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Table S1. Normalized expression values for proteomic biomarkers at baseline (N = 2045)

Protein names	Genenames	UniProt_ID
Immunoglobulin lambda constant 7 (Ig lambda-7 chain C region)	IGLC7	A0M8Q6
Transmembrane protein 131-like	TMEM131L	A2VDJ0
EF-hand calcium-binding domain-containing protein 5	EFCAB5	A4FU69
PH and SEC7 domain-containing protein 1 (Exchange factor for ADP-ribosylation factor guanine nucleotide factor 6) (Exchange factor for ARF6) (Exchange factor for ARF6 A) (Pleckstrin homology and SEC7 domain-containing protein 1)	PSD	A5PKW4
Transcription factor TFIIIB component B' homolog (Transcription factor IIIB 150) (TFIIIB150) (Transcription factor-like nuclear regulator)	BDP1	A6H8Y1
Rho GTPase-activating protein 42 (Rho GTPase-activating protein 10-like) (Rho-type GTPase-activating protein 42)	ARHGAP42	A6NI28
Golgin subfamily A member 6-like protein 10	GOLGA6L10	A6NI86
Leucine-rich repeat-containing protein 10B	LRRC10B	A6NIK2
Transmembrane protein 200C (Transmembrane protein TTMA) (Two transmembrane domain-containing family member A)	TMEM200C	A6NKL6
Sine oculis-binding protein homolog (Jackson circler protein 1)	SOBP	A7XYQ1
Putative WAS protein family homolog 4 (Protein FAM39CP)	WASH4P	A8MWX3
Melanoma-associated antigen B17	MAGEB17	A8MXT2
CMT1A duplicated region transcript 15 protein-like protein	CDRT15L2	A8MXV6
Forkhead-associated domain-containing protein 1 (FHA domain-containing protein 1)	FHAD1	B1AJZ9
Unconventional myosin-IXa (Unconventional myosin-9a)	MYO9A	B2RTY4
Uncharacterized protein encoded by LINC02881 (Long intergenic non-protein coding RNA 2881)	LINC02881	B7Z368
Zinc finger protein 814	ZNF814	B7Z6K7
Transmembrane protein 238	TMEM238	C9JI98
Ankyrin repeat domain-containing protein 65	ANKRD65	E5RJM6
RNA polymerase II elongation factor ELL2	ELL2	O00472
Probable ubiquitin carboxyl-terminal hydrolase FAF-Y (EC 3.4.19.12) (Deubiquitinating enzyme FAF-Y) (Fat facets protein-related, Y-linked) (Ubiquitin thioesterase FAF-Y) (Ubiquitin-specific protease 9, Y chromosome) (Ubiquitin-specific-processing protease FAF-Y)	USP9Y	O00507
Suppressor of cytokine signaling 2 (SOCS-2) (Cytokine-inducible SH2 protein 2) (CIS-2) (STAT-induced STAT inhibitor 2) (SSI-2)	SOCS2	O14508

Citron Rho-interacting kinase (CRIK) (EC 2.7.11.1) (Serine/threonine-protein kinase 21)	CIT	O14578
Histone-lysine N-methyltransferase 2D (Lysine N-methyltransferase 2D) (EC 2.1.1.364) (ALL1-related protein) (Myeloid/lymphoid or mixed-lineage leukemia protein 2)	KMT2D	O14686
Serine/threonine-protein kinase RIO3 (EC 2.7.11.1) (RIO kinase 3) (sudD homolog)	RIOK3	O14730
Apolipoprotein L1 (Apolipoprotein L) (Apo-L) (ApoL) (Apolipoprotein L-I) (ApoL-I)	APOL1	O14791
Protein unc-13 homolog B (Munc13-2) (munc13)	UNC13B	O14795
Microtubule-associated serine/threonine-protein kinase 4 (EC 2.7.11.1)	MAST4	O15021
Protein KHNYN (KH and NYN domain-containing protein)	KHNYN	O15037
Histone-lysine N-methyltransferase SETD1A (EC 2.1.1.364) (Lysine N-methyltransferase 2F) (SET domain-containing protein 1A) (hSET1A) (Set1/Ash2 histone methyltransferase complex subunit SET1)	SETD1A	O15047
Zinc finger and BTB domain-containing protein 5	ZBTB5	O15062
Rho guanine nucleotide exchange factor 11 (PDZ-RhoGEF)	ARHGEF11	O15085
Zinc finger protein 536	ZNF536	O15090
Nephrocystin-1 (Juvenile nephronophthisis 1 protein)	NPHP1	O15259
Ataxin-7 (Spinocerebellar ataxia type 7 protein)	ATXN7	O15265
Zinc finger ZZ-type and EF-hand domain-containing protein 1	ZZEF1	O43149
Signal-induced proliferation-associated 1-like protein 1 (SIPA1-like protein 1) (High-risk human papilloma viruses E6 oncoproteins targeted protein 1) (E6-targeted protein 1)	SIPA1L1	O43166
Rho GTPase-activating protein 6 (Rho-type GTPase-activating protein 6) (Rho-type GTPase-activating protein RhoGAPX-1)	ARHGAP6	O43182
Leucine-rich repeat transmembrane neuronal protein 2 (Leucine-rich repeat neuronal 2 protein)	LRRTM2	O43300
Protein CBFA2T2 (ETO homologous on chromosome 20) (MTG8-like protein) (MTG8-related protein 1) (Myeloid translocation-related protein 1) (p85)	CBFA2T2	O43439
CD5 antigen-like (Apoptosis inhibitor expressed by macrophages) (hAIM) (CT-2) (IgM-associated peptide) (SP-alpha)	CD5L	O43866
Protein phosphatase 1 regulatory subunit 12B (Myosin phosphatase-targeting subunit 2) (Myosin phosphatase target subunit 2)	PPP1R12B	O60237
Leucine zipper putative tumor suppressor 3 (ProSAP-interacting protein 1) (ProSAPiP1)	LZTS3	O60299
Phospholipid-transporting ATPase VA (EC 7.6.2.1) (ATPase class V type 10A) (Aminophospholipid translocase VA) (P4-ATPase flippase complex alpha subunit ATP10A)	ATP10A	O60312
Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma (PIP5K1gamma) (PtdIns(4)P-5-kinase 1 gamma) (EC 2.7.1.68) (Type I phosphatidylinositol 4-phosphate 5-kinase gamma)	PIP5K1C	O60331

Lymphocyte antigen 75 (Ly-75) (C-type lectin domain family 13 member B) (DEC-205) (gp200-MR6) (CD antigen CD205)	LY75	O60449
Cubilin (460 kDa receptor) (Intestinal intrinsic factor receptor) (Intrinsic factor-cobalamin receptor) (Intrinsic factor-vitamin B12 receptor)	CUBN	O60494
DNA/RNA-binding protein KIN17 (Binding to curved DNA) (KIN, antigenic determinant of recA protein homolog)	KIN	O60870
Kinesin-like protein KIF21B	KIF21B	O75037
Plexin-A2 (Semaphorin receptor OCT)	PLXNA2	O75051
Rho-associated protein kinase 2 (EC 2.7.11.1) (Rho kinase 2) (Rho-associated, coiled-coil-containing protein kinase 2) (Rho-associated, coiled-coil-containing protein kinase II) (ROCK-II) (p164 ROCK-2)	ROCK2	O75116
Low-density lipoprotein receptor-related protein 5 (LRP-5) (Low-density lipoprotein receptor-related protein 7) (LRP-7)	LRP5	O75197
Filamin-B (FLN-B) (ABP-278) (ABP-280 homolog) (Actin-binding-like protein) (Beta-filamin) (Filamin homolog 1) (Fh1) (Filamin-3) (Thyroid autoantigen) (Truncated actin-binding protein) (Truncated ABP)	FLNB	O75369
Nuclear receptor corepressor 1 (N-CoR) (N-CoR1)	NCOR1	O75376
GRB10-interacting GYF protein 1 (PERQ amino acid-rich with GYF domain-containing protein 1)	GIGYF1	O75420
KH domain-containing, RNA-binding, signal transduction-associated protein 3 (RNA-binding protein T-Star) (Sam68-like mammalian protein 2) (SLM-2) (Sam68-like phosphotyrosine protein)	KHDRBS3	O75525
Syntaxin-11	STX11	O75558
Ficolin-3 (Collagen/fibrinogen domain-containing lectin 3 p35) (Collagen/fibrinogen domain-containing protein 3) (Hakata antigen)	FCN3	O75636
Isocitrate dehydrogenase [NADP] cytoplasmic (IDH) (IDH1) (EC 1.1.1.42) (Cytosolic NADP-isocitrate dehydrogenase) (IDPc) (NADP(+)-specific ICDH) (Oxalosuccinate decarboxylase)	IDH1	O75874
Attractin (DPPT-L) (Mahogany homolog)	ATRN	O75882
Triple functional domain protein (EC 2.7.11.1) (PTPRF-interacting protein)	TRIO	O75962
Multiple PDZ domain protein (Multi-PDZ domain protein 1)	MPDZ	O75970
PHD finger protein 14	PHF14	O94880
Ubiquitin conjugation factor E4 B (EC 2.3.2.27) (Homozygously deleted in neuroblastoma 1) (RING-type E3 ubiquitin transferase E4 B) (Ubiquitin fusion degradation protein 2)	UBE4B	O95155
Chromosome-associated kinesin KIF4A (Chromokinesin-A)	KIF4A	O95239

Myotubularin-related protein 5 (Inactive phosphatidylinositol 3-phosphatase 5) (SET-binding factor 1) (Sbf1)	SBF1	O95248
Structural maintenance of chromosomes protein 2 (SMC protein 2) (SMC-2) (Chromosome-associated protein E) (hCAP-E) (XCAP-E homolog)	SMC2	O95347
Apolipoprotein M (Apo-M) (ApoM) (Protein G3a)	APOM	O95445
Keratin, type II cytoskeletal 75 (Cytokeratin-75) (CK-75) (Keratin-6 hair follicle) (hK6hf) (Keratin-75) (K75) (Type II keratin-K6hf) (Type-II keratin Kb18)	KRT75	O95678
E3 ubiquitin-protein ligase HERC2 (EC 2.3.2.26) (HECT domain and RCC1-like domain-containing protein 2) (HECT-type E3 ubiquitin transferase HERC2)	HERC2	O95714
Zinc finger MYM-type protein 6 (Transposon-derived Buster2 transposase-like protein) (Zinc finger protein 258)	ZMYM6	O95789
Megakaryocyte and platelet inhibitory receptor G6b (Protein G6b)	MPIG6B	O95866
G patch domain and ankyrin repeat-containing protein 1 (Ankyrin repeat domain-containing protein 59) (G patch domain-containing protein 10) (HLA-B-associated transcript 4) (Protein G5)	GPANK1	O95872
Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)	CP	P00450
Coagulation factor VIII (Antihemophilic factor) (AHF) (Procoagulant component) [Cleaved into: Factor VIIIa heavy chain, 200 kDa isoform; Factor VIIIa heavy chain, 92 kDa isoform; Factor VIII B chain; Factor VIIIa light chain]	F8	P00451
Coagulation factor XIII A chain (Coagulation factor XIIIa) (EC 2.3.2.13) (Protein-glutamine gamma-glutamyltransferase A chain) (Transglutaminase A chain)	F13A1	P00488
Prothrombin (EC 3.4.21.5) (Coagulation factor II) [Cleaved into: Activation peptide fragment 1; Activation peptide fragment 2; Thrombin light chain; Thrombin heavy chain]	F2	P00734
Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	HP	P00738
Haptoglobin-related protein	HPR	P00739
Coagulation factor IX (EC 3.4.21.22) (Christmas factor) (Plasma thromboplastin component) (PTC) [Cleaved into: Coagulation factor IXa light chain; Coagulation factor IXa heavy chain]	F9	P00740
Coagulation factor X (EC 3.4.21.6) (Stuart factor) (Stuart-Prower factor) [Cleaved into: Factor X light chain; Factor X heavy chain; Activated factor Xa heavy chain]	F10	P00742
Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	PLG	P00747
Coagulation factor XII (EC 3.4.21.38) (Hageman factor) (HAF) [Cleaved into: Coagulation factor XIIa heavy chain; Beta-factor XIIa part 1; Coagulation factor XIIa light chain (Beta-factor XIIa part 2)]	F12	P00748

Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I) (Cyanamide hydratase CA1) (EC 4.2.1.69)	CA1	P00915
Antithrombin-III (ATIII) (Serpine C1)	SERPINC1	P01008
Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serpine A1) [Cleaved into: Short peptide from AAT (SPAAT)]	SERPINA1	P01009
Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serpine A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	SERPINA3	P01011
Angiotensinogen (Serpine A8) [Cleaved into: Angiotensin-1 (Angiotensin 1-10) (Angiotensin I) (Ang I); Angiotensin-2 (Angiotensin 1-8) (Angiotensin II) (Ang II); Angiotensin-3 (Angiotensin 2-8) (Angiotensin III) (Ang III) (Des-Asp[1]-angiotensin II); Angiotensin-4 (Angiotensin 3-8) (Angiotensin IV) (Ang IV); Angiotensin 1-9; Angiotensin 1-7; Angiotensin 1-5; Angiotensin 1-4]	AGT	P01019
Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	A2M	P01023
Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]	C3	P01024
Complement C5 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 4) [Cleaved into: Complement C5 beta chain; Complement C5 alpha chain; C5a anaphylatoxin; Complement C5 alpha' chain]	C5	P01031
Kininogen-1 (Alpha-2-thiol proteinase inhibitor) (Fitzgerald factor) (High molecular weight kininogen) (HMWK) (Williams-Fitzgerald-Flaujeac factor) [Cleaved into: Kininogen-1 heavy chain; T-kinin (Ile-Ser-Bradykinin); Bradykinin (Kallidin I); Lysyl-bradykinin (Kallidin II); Kininogen-1 light chain; Low molecular weight growth-promoting factor]	KNG1	P01042
Immunoglobulin J chain (Joining chain of multimeric IgA and IgM)	JCHAIN	P01591
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin kappa variable 1-5 (Ig kappa chain V-I region CAR) (Ig kappa chain V-I region EU) (Ig kappa chain V-I region HK102) (Ig kappa chain V-I region Kue)	IGKV1-5	P01602
Immunoglobulin kappa variable 1-5 (Ig kappa chain V-I region CAR) (Ig kappa chain V-I region EU) (Ig kappa chain V-I region HK102) (Ig kappa chain V-I region Kue)	IGKV1-5	P01602

Immunoglobulin kappa variable 1-5 (Ig kappa chain V-I region CAR) (Ig kappa chain V-I region EU) (Ig kappa chain V-I region HK102) (Ig kappa chain V-I region Kue)	IGKV1-5	P01602
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin kappa variable 1-17 (Ig kappa chain V-I region Gal) (Ig kappa chain V-I region WEA)	IGKV1-17	P01599
Immunoglobulin kappa variable 1D-12 (Ig kappa chain V-I region Wes)	IGKV1D-12	P01611
Immunoglobulin kappa variable 1-39 (Ig kappa chain V-I region DEE) (Ig kappa chain V-I region Hau) (Ig kappa chain V-I region Mev) (Ig kappa chain V-I region OU) (Ig kappa chain V-I region Walker)	IGKV1-39	P01597
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin kappa variable 2D-40 (Ig kappa chain V-II region Cum)	IGKV2D-40	P01614
Immunoglobulin kappa variable 2D-28 (Ig kappa chain V-II region FR) (Ig kappa chain V-II region GM607) (Ig kappa chain V-II region MIL) (Ig kappa chain V-II region TEW)	IGKV2D-28	P01615
Immunoglobulin kappa variable 2D-28 (Ig kappa chain V-II region FR) (Ig kappa chain V-II region GM607) (Ig kappa chain V-II region MIL) (Ig kappa chain V-II region TEW)	IGKV2D-28	P01615
Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	IGKV3-20	P01619
Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	IGKV3-20	P01619

Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	IGKV3-20	P01619
Immunoglobulin kappa variable 3-15 (Ig kappa chain V-III region CLL) (Ig kappa chain V-III region POM)	IGKV3-15	P01624
Immunoglobulin kappa variable 4-1 (Ig kappa chain V-IV region B17) (Ig kappa chain V-IV region JI) (Ig kappa chain V-IV region Len) (Ig kappa chain V-IV region STH)	IGKV4-1	P06312
Immunoglobulin lambda variable 2-11 (Ig gamma lambda chain V-II region DOT) (Ig lambda chain V-II region BOH) (Ig lambda chain V-II region BUR) (Ig lambda chain V-II region NIG-58) (Ig lambda chain V-II region TRO) (Ig lambda chain V-II region WIN)	IGLV2-11	P01706
Immunoglobulin lambda variable 3-19 (Ig lambda chain V-III region SH)	IGLV3-19	P01714
Immunoglobulin lambda variable 3-25 (Ig lambda chain V-IV region Hil)	IGLV3-25	P01717
Immunoglobulin lambda variable 3-21 (Ig lambda chain V-III region LOI) (Ig lambda chain V-V region DEL) (Ig lambda chain V-VII region MOT)	IGLV3-21	P80748
Immunoglobulin heavy variable 3-48 (Ig heavy chain V-III region WEA)	IGHV3-48	P01763
Immunoglobulin heavy variable 3-13 (Ig heavy chain V-III region BRO)	IGHV3-13	P01766
Immunoglobulin heavy variable 3-30 (Ig heavy chain V-III region BUR) (Ig heavy chain V-III region CAM) (Ig heavy chain V-III region GA) (Ig heavy chain V-III region NIE)	IGHV3-30	P01768
Immunoglobulin heavy variable 3-23 (Ig heavy chain V-III region LAY) (Ig heavy chain V-III region POM) (Ig heavy chain V-III region TEI) (Ig heavy chain V-III region TIL) (Ig heavy chain V-III region TUR) (Ig heavy chain V-III region VH26) (Ig heavy chain V-III region WAS) (Ig heavy chain V-III region ZAP)	IGHV3-23	P01764
Immunoglobulin heavy variable 3-7 (Ig heavy chain V-III region GAL) (Ig heavy chain V-III region GAR) (Ig heavy chain V-III region JON)	IGHV3-7	P01780
Immunoglobulin heavy variable 3-7 (Ig heavy chain V-III region GAL) (Ig heavy chain V-III region GAR) (Ig heavy chain V-III region JON)	IGHV3-7	P01780
Polymeric immunoglobulin receptor (PIgR) (Poly-Ig receptor) (Hepatocellular carcinoma-associated protein TB6) [Cleaved into: Secretory component]	PIGR	P01833
Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	IGHA1	P01876
Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	APOA1	P02647
Apolipoprotein E (Apo-E)	APOE	P02649

Apolipoprotein C-III (Apo-CIII) (ApoC-III) (Apolipoprotein C3)	APOC3	P02656
Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	FGA	P02671
Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	FGB	P02675
Fibrinogen gamma chain	FGG	P02679
C-reactive protein [Cleaved into: C-reactive protein(1-205)]	CRP	P02741
Serum amyloid P-component (SAP) (9.5S alpha-1-glycoprotein) [Cleaved into: Serum amyloid P-component(1-203)]	APCS	P02743
Complement C1q subcomponent subunit A	C1QA	P02745
Complement C1q subcomponent subunit B	C1QB	P02746
Complement C1q subcomponent subunit C	C1QC	P02747
Complement component C9 [Cleaved into: Complement component C9a; Complement component C9b]	C9	P02748
Beta-2-glycoprotein 1 (APC inhibitor) (Activated protein C-binding protein) (Anticardiolipin cofactor) (Apolipoprotein H) (Apo-H) (Beta-2-glycoprotein I) (B2GPI) (Beta(2)GPI)	APOH	P02749
Leucine-rich alpha-2-glycoprotein (LRG)	LRG1	P02750
Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	FN1	P02751
Protein AMBP (Protein HC) [Cleaved into: Alpha-1-microglobulin (EC 1.6.2.-) (Alpha-1 microglycoprotein) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (EDC1) (HI-30) (Uronic-acid-rich protein); Trypstatin]	AMBP	P02760
Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	ORM1	P02763
Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	AHSG	P02765
Transthyretin (ATTR) (Prealbumin) (TBPA)	TTR	P02766
Albumin	ALB	P02768
Vitamin D-binding protein (DBP) (VDB) (Gc protein-derived macrophage activating factor) (Gc-MAF) (GcMAF) (Gc-globulin) (Group-specific component) (Gc) (Vitamin D-binding protein-macrophage activating factor) (DBP-maf)	GC	P02774
Platelet basic protein (PBP) (C-X-C motif chemokine 7) (Leukocyte-derived growth factor) (LDGF) (Macrophage-derived growth factor) (MDGF) (Small-inducible cytokine B7) [Cleaved into: Connective tissue-activating peptide III (CTAP-III) (LA-PF4) (Low-affinity platelet factor IV); TC-2; Connective tissue-activating peptide III(1-81) (CTAP-III(1-81)); Beta-thromboglobulin (Beta-TG); Neutrophil-activating peptide 2(74) (NAP-2(74)); Neutrophil-activating peptide 2(73) (NAP-2(73)); Neutrophil-activating peptide 2 (NAP-2); TC-1; Neutrophil-activating peptide 2(1-66) (NAP-2(1-66)); Neutrophil-activating peptide 2(1-63) (NAP-2(1-63))]	PPBP	P02775

Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	TF	P02787
Hemopexin (Beta-1B-glycoprotein)	HPX	P02790
Short-wave-sensitive opsin 1 (Blue cone photoreceptor pigment) (Blue-sensitive opsin) (BOP)	OPN1SW	P03999
C4b-binding protein alpha chain (C4bp) (Proline-rich protein) (PRP)	C4BPA	P04003
Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	VTN	P04004
Apolipoprotein B-100 (Apo B-100) [Cleaved into: Apolipoprotein B-48 (Apo B-48)]	APOB	P04114
Phosphatidylcholine-sterol acyltransferase (EC 2.3.1.43) (1-alkyl-2-acetylglycerophosphocholine esterase) (EC 3.1.1.47) (Lecithin-cholesterol acyltransferase) (Phospholipid-cholesterol acyltransferase) (Platelet-activating factor acetylhydrolase) (PAF acetylhydrolase)	LCAT	P04180
Histidine-rich glycoprotein (Histidine-proline-rich glycoprotein) (HPRG)	HRG	P04196
Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	IGKV3-20	P01619
Immunoglobulin kappa variable 3-15 (Ig kappa chain V-III region CLL) (Ig kappa chain V-III region POM)	IGKV3-15	P01624
Immunoglobulin lambda variable 1-47 (Ig lambda chain V-I region HA) (Ig lambda chain V-I region WAH)	IGLV1-47	P01700
Alpha-1B-glycoprotein (Alpha-1-B glycoprotein)	A1BG	P04217
Keratin, type II cytoskeletal 1 (67 kDa cytokeratin) (Cytokeratin-1) (CK-1) (Hair alpha protein) (Keratin-1) (K1) (Type-II keratin Kb1)	KRT1	P04264
von Willebrand factor (vWF) [Cleaved into: von Willebrand antigen 2 (von Willebrand antigen II)]	VWF	P04275
Immunoglobulin kappa variable 1-16 (Ig kappa chain V-I region BAN)	IGKV1-16	P04430
Immunoglobulin kappa variable 1-39 (Ig kappa chain V-I region DEE) (Ig kappa chain V-I region Hau) (Ig kappa chain V-I region Mev) (Ig kappa chain V-I region OU) (Ig kappa chain V-I region Walker)	IGKV1-39	P01597
Apolipoprotein D (Apo-D) (ApoD)	APOD	P05090
Plasma protease C1 inhibitor (C1 Inh) (C1Inh) (C1 esterase inhibitor) (C1-inhibiting factor) (Serpine G1)	SERPING1	P05155
Coagulation factor XIII B chain (Fibrin-stabilizing factor B subunit) (Protein-glutamine gamma-glutamyltransferase B chain) (Transglutaminase B chain)	F13B	P05160
Tetranectin (TN) (C-type lectin domain family 3 member B) (Plasminogen kringle 4-binding protein)	CLEC3B	P05452

Thyroxine-binding globulin (Serpina7) (T4-binding globulin)	SERPINA7	P05543
Heparin cofactor 2 (Heparin cofactor II) (HC-II) (Protease inhibitor leuserpin-2) (HLS2) (Serpina1)	SERPIND1	P05546
Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Butyrylcholine esterase) (Choline esterase II) (Pseudocholinesterase)	BCHE	P06276
Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	IGKV3-20	P01619
Immunoglobulin lambda variable 6-57 (Ig lambda chain V-VI region AR) (Ig lambda chain V-VI region EB4) (Ig lambda chain V-VI region NIG-48) (Ig lambda chain V-VI region SUT) (Ig lambda chain V-VI region WLT)	IGLV6-57	P01721
Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	GSN	P06396
Protein S100-A9 (Calgranulin-B) (Calprotectin L1H subunit) (Leukocyte L1 complex heavy chain) (Migration inhibitory factor-related protein 14) (MRP-14) (p14) (S100 calcium-binding protein A9)	S100A9	P06702
Apolipoprotein A-IV (Apo-AIV) (ApoA-IV) (Apolipoprotein A4)	APOA4	P06727
Immunoglobulin lambda variable 3-1 (Ig lambda chain V-IV region Bau) (Ig lambda chain V-IV region MOL) (Ig lambda chain V-IV region X)	IGLV3-1	P01715
Vitamin K-dependent protein S	PROS1	P07225
Complement component C8 alpha chain (Complement component 8 subunit alpha)	C8A	P07357
Complement component C8 gamma chain	C8G	P07360
Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	PFN1	P07737
Tyrosine-protein kinase Lyn (EC 2.7.10.2) (Lck/Yes-related novel protein tyrosine kinase) (V-yes-1 Yamaguchi sarcoma viral related oncogene homolog) (p53Lyn) (p56Lyn)	LYN	P07948
Corticosteroid-binding globulin (CBG) (Serpina6) (Transcortin)	SERPINA6	P08185
Apolipoprotein(a) (Apo(a)) (Lp(a)) (EC 3.4.21.-)	LPA	P08519
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (EC 1.2.4.1) (PDHE1-A type I)	PDHA1	P08559
Monocyte differentiation antigen CD14 (Myeloid cell-specific leucine-rich glycoprotein) (CD antigen CD14) [Cleaved into: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane-bound form]	CD14	P08571
Complement factor H (H factor 1)	CFH	P08603
Vimentin	VIM	P08670

Alpha-2-antiplasmin (Alpha-2-AP) (Alpha-2-plasmin inhibitor) (Alpha-2-PI) (Serpins F2)	SERPINF2	P08697
Complement C1s subcomponent (EC 3.4.21.42) (C1 esterase) (Complement component 1 subcomponent s) [Cleaved into: Complement C1s subcomponent heavy chain; Complement C1s subcomponent light chain]	C1S	P09871
Complement C4-A (Acidic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 2) [Cleaved into: Complement C4 beta chain; Complement C4-A alpha chain; C4a anaphylatoxin; C4b-A; C4d-A; Complement C4 gamma chain]	C4A	P0C0L4
Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	C4B	P0C0L5
RANBP2-like and GRIP domain-containing protein 2 (Ran-binding protein 2-like 2) (RanBP2-like 2) (RanBP2L2)	RGPD2	P0DJJ1
Serum amyloid A-2 protein (SAA2) [Cleaved into: Amyloid A2 protein (AA2)]	SAA2	P0DJI9
Complement component C7	C7	P10643
60 kDa heat shock protein, mitochondrial (EC 5.6.1.7) (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1	P10809
Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytolysis inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoJalpha) (Complement cytolysis inhibitor a chain) (SP-40,40 beta-chain); Clusterin alpha chain (ApoJbeta) (Complement cytolysis inhibitor b chain) (SP-40,40 alpha-chain)]	CLU	P10909
Microtubule-associated protein 2 (MAP-2)	MAP2	P11137
Spectrin beta chain, erythrocytic (Beta-I spectrin)	SPTB	P11277
DNA topoisomerase 2-alpha (EC 5.6.2.2) (DNA topoisomerase II, alpha isozyme)	TOP2A	P11388
Eosinophil peroxidase (EPO) (EC 1.11.1.7) [Cleaved into: Eosinophil peroxidase light chain; Eosinophil peroxidase heavy chain]	EPX	P11678
B-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Bp35) (Leukocyte surface antigen Leu-16) (Membrane-spanning 4-domains subfamily A member 1) (CD antigen CD20)	MS4A1	P11836
Coagulation factor V (Activated protein C cofactor) (Proaccelerin, labile factor) [Cleaved into: Coagulation factor V heavy chain; Coagulation factor V light chain]	F5	P12259
Proto-oncogene tyrosine-protein kinase Src (EC 2.7.10.2) (Proto-oncogene c-Src) (pp60c-src) (p60-Src)	SRC	P12931

Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	UNG	P13051
Complement component C6	C6	P13671
Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1	P14625
Insulin-degrading enzyme (EC 3.4.24.56) (Abeta-degrading protease) (Insulin protease) (Insulinase) (Insulysin)	IDE	P14735
Leukemia inhibitory factor (LIF) (Differentiation-stimulating factor) (D factor) (Melanoma-derived LPL inhibitor) (MLPLI) (Emfilermin)	LIF	P15018
Carboxypeptidase N catalytic chain (CPN) (EC 3.4.17.3) (Anaphylatoxin inactivator) (Arginine carboxypeptidase) (Carboxypeptidase N polypeptide 1) (Carboxypeptidase N small subunit) (Kininase-1) (Lysine carboxypeptidase) (Plasma carboxypeptidase B) (Serum carboxypeptidase N) (SCPN)	CPN1	P15169
Immunoglobulin lambda-like polypeptide 1 (CD179 antigen-like family member B) (Ig lambda-5) (Immunoglobulin omega polypeptide) (Immunoglobulin-related protein 14.1) (CD antigen CD179b)	IGLL1	P15814
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	DSP	P15924
Integrin beta-4 (GP150) (CD antigen CD104)	ITGB4	P16144
Ankyrin-1 (ANK-1) (Ankyrin-R) (Erythrocyte ankyrin)	ANK1	P16157
Carboxypeptidase E (CPE) (EC 3.4.17.10) (Carboxypeptidase H) (CPH) (Enkephalin convertase) (Prohormone-processing carboxypeptidase)	CPE	P16870
Integrin alpha-2 (CD49 antigen-like family member B) (Collagen receptor) (Platelet membrane glycoprotein Ia) (GPIa) (VLA-2 subunit alpha) (CD antigen CD49b)	ITGA2	P17301
Insulin-like growth factor-binding protein 3 (IBP-3) (IGF-binding protein 3) (IGFBP-3)	IGFBP3	P17936
Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	IGKV3-20	P01619
Vinculin (Metavinculin) (MV)	VCL	P18206
Lipopolysaccharide-binding protein (LBP)	LBP	P18428
Keratin, type I cytoskeletal 15 (Cytokeratin-15) (CK-15) (Keratin-15) (K15)	KRT15	P19012
Guanine nucleotide-binding protein G(z) subunit alpha (G(x) alpha chain) (Gz-alpha)	GNAZ	P19086

Tumor necrosis factor receptor superfamily member 1A (Tumor necrosis factor receptor 1) (TNF-R1) (Tumor necrosis factor receptor type I) (TNF-RI) (TNFR-I) (p55) (p60) (CD antigen CD120a) [Cleaved into: Tumor necrosis factor receptor superfamily member 1A, membrane form; Tumor necrosis factor-binding protein 1 (TBPI)]	TNFRSF1A	P19438
Alpha-1-acid glycoprotein 2 (AGP 2) (Orosomucoid-2) (OMD 2)	ORM2	P19652
Inter-alpha-trypsin inhibitor heavy chain H2 (ITI heavy chain H2) (ITI-HC2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor complex component II) (Serum-derived hyaluronan-associated protein) (SHAP)	ITIH2	P19823
Inter-alpha-trypsin inhibitor heavy chain H1 (ITI heavy chain H1) (ITI-HC1) (Inter-alpha-inhibitor heavy chain 1) (Inter-alpha-trypsin inhibitor complex component III) (Serum-derived hyaluronan-associated protein) (SHAP)	ITIH1	P19827
Plasma membrane calcium-transporting ATPase 1 (EC 7.2.2.10) (Plasma membrane calcium ATPase isoform 1) (PMCA1) (Plasma membrane calcium pump isoform 1)	ATP2B1	P20020
C4b-binding protein beta chain	C4BPB	P20851
Nebulin	NEB	P20929
Filaggrin	FLG	P20930
Neurofibromin (Neurofibromatosis-related protein NF-1) [Cleaved into: Neurofibromin truncated]	NF1	P21359
Fibroblast growth factor receptor 2 (FGFR-2) (EC 2.7.10.1) (K-sam) (KGFR) (Keratinocyte growth factor receptor) (CD antigen CD332)	FGFR2	P21802
Ryanodine receptor 1 (RYR-1) (RyR1) (Skeletal muscle calcium release channel) (Skeletal muscle ryanodine receptor) (Skeletal muscle-type ryanodine receptor) (Type 1 ryanodine receptor)	RYR1	P21817
Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	GPX3	P22352
Carboxypeptidase N subunit 2 (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N large subunit) (Carboxypeptidase N polypeptide 2) (Carboxypeptidase N regulatory subunit)	CPN2	P22792
Protein EVI2A (Ecotropic viral integration site 2A protein homolog) (EVI-2A)	EVI2A	P22794
Immunoglobulin heavy variable 1-2 (Ig heavy chain V-I region ND) (Ig heavy chain V-I region V35)	IGHV1-2	P23083
Fibulin-1 (FBL-1)	FBLN1	P23142
Inositol-trisphosphate 3-kinase A (EC 2.7.1.127) (Inositol 1,4,5-trisphosphate 3-kinase A) (IP3 3-kinase A) (IP3K A) (InsP 3-kinase A)	ITPKA	P23677
Laminin subunit alpha-2 (Laminin M chain) (Laminin-12 subunit alpha) (Laminin-2 subunit alpha) (Laminin-4 subunit alpha) (Merosin heavy chain)	LAMA2	P24043
Adenomatous polyposis coli protein (Protein APC) (Deleted in polyposis 2.5)	APC	P25054

Zinc-alpha-2-glycoprotein (Zn-alpha-2-GP) (Zn-alpha-2-glycoprotein)	AZGP1	P25311
Collagen alpha-3(V) chain	COL5A3	P25940
Integrin beta-8	ITGB8	P26012
Moesin (Membrane-organizing extension spike protein)	MSN	P26038
Serum paraoxonase/arylesterase 1 (PON 1) (EC 3.1.1.2) (EC 3.1.1.81) (EC 3.1.8.1) (Aromatic esterase 1) (A-esterase 1) (K-45) (Serum aryldialkylphosphatase 1)	PON1	P27169
Properdin (Complement factor P)	CFP	P27918
Inositol-trisphosphate 3-kinase B (EC 2.7.1.127) (Inositol 1,4,5-trisphosphate 3-kinase B) (IP3 3-kinase B) (IP3K B) (InsP 3-kinase B)	ITPKB	P27987
Collagen alpha-5(IV) chain	COL4A5	P29400
Kallistatin (Kallikrein inhibitor) (Peptidase inhibitor 4) (PI-4) (Serpina A4)	SERPINA4	P29622
Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPPp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1	P30086
Tyrosine-protein kinase receptor UFO (EC 2.7.10.1) (AXL oncogene)	AXL	P30530
G protein-coupled receptor kinase 4 (EC 2.7.11.16) (G protein-coupled receptor kinase GRK4) (ITI1)	GRK4	P32298
Cadherin-5 (7B4 antigen) (Vascular endothelial cadherin) (VE-cadherin) (CD antigen CD144)	CDH5	P33151
Kinesin-1 heavy chain (Conventional kinesin heavy chain) (Ubiquitous kinesin heavy chain) (UKHC)	KIF5B	P33176
Glypican-1 [Cleaved into: Secreted glypican-1]	GPC1	P35052
Thrombospondin-2	THBS2	P35442
Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9	P35579
RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	FUS	P35637
Insulin-like growth factor-binding protein complex acid labile subunit (ALS)	IGFALS	P35858
Pigment epithelium-derived factor (PEDF) (Cell proliferation-inducing gene 35 protein) (EPC-1) (Serpina F1)	SERPINF1	P36955
Sterol regulatory element-binding protein 1 (SREBP-1) (Class D basic helix-loop-helix protein 1) (bHLHd1) (Sterol regulatory element-binding transcription factor 1) [Cleaved into: Processed sterol regulatory element-binding protein 1 (Transcription factor SREBF1)]	SREBF1	P36956

Vasopressin V1a receptor (V1aR) (AVPR V1a) (Antidiuretic hormone receptor 1a) (Vascular/hepatic-type arginine vasopressin receptor)	AVPR1A	P37288
Homeobox protein cut-like 1 (CCAAT displacement protein) (CDP) (CDP/Cux p200) (Homeobox protein cux-1) [Cleaved into: CDP/Cux p110]	CUX1	P39880
Prostaglandin-H2 D-isomerase (EC 5.3.99.2) (Beta-trace protein) (Cerebrin-28) (Glutathione-independent PGD synthase) (Lipocalin-type prostaglandin-D synthase) (L-PGDS) (Prostaglandin-D2 synthase) (PGD2 synthase) (PGDS) (PGDS2)	PTGDS	P41222
Leukemia inhibitory factor receptor (LIF receptor) (LIF-R) (CD antigen CD118)	LIFR	P42702
Excitatory amino acid transporter 2 (Glutamate/aspartate transporter II) (Sodium-dependent glutamate/aspartate transporter 2) (Solute carrier family 1 member 2)	SLC1A2	P43004
Growth/differentiation factor 5 (GDF-5) (Bone morphogenetic protein 14) (BMP-14) (Cartilage-derived morphogenetic protein 1) (CDMP-1) (Lipopolysaccharide-associated protein 4) (LAP-4) (LPS-associated protein 4) (Radotermin)	GDF5	P43026
Netrin receptor DCC (Colorectal cancer suppressor) (Immunoglobulin superfamily DCC subclass member 1) (Tumor suppressor protein DCC)	DCC	P43146
Biotinidase (Biotinase) (EC 3.5.1.12)	BTD	P43251
Glycerol-3-phosphate dehydrogenase, mitochondrial (GPD-M) (GPDH-M) (EC 1.1.5.3) (mitochondrial glycerophosphate dehydrogenase gene) (mGDH) (mtGPD)	GPD2	P43304
Afamin (Alpha-albumin) (Alpha-Alb)	AFM	P43652
Proliferation marker protein Ki-67 (Antigen identified by monoclonal antibody Ki-67) (Antigen KI-67) (Antigen Ki67)	MKI67	P46013
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform (Phosphorylase kinase alpha M subunit)	PHKA1	P46020
Microtubule-associated protein 1B (MAP-1B) [Cleaved into: MAP1B heavy chain; MAP1 light chain LC1]	MAP1B	P46821
Utrophin (Dystrophin-related protein 1) (DRP-1)	UTRN	P46939
F-actin-capping protein subunit beta (CapZ beta)	CAPZB	P47756
Retinaldehyde dehydrogenase 3 (RALDH-3) (RaIDH3) (EC 1.2.1.36) (Aldehyde dehydrogenase 6) (Aldehyde dehydrogenase family 1 member A3) (ALDH1A3)	ALDH1A3	P47895
Sodium- and chloride-dependent glycine transporter 1 (GlyT-1) (GlyT1) (Solute carrier family 6 member 9)	SLC6A9	P48067
Heat shock 70 kDa protein 13 (Microsomal stress-70 protein ATPase core) (Stress-70 protein chaperone microsome-associated 60 kDa protein)	HSPA13	P48723
Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM	P49411

Centromere protein F (CENP-F) (AH antigen) (Kinetochore protein CENPF) (Mitotin)	CENPF	P49454
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCAD) (EC 1.3.8.9)	ACADVL	P49748
Tuberin (Tuberous sclerosis 2 protein)	TSC2	P49815
Selenoprotein P (SeP)	SELENOP	P49908
Histamine N-methyltransferase (HMT) (EC 2.1.1.8)	HNMT	P50135
Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2	P50395
Tubby protein homolog	TUB	P50607
Lipopolysaccharide-responsive and beige-like anchor protein (Beige-like protein) (CDC4-like protein)	LRBA	P50851
Sodium/potassium-transporting ATPase subunit alpha-2 (Na(+)/K(+) ATPase alpha-2 subunit) (EC 7.2.2.13) (Sodium pump subunit alpha-2)	ATP1A2	P50993
RNA-binding protein FXR1 (FMR1 autosomal homolog 1) (hFXR1p)	FXR1	P51114
Chloride channel protein CIC-Ka (Chloride channel Ka) (CIC-K1)	CLCNKA	P51800
Endoplasmic reticulum membrane adapter protein XK (Kell complex 37 kDa component) (Kx antigen) (Membrane transport protein XK) (XK-related protein 1)	XK	P51811
Zinc finger protein 75D (Zinc finger protein 75) (Zinc finger protein 82)	ZNF75D	P51815
Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	LUM	P51884
Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM	P52272
Ephrin-B2 (EPH-related receptor tyrosine kinase ligand 5) (LERK-5) (HTK ligand) (HTK-L)	EFNB2	P52799
Homeobox protein Nkx-2.5 (Cardiac-specific homeobox) (Homeobox protein CSX) (Homeobox protein NK-2 homolog E)	NKX2-5	P52952
Mismatch repair endonuclease PMS2 (EC 3.1.-.-) (DNA mismatch repair protein PMS2) (PMS1 protein homolog 2)	PMS2	P54278
Voltage-dependent L-type calcium channel subunit beta-3 (CAB3) (Calcium channel voltage-dependent subunit beta 3)	CACNB3	P54284
Myomesin-2 (165 kDa connectin-associated protein) (165 kDa titin-associated protein) (M-protein) (Myomesin family member 2)	MYOM2	P54296
Developmentally-regulated GTP-binding protein 2 (DRG-2) (Translation factor GTPase DRG2) (TRAFAC GTPase DRG2) (EC 3.6.5.-)	DRG2	P55039
Apolipoprotein C-IV (Apo-CIV) (ApoC-IV) (Apolipoprotein C4)	APOC4	P55056
Laminin subunit beta-2 (Laminin B1s chain) (Laminin-11 subunit beta) (Laminin-14 subunit beta) (Laminin-15 subunit beta) (Laminin-3 subunit beta) (Laminin-4 subunit beta) (Laminin-7 subunit beta) (Laminin-9 subunit beta) (S-laminin subunit beta) (S-LAM beta)	LAMB2	P55268

