Table S21: GO function analysis of ranked signals from YRI population using the T_1 test statistic.

Description	p-value	Enrichment	Genes
MHC class II receptor activity	1.3×10^{-9}	130.9	*HLA-DPA1, HLA-DQA1, HLA-DQB1, HLA-DRA, HLA-DRB1*
MHC class I receptor activity	1.2×10^{-7}	507.1	*HLA-A, HLA-B, HLA-C*
Phospholipid binding	2.4×10^{-7}	2.0	*ABCA1, AFAP1, APBB1IP, ARAP1, ARAP3, ARHGAP22, ARHGAP24, ARHGAP25, ARHGAP26, ARHGAP42, ARHGEF18, ARHGEF4, ASAP1, CADPS, CDC42BPA, CNKSR1, DAPP1, DGKH, DOCK10, DOK5, DOK6, DOK7, DYSF, ELMO1, FARP1, FGD5, FRMPD2, GRB10, HS1BP3, IQSEC1, KALRN, LANCL2, MCF2L2, MYO10, MYO1B, MYOF, PCLO, PHLDB2, PIK3C2G, PLA2G4C, PLCB1, PLCG2, PLCH1, PLEK, PLEKHG1, PLEKHH2, PON1, PREX2, PSD3, PXK, SCARB1, SGIP1, SKAP2, SNTB1, SNTG1, SNTG2, SNX16, SNX19, SNX29, SNX31, SNX4, SNX7, SPATA13, SWAP70, TEC, TIAM1, TIAM2, TULP3, VAV2, VAV3, VNN1, VPS36*
Ion gated channel activity	9.7×10^{-7}	2.2	*ANO2, ANO6, ASIC2, CACNA1A, CACNA1C, CACNA2D3, CACNG8, CATSPER4, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, PEX5L, RYR2, RYR3, SCN11A, SCN3A, SCN9A, SCNN1G, TPCN2, TRPC6*
Gated channel activity	9.7×10^{-7}	2.2	*ANO2, ANO6, ASIC2, CACNA1A, CACNA1C, CACNA2D3, CACNG8, CATSPER4, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, PEX5L, RYR2, RYR3, SCN11A, SCN3A, SCN9A, SCNN1G, TPCN2, TRPC6*
Metal ion binding	2.5×10^{-6}	1.3	*ABO, ACACB, ACSM2B, ACSM3, ACTN4, ACY3, ADARB2, ADCY2, ADCY3, ADCY5, ADD2, AGMAT, ANGPT2, APIP, APOA1BP, ARSB, ARSJ, ATP10B, ATP10D, ATP2C2, ATP8A1, ATP8A2, BMPR1B, BNIP2, C1GALT1, CACNA1A, CACNA1C, CACNA2D1, CACNA2D3, CADPS, CALN1, CAPN14, CAPN8, CAPN9, CARS2, CASQ2, CCBE1, CCDC155, CDC42BPA, CDH10, CDH13, CDH18, CDH23, CDH4, CDH7, CDH9, CDHR2, CDKAL1, CELSR1, CELSR2, CHN2, CLSTN2, COL11A1, COL27A1, COL2A1, COL5A1, COL9A1, CPQ, CRTAC1, CTDSPL, CUBN, CYBRD1, CYP11B1, CYP19A1, CYP27A1, CYP2E1, CYP4F11, CYP4F12, CYP4F2, CYP4F3, CYP4Z1, DCHS2, DDAH1, DGKH, DGKI, DMRT1, DNER, DSC1, DSC3, DSG1, DSG3, DTNA, EBF2, EFCAB11, EFEMP1, EFHB, EMR1, EMR2, ENPP1, EPHX2, EXO1, EYA2, EYS, F13A1, F5, FAHD1, FARS2, FAT2, FAT3, FBN2, FBP2, FCER2, FGD5, FHIT, FRAS1, FREM1, FSCB, FSTL4, FSTL5, FTO, FXN, GALNT10, GALNT2, GALNTL6, GCLC, GPHN, GPR39, GRM7, GUCA1A, GUCA1B, HAAO, HBD, HGD, HMGCLL1, HPCAL4, IDO2, IMPA2, INPP1, IQGAP1, ISCU, ITGA1, ITGA10, ITGA11, ITGA8, ITGA9, KALRN, KCND3, KCNIP1, KCNIP4, KCNMA1, KSR2, LCN2, LEPREL1, LHPP, LOXL2, LRP1B, LTBP1, LYAR, MAN1A1, MARC1, MARC2, MAST4, MCTP2, ME3, MGAT1, MGAT4C, MGAT5B, MIPEP, MOB2, MOB3B, MOCOS, MOXD1, MRE11A, MYL1, MYLK, MYO5A, NCALD, NECAB2, NELL1, NELL2, NID2, NME7, NOS1, NOTCH2, NOTCH4, NQO2, NRXN1, NRXN3, NUBPL, NUDT7, OAS2, OCM2, OMA1, PADI2, PADI4, PAM, PCDH15, PCLO, PDE11A, PDE1A, PDE1C, PDE2A, PDE3A, PDE4B, PDE4D, PDSS1, PELO, PHF2, PINK1, PKD1L2, PKDREJ, PLA2G4E, PLCB1, PLCB4, PLCH1, PLEKHF2, PLSCR1, POLD1, PON1, PPA1, PPEF2, PPP3CA, PRIM2, PRKCE, PRKCH, PRTFDC1, PRUNE2, PTGS1, PXDN, PXDNL, RELN, REPS1, RIMS1, RNPEP, RPS6KA2, RYR2, RYR3, SCD5, SCGN, SCIN, SCN9A, SCUBE1, SDF4, SIAH3, SLIT3, SMOC2, SNCA, SPARCL1, SPOCK1, STAC, STK32A, STK32B, SULF1, SULF2, SWAP70, SYT5, SYT6, SYT9, TEC, TESC, TF, THBS2, TIMP2, TLL1, TNFRSF11A, TPO, TYW1, UNC13C, USP32, UTRN, VAV2, VAV3, ZFYVE26*
Glutamate receptor activity	3.0×10^{-6}	6.3	*GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM1, GRM3, GRM5, GRM7, GRM8*

