

Supplemental Materials

Molecular Biology of the Cell

Hirata et al.

Table S1: Genome-wide screening in human haploid cell line

| Gene name | Inactivating insertion(s) in Sort 2 cells | Other insertion(s) in Sort 2 cells | Inactivating insertion(s) in control cells | Other insertion(s) in control cells | P-val (Fisher's exact) | FDR P-val(Fisher's exact) |
|--------------|---|------------------------------------|--|-------------------------------------|------------------------|---------------------------|
| HCG25 | 18 | 13997 | 3 | 43213 | 6.00E-09 | 0.000140462 |
| COG8 | 11 | 14004 | 0 | 43216 | 1.89E-07 | 0.001656277 |
| VPS52 | 19 | 13996 | 7 | 43209 | 2.53E-07 | 0.001656277 |
| VPS54 | 16 | 13999 | 4 | 43212 | 2.83E-07 | 0.001656277 |
| PGAP1 | 8 | 14007 | 1 | 43215 | 9.09E-05 | 0.425528998 |
| ATF7IP | 13 | 14002 | 7 | 43209 | 0.000146103 | 0.569751177 |
| JTB | 9 | 14006 | 3 | 43213 | 0.000330441 | 1 |
| FLNC | 5 | 14010 | 0 | 43216 | 0.000880187 | 1 |
| GSTO2 | 5 | 14010 | 0 | 43216 | 0.000880187 | 1 |
| FSTL4 | 8 | 14007 | 3 | 43213 | 0.001023554 | 1 |
| KIAA0182 | 7 | 14008 | 2 | 43214 | 0.001174045 | 1 |
| GPANK1 | 12 | 14003 | 10 | 43206 | 0.002373619 | 1 |
| LIPT1 | 4 | 14011 | 0 | 43216 | 0.003595064 | 1 |
| WDR12 | 4 | 14011 | 0 | 43216 | 0.003595064 | 1 |
| C11orf2 | 4 | 14011 | 0 | 43216 | 0.003595064 | 1 |
| CS | 4 | 14011 | 0 | 43216 | 0.003595064 | 1 |
| PGAP2 | 6 | 14009 | 2 | 43214 | 0.003772688 | 1 |
| GET4 | 5 | 14010 | 1 | 43215 | 0.004203689 | 1 |
| SETD1B | 5 | 14010 | 1 | 43215 | 0.004203689 | 1 |
| C2orf28 | 8 | 14007 | 5 | 43211 | 0.004922297 | 1 |
| MPPE1 | 7 | 14008 | 4 | 43212 | 0.006686019 | 1 |
| LOC100128675 | 10 | 14005 | 9 | 43207 | 0.007621102 | 1 |
| NRD1 | 6 | 14009 | 3 | 43213 | 0.008969972 | 1 |
| SORBS3 | 6 | 14009 | 3 | 43213 | 0.008969972 | 1 |
| ASTN2 | 6 | 14009 | 3 | 43213 | 0.008969972 | 1 |
| TRIP11 | 8 | 14007 | 6 | 43210 | 0.009033442 | 1 |
| ZSWIM6 | 5 | 14010 | 2 | 43214 | 0.011733186 | 1 |
| ADAM9 | 5 | 14010 | 2 | 43214 | 0.011733186 | 1 |
| C8orf34 | 5 | 14010 | 2 | 43214 | 0.011733186 | 1 |
| ARL3 | 5 | 14010 | 2 | 43214 | 0.011733186 | 1 |
| CDK17 | 5 | 14010 | 2 | 43214 | 0.011733186 | 1 |
| CLIC4 | 7 | 14008 | 5 | 43211 | 0.012672754 | 1 |
| C5orf44 | 7 | 14008 | 5 | 43211 | 0.012672754 | 1 |
| LRIG2 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| ATP1B1 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| GLB1L | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |

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|-----------|----|-------|----|-------|-------------|---|
| THBS4 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| PPARGC1B | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| PREP | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| C7orf55 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| NKAIN3 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| FEN1 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| KIRREL3 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| C16orf72 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| VPS53 | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| PIP4K2B | 4 | 14011 | 1 | 43215 | 0.014454575 | 1 |
| MTMR9LP | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| MTMR11 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| XPR1 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| KCTD3 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| ATG7 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| ASTE1 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| AFP | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| GPBP1 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| MRPS27 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| SKIV2L | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| MIR4283-1 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| ERLIN2 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| TMEM9B | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| TMEM109 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| CPT1A | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| RAP1B | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| BANP | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| LSMD1 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| ARHGEF18 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| GNRH2 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| MORC2 | 3 | 14012 | 0 | 43216 | 0.01468301 | 1 |
| DOCK2 | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| SLC29A2 | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| PPIB | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| KIAA0430 | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| SERPINF1 | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| C17orf48 | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| ACCN1 | 6 | 14009 | 4 | 43212 | 0.017800983 | 1 |
| LDB2 | 10 | 14005 | 11 | 43205 | 0.017859437 | 1 |
| BOLA2 | 11 | 14004 | 13 | 43203 | 0.018314878 | 1 |
| ALDH2 | 7 | 14008 | 6 | 43210 | 0.021714953 | 1 |

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|------------|----|-------|----|-------|-------------|---|
| PDE4A | 7 | 14008 | 6 | 43210 | 0.021714953 | 1 |
| MTA3 | 5 | 14010 | 3 | 43213 | 0.025000683 | 1 |
| LEPREL4 | 5 | 14010 | 3 | 43213 | 0.025000683 | 1 |
| SLC35E4 | 5 | 14010 | 3 | 43213 | 0.025000683 | 1 |
| HDAC4 | 12 | 14003 | 16 | 43200 | 0.025171751 | 1 |
| SMARCA2 | 9 | 14006 | 10 | 43206 | 0.025244373 | 1 |
| SETDB1 | 6 | 14009 | 5 | 43211 | 0.03113894 | 1 |
| MEIG1 | 6 | 14009 | 5 | 43211 | 0.03113894 | 1 |
| TSPEAR | 13 | 14002 | 19 | 43197 | 0.032220786 | 1 |
| BOLA2B | 12 | 14003 | 17 | 43199 | 0.033592516 | 1 |
| NTRK2 | 7 | 14008 | 7 | 43209 | 0.034396464 | 1 |
| ICMT | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| NR5A2 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| HOXD-AS2 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| BMPR2 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| NUP210 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| PDZRN3 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| ANAPC13 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| PRDM10 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| PTPN6 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| CNOT2 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| GGNBP2 | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| KAT2A | 4 | 14011 | 2 | 43214 | 0.034956345 | 1 |
| CTDSPL2 | 8 | 14007 | 9 | 43207 | 0.035839671 | 1 |
| GNG7 | 12 | 14003 | 18 | 43198 | 0.043838165 | 1 |
| RFWD2 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| RUVBL1 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| PLAC8 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| SERINC5 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| DENND2A | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| LINC00251 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| WDR74 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| ETV4 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| ZNF236 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| ZBTB32 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| PATZ1 | 5 | 14010 | 4 | 43212 | 0.045039072 | 1 |
| NT5C2 | 11 | 14004 | 16 | 43200 | 0.046055532 | 1 |
| MRPL20 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| PEF1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| DENND2C | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| HIST2H2AA3 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |

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|--------------|----|-------|----|-------|-------------|---|
| IL6R | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| OBSCN | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| TSSC1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| LOC100505876 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SPRED2 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SATB2 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| ULK4 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SEC22C | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| GATA2 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| GMPS | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| IL7R | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| C5orf39 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| BTBD9 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| PPP2R5D | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| GTF3C6 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| PTPN12 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SLC25A13 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| TFR2 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| LOC202781 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| TSPAN14 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| GBF1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| ZFP91-CNTF | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SUV420H1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| LAMTOR1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| FOXM1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| ZC3H10 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| VSIG10 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| ZBTB1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| LYSMD2 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| MYZAP | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| KIF7 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| CIAPIN1 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| MLKL | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SMG6 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| ME2 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| SLC13A3 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| HUNK | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| ZC3H7B | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| BCAP31 | 3 | 14012 | 1 | 43215 | 0.047946848 | 1 |
| EXOC4 | 14 | 14001 | 23 | 43193 | 0.049350092 | 1 |
| KIAA1797 | 6 | 14009 | 6 | 43210 | 0.049605127 | 1 |

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|--------|---|-------|---|-------|-------------|---|
| TAOK1 | 6 | 14009 | 6 | 43210 | 0.049605127 | 1 |
| HSF2BP | 6 | 14009 | 6 | 43210 | 0.049605127 | 1 |

Genes showing P-value > 0.05 were eliminated from this table.

