

SUPPLEMENTAL DATA

Whole-exome sequencing reveals rare genetic variations in ovarian granulosa cell tumor

Table S1. Summary statistics of sequencing quality

	Statistics					pre-alignment statistics					post-alignment statistics							
Sam ple Type	Sam ple name	Analy zeID	Q2 0(%)	Q3 0(%)	G C(%)	total read s	Av era ge Re ad Le	To tal Yi eld (M	Target Regions (bp)	average depth (pre- alignment)	Initi al Map pabl e	% Initi al Ma ppa ble	Non- Red und Rea ds	% Non - Red und ant	On- Targ et Rea ds	% O n- Targ et	On- Target Yield (bp)	mean depth (post- alignment)

							ngt h (bp)	bp)			Read s	Rea ds		Rea ds		Re ads		
Tumor	T1	S15-47822 F8	95.9	93.2	51.5	154,922,590	101.0	15,647	60,456,963	258.8	154,666,559	99.8	146,238,992	94.5	107,089,858	73.2	9519341374	157.4
	T2	S16-26915 B2	94.0	90.6	48.9	146,251,212	101.0	14,771	60,456,963	244.3	144,847,864	99.0	137,360,326	94.8	100,970,699	73.5	8776113111	145.1
	T3	S17-4139 B2	93.9	90.4	50.0	140,902,596	101.0	14,231	60,456,963	235.3	139,510,350	99.0	131,593,379	94.3	96,861,921	73.6	8377216650	138.5
	T4	S17-7934 RG1	94.2	90.8	51.5	139,881,802	101.0	14,128	60,456,963	233.6	138,620,243	99.0	126,740,170	91.4	97,819,824	77.1	8674285663	143.4
	T5	S17-16790 9	93.9	90.4	49.6	137,737,678	101.0	13,911	60,456,963	230.1	136,431,002	99.0	130,239,288	95.4	88,595,630	68.0	7656389803	126.6
	T6	S11-2891 RG5	96.0	93.4	50.6	141,676,368	101.0	14,309	60,456,963	236.6	141,487,308	99.8	129,578,037	91.5	98,568,622	76.0	8834348644	146.1

	T7	S11-23811 F3	94. 7	91. 5	51. 2	137, 817, 696	101 .0	13, 91 9	60,456,9 63	230.2	136,7 81,99 7	99.2	129, 567, 516	94.7	97,1 02,2 30	74. 9	8577862 313	141.8
	T8	S13-15636 E	94. 6	91. 3	53. 0	149, 231, 118	101 .0	15, 07 2	60,456,9 63	249.3	147,9 72,07 5	99.1	136, 115, 183	91.9	102, 461, 498	75. 2	9127763 553	150.9
	T9	S15-4531 F3	95. 2	92. 1	51. 2	186, 402, 720	101 .0	18, 82 6	60,456,9 63	311.4	185,7 64,68 3	99.6	162, 876, 676	87.6	121, 222, 036	74. 4	1085281 2049	179.5
	T10	S14-2813 F2	95. 0	91. 9	50. 6	176, 522, 844	101 .0	17, 82 8	60,456,9 63	294.9	175,7 12,74 2	99.5	164, 580, 604	93.6	120, 107, 606	72. 9	1059107 8346	175.1
	T11	S15-4343 F3	94. 5	91. 0	51. 0	187, 438, 318	101 .0	18, 93 1	60,456,9 63	313.1	186,6 51,21 3	99.5	172, 497, 815	92.4	130, 551, 091	75. 6	1161678 8824	192.1
average			94. 7	91. 5	50. 8	154, 434, 995	101 .0	15, 59 7.5	6045696 3	258.0	1534 9509 4	99.3	1424 8981 7	92.9	1055 7736 5	74. 0	9327636 394	154.2
normal	N1	S15-14897 7	96. 0	93. 7	51. 6	102, 506, 078	101 .0	10, 35 3	60,456,9 63	171.2	101,9 85,11 7	99.4	98,0 97,6 41	96.1	73,6 19,1 68	75. 0	6519310 788	107.8

N2	S16-26915 A2	95. 8	93. 1	49. 8	101, 839, 794	101 .0	10, 28 5	60,456,9 63	170.1	101,6 51,54 5	99.8	96,0 68,7 09	94.5	70,1 28,2 38	72. 9	6154444 800	101.8
N3	S17-4139 A9	96. 1	93. 6	50. 1	93,6 96,8 90	101 .0	9,4 63	60,456,9 63	156.5	93,55 9,850	99.8	89,1 09,5 81	95.2	66,5 61,9 45	74. 6	5865228 861	97.0
N4	S17-7934 6	95. 6	92. 8	50. 2	97,0 11,0 68	101 .0	9,7 98	60,456,9 63	162.0	96,81 6,305	99.7	92,0 12,2 19	95.0	67,2 43,2 31	73. 0	5905584 438	97.6
N5	S17-16790 6	95. 9	93. 3	50. 0	97,2 23,0 98	101 .0	9,8 19	60,456,9 63	162.4	97,04 9,431	99.8	91,6 54,4 93	94.4	67,3 67,4 23	73. 5	5908120 791	97.7
N6	S11-2891 1	94. 5	91. 3	51. 4	106, 083, 920	101 .0	10, 71 4	60,456,9 63	177.2	105,0 34,51 6	99.0	98,9 43,9 08	94.2	74,6 64,5 62	75. 4	6566599 356	108.6
N7	S11-23854 A7	95. 8	93. 1	51. 6	97,8 29,8 20	101 .0	9,8 80	60,456,9 63	163.4	97,68 6,402	99.8	92,1 29,7 98	94.3	70,4 22,8 77	76. 4	6284707 183	103.9
N8	S13-15636 A2	96. 2	93. 7	52. 9	99,2 17,5 86	101 .0	10, 02 0	60,456,9 63	165.7	99,09 9,123	99.8	92,1 98,0 33	93.0	71,9 28,4 73	78. 0	6470534 331	107.0

	N9	S14-28991	94.9	91.9	51.4	110,325,136	101.0	11,142	60,456,963	184.3	109,258,657	99.0	103,899,206	95.0	81,088,625	78.0	7178763168	118.7
	N10	S15-43944	95.0	92.0	51.1	111,616,652	101.0	11,273	60,456,963	186.4	110,682,424	99.1	105,490,521	95.3	79,443,664	75.3	7035610192	116.3
	N11	S15-4570	95.2	92.2	50.2	100,436,964	101.0	10,144	60,456,963	167.7	99,997,253	99.5	93,397,511	93.4	68,236,207	73.0	6036506480	99.8
average			95.5	92.8	50.9	101,617,001	101.0	10,262.8	60456963.0	169.7	101165511.2	99.5	95727420.0	94.6	71882219.4	75.0	6356855490	105.1

