	Module			Enriched Subset						
ID	Gene Count	Genes		Top Ontology	Gene Count	Genes	%	PValue	Bonferroni	
		ACBD6, C19orf70, ALOX5, ARHGAP4, C1QA, C1QB, C1QC, C1orf38, C2, CD300A, CD53,	ВР	immune response	18	PTPRC, LAIR1, LYN, LY96, GPSM3, TLR2, MYO1F, CTSS, C1QC, C1QA, C1QB, CD300A, FCER1G, CTSC, C2, FCGR3A, VSIG4, LCP1	34.62	8.50E-12	7.91E-09	
24	51	ADAP2, CD68, CTSC, CTSS, CTSZ, FCER1G, FCGR2A, FCGR3A, FERMT3, GPSM3, HCK, HCST, ITGB2, LAIR1, LAPTM5, LCP1, LY96, LYN, MANBA, MFSD1, MS4A4A, MS4A6A, MSR1, MYO1F, NPC2, P2RX4, PLA2G15, PLEK, PTPN6, PTPRC, PYCARD, RNASE6.	cc	lysosome	8	CTSZ, CD68, PLA2G15, LAPTM5, NPC2, CTSC, CTSS, MANBA	15.38	3.50E-06	4.55E-04	
		SASH3, SERPINB1, SLC7A7, SPI1, SYNGR2, TLR2, TYROBP, VAMP8, VSIG4	MF	IgG binding	3	FCER1G, FCGR2A, FCGR3A	5.77	2.08E-04	4.08E-02	
27	40	ACAP3, BRIX1, ALOX5, ARHGAP4, C2, CD300A, CD53, ADAP2, CD68, CTSS, FCER1G, FCGR2A, FERMT3, GPSM3, HCK, ITGB2, LAIR1, LAPTM5, LY96, LYN, MFSD1, MS4A4A,	BP	immune response	14	LAIR1, LYN, LY96, GPSM3, MYO1F, CTSS, TNFRSF1B, CD300A, FCER1G, CD4, C2, CD14, ARHGDIB, LCP2	29.79	5.57E-08	3.63E-05	
37	48	MS4A6A, MYO1F, NPC2, PTPN6, SASH3, SERPINB1, SLC7A7, SPI1, VAMP8, ARPC1B, CD14, FPR1, RAC2, SERPINA1, SQRDL, STAB1, ARHGDIB, CD4, HCLS1, LCP2, RHBDF2,	CC MF	receptor complex signal transducer activity	5 16	LYN, LY96, ITGB2, CD4, CD14 MS4A4A, LAIR1, PTPN6, LYN, LY96, FPR1, ITGB2, ARHGAP4, TNFRSF1B, CD300A,	10.64 34.04	3.18E-04 4.02E-04	3.98E-02 6.87E-02	
		TNFRSF1B, FUCA1, GMFG, GRN  ACADM, BCS1L, ACSL1, ALOX5, C1orf38, CD300A, CD68, CTSC, CTSS, CTSZ, FCER1G,	BP	response to external stimulus	14	STAB1, FCER1G, CD4, FCGR2A, MS4A6A, CD14  FPR1, TLR2, ITGB2, CD163, SLC11A1, ACSL1, RAC2, STAB1, CTSD, SERPINA1, ALOX5,	31.11	1.04E-06	7.68E-04	
34	46	FCGR2A, FERMT3, ITGB2, LAIR1, LAPTM5, LCP1, MS4A4A, MSR1, MYO1F, NPC2, SLC7A7, TLR2, VAMP8, VSIG4, ADPGK, ARPC1B, CD14, ALOX5AP, CD163, CTSB, CTSL1, FPR1, IFI30, RAC2, SERPINA1, SLC11A1, SQRDL, SRGN, STAB1, CREG1, CTSD, FTL,	<b>\</b> cc	lytic vacuole	12	CTSB, VSIG4, CD14 SLC11A1, CTSZ, CD68, LAPTM5, NPC2, IFI30, CTSD, CTSC, CTSB, CTSS, CTSL1, SRGN	26.67	6.83E-12	1.09E-09	
		MAFB, SLA	MF	cysteine-type endopeptidase activity	5	CTSZ, CTSC, CTSB, CTSS, CTSL1	11.11	4.16E-05	6.97E-03	
		ABHD8, APOC1, CCNB1, CDC20, CDK1, CDK2, CKS1B, CTPS, DNMT1, FOXM1, KPNA2,	ВР	cell cycle	21	CKS1B, CDK1, PRC1, FOXM1, TPX2, NUSAP1, CDC20, MCM2, PTTG1, UBE2C, MCM3, RCC1, RACGAP1, CDK2, SMC4, MCM6, CCNB1, UHRF1, MAD2L1, ZWINT, KPNA2	63.64	3.07E-19	1.58E-16	
1	34	LMNB1, LMNB2, MAD2L1, MCM2, MCM3, MCM4, MCM6, NUSAP1, PRC1, PTTG1, RACGAP1, RCC1, RNASEH2A, RRM2, SMC4, TOP2A, TPX2, TYMS, UBE2C, UBE2T,	<b>C</b> C CC	nucleus	27	CKS1B, LMNB1, PRC1, LMNB2, FOXM1, PTTG1, RCC1, TOP2A, CDK1, TPX2, NUSAP1, CDC20, MCM2, RNASEH2A, MCM3, UBE2C, RACGAP1, MCM4, CDK2, MCM6, SMC4,	81.82	7.73E-10	8.11E-08	
		UHRF1, ZWINT	MF	ATP binding	12	CCNB1, UHRF1, MAD2L1, ZWINT, DNMT1, KPNA2 CDK1, CTPS, TPX2, MCM2, MCM3, UBE2C, MCM4, TOP2A, UBE2T, CDK2, SMC4,	36.36	1.36E-04	1.90E-02	
			BP	extracellular matrix organization	12	MCM6  COL18A1, COL4A2, MMP9, LUM, COL3A1, COL1A2, HSPG2, LAMC1, COL1A1,	36.36	3.87E-17	1.79E-14	
22	2.4	ABHD8, APOD, BGN, CD248, CD93, COL18A1, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL5A1, COL5A2, FN1, HSPG2, IGFBP4, IKBIP, ITGA5, LAMB1, LAMC1,	₹ cc		19	SERPINH1, COL5A2, COL5A1  COL18A1, COL4A2, COL4A1, MMP9, CD248, LUM, COL3A1, HSPG2, MMP14, COL5A2,	57.58	2.90E-23	4.20E-21	
22	34	LEPRE1, LOXL2, LUM, MMP14, MMP9, MYL9, MYO1C, PCOLCE, PDGFRB, SERPINH1, SPON2, UACA, WIPI1		proteinaceous extracendiar matrix	19	COL5A1, BGN, LEPRE1, COL1A2, COL1A1, LAMC1, LAMB1, SPON2, FN1	37.38	2.90L-23	4.20L-21	
			MF	extracellular matrix structural constituent	13	COL18A1, COL4A2, COL4A1, LUM, COL3A1, COL5A2, COL5A1, BGN, COL1A2, LAMC1, COL1A1, LAMB1, FN1	39.39	6.50E-20	7.48E-18	
		ABHD2, ANKRD17, ADORA3, APBB1IP, APOC2, C3AR1, AIF1, CD37, CORO1A, CSF1R,	ВР	immune response	12	FYB, CORO1A, LAT2, CYBB, LST1, LY86, IL18, FCGR1A, LILRB4, HLA-DMB, TREM2, HLA- DMA	40.00	1.39E-08	7.17E-06	
23	31	CYBB, EVI2B, FCGR1A, FYB, HAVCR2, HLA-DMA, HLA-DMB, IL18, LAT2, LGALS9,  LILRB4, LST1, LY86, NCKAP1L, PARVG, RGS10, RNASET2, RPS6KA1, TBXAS1, TREM2	<b>c</b> c	plasma membrane	18	PARVG, C3AR1, ADORA3, AIF1, LY86, NCKAP1L, HLA-DMB, HLA-DMA, APBB1IP, CORO1A, LAT2, CD37, CYBB, FCGR1A, LILRB4, EVI2B, TREM2, CSF1R	60.00	3.18E-05	3.55E-03	