Blue; Genes encoding the subunit of GARP complex

Pink; Genes encoding GPI remodeling enzyme

Table S2: List of KO cells

| gene | cell | DNA sequence | amino acid sequence |
|-----------------|--|---|---|
| VPS51 | wild-type | GGCCCCGAGGGGAGGCTCCGGAGCGTCGCGCGGAAGGCGCACGGGATG | MAAAAAAGPSFGSGPGDSPEGPEGEAPERERRRKAHGM |
| | V51 KO | GGCCCCGAGGGGAGGCTCCGGAGCGT GCGGCGGAAGGCGCACGGGATG | MAAAAAAGPSFGSGPGDSPEGPEGEAPER AAEGARDAEALLRPLGRGGGGT PRGARPPGPD* |
| | | GGCCCCGAGGGGAGGCTCCGGAG-----GAAGGCGCACGGGATG | MAAAAAAGPSFGSGPGDSPEGPEGEAPER EGARDAEALLRPLGRGGGGT PRGARPPGPD* |
| VPS52 | wild-type | GCGGCTGCGGCCCGGAACTGGTGTTCGCGGCTGGGACCTCAGA | MAAAATMAAAARELVLRAGTS |
| | V52 KO | GCGGCTGCGGCCCGGAACTGGTGGTATTGGCGGCAA... | MAAAATMAAAARELGGIGGNQQQIRDANLCCGGGLQRGEQGV* |
| | | GCGGCTGCGGCCCGGAACTGGTGTATTGACGTCAATGGGTGGGGTTCGT TGGGC... | MAAAATMAAAARELVY* |
| VPS53 | wild-type | AGCCGTGCTGCAGCTCACGCCGAGGTGCAGCTGGCCATCGAGCAG | MMEEEEELEFVEELEAVLQLTPEVQLAIEQ |
| | V53 KO | AGCCGTGCTGCAGCTCACGCCGAGGTG-AGCTGGCCATCGAGCAG | MMEEEEELEFVEELEAVLQLTPEVSWPSSRCFQARTL* |
| | | AGCCGTGCTGCAGCTCACGCCGAGGTGCGTGTATGCTCGT... | MMEEEEELEFVEELEAVLQLTPEVRDARQGGGTRQD...PVTIVLSPTR* |
| | | AGCCGTGCTGCAGCTCACGCCGAGGTGTTTTGCTGGC... CCAGCAGGCCAGCTGGCCATCGAGCAG | MMEEEEELEFVEELEAVLQLTPEVLLLAFCSHVRAFFP* |
| VPS54 | wild-type | ATGGCTTCAAGCCACAGTTCTTCACCAGTGCCTCAAGGAAGCAGCA... ATTCGACCTGTGCCATCACTGCCAGATGTGTGTCCAAGGAACCCACAG | MASSHSSSPVPOGSSSDVFFKIEVDPSKHIRPVPSLPDVCPEPT |
| | V54 KO | ATGGCTTCAAGCCACAGTGCAGATGTGTGTCCAAGGAACCCACAG | MASSHSCQMCVPRNPQVIHIVYMLPHL* |
| | | ATGGCTTCAAGCCACAGCAGCAGATTGCGCTGGATGACCAGAAAGAGCGA GGAAACCACTGCCAGATGTGTGTCCAAGGAACCCACAG | MASSHSSRFAWMTRKSEETTARCVSQGTHR* |
| TMEM87A | wild-type | GCTAAGGAGAATGGAACAAACCTTACCTTTATTGGAGACAAAACC | MAAAALQVL...AKENGTNLTFIGDKTAMHEPL |
| | TM87A, B-DKO #1 | GCTAAGGAGAATGGAACAAACCTTACCTT-ATTGGAGACAAAACC | MAAAALQVL...AKENGTNLT LETKPQCMNHCKLGMHHTFLLYILAFHPQRNHQKKIH* |
| | TM87A, B-DKO #2 | GCTAAGGAGAATGGAACAAACCTTACCTT-ATTGGAGACAAAACC | MAAAALQVL...AKENGTNLT LETKPQCMNHCKLGMHHTFLLYILAFHPQRNHQKKIH* |
| TMEM87B | wild-type | GGCTCCTGCCACGCCCGCCGCTGCTTTCCCGCCCGGGCCCGCTGC TGCGCGTCGCCCTC | MVAACRSV...LCWTPAAVRAVPELGLWL |
| | TM87A, B-DKO #1 | GGCTCCTGCCACGCCCGCCGCTGCTTTCCCGGTGCTCCAGGTAATTA AACATTAATACCCCAACCAACGCCCGGGCCCGCTGCTGCGCGTCGC CCTC | MVAACRS...PRRRRCFP GAPGN* |
| | | GGCTCCTGCCACGCCCGCCGCTGCTTTCCCGCCCGGGCCCGCTGC TGCGCGTCGCCCTC | MVAACRS...PRRRRCFP RPGPAAARRPLPPVLDPGGCARGP* |
| | | GGCTCCTGCCACGCCCGCCGCTGCTTTCC----- -GCGCGTCGCCCTC | MVAACRS...PRRRRCFP ARRPLPPVLDPGGCARGP* |
| | wild-type | CTGTGCTGGACCCCGCGGCTGTGCGCGGTCCTGAGCTCGGGCTC | MVAACRSV...LCWTPAAVRAVPELGLWL |
| TM87A, B-DKO #2 | CTGTGCTGGACCCCGCGGCTGTGCGCGGTCCTGAGCTCGGGCTC CTGTGCTGGACCCCGCGGCTGTGCA CGCGCGGTCCTGAGCTCGGGCTC | MVAACRSV...LCWTPAAV PRGP* MVAACRSV...LCWTPAAV HARSLSSGSG* | |

* : stop

Table S3: The screening of suppressor gene in VPS54KO cells

| Feature ID | Test statistic (Kal's Z-test) | P-val (Kal's Z-test) | FDR P-val (Kal's Z-test) | Mapped reads in control cells | Mapped reads in the sorted cells |
|--------------|-------------------------------|----------------------|--------------------------|-------------------------------|----------------------------------|
| HIRA | 1933.132898 | 0 | 0 | 1412 | 1414790 |
| TMEM87A | 94.36592116 | 0 | 0 | 296 | 5082 |
| RILPL1 | 77.4144761 | 0 | 0 | 387 | 3742 |
| MAST3 | 75.14206296 | 0 | 0 | 566 | 3844 |
| WDR45 | 70.57010588 | 0 | 0 | 541 | 3454 |
| RAE1 | 69.17085541 | 0 | 0 | 19 | 2469 |
| PCYT2 | 66.03292299 | 0 | 0 | 582 | 3184 |
| FLII | 65.48859345 | 0 | 0 | 689 | 3297 |
| SPP1 | 64.58974783 | 0 | 0 | 3822 | 6651 |
| SLC2A6 | 64.40361367 | 0 | 0 | 69 | 2242 |
| GSN | 62.79882614 | 0 | 0 | 2739 | 5438 |
| CELF5 | 61.12261931 | 0 | 0 | 27 | 1952 |
| LOC100134015 | 59.37531078 | 0 | 0 | 27 | 1845 |
| SLC45A4 | 58.48234453 | 0 | 0 | 0 | 1738 |
| RYR2 | 57.99351265 | 0 | 0 | 79 | 1861 |
| PTTG1IP | 54.64473336 | 0 | 0 | 590 | 2446 |
| PIN1 | 52.49922621 | 0 | 0 | 652 | 2398 |
| CSNK1A1 | 52.42632839 | 0 | 0 | 359 | 1996 |
| NOMO3 | 52.40256127 | 0 | 0 | 394 | 2045 |
| ADAM9 | 51.86368367 | 0 | 0 | 50 | 1464 |
| UPF1 | 50.85851994 | 0 | 0 | 36 | 1385 |
| TBC1D10A | 50.18801777 | 0 | 0 | 280 | 1757 |
| C11orf73 | 49.73345027 | 0 | 0 | 0 | 1257 |
| IGSF5 | 48.91545798 | 0 | 0 | 0 | 1216 |
| TSPEAR | 48.77443097 | 0 | 0 | 0 | 1209 |
| LPCAT4 | 48.722533 | 0 | 0 | 1181 | 2788 |
| SLC27A4 | 48.00105338 | 0 | 0 | 1463 | 3039 |
| FJX1 | 46.70529024 | 0 | 0 | 96 | 1287 |
| DDX56 | 46.58348531 | 0 | 0 | 394 | 1731 |
| NFKBIL1 | 46.20793978 | 0 | 0 | 52 | 1185 |
| MED17 | 45.90566381 | 0 | 0 | 7 | 1085 |
| DROSHA | 45.53324578 | 0 | 0 | 173 | 1358 |
| ARPC1B | 44.75415159 | 0 | 0 | 202 | 1366 |
| C10orf103 | 44.33719532 | 0 | 0 | 93 | 1171 |
| SMARCC2 | 43.66864898 | 0 | 0 | 1131 | 2433 |
| COX6A1 | 43.34813994 | 0 | 0 | 209 | 1311 |
| NCEH1 | 43.09161658 | 0 | 0 | 277 | 1398 |
| SNX6 | 41.8582484 | 0 | 0 | 96 | 1066 |