Cathepsin W (EC 3.4.22.-) (Lymphopain)	CTSW	P56202
Potassium voltage-gated channel subfamily KQT member 4 (KQT-like 4) (Potassium channel subunit alpha KvLQT4) (Voltage-gated potassium channel subunit Kv7.4)	KCNQ4	P56696
A disintegrin and metalloproteinase with thrombospondin motifs 20 (ADAM-TS 20) (ADAM-TS20) (ADAMTS-20) (EC 3.4.24.-)	ADAMTS20	P59510
Actin, cytoplasmic 1 (EC 3.6.4.-) (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB	P60709
Signal recognition particle subunit SRP54 (EC 3.6.5.4) (Signal recognition particle 54 kDa protein)	SRP54	P61011
Actin-related protein 2 (Actin-like protein 2)	ACTR2	P61160
Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C)	LYZ	P61626
Beta-2-microglobulin [Cleaved into: Beta-2-microglobulin form pl 5.3]	B2M	P61769
Actin, alpha skeletal muscle (EC 3.6.4.-) (Alpha-actin-1) [Cleaved into: Actin, alpha skeletal muscle, intermediate form]	ACTA1	P68133
Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	HBB	P68871
Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain) [Cleaved into: Hemopressin]	HBA1;	P69905
Disintegrin and metalloproteinase domain-containing protein 8 (ADAM 8) (EC 3.4.24.-) (Cell surface antigen MS2) (CD antigen CD156a)	ADAM8	P78325
RNA-binding protein 6 (Lung cancer antigen NY-LU-12) (Protein G16) (RNA-binding motif protein 6) (RNA-binding protein DEF-3)	RBM6	P78332
Reelin (EC 3.4.21.-)	RELN	P78509
DENN domain-containing protein 2B (HeLa tumor suppression 1) (Suppression of tumorigenicity 5 protein)	DENND2B	P78524
Microtubule-associated protein 1A (MAP-1A) (Proliferation-related protein p80) [Cleaved into: MAP1A heavy chain; MAP1 light chain LC2]	MAP1A	P78559
Phosphatidylinositol-glycan-specific phospholipase D (PI-G PLD) (EC 3.1.4.50) (Glycoprotein phospholipase D) (Glycosyl-phosphatidylinositol-specific phospholipase D) (GPI-PLD) (GPI-specific phospholipase D)	GPLD1	P80108
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin heavy variable 3-7 (Ig heavy chain V-III region GAL) (Ig heavy chain V-III region GAR) (Ig heavy chain V-III region JON)	IGHV3-7	P01780

Immunoglobulin lambda variable 3-21 (Ig lambda chain V-III region LOI) (Ig lambda chain V-V region DEL) (Ig lambda chain V-VII region MOT)	IGLV3-21	P80748
TATA element modulatory factor (TMF) (Androgen receptor coactivator 160 kDa protein) (Androgen receptor-associated protein of 160 kDa)	TMF1	P82094
U7 snRNA-associated Sm-like protein LSM11	LSM11	P83369
Immunoglobulin kappa variable 4-1 (Ig kappa chain V-IV region B17) (Ig kappa chain V-IV region JI) (Ig kappa chain V-IV region Len) (Ig kappa chain V-IV region STH)	IGKV4-1	P06312
Enteropeptidase (EC 3.4.21.9) (Enterokinase) (Serine protease 7) (Transmembrane protease serine 15) [Cleaved into: Enteropeptidase non-catalytic heavy chain; Enteropeptidase catalytic light chain]	TMPRSS15	P98073
Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	HSPG2	P98160
Phospholipid-transporting ATPase IH (EC 7.6.2.1) (ATPase IS) (ATPase class VI type 11A) (P4-ATPase flippase complex alpha subunit ATP11A)	ATP11A	P98196
Phospholipid-transporting ATPase ID (EC 7.6.2.1) (ATPase class I type 8B member 2) (P4-ATPase flippase complex alpha subunit ATP8B2)	ATP8B2	P98198
Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (GRIP120) (Nuclear p120 ribonucleoprotein) (Scaffold-attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU	Q00839
Spectrin beta chain, non-erythrocytic 1 (Beta-II spectrin) (Fodrin beta chain) (Spectrin, non-erythroid beta chain 1)	SPTBN1	Q01082
AMP deaminase 2 (EC 3.5.4.6) (AMP deaminase isoform L)	AMPD2	Q01433
RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein)	EWSR1	Q01844
Collagen alpha-3(IV) chain (Goodpasture antigen) [Cleaved into: Tumstatin]	COL4A3	Q01955
Protein kinase C epsilon type (EC 2.7.11.13) (nPKC-epsilon)	PRKCE	Q02156
Centromere-associated protein E (Centromere protein E) (CENP-E) (Kinesin-7) (Kinesin-related protein CENPE)	CENPE	Q02224
Peptidyl-prolyl cis-trans isomerase FKBP4 (PPlase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	FKBP4	Q02790
Mucin-2 (MUC-2) (Intestinal mucin-2)	MUC2	Q02817

Dystonin (230 kDa bullous pemphigoid antigen) (230/240 kDa bullous pemphigoid antigen) (Bullous pemphigoid antigen 1) (BPA) (Bullous pemphigoid antigen) (Dystonia musculorum protein) (Hemidesmosomal plaque protein)	DST	Q03001
Histone-lysine N-methyltransferase 2A (Lysine N-methyltransferase 2A) (EC 2.1.1.364) (ALL-1) (CXXC-type zinc finger protein 7) (Cysteine methyltransferase KMT2A) (EC 2.1.1.-) (Myeloid/lymphoid or mixed-lineage leukemia) (Myeloid/lymphoid or mixed-lineage leukemia protein 1) (Trithorax-like protein) (Zinc finger protein HRX) [Cleaved into: MLL cleavage product N320 (N-terminal cleavage product of 320 kDa) (p320); MLL cleavage product C180 (C-terminal cleavage product of 180 kDa) (p180)]	KMT2A	Q03164
Hepatocyte growth factor activator (HGF activator) (HGFA) (EC 3.4.21.-) [Cleaved into: Hepatocyte growth factor activator short chain; Hepatocyte growth factor activator long chain]	HGFAC	Q04756
Inter-alpha-trypsin inhibitor heavy chain H3 (ITI heavy chain H3) (ITI-HC3) (Inter-alpha-inhibitor heavy chain 3) (Serum-derived hyaluronan-associated protein) (SHAP)	ITIH3	Q06033
Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1	Q06323
Cytoskeleton-associated protein 4 (63-kDa cytoskeleton-linking membrane protein) (Climp-63) (p63)	CKAP4	Q07065
Collagen alpha-1(XVI) chain	COL16A1	Q07092
Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	LGALS3BP	Q08380
Adenylate cyclase type 1 (EC 4.6.1.1) (ATP pyrophosphate-lyase 1) (Adenylate cyclase type I) (Adenylyl cyclase 1) (Ca(2+)/calmodulin-activated adenylyl cyclase)	ADCY1	Q08828
RNA cytosine C(5)-methyltransferase NSUN2 (EC 2.1.1.-) (Myc-induced SUN domain-containing protein) (Misu) (NOL1/NOP2/Sun domain family member 2) (Substrate of AIM1/Aurora kinase B) (mRNA cytosine C(5)-methyltransferase) (EC 2.1.1.-) (tRNA cytosine C(5)-methyltransferase) (EC 2.1.1.-, EC 2.1.1.203) (tRNA methyltransferase 4 homolog) (hTrm4)	NSUN2	Q08J23
Myotonin-protein kinase (MT-PK) (EC 2.7.11.1) (DM-kinase) (DMK) (DM1 protein kinase) (DMPK) (Myotonic dystrophy protein kinase)	DMPK	Q09013
Neuroblast differentiation-associated protein AHNAK (Desmoyokin)	AHNAK	Q09666
Apolipoprotein B receptor (Apolipoprotein B-100 receptor) (Apolipoprotein B-48 receptor) (Apolipoprotein B48 receptor) (apoB-48R)	APOBR	Q0VD83

Dynein axonemal heavy chain 14 (Axonemal beta dynein heavy chain 14) (Ciliary dynein heavy chain 14)	DNAH14	Q0VDD8
Potassium voltage-gated channel subfamily H member 2 (Eag homolog) (Ether-a-go-go-related gene potassium channel 1) (ERG-1) (Eag-related protein 1) (Ether-a-go-go-related protein 1) (H-ERG) (hERG-1) (hERG1) (Voltage-gated potassium channel subunit Kv11.1)	KCNH2	Q12809
Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha) (Zinc finger helicase) (hZFH)	CHD3	Q12873
Receptor-type tyrosine-protein phosphatase eta (Protein-tyrosine phosphatase eta) (R-PTP-eta) (EC 3.1.3.48) (Density-enhanced phosphatase 1) (DEP-1) (HPTP eta) (Protein-tyrosine phosphatase receptor type J) (R-PTP-J) (CD antigen CD148)	PTPRJ	Q12913
Forkhead box protein I1 (Forkhead-related protein FKHL10) (Forkhead-related transcription factor 6) (FREAC-6) (Hepatocyte nuclear factor 3 forkhead homolog 3) (HFH-3) (HNF-3/fork-head homolog 3)	FOXI1	Q12951
Heat shock protein beta-3 (HspB3) (Heat shock 17 kDa protein) (HSP 17) (Protein 3)	HSPB3	Q12988
Acetyl-CoA carboxylase 1 (ACC1) (EC 6.4.1.2) (Acetyl-Coenzyme A carboxylase alpha) (ACC-alpha)	ACACA	Q13085
Pappalysin-1 (EC 3.4.24.79) (Insulin-like growth factor-dependent IGF-binding protein 4 protease) (IGF-dependent IGFBP-4 protease) (IGFBP-4ase) (Pregnancy-associated plasma protein A) (PAPP-A)	PAPPA	Q13219
Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.11.25) (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1) (EC 2.3.2.27)	MAP3K1	Q13233
Dehydrogenase/reductase SDR family member 2, mitochondrial (EC 1.1.1.-) (Dicarbonyl reductase HEP27) (Protein D) (Short chain dehydrogenase/reductase family 25C member 1) (Protein SDR25C1)	DHRS2	Q13268
Receptor-type tyrosine-protein phosphatase S (R-PTP-S) (EC 3.1.3.48) (Receptor-type tyrosine-protein phosphatase sigma) (R-PTP-sigma)	PTPRS	Q13332
Beta-2-syntrophin (59 kDa dystrophin-associated protein A1 basic component 2) (Syntrophin-3) (SNT3) (Syntrophin-like) (SNTL)	SNTB2	Q13425
Serine/threonine-protein kinase PRP4 homolog (EC 2.7.11.1) (PRP4 kinase) (PRP4 pre-mRNA-processing factor 4 homolog)	PRPF4B	Q13523
Ras GTPase-activating-like protein IQGAP2	IQGAP2	Q13576
Myotubularin-related protein 2 (Phosphatidylinositol-3,5-bisphosphate 3-phosphatase) (EC 3.1.3.95) (Phosphatidylinositol-3-phosphate phosphatase) (EC 3.1.3.64)	MTMR2	Q13614
Apolipoprotein F (Apo-F) (Lipid transfer inhibitor protein) (LTIP)	APOF	Q13790
Tubulin beta-2A chain (Tubulin beta class IIa)	TUBB2A	Q13885

Cyclin-dependent kinase 13 (EC 2.7.11.22) (EC 2.7.11.23) (CDC2-related protein kinase 5) (Cell division cycle 2-like protein kinase 5) (Cell division protein kinase 13) (hCDK13) (Cholinesterase-related cell division controller)	CDK13	Q14004
Cytoskeleton-associated protein 5 (Colonic and hepatic tumor overexpressed gene protein) (Ch-TOG)	CKAP5	Q14008
Cold-inducible RNA-binding protein (A18 hnRNP) (Glycine-rich RNA-binding protein CIRP)	CIRBP	Q14011
Dynactin subunit 1 (150 kDa dynein-associated polypeptide) (DAP-150) (DP-150) (p135) (p150-glued)	DCTN1	Q14203
Hyaluronan-binding protein 2 (EC 3.4.21.-) (Factor VII-activating protease) (Factor seven-activating protease) (FSAP) (Hepatocyte growth factor activator-like protein) (Plasma hyaluronan-binding protein) [Cleaved into: Hyaluronan-binding protein 2 50 kDa heavy chain; Hyaluronan-binding protein 2 50 kDa heavy chain alternate form; Hyaluronan-binding protein 2 27 kDa light chain; Hyaluronan-binding protein 2 27 kDa light chain alternate form]	HABP2	Q14520
Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	ITIH4	Q14624
Early placenta insulin-like peptide (EPIL) (Insulin-like peptide 4) (Placentin) [Cleaved into: Early placenta insulin-like peptide B chain; Early placenta insulin-like peptide A chain]	INSL4	Q14641
Inositol 1,4,5-trisphosphate receptor type 1 (IP3 receptor isoform 1) (IP3R 1) (InsP3R1) (Type 1 inositol 1,4,5-trisphosphate receptor) (Type 1 InsP3 receptor)	ITPR1	Q14643
Ras GTPase-activating protein 3 (GAP1(IP4BP)) (Ins P4-binding protein)	RASA3	Q14644
E3 ubiquitin-protein ligase TRIP12 (EC 2.3.2.26) (E3 ubiquitin-protein ligase for Arf) (ULF) (HECT-type E3 ubiquitin transferase TRIP12) (Thyroid receptor-interacting protein 12) (TR-interacting protein 12) (TRIP-12)	TRIP12	Q14669
Kinesin-like protein KIF22 (Kinesin-like DNA-binding protein) (Kinesin-like protein 4)	KIF22	Q14807
Importin subunit beta-1 (Importin-90) (Karyopherin subunit beta-1) (Nuclear factor p97) (Pore targeting complex 97 kDa subunit) (PTAC97)	KPNB1	Q14974
Nuclear mitotic apparatus protein 1 (Nuclear matrix protein-22) (NMP-22) (Nuclear mitotic apparatus protein) (NuMA protein) (SP-H antigen)	NUMA1	Q14980
GTPase-activating protein and VPS9 domain-containing protein 1 (GAPex-5) (Rab5-activating protein 6)	GAPVD1	Q14C86
FERM and PDZ domain-containing protein 4 (PDZ domain-containing protein 10) (PSD-95-interacting regulator of spine morphogenesis) (Preso)	FRMPD4	Q14CM0

Squamous cell carcinoma antigen recognized by T-cells 3 (SART-3) (Tat-interacting protein of 110 kDa) (Tip110) (p110 nuclear RNA-binding protein)	SART3	Q15020
Ribosome biogenesis regulatory protein homolog	RRS1	Q15050
Kinesin-like protein KIF14	KIF14	Q15058
Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	POSTN	Q15063
Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain-containing protein 2)	EEA1	Q15075
Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6	Q15084
Phosphoglucosyltransferase-like protein 5 (Aciculin) (Phosphoglucosyltransferase-related protein) (PGM-RP)	PGM5	Q15124
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-4 (EC 3.1.4.11) (Phosphoinositide phospholipase C-beta-4) (Phospholipase C-beta-4) (PLC-beta-4)	PLCB4	Q15147
Plectin (PCN) (PLTN) (Hemidesmosomal protein 1) (HD1) (Plectin-1)	PLEC	Q15149
Serum paraoxonase/lactonase 3 (EC 3.1.1.2) (EC 3.1.1.81) (EC 3.1.8.1)	PON3	Q15166
Ficolin-2 (37 kDa elastin-binding protein) (Collagen/fibrinogen domain-containing protein 2) (EBP-37) (Ficolin-B) (Ficolin-beta) (Hucolin) (L-ficolin) (Serum lectin p35)	FCN2	Q15485
Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP)	TGFBI	Q15582
Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1	Q15691
Myosin light chain kinase, smooth muscle (MLCK) (smMLCK) (EC 2.7.11.18) (Kinase-related protein) (KRP) (Telokin) [Cleaved into: Myosin light chain kinase, smooth muscle, deglutamylated form]	MYLK	Q15746
Probable E3 ubiquitin-protein ligase HERC1 (EC 2.3.2.26) (HECT domain and RCC1-like domain-containing protein 1) (HECT-type E3 ubiquitin transferase HERC1) (p532) (p619)	HERC1	Q15751
Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (NPYY5-R) (Y5 receptor)	NPY5R	Q15761
Adiponectin (30 kDa adipocyte complement-related protein) (Adipocyte complement-related 30 kDa protein) (ACRP30) (Adipocyte, C1q and collagen domain-containing protein) (Adipose most abundant gene transcript 1 protein) (apM-1) (Gelatin-binding protein)	ADIPOQ	Q15848
Ecto-NOX disulfide-thiol exchanger 2 (APK1 antigen) (Cytosolic ovarian carcinoma antigen 1) (Tumor-associated hydroquinone oxidase) (tNOX) [Includes: Hydroquinone [NADH] oxidase (EC 1.-.-.-); Protein disulfide-thiol oxidoreductase (EC 1.-.-.-)]	ENOX2	Q16206

Cyclic nucleotide-gated cation channel alpha-3 (Cone photoreceptor cGMP-gated channel subunit alpha) (Cyclic nucleotide-gated channel alpha-3) (CNG channel alpha-3) (CNG-3) (CNG3)	CNGA3	Q16281
Extracellular matrix protein 1 (Secretory component p85)	ECM1	Q16610
Cleavage and polyadenylation specificity factor subunit 6 (Cleavage and polyadenylation specificity factor 68 kDa subunit) (CPSF 68 kDa subunit) (Cleavage factor Im complex 68 kDa subunit) (CFIm68) (Pre-mRNA cleavage factor Im 68 kDa subunit) (Protein HPBR11-4/7)	CPSF6	Q16630
2,4-dienoyl-CoA reductase [(3E)-enoyl-CoA-producing], mitochondrial (EC 1.3.1.124) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	DECR1	Q16698
Thioredoxin reductase 1, cytoplasmic (TR) (EC 1.8.1.9) (Gene associated with retinoic and interferon-induced mortality 12 protein) (GRIM-12) (Gene associated with retinoic and IFN-induced mortality 12 protein) (KM-102-derived reductase-like factor) (Peroxidase TXNRD1) (EC 1.11.1.2) (Thioredoxin reductase TR1)	TXNRD1	Q16881
Zinc finger protein 827	ZNF827	Q17R98
DNA-binding protein RFX7 (Regulatory factor X 7) (Regulatory factor X domain-containing protein 2)	RFX7	Q2KHR2
Kinesin-like protein KIF26B	KIF26B	Q2KJY2
Coiled-coil domain-containing protein 27	CCDC27	Q2M243
Kelch-like protein 40 (Kelch repeat and BTB domain-containing protein 5) (Sarcosynapsin)	KLHL40	Q2TBA0
Girdin (Akt phosphorylation enhancer) (APE) (Coiled-coil domain-containing protein 88A) (G alpha-interacting vesicle-associated protein) (GIV) (Girders of actin filament) (Hook-related protein 1) (HkRP1)	CCDC88A	Q3V6T2
Protein mono-ADP-ribosyltransferase PARP14 (EC 2.4.2.-) (ADP-ribosyltransferase diphtheria toxin-like 8) (ARTD8) (B aggressive lymphoma protein 2) (Poly [ADP-ribose] polymerase 14) (PARP-14)	PARP14	Q460N5
C2 domain-containing protein 3	C2CD3	Q4AC94
Probable ubiquitin carboxyl-terminal hydrolase MINDY-4 (EC 3.4.19.12) (Probable deubiquitinating enzyme MINDY-4)	MINDY4	Q4G0A6
Prolyl endopeptidase-like (EC 3.4.21.-) (Prolylendopeptidase-like)	PREPL	Q4J6C6
PAN2-PAN3 deadenylation complex catalytic subunit PAN2 (EC 3.1.13.4) (Inactive ubiquitin carboxyl-terminal hydrolase 52) (PAB1P-dependent poly(A)-specific ribonuclease) (Poly(A)-nuclease deadenylation complex subunit 2) (PAN deadenylation complex subunit 2)	PAN2	Q504Q3
Transmembrane protein 177	TMEM177	Q53S58

Actin maturation protease (EC 3.4.11.-) (Actin aminopeptidase ACTMAP)	ACTMAP	Q5BKX5
Probable E3 ubiquitin-protein ligase HERC4 (EC 2.3.2.26) (HECT domain and RCC1-like domain-containing protein 4) (HECT-type E3 ubiquitin transferase HERC4)	HERC4	Q5GLZ8
Dedicator of cytokinesis protein 11 (Activated Cdc42-associated guanine nucleotide exchange factor) (ACG) (Zizimin-2)	DOCK11	Q5JSL3
Cytospin-B (Nuclear structure protein 5) (NSP5) (Sperm antigen HCMOGT-1) (Sperm antigen with calponin homology and coiled-coil domains 1)	SPECC1	Q5M775
Zinc finger MYM-type protein 1	ZMYM1	Q5SVZ6
Putative hydroxypyruvate isomerase (EC 5.3.1.22) (Endothelial cell apoptosis protein E-CE1)	HYI	Q5T013
Uncharacterized protein C6orf118	C6orf118	Q5T5N4
Kinesin-like protein KIF24	KIF24	Q5T7B8
Tau-tubulin kinase 1 (EC 2.7.11.1) (Brain-derived tau kinase)	TTBK1	Q5TCY1
Rootletin (Ciliary rootlet coiled-coil protein)	CROCC	Q5TZA2
E3 ubiquitin-protein ligase RNF123 (EC 2.3.2.27) (Kip1 ubiquitination-promoting complex protein 1) (RING finger protein 123)	RNF123	Q5XPI4
Teashirt homolog 3 (Zinc finger protein 537)	TSHZ3	Q63HK5
Centrosomal protein of 135 kDa (Cep135) (Centrosomal protein 4)	CEP135	Q66GS9
Putative uncharacterized protein RUSC1-AS1 (RUSC1 antisense RNA 1) (RUSC1 antisense gene protein 1)	RUSC1-AS1	Q66K80
AT-rich interactive domain-containing protein 2 (ARID domain-containing protein 2) (BRG1-associated factor 200) (BAF200) (Zinc finger protein with activation potential) (Zipzap/p200)	ARID2	Q68CP9
Spermatogenesis-associated protein 31H1	SPATA31H1	Q68DN1
Very large A-kinase anchor protein (vIAKAP) (Beta/gamma crystallin domain-containing protein 3)	CRYBG3	Q68DQ2
Inositol 1,4,5-trisphosphate receptor-interacting protein-like 1	ITPRIPL1	Q6GPH6
OTU domain-containing protein 7B (EC 3.4.19.12) (Cellular zinc finger anti-NF-kappa-B protein) (Cezanne) (Zinc finger A20 domain-containing protein 1) (Zinc finger protein Cezanne)	OTUD7B	Q6GQQ9
Sulfotransferase 1C3 (ST1C3) (EC 2.8.2.1) (EC 2.8.2.2)	SULT1C3	Q6IMI6
Nipped-B-like protein (Delangin) (SCC2 homolog)	NIPBL	Q6KC79
Follistatin-related protein 4 (Follistatin-like protein 4)	FSTL4	Q6MZW2
Phospholipase B1, membrane-associated (Phospholipase B) (hPLB) (Lysophospholipase) (EC 3.1.1.5) (Phospholipase A2) (EC 3.1.1.4) (Phospholipase B/lipase) (PLB/LIP) (Triacylglycerol lipase) (EC 3.1.1.3)	PLB1	Q6P1J6
Protein arginine N-methyltransferase 9 (Protein arginine N-methyltransferase 10) (EC 2.1.1.320)	PRMT9	Q6P2P2

Inactive rhomboid protein 2 (iRhom2) (Rhomboid 5 homolog 2) (Rhomboid family member 2) (Rhomboid veinlet-like protein 5) (Rhomboid veinlet-like protein 6)	RHBDF2	Q6PJF5
ATPase family AAA domain-containing protein 2 (EC 3.6.1.-) (AAA nuclear coregulator cancer-associated protein) (ANCCA)	ATAD2	Q6PL18
Sperm-associated antigen 17 (Projection protein PF6 homolog)	SPAG17	Q6Q759
Rapamycin-insensitive companion of mTOR (AVO3 homolog) (hAVO3)	RICTOR	Q6R327
WD repeat-containing protein 74 (NOP seven-associated protein 1)	WDR74	Q6RFH5
Sterile alpha motif domain-containing protein 1 (SAM domain-containing protein 1) (Atherin)	SAMD1	Q6SPF0
Chondroitin sulfate proteoglycan 4 (Chondroitin sulfate proteoglycan NG2) (Melanoma chondroitin sulfate proteoglycan) (Melanoma-associated chondroitin sulfate proteoglycan)	CSPG4	Q6UVK1
Plexin domain-containing protein 2 (Tumor endothelial marker 7-related protein)	PLXDC2	Q6UX71
Protocadherin Fat 4 (hFat4) (Cadherin family member 14) (FAT tumor suppressor homolog 4) (Fat-like cadherin protein FAT-J)	FAT4	Q6V0I7
Protocadherin-23 (Cadherin-27) (Cadherin-like protein CDHJ) (Cadherin-like protein VR8) (Protein dachsous homolog 2) (Protocadherin PCDHJ)	DCHS2	Q6V1P9
SPOC domain-containing protein 1	SPOCD1	Q6ZMY3
Spermatogenesis-associated protein 31D1 (Protein FAM75D1)	SPATA31D1	Q6ZQQ2
Protein FAM83H	FAM83H	Q6ZRV2
Ras and Rab interactor-like protein	RINL	Q6ZS11
FYVE, RhoGEF and PH domain-containing protein 6 (Zinc finger FYVE domain-containing protein 24)	FGD6	Q6ZV73
Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 1	NYAP1	Q6ZVC0
Ubiquitin carboxyl-terminal hydrolase 31 (EC 3.4.19.12) (Deubiquitinating enzyme 31) (Ubiquitin thioesterase 31) (Ubiquitin-specific-processing protease 31)	USP31	Q70CQ4
E3 ubiquitin-protein ligase Hakai (EC 2.3.2.27) (Casitas B-lineage lymphoma-transforming sequence-like protein 1) (c-Cbl-like protein 1) (RING finger protein 188) (RING-type E3 ubiquitin transferase Hakai)	CBLL1	Q75N03
Nucleolar protein 8 (Nucleolar protein Nop132)	NOL8	Q76FK4
BEN domain-containing protein 5	BEND5	Q7L4P6
G protein-regulated inducer of neurite outgrowth 1 (GRIN1)	GPRIN1	Q7Z2K8
Keratin, type I cytoskeletal 28 (Cytokeratin-28) (CK-28) (Keratin-25D) (K25D) (Keratin-28) (K28) (Type I inner root sheath-specific keratin-K25irs4)	KRT28	Q7Z3Y7
FMR1-interacting protein NUFIP2 (82 kDa FMRP-interacting protein) (82-FIP) (Cell proliferation-inducing gene 1 protein) (FMRP-interacting protein 2) (Nuclear FMR1-interacting protein 2)	NUFIP2	Q7Z417

CLIP-associating protein 1 (Cytoplasmic linker-associated protein 1) (Multiple asters homolog 1) (Protein Orbit homolog 1) (hOrbit1)	CLASP1	Q7Z460
Nephrocystin-3	NPHP3	Q7Z494
Tetratricopeptide repeat protein 21B (TPR repeat protein 21B) (Intraflagellar transport 139 homolog)	TTC21B	Q7Z4L5
Mucin-19 (MUC-19)	MUC19	Q7Z5P9
Transmembrane emp24 domain-containing protein 4 (Endoplasmic reticulum stress-response protein 25) (ERS25) (GMP25iso) (Putative NF-kappa-B-activating protein 156) (p24 family protein alpha-3) (p24alpha3)	TMED4	Q7Z7H5
Transcriptional regulator Kaiso (Zinc finger and BTB domain-containing protein 33)	ZBTB33	Q86T24
Zinc finger homeobox protein 4 (Zinc finger homeodomain protein 4) (ZFH-4)	ZFHX4	Q86UP3
Pleckstrin homology-like domain family B member 1 (Protein LL5-alpha)	PHLDB1	Q86UU1
Calcium-dependent secretion activator 2 (Calcium-dependent activator protein for secretion 2) (CAPS-2)	CADPS2	Q86UW7
Leucine zipper protein 1	LUZP1	Q86V48
Thioredoxin domain-containing protein 2 (Spermatid-specific thioredoxin-1) (Sptrx-1)	TXNDC2	Q86VQ3
Ankyrin repeat and LEM domain-containing protein 2 (LEM domain-containing protein 4)	ANKLE2	Q86XL3
5'-3' DNA helicase ZGRF1 (EC 5.6.2.3) (GRF-type zinc finger domain-containing protein 1)	ZGRF1	Q86YA3
Protein AHNAK2	AHNAK2	Q8IVF2
Dynein axonemal heavy chain 10 (Axonemal beta dynein heavy chain 10) (Ciliary dynein heavy chain 10)	DNAH10	Q8IVF4
Aprataxin and PNK-like factor (EC 3.1.-.-) (Apyrimidinic endonuclease APLF) (PNK and APTX-like FHA domain-containing protein) (XRCC1-interacting protein 1)	APLF	Q8IW19
Rho guanine nucleotide exchange factor 19 (Ephexin-2)	ARHGEF19	Q8IW93
Testis-expressed protein 2 (Transmembrane protein 96)	TEX2	Q8IWB9
Zinc finger protein ZFPM1 (Friend of GATA protein 1) (FOG-1) (Friend of GATA 1) (Zinc finger protein 89A) (Zinc finger protein multitype 1)	ZFPM1	Q8IX07
Cell division cycle and apoptosis regulator protein 1 (Cell cycle and apoptosis regulatory protein 1) (CARP-1) (Death inducer with SAP domain)	CCAR1	Q8IX12
Serine/threonine-protein kinase NIM1 (EC 2.7.11.1) (NIM1 serine/threonine-protein kinase)	NIM1K	Q8IY84
Ras and EF-hand domain-containing protein (Ras-related protein Rab-45)	RASEF	Q8IZ41
Transcription initiation factor TFIID subunit 1-like (TAF(II)210) (TBP-associated factor 1-like) (TBP-associated factor 210 kDa) (Transcription initiation factor TFIID 210 kDa subunit)	TAF1L	Q8IZX4

Nesprin-4 (KASH domain-containing protein 4) (KASH4) (Nuclear envelope spectrin repeat protein 4)	SYNE4	Q8N205
Voltage-dependent calcium channel beta subunit-associated regulatory protein	CBARP	Q8N350
Cardiomyopathy-associated protein 5 (Dystrobrevin-binding protein 2) (Genethonin-3) (Myospryn) (SPRY domain-containing protein 2) (Tripartite motif-containing protein 76)	CMYA5	Q8N3K9
Ligand-dependent nuclear receptor corepressor-like protein (LCoR-like protein)	LCORL	Q8N3X6
Leucine-rich repeat-containing protein 71	LRRC71	Q8N4P6
Actin filament-associated protein 1-like 2 (AFAP1-like protein 2)	AFAP1L2	Q8N4X5
Refilin-B (Regulator of filamin protein B) (RefilinB)	RFLNB	Q8N5W9
Ligand-dependent corepressor (LCoR) (Mblk1-related protein 2)	LCOR	Q96JN0
ER membrane protein complex subunit 1	EMC1	Q8N766
FERM domain-containing protein 1	FRMD1	Q8N878
Exonuclease mut-7 homolog (EC 3.1.-.-) (Exonuclease 3'-5' domain-containing protein 3)	EXD3	Q8N9H8
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C (PP6-ARS-C) (Serine/threonine-protein phosphatase 6 regulatory subunit ARS-C) (Ankyrin repeat domain-containing protein 52)	ANKRD52	Q8NB46
Kremen protein 2 (Dickkopf receptor 2) (Kringle domain-containing transmembrane protein 2) (Kringle-containing protein marking the eye and the nose)	KREMEN2	Q8NCW0
Coiled-coil domain-containing protein 150	CCDC150	Q8NCX0
Basal body-orientation factor 1 (Coiled-coil domain-containing protein 176)	BBOF1	Q8ND07
Leucine-rich repeat transmembrane protein CCDC168 (Coiled-coil domain-containing protein 168)	CCDC168	Q8NDH2
Trinucleotide repeat-containing gene 6A protein (CAG repeat protein 26) (EMSY interactor protein) (GW182 autoantigen) (Protein GW1) (Glycine-tryptophan protein of 182 kDa)	TNRC6A	Q8NDV7
ATP-binding cassette sub-family F member 1 (ATP-binding cassette 50) (TNF-alpha-stimulated ABC protein)	ABCF1	Q8NE71
Microcephalin	MCPH1	Q8NEM0
Neuron navigator 1 (Pore membrane and/or filament-interacting-like protein 3) (Steerin-1) (Unc-53 homolog 1) (unc53H1)	NAV1	Q8NEY1
Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1	Q8NFC6
AT-rich interactive domain-containing protein 1B (ARID domain-containing protein 1B) (BRG1-associated factor 250b) (BAF250B) (BRG1-binding protein hELD/OSA1) (Osa homolog 2) (hOsa2) (p250R)	ARID1B	Q8NFD5
Collagen alpha-1(XXII) chain	COL22A1	Q8NFW1

Semaphorin-6D	SEMA6D	Q8NFY4
F-box DNA helicase 1 (hFBH1) (EC 5.6.2.4) (DNA 3'-5' helicase 1) (F-box only protein 18)	FBH1	Q8NFZ0
Olfactory receptor 51G1 (Olfactory receptor 51G3) (Olfactory receptor OR11-29)	OR51G1	Q8NGK1
Rhox homeobox family member 1 (Ovary-, testis- and epididymis-expressed gene protein) (Paired-like homeobox protein PEPP-1)	RHOXF1	Q8NHV9
Vang-like protein 1 (Loop-tail protein 2 homolog) (LPP2) (Strabismus 2) (Van Gogh-like protein 1)	VANGL1	Q8TAA9
SWI/SNF complex subunit SMARCC2 (BRG1-associated factor 170) (BAF170) (SWI/SNF complex 170 kDa subunit) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2)	SMARCC2	Q8TAQ2
F-box only protein 30	FBXO30	Q8TB52
E3 ubiquitin-protein ligase LNX (EC 2.3.2.27) (Ligand of Numb-protein X 1) (Numb-binding protein 1) (PDZ domain-containing RING finger protein 2) (RING-type E3 ubiquitin transferase LNX)	LNX1	Q8TBB1
Zinc finger protein 507	ZNF507	Q8TCN5
Chromodomain-helicase-DNA-binding protein 6 (CHD-6) (EC 3.6.4.12) (ATP-dependent helicase CHD6) (Radiation-induced gene B protein)	CHD6	Q8TD26
Dynein axonemal heavy chain 3 (Axonemal beta dynein heavy chain 3) (HsADHC3) (Ciliary dynein heavy chain 3) (Dnahc3-b)	DNAH3	Q8TD57
Serine/threonine-protein kinase BRSK1 (EC 2.7.11.1) (Brain-selective kinase 1) (EC 2.7.11.26) (Brain-specific serine/threonine-protein kinase 1) (BR serine/threonine-protein kinase 1) (Serine/threonine-protein kinase SAD-B) (Synapses of Amphids Defective homolog 1) (SAD1 homolog) (hSAD1)	BRSK1	Q8TDC3
Serine/threonine-protein kinase 35 (EC 2.7.11.1) (CLP-36-interacting kinase 1) (CLIK-1) (PDLIM1-interacting kinase 1) (Serine/threonine-protein kinase 35 L1)	STK35	Q8TDR2
[F-actin]-monooxygenase MICAL1 (EC 1.14.13.225) (EC 1.6.3.1) (Molecule interacting with CasL protein 1) (MICAL-1) (NEDD9-interacting protein with calponin homology and LIM domains)	MICAL1	Q8TDZ2
OTU domain-containing protein 7A (EC 3.4.19.12) (Zinc finger protein Cezanne 2)	OTUD7A	Q8TE49
Fas-binding factor 1 (FBF-1) (Protein albatross)	FBF1	Q8TES7
WASP homolog-associated protein with actin, membranes and microtubules (WAS protein homology region 2 domain-containing protein 1) (WH2 domain-containing protein 1)	WHAMM	Q8TF30
PHD finger protein 10 (BRG1-associated factor 45a) (BAF45a) (XAP135)	PHF10	Q8WUB8

Cytoplasmic dynein 2 intermediate chain 1 (Dynein 2 intermediate chain 1) (WD repeat-containing protein 60)	DYNC2I1	Q8WVS4
T-complex protein 11 homolog	TCP11	Q8WWU5
Nesprin-2 (KASH domain-containing protein 2) (KASH2) (Nuclear envelope spectrin repeat protein 2) (Nucleus and actin connecting element protein) (Protein NUANCE) (Synaptic nuclear envelope protein 2) (Syne-2)	SYNE2	Q8WXH0
Mucin-16 (MUC-16) (Ovarian cancer-related tumor marker CA125) (CA-125) (Ovarian carcinoma antigen CA125)	MUC16	Q8WXI7
HMG box transcription factor BBX (Bobby sox homolog) (HMG box-containing protein 2)	BBX	Q8WY36
Basic helix-loop-helix ARNT-like protein 2 (Aryl hydrocarbon receptor nuclear translocator-like protein 2) (Basic-helix-loop-helix-PAS protein MOP9) (Brain and muscle ARNT-like 2) (CYCLE-like factor) (CLIF) (Class E basic helix-loop-helix protein 6) (bHLHe6) (Member of PAS protein 9) (PAS domain-containing protein 9)	BMAL2	Q8WYA1
Contactin-associated protein-like 5 (Cell recognition molecule Caspr5)	CNTNAP5	Q8WYK1
Ryanodine receptor 2 (RYR-2) (RyR2) (hRYR-2) (Cardiac muscle ryanodine receptor) (Cardiac muscle ryanodine receptor-calcium release channel) (Type 2 ryanodine receptor)	RYR2	Q92736
Endoplasmic reticulum protein SC65 (Leprecan-like protein 4) (Nucleolar autoantigen No55) (Prolyl 3-hydroxylase family member 4) (Synaptonemal complex protein SC65)	P3H4	Q92791
Protein Jumonji (Jumonji/ARID domain-containing protein 2)	JARID2	Q92833
Probable ATP-dependent RNA helicase DDX17 (EC 3.6.4.13) (DEAD box protein 17) (DEAD box protein p72) (DEAD box protein p82) (RNA-dependent helicase p72)	DDX17	Q92841
Neogenin (Immunoglobulin superfamily DCC subclass member 2)	NEO1	Q92859
Regulator of nonsense transcripts 1 (EC 3.6.4.12) (EC 3.6.4.13) (ATP-dependent helicase RENT1) (Nonsense mRNA reducing factor 1) (NORF1) (Up-frameshift suppressor 1 homolog) (hUpf1)	UPF1	Q92900
GTP-binding protein Rit1 (EC 3.6.5.2) (Ras-like protein expressed in many tissues) (Ras-like without CAAX protein 1)	RIT1	Q92963
Protein naked cuticle homolog 2 (Naked-2) (hNkd2)	NKD2	Q969F2
Dapper homolog 3 (Antagonist of beta-catenin Dapper homolog 3) (Arginine-rich region 1 protein) (Dapper antagonist of catenin 3)	DACT3	Q96B18
Methyl-CpG-binding domain protein 6 (Methyl-CpG-binding protein MBD6)	MBD6	Q96DN6
Mdm2-binding protein (hMTBP)	MTBP	Q96DY7
CKLF-like MARVEL transmembrane domain-containing protein 7 (Chemokine-like factor superfamily member 7)	CMTM7	Q96FZ5

OTU domain-containing protein 5 (EC 3.4.19.12) (Deubiquitinating enzyme A) (DUBA)	OTUD5	Q96G74
Tonsoku-like protein (Inhibitor of kappa B-related protein) (I-kappa-B-related protein) (IkappaBR) (NF-kappa-B inhibitor-like protein 2) (Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2)	TONSL	Q96HA7
Carboxypeptidase B2 (EC 3.4.17.20) (Carboxypeptidase U) (CPU) (Plasma carboxypeptidase B) (pCPB) (Thrombin-activable fibrinolysis inhibitor) (TAFI)	CPB2	Q96IY4
Serine/threonine-protein kinase WNK4 (EC 2.7.11.1) (Protein kinase lysine-deficient 4) (Protein kinase with no lysine 4)	WNK4	Q96J92
Membrane-spanning 4-domains subfamily A member 14 (Testis development protein NYD-SP21)	MS4A14	Q96JA4
Protein SERAC1 (Serine active site-containing protein 1)	SERAC1	Q96JX3
Beta-Ala-His dipeptidase (EC 3.4.13.20) (CNDP dipeptidase 1) (Carnosine dipeptidase 1) (Glutamate carboxypeptidase-like protein 2) (Serum carnosinase)	CNDP1	Q96KN2
MAP/microtubule affinity-regulating kinase 4 (EC 2.7.11.1) (MAP/microtubule affinity-regulating kinase-like 1)	MARK4	Q96L34
E1A-binding protein p400 (EC 3.6.4.-) (CAG repeat protein 32) (Domino homolog) (hDomino) (Trinucleotide repeat-containing gene 12 protein) (p400 kDa SWI2/SNF2-related protein)	EP400	Q96L91
Dynein heavy chain domain-containing protein 1 (Coiled-coil domain-containing protein 35) (Dynein heavy chain domain 1-like protein)	DNHD1	Q96M86
Urocanate hydratase (Urocanase) (EC 4.2.1.49) (Imidazolonepropionate hydrolase)	UROC1	Q96N76
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 3 (Centaurin-beta-5) (Cnt-b5)	ACAP3	Q96P50
N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) (Peptidoglycan recognition protein 2) (Peptidoglycan recognition protein long) (PGRP-L)	PGLYRP2	Q96PD5
Serine/threonine-protein kinase SMG1 (SMG-1) (hSMG-1) (EC 2.7.11.1) (Lambda/iota protein kinase C-interacting protein) (Lambda-interacting protein) (Nonsense mediated mRNA decay-associated PI3K-related kinase SMG1)	SMG1	Q96Q15
Pannexin-2	PANX2	Q96RD6
Fc receptor-like protein 5 (FcR-like protein 5) (FcRL5) (BXMAS1) (Fc receptor homolog 5) (FcRH5) (Immune receptor translocation-associated protein 2) (CD antigen CD307e)	FCRL5	Q96RD9
Formin-binding protein 1 (Formin-binding protein 17) (hFBP17)	FNBP1	Q96RU3
Hemicentin-1 (Fibulin-6) (FIBL-6)	HMCN1	Q96RW7
JmjC domain-containing protein 8 (Jumonji domain-containing protein 8)	JMJD8	Q96S16
RNA-binding protein 15 (One-twenty two protein 1) (RNA-binding motif protein 15)	RBM15	Q96T37

