VEP annotated somatic variants

Hugo_Symbol	Entrez_Gene_Id	Center	NCBI_Build
AADACL2	0	.	GRCh37
AAED1	0	.	GRCh37
AASS	0	.	GRCh37
ABCA10	0	.	GRCh37
ABCA3	0	.	GRCh37
ABCA6	0	.	GRCh37
ABCA6	0	.	GRCh37
ABCA9	0	.	GRCh37
ABCC1	0	.	GRCh37
ABCC6	0	.	GRCh37
ABCC8	0	.	GRCh37
ABHD3	0	.	GRCh37
ABR	0	.	GRCh37
AC005013.5	0	.	GRCh37
AC026202.1	0	.	GRCh37
ACAD8	0	.	GRCh37
ACADM	0	.	GRCh37
ACADSB	0	.	GRCh37
ACBD3	0	.	GRCh37
ACER1	0	.	GRCh37
ACP2	0	.	GRCh37
ACPL2	0	.	GRCh37
ACSBG1	0	.	GRCh37
ACSF3	0	.	GRCh37
ACSM4	0	.	GRCh37
ACVR2B	0	.	GRCh37
ADAM15	0	.	GRCh37
ADAM17	0	.	GRCh37
ADAMTS14	0	.	GRCh37
ADAMTS2	0	.	GRCh37
ADAMTS20	0	.	GRCh37
ADAMTS4	0	.	GRCh37
ADAMTS6	0	.	GRCh37
ADAMTSL1	0	.	GRCh37
ADORA1	0	.	GRCh37
ADORA3	0	.	GRCh37
AFAP1L2	0	.	GRCh37
AFF1	0	.	GRCh37
AFF2	0	.	GRCh37
AGAP3	0	.	GRCh37
AGBL3	0	.	GRCh37
AGTR1	0	.	GRCh37
AHI1	0	.	GRCh37
AHSP	0	.	GRCh37
AIG1	0	.	GRCh37
AIM1L	0	.	GRCh37
AIM1L	0	.	GRCh37
AIPL1	0	.	GRCh37
AIRE	0	.	GRCh37
AIRE	0	.	GRCh37
AKAP9	0	.	GRCh37
AKAP9	0	.	GRCh37
AKR1B10	0	.	GRCh37
ALB	0	.	GRCh37

ALDH16A1	0	.	GRCh37
ALDH1A3	0	.	GRCh37
ALOX5	0	.	GRCh37
ALPK3	0	.	GRCh37
ALPK3	0	.	GRCh37
AMICA1	0	.	GRCh37
AMICA1	0	.	GRCh37
ANAPC1	0	.	GRCh37
ANK1	0	.	GRCh37
ANKAR	0	.	GRCh37
ANKK1	0	.	GRCh37
ANKLE2	0	.	GRCh37
ANKRD18B	0	.	GRCh37
ANKRD26	0	.	GRCh37
ANKRD28	0	.	GRCh37
ANKRD35	0	.	GRCh37
ANKRD52	0	.	GRCh37
ANKRD55	0	.	GRCh37
AOX1	0	.	GRCh37
AP002884.2	0	.	GRCh37
AP1B1	0	.	GRCh37
AP2A1	0	.	GRCh37
AP4E1	0	.	GRCh37
AP4E1	0	.	GRCh37
APBB1IP	0	.	GRCh37
APOOL	0	.	GRCh37
AQP12A	0	.	GRCh37
AQP12A	0	.	GRCh37
AQP4	0	.	GRCh37
AQPEP	0	.	GRCh37
ARF3	0	.	GRCh37
ARHGAP10	0	.	GRCh37
ARHGAP19-SLIT1	0	.	GRCh37
ARHGAP36	0	.	GRCh37
ARHGAP4	0	.	GRCh37
ARHGEF11	0	.	GRCh37
ARHGEF16	0	.	GRCh37
ARHGEF2	0	.	GRCh37
ARHGEF3	0	.	GRCh37
ARHGEF7	0	.	GRCh37
ARID3C	0	.	GRCh37
ARL5B	0	.	GRCh37
ARMC8	0	.	GRCh37
ARMCX4	0	.	GRCh37
ARMCX4	0	.	GRCh37
ARMCX4	0	.	GRCh37
ARMCX4	0	.	GRCh37
ARRB2	0	.	GRCh37
ARRDC2	0	.	GRCh37
ARRDC2	0	.	GRCh37
ARSA	0	.	GRCh37
ARVCF	0	.	GRCh37
ASB10	0	.	GRCh37
ASB14	0	.	GRCh37
ASB4	0	.	GRCh37

ASB6	0	.	GRCh37
ASIC4	0	.	GRCh37
ASPSCR1	0	.	GRCh37
ASTL	0	.	GRCh37
ASTL	0	.	GRCh37
ASTN2	0	.	GRCh37
ASXL3	0	.	GRCh37
ASZ1	0	.	GRCh37
ATG4C	0	.	GRCh37
ATL1	0	.	GRCh37
ATP11A	0	.	GRCh37
ATP13A2	0	.	GRCh37
ATP1A2	0	.	GRCh37
ATP1A4	0	.	GRCh37
ATP2C2	0	.	GRCh37
ATP5C1	0	.	GRCh37
ATP7A	0	.	GRCh37
ATP8B1	0	.	GRCh37
ATP9A	0	.	GRCh37
ATP9A	0	.	GRCh37
ATRIP	0	.	GRCh37
ATXN2L	0	.	GRCh37
AWAT1	0	.	GRCh37
AWAT2	0	.	GRCh37
AXDND1	0	.	GRCh37
AXIN1	0	.	GRCh37
B3GNT3	0	.	GRCh37
BAIAP2	0	.	GRCh37
BAIAP3	0	.	GRCh37
BBS12	0	.	GRCh37
BCKDHA	0	.	GRCh37
BCL7B	0	.	GRCh37
BCORL1	0	.	GRCh37
BEST1	0	.	GRCh37
BICD1	0	.	GRCh37
BLNK	0	.	GRCh37
BMP15	0	.	GRCh37
BNC1	0	.	GRCh37
BPIFB2	0	.	GRCh37
BPTF	0	.	GRCh37
BRCA1	0	.	GRCh37
BRCA1	0	.	GRCh37
BRCA1	0	.	GRCh37
BRCA2	0	.	GRCh37
BRD9	0	.	GRCh37
BRWD1	0	.	GRCh37
BSDC1	0	.	GRCh37
BSG	0	.	GRCh37
BSG	0	.	GRCh37
BTBD16	0	.	GRCh37
BTBD16	0	.	GRCh37
BTBD8	0	.	GRCh37
BTG1	0	.	GRCh37
BTNL9	0	.	GRCh37
BZRAP1	0	.	GRCh37

C10orf105	0	.	GRCh37
C10orf71	0	.	GRCh37
C10orf90	0	.	GRCh37
C11orf49	0	.	GRCh37
C12orf49	0	.	GRCh37
C12orf55	0	.	GRCh37
C12orf60	0	.	GRCh37
C14orf164	0	.	GRCh37
C17orf107	0	.	GRCh37
C17orf53	0	.	GRCh37
C19orf26	0	.	GRCh37
C19orf33	0	.	GRCh37
C1GALT1C1	0	.	GRCh37
C1orf101	0	.	GRCh37
C1orf141	0	.	GRCh37
C1orf168	0	.	GRCh37
C1orf173	0	.	GRCh37
C1QTNF1	0	.	GRCh37
C2orf54	0	.	GRCh37
C2orf81	0	.	GRCh37
C3	0	.	GRCh37
C4orf29	0	.	GRCh37
C5	0	.	GRCh37
C5	0	.	GRCh37
C6orf201	0	.	GRCh37
C7	0	.	GRCh37
CA10	0	.	GRCh37
CA5A	0	.	GRCh37
CABIN1	0	.	GRCh37
CACNA1A	0	.	GRCh37
CACNA1B	0	.	GRCh37
CACNA1C	0	.	GRCh37
CACNA2D2	0	.	GRCh37
CACNA2D2	0	.	GRCh37
CACNB2	0	.	GRCh37
CAGE1	0	.	GRCh37
CALD1	0	.	GRCh37
CALR	0	.	GRCh37
CAMK1D	0	.	GRCh37
CAMK2D	0	.	GRCh37
CAMKMT	0	.	GRCh37
CAMSAP3	0	.	GRCh37
CAPN11	0	.	GRCh37
CAPN9	0	.	GRCh37
CAPS	0	.	GRCh37
CARD10	0	.	GRCh37
CARD8	0	.	GRCh37
CASP14	0	.	GRCh37
CASQ1	0	.	GRCh37
CASZ1	0	.	GRCh37
CATSPERG	0	.	GRCh37
CAV3	0	.	GRCh37
CCDC102A	0	.	GRCh37
CCDC104	0	.	GRCh37
CCDC105	0	.	GRCh37

