**Supplementary Figure 1: Ancestry Proportions among Cases and Controls.** The Y-axis shows ancestry proportion, per individual, with all ancestry proportions adding up to 1.00. Each horizontal bar represents an individual. Individuals are sorted by proportion of indigenous ancestry from most on the left to least on the right. Ancestry was calculated using ADMIXTURE 1.3.
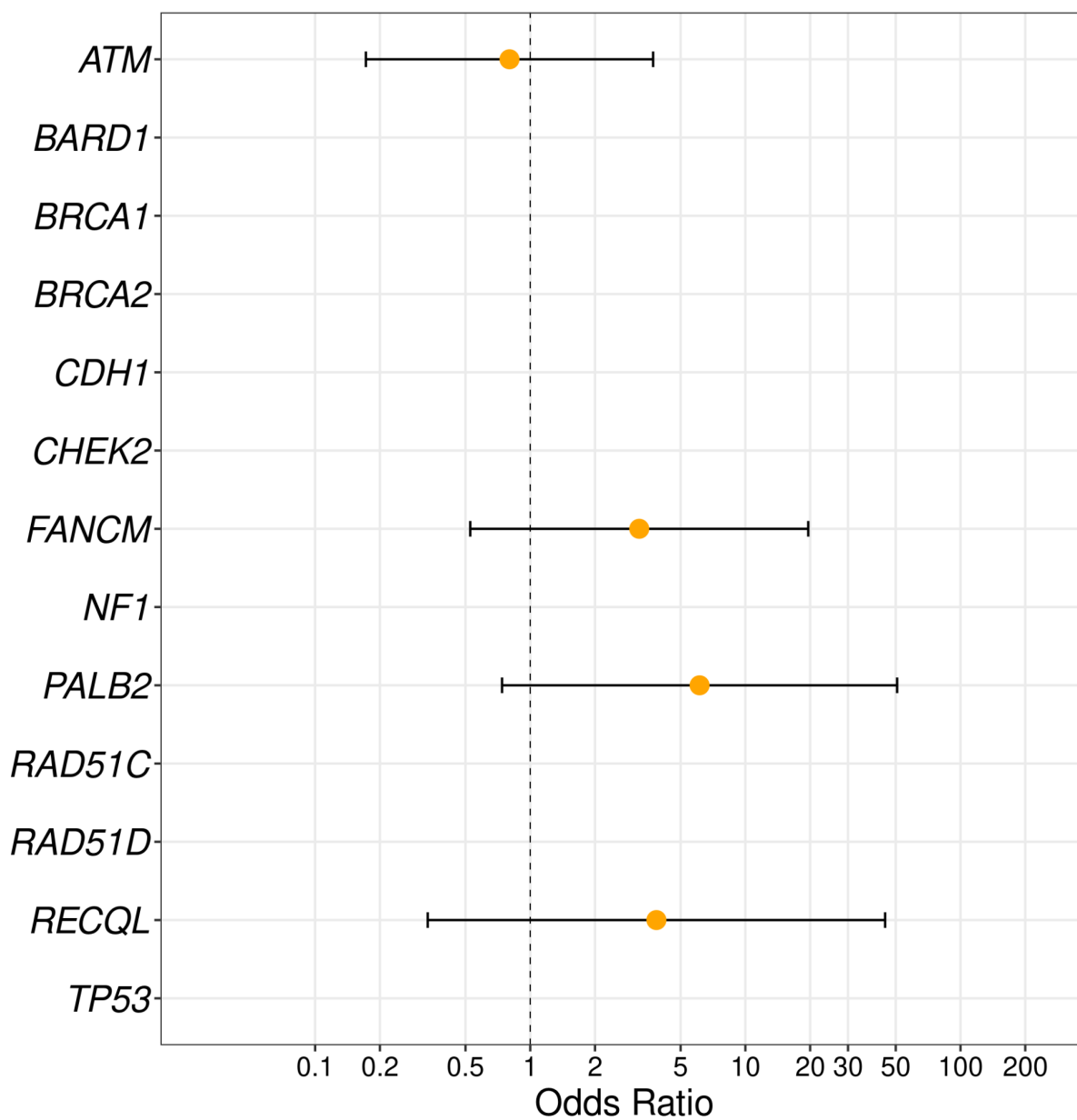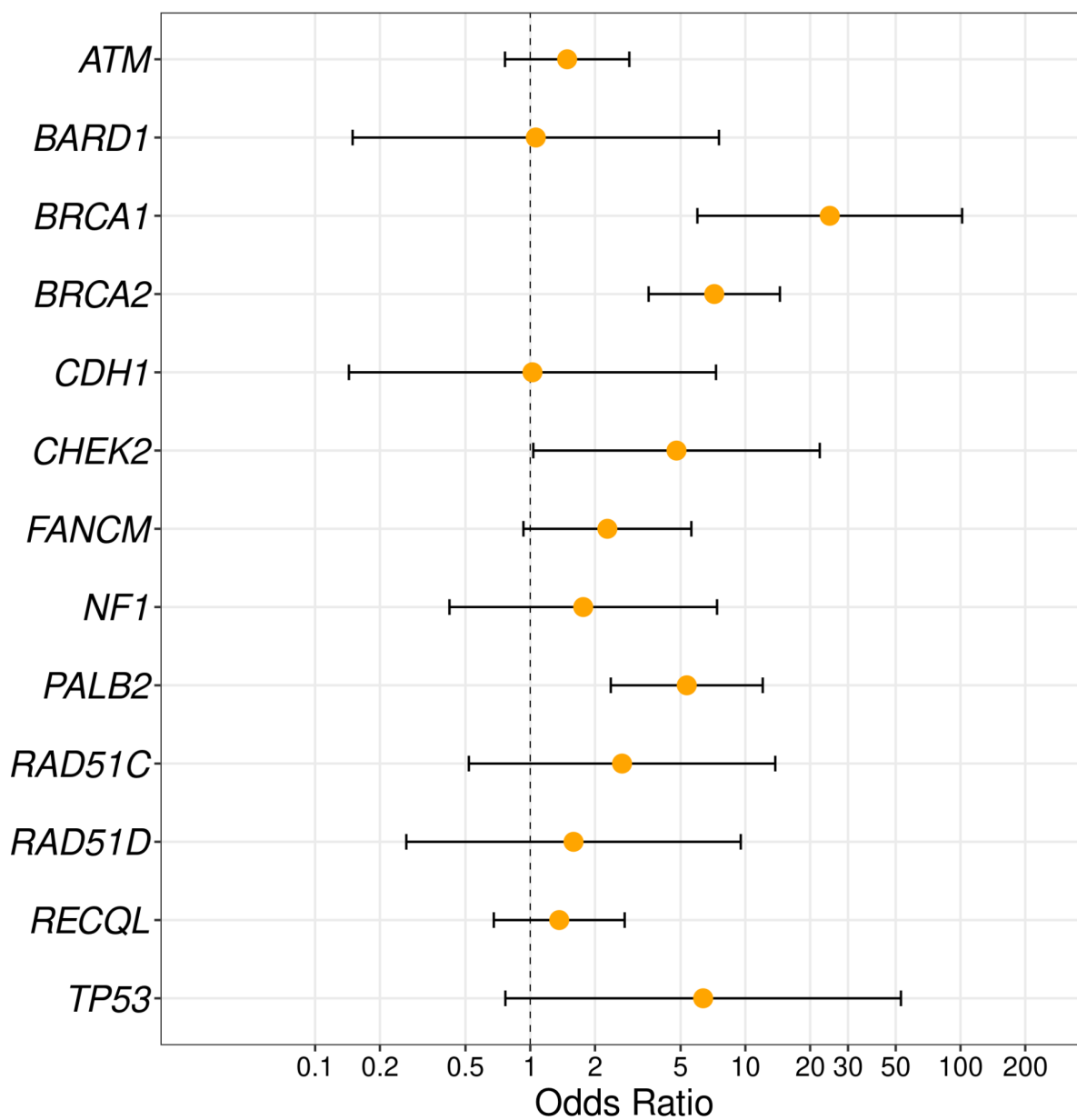
A. Hereditary Studies, Overall:
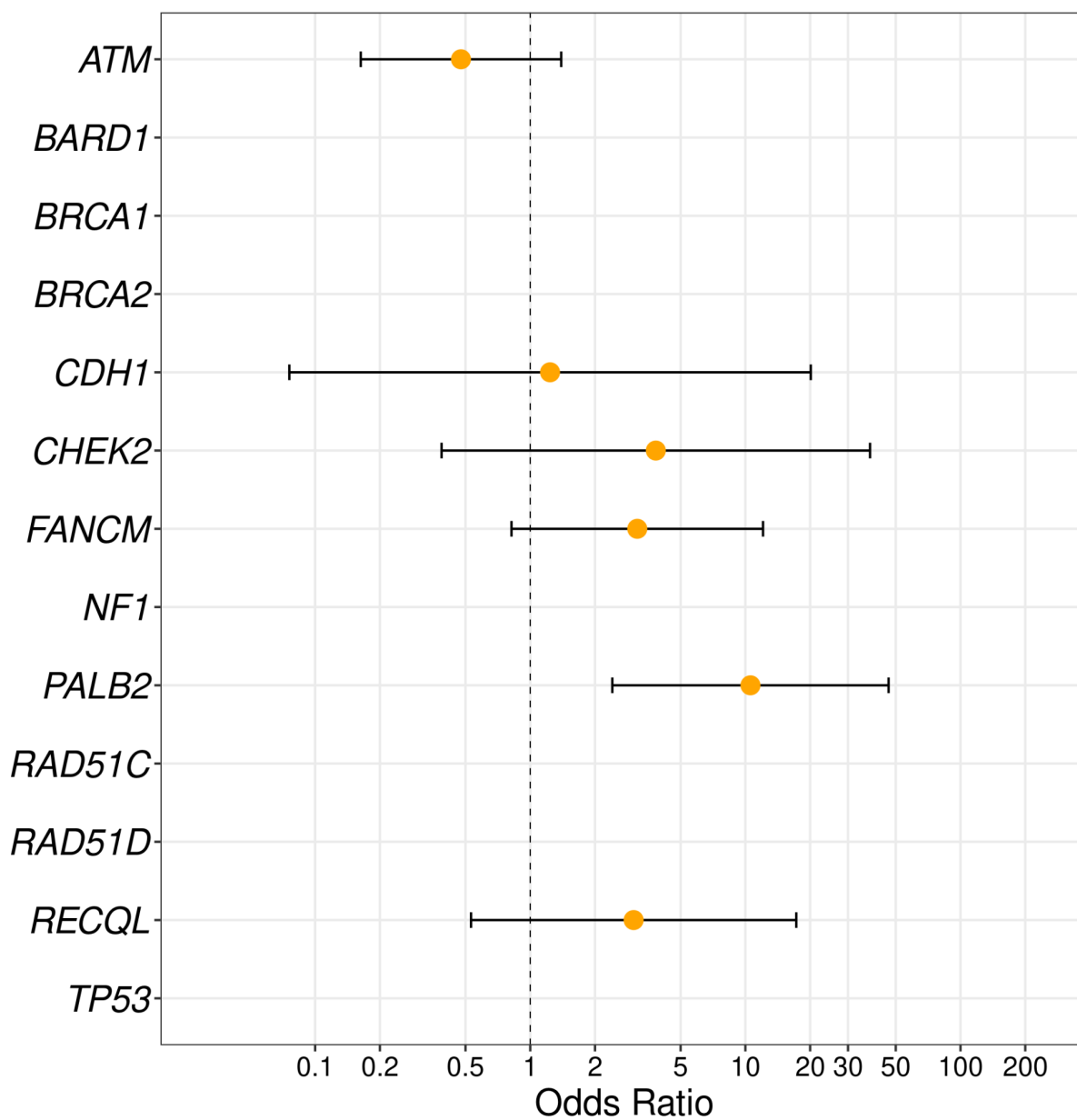
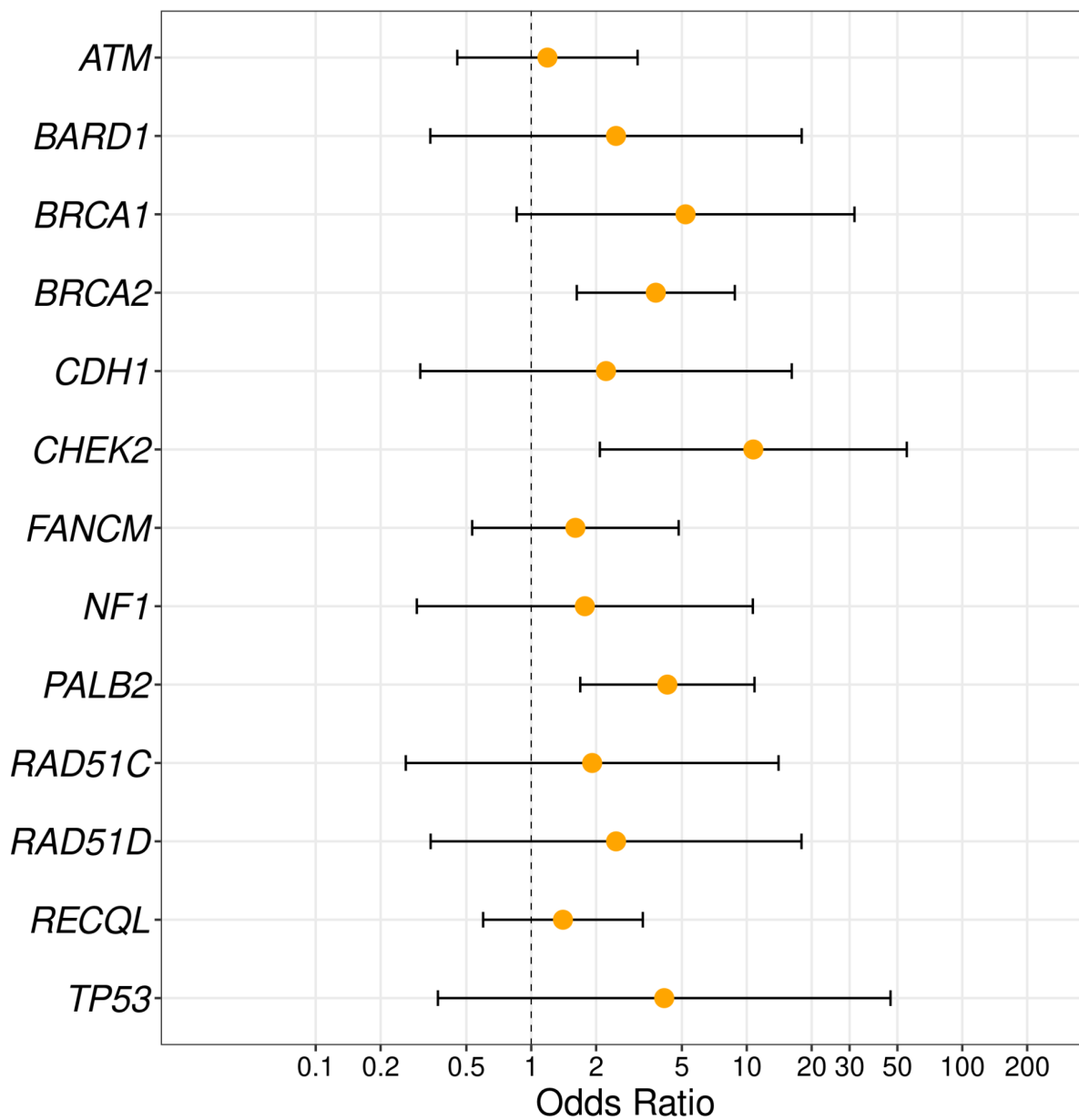**B. Hereditary Studies, Estrogen Receptor-Positive:**
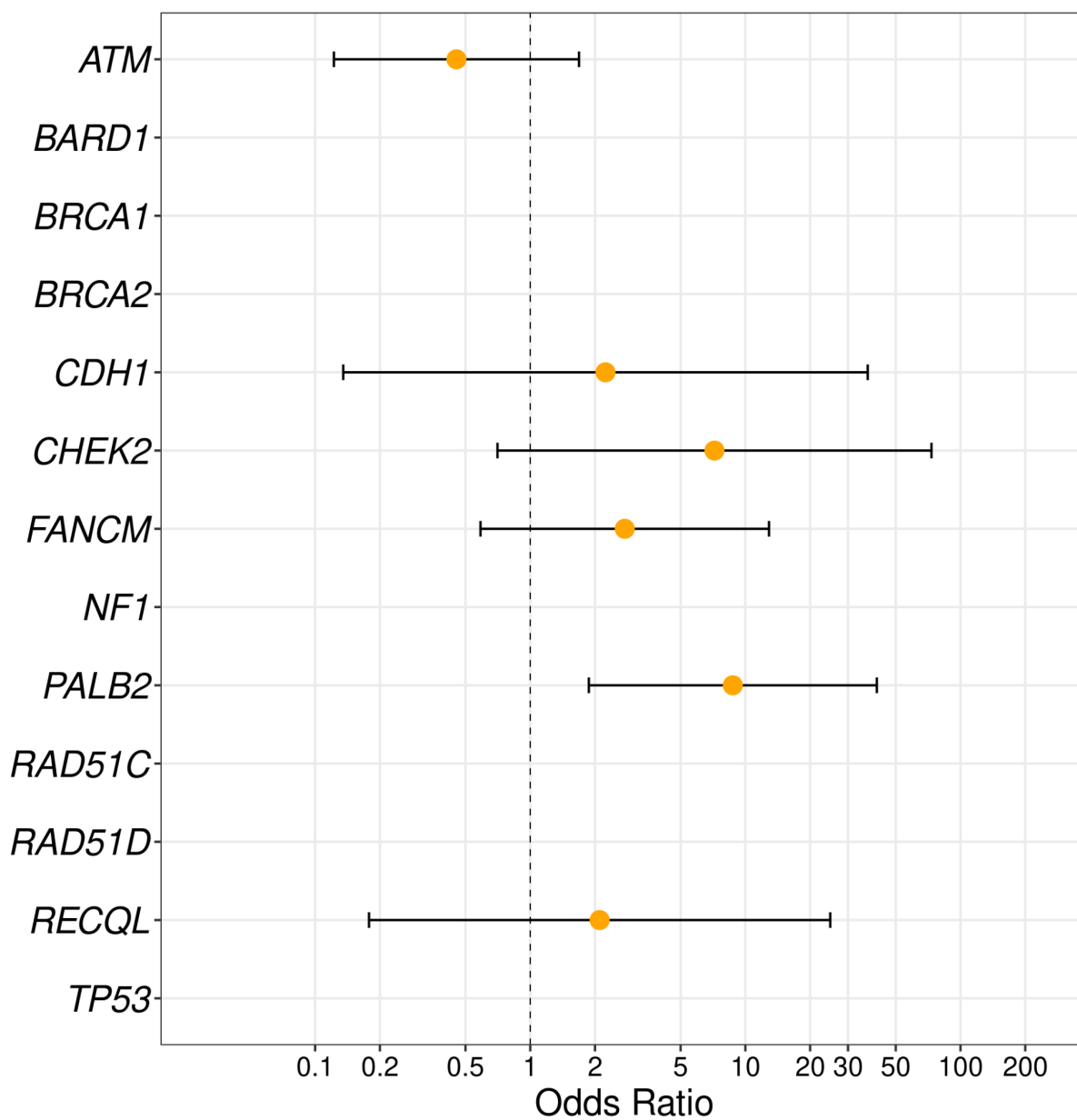
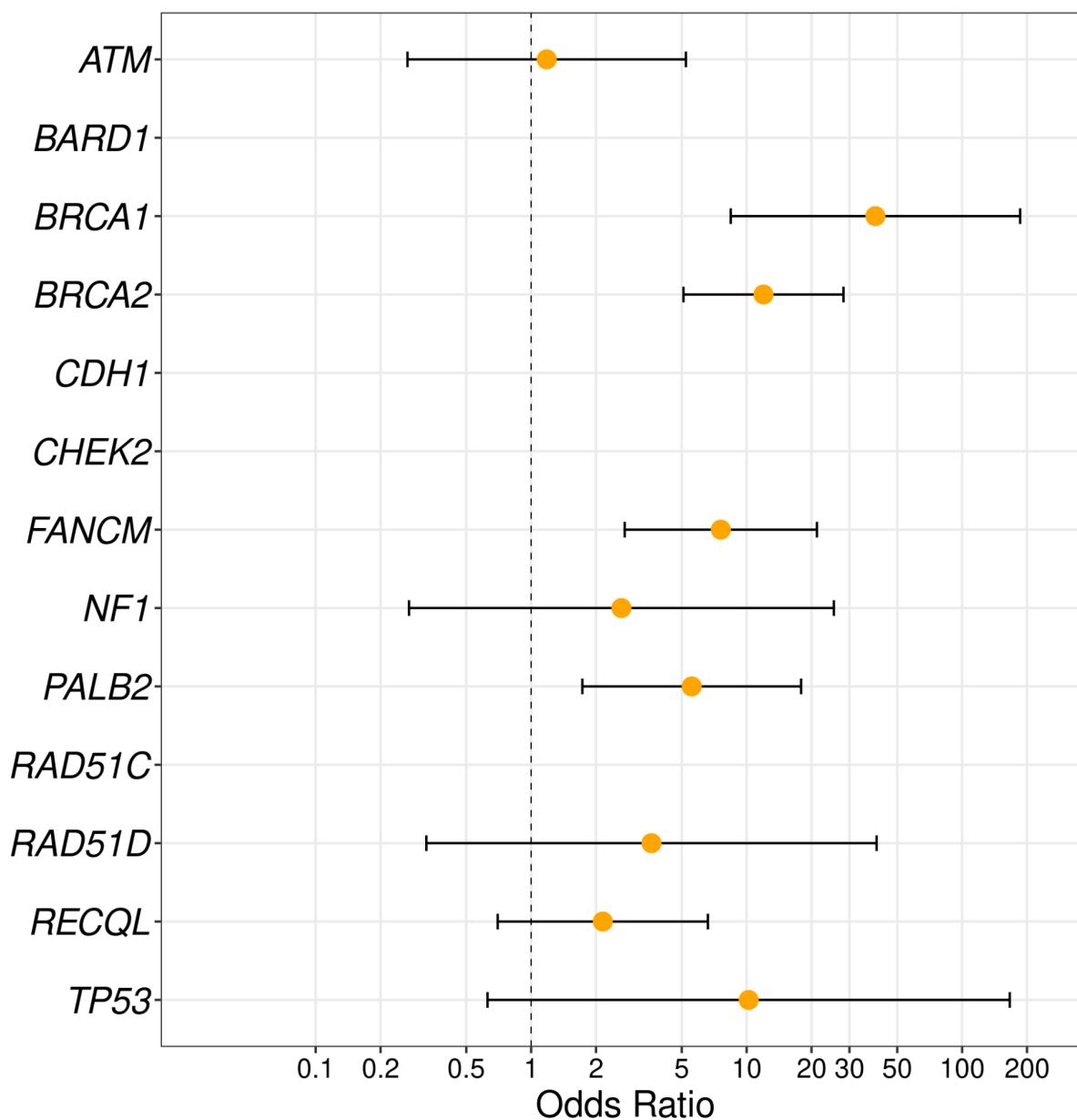**C. Hereditary Studies, Estrogen Receptor-Negative:**