Table S2. List of GO terms associated with tumor-specific genes in OGCT

(A) Cellular components

Group ID	Category	Term	Description	LogP	Log(q-value)	InTerm _InList	Symbols
1	GO Cellular Components	GO:0031012	extracellular matrix	-3.77659	-0.891	23/570	<i>CTSC, COL15A1, COL17A1, GLG1, MMP17, MUC4, MUC6, NID1, OVGPI, TPSAB1, HSP90B1, ADAMTSL2, POSTN, HPSE, ADAMTS20, ITIH5, FBN3, COL25A1, NAV2, COL24A1, LAMA1, EYS, MXRA7</i>
2	GO Cellular Components	GO:0005905	clathrin-coated pit	-3.69213	-0.891	7/70	<i>LDLR, ITSN1, CUBN, PICALM, AAK1, FCHO1, EPN3, BLK, PIK3C3, PTK2, GNA13, FERMT2, ATG14, WIPI2, VPS13C, WIPI1</i>
3	GO Cellular Components	GO:0005776	autophagosome	-3.43643	-0.850	8/101	<i>PEG3, PIK3C3, ATG14, WIPI2, TEX264, WIPI1, MCOLN3, MAP1LC3C</i>
4	GO Cellular Components	GO:0097546	ciliary base	-3.27694	-0.850	5/39	<i>GLI2, PRKARIA, PRKAR1B, TULP3, FANK1, PIK3C3, ATG14, CFAP46, CFAP54, CFAP221</i>
5	GO Cellular Components	GO:0031932	TORC2 complex	-3.25381	-0.850	3/10	<i>TTI1, SMG1, PRR5L</i>
6	GO Cellular Components	GO:0031414	N-terminal protein acetyltransferase complex	-3.25381	-0.850	3/10	<i>NAA25, NAA15, NAA38</i>

7	GO Cellular Components	GO:0030496	midbody	-3.19835	-0.850	11/196	<i>ECT2,PIK3C3,SAFB,HSP90B1,PKP4,TRIOBP,ZFYVE26,EXOC2,ZFYVE19,AGAP2,ASPM</i>
8	GO Cellular Components	GO:0005911	cell-cell junction	-2.97449	-0.737	19/494	<i>AQP7,COL17A1,CXADR,ECT2,NOTCH1,VAVI,SYMPK,PKP4,PTPRU,PATJ,FERMT2,EPB41L3,FRMD4B,ADGRL3,AH1,IQGAP3,PLEKHA7,PIKFYVE,LAMA1</i>
9	GO Cellular Components	GO:0032580	Golgi cisterna membrane	-2.88731	-0.713	7/95	<i>FUT2,B4GALT5,SCFD1,UXS1,COG3,GOLGA8IP,GOLGA8B,HOOK3</i>
10	GO Cellular Components	GO:0005770	late endosome	-2.8771	-0.713	13/282	<i>SLC31A1,DYNC1LI2,LDLR,CHMP1A,PIK3C3,PRKARIA,PRKAR1B,MAPK3,RNF13,MCOLN3,VIPAS39,GALNTL5,PIKFYVE</i>
11	GO Cellular Components	GO:0030894	replisome	-2.70284	-0.629	3/15	<i>PRIM2,RPA1,DONSON,BCL6,TEX264</i>
12	GO Cellular Components	GO:0016234	inclusion body	-2.69771	-0.629	6/76	<i>AGL,PICALM,XRN2,FBXO7,SFMBT2,PRDM16</i>
13	GO Cellular Components	GO:0005813	centrosome	-2.59469	-0.617	21/615	<i>BICD1,CTSC,CHD3,DYNC1LI2,PRKARIA,CIR1,KIAA0586,PATJ,CEP152,TLL5,BICD2,UBR4,ZFYVE26,AH1,CCDC77,HOOK3,ZFYVE19,CEP295,PLEKHA7,CEP120,ASPM</i>
14	GO Cellular Components	GO:0031143	pseudopodium	-2.46582	-0.549	3/18	<i>ACTN4,ACTN2,MAPK3</i>

15	GO Cellular Components	GO:0031258	lamellipodium membrane	-2.21213	-0.349	3/22	<i>NCKAP1,FERMT2,SYNE2</i>
16	GO Cellular Components	GO:0097060	synaptic membrane	-2.13866	-0.292	14/384	<i>ACTN2,DAGLA,GABRR2,PTPRD,PTPRS,ITSN1,PICALM,SLC6A5,DGKI,SLC4A8,RIMS1,SYNE1,GRIP1,CHRNA10</i>

(B) Molecular functions

Group ID	Category	Term	Description	LogP	Log(q-value)	InTerm _InList	Symbols
1	GO Molecular Functions	GO:0015318	inorganic molecular entity transmembrane transporter activity	-4.78765	-1.591	30/740	<i>AQP7,ATP4B,CFTR,SLC31A1,COX6B1,GABRR2,KCNH2,KCNJ12,FXYP3,KCNQ4,SLC6A5,SLC4A8,SLC12A7,DMAC2L,ANO7,SLC45A2,SLC38A2,MCOLN3,SLC2A9,CHRNA10,ANO2,SLC25A28,SLC12A8,CACNA2D4,PKD1L2,SLC5A11,ANO4,OTOP1,CCT8L2,KCNJ18,SLC30A9</i>
2	GO Molecular Functions	GO:0019901	protein kinase binding	-4.7295	-1.591	28/671	<i>BICD1,CBLB,ACE,KIF11,MEF2A,PPEF2,PRKARIA,PRKAR1B,MAP2K3,PTK2,WARS1,CIR1,SLC12A7,FERMT2,ATF7,RNF13,CEP152,SHC2,FBXO7,TRIB2,GPRC5B,EXO2,TRIM5,AGAP2,TRIM6,DUSP19,SIK1,GFRAL,LDHA</i>
3	GO Molecular Functions	GO:0004566	beta-glucuronidase activity	-4.69734	-1.591	3/4	<i>KL,HPSE,GUSBP3,AGL,GALC,OVGP1,GLBIL,ILIRAP</i>

4	GO Molecular Functions	GO:0005509	calcium ion binding	-4.6731	-1.591	29/713	<i>ACTN4,ACTN2,CBLB,CDH16,CLGN,F10,HABP2,LDLR,NID1,NOTCH1,PLCB2,PNLIPRP1,PPEF2,PRSS3,ITSN1,HSP90B1,CUBN,CELSR1,ADGRL3,HPCAL4,SYT17,LRP1B,MCTP1,SYT15,FBN3,PKD1L2,RASEF,EYS,NOTCH2NLA</i>
5	GO Molecular Functions	GO:0005201	extracellular matrix structural constituent	-4.3262	-1.446	12/172	<i>COL15A1,COL17A1,MUC3A,MUC4,MUC6,NID1,TUFT1,POSTN,FBN3,COL25A1,COL24A1,LAMA1,ACTN2,BICD1,COPB1,RPL4,TPM1,CCDC6,KRT38,EPB41L3,KLHL3,NUP54,NUP85,TLN2</i>
6	GO Molecular Functions	GO:0051020	GTPase binding	-4.23155	-1.446	16/294	<i>APIG1,BICD1,ECT2,PICALM,NCKAP1,TRIOBP,ATG14,RIMS1,BICD2,FNBP1L,EXOC2,FGD6,RANBP17,DOCK7,FMNL2,IQGAP3</i>
7	GO Molecular Functions	GO:0015144	carbohydrate transmembrane transporter activity	-4.22694	-1.446	6/40	<i>AQP7,SLC2A3,SLC45A2,SLC2A9,SLC5A11,SLC2A14,SLC6A5,SLC4A8,SLC12A7,SLC38A2,SLC12A8,ATP4B,CFTR,COX6B1</i>
8	GO Molecular Functions	GO:0004791	thioredoxin-disulfide reductase activity	-3.77215	-1.043	3/7	<i>SELENOT,NXN,TXNRD3,ERO1B</i>

