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Supplemental information

CD27^{hi}CD38^{hi} plasmablasts

are activated B cells of mixed

origin with distinct function

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Supplementary Figure S1: Clusters obtained using different algorithms and differences between clusters 0 and 1. A) Transcriptome from 890 single plasmablasts from 5 patients (1 primary and 4 secondary infections) were used for the analysis. tSNE plot (left) and UMAP plot (right) using the 400 most variable genes from Singular. B) Heatmap showing the DEGs between cluster 0 and 1. Related to Figure 1.







Supplementary Figure S2: Cluster distribution and heavy chain isotype usage in plasmablast clusters. A) Number of cells with scRNAseq data per patient sample and timepoint. The visit number is indicated in brackets for each sample. NA: not applicable. B) Normalized cluster size per patient sample and timt point. C) Violin plots of the expression of each antibody isotype IGHA1 (IgA1), IGHA2 (IgA2), IGM (IgM), IGHG1 (IgG1), IGHG2 (IgG2), IGHG3 (IgG3) and IGHG4 (IgG4) is represented for individual plasmablasts (n=890) according to their cluster (0/1:red, 2: green, 3:blue). Related to Figure 1.



Supplementary Figure S3: Specificity of antibodies secreted from bulk-sorted plasmablasts from primary and secondary patients. A-D) Plasmablasts (CD19⁺IgD⁻CD38⁺CD27⁺) from two primary and two secondary patients early after dengue-infection (6-10 days post-fever) were sorted and cultured for 24h before collection of cell culture supernatant containing secreted antibodies. ELISA was performed to detect DENV-specific IgG binding to UV-inactivated DENV (A and B) or E protein (C and D) of the serotype of the current infection. B and D: OD-values for specific binding at 5x dilution (linear range of the dilution curve) were normalized to the concentration of total IgG detected in the supernatants. Each symbol represents one patient, the mean is indicated with a bar in (B) and (D). Samples were tested in duplicates . Related to Figure 2.



Supplementary Figure S4: Fusion loop W101⁺F108⁻ plasmablast-derivate mAbs show a higher metabolic gene expression profile. A) Gene expression in W101⁺F108⁻ mAbs compared to others. B) Most significant pathways (left) for the 15 genes framed in panel A and the network (right) including the highest number of theses genes (n=6, genes of interest are indicated in grey). Ingenuity software (Qiagen) was used. For the network: dotted lines represent indirect interactions and solid lines represent direct interaction. Directions of the arrows represent the sense of the interaction. Related to Figure 2.



Supplementary Figure S5: VDJ usage of mAbs expressed from clusters 0/1, 2 and 3. A) Linkage of V gene and J gene usage for each cluster. Plots were generated with VDJtools (PlotFancyVJUsage) (https://vdjtools-doc.readthedocs.io). B) Individual V gene usage and J gene usage for antibodies per binding class: CE: complex epitope, FL-neg: fusionloop negative, FL-pos: fusionloop positive, neg: non-dengue. The color code for the heatmaps in indicated, units are number of antibodies. Related to Figure 2.

Supplementary Figure S6



Supplementary Figure S6: Surface expression of markers differentially expressed in cluster 2 and 3 compared to cluster 0/1. A) Plasmablast surface protein expression of seven markers that were differentially expressed in clusters 2 and 3 versus clusters 0/1. An overlay of surface marker expression on lymphocytes, monocytes and plasmablasts is shown for reference. B) Gating for CD47⁺ pasmablasts for a fully stained sample, stain without CD47 (fluorescence minus one FMO) and unstained control. CD47 expression on lymphocytes, monocytes was used as a reference to set the CD47 gate.



Supplementary Figure S7: Gating strategy for MT and TMRM content and antibody secretion of CD47⁺ and CD47⁻ plasmablasts detected by ELISPOT. A) Gating strategy for the identification of MT or TMRM high and –low plasmabasts. This gating was used for the data illustrated in Figure 4A-B and 4D-E. B) Total IgG-secreting cells, and DENV-1 E protein or DENV-2 E protein specific IgG secreting cells, calculated as a percentage of input sorted plasmablasts. Each symbol represents one donor; the lower panel of graphs links CD47⁺ and CD47⁻ plasmablasts from the same donor. Bars represent means±SD, ** p=0.0019. Students t test. Data are combined from three independent experiments. Related to Figure 4.



Supplementary Figure S8: Mutation analysis of antibodies from clusters 0/1, 2 and 3. The number of nucleotide mutations in the V region as determined by highV-Quest, IMGT, using sequences assembled from RNAseq data using basic algorithm. S: silent, NS: non-silent. Each symbol represents one antibody sequence. The mean is indicated with a bar. Related to Figure 6.



Supplementary Figure S9: Gating strategy for the sorting of plasmablasts based on Ig surface expression. IgA+, IgM+, IgG+ and IgG- populations were sorted for the analysis shown in Figure 7. Related to Figure 7.