TSC22 domain family protein 3 (DSIP-immunoreactive peptide) (Protein DIP) (hDIP) (Delta sleep-inducing peptide immunoreactor) (Glucocorticoid-induced leucine zipper protein) (GILZ) (TSC-22-like protein) (TSC-22-related protein) (TSC-22R)	TSC22D3	Q99576
Mitogen-activated protein kinase kinase kinase 5 (EC 2.7.11.25) (Apoptosis signal-regulating kinase 1) (ASK-1) (MAPK/ERK kinase kinase 5) (MEK kinase 5) (MEKK 5)	MAP3K5	Q99683
Endophilin-A3 (EEN-B2) (Endophilin-3) (SH3 domain protein 2C) (SH3 domain-containing GRB2-like protein 3)	SH3GL3	Q99963
Dihydropyrimidinase-related protein 5 (DRP-5) (CRMP3-associated molecule) (CRAM) (Collapsin response mediator protein 5) (CRMP-5) (UNC33-like phosphoprotein 6) (ULIP-6)	DPYSL5	Q9BPU6
Fermitin family homolog 1 (Kindlerin) (Kindlin syndrome protein) (Kindlin-1) (Unc-112-related protein 1)	FERMT1	Q9BQL6
Programmed cell death protein 2-like	PDCD2L	Q9BRP1
TERF1-interacting nuclear factor 2 (TRF1-interacting nuclear protein 2)	TINF2	Q9BSI4
Death-inducer obliterator 1 (DIO-1) (hDido1) (Death-associated transcription factor 1) (DATF-1)	DIDO1	Q9BTC0
Tubulin-specific chaperone D (Beta-tubulin cofactor D) (tfcD) (SSD-1) (Tubulin-folding cofactor D)	TBCD	Q9BTW9
Protein TALPID3	KIAA0586	Q9BVV6
Brother of CDO (Protein BOC)	BOC	Q9BWV1
Sorbin and SH3 domain-containing protein 1 (Ponsin) (SH3 domain protein 5) (SH3P12) (c-Cbl-associated protein) (CAP)	SORBS1	Q9BX66
Serrate RNA effector molecule homolog (Arsenite-resistance protein 2)	SRRT	Q9BXP5
RING finger protein 17 (Tudor domain-containing protein 4)	RNF17	Q9BXT8
EMILIN-2 (Elastin microfibril interface-located protein 2) (Elastin microfibril interfacier 2) (Protein FOAP-10)	EMILIN2	Q9BXX0
Uncharacterized protein KIAA1671	KIAA1671	Q9BY89
Partitioning defective 6 homolog gamma (PAR-6 gamma) (PAR6D)	PARD6G	Q9BYG4
Membrane-associated phosphatidylinositol transfer protein 2 (Phosphatidylinositol transfer protein, membrane-associated 2) (PITPnm 2) (Pyk2 N-terminal domain-interacting receptor 3) (NIR-3)	PITPNM2	Q9BZ72
Histone-lysine N-methyltransferase NSD3 (EC 2.1.1.370) (EC 2.1.1.371) (Nuclear SET domain-containing protein 3) (Protein whistle) (WHSC1-like 1 isoform 9 with methyltransferase activity to lysine) (Wolf-Hirschhorn syndrome candidate 1-like protein 1) (WHSC1-like protein 1)	NSD3	Q9BZ95
GTP-binding protein 4 (Chronic renal failure gene protein) (GTP-binding protein NGB) (Nucleolar GTP-binding protein 1)	GTPBP4	Q9BZE4

Tether containing UBX domain for GLUT4 (Alveolar soft part sarcoma chromosomal region candidate gene 1 protein) (Alveolar soft part sarcoma locus) (Renal papillary cell carcinoma protein 17) (UBX domain-containing protein 9)	ASPSCR1	Q9BZE9
Uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	Q9BZF9
Apoptosis inhibitor 5 (API-5) (Antiapoptosis clone 11 protein) (AAC-11) (Cell migration-inducing gene 8 protein) (Fibroblast growth factor 2-interacting factor) (FIF) (Protein XAGL)	API5	Q9BZZ5
Alpha-ketoglutarate-dependent dioxygenase FTO (Fat mass and obesity-associated protein) (U6 small nuclear RNA (2'-O-methyladenosine-N(6)-)-demethylase FTO) (EC 1.14.11.-) (U6 small nuclear RNA N(6)-methyladenosine-demethylase FTO) (EC 1.14.11.-) (mRNA (2'-O-methyladenosine-N(6)-)-demethylase FTO) (m6A(m)-demethylase FTO) (EC 1.14.11.-) (mRNA N(6)-methyladenosine demethylase FTO) (EC 1.14.11.53) (tRNA N1-methyl adenine demethylase FTO) (EC 1.14.11.-)	FTO	Q9C0B1
Zinc finger protein 407	ZNF407	Q9C0G0
Rho GTPase-activating protein 39	ARHGAP39	Q9C0H5
Ankyrin repeat domain-containing protein 2 (Skeletal muscle ankyrin repeat protein) (hArpp)	ANKRD2	Q9GZV1
Testis-specific Y-encoded-like protein 1 (TSPY-like protein 1)	TSPYL1	Q9H0U9
Presenilin-associated rhomboid-like protein, mitochondrial (EC 3.4.21.105) (Mitochondrial intramembrane cleaving protease PARL) [Cleaved into: P-beta (Pbeta)]	PARL	Q9H300
Tubulin beta-1 chain	TUBB1	Q9H4B7
Sentrin-specific protease 3 (EC 3.4.22.-) (SUMO-1-specific protease 3) (Sentrin/SUMO-specific protease SENP3)	SENP3	Q9H4L4
Proline-rich protein 36	PRR36	Q9H6K5
Pleckstrin homology domain-containing family G member 2 (PH domain-containing family G member 2)	PLEKHG2	Q9H7P9
Cysteine-rich protein 2-binding protein (CSRP2-binding protein) (ADA2A-containing complex subunit 2) (ATAC2) (CRP2-binding partner) (CRP2BP) (Lysine acetyltransferase 14)	KAT14	Q9H8E8
Probable ATP-dependent RNA helicase DDX31 (EC 3.6.4.13) (DEAD box protein 31) (Helicain)	DDX31	Q9H8H2
Interleukin-1 receptor accessory protein (IL-1 receptor accessory protein) (IL-1RAcP) (EC 3.2.2.6) (Interleukin-1 receptor 3) (IL-1R-3) (IL-1R3)	IL1RAP	Q9NPH3
Intraflagellar transport protein 46 homolog	IFT46	Q9NQC8
Cell death regulator Aven	AVEN	Q9NQS1
Spectrin beta chain, non-erythrocytic 5 (Beta-V spectrin)	SPTBN5	Q9NRC6
Kinesin-like protein KIF15 (Kinesin-like protein 2) (hKLP2) (Kinesin-like protein 7) (Serologically defined breast cancer antigen NY-BR-62)	KIF15	Q9NS87

Kinesin light chain 4 (KLC 4) (Kinesin-like protein 8)	KLC4	Q9NSK0
Stabilin-1 (Fasciclin, EGF-like, laminin-type EGF-like and link domain-containing scavenger receptor 1) (FEEL-1) (MS-1 antigen)	STAB1	Q9NY15
Tubulin alpha-8 chain (EC 3.6.5.-) (Alpha-tubulin 8) (Tubulin alpha chain-like 2) [Cleaved into: Dephenylalaninated tubulin alpha-8 chain]	TUBA8	Q9NY65
Dapper homolog 1 (hDPR1) (Dapper antagonist of catenin 1) (Hepatocellular carcinoma novel gene 3 protein)	DACT1	Q9NYF0
PH and SEC7 domain-containing protein 3 (Epididymis tissue protein Li 20mP) (Exchange factor for ADP-ribosylation factor guanine nucleotide factor 6 D) (Exchange factor for ARF6 D) (Hepatocellular carcinoma-associated antigen 67) (Pleckstrin homology and SEC7 domain-containing protein 3)	PSD3	Q9NYI0
Cadherin EGF LAG seven-pass G-type receptor 1 (Cadherin family member 9) (Flamingo homolog 2) (hFmi2)	CELSR1	Q9NYQ6
Sacsin (DnaJ homolog subfamily C member 29) (DNAJC29)	SACS	Q9NZJ4
Complement C1r subcomponent-like protein (C1r-LP) (C1r-like protein) (EC 3.4.21.-) (C1r-like serine protease analog protein) (CLSPa)	C1RL	Q9NZP8
Low-density lipoprotein receptor-related protein 1B (LRP-1B) (Low-density lipoprotein receptor-related protein-deleted in tumor) (LRP-DIT)	LRP1B	Q9NZR2
Calcium-binding protein 1 (CaBP1) (Calbrain) (Caldendrin)	CABP1	Q9NZU7
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 (Cell death regulatory protein GRIM-19) (Complex I-B16.6) (CI-B16.6) (Gene associated with retinoic and interferon-induced mortality 19 protein) (GRIM-19) (Gene associated with retinoic and IFN-induced mortality 19 protein) (NADH-ubiquinone oxidoreductase B16.6 subunit)	NDUFA13	Q9P0J0
Zinc finger and BTB domain-containing protein 4 (KAISO-like zinc finger protein 1) (KAISO-L1)	ZBTB4	Q9P1Z0
Calcium-binding and coiled-coil domain-containing protein 1 (Calphoglin) (Coiled-coil coactivator protein) (Sarcoma antigen NY-SAR-3)	CALCOCO1	Q9P1Z2
Whirlin (Autosomal recessive deafness type 31 protein)	WHRN	Q9P202
Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 2	NYAP2	Q9P242
Junctional cadherin 5-associated protein (Junctional protein associated with coronary artery disease) (JCAD)	JCAD	Q9P266
Cilia- and flagella-associated protein 97	CFAP97	Q9P2B7
Chromodomain-helicase-DNA-binding protein 7 (CHD-7) (EC 3.6.4.12) (ATP-dependent helicase CHD7)	CHD7	Q9P2D1

Ribosome-binding protein 1 (180 kDa ribosome receptor homolog) (RRp) (ES/130-related protein) (Ribosome receptor protein)	RRBP1	Q9P2E9
Zinc finger protein 219	ZNF219	Q9P2Y4
DNA repair protein REV1 (EC 2.7.7.-) (Alpha integrin-binding protein 80) (AIBP80) (Rev1-like terminal deoxycytidyl transferase)	REV1	Q9UBZ9
Alpha-amino adipic semialdehyde synthase, mitochondrial (LKR/SDH) [Includes: Lysine ketoglutarate reductase (LKR) (LOR) (EC 1.5.1.8); Saccharopine dehydrogenase (SDH) (EC 1.5.1.9)]	AASS	Q9UDR5
Solute carrier family 23 member 2 (Na(+)/L-ascorbic acid transporter 2) (Nucleobase transporter-like 1 protein) (Sodium-dependent vitamin C transporter 2) (hSVCT2) (Yolk sac permease-like molecule 2)	SLC23A2	Q9UGH3
Fetuin-B (16G2) (Fetuin-like protein IRL685) (Gugu)	FETUB	Q9UGM5
Probable ribosome biogenesis protein RLP24 (Ribosomal L24 domain-containing protein 1) (Ribosomal protein L24-like)	RSL24D1	Q9UHA3
LIM domain and actin-binding protein 1 (Epithelial protein lost in neoplasm)	LIMA1	Q9UHB6
Signal recognition particle subunit SRP68 (SRP68) (Signal recognition particle 68 kDa protein)	SRP68	Q9UHB9
FMR1-interacting protein NUFIP1 (Nuclear FMR1-interacting protein 1) (Nuclear FMRP-interacting protein 1)	NUFIP1	Q9UHK0
Death-associated protein kinase 2 (DAP kinase 2) (EC 2.7.11.1) (DAP-kinase-related protein 1) (DRP-1)	DAPK2	Q9UIK4
Serpin B13 (HaCaT UV-repressible serpin) (Hurpin) (Headpin) (Peptidase inhibitor 13) (PI-13) (Proteinase inhibitor 13)	SERPINB13	Q9UIV8
Probable E3 ubiquitin-protein ligase MID2 (EC 2.3.2.27) (Midin-2) (Midline defect 2) (Midline-2) (RING finger protein 60) (RING-type E3 ubiquitin transferase MID2) (Tripartite motif-containing protein 1)	MID2	Q9UJV3
Oxidative stress-induced growth inhibitor 1 (Bone marrow stromal cell-derived growth inhibitor) (BMSC-derived growth inhibitor) (Ovary, kidney and liver protein 38) (huOKL38) (Pregnancy-induced growth inhibitor OKL38)	OSGIN1	Q9UJX0
Protein TASOR (CTCL tumor antigen se89-1) (Retinoblastoma-associated protein RAP140) (Transgene activation suppressor protein)	TASOR	Q9UK61
F-box/LRR-repeat protein 5 (F-box and leucine-rich repeat protein 5) (F-box protein FBL4/FBL5) (p45SKP2-like protein)	FBXL5	Q9UKA1
TRAF2 and NCK-interacting protein kinase (EC 2.7.11.1)	TNIK	Q9UKE5

Myosin-13 (Myosin heavy chain 13) (Myosin heavy chain, skeletal muscle, extraocular) (MyHC-EO) (Myosin heavy chain, skeletal muscle, laryngeal) (MyHC-IIL) (Superfast myosin)	MYH13	Q9UKX3
Ras-related protein Rab-21	RAB21	Q9UL25
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2 (Brain cyclic nucleotide-gated channel 2) (BCNG-2)	HCN2	Q9UL51
Serine/threonine-protein kinase TAO2 (EC 2.7.11.1) (Kinase from chicken homolog C) (hKFC-C) (Prostate-derived sterile 20-like kinase 1) (PSK-1) (PSK1) (Prostate-derived STE20-like kinase 1) (Thousand and one amino acid protein kinase 2)	TAOK2	Q9UL54
Zinc finger protein 608 (Renal carcinoma antigen NY-REN-36)	ZNF608	Q9ULD9
Mediator of RNA polymerase II transcription subunit 23 (Activator-recruited cofactor 130 kDa component) (ARC130) (Cofactor required for Sp1 transcriptional activation subunit 3) (CRSP complex subunit 3) (Mediator complex subunit 23) (Protein sur-2 homolog) (hSur-2) (Transcriptional coactivator CRSP130) (Vitamin D3 receptor-interacting protein complex 130 kDa component) (DRIP130)	MED23	Q9ULK4
Pleckstrin homology domain-containing family H member 1 (PH domain-containing family H member 1)	PLEKHH1	Q9ULM0
Coronin-1C (Coronin-3) (hCRNN4)	CORO1C	Q9ULV4
Heat shock factor protein 4 (HSF 4) (hHSF4) (Heat shock transcription factor 4) (HSTF 4)	HSF4	Q9ULV5
Pre-mRNA-processing factor 19 (EC 2.3.2.27) (Nuclear matrix protein 200) (PRP19/PSO4 homolog) (hPso4) (RING-type E3 ubiquitin transferase PRP19) (Senescence evasion factor)	PRPF19	Q9UMS4
Transcription termination factor 2 (EC 3.6.4.-) (Lodestar homolog) (RNA polymerase II termination factor) (Transcription release factor 2) (F2) (HuF2)	TTF2	Q9UNY4
E3 ubiquitin-protein ligase TRIM33 (EC 2.3.2.27) (Ectodermin homolog) (RET-fused gene 7 protein) (Protein Rfg7) (RING-type E3 ubiquitin transferase TRIM33) (Transcription intermediary factor 1-gamma) (TIF1-gamma) (Tripartite motif-containing protein 33)	TRIM33	Q9UPN9
Trinucleotide repeat-containing gene 6B protein	TNRC6B	Q9UPQ9
RAC-gamma serine/threonine-protein kinase (EC 2.7.11.1) (Protein kinase Akt-3) (Protein kinase B gamma) (PKB gamma) (RAC-PK-gamma) (STK-2)	AKT3	Q9Y243
Exocyst complex component 6B (Exocyst complex component Sec15B) (SEC15-like protein 2)	EXOC6B	Q9Y2D4
E3 ubiquitin-protein ligase DTX4 (EC 2.3.2.27) (Protein deltex-4) (Deltex4) (RING finger protein 155) (RING-type E3 ubiquitin transferase DTX4)	DTX4	Q9Y2E6
Disks large-associated protein 4 (DAP-4) (PSD-95/SAP90-binding protein 4) (SAP90/PSD-95-associated protein 4) (SAPAP-4)	DLGAP4	Q9Y2H0

Serine/threonine-protein kinase 38-like (EC 2.7.11.1) (NDR2 protein kinase) (Nuclear Dbf2-related kinase 2)	STK38L	Q9Y2H1
Fanconi-associated nuclease 1 (EC 3.1.21.-) (EC 3.1.4.1) (FANCD2/FANCI-associated nuclease 1) (hFAN1) (Myotubularin-related protein 15)	FAN1	Q9Y2M0
Long-chain fatty acid transport protein 5 (FATP-5) (Fatty acid transport protein 5) (Bile acid-CoA ligase) (BA-CoA ligase) (BAL) (Bile acyl-CoA synthetase) (BACS) (EC 6.2.1.7) (Cholate--CoA ligase) (Fatty-acid-coenzyme A ligase, very long-chain 3) (Long-chain-fatty-acid--CoA ligase) (EC 6.2.1.3) (Solute carrier family 27 member 5) (Very long-chain acyl-CoA synthetase homolog 2) (VLCS-H2) (VLCSH2) (EC 6.2.1.-) (Very long-chain acyl-CoA synthetase-related protein) (VLACS-related) (VLACSR)	SLC27A5	Q9Y2P5
N-acetylglucosamine-6-phosphate deacetylase (GlcNAc 6-P deacetylase) (EC 3.5.1.25) (Amidohydrolase domain-containing protein 2)	AMDHD2	Q9Y303
V-type proton ATPase 116 kDa subunit a 2 (V-ATPase 116 kDa subunit a 2) (Lysosomal H(+)-transporting ATPase V0 subunit a 2) (TJ6) (Vacuolar proton translocating ATPase 116 kDa subunit a isoform 2)	ATP6V0A2	Q9Y487
Talin-1	TLN1	Q9Y490
Probable E3 ubiquitin-protein ligase HECTD4 (EC 2.3.2.26) (HECT domain-containing protein 4) (HECT-type E3 ubiquitin transferase HECTD4)	HECTD4	Q9Y4D8
AFG3-like protein 2 (EC 3.4.24.-) (Paraplegin-like protein)	AFG3L2	Q9Y4W6
Protocadherin gamma-A10 (PCDH-gamma-A10)	PCDHGA10	Q9Y5H3
Serine/threonine-protein kinase MRCK beta (EC 2.7.11.1) (CDC42-binding protein kinase beta) (CDC42BP-beta) (DMPK-like beta) (Myotonic dystrophy kinase-related CDC42-binding kinase beta) (MRCK beta) (Myotonic dystrophy protein kinase-like beta)	CDC42BPB	Q9Y5S2
NADPH oxidase 1 (NOX-1) (EC 1.6.3.-) (Mitogenic oxidase 1) (MOX-1) (NADH/NADPH mitogenic oxidase subunit P65-MOX) (NOH-1)	NOX1	Q9Y5S8
Glypican-6 [Cleaved into: Secreted glypican-6]	GPC6	Q9Y625
Brefeldin A-inhibited guanine nucleotide-exchange protein 2 (Brefeldin A-inhibited GEP 2) (ADP-ribosylation factor guanine nucleotide-exchange factor 2)	ARFGEF2	Q9Y6D5
Inositol 1,4,5-triphosphate receptor associated 1 (Inositol 1,4,5-trisphosphate receptor-associated cGMP kinase substrate) (JAW1-related protein MRV11) (Protein MRV11)	IRAG1	Q9Y6F6
SEC23-interacting protein (p125)	SEC23IP	Q9Y6Y8
Probable non-functional immunoglobulin kappa variable 3-7	IGKV3-7	A0A075B6H7
Immunoglobulin lambda variable 8-61	IGLV8-61	A0A075B6I0
Immunoglobulin lambda variable 1-40 (Ig lambda chain V-I region NEWM)	IGLV1-40	P01703

Immunoglobulin lambda variable 3-27 (Ig lambda chain V-IV region Kern)	IGLV3-27	P01718
Immunoglobulin lambda variable 2-14 (Ig lambda chain V-II region NIG-84) (Ig lambda chain V-II region TOG) (Ig lambda chain V-II region VIL)	IGLV2-14	P01704
Immunoglobulin lambda variable 3-10	IGLV3-10	A0A075B6K4
Immunoglobulin lambda constant 3 (Ig lambda chain C region DOT) (Ig lambda chain C region NEWM) (Ig lambda-3 chain C regions)	IGLC3	P0DOY3
Immunoglobulin heavy constant alpha 2 (Ig alpha-2 chain C region) (Ig alpha-2 chain C region BUT) (Ig alpha-2 chain C region LAN)	IGHA2	P01877
T cell receptor alpha joining 56	TRAJ56	A0A075B6Z2
Immunoglobulin heavy variable 3/OR16-12 (non-functional)	IGHV3OR16-12	A0A075B7B8
Immunoglobulin heavy variable 3/OR15-7 (pseudogene)	IGHV3OR15-7	A0A075B7D8
Immunoglobulin heavy variable 3-72	IGHV3-72	A0A0B4J1Y9
Phosphodiesterase 4D interacting protein	PDE4DIP	A0A087WX83
Vacuolar protein sorting-associated protein 11 homolog	VPS11	A0A087WXL6
Empty spiracles homeobox 1 (Empty spiracles homolog 1 (Drosophila), isoform CRA_a)	EMX1	A0A087WZF2
peptidylprolyl isomerase (EC 5.2.1.8)	FKBP1A	A0A087WZM5
RIB43A-like with coiled-coils protein 2	RIBC2	Q9H4K1
Immunoglobulin kappa variable 2D-29	IGKV2D-29	A0A075B6S2
Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	IGKC	P01834
Family with sequence similarity 184 member A	FAM184A	A0A087X2A7
SAA2-SAA4 readthrough	SAA2-SAA4	A0A096LPE2
Mitogen-activated protein kinase kinase kinase kinase 5 (EC 2.7.11.1) (Kinase homologous to SPS1/STE20) (KHS) (MAPK/ERK kinase kinase kinase 5) (MEK kinase kinase 5) (MEKKK 5)	MAP4K5	Q9Y4K4
Immunoglobulin heavy variable 4-34 (Ig heavy chain V-II region ARH-77)	IGHV4-34	P06331
Eukaryotic translation initiation factor 4 gamma 3	EIF4G3	A0A0A0MSA7

Immunoglobulin kappa variable 1-16 (Ig kappa chain V-I region BAN)	IGKV1-16	P04430
Titin	TTN	A0A0A0MTS7
Immunoglobulin kappa variable 1D-33 (Ig kappa chain V-I region AG) (Ig kappa chain V-I region Bi) (Ig kappa chain V-I region Lay) (Ig kappa chain V-I region Ni) (Ig kappa chain V-I region Rei) (Ig kappa chain V-I region Roy) (Ig kappa chain V-I region Scw) (Ig kappa chain V-I region WAT)	IGKV1D-33	P01593
Immunoglobulin lambda variable 1-44 (Ig lambda chain V-I region MEM) (Ig lambda chain V-I region VOR)	IGLV1-44	P01699
Immunoglobulin lambda variable 1-36	IGLV1-36	A0A0B4J1U3
Immunoglobulin heavy variable 3-15	IGHV3-15	A0A0B4J1V0
Immunoglobulin heavy variable 2-26	IGHV2-26	A0A0B4J1V2
Immunoglobulin heavy variable 1-46 (Ig heavy chain V-I region DOT) (Ig heavy chain V-I region HG3) (Ig heavy chain V-I region Mot)	IGHV1-46	P01743
Immunoglobulin heavy variable 1-69 (Ig heavy chain V-I region EU) (Ig heavy chain V-I region SIE) (Ig heavy chain V-I region WOL)	IGHV1-69	P01742
Immunoglobulin kappa variable 1-17 (Ig kappa chain V-I region Gal) (Ig kappa chain V-I region WEA)	IGKV1-17	P01599
Immunoglobulin heavy variable 3-30 (Ig heavy chain V-III region BUR) (Ig heavy chain V-III region CAM) (Ig heavy chain V-III region GA) (Ig heavy chain V-III region NIE)	IGHV3-30	P01768
EMILIN-1 (Elastin microfibril interface-located protein 1) (Elastin microfibril interfacer 1)	EMILIN1	Q9Y6C2
Immunoglobulin kappa variable 3D-20	IGKV3D-20	A0A0C4DH25
Immunoglobulin heavy variable 1-18	IGHV1-18	A0A0C4DH31
Immunoglobulin heavy variable 1-24	IGHV1-24	A0A0C4DH33
Probable non-functional immunoglobulin heavy variable 3-35	IGHV3-35	A0A0C4DH35
Probable non-functional immunoglobulin heavy variable 3-38	IGHV3-38	A0A0C4DH36
Immunoglobulin kappa variable 1-39 (Ig kappa chain V-I region DEE) (Ig kappa chain V-I region Hau) (Ig kappa chain V-I region Mev) (Ig kappa chain V-I region OU) (Ig kappa chain V-I region Walker)	IGKV1-39	P01597

Transcription factor 4	TCF4	A0A0D9SG44
Complement C2 (EC 3.4.21.43) (C3/C5 convertase)	C2	A0A0G2JL69
Solute carrier family 12 member 7	SLC12A7	A0A0G2JNW7
Immunoglobulin heavy variable 5-51	IGHV5-51	A0A0C4DH38
Nostrin	NOSTRIN	A0A0G2JPW3
Proteasome subunit beta	PSMB9	A2ACR1
Nuclear factor 1	NFIA	B1AKN8
complement subcomponent C1r (EC 3.4.21.41)	C1R	B4DPQ0
Bestrophin	BEST1	B7Z1N8
protein-serine/threonine phosphatase (EC 3.1.3.16)	PPM1B	B8ZZF0
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	MTHFD2	B9A062
Protein phosphatase 2 scaffold subunit Aalpha	PPP2R1A	C9J9C1
PR/SET domain 14	PRDM14	C9JMM8
Chromosome 10 open reading frame 47, isoform CRA_b (Proline and serine rich 2)	PROSER2	D3DRR9
Uncharacterized protein C4orf54 (Familial obliterative portal venopathy)	C4orf54	D6RIA3
Ankyrin repeat domain 31	ANKRD31	D6RJB7
Helicase, POLQ like	HELQ	E3W980
Dimethylglycine dehydrogenase	DMGDH	E5RGI4
Septin	SEPTIN7	E7EPK1
Propionyl-CoA carboxylase beta chain, mitochondrial (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit beta)	PCCB	E7EX59
Neurolysin, mitochondrial (EC 3.4.24.16) (Microsomal endopeptidase) (Mitochondrial oligopeptidase M) (Neurotensin endopeptidase)	NLN	E9PCB6
Structural maintenance of chromosomes protein	SMC4	E9PD53
Dystrophin	DMD	P11532
Serpin family G member 1	SERPING1	E9PGN7
Hypothetical LOC645967	LOC645967	F1T0L1
Pepsinogen A3 (Pepsinogen A4)	PGA3	F5GXL4
Centrosomal protein 112	CEP112	F5GYE8
Major histocompatibility complex, class II, DO alpha	HLA-DOA	F6WU08

FYVE, RhoGEF and PH domain containing 4	FGD4	F8VWL3
Keratin 18	KRT18	F8VZY9
Myosin XVI	MYO16	F8W883
Armadillo repeat-containing X-linked protein 4	ARMCX4	Q5H9R4
Transferrin receptor protein 1	TFRC	G3V0E5
GABA type A receptor associated protein like 1 (GABA(A) receptor-associated protein like 1, isoform CRA_e)	GABARAPL1	G3V1T7
Protein Z-dependent protease inhibitor (Serp family A member 10) (Serp peptidase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 10, isoform CRA_a)	SERPINA10	G3V2W1
ATP5MF-PTCD1 readthrough	ATP5MF-PTCD1	G3V325
SKI family transcriptional corepressor 1	SKOR1	G3V3E1
ZFP36 ring finger protein like 1	ZFP36L1	G3V515
Dihydrolipoamide S-succinyltransferase	DLST	G3V5L9
Zinc finger protein 766	ZNF766	G3XAE0
Complement factor I	CFI	G3XAM2
Cartilage oligomeric matrix protein	COMP	G3XAP6
ATPase family AAA domain containing 3A	ATAD3A	H0Y2W2
Dynein axonemal heavy chain 8	DNAH8	H0Y7V4
Plexin D1	PLXND1	H0YA64
RB transcriptional corepressor like 1	RBL1	H0YE05
ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	H0YEW4
Cysteinyl-tRNA synthetase 2, mitochondrial	CARS2	H0YFF0
Calbindin 2 (Calretinin)	CALB2	H3BN14
Protein phosphatase 4 catalytic subunit	PPP4C	H3BPN5
non-specific serine/threonine protein kinase (EC 2.7.11.1)	OBSCN	A6NGQ3
Microtubule actin crosslinking factor 1	MACF1	H3BQK9
Zinc finger FYVE-type containing 19	ZFYVE19	H3BS07
N-acetyl-D-glucosamine kinase (EC 2.7.1.59) (GlcNAc kinase)	NAGK	H7C3G9
ABI family member 3 binding protein	ABI3BP	H7C4H3
Proline rich transmembrane protein 4	PRRT4	H7C4Q3
Splicing factor 1	SF1	H7C561
Armadillo like helical domain containing 1	ARMH1	H7C5J1

Sex hormone-binding globulin (Sex steroid-binding protein) (Testis-specific androgen-binding protein)	SHBG	I3L145
Septin	SEPTIN1	J3KNL2
non-specific serine/threonine protein kinase (EC 2.7.11.1)	MARK3	J3KNR0
Mitogen-activated protein kinase kinase kinase (EC 2.7.11.25)	MAP3K9	J3KPI6
Synaptotagmin	SYT1	J3KQA0
Carnosine dipeptidase 1	CNDP1	J3KRP0
beta-N-acetylhexosaminidase (EC 3.2.1.52)	HEXD	J3QKL0
Golgi SNAP receptor complex member 1	GOSR1	K7EJC8
Adaptor related protein complex 1 subunit mu 2	AP1M2	K7EL08
Apolipoprotein C-II (Apo-CII) (ApoC-II) (Apolipoprotein C2)	APOC4-APOC2	K7ER74
Complement factor D (EC 3.4.21.46) (Adipsin) (C3 convertase activator) (Properdin factor D)	CFD	K7ERG9
Apolipoprotein C-I	APOC1	K7ERI9
Protein FAM210A	FAM210A	K7ERQ2
WW domain binding protein 2	WBP2	K7ESN4
Sterile alpha motif domain containing 4B	SAMD4B	M0QZ22
long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	SLC27A5	M0R075
Tubulin beta 4A class IVa	TUBB4A	M0R278
SURP and G-patch domain containing 2	SUGP2	M0R2Z9
HLA class II histocompatibility antigen, DR alpha chain (MHC cell surface glycoprotein) (Major histocompatibility complex, class II, DR alpha)	HLA-DRA	Q30118
Collagen alpha-2(XI) chain (Collagen type XI alpha 2)	COL11A2	Q4VXY6
Thromboxane-A synthase (EC 4.2.1.152) (EC 5.3.99.5) (Cytochrome P450 5A1) (Hydroperoxy icosatetraenoate dehydratase)	hCG_14925	Q53F23
Discs large MAGUK scaffold protein 3 (Discs, large homolog 3 (Neuroendocrine-dlg, Drosophila), isoform CRA_b)	DLG3	Q5JUW8
Myosin heavy chain 7B	MYH7B	Q5JW49
Heat shock protein family A (Hsp70) member 12B	HSPA12B	Q5JX83
Neurobeachin	NBEA	Q5T321
Retinol-binding protein	RBP4	Q5VY30
Ankyrin repeat domain-containing protein 30A	ANKRD30A	R4GNA2
Motor neuron and pancreas homeobox 1	MNX1	S4R364

PR/SET domain 2	PRDM2	S4R3F7
Motor neuron and pancreas homeobox 1	MNX1	S4R464
DDB1 and CUL4 associated factor 8	DCAF8	V9GY54
Complement factor H related 2	CFHR2	V9GYE7
Apolipoprotein A-II (Apolipoprotein A2)	APOA2	V9GYM3
Phospholipid phosphatase 7 (inactive)	PLPP7	X6R886

Table S2 Comprehensive results of basic logistic regression model on proteins related to obesity

Proteins	Estimate	SE	<i>p</i> value	adjusted <i>p</i> value	log10_adj_pval	log10_pval	OR (95% CI)
APOD	-0.634	0.057	1.83E-28	1.48E-25	24.830	27.738	0.53 (0.863; 1.048)
CRP	0.617	0.057	3.78E-27	3.06E-24	23.514	26.423	1.853 (0.883; 1.056)
LGALS3BP	0.652	0.073	2.62E-19	2.12E-16	15.674	18.582	1.919 (0.944; 1.156)
APOM	-0.494	0.057	4.17E-18	3.38E-15	14.471	17.380	0.61 (0.828; 0.994)
A2M	0.482	0.056	7.46E-18	6.04E-15	14.219	17.127	1.619 (0.905; 1.11)
APOF	-0.89	0.104	1.16E-17	9.40E-15	14.027	16.936	0.411 (0.832; 1.019)
CFH	0.468	0.056	9.37E-17	7.58E-14	13.120	16.028	1.597 (0.87; 1.049)
AFM	0.414	0.055	3.52E-14	2.85E-11	10.545	13.453	1.513 (0.889; 1.086)
SERPINF1	0.39	0.057	8.61E-12	6.96E-09	8.157	11.065	1.477 (0.966; 1.186)
ADIPOQ	-0.402	0.059	1.01E-11	8.20E-09	8.086	10.996	0.669 (0.899; 1.081)
APCS	0.394	0.058	1.36E-11	1.10E-08	7.959	10.866	1.483 (0.832; 0.989)
S100A9	0.424	0.065	5.46E-11	4.41E-08	7.356	10.263	1.528 (0.872; 1.051)
CFI	0.362	0.056	1.14E-10	9.23E-08	7.035	9.943	1.436 (0.9; 1.082)
SAA2-SAA4	0.332	0.055	1.71E-09	1.39E-06	5.857	8.767	1.394 (0.854; 1.028)
NFIA	0.328	0.056	3.37E-09	2.73E-06	5.564	8.472	1.388 (0.875; 1.051)
LBP	0.887	0.153	6.03E-09	4.88E-06	5.312	8.220	2.428 (0.918; 1.1)
SERPINA6	-0.295	0.059	4.99E-07	4.03E-04	3.395	6.302	0.745 (0.809; 0.974)
AZGP1	-0.255	0.051	7.20E-07	5.83E-04	3.234	6.143	0.775 (0.877; 1.073)
SERPIND1	0.258	0.053	9.47E-07	7.66E-04	3.116	6.024	1.294 (0.867; 1.039)
VTN	0.256	0.055	3.40E-06	2.75E-03	2.561	5.469	1.292 (0.905; 1.092)
GPX3	-0.24	0.052	4.68E-06	3.79E-03	2.421	5.330	0.787 (0.87; 1.075)
C4B	0.264	0.061	1.40E-05	1.13E-02	1.947	4.854	1.302 (0.954; 1.173)
SAA2	0.239	0.056	2.17E-05	1.75E-02	1.757	4.664	1.27 (0.86; 1.046)
C4A	0.225	0.053	2.51E-05	2.03E-02	1.693	4.600	1.252 (0.899; 1.096)
C3	0.227	0.054	3.15E-05	2.55E-02	1.593	4.502	1.255 (0.896; 1.086)
SERPINC1	-0.206	0.052	7.46E-05	6.04E-02	1.219	4.127	0.814 (0.992; 1.223)
APOA1	-0.197	0.052	1.49E-04	1.21E-01	0.917	3.827	0.821 (0.856; 1.035)
HPR	-0.191	0.052	2.21E-04	1.79E-01	0.747	3.656	0.826 (0.871; 1.059)
CBARP	-0.171	0.047	2.89E-04	2.34E-01	0.631	3.539	0.843 (0.834; 1.011)
NSD3	-0.16	0.044	2.94E-04	2.38E-01	0.623	3.532	0.852 (0.896; 1.093)

IGFALS	-0.192	0.054	3.74E-04	3.03E-01	0.519	3.427	0.825 (0.884; 1.08)
APOC1	-0.178	0.051	5.21E-04	4.21E-01	0.376	3.283	0.837 (0.951; 1.194)
CKAP5	-0.171	0.05	6.79E-04	5.49E-01	0.260	3.168	0.843 (0.891; 1.071)
PON3	-0.157	0.047	7.26E-04	5.87E-01	0.231	3.139	0.855 (0.919; 1.122)
PCCB	-0.172	0.051	8.49E-04	6.87E-01	0.163	3.071	0.842 (0.882; 1.08)
HP	0.176	0.054	1.24E-03	1.00E+00	0.000	2.907	1.192 (0.909; 1.105)
TTR	-0.166	0.052	1.45E-03	1.00E+00	0.000	2.839	0.847 (0.845; 1.018)
GSN	-0.171	0.054	1.46E-03	1.00E+00	0.000	2.836	0.843 (0.818; 0.999)
CLEC3B	-0.166	0.052	1.51E-03	1.00E+00	0.000	2.821	0.847 (0.901; 1.095)
HSPG2	-0.148	0.047	1.57E-03	1.00E+00	0.000	2.804	0.862 (0.853; 1.02)
ZFP36L1	-0.141	0.045	1.64E-03	1.00E+00	0.000	2.785	0.868 (0.789; 0.959)
FGB	0.191	0.061	1.66E-03	1.00E+00	0.000	2.780	1.21 (0.847; 1.019)
IGHV3-30.1	-0.163	0.052	1.91E-03	1.00E+00	0.000	2.719	0.85 (0.852; 1.012)
STAB1	-0.151	0.049	2.10E-03	1.00E+00	0.000	2.678	0.86 (0.899; 1.09)
F13A1	-0.132	0.044	2.70E-03	1.00E+00	0.000	2.569	0.876 (0.888; 1.063)
SERPINB13	-0.147	0.049	2.75E-03	1.00E+00	0.000	2.561	0.863 (0.894; 1.095)
F9	0.217	0.073	2.90E-03	1.00E+00	0.000	2.538	1.242 (0.879; 1.064)
APOA4	-0.152	0.051	2.91E-03	1.00E+00	0.000	2.536	0.859 (0.934; 1.139)
C8G	0.181	0.061	3.07E-03	1.00E+00	0.000	2.513	1.198 (0.816; 0.986)
GC	-0.157	0.054	3.37E-03	1.00E+00	0.000	2.472	0.855 (0.864; 1.044)
FN1	0.123	0.043	3.82E-03	1.00E+00	0.000	2.418	1.131 (0.901; 1.128)
ARMCX4	-0.14	0.05	4.86E-03	1.00E+00	0.000	2.313	0.869 (0.862; 1.047)
RBM6	-0.125	0.045	4.88E-03	1.00E+00	0.000	2.312	0.882 (0.903; 1.097)
PARL	-0.135	0.048	5.03E-03	1.00E+00	0.000	2.298	0.874 (0.884; 1.079)
CD5L	-0.14	0.05	5.08E-03	1.00E+00	0.000	2.294	0.869 (0.869; 1.047)
PON1	-0.139	0.05	5.66E-03	1.00E+00	0.000	2.247	0.87 (0.852; 1.026)
C1S	0.146	0.053	5.72E-03	1.00E+00	0.000	2.243	1.157 (0.917; 1.131)
ATP6V0A2	-0.143	0.052	5.74E-03	1.00E+00	0.000	2.241	0.867 (0.92; 1.135)
APOB	0.144	0.052	5.79E-03	1.00E+00	0.000	2.237	1.155 (0.864; 1.032)
IGKC	-0.14	0.051	5.91E-03	1.00E+00	0.000	2.228	0.869 (0.917; 1.148)
ORM2	0.146	0.053	6.13E-03	1.00E+00	0.000	2.213	1.157 (0.896; 1.08)
CENPF	-0.132	0.049	7.00E-03	1.00E+00	0.000	2.155	0.876 (0.965; 1.191)
CRYBG3	-0.129	0.048	7.45E-03	1.00E+00	0.000	2.128	0.879 (0.861; 1.022)

PROS1	0.141	0.053	7.73E-03	1.00E+00	0.000	2.112	1.151 (0.878; 1.049)
RASEF	-0.13	0.05	9.25E-03	1.00E+00	0.000	2.034	0.878 (0.884; 1.057)
FSTL4	-0.117	0.045	9.75E-03	1.00E+00	0.000	2.011	0.89 (0.883; 1.077)
SART3	-0.122	0.047	9.80E-03	1.00E+00	0.000	2.009	0.885 (0.846; 1.013)
SERPINA7	0.148	0.057	9.81E-03	1.00E+00	0.000	2.008	1.16 (0.545; 0.681)
MAP1B	-0.122	0.047	9.84E-03	1.00E+00	0.000	2.007	0.885 (0.906; 1.112)
C4BPA	0.136	0.053	1.01E-02	1.00E+00	0.000	1.996	1.146 (0.877; 1.083)
CFHR2	-0.132	0.052	1.06E-02	1.00E+00	0.000	1.975	0.876 (0.873; 1.085)
AMPD2	-0.12	0.047	1.08E-02	1.00E+00	0.000	1.967	0.887 (0.892; 1.075)
ZNF814	-0.119	0.047	1.10E-02	1.00E+00	0.000	1.959	0.888 (0.878; 1.08)
DTX4	-0.127	0.05	1.17E-02	1.00E+00	0.000	1.932	0.881 (0.894; 1.111)
ARID1B	-0.116	0.046	1.25E-02	1.00E+00	0.000	1.903	0.89 (0.857; 1.032)
FGA	0.143	0.057	1.28E-02	1.00E+00	0.000	1.893	1.154 (0.804; 0.956)
MYH13	-0.121	0.049	1.30E-02	1.00E+00	0.000	1.886	0.886 (0.938; 1.147)
CD14	0.158	0.065	1.49E-02	1.00E+00	0.000	1.827	1.171 (1.073; 1.329)
PANX2	-0.112	0.046	1.51E-02	1.00E+00	0.000	1.821	0.894 (0.746; 0.914)
C9	0.133	0.055	1.58E-02	1.00E+00	0.000	1.801	1.142 (1.085; 1.444)
ZNF75D	-0.112	0.046	1.58E-02	1.00E+00	0.000	1.801	0.894 (0.919; 1.111)
SELENOP	-0.115	0.048	1.59E-02	1.00E+00	0.000	1.799	0.891 (0.897; 1.099)
IGKV1D-33.3	-0.103	0.043	1.67E-02	1.00E+00	0.000	1.777	0.902 (0.907; 1.112)
FAM210A	-0.112	0.047	1.82E-02	1.00E+00	0.000	1.740	0.894 (0.881; 1.05)
APOE	0.123	0.053	1.95E-02	1.00E+00	0.000	1.710	1.131 (0.735; 0.901)
TSC2	-0.098	0.042	1.96E-02	1.00E+00	0.000	1.708	0.907 (0.875; 1.072)
ITGB8	-0.113	0.048	1.97E-02	1.00E+00	0.000	1.706	0.893 (0.917; 1.125)
IRAG1	-0.121	0.052	2.01E-02	1.00E+00	0.000	1.697	0.886 (0.819; 1.029)
KLHL40	-0.107	0.046	2.06E-02	1.00E+00	0.000	1.686	0.899 (1.452; 1.808)
ALB	-0.121	0.052	2.06E-02	1.00E+00	0.000	1.686	0.886 (1.128; 1.396)
MAP3K1	-0.107	0.047	2.12E-02	1.00E+00	0.000	1.674	0.899 (0.952; 1.171)
EMX1	-0.115	0.05	2.17E-02	1.00E+00	0.000	1.664	0.891 (0.89; 1.085)
KIF21B	-0.11	0.048	2.26E-02	1.00E+00	0.000	1.646	0.896 (0.851; 1.032)
BOC	-0.099	0.044	2.41E-02	1.00E+00	0.000	1.618	0.906 (0.864; 1.05)
WASH4P	-0.097	0.044	2.54E-02	1.00E+00	0.000	1.595	0.908 (0.887; 1.097)
CEP135	0.138	0.062	2.62E-02	1.00E+00	0.000	1.582	1.148 (0.922; 1.123)

