

Supplementary Tables

Table S1. List of upregulated unique genes for each population.

Population	Unique genes
Asian	AARS2, AATF, AC005332.3, ACBD6, ADM2, AL365181.3, ALG1L, AP5Z1, ASF1B, ATIC, AURKB, BANF1, BLOC1S3, C1orf35, CAD, CASC3, CCL25, CCNB2, CD2BP2, CDCA8, CDK1, CDKN2A, CDKN3, CDT1, CENPM, CHAF1A, CHTOP, COPS7B, CSE1L, CTHRC1, DAXX, DCAF13, DEDD, DHX34, DKK1, DVL2, DYNLL1, EHMT2, EPS8L3, FAM222A, FBL, FGF21, FN3KRP, GLA, GSDMB, HDAC11, HES6, HGS, HNRNPA1, HSPA1A, HSPA1B, IGF2BP2, ITGB1BP1, ITPKA, KIF22, KIFC1, LIG1, LYSMD1, METTL18, MROH1, NAA20, NCAPD2, NF2, NMB, NPM1, NT5DC2, NUP62, P3H4, PABPC1L, PLPP2, POC1A, PPOX, PYCR1, RBIS, RBMX, RECQL4, RFC4, RHNO1, RNPEPL1, RNU6-8, RPL23A, RRP1, RUSC1, SCARA3, SLC26A6, SNAPIN, SNHG1, SNHG25, SNHG7, SP5, SPC24, SPSB2, SREBF2, SUV39H1, TACC3, TAFAZZIN, TARBP1, TBC1D16, TCF19, TEAD3, TJAP1, TMED9, TOMM20, TPRKB, TRIM65, TRMT2A, TTC13, TUBB, TUFT1, UBE2O, UBE2T, USP21, VPS45, WDR5, XPO5, ZBED10P
Caucasian	NFYA, PLXND1, SPPL2B, TMEM98, GGCT, RPUSD1, CYB561, IL32, MVP, XYLT2, BIRC3, EHD2, RRAGD, TYMP, BTN3A1, BAK1, TMSB10, AIFM2, ATP6V1H, TPR, TSPAN17, CYBA, ATP2B4, CS, SUGP2, ME1, SMARCD1, ATP1B3, UFD1, NUCB2, GBA2, ATP6AP1, TRIB2, RHOBTB1, XRCC1, TEAD2, CA12, RAP1GAP, NFKB2, SIRT6, UBE2A, FBLN1, SCGN, COL5A3, DLGAP4, ATP8B1, FAT1, BAX, DNM1L, PIR, EPB41L1, ARHGAP4, STRN4, GOLGA3, SEL1L3, TMEM38B, PGC, ERMP1, TSPAN15, WASHC2A, CEP170B, RASSF7, LGALS1, PIK3IP1, TRIOBP, KDELR3, RHBDD3, FOXRED2, ABHD4, ABHD12, SLC17A9, C20orf27, CDC25B, ARFRP1, HM13, PXMP4, WFDC2, PSMD10, WDR13, ABCD1, MAGED2, MAPK3, CLCN7, PIEZO1, PYCARD, NIPAL2, EEF1D, ANXA13, RELB, ARHGEF18, YJU2B, PPP6R1, SLC1A5, TGFB1, RPS19, PLPPR2, BCAT2, ARRDC2, ISYNA1, TMEM147, ATP13A1, PON2, ABHD11, GARS1, SNX8, MOGAT3, BLVRA, YKT6, CA9, ABCA2, RASSF4, LZTS2, NPM3, CPD, COL1A1, RAB34, CPE, WFS1, MFSD10, GALNT18, TCIRG1, VWF, MLEC, MGP, TIMELESS, CILK1, VNN2, SLC39A7, SLC29A1, HARS2, APBB3, SPARC, SUB1, SLC12A7, GNPDA1, PDGFRB, CCL20, MPV17, PSMD14, EFEMP1, REG1A, TIA1, FAM20B, SRM, FBXO2, P3H1, RARRES1, IFI27L2, EPCAM, NUP43, CYSTM1, PDZD11, HSPH1, COPS5, SCPEP1, DESI2, TMEM54, OCRL, PAEP, GIPC1, TUBA1B, LPGAT1, PIGT, USP22, MYRF, DOK4, RAP2A, SOX9, MIF4GD, PPDPF, SDCBP2, BCL2L12, SSX1, MAP2K2, TSPAN8, TUBA4A, SDF2L1, GAL3ST1, ATP6V1F, SMO, MRPS12, DUT, PALLD, AP1M2, RNASE1, TOMM40, COL5A1, LAMA5, HIP1R, RAMP2, PRKAB2, SNRPA1, LGALS3, RAMP1, TRIM47, RHBG, AP3B1, FBXO44, CHI3L1, NTS, PTGFRN, FKBP11, RTL8C, GOLM1, CD36, TES, CDK4, GLUL, BZW2, TTYH3, SAP130, UGGT1, TXN, DAB2IP, CDK5RAP2, DPM2, ENPP2, GGH, PREB, SLC5A6, ITGAV, CXCL9, PAPSS1, COMMD4, ULK3, CMTM3, NOL3, OSGIN1, DEF8, G6PC3, SECTM1, CBX4, FKBP10, HSPG2, SLC44A3, ATP1B1, POGK, COP1, MRPL9, POGZ, EIF2D, INTS7, SMYD2, INTS3, PARP1, CCNA2, DCDC2, SLC17A4, FAM193B, RNF44, GNA12, C7orf50, OGT, PLPPR1, GSN, CIZ1, GPR107, CYP17A1, ST14, HYOU1, TAOX2, CCT5, AKR1C2, TMEM45B, HSPB8, GJA1, CLGN, RASSF3, LPCAT1, LY96, BTG3, LARP1, BATF, ODR4, MMP14, WASF2, LAD1, CYB5R1, PSKH1, NPR2,