Supplementary Ta	able S1: 100 top DEG	between cluster 3 and	clusters 0/1 and 2.	Related to Figure 1.
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	p_val	avg_logFC	pct.1	pct.2	p_val_adj	cluster	gene
MT-CYB.2	4.46E-09	0.23914208	1	0.997	8.82E-05	3	MT-CYB
GAPDH.2	1.38E-90	0.20292327	1	0.974	2.73E-86	3	GAPDH
ACTB.2	3.60E-61	0.19496342	1	0.984	7.13E-57	3	АСТВ
MT-ND4L.2	6.33E-11	0.18859622	1	1	1.25E-06	3	MT-ND4L
MT-CO1.2	4.62E-07	0.15491057	1	1	0.00914092	3	MT-CO1
	1.42E-						
TUBA1B.2	165	0.13086787	0.983	0.359	2.82E-161	3	TUBA1B
MT-RNR2.2	5.53E-07	0.12370244	1	1	0.01094717	3	MT-RNR2
MT-ND4.2	3.74E-12	0.11013875	1	1	7.40E-08	3	MT-ND4
ACTG1.2	1.07E-38	0.10025465	0.983	0.907	2.11E-34	3	ACTG1
MT-RNR1.1	4.99E-12	0.09711459	1	0.999	9.88E-08	3	MT-RNR1
	2.77E-						
HMGN2.2	111	0.0967229	1	0.766	5.49E-107	3	HMGN2
MT-ATP6.2	6.86E-07	0.09367726	1	0.997	0.01357116	3	MT-ATP6
MT-CO3.2	8.32E-07	0.07736197	1	0.994	0.01646792	3	MT-CO3
	3.65E-						
H2AFZ.2	160	0.07500873	0.974	0.702	7.22E-156	3	H2AFZ
MT-ATP8.2	1.29E-06	0.06642868	0.966	0.889	0.02558412	3	MT-ATP8
TMSB4X.2	6.24E-18	0.05974827	1	0.977	1.24E-13	3	TMSB4X
TPI1.2	9.38E-69	0.0566308	0.974	0.745	1.86E-64	3	TPI1
LDHA.2	2.02E-73	0.05621023	0.974	0.712	4.00E-69	3	LDHA
HIST1H4C.2	0	0.05490892	0.957	0.488	0	3	HIST1H4C
NPM1.2	1.78E-52	0.05438048	0.974	0.922	3.52E-48	3	NPM1
RAN.2	1.23E-73	0.05372681	0.983	0.691	2.44E-69	3	RAN
PPIA.2	1.51E-54	0.05370807	0.991	0.948	2.98E-50	3	PPIA
CFL1.2	1.24E-59	0.05249302	0.991	0.934	2.46E-55	3	CFL1
EIF4A1.2	6.19E-41	0.0521868	0.983	0.868	1.23E-36	3	EIF4A1
SLC25A5.2	1.01E-62	0.05071855	0.974	0.769	2.00E-58	3	SLC25A5
FTL.2	1.51E-29	0.0498335	0.983	0.994	2.98E-25	3	FTL
ALDOA.2	1.84E-48	0.04970299	0.983	0.82	3.65E-44	3	ALDOA
ARHGDIB.2	1.15E-17	0.04524813	1	0.941	2.28E-13	3	ARHGDIB
ANXA2.2	9.01E-12	0.04512537	0.991	0.924	1.78E-07	3	ANXA2
ATP5B.2	7.55E-26	0.04459195	0.974	0.913	1.49E-21	3	ATP5B
MT-ND5.2	6.82E-20	0.04432886	1	0.992	1.35E-15	3	MT-ND5
RPS2.2	3.88E-18	0.04286263	1	0.955	7.68E-14	3	RPS2
TAGLN2.2	1.34E-26	0.04220326	0.974	0.862	2.65E-22	3	TAGLN2
RPLP0.2	3.50E-17	0.04166771	1	0.987	6.93E-13	3	RPLPO
ENO1.2	7.33E-76	0.04120131	0.974	0.765	1.45E-71	3	ENO1
MCM7.2	5.21E-82	0.040564	0.94	0.233	1.03E-77	3	MCM7
PTMA.2	6.84E-88	0.04034366	1	0.979	1.35E-83	3	PTMA
HMGB1.2	5.17E-79	0.03977241	1	0.947	1.02E-74	3	HMGB1
UBB.2	1.00E-21	0.03976571	1	0.982	1.98E-17	3	UBB
GNB2L1.2	6.69E-13	0.0394505	1	0.957	1.32E-08	3	GNB2L1
HMGB2.2	6.14E-97	0.03837239	0.966	0.155	1.22E-92	3	HMGB2
PSME2.2	1.20E-26	0.03736866	0.991	0.926	2.37E-22	3	PSME2
RRM2.2	1.02E-88	0.03672434	0.853	0.071	2.02E-84	3	RRM2
TMSB10.2	4.77E-27	0.0365712	1	0.984	9.43E-23	3	TMSB10
	6.65E-						
TUBB.2	115	0.03608732	0.931	0.278	1.32E-110	3	TUBB
RPL4.2	3.92E-14	0.03441241	0.991	0.961	7.75E-10	3	RPL4
RPS3.2	6.30E-14	0.03359699	1	0.983	1.25E-09	3	RPS3
RPSA.2	1.02E-25	0.03358494	0.983	0.833	2.03E-21	3	RPSA
CORO1A.2	2.34E-32	0.03278004	0.966	0.677	4.63E-28	3	CORO1A

