

Figure S1. Summary of associations for three polygenic risk score (PRS) models of posttraumatic stress disorder re-experiencing (PTSD_{REX}) predicting traumatic loss-related PTSD: (**Model 1**) was covaried for age, sex, and 10 principal components of ancestry, (**Model 2**) was additionally covaried for attachment style, and (**Model 3**) was additionally covaried for attachment style and the interactive term of attachment style by PTSD_{REX} PRS. The most significant gene set is labeled.

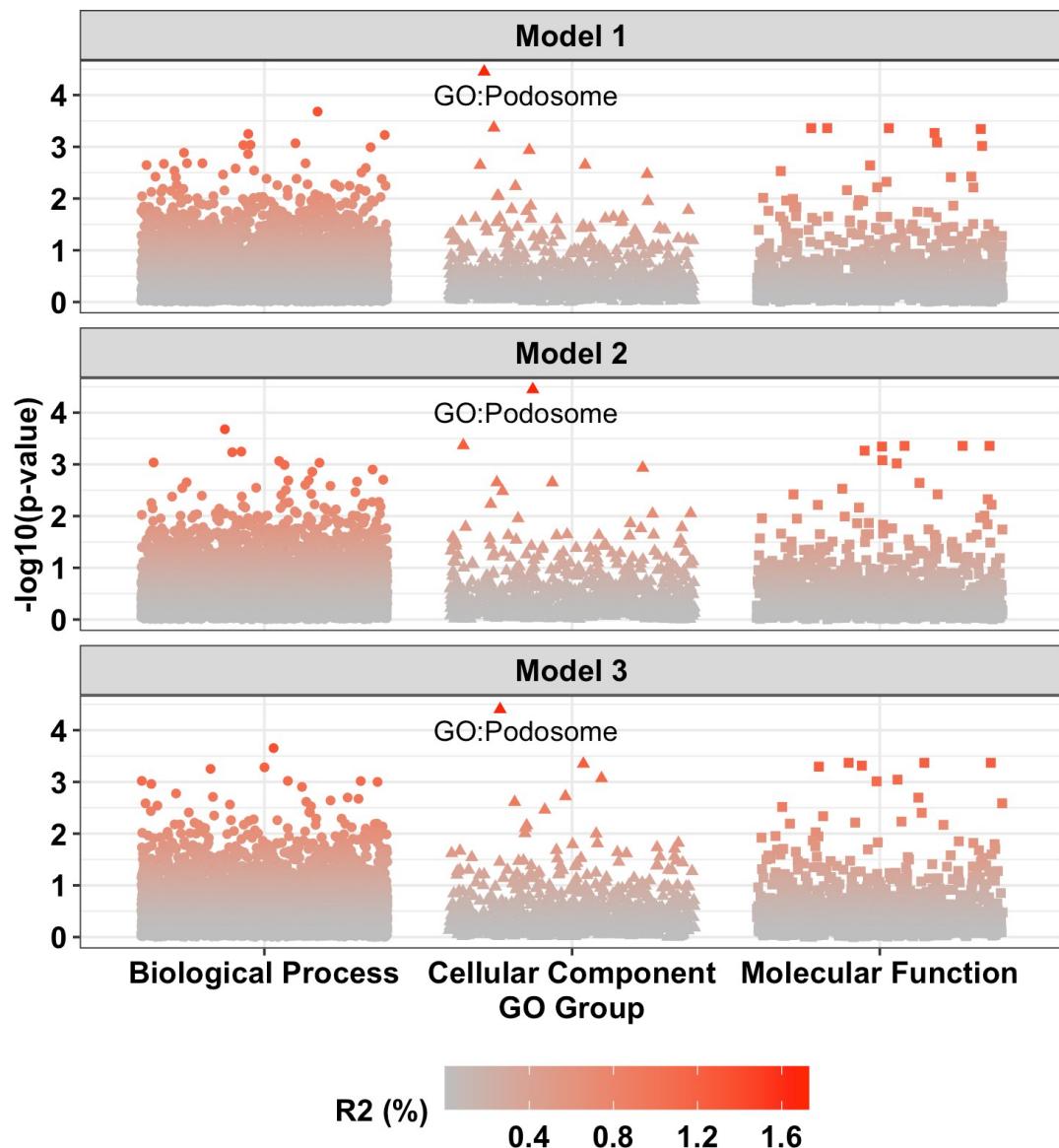


Figure S2. Representative Gene Ontology network for biological processes detected by models for PTSD_{REX} PRS predicting traumatic loss-related PTSD. Due to lack of distinct observational network sub-clusters, network node positions were adjusted to improve visual clarity.