TFF3, PDXK, SHKBP1, ZBTB7B, SHC1, ANO10, PMF1, GPATCH4, FGFR4, NACC1, PPP1R16A, SQSTM1, DVL3, ITGA5, JOSD2, FLYWCH2, KLHL21, SELENON, BROX, PKDCC, S100A11, COL6A3, NAXE, ATP1A1, ANKZF1, PRKCD, FOXQ1, SLC29A4, COL1A2, CDK5, SLC4A2, FASTK, COX6C, WASHC5, SPTSSA, INPPL1, ZNF503, ZMYND19, NSMF, IFI27, SPINT1, CKB, TRMT61A, MARS1, PRR15L, RRM1, MVD, LENG8, YIF1B, MFSD3, CD320, CYP7A1, FTH1, TAP1, REEP4, ATXN2L, COL3A1, PCSK9, PTK2, LRRC45, CENPX, ASPSCR1, FASN, RAC3, FABP4, COX7B2, GSTA4, BBLN, LGALS4, PWWP2B, CYP4F22, MRPL13, BPGM, MAB21L4, HCFC1, CORO1B, LRRC20, EGFL7, ADCK5, MTX1, GPR137, PPP1R14B, RNF213, PHLDA3, SLC16A11, SLC29A2, BRMS1, CD248, PDZK1, CSRP2, DCTN2, PNMA1, DEAF1, ERICH5, CD151, TMEM94, SOX12, PLEC, MSC, APOLD1, EXOSC4, RRS1, RCC2, SAMD4B, B3GNT3, DCTPP1, PPP1R14BP3, H2AC6, H2BC4, PHLDA2, CLDN7, CREB3L2, PLCXD1, LIMK2, MFSD5, SNORC, HMGN4, DDX41, FHL3, ALYREF, ZNF703, NUDT14, CRELD2, PGP, H2BC21, NRBP2, TCEAL9, UBALD2, NOTUM, TOR3A, C17orf58, TPCN1, RTN4RL2, BCAM, H1-2, AGRN, H1-0, CLDN4, S100A14, IARS1, MYL6B, NCOR2, LAMB3, FLNA, SRC, ATP6AP1-DT, ENTPD6, H2BC12, S100A6, ASPH, TXNRD1, DDX39B, MAGEA1, IPO9, GLMP, SHISA4, CCDC167, SOX18, HLA-DMA, COL5A2, PBX2, AGPAT1, FKBPL, VARS1, DDR1, HLA-F, NAT8B, LCMT1, HLA-A, MT-TL1, ARL2, SLC35F6, CLIC1, DDAH2, LYRM4, MAGEA3, CCNL2, BAIAP2-DT, RPL10P6, FTLP2, RPL10P9, PTGES3P1, APOC2, RPL39P3, HSPB1P1, RGL2, TMEM250, KMT2E-AS1, PSMB9, ARPC1A, NEAT1, H2AJ, MALAT1, TRNP1, PRKDC, LINC01419, MPV17L2, AC136475.3, SNHG9, GATD1-DT, AC006205.2, AC087482.1, DSP-AS1, PECAM1, AC009407.1, MYH4, MIR4664, AC027307.2, AL049840.5, H4C9, H2AC8, MRM1, AL606500.1