EFF10.2 1.78-16 0.034456 0.981 0.982 3.42E-12 3 EFF101 RPL7.2 S.09E-17 0.0314516 0.983 0.973 1.71E-12 3 RPL7 RPL41.2 7.71E-28 0.0313105 1 0.973 1.01E-12 3 RPL41 EBP.1 8.44E-34 0.0311768 0.81 0.389 1.67E-29 3 EFP PSMB4.2 2.02E-15 0.03001156 0.991 0.972 2.46E-87 3 PFN1 ATP5A1.2 1.34E-18 0.0299555 1 0.968 2.59E-14 3 ATP5A1 LDH8.2 1.20E-35 0.0298546 0.91 0.919 3.77E-09 3 CLIC1 LSP1.2 1.90E-13 0.02789509 0.991 0.925 6.01E-66 3 HPSA8 RPL8.2 6.39E-12 0.02789409 0.991 0.926 A.61E-79 3 QAC11 PCAA.2 2.33E-83 0.0274135 0.931 0.636 1.6374		4 705 46	0.00046006	0.004	0.000	0.405.40	•	
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RPL7.2 5.09E-17 0.03133074 1 0.977 1.52E-23 3 RPL7 EBP.1 8.44E-34 0.03131058 0.81 0.389 1.67E-29 3 EBP PSMB4.2 2.02E-15 0.03071009 0.991 0.841 4.00E-11 3 PSMB4 PFN1.2 1.31E-18 0.02999555 1 0.968 2.59E-14 3 ATPSA1 LDH8.2 1.20E-35 0.02982546 0.94 0.758 2.37E-31 3 LDH8 LSP1.2 2.42E-13 0.02980548 0.991 0.919 3.77E-09 3 LLC1 HSPA8.2 6.36E-12 0.02786900 0.991 0.99 1.26E-07 3 RPL8 QAZ1.2 4.19E-21 0.02780908 0.991 0.99 3.28E-17 3 QAZ1 PFNA.2 2.32E-83 0.02748150 0.931 0.603 1.63E-44 3 PGAM1 GAZ1.2 4.19E-21 0.02569133 1 0.977 7.35E-07	HNRNPA1.2	8.63E-17	0.0314516	0.983	0.937	1.71E-12	3	HNRNPA1
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ATP5A1.2 1.11E-18 0.0299555 1 0.968 2.59E-14 3 ATP5A1 LDHB.2 1.20E-35 0.02982546 0.94 0.758 2.37E-31 3 LDHB LSP1.2 2.42E-13 0.02796548 0.991 0.919 3.77E-09 3 CLIC1 HSPA8.2 3.04E-10 0.02785090 0.993 0.925 6.01E-06 3 HSPA8 RPL8.2 6.39E-12 0.02780908 0.991 0.99 8.28E-17 3 OAZ1 RPL5.2 9.26E-14 0.02728135 0.931 0.603 1.63E-44 3 PGAM1 FTH1.2 1.32E-16 0.02678318 1 0.97 7.55E-07 3 SUB1 NUR1.2 3.81E-11 0.02678318 1 0.977 1.40E-19 3 CALM1 GALM1.2 3.81E-11 0.0267023 0.991 0.82 5.67E-53 3 HNRNPA2B1.2 CALM1 GALM1.2 7.06E-23 0.025402 0.983 0.365	PFN1.2	1.24E-91	0.03001196	0.991	0.97	2.46E-87	3	PFN1
LDHB.2 1.20F-35 0.02982546 0.94 0.758 2.37E-31 3 LDHB LSP1.2 2.42E-13 0.02980548 0.919 3.77E-09 3 CLIC1 HSPA8.2 3.04E-10 0.02785909 0.983 0.925 6.01E-06 3 HSPA8 RPL8.2 6.39E-12 0.02784662 1 0.99 1.26E-07 3 RPL8 OAZ1.2 4.19E-21 0.02784060 0.991 0.953 1.83E-09 3 RPL5 PCNA.2 2.33E-83 0.0274815 0.802 0.076 4.61E-79 3 PCAM FGAM1.2 8.21E-14 0.02661373 1 0.97 7.55E-07 3 SUB1 SUB1.2 3.81E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 CALM2.2 7.09E-24 0.02594923 0.931 0.767 1.40E-19 3 CALM2 CALM2.2 7.09E-24 0.02594923 0.931 0.767 1.40E-19 3	ATP5A1.2	1.31E-18	0.02999555	1	0.968	2.59E-14	3	ATP5A1
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CLIC.12 1.90E-13 0.02796548 0.991 0.919 3.77E-09 3 CLIC1 HSPA8.2 3.04E-10 0.02785909 0.983 0.925 6.01E-06 3 HSPA8 RPL8.2 6.39E-12 0.02786462 1 0.99 8.28E-17 3 0A21 RPL5.2 9.26E-14 0.02768101 0.991 0.953 1.83E-09 3 RPL5 PCNA.2 2.33E-83 0.0274815 0.802 0.767 4.61E-79 3 PCNA PGAM1.2 8.21E-49 0.02729135 0.931 0.603 1.63E-44 3 PGAM1 FTH1.2 1.23E-16 0.0267813 1 0.977 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.02607023 0.991 0.822 5.67E-53 3 HNRNPA2B1 CALM1.2 4.06E-23 0.02594184 0.991 0.938 6.03E-193 CALM1 H3F38.2 2.63E-08 0.0252525 0.897 0.163 1.59E-82	LSP1.2	2.42E-13	0.02840182	1	0.93	4.79E-09	3	LSP1
HSPA8.2 3.04E-10 0.02785009 0.983 0.925 6.01E-06 3 HSPA8 RPL8.2 6.39E-12 0.0278080 0.991 1.26E-07 3 RPL8 OAZ1.2 4.19E-21 0.0278080 0.991 0.993 1.83E-09 3 RPL5 PCNA.2 2.33E-83 0.0274815 0.802 0.076 4.61E-79 3 PCNA PGAM1.2 8.21E-49 0.0276818 1 0.997 2.43E-12 3 FTH1 SUB1.2 3.83E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.709E-24 0.02564923 0.931 0.767 1.40E-19 3 CALM2 CALM2.2 7.09E-24 0.02564923 0.931 0.765 0.0051946 3 H3738 EIFAA3.1 1.22E-50 0.0252424 0.871 0.272-09 3 RP55 GAST 1.02E-491 0.994 0.61E-06 3 RP53A STMN1.2	CLIC1.2	1.90E-13	0.02796548	0.991	0.919	3.77E-09	3	CLIC1