9	GO Molecular Functions	GO:0015103	inorganic anion transmembrane transporter activity	-3.4719	-0.856	10/153	<i>CFTR,GABRR2,FXYP3,SLC4A8,SLC12A7,ANO7,ANO2,SLC12A8,ANO4,CCT8L2,SLC2A3,SLC6A5,SLC38A2,SFXN5,SLC2A14</i>
10	GO Molecular Functions	GO:0032266	phosphatidylinositol-3-phosphate binding	-3.07825	-0.737	5/43	<i>SNX13,ZFYVE26,WIPI2,WIPI1,ZFYVE19,ACTN2,TULP3,PICALM,FERMT2</i>
11	GO Molecular Functions	GO:0001784	phosphotyrosine residue binding	-3.03199	-0.710	5/44	<i>CBLB,MAPK3,VAV1,PTPN5,SHE</i>
12	GO Molecular Functions	GO:0034452	dynactin binding	-3.00173	-0.698	3/12	<i>BICD1,BICD2,HOOK3,EPB41L3,SMC3</i>
13	GO Molecular Functions	GO:0016757	glycosyltransferase activity	-2.91876	-0.650	13/279	<i>AGL,FUT2,RPN1,UGT8,UMPS,B4GALT5,UGT2A1,TIPARP,GALNTL5,STT3B,DPY19L2P2,UGT2A2,ALG1L2</i>

14	GO Molecular Functions	GO:0030276	clathrin binding	-2.8186	-0.612	6/72	<i>AP1G1,LDLR,PICALM,SYT17,EPN3,SYT15</i>
15	GO Molecular Functions	GO:0051015	actin filament binding	-2.79174	-0.599	11/220	<i>ACTN4,ACTN2,TPM1,FERMT2,TRIOBP,SYNE2,SYNE1,TLN2,FMNL2,MYOM3,IQGA P3</i>
16	GO Molecular Functions	GO:0043138	3''-5'' DNA helicase activity	-2.70284	-0.539	3/15	<i>FBH1,NAV2,HELQ</i>
17	GO Molecular Functions	GO:0008236	serine-type peptidase activity	-2.68268	-0.539	10/194	<i>CTSC,ACE,DPP6,F10,HABP2,HGF,PRSS3,TPSAB1,TPSD1,PRSS3P2,MMP17,CHMP1A,CPZ,ADAM21,ADAMTSL2,PSMD14,UFSP2,ADGRG6,ADAMTS20,TRABD2A</i>
18	GO Molecular Functions	GO:0030674	protein-macromolecule adaptor activity	-2.67848	-0.539	13/297	<i>AP1G1,BICD1,UBXN8,SEC22B,EPB41L3,SYNE2,BICD2,SYNE1,GRIP1,FBXO7,TRIM5,TRIM6,DUSP19,ITSN1</i>

19	GO Molecular Functions	GO:0004725	protein tyrosine phosphatase activity	-2.66071	-0.533	7/104	<i>CDKN3,PTPRD,PTPRS,PTPRU,PTPN5,TPTE2,DUSP19,PPEF2,PHLPP2,MTMR9,PIKFYVE</i>
20	GO Molecular Functions	GO:0003951	NAD+ kinase activity	-2.53945	-0.458	3/17	<i>DGKI,NADK,DGKH</i>

(C) Biological processes

Group ID	Category	Term	Description	LogP	Log(q-value)	InTerm _InList	Symbols
1	GO Biological Processes	GO:0042594	response to starvation	-5.03962	-1.021	14/197	<i>ACAT1,ASNS,PIK3C3,MAPK3,ATG14,WIP12,SLC38A2,MIOS,WIP11,EIF2A,SIK1,EIF2AK4,MAP1LC3C,LOC102724428,POSTN,AGL,BCHE,LDHA,LDLR,GFRAL</i>
2	GO Biological Processes	GO:1902476	chloride transmembrane transport	-4.70628	-1.021	8/67	<i>CFTR,GABRR2,SLC4A8,SLC12A7,ANO7,ANO2,SLC12A8,ANO4,FXD3,CD47,ACE,SLC2A3,SLC6A5,PLA2R1,SLC38A2,SLC2A9,SFXN5,SLC51B,SLC2A14,CCT8L2,SLC51A</i>
3	GO Biological Processes	GO:0061912	selective autophagy	-4.61147	-1.021	8/69	<i>MAPK3,CERS1,ATG14,WIP12,KLHL3,TEX264,VPS13C,MAP1LC3C,PIK3C3,SEC22B,FEZ2,SCFD1,WIP11,PIKFYVE,SMG1,VIPAS39,HGF,FBXO7,FNBP1L,MTMR9,TRIM5,TRIM6,RAB20,HOOK3,ACTN2,CHMP1A,SMARCE1,TPSAB1,TRIOBP,SUPT16H,NAV3</i>
4	GO Biological Processes	GO:0022604	regulation of cell morphogenesis	-4.51809	-1.021	17/309	<i>ACTN4,ITGA7,PTK2,PTPRD,TPM1,SEMA3E,POSTN,FERMT2,TRIOBP,RIMS1,EPB41L3,GRIP1,SYT17,FGD6,DOCK5,LARP4,FMNL2,ACTN2,BCL6,COL17A1,MUC4,NID</i>

