

**Supplementary table 1** Significantly differently expressed genes between pre- and postoperative samples. All probes with FDR < 2.5% ranked according to SAM. Systematic names shown in brackets.

Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
PACSIN2	A_32_P38145	cDNA DKFZp434H1130 (from clone DKFZp434H1130), [AL136845]	1	0	0	0	2,03	0,53-2,55
PLA2G3	A_23_P17814	phospholipase A2, group III (PLA2G3), mRNA [NM_015715]	2	0	0	0	2,2	0,11-4,07
MALAT1	A_24_P497244	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding) (MALAT1), non-coding RNA [NR_002819]	3	0	0	0	3,54	1,31-9,97
DAK	A_23_P36129	dihydroxyacetone kinase 2 homolog (S, cerevisiae) (DAK), mRNA [NM_015533]	4	0	0	0	1,71	0,36-2,65
HISPPD2A	A_23_P205818	histidine acid phosphatase domain containing 2A (HISPPD2A), transcript variant 4, mRNA [NM_001024463]	5	0	0	0	1,71	0,76-3,01
PCDH1	A_23_P213359	protocadherin 1 (PCDH1), transcript variant 1, mRNA [NM_002587]	6	0	0	0	1,64	0,38-3,45
DUSP9	A_24_P417189	dual specificity phosphatase 9 (DUSP9), mRNA [NM_001395]	7	0	0	0	2,12	1,15-2,88
DFNB31	A_24_P376129	cDNA FLJ31628 fis, clone NT2R12003344, [AK056190]	8	0	0	0	3,15	1,30-5,69
KIAA1305	A_23_P129005	KIAA1305 (KIAA1305), mRNA [NM_025081]	9	0	0	0	1,65	1,11-2,19
RAB17	A_23_P5778	RAB17, member RAS oncogene family (RAB17), mRNA [NM_022449]	10	0	0	0	1,84	0,23-4,36
NCK2	A_23_P50962	NCK adaptor protein 2 (NCK2), transcript variant 1, mRNA [NM_003581]	11	0	0	0	1,9	1,00-4,13
LMBRD2	A_32_P8952	LMBR1 domain containing 2 (LMBRD2), mRNA [NM_001007527]	12	0	0	0	1,79	1,08-3,63
THC2610143	A_32_P124580	aa43f10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:823723 5', mRNA sequence [AA490192]	13	0	0	0	1,61	1,01-2,43
HES1	A_23_P6596	hairy and enhancer of split 1, (Drosophila) (HES1), mRNA [NM_005524]	14	0	0	0	1,87	0,77-4,18
STARD13	A_24_P210420	StAR-related lipid transfer (START) domain containing 13 (STARD13), transcript variant alpha, mRNA [NM_178006]	15	0	0	0	1,44	0,28-2,15
RHOB	A_23_P51136	ras homolog gene family, member B (RHOB), mRNA [NM_004040]	16	0	0	0	1,99	0,51-2,96
AK075052	A_24_P726399	cDNA FLJ90571 fis, clone OVARC1001725, highly similar to Homo sapiens patched related protein TRC8 (TRC8) gene, [AK075052]	17	0	0	0	2,52	0,88-2,97
CYP2D6	A_23_P143734	cytochrome P450, family 2, subfamily D, polypeptide 6 (CYP2D6), transcript variant 1, mRNA [NM_000106]	18	0	0	0	1,65	0,58-3,55
C10orf10	A_24_P329795	chromosome 10 open reading frame 10 (C10orf10), mRNA [NM_007021]	19	0	0	0	2,08	0,88-18,37
EEA1	A_23_P76159	early endosome antigen 1 (EEA1), mRNA [NM_003566]	20	0	0	0	1,4	0,33-1,84
CX3CL1	A_24_P390495	chemokine (C-X3-C motif) ligand 1 (CX3CL1), mRNA [NM_002996]	21	0	0	0	2,99	0,90-4,09

Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
BC039457	A_24_P368023	cDNA clone IMAGE:5312122, [BC039457]	22	0	0	0	1,56	0,95-2,09
A_23_P206135	A_23_P206135	Unknown	23	0	0	0	1,71	0,51-2,51
ANAPC2	A_23_P253068	anaphase promoting complex subunit 2 (ANAPC2), mRNA [NM_013366]	24	0	0	0	1,74	0,45-3,58
BCR	A_24_P15270	breakpoint cluster region (BCR), transcript variant 1, mRNA [NM_004327]	25	0	0	0	1,6	0,63-2,90
A_24_P593733	A_24_P593733	Unknown	26	0	0	0	1,9	0,55-3,66
RASD1	A_24_P348006	RAS, dexamethasone-induced 1 (RASD1), mRNA [NM_016084]	27	0	0	0	2,69	0,85-12,90
PQLC1	A_24_P181677	PQ loop repeat containing 1 (PQLC1), mRNA [NM_025078]	28	0	0	0	1,6	0,97-2,25
CIITA	A_23_P353478	CIITA-8 MHC class II transactivator CIITA mRNA, complete cds, [U18259]	29	0,713	2,458	1,485	0,52	0,15-3,01
ANKRD35	A_23_P325690	ankyrin repeat domain 35 (ANKRD35), mRNA [NM_144698]	30	0,713	2,377	1,296	1,93	0,11-3,82
LRRC1	A_23_P377350	cDNA FLJ11834 fis, clone HEMBA1006583, weakly similar to Drosophila melanogaster Scribble (scrib) mRNA, [AK021896]	31	0,713	2,3	1,296	1,79	0,99-4,69
BX110908	A_32_P4172	Soares_testis_NHT Homo sapiens cDNA clone IMAGp998G162577, mRNA sequence [BX110908]	32	0,713	2,228	1,485	0,54	0,19-4,04
C21orf58	A_23_P132139	chromosome 21 open reading frame 58 (C21orf58), mRNA [NM_058180]	33	0,713	2,16	1,296	1,96	0,68-3,73
AK098372	A_24_P238649	cDNA FLJ25506 fis, clone CBR05185, [AK098372]	34	0,713	2,097	1,296	1,66	0,42-5,33
AB040974	A_24_P940218	mRNA for KIAA1541 protein, partial cds, [AB040974]	35	0,713	2,037	1,296	1,91	1,20-6,61
FBXW4P1	A_23_P252603	F-box protein Fbw3 (FBW3) mRNA, complete cds, [AF174606]	36	0,713	1,98	1,296	2,1	0,39-5,90
NCAPG2	A_23_P168747	non-SMC condensin II complex, subunit G2 (NCAPG2), mRNA [NM_017760]	37	0,713	1,927	1,296	2,81	0,77-8,76
ADAMTS1	A_23_P211039	ADAM metalloproteinase with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA [NM_006988]	38	0,713	1,876	1,296	2,45	0,80-11,37
THC2505349	A_32_P48856	ALU6_HUMAN (P39193) Alu subfamily SP sequence contamination warning entry, partial (13%) [THC2505349]	39	0,713	1,828	1,485	0,77	0,70-1,67
TRIB1	A_23_P123503	tribbles homolog 1 (Drosophila) (TRIB1), mRNA [NM_025195]	40	0,713	1,782	1,296	1,69	0,82-3,72
LOC392335	A_32_P223173	PREDICTED: Homo sapiens misc_RNA (LOC392335), miscRNA [XR_037043]	41	0,713	1,739	1,296	1,72	0,52-3,00
MAPK3	A_23_P37910	mitogen-activated protein kinase 3 (MAPK3), transcript variant 1, mRNA [NM_002746]	42	0,713	1,698	1,296	2,01	0,40-2,55
C4orf23	A_24_P320171	chromosome 4 open reading frame 23 (C4orf23), transcript variant 2, mRNA [NM_152544]	43	0,713	1,658	1,296	1,87	0,50-4,59
TMEM49	A_32_P9753	transmembrane protein 49, mRNA (cDNA clone IMAGE:4295896), with apparent retained intron, [BC024020]	44	0,713	1,62	1,296	2,09	1,10-5,02
PTPRE	A_24_P213494	protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA [NM_006504]	45	0,713	1,584	1,485	0,38	0,16-1,10
SH2D3A	A_24_P262728	SH2 domain containing 3A (SH2D3A), mRNA [NM_005490]	46	0,713	1,55	1,296	1,5	0,30-2,74
BC036645	A_24_P570806	cDNA clone IMAGE:4814437, [BC036645]	47	0,713	1,517	1,296	1,57	0,74-2,54

Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
AA455656	A_32_P92415	aa22e03,s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814012 3', mRNA sequence [AA455656]	48	0,713	1,485	1,485	0,6	0,43-1,81
RXRΒ	A_23_P59179	retinoid X receptor, beta (RXRB), mRNA [NM_021976]	49	0,713	1,455	1,296	1,97	0,70-3,71
ECHDC2	A_24_P225477	enoyl Coenzyme A hydratase domain containing 2 (ECHDC2), mRNA [NM_018281]	50	0,713	1,426	1,296	1,85	0,59-3,37
EDC4	A_24_P399009	enhancer of mRNA decapping 4 (EDC4), mRNA [NM_014329]	51	0,713	1,398	1,296	1,77	0,59-2,60
CASKIN2	A_24_P48187	CASK interacting protein 2 (CASKIN2), transcript variant 1, mRNA [NM_020753]	52	0,713	1,371	1,296	1,77	0,82-2,78
HSPG2	A_23_P23191	heparan sulfate proteoglycan 2 (HSPG2), mRNA [NM_005529]	53	0,713	1,345	1,296	2,01	0,45-2,77
SF3B3	A_23_P135914	splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA [NM_012426]	54	0,713	1,32	1,296	1,4	0,92-2,85
CTA-216E10,6	A_23_P132341	hypothetical FLJ23584 (FLJ23584), mRNA [NM_001142964]	55	0,713	1,296	1,296	1,37	0,45-3,12
PRDM11	A_23_P13057	PR domain containing 11 (PRDM11), mRNA [NM_020229]	56	1,426	2,546	1,44	1,65	0,50-2,84
A_24_P900555	A_24_P900555	Unknown	57	1,426	2,502	1,44	1,59	0,72-3,87
ITPKC	A_23_P208369	inositol 1,4,5-trisphosphate 3-kinase C (ITPKC), mRNA [NM_025194]	58	1,426	2,458	1,44	1,47	0,71-2,04
ZZEF1	A_23_P130107	cDNA FLJ10821 fis, clone NT2RP4001057, [AK001683]	59	1,426	2,417	1,44	1,48	1,04-2,55
AZI1	A_24_P66522	5-azacytidine induced 1 (AZI1), transcript variant 1, mRNA [NM_014984]	60	1,426	2,377	1,44	1,76	0,28-3,90
C1orf183	A_24_P336577	chromosome 1 open reading frame 183 (C1orf183), transcript variant 1, mRNA [NM_019099]	61	1,426	2,338	1,44	1,65	1,02-2,14
AK123264	A_24_P930088	cDNA FLJ41270 fis, clone BRAMY2036387, [AK123264]	62	1,426	2,3	1,55	0,27	0,07-1,41
SIK2	A_23_P138957	salt-inducible kinase 2 (SIK2), mRNA [NM_015191]	63	1,426	2,263	1,44	2,3	0,99-10,33
FLJ38359	A_24_P163009	cDNA FLJ38359 fis, clone FEBRA2000321, [AK095678]	64	1,426	2,228	1,44	3,04	0,80-25,23
HEATR5B	A_32_P389118	HEAT repeat containing 5B (HEATR5B), mRNA [NM_019024]	65	1,426	2,194	1,44	1,33	1,05-2,25
SC4MOL	A_23_P110184	sterol-C4-methyl oxidase-like (SC4MOL), transcript variant 1, mRNA [NM_006745]	66	1,426	2,16	1,44	1,76	0,52-2,25
ERO1LB	A_23_P347618	ERO1-like beta (S, cerevisiae) (ERO1LB), mRNA [NM_019891]	67	1,426	2,128	1,44	1,54	0,57-2,29
TAX1BP3	A_23_P38468	Tax1 (human T-cell leukemia virus type I) binding protein 3 (TAX1BP3), mRNA [NM_014604]	68	1,426	2,097	1,44	1,39	0,45-2,49
MBD6	A_32_P411592	methyl-CpG binding domain protein 6 (MBD6), mRNA [NM_052897]	69	1,426	2,067	1,44	1,76	0,72-3,95
WDR26	A_24_P42803	WD repeat domain 26 (WDR26), transcript variant 1, mRNA [NM_025160]	70	1,426	2,037	1,44	1,97	0,62-2,74
A_32_P82119	A_32_P82119	Unknown	71	1,426	2,008	1,44	1,73	0,82-4,26
MYO10	A_24_P46357	myosin X (MYO10), mRNA [NM_012334]	72	1,426	1,98	1,44	2,68	1,08-5,29
GOLGA2	A_24_P910297	golgi autoantigen, golgin subfamily a, 2 (GOLGA2), mRNA [NM_004486]	73	1,426	1,953	1,44	1,75	0,73-2,63

Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
MTMR14	A_24_P388502	myotubularin related protein 14 (MTMR14), transcript variant 3, mRNA [NM_022485]	74	1,426	1,927	1,44	1,37	0,88-4,14
TMEM97	A_32_P201521	transmembrane protein 97 (TMEM97), mRNA [NM_014573]	75	1,426	1,901	1,55	0,58	0,27-1,03
FLJ36031	A_23_P377982	hypothetical protein FLJ36031 (FLJ36031), mRNA [NM_175884]	76	1,426	1,876	1,44	2,06	0,63-5,49
FOXD3	A_23_P46560	forkhead box D3 (FOXD3), mRNA [NM_012183]	77	1,426	1,852	1,44	1,61	0,84-2,49
GPR155	A_23_P335958	G protein-coupled receptor 155 (GPR155), transcript variant 9, mRNA [NM_001033045]	78	1,426	1,828	1,55	0,65	0,31-1,62
THC2537951	A_32_P217330	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (27%) [THC2537674]	79	1,426	1,805	1,44	1,52	0,95-2,22
DIS3L2	A_23_P113888	DIS3 mitotic control homolog (S, cerevisiae)-like 2 (DIS3L2), mRNA [NM_152383]	80	1,426	1,782	1,44	1,49	0,74-2,27
THC2708124	A_32_P73304	Unknown	81	1,426	1,76	1,55	0,65	0,26-2,75
AK024470	A_24_P84370	mRNA for FLJ00063 protein, partial cds, [AK024470]	82	1,426	1,739	1,44	1,92	1,12-6,35
WASF2	A_32_P41461	WAS protein family, member 2 (WASF2), mRNA [NM_006990]	83	1,426	1,718	1,55	0,59	0,25-3,08
INPPL1	A_23_P36322	inositol polyphosphate phosphatase-like 1 (INPPL1), mRNA [NM_001567]	84	1,426	1,698	1,44	1,61	0,71-2,16
LOC344382	A_24_P135579	PREDICTED: Homo sapiens similar to uninteracting protein (LOC344382), mRNA [XM_293026]	85	1,426	1,678	1,44	1,24	1,05-2,29
BC031320	A_24_P523061	cDNA clone IMAGE:5278682, [BC031320]	86	1,426	1,658	1,44	1,32	0,78-1,98
ZW10	A_23_P64204	ZW10, kinetochore associated, homolog (Drosophila) (ZW10), mRNA [NM_004724]	87	1,426	1,639	1,44	1,35	0,83-2,69
COBRA1	A_23_P148150	cofactor of BRCA1 (COBRA1), mRNA [NM_015456]	88	1,426	1,62	1,44	1,33	0,65-1,86
SUZ12P	A_24_P889103	full-length cDNA clone CS0DC012YL18 of Neuroblastoma Cot 25-normalized of Homo sapiens (human), [CR597846]	89	1,426	1,602	1,44	1,73	0,91-2,96
GRB7	A_23_P163992	growth factor receptor-bound protein 7 (GRB7), transcript variant 1, mRNA [NM_005310]	90	1,426	1,584	1,44	1,62	0,55-3,23
DTNB	A_24_P216421	dystrobrevin, beta (DTNB), transcript variant 3, mRNA [NM_033148]	91	1,426	1,567	1,44	1,66	0,23-2,53
A_32_P194182	A_32_P194182	Unknown	92	1,426	1,55	1,55	0,68	0,43-1,52
F11R	A_24_P319369	F11 receptor (F11R), mRNA [NM_016946]	93	1,426	1,533	1,44	1,48	0,21-2,39
BC016384	A_24_P677890	clone IMAGE:4703872, mRNA, [BC016384]	94	1,426	1,517	1,44	1,35	1,07-3,74
ALS2CL	A_32_P420009	ALS2 C-terminal like (ALS2CL), transcript variant 1, mRNA [NM_147129]	95	1,426	1,501	1,44	1,82	0,60-2,76
SLC25A4	A_24_P206047	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 (SLC25A4), nuclear gene encoding mitochondrial protein, mRNA [NM_001151]	96	1,426	1,485	1,44	1,48	0,56-2,06
TSC22D3	A_23_P217688	TSC22 domain family, member 3 (TSC22D3), transcript variant 2, mRNA [NM_004089]	97	1,426	1,47	1,44	1,91	0,55-3,56
A_24_P195528	A_24_P195528	Unknown	98	1,426	1,455	1,44	1,58	0,59-2,98
BAG3	A_23_P47077	BCL2-associated athanogene 3 (BAG3), mRNA [NM_004281]	99	1,426	1,44	1,44	1,82	0,44-3,50

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PTPRE	A_24_P213503	protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA [NM_006504]	100	2,139	2,139	1,678	0,58	0,10-1,94
VPRBP	A_23_P212595	Vpr (HIV-1) binding protein (VPRBP), mRNA [NM_014703]	101	2,139	2,118	1,55	1,47	1,03-3,20
FXR2	A_23_P4007	fragile X mental retardation, autosomal homolog 2 (FXR2), mRNA [NM_004860]	102	2,139	2,097	1,55	1,83	0,25-4,84
CYP2D6	A_23_P155123	cytochrome P450, family 2, subfamily D, polypeptide 6 (CYP2D6), transcript variant 1, mRNA [NM_000106]	103	2,139	2,077	1,55	1,51	0,46-3,38
A_24_P812172	A_24_P812172	Unknown	104	2,139	2,057	1,55	1,94	0,57-4,80
RASD1	A_23_P118392	RAS, dexamethasone-induced 1 (RASD1), mRNA [NM_016084]	105	2,139	2,037	1,55	3,14	0,88-21,55
C8orf73	A_23_P369641	chromosome 8 open reading frame 73 (C8orf73), mRNA [NM_001100878]	106	2,139	2,018	1,55	1,7	0,43-4,02
SLC13A2	A_23_P107307	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA [NM_003984]	107	2,139	1,999	1,55	1,62	0,87-2,71
HIRIP3	A_24_P142269	HIRA interacting protein 3 (HIRIP3), mRNA [NM_003609]	108	2,139	1,98	1,55	1,51	0,36-2,84
ENST00000307533	A_24_P89038	LOC93622 protein (Putative uncharacterized protein LOC93622) (cDNA, FLJ95718) [Source:UniProtKB/TrEMBL;Acc:Q8WU25] [ENST00000307533]	109	2,139	1,962	1,55	1,79	0,59-2,38
RGMB	A_24_P363100	RGM domain family, member B (RGMB), transcript variant 2, mRNA [NM_173670]	110	2,139	1,944	1,55	1,41	0,82-2,36
ARID5B	A_23_P97871	AT rich interactive domain 5B (MRF1-like) (ARID5B), mRNA [NM_032199]	111	2,139	1,927	1,55	2,11	0,81-3,00
IGF2BP2	A_23_P250156	insulin-like growth factor 2 mRNA binding protein 2 (IGF2BP2), transcript variant 1, mRNA [NM_006548]	112	2,139	1,91	1,55	1,6	1,09-3,09
SP100	A_24_P916816	nuclear autoantigen mRNA, partial cds; alternatively spliced, [L79989]	113	2,139	1,893	1,678	0,49	0,15-3,15
A_24_P349580	A_24_P349580	Unknown	114	2,139	1,876	1,55	1,38	0,75-2,38
A_24_P920081	A_24_P920081	Unknown	115	2,139	1,86	1,55	1,57	0,76-4,11
H6PD	A_24_P626850	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA [NM_004285]	116	2,139	1,844	1,55	2,6	0,26-4,61
SAPS2	A_23_P95353	SAPS domain family, member 2 (SAPS2), mRNA [NM_014678]	117	2,139	1,828	1,55	1,51	0,86-2,13
SPAG9	A_24_P365025	sperm associated antigen 9 (SPAG9), transcript variant 3, mRNA [NM_003971]	118	2,139	1,813	1,55	1,42	0,93-1,94
NDRG1	A_24_P38387	N-myc downstream regulated 1 (NDRG1), transcript variant 2, mRNA [NM_006096]	119	2,139	1,797	1,55	1,67	0,98-4,09
ENST00000312412	A_24_P690235	cDNA FLJ43844 fis, clone TEST14006308, highly similar to Puromycin-sensitive aminopeptidase (EC 3,4,11,-), [AK125832]	120	2,139	1,782	1,55	1,49	0,14-2,16
A_24_P170365	A_24_P170365	Unknown	121	2,139	1,768	1,55	1,85	0,68-4,24
RHOU	A_23_P114814	ras homolog gene family, member U (RHOU), mRNA [NM_021205]	122	2,139	1,753	1,55	2,68	0,71-3,65
DHRS11	A_23_P27005	dehydrogenase/reductase (SDR family) member 11 (DHRS11), mRNA [NM_024308]	123	2,139	1,739	1,55	1,38	1,02-3,10

