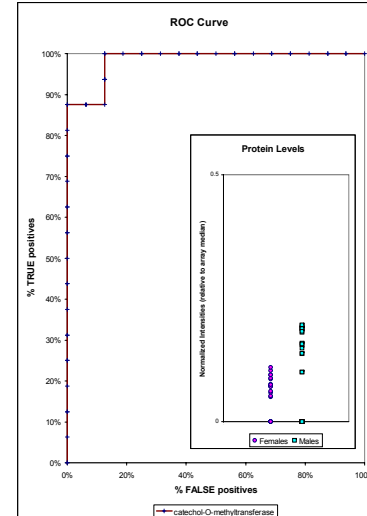
caspase 7, apoptosis-related cysteine protease



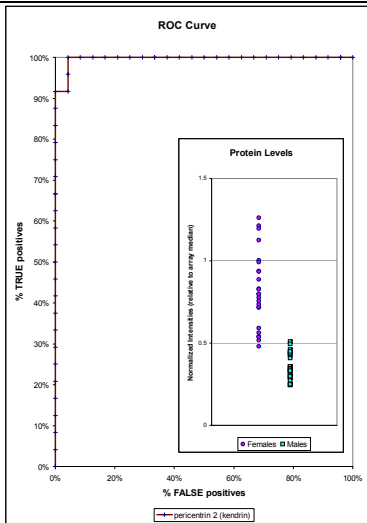
dynamin 2



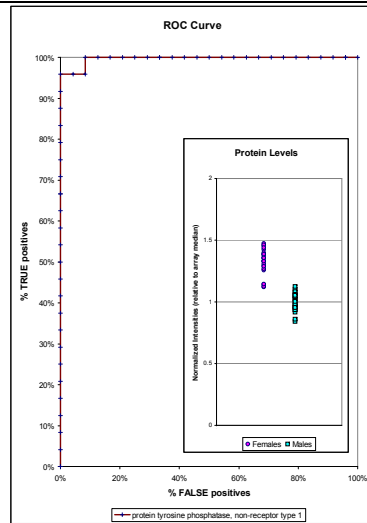
huntingtin-associated protein 1 (neuroan 1)



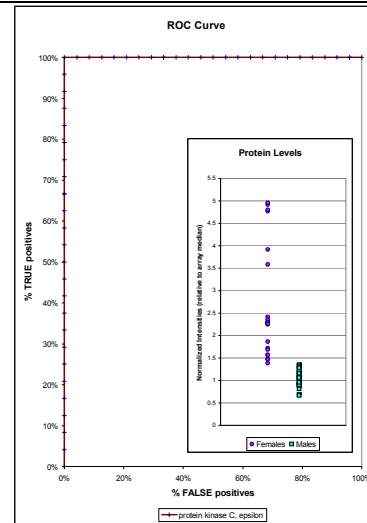
catechol-O-methyltransferase



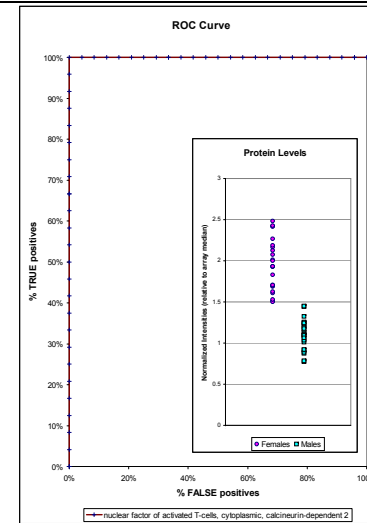
pericentrin 2 (kendrin)



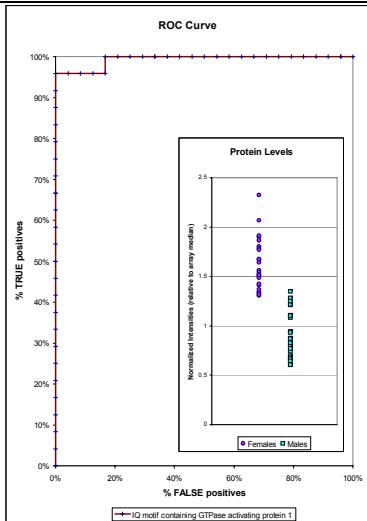
protein tyrosine phosphatase, non-receptor type 1