							<i>1,NOTCH1,HPSE,BMPRIA,LDLR,PTPRS,CLOCK,TRAK1,ADGRA2,TENM4,HOOK3,DOCK7,ASPM,BDKRB1,CD47,F10,HGF,MAPK3,MAP2K3,SPN,SYNE2,ELP5</i>
5	GO Biological Processes	GO:0072385	minus-end-directed organelle transport along microtubule	-4.30501	-0.972	3/5	<i>BICD1,RAB6A,BICD2,HOOK3</i>
6	GO Biological Processes	GO:0022027	interkinetic nuclear migration	-4.30501	-0.972	3/5	<i>HOOK3,DOCK7,CEP120,SYNE2,ACTN4,BICD1,BLK,CFTR,MEF2A,CHMP1A,RAB6A,PICALM,ATG14,TRAK1,BICD2,FNBP1L,WIPI1,ASPM</i>
7	GO Biological Processes	GO:0010927	cellular component assembly involved in morphogenesis	-3.99831	-0.886	9/107	<i>ACTN2,MEF2A,PRKARIA,TPM1,UGT8,ZPBP,EPB41L3,TENM4,PIKFYVE,CTSC,GALC,HGF,B4GALT5,ADGRG6</i>
8	GO Biological Processes	GO:0048232	male gamete generation	-3.96841	-0.886	24/590	<i>BCL6,CFTR,ACE,FANCA,MSH4,NOTCH1,CCNA1,CLOCK,ZPBP,XRN2,UBR2,SYNE1,MORC1,SPATA6L,STRBP,VIPAS39,TXNRD3,TDRD9,SLC2A14,CFAP54,GALNTL5,ASPM,C14orf39,DPY19L2P2,CXADR,PRKARIA,RXFP2,EQTN</i>
9	GO Biological Processes	GO:0006898	receptor-mediated endocytosis	-3.92374	-0.886	14/249	<i>AP1G1,BICD1,LDLR,ITSN1,CUBN,PICALM,CALCRL,AAK1,PLA2R1,FCHO1,LRP1B</i>

							, <i>AH11,FNBP1L,PIKFYVE,PIK3C3,MAPK3,EQTN,EPN3,MTMR9,MCTP1,ARHGAP12</i>
10	GO Biological Processes	GO:0140694	non-membrane-bounded organelle assembly	-3.78465	-0.867	18/389	<i>ACTN2,BICD1,KIF11,MEF2A,CHMP1A,PRKARIA,TPM1,SMC3,CEP152,MRTO4,EIF2A,CEP295,CEP120,DEUP1,ASPM,GOLGA8IP,MCIDAS,GOLGA8B,CHD3,PATJ,DYNC1LI2,TLL5,BICD2,CFAP46,ULK4,HOOK3,DOCK7,NAV3</i>
11	GO Biological Processes	GO:1990573	potassium ion import across plasma membrane	-3.72229	-0.849	6/49	<i>ATP4B,KCNH2,KCNJ12,SLC12A7,SLC12A8,KCNJ18,ACTN2,DPP6,FXD3,SUMO1,KCNQ4,CCT8L2,ACTN4,BDKRB1,SLC31A1,COX6B1,SLC6A5,SLC4A8,DMAC2L,MCOLN3,SLC2A9,CHRNA10,SLC25A28,CACNA2D4,PKD1L2,OTOP1,SLC2A3,CFTR,MAPK3,RAB20</i>
12	GO Biological Processes	GO:0032989	cellular component morphogenesis	-3.58157	-0.784	27/744	<i>ACTN2,GLI2,MEF2A,NOTCH1,PRKARIA,PTK2,PTPRD,PTPRS,TPM1,UGT8,PICALM,B4GALT5,FEZ2,SEMA3E,POSTN,NCKAIP1,ZBPB,TRAK1,RIMS1,EPB41L3,GRIP1,TENM4,SYT17,DOCK7,PIKFYVE,LAMA1,EIF2AK4</i>
13	GO Biological Processes	GO:0030155	regulation of cell adhesion	-3.51805	-0.746	27/751	<i>ACTN4,BCL6,BLK,CBLB,CD47,FUT2,GLI2,NID1,NOTCH1,PRKARIA,PTK2,SPN,TP</i>

							<i>M1, VAV1, PKP4, SEMA3E, PTPRU, POSTN, NFAT5, FERMT2, TRIOBP, TMEM131L, ABCA12, GPAM, DOCK5, CARD11, LAMA1</i>
14	GO Biological Processes	GO:0042733	embryonic digit morphogenesis	-3.40055	-0.696	6/56	<i>BMPRIA, GLI2, NOTCH1, TULP3, LMBR1, TBC1D32</i>
15	GO Biological Processes	GO:0048246	macrophage chemotaxis	-3.33039	-0.666	5/38	<i>MAPK3, PTK2, MTUS1, NUP85, TAF4A</i>
16	GO Biological Processes	GO:0030866	cortical actin cytoskeleton organization	-3.22508	-0.635	5/40	<i>ECT2, NCKAP1, AKAP11, EPB41L3, FMNL2</i>
17	GO Biological Processes	GO:2000209	regulation of anoikis	-3.15263	-0.590	4/24	<i>NOTCH1, PTK2, BRMS1, SIK1</i>
18	GO Biological Processes	GO:0046339	diacylglycerol metabolic process	-3.08282	-0.540	4/25	<i>DAGLA, DGKI, GPAM, DGKH, LDLR, ATG14, SIK1, PIK3C3, PLCB2, SMG1, TTC7A, MTMR9, TPTE2, PIKFYVE</i>
19	GO Biological Processes	GO:0014910	regulation of smooth muscle cell migration	-3.05418	-0.521	7/89	<i>BMPRIA, ACE, TPM1, POSTN, GNAI3, DOCK5, DOCK7</i>
20	GO Biological Processes	GO:0051493	regulation of cytoskeleton organization	-3.01088	-0.513	20/529	<i>ACTN2, BICD1, CD47, ECT2, CHMP1A, MAPK3, PTK2, TPM1, CELSR1, SEMA3E, PATJ, NCKAP1, FERMT2, TRIOBP, BICD2, CEP295, NAV3, IQGAP3, CEP120, WHAMMP3, ACTN4, BCL6, CXADR, KCNH2, MEF2A, PRKAR1</i>

						<i>A,HSP90B1,AKAP11,EPB41L3,SYNE2,FN BP1L,FGD6,ARHGAP12,FMNL2,AGAP2</i>
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Table S3. List of biological network analysis with cytoscape

ID	Term	Ontology Source	Term PValue	Term PValue Corrected with Benjamini-Hochberg	Group PValue	Group PValue Corrected with Benjamini-Hochberg	GO Levels	GO Groups	% Associated Genes	Nr. Genes	Associated Genes Found
GO:0005509	calcium ion binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.01	[5]	Group00	4.12	31.00	<i>ACTN2, ACTN4, ADGRL3, CBLB, CDH16, CELSR1, CLGN, CUBN, EYS, F10, FBN3, HABP2, HPCAL4, HSP90B1, ITSN1, LDLR, LRP1B, MCTP1, NBP26,</i>

											<i>NID1, NOTCH1, NOTCH2NLA, PKD1L2, PLCB2, PNLIPRP1, PPEF2, PRSS3, RASEF, SYT15, SYT17, VWDE</i>
GO:0016266	O-glycan processing	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.04	0.00	0.01	[6, 8, 9]	Group01	9.09	6.00	<i>B4GALT5, GALNTL5, MUC12, MUC3A, MUC4, MUC6</i>
GO:0016410	N-acyltransferase activity	GO_MolecularFunction-EBI-	0.00	0.04	0.00	0.01	[5]	Group02	7.21	8.00	<i>BRPF3, CERS1, CLOCK,</i>

		UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									<i>GDF1,</i> <i>NAA15,</i> <i>NAA25,</i> <i>SLC38A2,</i> <i>SMARCE1</i>
GO:0019901	protein kinase binding	GO_Mole cularFunct ion-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.01	0.01	[5]	Group03	4.09	29.00	<i>ACE, AGAP2,</i> <i>ATF7, BICD1,</i> <i>CBLB,</i> <i>CEP152,</i> <i>CIR1,</i> <i>DUSP19,</i> <i>EXOC2,</i> <i>FBXO7,</i> <i>FERMT2,</i> <i>GFRAL,</i> <i>GPRC5B,</i> <i>KIF11,</i> <i>MAP2K3,</i> <i>MEF2A,</i> <i>PPEF2,</i> <i>PRKAR1A,</i> <i>PRKAR1B,</i>

											<i>PTK2, RNF13, SHC2, SIK1, SLC12A7, TRIB2, TRIM5, TRIM6, TRIM6-TRIM34, WARS1</i>
GO:0030866	cortical actin cytoskeleton organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.01	[4, 7]	Group04	12.50	5.00	<i>AKAP11, ECT2, EPB41L3, FMNL2, NCKAP1</i>
GO:0031349	positive regulation of defense response	GO_BiologicalProcess-EBI-UniProt-GOA-	0.00	0.03	0.00	0.01	[3, 4, 5, 6]	Group05	4.92	19.00	<i>APIG1, CARD11, CD47, CLOCK, CTSC,</i>

		ACAP-ARAP_13 .05.2021_ 00h00									<i>GPRC5B, KLRC2, LDLR, MAPK3, MUC12, MUC3A, MUC4, MUC6, OSMR, PSMD14, TRIM5, TRIM6, TRIM6- TRIM34, VAV1</i>
GO:0031414	N-terminal protein acetyltransf er ase complex	GO_Cellu larCompo nent-EBI- UniProt- GOA- ACAP- ARAP_13	0.00	0.03	0.00	0.01	[3, 4, 6]	Group06	27.27	3.00	<i>NAA15, NAA25, NAA38</i>

		.05.2021_00h00									
GO:0004566	beta-glucuronidase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.04	0.00	0.00	[5]	Group07	60.00	3.00	<i>GUSBP3, HPSE, KL</i>
GO:0032580	Golgi cisterna membrane	GO_CellularComponent-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.01	0.01	[5, 6, 7, 8, 9]	Group08	7.22	7.00	<i>B4GALT5, COG3, FUT2, GOLGA8B, GOLGA8IP, SCFD1, UXS1</i>
GO:0048246	macrophage chemotaxis	GO_BiologicalProcess-EBI-	0.01	0.04	0.01	0.01	[4, 5, 6, 7, 8]	Group09	10.20	5.00	<i>MAPK3, MTUS1,</i>

		UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									<i>NUP85, PTK2, TAFA4</i>
GO:0051642	centrosome localization	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.01	0.01	[3]	Group10	12.12	4.00	<i>ASPM, BICD2, DYNC1LI2, SYNE2</i>
GO:0060038	cardiac muscle cell proliferation	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13	0.01	0.04	0.01	0.01	[4, 5, 6, 7, 8, 9]	Group11	9.80	5.00	<i>BMPRIA, NOTCH1, PRKARIA, TENM4, ZFPM2</i>

		.05.2021_00h00									
GO:0070925	organelle assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.00	[5]	Group12	4.11	41.00	<i>ACTN2, AH11, ASPM, ATG14, BICD1, CEP120, CEP152, CEP295, CFAP221, CFAP46, CFAP54, CHMP1A, DEUP1, EIF2A, EXOC2, FEZ2, GOLGA8B, GOLGA8IP, IL1RAP, KIAA0586, KIF11, MAP1LC3C,</i>

											<i>MCIDAS,</i> <i>MEF2A,</i> <i>MRT04,</i> <i>NOTCH1,</i> <i>PIK3C3,</i> <i>PIKFYVE,</i> <i>PRKARIA,</i> <i>PTPRD,</i> <i>PTPRS,</i> <i>RAB20,</i> <i>SCFD1,</i> <i>SEC22B,</i> <i>SMC3,</i> <i>SYNE2,</i> <i>TBC1D32,</i> <i>TPM1, WIPI1,</i> <i>WIPI2, ZPBP</i>
GO:1903305	regulation of regulated secretory pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-	0.01	0.05	0.01	0.01	[5, 6, 7, 8]	Group13	5.96	9.00	<i>AP1G1, BLK,</i> <i>DGKI,</i> <i>KLRC2,</i> <i>NOTCH1,</i> <i>RIMS1,</i>

		ARAP_13 .05.2021_ 00h00									<i>SLC4A8, SYT15, SYT17</i>
GO:2000104	negative regulation of DNA- dependent DNA replication	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.01	0.01	[7, 8, 9]	Group14	17.65	3.00	<i>BCL6, DONSON, FBH1</i>
GO:0010669	epithelial structure maintenanc e	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.01	0.01	[4, 6]	Group15	12.50	4.00	<i>CXADR, MUC4, MUC6, SRFBP1</i>
GO:0010812	negative regulation	GO_Biolo gicalProce	0.00	0.04	0.00	0.01	[4, 5, 6]	Group16	9.09	6.00	<i>ACTN4, BCL6,</i>

	of cell-substrate adhesion	ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									<i>NOTCH1, POSTN, PTPRU, SEMA3E</i>
GO:0001784	phosphotyrosine residue binding	GO_MolecularFunction-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.04	0.00	0.01	[5]	Group17	10.87	5.00	<i>CBLB, MAPK3, PTPN5, SHE, VAV1</i>
GO:0016234	inclusion body	GO_CellularComponent-EBI- UniProt- GOA- ACAP- ARAP_13	0.01	0.05	0.01	0.01	[3]	Group18	7.69	6.00	<i>AGL, FBXO7, PICALM, PRDM16, SFMBT2, XRN2</i>

		.05.2021_00h00									
GO:0035335	peptidyl-tyrosine dephosphorylation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.01	0.01	[7, 8]	Group19	6.78	8.00	<i>CDKN3, DUSP19, MTMR9, PTPN5, PTPRD, PTPRS, PTPRU, TPTE2</i>
GO:0004725	protein tyrosine phosphatase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.01	0.01	[8, 9]	Group19	6.78	8.00	<i>CDKN3, DUSP19, MTMR9, PTPN5, PTPRD, PTPRS, PTPRU, TPTE2</i>
GO:0038201	TOR complex	GO_CellularComponent-EBI-	0.00	0.04	0.00	0.01	[3]	Group20	21.43	3.00	<i>PRR5L, SMG1, TTI1</i>

		UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									
GO:0031932	TORC2 complex	GO_CellularComponent-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.03	0.00	0.01	[4]	Group20	27.27	3.00	<i>PRR5L, SMG1, TTI1</i>
GO:0046339	diacylglycerol metabolic process	GO_BiologicalProcess-EBI- UniProt- GOA- ACAP- ARAP_13	0.00	0.03	0.00	0.00	[6, 7]	Group21	15.38	4.00	<i>DAGLA, DGKH, DGKI, GPAM</i>

