

	Symptoms		C4a		MMP-9		TGFβ1		VEGF	
	Pre	Post	Pre	Post	Pre	Post	Pre	Post	Pre	Post
<b>Mean</b>	12.87	3.33	9269	3903	357.8	249.1	9373	4328	57.6	66.0
<b>StD</b>	4.23	3.42	8376	3040	214.5	165.7	7579	3201	38.4	22.7
<b>p (t test)</b>	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
<b>Cluster 1</b>		<b>Enrichment Score: 32.75</b>			
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
<b>Cluster 2</b>		<b>Enrichment Score: 4.95</b>			
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
<b>Cluster 3</b>		<b>Enrichment Score: 3.22</b>			
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
<b>Cluster 4</b>		<b>Enrichment Score: 2.67</b>			
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

<b>Name</b>	<b># of Entities</b>	<b># Measured</b>	<b>change</b>	<b>p-value</b>	<b>Hit type</b>
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