CCDC11	0	.	GRCh37
CCDC120	0	.	GRCh37
CCDC132	0	.	GRCh37
CCDC137	0	.	GRCh37
CCDC147	0	.	GRCh37
CCDC158	0	.	GRCh37
CCDC169-SOHLH2	0	.	GRCh37
CCDC18	0	.	GRCh37
CCDC57	0	.	GRCh37
CCDC6	0	.	GRCh37
CCDC81	0	.	GRCh37
CCL19	0	.	GRCh37
CCR2	0	.	GRCh37
CD109	0	.	GRCh37
CD200R1L	0	.	GRCh37
CD244	0	.	GRCh37
CD300A	0	.	GRCh37
CD3EAP	0	.	GRCh37
CD46	0	.	GRCh37
CD7	0	.	GRCh37
CDC23	0	.	GRCh37
CDC42BPG	0	.	GRCh37
CDC45	0	.	GRCh37
CDCP1	0	.	GRCh37
CDH18	0	.	GRCh37
CDK19	0	.	GRCh37
CDK3	0	.	GRCh37
CDK7	0	.	GRCh37
CDKAL1	0	.	GRCh37
CDKL5	0	.	GRCh37
CDS2	0	.	GRCh37
CDSN	0	.	GRCh37
CDSN	0	.	GRCh37
CEACAM21	0	.	GRCh37
CEACAM3	0	.	GRCh37
CECR1	0	.	GRCh37
CECR2	0	.	GRCh37
CECR2	0	.	GRCh37
CECR5	0	.	GRCh37
CECR6	0	.	GRCh37
CENPI	0	.	GRCh37
CENPW	0	.	GRCh37
CEP250	0	.	GRCh37
CEP250	0	.	GRCh37
CEP63	0	.	GRCh37
CEP63	0	.	GRCh37
CEP70	0	.	GRCh37
CEP95	0	.	GRCh37
CERCAM	0	.	GRCh37
CES2	0	.	GRCh37
CFH	0	.	GRCh37
CFTR	0	.	GRCh37
CGB7	0	.	GRCh37
CHD1L	0	.	GRCh37
CHFR	0	.	GRCh37

CHFR	0	.	GRCh37
CHI3L2	0	.	GRCh37
CHRNB1	0	.	GRCh37
CHST14	0	.	GRCh37
CIITA	0	.	GRCh37
CINP	0	.	GRCh37
CIT	0	.	GRCh37
CITED1	0	.	GRCh37
CKMT2	0	.	GRCh37
CLCN6	0	.	GRCh37
CLCNKA	0	.	GRCh37
CLDN15	0	.	GRCh37
CLEC4E	0	.	GRCh37
CLIC2	0	.	GRCh37
CLIC4	0	.	GRCh37
CLIP1	0	.	GRCh37
CLIP4	0	.	GRCh37
CNKSR2	0	.	GRCh37
CNNM1	0	.	GRCh37
CNOT1	0	.	GRCh37
CNOT11	0	.	GRCh37
CNR1	0	.	GRCh37
CNTN4	0	.	GRCh37
CNTNAP2	0	.	GRCh37
CNTNAP2	0	.	GRCh37
CNTRL	0	.	GRCh37
COBL	0	.	GRCh37
COG4	0	.	GRCh37
COG5	0	.	GRCh37
COL17A1	0	.	GRCh37
COL23A1	0	.	GRCh37
COL24A1	0	.	GRCh37
COL24A1	0	.	GRCh37
COL26A1	0	.	GRCh37
COL4A6	0	.	GRCh37
COL5A3	0	.	GRCh37
COL6A1	0	.	GRCh37
COL6A3	0	.	GRCh37
COMT	0	.	GRCh37
COX20	0	.	GRCh37
CP	0	.	GRCh37
CPEB1	0	.	GRCh37
CPEB4	0	.	GRCh37
CR2	0	.	GRCh37
CRB2	0	.	GRCh37
CRHR2	0	.	GRCh37
CRIM1	0	.	GRCh37
CRIM1	0	.	GRCh37
CRISP3	0	.	GRCh37
CRNKL1	0	.	GRCh37
CRTC3	0	.	GRCh37
CRYBG3	0	.	GRCh37
CRYBG3	0	.	GRCh37
CSAG1	0	.	GRCh37
CSNK2A1	0	.	GRCh37

CSPG4	0	.	GRCh37
CTCFL	0	.	GRCh37
CTD-3088G3.8	0	.	GRCh37
CTNNA3	0	.	GRCh37
CTNNAL1	0	.	GRCh37
CUBN	0	.	GRCh37
CUL2	0	.	GRCh37
CUL7	0	.	GRCh37
CUX1	0	.	GRCh37
CUX1	0	.	GRCh37
CWC22	0	.	GRCh37
CWC22	0	.	GRCh37
CWF19L2	0	.	GRCh37
CXCR3	0	.	GRCh37
CYB561A3	0	.	GRCh37
CYB5R2	0	.	GRCh37
CYP2A13	0	.	GRCh37
CYP2A13	0	.	GRCh37
CYP3A4	0	.	GRCh37
CYP4F12	0	.	GRCh37
CYP51A1	0	.	GRCh37
DAGLA	0	.	GRCh37
DARS	0	.	GRCh37
DBR1	0	.	GRCh37
DCAF15	0	.	GRCh37
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DCAF15	0	.	GRCh37
DCC	0	.	GRCh37
DCDC2	0	.	GRCh37
DCHS2	0	.	GRCh37
DCTD	0	.	GRCh37
DDX11	0	.	GRCh37
DDX11	0	.	GRCh37
DDX59	0	.	GRCh37
DENND1A	0	.	GRCh37
DENND5A	0	.	GRCh37
DEPDC1B	0	.	GRCh37
DGCR2	0	.	GRCh37
DGKB	0	.	GRCh37
DHRS3	0	.	GRCh37
DHX32	0	.	GRCh37
DHX37	0	.	GRCh37
DHX8	0	.	GRCh37
DHX8	0	.	GRCh37
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DIAPH1	0	.	GRCh37
DIP2B	0	.	GRCh37
DIS3L	0	.	GRCh37
DISC1	0	.	GRCh37
DISC1	0	.	GRCh37
DKK4	0	.	GRCh37
DLG2	0	.	GRCh37
DLG3	0	.	GRCh37
DLG5	0	.	GRCh37
DLK2	0	.	GRCh37

DMKN	0	.	GRCh37
DNA2	0	.	GRCh37
DNAH11	0	.	GRCh37
DNAH12	0	.	GRCh37
DNAH14	0	.	GRCh37
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DNAH14	0	.	GRCh37
DNAH17	0	.	GRCh37
DNAH8	0	.	GRCh37
DNAH9	0	.	GRCh37
DNALI1	0	.	GRCh37
DNASE2B	0	.	GRCh37
DNMBP	0	.	GRCh37
DOCK2	0	.	GRCh37
DOCK3	0	.	GRCh37
DOT1L	0	.	GRCh37
DPEP1	0	.	GRCh37
DPF1	0	.	GRCh37
DPH5	0	.	GRCh37
DPY19L2	0	.	GRCh37
DRAXIN	0	.	GRCh37
DRP2	0	.	GRCh37
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DRP2	0	.	GRCh37
DSCAML1	0	.	GRCh37
DSG3	0	.	GRCh37
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DSP	0	.	GRCh37
DST	0	.	GRCh37
DTD2	0	.	GRCh37
DTNBP1	0	.	GRCh37
DTWD2	0	.	GRCh37
DTX2	0	.	GRCh37
DUSP18	0	.	GRCh37
DUSP6	0	.	GRCh37
DYNC1I1	0	.	GRCh37
DYNC2H1	0	.	GRCh37
EBNA1BP2	0	.	GRCh37
EBP	0	.	GRCh37
ECE1	0	.	GRCh37
ECEL1	0	.	GRCh37
ECT2	0	.	GRCh37
ECT2L	0	.	GRCh37
EDEM3	0	.	GRCh37
EDN1	0	.	GRCh37
EDNRB	0	.	GRCh37
EEA1	0	.	GRCh37
EEF1A2	0	.	GRCh37
EEF1E1	0	.	GRCh37
EFCAB13	0	.	GRCh37
EFCAB3	0	.	GRCh37
EFCAB4B	0	.	GRCh37