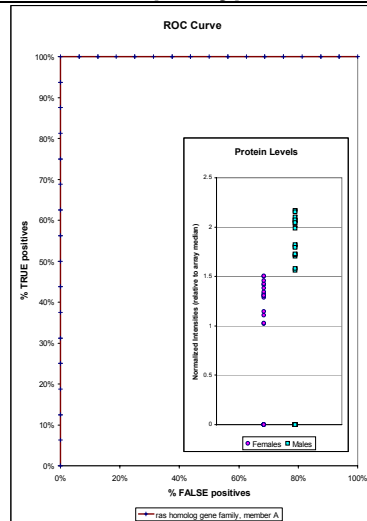
protein kinase C, epsilon



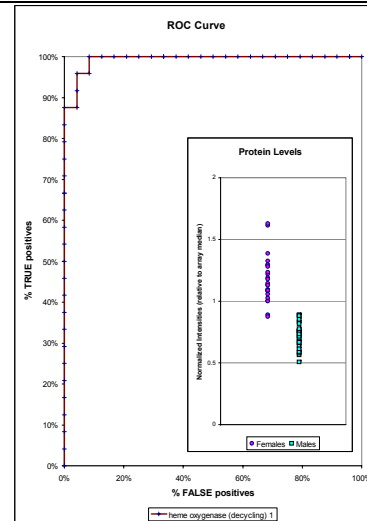
nuclear factor of activated T-cells, cytoplasmic, calcineurin-dep.2



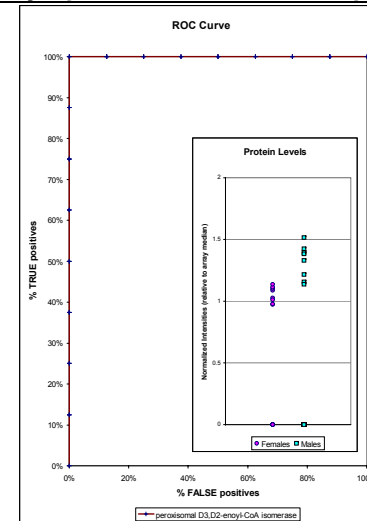
IQ motif containing GTPase activating protein 1



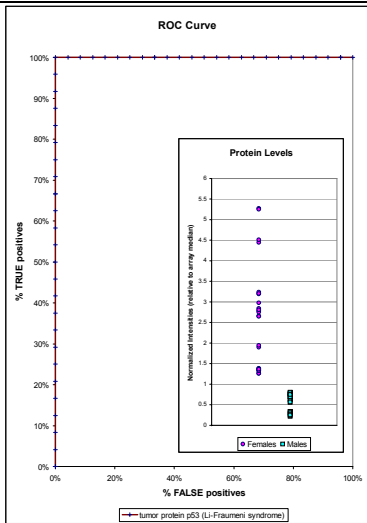
ras homolog gene family, member A



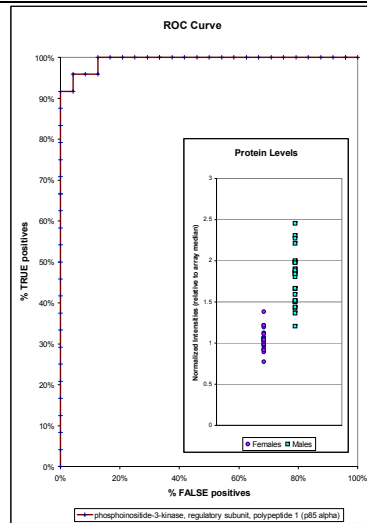
heme oxygenase (decycling) 1



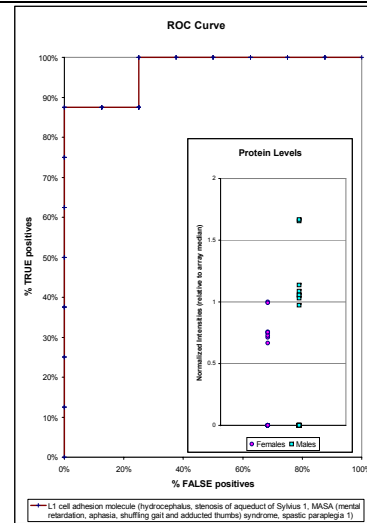
peroxisomal D3,D2-enoyl-CoA isomerase



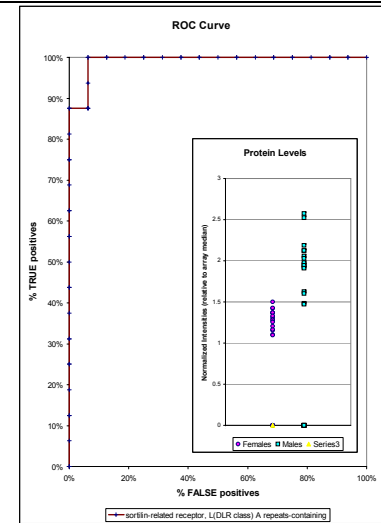
**tumor protein p53
(Li-Fraumeni syndrome)**



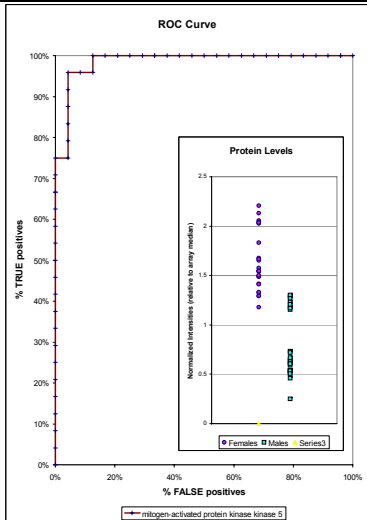
**phosphoinositide-3-kinase,
regulatory subunit, polypeptide 1**