Table S2. List of downregulated unique genes for each population.

Population	Unique genes
Asian	LAP3, PDK4, AASS, SEC62, HEBP1, TNFRSF1B, PI4K2B, TAB2, OAT, ISOC1, MAOB, LMAN1, TTC38, MCCC1, STRADB, TGDS, F11, CMTM6, COMT, SORBS1, CREM, SUN2, LGMN, DCAF11, SEC23A, LPIN2, NDFIP2, FNDC3A, SLC25A15, LONP2, FCGRT, HIBADH, ENG, PHYH, PPIF, ZNF330, KLHL2, SEPSECS, SC5D, DUSP16, SERINC1, CPEB4, EHBP1, PCYOX1, GADD45A, CTH, SDHB, MTARC2, ELL2, IRF2BPL, AVPI1, GOT1, RAMP3, ACO1, SRGN, FAM210B, TTPAL, PEPD, TMEM53, ASL, SGPP1, MCCC2, IL6ST, CTSL, NIPSNAP3A, CDK9, SLC31A1, SLCO2B1, PRCP, ITPRID2, ENPEP, HADH, SEC24B, GABARAPL1, SUOX, TMBIM6, RAB20, BNIP2, ABHD2, ALDH9A1, PIK3R1, IQGAP2, AK3, STOM, EI24, SEC24D, UBALD1, SORBS2, TSPAN7, PAFAH2, ALDH4A1, ACOX1, ZYG11B, PDLIM5, FBXO8, SFXN1, PDSS2, ARL5B, CLPX, CYB5D2, MMADHC, PPID, SUCLG2, MYD88, PCCA, SLC25A20, MAF, PER1, CSF1R, FAM167B, ACOT1, SOWAHB, CHP1, TSPYL1, ARHGEF12, ENPP1, PIM3, PAPSS2, GK, SDHD, ETRF1, APOL6, CTSO, SRSF8, NCOA4, AL354872.2
Caucasian	AADAT, ABLIM3, AC008549.1, AC026803.3, AC115619.1, ACOT12, ACSM2A, ACSM3, ACSM5, AD000090.1, ADAMTS1, ADAMTSL2, ADGRG6, ADH1C, ADI1, ADRB2, AGL, AGTR1, AGXT, AHSG, AKR7A3, AL360013.3, AL391095.2, ALDOB, ALPL, AMBP, AMN, ANG, ANGPTL3, ANKS4B, ANO1, ANXA10, AOX1, APCS, APOA1, APOA5, APOC1P1, APOC3, APOH, APOL1, AR, ARSD, ART4, ASPDH, ASPG, ATF5, ATP11C, AVPR1A, AZGP1P1, BBOX1, BCHE, BGN, BHMT, C1QB, C1QTNF1, C3P1, C7, C9, CA2, CCDC3, CCDC71L, CCL19, CCL2, CCL21, CCND2P1, CDA, CDO1, CEBPD, CES3, CFHR3, CFI, CISH, CLRN3, CLU, CMBL, CNGA1, COLEC11, CPB2, CPN2, CREB3L3, CRHBP, CXCL14, CXCL2, CYB5A, CYP1A2, CYP27A1, CYP2A6, CYP2B6, CYP2C18, CYP2C19, CYP2C9, CYP2E1, CYP2J2, CYP3A4, CYP4F12, CYP4F2, CYP8B1, DCN, DCXR, DGAT2, DHRS1, DNAJC12, DPYS, DTX1, DUSP10, DUSP14, ECM1, EDNRB, EFHD1, EVA1A, F2, FABP1, FAM110C, FAM99A, FAXDC2, FCGR3A, FETUB, FGG, FGL1, FMO3, FNIP2, FOSB, FTCD, G6PC1, GADD45G, GATA4, GATM, GBP1, GBP7, GCGR, GCKR, GGT5, GJB2, GLYAT, GPAT3, GPD1, GSTA2, HAAO, HABP2, HAO2, HBA2, HES1, HGFAC, HMGCS2, HNF4A-AS1, HP, HRG, HS3ST3B1, HSD17B13, HSD17B6, IER2, IGFBP1, IGFBP2, IGHA1, IGHA2, IGHM, IL1RAP, IL27, INHBC, INMT, IRF8, ITIH1, JCHAIN, JUND, KDSR, KIAA0040, LEAP2, LECT2, LINC01018, LINC01093, LINC01702, LIPC, LRCOL1, LRG1, LY6E, MFAP4, MFSD2A, MOGAT2, MST1, MT1A, MT1DP, MT1E, MT1F, MT1G, MT1H, MT1L, MT1M, MT1X, MT-ATP8, MT-CO2, MTND2P28, MT-ND3, MT-ND6, MTPP, MYC, N4BP2L1, NAAA, NBPF13P, NCOR1, NNMT, NR0B2, NR1I2, NR4A1, NRB2F2, NUGGC, OGDHL, OLFML3, ORM1, ORM2, OTC, PGLYRP2, PHGDH, PHYHD1, PIGV, PLAAT3, PLEK2, PLSCR4, PON1, PPP1R1A, PRG4, PRODH2, PROZ, PRRG4, PTMS, PTPN3, PZP, RBP4, RBP5, RETREG1, RGN, RN7SL1, RND1, RNF152, S100A8, SAA1, SAA2, SERPINA1, SERPINA10, SERPINA4, SERPINF2, SFRP5, SHBG, SIK1B, SLC10A1, SLC13A5, SLC16A2, SLC1A1, SLC22A1, SLC22A10, SLC25A47, SLC27A2, SLC27A5, SLC28A1, SLC2A2, SLC39A5, SLC4A4, SLC6A12, SLC9B2, SLCO1B1, SLCO1B3, SMIM19, SMIM24, SOCS2, SPP2, SPRY2, SRD5A2, ST3GAL6, SULT1A1, SULT2A1, TBX15, TENT5A, TF, THBS1, THRSP, TKFC, TM6SF2, TMEM45A, TMEM47, TMEM82, TMPRSS2, TTC36, TTPA, TTR, UPB1, VMO1, VNN1, XDH, ZG16

Table S3. List of common upregulated and downregulated genes in Asian and Caucasian populations.

