

	Symptoms		C4a		MMP-9		TGFβ1		VEGF	
	Pre	Post	Pre	Post	Pre	Post	Pre	Post	Pre	Post
Mean	12.87	3.33	9269	3903	357.8	249.1	9373	4328	57.6	66.0
StD	4.23	3.42	8376	3040	214.5	165.7	7579	3201	38.4	22.7
p (t test)	5.25E-08		1.96E-02		1.94E-01		1.55E-02		5.72E-01	

Feature ID	Fold	P Value	Pre Vip	Post Vip
A1BG	-1.36	6.71E-04	6.67	4.91
ABCC4	1.34	5.51E-04	8.01	10.76
AC133528.2	-1.37	3.65E-04	4.29	3.12
ARHGAP21	1.40	5.45E-04	12.88	17.97
ARID1B	1.30	9.98E-04	53.12	68.85
BCL2L13	1.10	7.41E-04	42.34	46.38
BCOR	1.39	6.26E-04	21.89	30.37
C6orf48	-1.31	8.28E-04	96.87	74.05
CD3D	-1.39	1.03E-03	91.35	65.95
CDC42BPA	1.30	3.69E-04	1.30	1.69
CHAMP1	1.32	4.07E-05	15.17	20.08
CITED2	1.17	6.64E-04	51.12	59.96
COX7A2L	-1.25	9.22E-04	59.06	47.29
CTCF	1.19	9.57E-04	70.63	84.25
CTR9	1.19	4.43E-04	68.17	81.31
DAP3	-1.14	1.02E-03	82.46	72.16
DARS2	1.24	4.26E-05	8.74	10.84
EEF1D	-1.23	5.88E-04	564.04	458.11
ELAVL1	1.12	6.36E-04	51.15	57.38
EPB41	1.21	8.38E-04	352.89	427.25
EPB41L2	1.26	3.18E-04	11.66	14.69
EXOSC6	1.22	8.42E-04	11.03	13.48
EZH1	-1.12	8.91E-04	191.16	170.81
FAM225A	1.36	5.46E-04	1.78	2.41
FBXO21	1.16	9.81E-04	24.11	28.01
FKBP3	-1.27	6.19E-04	28.99	22.74
GEMIN6	-1.23	5.50E-04	12.89	10.52
GUCY1B3	1.60	8.57E-04	2.32	3.71
HFE	1.23	3.79E-05	7.71	9.50
IFIH1	1.21	1.01E-03	33.69	40.79
IKZF4	1.38	7.01E-04	3.38	4.67
ING4	-1.25	1.91E-04	54.23	43.25
INO80	1.18	5.79E-04	39.33	46.43
IRS1	1.64	5.59E-04	2.16	3.53
KIAA0196	1.17	2.77E-04	38.15	44.63
KIF3B	1.20	7.05E-04	26.35	31.74
KIF5C	1.28	9.50E-04	5.94	7.63
MAPKAPK5-AS1	-1.13	9.96E-04	18.30	16.14
MAPRE2	1.12	8.70E-04	74.12	83.26
MRPL48	-1.26	3.87E-04	14.49	11.50
MTBP	1.32	6.92E-04	2.39	3.17
MTCH1	-1.17	9.99E-04	208.08	177.21
NDRG1	1.13	9.46E-04	125.88	142.23
NFKB1	1.19	7.13E-04	98.53	116.92
PDZD3	-1.37	6.61E-04	1.91	1.40
PTK2	1.22	4.07E-04	8.93	10.91