GO categories in which false discovery rate is less than 0.01.

Table S21 continued.

Description	p-value	Enrichment	Genes
Ion channel activity	4.2×10^{-6}	1.8	*ANO2, ANO6, ASIC2, CACNA1A, CACNA1C, CACNA2D1, CACNA2D3, CACNG8, CATSPER3, CATSPER4, CHRNA2, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA1, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GLRA3, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNB2, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK18, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, LRRC52, MCOLN2, NALCN, PDE2A, PEX5L, PIEZO2, PKD1L2, PKDREJ, RYR2, RYR3, SCN11A, SCN3A, SCN5A, SCN9A, SCNN1G, SLC24A2, TPCN2, TRPC6, TRPM3, TRPM4*
Substrate-specific channel activity	4.8×10^{-6}	1.8	*ANO2, ANO6, AQP8, ASIC2, CACNA1A, CACNA1C, CACNA2D1, CACNA2D3, CACNG8, CATSPER3, CATSPER4, CHRNA2, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA1, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GLRA3, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNB2, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK18, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, LRRC52, MCOLN2, NALCN, PDE2A, PEX5L, PIEZO2, PKD1L2, PKDREJ, RYR2, RYR3, SCN11A, SCN3A, SCN5A, SCN9A, SCNN1G, SLC24A2, TPCN2, TRPC6, TRPM3, TRPM4*
Actin binding	7.9×10^{-6}	1.9	*ABLIM1, ABLIM3, ACTN4, ACTR2, ADD2, AFAP1, ARPC5, CAP1, CLMN, COBLL1, CORO2B, DAAM2, EPB41L2, FER, FHOD3, FKBP15, FMN1, FMN2, FMNL2, GAS7, IQGAP2, KCNMA1, KLHL1, KLHL5, LIMCH1, MAEA, MICAL2, MTSS1, MYLK, MYO10, MYO16, MYO18B, MYO1B, MYO3B, MYO5A, MYO5B, MYO7A, MYOZ2, MYPN, MYRIP, NCALD, NRAP, PALLD, PARVA, PDLIM5, PHACTR1, PRKCE, PXK, RCSD1, SCIN, SHROOM3, SNTB1, SNTG1, SNTG2, SORBS1, SPTB, SVIL, SYNE1, TNS1, UTRN, WASF3, XIRP2*
Signaling receptor activity	1.6×10^{-5}	6.2	*DMBT1, HLA-A, HLA-B, HLA-C, HLA-DPA1, HLA-DQA1, HLA-DQB1, HLA-DRB1, OR4C3, OR4C45*
Phospholipid-translocating ATPase activity	1.7×10^{-5}	20.1	*ABCA4, ATP10B, ATP10D, ATP8A1, ATP8A2*