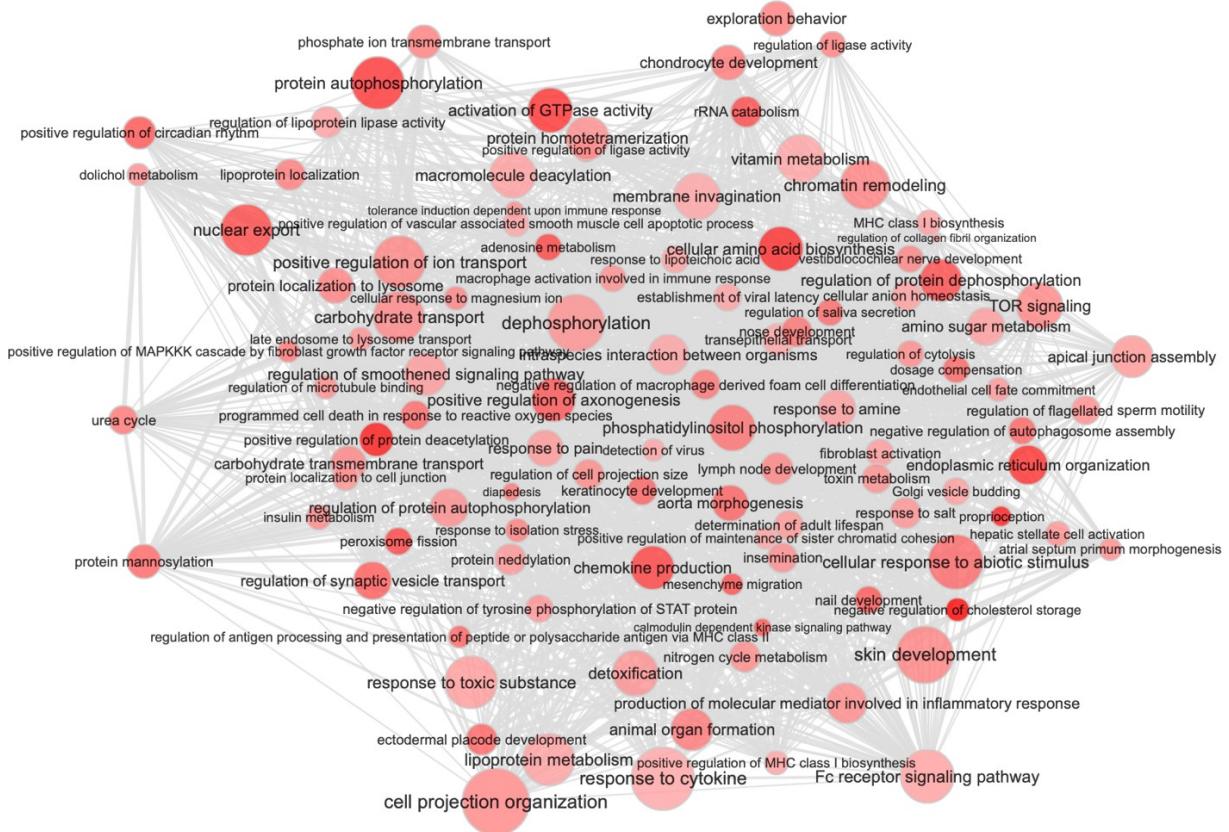


Figure S3. Representative Gene Ontology network for cellular components detected by models for PTSD_{REX} PRS predicting traumatic loss-related PTSD.