PTRH2	-1.25	1.37E-05	17.39	13.97
RER1	-1.12	9.75E-04	185.05	165.32
RP11-1084J3.4	1.18	1.02E-03	8.31	9.82
RP11-231C14.4	1.97	8.90E-04	1.54	3.04
RPL35	-1.50	7.59E-04	252.96	169.01
RPLP0	-1.37	7.91E-04	1222.24	892.22
RPS21	-1.55	5.52E-04	141.95	91.57
RPS3	-1.30	8.17E-04	1377.21	1059.56
RPS9	-1.37	1.23E-04	1073.48	782.86
SALL2	1.18	1.00E-03	2.39	2.82
SAV1	1.30	7.12E-04	9.14	11.87
SEC23B	1.18	3.97E-04	45.87	54.04
SEC23IP	1.23	4.73E-04	30.71	37.80
SIK3	1.17	7.23E-04	76.70	89.99
SNHG6	-1.31	2.20E-04	39.81	30.38
SNHG8	-1.26	9.99E-04	14.39	11.44
SNX29	1.36	4.94E-04	28.66	39.08
SOGA1	1.27	6.41E-04	13.35	17.01
STARD8	1.29	7.41E-04	6.09	7.89
STIL	1.58	7.50E-05	1.21	1.91
TBC1D5	1.24	6.94E-04	46.17	57.10
TFG	1.11	2.65E-04	36.33	40.50
TJP2	1.30	4.69E-04	13.35	17.38
TMEM259	-1.19	9.40E-04	340.09	286.69
TOMM7	-1.41	6.22E-04	66.14	46.77
TRIM24	1.16	6.36E-04	20.11	23.37
TSC22D1	1.26	7.87E-04	21.75	27.42
UFD1L	-1.19	3.85E-04	71.59	60.12
UNC13B	1.47	2.90E-04	1.09	1.61
WBP11	1.16	8.41E-04	63.51	73.38
WDR3	1.23	7.56E-04	19.55	24.08
WIPF1	1.31	2.42E-04	182.09	238.07
XPC	1.15	8.04E-04	77.69	89.60
ZNF407	1.22	6.86E-04	17.98	21.88

Category	Term	Count	%	Enrichment	Benjamini
Cluster 1		Enrichment Score: 32.75			
GOTERM_BP_DIRECT	Translational elongation	51	7.35	14.29	1.32E-42
GOTERM_BP_DIRECT	Translational termination	47	6.77	15.02	8.87E-41
GOTERM_BP_DIRECT	Translational initiation	52	7.49	10.54	5.74E-36
KEGG_PATHWAY	Ribosome	52	7.49	8.65	7.61E-33
Cluster 2		Enrichment Score: 4.95			
UP_KEYWORDS	Mitochondrion	68	9.80	1.79	1.14E-04
UP_KEYWORDS	Transit peptide	37	5.33	2.07	1.10E-03
UP_SEQ_FEATURE	Transit peptide:Mitochondrion	37	5.33	2.30	5.86E-03
Cluster 3		Enrichment Score: 3.22			
GOTERM_BP_DIRECT	mRNA splicing, via spliceosome	24	3.46	3.15	2.94E-04
UP_KEYWORDS	mRNA splicing	23	3.31	2.65	1.11E-03
UP_KEYWORDS	mRNA processing	24	3.46	2.19	1.02E-02
Cluster 4		Enrichment Score: 2.67			
GOTERM_BP_DIRECT	Respiratory electron transport chair	17	2.45	4.40	1.92E-04
GOTERM_CC_DIRECT	Mitochondrial inner membrane	35	5.04	2.34	3.00E-04
KEGG_PATHWAY	Oxidative phosphorylation	20	2.88	3.38	6.55E-04
KEGG_PATHWAY	Alzheimer's disease	19	2.74	2.54	2.08E-02

Name	# of Entities	# Measured	change	p-value	Hit type
Killing of cells of other organism	17	7	-1.40	1.17E-03	biological_process
Innate immune response in mucosa	32	13	-1.35	3.13E-03	biological_process
Mitochondrial proton-transporting ATP synthase complex	14	8	-1.33	1.01E-05	cellular_component
Cytochrome c oxidase	15	9	-1.33	2.35E-06	Pathway Studio Ontology
Small Tim family	7	5	-1.32	2.06E-02	Pathway Studio Ontology
Defense response to fungus	32	16	-1.31	7.65E-05	biological_process
Small ribosomal subunit	32	32	-1.30	1.64E-16	Pathway Studio Ontology
DOCK	11	10	1.24	3.25E-04	Pathway Studio Ontology
Sp1 C2H2-type zinc-finger protein family	9	7	1.24	7.20E-03	Pathway Studio Ontology
Mutations Associated with Hereditary Thrombophilia	8	6	1.24	6.00E-03	Disease Collections
Hemidesmosome	12	8	1.25	1.11E-02	cellular_component
Negative regulation of protein localization to plasma membra	5	5	1.25	1.73E-02	biological_process
mRNA 3'-UTR AU-rich region binding	7	5	1.26	9.67E-03	molecular_function
Ikaros C2H2-type zinc-finger protein family	5	5	1.38	4.91E-04	Pathway Studio Ontology