		.05.2021_00h00									
GO:0003951	NAD+ kinase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.00	0.00	[7]	Group21	17.65	3.00	<i>DGKH, DGKI, NADK</i>
GO:0051020	GTPase binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.02	0.00	0.00	[4]	Group22	5.83	18.00	<i>APIG1, ATG14, BICD1, BICD2, DGKI, DOCK7, ECT2, EXOC2, FGD6, FMNL2, FNBP1L, GOLGA8B, IQGAP3,</i>

											<i>NCKAPI,</i> <i>PICALM,</i> <i>RANBP17,</i> <i>RIMS1,</i> <i>TRIOBP</i>
GO:0031267	small GTPase binding	GO_Mole cularFunct ion-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.03	0.00	0.00	[5]	Group22	5.82	16.00	<i>APIG1,</i> <i>BICD1,</i> <i>BICD2, DGKI,</i> <i>DOCK7,</i> <i>ECT2,</i> <i>EXOC2,</i> <i>FGD6,</i> <i>FMNL2,</i> <i>GOLGA8B,</i> <i>IQGAP3,</i> <i>NCKAPI,</i> <i>PICALM,</i> <i>RANBP17,</i> <i>RIMS1,</i> <i>TRIOBP</i>
GO:0042733	embryonic digit	GO_Biolo gicalProce ss-EBI-	0.00	0.03	0.01	0.01	[4, 5, 6, 7, 8]	Group23	10.00	6.00	<i>BMPRIA,</i> <i>GLI2, LMBR1,</i> <i>NOTCH1,</i>

	morphogenesis	UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									<i>TBC1D32,</i> <i>TULP3</i>
GO:0060831	smoothened signaling pathway involved in dorsal/ventral neural tube patterning	GO_BiologicalProcess-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.03	0.01	0.01	[5, 6, 7, 8, 9, 10]	Group23	23.08	3.00	<i>GLI2,</i> <i>TBC1D32,</i> <i>TULP3</i>
GO:1903251	multiciliated epithelial cell differentiation	GO_BiologicalProcess-EBI- UniProt- GOA- ACAP- ARAP_13	0.00	0.03	0.01	0.01	[5, 6]	Group24	33.33	3.00	<i>CEP152,</i> <i>DEUP1,</i> <i>MCIDAS</i>

		.05.2021_00h00									
GO:0098534	centriole assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.04	0.01	0.01	[4, 5, 6, 8]	Group24	10.64	5.00	<i>CEP120, CEP152, CEP295, DEUPI, MCIDAS</i>
GO:0043276	anoikis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.05	0.01	0.01	[5]	Group25	11.43	4.00	<i>BRMS1, NOTCH1, PTK2, SIK1</i>
GO:2000209	regulation of anoikis	GO_BiologicalProcess-EBI-	0.00	0.03	0.01	0.01	[6, 7]	Group25	15.38	4.00	<i>BRMS1, NOTCH1, PTK2, SIK1</i>

		UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									
GO:0030276	clathrin binding	GO_Mole cularFunct ion-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.00	0.00	[3]	Group26	8.33	6.00	<i>APIG1, EPN3, LDLR, PICALM, SYT15, SYT17</i>
GO:0005905	clathrin- coated pit	GO_Cellu larCompo nent-EBI- UniProt- GOA- ACAP- ARAP_13	0.00	0.03	0.00	0.00	[3, 4, 5]	Group26	9.21	7.00	<i>AAK1, CUBN, EPN3, FCHO1, ITSN1, LDLR, PICALM</i>

		.05.2021_00h00									
GO:0072583	clathrin-dependent endocytosis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.00	0.00	[5, 7]	Group26	9.43	5.00	<i>AAK1, FCHO1, FNBP1L, ITSN1, PICALM</i>
GO:0016668	oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.04	0.00	0.01	[4]	Group27	20.00	3.00	<i>NXN, SELENOT, TXNRD3</i>
GO:0047134	protein-disulfide reductase	GO_MolecularFunction-EBI-	0.00	0.03	0.00	0.01	[4, 5, 6]	Group27	27.27	3.00	<i>NXN, SELENOT, TXNRD3</i>

	(NAD(P)) activity	UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									
GO:0004791	thioredoxin- disulfide reductase activity	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.03	0.00	0.01	[5, 8]	Group27	50.00	3.00	<i>NXN, SELENOT, TXNRD3</i>
GO:0051647	nucleus localization	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13	0.00	0.04	0.00	0.01	[4]	Group28	14.29	4.00	<i>CEP120, DOCK7, HOOK3, SYNE2</i>

		.05.2021_00h00									
GO:0007097	nuclear migration	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.01	[4, 5]	Group28	18.18	4.00	<i>CEP120, DOCK7, HOOK3, SYNE2</i>
GO:0022027	interkinetic nuclear migration	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.01	[5, 6, 7, 8, 9, 10]	Group28	50.00	3.00	<i>CEP120, DOCK7, HOOK3</i>
GO:0022604	regulation of cell	GO_BiologicalProcess-EBI-	0.00	0.03	0.00	0.01	[4, 5]	Group29	5.20	17.00	<i>ACTN4, DOCK5, EPB41L3,</i>

	morphogenesis	UniProt-GOA-ACAP-ARAP_13.05.2021_00h00									<i>FERMT2, FGD6, FMNL2, GRIP1, ITGA7, LARP4, POSTN, PTK2, PTPRD, RIMS1, SEMA3E, SYT17, TPM1, TRIOBP</i>
GO:0010769	regulation of cell morphogenesis involved in differentiation	GO_BiologicalProcess-EBI- UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.05	0.00	0.01	[5, 6]	Group29	7.00	7.00	<i>ACTN4, DOCK5, FERMT2, POSTN, PTK2, PTPRD, TRIOBP</i>

GO:1900024	regulation of substrate adhesion-dependent cell spreading	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.01	[5, 6, 7]	Group29	9.68	6.00	<i>ACTN4, DOCK5, FERMT2, POSTN, PTK2, TRIOBP</i>
GO:0014812	muscle cell migration	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.01	0.01	[4, 5]	Group30	7.61	7.00	<i>ACE, BMPR1A, DOCK5, DOCK7, POSTN, SLC6A5, TPM1</i>
GO:0014909	smooth muscle cell migration	GO_BiologicalProcess-EBI-UniProt-GOA-	0.01	0.05	0.01	0.01	[5, 6]	Group30	8.11	6.00	<i>ACE, BMPR1A, DOCK5, DOCK7,</i>

		ACAP-ARAP_13 .05.2021_ 00h00									<i>POSTN, TPM1</i>
GO:0014910	regulation of smooth muscle cell migration	GO_BiologicalProcesses-EBI- UniProt-GOA- ACAP-ARAP_13 .05.2021_ 00h00	0.00	0.04	0.01	0.01	[5, 6, 7]	Group30	9.09	6.00	<i>ACE, BMPRI1A, DOCK5, DOCK7, POSTN, TPM1</i>
GO:0099587	inorganic ion import across plasma membrane	GO_BiologicalProcesses-EBI- UniProt-GOA- ACAP-ARAP_13 .05.2021_ 00h00	0.01	0.05	0.02	0.02	[4, 5, 6, 7]	Group31	6.93	7.00	<i>ATP4B, KCNH2, KCNJ12, KCNJ18, SLC12A7, SLC12A8, SLC31A1</i>