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|--------------|-------------|---|---|------|------|
| YKT6 | 41.74728209 | 0 | 0 | 80 | 1034 |
| GEMIN6 | 41.20698477 | 0 | 0 | 0 | 863 |
| ABCC12 | 40.75855189 | 0 | 0 | 150 | 1106 |
| SLC2A12 | 39.53794623 | 0 | 0 | 195 | 1122 |
| TRIM44 | 38.83210063 | 0 | 0 | 45 | 852 |
| KHDRBS1 | 38.63486095 | 0 | 0 | 133 | 991 |
| POLD2 | 38.56621994 | 0 | 0 | 684 | 1686 |
| UBOX5 | 38.47102777 | 0 | 0 | 12 | 776 |
| TMEM132A | 38.22799265 | 0 | 0 | 2122 | 3035 |
| C7orf43 | 37.9698684 | 0 | 0 | 472 | 1416 |
| GLDC | 37.88978894 | 0 | 0 | 348 | 1260 |
| FAU | 37.71889437 | 0 | 0 | 9 | 741 |
| LRSAM1 | 37.54132581 | 0 | 0 | 409 | 1321 |
| ANKRD12 | 37.12187855 | 0 | 0 | 102 | 882 |
| NLE1 | 36.90133546 | 0 | 0 | 22 | 735 |
| UBE2I | 36.45873236 | 0 | 0 | 413 | 1279 |
| MRFAP1L1 | 36.13638336 | 0 | 0 | 219 | 1017 |
| ZNF282 | 35.9613341 | 0 | 0 | 54 | 758 |
| DLG3 | 35.92557454 | 0 | 0 | 292 | 1106 |
| DDX19A | 35.68071482 | 0 | 0 | 21 | 688 |
| NUP160 | 35.63728296 | 0 | 0 | 218 | 996 |
| ALG12 | 35.59806171 | 0 | 0 | 21 | 685 |
| ATAD3B | 35.52781142 | 0 | 0 | 272 | 1064 |
| CLCN6 | 35.34624848 | 0 | 0 | 0 | 635 |
| SART3 | 34.76815376 | 0 | 0 | 286 | 1052 |
| CTNNB1 | 33.57217483 | 0 | 0 | 1346 | 2086 |
| PEAK1 | 33.36994838 | 0 | 0 | 2 | 570 |
| WDR45L | 33.08259217 | 0 | 0 | 360 | 1077 |
| NR3C1 | 32.73425575 | 0 | 0 | 243 | 919 |
| MFHAS1 | 32.67387671 | 0 | 0 | 197 | 856 |
| SLC39A13 | 32.67290193 | 0 | 0 | 69 | 667 |
| GUSBP9 | 32.64315644 | 0 | 0 | 23 | 586 |
| LOC100130581 | 32.59452942 | 0 | 0 | 1 | 542 |
| HLA-B | 32.36861113 | 0 | 0 | 1825 | 2433 |
| HMOX2 | 32.32683817 | 0 | 0 | 156 | 787 |
| NCAPH2 | 31.95552222 | 0 | 0 | 5 | 529 |
| AGPAT5 | 31.44923697 | 0 | 0 | 181 | 791 |
| DDX25 | 30.98762321 | 0 | 0 | 369 | 1007 |
| LMBR1L | 30.78969757 | 0 | 0 | 186 | 775 |
| CLDND1 | 30.61540239 | 0 | 0 | 265 | 870 |
| NFS1 | 30.4673864 | 0 | 0 | 321 | 932 |

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|-------------|-------------|---|---|------|------|
| SMAD1 | 30.24689002 | 0 | 0 | 29 | 520 |
| SYF2 | 30.21439021 | 0 | 0 | 4 | 472 |
| FAM96B | 29.80635962 | 0 | 0 | 87 | 602 |
| YTHDC1 | 29.09743845 | 0 | 0 | 59 | 536 |
| PRKCH | 28.8011563 | 0 | 0 | 13 | 447 |
| GNAO1 | 28.76533447 | 0 | 0 | 1319 | 1819 |
| ULK3 | 28.42220182 | 0 | 0 | 1222 | 1720 |
| HEATR5B | 27.69431856 | 0 | 0 | 200 | 691 |
| C16orf89 | 27.61378154 | 0 | 0 | 12 | 411 |
| MYH9 | 27.39959017 | 0 | 0 | 12 | 405 |
| U2AF1 | 27.36463046 | 0 | 0 | 554 | 1067 |
| VIT | 27.0531338 | 0 | 0 | 0 | 372 |
| CHRNE | 26.61318718 | 0 | 0 | 0 | 360 |
| PHB | 26.52264644 | 0 | 0 | 944 | 1394 |
| PLXNB2 | 26.43906743 | 0 | 0 | 498 | 977 |
| PPM1K | 26.42476823 | 0 | 0 | 182 | 629 |
| TMEFF2 | 26.34087061 | 0 | 0 | 537 | 1012 |
| SPOCK3 | 26.29614335 | 0 | 0 | 117 | 540 |
| AMPD2 | 26.10234123 | 0 | 0 | 967 | 1396 |
| RAB20 | 25.90095713 | 0 | 0 | 1 | 343 |
| ZFPM2 | 25.77276434 | 0 | 0 | 147 | 565 |
| SOWAHA | 25.76412658 | 0 | 0 | 624 | 1074 |
| SEC14L2 | 25.52064825 | 0 | 0 | 170 | 587 |
| ZC3H18 | 25.47621428 | 0 | 0 | 156 | 568 |
| DCUN1D4 | 25.39346168 | 0 | 0 | 58 | 429 |
| HLTF | 24.77726602 | 0 | 0 | 4 | 320 |
| SHMT2 | 24.58410663 | 0 | 0 | 363 | 776 |
| C17orf107 | 24.49589957 | 0 | 0 | 0 | 305 |
| DYRK4 | 24.41610135 | 0 | 0 | 3 | 309 |
| DERL2 | 24.13175872 | 0 | 0 | 0 | 296 |
| CRTAC1 | 24.06373845 | 0 | 0 | 704 | 1083 |
| HADH | 23.72894458 | 0 | 0 | 77 | 414 |
| TSC22D3 | 23.20399646 | 0 | 0 | 1133 | 1410 |
| TMX2-CTNND1 | 22.96163723 | 0 | 0 | 1 | 270 |
| NCBP2 | 22.87315337 | 0 | 0 | 69 | 381 |
| CLCN7 | 22.68133735 | 0 | 0 | 1246 | 1477 |
| C9orf41 | 22.66855359 | 0 | 0 | 6 | 273 |
| ST18 | 22.51428462 | 0 | 0 | 16 | 288 |
| ABHD16A | 22.24330882 | 0 | 0 | 644 | 963 |
| EXOSC5 | 22.21403501 | 0 | 0 | 95 | 401 |
| YEATS2 | 22.18509506 | 0 | 0 | 66 | 360 |

| | | | | | |
|-------------|-------------|---|---|------|------|
| FAM21C | 22.03541177 | 0 | 0 | 170 | 490 |
| TOB1 | 21.97979509 | 0 | 0 | 40 | 316 |
| PLEKHB1 | 21.82956921 | 0 | 0 | 2763 | 2537 |
| ACCN2 | 21.68402132 | 0 | 0 | 0 | 239 |
| NHS | 21.54357334 | 0 | 0 | 24 | 280 |
| COPB2 | 21.48159005 | 0 | 0 | 354 | 670 |
| ANKRD11 | 21.4648381 | 0 | 0 | 147 | 448 |
| SYS1-DBNDD2 | 21.46112531 | 0 | 0 | 420 | 733 |
| KIF13A | 21.41009525 | 0 | 0 | 0 | 233 |
| FAM182B | 21.23953634 | 0 | 0 | 341 | 650 |
| PINK1 | 20.95179848 | 0 | 0 | 4423 | 3584 |
| RNF26 | 20.93010957 | 0 | 0 | 98 | 374 |
| UFSP2 | 20.80422143 | 0 | 0 | 0 | 220 |
| CBFB | 20.77255634 | 0 | 0 | 97 | 369 |
| UBR4 | 20.74758097 | 0 | 0 | 1238 | 1387 |
| SMO | 20.60957428 | 0 | 0 | 23 | 258 |
| ATXN2L | 20.28526851 | 0 | 0 | 162 | 436 |
| MED9 | 19.98423265 | 0 | 0 | 0 | 203 |
| C12orf51 | 19.87587481 | 0 | 0 | 35 | 262 |
| FOXRED1 | 19.83655431 | 0 | 0 | 85 | 332 |
| PSMD12 | 19.83601088 | 0 | 0 | 0 | 200 |
| SND1 | 19.78152709 | 0 | 0 | 1888 | 1818 |
| CNTNAP4 | 19.75164953 | 0 | 0 | 204 | 469 |
| GRB10 | 19.63791725 | 0 | 0 | 11 | 217 |
| TECR | 19.60125915 | 0 | 0 | 627 | 857 |
| GDAP1L1 | 19.52165624 | 0 | 0 | 326 | 586 |
| CAMKK1 | 19.46224944 | 0 | 0 | 353 | 610 |
| SLC44A1 | 19.39825405 | 0 | 0 | 222 | 479 |
| ATP6AP1 | 19.35041521 | 0 | 0 | 3791 | 3069 |
| XYLT2 | 19.12913186 | 0 | 0 | 0 | 186 |
| SPSB3 | 19.03727684 | 0 | 0 | 640 | 849 |
| ANKRD9 | 18.62484917 | 0 | 0 | 6 | 188 |
| SFMBT1 | 18.36578559 | 0 | 0 | 101 | 320 |
| PTPRB | 18.00040684 | 0 | 0 | 79 | 285 |
| FAM65A | 17.97827092 | 0 | 0 | 975 | 1076 |
| SERF1B | 17.85620948 | 0 | 0 | 3 | 168 |
| FZD3 | 17.7953928 | 0 | 0 | 23 | 202 |
| ZNF324B | 17.74180317 | 0 | 0 | 0 | 160 |
| CWC15 | 17.68627153 | 0 | 0 | 0 | 159 |
| PI4KAP1 | 17.29368519 | 0 | 0 | 25 | 196 |
| COPS5 | 17.26955416 | 0 | 0 | 78 | 269 |