D. Unselected Studies, Overall:

E. Unselected Studies, Estrogen Receptor-Positive:

F. Unselected Studies, Estrogen Receptor-Negative:

Supplementary Figure 2: Gene-Based Odds Ratios from Joint Analysis for Breast Cancer Overall, ER-Positive, and ER-Negative Disease, in Hereditary Studies and Unselected Studies Separately. Odds ratios and confidence intervals are presented for participants in hereditary studies with overall breast cancer (Panel A), estrogen receptor (ER)-positive (Panel B), and ER-negative (Panel C) disease, and for participants in unselected studies with overall breast cancer (Panel D), estrogen receptor-positive (Panel E), and estrogen receptor-negative (Panel F) disease. The orange dot represents the point estimate and the bars represent the upper and lower bounds of the 95% confidence intervals. The X-axis describes the odds ratio on a log scale, the Y-axis represents the individual genes. Genes are listed in alphabetical order. *BRCA1* and *BRCA2* are not included for hereditary studies as participants in these studies were

selected for being *BRCA1/2* negative. Participants selected for hereditary risk in the Northern California Breast Cancer Family Registry were excluded from this analysis as the selection criteria were different than those used in other studies.

Supplementary Table 1: Gene-Based Results for Known Genes from Joint Analysis without Exome-Wide Significance, for Breast Cancer Overall, ER-Positive, and ER-Negative Disease

Gene	Chr	All Studies		
		Overall	ER-Positive	ER-Negative
ATM	11	0.73	0.63	0.81
BARD1	2	0.44	0.17	0.67
CDH1	16	0.78	0.55	N/A
CHEK2	22	0.01	3.6×10^{-5}	0.71
NF1	17	0.62	0.46	0.37
RAD51C	17	0.39	0.34	N/A
RAD51D	17	0.27	0.27	1.9×10^{-3}
RECQL	12	0.52	0.75	0.40
TP53	17	0.11	1.00	1.6×10^{-3}

Chr=Chromosome; ER=estrogen receptor.

P-values are from gene-based SKAT-O analyses.