GO:0098659	inorganic cation import across plasma membrane	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.05	0.02	0.02	[5, 6, 7, 8]	Group31	6.93	7.00	<i>ATP4B, KCNH2, KCNJ12, KCNJ18, SLC12A7, SLC12A8, SLC31A1</i>
GO:1990573	potassium ion import across plasma membrane	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.02	0.02	[6, 7, 8, 9]	Group31	12.50	6.00	<i>ATP4B, KCNH2, KCNJ12, KCNJ18, SLC12A7, SLC12A8</i>
GO:0055075	potassium ion homeostasis	GO_BiologicalProcesses-EBI-UniProt-GOA-	0.01	0.04	0.02	0.02	[8]	Group31	12.50	4.00	<i>ATP4B, KCNH2, SLC12A7, SLC12A8</i>

		ACAP-ARAP_13 .05.2021_00h00									
GO:0010927	cellular component assembly involved in morphogenesis	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[3, 4, 5]	Group32	8.33	9.00	<i>ACTN2, EPB41L3, MEF2A, PIKFYVE, PRKARIA, TENM4, TPM1, UGT8, ZPBP</i>
GO:0007272	myelination of neurons	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.00	0.00	[2, 5, 6]	Group32	6.29	9.00	<i>ADGRG6, B4GALT5, CTSC, EPB41L3, GALC, HGF, PIKFYVE, TENM4, UGT8</i>

GO:0008366	axon ensheathme nt	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.00	0.00	[3, 6, 7]	Group32	6.29	9.00	<i>ADGRG6, B4GALT5, CTSC, EPB41L3, GALC, HGF, PIKFYVE, TENM4, UGT8</i>
GO:0042552	myelination	GO_Biolo gicalProce ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.04	0.00	0.00	[4, 7, 8]	Group32	6.38	9.00	<i>ADGRG6, B4GALT5, CTSC, EPB41L3, GALC, HGF, PIKFYVE, TENM4, UGT8</i>
GO:0032288	myelin assembly	GO_Biolo gicalProce ss-EBI- UniProt- GOA-	0.00	0.03	0.00	0.00	[4, 5, 6, 8, 9]	Group32	18.18	4.00	<i>EPB41L3, PIKFYVE, TENM4, UGT8</i>

		ACAP-ARAP_13 .05.2021_00h00									
GO:0034452	dynactin binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[4]	Group33	25.00	3.00	<i>BICD1, BICD2, HOOK3</i>
GO:0006890	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[4, 6]	Group33	8.42	8.00	<i>BICD2, COG3, COPB1, KIF11, RAB6A, SCFD1, SEC22B, TMED10P1</i>

GO:0006891	intra-Golgi vesicle-mediated transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.05	0.00	0.00	[4, 6]	Group33	11.11	4.00	<i>COG3, COPB1, GOLGA8B, RAB6A</i>
GO:0034067	protein localization to Golgi apparatus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.00	0.00	[6]	Group33	13.33	4.00	<i>BICD2, RAB6A, TMED10P1, VPS13C</i>
GO:0072385	minus-end-directed organelle transport	GO_BiologicalProcess-EBI-UniProt-GOA-	0.00	0.04	0.00	0.00	[5, 6, 7, 8]	Group33	60.00	3.00	<i>BICD1, BICD2, RAB6A</i>

	along microtubule	ACAP-ARAP_13 .05.2021_00h00									
GO:0072393	microtubule anchoring at microtubule organizing center	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.04	0.00	0.00	[5, 8]	Group33	21.43	3.00	<i>BICD1, BICD2, HOOK3</i>
GO:0005229	intracellular calcium activated chloride channel activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.05	0.01	0.01	[8, 9, 10, 11, 12]	Group34	15.79	3.00	<i>ANO2, ANO4, ANO7</i>

GO:0098661	inorganic anion transmembrane transport	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.01	0.01	[5, 7]	Group34	8.70	8.00	<i>ANO2, ANO4, ANO7, CFTR, GABRR2, SLC12A7, SLC12A8, SLC4A8</i>
GO:0015103	inorganic anion transmembrane transporter activity	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.01	0.01	[5, 6, 7, 8]	Group34	5.88	10.00	<i>ANO2, ANO4, ANO7, CCT8L2, CFTR, FXYD3, GABRR2, SLC12A7, SLC12A8, SLC4A8</i>
GO:0006821	chloride transport	GO_BiologicalProcesses-EBI-UniProt-GOA-	0.00	0.03	0.01	0.01	[7]	Group34	8.11	9.00	<i>ANO2, ANO4, ANO7, CFTR, FXYD3, GABRR2, SLC12A7,</i>

		ACAP-ARAP_13 .05.2021_00h00									<i>SLC12A8, SLC4A8</i>
GO:1902476	chloride transmembrane transport	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.01	0.01	[6, 8]	Group34	12.12	8.00	<i>ANO2, ANO4, ANO7, CFTR, GABRR2, SLC12A7, SLC12A8, SLC4A8</i>
GO:0061778	intracellular chloride channel activity	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.05	0.01	0.01	[8, 9, 10, 11]	Group34	15.79	3.00	<i>ANO2, ANO4, ANO7</i>

GO:0099084	postsynaptic specialization organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.05	0.01	0.01	[5, 7]	Group35	11.11	4.00	<i>IL1RAP, MPP2, PTPRD, PTPRS</i>
GO:0097106	postsynaptic density organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.01	0.01	[6, 8]	Group35	11.76	4.00	<i>IL1RAP, MPP2, PTPRD, PTPRS</i>
GO:0099150	regulation of postsynaptic specialization assembly	GO_BiologicalProcess-EBI-UniProt-GOA-	0.00	0.04	0.01	0.01	[5, 6, 7, 8, 9]	Group35	21.43	3.00	<i>IL1RAP, PTPRD, PTPRS</i>

		ACAP-ARAP_13.05.2021_00h00									
GO:1904889	regulation of excitatory synapse assembly	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.01	0.01	[6, 7, 8]	Group35	18.75	3.00	<i>ILIRAP, PTPRD, PTPRS</i>
GO:1905874	regulation of postsynaptic density organization	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.01	0.01	[5, 6, 7, 8, 9]	Group35	17.65	3.00	<i>ILIRAP, PTPRD, PTPRS</i>