| | | | | | |
|------------|-------------|---|---|------|------|
| SMN1 | 17.25701812 | 0 | 0 | 225 | 429 |
| OXSM | 17.00567455 | 0 | 0 | 1 | 149 |
| ADSS | 16.97208308 | 0 | 0 | 412 | 593 |
| CRSP8P | 16.89931271 | 0 | 0 | 4 | 153 |
| USP32P2 | 16.83132793 | 0 | 0 | 0 | 144 |
| BABAM1 | 16.79879398 | 0 | 0 | 406 | 583 |
| SF3A3 | 16.77278249 | 0 | 0 | 0 | 143 |
| EIF4G2 | 16.69551092 | 0 | 0 | 999 | 1046 |
| STYK1 | 16.48746377 | 0 | 0 | 4 | 146 |
| NALCN | 16.37829917 | 0 | 0 | 472 | 627 |
| SERF1A | 16.30243156 | 0 | 0 | 3 | 141 |
| TTC7B | 16.30024395 | 0 | 0 | 760 | 853 |
| RAB11B | 16.25346119 | 0 | 0 | 3244 | 2529 |
| BCAP31 | 16.24590897 | 0 | 0 | 731 | 829 |
| PPAP2A | 16.23049312 | 0 | 0 | 108 | 284 |
| ZDHC4 | 16.13248686 | 0 | 0 | 210 | 388 |
| PSMB1 | 15.95261065 | 0 | 0 | 885 | 935 |
| TRIM8 | 15.90072442 | 0 | 0 | 1168 | 1138 |
| KIAA1244 | 15.70062924 | 0 | 0 | 96 | 260 |
| CD14 | 15.56121244 | 0 | 0 | 9 | 140 |
| OGDHL | 15.49487005 | 0 | 0 | 2065 | 1730 |
| GYS1 | 15.49204486 | 0 | 0 | 83 | 241 |
| DGCR6L | 15.46934572 | 0 | 0 | 166 | 330 |
| CDK16 | 15.36841602 | 0 | 0 | 1213 | 1149 |
| FUS | 15.18774898 | 0 | 0 | 557 | 661 |
| HSD17B4 | 15.05560202 | 0 | 0 | 184 | 339 |
| RUNX1T1 | 15.04370892 | 0 | 0 | 148 | 303 |
| ATHL1 | 14.84400525 | 0 | 0 | 1 | 114 |
| EIF3B | 14.70995773 | 0 | 0 | 643 | 713 |
| DHX16 | 14.70104744 | 0 | 0 | 248 | 391 |
| C11orf49 | 14.61872829 | 0 | 0 | 315 | 448 |
| VDAC3 | 14.50026189 | 0 | 0 | 361 | 484 |
| GPR75-ASB3 | 14.41043116 | 0 | 0 | 47 | 178 |
| PDE6B | 14.40339392 | 0 | 0 | 376 | 494 |
| SALL1 | 14.38916293 | 0 | 0 | 738 | 774 |
| TST | 14.28111972 | 0 | 0 | 114 | 253 |
| CDK20 | 14.22572127 | 0 | 0 | 471 | 566 |
| KANSL3 | 14.1305717 | 0 | 0 | 24 | 142 |
| AP2S1 | 14.11547146 | 0 | 0 | 471 | 563 |
| CTSZ | 13.84728836 | 0 | 0 | 285 | 404 |
| GPR75 | 13.75632471 | 0 | 0 | 45 | 165 |

| | | | | | |
|----------|-------------|---|---|------|------|
| EXD2 | 13.55184374 | 0 | 0 | 164 | 289 |
| P4HA2 | 13.45891048 | 0 | 0 | 94 | 217 |
| SYNJ2 | 13.45235021 | 0 | 0 | 278 | 389 |
| KNDC1 | 13.44789223 | 0 | 0 | 327 | 430 |
| PHF20 | 13.20546217 | 0 | 0 | 23 | 127 |
| VPS13D | 13.13328919 | 0 | 0 | 465 | 532 |
| CCT2 | 13.07470784 | 0 | 0 | 328 | 422 |
| BRD4 | 13.02341958 | 0 | 0 | 16 | 114 |
| DRG2 | 12.93179244 | 0 | 0 | 280 | 379 |
| DNAJB5 | 12.77907954 | 0 | 0 | 1 | 85 |
| PORCN | 12.73435737 | 0 | 0 | 696 | 692 |
| NAF1 | 12.59248386 | 0 | 0 | 252 | 348 |
| CREM | 12.51024939 | 0 | 0 | 95 | 202 |
| RCAN2 | 12.49336683 | 0 | 0 | 293 | 380 |
| FADS1 | 12.37285782 | 0 | 0 | 406 | 467 |
| UBA6 | 12.36948439 | 0 | 0 | 49 | 149 |
| ASNSD1 | 12.30398403 | 0 | 0 | 36 | 132 |
| RRBP1 | 12.2333768 | 0 | 0 | 172 | 271 |
| SLC25A16 | 12.2276009 | 0 | 0 | 0 | 76 |
| EBNA1BP2 | 12.20655743 | 0 | 0 | 75 | 176 |
| B4GALNT4 | 12.09127108 | 0 | 0 | 1104 | 952 |
| CERS2 | 12.07145162 | 0 | 0 | 918 | 826 |
| KIN | 12.06563658 | 0 | 0 | 0 | 74 |
| AKAP1 | 11.90836494 | 0 | 0 | 2 | 76 |
| C4orf34 | 11.83567353 | 0 | 0 | 3 | 77 |
| ASPH | 11.64249489 | 0 | 0 | 902 | 801 |
| TRAF4 | 11.4886157 | 0 | 0 | 2 | 71 |
| MTBP | 11.39619515 | 0 | 0 | 1 | 68 |
| ELOVL5 | 11.34634372 | 0 | 0 | 698 | 652 |
| HNMT | 11.2681065 | 0 | 0 | 8 | 79 |
| SON | 11.21840478 | 0 | 0 | 522 | 524 |
| ST3GAL5 | 11.17313577 | 0 | 0 | 1050 | 884 |
| SERINC3 | 10.95897609 | 0 | 0 | 2266 | 1640 |
| EXOSC8 | 10.70540864 | 0 | 0 | 3 | 64 |
| DUSP1 | 10.63290576 | 0 | 0 | 28 | 100 |
| AP3B2 | 10.50216464 | 0 | 0 | 246 | 300 |
| GOLPH3 | 10.44878874 | 0 | 0 | 408 | 422 |
| AS3MT | 10.30695721 | 0 | 0 | 0 | 54 |
| C11orf2 | 10.09992629 | 0 | 0 | 269 | 310 |
| FAM108A1 | 10.03519079 | 0 | 0 | 585 | 537 |
| ABCA7 | 9.96113987 | 0 | 0 | 68 | 136 |