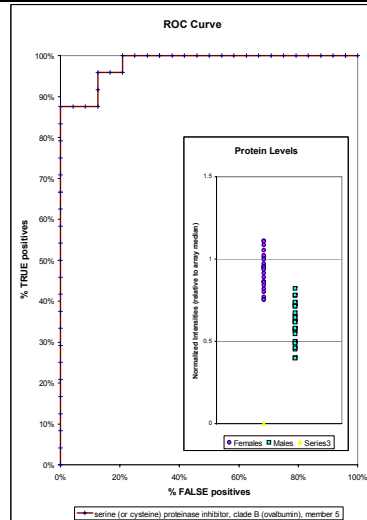
L1 cell adhesion molecule



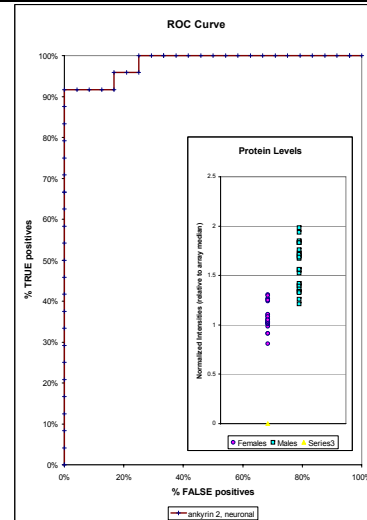
**sortilin-related receptor, L(DLR
class) A repeats-containing**



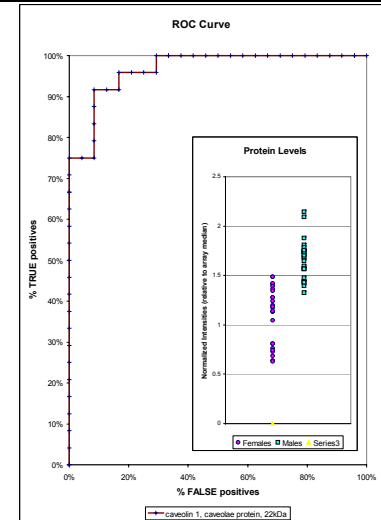
**mitogen-activated protein kinase
kinase 5**



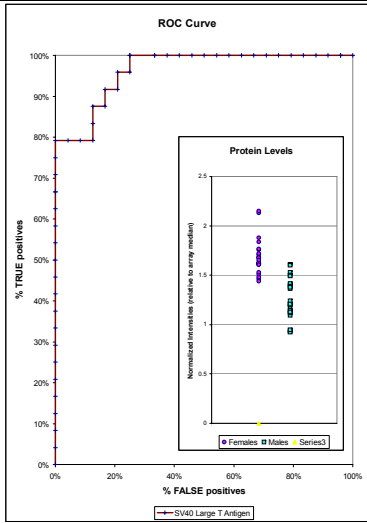
**serine (or cysteine) proteinase
inhibitor, member 5**