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RNPEP	A_24_P68649	arginyl aminopeptidase (aminopeptidase B) (RNPEP), mRNA [NM_020216]	124	2,139	1,725	1,55	2,35	0,27-3,54
CHST10	A_23_P102351	carbohydrate sulfotransferase 10 (CHST10), mRNA [NM_004854]	125	2,139	1,711	1,55	1,5	0,33-3,35
CA314936	A_32_P140228	UI-CF-FN0-afi-d-17-0-UI,s1 UI-CF-FN0 Homo sapiens cDNA clone UI-CF-FN0-afi-d-17-0-UI 3', mRNA sequence [CA314936]	126	2,139	1,698	1,55	2,16	0,39-4,08
SSBP2	A_23_P33791	single-stranded DNA binding protein 2 (SSBP2), mRNA [NM_012446]	127	2,139	1,684	1,55	1,33	0,71-1,76
BRCC3	A_23_P217659	BRCA1/BRCA2-containing complex, subunit 3 (BRCC3), transcript variant 2, mRNA [NM_001018055]	128	2,139	1,671	1,55	1,47	0,89-3,17
SPG7	A_24_P5305	spastic paraplegia 7 (pure and complicated autosomal recessive) (SPG7), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_003119]	129	2,139	1,658	1,55	1,83	0,84-3,97
MFGE8	A_24_P133584	milk fat globule-EGF factor 8 protein (MFGE8), transcript variant 1, mRNA [NM_005928]	130	2,139	1,645	1,55	1,56	0,85-2,51
A_24_P152144	A_24_P152144	Unknown	131	2,139	1,633	1,55	1,51	0,63-2,53
CHKA	A_23_P136135	choline kinase alpha (CHKA), transcript variant 1, mRNA [NM_001277]	132	2,139	1,62	1,55	1,45	0,50-2,57
RBM8A	A_23_P305335	RNA binding motif protein 8A, mRNA (cDNA clone IMAGE:4687764), complete cds, [BC017770]	133	2,139	1,608	1,55	1,95	0,85-3,33
BC063542	A_32_P135790	cDNA clone IMAGE:4525305, **** WARNING: chimeric clone ****, [BC063542]	134	2,139	1,596	1,55	1,93	0,71-3,76
A_24_P460195	A_24_P460195	Unknown	135	2,139	1,584	1,55	2,36	0,37-5,36
DFNB31	A_23_P83351	deafness, autosomal recessive 31 (DFNB31), transcript variant 1, mRNA [NM_015404]	136	2,139	1,573	1,55	1,51	0,40-3,71
LOC388152	A_23_P305981	cDNA FLJ90297 fis, clone NT2RP2000447, moderately similar to GOLGIN-95, [AK074778]	137	2,139	1,561	1,55	1,68	0,84-2,65
CARS	A_24_P95439	cysteinyI-tRNA synthetase (CARS), transcript variant 4, mRNA [NM_001014438]	138	2,139	1,55	1,55	1,66	0,66-3,26
BI024548	A_32_P74942	BI024548 PM3-MT0205-300101-005-f07 MT0205 Homo sapiens cDNA, mRNA sequence [BI024548]	139	2,852	2,052	1,678	0,67	0,14-2,80
RASAL1	A_23_P139600	RAS protein activator like 1 (GAP1 like) (RASAL1), mRNA [NM_004658]	140	2,852	2,037	1,648	1,46	0,38-2,41
A_24_P33055	A_24_P33055	Unknown	141	2,852	2,023	1,648	1,38	0,92-2,47
CAMK1D	A_23_P124252	calcium/calmodulin-dependent protein kinase ID (CAMK1D), transcript variant 1, mRNA [NM_020397]	142	2,852	2,008	1,648	1,58	1,00-3,03
TMEM19	A_24_P358976	transmembrane protein 19 (TMEM19), mRNA [NM_018279]	143	2,852	1,994	1,678	0,71	0,40-0,93
ATP1A4	A_23_P160177	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 4 polypeptide (ATP1A4), transcript variant 1, mRNA [NM_144699]	144	2,852	1,98	1,648	1,64	0,77-3,35
ANO1	A_23_P98304	anoctamin 1, calcium activated chloride channel (ANO1), mRNA [NM_018043]	145	2,852	1,967	1,648	1,48	0,59-2,05
A_32_P78488	A_32_P78488	Unknown	146	2,852	1,953	1,648	1,35	0,90-1,96
UBL4A	A_23_P62361	ubiquitin-like 4A (UBL4A), mRNA [NM_014235]	147	2,852	1,94	1,648	1,64	0,36-3,54