EFHB	0	.	GRCh37
EFTUD1	0	.	GRCh37
EFTUD2	0	.	GRCh37
EIF2S3	0	.	GRCh37
ELF4	0	.	GRCh37
ELFN2	0	.	GRCh37
ELFN2	0	.	GRCh37
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ELN	0	.	GRCh37
ELOVL2	0	.	GRCh37
EMC1	0	.	GRCh37
EMC2	0	.	GRCh37
EMC2	0	.	GRCh37
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EML1	0	.	GRCh37
EN1	0	.	GRCh37
ENG	0	.	GRCh37
ENOX1	0	.	GRCh37
ENTPD1	0	.	GRCh37
ENTPD5	0	.	GRCh37
EP400	0	.	GRCh37
EPHB6	0	.	GRCh37
EPHX1	0	.	GRCh37
EPHX2	0	.	GRCh37
ERN1	0	.	GRCh37
ESPL1	0	.	GRCh37
ESYT3	0	.	GRCh37
ETFA	0	.	GRCh37
ETFB	0	.	GRCh37
ETHE1	0	.	GRCh37
EVI5	0	.	GRCh37
EVI5L	0	.	GRCh37
EVI5L	0	.	GRCh37
EVPL	0	.	GRCh37
EVPL	0	.	GRCh37
EXD2	0	.	GRCh37
EXO1	0	.	GRCh37
EXOC1	0	.	GRCh37
EZR	0	.	GRCh37
F8	0	.	GRCh37
F8	0	.	GRCh37
F9	0	.	GRCh37
FAAH2	0	.	GRCh37
FADS2	0	.	GRCh37
FADS3	0	.	GRCh37
FAH	0	.	GRCh37
FAM118A	0	.	GRCh37
FAM122C	0	.	GRCh37
FAM122C	0	.	GRCh37
FAM127C	0	.	GRCh37
FAM127C	0	.	GRCh37
FAM135B	0	.	GRCh37
FAM162B	0	.	GRCh37
FAM168A	0	.	GRCh37

FAM181B	0	.	GRCh37
FAM184B	0	.	GRCh37
FAM186A	0	.	GRCh37
FAM187B	0	.	GRCh37
FAM189B	0	.	GRCh37
FAM21C	0	.	GRCh37
FAM63A	0	.	GRCh37
FAM65B	0	.	GRCh37
FAM81B	0	.	GRCh37
FANCA	0	.	GRCh37
FANCE	0	.	GRCh37
FANCE	0	.	GRCh37
FANCE	0	.	GRCh37
FAR2	0	.	GRCh37
FARP2	0	.	GRCh37
FARP2	0	.	GRCh37
FASN	0	.	GRCh37
FASN	0	.	GRCh37
FASN	0	.	GRCh37
FASN	0	.	GRCh37
FBLN2	0	.	GRCh37
FBN3	0	.	GRCh37
FBRSL1	0	.	GRCh37
FBXL21	0	.	GRCh37
FBXO10	0	.	GRCh37
FBXO10	0	.	GRCh37
FBXO17	0	.	GRCh37
FBXW12	0	.	GRCh37
FBXW4	0	.	GRCh37
FCAMR	0	.	GRCh37
FCHO1	0	.	GRCh37
FGFR4	0	.	GRCh37
FGG	0	.	GRCh37
FHOD3	0	.	GRCh37
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FHOD3	0	.	GRCh37
FIGN	0	.	GRCh37
FIP1L1	0	.	GRCh37
FKBP6	0	.	GRCh37
FKBP7	0	.	GRCh37
FLNA	0	.	GRCh37
FLNB	0	.	GRCh37
FLT4	0	.	GRCh37
FMN2	0	.	GRCh37
FMN2	0	.	GRCh37
FMO3	0	.	GRCh37
FNBP4	0	.	GRCh37
FNBP4	0	.	GRCh37
FNDC1	0	.	GRCh37
FNDC1	0	.	GRCh37
FOXF2	0	.	GRCh37
FOXP4	0	.	GRCh37
FPGS	0	.	GRCh37
FRAS1	0	.	GRCh37
FRAS1	0	.	GRCh37

FRAS1	0	.	GRCh37
FRAS1	0	.	GRCh37
FRAS1	0	.	GRCh37
FREM3	0	.	GRCh37
FRMD4A	0	.	GRCh37
FSIP1	0	.	GRCh37
FSTL5	0	.	GRCh37
FUBP3	0	.	GRCh37
FUT1	0	.	GRCh37
FUT6	0	.	GRCh37
FXYD2	0	.	GRCh37
FYCO1	0	.	GRCh37
GADL1	0	.	GRCh37
GAK	0	.	GRCh37
GAK	0	.	GRCh37
GALC	0	.	GRCh37
GALC	0	.	GRCh37
GALK1	0	.	GRCh37
GALNT10	0	.	GRCh37
GALNT14	0	.	GRCh37
GALNT8	0	.	GRCh37
GALNT8	0	.	GRCh37
GAREM	0	.	GRCh37
GAREM	0	.	GRCh37
GAREM	0	.	GRCh37
GARNL3	0	.	GRCh37
GBP5	0	.	GRCh37
GBP5	0	.	GRCh37
GBP5	0	.	GRCh37
GCGR	0	.	GRCh37
GCNT2	0	.	GRCh37
GDA	0	.	GRCh37
GDAP1L1	0	.	GRCh37
GDF2	0	.	GRCh37
GEMIN2	0	.	GRCh37
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GINS1	0	.	GRCh37
GLG1	0	.	GRCh37
GLG1	0	.	GRCh37
GLIS2	0	.	GRCh37
GLO1	0	.	GRCh37
GLRA4	0	.	GRCh37
GLRA4	0	.	GRCh37
GLT8D2	0	.	GRCh37
GLYATL2	0	.	GRCh37
GMCL1	0	.	GRCh37
GNAZ	0	.	GRCh37
GNB1L	0	.	GRCh37
GNRHR	0	.	GRCh37
GOLGA3	0	.	GRCh37

GP1BA	0	.	GRCh37
GPC6	0	.	GRCh37
GPLD1	0	.	GRCh37
GPM6B	0	.	GRCh37
GPN1	0	.	GRCh37
GPR101	0	.	GRCh37
GPR123	0	.	GRCh37
GPR123	0	.	GRCh37
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RP3-467K16.2	0	.	GRCh37
RPAP3	0	.	GRCh37
RPH3AL	0	.	GRCh37
RPL18A	0	.	GRCh37
RPL23A	0	.	GRCh37
RPL23A	0	.	GRCh37
RPL3	0	.	GRCh37
RPS4X	0	.	GRCh37
RPS6KA2	0	.	GRCh37
RPTOR	0	.	GRCh37
RPTOR	0	.	GRCh37
RRP1B	0	.	GRCh37
RRP1B	0	.	GRCh37
RSAD1	0	.	GRCh37
RSU1	0	.	GRCh37
RTN3	0	.	GRCh37
RUFY1	0	.	GRCh37
RUFY1	0	.	GRCh37
RUFY2	0	.	GRCh37
RXRA	0	.	GRCh37
RYR1	0	.	GRCh37
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RYR1	0	.	GRCh37
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RYR2	0	.	GRCh37
RYR3	0	.	GRCh37
SAP18	0	.	GRCh37
SARDH	0	.	GRCh37
SBDS	0	.	GRCh37
SBF1	0	.	GRCh37
SBF2	0	.	GRCh37
SCAF1	0	.	GRCh37
SCAMP3	0	.	GRCh37
SCARF2	0	.	GRCh37
SCEL	0	.	GRCh37
SCIN	0	.	GRCh37
SCLT1	0	.	GRCh37
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SCML4	0	.	GRCh37
SCN3A	0	.	GRCh37
SCN9A	0	.	GRCh37

SCN9A	0	.	GRCh37
SDE2	0	.	GRCh37
SDK1	0	.	GRCh37
SEC13	0	.	GRCh37
SEC14L6	0	.	GRCh37
SEC16B	0	.	GRCh37
SEC23B	0	.	GRCh37
SEC24D	0	.	GRCh37
SEC31B	0	.	GRCh37
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SEC31B	0	.	GRCh37
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SECISBP2	0	.	GRCh37
SECTM1	0	.	GRCh37
SELE	0	.	GRCh37
SELP	0	.	GRCh37
SEMA3A	0	.	GRCh37
SEMA3A	0	.	GRCh37
SEMA3F	0	.	GRCh37
SEPT3	0	.	GRCh37
SERPINA3	0	.	GRCh37
SERTAD1	0	.	GRCh37
SETD1B	0	.	GRCh37
SETD1B	0	.	GRCh37
SETD5	0	.	GRCh37
SEZ6L	0	.	GRCh37
SF3B3	0	.	GRCh37
SF3B5	0	.	GRCh37
SGPL1	0	.	GRCh37
SGSM2	0	.	GRCh37
SGSM2	0	.	GRCh37
SGSM3	0	.	GRCh37
SH3GLB1	0	.	GRCh37
SH3PXD2A	0	.	GRCh37
SHANK1	0	.	GRCh37
SHANK1	0	.	GRCh37
SHH	0	.	GRCh37
SHROOM2	0	.	GRCh37
SIGLEC12	0	.	GRCh37
SIK1	0	.	GRCh37
SIM2	0	.	GRCh37
SIPA1L2	0	.	GRCh37
SLAMF7	0	.	GRCh37
SLC10A4	0	.	GRCh37
SLC10A6	0	.	GRCh37
SLC12A7	0	.	GRCh37
SLC13A1	0	.	GRCh37
SLC16A2	0	.	GRCh37
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SLC1A6	0	.	GRCh37
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SLC23A1	0	.	GRCh37
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SLC25A39	0	.	GRCh37