GO:0097107	postsynaptic density assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.01	0.01	[7, 8, 9]	Group35	16.67	3.00	<i>IL1RAP, PTPRD, PTPRS</i>
GO:0099151	regulation of postsynaptic density assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.01	0.01	[6, 7, 8, 9, 10]	Group35	23.08	3.00	<i>IL1RAP, PTPRD, PTPRS</i>
GO:0015144	carbohydrate transmembrane	GO_BiologicalProcess-EBI-UniProt-GOA-	0.00	0.02	0.00	0.00	[4, 6, 7]	Group36	15.38	6.00	<i>AQP7, SLC2A14, SLC2A3, SLC2A9,</i>

	transporter activity	ACAP-ARAP_13.05.2021_00h00									<i>SLC45A2, SLC5A11</i>
GO:0051119	sugar transmembrane transporter activity	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.00	[5, 7, 8]	Group36	16.00	4.00	<i>SLC2A14, SLC2A3, SLC2A9, SLC5A11</i>
GO:0015145	monosaccharide transmembrane transporter activity	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.00	[5, 6, 7, 8, 9]	Group36	16.67	4.00	<i>SLC2A14, SLC2A3, SLC2A9, SLC5A11</i>

GO:0015294	solute:cation symporter activity	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.00	[6, 7, 8, 9]	Group36	8.16	8.00	<i>SLC12A7, SLC12A8, SLC2A9, SLC38A2, SLC45A2, SLC4A8, SLC5A11, SLC6A5</i>
GO:0005402	carbohydrate:cation symporter activity	GO_BiologicalProcesses-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.00	0.00	[5, 7, 8, 9, 10]	Group36	18.75	3.00	<i>SLC2A9, SLC45A2, SLC5A11</i>
GO:0015149	hexose transmembrane transporter activity	GO_BiologicalProcesses-EBI-UniProt-GOA-	0.00	0.03	0.00	0.00	[6, 7, 8, 9, 10]	Group36	18.18	4.00	<i>SLC2A14, SLC2A3, SLC2A9, SLC5A11</i>

		ACAP-ARAP_13 .05.2021_00h00									
GO:0005355	glucose transmembrane transporter activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[7, 8, 9, 10, 11]	Group36	18.18	4.00	<i>SLC2A14, SLC2A3, SLC2A9, SLC5A11</i>
GO:0000407	phagophore assembly site	GO_CellularComponent-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.00	0.00	[2, 3, 4]	Group37	12.12	4.00	<i>ATG14, PIK3C3, WIPI1, WIPI2</i>

GO:0006914	autophagy	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.00	0.00	[3, 4]	Group37	4.24	25.00	<i>ATG14, CFTR, DYNC1LI2, EIF2AK4, FBXO7, FEZ2, FNBP1L, HGF, KLHL3, MAP1LC3C, MAPK3, MTMR9, PIK3C3, PIKFYVE, SCFD1, SEC22B, SMG1, TEX264, TRIM5, TRIM6, TRIM6-TRIM34, VIPAS39,</i>
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											<i>VPS13C, WIPI1, WIPI2</i>
GO:0034045	phagophore assembly site membrane	GO_CellularComponent-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.04	0.00	0.00	[3, 4, 5]	Group37	20.00	3.00	<i>ATG14, WIPI1, WIPI2</i>
GO:0042594	response to starvation	GO_BiologicalProcess-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.01	0.05	0.00	0.00	[3, 5]	Group37	5.22	13.00	<i>ACAT1, ASNS, ATG14, EIF2A, EIF2AK4, MAP1LC3C, MAPK3, MIOS, PIK3C3, SIK1, SLC38A2, WIPI1, WIPI2</i>
GO:0016236	macroautophagy	GO_BiologicalProcess	0.00	0.03	0.00	0.00	[4, 5]	Group37	5.16	18.00	<i>ATG14, CFTR,</i>

		ss-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00									<i>DYNC1L2, FEZ2, KLHL3, MAP1LC3C, MAPK3, MTMR9, PIK3C3, PIKFYVE, SCFD1, SEC22B, SMG1, TEX264, VIPAS39, VPS13C, WIPI1, WIPI2</i>
GO:0005776	autophagosome	GO_CellularComponent-EBI- UniProt- GOA- ACAP- ARAP_13 .05.2021_ 00h00	0.00	0.03	0.00	0.00	[4, 5, 6]	Group37	8.16	8.00	<i>ATG14, MAP1LC3C, MCOLN3, PEG3, PIK3C3, TEX264, WIPI1, WIPI2</i>

GO:0007033	vacuole organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.00	0.00	[5]	Group37	5.85	11.00	<i>ATG14, FEZ2, HOOK3, MAP1LC3C, PIK3C3, PIKFYVE, RAB20, SCFD1, SEC22B, WIPI1, WIPI2</i>
GO:0009267	cellular response to starvation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.01	0.04	0.00	0.00	[4, 5, 6]	Group37	5.64	11.00	<i>ASNS, ATG14, EIF2AK4, MAP1LC3C, MAPK3, MIOS, PIK3C3, SIK1, SLC38A2, WIPI1, WIPI2</i>
GO:0061912	selective autophagy	GO_BiologicalProcess-EBI-UniProt-GOA-	0.00	0.02	0.00	0.00	[5, 6]	Group37	9.89	9.00	<i>ATG14, CFTR, DYNC1LI2, KLHL3, MAP1LC3C,</i>

		ACAP-ARAP_13 .05.2021_00h00									<i>MAPK3, TEX264, VPS13C, WIPI2</i>
GO:1905037	autophagosome organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[5, 6]	Group37	8.57	9.00	<i>ATG14, FEZ2, MAP1LC3C, PIK3C3, PIKFYVE, SCFD1, SEC22B, WIPI1, WIPI2</i>
GO:0000421	autophagosome membrane	GO_CellularComponent-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[5, 6, 7]	Group37	13.16	5.00	<i>ATG14, MAP1LC3C, MCOLN3, TEX264, WIPI1</i>

GO:0032266	phosphatidylinositol-3-phosphate binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.00	[6]	Group37	11.63	5.00	<i>SNX13, WIPI1, WIPI2, ZFYVE19, ZFYVE26</i>
GO:0000045	autophagosome assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13.05.2021_00h00	0.00	0.03	0.00	0.00	[6, 7]	Group37	9.00	9.00	<i>ATG14, FEZ2, MAP1LC3C, PIK3C3, PIKFYVE, SCFD1, SEC22B, WIPI1, WIPI2</i>
GO:0016242	negative regulation of macroautophagy	GO_BiologicalProcess-EBI-UniProt-GOA-	0.01	0.05	0.00	0.00	[5, 6, 7, 8]	Group37	11.43	4.00	<i>FEZ2, SCFD1, SEC22B, SMG1</i>

		ACAP-ARAP_13 .05.2021_00h00									
GO:0034497	protein localization to phagophore assembly site	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.00	0.03	0.00	0.00	[5, 7, 8]	Group37	30.00	3.00	<i>PIK3C3, WIPI1, WIPI2</i>
GO:1902902	negative regulation of autophagosome assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_13 .05.2021_00h00	0.01	0.04	0.00	0.00	[6, 7, 8, 9]	Group37	18.75	3.00	<i>FEZ2, SCFD1, SEC22B</i>