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|--------------------|-------------|------------|------------|------|------|
| ZC3H13 | 9.9178706 | 0 | 0 | 0 | 50 |
| NSFP1 | 9.895690667 | 0 | 0 | 61 | 128 |
| DUSP14 | 9.890381968 | 0 | 0 | 192 | 245 |
| ZNF721 | 9.398049338 | 0 | 0 | 130 | 185 |
| TMCC2 | 9.039320956 | 0 | 0 | 700 | 587 |
| DDX39A | 8.924289949 | 0 | 0 | 75 | 129 |
| RNF187 | 8.542715161 | 0 | 0 | 602 | 509 |
| PCDH17 | 8.504650141 | 0 | 0 | 120 | 163 |
| RAB19 | 8.415581589 | 0 | 0 | 0 | 36 |
| INSR | 8.324215062 | 0 | 0 | 302 | 299 |
| APBB3 | 8.281271292 | 0 | 0 | 529 | 454 |
| SOSTDC1 | 8.178473753 | 4.4409E-16 | 2.3355E-15 | 0 | 34 |
| PAPSS1 | 8.174040169 | 4.4409E-16 | 2.3355E-15 | 1893 | 1291 |
| LOH12CR1 | 8.116208411 | 4.4409E-16 | 2.3355E-15 | 39 | 84 |
| SRPR | 8.031407166 | 8.8818E-16 | 4.6243E-15 | 187 | 209 |
| MYBPC1 | 7.981503895 | 1.3323E-15 | 6.9027E-15 | 63 | 106 |
| CORO2B | 7.953867013 | 1.7764E-15 | 9.167E-15 | 1719 | 1179 |
| ARAF | 7.939170639 | 1.9984E-15 | 1.0292E-14 | 213 | 227 |
| KLHL22 | 7.93452354 | 2.2204E-15 | 1.1429E-14 | 1375 | 973 |
| RPL4 | 7.92571875 | 2.2204E-15 | 1.1429E-14 | 3617 | 2272 |
| C8orf46 | 7.820058159 | 5.3291E-15 | 2.7148E-14 | 185 | 204 |
| SLC25A6 (chrY 145) | 7.53167626 | 5.0182E-14 | 2.4724E-13 | 2739 | 1752 |
| VRK3 | 7.50906726 | 5.9508E-14 | 2.9178E-13 | 219 | 224 |
| WDR17 | 7.476195513 | 7.6383E-14 | 3.7335E-13 | 64 | 101 |
| FUNDC2 | 7.343717149 | 2.0783E-13 | 1.0037E-12 | 275 | 261 |
| CDH15 | 7.343625755 | 2.0783E-13 | 1.0037E-12 | 425 | 363 |
| RLIM | 7.296088298 | 2.9621E-13 | 1.4162E-12 | 1 | 29 |
| SLIT2 | 7.207561934 | 5.6977E-13 | 2.6981E-12 | 132 | 154 |
| CKAP5 | 7.126728767 | 1.0278E-12 | 4.8089E-12 | 188 | 195 |
| ADIPOR1 | 6.967952987 | 3.2159E-12 | 1.4795E-11 | 307 | 276 |
| DDX5 | 6.928161738 | 4.2635E-12 | 1.9522E-11 | 750 | 560 |
| RAB4A | 6.924062356 | 4.3887E-12 | 2.0091E-11 | 279 | 256 |
| INPP5F | 6.920608965 | 4.4971E-12 | 2.0583E-11 | 282 | 258 |
| TTC19 | 6.804128451 | 1.0166E-11 | 4.5965E-11 | 524 | 415 |
| LMAN2L | 6.643599458 | 3.0612E-11 | 1.3555E-10 | 291 | 259 |
| ASB6 | 6.638663154 | 3.1654E-11 | 1.4014E-10 | 152 | 161 |
| HAPLN4 | 6.578754404 | 4.7441E-11 | 2.0908E-10 | 0 | 22 |
| SLC25A6 (chrX 150) | 6.470520271 | 9.7666E-11 | 4.2515E-10 | 3009 | 1851 |
| ATF4 | 6.332758776 | 2.4082E-10 | 1.0269E-09 | 394 | 321 |
| PAPOLA | 6.294272284 | 3.0885E-10 | 1.3108E-09 | 117 | 130 |
| NUAK2 | 6.272595071 | 3.5508E-10 | 1.5062E-09 | 0 | 20 |

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| ODZ1 | 6.272595071 | 3.5508E-10 | 1.5062E-09 | 0 | 20 |
| LOC100505666 | 6.186162198 | 6.1647E-10 | 2.5896E-09 | 79 | 99 |
| CNNM2 | 6.113768863 | 9.7305E-10 | 4.0526E-09 | 0 | 19 |
| GNB1 | 5.768640953 | 7.9913E-09 | 3.2034E-08 | 1751 | 1110 |
| OS9 | 5.542138941 | 2.988E-08 | 1.1666E-07 | 1174 | 771 |
| STMN2 | 5.515783543 | 3.4723E-08 | 1.3498E-07 | 432 | 328 |
| ICA1 | 5.368377859 | 7.9448E-08 | 3.0399E-07 | 87 | 96 |
| PWP2 | 5.305423754 | 1.1241E-07 | 4.2768E-07 | 653 | 458 |
| SYNGAP1 | 5.29243761 | 1.207E-07 | 4.5905E-07 | 37 | 55 |
| GAS6 | 5.276658579 | 1.3156E-07 | 4.9786E-07 | 1118 | 730 |
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| HERC1 | 5.165731146 | 2.395E-07 | 8.9433E-07 | 1870 | 1153 |
| CORO1B | 5.163434644 | 2.4246E-07 | 9.0523E-07 | 1262 | 809 |
| PHKG1 | 5.10895728 | 3.2394E-07 | 1.2025E-06 | 52 | 66 |
| NSUN2 | 5.076892335 | 3.8366E-07 | 1.4137E-06 | 320 | 249 |
| EPB49 | 5.065471325 | 4.0739E-07 | 1.5009E-06 | 1382 | 874 |
| FLJ45340 | 5.048905479 | 4.4435E-07 | 1.6365E-06 | 294 | 232 |
| FKBP8 | 5.021456733 | 5.1281E-07 | 1.8769E-06 | 2518 | 1507 |
| H2AFY2 | 4.837002135 | 1.3181E-06 | 4.7507E-06 | 19 | 35 |
| CHRD | 4.801661342 | 1.5735E-06 | 5.6365E-06 | 293 | 227 |
| CPEB1 | 4.742446918 | 2.1115E-06 | 7.5221E-06 | 393 | 288 |
| TUBG2 | 4.634964295 | 3.57E-06 | 1.2555E-05 | 1709 | 1042 |
| C1orf96 | 4.593554467 | 4.3576E-06 | 1.5254E-05 | 62 | 69 |
| DNAJB6 | 4.578710164 | 4.6785E-06 | 1.6373E-05 | 1548 | 950 |
| PLEKHO1 | 4.434787122 | 9.2163E-06 | 3.1684E-05 | 165 | 139 |
| SAP30BP | 4.413965712 | 1.0149E-05 | 3.4882E-05 | 170 | 142 |
| SUCLA2 | 4.362990503 | 1.283E-05 | 4.3804E-05 | 818 | 530 |
| CLEC16A | 4.339753339 | 1.4264E-05 | 4.8695E-05 | 2 | 13 |
| GLRX5 | 4.276064426 | 1.9023E-05 | 6.419E-05 | 54 | 60 |
| GLIS3 | 4.207780497 | 2.5789E-05 | 8.6437E-05 | 0 | 9 |
| SCD5 | 3.991633148 | 6.562E-05 | 0.00021582 | 48 | 53 |
| SYCE2 | 3.967133138 | 7.2742E-05 | 0.00023785 | 0 | 8 |
| CRBN | 3.869568112 | 0.00010903 | 0.00035358 | 35 | 42 |
| TERF1 | 3.85989038 | 0.00011344 | 0.00036772 | 83 | 77 |
| ATP1A1OS | 3.710912917 | 0.00020651 | 0.00065966 | 0 | 7 |
| REEP2 | 3.604624203 | 0.0003126 | 0.0009839 | 486 | 320 |
| BCAN | 3.419059886 | 0.00062838 | 0.00193153 | 1295 | 769 |
| GSTT2 | 3.416883252 | 0.00063342 | 0.00194678 | 19 | 26 |
| THYN1 | 3.296871979 | 0.00097768 | 0.0029825 | 3 | 10 |
| ABHD12 | 3.266648152 | 0.00108829 | 0.00329671 | 1028 | 617 |
| MRAS | 3.225129466 | 0.00125916 | 0.00381382 | 500 | 320 |