			MF	molecular transducer activity	10	RGS10, C3AR1, ADORA3, IL18, FCGR1A, LILRB4, TREM2, HLA-DMA, LGALS9, CSF1R	33.33	5.81E-03	5.39E-01	
		ABHD10, AK4, CNN2, COL1A1, COL1A2, COL3A1, CLIC1, COL6A1, COL5A1, COL6A2,	ВР	collagen fibril organization	5	LUM, COL3A1, COL1A2, COL1A1, COL5A1  LEPRE1, LUM, COL3A1, COL1A2, COL6A2, COL6A1, COL1A1, MMP14, THBS1, COL5A1,	20.83	6.80E-08	3.51E-05	
46	26	FBLIM1, FN1, IKBIP, ITGA5, LEPRE1, LUM, MMP14, MYL9, MYO1C, NRP1, PCOLCE,  RCN3, THBS1, TPM4, VASP	<b>1</b> cc	extracellular matrix	11	FN1	45.83	1.80E-11	2.39E-09	
		,	MF	platelet-derived growth factor binding	5	COL3A1, COL1A2, COL6A1, COL1A1, COL5A1	20.83	1.09E-09	1.29E-07	
26	24	ABCF3, AGGF1, ADPGK, ARPC1B, CD14, ALOX5AP, CD163, CTSB, CTSL1, F13A1, FPR1,	ВР	response to external stimulus	12	SLC11A1, S100A8, RAC2, STAB1, HMOX1, F13A1, S100A9, FPR1, SERPINA1, CTSB, CD14, CD163	52.17	1.53E-08	9.49E-06	
26	24	HMOX1, IFI30, RAC2, RNF149, S100A8, S100A9, SERPINA1, SLC11A1, SQRDL, SRGN, STAB1, TCIRG1	CC MF	extracellular region kininogen binding	11 2	AGGF1, ADPGK, HMOX1, F13A1, IFI3O, SERPINA1, CTSB, CTSL1, CD14, SRGN, CD163  CTSB, CTSL1	47.83 8.70	5.61E-05 4.35E-03	5.60E-03 4.45E-01	
			BP	translational elongation	16	RPL17, RPL27, RPS15A, RPL24, RPL39, RPS8, RPS27, RPS3A, RPL31, RPL34, RPL9, RPS13, RPL10, RPL5, RPL37A, RPS27A	80.00	3.54E-32	8.46E-30	
4	21	ABCE1, ADD3, GAS5, RPL10, RPL17, RPL24, RPL27, RPL31, RPL34, RPL37A, RPL39, RPL5, RPL9, RPS13, RPS15A, RPS27, RPS27A, RPS3A, RPS8, SNHG6	<b>C</b> CC	ribosome	16	RPL17, RPL27, RPS15A, RPL24, RPL39, RPS8, RPS27, RPS3A, RPL31, RPL34, RPL9,  RPS13, RPL10, RPL5, RPL37A, RPS27A	80.00	7.43E-27	3.56E-25	
			MF	structural constituent of ribosome	16	RPL17, RPL27, RPS15A, RPL24, RPL39, RPS8, RPS27, RPS3A, RPL31, RPL34, RPL9, RPS13, RPL10, RPL5, RPL37A, RPS27A	80.00	3.35E-28	1.51E-26	
20	17	ABCB7, ACOX1, CD248, CD93, HSPG2, LAMC1, PDGFRB, UACA, ANGPT2, LAMA4,	BP CC	anatomical structure morphogenesis basal lamina	9	NOTCH3, HSPG2, PDGFRB, LAMC1, MYH9, MCAM, PLXND1, ENG, ANGPT2  LAMA4, HSPG2, LAMC1	56.25 18.75	2.28E-06 1.12E-04	1.14E-03 1.12E-02	
39	17	MCAM, ENG, MYH9, MYO1B, NOTCH3, PLXND1	MF		14	ACOX1, MYO1B, HSPG2, MYH9, MCAM, NOTCH3, LAMA4, UACA, CD93, PDGFRB, LAMC1, PLXND1, ENG, ANGPT2	87.50	8.42E-03	5.56E-01	
		ADCDC ACD3 COLCAA COLAAA ITCAF LAMBA LOVIS CEDDINIIA COLCAS EDILMA	BP CC	cell adhesion proteinaceous extracellular matrix	7 4	NRP1, ITGA5, COL6A2, FBLIM1, COL6A1, LAMB1, LOXL2  COL6A2, COL6A1, COL1A1, LAMB1	46.67 26.67	1.85E-05 2.49E-03	5.13E-03 2.38E-01	
43	16	ABCB6, ACP2, COL6A1, COL1A1, ITGA5, LAMB1, LOXL2, SERPINH1, COL6A2, FBLIM1, PLEKHB1, NRP1, RCN3, TPM4, VASP	1 MF		3	COL6A2, COL1A1, LAMB1	20.00	2.49L-03 2.78E-03	1.99E-01	
			BP	NONE	-	NONE	-	-	-	
10	15	ABCA3, ACAD11, ACBD5, ARHGAP12, CBARA1, CLASP2, CNTN1, CSTF2T, DIP2B, FAM190B, KIAA1279, RAB18, WAC, ZMYND11	CC MF	NONE NONE	-	NONE NONE	-	-	-	
	4 =	ABCA3, ACAD9, CKAP4, FNDC3B, FAM114A1, FURIN, P4HB, PDIA3, RBMS1, SEC24D,	BP	establishment of localization in cell	6	SEC31A, PDIA3, SRPR, TXNDC5, FURIN, SEC24D	42.86	1.55E-04	2.91E-02	
21	15	SEC31A, SRPR, TMEM214, TXNDC5	CC MF	endoplasmic reticulum isomerase activity	9	P4HB, SEC31A, PDIA3, SRPR, TXNDC5, CKAP4, FURIN, SEC24D, FNDC3B  P4HB, PDIA3, TXNDC5	64.29 21.43	1.68E-07 3.29E-03	1.36E-05 2.59E-01	
18	13	ABCA1, ABHD4, KIAA1949, MAP2K3, CLIC1, METRNL, PLAU, PLAUR, SLC16A3, SOCS3,	BP CC	response to external stimulus plasma membrane	6 6	SOCS3, MAP2K3, CLIC1, THBS1, PLAU, PLAUR SLC16A3, CLIC1, ABCA1, THBS1, PLAU, PLAUR	50.00 50.00	1.14E-04 3.97E-02	5.31E-02 9.28E-01	
10	13	TAGLN, THBS1	MF	anion transmembrane transporter activity	2	CLIC1, ABCA1	16.67	9.30E-02	1.00E+00	
	_	ABCA1, ABTB1, GIMAP4, HLA-DMA, HLA-DMB, CD74, HLA-DOA, HLA-DPB1, HLA-	BP	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	9	HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DMA, CD74, HLA-DRA	75.00	1.60E-20	4.37E-18	
38	13	DPA1, HLA-DQB1, HLA-DRA, HLA-DRB1	CC	MHC class II protein complex	8	HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DMA, HLA- DRA	66.67	3.65E-18	1.94E-16	
			MF BP	MHC class II receptor activity  NONE		HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DMA, HLA-DRA  NONE	58.33	7.46E-16	4.66E-14 -	