RPL8.2 6.39E-12 0.02780662 1 0.99 1.26E-07 3 RPL8 OAZ1.2 4.19E-21 0.0278008 0.991 0.99 8.28E-17 3 OAZ1 PRL5.2 9.26E-14 0.02763101 0.991 0.953 1.83E-09 3 RPL5 PCNA.2 2.33E-83 0.0274815 0.802 0.076 4.61E-79 3 PCNA PGAM1.2 8.21E-49 0.02729135 0.931 0.603 1.63E-44 3 PGAM1 FTH1.2 1.23E-16 0.0267023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM2.2 7.09E-24 0.02594184 0.991 0.938 8.03E-19 3 CALM1 H3F38.2 2.63E-08 0.0256402 0.983 0.965 0.00051946 3 H3F38 EIF4A3.1 1.22E-55 0.0253253 0.897 0.163 1.59E-82 3 STMN1 RPS53.2 1.37E-13 0.02457921 0.994 3.61E-06 3	HSPA8.2	3.04E-10	0.02785909	0.983	0.925	6.01E-06	3	HSPA8
OAZ1.2 4.19E-21 0.02780908 0.991 0.99 8.28E-17 3 OAZ1 RPLS.2 9.26E-14 0.02768101 0.991 0.953 1.83E-09 3 RPLS PCNA.2 2.33E-83 0.0274815 0.802 0.076 4.61E-79 3 PCNA PGAM1.2 8.21E-49 0.02729135 0.931 0.603 1.63E-44 3 PGAM1 SUB1 3.81E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.02607023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM2.2 7.09E-24 0.02594923 0.931 0.767 1.40E-19 3 CALM2 CALM2.2 7.09E-24 0.0259402 0.983 0.965 0.000501946 3 H3F3B EIF4A3.1 1.22E-55 0.0226425 0.887 0.163 1.59E-82 3 STMN1 RPS52.2 1.37E-13 0.02463792 1 0.996 2	RPL8.2	6.39E-12	0.02784662	1	0.99	1.26E-07	3	RPL8
RPL5.2 9.26E-14 0.02768101 0.991 0.953 1.83E-09 3 RPL5 PGAM1.2 2.33E-83 0.0274815 0.802 0.076 4.61E-79 3 PCNA PGAM1.2 8.21E-49 0.02729135 0.931 0.603 1.63E-44 3 PGAM1 FTH1.2 1.23E-16 0.02678318 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.02607023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM2.2 7.09E-24 0.02594184 0.991 0.938 8.03E-19 3 CALM2 CALM1.2 4.06E-23 0.02594184 0.991 0.938 8.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.0250253 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02464906 0.974 0.95 2.72E-09 3 RPS58 RPS3A.2 1.82E-10 0.0243792 1 0.996 2	OAZ1.2	4.19E-21	0.02780908	0.991	0.99	8.28E-17	3	OAZ1
PCNA.2 2.33E-83 0.0274815 0.802 0.076 4.61E-79 3 PCNA PGAM1.2 8.21E-49 0.02729135 0.931 0.603 1.63E-44 3 PGAM1 FTH1.2 1.23E-16 0.02678318 1 0.97 2.43E-12 3 FTH1 SUB1.2 3.81E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.02607023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM1.2 4.06E-23 0.02594184 0.991 0.938 8.03E-19 3 CALM2 CALM1.2 4.06E-87 0.0250253 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02464906 0.974 0.95 2.72E-09 3 RP53A RPS18.2 1.30E-18 0.02437202 0.931 0.612 5.06E-30 3 CYC1.2 SGC2SA3.2 4.47E-10 0.0234873 0.94 0.779 8	RPL5.2	9.26E-14	0.02768101	0.991	0.953	1.83E-09	3	RPL5
PGAM1.2 8.21E-49 0.02729135 0.931 0.603 1.63E-44 3 PGAM1 FTH1.2 1.33E-16 0.02678318 1 0.97 2.43E-12 3 FTH1 SUB1.2 3.81E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.02607023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM1.2 4.06E-23 0.02594923 0.931 0.767 1.40E-19 3 CALM1 H3F3B.2 2.63E-08 0.025294184 0.991 0.938 8.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.02502553 0.897 0.163 1.59E-82 3 STMN1 RPS55.2 1.37E-13 0.02463792 1 0.996 2.18E-14 3 RP518 CYC1.2 2.56E-34 0.02432702 0.931 0.612 5.06E-30 3 CYC1 SLC25A3.2 4.47E-10 0.02334873 0.991 0.974 <td< td=""><td>PCNA.2</td><td>2.33E-83</td><td>0.0274815</td><td>0.802</td><td>0.076</td><td>4.61E-79</td><td>3</td><td>PCNA</td></td<>	PCNA.2	2.33E-83	0.0274815	0.802	0.076	4.61E-79	3	PCNA
FTH1.2 1.23E-16 0.02678318 1 0.97 2.43E-12 3 FTH1 SUB1.2 3.81E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.0207023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM2.2 7.09E-24 0.02594184 0.991 0.938 8.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.0256402 0.983 0.965 0.00051946 3 HJF3B EIF4A3.1 1.22E-55 0.0250253 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02464906 0.974 0.95 2.72E-09 3 RP55 RPS18.2 1.10E-18 0.02437021 1 0.996 2.18E-14 3 RP518 CYC1.2 2.56E-34 0.0243702 0.931 0.612 5.06E-30 3 CYC1 SLC25A3.2 4.47E-10 0.0231593 0.94 0.779 8.84E-	PGAM1.2	8.21E-49	0.02729135	0.931	0.603	1.63E-44	3	PGAM1