Supplementary Table 2: Gene-Based P-Values from Joint Analysis with Suggestive Significance, for Breast Cancer Overall, ER-Positive, and ER-Negative Disease

Gene	Chr	Overall	ER-Positive	ER-Negative
ACSM6	10	0.04	0.23	3.20E-03
BRCA1	17	2.30E-10	0.03	4.40E-16
BRCA2	13	8.40E-10	3.30E-04	8.00E-15
CCDC40	17	0.15	0.12	1.60E-03
CDHR2	5	0.13	0.47	3.00E-03
CEACAM8	19	0.22	0.19	4.90E-03
CHEK2	22	0.01	3.60E-05	0.71
DHRS4L2	14	3.60E-03	0.1	0.19
FANCG	9	0.15	0.29	3.50E-03
FANCM	14	9.80E-03	0.11	4.10E-07
FBP1	9	0.37	N/A	6.10E-03
FSHR	2	0.13	3.80E-03	N/A
GEMIN2	14	6.60E-03	0.07	N/A
GSTA1	6	7.90E-03	7.60E-03	0.26
LCP2	5	0.15	0.31	1.80E-03
MAPK12	22	8.30E-03	0.05	0.05
MBP	18	3.90E-04	7.60E-04	0.51
MKI67	10	0.42	0.57	3.20E-04
PALB2	16	1.80E-08	1.30E-05	5.90E-05
PRDM2	1	6.30E-03	0.02	0.57
RAD51D	17	0.27	0.27	1.90E-03
SAMD15	14	0.02	0.01	2.90E-03
SELP	1	7.10E-03	0.05	0.17
SLC26A5	7	0.06	0.02	4.40E-03

TP53	17	0.11	1	1.60E-03
TTC4	1	7.00E-03	6.00E-04	0.2
TTLL9	20	3.80E-03	4.40E-03	N/A
WDR93	15	0.03	0.56	1.60E-03
ZNF404	19	0.01	1.20E-04	N/A
ZSCAN22	19	0.03	4.60E-03	0.93

Chr=Chromosome; ER=estrogen receptor;

P-values are from gene-based SKAT-O analyses. Genes with P<0.01 in any of the three analyses are included in the table.

* Discovery participants were selected for being *BRCA1/2* negative (see methods), replication results are presented for *BRCA1/2*.

Supplementary Table 3: Gene-Based Odds Ratios and 95% Confidence Intervals from Joint Analysis for Breast Cancer Overall, ER-Positive, and ER-Negative Disease, for Genes with Suggestive Significance

Gene	Chromosome	Overall	ER-Positive	ER-Negative
ACSM6	10	1.81 (0.72 - 4.54)	1.44 (0.47 - 4.39)	4.29 (1.34 - 13.74)
BRCA1*	17	24.90 (6.05 - 102.50)	6.00 (1.08 - 33.41)	40.73 (8.90 - 186.50)
BRCA2*	13	6.96 (3.45 - 14.03)	3.89 (1.70 - 8.89)	10.51 (4.47 - 24.73)
CCDC40	17	0.62 (0.52 - 0.74)	0.57 (0.46 - 0.70)	0.51 (0.36 - 0.73)
CDHR2	5	2.61 (0.51 - 13.46)	0.73 (0.07 - 8.06)	6.52 (0.89 - 47.68)
CEACAM8	19	2.61 (0.51 - 13.46)	2.81 (0.38 - 20.86)	7.06 (0.98 - 50.60)
CHEK2	22	4.75 (1.35 - 16.69)	9.77 (2.61 - 36.52)	NA (NA - NA)
DHRS4L2	14	1.10 (0.99 - 1.23)	1.06 (0.93 - 1.21)	1.21 (1.00 - 1.47)
FANCG	9	1.80 (0.53 - 6.16)	0.91 (0.16 - 5.10)	6.44 (1.60 - 25.98)
FANCM	14	2.68 (1.29 - 5.54)	2.20 (0.94 - 5.16)	6.69 (2.86 - 15.65)
FBP1	9	1.42 (0.24 - 8.49)	N/A	4.93 (0.69 - 35.41)
FSHR	2	5.16 (0.60 - 44.26)	12.04 (1.35 - 107.49)	N/A
GEMIN2	14	0.14 (0.02 - 1.10)	0.35 (0.04 - 2.83)	N/A
GSTA1	6	2.87 (1.28 - 6.43)	3.20 (1.32 - 7.80)	2.13 (0.56 - 8.14)
LCP2	5	5.01 (0.58 - 42.93)	4.30 (0.38 - 49.03)	12.46 (1.11 - 140.47)
MAPK12	22	0.48 (0.28 - 0.80)	0.42 (0.20 - 0.90)	0.29 (0.07 - 1.19)
MBP	18	4.05 (1.66 - 9.89)	4.31 (1.64 - 11.36)	1.80 (0.36 - 9.09)
MKI67	10	1.24 (0.53 - 2.87)	1.49 (0.56 - 3.99)	2.44 (0.76 - 7.87)
PALB2	16	6.47 (3.19 - 13.11)	5.11 (2.33 - 11.19)	6.43 (2.51 - 16.48)
PRDM2	1	1.95 (1.04 - 3.65)	2.27 (1.12 - 4.61)	1.06 (0.30 - 3.69)
RAD51D	17	2.00 (0.37 - 10.91)	2.08 (0.29 - 15.18)	5.35 (0.75 - 38.18)
SAMD15	14	1.45 (0.73 - 2.88)	1.66 (0.72 - 3.82)	3.12 (1.24 - 7.87)
SELP	1	0.23 (0.08 - 0.69)	0.23 (0.05 - 0.98)	N/A

SLC26A5	7	2.06 (1.21 - 3.52)	1.94 (1.04 - 3.59)	2.04 (0.89 - 4.67)
TP53	17	7.22 (0.89 - 58.53)	3.42 (0.30 - 38.46)	15.47 (1.39 - 172.75)
TTC4	1	2.94 (0.80 - 10.87)	4.98 (1.30 - 18.99)	1.56 (0.16 - 15.24)
TTLL9	20	0.26 (0.10 - 0.70)	0.09 (0.01 - 0.68)	N/A
WDR93	15	2.62 (0.82 - 8.35)	1.21 (0.22 - 6.68)	4.84 (1.07 - 21.91)
ZNF404	19	4.78 (1.36 - 16.80)	7.35 (1.94 - 27.90)	N/A
ZSCAN22	19	1.90 (0.95 - 3.82)	2.50 (1.18 - 5.31)	0.94 (0.21 - 4.22)

ER=estrogen receptor

* Discovery participants were selected for being *BRCA1/2* negative (see methods), replication
results are presented for *BRCA1/2*.