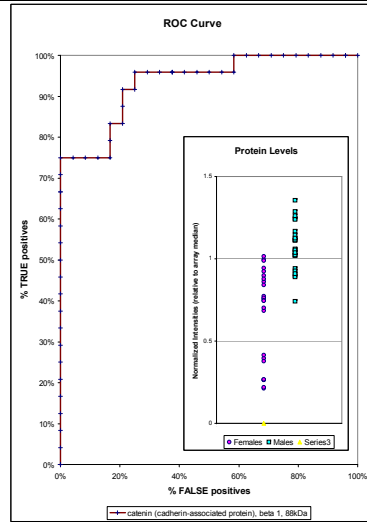
ankyrin 2, neuronal



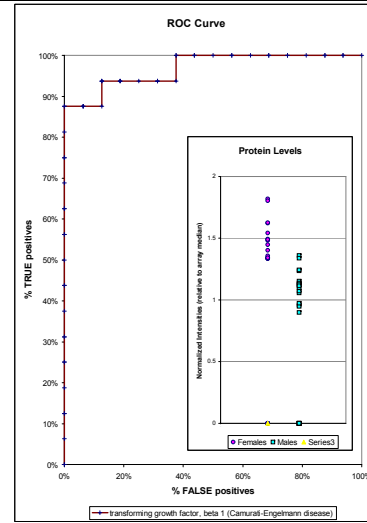
caveolin 1, caveolae protein, 22kDa



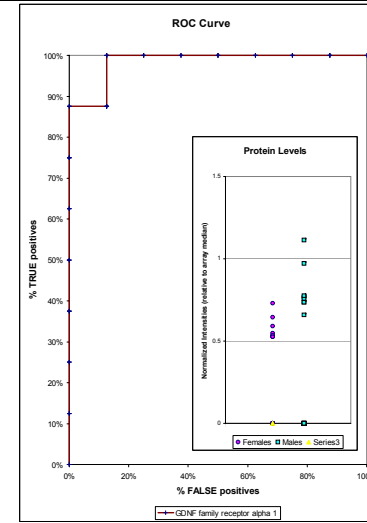
SV40 Large T Antigen



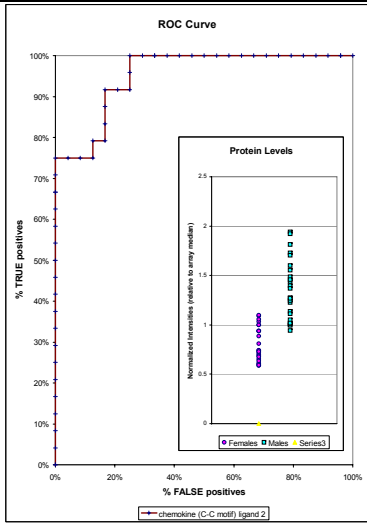
catenin (cadherin-associated protein), beta 1, 88kDa



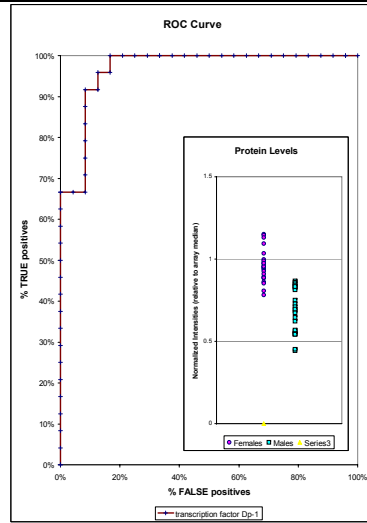
**TGF β 1
(Camurati-Engelmann disease)**



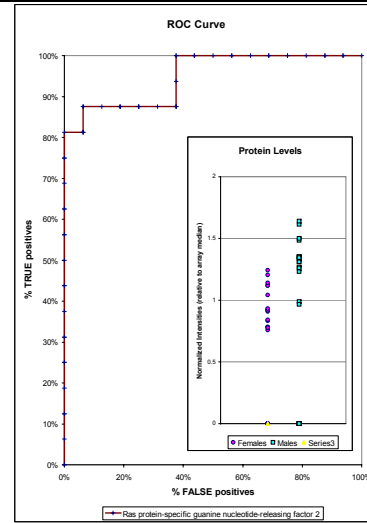
GDNF family receptor alpha 1



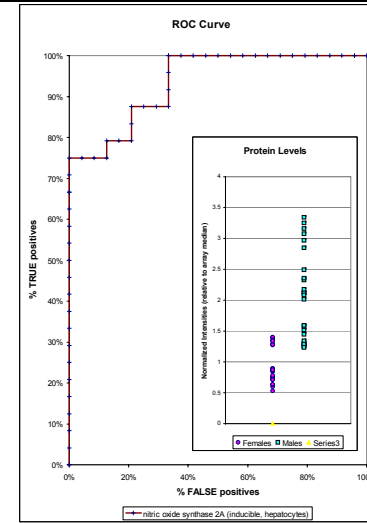
chemokine (C-C motif) ligand 2



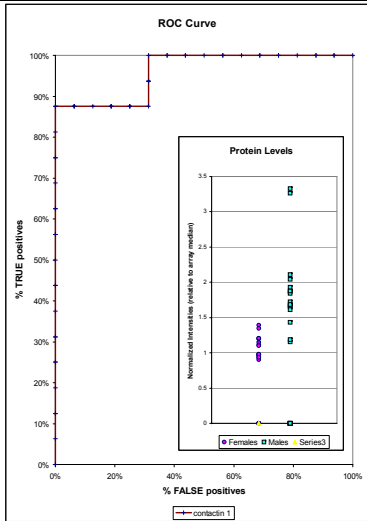
transcription factor Dp-1



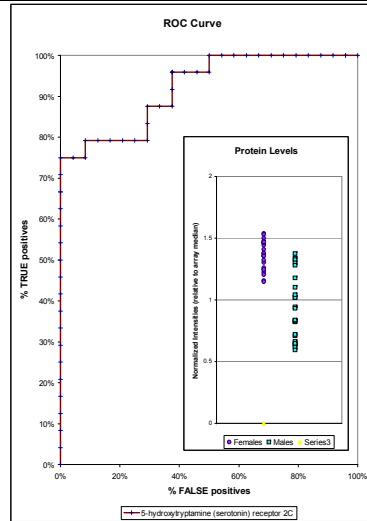
Ras protein-specific guanine nucleotide-releasing factor 2