SUB1.2 3.81E-11 0.02661373 1 0.997 7.55E-07 3 SUB1 HNRNPA2B1.2 2.87E-57 0.02607023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM2.2 7.09E-24 0.02594923 0.931 0.767 1.40E-19 3 CALM1 HAF3B.2 2.63E-08 0.0256402 0.983 0.965 0.00051946 3 H37B EIF4A3.1 1.22E-55 0.02532284 0.871 0.274 2.41E-51 3 EIF4A3 STMN1.2 8.06E-87 0.02463906 0.974 0.95 2.72E-09 3 RPS5 RPS3A.2 1.82E-10 0.02453792 1 0.994 3.61E-06 3 RPS3A RPS18.2 1.10E-18 0.02437291 1 0.994 3.61E-06 3 RPS3A SMC4.2 1.07E-52 0.02324373 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02324847 0.94 0.363 <td< td=""><td>FTH1.2</td><td>1.23E-16</td><td>0.02678318</td><td>1</td><td>0.97</td><td>2.43E-12</td><td>3</td><td>FTH1</td></td<>	FTH1.2	1.23E-16	0.02678318	1	0.97	2.43E-12	3	FTH1
INRNPA2B1.2 2.87E-57 0.02607023 0.991 0.82 5.67E-53 3 HNRNPA2B1 CALM2.2 7.09E-24 0.02594134 0.991 0.938 8.03E-19 3 CALM2 CALM1.2 4.06E-23 0.025594184 0.991 0.938 8.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.02550224 0.871 0.274 2.41E-51 3 EIF4A3 STMN1.2 8.06E-87 0.02532284 0.871 0.274 2.41E-51 3 EIF4A3 STMN1.2 8.06E-87 0.02453792 1 0.994 3.61E-06 3 RPS3A RPS18.2 1.10E-18 0.02437291 1 0.996 2.18E-14 3 RPS18 CYC1.2 2.56E-34 0.02335933 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.0231473 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.02214877 0.991 0.897	SUB1.2	3.81F-11	0.02661373	1	0.997	7.55E-07	3	SUB1
International construction Instruction Instruction Instruction Instruction CALM2.2 7.09F-24 0.02594923 0.931 0.767 1.40E-19 3 CALM2 CALM1.2 4.06E-23 0.02594184 0.991 0.938 8.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.0255402 0.983 0.965 0.00051946 3 H3F3B EIF4A3.1 1.22E-55 0.02502553 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02464906 0.974 0.995 2.72E-09 3 RPS5 RPS18.2 1.10E-18 0.02453792 1 0.996 2.18E-14 3 RPS18 CYC1.2 2.56E-34 0.02335933 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02324347 0.94 0.363 2.12E-48 3 SMC4 PDIA6.2 5.30E-10 0.02314873 0.991 0.974 1.05E-05 3 <td>HNRNPA2B1 2</td> <td>2 87F-57</td> <td>0.02607023</td> <td>0.991</td> <td>0.82</td> <td>5.67E-53</td> <td>3</td> <td>HNRNPA2R1</td>	HNRNPA2B1 2	2 87F-57	0.02607023	0.991	0.82	5.67E-53	3	HNRNPA2R1
CALMI-12 ADGE 23 O.02594184 O.991 O.938 R.03E-19 S CALM1 H3F3B.2 2.63E-08 0.02594184 0.991 0.938 R.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.02594184 0.991 0.938 R.03E-19 3 CALM1 H3F3B.2 2.63E-08 0.02502553 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02463792 1 0.994 3.61E-06 3 RPS53 RPS18.2 1.10E-18 0.02437291 1 0.996 2.18E-14 3 RPS18 CYC1.2 2.56E-34 0.02432702 0.931 0.612 5.06E-30 3 CYC1 SLC2SA3.2 4.47E-10 0.02314973 0.94 0.363 2.12E-48 3 SMC4 PDIA6.2 5.30E-10 0.02314973 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.02214873 0.991 0.897 4		7.09F-24	0.02594923	0.931	0.767	1 40F-19	3	
CNLIMIZ NODE 25 O.0256402 O.983 O.965 O.00051946 3 H3F3B. EIF4A3.1 1.22E-55 0.0256402 0.983 0.965 0.00051946 3 H3F3B EIF4A3.1 1.22E-55 0.02502553 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02464906 0.974 0.95 2.72E-09 3 RPS5 RPS3A.2 1.82E-10 0.02453792 1 0.996 2.18E-14 3 RPS18 CYC1.2 2.56E-34 0.02432702 0.931 0.612 5.06E-30 3 CYC1 SLC25A3.2 4.47E-10 0.02335933 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.022195726 0.991 0.897 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.0228040 0.887 4.00E-28	CALM1 2	1.05E 24	0.02594525	0.991	0.707	8 03F-19	3	