SLC25A39	0	.	GRCh37
SLC26A11	0	.	GRCh37
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SLC28A2	0	.	GRCh37
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SLC35B4	0	.	GRCh37
SLC35F1	0	.	GRCh37
SLC35F3	0	.	GRCh37
SLC37A2	0	.	GRCh37
SLC38A3	0	.	GRCh37
SLC38A7	0	.	GRCh37
SLC45A4	0	.	GRCh37
SLC4A2	0	.	GRCh37
SLC5A5	0	.	GRCh37
SLC6A14	0	.	GRCh37
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SLC6A9	0	.	GRCh37
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SLC9A7	0	.	GRCh37
SLCO2A1	0	.	GRCh37
SMARCA1	0	.	GRCh37
SMARCA5	0	.	GRCh37
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SMOC1	0	.	GRCh37
SMTN	0	.	GRCh37
SMYD3	0	.	GRCh37
SORBS1	0	.	GRCh37
SORCS2	0	.	GRCh37
SPAG17	0	.	GRCh37
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SPANXN2	0	.	GRCh37
SPATC1	0	.	GRCh37
SPEG	0	.	GRCh37
SPEG	0	.	GRCh37
SPINT2	0	.	GRCh37
SPOCK2	0	.	GRCh37
SPTBN5	0	.	GRCh37
SPTBN5	0	.	GRCh37
SRCAP	0	.	GRCh37
SSPO	0	.	GRCh37
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SSUH2	0	.	GRCh37
ST3GAL2	0	.	GRCh37
ST6GALNAC2	0	.	GRCh37
ST6GALNAC2	0	.	GRCh37
ST6GALNAC4	0	.	GRCh37
STAB2	0	.	GRCh37
STAMBP	0	.	GRCh37
STAP1	0	.	GRCh37
STARD9	0	.	GRCh37
STAT4	0	.	GRCh37
STAT5B	0	.	GRCh37

STAU2	0	.	GRCh37
STOML1	0	.	GRCh37
STRA13	0	.	GRCh37
STRA8	0	.	GRCh37
STRBP	0	.	GRCh37
STRIP1	0	.	GRCh37
STRIP2	0	.	GRCh37
STXBP5	0	.	GRCh37
STYK1	0	.	GRCh37
STYXL1	0	.	GRCh37
SUCNR1	0	.	GRCh37
SUMO3	0	.	GRCh37
SUMO4	0	.	GRCh37
SUPT5H	0	.	GRCh37
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SUSD3	0	.	GRCh37
SWAP70	0	.	GRCh37
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SYN2	0	.	GRCh37
SYNE2	0	.	GRCh37
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SYNJ2	0	.	GRCh37
SYNM	0	.	GRCh37
SYNPO2	0	.	GRCh37
TAB2	0	.	GRCh37
TAB2	0	.	GRCh37
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TAGAP	0	.	GRCh37
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TARSL2	0	.	GRCh37
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TATDN2	0	.	GRCh37
TATDN2	0	.	GRCh37
TBC1D22A	0	.	GRCh37
TBC1D4	0	.	GRCh37
TBC1D5	0	.	GRCh37
TBCK	0	.	GRCh37
TBX10	0	.	GRCh37
TCEAL2	0	.	GRCh37
TCEB3	0	.	GRCh37
TCERG1	0	.	GRCh37
TCN2	0	.	GRCh37
TDRD9	0	.	GRCh37
TENM1	0	.	GRCh37
TENM2	0	.	GRCh37
TERF2	0	.	GRCh37
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TEX14	0	.	GRCh37
TEX2	0	.	GRCh37
TEX26	0	.	GRCh37
TFB1M	0	.	GRCh37
TFDP3	0	.	GRCh37
TFPT	0	.	GRCh37
TGFBR3	0	.	GRCh37

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THEG	0	.	GRCh37
THSD7A	0	.	GRCh37
THTPA	0	.	GRCh37
THUMPD2	0	.	GRCh37
TIAM1	0	.	GRCh37
TIAM2	0	.	GRCh37
TICAM1	0	.	GRCh37
TIMM21	0	.	GRCh37
TKT	0	.	GRCh37
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TLX2	0	.	GRCh37
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TMEM131	0	.	GRCh37
TMEM140	0	.	GRCh37
TMEM150C	0	.	GRCh37
TMEM185A	0	.	GRCh37
TMEM216	0	.	GRCh37
TMEM220	0	.	GRCh37
TMPRSS11A	0	.	GRCh37
TNFAIP3	0	.	GRCh37
TNFSF8	0	.	GRCh37
TNRC18	0	.	GRCh37
TNS4	0	.	GRCh37
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TPGS2	0	.	GRCh37
TPM4	0	.	GRCh37
TPPP	0	.	GRCh37
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TPRG1	0	.	GRCh37
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TRAPPC6B	0	.	GRCh37
TRAPPC6B	0	.	GRCh37
TRERF1	0	.	GRCh37
TREX2	0	.	GRCh37
TRIM15	0	.	GRCh37
TRIM27	0	.	GRCh37
TRIM46	0	.	GRCh37
TRIM62	0	.	GRCh37
TRIM67	0	.	GRCh37
TRIM9	0	.	GRCh37

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TRIO	0	.	GRCh37
TRIP6	0	.	GRCh37
TRMT1	0	.	GRCh37
TRMT2B	0	.	GRCh37
TRPC4AP	0	.	GRCh37
TRPM1	0	.	GRCh37
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TSPAN1	0	.	GRCh37
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TSPAN7	0	.	GRCh37
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TTC18	0	.	GRCh37
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TTC28	0	.	GRCh37
TTC40	0	.	GRCh37
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TTLL1	0	.	GRCh37
TTLL6	0	.	GRCh37
TUB	0	.	GRCh37
TUBGCP5	0	.	GRCh37
TUBGCP6	0	.	GRCh37
TULP4	0	.	GRCh37
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TWF1	0	.	GRCh37
TYMP	0	.	GRCh37
UBASH3A	0	.	GRCh37
UBASH3B	0	.	GRCh37
UBE3C	0	.	GRCh37
UBR4	0	.	GRCh37
UBXN2B	0	.	GRCh37
UCP3	0	.	GRCh37
UHRF1	0	.	GRCh37
UHRF2	0	.	GRCh37
ULK4	0	.	GRCh37
UMODL1	0	.	GRCh37
UMODL1	0	.	GRCh37
UMODL1	0	.	GRCh37
UNC45B	0	.	GRCh37
UNKL	0	.	GRCh37
Unknown	0	.	GRCh37
UPB1	0	.	GRCh37
UPRT	0	.	GRCh37
USH2A	0	.	GRCh37
USHBP1	0	.	GRCh37

USP10	0	.	GRCh37
USP11	0	.	GRCh37
USP18	0	.	GRCh37
USP20	0	.	GRCh37
USP22	0	.	GRCh37
USP34	0	.	GRCh37
UTP15	0	.	GRCh37
UTP20	0	.	GRCh37
UTP20	0	.	GRCh37
UTY	0	.	GRCh37
VIM	0	.	GRCh37
VIPR2	0	.	GRCh37
VRK2	0	.	GRCh37
VTI1B	0	.	GRCh37
WBSCR22	0	.	GRCh37
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WBSCR27	0	.	GRCh37
WDFY4	0	.	GRCh37
WDR11	0	.	GRCh37
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WDR26	0	.	GRCh37
WDR43	0	.	GRCh37
WDR48	0	.	GRCh37
WDR60	0	.	GRCh37
WDR87	0	.	GRCh37
WDR91	0	.	GRCh37
WIPI2	0	.	GRCh37
WNK1	0	.	GRCh37
WNT2B	0	.	GRCh37
WNT8B	0	.	GRCh37
WRNIP1	0	.	GRCh37
WSB2	0	.	GRCh37
WWC1	0	.	GRCh37
WWP2	0	.	GRCh37
XAB2	0	.	GRCh37
XKR8	0	.	GRCh37
XPNPEP1	0	.	GRCh37
XPNPEP3	0	.	GRCh37
XPO5	0	.	GRCh37
XRCC1	0	.	GRCh37
XRCC1	0	.	GRCh37
YBX2	0	.	GRCh37
YY1AP1	0	.	GRCh37
YY1AP1	0	.	GRCh37
ZBTB2	0	.	GRCh37
ZC2HC1B	0	.	GRCh37
ZC3H12D	0	.	GRCh37
ZC3H12D	0	.	GRCh37
ZC3H12D	0	.	GRCh37
ZC3H3	0	.	GRCh37
ZC3H7B	0	.	GRCh37