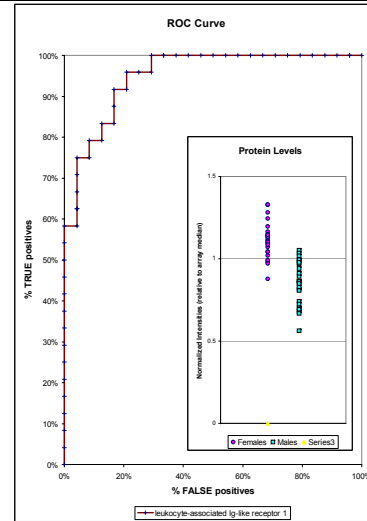
nitric oxide synthase 2A (inducible, hepatocytes)



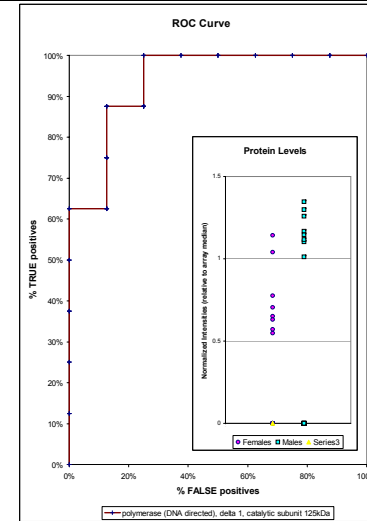
contactin 1



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 No.	Ave Male		Ave Female		Ratio	T-test (p)
	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
	Q9y4P1	Cysteine protease ATG4B	ATG4B	42	5.2	6	17	1.599	0.009	3.18E+03
1583	Q8WZ19	Potassium channel tetramerization domain								
		containing protein 13	KCTD13	36	6.3	7	19	3.246	0.003	1.31E+03
	P78417	Glutathione transferase omega 1	GSTO1	28	6.2	8	30	3.246	0.003	1.33E+03
1140	Q9ULV4	Coronin-1C	CORD1C	53	6.6	10	22	-1.698	0.003	3.08E+03
1476	P30519	Heme oxygenase 2	HMOX2	36	5.3	6	30	2.015	0.003	2.08E+03
1556	P29992	Guanine nucleotide-binding protein G(Y), alpha subunit	GNA11	41	5.5	6	34	1.922	0.005	1.16E+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		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					Females	Males	Delta
v-myc myelocytomatosis viral oncogene homolog avian	0.00%	0.00%	3.5E-20	P01106	-1	MYC	91 ± 2 %	25 ± 2 %	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	37 ± 2 %	83 ± 3 %	46%
polymerase DNA directed , epsilon	0.00%	0.00%	1.7E-14	Q07864	-1	DPOE1	60 ± 1 %	14 ± 1 %	47%
proteasome prosome, macropain 26S subunit, ATPase, 5	0.00%	0.00%	2.2E-14	P62195	-1	PSMC5	90 ± 2 %	27 ± 1 %	63%
synapsin II	0.00%	0.00%	3.2E-14	Q92777	-1	SYN2	94 ± 1 %	34 ± 2 %	60%
synaptotagmin I	0.00%	0.00%	4.2E-14	P21579	-1	SYT1	88 ± 1 %	33 ± 2 %	55%
A kinase PRKA anchor protein yotiao 9	0.00%	0.00%	2.6E-13	Q99996	1	AKAP9	41 ± 3 %	86 ± 3 %	45%
phosphatidylinositol 4-kinase, catalytic, beta polypeptide	0.00%	0.00%	1.1E-12	Q9UBF8	-1	PIK4CB	86 ± 1 %	38 ± 2 %	48%
protein tyrosine phosphatase, non-receptor type 11 Noonan syndrome 1	0.00%	0.00%	3.6E-12	Q06124	-1	PTPN11	82 ± 3 %	28 ± 1 %	55%
A kinase PRKA anchor protein gravin 12	0.00%	0.00%	5.2E-11	Q02952	1	AKAP12	32 ± 1 %	83 ± 3 %	52%
RAB5A, member RAS oncogene family	0.00%	0.00%	1.3E-10	P20339	-1	RAB5A	86 ± 2 %	59 ± 2 %	27%
lymphocyte cytosolic protein 2 SH2 domain containing leukocyte protein of 76kDa	0.00%	0.00%	1.3E-10	Q13094	-1	LCP2	79 ± 4 %	38 ± 4 %	41%
amphiphysin Stiff-Man syndrome with breast cancer 128kDa autoantigen	0.00%	0.00%	9.8E-10	P49418	-1	AMPH	89 ± 4 %	48 ± 4 %	41%
TRAF family member-associated NFkB activator	0.00%	0.00%	1.6E-09	Q92844	-1	TANK	55 ± 2 %	36 ± 2 %	18%
solute carrier family 9 sodium/hydrogen exchanger , isoform 3 regulatory factor 1	0.00%	0.00%	4.1E-09	Q9JJ19	1	NHERF-1	32 ± 2 %	75 ± 5 %	43%
leukocyte-associated Ig-like receptor 1 annexin A11	0.00%	0.00%	4.9E-09	n/d	-1	LAIR1	60 ± 2 %	40 ± 2 %	20%
annexin A11	0.00%	0.00%	5.5E-09	P50995	-1	ANXA11	84 ± 5 %	19 ± 1 %	65%
dynein, cytoplasmic, light polypeptide 1	0.00%	0.00%	7.5E-09	Q15701	1	DYNLL1	49 ± 3 %	73 ± 2 %	24%
retinol binding protein 4, plasma	0.00%	0.00%	7.6E-09	P02753	1	RETBP	56 ± 3 %	81 ± 2 %	25%
scavenger receptor class B, member 1	0.00%	0.00%	1.1E-08	Q14016	-1	SCRB1	93 ± 2 %	42 ± 7 %	51%