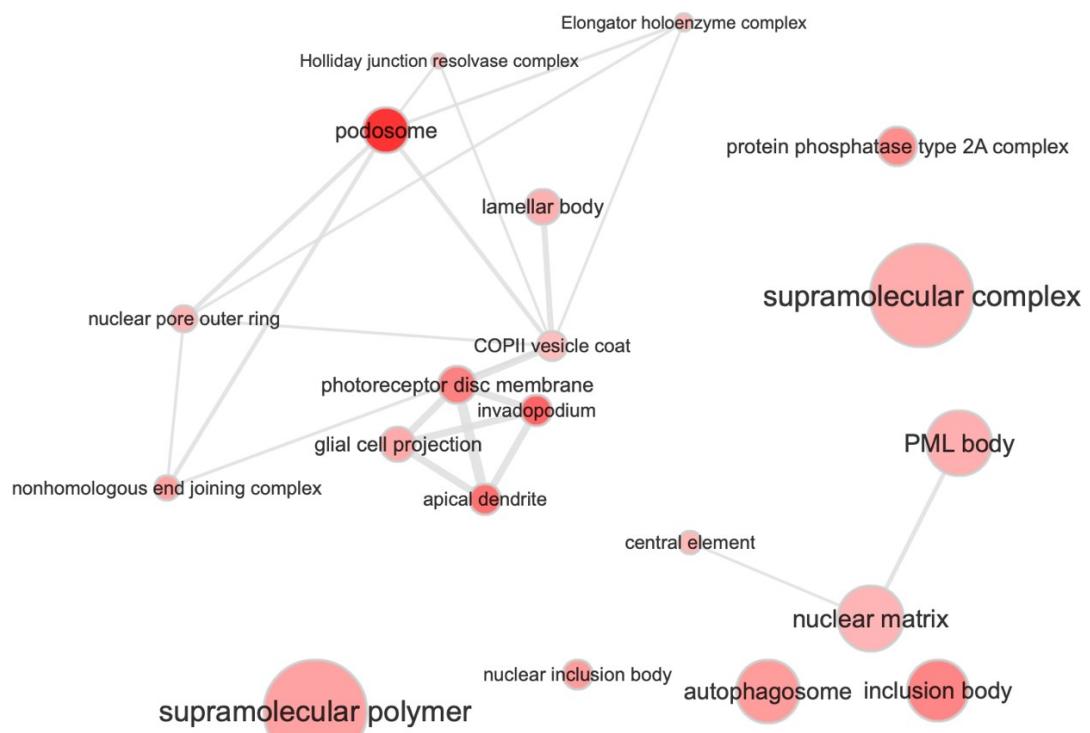


Figure S4. Representative Gene Ontology network for molecular functions detected by models for PTSD_{REX} PRS predicting traumatic loss-related PTSD.