ITIH2	-0.113	0.051	2.67E-02	1.00E+00	0.000	1.573	0.893 (0.903; 1.118)
CADPS2	-0.11	0.05	2.75E-02	1.00E+00	0.000	1.561	0.896 (0.884; 1.094)
SPATA31H1	-0.133	0.06	2.75E-02	1.00E+00	0.000	1.561	0.875 (0.86; 1.044)
FAM83H	0.121	0.055	2.77E-02	1.00E+00	0.000	1.558	1.129 (0.829; 0.983)
PDHA1	-0.098	0.045	3.07E-02	1.00E+00	0.000	1.513	0.907 (0.992; 1.242)
DSP	-0.097	0.045	3.11E-02	1.00E+00	0.000	1.507	0.908 (0.909; 1.103)
PARP14	-0.093	0.043	3.19E-02	1.00E+00	0.000	1.496	0.911 (0.852; 1.038)
PSD	-0.098	0.046	3.36E-02	1.00E+00	0.000	1.474	0.907 (0.88; 1.077)
C7	-0.11	0.052	3.37E-02	1.00E+00	0.000	1.472	0.896 (0.879; 1.074)
FGG	0.12	0.057	3.45E-02	1.00E+00	0.000	1.462	1.127 (0.85; 1.03)
IFT46	0.12	0.057	3.46E-02	1.00E+00	0.000	1.461	1.127 (0.915; 1.121)
SHBG	0.135	0.064	3.48E-02	1.00E+00	0.000	1.458	1.145 (0.874; 1.069)
TRAJ56	-0.101	0.048	3.52E-02	1.00E+00	0.000	1.453	0.904 (0.857; 1.049)
TSC22D3	-0.099	0.047	3.53E-02	1.00E+00	0.000	1.452	0.906 (0.829; 1.002)
SERPING1.1	-0.124	0.059	3.62E-02	1.00E+00	0.000	1.441	0.883 (0.867; 1.053)
APOC4	0.125	0.06	3.65E-02	1.00E+00	0.000	1.438	1.133 (0.875; 1.07)
PLEKHH1	-0.099	0.047	3.65E-02	1.00E+00	0.000	1.438	0.906 (0.886; 1.076)
C1QC	0.113	0.054	3.66E-02	1.00E+00	0.000	1.437	1.12 (0.948; 1.154)
IGKV2D-29	-0.103	0.049	3.67E-02	1.00E+00	0.000	1.435	0.902 (0.876; 1.058)
TLN1	-0.101	0.049	3.71E-02	1.00E+00	0.000	1.431	0.904 (0.85; 1.034)
CCDC27	-0.104	0.05	3.78E-02	1.00E+00	0.000	1.423	0.901 (0.896; 1.096)
C1QB	0.107	0.052	3.85E-02	1.00E+00	0.000	1.415	1.113 (0.901; 1.098)
REV1	-0.099	0.048	3.94E-02	1.00E+00	0.000	1.405	0.906 (0.917; 1.12)
HPX	0.109	0.053	4.02E-02	1.00E+00	0.000	1.396	1.115 (0.882; 1.18)
IGHV3OR16-12	-0.102	0.05	4.09E-02	1.00E+00	0.000	1.388	0.903 (0.848; 1.028)
IGHV5-51	-0.088	0.043	4.11E-02	1.00E+00	0.000	1.386	0.916 (0.898; 1.095)
DNAH3	-0.102	0.05	4.14E-02	1.00E+00	0.000	1.383	0.903 (0.924; 1.101)
SLC27A5.1	-0.102	0.051	4.37E-02	1.00E+00	0.000	1.360	0.903 (0.965; 1.289)
ARHGAP6	-0.102	0.051	4.37E-02	1.00E+00	0.000	1.360	0.903 (0.742; 0.909)
OBSCN	-0.097	0.048	4.61E-02	1.00E+00	0.000	1.336	0.908 (1.02; 1.254)
MAP1A	-0.094	0.047	4.67E-02	1.00E+00	0.000	1.331	0.91 (0.868; 1.052)
GPD2	-0.101	0.052	5.15E-02	1.00E+00	0.000	1.288	0.904 (1.032; 1.292)
IGKV3-20.2	-0.094	0.048	5.22E-02	1.00E+00	0.000	1.282	0.91 (1.078; 1.368)

CARS2	-0.088	0.046	5.25E-02	1.00E+00	0.000	1.280	0.916 (1.012; 1.264)
SMG1	-0.091	0.047	5.30E-02	1.00E+00	0.000	1.276	0.913 (1.658; 2.075)
MTMR2	-0.08	0.042	5.50E-02	1.00E+00	0.000	1.260	0.923 (1.324; 1.664)
LUM	0.112	0.058	5.57E-02	1.00E+00	0.000	1.254	1.119 (0.984; 1.234)
SPTB	-0.085	0.045	5.76E-02	1.00E+00	0.000	1.240	0.919 (1.006; 1.233)
PRPF4B	-0.087	0.046	5.79E-02	1.00E+00	0.000	1.237	0.917 (1.007; 1.245)
PMS2	-0.098	0.052	5.89E-02	1.00E+00	0.000	1.230	0.907 (1.026; 1.274)
FRMPD4	-0.083	0.044	5.89E-02	1.00E+00	0.000	1.230	0.92 (0.888; 1.101)
DYNC2I1	-0.087	0.046	5.95E-02	1.00E+00	0.000	1.225	0.917 (0.873; 1.081)
NOSTRIN	-0.09	0.048	6.06E-02	1.00E+00	0.000	1.218	0.914 (1.041; 1.23)
MYLK	-0.084	0.045	6.07E-02	1.00E+00	0.000	1.217	0.919 (0.909; 1.113)
C6orf118	-0.089	0.048	6.35E-02	1.00E+00	0.000	1.197	0.915 (0.967; 1.186)
SULT1C3	-0.088	0.047	6.38E-02	1.00E+00	0.000	1.195	0.916 (0.904; 1.105)
CFP	0.119	0.064	6.48E-02	1.00E+00	0.000	1.188	1.126 (0.764; 0.938)
JCAD	-0.081	0.044	6.61E-02	1.00E+00	0.000	1.180	0.922 (0.8; 0.982)
TTN	-0.091	0.05	6.73E-02	1.00E+00	0.000	1.172	0.913 (0.769; 0.949)
FXR1	-0.094	0.051	6.74E-02	1.00E+00	0.000	1.171	0.91 (0.923; 1.134)
ZNF608	-0.089	0.049	6.80E-02	1.00E+00	0.000	1.167	0.915 (0.853; 1.044)
NUFIP2	-0.078	0.043	6.86E-02	1.00E+00	0.000	1.164	0.925 (1.005; 1.238)
APOL1	0.096	0.053	7.06E-02	1.00E+00	0.000	1.151	1.101 (0.9; 1.081)
COL4A3	-0.079	0.044	7.09E-02	1.00E+00	0.000	1.149	0.924 (1.033; 1.271)
ENOX2	-0.086	0.048	7.17E-02	1.00E+00	0.000	1.144	0.918 (1.161; 1.441)
PHF10	0.097	0.054	7.24E-02	1.00E+00	0.000	1.140	1.102 (1.043; 1.28)
ITPR1	-0.082	0.046	7.25E-02	1.00E+00	0.000	1.140	0.921 (0.883; 1.076)
FRMD1	-0.078	0.043	7.26E-02	1.00E+00	0.000	1.139	0.925 (0.939; 1.156)
TINF2	-0.082	0.046	7.29E-02	1.00E+00	0.000	1.137	0.921 (0.874; 1.066)
CPSF6	-0.086	0.048	7.30E-02	1.00E+00	0.000	1.137	0.918 (0.958; 1.206)
DST	-0.084	0.047	7.41E-02	1.00E+00	0.000	1.130	0.919 (0.913; 1.14)
KHNYN	-0.087	0.049	7.52E-02	1.00E+00	0.000	1.124	0.917 (0.881; 1.08)
PTPRJ	-0.078	0.044	7.70E-02	1.00E+00	0.000	1.114	0.925 (0.927; 1.12)
GPRIN1	0.099	0.056	7.81E-02	1.00E+00	0.000	1.107	1.104 (0.875; 1.065)
FBXO30	-0.08	0.046	7.83E-02	1.00E+00	0.000	1.106	0.923 (0.853; 1.04)
ABCF1	-0.079	0.045	7.92E-02	1.00E+00	0.000	1.101	0.924 (0.888; 1.089)

RASA3	-0.084	0.048	8.02E-02	1.00E+00	0.000	1.096	0.919 (0.473; 0.593)
IGHV1-24	-0.081	0.046	8.04E-02	1.00E+00	0.000	1.095	0.922 (0.907; 1.152)
CAPZB	-0.082	0.047	8.10E-02	1.00E+00	0.000	1.092	0.921 (0.83; 1.02)
IGKV1-17	0.1	0.057	8.14E-02	1.00E+00	0.000	1.089	1.105 (0.765; 0.938)
DNAH8	-0.081	0.047	8.24E-02	1.00E+00	0.000	1.084	0.922 (1.038; 1.298)
LZTS3	-0.075	0.043	8.31E-02	1.00E+00	0.000	1.080	0.928 (1.168; 1.436)
AMDHD2	-0.086	0.05	8.52E-02	1.00E+00	0.000	1.070	0.918 (0.936; 1.174)
SMC2	-0.078	0.045	8.56E-02	1.00E+00	0.000	1.068	0.925 (0.957; 1.164)
SAMD4B	-0.084	0.049	8.68E-02	1.00E+00	0.000	1.061	0.919 (0.909; 1.103)
KIF5B	0.105	0.061	8.83E-02	1.00E+00	0.000	1.054	1.111 (0.758; 0.936)
MCPH1	-0.076	0.045	8.92E-02	1.00E+00	0.000	1.050	0.927 (1.347; 1.735)
F5	-0.113	0.067	8.98E-02	1.00E+00	0.000	1.047	0.893 (0.776; 0.949)
WNK4	-0.077	0.046	9.12E-02	1.00E+00	0.000	1.040	0.926 (0.888; 1.077)
SLC12A7	-0.087	0.051	9.15E-02	1.00E+00	0.000	1.039	0.917 (1.039; 1.278)
HBB	0.119	0.071	9.19E-02	1.00E+00	0.000	1.037	1.126 (0.983; 1.216)
RBP4	-0.087	0.052	9.29E-02	1.00E+00	0.000	1.032	0.917 (1.065; 1.352)
LNK1	0.097	0.058	9.37E-02	1.00E+00	0.000	1.028	1.102 (0.984; 1.197)
PITPNM2	-0.083	0.049	9.41E-02	1.00E+00	0.000	1.026	0.92 (0.895; 1.09)
LIF	-0.079	0.047	9.44E-02	1.00E+00	0.000	1.025	0.924 (0.663; 0.834)
HSPA13	-0.077	0.046	9.53E-02	1.00E+00	0.000	1.021	0.926 (0.832; 1.028)
IGKV3D-20	-0.083	0.05	9.56E-02	1.00E+00	0.000	1.020	0.92 (0.829; 0.992)
SRP54	-0.072	0.043	9.58E-02	1.00E+00	0.000	1.019	0.931 (1.041; 1.344)
LIMA1	-0.079	0.047	9.63E-02	1.00E+00	0.000	1.016	0.924 (1.432; 1.786)
EWSR1	-0.081	0.049	9.79E-02	1.00E+00	0.000	1.009	0.922 (0.945; 1.158)
MAP3K5	-0.077	0.047	9.95E-02	1.00E+00	0.000	1.002	0.926 (0.945; 1.179)
IL1RAP	-0.072	0.044	9.98E-02	1.00E+00	0.000	1.001	0.931 (1.044; 1.283)
C8A	0.089	0.054	1.00E-01	1.00E+00	0.000	1.000	1.093 (1.129; 1.392)
PHLDB1	-0.08	0.049	1.01E-01	1.00E+00	0.000	0.996	0.923 (1.157; 1.469)
ARHGAP42	-0.083	0.051	1.03E-01	1.00E+00	0.000	0.987	0.92 (0.866; 1.073)
RYR1	-0.073	0.045	1.04E-01	1.00E+00	0.000	0.983	0.93 (1.139; 1.421)
SIPA1L1	-0.077	0.047	1.04E-01	1.00E+00	0.000	0.983	0.926 (0.809; 0.992)
DNAH14	-0.075	0.046	1.06E-01	1.00E+00	0.000	0.975	0.928 (0.865; 1.058)
F13B	-0.084	0.052	1.07E-01	1.00E+00	0.000	0.971	0.919 (0.872; 1.079)

DMPK	-0.076	0.047	1.07E-01	1.00E+00	0.000	0.971	0.927 (0.903; 1.08)
FETUB	0.1	0.062	1.08E-01	1.00E+00	0.000	0.967	1.105 (0.842; 1.004)
RAB21	-0.076	0.047	1.08E-01	1.00E+00	0.000	0.967	0.927 (0.962; 1.227)
EXOC6B	-0.075	0.046	1.09E-01	1.00E+00	0.000	0.963	0.928 (0.845; 1.055)
VPS11	-0.075	0.047	1.09E-01	1.00E+00	0.000	0.963	0.928 (0.868; 1.054)
PPP1R12B	-0.075	0.047	1.09E-01	1.00E+00	0.000	0.963	0.928 (0.778; 1.018)
AKT3	-0.067	0.042	1.10E-01	1.00E+00	0.000	0.959	0.935 (0.889; 1.079)
PFN1	0.08	0.05	1.11E-01	1.00E+00	0.000	0.955	1.083 (0.871; 1.056)
CBFA2T2	-0.071	0.045	1.14E-01	1.00E+00	0.000	0.943	0.931 (0.968; 1.199)
FKBP1A	-0.082	0.052	1.14E-01	1.00E+00	0.000	0.943	0.921 (0.98; 1.214)
SPTBN5	-0.074	0.047	1.15E-01	1.00E+00	0.000	0.939	0.929 (0.919; 1.114)
C1QA	0.091	0.058	1.15E-01	1.00E+00	0.000	0.939	1.095 (0.842; 1.016)
IGKV3-7	-0.071	0.046	1.18E-01	1.00E+00	0.000	0.928	0.931 (0.851; 1.052)
LIFR	-0.077	0.049	1.18E-01	1.00E+00	0.000	0.928	0.926 (0.846; 1.04)
MID2	-0.067	0.043	1.18E-01	1.00E+00	0.000	0.928	0.935 (0.831; 0.993)
KRT18	-0.069	0.044	1.19E-01	1.00E+00	0.000	0.924	0.933 (0.937; 1.159)
LCOR	-0.072	0.046	1.20E-01	1.00E+00	0.000	0.921	0.931 (0.904; 1.097)
GDF5	-0.074	0.048	1.23E-01	1.00E+00	0.000	0.910	0.929 (0.853; 1.042)
DCTN1	-0.068	0.045	1.26E-01	1.00E+00	0.000	0.900	0.934 (0.933; 1.152)
NIM1K	-0.079	0.052	1.28E-01	1.00E+00	0.000	0.893	0.924 (0.844; 1.026)
EIF4G3	-0.072	0.047	1.28E-01	1.00E+00	0.000	0.893	0.931 (0.876; 1.055)
ACTA1	0.081	0.054	1.28E-01	1.00E+00	0.000	0.893	1.084 (0.918; 1.116)
BEND5	-0.06	0.039	1.29E-01	1.00E+00	0.000	0.889	0.942 (1.819; 3.302)
SORBS1	-0.074	0.049	1.29E-01	1.00E+00	0.000	0.889	0.929 (0.932; 1.137)
ITIH3	-0.078	0.051	1.31E-01	1.00E+00	0.000	0.883	0.925 (0.871; 1.061)
PHF14	-0.065	0.043	1.32E-01	1.00E+00	0.000	0.879	0.937 (0.874; 1.08)
C2CD3	-0.087	0.058	1.33E-01	1.00E+00	0.000	0.876	0.917 (1.043; 1.286)
LPA	-0.08	0.054	1.36E-01	1.00E+00	0.000	0.866	0.923 (0.809; 0.987)
PSMB9	0.079	0.053	1.36E-01	1.00E+00	0.000	0.866	1.082 (0.849; 1.037)
HSP90B1	0.081	0.055	1.37E-01	1.00E+00	0.000	0.863	1.084 (0.882; 1.096)
COL11A2	0.086	0.058	1.39E-01	1.00E+00	0.000	0.857	1.09 (0.947; 1.19)
FLG	-0.076	0.052	1.41E-01	1.00E+00	0.000	0.851	0.927 (0.842; 1.032)
ADAMTS20	-0.073	0.05	1.41E-01	1.00E+00	0.000	0.851	0.93 (0.838; 1.027)

IGFBP3	-0.073	0.05	1.42E-01	1.00E+00	0.000	0.848	0.93 (0.924; 1.131)
VANGL1	-0.075	0.051	1.43E-01	1.00E+00	0.000	0.845	0.928 (0.928; 1.128)
IGHV1-46	-0.069	0.047	1.46E-01	1.00E+00	0.000	0.836	0.933 (0.85; 1.018)
AGT	-0.085	0.058	1.46E-01	1.00E+00	0.000	0.836	0.919 (0.709; 0.871)
KHDRBS3	-0.069	0.047	1.47E-01	1.00E+00	0.000	0.833	0.933 (0.956; 1.196)
EP400	-0.063	0.044	1.49E-01	1.00E+00	0.000	0.827	0.939 (0.892; 1.072)
FAN1	-0.071	0.049	1.49E-01	1.00E+00	0.000	0.827	0.931 (0.912; 1.124)
IGHV3-7	-0.069	0.048	1.51E-01	1.00E+00	0.000	0.821	0.933 (0.88; 1.093)
GPC6	-0.073	0.051	1.53E-01	1.00E+00	0.000	0.815	0.93 (0.891; 1.077)
PLEKHG2	-0.063	0.044	1.53E-01	1.00E+00	0.000	0.815	0.939 (0.855; 1.103)
CDK13	-0.067	0.047	1.56E-01	1.00E+00	0.000	0.807	0.935 (0.873; 1.053)
HBA1;	0.101	0.071	1.58E-01	1.00E+00	0.000	0.801	1.106 (0.7; 0.857)
FUS	-0.07	0.049	1.59E-01	1.00E+00	0.000	0.799	0.932 (0.849; 1.042)
PLEC	-0.071	0.051	1.59E-01	1.00E+00	0.000	0.799	0.931 (0.811; 0.983)
ACTR2	0.078	0.056	1.60E-01	1.00E+00	0.000	0.796	1.081 (0.887; 1.067)
SRP68	0.075	0.053	1.60E-01	1.00E+00	0.000	0.796	1.078 (0.788; 0.96)
RNF123	-0.066	0.047	1.61E-01	1.00E+00	0.000	0.793	0.936 (0.999; 1.284)
FHAD1	-0.066	0.047	1.62E-01	1.00E+00	0.000	0.790	0.936 (0.961; 1.187)
CNTNAP5	-0.063	0.045	1.63E-01	1.00E+00	0.000	0.788	0.939 (0.917; 1.12)
MS4A14	-0.066	0.047	1.64E-01	1.00E+00	0.000	0.785	0.936 (0.876; 1.081)
TNRC6A	-0.067	0.048	1.65E-01	1.00E+00	0.000	0.783	0.935 (0.891; 1.073)
IGHV2-26	-0.076	0.055	1.65E-01	1.00E+00	0.000	0.783	0.927 (0.864; 1.049)
GDI2	-0.062	0.045	1.68E-01	1.00E+00	0.000	0.775	0.94 (0.881; 1.066)
HNMT	-0.061	0.044	1.69E-01	1.00E+00	0.000	0.772	0.941 (0.867; 1.07)
IGKV2D-28	-0.067	0.049	1.70E-01	1.00E+00	0.000	0.770	0.935 (0.992; 1.264)
HERC4	-0.063	0.046	1.71E-01	1.00E+00	0.000	0.767	0.939 (0.899; 1.086)
MUC2	-0.066	0.048	1.72E-01	1.00E+00	0.000	0.764	0.936 (0.867; 1.031)
C6	0.074	0.054	1.75E-01	1.00E+00	0.000	0.757	1.077 (0.901; 1.096)
KPNB1	-0.063	0.046	1.75E-01	1.00E+00	0.000	0.757	0.939 (0.847; 1.03)
NEB	-0.07	0.052	1.75E-01	1.00E+00	0.000	0.757	0.932 (0.742; 0.917)
APLF	-0.058	0.043	1.76E-01	1.00E+00	0.000	0.754	0.944 (1.322; 1.654)
F8	-0.063	0.047	1.77E-01	1.00E+00	0.000	0.752	0.939 (0.877; 1.067)
CEP112	0.072	0.054	1.79E-01	1.00E+00	0.000	0.747	1.075 (0.862; 1.061)

SAMD1	-0.063	0.047	1.84E-01	1.00E+00	0.000	0.735	0.939 (0.906; 1.078)
ITPRIPL1	-0.064	0.048	1.84E-01	1.00E+00	0.000	0.735	0.938 (0.887; 1.084)
IDH1	-0.06	0.045	1.84E-01	1.00E+00	0.000	0.735	0.942 (0.842; 1.022)
IGLV3-21	-0.066	0.05	1.85E-01	1.00E+00	0.000	0.733	0.936 (0.889; 1.082)
IGLV1-36	-0.064	0.048	1.85E-01	1.00E+00	0.000	0.733	0.938 (0.847; 1.023)
JCHAIN	-0.065	0.049	1.85E-01	1.00E+00	0.000	0.733	0.937 (0.876; 1.055)
THBS2	-0.058	0.044	1.86E-01	1.00E+00	0.000	0.730	0.944 (0.866; 1.101)
KIAA0586	-0.061	0.047	1.91E-01	1.00E+00	0.000	0.719	0.941 (0.816; 1.002)
ORM1	0.068	0.052	1.92E-01	1.00E+00	0.000	0.717	1.07 (1.36; 1.684)
RHOXF1	-0.062	0.048	1.93E-01	1.00E+00	0.000	0.714	0.94 (0.903; 1.087)
TEX2	-0.066	0.05	1.94E-01	1.00E+00	0.000	0.712	0.936 (0.943; 1.144)
MED23	-0.06	0.046	1.94E-01	1.00E+00	0.000	0.712	0.942 (0.806; 0.971)
KIF15	-0.059	0.045	1.94E-01	1.00E+00	0.000	0.712	0.943 (0.953; 1.167)
ATP1A2	-0.056	0.043	1.95E-01	1.00E+00	0.000	0.710	0.946 (0.838; 1.012)
NSUN2	-0.057	0.044	1.97E-01	1.00E+00	0.000	0.706	0.945 (0.898; 1.085)
UNC13B	-0.062	0.048	1.99E-01	1.00E+00	0.000	0.701	0.94 (0.906; 1.105)
IGHA1	0.098	0.076	1.99E-01	1.00E+00	0.000	0.701	1.103 (0.846; 1.016)
IGKV1D-33.5	-0.06	0.047	2.01E-01	1.00E+00	0.000	0.697	0.942 (0.891; 1.085)
ACAP3	-0.063	0.05	2.02E-01	1.00E+00	0.000	0.695	0.939 (0.794; 0.963)
HMCN1	-0.063	0.05	2.02E-01	1.00E+00	0.000	0.695	0.939 (0.89; 1.088)
ZFHX4	0.064	0.05	2.03E-01	1.00E+00	0.000	0.693	1.066 (0.834; 0.985)
CIRBP	-0.06	0.047	2.03E-01	1.00E+00	0.000	0.693	0.942 (0.811; 0.979)
NKD2	-0.059	0.046	2.04E-01	1.00E+00	0.000	0.690	0.943 (0.864; 1.029)
CCDC150	0.074	0.058	2.05E-01	1.00E+00	0.000	0.688	1.077 (0.861; 1.029)
SPOCD1	-0.064	0.05	2.05E-01	1.00E+00	0.000	0.688	0.938 (0.873; 1.069)
IGLL1	-0.066	0.052	2.06E-01	1.00E+00	0.000	0.686	0.936 (0.943; 1.22)
IGKV1-16.1	0.073	0.058	2.06E-01	1.00E+00	0.000	0.686	1.076 (0.869; 1.032)
ITIH1	-0.064	0.051	2.08E-01	1.00E+00	0.000	0.682	0.938 (0.823; 1.009)
SKOR1	-0.064	0.051	2.09E-01	1.00E+00	0.000	0.680	0.938 (0.963; 1.206)
NAGK	-0.061	0.049	2.10E-01	1.00E+00	0.000	0.678	0.941 (0.874; 1.043)
TMEM200C	0.065	0.052	2.13E-01	1.00E+00	0.000	0.672	1.067 (0.815; 0.98)
MPDZ	0.067	0.054	2.13E-01	1.00E+00	0.000	0.672	1.069 (0.998; 1.254)
ZNF766	-0.063	0.05	2.14E-01	1.00E+00	0.000	0.670	0.939 (0.91; 1.102)

KAT14	0.066	0.053	2.14E-01	1.00E+00	0.000	0.670	1.068 (0.924; 1.104)
CFAP97	-0.061	0.049	2.15E-01	1.00E+00	0.000	0.668	0.941 (0.912; 1.111)
TCF4	0.074	0.06	2.15E-01	1.00E+00	0.000	0.668	1.077 (0.818; 1.005)
DNHD1	-0.06	0.049	2.16E-01	1.00E+00	0.000	0.666	0.942 (0.887; 1.056)
TOP2A	0.076	0.062	2.17E-01	1.00E+00	0.000	0.664	1.079 (0.896; 1.085)
KMT2A	0.077	0.062	2.18E-01	1.00E+00	0.000	0.662	1.08 (0.925; 1.144)
IGKV1-39	-0.062	0.05	2.18E-01	1.00E+00	0.000	0.662	0.94 (1.013; 1.28)
FOXI1	-0.061	0.05	2.20E-01	1.00E+00	0.000	0.658	0.941 (0.886; 1.071)
RFX7	-0.053	0.044	2.21E-01	1.00E+00	0.000	0.656	0.948 (0.89; 1.048)
CCDC88A	-0.063	0.052	2.22E-01	1.00E+00	0.000	0.654	0.939 (0.912; 1.121)
COL5A3	-0.063	0.052	2.24E-01	1.00E+00	0.000	0.650	0.939 (0.844; 1.028)
CLCNKA	0.069	0.057	2.24E-01	1.00E+00	0.000	0.650	1.071 (0.948; 1.222)
CKAP4	-0.059	0.049	2.25E-01	1.00E+00	0.000	0.648	0.943 (0.856; 1.016)
CPE	-0.061	0.051	2.26E-01	1.00E+00	0.000	0.646	0.941 (0.974; 1.213)
RFLNB	-0.054	0.045	2.32E-01	1.00E+00	0.000	0.635	0.947 (0.92; 1.099)
PDCD2L	-0.053	0.045	2.32E-01	1.00E+00	0.000	0.635	0.948 (0.909; 1.115)
FBXL5	-0.054	0.045	2.34E-01	1.00E+00	0.000	0.631	0.947 (0.979; 1.208)
RUSC1-AS1	0.071	0.059	2.34E-01	1.00E+00	0.000	0.631	1.074 (0.98; 1.294)
IGKV1-16	-0.06	0.051	2.37E-01	1.00E+00	0.000	0.625	0.942 (0.961; 1.272)
ANKRD65	-0.053	0.045	2.37E-01	1.00E+00	0.000	0.625	0.948 (0.874; 1.057)
PRDM14	-0.056	0.048	2.39E-01	1.00E+00	0.000	0.622	0.946 (0.807; 0.963)
DECR1	-0.056	0.048	2.41E-01	1.00E+00	0.000	0.618	0.946 (0.868; 1.076)
KRT28	-0.055	0.047	2.42E-01	1.00E+00	0.000	0.616	0.946 (0.872; 1.053)
TMEM177	0.065	0.055	2.44E-01	1.00E+00	0.000	0.613	1.067 (0.829; 1)
ITPKB	0.063	0.054	2.44E-01	1.00E+00	0.000	0.613	1.065 (0.928; 1.149)
CDC42BPB	-0.055	0.047	2.45E-01	1.00E+00	0.000	0.611	0.946 (0.861; 1.036)
FAM184A	0.058	0.05	2.45E-01	1.00E+00	0.000	0.611	1.06 (0.902; 1.103)
ARFGEF2	0.061	0.052	2.46E-01	1.00E+00	0.000	0.609	1.063 (0.892; 1.085)
IGHV3-35	0.059	0.051	2.46E-01	1.00E+00	0.000	0.609	1.061 (0.919; 1.099)
CPB2	-0.064	0.056	2.49E-01	1.00E+00	0.000	0.604	0.938 (0.91; 1.093)
NOL8	-0.056	0.049	2.49E-01	1.00E+00	0.000	0.604	0.946 (0.889; 1.091)
MICAL1	-0.053	0.047	2.51E-01	1.00E+00	0.000	0.600	0.948 (0.948; 1.167)
PLXNA2	-0.055	0.048	2.52E-01	1.00E+00	0.000	0.599	0.946 (0.786; 0.945)

C4orf54	-0.061	0.053	2.55E-01	1.00E+00	0.000	0.593	0.941 (0.886; 1.064)
ATAD2	-0.056	0.05	2.56E-01	1.00E+00	0.000	0.592	0.946 (0.888; 1.071)
CPN2	0.065	0.057	2.58E-01	1.00E+00	0.000	0.588	1.067 (0.905; 1.109)
TF	-0.058	0.051	2.59E-01	1.00E+00	0.000	0.587	0.944 (0.879; 1.072)
TMED4	-0.055	0.049	2.59E-01	1.00E+00	0.000	0.587	0.946 (0.807; 0.973)
MNX1.1	-0.05	0.045	2.60E-01	1.00E+00	0.000	0.585	0.951 (0.839; 1.015)
WHAMM	-0.058	0.052	2.61E-01	1.00E+00	0.000	0.583	0.944 (0.848; 1.008)
CIT	-0.055	0.049	2.61E-01	1.00E+00	0.000	0.583	0.946 (0.927; 1.123)
XK	-0.049	0.044	2.64E-01	1.00E+00	0.000	0.578	0.952 (0.89; 1.08)
ACTB	0.072	0.065	2.67E-01	1.00E+00	0.000	0.573	1.075 (0.894; 1.091)
PRPF19	-0.054	0.049	2.68E-01	1.00E+00	0.000	0.572	0.947 (0.852; 1.032)
CNGA3	-0.052	0.047	2.68E-01	1.00E+00	0.000	0.572	0.949 (0.838; 1.01)
LRP5	-0.054	0.049	2.73E-01	1.00E+00	0.000	0.564	0.947 (0.963; 1.233)
ZNF219	0.059	0.054	2.73E-01	1.00E+00	0.000	0.564	1.061 (0.875; 1.081)
C1R	-0.054	0.049	2.74E-01	1.00E+00	0.000	0.562	0.947 (0.836; 1.024)
CPN1	-0.058	0.053	2.75E-01	1.00E+00	0.000	0.561	0.944 (0.891; 1.093)
IGKV1D-33.2	-0.054	0.05	2.76E-01	1.00E+00	0.000	0.559	0.947 (0.858; 1.04)
EPX	-0.061	0.056	2.79E-01	1.00E+00	0.000	0.554	0.941 (0.917; 1.123)
MINDY4	-0.049	0.046	2.83E-01	1.00E+00	0.000	0.548	0.952 (1.667; 2.215)
IGKV3-20.4	0.053	0.05	2.89E-01	1.00E+00	0.000	0.539	1.054 (0.91; 1.109)
GIGYF1	-0.05	0.047	2.90E-01	1.00E+00	0.000	0.538	0.951 (0.864; 1.034)
APOC4-APOC2	0.054	0.051	2.91E-01	1.00E+00	0.000	0.536	1.055 (0.846; 1.019)
PCDHGA10	-0.05	0.047	2.93E-01	1.00E+00	0.000	0.533	0.951 (0.875; 1.074)
EMILIN1	-0.05	0.048	2.96E-01	1.00E+00	0.000	0.529	0.951 (0.876; 1.073)
C1RL	0.059	0.057	2.98E-01	1.00E+00	0.000	0.526	1.061 (0.847; 1.018)
NUMA1	-0.049	0.048	3.01E-01	1.00E+00	0.000	0.521	0.952 (0.884; 1.054)
AXL	-0.051	0.049	3.01E-01	1.00E+00	0.000	0.521	0.95 (0.908; 1.12)
SERPINA10	0.061	0.059	3.02E-01	1.00E+00	0.000	0.520	1.063 (0.848; 1.01)
FBF1	-0.052	0.051	3.04E-01	1.00E+00	0.000	0.517	0.949 (0.854; 1.04)
IGKV3-20.1	-0.053	0.052	3.04E-01	1.00E+00	0.000	0.517	0.948 (0.878; 1.07)
IGLC7	-0.051	0.049	3.05E-01	1.00E+00	0.000	0.516	0.95 (0.89; 1.063)
MARK4	-0.046	0.045	3.05E-01	1.00E+00	0.000	0.516	0.955 (0.918; 1.109)
AFAP1L2	-0.048	0.047	3.06E-01	1.00E+00	0.000	0.514	0.953 (0.819; 0.985)

IGKV3-15.1	0.06	0.059	3.07E-01	1.00E+00	0.000	0.513	1.062 (0.937; 1.15)
KIF24	0.059	0.058	3.08E-01	1.00E+00	0.000	0.511	1.061 (0.916; 1.117)
PDIA6	-0.046	0.046	3.10E-01	1.00E+00	0.000	0.509	0.955 (0.858; 1.059)
C5	0.054	0.053	3.11E-01	1.00E+00	0.000	0.507	1.055 (0.836; 1.005)
MAGEB17	-0.047	0.046	3.12E-01	1.00E+00	0.000	0.506	0.954 (0.945; 1.179)
PROSER2	-0.05	0.05	3.14E-01	1.00E+00	0.000	0.503	0.951 (0.85; 1.004)
CLASP1	0.053	0.053	3.17E-01	1.00E+00	0.000	0.499	1.054 (0.334; 0.502)
MNX1	-0.045	0.045	3.17E-01	1.00E+00	0.000	0.499	0.956 (0.875; 1.064)
IGKV3-15	-0.049	0.049	3.17E-01	1.00E+00	0.000	0.499	0.952 (0.853; 1.029)
CHD6	-0.049	0.049	3.17E-01	1.00E+00	0.000	0.499	0.952 (0.762; 0.93)
IGLV8-61	-0.046	0.046	3.19E-01	1.00E+00	0.000	0.496	0.955 (0.859; 1.035)
GOLGA6L10	-0.047	0.047	3.19E-01	1.00E+00	0.000	0.496	0.954 (0.856; 1.021)
IGHA2	0.052	0.052	3.19E-01	1.00E+00	0.000	0.496	1.053 (0.925; 1.113)
IGLC3	-0.05	0.05	3.20E-01	1.00E+00	0.000	0.495	0.951 (0.929; 1.149)
LUZP1	0.051	0.051	3.22E-01	1.00E+00	0.000	0.492	1.052 (0.907; 1.108)
SOCS2	0.052	0.052	3.23E-01	1.00E+00	0.000	0.491	1.053 (0.842; 1.008)
IGKV1D-33	-0.049	0.05	3.24E-01	1.00E+00	0.000	0.489	0.952 (0.837; 1.013)
LRRC71	0.052	0.053	3.28E-01	1.00E+00	0.000	0.484	1.053 (0.878; 1.064)
DLG3	-0.049	0.05	3.28E-01	1.00E+00	0.000	0.484	0.952 (0.905; 1.1)
KIF26B	-0.048	0.049	3.29E-01	1.00E+00	0.000	0.483	0.953 (0.858; 1.031)
ZBTB4	-0.047	0.048	3.30E-01	1.00E+00	0.000	0.481	0.954 (0.868; 1.049)
UBE4B	-0.043	0.045	3.30E-01	1.00E+00	0.000	0.481	0.958 (0.891; 1.093)
SNTB2	-0.051	0.053	3.31E-01	1.00E+00	0.000	0.480	0.95 (0.845; 1.005)
TTC21B	-0.044	0.045	3.33E-01	1.00E+00	0.000	0.478	0.957 (0.805; 0.971)
POSTN	-0.04	0.042	3.33E-01	1.00E+00	0.000	0.478	0.961 (0.904; 1.128)
KLC4	-0.043	0.045	3.35E-01	1.00E+00	0.000	0.475	0.958 (0.88; 1.065)
TSPYL1	-0.046	0.048	3.35E-01	1.00E+00	0.000	0.475	0.955 (0.887; 1.046)
UTRN	0.05	0.052	3.35E-01	1.00E+00	0.000	0.475	1.051 (0.95; 1.179)
C4BPB	0.056	0.058	3.35E-01	1.00E+00	0.000	0.475	1.058 (0.874; 1.048)
CFD	0.062	0.064	3.36E-01	1.00E+00	0.000	0.474	1.064 (0.909; 1.099)
ARHGEF11	0.056	0.058	3.37E-01	1.00E+00	0.000	0.472	1.058 (0.881; 1.064)
MYH7B	-0.042	0.044	3.38E-01	1.00E+00	0.000	0.471	0.959 (0.843; 1.029)
BBOF1	-0.044	0.046	3.39E-01	1.00E+00	0.000	0.470	0.957 (0.777; 0.933)

SERPINF2	0.054	0.056	3.39E-01	1.00E+00	0.000	0.470	1.055 (0.946; 1.162)
MYO9A	-0.044	0.046	3.41E-01	1.00E+00	0.000	0.467	0.957 (0.904; 1.079)
PLXND1	-0.05	0.053	3.42E-01	1.00E+00	0.000	0.466	0.951 (0.915; 1.1)
SLC27A5	0.049	0.052	3.44E-01	1.00E+00	0.000	0.463	1.05 (0.84; 1.005)
LRP1B	-0.044	0.046	3.44E-01	1.00E+00	0.000	0.463	0.957 (0.887; 1.071)
STK35	0.05	0.053	3.46E-01	1.00E+00	0.000	0.461	1.051 (0.905; 1.107)
HSPD1	-0.048	0.051	3.46E-01	1.00E+00	0.000	0.461	0.953 (0.594; 0.749)
MACF1	-0.043	0.046	3.46E-01	1.00E+00	0.000	0.461	0.958 (0.835; 1.01)
APOC3	-0.046	0.049	3.50E-01	1.00E+00	0.000	0.456	0.955 (0.866; 1.043)
AHNAK2	-0.046	0.049	3.50E-01	1.00E+00	0.000	0.456	0.955 (0.936; 1.139)
CA1	-0.042	0.045	3.52E-01	1.00E+00	0.000	0.453	0.959 (0.836; 1.01)
LRBA	0.06	0.065	3.53E-01	1.00E+00	0.000	0.452	1.062 (0.862; 1.041)
SACS	-0.046	0.05	3.53E-01	1.00E+00	0.000	0.452	0.955 (0.904; 1.099)
MS4A1	-0.046	0.049	3.53E-01	1.00E+00	0.000	0.452	0.955 (0.896; 1.087)
DENND2B	-0.044	0.048	3.54E-01	1.00E+00	0.000	0.451	0.957 (0.87; 1.036)
EEA1	0.051	0.055	3.56E-01	1.00E+00	0.000	0.449	1.052 (0.868; 1.052)
APC	-0.044	0.048	3.56E-01	1.00E+00	0.000	0.449	0.957 (0.814; 0.994)
CTSW	-0.038	0.041	3.61E-01	1.00E+00	0.000	0.442	0.963 (0.82; 0.984)
HELQ	-0.046	0.05	3.65E-01	1.00E+00	0.000	0.438	0.955 (0.848; 1.043)
IGLV2-14	-0.044	0.049	3.65E-01	1.00E+00	0.000	0.438	0.957 (0.837; 0.993)
SPAG17	0.049	0.054	3.67E-01	1.00E+00	0.000	0.435	1.05 (0.819; 1.03)
LOC645967	0.055	0.062	3.73E-01	1.00E+00	0.000	0.428	1.057 (0.872; 1.044)
IGLV3-19	0.045	0.05	3.73E-01	1.00E+00	0.000	0.428	1.046 (0.888; 1.082)
ADAM8	-0.043	0.048	3.74E-01	1.00E+00	0.000	0.427	0.958 (0.895; 1.112)
TMPRSS15	0.047	0.053	3.78E-01	1.00E+00	0.000	0.423	1.048 (0.96; 1.193)
DCC	-0.042	0.047	3.78E-01	1.00E+00	0.000	0.423	0.959 (0.902; 1.083)
PGLYRP2	-0.047	0.054	3.81E-01	1.00E+00	0.000	0.419	0.954 (0.858; 1.03)
AVPR1A	-0.046	0.053	3.82E-01	1.00E+00	0.000	0.418	0.955 (0.866; 1.081)
IGKV3-20.5	-0.041	0.047	3.83E-01	1.00E+00	0.000	0.417	0.96 (0.873; 1.067)
SLC23A2	-0.043	0.049	3.86E-01	1.00E+00	0.000	0.413	0.958 (0.921; 1.127)
IGHV1-69	-0.041	0.048	3.87E-01	1.00E+00	0.000	0.412	0.96 (0.876; 1.062)
GNAZ	-0.043	0.05	3.87E-01	1.00E+00	0.000	0.412	0.958 (0.832; 1.007)
KCNH2	-0.038	0.044	3.88E-01	1.00E+00	0.000	0.411	0.963 (0.952; 1.196)