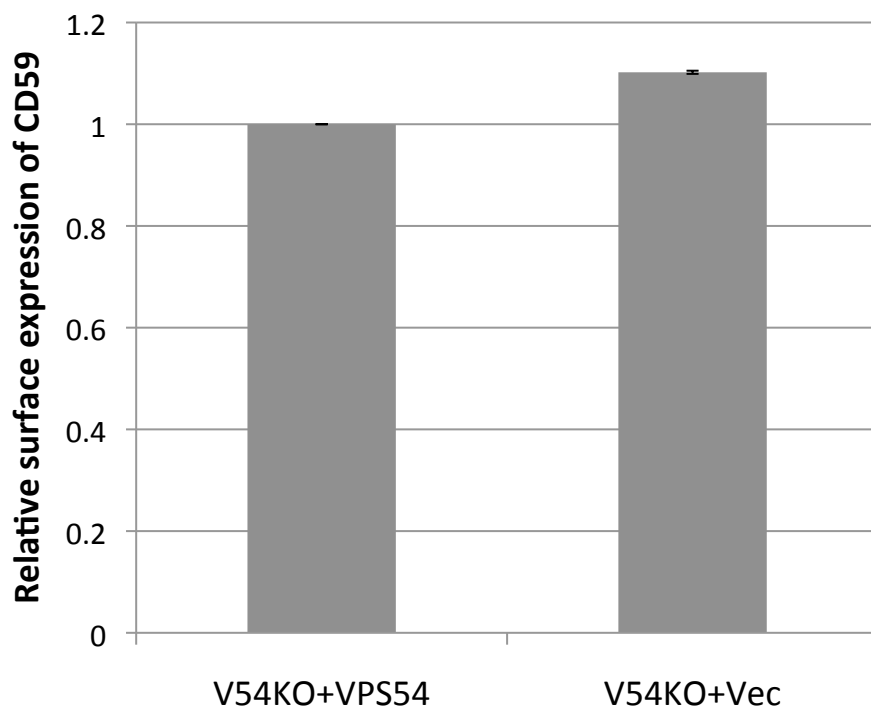
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|-----------|-------------|------------|------------|------|------|
| SYS1 | 3.219169933 | 0.00128562 | 0.00389247 | 1 | 7 |
| ETV1 | 3.188216406 | 0.00143153 | 0.0043003 | 137 | 105 |
| CACNA1G | 3.133932622 | 0.0017248 | 0.00517995 | 94 | 77 |
| SUPT6H | 3.084728909 | 0.00203738 | 0.00605725 | 160 | 118 |
| ZNF692 | 3.031985327 | 0.00242951 | 0.00722217 | 140 | 105 |
| SLC25A1 | 3.030439309 | 0.00244198 | 0.00725832 | 383 | 249 |
| MUC4 | 2.93006467 | 0.00338891 | 0.00987593 | 59 | 52 |
| BEND5 | 2.809558189 | 0.00496096 | 0.01430746 | 11 | 16 |
| RPS23 | 2.805185727 | 0.00502876 | 0.01449943 | 0 | 4 |
| TPCN2 | 2.805185727 | 0.00502876 | 0.01449943 | 0 | 4 |
| XPNPEP1 | 2.703874958 | 0.00685361 | 0.01956095 | 468 | 291 |
| CELF1 | 2.480696577 | 0.01311259 | 0.03657707 | 297 | 190 |
| MAP7 | 2.429985112 | 0.01509944 | 0.04162799 | 112 | 81 |
| UBE2E1 | 2.429361882 | 0.01512543 | 0.04169471 | 0 | 3 |
| SNRPN | 2.379511197 | 0.01733558 | 0.04777596 | 1385 | 783 |
| LAMTOR1 | 2.292565044 | 0.02187306 | 0.05948231 | 1009 | 578 |
| SENP5 | 2.164944407 | 0.03039194 | 0.08146531 | 16 | 17 |
| C14orf180 | 1.983565491 | 0.0473043 | 0.12299433 | 0 | 2 |
| IGSF3 | 1.983565491 | 0.0473043 | 0.12299433 | 0 | 2 |
| LOC728989 | 1.983565491 | 0.0473043 | 0.12299433 | 0 | 2 |
| LRRC4 | 1.983565491 | 0.0473043 | 0.12299433 | 0 | 2 |
| PAX5 | 1.983565491 | 0.0473043 | 0.12299433 | 0 | 2 |
| KCMF1 | 1.908215915 | 0.05636332 | 0.14649954 | 22 | 20 |
| UBB | 1.850700225 | 0.06421269 | 0.16430977 | 4700 | 2501 |
| CACNB3 | 1.815957476 | 0.0693769 | 0.17750471 | 760 | 431 |
| NCKAP1 | 1.672672557 | 0.09439177 | 0.23748158 | 2556 | 1374 |
| AK3 | 1.662902652 | 0.09633192 | 0.24231072 | 81 | 55 |
| ANK3 | 1.635837625 | 0.10187358 | 0.25619496 | 647 | 366 |
| MAGED1 | 1.623743716 | 0.10443052 | 0.26259702 | 1418 | 775 |
| CLIP3 | 1.541396938 | 0.12322021 | 0.30393279 | 1353 | 738 |
| PFKP | 1.486071368 | 0.13726024 | 0.33852801 | 3676 | 1948 |
| SEPT7 | 1.42847392 | 0.1531555 | 0.3711652 | 899 | 495 |
| C9orf89 | 1.41148021 | 0.15810307 | 0.38129206 | 127 | 79 |
| P2RX7 | 1.411292536 | 0.15815837 | 0.38138613 | 349 | 201 |
| ANAPC10 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| ANXA13 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| C1QTNF6 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| CATSPERB | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| CCDC60 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| DCAF4L1 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| DEPDC1B | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |

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| FAM46D | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
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| HLA-DMB | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
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| HOTAIR | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| LINC00265 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| LOC100130480 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
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| LOC399829 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| LOC730091 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| LOC731275 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| MARCO | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| MEX3D | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| MGAT4C | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| MRPS16 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| MST4 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| NHSL1 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| PDSS2 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| PIGO | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| PKP2 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| POLR2K | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| SEC16B | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| SLC16A10 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| TRAPPC2 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| TSTD2 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| USP49 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| VPS16 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| XRCC1 | 1.402592482 | 0.16073839 | 0.38621452 | 0 | 1 |
| ROBO2 | 1.396928108 | 0.16243519 | 0.39021136 | 99 | 63 |
| ARL1 | 1.387743158 | 0.16521527 | 0.39684908 | 61 | 41 |
| NRXN2 | 1.382242853 | 0.16689715 | 0.40084782 | 439 | 249 |
| MANBAL | 1.349309846 | 0.17723746 | 0.42559546 | 11 | 10 |
| CDK11A | 1.312094233 | 0.18948834 | 0.45491978 | 3 | 4 |
| SETD1A | 1.259603406 | 0.20781247 | 0.49886079 | 166 | 99 |
| DCHS2 | 1.207943636 | 0.22706894 | 0.53050016 | 1 | 2 |
| CEBPD | 1.146429477 | 0.25161749 | 0.58779414 | 268 | 153 |
| TMX2 | 1.127083093 | 0.25970735 | 0.60663199 | 1792 | 953 |
| WDR1 | 1.007195989 | 0.3138406 | 0.70750962 | 957 | 514 |
| CYTH3 | 0.975280318 | 0.32942123 | 0.74256242 | 4 | 4 |
| RIPK1 | 0.919127364 | 0.35802896 | 0.80673744 | 98 | 58 |
| ADC | 0.894538071 | 0.37103407 | 0.83596102 | 777 | 417 |

| | | | | | |
|---------|-------------|------------|------------|------|------|
| CCBL1 | 0.888227911 | 0.37441817 | 0.84350436 | 115 | 67 |
| CHCHD5 | 0.809307926 | 0.41833805 | 0.9419047 | 26 | 17 |
| SKP1 | 0.658557426 | 0.51018001 | 1 | 1196 | 628 |
| ARRB1 | 0.621500986 | 0.53427005 | 1 | 239 | 130 |
| SLC41A3 | 0.586252685 | 0.55770572 | 1 | 1571 | 819 |
| HSPB8 | 0.551393227 | 0.58136414 | 1 | 178 | 97 |
| AGMO | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| CDKAL1 | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| DCAF7 | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| FAT3 | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| GCSH | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| KLHL1 | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| MMP23A | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| TRIM26 | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| UGT1A6 | 0.487639894 | 0.62580493 | 1 | 1 | 1 |
| NLRX1 | 0.264877292 | 0.79110399 | 1 | 117 | 62 |
| KDM5C | 0.23072418 | 0.81752909 | 1 | 35 | 19 |
| SDHA | 0.222884589 | 0.82362533 | 1 | 4907 | 2508 |
| CAPZA2 | 0.209102463 | 0.83436825 | 1 | 519 | 268 |
| RPLP0 | 0.132860089 | 0.89430403 | 1 | 1349 | 690 |
| DLST | 0.064965166 | 0.94820174 | 1 | 507 | 259 |

Genes showing test statistics < 0 were eliminated from this table.