ID	SAM		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					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 1	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	O60484	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	O15111	-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		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					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 SFFV proviral integration oncogene spi1	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	P30260	-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		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					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	F11R	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	O15075	-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 UBC4/5 homolog, yeast	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		
	q-value	local-FDR					Females	Males	Delta
calnexin	0.00%	0.00%	1.5E-04	P27824	-1	CANX	69 ± 7 %	36 ± 3 %	34%
interleukin 6 interferon, beta 2	0.00%	0.00%	1.6E-04	P05231	1	IL6	40 ± 2 %	58 ± 4 %	18%
sorting nexin 2	0.00%	0.00%	1.8E-04	O60749	-1	SNX2	57 ± 3 %	40 ± 3 %	17%
caspase 4, apoptosis-related cysteine protease	0.00%	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%	0.00%	2.0E-04	Q9UMT8	1	MDM2	78 ± 4 %	95 ± 1 %	17%
ribosomal protein S6 kinase, 70kDa, polypeptide 1	0.00%	0.00%	2.0E-04	P23443	1	RPS6KB1	59 ± 5 %	83 ± 3 %	24%
thymopoietin	0.00%	0.00%	2.1E-04	P42166	1	TMPO	41 ± 3 %	54 ± 2 %	13%
deleted in colorectal carcinoma	0.00%	0.00%	2.1E-04	P43146	-1	DCC	70 ± 5 %	36 ± 6 %	34%
density-regulated protein	0.00%	0.00%	2.3E-04	O43583	1	DENR	72 ± 3 %	84 ± 2 %	12%
COP9 constitutive photomorphogenic homolog subunit 5 Arabidopsis	0.00%	0.00%	2.3E-04	Q92905	1	COPS5	55 ± 4 %	75 ± 3 %	20%
myogenin myogenic factor 4	0.00%	0.00%	2.4E-04	P15173	1	MYOG	72 ± 3 %	87 ± 2 %	14%
likely ortholog of mouse rabphilin 3A	0.00%	0.00%	2.6E-04	Q9Y2J0	1	RPH3A	21 ± 3 %	50 ± 7 %	29%
cyclin D3	0.00%	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%	0.00%	2.9E-04	P10644	-1	PRKAR1A	77 ± 2 %	66 ± 2 %	11%
polyamine-modulated factor 1	0.00%	0.00%	3.0E-04	Q9UBQ3	1	PMF1	64 ± 3 %	82 ± 3 %	18%
ribosomal protein S6 kinase, 90kDa, polypeptide 1	0.00%	0.00%	3.1E-04	Q15418	1	RPS6KA1	50 ± 6 %	80 ± 5 %	30%
tubulin, beta polypeptide	0.00%	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%	0.00%	3.4E-04	P04150	-1	NR3C1	88 ± 3 %	57 ± 7 %	31%
Rho-associated, coiled-coil containing protein kinase 2	0.00%	0.00%	4.1E-04	O75116	-1	ROCK2	47 ± 3 %	34 ± 2 %	12%
leucine zipper, putative tumor suppressor 1	0.00%	0.00%	4.1E-04	Q9Y250	1	LZTS1	62 ± 4 %	79 ± 3 %	17%
elongation factor-2 kinase	0.00%	0.00%	4.5E-04	O00418	-1	EEF2K	59 ± 3 %	43 ± 3 %	16%
topoisomerase DNA I	0.00%	0.00%	4.8E-04	P11387	1	TOP1	37 ± 5 %	63 ± 5 %	26%
ubiquitin-conjugating enzyme E2L 3	0.00%	0.00%	5.0E-04	P51966	1	UBE2L3	79 ± 2 %	87 ± 1 %	9%

ID	SAM		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					Females	Males	Delta
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	TGFB111	41 ± 2 %	33 ± 1 %	8%
MCM4 minichromosome maintenance deficient 4 <i>S. cerevisiae</i>	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%
adenomatous polyposis coli	0.00%	0.00%	5.8E-03	P25054	1	APC	7 ± 1 %	15 ± 2 %	8%