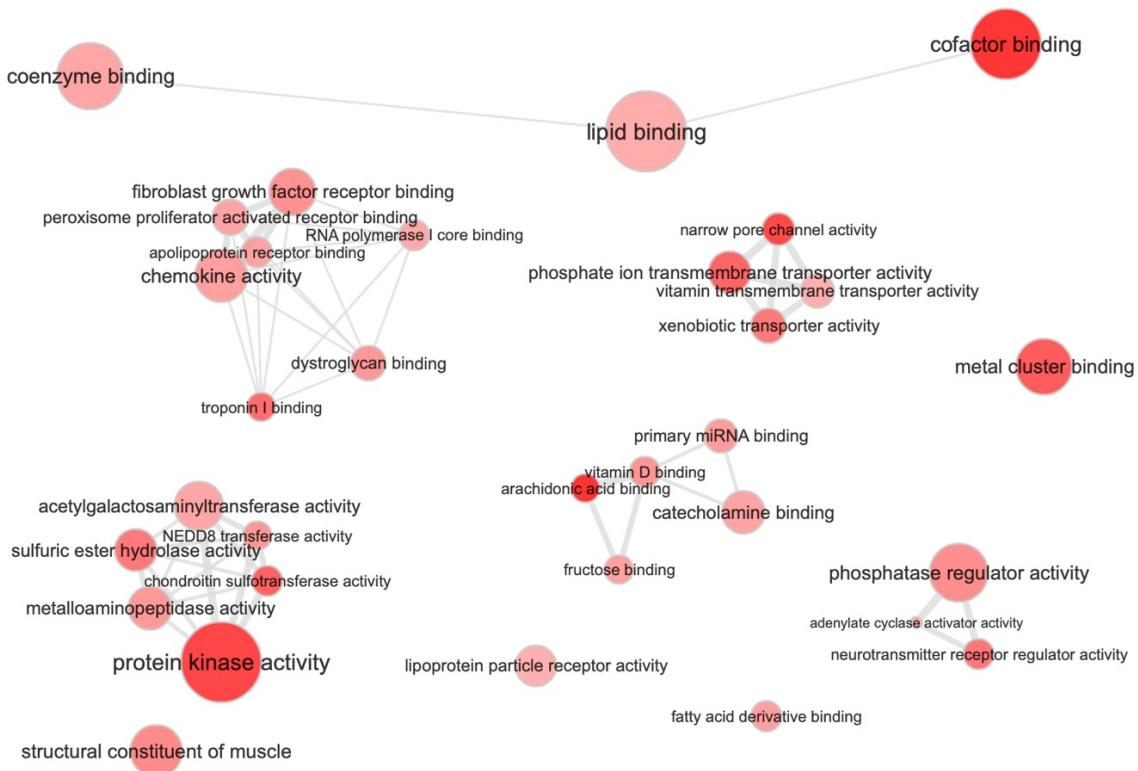


Table S1. Full list of genes represented in gene ontologies (GO) from **Table 2** and **Figures S1-S4** for gene-sets identified by polygenic risk score (PRS) models of posttraumatic stress disorder re-experiencing (PTSDREX).