Supplementary Table 4: Gene-Based P-Values from Joint Analysis Including Missense Variants with Suggestive Significance for Breast Cancer Overall, ER-Positive, and ER-Negative Disease

Gene	Chr	Overall	ER-Positive	ER-Negative
ACSM6	10	0.04	0.23	3.20E-03
ATR	3	0.02	9.20E-04	0.29
BRCA1	17	2.30E-10	0.03	4.40E-16
BRCA2	13	6.70E-10	2.30E-04	1.30E-14
CASP8AP2	6	2.90E-03	0.58	0.13
CCDC40	17	0.1	0.12	1.20E-04
CDHR2	5	0.13	0.47	3.00E-03
CEACAM8	19	0.22	0.19	4.90E-03
CHEK2	22	4.10E-03	1.00E-04	0.4
DDX56	7	0.09	6.00E-03	N/A
DHRS4L2	14	3.60E-03	0.1	0.19
DSTYK	1	8.70E-03	0.13	N/A
FANCG	9	0.15	0.35	8.60E-03
FANCM	14	0.04	0.2	2.90E-06
FAT3	11	0.29	0.49	6.60E-03
GEMIN2	14	7.10E-03	0.07	0.25
GSTA1	6	7.90E-03	7.60E-03	0.26
LCP2	5	0.15	0.31	1.80E-03
MBP	18	3.90E-04	7.60E-04	0.51
MKI67	10	0.42	0.57	3.20E-04
MSH6	2	4.20E-03	3.90E-03	0.04
NDOR1	9	4.70E-03	3.10E-03	0.07
PALB2	16	1.80E-08	1.30E-05	5.90E-05

PCDHGC5	5	0.21	1.0	6.50E-03
PRDM2	1	4.60E-03	0.02	0.85
PREX2	8	0.25	0.44	8.60E-03
RAD51D	17	0.44	0.17	5.40E-03
SAMD15	14	0.02	0.01	2.90E-03
SDK2	17	0.02	9.60E-03	3.00E-03
SERINC3	20	0.37	1.0	1.50E-03
SLC26A5	7	0.03	0.02	4.40E-03
TTC4	1	7.00E-03	6.00E-04	0.2
TTLL9	20	6.00E-03	4.30E-03	0.1
WDR93	15	0.03	0.56	1.60E-03
ZNF404	19	0.01	1.20E-04	N/A

Chr=Chromosome; ER=estrogen receptor; LoF=loss of function.

P-values are from gene-based SKAT-O analyses that include LoF and missense variants.

Genes with P<0.01 in any of the three analyses are included in the table.

* Discovery participants were selected for being *BRCA1/2* negative (see methods), replication results are presented for *BRCA1/2*.

Supplementary Table 5: Gene-Based Odds Ratios and 95% Confidence Intervals from Joint Analysis Including Missense Variants for Breast Cancer Overall, ER-Positive, and ER-Negative Disease, for Genes with Suggestive Significance

Gene	Chromosome	Overall	ER-Positive	ER-Negative
ACSM6	10	1.81 (0.72 - 4.54)	1.44 (0.47 - 4.39)	4.29 (1.34 - 13.74)
ATR	3	2.58 (1.14 - 5.87)	3.84 (1.56 - 9.45)	1.51 (0.32 - 7.20)
BRCA1	17	24.90 (6.05 - 102.50)	6.00 (1.08 - 33.41)	40.73 (8.90 - 186.50)
BRCA2	13	6.47 (3.32 - 12.63)	3.84 (1.74 - 8.46)	9.53 (4.15 - 21.85)
CASP8AP2	6	1.15 (1.05 - 1.27)	1.02 (0.90 - 1.15)	0.88 (0.73 - 1.07)
CCDC40	17	0.62 (0.53 - 0.74)	0.57 (0.46 - 0.70)	0.53 (0.37 - 0.75)
CDHR2	5	3.12 (0.63 - 15.48)	1.63 (0.23 - 11.69)	6.52 (0.89 - 47.68)
CEACAM8	19	2.61 (0.51 - 13.46)	2.81 (0.38 - 20.86)	7.06 (0.98 - 50.60)
CHEK2	22	4.01 (1.50 - 10.77)	5.98 (2.04 - 17.50)	1.31 (0.15 - 11.44)
DDX56	7	6.20 (0.75 - 51.53)	11.81 (1.34 - 104.03)	N/A
DHRS4L2	14	1.11 (1.00 - 1.23)	1.06 (0.93 - 1.21)	1.21 (1.00 - 1.47)
DSTYK	1	0.09 (0.01 - 0.70)	0.18 (0.02 - 1.37)	N/A
FANCG	9	1.43 (0.45 - 4.51)	0.72 (0.14 - 3.80)	5.01 (1.33 - 18.83)
FANCM	14	2.01 (1.08 - 3.74)	1.79 (0.85 - 3.77)	4.61 (2.13 - 9.96)
FAT3	11	1.58 (0.71 - 3.49)	1.46 (0.54 - 3.89)	3.60 (1.34 - 9.62)
GEMIN2	14	0.27 (0.06 - 1.27)	0.35 (0.04 - 2.83)	0.86 (0.11 - 6.88)
GSTA1	6	2.87 (1.28 - 6.43)	3.20 (1.32 - 7.80)	2.13 (0.56 - 8.14)
LCP2	5	5.01 (0.58 - 42.93)	4.30 (0.38 - 49.03)	12.46 (1.11 - 140.47)
MBP	18	4.05 (1.66 - 9.89)	4.31 (1.64 - 11.36)	1.80 (0.36 - 9.09)
MKI67	10	1.24 (0.53 - 2.87)	1.49 (0.56 - 3.99)	2.44 (0.76 - 7.87)
MSH6	2	0.90 (0.81 - 0.99)	1.34 (1.19 - 1.51)	1.61 (1.34 - 1.92)
NDOR1	9	3.09 (1.51 - 6.33)	3.61 (1.63 - 7.97)	3.23 (1.09 - 9.51)
PALB2	16	6.47 (3.19 - 13.11)	5.11 (2.33 - 11.19)	6.43 (2.51 - 16.48)
PCDHGC5	5	1.07 (0.98 - 1.16)	0.88 (0.79 - 0.98)	0.86 (0.73 - 1.02)

PRDM2	1	1.17 (0.71 - 1.94)	1.33 (0.73 - 2.43)	1.05 (0.40 - 2.74)
PREX2	8	1.07 (0.50 - 2.29)	0.43 (0.12 - 1.53)	2.68 (1.01 - 7.15)
RAD51D	17	1.53 (0.43 - 5.45)	2.31 (0.57 - 9.38)	2.98 (0.54 - 16.44)
SAMD15	14	1.45 (0.73 - 2.88)	1.66 (0.72 - 3.82)	3.12 (1.24 - 7.87)
SDK2	17	4.20 (0.89 - 19.78)	5.14 (0.93 - 28.36)	6.71 (0.94 - 48.04)
SERINC3	20	1.40 (0.44 - 4.41)	0.81 (0.15 - 4.34)	4.67 (1.23 - 17.76)
SLC26A5	7	2.12 (1.25 - 3.62)	1.94 (1.04 - 3.59)	2.04 (0.89 - 4.67)
TTC4	1	2.94 (0.80 - 10.87)	4.98 (1.30 - 18.99)	1.56 (0.16 - 15.24)
TTLL9	20	0.43 (0.21 - 0.91)	0.15 (0.04 - 0.64)	0.48 (0.11 - 2.03)
WDR93	15	2.84 (0.90 - 8.94)	1.65 (0.36 - 7.53)	4.84 (1.07 - 21.91)
ZNF404	19	4.78 (1.36 - 16.80)	7.35 (1.94 - 27.90)	N/A

ER=estrogen receptor

* Discovery participants were selected for being *BRCA1/2* negative (see methods), replication results are presented for *BRCA1/2*.