HSF35.2 2.051-06 0.0230402 0.933 0.903 0.00444 3 HSF35 EIF4A3.1 1.22E-55 0.02532284 0.871 0.274 2.41E-51 3 EIF4A3 STMN1.2 8.06E-87 0.02502553 0.897 0.163 1.59E-82 3 STMN1 RPS5.2 1.37E-13 0.02464906 0.974 0.95 2.72E-09 3 RPS5 RPS18.2 1.10E-18 0.02432702 0.931 0.612 5.06E-30 3 CYC1 SLC25A3.2 4.47E-10 0.02335933 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.0214873 0.991 0.897 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.02233093 0.983 0.966 5.40E-09 3 ARPC2 CHCHD2.2 2.02E-32 0.02295726 0.991 0.837 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.0228		4.00L-23	0.02594184	0.991	0.958	0.00051046	2	
Elf4AS.1 1.22E+33 0.0233224 0.071 0.274 2.41E+31 3 Elf4AS STMN1.2 8.06E+87 0.02502553 0.897 0.163 1.59E+82 3 STMN1 RPS5.2 1.37E+13 0.02464906 0.974 0.95 2.72E-09 3 RPS3A RPS18.2 1.10E+18 0.02437291 1 0.996 2.18E+14 3 RPS18 CYC1.2 2.56E+34 0.02432702 0.931 0.612 5.06E+30 3 CYC1 SLC25A3.2 4.47E+10 0.02335933 0.94 0.779 8.84E+06 3 SLC25A3 SMC4.2 1.07E+52 0.02314873 0.991 0.974 1.05E+05 3 PDIA6 ARPC2.2 2.73E+13 0.02313993 0.983 0.966 5.40E+09 3 ARPC2 CHCHD2.2 2.02E+32 0.02295726 0.991 0.897 4.00E+28 3 DHA6 ANP322 1.99E+81 0.02250432 0.883 2.67E+13		2.03E-08	0.0250402	0.965	0.903	2 415 51	<u></u> э	
STMIN1.2 8.06E-87 0.02502535 0.897 0.163 1.59E-82 3 STMIN1 RPS5.2 1.37E-13 0.02464906 0.974 0.95 2.72E-09 3 RPS5 RPS3A.2 1.82E-10 0.02453792 1 0.994 3.61E-06 3 RPS3A RPS18.2 1.10E-18 0.02437291 1 0.996 2.18E-14 3 RPS18 CYC1.2 2.56E-34 0.02432702 0.931 0.612 5.06E-30 3 CYC1 SLC25A3.2 4.47E-10 0.02335933 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.0214873 0.991 0.897 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.02239576 0.991 0.897 4.00E-28 3 DX39A HNRNPC.2 1.35E-17 0.02261847 0.983 0.833 <		1.22E-55	0.02532284	0.871	0.274	2.41E-51	3	EIF4A3
RFS3.2 1.37E-13 0.0246306 0.974 0.95 2.72E-09 3 RP53 RPS3A.2 1.82E-10 0.02453792 1 0.994 3.61E-06 3 RP53A RP518.2 1.10E-18 0.02437291 1 0.994 0.612 5.06E-30 3 CYC1 SLC25A3.2 4.47E-10 0.02335933 0.94 0.779 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02324347 0.94 0.363 2.12E-48 3 SMC4 PDIA6.2 5.30E-10 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.02295726 0.991 0.897 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.0228055 0.836 0.619 3.19E-12 3 UQCRC1 DDX39A.2 4.77E-38 0.02270163 0.879 0.411 9.43E-34 3 DDX39A HNRNPC.2 1.35E-17 0.02261847 0.983 0.685 9.99E-20 3 PSMA4 RP56.2 1.77E-14		8.06E-87	0.02502553	0.897	0.163	1.59E-82	3	
RPS3A.2 1.82E+10 0.02433792 1 0.994 3.61E+06 3 RPS3A RPS18.2 1.10E+18 0.02437291 1 0.996 2.18E+14 3 RPS18 CYC1.2 2.56E+34 0.02432702 0.931 0.612 5.06E+30 3 CYC1 SLC2SA3.2 4.47E+10 0.02335933 0.94 0.779 8.84E+06 3 SLC2SA3 SMC4.2 1.07E+52 0.02324347 0.94 0.363 2.12E+48 3 SMC4 PDIA6.2 5.30E+10 0.02314873 0.991 0.974 1.05E+05 3 PDIA6 ARPC2.2 2.73E+13 0.02295726 0.991 0.897 4.00E+28 3 CHCHD2 UQCRC1.2 1.61E+16 0.0228305 0.836 0.619 3.19E+12 3 UQCRC1 DX39A.2 4.77E+38 0.02270163 0.879 0.411 9.43E+34 3 DDX39A HNRNPC.2 1.35E+17 0.02261847 0.983 0.833 2.67E+13 3 HNRNPC ANP32E 2.99E+81 0.02250432 <td>RPS5.2</td> <td>1.37E-13</td> <td>0.02464906</td> <td>0.974</td> <td>0.95</td> <td>2.72E-09</td> <td>3</td> <td>RPS5</td>	RPS5.2	1.37E-13	0.02464906	0.974	0.95	2.72E-09	3	RPS5
RFS18.2 1.10E+18 0.02437291 1 0.996 2.18E+14 3 RFS18 CYC1.2 2.56E+34 0.02432702 0.931 0.612 5.06E+30 3 CYC1 SLC25A3.2 4.47E+10 0.02335933 0.94 0.779 8.84E+06 3 SLC25A3 SMC4.2 1.07E+52 0.02324347 0.94 0.363 2.12E+48 3 SMC4 PDIA6.2 5.30E+10 0.02314873 0.991 0.974 1.05E+05 3 PDIA6 ARPC2.2 2.73E+13 0.02314873 0.991 0.897 4.00E+28 3 CHCHD2 UQCRC1.2 1.61E+16 0.0228305 0.836 0.619 3.19E+12 3 UQCRC1 DDX39A.2 4.77E+38 0.02270163 0.879 0.411 9.43E+34 3 DDX39A HNRNPC.2 1.35E+17 0.02261847 0.983 0.833 2.67E+13 3 HNRNPC ANP32E.2 2.99E+81 0.02250432 0.94 0.654 5.91E+77 3 ANP32E PSMA4.2 5.05E+24 0.02177	RPS3A.2	1.82E-10	0.02453792	1	0.994	3.61E-06	3	RPS3A