11	12	ABAT, ABHD11, GPM6B, GPRC5B, C5orf4, ITPK1, KCNJ10, PAQR8, PHLPP1, PLEKHB1, USP54	<b>८</b>	membrane part	7	PHLPP1, PLEKHB1, C5ORF4, KCNJ10, PAQR8, GPM6B, GPRC5B	63.64	5.87E-02	9.11E-01	
			MF BP	NONE synaptic transmission	3	NONE PLP1, ABAT, MBP	27.27	8.70E-03	- 8.59E-01	
13	12	ABAT, ABHD12, CAPN3, DBNDD2, MBP, C7orf41, PLP1, QDPR, RAB40B, SEPT4, TF	< cc	compact myelin	2	PLP1, MBP	18.18	2.26E-03	1.35E-01	
			MF	•	2	PLP1, MBP	18.18	2.97E-03	1.81E-01	
17	12	ABAT, ABCG1, ARID1A, CREBBP, CNOT1, HCFC1, PHF12, SAP130, SNRNP200, SRCAP, UBAP2L	BP CC	nitrogen compound metabolic process  macromolecular complex	9 8	SAP130, SNRNP200, CREBBP, ABAT, HCFC1, ARID1A, CNOT1, PHF12, SRCAP SAP130, SNRNP200, CREBBP, ABAT, HCFC1, ARID1A, PHF12, SRCAP	81.82 72.73	1.80E-04 7.94E-05	4.60E-02 5.62E-03	
	<b></b>	UDAPZL	MF BP	transcription activator activity	5	SAP130, CREBBP, HCFC1, ARID1A, SRCAP TNFRSF1B, HCLS1, TGFBR2, CD4, ARHGDIB, LCP2	45.45	5.99E-05 3.26E-05	5.67E-03	
25	12	ABAT, ABHD10, ARHGDIB, CD4, HCLS1, C1orf162, LCP2, RHBDF2, STAT6, TGFBR2, TNFRSF1B	cc	immune system process membrane raft	3	TNFRSF1B, HCLS1, TGFBR2, CD4, ARHGDIB, LCP2  TNFRSF1B, TGFBR2, CD4	54.55 27.27	3.44E-03	1.30E-02 1.98E-01	
			MF BP	enzyme binding  RNA splicing	3 6	TGFBR2, ABAT, CD4  HNRNPA3, DHX9, SFPQ, RBMX, HNRNPR, HNRNPU	27.27 60.00	2.90E-02 3.75E-07	9.27E-01 4.84E-05	
2	11	AATF, ABCF1, CCT3, DHX9, HNRNPA3, HNRNPR, HNRNPU, ILF2, RBMX, SFPQ	<b>\</b> cc	ribonucleoprotein complex	7	ABCF1, HNRNPA3, DHX9, ILF2, RBMX, HNRNPR, HNRNPU	70.00	8.65E-08	4.06E-06	
			MF BP	RNA binding RNA metabolic process	7 5	HNRNPA3, DHX9, ILF2, SFPQ, RBMX, HNRNPR, HNRNPU  ABCE1, CHERP, MED16, C19ORF29, KHSRP	70.00 50.00	8.27E-07 5.76E-04	4.38E-05 1.11E-01	
3	11	AATF, ABCE1, AP1M1, C19orf29, CHERP, FZR1, KHSRP, MED16, RAVER1, WIZ	cc	intracellular membrane-bounded organelle	10	ABCE1, AP1M1, FZR1, CHERP, MED16, RAVER1, C19ORF29, KHSRP, AATF, WIZ	100.00	2.01E-03	9.94E-02	
			MF	3	3	CHERP, RAVER1, KHSRP	30.00	6.48E-02	9.78E-01	
29	11	AATF, ABCF1, BCAN, NKAIN4, LMF1, OLIG1, OLIG2, SCHIP1, SOX8, TNK2	BP CC	cell fate commitment NONE	3 -	OLIG1, OLIG2, SOX8  NONE	30.00	1.96E-03 -	3.41E-01 -	
			MF	transcription regulator activity	4	OLIG1, AATF, OLIG2, SOX8	40.00	2.56E-02	8.24E-01	

				ВР	response to biotic stimulus	3 ABCE1, HSPA5, MANF	30.00	1.85E-02	9.96E-01
40	11	AATF, ABCE1, ANXA2, CALR, CHPF2, HSPA5, MANF, PDIA4, PLOD3, TUBA1C	<b>1</b>	CC	endoplasmic reticulum lumen	3 PDIA4, HSPA5, CALR	30.00	8.79E-04	7.12E-02
			$\rightarrow$	MF BP	enzyme inhibitor activity  NONE	ABCE1, HSPA5, ANXA2  NONE	30.00	1.05E-02 -	6.77E-01 -
5	10	AASS, ABCB7, RPL13AP5, RPL18, RPS15, RPS16, RPS19, RPS5, RPS9	$\prec$	CC	NONE	- NONE	-	-	-
			<u> </u>	MF	NONE	- NONE	_	-	_
7	10	AASS, ABCD3, B2M, HLA-B, HLA-A, HLA-C, PSMB8, PSMB9, TAP1	S	BP CC	antigen processing and presentation  MHC class I protein complex	5 HLA-A, HLA-C, HLA-B, PSMB8, PSMB9 3 HLA-A, HLA-C, HLA-B, B2M	9, B2M 62.50 37.50	3.84E-08 6.24E-05	6.33E-06 3.55E-03
,	10	AA33, ABCD3, BZIVI, IILA-B, IILA-A, IILA-C, F3IVIBO, F3IVIBO, FAFT	1	MF	MHC class I receptor activity	2 HLA-A, HLA-C, HLA-B	25.00	7.83E-03	3.61E-01
			7	ВР	NONE	- NONE	-	-	-
20	10	AACC ADCDZ ATD4A2 ATD6V4C2 LINCO4 DDVD CCDT2 CVNCD4 WASC4	ر	CC	synaptic vesicle membrane	2 ATP6V1G2, SYNGR1	2.27	1.15E-02	6.17E-01
30	10	AASS, ABCB7, ATP1A3, ATP6V1G2, LINGO1, PDXP, SEPT3, SYNGR1, WASF1	1	MF	ATPase activity, coupled to transmembrane	3 ATP1A3, ATP6V1G2, ABCB7	3.41	1.05E-03	6.52E-02
			Ĺ		movement of substances		3.11	1.032 03	0.022 02
	10	AASS, ABCF2, CLASP2, GATS, GNAO1, MAPT, NCAM1, PHYHIPL, SEPT8	$\left\{ \right.$	BP	regulation of microtubule depolymerization	2 MAPT, CLASP2	22.22	6.78E-03	7.42E-01
41				СС	protein complex	5 ABCF2, GNAO1, MAPT, CLASP2, SE	PT8 55.56	1.62E-02	6.64E-01
			L	MF	microtubule binding	2 MAPT, CLASP2	22.22	2.82E-02	7.98E-01
4.7	4.0			BP	cellular component organization	6 CD93, CALD1, HSPG2, ABCD3, AASS,		2.64E-03	3.71E-01
47	10	AASS, ABCD3, CD248, CD93, HSPG2, LAMC1, CALD1, FSTL1, PLOD1	1	CC MF	basal lamina carbohydrate binding	2 HSPG2, LAMC1 3 CD93, CD248, FSTL1	22.22 33.33	8.52E-03 1.39E-02	4.60E-01 6.30E-01
	9	AASDHPPT, ABCA1, ATPSD, GADD45GIP1, NDUFA11, NDUFA13, NDUFA7, NDUFB	$\overline{}$		generation of precursor metabolites and				
			7	BP	energy	5 ATP5D, NDUFB7, NDUFA7, NDUFA13, N		7.87E-06	2.20E-03