ZCCHC18	0	.	GRCh37
ZDHHC16	0	.	GRCh37
ZDHHC6	0	.	GRCh37
ZDHHC7	0	.	GRCh37
ZFAND2A	0	.	GRCh37
ZFHX2	0	.	GRCh37
ZFPM2	0	.	GRCh37
ZFYVE19	0	.	GRCh37
ZKSCAN5	0	.	GRCh37
ZMYND10	0	.	GRCh37
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ZNF185	0	.	GRCh37
ZNF275	0	.	GRCh37
ZNF304	0	.	GRCh37
ZNF324	0	.	GRCh37
ZNF365	0	.	GRCh37
ZNF414	0	.	GRCh37
ZNF420	0	.	GRCh37
ZNF432	0	.	GRCh37
ZNF441	0	.	GRCh37
ZNF449	0	.	GRCh37
ZNF493	0	.	GRCh37
ZNF512B	0	.	GRCh37
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ZNF598	0	.	GRCh37
ZNF614	0	.	GRCh37
ZNF626	0	.	GRCh37
ZNF676	0	.	GRCh37
ZNF697	0	.	GRCh37
ZNF708	0	.	GRCh37
ZNF717	0	.	GRCh37
ZNF75D	0	.	GRCh37
ZNF785	0	.	GRCh37
ZNF816	0	.	GRCh37
ZNF839	0	.	GRCh37
ZP1	0	.	GRCh37
ZSCAN2	0	.	GRCh37
ZSWIM4	0	.	GRCh37
ZZEF1	0	.	GRCh37

Chromosome	Start_Position	End_Position	Strand
3	151458754	151458755	+
9	99408152	99408152	+
7	121758290	121758290	+
17	67212031	67212031	+
16	2326640	2326640	+
17	67133352	67133352	+
17	67099129	67099129	+
17	67023755	67023755	+
16	16228278	16228278	+
16	16278976	16278976	+
11	17419279	17419279	+
18	19284677	19284678	+
17	912914	912914	+
7	28996944	28996944	+
3	5229643	5229643	+
11	134132364	134132364	+
1	76190569	76190569	+
10	124813127	124813127	+
1	226334605	226334605	+
19	6333604	6333604	+
11	47266762	47266762	+
3	140998214	140998214	+
15	78473309	78473309	+
16	89167828	89167828	+
12	7457217	7457217	+
3	38520767	38520767	+
1	155033918	155033918	+
2	9650350	9650351	+
10	72513635	72513635	+
5	178557142	178557142	+
12	43887065	43887065	+
1	161163633	161163633	+
5	64625166	64625166	+
9	18753529	18753529	+
1	203119929	203119943	+
1	112046197	112046197	+
10	116073801	116073801	+
4	88052219	88052219	+
X	147967544	147967544	+
7	150814340	150814341	+
7	134673958	134673958	+
3	148459395	148459395	+
6	135749682	135749682	+
16	31539386	31539386	+
6	143382110	143382110	+
1	26662774	26662774	+
1	26662904	26662904	+
17	6331817	6331817	+
21	45708277	45708277	+
21	45710107	45710107	+
7	91707197	91707197	+
7	91659150	91659150	+
7	134225788	134225788	+
4	74279398	74279398	+

19	49962892	49962892	+
15	101448571	101448571	+
10	45938746	45938746	+
15	85360004	85360004	+
15	85403340	85403340	+
11	118071097	118071097	+
11	118074117	118074117	+
2	112552427	112552427	+
8	41585384	41585384	+
2	190593169	190593173	+
11	113264521	113264521	+
12	133304126	133304126	+
9	33572347	33572347	+
10	27326999	27326999	+
3	15727823	15727823	+
1	145561116	145561116	+
12	56648777	56648777	+
5	55455600	55455600	+
2	201501857	201501857	+
11	112131049	112131049	+
22	29737823	29737823	+
19	50303459	50303459	+
15	51222966	51222966	+
15	51233761	51233761	+
10	26781157	26781157	+
X	84322103	84322103	+
2	241631413	241631413	+
2	241631267	241631267	+
18	24442056	24442056	+
5	115338958	115338958	+
12	49334639	49334640	+
4	148984321	148984321	+
10	99024572	99024572	+
X	130219723	130219723	+
X	153176284	153176284	+
1	156929023	156929023	+
1	3383665	3383665	+
1	155948438	155948438	+
3	56771251	56771251	+
13	111870037	111870037	+
9	34623338	34623338	+
10	18964097	18964097	+
3	137958438	137958438	+
X	100743037	100743037	+
X	100743826	100743826	+
X	100742551	100742551	+
X	100749585	100749585	+
17	4622551	4622551	+
19	18119678	18119678	+
19	18119399	18119399	+
22	51065361	51065361	+
22	19965428	19965428	+
7	150883761	150883761	+
3	57314594	57314594	+
7	95115500	95115500	+

9	132404347	132404347	+
2	220380125	220380125	+
17	79972901	79972901	+
2	96798510	96798510	+
2	96795944	96795944	+
9	119449230	119449230	+
18	31263320	31263320	+
7	117008580	117008580	+
1	63269580	63269580	+
14	51062270	51062270	+
13	113536467	113536467	+
1	17326540	17326540	+
1	160105367	160105367	+
1	160156027	160156027	+
16	84459424	84459424	+
10	7849054	7849054	+
X	77276413	77276413	+
18	55399089	55399089	+
20	50273749	50273749	+
20	50225206	50225206	+
3	48505302	48505302	+
16	28845584	28845584	+
X	69459945	69459945	+
X	69261818	69261818	+
1	179414105	179414105	+
16	338332	338333	+
19	17922795	17922795	+
17	79060180	79060180	+
16	1393575	1393575	+
4	123664204	123664204	+
19	41903699	41903699	+
7	72966638	72966638	+
X	129186012	129186012	+
11	61724787	61724787	+
12	32491915	32491915	+
10	97987378	97987378	+
X	50654091	50654091	+
15	83951807	83951807	+
20	31609246	31609246	+
17	65936805	65936805	+
17	41215825	41215825	+
17	41219560	41219560	+
17	41226601	41226601	+
13	32903685	32903685	+
5	870740	870740	+
21	40652142	40652142	+
1	32832292	32832292	+
19	577760	577760	+
19	580575	580575	+
10	124097427	124097427	+
10	124089075	124089075	+
1	92568304	92568304	+
12	92539105	92539105	+
5	180486247	180486247	+
17	56384374	56384374	+

10	73483954	73483955	+
10	50534862	50534862	+
10	128153623	128153623	+
11	47182926	47182926	+
12	117160976	117160976	+
12	96927817	96927817	+
12	14976418	14976419	+
14	23729976	23729979	+
17	4806428	4806428	+
17	42239349	42239349	+
19	1231142	1231142	+
19	38794895	38794895	+
X	119760629	119760629	+
1	244735858	244735858	+
1	67569129	67569132	+
1	57216949	57216949	+
1	75086412	75086412	+
17	77043574	77043574	+
2	241826477	241826477	+
2	74643451	74643451	+
19	6697829	6697829	+
4	128905672	128905672	+
9	123744252	123744252	+
9	123737040	123737040	+
6	4079875	4079875	+
5	40937863	40937863	+
17	49711045	49711045	+
16	87925534	87925534	+
22	24466964	24466964	+
19	13323642	13323647	+
9	140881314	140881314	+
12	2702590	2702590	+
3	50416785	50416785	+
3	50402309	50402309	+
10	18787195	18787195	+
6	7329987	7329987	+
7	134635040	134635040	+
19	13049423	13049423	+
10	12870927	12870927	+
4	114458402	114458402	+
2	44931520	44931520	+
19	7675369	7675369	+
6	44144798	44144798	+
1	230891248	230891248	+
19	5914938	5914938	+
22	37902177	37902177	+
19	48734018	48734018	+
19	15166997	15166997	+
1	160163449	160163449	+
1	10704876	10704876	+
19	38848861	38848861	+
3	8775589	8775589	+
16	57550331	57550331	+
2	55764755	55764764	+
19	15131330	15131330	+