Passive transmembrane transporter activity	2.0×10^{-5}	1.7	*ANO2, ANO6, AQP8, ASIC2, CACNA1A, CACNA1C, CACNA2D1, CACNA2D3, CACNG8, CATSPER3, CATSPER4, CHRNA2, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA1, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GLRA3, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNB2, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK18, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, LRRC52, MCOLN2, NALCN, PDE2A, PEX5L, PIEZO2, PKD1L2, PKDREJ, RYR2, RYR3, SCN11A, SCN3A, SCN5A, SCN9A, SCNN1G, SLC24A2, TPCN2, TRPC6, TRPM3, TRPM4*
Channel activity	2.0×10^{-5}	1.7	*ANO2, ANO6, AQP8, ASIC2, CACNA1A, CACNA1C, CACNA2D1, CACNA2D3, CACNG8, CATSPER3, CATSPER4, CHRNA2, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA1, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GLRA3, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNB2, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK18, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, LRRC52, MCOLN2, NALCN, PDE2A, PEX5L, PIEZO2, PKD1L2, PKDREJ, RYR2, RYR3, SCN11A, SCN3A, SCN5A, SCN9A, SCNN1G, SLC24A2, TPCN2, TRPC6, TRPM3, TRPM4*
Transmembrane transporter activity	2.7×10^{-5}	1.5	*ABCA1, ABCA4, ABCB5, ABCC12, ABCC4, ABCD4, ABCG1, ANKH, ANO2, ANO6, AQP8, ASIC2, ATP10B, ATP10D, ATP2C2, ATP6V0A2, ATP6V0A4, ATP6V0E2, ATP8A1, ATP8A2, CACNA1A, CACNA1C, CACNA2D1, CACNA2D3, CACNG8, CATSPER3, CATSPER4, CHRNA2, CHRNB3, CLCA2, CLCNKB, CLIC5, CNGA1, CNGA3, FGF2, GABRB3, GABRG3, GABRR1, GLRA3, GRIA1, GRID1, GRID2, GRIK2, GRIK4, GRIN2A, GRM7, JPH3, KCNAB1, KCNB2, KCNC2, KCND3, KCNE1, KCNE3, KCNIP1, KCNIP4, KCNJ12, KCNJ15, KCNJ6, KCNK18, KCNK2, KCNMA1, KCNMB1, KCNMB2, KCNMB3, KCNQ4, KCNQ5, LRRC52, MCOLN2, NALCN, NIPAL3, OCA2, PDE2A, PEX5L, PIEZO2, PKD1L2, PKDREJ, RYR2, RYR3, SCN11A, SCN3A, SCN5A, SCN9A, SCNN1G, SIDT1, SLC12A6, SLC12A8, SLC15A2, SLC15A5, SLC16A14, SLC17A5, SLC19A3, SLC1A2, SLC1A6, SLC1A7, SLC22A16, SLC24A2, SLC24A3, SLC24A4, SLC26A11, SLC26A9, SLC28A3, SLC2A1, SLC2A9, SLC30A9, SLC35A1, SLC36A1, SLC36A2, SLC39A11, SLC39A12, SLC39A8, SLC4A4, SLC5A12, SLC7A1, SLC7A13, SLC7A5, SLC8A3, SLC9A2, SLC9A4, SLC9A9, SLC9C1, SLCO1B1, SLCO1B3, SV2C, TAP1, TAP2, TPCN2, TRPC6, TRPM3, TRPM4, ZDHHC13*

GO categories in which false discovery rate is less than 0.01.