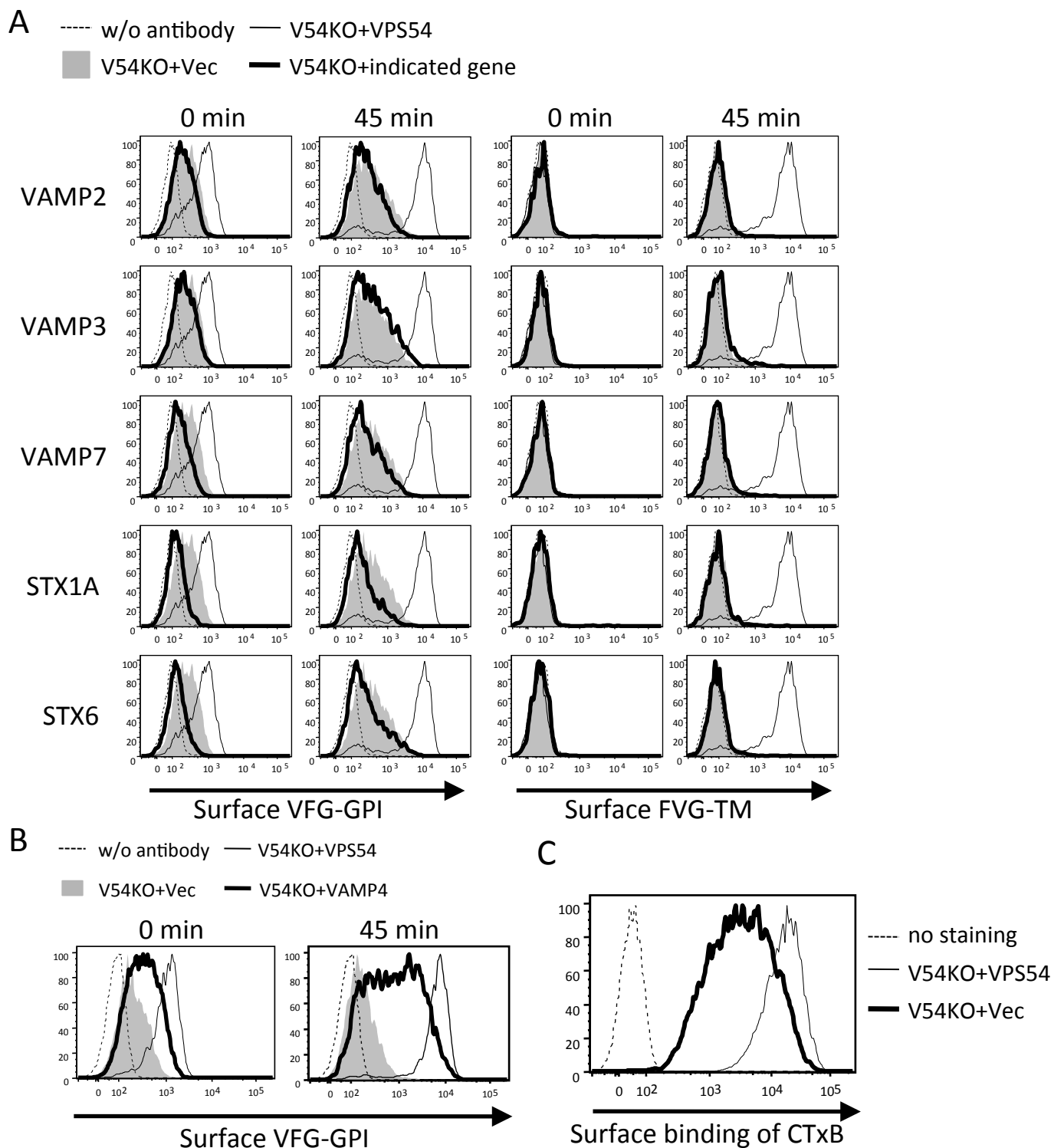
Supplemental figure 1



Supplemental Fig. 1. Supporting data for Fig. 4

Relative surface expression of CD59. Surface expression of CD59 was analyzed by flow cytometry. The geometric mean fluorescence of surface CD59 in cells was quantified and relative expression was calculated. Error bars represent the SDs (n=2).

Supplemental figure 2



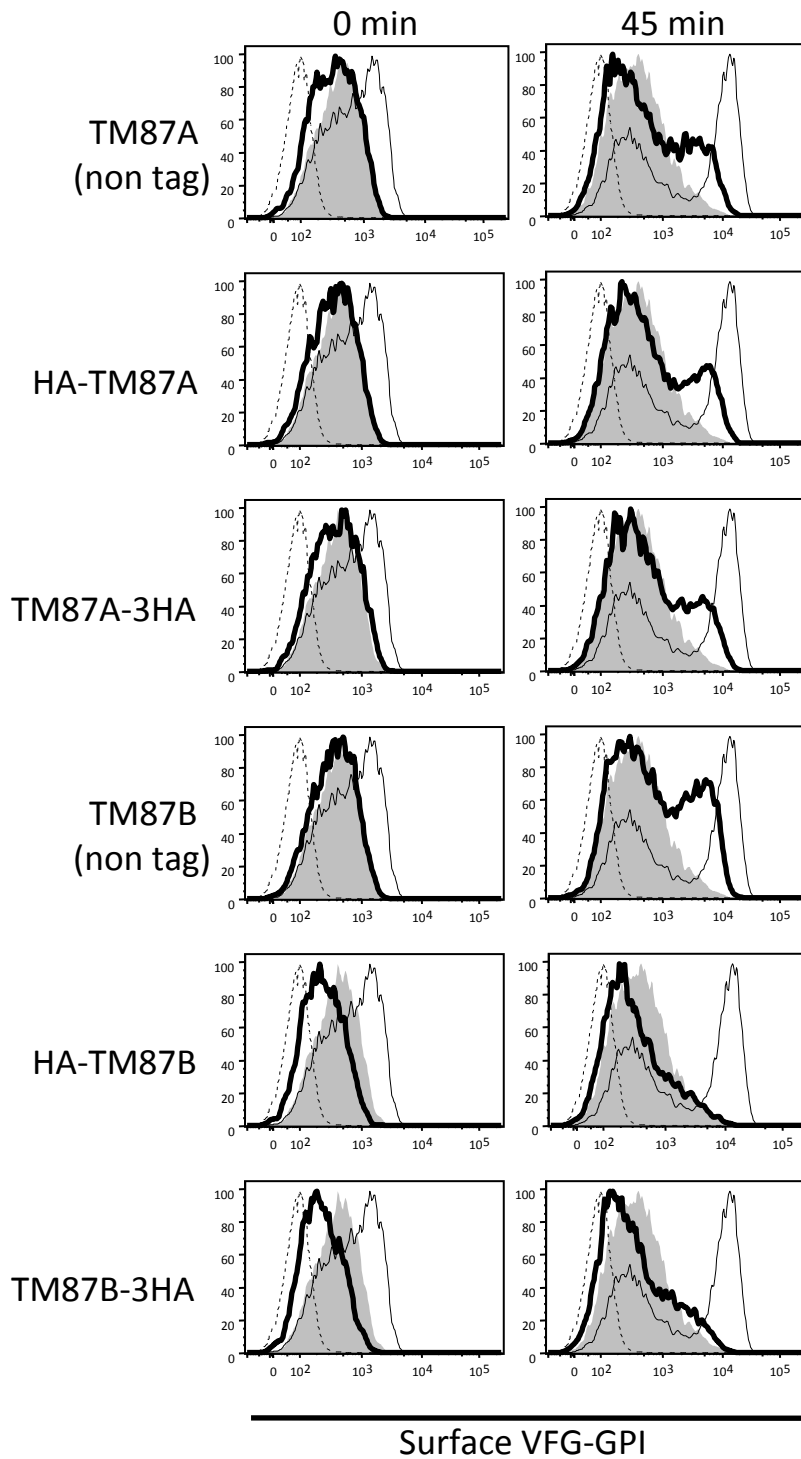
Supplemental Fig. 2. Supporting data for Fig. 5

A. Transport assay of VFG-GPI (left) and FVG-TM (right) in V54KO cells transiently transfected with the indicated genes. B. V54KO cells stably expressing VAMP4 (V54KO+VAMP4) in which the anterograde transport of VFG-GPI was efficiently restored were collected twice by cell sorting. VFG-GPI transport was assayed in V54KO+VAMP4 cells after sorting. C. Cell-surface binding of CTxB. The cells were incubated with Alexa Fluor 488-conjugated CTxB on ice for 15 min. Fluorescent intensity was analyzed by flow cytometry.