18	47777358	47777358	+
X	48926261	48926261	+
7	92987771	92987771	+
17	79637548	79637548	+
10	106124620	106124620	+
4	77278676	77278676	+
13	36788758	36788758	+
1	93712532	93712532	+
17	80159665	80159665	+
10	61665842	61665842	+
11	86098732	86098732	+
9	34690400	34690400	+
3	46400062	46400062	+
6	74497009	74497009	+
3	112545911	112545911	+
1	160803802	160803802	+
17	72478031	72478031	+
19	45912002	45912002	+
1	207934849	207934849	+
17	80274142	80274168	+
5	137549089	137549089	+
11	64602757	64602757	+
22	19506456	19506456	+
3	45134822	45134822	+
5	19747396	19747396	+
6	110942653	110942653	+
17	73997639	73997639	+
5	68557958	68557958	+
6	21065450	21065450	+
X	18668769	18668769	+
20	5107809	5107809	+
6	31085340	31085340	+
6	31088202	31088202	+
19	42083495	42083495	+
19	42311060	42311061	+
22	17669151	17669151	+
22	18018604	18018604	+
22	17990852	17990852	+
22	17619378	17619378	+
22	17601466	17601466	+
X	100375371	100375371	+
6	126661502	126661502	+
20	34060062	34060062	+
20	34082583	34082583	+
3	134214042	134214042	+
3	134226159	134226159	+
3	138289221	138289221	+
17	62517456	62517456	+
9	131191403	131191403	+
16	66976249	66976249	+
1	196659237	196659237	+
7	117307108	117307108	+
19	49558667	49558667	+
1	146714392	146714392	+
12	133448815	133448815	+

12	133447242	133447242	+
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17	7360110	7360110	+
15	40764549	40764549	+
16	11004150	11004150	+
14	102814945	102814945	+
12	120135717	120135717	+
X	71521867	71521867	+
5	80561943	80561943	+
1	11893715	11893715	+
1	16355877	16355877	+
7	100875598	100875598	+
12	8693418	8693418	+
X	154507173	154507173	+
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12	122839909	122839909	+
2	29383374	29383374	+
X	21619305	21619305	+
10	101137063	101137063	+
16	58575489	58575489	+
2	101883046	101883046	+
6	88853635	88853635	+
3	3030223	3030223	+
7	147926888	147926888	+
7	147926734	147926734	+
9	123929686	123929686	+
7	51093049	51093049	+
16	70530359	70530359	+
7	106965009	106965009	+
10	105796465	105796466	+
5	177686815	177686815	+
1	86435850	86435850	+
1	86482958	86482958	+
7	101200727	101200727	+
X	107420287	107420287	+
19	10080194	10080194	+
21	47417303	47417303	+
2	238289490	238289492	+
22	19951207	19951207	+
1	245005373	245005373	+
3	148902954	148902954	+
15	83240441	83240441	+
5	173383194	173383194	+
1	207653364	207653364	+
9	126131161	126131161	+
7	30706799	30706799	+
2	36624021	36624021	+
2	36669670	36669670	+
6	49696473	49696473	+
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15	91162945	91162945	+
3	97611916	97611916	+
3	97541018	97541018	+
X	151904488	151904488	+
20	472855	472855	+

15	75977920	75977920	+
20	56099305	56099305	+
16	11540760	11540760	+
10	69366602	69366602	+
9	111755008	111755008	+
10	17130199	17130199	+
10	35362977	35362977	+
6	43006408	43006408	+
7	101559302	101559302	+
7	101845476	101845476	+
2	180815528	180815528	+
2	180810180	180810180	+
11	107299631	107299631	+
X	70837517	70837517	+
11	61118437	61118437	+
11	7691019	7691019	+
19	41601609	41601609	+
19	41600800	41600800	+
7	99364703	99364704	+
19	15784377	15784377	+
7	91758422	91758422	+
11	61487690	61487690	+
2	136740900	136740900	+
3	137882752	137882752	+
19	14065534	14065534	+
19	14065341	14065341	+
19	14065074	14065074	+
18	50832102	50832102	+
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4	155412587	155412587	+
4	183815688	183815688	+
12	31246086	31246086	+
12	31242725	31242725	+
1	200617533	200617533	+
9	126202551	126202551	+
11	9225486	9225486	+
5	59995820	59995820	+
22	19050635	19050635	+
7	14737676	14737676	+
1	12639018	12639018	+
10	127529756	127529757	+
12	125465023	125465023	+
17	41603882	41603882	+
17	41582284	41582284	+
17	41599383	41599383	+
5	140956464	140956464	+
12	51093032	51093032	+
15	66625725	66625728	+
1	232002392	232002392	+
1	231954872	231954872	+
8	42233448	42233448	+
11	83497637	83497637	+
X	69668463	69668463	+
10	79571843	79571843	+
6	43422698	43422698	+

19	35993661	35993661	+
10	70190155	70190155	+
7	21827297	21827297	+
3	57422824	57422824	+
1	225492845	225492845	+
1	225477793	225477793	+
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1	225541666	225541666	+
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17	76569056	76569056	+
6	38796135	38796135	+
17	11837161	11837161	+
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1	84876501	84876501	+
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5	169472765	169472765	+
3	51393457	51393457	+
19	2223327	2223327	+
16	89704365	89704365	+
19	38708398	38708398	+
1	101458396	101458396	+
12	63974439	63974439	+
1	11772491	11772491	+
X	100511098	100511098	+
X	100505617	100505617	+
X	100514986	100514986	+
11	117375596	117375596	+
18	29036519	29036522	+
18	28993501	28993501	+
18	28956904	28956904	+
6	7556063	7556063	+
6	56496904	56496904	+
14	31922408	31922408	+
6	15652266	15652266	+
5	118280395	118280395	+
7	76111835	76111835	+
22	31060029	31060029	+
12	89744773	89744773	+
7	95616330	95616330	+
11	103192039	103192039	+
1	43638185	43638185	+
X	48382236	48382236	+
1	21573855	21573855	+
2	233347919	233347919	+
3	172486964	172486964	+
6	139134558	139134558	+
1	184706920	184706920	+
6	12292772	12292772	+
13	78477256	78477256	+
12	93202726	93202726	+
20	62127121	62127121	+
6	8102361	8102362	+
17	45447734	45447734	+
17	60464839	60464842	+
12	3768705	3768705	+

3	19975139	19975139	+
15	82545188	82545188	+
17	42945296	42945296	+
X	24073761	24073761	+
X	129201179	129201179	+
22	37771158	37771158	+
22	37770066	37770066	+
22	37770357	37770357	+
7	73469169	73469169	+
6	10990074	10990074	+
1	19565344	19565344	+
8	109491399	109491399	+
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14	100380948	100380948	+
14	100363671	100363671	+
14	100363672	100363672	+
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9	130578404	130578404	+
13	43985992	43985992	+
10	97582968	97582968	+
14	74426375	74426375	+
12	132464406	132464406	+
7	142564854	142564854	+
1	226026406	226026406	+
8	27394366	27394366	+
17	62144344	62144344	+
12	53671549	53671549	+
3	138191232	138191232	+
15	76578762	76578762	+
19	51850290	51850290	+
19	44031324	44031324	+
1	93101670	93101670	+
19	7912816	7912816	+
19	7917919	7917919	+
17	74015819	74015819	+
17	74006136	74006136	+
14	69695888	69695888	+
1	242042301	242042301	+
4	56770438	56770438	+
6	159210283	159210283	+
X	154158285	154158285	+
X	154194989	154194989	+
X	138643964	138643964	+
X	57318907	57318907	+
11	61615803	61615803	+
11	61645967	61645967	+
15	80452886	80452886	+
22	45728370	45728370	+
X	133955848	133955849	+
X	133955849	133955850	+
X	134156121	134156121	+
X	134155904	134155904	+
8	139277934	139277934	+
6	117083182	117083182	+
11	73179426	73179426	+