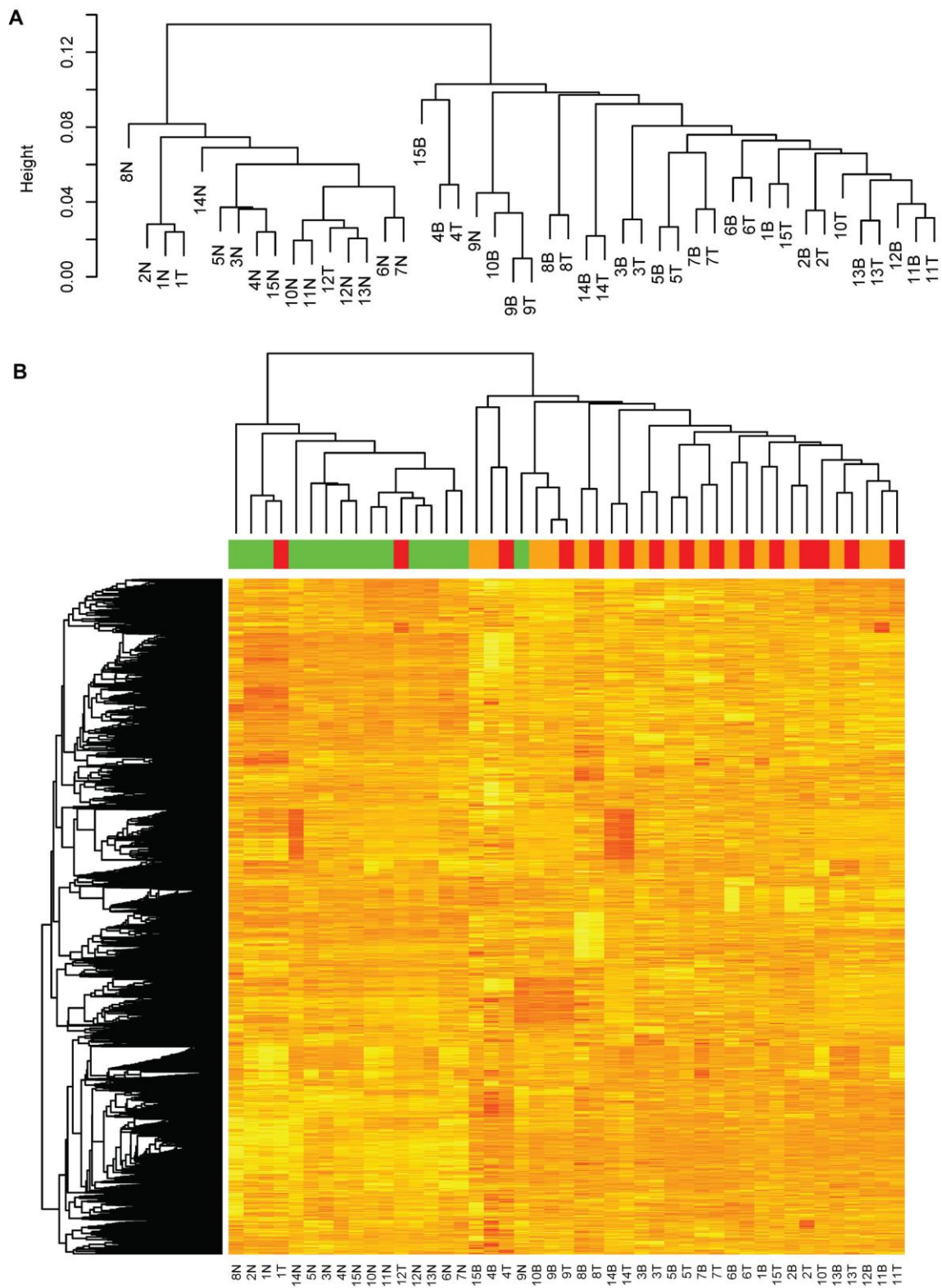
Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
SDHA	A_32_P67259	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (SDHA), nuclear gene encoding mitochondrial protein, mRNA [NM_004168]	148	2,852	1,927	1,648	1,42	0,54-2,68
CNOT3	A_23_P38987	CCR4-NOT transcription complex, subunit 3 (CNOT3), mRNA [NM_014516]	149	2,852	1,914	1,648	1,3	0,75-2,22
ARHGEF9	A_24_P254551	Cdc42 guanine nucleotide exchange factor (GEF) 9 (ARHGEF9), mRNA [NM_015185]	150	2,852	1,901	1,648	1,8	0,76-4,15
STK35	A_24_P940537	serine/threonine kinase 35 (STK35), mRNA [NM_080836]	151	2,852	1,889	1,648	1,6	0,52-3,00
DDR1	A_23_P93311	discoidin domain receptor tyrosine kinase 1 (DDR1), transcript variant 1, mRNA [NM_013993]	152	2,852	1,876	1,648	1,74	0,40-3,20
C3orf39	A_24_P217330	chromosome 3 open reading frame 39 (C3orf39), mRNA [NM_032806]	153	2,852	1,864	1,648	1,42	0,48-2,69
ZKSCAN5	A_24_P317637	zinc finger with KRAB and SCAN domains 5 (ZKSCAN5), transcript variant 1, mRNA [NM_014569]	154	2,852	1,852	1,648	1,61	0,73-2,22
TBC1D17	A_23_P130731	TBC1 domain family, member 17 (TBC1D17), mRNA [NM_024682]	155	2,852	1,84	1,648	1,26	0,36-2,11
RNF215	A_32_P420563	ring finger protein 215 (RNF215), mRNA [NM_001017981]	156	2,852	1,828	1,648	1,79	0,61-2,98
LOC100130713	A_24_P119405	cDNA FLJ39247 fis, clone OCBBF2008520, [AK096566]	157	2,852	1,816	1,648	1,81	0,96-3,49
PPP2R3B	A_23_P45517	protein phosphatase 2 (formerly 2A), regulatory subunit B", beta (PPP2R3B), transcript variant 1, mRNA [NM_013239]	158	2,852	1,805	1,648	1,29	0,54-2,17
EPHA1	A_23_P157333	EPH receptor A1 (EPHA1), mRNA [NM_005232]	159	2,852	1,794	1,648	1,67	0,55-2,95
GPR65	A_23_P14564	G protein-coupled receptor 65 (GPR65), mRNA [NM_003608]	160	2,852	1,782	1,678	0,61	0,35-4,64
RMND5A	A_24_P114339	required for meiotic nuclear division 5 homolog A (S. cerevisiae) (RMND5A), mRNA [NM_022780]	161	2,852	1,771	1,648	2,08	0,76-4,92
CR616003	A_24_P65597	gb full-length cDNA clone CS0DM012YB14 of Fetal liver of Homo sapiens (human), [CR616003]	162	2,852	1,76	1,648	2,41	0,21-15,71
CYR61	A_23_P46426	cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA [NM_001554]	163	2,852	1,75	1,648	4,07	0,61-12,88
ANGEL2	A_24_P28622	angel homolog 2 (Drosophila) (ANGEL2), mRNA [NM_144567]	164	2,852	1,739	1,678	0,79	0,54-0,98
RNF185	A_32_P15421	ring finger protein 185 (RNF185), transcript variant 1, mRNA [NM_152267]	165	2,852	1,728	1,648	1,5	0,62-2,03
UBE2MP1	A_24_P239017	ubiquitin-conjugating enzyme E2M pseudogene 1 (UBE2MP1), non-coding RNA [NR_002837]	166	2,852	1,718	1,648	1,31	0,42-9,42
TUBA4A	A_23_P102109	tubulin, alpha 4a (TUBA4A), mRNA [NM_006000]	167	2,852	1,708	1,648	1,46	0,39-3,22
TSPAN12	A_23_P145984	tetraspanin 12 (TSPAN12), mRNA [NM_012338]	168	2,852	1,698	1,648	1,64	1,04-3,43
DDR1	A_24_P367289	discoidin domain receptor tyrosine kinase 1 (DDR1), transcript variant 1, mRNA [NM_013993]	169	2,852	1,687	1,648	1,51	0,29-6,52
X05126	A_32_P64936	Human fibroblast mRNA fragment with Alu sequence (pRHF11), [X05126]	170	2,852	1,678	1,678	0,66	0,39-1,43
GLTPD2	A_24_P392925	glycolipid transfer protein domain containing 2 (GLTPD2), mRNA [NM_001014985]	171	2,852	1,668	1,648	1,57	0,77-3,48

Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
SLC22A12	A_23_P35809	solute carrier family 22 (organic anion/urate transporter), member 12 (SLC22A12), transcript variant 1, mRNA [NM_144585]	172	2,852	1,658	1,648	1,68	0,91-3,22
SIX5	A_23_P328687	SIX homeobox 5 (SIX5), mRNA [NM_175875]	173	2,852	1,648	1,648	1,43	0,60-2,08
IMMT	A_24_P351304	inner membrane protein, mitochondrial (mitofilin) (IMMT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_006839]	174	3,565	2,049	1,791	1,23	0,59-1,54
ZNF628	A_32_P409222	zinc finger protein 628 (ZNF628), mRNA [NM_033113]	175	3,565	2,037	1,791	1,25	0,63-1,73
L3MBTL	A_23_P501961	I(3)mbt-like (Drosophila) (L3MBTL), transcript variant II, mRNA [NM_032107]	176	3,565	2,025	1,791	1,63	0,85-2,52
DGCR2	A_24_P125881	DiGeorge syndrome critical region gene 2 (DGCR2), mRNA [NM_005137]	177	3,565	2,014	1,791	1,31	0,58-1,59
WAPAL	A_23_P342185	wings apart-like homolog (Drosophila) (WAPAL), mRNA [NM_015045]	178	3,565	2,003	1,791	1,31	0,87-1,91
B4GALT4	A_32_P103945	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), transcript variant 1, mRNA [NM_212543]	179	3,565	1,992	1,791	1,45	0,82-2,35
SPRY1	A_23_P144476	sprouty homolog 1, antagonist of FGF signaling (Drosophila) (SPRY1), transcript variant 2, mRNA [NM_199327]	180	3,565	1,98	1,791	1,69	0,77-8,90
LRP5L	A_24_P387514	low density lipoprotein receptor-related protein 5-like (LRP5L), transcript variant 1, mRNA [NM_182492]	181	3,565	1,97	1,791	1,56	0,98-3,46
ARHGEF5	A_24_P389218	Rho guanine nucleotide exchange factor (GEF) 5 (ARHGEF5), mRNA [NM_005435]	182	3,565	1,959	1,791	1,9	0,43-4,10
NFRKB	A_23_P24485	nuclear factor related to kappaB binding protein (NFRKB), transcript variant 2, mRNA [NM_006165]	183	3,565	1,948	1,791	1,61	0,63-3,25
RHOV	A_23_P117912	Rho-related GTP-binding protein RhoV (Wnt-1 responsive Cdc42 homolog 2)(WRCH-2)(CDC42-like GTPase 2)(GTP-binding protein-like 2)(Rho GTPase-like protein ARHV) [Source:UniProtKB/Swiss-Prot;Acc:Q96L33] [ENST00000220507]	184	3,565	1,937	1,791	1,6	0,25-5,45
CCDC52	A_23_P109733	coiled-coil domain containing 52 (CCDC52), mRNA [NM_144718]	185	3,565	1,927	1,791	1,47	0,52-1,90
SLC25A27	A_23_P81721	solute carrier family 25, member 27 (SLC25A27), nuclear gene encoding mitochondrial protein, mRNA [NM_004277]	186	3,565	1,917	1,791	1,82	0,86-2,93
SCRN2	A_23_P4323	secernin 2 (SCRN2), mRNA [NM_138355]	187	3,565	1,906	1,791	1,35	0,82-2,17
AK022337	A_24_P825969	cDNA FLJ12275 fis, clone MAMMA1001686, [AK022337]	188	3,565	1,896	1,791	1,6	0,95-3,98
C20orf151	A_32_P331052	chromosome 20 open reading frame 151 (C20orf151), mRNA [NM_080833]	189	3,565	1,886	1,791	1,32	0,38-2,32
GABARAP	A_23_P27075	GABA(A) receptor-associated protein (GABARAP), mRNA [NM_007278]	190	3,565	1,876	1,81	0,79	0,57-1,43
CYTH2	A_23_P119377	cytohesin 2 (CYTH2), transcript variant 2, mRNA [NM_004228]	191	3,565	1,866	1,791	1,58	0,48-4,52
THC2564025	A_24_P936051	BC065015 transmembrane protein 4 {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (8%) [THC2564025]	192	3,565	1,857	1,791	1,42	0,79-2,76
SETD1A	A_23_P129678	SET domain containing 1A (SETD1A), mRNA [NM_014712]	193	3,565	1,847	1,791	1,44	0,32-2,89