6			В7	CC	respiratory chain	4 NDUFB7, NDUFA7, NDUFA13, NDU		3.48E-06	2.22E-04
				MF	NADH dehydrogenase (quinone) activity	3 NDUFB7, NDUFA7, NDUFA13	37.50	1.17E-04	8.88E-03
4.0			5	ВР	regulation of cell differentiation	3 ZFP91, BMPR2, ABCA1	37.50	1.66E-02	9.98E-01
16	9	AASDHPPT, ABCA1, BMPR2, CAMSAP1L1, NCKAP1, NDUFS1, USP34, ZFP91	1	CC MF	membrane raft NONE	2 BMPR2, ABCA1 NONE	25.00	5.27E-02 -	9.79E-01 -
			7	BP	NONE	- NONE	-	-	-
19	9	AASDHPPT, ABCA3, GLUD1, PEA15, RFTN2, SYT11, TIMP1, TMSB10	Į	СС	cytoplasmic membrane-bounded vesicle	3 SYT11, ABCA3, TIMP1	37 50	2.23E-02	7.48E-01
13	9	, v. d. 1. 1, 7, d.				- NONE	37.30		
			_	MF	NONE				-
20	9	AASDHPPT, ABCA1, ALDOC, IL17D, NDRG2, GLT25D1, PMM2, THRA	ر	BP	cellular carbohydrate metabolic process	3 GLT25D1, ALDOC, PMM2	37.50	1.44E-02	9.81E-01
20	Э			CC	cytoplasmic part	6 GLT25D1, AASDHPPT, THRA, ALDOC, ABC	A1, NDRG2 75.00	3.21E-02	8.28E-01
			<del></del>	MF BP	NONE macromolecule metabolic process	- NONE 4 AASDHPPT, CLPP, CDC34, ABCA	50.00	6.62E-02	1.00E+00
27	9	AASDHPPT, ABCA1, CCDC124, CLPP, ARMC6, DDX49, CDC34, HDGFRP2	$\prec$	CC	NONE	- NONE	-	-	-
			>	MF	ATP binding	4 DDX49, CLPP, CDC34, ABCA1	50.00	1.48E-02	6.47E-01
44	9	AASDHPPT, ABCA1, CALD1, CALU, FLNA, LMAN1, MRC2, PTPN12	$\downarrow$	BP CC	vesicle-mediated transport cytoplasmic part	4 MRC2, ABCA1, LMAN1, FLNA 7 AASDHPPT, CALD1, ABCA1, LMAN1, FLNA, P	50.00 TPN12, CALU 87.50	1.23E-03 4.37E-03	2.68E-01 3.02E-01
			Ţ	MF	small GTPase binding	2 ABCA1, FLNA	25.00	4.58E-02	9.84E-01
	0		5	ВР	cellular amino acid metabolic process	2 AASS, AARSD1	28.57	7.75E-02	1.00E+00
8	8	AARSD1, AASS, CDC42BPB, CHD8, HECTD1, PPP2R5E, YLPM1	1	CC MF	NONE catalytic activity	- NONE 5 CHD8, AASS, AARSD1, CDC42BPB, HI	- ECTD1 71.43	- 5.03E-02	- 9.77E-01
9		AARSD1, AASS, ALDH6A1, ARHGAP5, EXD2, KIAA1737, MUDENG	7	BP	cellular amino acid metabolic process	3 ALDH6A1, AASS, AARSD1	42.86	2.47E-03	2.55E-01
	8		1	СС	NONE	- NONE	-	-	-
			$\rightarrow$	MF BP	catalytic activity cellular amino acid metabolic process	5 ALDH6A1, ARHGAP5, AASS, EXD2, AA 2 AASS, AARSD1	ARSD1 71.43 28.57	5.03E-02	9.52E-01
12		AARSD1, AASS, DDX50, MRPS16, MARCH5, SAR1A, VPS26A			•	2		7 75F-N2	9 991-01
12	8	AARSD1, AASS, DDX50, MRPS16, MARCH5, SAR1A, VPS26A	$\prec$	CC	mitochondrion	3 MRPS16, AASS, MARCH5	42.86	7.75E-02 5.82E-02	9.99E-01 9.65E-01
12	8	AARSD1, AASS, DDX50, MRPS16, MARCH5, SAR1A, VPS26A	1	MF	NONE	- NONE	42.86 -	5.82E-02 -	9.65E-01 -
			}	MF BP	NONE cellular component organization	- NONE 4 HPS4, HIRA, CABIN1, AASS			
12	8	AARSD1, AASS, DDX50, MRPS16, MARCH5, SAR1A, VPS26A  AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4	{	MF	NONE	- NONE	42.86 -	5.82E-02 -	9.65E-01 -
14	8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	MF BP CC MF	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1	42.86 - 57.14 - - 33.33	5.82E-02 - 7.26E-02 - - 7.75E-02	9.65E-01 - 1.00E+00 - - 1.00E+00
			\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	MF BP CC MF BP CC	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process  perinuclear region of cytoplasm	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1	42.86 - 57.14 - -	5.82E-02 - 7.26E-02 - -	9.65E-01 - 1.00E+00 - -
14 15	8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	MF BP CC MF CC MF BP CC MF	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1	42.86 - 57.14 - - 33.33 33.33 -	5.82E-02 - 7.26E-02 - - 7.75E-02 8.73E-02 - 2.61E-04	9.65E-01 - 1.00E+00 - - 1.00E+00 9.94E-01 - 3.56E-02
14	8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	MF BP CC MF BP CC MF CC CC	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process  perinuclear region of cytoplasm  NONE  RNA metabolic process  nuclear lumen	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP	42.86 - 57.14 - - 33.33 33.33 - APEX1 71.43 2 57.14	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02	9.65E-01 - 1.00E+00 - - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01
14 15	8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1	\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	MF BP CC MF BP CC MF BP CC MF	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process perinuclear region of cytoplasm  NONE  RNA metabolic process  nuclear lumen catalytic activity	-         NONE           4         HPS4, HIRA, CABIN1, AASS           -         NONE           -         NONE           2         AASS, AARSD1           2         ATXN10, RANGAP1           -         NONE           5         RBM23, PRMT5, SUPT16H, AARSD1,	42.86 - 57.14 - 33.33 33.33 - APEX1 71.43 2 57.14 1, PARP2 85.71	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02	9.65E-01 - 1.00E+00 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01