JARID2	-0.038	0.044	3.88E-01	1.00E+00	0.000	0.411	0.963 (0.91; 1.113)
IQGAP2	0.048	0.056	3.89E-01	1.00E+00	0.000	0.410	1.049 (0.898; 1.068)
COMP	-0.038	0.044	3.93E-01	1.00E+00	0.000	0.406	0.963 (0.855; 1.029)
UNG	-0.042	0.049	3.95E-01	1.00E+00	0.000	0.403	0.959 (0.88; 1.076)
ZFPM1	-0.041	0.048	3.95E-01	1.00E+00	0.000	0.403	0.96 (1.022; 1.305)
MAST4	-0.042	0.05	3.98E-01	1.00E+00	0.000	0.400	0.959 (0.963; 1.218)
FBH1	0.045	0.054	3.99E-01	1.00E+00	0.000	0.399	1.046 (0.879; 1.065)
IGHV3-38	-0.04	0.047	3.99E-01	1.00E+00	0.000	0.399	0.961 (0.775; 0.983)
TMEM131L	-0.038	0.045	4.00E-01	1.00E+00	0.000	0.398	0.963 (0.799; 0.966)
NLN	-0.041	0.049	4.04E-01	1.00E+00	0.000	0.394	0.96 (0.854; 1.033)
SYT1	0.045	0.054	4.05E-01	1.00E+00	0.000	0.393	1.046 (0.881; 1.068)
SEMA6D	-0.04	0.048	4.06E-01	1.00E+00	0.000	0.391	0.961 (0.835; 1.007)
HSF4	-0.042	0.051	4.09E-01	1.00E+00	0.000	0.388	0.959 (0.901; 1.089)
UROC1	-0.039	0.047	4.09E-01	1.00E+00	0.000	0.388	0.962 (0.814; 0.973)
KIF4A	-0.037	0.045	4.10E-01	1.00E+00	0.000	0.387	0.964 (0.878; 1.066)
GTPBP4	-0.04	0.049	4.11E-01	1.00E+00	0.000	0.386	0.961 (0.867; 1.07)
JMJD8	-0.037	0.045	4.13E-01	1.00E+00	0.000	0.384	0.964 (0.879; 1.062)
MTHFD2	-0.039	0.047	4.13E-01	1.00E+00	0.000	0.384	0.962 (0.858; 1.043)
AP1M2	0.049	0.06	4.15E-01	1.00E+00	0.000	0.382	1.05 (0.948; 1.172)
SYNE4	-0.043	0.053	4.18E-01	1.00E+00	0.000	0.379	0.958 (0.901; 1.097)
FCN2	0.042	0.052	4.18E-01	1.00E+00	0.000	0.379	1.043 (0.915; 1.108)
TAOK2	-0.036	0.045	4.20E-01	1.00E+00	0.000	0.377	0.965 (0.856; 1.034)
IGHV3OR15-7	0.04	0.049	4.21E-01	1.00E+00	0.000	0.376	1.041 (0.905; 1.082)
RNF17	-0.037	0.046	4.21E-01	1.00E+00	0.000	0.376	0.964 (0.924; 1.119)
VWF	-0.04	0.049	4.21E-01	1.00E+00	0.000	0.376	0.961 (0.885; 1.088)
HEXD	-0.034	0.043	4.22E-01	1.00E+00	0.000	0.375	0.967 (0.889; 1.076)
IGLV3-25	-0.039	0.048	4.22E-01	1.00E+00	0.000	0.375	0.962 (0.851; 1.039)
VIM	0.041	0.051	4.22E-01	1.00E+00	0.000	0.375	1.042 (0.931; 1.168)
hCG_14925	0.046	0.058	4.22E-01	1.00E+00	0.000	0.375	1.047 (1.017; 1.262)
MUC19	-0.039	0.049	4.24E-01	1.00E+00	0.000	0.373	0.962 (0.882; 1.061)
HYI	-0.039	0.049	4.24E-01	1.00E+00	0.000	0.373	0.962 (0.901; 1.106)
CACNB3	-0.035	0.044	4.27E-01	1.00E+00	0.000	0.370	0.966 (0.911; 1.109)
DMGDH	-0.037	0.047	4.28E-01	1.00E+00	0.000	0.369	0.964 (0.894; 1.087)

PRMT9	-0.042	0.053	4.32E-01	1.00E+00	0.000	0.365	0.959 (0.891; 1.082)
AFG3L2	-0.039	0.05	4.33E-01	1.00E+00	0.000	0.364	0.962 (0.86; 1.044)
IGLV1-44	0.041	0.053	4.33E-01	1.00E+00	0.000	0.364	1.042 (0.872; 1.02)
TUBB2A	-0.039	0.049	4.35E-01	1.00E+00	0.000	0.362	0.962 (0.993; 1.238)
EFCAB5	0.04	0.052	4.36E-01	1.00E+00	0.000	0.361	1.041 (0.865; 1.041)
CDH5	-0.041	0.053	4.39E-01	1.00E+00	0.000	0.358	0.96 (0.851; 1.008)
SEPTIN7	-0.039	0.051	4.39E-01	1.00E+00	0.000	0.358	0.962 (0.954; 1.176)
RHBDF2	-0.037	0.048	4.41E-01	1.00E+00	0.000	0.356	0.964 (0.922; 1.125)
PSD3	0.042	0.056	4.47E-01	1.00E+00	0.000	0.350	1.043 (0.877; 1.047)
MBD6	-0.035	0.046	4.47E-01	1.00E+00	0.000	0.350	0.966 (0.875; 1.062)
HRG	0.04	0.053	4.47E-01	1.00E+00	0.000	0.350	1.041 (0.86; 1.045)
TRIP12	-0.036	0.048	4.51E-01	1.00E+00	0.000	0.346	0.965 (0.939; 1.146)
PLB1	-0.037	0.049	4.53E-01	1.00E+00	0.000	0.344	0.964 (0.968; 1.178)
IGLV3-27	-0.036	0.048	4.55E-01	1.00E+00	0.000	0.342	0.965 (0.839; 1.018)
SPECC1	-0.038	0.051	4.55E-01	1.00E+00	0.000	0.342	0.963 (0.811; 0.989)
RINL	-0.035	0.047	4.57E-01	1.00E+00	0.000	0.340	0.966 (0.956; 1.171)
EMC1	0.041	0.055	4.59E-01	1.00E+00	0.000	0.338	1.042 (0.893; 1.094)
PLCB4	-0.035	0.048	4.59E-01	1.00E+00	0.000	0.338	0.966 (0.894; 1.096)
SREBF1	-0.037	0.05	4.61E-01	1.00E+00	0.000	0.336	0.964 (0.908; 1.096)
PARD6G	0.037	0.051	4.62E-01	1.00E+00	0.000	0.335	1.038 (0.868; 1.056)
C2	-0.036	0.05	4.63E-01	1.00E+00	0.000	0.334	0.965 (0.882; 1.079)
STK38L	-0.029	0.039	4.64E-01	1.00E+00	0.000	0.333	0.971 (0.867; 1.029)
CUBN	-0.035	0.048	4.65E-01	1.00E+00	0.000	0.333	0.966 (0.917; 1.115)
NEO1	-0.035	0.048	4.68E-01	1.00E+00	0.000	0.330	0.966 (0.848; 1.037)
TUB	-0.037	0.051	4.68E-01	1.00E+00	0.000	0.330	0.964 (0.875; 1.059)
ARID2	-0.035	0.049	4.70E-01	1.00E+00	0.000	0.328	0.966 (0.896; 1.098)
RYR2	-0.032	0.044	4.70E-01	1.00E+00	0.000	0.328	0.969 (0.836; 1.027)
ANKRD52	0.035	0.048	4.72E-01	1.00E+00	0.000	0.326	1.036 (0.796; 0.969)
PHKA1	0.035	0.049	4.74E-01	1.00E+00	0.000	0.324	1.036 (0.888; 1.094)
PIP5K1C	-0.032	0.045	4.75E-01	1.00E+00	0.000	0.323	0.969 (0.866; 1.066)
BOD1L1	-0.032	0.044	4.75E-01	1.00E+00	0.000	0.323	0.969 (0.767; 0.924)
IGKV3-20.3	-0.036	0.051	4.76E-01	1.00E+00	0.000	0.322	0.965 (0.887; 1.084)
F2	0.036	0.051	4.77E-01	1.00E+00	0.000	0.321	1.037 (0.894; 1.105)

RGPD2	-0.039	0.054	4.77E-01	1.00E+00	0.000	0.321	0.962 (0.953; 1.176)
KIF14	-0.034	0.049	4.78E-01	1.00E+00	0.000	0.321	0.967 (0.87; 1.047)
GRK4	-0.034	0.048	4.78E-01	1.00E+00	0.000	0.321	0.967 (0.868; 1.038)
BRSK1	-0.035	0.049	4.83E-01	1.00E+00	0.000	0.316	0.966 (0.851; 1.021)
DDX31	-0.033	0.047	4.85E-01	1.00E+00	0.000	0.314	0.968 (0.938; 1.165)
ACACA	-0.031	0.045	4.89E-01	1.00E+00	0.000	0.311	0.969 (0.851; 1.009)
USP9Y	-0.037	0.053	4.91E-01	1.00E+00	0.000	0.309	0.964 (0.898; 1.091)
ATP11A	-0.032	0.047	4.92E-01	1.00E+00	0.000	0.308	0.969 (0.944; 1.141)
DPYSL5	-0.031	0.045	4.93E-01	1.00E+00	0.000	0.307	0.969 (0.93; 1.124)
PRDM2	-0.033	0.048	4.98E-01	1.00E+00	0.000	0.303	0.968 (0.967; 1.217)
OTUD7B	-0.033	0.049	5.00E-01	1.00E+00	0.000	0.301	0.968 (0.876; 1.051)
RELN	-0.037	0.055	5.01E-01	1.00E+00	0.000	0.300	0.964 (0.889; 1.08)
IGKV3-20	-0.034	0.051	5.04E-01	1.00E+00	0.000	0.298	0.967 (0.853; 1.031)
SPATA31D1	0.038	0.058	5.05E-01	1.00E+00	0.000	0.297	1.039 (0.847; 1.011)
ZBTB33	0.034	0.051	5.05E-01	1.00E+00	0.000	0.297	1.035 (0.85; 1.013)
SPTBN1	-0.033	0.05	5.07E-01	1.00E+00	0.000	0.295	0.968 (0.93; 1.138)
APOBR	-0.034	0.051	5.11E-01	1.00E+00	0.000	0.292	0.967 (0.89; 1.062)
DOCK11	-0.037	0.056	5.11E-01	1.00E+00	0.000	0.292	0.964 (0.813; 0.976)
HSPB3	-0.033	0.05	5.12E-01	1.00E+00	0.000	0.291	0.968 (0.898; 1.1)
BCHE	0.037	0.057	5.12E-01	1.00E+00	0.000	0.291	1.038 (0.876; 1.059)
SEPTIN1	0.033	0.05	5.13E-01	1.00E+00	0.000	0.290	1.034 (0.946; 1.168)
IGHV3-15	0.034	0.053	5.13E-01	1.00E+00	0.000	0.290	1.035 (0.893; 1.085)
ABI3BP	-0.033	0.05	5.14E-01	1.00E+00	0.000	0.289	0.968 (0.856; 1.035)
MSN	-0.03	0.047	5.14E-01	1.00E+00	0.000	0.289	0.97 (0.841; 1.029)
ITGB4	0.035	0.054	5.14E-01	1.00E+00	0.000	0.289	1.036 (0.934; 1.154)
HCN2	0.033	0.051	5.15E-01	1.00E+00	0.000	0.288	1.034 (0.844; 1.012)
TMEM238	-0.033	0.051	5.16E-01	1.00E+00	0.000	0.287	0.968 (0.988; 1.24)
NYAP2	-0.03	0.047	5.22E-01	1.00E+00	0.000	0.282	0.97 (0.901; 1.118)
IGKV4-1	-0.033	0.051	5.22E-01	1.00E+00	0.000	0.282	0.968 (0.865; 1.048)
ATAD3A	0.035	0.054	5.22E-01	1.00E+00	0.000	0.282	1.036 (0.819; 0.997)
SMARCC2	0.034	0.054	5.24E-01	1.00E+00	0.000	0.281	1.035 (0.879; 1.067)
FGD4	-0.026	0.041	5.27E-01	1.00E+00	0.000	0.278	0.974 (0.951; 1.171)
IGKV1-39.2	-0.031	0.049	5.30E-01	1.00E+00	0.000	0.276	0.969 (0.866; 1.04)

DHRS2	0.033	0.052	5.32E-01	1.00E+00	0.000	0.274	1.034 (0.909; 1.104)
RIT1	-0.031	0.05	5.32E-01	1.00E+00	0.000	0.274	0.969 (0.86; 1.053)
SERPINA1	-0.032	0.052	5.36E-01	1.00E+00	0.000	0.271	0.969 (0.853; 1.047)
TSHZ3	-0.031	0.051	5.39E-01	1.00E+00	0.000	0.268	0.969 (0.994; 1.23)
HGFAC	-0.032	0.053	5.40E-01	1.00E+00	0.000	0.268	0.969 (0.838; 1.006)
P3H4	0.033	0.054	5.46E-01	1.00E+00	0.000	0.263	1.034 (0.874; 1.082)
AHNAK	-0.031	0.052	5.47E-01	1.00E+00	0.000	0.262	0.969 (0.924; 1.131)
ITGA2	0.032	0.054	5.49E-01	1.00E+00	0.000	0.260	1.033 (0.925; 1.148)
TNFRSF1A	-0.032	0.054	5.53E-01	1.00E+00	0.000	0.257	0.969 (0.935; 1.147)
LCAT	-0.03	0.05	5.53E-01	1.00E+00	0.000	0.257	0.97 (0.9; 1.084)
MTBP	0.03	0.05	5.54E-01	1.00E+00	0.000	0.256	1.03 (0.861; 1.028)
ATP8B2	-0.028	0.047	5.54E-01	1.00E+00	0.000	0.256	0.972 (0.89; 1.06)
HSPA12B	-0.029	0.049	5.55E-01	1.00E+00	0.000	0.256	0.971 (0.933; 1.155)
ITIH4	0.032	0.054	5.56E-01	1.00E+00	0.000	0.255	1.033 (0.886; 1.054)
ECM1	0.029	0.05	5.56E-01	1.00E+00	0.000	0.255	1.029 (0.912; 1.099)
DCAF8	-0.03	0.051	5.56E-01	1.00E+00	0.000	0.255	0.97 (0.881; 1.064)
GPLD1	0.032	0.054	5.57E-01	1.00E+00	0.000	0.254	1.033 (0.929; 1.119)
LAMB2	-0.028	0.048	5.57E-01	1.00E+00	0.000	0.254	0.972 (0.879; 1.073)
GPANK1	-0.031	0.052	5.60E-01	1.00E+00	0.000	0.252	0.969 (0.863; 1.035)
TCP11	-0.031	0.054	5.60E-01	1.00E+00	0.000	0.252	0.969 (0.93; 1.121)
TUBB1	-0.027	0.047	5.63E-01	1.00E+00	0.000	0.249	0.973 (0.883; 1.061)
BBX	0.03	0.052	5.64E-01	1.00E+00	0.000	0.249	1.03 (0.938; 1.143)
IGKV2D-40	-0.029	0.051	5.64E-01	1.00E+00	0.000	0.249	0.971 (0.919; 1.129)
ZNF536	-0.027	0.047	5.67E-01	1.00E+00	0.000	0.246	0.973 (0.921; 1.128)
HLA-DOA	0.028	0.049	5.67E-01	1.00E+00	0.000	0.246	1.028 (0.916; 1.124)
RBL1	-0.029	0.051	5.74E-01	1.00E+00	0.000	0.241	0.971 (0.841; 1.048)
CLU	-0.031	0.054	5.74E-01	1.00E+00	0.000	0.241	0.969 (0.846; 1.014)
NCOR1	-0.028	0.05	5.77E-01	1.00E+00	0.000	0.239	0.972 (0.854; 1.03)
IGLV3-10	-0.024	0.043	5.78E-01	1.00E+00	0.000	0.238	0.976 (0.902; 1.102)
MYO16	0.027	0.049	5.78E-01	1.00E+00	0.000	0.238	1.027 (0.919; 1.154)
EVI2A	-0.026	0.046	5.78E-01	1.00E+00	0.000	0.238	0.974 (0.876; 1.046)
ATP5MF-PTCD	-0.026	0.048	5.81E-01	1.00E+00	0.000	0.236	0.974 (0.862; 1.026)
CROCC	-0.024	0.044	5.81E-01	1.00E+00	0.000	0.236	0.976 (0.857; 1.038)

HERC1	-0.026	0.048	5.81E-01	1.00E+00	0.000	0.236	0.974 (0.88; 1.058)
NBEA	-0.027	0.049	5.84E-01	1.00E+00	0.000	0.234	0.973 (0.853; 1.037)
DNAH10	-0.028	0.051	5.91E-01	1.00E+00	0.000	0.228	0.972 (0.859; 1.061)
IGLV2-11	-0.026	0.049	5.93E-01	1.00E+00	0.000	0.227	0.974 (0.833; 1.002)
TTF2	0.028	0.053	5.94E-01	1.00E+00	0.000	0.226	1.028 (0.817; 0.979)
HERC2	-0.029	0.054	5.94E-01	1.00E+00	0.000	0.226	0.971 (0.89; 1.077)
ZMYM6	-0.029	0.055	5.96E-01	1.00E+00	0.000	0.225	0.971 (0.903; 1.084)
LRG1	-0.029	0.054	5.98E-01	1.00E+00	0.000	0.223	0.971 (0.852; 1.035)
LAMA2	-0.034	0.064	5.98E-01	1.00E+00	0.000	0.223	0.967 (0.884; 1.057)
ANKRD30A	-0.026	0.049	5.98E-01	1.00E+00	0.000	0.223	0.974 (0.908; 1.12)
SBF1	-0.027	0.051	6.00E-01	1.00E+00	0.000	0.222	0.973 (0.827; 0.995)
SERPINA4	-0.028	0.054	6.01E-01	1.00E+00	0.000	0.221	0.972 (0.845; 1.016)
SRC	-0.025	0.049	6.02E-01	1.00E+00	0.000	0.220	0.975 (0.914; 1.11)
DCHS2	-0.025	0.048	6.02E-01	1.00E+00	0.000	0.220	0.975 (0.889; 1.063)
IGLV3-1	-0.025	0.049	6.04E-01	1.00E+00	0.000	0.219	0.975 (0.919; 1.12)
KIN	0.026	0.05	6.04E-01	1.00E+00	0.000	0.219	1.026 (0.87; 1.037)
MUC16	0.028	0.055	6.05E-01	1.00E+00	0.000	0.218	1.028 (0.842; 1.009)
PEBP1	-0.024	0.047	6.05E-01	1.00E+00	0.000	0.218	0.976 (0.906; 1.09)
NAV1	0.027	0.051	6.05E-01	1.00E+00	0.000	0.218	1.027 (0.9; 1.109)
ATXN7	-0.026	0.051	6.06E-01	1.00E+00	0.000	0.218	0.974 (0.859; 1.034)
IGKV1D-33.4	-0.027	0.052	6.06E-01	1.00E+00	0.000	0.218	0.973 (0.832; 0.988)
ZBTB5	-0.026	0.051	6.10E-01	1.00E+00	0.000	0.215	0.974 (0.845; 1.024)
TNIK	-0.024	0.047	6.11E-01	1.00E+00	0.000	0.214	0.976 (0.888; 1.078)
NDUFA13	0.027	0.053	6.13E-01	1.00E+00	0.000	0.213	1.027 (0.883; 1.06)
PPP4C	-0.022	0.044	6.15E-01	1.00E+00	0.000	0.211	0.978 (0.881; 1.096)
SRRT	-0.025	0.049	6.16E-01	1.00E+00	0.000	0.210	0.975 (0.912; 1.111)
ITPKA	-0.024	0.048	6.18E-01	1.00E+00	0.000	0.209	0.976 (0.943; 1.153)
UACA	-0.026	0.053	6.19E-01	1.00E+00	0.000	0.208	0.974 (0.836; 1.016)
A1BG	-0.026	0.052	6.20E-01	1.00E+00	0.000	0.208	0.974 (0.779; 0.928)
SENP3	-0.025	0.05	6.21E-01	1.00E+00	0.000	0.207	0.975 (0.875; 1.06)
CCDC168	-0.024	0.049	6.25E-01	1.00E+00	0.000	0.204	0.976 (0.911; 1.119)
MPIG6B	-0.023	0.047	6.25E-01	1.00E+00	0.000	0.204	0.977 (0.881; 1.085)
KRT15	0.024	0.05	6.27E-01	1.00E+00	0.000	0.203	1.024 (0.903; 1.087)

HLA-DRA	-0.025	0.052	6.27E-01	1.00E+00	0.000	0.203	0.975 (0.892; 1.081)
IGHV4-34	-0.021	0.044	6.28E-01	1.00E+00	0.000	0.202	0.979 (0.914; 1.122)
NUFIP1	-0.025	0.051	6.31E-01	1.00E+00	0.000	0.200	0.975 (0.905; 1.107)
MAP4K5	0.024	0.05	6.36E-01	1.00E+00	0.000	0.197	1.024 (0.915; 1.124)
BTD	-0.028	0.06	6.36E-01	1.00E+00	0.000	0.197	0.972 (0.871; 1.053)
CELSR1	0.026	0.054	6.38E-01	1.00E+00	0.000	0.195	1.026 (0.794; 0.96)
ATPAF1	-0.023	0.05	6.38E-01	1.00E+00	0.000	0.195	0.977 (0.888; 1.072)
FCRL5	-0.023	0.048	6.39E-01	1.00E+00	0.000	0.194	0.977 (0.885; 1.075)
AVEN	-0.024	0.05	6.39E-01	1.00E+00	0.000	0.194	0.976 (0.911; 1.113)
PREPL	-0.023	0.05	6.41E-01	1.00E+00	0.000	0.193	0.977 (0.861; 1.027)
DLGAP4	-0.022	0.047	6.43E-01	1.00E+00	0.000	0.192	0.978 (0.964; 1.189)
LRRC10B	-0.023	0.05	6.43E-01	1.00E+00	0.000	0.192	0.977 (0.885; 1.066)
PPM1B	0.024	0.052	6.46E-01	1.00E+00	0.000	0.190	1.024 (0.856; 1.016)
APOA2	-0.021	0.046	6.48E-01	1.00E+00	0.000	0.188	0.979 (1.013; 1.265)
TNRC6B	-0.021	0.048	6.56E-01	1.00E+00	0.000	0.183	0.979 (0.887; 1.081)
CENPE	-0.022	0.049	6.57E-01	1.00E+00	0.000	0.182	0.978 (0.847; 1.02)
PDE4DIP	0.02	0.046	6.60E-01	1.00E+00	0.000	0.180	1.02 (0.864; 1.034)
CBLL1	-0.022	0.049	6.61E-01	1.00E+00	0.000	0.180	0.978 (0.878; 1.049)
PTGDS	-0.022	0.051	6.62E-01	1.00E+00	0.000	0.179	0.978 (0.781; 0.947)
DRG2	0.024	0.054	6.62E-01	1.00E+00	0.000	0.179	1.024 (0.928; 1.124)
PLPP7	-0.022	0.051	6.63E-01	1.00E+00	0.000	0.178	0.978 (0.916; 1.107)
FTO	-0.021	0.049	6.64E-01	1.00E+00	0.000	0.178	0.979 (0.939; 1.169)
CMYA5	-0.022	0.051	6.65E-01	1.00E+00	0.000	0.177	0.978 (0.926; 1.147)
CNDP1	0.025	0.058	6.71E-01	1.00E+00	0.000	0.173	1.025 (0.868; 1.058)
TUFM	-0.021	0.05	6.72E-01	1.00E+00	0.000	0.173	0.979 (0.954; 1.192)
TRIO	-0.02	0.047	6.73E-01	1.00E+00	0.000	0.172	0.98 (0.876; 1.052)
FAT4	-0.022	0.052	6.78E-01	1.00E+00	0.000	0.169	0.978 (0.905; 1.11)
FBLN1	-0.023	0.055	6.80E-01	1.00E+00	0.000	0.167	0.977 (0.928; 1.143)
TUBA8	0.02	0.049	6.80E-01	1.00E+00	0.000	0.167	1.02 (0.87; 1.052)
PPBP	0.022	0.052	6.82E-01	1.00E+00	0.000	0.166	1.022 (0.926; 1.121)
CALB2	-0.019	0.047	6.85E-01	1.00E+00	0.000	0.164	0.981 (0.905; 1.095)
MARK3	-0.02	0.05	6.85E-01	1.00E+00	0.000	0.164	0.98 (0.886; 1.067)
SYNE2	0.021	0.052	6.87E-01	1.00E+00	0.000	0.163	1.021 (0.844; 1.006)

KNG1	-0.02	0.05	6.89E-01	1.00E+00	0.000	0.162	0.98 (0.855; 1.037)
OPN1SW	-0.018	0.046	6.93E-01	1.00E+00	0.000	0.159	0.982 (0.914; 1.115)
ATP2B1	-0.021	0.055	6.95E-01	1.00E+00	0.000	0.158	0.979 (0.906; 1.103)
ANKRD31	0.02	0.052	6.96E-01	1.00E+00	0.000	0.157	1.02 (0.958; 1.183)
ACADVL	-0.02	0.051	6.96E-01	1.00E+00	0.000	0.157	0.98 (0.82; 0.995)
IGHV3-72	-0.02	0.051	6.97E-01	1.00E+00	0.000	0.157	0.98 (0.92; 1.139)
SLC1A2	-0.019	0.05	6.97E-01	1.00E+00	0.000	0.157	0.981 (0.871; 1.059)
NF1	0.02	0.052	6.98E-01	1.00E+00	0.000	0.156	1.02 (0.987; 1.258)
CALCOCO1	0.018	0.049	7.04E-01	1.00E+00	0.000	0.152	1.018 (0.909; 1.098)
FGFR2	0.019	0.049	7.06E-01	1.00E+00	0.000	0.151	1.019 (0.843; 1.015)
DACT3	0.018	0.047	7.06E-01	1.00E+00	0.000	0.151	1.018 (0.975; 1.202)
EMILIN2	-0.021	0.055	7.06E-01	1.00E+00	0.000	0.151	0.979 (0.885; 1.087)
MAP2	-0.017	0.045	7.07E-01	1.00E+00	0.000	0.151	0.983 (0.903; 1.102)
IGKV1D-33.1	-0.02	0.054	7.12E-01	1.00E+00	0.000	0.148	0.98 (0.782; 0.949)
CUX1	-0.016	0.044	7.14E-01	1.00E+00	0.000	0.146	0.984 (0.861; 1.02)
TAF1L	-0.019	0.052	7.15E-01	1.00E+00	0.000	0.146	0.981 (0.896; 1.089)
IGKV1D-33.6	-0.019	0.054	7.17E-01	1.00E+00	0.000	0.144	0.981 (0.923; 1.13)
TASOR	0.019	0.052	7.17E-01	1.00E+00	0.000	0.144	1.019 (0.868; 1.038)
IGKV1-39.1	-0.019	0.052	7.18E-01	1.00E+00	0.000	0.144	0.981 (0.892; 1.076)
CDRT15L2	-0.017	0.046	7.20E-01	1.00E+00	0.000	0.143	0.983 (0.805; 0.975)
IGKV4-1.1	-0.019	0.052	7.20E-01	1.00E+00	0.000	0.143	0.981 (0.846; 1.018)
SUGP2	0.018	0.051	7.20E-01	1.00E+00	0.000	0.143	1.018 (0.939; 1.148)
ATRN	0.02	0.057	7.22E-01	1.00E+00	0.000	0.141	1.02 (0.885; 1.057)
SOBP	-0.017	0.047	7.23E-01	1.00E+00	0.000	0.141	0.983 (0.83; 1.009)
PSME1	-0.018	0.051	7.25E-01	1.00E+00	0.000	0.140	0.982 (0.861; 1.034)
USP31	-0.017	0.05	7.26E-01	1.00E+00	0.000	0.139	0.983 (0.824; 0.995)
MYOM2	-0.017	0.048	7.27E-01	1.00E+00	0.000	0.138	0.983 (0.896; 1.101)
OR51G1	-0.017	0.05	7.28E-01	1.00E+00	0.000	0.138	0.983 (0.87; 1.063)
KREMEN2	0.017	0.048	7.28E-01	1.00E+00	0.000	0.138	1.017 (0.863; 1.045)
IGKV1-5.1	0.018	0.05	7.28E-01	1.00E+00	0.000	0.138	1.018 (0.93; 1.144)
PRKCE	0.017	0.049	7.33E-01	1.00E+00	0.000	0.135	1.017 (0.903; 1.09)
FNBP1	-0.015	0.046	7.37E-01	1.00E+00	0.000	0.133	0.985 (0.892; 1.08)
IGLV3-21.1	-0.017	0.05	7.38E-01	1.00E+00	0.000	0.132	0.983 (0.862; 1.018)

BMAL2	-0.015	0.047	7.44E-01	1.00E+00	0.000	0.128	0.985 (0.847; 1.02)
GAPVD1	-0.017	0.052	7.44E-01	1.00E+00	0.000	0.128	0.983 (0.794; 0.97)
ALDH1A3	-0.016	0.048	7.45E-01	1.00E+00	0.000	0.128	0.984 (0.894; 1.077)
UPF1	0.015	0.047	7.46E-01	1.00E+00	0.000	0.127	1.015 (0.901; 1.055)
RIOK3	-0.016	0.049	7.48E-01	1.00E+00	0.000	0.126	0.984 (0.846; 1.028)
GPC1	-0.015	0.048	7.49E-01	1.00E+00	0.000	0.126	0.985 (0.951; 1.166)
DLST	0.015	0.047	7.49E-01	1.00E+00	0.000	0.126	1.015 (0.831; 1.015)
OTUD5	0.016	0.052	7.52E-01	1.00E+00	0.000	0.124	1.016 (0.779; 0.956)
CSPG4	-0.014	0.045	7.52E-01	1.00E+00	0.000	0.124	0.986 (0.822; 0.996)
AASS	0.017	0.054	7.53E-01	1.00E+00	0.000	0.123	1.017 (0.9; 1.096)
IGLV1-40	0.016	0.051	7.55E-01	1.00E+00	0.000	0.122	1.016 (0.873; 1.064)
TGFBI	-0.014	0.045	7.56E-01	1.00E+00	0.000	0.121	0.986 (0.869; 1.048)
OSGIN1	-0.015	0.05	7.58E-01	1.00E+00	0.000	0.120	0.985 (0.864; 1.041)
LYN	-0.015	0.05	7.58E-01	1.00E+00	0.000	0.120	0.985 (0.905; 1.108)
SF1	-0.014	0.047	7.59E-01	1.00E+00	0.000	0.120	0.986 (0.843; 1.029)
ACTMAP	-0.014	0.047	7.63E-01	1.00E+00	0.000	0.117	0.986 (0.963; 1.183)
TXNDC2	-0.015	0.051	7.63E-01	1.00E+00	0.000	0.117	0.985 (0.799; 0.982)
SERPINA3	0.016	0.052	7.65E-01	1.00E+00	0.000	0.116	1.016 (0.912; 1.113)
GOSR1	-0.015	0.05	7.67E-01	1.00E+00	0.000	0.115	0.985 (0.85; 1.018)
IGKV1-5	-0.016	0.054	7.68E-01	1.00E+00	0.000	0.115	0.984 (0.873; 1.048)
NIPBL	-0.014	0.048	7.69E-01	1.00E+00	0.000	0.114	0.986 (0.923; 1.127)
SMC4	-0.015	0.053	7.70E-01	1.00E+00	0.000	0.114	0.985 (0.879; 1.065)
STX11	0.016	0.053	7.71E-01	1.00E+00	0.000	0.113	1.016 (0.871; 1.054)
ZNF827	-0.014	0.049	7.71E-01	1.00E+00	0.000	0.113	0.986 (0.899; 1.068)
LY75	-0.015	0.051	7.71E-01	1.00E+00	0.000	0.113	0.985 (0.863; 1.049)
CMTM7	0.015	0.052	7.76E-01	1.00E+00	0.000	0.110	1.015 (0.953; 1.168)
KRT1	0.014	0.048	7.76E-01	1.00E+00	0.000	0.110	1.014 (0.824; 0.994)
ZMYM1	0.015	0.051	7.78E-01	1.00E+00	0.000	0.109	1.015 (0.819; 0.998)
ZFYVE19	-0.013	0.046	7.79E-01	1.00E+00	0.000	0.108	0.987 (0.95; 1.155)
FKBP4	-0.014	0.051	7.80E-01	1.00E+00	0.000	0.108	0.986 (0.886; 1.084)
ATP10A	-0.013	0.049	7.82E-01	1.00E+00	0.000	0.107	0.987 (0.936; 1.121)
EXD3	-0.013	0.05	7.88E-01	1.00E+00	0.000	0.103	0.987 (0.847; 1.019)
FCN3	0.014	0.053	7.88E-01	1.00E+00	0.000	0.103	1.014 (0.808; 0.984)

PLXDC2	0.013	0.049	7.91E-01	1.00E+00	0.000	0.102	1.013 (0.832; 1.02)
IGKV1-17.1	-0.014	0.051	7.91E-01	1.00E+00	0.000	0.102	0.986 (0.913; 1.091)
CCAR1	-0.013	0.051	7.93E-01	1.00E+00	0.000	0.101	0.987 (0.818; 0.994)
TFRC	0.014	0.053	7.96E-01	1.00E+00	0.000	0.099	1.014 (0.787; 0.96)
ANKLE2	-0.013	0.052	7.99E-01	1.00E+00	0.000	0.097	0.987 (0.966; 1.174)
IGKV2D-28.1	0.013	0.052	7.99E-01	1.00E+00	0.000	0.097	1.013 (1.252; 1.554)
TUBB4A	-0.012	0.048	8.00E-01	1.00E+00	0.000	0.097	0.988 (0.929; 1.131)
DIDO1	-0.012	0.046	8.03E-01	1.00E+00	0.000	0.095	0.988 (0.901; 1.069)
KMT2D	-0.012	0.05	8.07E-01	1.00E+00	0.000	0.093	0.988 (0.849; 1.023)
NPHP3	0.012	0.05	8.09E-01	1.00E+00	0.000	0.092	1.012 (0.962; 1.208)
NPHP1	0.012	0.051	8.09E-01	1.00E+00	0.000	0.092	1.012 (0.828; 1.006)
MKI67	-0.011	0.047	8.10E-01	1.00E+00	0.000	0.092	0.989 (0.885; 1.092)
API5	-0.011	0.047	8.11E-01	1.00E+00	0.000	0.091	0.989 (0.943; 1.16)
IGLV1-47	0.013	0.056	8.13E-01	1.00E+00	0.000	0.090	1.013 (0.854; 1.032)
TRIM33	-0.011	0.048	8.15E-01	1.00E+00	0.000	0.089	0.989 (0.937; 1.153)
SETD1A	-0.012	0.051	8.19E-01	1.00E+00	0.000	0.087	0.988 (0.833; 1.034)
SERPING1	0.014	0.06	8.19E-01	1.00E+00	0.000	0.087	1.014 (0.851; 1.027)
HECTD4	-0.011	0.05	8.21E-01	1.00E+00	0.000	0.086	0.989 (0.875; 1.056)
HABP2	0.011	0.047	8.22E-01	1.00E+00	0.000	0.085	1.011 (0.893; 1.092)
IGHV3-7.1	-0.011	0.05	8.24E-01	1.00E+00	0.000	0.084	0.989 (0.767; 0.942)
FERMT1	0.011	0.05	8.26E-01	1.00E+00	0.000	0.083	1.011 (0.867; 1.049)
APOH	-0.012	0.055	8.29E-01	1.00E+00	0.000	0.081	0.988 (0.835; 1.017)
COL16A1	0.011	0.051	8.31E-01	1.00E+00	0.000	0.080	1.011 (0.908; 1.092)
IGHV3-23	0.016	0.074	8.32E-01	1.00E+00	0.000	0.080	1.016 (0.843; 1.011)
ANK1	-0.01	0.048	8.34E-01	1.00E+00	0.000	0.079	0.99 (0.96; 1.174)
COL22A1	-0.011	0.051	8.36E-01	1.00E+00	0.000	0.078	0.989 (0.879; 1.057)
TONSL	0.01	0.052	8.40E-01	1.00E+00	0.000	0.076	1.01 (0.883; 1.073)
WBP2	-0.01	0.051	8.40E-01	1.00E+00	0.000	0.076	0.99 (0.962; 1.215)
IGHV3-30	0.01	0.051	8.41E-01	1.00E+00	0.000	0.075	1.01 (0.876; 1.068)
LRRTM2	-0.01	0.049	8.43E-01	1.00E+00	0.000	0.074	0.99 (0.829; 1.014)
CORO1C	-0.01	0.052	8.46E-01	1.00E+00	0.000	0.073	0.99 (0.841; 0.998)
IGHV3-48	-0.01	0.051	8.46E-01	1.00E+00	0.000	0.073	0.99 (0.832; 1.005)
IGHV3-13	-0.01	0.05	8.48E-01	1.00E+00	0.000	0.072	0.99 (0.976; 1.203)

LCORL	-0.01	0.053	8.50E-01	1.00E+00	0.000	0.071	0.99 (1.246; 1.549)
ELL2	-0.009	0.048	8.54E-01	1.00E+00	0.000	0.069	0.991 (0.861; 1.048)
COL4A5	0.009	0.051	8.60E-01	1.00E+00	0.000	0.066	1.009 (0.914; 1.103)
ANKRD2	0.009	0.052	8.60E-01	1.00E+00	0.000	0.066	1.009 (0.928; 1.138)
RICTOR	-0.009	0.05	8.64E-01	1.00E+00	0.000	0.063	0.991 (0.878; 1.058)
ZGRF1	-0.008	0.047	8.64E-01	1.00E+00	0.000	0.063	0.992 (0.907; 1.098)
ZNF407	0.009	0.052	8.65E-01	1.00E+00	0.000	0.063	1.009 (0.863; 1.041)
IDE	0.008	0.049	8.70E-01	1.00E+00	0.000	0.060	1.008 (0.863; 1.051)
WHRN	-0.008	0.048	8.71E-01	1.00E+00	0.000	0.060	0.992 (0.849; 1.05)
IGHV1-2	0.008	0.053	8.76E-01	1.00E+00	0.000	0.057	1.008 (0.924; 1.135)
IGHV1-18	-0.007	0.047	8.76E-01	1.00E+00	0.000	0.057	0.993 (0.867; 1.058)
FLNB	-0.008	0.049	8.77E-01	1.00E+00	0.000	0.057	0.992 (0.881; 1.06)
F10	0.007	0.048	8.77E-01	1.00E+00	0.000	0.057	1.007 (0.873; 1.065)
PGA3	0.007	0.047	8.78E-01	1.00E+00	0.000	0.057	1.007 (0.761; 0.931)
ARHGEF19	0.007	0.049	8.80E-01	1.00E+00	0.000	0.056	1.007 (0.872; 1.06)
KCNQ4	0.008	0.052	8.85E-01	1.00E+00	0.000	0.053	1.008 (0.891; 1.098)
VCL	0.007	0.049	8.86E-01	1.00E+00	0.000	0.053	1.007 (0.907; 1.108)
PLG	-0.007	0.052	8.87E-01	1.00E+00	0.000	0.052	0.993 (0.786; 0.992)
MYH9	-0.007	0.05	8.88E-01	1.00E+00	0.000	0.052	0.993 (0.943; 1.205)
LSM11	-0.006	0.046	8.89E-01	1.00E+00	0.000	0.051	0.994 (0.922; 1.109)
CHD7	0.007	0.051	8.90E-01	1.00E+00	0.000	0.051	1.007 (0.968; 1.195)
PRRT4	0.006	0.046	8.91E-01	1.00E+00	0.000	0.050	1.006 (0.935; 1.131)
RSL24D1	-0.006	0.048	8.94E-01	1.00E+00	0.000	0.049	0.994 (0.901; 1.06)
TXNRD1	-0.007	0.05	8.96E-01	1.00E+00	0.000	0.048	0.993 (0.857; 1.02)
DAPK2	-0.007	0.05	8.96E-01	1.00E+00	0.000	0.048	0.993 (0.937; 1.136)
EFNB2	0.006	0.045	9.00E-01	1.00E+00	0.000	0.046	1.006 (0.785; 0.956)
PAPPA	0.006	0.048	9.04E-01	1.00E+00	0.000	0.044	1.006 (0.916; 1.126)
PAN2	-0.006	0.055	9.07E-01	1.00E+00	0.000	0.042	0.994 (0.917; 1.11)
GABARAPL1	0.006	0.049	9.08E-01	1.00E+00	0.000	0.042	1.006 (0.953; 1.201)
SERAC1	-0.006	0.051	9.09E-01	1.00E+00	0.000	0.041	0.994 (0.89; 1.074)
FGD6	-0.006	0.052	9.10E-01	1.00E+00	0.000	0.041	0.994 (0.85; 1.04)
ASPSCR1	0.006	0.052	9.10E-01	1.00E+00	0.000	0.041	1.006 (0.794; 0.947)
PTPRS	0.006	0.05	9.12E-01	1.00E+00	0.000	0.040	1.006 (0.929; 1.118)

KIF22	-0.005	0.05	9.16E-01	1.00E+00	0.000	0.038	0.995 (0.852; 1.04)
AMBP	0.005	0.052	9.18E-01	1.00E+00	0.000	0.037	1.005 (1.287; 1.604)
PGM5	-0.005	0.048	9.19E-01	1.00E+00	0.000	0.037	0.995 (0.884; 1.053)
PPP2R1A	-0.005	0.049	9.20E-01	1.00E+00	0.000	0.036	0.995 (0.935; 1.157)
IGLV6-57	-0.005	0.048	9.25E-01	1.00E+00	0.000	0.034	0.995 (0.842; 1.012)
RBM15	0.005	0.053	9.28E-01	1.00E+00	0.000	0.032	1.005 (0.858; 1.055)
CHD3	0.005	0.053	9.30E-01	1.00E+00	0.000	0.032	1.005 (0.882; 1.078)
RIBC2	-0.004	0.045	9.32E-01	1.00E+00	0.000	0.031	0.996 (0.888; 1.082)
DDX17	-0.004	0.047	9.32E-01	1.00E+00	0.000	0.031	0.996 (0.837; 1.003)
NKX2-5	0.004	0.05	9.33E-01	1.00E+00	0.000	0.030	1.004 (0.898; 1.082)
RRS1	0.005	0.056	9.33E-01	1.00E+00	0.000	0.030	1.005 (0.899; 1.07)
IGHV3-7.2	-0.004	0.051	9.33E-01	1.00E+00	0.000	0.030	0.996 (0.825; 0.999)
SH3GL3	0.004	0.049	9.35E-01	1.00E+00	0.000	0.029	1.004 (0.876; 1.052)
B2M	0.004	0.052	9.36E-01	1.00E+00	0.000	0.029	1.004 (0.903; 1.082)
SEC23IP	0.004	0.05	9.40E-01	1.00E+00	0.000	0.027	1.004 (0.857; 1.037)
F12	0.004	0.052	9.41E-01	1.00E+00	0.000	0.026	1.004 (0.878; 1.07)
CNDP1.1	-0.004	0.049	9.42E-01	1.00E+00	0.000	0.026	0.996 (0.921; 1.105)
ZZEF1	-0.004	0.049	9.43E-01	1.00E+00	0.000	0.025	0.996 (0.902; 1.086)
WDR74	0.003	0.049	9.44E-01	1.00E+00	0.000	0.025	1.003 (0.917; 1.105)
TBCD	-0.003	0.053	9.49E-01	1.00E+00	0.000	0.023	0.997 (1.018; 1.309)
LINC02881	0.003	0.046	9.50E-01	1.00E+00	0.000	0.022	1.003 (0.938; 1.143)
PIGR	0.003	0.044	9.51E-01	1.00E+00	0.000	0.022	1.003 (0.891; 1.086)
RRBP1	-0.003	0.05	9.51E-01	1.00E+00	0.000	0.022	0.997 (0.91; 1.11)
OTUD7A	-0.003	0.049	9.51E-01	1.00E+00	0.000	0.022	0.997 (0.945; 1.172)
CP	-0.003	0.055	9.52E-01	1.00E+00	0.000	0.021	0.997 (0.906; 1.1)
ARMH1	0.003	0.047	9.53E-01	1.00E+00	0.000	0.021	1.003 (0.89; 1.055)
DACT1	0.003	0.048	9.57E-01	1.00E+00	0.000	0.019	1.003 (0.896; 1.09)
HNRNPM	-0.003	0.049	9.58E-01	1.00E+00	0.000	0.019	0.997 (0.94; 1.192)
SLC6A9	-0.003	0.05	9.59E-01	1.00E+00	0.000	0.018	0.997 (0.955; 1.165)
PRR36	0.003	0.051	9.61E-01	1.00E+00	0.000	0.017	1.003 (0.947; 1.222)
KRT75	-0.002	0.051	9.63E-01	1.00E+00	0.000	0.016	0.998 (0.757; 0.925)
INSL4	-0.002	0.051	9.64E-01	1.00E+00	0.000	0.016	0.998 (0.815; 0.982)
ARHGAP39	-0.002	0.051	9.64E-01	1.00E+00	0.000	0.016	0.998 (0.899; 1.1)

ADCY1	0.002	0.05	9.66E-01	1.00E+00	0.000	0.015	1.002 (0.835; 1.015)
MAP3K9	0.002	0.05	9.72E-01	1.00E+00	0.000	0.012	1.002 (0.819; 0.999)
KIAA1671	0.002	0.05	9.74E-01	1.00E+00	0.000	0.011	1.002 (0.901; 1.089)
NPY5R	-0.002	0.051	9.75E-01	1.00E+00	0.000	0.011	0.998 (0.924; 1.13)
BDP1	-0.002	0.052	9.76E-01	1.00E+00	0.000	0.011	0.998 (0.884; 1.085)
IGKV1D-12	0.001	0.049	9.77E-01	1.00E+00	0.000	0.010	1.001 (0.977; 1.229)
ROCK2	0.001	0.056	9.80E-01	1.00E+00	0.000	0.009	1.001 (0.944; 1.188)
ZNF507	-0.001	0.055	9.81E-01	1.00E+00	0.000	0.008	0.999 (0.866; 1.054)
AHSG	-0.001	0.051	9.82E-01	1.00E+00	0.000	0.008	0.999 (0.881; 1.048)
NOX1	-0.001	0.051	9.82E-01	1.00E+00	0.000	0.008	0.999 (0.886; 1.074)
IGKV1-5.2	0.001	0.054	9.83E-01	1.00E+00	0.000	0.007	1.001 (0.885; 1.076)
TMF1	0.001	0.045	9.83E-01	1.00E+00	0.000	0.007	1.001 (0.828; 1.015)
DMD	-0.001	0.051	9.86E-01	1.00E+00	0.000	0.006	0.999 (0.888; 1.076)
HNRNPU	0.001	0.052	9.87E-01	1.00E+00	0.000	0.006	1.001 (0.875; 1.049)
TTBK1	0.001	0.051	9.89E-01	1.00E+00	0.000	0.005	1.001 (0.883; 1.066)
LYZ	0.001	0.045	9.90E-01	1.00E+00	0.000	0.004	1.001 (0.872; 1.041)
MAPRE1	-0.001	0.047	9.90E-01	1.00E+00	0.000	0.004	0.999 (0.88; 1.077)
CABP1	0	0.052	9.94E-01	1.00E+00	0.000	0.003	1 (0.792; 0.97)
BEST1	0	0.047	9.96E-01	1.00E+00	0.000	0.002	1 (0.898; 1.075)
NYAP1	0	0.05	9.96E-01	1.00E+00	0.000	0.002	1 (0.887; 1.086)

1. Full names of the biomarkers can be found in Additional file 1: Table S1. Abbreviations: OR: odds ratio; CI: confident interval.