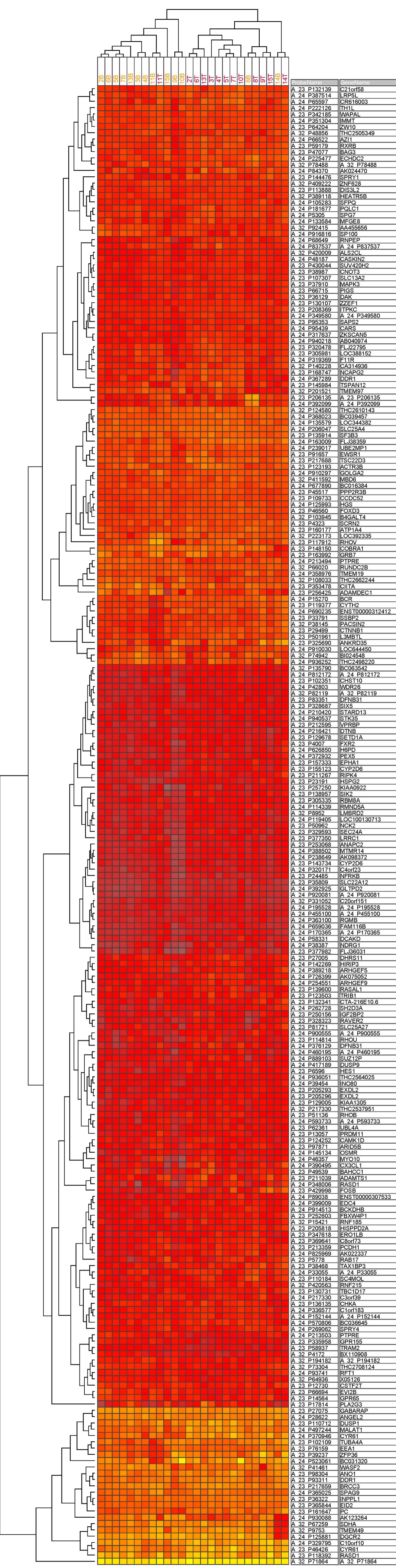


Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
EXDL2	A_23_P205296	exonuclease 3'-5' domain-like 2 (EXDL2), mRNA [NM_018199]	194	3,565	1,838	1,791	1,48	0,57-2,63
EID2	A_23_P365844	EP300 interacting inhibitor of differentiation 2 (EID2), mRNA [NM_153232]	195	3,565	1,828	1,791	1,3	0,73-2,81
CYR61	A_24_P370946	cysteine-rich, angiogenic inducer, 61 (CYR61), mRNA [NM_001554]	196	3,565	1,819	1,791	5,51	0,36-22,80
RFT1	A_24_P93741	RFT1 homolog (S, cerevisiae) (RFT1), mRNA [NM_052859]	197	3,565	1,81	1,81	0,64	0,49-1,18
BAHCC1	A_23_P49539	BAH domain and coiled-coil containing 1 (BAHCC1), mRNA [NM_001080519]	198	3,565	1,8	1,791	1,55	0,74-5,59
RIPK4	A_23_P211267	receptor-interacting serine-threonine kinase 4 (RIPK4), mRNA [NM_020639]	199	3,565	1,791	1,791	2,08	0,64-4,59
HGS	A_24_P125993	hepatocyte growth factor-regulated tyrosine kinase substrate (HGS), mRNA [NM_004712]	200	4,278	2,139	2,008	1,76	0,59-2,60
A_24_P392099	A_24_P392099	Unknown	201	4,278	2,128	2,008	1,44	0,38-3,60
A_24_P455100	A_24_P455100	Unknown	202	4,278	2,118	2,008	1,38	1,02-2,06
FOSB	A_23_P429998	FBJ murine osteosarcoma viral oncogene homolog B (FOSB), transcript variant 1, mRNA [NM_006732]	203	4,278	2,107	2,008	2,79	0,96-24,26
DCAKD	A_24_P58331	dephospho-CoA kinase domain containing (DCAKD), transcript variant 1, mRNA [NM_024819]	204	4,278	2,097	2,008	1,89	0,41-4,80
SUV420H2	A_23_P430044	suppressor of variegation 4-20 homolog 2 (Drosophila) (SUV420H2), mRNA [NM_032701]	205	4,278	2,087	2,008	1,41	0,89-2,29
EWSR1	A_23_P91657	Ewing sarcoma breakpoint region 1 (EWSR1), transcript variant EWS-b, mRNA [NM_013986]	206	4,278	2,077	2,008	1,57	0,38-2,43
OSMR	A_24_P145134	oncostatin M receptor, mRNA (cDNA clone IMAGE:4043935), complete cds, [BC010943]	207	4,278	2,067	2,008	1,32	0,54-2,17
SFPQ	A_24_P105283	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA [NM_005066]	208	4,278	2,057	2,008	1,82	0,64-3,83
BCKDHB	A_24_P914513	branched chain keto acid dehydrogenase E1, beta polypeptide (BCKDHB), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_183050]	209	4,278	2,047	2,008	1,55	0,62-2,08
SEC24A	A_23_P329593	SEC24 related gene family, member A (S, cerevisiae), mRNA (cDNA clone MGC:12985 IMAGE:3355949), complete cds, [BC019341]	210	4,278	2,037	2,008	1,69	0,95-4,92
SPRY4	A_24_P269062	sprouty homolog 4 (Drosophila) (SPRY4), transcript variant 1, mRNA [NM_030964]	211	4,278	2,027	2,008	1,47	0,61-2,20
A_24_P837537	A_24_P837537	Unknown	212	4,278	2,018	2,008	1,67	0,81-3,35
PC	A_23_P161647	pyruvate carboxylase (PC), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA [NM_001040716]	213	4,278	2,008	2,008	2,22	0,72-9,75
THC2662244	A_32_P108033	Q26SG8_XANP2 (Q26SG8) Cytochrome C-type biogenesis protein CycL precursor, partial (8%) [THC2662244]	214	4,278	1,999	1,999	0,48	0,22-2,06
ACTR3B	A_23_P123193	ARP3 actin-related protein 3 homolog B (yeast) (ACTR3B), transcript variant 1, mRNA [NM_020445]	215	4,991	2,321	2,199	1,54	0,79-2,04
RUNDC2B	A_32_P66020	RUN domain containing 2B (RUNDC2B), mRNA [NM_001012391]	216	4,991	2,311	2,189	0,74	0,40-1,69

Gene Name	Agilent ID	Description	SAM				Fold change	
			Called	FSN	FDR	q-val	mean	Range
DUSP1	A_23_P110712	dual specificity phosphatase 1 (DUSP1), mRNA [NM_004417]	217	4,991	2,3	2,199	3,18	0,49-12,69
EXDL2	A_23_P205293	exonuclease 3'-5' domain-like 2 (EXDL2), mRNA [NM_018199]	218	4,991	2,289	2,199	1,31	0,58-2,17
KIAA0922	A_23_P257250	KIAA0922 (KIAA0922), transcript variant 2, mRNA [NM_015196]	219	4,991	2,279	2,199	1,75	0,83-6,14
ADAMDEC1	A_23_P256425	ADAM-like, decysin 1 (ADAMDEC1), mRNA [NM_014479]	220	4,991	2,269	2,189	0,59	0,11-6,10
LOC644450	A_24_P910030	hypothetical protein LOC644450, mRNA (cDNA clone IMAGE:4606942), partial cds, [BC022881]	221	4,991	2,258	2,189	0,63	0,41-1,24
ZFP36	A_23_P39237	zinc finger protein 36, C3H type, homolog (mouse) (ZFP36), mRNA [NM_003407]	222	4,991	2,248	2,199	2,21	0,07-23,35
PIGS	A_23_P66715	phosphatidylinositol glycan anchor biosynthesis, class S (PIGS), mRNA [NM_033198]	223	4,991	2,238	2,199	1,45	0,45-2,59
TRAM2	A_23_P58937	translocation associated membrane protein 2 (TRAM2), mRNA [NM_012288]	224	4,991	2,228	2,189	0,7	0,36-1,18
CTNNB1	A_23_P29499	catenin (cadherin-associated protein), beta 1, 88kDa (CTNNB1), mRNA [NM_001904]	225	4,991	2,218	2,199	1,63	0,79-5,30
PEX5	A_24_P372932	peroxisomal biogenesis factor 5 (PEX5), transcript variant 2, mRNA [NM_000319]	226	4,991	2,208	2,199	1,7	0,56-5,88
TH1L	A_24_P222126	TH1-like (Drosophila) (TH1L), transcript variant 1, mRNA [NM_198976]	227	4,991	2,199	2,199	1,3	0,47-2,10
THC2498220	A_24_P936252	thc Q30VC0_DESDG (Q30VC0) Flagellar biosynthetic protein FlIP, partial (8%) [THC2498220]	228	4,991	2,189	2,189	0,43	0,11-1,25
A_32_P71864	A_32_P71864	Unknown	229	5,704	2,491	2,427	1,28	0,96-2,05
RAVER2	A_23_P328323	ribonucleoprotein, PTB-binding 2 (RAVER2), mRNA [NM_018211]	230	5,704	2,48	2,427	1,66	0,99-3,04
CSTF2T	A_23_P12730	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant (CSTF2T), mRNA [NM_015235]	231	5,704	2,469	2,437	0,62	0,39-1,09
FAM116B	A_24_P659036	family with sequence similarity 116, member B (FAM116B), mRNA [NM_001001794]	232	5,704	2,458	2,427	1,42	0,28-2,78
FLJ22795	A_23_P320478	similar to cis-Golgi matrix protein GM130, mRNA (cDNA clone MGC:70902 IMAGE:6144741), complete cds, [BC065260]	233	5,704	2,448	2,427	1,78	0,74-3,57
EVI2B	A_23_P66694	ecotropic viral integration site 2B (EVI2B), mRNA [NM_006495]	234	5,704	2,437	2,437	0,56	0,15-3,17
INO80	A_24_P39454	INO80 homolog (S. cerevisiae) (INO80), mRNA [NM_017553]	235	5,704	2,427	2,427	1,51	0,63-2,66