ID	SAM		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					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	VTI1B	62 ± 2 %	54 ± 3 %	8%
MCM2 minichromosome maintenance deficient 2, mitotin <i>S. cerevisiae</i>	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 <i>Drosophila</i>	0.00%	0.01%	5.9E-04	O60610	-1	DIAPH1	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	O08961	-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	O14980	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		t-test	Swiss-Prot	Gen* code	HUGO	RANK		
	q-value	local-FDR					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, polypeptide 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	O75970	-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%	HSPCA
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 1)	(35.8 ± 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%	COPS5
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 (<i>S. cerevisiae</i>)	(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 likely ortholog of mouse rabphilin 3A	(23.0 ± 1.2)%	(51.3 ± 5.2)%	↓ 28.3%	0%	NME1
son of sevenless homolog 1 (<i>Drosophila</i>)	(21.0 ± 2.6)%	(50.2 ± 7.1)%	↓ 29.2%	0%	RPH3A
ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)	(4.0 ± 0.1)%	(5.0 ± 0.2)%	↓ 1.0%	0%	SOS1
CrmA	(23.1 ± 2.3)%	(39.0 ± 3.2)%	↓ 16.0%	0%	UBE2E1
MCM2 minichromosome maintenance deficient 2, mitotin (<i>S. cerevisiae</i>)	(21.6 ± 0.4)%	(35.9 ± 2.8)%	↓ 14.3%	0%	CRMA
spleen focus forming virus (SFFV) proviral integration oncogene spi1	(20.4 ± 4.1)%	(34.3 ± 7.6)%	↓ 13.9%	0%	MCM2
growth associated protein 43	(13.5 ± 0.8)%	(23.2 ± 1.8)%	↓ 9.6%	0%	SPI1
baculoviral IAP repeat-containing 6 (apollon)	(0.9 ± 0.2)%	(2.3 ± 0.2)%	↓ 1.4%	0%	GAP43
adenomatous polyposis coli	(12.0 ± 0.5)%	(17.0 ± 0.7)%	↓ 5.0%	0%	BIRC6
	(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%	DDX1
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 I	(87.5 ± 1.2)%	(32.5 ± 1.5)%	↑ 55.0%	0%	SYT1
neuronal Shc	(87.2 ± 1.7)%	(26.5 ± 2.3)%	↑ 60.7%	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%	1%	TGFB1
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
gephyrin	(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 (<i>S. cerevisiae</i>)	(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	★	Mxi1	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	★	TFII-I	6	2	4
11	★	TIF1-beta	1	0	1

b. Transcription Factor Enrichment in Female Platelets

#		Name	Edges	Edges In	Edges Out
1	★	c-Myc	41	4	36
2	★	DP1	1	0	1
3	★	E2F2	4	1	3
4	★	E2F2/DP1 complex *	0	0	0
5	★	E2F2/DP1 complex	2	2	0
6	★	Max	5	2	3
7	★	MYOD	5	0	5
8	★	NeuroD3	0	0	0
9	★	NF-AT1(NFATC2)	3	0	2
10	★	NUR77	5	1	4
11	★	p53	24	10	14
12	★	p73	8	6	2
13	★	PAX5	2	1	1
14	★	SMAD2	5	3	2
15	★	ZFP37	1	1	0
16	★	ZNF423	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 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**