14 15 28	8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	MF BP CC MF BP CC MF CC CC	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process  perinuclear region of cytoplasm  NONE  RNA metabolic process  nuclear lumen	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02	9.65E-01 - 1.00E+00 - - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01
14 15	8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	MF BP CC MF BP CC MF BP CC MF BP	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process  perinuclear region of cytoplasm  NONE  RNA metabolic process  nuclear lumen  catalytic activity  regulation of developmental process	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01
14 15 28	8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	MF BP CC MF BP CC MF BP CC MF CC MF	Cellular component organization NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 4 LAMA4, COL4A2, COL4A1	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 42.86 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02
14 15 28 31	8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	MF BP CC MF BP CC MF BP CC MF CC CC MF CC	NONE  cellular component organization NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02
14 15 28	8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	MF BP CC MF BP CC MF BP CC MF BP CC	Cellular component organization NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane	- NONE 4 HPS4, HIRA, CABIN1, AASS NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 MP5 71.43	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01
14 15 28 31	8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	MF BP CC MF BP CC MF BP CC MF BP CC MF	NONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process perinuclear region of cytoplasm  NONE  RNA metabolic process nuclear lumen catalytic activity  regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding	- NONE 4 HPS4, HIRA, CABIN1, AASS NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02
14 15 28 31 32	8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP		MF BP CC MF BP CC MF BP CC MF BP CC	Cellular component organization NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome	- NONE 4 HPS4, HIRA, CABIN1, AASS NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 MP5 71.43	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01
14 15 28 31	8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM		MF BP CC MF	cellular component organization NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 6 SYP, GNAO1, SHC1 - NONE	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 MP5 71.43 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01
14 15 28 31 32	8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP		MF BP CC MF BP CC MF BP CC MF BP CC MF CC	cellular component organization NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 6 SYP, GNAO1, SHC1 7 NONE 7 NONE	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 57.14	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03
14 15 28 31 32	8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP		MF BP CC MF BP CC MF BP CC MF BP CC MF CC	cellular component organization NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding  NONE lysosome hydrolase activity, hydrolyzing O-glycosyl	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 6 SYP, GNAO1, SHC1 7 NONE 7 NONE	42.86 - 57.14 - 33.33 33.33 - APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86 42.86 - 57.14 28.57	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03
14 15 28 31 32	8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP		MF BP CC MF BP	cellular component organization NONE NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	- NONE 4 HPS4, HIRA, CABIN1, AASS NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C1ORF85, HEXA, NEU1, CTSA 2 HEXA, NEU1	42.86 - 57.14 - 33.33 33.33 - APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 - 57.14 28.57	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02	9.65E-01 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07