Type	Biological Process				Cellular Component				Molecular Function									
GO	7029	10887	19230	35640	2102	99080	99081	71437	4672	8307	22842	30228	50544	99602	31013	48037	1901567	
Description	Endo-plasmic reticulum organization	Negative regulation of cholesterol storage	Proprioception	Exploration behavior	Podosome	Supra-molecular complex	Supra-molecular polymer	Invadopodium	Protein kinase activity	Structural constituent of muscle	Narrow-pore channel activity	Lipo-protein particle receptor activity	Arachidonic acid binding	Neuro-transmitter receptor regulator activity	Trop-onin I binding	Cofactor binding	Fatty acid derivative binding	
Genes	RTN3	NR1H3	FXN	CHL1	ACTR2	ARHGEF2	KIF28P	ACTR2	BK3	NEBL	KCNK7	STAB1	ALOX5AP	RTN4	NR1H4	RTN4	ACOT7	
	TRDN	TTC39B	GBX1	CHRNA4	ADAM8	ACTL8	KRTAP4_9	PDPN	SGK2	MYOM3	PANX1	LRP10	PPARG	TRDN	TTC39B	TRDN	ACOT12	
	RAB10	ABC1	TMEM150C	LRRK2	AFAP1L1	ACTN2	DNAJB6	AFAP1L	HIPK3	MYL6B	NALCN	ILDR1	S100A8	RAB11	ABC2	RAB11	DBI	
	LMAN2	MIR146A	POU4F1	BRINP1	PALLD	AGO1	KRTAP9_7	DPP4	CDK2	CSRP1	KCNK18	LRP12	STX3	LMAN3	MIR146A	LMAN3	ALOX5AP	
	ZFYVE27	PPAR	DLG4	SH3PXD2B	AGO3	KRTAP16_1	FAP	CDK3	DAG1	KCNK1	LDLR	ZFYVE28	PPARA	ZFYVE28	ZFYVE28	ZFYVE28	ZFYVE28	
	LRRK2	PPARD	ABAT	GSN	AHCTF1	KRTAP9_6	RUFY3	TNK2	SYNM	KCNK2	LRP1	LPK3	PPARD	LRRK3	PPARD	LRRK3	GCDH	
	TOR1AIP2	PPARG	DPP4	HNRNPK	ASPM	KRTAP29_1	ITGA3	CDK4	PDLIM3	KCNK3	LRP6	TOR1AIP3	PPARG	TOR1AIP3	TOR1AIP3	ACAD9		
	SPTSSB	NR1H2	GADI	LCPI	ATP2B4	DNM1L	ITGB1	CDK6	MYLPF	KCNK4	STAB2	SPTSSB	NR1H3	SPTSSB	SPTSSB	HADHA		
	MAPK15	ABCG1	GIP	ASAPI	BCL10	ABC9	PAK1	CDK7	KRT19	KCNK9	CXCL16	MAPK16	ABCG2	MAPK16	MAPK16	ACADL		
	SEC31A	ABL2	BIN2	CACNA1S	MYZAP	PLAUR	CDK8	ASPH	KCNK10	SORL1	SEC31A	SEC31A	ACBD7	RAB3GAP2	RAB3GAP2	RAB3GAP2		
	RAB3GAP1	APOE	PTPN12	CAMSAP2	ARP3	FSCN1	CDK9	MYBPC1	KCNK13	VLDLR	RAB3GAP2	RAB3GAP2	ALDH6A1	RAB3GAP2	RAB3GAP2	RAB3GAP2		
	RAB18	ITGA3	KIF9	CAPZB	KIF20A	SVIL	CDKN1A	MYBPC2	KCNK12	LRP8	RAB19	RAB19	PPARG	RAB19	RAB19	RAB19		
	TMCC1	PRKCE	SH3GL1	CASQ1	DNAL4	EZR	SPEG	MYBPC3	RHAG	CD36	TMCC2	TMCC2	S100A8	TMCC2	TMCC2	TMCC2		
	ARL6IP1	SLC4A10	FSCN1	CASQ2	LRPPRC		PAK4	MYBPH	KCNK16	SCARB1	ARL6IP2	ARL6IP2	SCP2	ARL6IP2	ARL6IP2	ARL6IP2		
	RAB3GAP2	JPHB	SRC	CCDC181	SPRY2		TESK2	MYH8	TMEM175		RAB3GAP3	RAB3GAP3	ACBD3	RAB3GAP3	RAB3GAP3	RAB3GAP3		
	GAK	C12orf10	SVIL	CCSAP	CDK2AP2		MERTK	MYH11	KCNK5		GAK	GAK	SOAT1	GAK	GAK	GAK		
	ATL3	TNR	TJPI	CCT3	APC2		STK25	MYL1	KCNK17		ATL4	ATL4	STX3	ATL4	ATL4	ATL4		
	SEC31B	EIF4A3	VCAM1	CDC42	KATNB1		CAMKK2	MYL2	KCNK6		SEC31B	SEC31B	ACBD4	SEC31B	SEC31B	SEC31B		
	TOR1B	VCL	CENPF	KLHL41			MAP3K2	MYL3			TOR1B	TOR1B	PNPLA3	TOR1B	TOR1B	TOR1B		
	SEC61A1	FERMT3	CEP170	TUBA1B			PLK2	MYL5			SEC61A2	SEC61A2	ACBD6	SEC61A2	SEC61A2	SEC61A2		
	MIA3	SCIN	CHTOP	TUBB3			NEK6	MYL6			MIA4	MIA4	ACBD5	MIA4	MIA4	MIA4		
	ATL1	ARHGEF2	COL11A1	MYL12B			CCNI	NEB			ATL2	ATL2	ATL2	ATL2	ATL2	ATL2		
	REEP2	LPXN	CSR1	NDRG1			TLK2	PLEC			REEP3	REEP3	REEP3	REEP3	REEP3	REEP3		
	STX18	SH3PXD2A	DHX9	TUBGCP3			RIPK3	JPH1			STX19	STX19	STX19	STX19	STX19	STX19		
	TMEM38B	WDR1	DISC1	BAIAP2			CHEK1	SMTN			TMEM38B	TMEM38B	TMEM38B	TMEM38B	TMEM38B	TMEM38B		
	TMEM33		DNAH14	APPBP2			CIT	TPM1			TMEM34	TMEM34	TMEM34	TMEM34	TMEM34	TMEM34		
	CCDC47		DNM3	FBLN5			MAP4K5	TPM2			CCDC48	CCDC48	CCDC48	CCDC48	CCDC48	CCDC48		
	RTN4		DVL1	NEBL			MAP4K1	TPM4			RTN5	RTN5	RTN5	RTN5	RTN5	RTN5		
	ATL2		DYRK3	GLRX3			CHEK2	TTN			ATL3	ATL3	ATL3	ATL3	ATL3	ATL3		
	SGTA		ENO1	DCTN2			IRAK3	CSRP3			SGTA	SGTA	SGTA	SGTA	SGTA	SGTA		
	REEP1		ESPN	ARFGEF2			AKAP13	CAPN3			REEP2	REEP2	REEP2	REEP2	REEP2	REEP2		
	BNIP1		FBXO28	CCT7			STK38	OBSCN			BNIP2	BNIP2	BNIP2	BNIP2	BNIP2	BNIP2		
	TMEM38A		FLG	CCT4			CHUK	SORBS2			TMEM38A	TMEM38A	TMEM38A	TMEM38A	TMEM38A	TMEM38A		
	BAG6		GNG12	CCT2			ALPK2	MYOM1			BAG7	BAG7	BAG7	BAG7	BAG7	BAG7		
	LMAN1L		HAX1	PDLIM5			CLK1	ACTN2			LMAN1L	LMAN1L	LMAN1L	LMAN1L	LMAN1L	LMAN1L		
	LMAN2L		HOOK1	SPAG5			CLK2	ACTN3			LMAN2L	LMAN2L	LMAN2L	LMAN2L	LMAN2L	LMAN2L		
	CASQ1		IFFO2	CENPE			CLK3	NEXN			CASQ2	CASQ2	CASQ2	CASQ2	CASQ2	CASQ2		
	JAGN1		IGFN1	GAS2L1			LRRK2	MYOM2			JAGN2	JAGN2	JAGN2	JAGN2	JAGN2	JAGN2		
	CAV2		ITGB3BP	RGS14			CSNK1A1L				CAV3	CAV3	CAV3	CAV3	CAV3	CAV3		