Supplementary Methods: Genes Selected for Replication Based on Discovery Findings

AAMDC	*APCDD1*	*BRIP1*
AARS	*APEX1*	*BTN3A2*
ABCA1	*APOC3*	*BUB1B*
ABCA4	*AR*	*C12orf10*
ABCB5	*AREL1*	*C12orf80*
ABCC1	*ARHGAP28*	*C16orf45*
ABCC10	*ARHGAP35*	*C17orf77*
ACOT11	*ARHGEF10L*	*C17orf82*
ACOXL	*ARHGEF2*	*C2*
ACSBG2	*ARI1B*	*C2orf47*
ACSL1	*ARID1A*	*C3*
ACSM5	*ARID4A*	*C4orf46*
ACSM6	*ARID5B*	*C5orf60*
ACTR1B	*ARL5C*	*C7*
ADAM20	*ARPC1B*	*C9*
ADAM8	*ASCC1*	*CA9*
ADAMTS5	*ASIC3*	*CACNA2D1*
ADCY10	*ASPM*	*CAPN15*
ADCY4	*ASTN2*	*CAPN5*
ADGRG7	*ATAD3C*	*CARD14*
ADH7	*ATM*	*CASP8*
AGL	*ATP1A4*	*CASP8AP2*
AIF1	*ATP2B2*	*CATSPERB*
AKT1	*ATR*	*CAV3*
ALCAM	*ATXN7*	*CBWD1*
ALDH1B1	*B4GALT7*	*CBX2*
ALKBH8	*BABAM1*	*CBX8*
ALOX15	*BAG1*	*CCAR1*
ALPK1	*BAHD1*	*CCDC110*
AMZ1	*BAP1*	*CCDC40*
ANKDD1B	*BARD1*	*CCHCR1*
ANKRD2	*BATF2*	*CCL5*
ANKRD23	*BAZ1A*	*CCM2L*
ANKRD54	*BCHE*	*CCND1*
ANKS4B	*BCL9*	*CCNT1*
ANP32E	*BIN1*	*CCNT2*
ANXA3	*BIN2*	*CCR3*
ANXA4	*BLM*	*CCT6B*
AOC2	*BMP5*	*CD101*
AP2S1	*BOC*	*CD109*
APAF1	*BRCA1*	*CD244*
APBB2	*BRCA2*	*CD44*

CD46	CNTN5	DNAJC9
CD96	CNTN6	DNTT
CDC20	CPT1B	DOCK1
CDCA5	CRACR2B	DOK4
CDH1	CREB3L3	DPF3
CDH18	CREB3L4	DPPA3
CDH26	CRIPAK	DSG1
CDH3	CRLF3	DSG2
CDHR2	CSF2RB	DSP
CDIP1	CTBP2	DSTYK
CDK13	CTC1	DTNA
CDK5R2	CTCF	DUOX2
CDK5RAP2	CTNNB1	DUOXA2
CDKN1B	CTSH	DUSP10
CDKN2A	CXCL10	DUSP12
CDNF	CYFIP2	DUSP16
CEACAM1	CYP26B1	E2F3
CEACAM21	CYP2R1	ECD
CECR1	DARS2	ECM1
CELSR2	DCHS2	ECSIT
CENPT	DCLK1	ECT2
CEP152	DCTN1	EGFR
CEP250	DDX25	EID2
CFAP206	DDX39B	EIF2A
CFAP70	DDX43	EIF2B3
CFAP99	DDX56	EIF2S2
CFH	DDX58	EIF4EBP2
CGNL1	DEFB115	EIF4G2
CHAC1	DEFB128	ELAC2
CHAF1B	DEFB132	ELMO2
CHD6	DEPDC5	ELP3
CHEK2	DGKZ	EMP1
CHRND	DGUOK	ENAH
CITED2	DHRS4	EP300
CLDN3	DHX37	EPCAM
CLEC10A	DIAPH3	EQTN
CLEC11A	DICER1	ERAP2
CLSTN1	DKK3	ERBB3
CLSTN2	DLD	ERCC2
CLSTN3	DLG1	ERCC3
CMA1	DLGAP1	ERCC4
CNKSR1	DNAJA4	ERCC6
CNR2	DNAJC10	ERCC8
CNTD1	DNAJC5B	ETV4

ETV5	FSHR	HNF1A
EVPL	FSTL1	HNF1B
EXO1	FUZ	HNRNPCL3
EXOC6	FZD2	HOXC11
EXOSC1	GALNT2	HPCA
EXOSC10	GAPDHS	HPGDS
EYA3	GART	HPS6
EZH2	GATA3	HRG
FAM120A	GCNT3	ICAM1
FAM160A2	GEMIN2	IFIH1
FAM219B	GEMIN4	IFIT1
FANCA	GFM2	IFIT2
FANCC	GFRAL	IFNA10
FANCD2	GHR	IFNAR2
FANCG	GHSR	IFNW1
FANCL	GJA10	IGF2BP1
FANCM	GJB2	IK
FARP1	GK2	IL10RA
FASTKD2	GLI2	IL18RAP
FAT2	GLMP	IL23R
FAT3	GLP2R	IL2RB
FBN1	GLT1D1	IL33
FBP1	GMFG	IL5RA
FBXO18	GNA14	ILK
FBXW7	GOT1	IQCA1
FCGR1A	GP6	IRAK2
FCGR2B	GPR155	IRF3
FCGR3B	GPR55	ITGA2B
FDFT1	GPRC6A	ITGA3
FECH	GRB7	ITGB3
FERMT2	GRHL3	JAK2
FES	GRIP1	JAM2
FGF19	GSN	JMJD8
FKBP1B	GSTA1	KARS
FLRT2	GTF2H1	KHNYN
FLT4	GTF2H3	KIAA0319L
FMO1	GYS1	KIAA0368
FOLR1	HABP2	KIAA1524
FOXA3	HBP1	KIF26B
FPGS	HDAC1	KIRREL2
FPGT-TNNI3K	HEATR1	KLF12
FREM1	HIST1H2BO	KLF3
FRRS1L	HIST4H4	KLHL17
FRS3	HLTF	KLK7