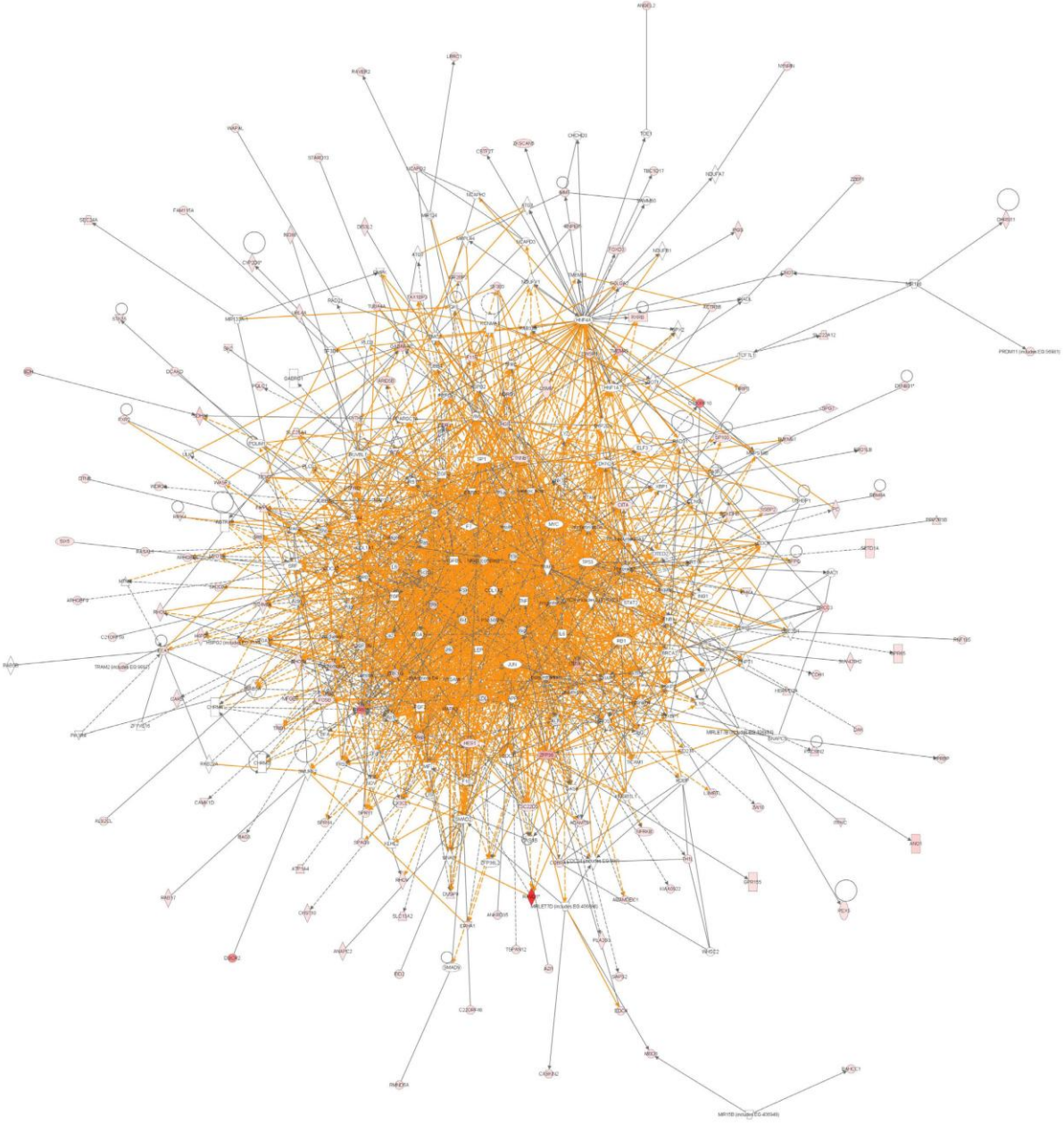


Supplementary fig 1



ProbeName	GeneName
A 23 P132139	C21orf58
A 24 P387514	LRP5L
A 24 P65597	CR616003
A 24 P222126	TH1L
A 23 P342185	WAPAL
A 24 P351304	IMMT
A 23 P64204	ZW10
A 32 P48856	THC2505349
A 24 P66522	AZI1
A 23 P59179	RXR8
A 23 P47077	BAG3
A 24 P225477	ECHDC2
A 32 P78488	A 32 P78488
A 24 P84370	AK024470
A 23 P144476	SPRY1
A 32 P409222	ZNF628
A 23 P113888	DIS3L2
A 32 P389118	HEATR5B
A 24 P105283	SFPQ
A 24 P181677	PQLC1
A 24 P5305	SPG7
A 24 P133584	MFGE8
A 32 P92415	AA455656
A 24 P916816	SP100
A 24 P68649	RNPEP
A 24 P837537	A 24 P837537
A 32 P420009	ALS2CL
A 24 P48187	CASKIN2
A 23 P430044	SUV420H2
A 23 P38987	CNOT3
A 23 P107307	SLC13A2
A 23 P37910	MAPK3
A 23 P66715	PIGS
A 23 P36129	DAK
A 23 P130107	ZZEF1
A 23 P208369	ITPKC
A 24 P349580	A 24 P349580
A 23 P95353	SAPS2
A 24 P95439	CARS
A 24 P317637	ZKSCAN5
A 24 P940218	AB040974
A 23 P320478	FLJ22795
A 23 P305981	LOC388152
A 24 P319369	F11R
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Supplementary fig 2



Supplementary fig 3