Expression	Genes
Upregulated	<i>REG3A, S100P, AKR1B10, AFP, PEG10, DUSP9, UPK3A, CPLX2, GPC3, EEF1A2, MYBL2, NQO1, MUC13, CDC20, C1QL1, BIRC5, ETV4, MMP11, UBE2C, ACSL4, LCN2, MPZ, TOP2A, ALDH3A1, SEZ6L2, PTTG1, PDZK1IP1, KRT23, SLC6A8, SPINK1, UGT2B11, CCNB1, SNCG, BAIAP2L2, SPP1, E2F1, THY1, MDK, ROBO1, CGREF1, AC092535.5, SLC51B, BEX2, SFN, PTP4A3, TRIM16L, HRCT1, CENPW, TMEM150B, C12orf75, NDUFA4L2, PLVAP, TESC, TPX2, G6PD, SNORD104, OR2I1P, SPARCL1, NOTCH3, CAP2, PDGFA, CD34, HKDC1, ZWINT, FAM83D, CDKN2C, AURKA, GMNN</i>
Downregulated	<i>FCN2, MARCO, FCN3, HAMP, OIT3, CD5L, NAT2, MT2P1, DNASE1L3, IGFALS, APOF, ADH4, GHR, CYP2C8, RND3, CYP39A1, CXCL12, RCAN1, UROC1, PHLDA1, PCK1, LCAT, GBA3, KDM8, FOS, MT2A, LPA, EGR1, CSRNP1, CYP4A11, CYP4A22, TCIM, RDH16</i>

Table S4. The top 20 enriched biological processes associated with common upregulated genes in both populations.

Category	Biological Processes Unique
Biological Process	• mRNA splicing, via spliceosome (GO: 0000398) • regulation of DNA-templated DNA replication initiation (GO: 0030174) • DNA unwinding involved in DNA replication (GO: 0006268) • double-strand break repair via break-induced replication (GO: 0000727) • U2-type prespliceosome assembly (GO: 1903241) • spliceosomal snRNP assembly (GO: 0000387) • cell division (GO: 0051301) • 7-methylguanosine cap hypermethylation (GO: 0036261) • regulation of cell cycle (GO: 0051726) • chaperone-mediated gene folding (GO: 0061077) • positive regulation of mitotic metaphase/anaphase transition (GO: 0045842) • RNA splicing (GO: 0008380) • DNA replication initiation (GO: 0006270) • heterochromatin formation (GO: 0031507) • mRNA processing (GO: 0006397) • positive regulation of DNA-templated transcription (GO: 0045893) • nuclear pore localization (GO: 0051664) • nuclear envelope organization (GO: 0006998) • anaphase-promoting complex-dependent catabolic process (GO: 0031145) • regulation of mitotic cell cycle (GO: 0007346)
Cellular Component	• nucleoplasm (GO: 0005654) • cytosol (GO: 0005829) • nucleus (GO: 0005634) • spliceosomal complex (GO: 0005681) • cytoplasm (GO: 0005737) • U2-type precatalytic spliceosome (GO: 0071005) • extracellular exosome (GO: 0070062) • U4/U6 x U5 tri-snRNP complex (GO: 0046540) • precatalytic spliceosome (GO: 0071011) • U1 snRNP (GO: 0005685) • CMG complex (GO: 0071162) • MCM complex (GO: 0042555) • nuclear laminanuclear lamina (GO: 0005652) • chromosome, telomeric region chromosome, telomeric region (GO: 0000781) • spindle (GO: 0005819) • small nuclear ribonucleogene complex (GO: 0030532) • U2 snRNP (GO: 0005686) • U2-type spliceosomal complex (GO: 0005684) • gene folding chaperone complex (GO: 0101031) • catalytic step 2 spliceosome (GO: 0071013)
Molecular Function	• gene binding (GO: 0005515) • RNA binding (GO: 0003723) • identical gene binding (GO: 0042802) • gene homodimerization activity (GO: 0042803) • gene kinase binding (GO: 0019901) • ubiquitin binding (GO: 0043130)