CYC1.2 2.56E-34 0.02432/02 0.931 0.612 5.06E-30 3 CYC1 SLC2SA3.2 4.47E-10 0.02335933 0.94 0.779 8.84E-06 3 SLC2SA3 SMC4.2 1.07E-52 0.02324347 0.94 0.363 2.12E-48 3 SMC4 PDIA6.2 5.30E-10 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.02313993 0.983 0.966 5.40E-09 3 ARPC2 CHCHD2.2 2.02E-32 0.0228305 0.836 0.619 3.19E-12 3 UQCRC1 DDX39A.2 4.77E-38 0.02270163 0.879 0.411 9.43E-34 3 DDX39A HNRNPC.2 1.35E-17 0.02261847 0.983 0.833 2.67E-13 3 HNRNPC ANP32E.2 2.99E-81 0.02228402 0.931 0.685 9.99E-20 3 PSMA4 RPS6.2 1.77E-14 0.02177789 1 0.987	RPS18.2	1.10E-18	0.02437291	1	0.996	2.18E-14	3	RPS18
SLC25A3.2 4.4/E-10 0.02335933 0.94 0.7/9 8.84E-06 3 SLC25A3 SMC4.2 1.07E-52 0.02324347 0.94 0.363 2.12E-48 3 SMC4 PDIA6.2 5.30E-10 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.02313993 0.983 0.966 5.40E-09 3 ARPC2 CHCHD2.2 2.02E-32 0.02295726 0.991 0.897 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.022805 0.836 0.619 3.19E-12 3 UQCRC1 DX39A.2 4.77E-38 0.02270163 0.879 0.411 9.43E-34 3 DDX39A HNRNPC.2 1.35E-17 0.02261847 0.983 0.833 2.67E-13 3 HNRNPC ANP32E 2.99E-81 0.02228402 0.931 0.665 9.99E-20 3 PSMA4 RPS6.2 1.77E-14 0.02177789 1 0.987	CYC1.2	2.56E-34	0.02432702	0.931	0.612	5.06E-30	3	CYCI
SMC4.2 1.07E-52 0.02324347 0.94 0.363 2.12E-48 3 SMC4 PDIA6.2 5.30E-10 0.02314873 0.991 0.974 1.05E-05 3 PDIA6 ARPC2.2 2.73E-13 0.02313993 0.983 0.966 5.40E-09 3 ARPC2 CHCHD2.2 2.02E-32 0.02295726 0.991 0.897 4.00E-28 3 CHCHD2 UQCRC1.2 1.61E-16 0.0228305 0.836 0.619 3.19E-12 3 UQCRC1 DX39A.2 4.77E-38 0.02270163 0.879 0.411 9.43E-34 3 DDX39A HNRNPC.2 1.35E-17 0.02261847 0.983 0.833 2.67E-13 3 HNRNPC ANP32E.2 2.99E-81 0.02228402 0.931 0.685 9.99E-20 3 PSMA4 RPS6.2 1.77E-14 0.02177789 1 0.987 3.50E-10 3 REIT PSMB8.2 9.47E-09 0.02101971 0.905 0.798	SLC25A3.2	4.47E-10	0.02335933	0.94	0.779	8.84E-06	3	SLC25A3
PDIA6.25.30E-100.023148730.9910.9741.05E-053PDIA6ARPC2.22.73E-130.023139930.9830.9665.40E-093ARPC2CHCHD2.22.02E-320.022957260.9910.8974.00E-283CHCHD2UQCRC1.21.61E-160.02283050.8360.6193.19E-123UQCRC1DDX39A.24.77E-380.022701630.8790.4119.43E-343DDX39AHNRNPC.21.35E-170.022618470.9830.8332.67E-133HNRNPCANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021001660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-06 </td <td>SMC4.2</td> <td>1.07E-52</td> <td>0.02324347</td> <td>0.94</td> <td>0.363</td> <td>2.12E-48</td> <td>3</td> <td>SMC4</td>	SMC4.2	1.07E-52	0.02324347	0.94	0.363	2.12E-48	3	SMC4
ARPC2.22.73E-130.023139930.9830.9665.40E-093ARPC2CHCHD2.22.02E-320.022957260.9910.8974.00E-283CHCHD2UQCRC1.21.61E-160.02283050.8360.6193.19E-123UQCRC1DDX39A.24.77E-380.022701630.8790.4119.43E-343DDX39AHNRNPC.21.35E-170.022618470.9830.8332.67E-133HNRNPCANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSM88.29.47E-090.021019710.9050.7980.000187283PSM88MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9590.000380893EIF1RPL19.24.03E-130.020673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATPSF1.25.79E-080.019678730.8280.630.00114544<	PDIA6.2	5.30E-10	0.02314873	0.991	0.974	1.05E-05	3	PDIA6
CHCHD2.22.02E-320.022957260.9910.8974.00E-283CHCHD2UQCRC1.21.61E-160.02283050.8360.6193.19E-123UQCRC1DDX39A.24.77E-380.022701630.8790.4119.43E-343DDX39AHNRNPC.21.35E-170.022618470.9830.8332.67E-133HNRNPCANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RP56.21.77E-140.0217778910.9873.50E-103RP56SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-08 <td>ARPC2.2</td> <td>2.73E-13</td> <td>0.02313993</td> <td>0.983</td> <td>0.966</td> <td>5.40E-09</td> <td>3</td> <td>ARPC2</td>	ARPC2.2	2.73E-13	0.02313993	0.983	0.966	5.40E-09	3	ARPC2