2.Adjusted for variables in basic model (age, sex).

Table S3 Significant associations of 25 proteomic biomarkers with obesity in the basic model

Proteins	UniProt_ID	Estimate	SE	p value	adjusted p value	log10_adj_pval	log10_pval	OR (95% CI)
APOD	P05090	-0.634	0.057	1.83E-28	1.48E-25	24.830	27.738	0.53 (0.863, 1.048)
CRP	P02741	0.617	0.057	3.78E-27	3.06E-24	23.514	26.423	1.853 (0.883, 1.056)
LGALS3BP	Q08380	0.652	0.073	2.62E-19	2.12E-16	15.674	18.582	1.919 (0.944, 1.156)
APOM	O95445	-0.494	0.057	4.17E-18	3.38E-15	14.471	17.380	0.61 (0.828, 0.994)
A2M	P01023	0.482	0.056	7.46E-18	6.04E-15	14.219	17.127	1.619 (0.905, 1.11)
APOF	Q13790	-0.89	0.104	1.16E-17	9.40E-15	14.027	16.936	0.411 (0.832, 1.019)
CFH	P08603	0.468	0.056	9.37E-17	7.58E-14	13.120	16.028	1.597 (0.87, 1.049)
AFM	P43652	0.414	0.055	3.52E-14	2.85E-11	10.545	13.453	1.513 (0.889, 1.086)
SERPINF1	P36955	0.39	0.057	8.61E-12	6.96E-09	8.157	11.065	1.477 (0.966, 1.186)
ADIPOQ	Q15848	-0.402	0.059	1.01E-11	8.20E-09	8.086	10.996	0.669 (0.899, 1.081)
APCS	P02743	0.394	0.058	1.36E-11	1.10E-08	7.959	10.866	1.483 (0.832, 0.989)
S100A9	P06702	0.424	0.065	5.46E-11	4.41E-08	7.356	10.263	1.528 (0.872, 1.051)
CFI	G3XAM2	0.362	0.056	1.14E-10	9.23E-08	7.035	9.943	1.436 (0.9, 1.082)
SAA2-SAA4	A0A096LPE2	0.332	0.055	1.71E-09	1.39E-06	5.857	8.767	1.394 (0.854, 1.028)
NFIA	B1AKN8	0.328	0.056	3.37E-09	2.73E-06	5.564	8.472	1.388 (0.875, 1.051)
LBP	P18428	0.887	0.153	6.03E-09	4.88E-06	5.312	8.220	2.428 (0.918, 1.1)
SERPINA6	P08185	-0.295	0.059	4.99E-07	4.03E-04	3.395	6.302	0.745 (0.809, 0.974)
AZGP1	P25311	-0.255	0.051	7.20E-07	5.83E-04	3.234	6.143	0.775 (0.877, 1.073)
SERPIND1	P05546	0.258	0.053	9.47E-07	7.66E-04	3.116	6.024	1.294 (0.867, 1.039)
VTN	P04004	0.256	0.055	3.40E-06	2.75E-03	2.561	5.469	1.292 (0.905, 1.092)
GPX3	P22352	-0.24	0.052	4.68E-06	3.79E-03	2.421	5.330	0.787 (0.87, 1.075)
C4B	P0C0L5	0.264	0.061	1.40E-05	1.13E-02	1.947	4.854	1.302 (0.954, 1.173)
SAA2	P0DJ19	0.239	0.056	2.17E-05	1.75E-02	1.757	4.664	1.27 (0.86, 1.046)
C4A	P0C0L4	0.225	0.053	2.51E-05	2.03E-02	1.693	4.600	1.252 (0.899, 1.096)
C3	P01024	0.227	0.054	3.15E-05	2.55E-02	1.593	4.502	1.255 (0.896, 1.086)

1. Full names of the biomarkers can be found in Additional file 1: Table S1. The 25 proteins significantly associated with obesity (FDR < 0.05) using the logistic regression model are presented in this table.
Abbreviations: FDR, Bonferroni false-discovery rate; OR: odds ratio; CI: confident interval.

2.Adjusted for variables in basic model (age, sex).

Table S4 Comprehensive results of full logistic regression model on proteins related to obesity

Proteins	Estimate	SE	<i>p</i> value	adjusted <i>p</i> value	log10_adj_pval	log10_pval	OR (95% CI)
CRP	0.488	0.062	2.49E-15	2.02E-12	11.695	14.604	1.629 (0.854; 1.059)
APOD	-0.403	0.063	1.49E-10	1.20E-07	6.921	9.827	0.668 (0.835; 1.012)
SAA2-SAA4	0.343	0.061	2.33E-08	1.88E-05	4.726	7.633	1.409 (0.892; 1.103)
APOM	-0.329	0.062	1.16E-07	9.37E-05	4.028	6.936	0.72 (0.811; 0.989)
CFH	0.321	0.061	1.35E-07	1.09E-04	3.963	6.870	1.379 (0.89; 1.11)
LGALS3BP	0.415	0.079	1.51E-07	1.22E-04	3.914	6.821	1.514 (0.8; 1.001)
A2M	0.306	0.061	5.01E-07	4.06E-04	3.391	6.300	1.358 (0.889; 1.096)
APOF	-0.533	0.107	6.27E-07	5.07E-04	3.295	6.203	0.587 (0.837; 1.028)
AFM	0.266	0.059	7.24E-06	5.86E-03	2.232	5.140	1.305 (0.908; 1.133)
SERPINA6	-0.257	0.064	5.80E-05	4.69E-02	1.329	4.237	0.773 (0.879; 1.077)
CKAP5	-0.216	0.054	6.08E-05	4.92E-02	1.308	4.216	0.806 (0.809; 0.974)
ZFP36L1	-0.196	0.049	6.44E-05	5.21E-02	1.283	4.191	0.822 (0.823; 0.999)
APCS	0.25	0.064	8.37E-05	6.77E-02	1.169	4.077	1.284 (0.869; 1.067)
SERPINC1	-0.212	0.056	1.73E-04	1.40E-01	0.854	3.762	0.809 (0.855; 1.049)
ADIPOQ	-0.233	0.062	1.85E-04	1.50E-01	0.824	3.733	0.792 (0.84; 1.028)
S100A9	0.262	0.07	1.88E-04	1.52E-01	0.818	3.726	1.3 (0.906; 1.109)
AZGP1	-0.206	0.056	2.13E-04	1.73E-01	0.762	3.672	0.814 (0.775; 0.944)
NSD3	-0.172	0.047	2.75E-04	2.22E-01	0.654	3.561	0.842 (0.841; 1.048)
CFI	0.218	0.061	3.34E-04	2.70E-01	0.569	3.476	1.244 (0.846; 1.035)
PON3	-0.166	0.048	5.21E-04	4.21E-01	0.376	3.283	0.847 (0.875; 1.076)
SERPINF1	0.208	0.062	7.64E-04	6.18E-01	0.209	3.117	1.231 (0.839; 1.058)
CBARP	-0.168	0.051	1.04E-03	8.41E-01	0.075	2.983	0.845 (0.923; 1.163)
LBP	0.46	0.14	1.07E-03	8.66E-01	0.062	2.971	1.584 (0.836; 1.041)
NFIA	0.195	0.06	1.24E-03	1.00E+00	0.000	2.907	1.215 (0.858; 1.065)
PANX2	-0.16	0.05	1.25E-03	1.00E+00	0.000	2.903	0.852 (0.869; 1.073)

HSPG2	-0.167	0.052	1.29E-03	1.00E+00	0.000	2.889	0.846 (0.899; 1.139)
PARL	-0.167	0.053	1.52E-03	1.00E+00	0.000	2.818	0.846 (0.854; 1.055)
ZNF814	-0.157	0.05	1.72E-03	1.00E+00	0.000	2.764	0.855 (0.841; 1.039)
APOC4-APOC2	-0.206	0.066	1.75E-03	1.00E+00	0.000	2.757	0.814 (0.804; 0.99)
CRYBG3	-0.161	0.052	1.92E-03	1.00E+00	0.000	2.717	0.851 (0.881; 1.103)
C7	-0.177	0.057	2.01E-03	1.00E+00	0.000	2.697	0.838 (0.842; 1.047)
RASEF	-0.166	0.054	2.23E-03	1.00E+00	0.000	2.652	0.847 (0.905; 1.147)
ARID1B	-0.152	0.05	2.24E-03	1.00E+00	0.000	2.650	0.859 (0.872; 1.064)
RASA3	-0.16	0.053	2.38E-03	1.00E+00	0.000	2.623	0.852 (0.873; 1.09)
BOC	-0.144	0.048	2.63E-03	1.00E+00	0.000	2.580	0.866 (0.861; 1.078)
DTX4	-0.159	0.053	2.69E-03	1.00E+00	0.000	2.570	0.853 (0.88; 1.093)
APOA4	-0.168	0.056	2.75E-03	1.00E+00	0.000	2.561	0.845 (0.792; 0.971)
C4B	0.198	0.066	2.90E-03	1.00E+00	0.000	2.538	1.219 (0.82; 1.025)
SERPIND1	0.171	0.058	3.26E-03	1.00E+00	0.000	2.487	1.186 (0.864; 1.063)
IGHV3OR16-12	-0.156	0.053	3.27E-03	1.00E+00	0.000	2.485	0.856 (0.798; 0.966)
MAP1B	-0.15	0.051	3.56E-03	1.00E+00	0.000	2.449	0.861 (0.806; 1.001)
SART3	-0.144	0.05	3.87E-03	1.00E+00	0.000	2.412	0.866 (0.887; 1.106)
APOC3	-0.168	0.059	4.02E-03	1.00E+00	0.000	2.396	0.845 (0.818; 0.981)
FXR1	-0.164	0.057	4.21E-03	1.00E+00	0.000	2.376	0.849 (0.844; 1.039)
JCAD	-0.132	0.046	4.23E-03	1.00E+00	0.000	2.374	0.876 (0.875; 1.071)
GPX3	-0.163	0.057	4.23E-03	1.00E+00	0.000	2.374	0.85 (0.864; 1.075)
C6orf118	-0.149	0.052	4.50E-03	1.00E+00	0.000	2.347	0.862 (0.851; 1.051)
FSTL4	-0.14	0.049	4.56E-03	1.00E+00	0.000	2.341	0.869 (0.896; 1.113)
SERPINB13	-0.144	0.051	4.68E-03	1.00E+00	0.000	2.330	0.866 (0.783; 0.965)
STAB1	-0.155	0.055	4.71E-03	1.00E+00	0.000	2.327	0.856 (0.807; 0.985)
GPC1	-0.141	0.05	4.91E-03	1.00E+00	0.000	2.309	0.868 (0.856; 1.088)
ZNF75D	-0.142	0.051	5.62E-03	1.00E+00	0.000	2.250	0.868 (0.813; 1.003)

RBP4	-0.161	0.058	5.63E-03	1.00E+00	0.000	2.249	0.851 (0.878; 1.085)
DNAH14	-0.139	0.051	5.77E-03	1.00E+00	0.000	2.239	0.87 (0.834; 1.032)
ATP6V0A2	-0.155	0.057	6.19E-03	1.00E+00	0.000	2.208	0.856 (0.826; 1.012)
HSPA13	-0.137	0.05	6.45E-03	1.00E+00	0.000	2.190	0.872 (0.835; 1.022)
PARP14	-0.126	0.046	6.63E-03	1.00E+00	0.000	2.178	0.882 (0.904; 1.134)
RBM6	-0.13	0.048	6.69E-03	1.00E+00	0.000	2.175	0.878 (0.858; 1.059)
ITIH2	-0.151	0.056	6.85E-03	1.00E+00	0.000	2.164	0.86 (0.848; 1.035)
CBFA2T2	-0.131	0.048	6.89E-03	1.00E+00	0.000	2.162	0.877 (0.84; 1.053)
CPSF6	-0.143	0.053	6.93E-03	1.00E+00	0.000	2.159	0.867 (0.864; 1.056)
MTMR2	-0.119	0.044	7.17E-03	1.00E+00	0.000	2.144	0.888 (0.897; 1.129)
TSC22D3	-0.142	0.053	7.40E-03	1.00E+00	0.000	2.131	0.868 (0.859; 1.04)
REV1	-0.146	0.055	7.45E-03	1.00E+00	0.000	2.128	0.864 (0.826; 0.999)
C3	0.159	0.06	7.48E-03	1.00E+00	0.000	2.126	1.172 (0.855; 1.037)
HPR	-0.153	0.057	7.54E-03	1.00E+00	0.000	2.123	0.858 (0.874; 1.086)
KIF21B	-0.142	0.053	7.80E-03	1.00E+00	0.000	2.108	0.868 (0.835; 1.021)
SREBF1	-0.136	0.051	8.14E-03	1.00E+00	0.000	2.089	0.873 (0.637; 0.812)
TTR	-0.151	0.058	8.78E-03	1.00E+00	0.000	2.057	0.86 (0.864; 1.075)
TLN1	-0.137	0.052	8.88E-03	1.00E+00	0.000	2.052	0.872 (0.885; 1.123)
FAM210A	-0.136	0.052	9.11E-03	1.00E+00	0.000	2.040	0.873 (0.796; 1.006)
TSC2	-0.119	0.046	9.12E-03	1.00E+00	0.000	2.040	0.888 (0.881; 1.082)
SULT1C3	-0.141	0.054	9.28E-03	1.00E+00	0.000	2.032	0.868 (0.815; 1.017)
SPATA31H1	-0.188	0.072	9.28E-03	1.00E+00	0.000	2.032	0.829 (0.892; 1.13)
ZNF608	-0.134	0.052	9.40E-03	1.00E+00	0.000	2.027	0.875 (0.848; 1.046)
C4A	0.149	0.057	9.49E-03	1.00E+00	0.000	2.023	1.161 (0.807; 0.978)
IGFALS	-0.155	0.06	9.53E-03	1.00E+00	0.000	2.021	0.856 (0.924; 1.152)
TRAJ56	-0.131	0.051	9.64E-03	1.00E+00	0.000	2.016	0.877 (1.008; 1.26)
LIFR	-0.134	0.052	9.77E-03	1.00E+00	0.000	2.010	0.875 (0.767; 0.96)

WASH4P	-0.12	0.047	9.85E-03	1.00E+00	0.000	2.007	0.887 (0.942; 1.223)
MYH13	-0.138	0.054	1.02E-02	1.00E+00	0.000	1.991	0.871 (0.897; 1.099)
PRPF4B	-0.122	0.048	1.03E-02	1.00E+00	0.000	1.987	0.885 (0.869; 1.089)
SMG1	-0.128	0.05	1.11E-02	1.00E+00	0.000	1.955	0.88 (0.885; 1.109)
GDF5	-0.132	0.052	1.11E-02	1.00E+00	0.000	1.955	0.876 (0.836; 1.011)
SIPA1L1	-0.132	0.052	1.12E-02	1.00E+00	0.000	1.951	0.876 (0.724; 0.903)
PLEKHH1	-0.128	0.051	1.12E-02	1.00E+00	0.000	1.951	0.88 (0.852; 1.062)
NUMA1	-0.128	0.051	1.13E-02	1.00E+00	0.000	1.947	0.88 (0.897; 1.123)
NIM1K	-0.14	0.055	1.15E-02	1.00E+00	0.000	1.939	0.869 (0.76; 0.985)
CENPF	-0.129	0.051	1.18E-02	1.00E+00	0.000	1.928	0.879 (1.206; 1.531)
ENOX2	-0.129	0.051	1.21E-02	1.00E+00	0.000	1.917	0.879 (1.044; 1.319)
IGKV2D-29	-0.133	0.053	1.22E-02	1.00E+00	0.000	1.914	0.875 (0.884; 1.109)
ALB	-0.143	0.057	1.23E-02	1.00E+00	0.000	1.910	0.867 (0.834; 1.03)
AMPD2	-0.127	0.051	1.24E-02	1.00E+00	0.000	1.907	0.881 (0.88; 1.089)
LZTS3	-0.113	0.046	1.35E-02	1.00E+00	0.000	1.870	0.893 (0.861; 1.066)
MAP3K1	-0.126	0.051	1.36E-02	1.00E+00	0.000	1.866	0.882 (0.824; 1.039)
SAMD4B	-0.13	0.053	1.40E-02	1.00E+00	0.000	1.854	0.878 (0.908; 1.128)
ARMCX4	-0.125	0.051	1.41E-02	1.00E+00	0.000	1.851	0.882 (0.859; 1.078)
C9	0.149	0.061	1.43E-02	1.00E+00	0.000	1.845	1.161 (0.856; 1.074)
CADPS2	-0.132	0.054	1.44E-02	1.00E+00	0.000	1.842	0.876 (0.836; 1.033)
AMDHD2	-0.13	0.053	1.45E-02	1.00E+00	0.000	1.839	0.878 (0.836; 1.009)
F13A1	-0.119	0.049	1.46E-02	1.00E+00	0.000	1.836	0.888 (0.902; 1.142)
DMPK	-0.122	0.05	1.50E-02	1.00E+00	0.000	1.824	0.885 (0.86; 1.064)
DSP	-0.117	0.049	1.67E-02	1.00E+00	0.000	1.777	0.89 (0.834; 1.036)
FLG	-0.138	0.058	1.69E-02	1.00E+00	0.000	1.772	0.871 (0.859; 1.072)
DYNC2I1	-0.122	0.052	1.76E-02	1.00E+00	0.000	1.754	0.885 (0.874; 1.087)
CAPZB	-0.124	0.052	1.76E-02	1.00E+00	0.000	1.754	0.883 (0.834; 1.03)

OBSCN	-0.125	0.053	1.81E-02	1.00E+00	0.000	1.742	0.882 (0.881; 1.104)
MYLK	-0.114	0.048	1.85E-02	1.00E+00	0.000	1.733	0.892 (0.876; 1.091)
NEB	-0.134	0.057	1.87E-02	1.00E+00	0.000	1.728	0.875 (0.846; 1.061)
TINF2	-0.118	0.05	1.88E-02	1.00E+00	0.000	1.726	0.889 (0.804; 0.993)
PLXNA2	-0.118	0.05	1.92E-02	1.00E+00	0.000	1.717	0.889 (0.841; 1.037)
C2CD3	-0.147	0.063	1.92E-02	1.00E+00	0.000	1.717	0.863 (0.844; 1.051)
IGHV5-51	-0.11	0.047	1.92E-02	1.00E+00	0.000	1.717	0.896 (0.878; 1.084)
TNRC6A	-0.122	0.052	1.99E-02	1.00E+00	0.000	1.701	0.885 (0.901; 1.119)
ITGB8	-0.125	0.054	1.99E-02	1.00E+00	0.000	1.701	0.882 (0.833; 1.023)
APC	-0.119	0.051	2.03E-02	1.00E+00	0.000	1.693	0.888 (0.838; 1.042)
PMS2	-0.13	0.056	2.04E-02	1.00E+00	0.000	1.690	0.878 (0.881; 1.096)
APOC1	-0.134	0.058	2.08E-02	1.00E+00	0.000	1.682	0.875 (0.914; 1.13)
IRAG1	-0.13	0.056	2.09E-02	1.00E+00	0.000	1.680	0.878 (0.909; 1.134)
FBXO30	-0.115	0.05	2.10E-02	1.00E+00	0.000	1.678	0.891 (0.842; 1.14)
PSD	-0.114	0.05	2.28E-02	1.00E+00	0.000	1.642	0.892 (0.841; 1.037)
PITPNM2	-0.123	0.054	2.32E-02	1.00E+00	0.000	1.635	0.884 (0.877; 1.091)
GPD2	-0.131	0.058	2.33E-02	1.00E+00	0.000	1.633	0.877 (0.895; 1.082)
COL4A3	-0.108	0.048	2.41E-02	1.00E+00	0.000	1.618	0.898 (0.902; 1.228)
XK	-0.105	0.047	2.42E-02	1.00E+00	0.000	1.616	0.9 (0.837; 1.052)
ITPR1	-0.113	0.05	2.42E-02	1.00E+00	0.000	1.616	0.893 (0.86; 1.101)
GC	-0.132	0.059	2.43E-02	1.00E+00	0.000	1.614	0.876 (0.753; 0.947)
LIMA1	-0.118	0.053	2.54E-02	1.00E+00	0.000	1.595	0.889 (0.965; 1.225)
JMJD8	-0.103	0.047	2.75E-02	1.00E+00	0.000	1.561	0.902 (0.998; 1.275)
CFAP97	-0.12	0.054	2.76E-02	1.00E+00	0.000	1.559	0.887 (0.94; 1.188)
EMX1	-0.123	0.056	2.81E-02	1.00E+00	0.000	1.551	0.884 (1.444; 1.839)
KHNYN	-0.115	0.053	2.91E-02	1.00E+00	0.000	1.536	0.891 (1.134; 1.456)
APLF	-0.102	0.047	2.91E-02	1.00E+00	0.000	1.536	0.903 (0.913; 1.146)

AGT	-0.144	0.066	2.97E-02	1.00E+00	0.000	1.527	0.866 (0.906; 1.13)
EP400	-0.101	0.047	3.02E-02	1.00E+00	0.000	1.520	0.904 (0.891; 1.124)
CARS2	-0.109	0.05	3.07E-02	1.00E+00	0.000	1.513	0.897 (1.031; 1.308)
NSUN2	-0.1	0.047	3.22E-02	1.00E+00	0.000	1.492	0.905 (0.812; 1.027)
CIRBP	-0.111	0.052	3.26E-02	1.00E+00	0.000	1.487	0.895 (0.891; 1.128)
PDIA6	-0.103	0.049	3.30E-02	1.00E+00	0.000	1.481	0.902 (0.983; 1.183)
CDK13	-0.108	0.051	3.33E-02	1.00E+00	0.000	1.478	0.898 (0.831; 1.035)
IGHV1-46	-0.112	0.053	3.34E-02	1.00E+00	0.000	1.476	0.894 (0.902; 1.128)
DNAH8	-0.108	0.051	3.37E-02	1.00E+00	0.000	1.472	0.898 (0.874; 1.088)
MAGEB17	-0.102	0.048	3.48E-02	1.00E+00	0.000	1.458	0.903 (0.768; 0.963)
IGKV3-20.2	-0.113	0.054	3.49E-02	1.00E+00	0.000	1.457	0.893 (0.775; 0.969)
AHNAK2	-0.115	0.054	3.51E-02	1.00E+00	0.000	1.455	0.891 (0.781; 0.983)
IGHV2-26	-0.127	0.061	3.59E-02	1.00E+00	0.000	1.445	0.881 (0.87; 1.091)
KIF15	-0.102	0.049	3.62E-02	1.00E+00	0.000	1.441	0.903 (0.82; 1.023)
NOL8	-0.11	0.053	3.72E-02	1.00E+00	0.000	1.429	0.896 (0.945; 1.183)
PLEKHG2	-0.097	0.046	3.72E-02	1.00E+00	0.000	1.429	0.908 (0.885; 1.088)
SPOCD1	-0.114	0.055	3.72E-02	1.00E+00	0.000	1.429	0.892 (0.99; 1.245)
HP	0.118	0.057	3.73E-02	1.00E+00	0.000	1.428	1.125 (0.962; 1.215)
IGHV1-24	-0.107	0.051	3.78E-02	1.00E+00	0.000	1.423	0.899 (0.795; 1.016)
BEND5	-0.088	0.043	3.79E-02	1.00E+00	0.000	1.421	0.916 (0.849; 1.054)
UBE4B	-0.099	0.048	3.91E-02	1.00E+00	0.000	1.408	0.906 (0.89; 1.118)
SPTBN5	-0.108	0.053	3.92E-02	1.00E+00	0.000	1.407	0.898 (0.888; 1.104)
MED23	-0.102	0.05	3.93E-02	1.00E+00	0.000	1.406	0.903 (0.928; 1.203)
TCP11	-0.119	0.058	3.95E-02	1.00E+00	0.000	1.403	0.888 (0.867; 1.106)
CCDC88A	-0.114	0.055	4.01E-02	1.00E+00	0.000	1.397	0.892 (0.848; 1.059)
IGKC	-0.115	0.056	4.02E-02	1.00E+00	0.000	1.396	0.891 (0.872; 1.067)
EWSR1	-0.11	0.054	4.09E-02	1.00E+00	0.000	1.388	0.896 (0.823; 1.014)

PDHA1	-0.103	0.051	4.25E-02	1.00E+00	0.000	1.372	0.902 (0.845; 1.048)
CD14	0.149	0.073	4.28E-02	1.00E+00	0.000	1.369	1.161 (0.866; 1.084)
IGHV3-30.1	-0.117	0.058	4.29E-02	1.00E+00	0.000	1.368	0.89 (0.59; 0.755)
HECTD4	-0.106	0.053	4.32E-02	1.00E+00	0.000	1.365	0.899 (0.857; 1.123)
FKBP1A	-0.114	0.057	4.51E-02	1.00E+00	0.000	1.346	0.892 (0.813; 1.019)
EXOC6B	-0.101	0.051	4.58E-02	1.00E+00	0.000	1.339	0.904 (0.818; 1.024)
ABCF1	-0.097	0.049	4.62E-02	1.00E+00	0.000	1.335	0.908 (0.931; 1.18)
STK38L	-0.083	0.042	4.63E-02	1.00E+00	0.000	1.334	0.92 (1.059; 1.331)
FRMPD4	-0.098	0.049	4.66E-02	1.00E+00	0.000	1.332	0.907 (0.868; 1.094)
KLHL40	-0.1	0.05	4.72E-02	1.00E+00	0.000	1.326	0.905 (0.949; 1.175)
RBL1	-0.108	0.055	4.77E-02	1.00E+00	0.000	1.321	0.898 (0.844; 1.035)
ARHGAP42	-0.113	0.057	4.78E-02	1.00E+00	0.000	1.321	0.893 (0.812; 1.023)
VPS11	-0.1	0.051	4.96E-02	1.00E+00	0.000	1.305	0.905 (1.133; 1.492)
LRP5	-0.105	0.053	4.97E-02	1.00E+00	0.000	1.304	0.9 (0.757; 0.943)
C4orf54	-0.115	0.059	5.13E-02	1.00E+00	0.000	1.290	0.891 (0.858; 1.053)
CD5L	-0.107	0.055	5.22E-02	1.00E+00	0.000	1.282	0.899 (0.977; 1.223)
CDH5	-0.111	0.057	5.24E-02	1.00E+00	0.000	1.281	0.895 (0.945; 1.191)
NOSTRIN	-0.103	0.053	5.27E-02	1.00E+00	0.000	1.278	0.902 (0.998; 1.289)
SERPING1.1	-0.125	0.065	5.28E-02	1.00E+00	0.000	1.277	0.882 (0.94; 1.165)
FOXI1	-0.105	0.054	5.31E-02	1.00E+00	0.000	1.275	0.9 (0.883; 1.103)
SLC27A5.1	-0.108	0.056	5.35E-02	1.00E+00	0.000	1.272	0.898 (0.682; 0.876)
ZMYM6	-0.114	0.059	5.47E-02	1.00E+00	0.000	1.262	0.892 (0.817; 1.036)
KRT28	-0.097	0.05	5.57E-02	1.00E+00	0.000	1.254	0.908 (0.818; 0.998)
THBS2	-0.092	0.048	5.60E-02	1.00E+00	0.000	1.252	0.912 (1.015; 1.354)
GTPBP4	-0.101	0.053	5.62E-02	1.00E+00	0.000	1.250	0.904 (1.225; 1.555)
PLEC	-0.107	0.056	5.65E-02	1.00E+00	0.000	1.248	0.899 (0.93; 1.158)
GPRIN1	0.124	0.065	5.67E-02	1.00E+00	0.000	1.246	1.132 (0.851; 1.085)

C8G	0.124	0.066	5.81E-02	1.00E+00	0.000	1.236	1.132 (0.955; 1.199)
FUS	-0.103	0.055	5.85E-02	1.00E+00	0.000	1.233	0.902 (1.038; 1.3)
CPE	-0.105	0.056	5.89E-02	1.00E+00	0.000	1.230	0.9 (1.071; 1.39)
DLG3	-0.103	0.054	5.92E-02	1.00E+00	0.000	1.228	0.902 (0.841; 1.061)
SACS	-0.099	0.052	5.95E-02	1.00E+00	0.000	1.225	0.906 (0.99; 1.253)
MID2	-0.087	0.046	6.01E-02	1.00E+00	0.000	1.221	0.917 (0.748; 0.937)
AKT3	-0.086	0.046	6.05E-02	1.00E+00	0.000	1.218	0.918 (0.818; 1.017)
TMED4	-0.102	0.054	6.10E-02	1.00E+00	0.000	1.215	0.903 (0.817; 1.031)
PLB1	-0.098	0.052	6.17E-02	1.00E+00	0.000	1.210	0.907 (0.9; 1.094)
FGB	0.117	0.063	6.20E-02	1.00E+00	0.000	1.208	1.124 (0.83; 1.012)
CACNB3	-0.09	0.048	6.23E-02	1.00E+00	0.000	1.206	0.914 (0.906; 1.172)
FAN1	-0.101	0.054	6.28E-02	1.00E+00	0.000	1.202	0.904 (0.805; 1.026)
RNF17	-0.089	0.048	6.32E-02	1.00E+00	0.000	1.199	0.915 (0.843; 1.046)
KIAA0586	-0.094	0.051	6.35E-02	1.00E+00	0.000	1.197	0.91 (0.76; 1.013)
ADAMTS20	-0.102	0.055	6.41E-02	1.00E+00	0.000	1.193	0.903 (0.862; 1.074)
NKD2	-0.094	0.051	6.46E-02	1.00E+00	0.000	1.190	0.91 (0.853; 1.053)
LIF	-0.097	0.052	6.48E-02	1.00E+00	0.000	1.188	0.908 (0.949; 1.2)
CFHR2	-0.104	0.057	6.66E-02	1.00E+00	0.000	1.177	0.901 (0.922; 1.14)
ITPRIPL1	-0.097	0.053	6.67E-02	1.00E+00	0.000	1.176	0.908 (0.92; 1.131)
IGKV1D-33.5	-0.094	0.051	6.73E-02	1.00E+00	0.000	1.172	0.91 (0.821; 1.01)
SERPINA4	-0.108	0.059	6.75E-02	1.00E+00	0.000	1.171	0.898 (0.82; 1.035)
TMEM131L	-0.088	0.048	6.82E-02	1.00E+00	0.000	1.166	0.916 (0.811; 1.017)
ITIH1	-0.101	0.056	6.94E-02	1.00E+00	0.000	1.159	0.904 (0.809; 0.981)
MACF1	-0.09	0.05	7.00E-02	1.00E+00	0.000	1.155	0.914 (0.892; 1.129)
SKOR1	-0.1	0.055	7.06E-02	1.00E+00	0.000	1.151	0.905 (0.867; 1.064)
SELENOP	-0.097	0.054	7.10E-02	1.00E+00	0.000	1.149	0.908 (0.808; 1.006)
IGKV1D-33.3	-0.086	0.048	7.11E-02	1.00E+00	0.000	1.148	0.918 (0.911; 1.15)

PLPP7	-0.099	0.055	7.17E-02	1.00E+00	0.000	1.144	0.906 (0.816; 1.011)
SPTB	-0.09	0.05	7.20E-02	1.00E+00	0.000	1.143	0.914 (0.834; 1.021)
GIGYF1	-0.092	0.051	7.21E-02	1.00E+00	0.000	1.142	0.912 (0.872; 1.074)
IGFBP3	-0.098	0.055	7.30E-02	1.00E+00	0.000	1.137	0.907 (1.221; 2.114)
RYR1	-0.091	0.051	7.32E-02	1.00E+00	0.000	1.135	0.913 (0.882; 1.095)
CA1	-0.086	0.048	7.38E-02	1.00E+00	0.000	1.132	0.918 (0.84; 1.042)
C4BPA	0.104	0.058	7.40E-02	1.00E+00	0.000	1.131	1.11 (0.837; 1.054)
VWF	-0.093	0.052	7.46E-02	1.00E+00	0.000	1.127	0.911 (0.966; 1.211)
PRPF19	-0.095	0.053	7.54E-02	1.00E+00	0.000	1.123	0.909 (0.77; 0.959)
SNTB2	-0.102	0.058	7.70E-02	1.00E+00	0.000	1.114	0.903 (0.81; 1.008)
KPNB1	-0.09	0.051	7.71E-02	1.00E+00	0.000	1.113	0.914 (0.82; 1.036)
SAA2	0.106	0.06	7.75E-02	1.00E+00	0.000	1.111	1.112 (0.886; 1.133)
CCDC168	-0.093	0.053	7.87E-02	1.00E+00	0.000	1.104	0.911 (0.782; 0.978)
TNRC6B	-0.091	0.052	8.13E-02	1.00E+00	0.000	1.090	0.913 (0.778; 0.977)
TSHZ3	-0.095	0.055	8.16E-02	1.00E+00	0.000	1.088	0.909 (0.867; 1.085)
F5	-0.125	0.072	8.16E-02	1.00E+00	0.000	1.088	0.882 (0.884; 1.088)
TSPYL1	-0.089	0.051	8.21E-02	1.00E+00	0.000	1.086	0.915 (0.827; 1.01)
CEP135	0.115	0.066	8.44E-02	1.00E+00	0.000	1.074	1.122 (0.759; 0.949)
NAGK	-0.091	0.053	8.55E-02	1.00E+00	0.000	1.068	0.913 (0.91; 1.165)
IL1RAP	-0.082	0.048	8.64E-02	1.00E+00	0.000	1.063	0.921 (0.859; 1.05)
GPANK1	-0.096	0.056	8.69E-02	1.00E+00	0.000	1.061	0.908 (0.892; 1.12)
HSPD1	-0.094	0.055	8.75E-02	1.00E+00	0.000	1.058	0.91 (0.863; 1.097)
EIF4G3	-0.089	0.052	8.79E-02	1.00E+00	0.000	1.056	0.915 (0.844; 1.036)
LCOR	-0.09	0.053	8.91E-02	1.00E+00	0.000	1.050	0.914 (0.846; 1.122)
IGKV1-39.2	-0.089	0.052	8.92E-02	1.00E+00	0.000	1.050	0.915 (0.803; 0.984)
CNTNAP5	-0.084	0.049	8.92E-02	1.00E+00	0.000	1.050	0.919 (0.73; 0.908)
APOB	-0.107	0.063	8.92E-02	1.00E+00	0.000	1.050	0.899 (0.82; 1.027)

CTSW	-0.075	0.044	8.93E-02	1.00E+00	0.000	1.049	0.928 (0.795; 0.982)
MS4A14	-0.09	0.053	8.98E-02	1.00E+00	0.000	1.047	0.914 (0.84; 1.022)
MUC2	-0.09	0.053	9.08E-02	1.00E+00	0.000	1.042	0.914 (0.848; 1.058)
IGLL1	-0.097	0.058	9.13E-02	1.00E+00	0.000	1.040	0.908 (0.905; 1.154)
SORBS1	-0.089	0.053	9.46E-02	1.00E+00	0.000	1.024	0.915 (0.891; 1.119)
CCDC27	-0.094	0.057	9.49E-02	1.00E+00	0.000	1.023	0.91 (0.887; 1.103)
SAMD1	-0.087	0.052	9.51E-02	1.00E+00	0.000	1.022	0.917 (0.799; 1.008)
SRP54	-0.08	0.048	9.70E-02	1.00E+00	0.000	1.013	0.923 (0.862; 1.056)
MCPH1	-0.082	0.05	9.73E-02	1.00E+00	0.000	1.012	0.921 (0.825; 1.022)
ZFPM1	-0.086	0.052	9.76E-02	1.00E+00	0.000	1.011	0.918 (0.843; 1.041)
PCCB	-0.094	0.057	9.77E-02	1.00E+00	0.000	1.010	0.91 (0.802; 1.006)
KIF26B	-0.088	0.053	9.84E-02	1.00E+00	0.000	1.007	0.916 (0.967; 1.27)
FBXL5	-0.081	0.049	9.94E-02	1.00E+00	0.000	1.003	0.922 (0.789; 0.961)
IGKV3D-20	-0.088	0.054	1.00E-01	1.00E+00	0.000	1.000	0.916 (0.832; 1.005)
SMC2	-0.083	0.051	1.01E-01	1.00E+00	0.000	0.996	0.92 (0.892; 1.103)
EPX	-0.1	0.061	1.01E-01	1.00E+00	0.000	0.996	0.905 (0.811; 1.005)
ACAP3	-0.09	0.055	1.02E-01	1.00E+00	0.000	0.991	0.914 (0.761; 0.963)
F13B	-0.093	0.057	1.03E-01	1.00E+00	0.000	0.987	0.911 (1.092; 1.391)
PHLDB1	-0.09	0.055	1.03E-01	1.00E+00	0.000	0.987	0.914 (0.79; 0.968)
TEX2	-0.09	0.056	1.04E-01	1.00E+00	0.000	0.983	0.914 (0.866; 1.091)
MUC19	-0.088	0.054	1.05E-01	1.00E+00	0.000	0.979	0.916 (0.893; 1.081)
AXL	-0.088	0.054	1.05E-01	1.00E+00	0.000	0.979	0.916 (0.826; 1.027)
JARID2	-0.075	0.046	1.08E-01	1.00E+00	0.000	0.967	0.928 (0.791; 0.971)
MNX1	-0.08	0.05	1.08E-01	1.00E+00	0.000	0.967	0.923 (0.86; 1.067)
FN1	0.076	0.047	1.09E-01	1.00E+00	0.000	0.963	1.079 (0.793; 0.973)
PDCD2L	-0.079	0.049	1.09E-01	1.00E+00	0.000	0.963	0.924 (0.845; 1.037)
FGD4	-0.07	0.044	1.10E-01	1.00E+00	0.000	0.959	0.932 (0.797; 1.027)