14 15 28 31 32	8 8 8 8	AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1		MF BP CC CC CC MF BP CC	cellular component organization NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex	- NONE 4 HPS4, HIRA, CABIN1, AASS NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C1ORF85, HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, F	42.86 - 57.14 - 33.33 33.33 - APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86 42.86 - 57.14 28.57 HLA-DQA1 71.43	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02 3.70E-10 1.09E-07	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06
14 15 28 31 32 33	8 8 8 8 8	AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1		MF BP CC MF BP	cellular component organization NONE NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	- NONE 4 HPS4, HIRA, CABIN1, AASS NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C1ORF85, HEXA, NEU1, CTSA 2 HEXA, NEU1	42.86 - 57.14 - 33.33 33.33 - APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86 42.86 - 57.14 28.57 HLA-DQA1 71.43	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07
14 15 28 31 32	8 8 8 8	AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1		MF BP CC CC	cellular component organization NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity carboxylic acid metabolic process cytoplasm	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1, CTSA 2 HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, H 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 5 AASS, QKI, AARSD1, F	42.86 - 57.14 - 33.33 33.33 33.33 - APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 - 57.14 28.57 HLA-DQA1 71.43 -DQA1 57.14 -DQA1 57.14 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04  5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02  3.70E-10 1.09E-07 3.34E-08	9.65E-01 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06
14 15 28 31 32 33	8 8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1		MF BP CC MF BP	cellular component organization NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity carboxylic acid metabolic process cytoplasm NONE	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, H 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 5 AASS, QKI, AARSD1	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86 42.86 57.14 28.57 HLA-DQA1 71.43 -DQA1 57.14 -DQA1 57.14 42.86 BXW11 85.71	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04  5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02  3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 -	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 -
14 15 28 31 32 33 35	8 8 8 8 8	AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1  AARSD1, AASS, FBXW11, HINT3, GMFB, LANCL1, QKI		MF BP CC CC	cellular component organization NONE NONE  cellular amino acid metabolic process perinuclear region of cytoplasm NONE  RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity carboxylic acid metabolic process cytoplasm	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1, CTSA 2 HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, H 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 5 AASS, QKI, AARSD1, F	42.86 57.14 33.33 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 57.14 28.57  HLA-DQA1 71.43 -DQA1 57.14 -DQA1 57.14 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04  5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02  3.70E-10 1.09E-07 3.34E-08 1.43E-02	9.65E-01 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01
14 15 28 31 32 33	8 8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1		MF BP CC MF CC MF CC MF CC MF CC CC CC CC MF CC	Cellular component organization NONE NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity carboxylic acid metabolic process cytoplasm NONE G-protein coupled receptor protein signaling pathway plasma membrane	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1, CTSA 2 HEXA, NEU1  5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, FLA-DMA, HLA-DB1, HLA-DOA, HLA-DMA, HLA-DB1, H	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 57.14 28.57  HLA-DQA1 71.43 -DQA1 57.14 42.86 BXW11 57.14 42.86 BXW11 85.71 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02 3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 - 5.38E-02 3.62E-03	9.65E-01 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 - 1.00E+00 1.66E-01