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- gene heterodimerization activity (GO: 0046982)
 - cadherin binding (GO: 0045296)
 - ATP-dependent gene binding (GO: 0043008)
 - single-stranded DNA helicase activity (GO: 0017116)
 - gene-containing complex binding (GO: 0044877)
 - DNA polymerase binding (GO: 0070182)
 - ATP-dependent H2AZ histone chaperone activity (GO: 0140849)
 - DNA binding (GO: 0003677)
 - tubulin binding (GO: 0015631)
 - U1 snRNP binding (GO: 1990446)
 - U1 snRNA binding (GO: 0030619)
 - structural constituent of ribosome (GO: 0003735)
 - histone deacetylase binding (GO: 0042826)
 - unfolded gene binding (GO: 0051082)
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Table S5. The top 20 enriched biological processes associated with common down-regulated genes in both populations.

Category	Biological Processes Unique
Biological Process	• fibrinolysis (GO: 0042730) • complement activation, classical pathway (GO: 0006958) • fatty acid beta-oxidation (GO: 0006635) • fatty acid beta-oxidation using acyl-CoA dehydrogenase (GO: 0033539) • zymogen activation (GO: 0031638) • response to hypoxia (GO: 0001666) • lipid metabolic process (GO: 0006629) • electron transport coupled proton transport (GO: 0015990) • gluconeogenesis (GO: 0006094) • response to organic cyclic compound (GO: 0014070) • complement activation, lectin pathway (GO: 0001867) • cellular response to insulin stimulus (GO: 0032869) • response to starvation (GO: 0042594) • aerobic respiration (GO: 0009060) • retinoic acid metabolic process (GO: 0042573) • cell surface pattern recognition receptor signaling pathway (GO: 0002752) • fatty acid metabolic process (GO: 0006631) • bile acid biosynthetic process (GO: 0006699) • response to xenobiotic stimulus (GO: 0009410) • regulation of keratinocyte differentiation (GO: 0045616)
Cellular Component	• mitochondrion (GO: 0005739) • mitochondrial matrix (GO: 0005759) • blood microparticle (GO: 0072562) • extracellular exosome (GO: 0070062) • peroxisomal matrix (GO: 0005782) • extracellular space (GO: 0005615) • peroxisome (GO: 0005777) • cytosol (GO: 0005829) • extracellular region (GO: 0005576) • platelet alpha granule lumen (GO: 0031093) • collagen-containing extracellular matrix (GO: 0062023) • mitochondrial membrane (GO: 0031966) • external side of plasma membrane (GO: 0009897) • transcription factor AP-1 complex (GO: 0035976) • respiratory chain complex I (GO: 0045271) • membrane attack complex (GO: 0005579) • serine-type endopeptidase complex (GO: 1905370) • mitochondrial inner membrane (GO: 0005743) • RNA polymerase II transcription regulator complex (GO: 0090575) • endoplasmic reticulum membrane (GO: 0005789)
Molecular Function	• oxidoreductase activity (GO: 0016491) • heme binding (GO: 0020037) • acyl-CoA dehydrogenase activity (GO: 0003995) • pyridoxal phosphate binding (GO: 0030170) • identical gene binding (GO: 0042802) • flavin adenine dinucleotide binding (GO: 0050660)

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- oxidoreductase activity, acting on the CH-CH group of donors (GO: 0016627)
 - acetyl-CoA C-acyltransferase activity (GO: 0003988)
 - all-trans-retinol dehydrogenase (NAD⁺) activity (GO: 0004745)
 - electron transfer activity (GO: 0009055)
 - alcohol dehydrogenase (NAD⁺) activity (GO: 0004022)
 - NADH dehydrogenase (ubiquinone) activity (GO: 0008137)
 - NAD binding (GO: 0051287)
 - signaling receptor binding (GO: 0005102)
 - NADPH binding (GO: 0070402)
 - acetyl-CoA C-acetyltransferase activity (GO: 0003985)
 - serine-type endopeptidase activity (GO: 0004252)
 - gene homodimerization activity (GO: 0042803)
 - long-chain fatty acid omega-hydroxylase activity (GO: 0102033)
 - oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO: 0016705)
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