IGKV3-20.5	-0.082	0.051	1.11E-01	1.00E+00	0.000	0.955	0.921 (0.785; 0.985)
PRDM14	-0.083	0.052	1.11E-01	1.00E+00	0.000	0.955	0.92 (1.163; 1.467)
MSN	-0.079	0.05	1.12E-01	1.00E+00	0.000	0.951	0.924 (0.887; 1.093)
KHDRBS3	-0.081	0.052	1.14E-01	1.00E+00	0.000	0.943	0.922 (0.944; 1.171)
COL5A3	-0.09	0.057	1.14E-01	1.00E+00	0.000	0.943	0.914 (0.777; 0.952)
SLC23A2	-0.084	0.053	1.15E-01	1.00E+00	0.000	0.939	0.919 (0.893; 1.108)
EMILIN1	-0.082	0.052	1.16E-01	1.00E+00	0.000	0.936	0.921 (0.795; 0.979)
RFLNB	-0.08	0.051	1.16E-01	1.00E+00	0.000	0.936	0.923 (0.878; 1.08)
GSN	-0.093	0.059	1.16E-01	1.00E+00	0.000	0.936	0.911 (0.863; 1.071)
BTD	-0.1	0.064	1.16E-01	1.00E+00	0.000	0.936	0.905 (0.791; 0.964)
TTN	-0.087	0.055	1.17E-01	1.00E+00	0.000	0.932	0.917 (0.856; 1.064)
POSTN	-0.07	0.045	1.17E-01	1.00E+00	0.000	0.932	0.932 (0.794; 0.974)
PTPRJ	-0.077	0.049	1.18E-01	1.00E+00	0.000	0.928	0.926 (0.852; 1.06)
DNAH3	-0.087	0.056	1.18E-01	1.00E+00	0.000	0.928	0.917 (0.811; 0.972)
TF	-0.088	0.056	1.18E-01	1.00E+00	0.000	0.928	0.916 (0.817; 1.01)
LRRC10B	-0.08	0.052	1.19E-01	1.00E+00	0.000	0.924	0.923 (0.847; 1.029)
ARHGAP6	-0.089	0.057	1.20E-01	1.00E+00	0.000	0.921	0.915 (0.846; 1.029)
CLEC3B	-0.089	0.057	1.23E-01	1.00E+00	0.000	0.910	0.915 (0.853; 1.063)
PROS1	0.088	0.057	1.23E-01	1.00E+00	0.000	0.910	1.092 (0.898; 1.178)
CABP1	-0.086	0.056	1.25E-01	1.00E+00	0.000	0.903	0.918 (0.857; 1.044)
INSL4	-0.082	0.053	1.25E-01	1.00E+00	0.000	0.903	0.921 (0.758; 0.95)
IGLV3-25	-0.08	0.052	1.25E-01	1.00E+00	0.000	0.903	0.923 (0.921; 1.176)
PTGDS	-0.085	0.055	1.26E-01	1.00E+00	0.000	0.900	0.919 (0.822; 0.991)
APOH	-0.092	0.06	1.26E-01	1.00E+00	0.000	0.900	0.912 (0.786; 0.962)
PHF10	0.089	0.058	1.26E-01	1.00E+00	0.000	0.900	1.093 (0.963; 1.236)
PSME1	-0.083	0.055	1.27E-01	1.00E+00	0.000	0.896	0.92 (0.899; 1.124)
LRP1B	-0.075	0.05	1.28E-01	1.00E+00	0.000	0.893	0.928 (0.898; 1.09)

RHBDF2	-0.079	0.052	1.29E-01	1.00E+00	0.000	0.889	0.924 (0.883; 1.097)
DECR1	-0.081	0.054	1.29E-01	1.00E+00	0.000	0.889	0.922 (0.787; 0.984)
NCOR1	-0.08	0.053	1.30E-01	1.00E+00	0.000	0.886	0.923 (0.833; 1.008)
CCAR1	-0.082	0.054	1.30E-01	1.00E+00	0.000	0.886	0.921 (0.853; 1.049)
ABI3BP	-0.083	0.055	1.33E-01	1.00E+00	0.000	0.876	0.92 (0.872; 1.098)
KCNH2	-0.072	0.048	1.33E-01	1.00E+00	0.000	0.876	0.931 (0.818; 1.04)
CROCC	-0.071	0.047	1.34E-01	1.00E+00	0.000	0.873	0.931 (0.847; 1.044)
MYO9A	-0.077	0.051	1.35E-01	1.00E+00	0.000	0.870	0.926 (0.853; 1.018)
PRMT9	-0.086	0.058	1.35E-01	1.00E+00	0.000	0.870	0.918 (0.912; 1.154)
KRT18	-0.072	0.049	1.36E-01	1.00E+00	0.000	0.866	0.931 (0.813; 1.011)
OSGIN1	-0.079	0.053	1.36E-01	1.00E+00	0.000	0.866	0.924 (0.921; 1.218)
SPECC1	-0.082	0.055	1.37E-01	1.00E+00	0.000	0.863	0.921 (0.843; 1.02)
ATP2B1	-0.087	0.059	1.37E-01	1.00E+00	0.000	0.863	0.917 (0.94; 1.2)
WNK4	-0.075	0.05	1.38E-01	1.00E+00	0.000	0.860	0.928 (0.918; 1.125)
IGLV1-36	-0.078	0.053	1.39E-01	1.00E+00	0.000	0.857	0.925 (0.858; 1.068)
HYI	-0.076	0.052	1.41E-01	1.00E+00	0.000	0.851	0.927 (0.925; 1.161)
DCTN1	-0.071	0.049	1.42E-01	1.00E+00	0.000	0.848	0.931 (0.863; 1.172)
C1R	-0.077	0.053	1.43E-01	1.00E+00	0.000	0.845	0.926 (0.829; 1.131)
TAOK2	-0.073	0.05	1.43E-01	1.00E+00	0.000	0.845	0.93 (0.873; 1.083)
HNMT	-0.072	0.049	1.45E-01	1.00E+00	0.000	0.839	0.931 (0.799; 0.966)
CLU	-0.086	0.059	1.46E-01	1.00E+00	0.000	0.836	0.918 (0.843; 1.062)
AFG3L2	-0.078	0.054	1.46E-01	1.00E+00	0.000	0.836	0.925 (0.849; 1.051)
CPN1	-0.085	0.059	1.49E-01	1.00E+00	0.000	0.827	0.919 (0.848; 1.043)
CHD6	-0.078	0.054	1.50E-01	1.00E+00	0.000	0.824	0.925 (0.894; 1.132)
AFAP1L2	-0.075	0.052	1.50E-01	1.00E+00	0.000	0.824	0.928 (0.825; 1.011)
RIT1	-0.08	0.056	1.51E-01	1.00E+00	0.000	0.821	0.923 (0.899; 1.118)
GDI2	-0.071	0.05	1.52E-01	1.00E+00	0.000	0.818	0.931 (0.859; 1.062)

NUFIP2	-0.069	0.048	1.52E-01	1.00E+00	0.000	0.818	0.933 (0.876; 1.06)
KNG1	-0.077	0.054	1.52E-01	1.00E+00	0.000	0.818	0.926 (0.872; 1.074)
CALB2	-0.072	0.05	1.52E-01	1.00E+00	0.000	0.818	0.931 (0.858; 1.074)
FAT4	-0.082	0.057	1.52E-01	1.00E+00	0.000	0.818	0.921 (0.915; 1.138)
FRMD1	-0.069	0.048	1.53E-01	1.00E+00	0.000	0.815	0.933 (0.764; 0.937)
BOD1L1	-0.067	0.047	1.53E-01	1.00E+00	0.000	0.815	0.935 (0.854; 1.041)
IGKV2D-28	-0.076	0.053	1.54E-01	1.00E+00	0.000	0.812	0.927 (0.874; 1.07)
TFRC	-0.08	0.057	1.56E-01	1.00E+00	0.000	0.807	0.923 (0.882; 1.104)
ZNF766	-0.079	0.056	1.58E-01	1.00E+00	0.000	0.801	0.924 (0.834; 1.04)
PGLYRP2	-0.083	0.059	1.58E-01	1.00E+00	0.000	0.801	0.92 (0.797; 0.976)
DDX31	-0.072	0.051	1.59E-01	1.00E+00	0.000	0.799	0.931 (0.806; 0.996)
LPA	-0.085	0.061	1.59E-01	1.00E+00	0.000	0.799	0.919 (0.817; 0.988)
KLC4	-0.069	0.049	1.59E-01	1.00E+00	0.000	0.799	0.933 (0.902; 1.117)
HEXD	-0.066	0.047	1.60E-01	1.00E+00	0.000	0.796	0.936 (0.845; 1.045)
HERC4	-0.074	0.053	1.62E-01	1.00E+00	0.000	0.790	0.929 (0.922; 1.148)
ANKRD65	-0.07	0.05	1.63E-01	1.00E+00	0.000	0.788	0.932 (0.825; 1.017)
IDH1	-0.07	0.051	1.63E-01	1.00E+00	0.000	0.788	0.932 (0.857; 1.055)
SEMA6D	-0.074	0.053	1.64E-01	1.00E+00	0.000	0.785	0.929 (0.894; 1.164)
RSL24D1	-0.069	0.05	1.66E-01	1.00E+00	0.000	0.780	0.933 (0.864; 1.085)
FBF1	-0.076	0.055	1.67E-01	1.00E+00	0.000	0.777	0.927 (0.845; 1.062)
BBOF1	-0.07	0.051	1.71E-01	1.00E+00	0.000	0.767	0.932 (0.83; 1.031)
KIF5B	0.094	0.069	1.72E-01	1.00E+00	0.000	0.764	1.099 (0.853; 1.058)
IGKV1D-33.2	-0.074	0.054	1.72E-01	1.00E+00	0.000	0.764	0.929 (0.912; 1.138)
FGA	0.083	0.061	1.73E-01	1.00E+00	0.000	0.762	1.087 (1.299; 1.77)
ITPKA	-0.071	0.052	1.74E-01	1.00E+00	0.000	0.759	0.931 (0.886; 1.105)
LUM	0.087	0.064	1.74E-01	1.00E+00	0.000	0.759	1.091 (0.826; 0.997)
AMBP	-0.076	0.056	1.76E-01	1.00E+00	0.000	0.754	0.927 (0.802; 0.979)

ORM2	0.078	0.058	1.76E-01	1.00E+00	0.000	0.754	1.081 (0.88; 1.105)
APOC4	-0.082	0.061	1.76E-01	1.00E+00	0.000	0.754	0.921 (0.886; 1.123)
IGKV1-5	-0.08	0.059	1.77E-01	1.00E+00	0.000	0.752	0.923 (0.787; 0.962)
MYH7B	-0.065	0.048	1.77E-01	1.00E+00	0.000	0.752	0.937 (0.85; 1.028)
SPTBN1	-0.075	0.056	1.77E-01	1.00E+00	0.000	0.752	0.928 (0.849; 1.069)
CPB2	-0.082	0.061	1.79E-01	1.00E+00	0.000	0.747	0.921 (0.84; 1.02)
IGKV3-15	-0.071	0.053	1.80E-01	1.00E+00	0.000	0.745	0.931 (0.811; 1.006)
IGLV6-57	-0.067	0.05	1.80E-01	1.00E+00	0.000	0.745	0.935 (0.841; 1.049)
RINL	-0.068	0.051	1.81E-01	1.00E+00	0.000	0.742	0.934 (0.856; 1.035)
IGLV2-14	-0.072	0.054	1.81E-01	1.00E+00	0.000	0.742	0.931 (0.868; 1.067)
CIT	-0.074	0.056	1.82E-01	1.00E+00	0.000	0.740	0.929 (0.797; 0.975)
IGKV1-39	-0.073	0.055	1.86E-01	1.00E+00	0.000	0.730	0.93 (0.894; 1.123)
PCDHGA10	-0.067	0.051	1.87E-01	1.00E+00	0.000	0.728	0.935 (0.866; 1.068)
ACACA	-0.063	0.048	1.88E-01	1.00E+00	0.000	0.726	0.939 (0.809; 1.018)
DCC	-0.069	0.052	1.89E-01	1.00E+00	0.000	0.724	0.933 (0.806; 0.976)
GPC6	-0.074	0.056	1.89E-01	1.00E+00	0.000	0.724	0.929 (0.905; 1.138)
IGHV1-18	-0.066	0.051	1.90E-01	1.00E+00	0.000	0.721	0.936 (0.814; 0.971)
BRSK1	-0.071	0.055	1.94E-01	1.00E+00	0.000	0.712	0.931 (0.474; 0.719)
ATP10A	-0.069	0.053	1.94E-01	1.00E+00	0.000	0.712	0.933 (0.851; 1.059)
PLXND1	-0.076	0.059	1.94E-01	1.00E+00	0.000	0.712	0.927 (0.815; 0.996)
DLGAP4	-0.065	0.05	1.95E-01	1.00E+00	0.000	0.710	0.937 (0.724; 0.896)
VTN	0.077	0.06	1.95E-01	1.00E+00	0.000	0.710	1.08 (0.81; 0.993)
NUFIP1	-0.07	0.055	1.97E-01	1.00E+00	0.000	0.706	0.932 (0.847; 1.026)
KIF4A	-0.063	0.049	1.97E-01	1.00E+00	0.000	0.706	0.939 (0.893; 1.085)
IGHV3-7	-0.068	0.053	1.97E-01	1.00E+00	0.000	0.706	0.934 (0.909; 1.146)
SEPTIN7	-0.072	0.056	1.99E-01	1.00E+00	0.000	0.701	0.931 (0.834; 1.029)
SRP68	0.074	0.058	1.99E-01	1.00E+00	0.000	0.701	1.077 (0.81; 0.987)

TNIK	-0.067	0.052	2.01E-01	1.00E+00	0.000	0.697	0.935 (0.769; 0.947)
DOCK11	-0.078	0.061	2.03E-01	1.00E+00	0.000	0.693	0.925 (0.872; 1.082)
GNAZ	-0.069	0.054	2.03E-01	1.00E+00	0.000	0.693	0.933 (0.881; 1.089)
IGLV3-21	-0.07	0.055	2.07E-01	1.00E+00	0.000	0.684	0.932 (0.828; 1.013)
MAST4	-0.068	0.054	2.08E-01	1.00E+00	0.000	0.682	0.934 (0.797; 0.975)
GRK4	-0.067	0.054	2.09E-01	1.00E+00	0.000	0.680	0.935 (0.851; 1.067)
RAB21	-0.065	0.052	2.11E-01	1.00E+00	0.000	0.676	0.937 (0.826; 1.002)
HMCN1	-0.07	0.056	2.11E-01	1.00E+00	0.000	0.676	0.932 (0.785; 0.957)
FTO	-0.066	0.053	2.11E-01	1.00E+00	0.000	0.676	0.936 (0.857; 1.089)
SRRT	-0.067	0.054	2.13E-01	1.00E+00	0.000	0.672	0.935 (0.856; 1.057)
ATP1A2	-0.062	0.049	2.14E-01	1.00E+00	0.000	0.670	0.94 (0.856; 1.022)
PHF14	-0.06	0.048	2.17E-01	1.00E+00	0.000	0.664	0.942 (0.893; 1.128)
DAPK2	-0.066	0.054	2.22E-01	1.00E+00	0.000	0.654	0.936 (0.82; 0.996)
DNHD1	-0.064	0.053	2.26E-01	1.00E+00	0.000	0.646	0.938 (0.88; 1.086)
RYR2	-0.061	0.05	2.26E-01	1.00E+00	0.000	0.646	0.941 (0.876; 1.078)
MAP1A	-0.063	0.052	2.28E-01	1.00E+00	0.000	0.642	0.939 (0.806; 1.005)
ATP11A	-0.06	0.05	2.28E-01	1.00E+00	0.000	0.642	0.942 (0.769; 0.93)
RHOXF1	-0.063	0.053	2.30E-01	1.00E+00	0.000	0.638	0.939 (0.874; 1.082)
PREPL	-0.066	0.055	2.31E-01	1.00E+00	0.000	0.636	0.936 (0.865; 1.051)
ZBTB5	-0.066	0.055	2.33E-01	1.00E+00	0.000	0.633	0.936 (0.888; 1.085)
F8	-0.063	0.053	2.34E-01	1.00E+00	0.000	0.631	0.939 (0.811; 0.984)
HSPB3	-0.067	0.056	2.35E-01	1.00E+00	0.000	0.629	0.935 (0.919; 1.139)
TMEM238	-0.066	0.056	2.35E-01	1.00E+00	0.000	0.629	0.936 (0.882; 1.1)
LAMB2	-0.063	0.053	2.35E-01	1.00E+00	0.000	0.629	0.939 (0.7; 0.894)
TTC21B	-0.059	0.05	2.35E-01	1.00E+00	0.000	0.629	0.943 (0.795; 0.975)
ATPAF1	-0.065	0.054	2.36E-01	1.00E+00	0.000	0.627	0.937 (0.867; 1.061)
CENPE	-0.064	0.054	2.36E-01	1.00E+00	0.000	0.627	0.938 (0.908; 1.127)

ANKLE2	-0.066	0.056	2.37E-01	1.00E+00	0.000	0.625	0.936 (0.783; 0.963)
RFX7	-0.055	0.047	2.38E-01	1.00E+00	0.000	0.623	0.946 (0.832; 1.027)
IGLV3-27	-0.064	0.054	2.38E-01	1.00E+00	0.000	0.623	0.938 (0.873; 1.081)
MS4A1	-0.065	0.055	2.39E-01	1.00E+00	0.000	0.622	0.937 (0.869; 1.078)
TAF1L	-0.066	0.056	2.42E-01	1.00E+00	0.000	0.616	0.936 (0.863; 1.041)
IFT46	0.068	0.058	2.43E-01	1.00E+00	0.000	0.614	1.07 (0.826; 1.018)
C1S	0.068	0.058	2.43E-01	1.00E+00	0.000	0.614	1.07 (0.815; 1.019)
MBD6	-0.059	0.051	2.50E-01	1.00E+00	0.000	0.602	0.943 (0.821; 1.001)
OTUD7B	-0.061	0.054	2.52E-01	1.00E+00	0.000	0.599	0.941 (0.801; 0.999)
TUBB1	-0.06	0.052	2.52E-01	1.00E+00	0.000	0.599	0.942 (0.806; 0.968)
SF1	-0.056	0.049	2.55E-01	1.00E+00	0.000	0.593	0.946 (0.765; 0.98)
FGD6	-0.064	0.056	2.59E-01	1.00E+00	0.000	0.587	0.938 (0.862; 1.047)
DENND2B	-0.061	0.054	2.60E-01	1.00E+00	0.000	0.585	0.941 (0.842; 1.047)
MYOM2	-0.059	0.052	2.61E-01	1.00E+00	0.000	0.583	0.943 (0.866; 1.105)
MNX1.1	-0.056	0.05	2.61E-01	1.00E+00	0.000	0.583	0.946 (0.937; 1.186)
MICAL1	-0.058	0.052	2.62E-01	1.00E+00	0.000	0.582	0.944 (0.87; 1.061)
ZGRF1	-0.058	0.052	2.64E-01	1.00E+00	0.000	0.578	0.944 (0.838; 1.031)
TNFRSF1A	-0.065	0.058	2.64E-01	1.00E+00	0.000	0.578	0.937 (0.823; 1.047)
DCHS2	-0.059	0.053	2.65E-01	1.00E+00	0.000	0.577	0.943 (0.829; 1.03)
IGKV1-16	-0.061	0.055	2.67E-01	1.00E+00	0.000	0.573	0.941 (0.882; 1.101)
ATRN	-0.063	0.057	2.70E-01	1.00E+00	0.000	0.569	0.939 (0.838; 1.029)
EVI2A	-0.056	0.051	2.73E-01	1.00E+00	0.000	0.564	0.946 (0.777; 0.956)
APOA1	-0.064	0.058	2.75E-01	1.00E+00	0.000	0.561	0.938 (0.854; 1.082)
MINDY4	-0.054	0.049	2.77E-01	1.00E+00	0.000	0.558	0.947 (0.894; 1.128)
PRR36	-0.057	0.053	2.78E-01	1.00E+00	0.000	0.556	0.945 (0.851; 1.027)
USP9Y	-0.064	0.059	2.78E-01	1.00E+00	0.000	0.556	0.938 (0.881; 1.091)
C6	0.065	0.06	2.78E-01	1.00E+00	0.000	0.556	1.067 (0.82; 1.018)

LCAT	-0.059	0.055	2.79E-01	1.00E+00	0.000	0.554	0.943 (0.99; 1.286)
IGKV4-1	-0.06	0.056	2.82E-01	1.00E+00	0.000	0.550	0.942 (0.927; 1.202)
VANGL1	-0.061	0.056	2.82E-01	1.00E+00	0.000	0.550	0.941 (0.857; 1.06)
DPYSL5	-0.053	0.049	2.84E-01	1.00E+00	0.000	0.547	0.948 (0.72; 0.954)
CUBN	-0.057	0.054	2.84E-01	1.00E+00	0.000	0.547	0.945 (0.767; 0.943)
DIDO1	-0.054	0.051	2.84E-01	1.00E+00	0.000	0.547	0.947 (0.819; 1.009)
PRDM2	-0.056	0.052	2.85E-01	1.00E+00	0.000	0.545	0.946 (0.849; 1.048)
EMILIN2	-0.064	0.06	2.85E-01	1.00E+00	0.000	0.545	0.938 (0.781; 0.967)
HSF4	-0.059	0.055	2.85E-01	1.00E+00	0.000	0.545	0.943 (0.869; 1.065)
FHAD1	-0.056	0.052	2.87E-01	1.00E+00	0.000	0.542	0.946 (0.79; 0.959)
IGLC3	-0.058	0.054	2.89E-01	1.00E+00	0.000	0.539	0.944 (0.82; 1.009)
UROC1	-0.054	0.051	2.90E-01	1.00E+00	0.000	0.538	0.947 (0.822; 1.033)
ZBTB4	-0.057	0.054	2.90E-01	1.00E+00	0.000	0.538	0.945 (0.836; 1.027)
PROSER2	-0.059	0.056	2.94E-01	1.00E+00	0.000	0.532	0.943 (0.864; 1.077)
SLC12A7	-0.059	0.056	2.95E-01	1.00E+00	0.000	0.530	0.943 (0.912; 1.148)
IGLV1-40	-0.056	0.054	2.98E-01	1.00E+00	0.000	0.526	0.946 (0.854; 1.059)
TUBB2A	-0.057	0.055	3.04E-01	1.00E+00	0.000	0.517	0.945 (0.865; 1.062)
DDX17	-0.052	0.05	3.05E-01	1.00E+00	0.000	0.516	0.949 (0.83; 1.022)
IGLV3-1	-0.053	0.052	3.05E-01	1.00E+00	0.000	0.516	0.948 (0.893; 1.095)
WHAMM	-0.059	0.058	3.06E-01	1.00E+00	0.000	0.514	0.943 (0.903; 1.125)
UNG	-0.054	0.054	3.16E-01	1.00E+00	0.000	0.500	0.947 (0.826; 1.035)
RGPD2	-0.059	0.059	3.17E-01	1.00E+00	0.000	0.499	0.943 (0.852; 1.049)
UNC13B	-0.054	0.054	3.18E-01	1.00E+00	0.000	0.498	0.947 (0.801; 0.995)
C8A	0.059	0.059	3.19E-01	1.00E+00	0.000	0.496	1.061 (0.882; 1.124)
TRIM33	-0.052	0.053	3.21E-01	1.00E+00	0.000	0.493	0.949 (0.888; 1.11)
DST	-0.052	0.053	3.21E-01	1.00E+00	0.000	0.493	0.949 (0.846; 1.034)
CKAP4	-0.054	0.055	3.22E-01	1.00E+00	0.000	0.492	0.947 (0.843; 1.053)

CBLL1	-0.054	0.055	3.23E-01	1.00E+00	0.000	0.491	0.947 (0.86; 1.068)
TGFB1	-0.049	0.05	3.25E-01	1.00E+00	0.000	0.488	0.952 (0.886; 1.103)
COL11A2	0.062	0.063	3.26E-01	1.00E+00	0.000	0.487	1.064 (0.853; 1.06)
RELN	-0.058	0.059	3.27E-01	1.00E+00	0.000	0.485	0.944 (0.809; 0.999)
IGKV3-20.4	0.053	0.055	3.27E-01	1.00E+00	0.000	0.485	1.054 (0.843; 0.998)
RICTOR	-0.053	0.055	3.29E-01	1.00E+00	0.000	0.483	0.948 (1; 1.288)
KIF14	-0.052	0.054	3.30E-01	1.00E+00	0.000	0.481	0.949 (0.824; 1.007)
ANKRD2	-0.054	0.056	3.30E-01	1.00E+00	0.000	0.481	0.947 (0.85; 1.029)
UACA	-0.057	0.059	3.31E-01	1.00E+00	0.000	0.480	0.945 (0.896; 1.122)
PON1	-0.055	0.056	3.32E-01	1.00E+00	0.000	0.479	0.946 (0.879; 1.088)
F9	0.064	0.066	3.32E-01	1.00E+00	0.000	0.479	1.066 (0.856; 1.041)
ACADVL	-0.054	0.056	3.32E-01	1.00E+00	0.000	0.479	0.947 (0.827; 1.024)
HPX	0.056	0.057	3.33E-01	1.00E+00	0.000	0.478	1.058 (0.813; 1.007)
ITIH3	-0.056	0.058	3.33E-01	1.00E+00	0.000	0.478	0.946 (0.91; 1.134)
PEBP1	-0.05	0.052	3.35E-01	1.00E+00	0.000	0.475	0.951 (0.926; 1.151)
TRIO	-0.049	0.051	3.37E-01	1.00E+00	0.000	0.472	0.952 (0.821; 1.019)
SYNE4	-0.055	0.058	3.42E-01	1.00E+00	0.000	0.466	0.946 (0.789; 0.978)
ARID2	-0.051	0.054	3.43E-01	1.00E+00	0.000	0.465	0.95 (0.888; 1.096)
A1BG	-0.054	0.057	3.43E-01	1.00E+00	0.000	0.465	0.947 (0.865; 1.091)
SHBG	0.061	0.065	3.46E-01	1.00E+00	0.000	0.461	1.063 (0.84; 1.048)
FCN3	-0.05	0.053	3.46E-01	1.00E+00	0.000	0.461	0.951 (0.851; 1.045)
BEST1	-0.048	0.051	3.50E-01	1.00E+00	0.000	0.456	0.953 (0.801; 0.994)
IGKV3-20.1	-0.054	0.058	3.51E-01	1.00E+00	0.000	0.455	0.947 (0.854; 1.067)
TUFM	-0.051	0.055	3.52E-01	1.00E+00	0.000	0.453	0.95 (0.824; 0.993)
MAP3K5	-0.049	0.053	3.53E-01	1.00E+00	0.000	0.452	0.952 (0.865; 1.065)
IGLC7	-0.051	0.055	3.54E-01	1.00E+00	0.000	0.451	0.95 (0.82; 1.024)
TUB	-0.052	0.056	3.54E-01	1.00E+00	0.000	0.451	0.949 (0.831; 1.02)

GAPVD1	-0.053	0.057	3.55E-01	1.00E+00	0.000	0.450	0.948 (0.831; 1.031)
MARK3	-0.05	0.055	3.61E-01	1.00E+00	0.000	0.442	0.951 (0.781; 0.972)
WBP2	-0.051	0.055	3.61E-01	1.00E+00	0.000	0.442	0.95 (0.761; 0.943)
KMT2D	-0.05	0.055	3.62E-01	1.00E+00	0.000	0.441	0.951 (0.84; 1.052)
FNBP1	-0.046	0.051	3.69E-01	1.00E+00	0.000	0.433	0.955 (0.847; 1.064)
NYAP1	-0.049	0.055	3.69E-01	1.00E+00	0.000	0.433	0.952 (0.765; 0.936)
CHD3	-0.053	0.059	3.69E-01	1.00E+00	0.000	0.433	0.948 (0.891; 1.117)
ANK1	-0.046	0.051	3.71E-01	1.00E+00	0.000	0.431	0.955 (0.865; 1.091)
SERPINA1	-0.05	0.056	3.73E-01	1.00E+00	0.000	0.428	0.951 (0.917; 1.147)
MTHFD2	-0.047	0.053	3.74E-01	1.00E+00	0.000	0.427	0.954 (0.838; 1.029)
WDR74	-0.046	0.052	3.76E-01	1.00E+00	0.000	0.425	0.955 (0.838; 1.023)
IGLV3-10	-0.04	0.045	3.78E-01	1.00E+00	0.000	0.423	0.961 (0.826; 1.017)
ACTR2	0.055	0.062	3.79E-01	1.00E+00	0.000	0.421	1.057 (0.91; 1.152)
CDC42BPB	-0.045	0.052	3.81E-01	1.00E+00	0.000	0.419	0.956 (0.85; 1.028)
FGG	0.052	0.06	3.82E-01	1.00E+00	0.000	0.418	1.053 (0.864; 1.066)
DNAH10	-0.05	0.057	3.82E-01	1.00E+00	0.000	0.418	0.951 (0.889; 1.088)
SENP3	-0.047	0.054	3.85E-01	1.00E+00	0.000	0.415	0.954 (0.895; 1.092)
PHKA1	0.048	0.055	3.85E-01	1.00E+00	0.000	0.415	1.049 (0.904; 1.14)
TTF2	-0.049	0.057	3.86E-01	1.00E+00	0.000	0.413	0.952 (0.847; 1.035)
NYAP2	-0.046	0.053	3.87E-01	1.00E+00	0.000	0.412	0.955 (0.824; 1.016)
LRRTM2	-0.046	0.053	3.87E-01	1.00E+00	0.000	0.412	0.955 (0.8; 0.984)
PTPRS	-0.045	0.053	3.91E-01	1.00E+00	0.000	0.408	0.956 (0.826; 1.001)
IGHV1-69	-0.045	0.052	3.92E-01	1.00E+00	0.000	0.407	0.956 (0.838; 1.018)
IGLV3-21.1	-0.046	0.054	3.92E-01	1.00E+00	0.000	0.407	0.955 (0.891; 1.114)
TMF1	-0.041	0.048	3.92E-01	1.00E+00	0.000	0.407	0.96 (0.855; 1.031)
ACTMAP	-0.043	0.05	3.96E-01	1.00E+00	0.000	0.402	0.958 (0.779; 0.949)
NIPBL	-0.044	0.051	3.96E-01	1.00E+00	0.000	0.402	0.957 (0.87; 1.088)

SRC	-0.047	0.055	3.96E-01	1.00E+00	0.000	0.402	0.954 (0.839; 1.034)
COMP	-0.042	0.05	3.96E-01	1.00E+00	0.000	0.402	0.959 (0.892; 1.121)
MAP4K5	0.047	0.055	3.99E-01	1.00E+00	0.000	0.399	1.048 (0.864; 1.071)
CEP112	0.049	0.059	4.00E-01	1.00E+00	0.000	0.398	1.05 (0.847; 1.044)
DMGDH	-0.043	0.052	4.02E-01	1.00E+00	0.000	0.396	0.958 (0.844; 1.055)
B2M	-0.047	0.056	4.03E-01	1.00E+00	0.000	0.395	0.954 (0.891; 1.136)
DCAF8	-0.046	0.055	4.06E-01	1.00E+00	0.000	0.391	0.955 (0.81; 0.986)
CDRT15L2	-0.043	0.052	4.06E-01	1.00E+00	0.000	0.391	0.958 (0.93; 1.193)
TMEM177	0.05	0.06	4.06E-01	1.00E+00	0.000	0.391	1.051 (0.881; 1.112)
CNGA3	-0.042	0.051	4.09E-01	1.00E+00	0.000	0.388	0.959 (0.833; 1.029)
ARHGEF19	-0.044	0.053	4.09E-01	1.00E+00	0.000	0.388	0.957 (0.823; 1.024)
ASPSCR1	-0.047	0.057	4.10E-01	1.00E+00	0.000	0.387	0.954 (0.839; 1.04)
MAP3K9	-0.044	0.054	4.12E-01	1.00E+00	0.000	0.385	0.957 (0.905; 1.131)
TUBA8	0.043	0.054	4.17E-01	1.00E+00	0.000	0.380	1.044 (0.853; 1.047)
EXD3	-0.043	0.053	4.17E-01	1.00E+00	0.000	0.380	0.958 (0.882; 1.096)
IGKV1D-12	-0.044	0.054	4.19E-01	1.00E+00	0.000	0.378	0.957 (0.833; 1.036)
PFN1	0.044	0.055	4.22E-01	1.00E+00	0.000	0.375	1.045 (0.844; 1.059)
ZNF536	-0.04	0.051	4.26E-01	1.00E+00	0.000	0.371	0.961 (0.978; 1.23)
PAPPA	-0.042	0.052	4.28E-01	1.00E+00	0.000	0.369	0.959 (0.8; 0.98)
IGHV3-72	-0.044	0.056	4.28E-01	1.00E+00	0.000	0.369	0.957 (0.795; 0.999)
PPP2R1A	-0.042	0.053	4.30E-01	1.00E+00	0.000	0.367	0.959 (0.895; 1.122)
KRT75	-0.043	0.055	4.30E-01	1.00E+00	0.000	0.367	0.958 (0.883; 1.122)
IGKV1D-33	-0.043	0.054	4.31E-01	1.00E+00	0.000	0.366	0.958 (0.899; 1.122)
KRT1	-0.04	0.051	4.33E-01	1.00E+00	0.000	0.364	0.961 (0.874; 1.073)
ACTB	0.056	0.071	4.34E-01	1.00E+00	0.000	0.363	1.058 (0.836; 1.016)
IGKV1D-33.1	-0.045	0.057	4.35E-01	1.00E+00	0.000	0.362	0.956 (0.856; 1.043)
C2	-0.043	0.055	4.38E-01	1.00E+00	0.000	0.359	0.958 (0.897; 1.132)

SLC1A2	-0.043	0.055	4.38E-01	1.00E+00	0.000	0.359	0.958 (0.849; 1.021)
ATAD3A	-0.044	0.056	4.39E-01	1.00E+00	0.000	0.358	0.957 (0.863; 1.054)
SLC6A9	-0.042	0.055	4.44E-01	1.00E+00	0.000	0.353	0.959 (0.874; 1.073)
HLA-DRA	-0.044	0.057	4.46E-01	1.00E+00	0.000	0.351	0.957 (0.916; 1.123)
NBEA	-0.042	0.055	4.52E-01	1.00E+00	0.000	0.345	0.959 (0.83; 1.033)
IGKV4-1.1	-0.043	0.057	4.52E-01	1.00E+00	0.000	0.345	0.958 (0.827; 1.01)
HELQ	-0.044	0.059	4.55E-01	1.00E+00	0.000	0.342	0.957 (0.89; 1.09)
KIF24	-0.045	0.06	4.55E-01	1.00E+00	0.000	0.342	0.956 (0.855; 1.047)
ANKRD31	-0.042	0.056	4.57E-01	1.00E+00	0.000	0.340	0.959 (0.894; 1.109)
LNX1	0.047	0.063	4.57E-01	1.00E+00	0.000	0.340	1.048 (0.875; 1.094)
SERPINA7	0.045	0.061	4.58E-01	1.00E+00	0.000	0.339	1.046 (0.896; 1.127)
CNDP1	-0.045	0.061	4.60E-01	1.00E+00	0.000	0.337	0.956 (0.872; 1.09)
TBCD	-0.043	0.058	4.60E-01	1.00E+00	0.000	0.337	0.958 (0.818; 1.04)
WHRN	-0.04	0.054	4.61E-01	1.00E+00	0.000	0.336	0.961 (0.842; 1.027)
OR51G1	-0.04	0.055	4.62E-01	1.00E+00	0.000	0.335	0.961 (0.825; 1.017)
LY75	-0.04	0.055	4.65E-01	1.00E+00	0.000	0.333	0.961 (0.869; 1.081)
IGKV1D-33.4	-0.041	0.056	4.66E-01	1.00E+00	0.000	0.332	0.96 (0.851; 1.081)
TCF4	-0.043	0.059	4.68E-01	1.00E+00	0.000	0.330	0.958 (0.888; 1.076)
ZFYVE19	-0.036	0.05	4.71E-01	1.00E+00	0.000	0.327	0.965 (0.826; 0.994)
APOA2	-0.036	0.05	4.72E-01	1.00E+00	0.000	0.326	0.965 (0.846; 1.043)
PIP5K1C	-0.037	0.051	4.75E-01	1.00E+00	0.000	0.323	0.964 (0.857; 1.049)
LSM11	-0.038	0.053	4.78E-01	1.00E+00	0.000	0.321	0.963 (0.821; 1.02)
IGKV1-5.2	-0.041	0.058	4.79E-01	1.00E+00	0.000	0.320	0.96 (0.82; 1.033)
ATP8B2	-0.036	0.051	4.80E-01	1.00E+00	0.000	0.319	0.965 (0.798; 0.974)
ATXN7	-0.04	0.057	4.83E-01	1.00E+00	0.000	0.316	0.961 (0.773; 0.941)
BMAL2	-0.036	0.052	4.85E-01	1.00E+00	0.000	0.314	0.965 (0.905; 1.128)
RIOK3	-0.037	0.054	4.86E-01	1.00E+00	0.000	0.313	0.964 (0.869; 1.064)

VCL	-0.037	0.053	4.87E-01	1.00E+00	0.000	0.312	0.964 (0.837; 1.042)
ROCK2	-0.042	0.06	4.89E-01	1.00E+00	0.000	0.311	0.959 (0.824; 0.991)
RUSC1-AS1	0.045	0.066	4.93E-01	1.00E+00	0.000	0.307	1.046 (0.886; 1.12)
TRIP12	-0.037	0.054	5.00E-01	1.00E+00	0.000	0.301	0.964 (0.782; 0.964)
IGKV1-17.1	-0.037	0.056	5.04E-01	1.00E+00	0.000	0.298	0.964 (0.86; 1.057)
AVEN	-0.037	0.056	5.05E-01	1.00E+00	0.000	0.297	0.964 (0.872; 1.079)
ATAD2	-0.037	0.056	5.08E-01	1.00E+00	0.000	0.294	0.964 (0.863; 1.05)
CALCOCO1	-0.035	0.054	5.11E-01	1.00E+00	0.000	0.292	0.966 (0.89; 1.106)
NEO1	-0.034	0.052	5.12E-01	1.00E+00	0.000	0.291	0.967 (0.84; 1.021)
SERPINF2	-0.04	0.062	5.18E-01	1.00E+00	0.000	0.286	0.961 (0.805; 0.982)
RRS1	-0.039	0.061	5.20E-01	1.00E+00	0.000	0.284	0.962 (0.862; 1.054)
ARHGAP39	-0.036	0.057	5.24E-01	1.00E+00	0.000	0.281	0.965 (0.857; 1.077)
GOSR1	-0.035	0.055	5.28E-01	1.00E+00	0.000	0.277	0.966 (0.825; 1.01)
ELL2	-0.033	0.052	5.29E-01	1.00E+00	0.000	0.277	0.968 (0.788; 0.952)
IGKV3-15.1	0.042	0.066	5.29E-01	1.00E+00	0.000	0.277	1.043 (0.826; 1.019)
SEPTIN1	0.034	0.055	5.32E-01	1.00E+00	0.000	0.274	1.035 (0.843; 1.044)
SH3GL3	-0.034	0.054	5.35E-01	1.00E+00	0.000	0.272	0.967 (0.834; 1.011)
ZNF827	-0.034	0.055	5.36E-01	1.00E+00	0.000	0.271	0.967 (0.834; 1.058)
SERAC1	-0.034	0.055	5.37E-01	1.00E+00	0.000	0.270	0.967 (0.907; 1.147)
HGFAC	-0.035	0.057	5.38E-01	1.00E+00	0.000	0.269	0.966 (0.904; 1.133)
ATP5MF-PTCD1	-0.033	0.054	5.44E-01	1.00E+00	0.000	0.264	0.968 (0.797; 0.986)
ADAM8	-0.033	0.055	5.44E-01	1.00E+00	0.000	0.264	0.968 (0.767; 0.925)
PLCB4	-0.032	0.053	5.46E-01	1.00E+00	0.000	0.263	0.969 (0.817; 1.006)
VIM	0.033	0.056	5.51E-01	1.00E+00	0.000	0.259	1.034 (0.855; 1.072)
TXNRD1	-0.032	0.054	5.52E-01	1.00E+00	0.000	0.258	0.969 (0.845; 1.065)
GABARAPL1	-0.031	0.053	5.52E-01	1.00E+00	0.000	0.258	0.969 (0.904; 1.111)
NF1	-0.034	0.057	5.55E-01	1.00E+00	0.000	0.256	0.967 (0.846; 1.043)

TXNDC2	-0.035	0.059	5.59E-01	1.00E+00	0.000	0.253	0.966 (0.912; 1.153)
BCHE	-0.034	0.058	5.59E-01	1.00E+00	0.000	0.253	0.967 (0.865; 1.082)
PGA3	-0.03	0.051	5.60E-01	1.00E+00	0.000	0.252	0.97 (0.852; 1.062)
FCN2	-0.031	0.054	5.61E-01	1.00E+00	0.000	0.251	0.969 (0.829; 1.016)
SOBP	-0.03	0.052	5.63E-01	1.00E+00	0.000	0.249	0.97 (0.762; 0.938)
IGKV1-39.1	-0.033	0.057	5.63E-01	1.00E+00	0.000	0.249	0.968 (0.852; 1.046)
IGLV8-61	-0.028	0.05	5.68E-01	1.00E+00	0.000	0.246	0.972 (0.857; 1.061)
LCORL	-0.033	0.059	5.68E-01	1.00E+00	0.000	0.246	0.968 (0.854; 1.052)
NOX1	-0.033	0.058	5.69E-01	1.00E+00	0.000	0.245	0.968 (0.83; 0.999)
ACTA1	0.033	0.058	5.69E-01	1.00E+00	0.000	0.245	1.034 (0.913; 1.145)
IGHV3-38	-0.029	0.052	5.76E-01	1.00E+00	0.000	0.240	0.971 (0.846; 1.035)
COL22A1	-0.032	0.057	5.77E-01	1.00E+00	0.000	0.239	0.969 (0.84; 1.014)
F2	0.031	0.056	5.77E-01	1.00E+00	0.000	0.239	1.031 (0.958; 1.204)
ALDH1A3	-0.029	0.053	5.77E-01	1.00E+00	0.000	0.239	0.971 (0.866; 1.078)
SMC4	-0.033	0.06	5.78E-01	1.00E+00	0.000	0.238	0.968 (0.809; 0.995)
CLCNKA	0.034	0.062	5.81E-01	1.00E+00	0.000	0.236	1.035 (0.822; 0.997)
ZFHX4	0.03	0.056	5.86E-01	1.00E+00	0.000	0.232	1.03 (0.85; 1.032)
NPHP3	-0.028	0.054	5.97E-01	1.00E+00	0.000	0.224	0.972 (0.769; 0.954)
PGM5	-0.028	0.053	6.03E-01	1.00E+00	0.000	0.220	0.972 (0.941; 1.161)
SOCS2	0.031	0.059	6.03E-01	1.00E+00	0.000	0.220	1.031 (0.928; 1.139)
FLNB	-0.027	0.054	6.08E-01	1.00E+00	0.000	0.216	0.973 (0.882; 1.117)
TUBB4A	-0.027	0.053	6.09E-01	1.00E+00	0.000	0.215	0.973 (0.877; 1.105)
SUGP2	-0.028	0.055	6.09E-01	1.00E+00	0.000	0.215	0.972 (0.819; 1.009)
MARK4	-0.025	0.049	6.10E-01	1.00E+00	0.000	0.215	0.975 (0.879; 1.095)
AVPR1A	-0.03	0.059	6.10E-01	1.00E+00	0.000	0.215	0.97 (0.844; 1.027)
FBLN1	-0.031	0.061	6.11E-01	1.00E+00	0.000	0.214	0.969 (0.824; 1.027)
TONSL	-0.029	0.056	6.12E-01	1.00E+00	0.000	0.213	0.971 (0.892; 1.124)