Supplemental figure 3

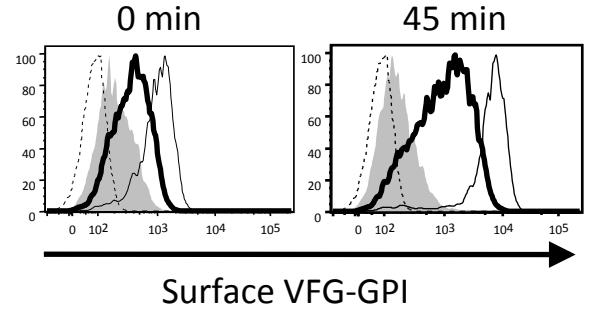
A

- w/o antibody
- V54KO+VPS54
- V54KO+Vec
- V54KO+TM87A/B



B

- w/o antibody
- V54KO+VPS54
- V54KO+Vec
- V54KO+TM87A

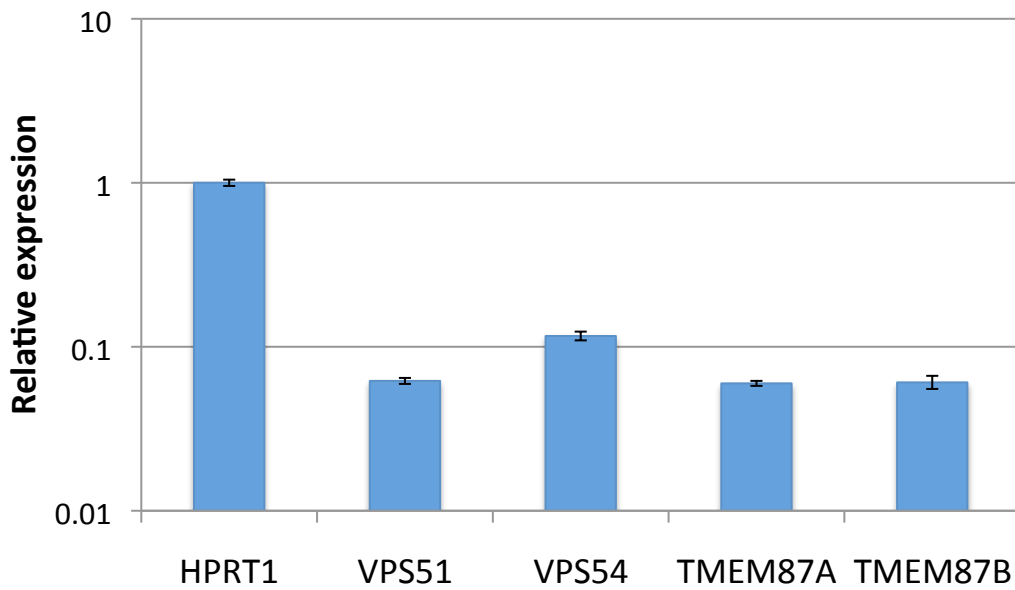


Supplemental Fig. 3. Supporting data 1 for Fig. 6

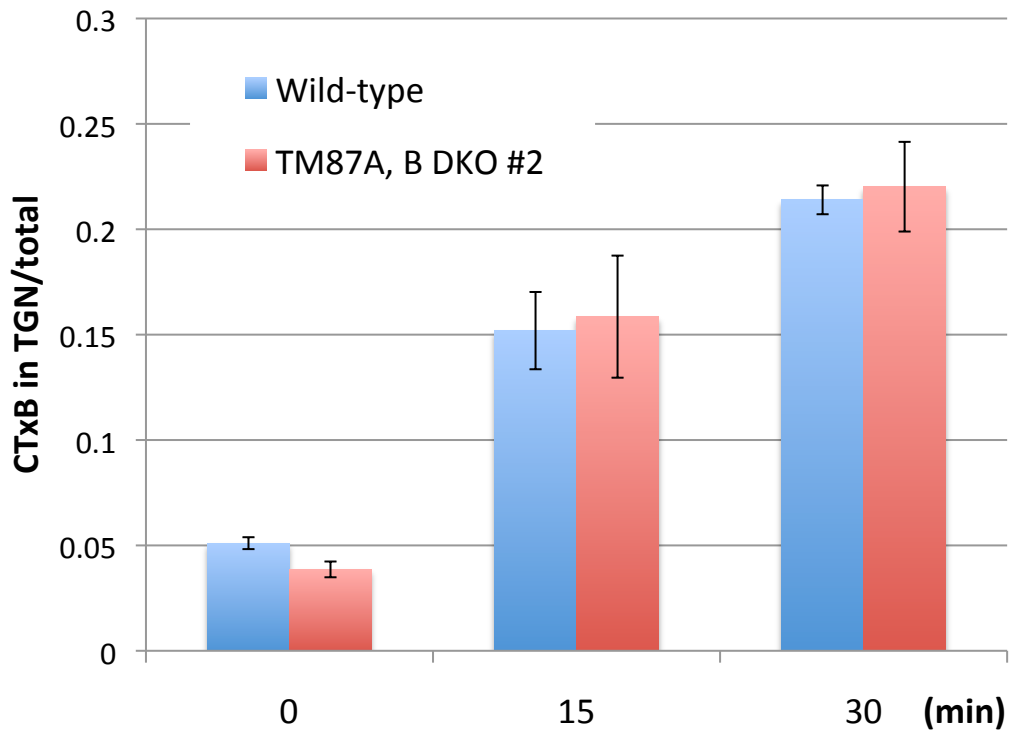
A. Transport assay of VFG-GPI in V54KO cells transiently transfected with the indicated genes. B. V54KO cells stably expressing HA-TMEM87A (V54KO+TM87A) in which the anterograde transport of VFG-GPI was efficiently restored were collected twice by cell sorting. VFG-GPI transport was assayed in V54KO+TM87A cells after sorting.

Supplemental figure 4

A



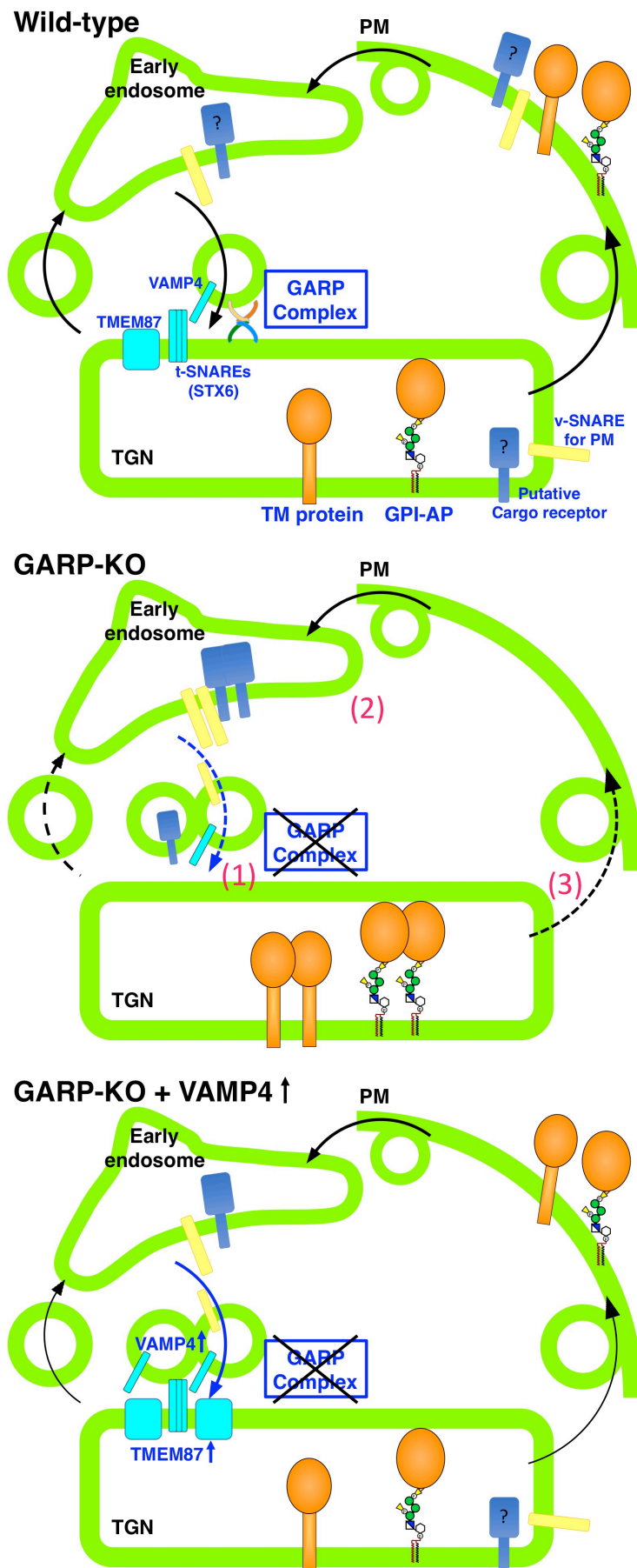
B



Supplemental Fig. 4. Supporting data 2 for Fig. 6

A. Relative expression of TMEM87A and B in wild-type HEK293 cells. The expression of TMEM87A and B relative to HPRT1 expression was analyzed by qRT-PCR. Both TMEM87A and B were expressed at levels comparable to VPS51 and VPS54 in HEK293 cells. B. Retrograde transport assay in TMEM87A- and TMEM87B-double knockout HEK293 cells using CTxB. CTxB retrograde transport at 0, 15 and 30 min in wild-type HEK293 cells and TMEM87A- and TMEM87B-double knockout HEK293 cells were similar.

Supplemental figure 5



Supplemental Fig. 5. The coupling between anterograde and retrograde pathway in post-Golgi compartment.

(Top panel) Vesicular transport in post-Golgi compartment in wild-type cells. GPI-APs and transmembrane (TM) proteins are transported by putative cargo receptors. Transport carriers contain v-SNAREs required for fusion with the plasma membrane (PM). Putative cargo receptors and v-SNAREs are then endocytosed and recycled back to the TGN in GARP complex- and VAMP4- dependent manner. TMEM87A might be involved in this step. (Middle panel) Vesicle transport in GARP-KO cells. (1) Recycling from the endosomes to the TGN is defective because of GARP-KO (retrograde transport defect). (2) Transport machineries including putative cargo receptors and v-SNAREs required for anterograde transport are accumulated in the endosomes or transport vesicles derived from the endosomes. (3) Post-Golgi anterograde transport is defective because of the reduced availability of transport machineries. (Bottom panel) Vesicle transport in GARP-KO+VAMP4 cells. Because overexpression of VAMP4 partially restores endosome-to-TGN retrograde transport, levels of TGN localized transport machineries slightly increase. This increase leads to enhancement of post-Golgi anterograde transport.