Table S21 continued.

Description	p-value	Enrichment	Genes
Lipid binding	3.0×10^{-5}	1.5	*ABCA1, ABCG1, ACBD5, ADH4, ADH5, AFAP1, AKR1C2, ALS2, APBB1IP, APOC2, ARAP1, ARAP3, ARHGAP15, ARHGAP22, ARHGAP24, ARHGAP25, ARHGAP26, ARHGAP42, ARHGEF18, ARHGEF4, ASAP1, BCR, BPIFB2, BPIFB6, CADPS, CDC42BPA, CMIP, CNKSR1, DAPP1, DGKH, DNM3, DOCK10, DOK5, DOK6, DOK7, DYSF, ELMO1, ESR1, ESRRG, FARP1, FER, FGD5, FRMPD2, GRB10, HS1BP3, IQSEC1, KALRN, KL, LAMC1, LANCL2, LPAR3, MAP3K1, MCF2L2, MYO10, MYO1B, MYOF, NR3C1, NR3C2, O3FAR1, PCLO, PGR, PHLDB2, PIK3C2G, PLA2G4C, PLCB1, PLCG2, PLCH1, PLEK, PLEKHA6, PLEKHF2, PLEKHG1, PLEKHH2, PON1, PREX2, PSD3, PTGS1, PXK, RASGRF2, RBP4, SCARB1, SCIN, SCP2, SELL, SGIP1, SH3GL2, SKAP2, SNTB1, SNTG1, SNTG2, SNX16, SNX19, SNX29, SNX31, SNX4, SNX7, SNX9, SOAT1, SPATA13, SWAP70, TEC, TIAM1, TIAM2, TULP3, UGT1A7, UGT1A8, UGT1A9, VAV2, VAV3, VNN1, VPS36, ZFYVE26*
Cytoskeletal protein binding	3.8×10^{-5}	1.6	*ABLIM1, ABLIM3, ACTN4, ACTR2, ADD2, AFAP1, AGBL1, AGBL4, AGTPBP1, ANK1, ANK2, ANK3, ARHGAP26, ARHGAP42, ARPC5, ASAP1, BICD1, CACNA1C, CAP1, CCDC88C, CLMN, COBLL1, CORO2B, DAAM2, DLC1, DYNC1I1, EPB41L2, EPB41L4A, FARP1, FBXO25, FER, FHOD3, FKBP15, FMN1, FMN2, FMNL2, FRMD3, GAS7, IQGAP2, JAKMIP2, JAKMIP3, KCNE1, KCNMA1, KLHL1, KLHL5, LDB3, LIMCH1, LRPPRC, MAEA, MAGI1, MAP2, MICAL2, MTSS1, MTUS2, MYLK, MYO10, MYO16, MYO18B, MYO1B, MYO3B, MYO5A, MYO5B, MYO7A, MYOZ2, MYPN, MYRIP, NCALD, NRAP, NRCAM, PACSIN2, PALLD, PARVA, PDLIM5, PHACTR1, PRKCE, PTPRT, PXK, RCSD1, SCIN, SCN5A, SDC2, SGIP1, SHROOM3, SKA1, SNCA, SNTB1, SNTG1, SNTG2, SORBS1, SPTB, SVIL, SYBU, SYNE1, TBCD, TNS1, UTRN, WASF3, XIRP2*
Rho guanyl-nucleotide exchange factor activity	3.9×10^{-5}	3.1	*ALS2, ARHGEF18, ARHGEF37, ARHGEF4, BCR, DOCK10, DOCK2, ECT2L, FARP1, FGD5, KALRN, MCF2L2, PLEKHG1, PREX2, RASGRF2, SPATA13, TIAM1, TIAM2, VAV2, VAV3*
Transmembrane signaling receptor activity	4.4×10^{-5}	8.6	*HLA-A, HLA-B, HLA-C, HLA-DPA1, HLA-DQA1, HLA-DQB1, OR4C3*

GO categories in which false discovery rate is less than 0.01.