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	ITGA3	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 \pm Standard Deviation for the normalized fluorescent signals in the female cohort
- h. Average \pm 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
a	b	c	d	e	f	g	h	i
tumor protein p53 binding protein, 2	4	100%	1.2E-27	0.1%	1.000	2.0 ± 0.1	0.4 ± 0.1	1.564
polymerase (DNA directed), epsilon	5	100%	1.2E-15	0.0%	1.000	1.1 ± 0.1	0.3 ± 0.0	0.893
stathmin 1/oncoprotein 18	5	100%	3.0E-11	2.1%	1.000	2.3 ± 0.2	1.0 ± 0.0	1.906
proteasome (prosome, macropain) 26S subunit, ATPase, 5	9	90%	3.2E-11	0.0%	1.000	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%	1.000	1.4 ± 0.1	0.6 ± 0.0	1.118
RAS p21 protein activator 2	12	68%	1.0E-10	10.1%	1.000	0.6 ± 0.1	1.8 ± 0.2	1.412
thyroid autoantigen 70kDa (Ku antigen)	12	67%	6.0E-11	10.1%	1.000	0.6 ± 0.1	1.5 ± 0.1	1.290
synapsin II	13	60%	3.9E-10	0.0%	1.000	1.7 ± 0.2	0.8 ± 0.1	1.427
phospholipase C, beta 1 (phosphoinositide-specific)	14	58%	1.4E-19	0.1%	1.000	0.6 ± 0.2	1.8 ± 0.2	1.427
synaptotagmin I	14	54%	1.9E-12	0.0%	1.000	1.5 ± 0.1	0.7 ± 0.1	1.275
phosphatidylinositol 4-kinase, catalytic, beta polypeptide	17	40%	3.4E-12	0.0%	1.000	1.4 ± 0.1	0.8 ± 0.1	1.269
annexin A11	21	26%	4.1E-06	0.0%	1.000	1.8 ± 0.5	0.5 ± 0.1	1.142
general transcription factor II, i	22	22%	2.4E-15	0.1%	1.000	0.9 ± 0.2	2.0 ± 0.2	1.608
A kinase (PRKA) anchor protein (gravin) 12	22	22%	6.3E-10	0.0%	1.000	0.7 ± 0.1	1.6 ± 0.2	1.280
multiple PDZ domain protein	23	20%	5.3E-16	0.1%	1.000	2.1 ± 0.6	0.4 ± 0.2	1.396
cyclin D-type binding-protein 1	25	17%	7.3E-08	1.4%	1.000	1.1 ± 0.1	0.7 ± 0.0	0.940
G protein-coupled receptor kinase-interactor 1	32	9%	3.4E-08	75.7%	1.000	1.9 ± 0.1	1.2 ± 0.1	1.684
neuronal Shc	35	7%	5.8E-15	0.1%	1.000	1.7 ± 0.4	0.6 ± 0.2	1.284
chromogranin A (parathyroid secretory protein 1)	46	3%	1.3E-10	0.1%	1.000	1.6 ± 0.2	0.9 ± 0.2	1.288
RAB5A, member RAS oncogene family	68	1%	4.6E-07	0.0%	1.000	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%	1.000	0.9 ± 0.0	1.2 ± 0.1	1.141
antigen identified by monoclonal antibody Ki-67	39	5%	9.3E-14	0.1%	1.000	1.3 ± 0.1	0.8 ± 0.1	1.100
caspase 14, apoptosis-related cysteine protease	135	0%	1.6E-05	0.9%	1.000	1.2 ± 0.1	0.9 ± 0.1	1.072
FK506 binding protein 5	158	0%	1.6E-04	97.4%	1.000	1.2 ± 0.1	1.5 ± 0.2	1.321
topoisomerase (DNA) II beta 180kDa	41	5%	1.3E-12	0.1%	0.999	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%	0.999	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%	0.996	1.0 ± 0.1	0.7 ± 0.1	0.915

Protein	n for 80% power	Power for n = 10	t-test (values)	local FDR (ranks)	AUC	Female cohort	Male cohort	cutoff
a	b	c	d	e	f	g	h	i
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
a	b	c	d	e	f	g	h	i
phosphoinositide-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	cutoff
a	b	c	d	e	f	g	h	i
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
BTAF1 RNA polymerase II, B-TFIID 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-monooxygenase/tryptophan 5-monooxygenase 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
a	b	c	d	e	f	g	h	i
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
a	b	c	d	e	f	g	h	i
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
synapsin II	13	60%	3.9E-10	0.0%	1.000	1.7 ± 0.2	0.8 ± 0.1	1.420
phospholipase C, beta 1 (phosphoinositide-specific)	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
a	b	c	d	e	f	g	h	i
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 ± 0.4	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
dynammin 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	n for 80% power	Power for n = 10	t-test (values)	local FDR (ranks)	AUC	Female cohort	Male cohort	cutoff
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 (neuroan 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 regulatory factor 1	86	1%	2.9E-06	0.0%	0.988	0.7 ± 0.2	1.5 ± 0.5	0.968
mitogen-activated protein kinase kinase 5	60	2%	4.1E-12	0.1%	0.986	1.6 ± 0.3	0.8 ± 0.3	1.292
ubiquitin fusion degradation 1-like	96	1%	8.7E-09	0.1%	0.984	1.0 ± 0.3	1.7 ± 0.4	1.355
GDNF family receptor alpha 1	284	0%	1.4E-03	85.1%	0.984	0.6 ± 0.1	0.8 ± 0.2	0.715
catechol-O-methyltransferase	439	0%	1.5E-10	83.4%	0.984	0.1 ± 0.0	0.2 ± 0.0	0.104
ankyrin 2, neuronal	96	1%	2.1E-12	0.1%	0.983	1.1 ± 0.1	1.6 ± 0.2	1.291
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	134	0%	1.7E-12	0.0%	0.981	0.9 ± 0.1	0.6 ± 0.1	0.777
transforming growth factor, beta 1 (Camurati-Engelmann disease)	118	0%	6.4E-08	0.0%	0.969	1.5 ± 0.2	1.1 ± 0.1	1.338
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%	0.969	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 of 76kDa)	87	1%	1.2E-10	0.0%	0.957	1.4 ± 0.3	0.8 ± 0.3	1.145
recombination 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
a	b	c	d	e	f	g	h	i
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