14 15 28 31 32 33 35	8 8 8 8 8	AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1  AARSD1, AASS, FBXW11, HINT3, GMFB, LANCL1, QKI		MF BP CC MF	cellular component organization NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity carboxylic acid metabolic process cytoplasm NONE G-protein coupled receptor protein signaling pathway plasma membrane receptor activity	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGPT 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C1ORF85, HEXA, NEU1, CTSA 2 HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, H 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 5 AASS, QKI, AARSD1 6 HINT3, LANCL1, AASS, QKI, AARSD1, F NONE 3 C3AR1, GPR34, ABCA1, TREM2, CSB	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 57.14 28.57 HLA-DQA1 71.43 -DQA1 57.14 -DQA1 57.14 42.86 BXW11 85.71 42.86 P, CSF2RA 85.71 71.43	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04  5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02  3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 - 5.38E-02 3.62E-03 9.77E-04	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 - 1.00E+00 1.66E-01 7.52E-02
14 15 28 31 32 33 35	8 8 8 8 8	AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1  AARSD1, AASS, FBXW11, HINT3, GMFB, LANCL1, QKI		MF BP CC MF CC MF CC MF CC MF CC CC CC CC MF CC	Cellular component organization NONE NONE NONE Cellular amino acid metabolic process perinuclear region of cytoplasm NONE RNA metabolic process nuclear lumen catalytic activity regulation of developmental process basement membrane extracellular matrix structural constituent regulation of multicellular organismal process plasma membrane protein complex binding NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity carboxylic acid metabolic process cytoplasm NONE G-protein coupled receptor protein signaling pathway plasma membrane	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, APEX1, PARP 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1, CTSA 2 HEXA, NEU1  5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, FLA-DMA, HLA-DB1, HLA-DOA, HLA-DMA, HLA-DB1, H	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 42.86 42.86 42.86 42.86 57.14 28.57  ALA-DQA1 71.43 -DQA1 57.14 -DQA1 57.14 -DQA1 57.14 -DQA1 57.14 -DQA1 57.14 -DQA1 57.14 42.86 BXW11 85.71 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02 3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 - 5.38E-02 3.62E-03	9.65E-01 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 - 1.00E+00 1.66E-01
14 15 28 31 32 33 35 42	8 8 8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1  AARSD1, AASS, FBXW11, HINT3, GMFB, LANCL1, QKI  AARSD1, ABCA1, CSF2RA, APBB1IP, C3AR1, TREM2, GPR34		MF BP CC MF	RONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process perinuclear region of cytoplasm  NONE  RNA metabolic process nuclear lumen catalytic activity  regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding  NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds  antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity  carboxylic acid metabolic process cytoplasm NONE  G-protein coupled receptor protein signaling pathway plasma membrane receptor activity  NONE cytoplasm calmodulin binding	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, AASS, AARSD1, APEX 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 9 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1, CTSA 2 HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, HLA-DMA, HLA-DMB1, HLA-DM	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86 42.86 57.14 28.57 HLA-DQA1 71.43 DQA1 57.14 DQA1 57.14 42.86 BXW11 85.71 42.86 42.86 42.86 57.14 42.86 42.86 57.14 42.86 42.86 42.86 57.14 42.86 42.86 42.86 42.86 57.14 42.86 4	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02 3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 - 5.38E-02 3.62E-03 9.77E-04 - 7.62E-02 4.54E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 - 1.00E+00 1.66E-01 7.52E-02 - 9.79E-01 9.15E-01