UQCRC1.21.61E-160.02283050.8360.6193.19E-123UQCRC1DDX39A.24.77E-380.022701630.8790.4119.43E-343DDX39AHNRNPC.21.35E-170.022618470.9830.8332.67E-133HNRNPCANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02009080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020069440.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-24	CHCHD2.2	2.02E-32	0.02295726	0.991	0.897	4.00E-28	3	CHCHD2
DDX39A.24.77E-380.022701630.8790.4119.43E-343DDX39AHNRNPC.21.35E-170.022618470.9830.8332.67E-133HNRNPCANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.01922590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	UQCRC1.2	1.61E-16	0.0228305	0.836	0.619	3.19E-12	3	UQCRC1
HNRNPC.21.35E-170.022618470.9830.8332.67E-133HNRNPCANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	DDX39A.2	4.77E-38	0.02270163	0.879	0.411	9.43E-34	3	DDX39A
ANP32E.22.99E-810.022504320.940.6545.91E-773ANP32EPSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	HNRNPC.2	1.35E-17	0.02261847	0.983	0.833	2.67E-13	3	HNRNPC
PSMA4.25.05E-240.022284020.9310.6859.99E-203PSMA4RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	ANP32E.2	2.99E-81	0.02250432	0.94	0.654	5.91E-77	3	ANP32E
RPS6.21.77E-140.0217778910.9873.50E-103RPS6SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	PSMA4.2	5.05E-24	0.02228402	0.931	0.685	9.99E-20	3	PSMA4
SELT.24.22E-110.021601660.940.7988.35E-073SELTPSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	RPS6.2	1.77E-14	0.02177789	1	0.987	3.50E-10	3	RPS6
PSMB8.29.47E-090.021019710.9050.7980.000187283PSMB8MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	SELT.2	4.22E-11	0.02160166	0.94	0.798	8.35E-07	3	SELT
MYL6.21.12E-100.0209064910.9842.21E-063MYL6PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	PSMB8.2	9.47E-09	0.02101971	0.905	0.798	0.00018728	3	PSMB8
PGK1.25.42E-160.02069080.9660.7821.07E-113PGK1MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	MYL6.2	1.12E-10	0.02090649	1	0.984	2.21E-06	3	MYL6
MT-ND6.22.72E-170.020193910.9830.9155.39E-133MT-ND6EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	PGK1.2	5.42E-16	0.0206908	0.966	0.782	1.07E-11	3	PGK1
EIF1.21.93E-080.020069640.9830.9590.000380893EIF1RPL19.24.03E-130.0200673710.9777.98E-093RPL19EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	MT-ND6.2	2.72E-17	0.02019391	0.983	0.915	5.39E-13	3	MT-ND6
RPL19.2 4.03E-13 0.02006737 1 0.977 7.98E-09 3 RPL19 EWSR1.2 4.06E-10 0.01992959 0.948 0.827 8.02E-06 3 EWSR1 ATP5F1.2 5.79E-08 0.01967873 0.828 0.63 0.00114544 3 ATP5F1 RPL7A.2 1.59E-12 0.01912488 1 0.926 3.14E-08 3 RPL7A SRSF3.2 1.69E-28 0.01911537 0.983 0.867 3.35E-24 3 SRSF3	EIF1.2	1.93E-08	0.02006964	0.983	0.959	0.00038089	3	EIF1
EWSR1.24.06E-100.019929590.9480.8278.02E-063EWSR1ATP5F1.25.79E-080.019678730.8280.630.001145443ATP5F1RPL7A.21.59E-120.0191248810.9263.14E-083RPL7ASRSF3.21.69E-280.019115370.9830.8673.35E-243SRSF3	RPL19.2	4.03E-13	0.02006737	1	0.977	7.98E-09	3	RPL19
ATP5F1.2 5.79E-08 0.01967873 0.828 0.63 0.00114544 3 ATP5F1 RPL7A.2 1.59E-12 0.01912488 1 0.926 3.14E-08 3 RPL7A SRSF3.2 1.69E-28 0.01911537 0.983 0.867 3.35E-24 3 SRSF3	EWSR1.2	4.06E-10	0.01992959	0.948	0.827	8.02E-06	3	EWSR1
RPL7A.2 1.59E-12 0.01912488 1 0.926 3.14E-08 3 RPL7A SRSF3.2 1.69E-28 0.01911537 0.983 0.867 3.35E-24 3 SRSF3	ATP5F1.2	5.79E-08	0.01967873	0.828	0.63	0.00114544	3	ATP5F1
SRSF3.2 1.69E-28 0.01911537 0.983 0.867 3.35E-24 3 SRSF3	RPL7A.2	1.59E-12	0.01912488	1	0.926	3.14E-08	3	RPL7A
	SRSF3.2	1.69E-28	0.01911537	0.983	0.867	3.35E-24	3	SRSF3