

Supplementary Table SIV Gene ontology (GO) enrichment analysis results.

Category	Term	P-value	Genes	Fold enrichment	Bonferroni	FDR
Cellular Component	axon	0.0023	<i>IGHMBP2, TNFRSF21, DAB2IP, APP, AVIL, KATNB1, CNTN4, SPTA1, IGSF9, LRFN3, DISC1, DSCAM</i>	3.01	0.51	3.00
	spectrin-associated cytoskeleton	0.0083	<i>ANK1, EPB41, SPTA1</i>	20.90	0.93	10.65
	centriole	0.0160	<i>CEP120, NIN, PCNT, TUBD1, LRRCC1, HERC2, PCM1</i>	3.45	0.99	19.56
	membrane	0.0215	<i>ABCF3, RPL14, SLC20A2, ATP5B, STRN, IGHMBP2, CHST10, ELOVL5, PRRT2, MGRN1, INSR, DSCAM, ICAM3, HLA-C, HERC2, GZMH, PCM1, PCLO, FLNA, MCM5, PITPNM1, NPC1, SBF2, IGF2R, MGEA5, EMP1, KCNMB3, GLG1, GANAB, KATNB1, SFXN1, IL12RB2, PSMF1, NPHP4, ABCD3, NBEAL2, IQSECI, ACSL5, SVEP1, OSBPL3, MSH3, MSH2, PCNT, ACLY, ABCB4, MUC4, NTRK3, APOL3, LOXHD1, SLC16A4, KREMEN2, ABCC3, DDX51</i>	1.34	1.00	25.44
	centrosome	0.0219	<i>CEP97, ZNF274, CEP120, XRCC2, NIN, PCNT, LRRCC1, KATNB1, VPS37A, PCM1, NPHP4, ZFYVE19, WDR35, TRAF5, DISC1</i>	1.96	1.00	25.77
Biological Process	plasma membrane	0.0347	<i>SLC16A14, TLN1, SLC6A20, SLC20A2, ATP5B, OR4S1, LGR6, SLC26A1, GLDC, SLC2A7, APP, ANK1, CD44, MGRN1, PRRT2, BAG3, RAB23, RHOD, KIRREL2, CDH26, NRG2, INSR, BOC, DSCAM, DAB2IP, RXFP1, CNTN6, STRN3, ICAM3, SIGLEC10, HLA-C, SPIRE1, OXGR1, OR4M1, FLNA, LRPAP1, AMBP, OR2H1, KIR3DL3, CNTN4, CD226, IGSF9, KCNH4, EMP1, KCNMB3, GLG1, ABCA7, TNFRSF21, RALGPS1, FFAR3, PPP1R12B, PRND, KATNB1, CACNB4, FPR2, OR1G1, IL12RB2, TTYH2, HRH4, OR5F1, HTR3C, LRFN3, OSBPL3, OR5M10, KLF9, EPB41, LPP, ADAM23, OR2Y1, CACNA1I, NSFL1C, TMPRSS7, ACLY, OR10H5, TAB2, ABCG2, ABCB4, CDH12, DSG4, DYTN, ABCG5, C21ORF2, KREMEN2, ZACN, ABCC3, ADAM20, CHRNB3, RGS9, SLC46A2</i>	1.20	1.00	37.87
	MutSbeta complex synapse	0.0355	<i>MSH3, MSH2</i>	55.73	1.00	38.52
		0.0445	<i>APP, DACT1, LAMB2, PRRT2, HRH4, CACNB4, PCLO, DSCAM</i>	2.46	1.00	45.88
	cell adhesion	0.0000	<i>SVEP1, LPP, CNTN6, ADAM23, ICAM3, SIGLEC10, COL15A1, NEDD9, FPR2, EMILIN1, AMBP, LAMB4, AMBN, APP, LAMB2, LAMA3, CD44, CHST10, CNTN4, KIRREL2, BOC, THBS2, CD226, LRFN3, DSCAM</i>	2.89	0.01	0.01
	extracellular matrix organization	0.0004	<i>RXFP1, ICAM3, OLFML2A, NFKB2, EMILIN1, COL4A5, APP, LAMB2, LAMA3, CD44, POMT1, VWA1, COL11A1</i>	3.51	0.37	0.57
	cholesterol efflux	0.0112	<i>ABCA7, NPC1, ABCG5, ABCA5</i>	8.48	1.00	16.80
	neuromuscular junction development	0.0153	<i>LAMB2, ZC4H2, CACNB4, COL4A5</i>	7.57	1.00	22.26
	nervous system development	0.0205	<i>APP, BDNF, CHRDL1, ZC4H2, DOK5, AVIL, CNTN4, ZEB2, VPS13A, RGS9, DGCR14, DSCAM</i>	2.21	1.00	28.76
	synaptic transmission, cholinergic	0.0320	<i>ZACN, HRH4, CHRNB3, HTR3C</i>	5.73	1.00	41.29
	DNA repair	0.0345	<i>IGHMBP2, POLK, POLI, XRCC2, MSH3, MSH2, CINP, HINFP, RAD9B, ERCC4</i>	2.25	1.00	43.75
	transmembrane transport	0.0420	<i>ABCA7, SLC16A14, ABCG5, SLC25A23, ABCC3, ABCD3, SLC25A18, ABCA5, ABCB4, SLC46A2</i>	2.17	1.00	50.46

(continued)

Supplementary Table SIV Continued

Category	Term	P-value	Genes	Fold enrichment	Bonferroni	FDR
Molecular Function	ATPase activity, coupled to transmembrane movement of substances	0.0002	<i>ABCA7, ABCG5, ABCC3, ABCD3, ABCA5, ABCG2, ABCB4</i>	8.39	0.08	0.24
	ATPase activity	0.0026	<i>ABCA7, ABCF3, ABCG5, MSH2, ATP5B, DHX16, ABCD3, MYH6, ABCA5, ABCG2, ABCB4</i>	3.17	0.71	3.62
	phosphatase regulator activity	0.0070	<i>SBF2, PPP1R12B, ZEB2</i>	22.61	0.97	9.61
	damaged DNA binding	0.0312	<i>POLK, POLI, MSH3, MSH2, ERCC4</i>	4.19	1.00	36.51
	dinucleotide repeat insertion binding	0.0374	<i>MSH3, MSH2</i>	52.75	1.00	42.13
	protein complex binding	0.0423	<i>DAB2IP, STRN3, BAG3, GIT2, MAPK8IP2, STRN, RGS9, LZTFL1, DISC1</i>	2.30	1.00	46.20
	structural molecule activity	0.0456	<i>KRT75, NPHP4, LAMA3, ANK1, LAMB2, EPB41, FLG, MAPK8IP2, COL15A1, MAP7</i>	2.14	1.00	48.76
	integrin binding	0.0490	<i>TLN1, LAMB2, ADAM23, ICAM3, CD226, ADAMTS5</i>	3.01	1.00	51.32
	K63-linked polyubiquitin binding	0.0493	<i>RNF169, TAB2, UIMC1</i>	8.33	1.00	51.53

Columns are from DAVID GO enrichment analysis output. For detailed explanation, please see: <https://david.ncifcrf.gov>.