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Genes	SEC16B VAPB EIF2AK3 TRAM2 SEC16A	KCNAB2 KIF14 KIF17 KIF1B KIF21B KIF26B KIF28P KIF2C KIFAP3 KLHL21 LDLRAP1 LIN28A LMNA LMOD1 MACF1 MAEL MAP10 MEAF6 MOV10 MYBPH MYOM3 NAV1 NEK2 NEK7 NEXN NOS1AP NSL1 NUDC NUP2 NUP133 OBSCN PABPC4 PBXIP1 PDE4B PDE4DIP PKP1 PMF1 PPP1R12B PPP2R5A PSEN2 PSRC1 PUMI RASSF5 RC3H1 RCC2 RCSD1 RYR2 SLC2A1 STMN1 SYNC TAF5L TARDBP	NUDC KIF1C NEK6 NCKAP1 GJB6 HSPH1 TUBGCP2 FERMT2 MAPRE2 KIF2C TLK2 TPPP KATNA1 KIF3A LDB3 RASSF1 AKAP13 DCTN3 KRT71 AHNAK2 KIF12 TWF2 SYNPO TUBGCP5 	PLK5 UHMK1 ACVR1C GRK7 MAP3K8 TAF1L MYO3B NEK7 TRPM6 STK35 MAPK14 CSF1R CSK CSNK1A1 CSNK1E CSNK1G2 CSNK1G3 CSNK2A1 CSNK2A2 CSNK2B TTBK2 HIPK4 PDIK1L SIK1 NEK10 DAPK1 DAPK3 DCLK2 NIMIK DYRK1A EFNA3 EFNA4 EGFR EPHA2 MARK2 STK32A EPHA1 	SEC16B VAPB EIF2AK4 TRAM3 SEC16A	SEC16B VAPB EIF2AK4 TRAM3 SEC16A											

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GO	7029	10887	19230	35640	2102	99080	99081	71437	4672	8307	22842	30228	50544	99602	31013	48037	1901567	
Genes	CAPN3	LMBNB2	CPEB1	KLHL22	CTSH	TIGD5	EDC3	KCNAB2	EID1	KRTAP9_4	EXD1	KRTAP4_5	FBN1	KRTAP3_3	FBXL22	COL27A1	FBXO22	FBF1
	FMN1	MYLK2	GABPB1	TUBGCP6	INO80	FHD1C1	IQGAP1	PDLIM4	KIF23	CAV3	KIF7	SKAPI	KNSTRN	DNAH17	LRRC49	DYNLL1	MAP1A	MARCO
	MFAP1	KRT38	MNS1	KRT37	MYO5A	KRT36	MYZAP	ACTN1	NUSAP1	DNAH11	PATL2	MYH13	PRC1	MYOM1	PSMA4	RAB11A	RAB11A	FBP2
	RMDN3	ACTN2	RYR3	IQGAP1	SIN3A	NRP1	SYNM	KAT2B	THSD4	CDK5R1	TMOD2	SYNJ1	TMOD3	SQSTM1	TP53BP1	CDC16	TPM1	ACTN3
	TUBGCP4	BCL10	TUBGCP5	WASL	USP3	RSPH1	VPS18	NAV3	WHAMM	NAV1	ZWILCH	KLC4	ALDOA	KNSTRN	ATXN2L	MAP7	CARHSP1	PRC1
	CDT1	CCT6A	CENPN	DNAJA3	CENPT	KIFC2	CFDP1	IGFN1	CNOT1	INA	COTL1	KRT75	CYLD	PDLIM1				