14 15 28 31 32 33 35 42 45	8 8 8 8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1  AARSD1, AASS, FBXW11, HINT3, GMFB, LANCL1, QKI  AARSD1, ABCA1, CSF2RA, APBB1IP, C3AR1, TREM2, GPR34  AARSD1, AATF, ASCC1, ZMYND11, ADD3, CAMK2G, PHYHIPL		MF BP CC MF BP	RONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process perinuclear region of cytoplasm  NONE  RNA metabolic process nuclear lumen catalytic activity  regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding  NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds  antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity  carboxylic acid metabolic process cytoplasm NONE  G-protein coupled receptor protein signaling pathway plasma membrane receptor activity  NONE cytoplasm calmodulin binding cell motion	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, AASS, AARSD1, APEX 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 4 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 LAMA4, COL4A2, COL4A1 4 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, CD74, H 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 4 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 5 HLA-DPB1, HLA-DOA, HLA-DMA, HLA 6 HINT3, LANCL1, AASS, QKI, AARSD1, F NONE 3 C3AR1, GPR34, ABCA1 6 C3AR1, GPR34, ABCA1, TREM2, APBB1II 5 C3AR1, GPR34, ABCA1, TREM2, CSI 6 PHYHIPL, CAMK2G, ASCC1, AATF, AARSI 7 CAMK2G, ADD3 8 ARPC2, CAPZA1, TPM3	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 72 57.14 42.86 42.86 42.86 42.86 42.86 57.14 28.57 42.86 57.14 28.57 42.86 85.71 42.86 85.71 42.86 85.71 42.86 85.71 42.86 85.71 42.86 85.71 42.86 85.71 42.86 85.71 42.86	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04  5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02  3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 - 5.38E-02 3.62E-03 9.77E-04 - 7.62E-02 4.54E-02 1.55E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 - 1.00E+00 1.66E-01 7.52E-02 - 9.79E-01 9.15E-01 8.29E-01
14 15 28 31 32 33 35 42	8 8 8 8 8 8	AARSD1, AASS, CABIN1, CRKL, DGCR2, HIRA, HPS4  AARSD1, AASS, ATXN10, NHP2L1, L3MBTL2, PPP6R2, RANGAP1  AARSD1, AASS, APEX1, PARP2, PRMT5, RBM23, SUPT16H  AARSD1, ABCA1, ANGPT2, COL4A1, COL4A2, LAMA4, MCAM  AARSD1, AASS, GNAO1, RUNDC3A, SCAMP5, SHC1, SYP  AARSD1, AATF, C1orf85, CTSA, GRN, HEXA, NEU1  AARSD1, ABCA1, HLA-DMA, CD74, HLA-DOA, HLA-DPB1, HLA-DQA1  AARSD1, AASS, FBXW11, HINT3, GMFB, LANCL1, QKI  AARSD1, ABCA1, CSF2RA, APBB1IP, C3AR1, TREM2, GPR34		MF BP CC MF	RONE  cellular component organization  NONE  NONE  cellular amino acid metabolic process perinuclear region of cytoplasm  NONE  RNA metabolic process nuclear lumen catalytic activity  regulation of developmental process basement membrane  extracellular matrix structural constituent  regulation of multicellular organismal process plasma membrane  protein complex binding  NONE lysosome hydrolase activity, hydrolyzing O-glycosyl compounds  antigen processing and presentation of peptide or polysaccharide antigen via MHC class II MHC class II protein complex MHC class II receptor activity  carboxylic acid metabolic process cytoplasm NONE  G-protein coupled receptor protein signaling pathway plasma membrane receptor activity  NONE cytoplasm calmodulin binding	- NONE 4 HPS4, HIRA, CABIN1, AASS - NONE - NONE - NONE 2 AASS, AARSD1 2 ATXN10, RANGAP1 - NONE 5 RBM23, PRMT5, SUPT16H, AARSD1, 4 RBM23, SUPT16H, AASS, AARSD1, APEX 6 PRMT5, SUPT16H, AASS, AARSD1, APEX 9 LAMA4, COL4A2, ABCA1, ANGP1 3 LAMA4, COL4A2, COL4A1 3 LAMA4, COL4A2, COL4A1 3 SYP, GNAO1, SCAMP5 5 SYP, GNAO1, RUNDC3A, SHC1, SCA 3 SYP, GNAO1, SHC1 - NONE 4 C10RF85, HEXA, NEU1, CTSA 2 HEXA, NEU1 5 HLA-DPB1, HLA-DOA, HLA-DMA, HLA-DMA, HLA-DMB1, HLA-DM	42.86 57.14 33.33 33.33 APEX1 71.43 2 57.14 1, PARP2 85.71 2 57.14 42.86 42.86 42.86 42.86 57.14 28.57 HLA-DQA1 71.43 DQA1 57.14 DQA1 57.14 42.86 BXW11 85.71 42.86 42.86 42.86 57.14 42.86 42.86 57.14 42.86 42.86 42.86 57.14 42.86 42.86 42.86 42.86 57.14 42.86 4	5.82E-02 - 7.26E-02 - 7.75E-02 8.73E-02 - 2.61E-04 1.22E-02 2.04E-02 1.01E-03 3.52E-04 4.71E-04 5.52E-02 3.13E-02 2.42E-03 - 4.47E-05 3.07E-02 3.70E-10 1.09E-07 3.34E-08 1.43E-02 7.62E-02 - 5.38E-02 3.62E-03 9.77E-04 - 7.62E-02 4.54E-02	9.65E-01 - 1.00E+00 - 1.00E+00 9.94E-01 - 3.56E-02 3.42E-01 7.95E-01 1.70E-01 1.53E-02 2.60E-02 1.00E+00 8.56E-01 1.52E-01 - 1.87E-03 7.83E-01 1.07E-07 5.75E-06 2.00E-06 8.94E-01 9.33E-01 - 1.00E+00 1.66E-01 7.52E-02 - 9.79E-01 9.15E-01