11	82443417	82443417	+
4	17649233	17649233	+
12	50724267	50724267	+
19	35719644	35719644	+
1	155224091	155224091	+
10	46222724	46222724	+
1	150974162	150974162	+
6	24818785	24818785	+
5	94756010	94756010	+
16	89865650	89865650	+
6	35423489	35423489	+
6	35424188	35424188	+
6	35423662	35423662	+
12	29486745	29486745	+
2	242374358	242374358	+
2	242405021	242405021	+
17	80044211	80044211	+
17	80044078	80044078	+
17	80045147	80045147	+
17	80059487	80059487	+
3	13612319	13612319	+
19	8159339	8159339	+
12	133102462	133102462	+
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9	37512734	37512734	+
9	37529344	37529344	+
19	39437014	39437014	+
3	48419723	48419723	+
10	103432635	103432635	+
1	207135991	207135991	+
19	17886940	17886940	+
5	176520243	176520243	+
4	155525970	155525970	+
18	34232952	34232952	+
18	34310668	34310668	+
18	34233231	34233231	+
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7	72754645	72754645	+
2	179341953	179341953	+
X	153594535	153594535	+
3	58092346	58092346	+
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1	240497598	240497598	+
1	240492543	240492543	+
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11	47776283	47776283	+
6	159682206	159682206	+
6	159653635	159653635	+
6	1395043	1395043	+
6	41552429	41552429	+
9	130576075	130576075	+
4	79238649	79238649	+
4	79394836	79394836	+

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4	79238496	79238496	+
4	79403146	79403146	+
4	144617842	144617842	+
10	13702231	13702231	+
15	40055973	40055973	+
4	162421109	162421109	+
9	133511390	133511390	+
19	49254573	49254573	+
19	5832589	5832589	+
11	117693255	117693255	+
3	46007702	46007702	+
3	30769948	30769948	+
4	871624	871624	+
4	905401	905401	+
14	88407917	88407917	+
14	88459656	88459656	+
17	73759061	73759061	+
5	153783587	153783587	+
2	31135184	31135184	+
12	4830000	4830000	+
12	4873163	4873163	+
18	29867504	29867504	+
18	29867091	29867091	+
18	29847739	29847740	+
9	130027009	130027009	+
1	89735314	89735314	+
1	89727870	89727870	+
1	89732237	89732237	+
17	79770740	79770740	+
6	10587056	10587056	+
9	74846104	74846104	+
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14	39587348	39587348	+
3	158380546	158380546	+
2	85788140	85788140	+
19	38876464	38876464	+
19	38876352	38876352	+
17	40341909	40341909	+
6	149899916	149899916	+
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16	74499589	74499589	+
16	74503860	74503860	+
16	4386645	4386645	+
6	38670837	38670837	+
X	102979486	102979486	+
X	102978965	102978965	+
12	104387138	104387138	+
11	58605673	58605673	+
2	70076954	70076954	+
22	23438191	23438191	+
22	19808769	19808769	+
4	68619601	68619601	+
12	133363006	133363006	+

17	4835895	4835895	+
13	95034763	95034763	+
6	24463055	24463055	+
X	13795394	13795395	+
2	27851904	27851904	+
X	136113464	136113464	+
10	134886618	134886618	+
10	134902253	134902253	+
10	134910629	134910629	+
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15	40212031	40212031	+
11	123480981	123480981	+
3	113601761	113601761	+
22	47064164	47064164	+
22	47070747	47070747	+
22	47061659	47061659	+
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5	152871721	152871721	+
4	158242540	158242540	+
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3	7620382	7620382	+
16	85682071	85682071	+
9	124089692	124089692	+
X	51486659	51486659	+
11	67353844	67353844	+
14	77787844	77787844	+
10	1055055	1055055	+
10	1065406	1065406	+
X	108628579	108628579	+
3	73024350	73024350	+
12	96384345	96384345	+
19	35775594	35775594	+
12	48192062	48192062	+
12	48181778	48181778	+
7	19015652	19015652	+
6	125598408	125598408	+
X	6995315	6995315	+
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1	236746511	236746511	+
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7	810219	810219	+
14	31619121	31619121	+
14	31647519	31647519	+
10	96341336	96341336	+
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3	50617502	50617502	+
15	64050665	64050665	+
6	26091179	26091179	+
7	81358953	81358953	+
3	42740492	42740492	+
14	100135306	100135306	+
17	42925559	42925559	+
5	130497976	130497976	+
6	26200256	26200256	+
6	26198980	26198980	+

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10	70998925	70998925	+
6	33052981	33052981	+
21	38132172	38132172	+
3	148777446	148777448	+
11	118962230	118962230	+
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12	121431272	121431272	+
19	41807363	41807363	+
19	12877042	12877042	+
19	35551225	35551226	+
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19	36247708	36247708	+
7	154862621	154862621	+
X	53641647	53641647	+
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21	45643008	45643008	+
15	90634691	90634691	+
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21	34614255	34614255	+
15	99473606	99473606	+
6	160465753	160465753	+
6	160524773	160524773	+
6	160479882	160479882	+
19	51825238	51825238	+
X	130415818	130415818	+
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11	18741260	18741260	+
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9	111653574	111653574	+
3	9969933	9969934	+
6	137330503	137330503	+
1	24463854	24463854	+
10	6054765	6054765	+
16	30016820	30016820	+
11	2181073	2181073	+
11	2169110	2169110	+
19	7166376	7166376	+
19	7167951	7167951	+
7	1538021	1538021	+
7	1510719	1510719	+
13	51956067	51956067	+
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1	156505079	156505079	+
12	280349	280349	+
7	128588475	128588475	+
19	44223667	44223667	+

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2	182360182	182360182	+
3	37695192	37695192	+
3	52855229	52855229	+
3	52860936	52860936	+
3	52851137	52851137	+
X	78618050	78618050	+
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12	26869233	26869233	+
12	26572244	26572245	+
6	33635565	33635565	+
10	106075081	106075081	+
21	35247611	35247611	+
21	35230921	35230921	+
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X	46884050	46884050	+
10	133963466	133963466	+
6	15374533	15374533	+
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6	15496662	15496662	+
11	96125436	96125437	+
9	745289	745289	+
1	62704134	62704134	+
1	62739198	62739198	+
1	62713246	62713246	+
6	149953981	149953981	+
19	49574125	49574125	+
3	156233996	156233996	+
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7	128533818	128533818	+
12	109907308	109907308	+
13	45768759	45768759	+
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19	5135337	5135337	+
Y	21905008	21905008	+
X	44929077	44929077	+
7	139820354	139820354	+
7	139801777	139801777	+
7	139797431	139797431	+
22	45608192	45608192	+
4	123111354	123111354	+
6	138584685	138584685	+
8	95521854	95521861	+
19	18368608	18368608	+
6	111583381	111583381	+
1	200577919	200577919	+
1	21042094	21042094	+
17	72339369	72339369	+
2	241722621	241722622	+
17	4910485	4910485	+
10	91505816	91505817	+
1	169993762	169993762	+
10	7808086	7808086	+

8	103663912	103663912	+
4	166141086	166141086	+
4	88091449	88091449	+
12	9147926	9147926	+
7	151836397	151836397	+
10	135015427	135015427	+
12	123087442	123087442	+
7	98782750	98782750	+
17	45747277	45747277	+
22	29533275	29533275	+
17	38974814	38974814	+
17	39620733	39620733	+
17	39642561	39642561	+
21	46047971	46047971	+
21	46078220	46078220	+
21	46074202	46074202	+
22	41620825	41620825	+
6	129674562	129674562	+
6	129380844	129380844	+
6	112506375	112506375	+
6	112506583	112506583	+
1	183099701	183099701	+
1	183079853	183079853	+
1	183104013	183104013	+
1	183155482	183155482	+
6	150004779	150004779	+
1	152573162	152573162	+
9	139649217	139649218	+
1	22148164	22148164	+
12	65612499	65612499	+
7	2565268	2565268	+
19	54848986	54848986	+
7	73522361	73522361	+
19	2290499	2290499	+
12	49494854	49494854	+
13	76395278	76395278	+
5	96349590	96349590	+
8	12600837	12600837	+
X	118108785	118108785	+
X	118120908	118120908	+
15	74238734	74238734	+
3	188426256	188426256	+
12	25249785	25249785	+
2	140992337	140992337	+
11	68179125	68179125	+
22	25750656	25750656	+
22	25747923	25747923	+
4	3521939	3521939	+
14	50069282	50069282	+
10	50122181	50122181	+
8	86057798	86057798	+
12	85547008	85547008	+
3	194387253	194387253	+
19	34706203	34706203	+
4	147110891	147110891	+