KRTAP25-1	MBP	NCF1
LACTB2	MC1R	NCOA6
LAMC2	MCL1	NCR3LG1
LAMP1	MCM4	NDOR1
LAMP5	MCM6	NEDD9
LARP4	MCTP1	NEIL1
LCN2	MDC1	NEK1
LCNL1	MDM4	NEK8
LCP2	ME1	NEK9
LDLR	MED1	NELL1
LHX1	MED16	NF1
LIF	MELK	NHP2
LIM2	MEOX2	NID2
LIPM	METTL17	NLRP1
LMO4	METTL21A	NLRP11
LOC100129697	MFAP5	NLRP12
LOC107984974	MFN1	NLRP2
LONP1	MISP3	NLRP7
LOXL4	MKI67	NOG
LPL	MLANA	NOTCH3
LRBA	MLH1	NOTCH4
LRP4	MLH3	NOTO
LRRCC1	MLN	NPR3
LRRK1	MME	NR0B2
LRRK2	MMP1	NRBP2
LRTOMT	MMP21	NRCAM
LSM14A	MOS	NRN1
LTA4H	MPND	NRXN1
LY96	MPZL2	NSA2
MAD1L1	MRE11A	NT5C
MAGOHB	MRPS9	NTRK1
MANSC4	MSH2	NTRK2
MAP2K4	MSH4	NUP188
MAP3K1	MSH6	NUP210
MAP3K11	MTFR1L	NUP210L
MAP3K5	MTHFD1	NUP58
MAP3K9	MTHFR	NUPR1
MAP4	MUTYH	NWD1
MAPK12	MXRA7	NXPE2
MAPK14	N4BP2	OBSL1
MAPK9	NAE1	OGG1
MARC2	NAP1L4	OSBPL1A
MASP2	NBN	OSBPL9
MBD2	NBPF3	OXSR1

PAFAH1B2	PLAT	PTPRF
PALB2	PLCG2	PVRL2
PAPOLA	PLCH1	PXDN
PAPOLG	PLCL2	PXK
PAPSS1	PLEKHG5	PYGO2
PAQR3	PLG	QRSL1
PARN	PLGRKT	R3HCC1L
PARP2	PLPPR3	RAB25
PATE3	PMS1	RAB34
PBK	POLG	RAB42
PBX4	POLQ	RABL6
PCDH20	POM121C	RAD17
PCDHA11	PPFIBP1	RAD18
PCDHB3	PPIE	RAD21
PCDHGA3	PPIP5K1	RAD50
PCDHGA4	PPP1R12A	RAD51B
PCDHGA5	PPP1R42	RAD51C
PCDHGA9	PPP2R1A	RAD51D
PCDHGB2	PPP2R3A	RAD52
PCDHGB5	PPP3CA	RARS
PCDHGC3	PRAC2	RASAL2
PCDHGC5	PRAMEF17	RASIP1
PCSK4	PRDM2	RB1
PDCD6IP	PRDM7	RBBP8
PDE4B	PRELP	RBBP8NL
PDIA3	PREX1	RBKS
PDIA4	PREX2	RBM19
PDIA5	PRKAR2A	RBM6
PDLIM1	PRKCE	RCHY1
PDZD8	PRKRA	RECQL
PELO	PRMT9	RECQL5
PER3	PRODH	REST
PFDN6	PRPF19	RHNO1
PGLYRP3	PSAP	RHOBTB1
PGLYRP4	PSMC3IP	RHOF
PGM5	PSMD13	RIC1
PHC2	PTEN	RIPK4
PIK3C2G	PTGDR2	RLF
PIK3CA	PTGER4	RMDN1
PIK3CG	PTGES3	RNASE7
PIK3R1	PTGIS	RNASEL
PIK3R3	PTGS1	RNF135
PKLR	PTPN11	RNF138
PKP4	PTPRD	RNF187

RNF34	SLC12A4	SYT1
RNF44	SLC16A1	SZT2
ROBO2	SLC19A1	TAB2
ROBO4	SLC26A5	TACC2
RORA	SLC27A5	TAF6
RP1L1	SLC36A1	TARSL2
RRBP1	SLC37A4	TAX1BP3
RREB1	SLC44A2	TBC1D2
RTEL1	SLC6A2	TBC1D23
RTTN	SLX4	TBX3
S100A13	SMARCE1	TCEA1
SALL1	SMPDL3A	TCF7L1
SAMD15	SNAPC1	TEK
SASH1	SNRNP200	TF
SAXO1	SNX8	TFAP4
SAXO2	SORD	THAP5
SBF2	SPAST	THBS4
SCMH1	SPATA18	THPO
SCYL3	SPHK1	THRA
SDCBP2	SPINK5	TIMELESS
SDCCAG3	SPINT1	TIMM44
SDHB	SPIRE2	TINAG
SDK1	SPOP	TLDC2
SDK2	SPPL2A	TLN2
SECTM1	SPSB2	TLR4
SELP	SPTBN5	TMEM221
SEMA6D	SQRDL	TMEM254
SERGEF	SQSTM1	TMEM59
SERINC3	SRA1	TNFAIP6
SERINC5	SRGAP1	TNFSF18
SETD2	SSC5D	TNS1
SETSIP	STAB1	TOB2
SETX	STAG3	TP53
SF3A3	STARD5	TRAK1
SFPQ	STARD9	TRIM31
SFRP5	STC2	TRIM32
SH2D3C	STK11	TRIM6
SHC2	STK31	TRIM63
SHCBP1	STK36	TRIM71
SIDT2	STMND1	TRIO
SIGLEC1	SUCLG2	TRIOBP
SIVA1	SUCO	TRIP13
SKA2	SVIL	TRMU
SKA3	SYN3	TROAP

TRPV1	USP19	XYLB
TSC2	USP25	ZBTB40
TSPAN15	USP49	ZDHHC2
TSPO	USP54	ZFP36L2
TTC21B	USP6	ZFR2
TTC4	VANGL2	ZFYVE1
TTC7A	VARS2	ZHX1-C8orf76
TTLL9	VCL	ZNF195
TUB	VLDLR	ZNF257
TUBE1	VRK2	ZNF266
TUBGCP2	WDHD1	ZNF335
TUT1	WDR7	ZNF358
TXLNA	WDR93	ZNF385B
TXNDC11	WEE2	ZNF404
TYK2	WRAP53	ZNF510
TYR	WRN	ZNF521
UBA7	WTAP	ZNF528
UBE2U	XAB2	ZNF560
UFM1	XAF1	ZNF778
UGT1A1	XPC	ZNF8
UMODL1	XPNPEP1	ZNF816
URB2	XRCC1	ZNF880
USH1C	XRCC2	ZSCAN22
USP17L1	XRCC3	