MPIG6B	-0.026	0.052	6.20E-01	1.00E+00	0.000	0.208	0.974 (0.853; 1.053)
SBF1	-0.027	0.055	6.21E-01	1.00E+00	0.000	0.207	0.973 (0.869; 1.073)
FKBP4	0.027	0.056	6.22E-01	1.00E+00	0.000	0.206	1.027 (0.867; 1.071)
ZZEF1	-0.027	0.055	6.24E-01	1.00E+00	0.000	0.205	0.973 (0.864; 1.062)
OPN1SW	-0.026	0.052	6.24E-01	1.00E+00	0.000	0.205	0.974 (0.799; 0.961)
IGLV2-11	-0.026	0.053	6.25E-01	1.00E+00	0.000	0.204	0.974 (0.798; 0.988)
IGHA1	0.04	0.082	6.25E-01	1.00E+00	0.000	0.204	1.041 (0.889; 1.103)
NPHP1	-0.027	0.057	6.28E-01	1.00E+00	0.000	0.202	0.973 (0.893; 1.112)
IGKV3-7	-0.024	0.049	6.29E-01	1.00E+00	0.000	0.201	0.976 (0.893; 1.121)
IGHA2	0.028	0.058	6.31E-01	1.00E+00	0.000	0.200	1.028 (0.773; 0.961)
PLG	-0.028	0.057	6.32E-01	1.00E+00	0.000	0.199	0.972 (0.891; 1.119)
PPBP	-0.028	0.058	6.32E-01	1.00E+00	0.000	0.199	0.972 (0.83; 1.026)
PIGR	-0.023	0.048	6.34E-01	1.00E+00	0.000	0.198	0.977 (0.915; 1.155)
CUX1	-0.023	0.048	6.35E-01	1.00E+00	0.000	0.197	0.977 (0.85; 1.035)
IGKV2D-40	-0.026	0.056	6.35E-01	1.00E+00	0.000	0.197	0.974 (0.802; 0.987)
IGLV1-47	-0.028	0.061	6.44E-01	1.00E+00	0.000	0.191	0.972 (0.966; 1.213)
CMTM7	-0.026	0.057	6.46E-01	1.00E+00	0.000	0.190	0.974 (0.841; 1.046)
hCG_14925	0.029	0.063	6.46E-01	1.00E+00	0.000	0.190	1.029 (0.844; 1.044)
CNDP1.1	-0.025	0.055	6.46E-01	1.00E+00	0.000	0.190	0.975 (0.783; 0.958)
DRG2	-0.027	0.059	6.50E-01	1.00E+00	0.000	0.187	0.973 (0.838; 1.008)
IGHV3-7.1	-0.025	0.056	6.53E-01	1.00E+00	0.000	0.185	0.975 (0.835; 1.028)
FGFR2	-0.024	0.053	6.53E-01	1.00E+00	0.000	0.185	0.976 (0.908; 1.139)
DACT1	0.023	0.052	6.54E-01	1.00E+00	0.000	0.184	1.023 (0.839; 1.02)
AHSG	-0.025	0.056	6.55E-01	1.00E+00	0.000	0.184	0.975 (0.848; 1.042)
LAMA2	-0.032	0.072	6.57E-01	1.00E+00	0.000	0.182	0.969 (0.784; 0.969)
CPN2	0.027	0.063	6.64E-01	1.00E+00	0.000	0.178	1.027 (0.847; 1.039)
APOE	-0.027	0.063	6.65E-01	1.00E+00	0.000	0.177	0.973 (0.884; 1.097)

OTUD7A	-0.024	0.055	6.66E-01	1.00E+00	0.000	0.177	0.976 (0.845; 1.03)
MAPRE1	-0.022	0.051	6.67E-01	1.00E+00	0.000	0.176	0.978 (0.791; 0.971)
RNF123	-0.023	0.054	6.68E-01	1.00E+00	0.000	0.175	0.977 (0.819; 0.997)
KIF22	-0.023	0.054	6.69E-01	1.00E+00	0.000	0.175	0.977 (0.797; 0.975)
PAN2	-0.026	0.062	6.75E-01	1.00E+00	0.000	0.171	0.974 (0.877; 1.098)
IGKV3-20	-0.023	0.056	6.79E-01	1.00E+00	0.000	0.168	0.977 (0.849; 1.053)
KRT15	-0.022	0.055	6.82E-01	1.00E+00	0.000	0.166	0.978 (0.821; 1.013)
SERPING1	-0.028	0.068	6.83E-01	1.00E+00	0.000	0.166	0.972 (0.854; 1.067)
SERPINA10	0.023	0.057	6.83E-01	1.00E+00	0.000	0.166	1.023 (0.859; 1.057)
HLA-DOA	-0.022	0.054	6.87E-01	1.00E+00	0.000	0.163	0.978 (0.827; 1.016)
PRRT4	-0.02	0.05	6.90E-01	1.00E+00	0.000	0.161	0.98 (0.84; 1.007)
CORO1C	-0.022	0.057	6.94E-01	1.00E+00	0.000	0.159	0.978 (0.82; 1.004)
HBA1;	-0.031	0.079	6.94E-01	1.00E+00	0.000	0.159	0.969 (0.766; 0.946)
HERC1	0.021	0.055	6.95E-01	1.00E+00	0.000	0.158	1.021 (0.85; 1.037)
JCHAIN	-0.021	0.054	7.01E-01	1.00E+00	0.000	0.154	0.979 (0.85; 1.004)
DMD	-0.022	0.057	7.01E-01	1.00E+00	0.000	0.154	0.978 (0.814; 1.007)
PPP4C	-0.019	0.05	7.04E-01	1.00E+00	0.000	0.152	0.981 (0.914; 1.139)
HABP2	-0.019	0.05	7.07E-01	1.00E+00	0.000	0.151	0.981 (0.791; 0.978)
HSP90B1	0.02	0.054	7.08E-01	1.00E+00	0.000	0.150	1.02 (0.764; 0.956)
LRRC71	0.021	0.057	7.15E-01	1.00E+00	0.000	0.146	1.021 (0.788; 0.968)
FETUB	0.021	0.059	7.16E-01	1.00E+00	0.000	0.145	1.021 (0.813; 1.001)
C1RL	-0.02	0.055	7.19E-01	1.00E+00	0.000	0.143	0.98 (0.833; 1.03)
ANKRD52	-0.018	0.051	7.19E-01	1.00E+00	0.000	0.143	0.982 (0.847; 1.037)
KCNQ4	0.021	0.06	7.21E-01	1.00E+00	0.000	0.142	1.021 (0.866; 1.06)
HCN2	-0.019	0.055	7.23E-01	1.00E+00	0.000	0.141	0.981 (0.866; 1.087)
ZNF407	0.021	0.06	7.25E-01	1.00E+00	0.000	0.140	1.021 (0.833; 1.038)
DACT3	-0.018	0.052	7.26E-01	1.00E+00	0.000	0.139	0.982 (0.916; 1.137)

TOP2A	0.023	0.065	7.26E-01	1.00E+00	0.000	0.139	1.023 (0.787; 0.983)
KAT14	0.02	0.058	7.28E-01	1.00E+00	0.000	0.138	1.02 (0.882; 1.102)
CELSR1	-0.02	0.058	7.31E-01	1.00E+00	0.000	0.136	0.98 (0.883; 1.076)
SEC23IP	-0.019	0.056	7.31E-01	1.00E+00	0.000	0.136	0.981 (0.883; 1.074)
EMC1	0.02	0.06	7.32E-01	1.00E+00	0.000	0.135	1.02 (0.854; 1.056)
LUZP1	-0.018	0.053	7.33E-01	1.00E+00	0.000	0.135	0.982 (0.845; 1.047)
ITIH4	0.02	0.059	7.33E-01	1.00E+00	0.000	0.135	1.02 (0.839; 1.035)
MKI67	-0.018	0.053	7.34E-01	1.00E+00	0.000	0.134	0.982 (0.879; 1.055)
ZMYM1	-0.019	0.056	7.36E-01	1.00E+00	0.000	0.133	0.981 (0.848; 1.05)
ITGA2	0.02	0.059	7.36E-01	1.00E+00	0.000	0.133	1.02 (0.921; 1.153)
NKX2-5	-0.019	0.055	7.37E-01	1.00E+00	0.000	0.133	0.981 (0.794; 0.97)
KREMEN2	-0.017	0.05	7.39E-01	1.00E+00	0.000	0.131	0.983 (0.771; 0.952)
IGHV3-35	0.018	0.056	7.41E-01	1.00E+00	0.000	0.130	1.018 (0.917; 1.124)
SPAG17	0.019	0.058	7.41E-01	1.00E+00	0.000	0.130	1.019 (0.857; 1.068)
NPY5R	-0.018	0.056	7.51E-01	1.00E+00	0.000	0.124	0.982 (0.916; 1.117)
IDE	0.017	0.052	7.51E-01	1.00E+00	0.000	0.124	1.017 (0.821; 1.004)
IGHV3-23	-0.024	0.077	7.51E-01	1.00E+00	0.000	0.124	0.976 (0.792; 0.988)
SLC27A5	0.018	0.056	7.53E-01	1.00E+00	0.000	0.123	1.018 (0.798; 0.997)
EFNB2	-0.015	0.049	7.54E-01	1.00E+00	0.000	0.123	0.985 (0.9; 1.094)
MYO16	-0.016	0.052	7.57E-01	1.00E+00	0.000	0.121	0.984 (0.789; 0.974)
DLST	-0.016	0.052	7.57E-01	1.00E+00	0.000	0.121	0.984 (0.798; 0.995)
CSPG4	-0.016	0.052	7.60E-01	1.00E+00	0.000	0.119	0.984 (0.896; 1.103)
LYN	-0.017	0.057	7.60E-01	1.00E+00	0.000	0.119	0.983 (1.25; 1.591)
ARFGEF2	0.017	0.055	7.61E-01	1.00E+00	0.000	0.119	1.017 (0.94; 1.169)
TMPRSS15	0.017	0.056	7.61E-01	1.00E+00	0.000	0.119	1.017 (0.899; 1.086)
IGHV3-48	-0.017	0.055	7.63E-01	1.00E+00	0.000	0.117	0.983 (0.828; 1.016)
IGHV4-34	-0.014	0.048	7.68E-01	1.00E+00	0.000	0.115	0.986 (0.895; 1.144)

CFP	0.018	0.062	7.70E-01	1.00E+00	0.000	0.114	1.018 (0.823; 1.022)
ARMH1	-0.015	0.053	7.71E-01	1.00E+00	0.000	0.113	0.985 (0.901; 1.136)
IGLV1-44	-0.016	0.057	7.73E-01	1.00E+00	0.000	0.112	0.984 (0.883; 1.103)
C1QA	0.016	0.058	7.75E-01	1.00E+00	0.000	0.111	1.016 (0.835; 1.027)
SETD1A	-0.016	0.057	7.78E-01	1.00E+00	0.000	0.109	0.984 (0.903; 1.129)
COL4A5	-0.016	0.055	7.79E-01	1.00E+00	0.000	0.108	0.984 (0.782; 0.992)
GOLGA6L10	-0.015	0.053	7.85E-01	1.00E+00	0.000	0.105	0.985 (0.807; 0.993)
USP31	-0.015	0.056	7.87E-01	1.00E+00	0.000	0.104	0.985 (0.864; 1.06)
LRBA	0.018	0.068	7.89E-01	1.00E+00	0.000	0.103	1.018 (0.864; 1.075)
HSPA12B	-0.015	0.059	7.92E-01	1.00E+00	0.000	0.101	0.985 (0.795; 0.997)
SYT1	-0.015	0.057	7.93E-01	1.00E+00	0.000	0.101	0.985 (0.833; 1.025)
COL16A1	0.015	0.056	7.94E-01	1.00E+00	0.000	0.100	1.015 (0.825; 1.02)
ZNF507	-0.015	0.059	7.94E-01	1.00E+00	0.000	0.100	0.985 (0.849; 1.037)
HNRNPU	-0.015	0.057	7.98E-01	1.00E+00	0.000	0.098	0.985 (0.813; 0.994)
PPP1R12B	-0.014	0.056	8.04E-01	1.00E+00	0.000	0.095	0.986 (0.913; 1.137)
AHNAK	-0.014	0.058	8.07E-01	1.00E+00	0.000	0.093	0.986 (0.879; 1.079)
TASOR	0.014	0.058	8.07E-01	1.00E+00	0.000	0.093	1.014 (0.828; 1.02)
IGKV2D-28.1	-0.014	0.057	8.11E-01	1.00E+00	0.000	0.091	0.986 (0.854; 1.08)
ZBTB33	0.013	0.056	8.16E-01	1.00E+00	0.000	0.088	1.013 (0.861; 1.072)
ADCY1	-0.013	0.056	8.19E-01	1.00E+00	0.000	0.087	0.987 (0.844; 1.053)
ANKRD30A	-0.013	0.055	8.19E-01	1.00E+00	0.000	0.087	0.987 (0.819; 0.986)
IGHV3-13	0.012	0.054	8.23E-01	1.00E+00	0.000	0.085	1.012 (0.814; 1.003)
CHD7	-0.012	0.055	8.24E-01	1.00E+00	0.000	0.084	0.988 (0.889; 1.113)
MAP2	-0.011	0.049	8.28E-01	1.00E+00	0.000	0.082	0.989 (1.08; 1.369)
EFCAB5	-0.012	0.054	8.31E-01	1.00E+00	0.000	0.080	0.988 (0.836; 1.031)
IGHV3-30	0.012	0.056	8.32E-01	1.00E+00	0.000	0.080	1.012 (0.865; 1.057)
TMEM200C	0.012	0.056	8.32E-01	1.00E+00	0.000	0.080	1.012 (0.888; 1.108)

IGKV1-5.1	0.012	0.055	8.33E-01	1.00E+00	0.000	0.079	1.012 (0.861; 1.062)
FERMT1	-0.012	0.055	8.34E-01	1.00E+00	0.000	0.079	0.988 (0.866; 1.068)
FAM184A	-0.011	0.053	8.37E-01	1.00E+00	0.000	0.077	0.989 (0.832; 1.023)
C1QB	0.011	0.056	8.39E-01	1.00E+00	0.000	0.076	1.011 (0.847; 1.055)
PSD3	-0.012	0.06	8.40E-01	1.00E+00	0.000	0.076	0.988 (0.795; 1.004)
PPM1B	-0.011	0.056	8.40E-01	1.00E+00	0.000	0.076	0.989 (0.861; 1.075)
FAM83H	-0.011	0.057	8.42E-01	1.00E+00	0.000	0.075	0.989 (0.856; 1.081)
UPF1	0.01	0.052	8.43E-01	1.00E+00	0.000	0.074	1.01 (0.868; 1.065)
RIBC2	-0.01	0.05	8.45E-01	1.00E+00	0.000	0.073	0.99 (0.836; 1.043)
APOL1	0.012	0.06	8.45E-01	1.00E+00	0.000	0.073	1.012 (0.815; 1.019)
KIAA1671	0.012	0.06	8.47E-01	1.00E+00	0.000	0.072	1.012 (0.894; 1.109)
LYZ	0.01	0.051	8.48E-01	1.00E+00	0.000	0.072	1.01 (0.865; 1.097)
IGKV3-20.3	-0.01	0.055	8.52E-01	1.00E+00	0.000	0.070	0.99 (0.878; 1.099)
IGHV3OR15-7	0.01	0.051	8.53E-01	1.00E+00	0.000	0.069	1.01 (0.777; 1.002)
F10	-0.01	0.052	8.53E-01	1.00E+00	0.000	0.069	0.99 (0.878; 1.144)
CFD	-0.012	0.063	8.53E-01	1.00E+00	0.000	0.069	0.988 (0.882; 1.078)
C5	-0.01	0.058	8.58E-01	1.00E+00	0.000	0.067	0.99 (0.937; 1.179)
IGKV1-17	0.01	0.06	8.61E-01	1.00E+00	0.000	0.065	1.01 (0.881; 1.088)
STX11	0.01	0.058	8.62E-01	1.00E+00	0.000	0.064	1.01 (0.856; 1.019)
ARHGEF11	0.01	0.06	8.63E-01	1.00E+00	0.000	0.064	1.01 (0.847; 1.026)
IQGAP2	0.01	0.058	8.66E-01	1.00E+00	0.000	0.062	1.01 (0.891; 1.095)
IGKV1D-33.6	0.01	0.059	8.67E-01	1.00E+00	0.000	0.062	1.01 (0.797; 0.978)
F12	-0.01	0.057	8.68E-01	1.00E+00	0.000	0.061	0.99 (0.826; 1.032)
MTBP	-0.009	0.055	8.70E-01	1.00E+00	0.000	0.060	0.991 (0.877; 1.078)
IGKV1-16.1	0.01	0.063	8.72E-01	1.00E+00	0.000	0.059	1.01 (0.918; 1.152)
ECM1	0.009	0.055	8.73E-01	1.00E+00	0.000	0.059	1.009 (0.875; 1.081)
CCDC150	0.009	0.059	8.74E-01	1.00E+00	0.000	0.058	1.009 (0.812; 1.01)

UTRN	-0.009	0.055	8.77E-01	1.00E+00	0.000	0.057	0.991 (0.744; 0.904)
ORM1	0.009	0.057	8.77E-01	1.00E+00	0.000	0.057	1.009 (0.893; 1.095)
KMT2A	0.01	0.067	8.79E-01	1.00E+00	0.000	0.056	1.01 (0.828; 1.032)
BDP1	-0.008	0.056	8.81E-01	1.00E+00	0.000	0.055	0.992 (1.105; 1.401)
MYH9	-0.008	0.054	8.83E-01	1.00E+00	0.000	0.054	0.992 (0.872; 1.061)
PDE4DIP	0.007	0.05	8.85E-01	1.00E+00	0.000	0.053	1.007 (0.861; 1.075)
RBM15	-0.008	0.06	8.87E-01	1.00E+00	0.000	0.052	0.992 (0.813; 0.994)
FCRL5	0.008	0.056	8.90E-01	1.00E+00	0.000	0.051	1.008 (0.825; 1.039)
STK35	0.007	0.057	8.97E-01	1.00E+00	0.000	0.047	1.007 (0.809; 1.003)
APOBR	-0.008	0.06	8.98E-01	1.00E+00	0.000	0.047	0.992 (0.845; 1.047)
NLN	-0.007	0.055	8.99E-01	1.00E+00	0.000	0.046	0.993 (0.813; 0.992)
RRBP1	-0.007	0.056	9.01E-01	1.00E+00	0.000	0.045	0.993 (0.845; 1.033)
SPATA31D1	-0.008	0.062	9.02E-01	1.00E+00	0.000	0.045	0.992 (0.893; 1.088)
PARD6G	0.007	0.058	9.04E-01	1.00E+00	0.000	0.044	1.007 (0.795; 0.98)
KIN	-0.006	0.055	9.09E-01	1.00E+00	0.000	0.041	0.994 (0.83; 1.011)
AASS	-0.006	0.057	9.12E-01	1.00E+00	0.000	0.040	0.994 (0.874; 1.066)
MUC16	-0.006	0.061	9.17E-01	1.00E+00	0.000	0.038	0.994 (0.824; 1.015)
PSMB9	-0.006	0.057	9.18E-01	1.00E+00	0.000	0.037	0.994 (0.827; 1.027)
NAV1	-0.006	0.057	9.19E-01	1.00E+00	0.000	0.037	0.994 (0.891; 1.084)
IGHV3-15	0.006	0.057	9.21E-01	1.00E+00	0.000	0.036	1.006 (0.86; 1.046)
LOC645967	-0.007	0.067	9.21E-01	1.00E+00	0.000	0.036	0.993 (0.892; 1.097)
HERC2	-0.006	0.061	9.22E-01	1.00E+00	0.000	0.035	0.994 (0.943; 1.216)
GPLD1	0.006	0.06	9.25E-01	1.00E+00	0.000	0.034	1.006 (0.931; 1.154)
TTBK1	-0.005	0.059	9.31E-01	1.00E+00	0.000	0.031	0.995 (0.858; 1.064)
FBH1	-0.005	0.058	9.37E-01	1.00E+00	0.000	0.028	0.995 (0.862; 1.067)
CMYA5	-0.004	0.058	9.38E-01	1.00E+00	0.000	0.028	0.996 (0.885; 1.108)
HBB	0.006	0.078	9.39E-01	1.00E+00	0.000	0.027	1.006 (0.877; 1.088)

IGHV1-2	-0.004	0.058	9.39E-01	1.00E+00	0.000	0.027	0.996 (0.856; 1.032)
ITPKB	-0.004	0.058	9.40E-01	1.00E+00	0.000	0.027	0.996 (0.87; 1.079)
MPDZ	0.004	0.059	9.41E-01	1.00E+00	0.000	0.026	1.004 (0.892; 1.151)
AP1M2	0.005	0.064	9.43E-01	1.00E+00	0.000	0.025	1.005 (0.715; 0.925)
IGLV3-19	0.004	0.055	9.44E-01	1.00E+00	0.000	0.025	1.004 (0.878; 1.128)
PLXDC2	0.004	0.056	9.47E-01	1.00E+00	0.000	0.024	1.004 (0.78; 0.98)
SERPINA3	0.004	0.057	9.49E-01	1.00E+00	0.000	0.023	1.004 (0.788; 0.968)
CP	0.004	0.06	9.52E-01	1.00E+00	0.000	0.021	1.004 (0.856; 1.066)
DHRS2	-0.003	0.058	9.53E-01	1.00E+00	0.000	0.021	0.997 (0.792; 0.978)
ZNF219	-0.003	0.058	9.55E-01	1.00E+00	0.000	0.020	0.997 (0.806; 1.004)
ITGB4	-0.003	0.06	9.58E-01	1.00E+00	0.000	0.019	0.997 (0.879; 1.084)
P3H4	0.003	0.059	9.60E-01	1.00E+00	0.000	0.018	1.003 (0.875; 1.087)
HRG	-0.003	0.058	9.63E-01	1.00E+00	0.000	0.016	0.997 (0.86; 1.078)
LRG1	0.002	0.06	9.70E-01	1.00E+00	0.000	0.013	1.002 (0.945; 1.211)
EEA1	-0.002	0.059	9.73E-01	1.00E+00	0.000	0.012	0.998 (0.919; 1.184)
OTUD5	0.002	0.058	9.74E-01	1.00E+00	0.000	0.011	1.002 (0.813; 1.008)
SMARCC2	0.002	0.062	9.79E-01	1.00E+00	0.000	0.009	1.002 (0.854; 1.033)
NDUFA13	-0.001	0.059	9.80E-01	1.00E+00	0.000	0.009	0.999 (0.884; 1.115)
BBX	-0.001	0.056	9.81E-01	1.00E+00	0.000	0.008	0.999 (0.863; 1.073)
C4BPB	-0.001	0.062	9.83E-01	1.00E+00	0.000	0.007	0.999 (0.759; 0.954)
SYNE2	0.001	0.058	9.85E-01	1.00E+00	0.000	0.007	1.001 (0.89; 1.104)
CLASP1	-0.001	0.057	9.87E-01	1.00E+00	0.000	0.006	0.999 (0.839; 1.025)
HNRNPM	-0.001	0.057	9.92E-01	1.00E+00	0.000	0.003	0.999 (0.855; 1.05)
IGHV3-7.2	0.001	0.056	9.93E-01	1.00E+00	0.000	0.003	1.001 (0.859; 1.046)
PRKCE	0	0.054	9.94E-01	1.00E+00	0.000	0.003	1 (0.859; 1.068)
C1QC	0	0.059	9.95E-01	1.00E+00	0.000	0.002	1 (0.807; 1.007)
LINC02881	0	0.051	9.98E-01	1.00E+00	0.000	0.001	1 (0.878; 1.067)

API5	0	0.052	9.98E-01	1.00E+00	0.000	0.001	1 (0.815; 1.013)
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1. Full names of the biomarkers can be found in Additional file 1: Table S1. Abbreviations: FDR, Bonferroni false-discovery rate; OR: odds ratio; CI: confident interval.

2. Adjusted for variables in full model (age, sex, smoking status, physical activity, HDL-C, systolic BP, naturally log-transformed triglycerides, fasting glucose, and T2D status).

Table S5 Significant associations of 11 protein biomarkers with obesity in the full model

Proteins	UniProt_ID	Estimate	SE	<i>p</i> value	adjusted <i>p</i> value	log10_adj_pval	log10_pval	OR (95% CI)
CRP	P02741	0.488	0.062	2.49E-15	2.02E-12	11.695	14.604	1.629 (0.854; 1.059)
APOD	P05090	-0.403	0.063	1.49E-10	1.20E-07	6.921	9.827	0.668 (0.835; 1.012)
SAA2-SAA4	A0A096LPE2	0.343	0.061	2.33E-08	1.88E-05	4.726	7.633	1.409 (0.892; 1.103)
APOM	O95445	-0.329	0.062	1.16E-07	9.37E-05	4.028	6.936	0.72 (0.811; 0.989)
CFH	P08603	0.321	0.061	1.35E-07	1.09E-04	3.963	6.870	1.379 (0.89; 1.11)
LGALS3BP	Q08380	0.415	0.079	1.51E-07	1.22E-04	3.914	6.821	1.514 (0.8; 1.001)
A2M	P01023	0.306	0.061	5.01E-07	4.06E-04	3.391	6.300	1.358 (0.889; 1.096)
APOF	Q13790	-0.533	0.107	6.27E-07	5.07E-04	3.295	6.203	0.587 (0.837; 1.028)
AFM	P43652	0.266	0.059	7.24E-06	5.86E-03	2.232	5.140	1.305 (0.908; 1.133)
SERPINA6	P08185	-0.257	0.064	5.80E-05	4.69E-02	1.329	4.237	0.773 (0.879; 1.077)
CKAP5	Q14008	-0.216	0.054	6.08E-05	4.92E-02	1.308	4.216	0.806 (0.809; 0.974)

1. Full names of the biomarkers can be found in Additional file 1: Table S1. The 11 proteins significantly associated with obesity (FDR < 0.05) using the logistic regression model are presented in this table.

Abbreviations: FDR, Bonferroni false-discovery rate; OR: odds ratio; CI: confident interval.

2. Adjusted for variables in full model (age, sex, smoking status, physical activity, HDL-C, systolic BP, naturally log-transformed triglycerides, fasting glucose, and T2D status).

Table S6 Frequency of significant proteins identified by priority-lasso in 1000 rounds of basic model

Biomarkers	Frequency
A2M	1000
ADIPOQ	1000
AFM	1000
APCS	1000
APOD	1000
APOF	1000
APOM	1000
AZGP1	1000
C4B	892
CFH	1000
CRP	1000
GPX3	1000
LGALS3BP	1000
S100A9	632
SERPINA6	1000
SERPINF1	1000
VTN	13

Table S7 The *p* value of correlation analysis between obesity-related phenotype and significant proteins

Proteins	BMI	WHR	WC	BFP	age	SBP	DBP	alcohol	FPG	TG	HDL	LDL	TCHO
A2M	4.07E-33	2.25E-14	2.54E-26	2.67E-20	9.35E-05	1.96E-07	2.12E-04	8.26E-03	7.78E-15	1.79E-36	1.04E-11	0.01593	1.61E-02
ADIPOQ	7.95E-31	3.80E-73	8.28E-54	1.28E-15	1.26E-09	2.38E-13	2.98E-18	1.75E-01	1.58E-24	5.19E-38	4.63E-103	0.28396	1.22E-08
AFM	1.39E-31	7.05E-27	6.05E-33	1.62E-08	1.83E-06	2.02E-12	6.90E-06	2.71E-01	3.17E-30	1.08E-39	4.14E-10	0.18635	6.74E-02
APCS	2.51E-32	1.09E-64	1.67E-55	1.42E-03	4.54E-02	1.65E-19	2.45E-13	6.12E-08	8.25E-22	5.30E-41	1.76E-38	2.7E-10	2.22E-04
APOD	2.61E-32	5.19E-04	6.96E-20	2.33E-32	8.98E-02	9.32E-01	1.88E-01	1.16E-13	1.24E-10	4.07E-11	3.01E-28	0.78674	3.62E-04
APOF	1.71E-33	3.44E-22	4.01E-37	5.46E-06	3.72E-02	2.81E-04	1.71E-06	2.28E-02	3.95E-18	1.66E-19	2.03E-30	0.37697	1.65E-04
APOM	5.60E-30	7.38E-15	2.38E-31	5.77E-04	1.66E-04	2.67E-01	7.60E-02	1.00E-08	8.27E-12	3.24E-02	2.21E-43	1.9E-09	2.15E-35
AZGP1	3.35E-05	5.77E-02	6.48E-02	4.82E-14	6.09E-06	1.60E-01	7.12E-02	2.43E-05	3.11E-01	8.87E-01	2.25E-01	0.04713	5.34E-01
C4B	3.57E-09	9.68E-04	2.00E-06	1.22E-07	2.42E-03	6.41E-02	5.69E-01	8.22E-01	2.60E-04	7.05E-08	2.35E-02	0.24526	5.01E-02
CFH	6.62E-31	1.91E-16	1.00E-26	8.16E-18	4.26E-07	1.47E-06	2.70E-03	3.32E-04	6.38E-13	1.29E-26	1.00E-13	0.00324	6.33E-02
CRP	1.40E-41	5.41E-17	1.16E-37	1.66E-28	4.49E-07	5.37E-05	2.07E-02	7.45E-01	4.05E-13	9.20E-18	3.73E-13	0.03688	5.06E-01
LGALS3BP	2.61E-45	8.92E-24	1.07E-39	4.75E-26	6.58E-12	1.91E-11	3.63E-03	1.09E-02	6.28E-22	9.72E-22	3.39E-13	0.80572	4.15E-01
GPX3	7.65E-13	4.89E-06	9.90E-13	4.39E-09	1.03E-04	1.37E-01	8.67E-01	4.21E-03	4.45E-04	5.25E-08	6.06E-07	0.01352	2.42E-01
SERPINF1	2.16E-31	1.21E-37	2.00E-43	3.82E-01	1.74E-10	1.70E-15	3.13E-04	1.56E-02	2.02E-28	6.71E-37	2.75E-23	0.73523	1.33E-01
SERPINA6	2.29E-18	3.38E-28	2.81E-28	2.18E-01	1.67E-10	5.33E-06	3.04E-02	1.06E-02	6.22E-06	1.03E-01	1.91E-19	0.03877	9.20E-04
S100A9	8.56E-21	6.63E-16	6.45E-25	1.40E-04	3.99E-06	9.98E-07	1.90E-03	3.62E-01	6.72E-15	5.88E-17	3.47E-15	0.00115	1.01E-01

The *p* value of correlation analysis between obesity-related indexes

Indexes	BMI	WHR	WC	BFP
BMI	0.00E+00	1.25E-155	0.00E+00	4.55E-130

Table S8 The coefficient of correlation analysis between obesity-related phenotype and significant proteins

Proteins	BMI	WHR	WC	BFP	age	SBP	DBP	alcohol	FPG	TG	HDL	LDL	TCHO
A2M	0.261	0.168	0.232	0.202	0.086	0.115	0.082	-0.058	0.171	0.274	-0.150	0.053	0.053
ADIPOQ	-0.251	-0.385	-0.332	0.176	0.134	-0.161	-0.191	-0.030	-0.223	-0.279	0.451	-0.024	0.126
AFM	0.254	0.234	0.260	0.125	0.105	0.155	0.099	0.024	0.249	0.286	-0.138	0.029	0.040
APCS	0.257	0.363	0.337	-0.070	0.044	0.198	0.161	0.119	0.210	0.290	-0.281	0.139	0.082
APOD	-0.257	-0.077	-0.200	-0.258	0.038	0.002	-0.029	0.163	-0.142	-0.145	0.240	-0.006	0.079
APOF	-0.262	-0.212	-0.276	-0.100	0.046	-0.080	-0.106	0.050	-0.190	-0.198	0.250	0.020	0.083
APOM	-0.248	-0.171	-0.253	-0.076	-0.083	-0.025	0.039	0.126	-0.150	-0.047	0.299	0.132	0.270
AZGP1	-0.092	0.042	-0.041	-0.166	0.100	0.031	-0.040	0.093	0.022	0.003	0.027	-0.044	-0.014
C4B	0.130	0.073	0.105	0.117	0.067	0.041	0.013	-0.005	0.081	0.119	-0.050	0.026	0.043
CFH	0.252	0.181	0.234	0.189	0.112	0.106	0.066	-0.079	0.158	0.233	-0.164	0.065	0.041
CRP	0.292	0.184	0.278	0.241	0.111	0.089	0.051	-0.007	0.159	0.188	-0.160	0.046	0.015
LGALS3BP	0.305	0.220	0.286	0.230	0.151	0.148	0.064	-0.056	0.211	0.210	-0.160	0.005	-0.018
GPX3	-0.158	-0.101	-0.157	-0.129	-0.086	-0.033	-0.004	0.063	-0.078	-0.120	0.110	-0.055	-0.026
SERPINF1	0.254	0.278	0.299	0.019	0.141	0.175	0.080	0.053	0.241	0.275	-0.217	-0.007	-0.033
SERPINA6	-0.192	-0.240	-0.240	0.027	-0.141	-0.100	-0.048	0.056	-0.100	-0.036	0.198	-0.046	0.073
S100A9	0.205	0.177	0.225	0.084	0.102	0.108	0.069	-0.020	0.171	0.184	-0.173	0.072	0.036

**The coefficient of correlation analysis between
obesity-related indexes**

Indexes	BMI	WHR	WC	BFP
BMI	1.000	0.542	0.865	0.501

Table S9 Function enrichment analysis of the 16 protein biomarkers showing the top 16 gene ontology (GO) terms related to obesity

ONTOLOGY	ID	Description	GeneRatio	BgRatio	p value	adjusted p value	q value	geneID	Count
BP	GO:0006953	acute-phase response	3/16	48/18870	8.45E-06	5.32E-03	3.13E-03	A2M/APCS/CRP	3
BP	GO:0006956	complement activation	3/16	67/18870	2.32E-05	1.46E-02	4.24E-03	A2M/C4B/CFH	3
BP	GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	2/16	13/18870	5.23E-05	3.29E-02	4.24E-03	..	2
BP	GO:0006959	humoral immune response	4/16	258/18870	5.46E-05	3.44E-02	4.24E-03	A2M/C4B/CFH/S100A9	4
BP	GO:0010745	negative regulation of macrophage derived foam cell differentiation	2/16	14/18870	6.10E-05	3.84E-02	4.24E-03	ADIPOQ/CRP	2
BP	GO:0098869	cellular oxidant detoxification	3/16	99/18870	7.46E-05	4.70E-02	4.24E-03	APOM/GPX3/S100A9	3
CC	GO:0072562	blood microparticle	6/16	144/19886	9.80E-10	2.74E-08	1.24E-08	A2M/AFM/APCS/C4B/CFH/LGALS3BP	6
CC	GO:0062023	collagen-containing extracellular matrix	7/16	429/19886	2.00E-08	5.61E-07	1.27E-07	A2M/ADIPOQ/APCS/AZGP1/LGALS3BP/SERPINF1/S100A9	7
CC	GO:0034362	low-density lipoprotein particle	2/16	12/19886	3.99E-05	1.12E-03	1.68E-04	APOF/APOM	2
CC	GO:1990777	lipoprotein particle	2/16	36/19886	3.76E-04	1.05E-02	7.92E-04	APOF/APOM	2
MF	GO:0001848	complement binding	4/16	26/18496	5.52E-09	3.64E-07	1.39E-07	APCS/C4B/CFH/CRP	4
MF	GO:0001846	opsonin binding	3/16	21/18496	7.00E-07	4.62E-05	8.84E-06	APCS/CFH/CRP	3
MF	GO:0004866	endopeptidase inhibitor activity	4/16	168/18496	1.10E-05	7.24E-04	7.94E-05	A2M/C4B/SERPINF1/SERPINA6	4
MF	GO:0016209	antioxidant activity	3/16	83/18496	4.68E-05	3.09E-03	1.69E-04	APOM/GPX3/S100A9	3
MF	GO:0005496	steroid binding	3/16	102/18496	8.65E-05	5.71E-03	2.43E-04	APOD/APOF/SERPINA6	3
MF	GO:0005319	lipid transporter activity	3/16	172/18496	4.05E-04	2.67E-02	9.30E-04	APOD/APOF/APOM	3

The 16 proteins significantly associated with obesity, were included in the function enrichment analysis.

Table S10 KEGG Pathway Enrichment Analysis of the 16 Identified Biomarkers Related to Obesity

category	subcategory	ID	Description	GeneRatio	BgRatio	<i>p</i> value	adjust <i>p</i> value	q value	geneID	Count
Organismal Systems	Immune system	hsa04610	Complement and coagulation cascades	3/7	86/8772	3.10E-05	5.88E-04	4.56E-04	2/721/3075	3
Human Diseases	Infectious disease: bacterial	hsa05150	Staphylococcus aureus infection	2/7	96/8772	2.40E-03	4.56E-02	1.77E-02	721/3075	2

Table S11 Mendelian randomisation analysis results of the proteins as the exposure, and BMI as outcome

Outcomes	Protein ^a	MR main results					Heterogeneity		Horizontal pleiotropy		Exposure database	Outcome database
		Method	No.IVs	Beta	SE	p value	Q statistic	p value	Egger intercept	p value		
BMI $p_{sig.} = 0.05/12 = 0.00417$	ADIPOQ	Inverse variance weighted	16	0.037	0.017	2.65E-02	120.775	1.34E-18	0.007	3.32E-03	Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	AFM	Inverse variance weighted	7	0.012	0.019	5.17E-01	40.890	3.04E-07	-0.004	2.42E-01	Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	APCS	Inverse variance weighted	6	-0.001	0.010	9.54E-01	7.972	1.58E-01	0.007	3.32E-03	Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	APOD	Inverse variance weighted	6	-0.010	0.020	5.96E-01	38.771	2.64E-07	-0.004	2.42E-01	Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	AZGP1	Wald ratio	1	-0.011	0.030	7.29E-01	-		-		Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	CRP	Inverse variance weighted	14	0.030	0.021	1.53E-01	171.989	7.28E-30	-0.004	4.10E-01	Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	S100A9	Inverse variance weighted	2	-0.100	0.043	2.13E-02	2.504	1.14E-01	-		Ferkingstad, E. et al. [x]	GWAS ID: ebi-a-GCST90029007
	LGALS3BP	Inverse variance weighted	32	-0.004	0.011	7.34E-01	120.748	1.56E-12	0.002	7.64E-01	PMID:38412862	GWAS ID: ebi-a-GCST90029007
	APOM	Inverse variance weighted	2	0.007	0.008	3.57E-01	0.781	3.77E-01	-		PMID:29875488	GWAS ID: ebi-a-GCST90029007
	CFH	Inverse variance weighted	2	0.004	0.010	6.92E-01	4.619	3.16E-02	-		PMID:29875488	GWAS ID: ebi-a-GCST90029007
	SERPINF1	Wald ratio	1	0.001	0.005	7.53E-01	-		-		PMID:29875488	GWAS ID: ebi-a-GCST90029007
	A2M	Inverse variance weighted	4	-0.007	0.008	3.85E-01	13.544	0.0036	0.007	7.21E-01	PMID:29875488	GWAS ID: ebi-a-GCST90029007

IVs: Instrumental variables

^a The causal effect of 2 proteins (APOF) on BMI was not explored in this study since the IVs identified for the proteins were not found in the GWAS of outcomes. SERPINA6 doesn't have SNP's p value is lower than 5e-08.

Mendelian randomisation analysis results of BMI as the exposure, and the proteins as outcome

Outcomes	Protein ^a	MR main results					Heterogeneity		Horizontal pleiotropy		Exposure database	Outcome database
		Method	No.IVs	Beta	SE	p value	Q statistic	p value	Egger intercept	p value		
proteins $p_{sig.} = 0.05/6 = 0.00833$	AFM	Wald ratio	1	3.063	0.507	1.58E-09	-		-		GWAS ID: ebi-a-GCST90029007	Ferkingstad, E. et al. [x]
	CRP	Wald ratio	1	9.962	0.422	5.44E-123	-		-		GWAS ID: ebi-a-GCST90029007	Ferkingstad, E. et al. [x]
	APOF	Inverse variance weighted	447	-0.128	0.075	8.62E-02	429.382	0.7058	0.003	6.57E-01	GWAS ID: ebi-a-GCST90029007	PMID:29875488
	APOM	Inverse variance weighted	447	-0.104	0.078	1.81E-01	479.930	0.1291	-0.002	5.01E-01	GWAS ID: ebi-a-GCST90029007	PMID:29875488
	CFH	Inverse variance weighted	447	0.243	0.075	1.16E-03	422.692	0.7800	-0.002	5.34E-01	GWAS ID: ebi-a-GCST90029007	PMID:29875488
	A2M	Inverse variance weighted	447	0.063	0.075	3.99E-01	449.442	0.4454	-0.007	4.11E-02	GWAS ID: ebi-a-GCST90029007	PMID:29875488

^a The causal effect of 1 proteins (LGALS3BP) on BMI was not explored in this study since SNPs identified for the proteins were not found in the GWAS of exposures.