21	47630550	47630550	+
21	30315730	30315730	+
11	24998286	24998286	+
19	42343155	42343155	+
1	151137793	151137793	+
10	102770082	102770082	+
10	102762256	102762256	+
7	2108982	2108982	+
4	120983259	120983259	+
X	152483088	152483088	+
X	151899913	151899913	+
X	30260217	30260217	+
X	140993150	140993150	+
X	141290865	141290865	+
X	54836127	54836127	+
9	139752333	139752333	+
X	149680539	149680539	+
6	119509785	119509785	+
5	109110537	109110537	+
4	6594947	6594947	+
19	17838787	17838787	+
X	19482476	19482476	+
17	61770856	61770856	+
19	39100297	39100297	+
2	102445893	102445893	+
3	50679045	50679047	+
19	12958360	12958360	+
19	12963143	12963143	+
5	65892448	65892448	+
20	43933021	43933021	+
3	182754967	182754967	+
21	47674275	47674275	+
6	37623626	37623626	+
6	90363802	90363802	+
6	90363803	90363803	+
X	153296337	153296337	+
X	40514122	40514122	+
9	136213521	136213521	+
19	50335510	50335510	+
19	39884273	39884273	+
19	19297630	19297630	+
1	3415657	3415657	+
18	29800119	29800119	+
2	112786523	112786524	+
14	21970091	21970091	+
2	172188368	172188368	+
19	3546185	3546185	+
17	74936576	74936576	+
17	74921257	74921257	+
17	74928758	74928758	+
10	131506283	131506283	+
22	18379160	18379160	+
22	18368548	18368548	+
22	18372020	18372020	+
X	10437968	10437968	+

17	4784249	4784249	+
17	4796656	4796656	+
12	121132100	121132100	+
1	233512362	233512362	+
19	6262355	6262355	+
10	127460753	127460753	+
7	156801661	156801661	+
19	2076974	2076974	+
X	106221490	106221490	+
X	106200202	106200202	+
15	79133026	79133026	+
11	118108003	118108003	+
11	94225807	94225807	+
1	55119515	55119515	+
1	55139741	55139741	+
1	55136529	55136529	+
17	45904163	45904163	+
9	140446449	140446449	+
10	102746829	102746829	+
6	42176544	42176544	+
11	10655623	10655623	+
2	47635776	47635777	+
4	166259161	166259161	+
1	11181327	11181327	+
1	237054569	237054569	+
1	237060433	237060433	+
1	237001926	237001926	+
1	237057608	237057608	+
4	100513028	100513031	+
19	8997189	8997190	+
19	9084216	9084216	+
12	40805948	40805948	+
12	40954482	40954482	+
11	1101649	1101649	+
16	88721012	88721012	+
X	3228891	3228891	+
17	79899495	79899495	+
11	47371485	47371485	+
16	15820863	15820863	+
3	108174537	108174537	+
14	23899027	23899027	+
14	23895893	23895893	+
14	23887645	23887645	+
22	36691526	36691526	+
3	123411589	123411589	+
17	18058371	18058371	+
22	26241994	26241994	+
17	34863439	34863439	+
19	8587782	8587782	+
15	52629950	52629950	+
19	17283491	17283491	+
1	203055101	203055101	+
10	69908113	69908113	+
11	61551927	61551927	+
1	59134792	59134792	+

9	88633829	88633829	+
9	138908250	138908250	+
16	5083982	5083982	+
19	50862768	50862768	+
17	72769694	72769694	+
2	15448311	15448311	+
17	41361960	41361960	+
17	41352643	41352643	+
17	41330024	41330024	+
17	41331460	41331460	+
19	19329924	19329924	+
12	6620226	6620226	+
11	134031588	134031588	+
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20	33342477	33342477	+
17	15950198	15950198	+
1	161183516	161183516	+
2	152474076	152474076	+
2	152552062	152552062	+
2	152581866	152581866	+
4	1986542	1986542	+
1	212619339	212619339	+
1	212617829	212617829	+
1	78395131	78395131	+
4	103518843	103518843	+
10	104155836	104155836	+
3	101571550	101571550	+
6	18122526	18122526	+
6	138820324	138820324	+
1	236176623	236176623	+
14	51214888	51214888	+
1	24782847	24782847	+
5	156898690	156898690	+
5	37064164	37064164	+
22	29966083	29966083	+
3	52514529	52514529	+
14	37050642	37050642	+
X	70386825	70386825	+
2	32449872	32449875	+
19	56565263	56565263	+
19	56552456	56552456	+
19	56520125	56520125	+
19	56228067	56228067	+
12	132635989	132635989	+
9	33469427	33469427	+
4	2941418	2941418	+
20	2638982	2638982	+
1	162335052	162335052	+
7	150696111	150696111	+
7	150703675	150703675	+
9	139396983	139396983	+
9	139405530	139405530	+
7	44553238	44553238	+
10	72015573	72015573	+
7	34874038	34874038	+

7	98254560	98254561	+
3	23986983	23986983	+
1	161208255	161208258	+
14	90752619	90752619	+
5	176639105	176639105	+
5	6605532	6605532	+
3	52558768	52558768	+
19	49559693	49559693	+
7	44444122	44444122	+
13	45540136	45540136	+
8	27925796	27925796	+
12	69109579	69109579	+
9	134103759	134103759	+
6	150067675	150067675	+
22	45580592	45580597	+
4	77045986	77045990	+
4	77038807	77038807	+
17	5289676	5289676	+
17	5290824	5290824	+
X	102339606	102339606	+
X	101087618	101087618	+
X	101087497	101087497	+
X	101087498	101087498	+
17	708531	708531	+
6	41036770	41036770	+
2	220431802	220431802	+
17	80350331	80350331	+
19	46056620	46056620	+
7	99473624	99473624	+
17	3195503	3195503	+
11	55111222	55111222	+
11	51412353	51412353	+
11	55340552	55340552	+
11	5322520	5322520	+
11	5809477	5809477	+
14	21623290	21623290	+
3	97888302	97888302	+
11	55703247	55703247	+
11	56043056	56043056	+
20	60847086	60847086	+
16	83998662	83998662	+
16	83999033	83999033	+
5	38921662	38921663	+
15	31823062	31823062	+
14	23240713	23240714	+
X	69478942	69478942	+
17	79805134	79805134	+
1	40035320	40035320	+
11	65994941	65994941	+
X	55248320	55248320	+
19	726200	726200	+
10	91358943	91358943	+
10	91404448	91404448	+
1	2444414	2444414	+
2	61021342	61021342	+

1	55224751	55224751	+
11	12525925	12525925	+
22	44547355	44547355	+
2	114001921	114001921	+
6	138539315	138539315	+
10	55826470	55826470	+
13	66879139	66879139	+
7	82546282	82546282	+
6	150114745	150114745	+
21	47851424	47851424	+
3	57542173	57542173	+
2	183387446	183387446	+
11	72290629	72290629	+
10	95372734	95372734	+
4	55139638	55139638	+
5	149495395	149495395	+
5	149497177	149497177	+
10	26994150	26994150	+
16	15129459	15129459	+
16	15132108	15132108	+
10	102775350	102775350	+
15	77407114	77407114	+
1	156875037	156875037	+
1	156873727	156873727	+
1	156878737	156878737	+
19	33878837	33878837	+
19	33878198	33878198	+
10	3154534	3154534	+
10	3154339	3154339	+
2	197737842	197737842	+
X	77380307	77380307	+
19	15582863	15582863	+
1	153283179	153283179	+
9	96415653	96415653	+
6	79651133	79651134	+
X	71876187	71876187	+
11	118520918	118520918	+
11	587425	587425	+
1	111893958	111893958	+
1	77588131	77588131	+
18	59768375	59768375	+
17	34893326	34893326	+
17	8784361	8784361	+
2	209150361	209150361	+
22	50354819	50354819	+
22	25158326	25158326	+
X	68381912	68381912	+
16	81193433	81193433	+
6	51712492	51712492	+
12	32974218	32974218	+
6	46684925	46684925	+
8	42037630	42037630	+
2	28771854	28771854	+
10	96053239	96053239	+
10	96014622	96014622	+

10	96084372	96084373	+
10	96058298	96058298	+
16	81887957	81887957	+
1	2409892	2409892	+
1	2420590	2420590	+
8	145001031	145001031	+
8	145011204	145011204	+
8	144990335	144990335	+
8	144995736	144995736	+
8	144990528	144990528	+
8	144992862	144992862	+
1	6533599	6533599	+
14	68046602	68046602	+
14	68041124	68041124	+
14	68053149	68053149	+
1	908823	908823	+
19	1528149	1528150	+
17	37234111	37234111	+
22	50724733	50724733	+
6	99862600	99862601	+
6	36274153	36274153	+
22	44341986	44341986	+
19	7615903	7615903	+
12	89919631	89919632	+
11	62529460	62529460	+
20	18453391	18453391	+
20	18464101	18464101	+
13	38154189	38154189	+
8	128428656	128428656	+
3	12393125	12393125	+
3	12475557	12475557	+
22	22036832	22036832	+
17	56833457	56833458	+
1	161136843	161136843	+
17	79791792	79791792	+
10	133769482	133769482	+
3	135742057	135742058	+
X	48759204	48759204	+
4	121737767	121737767	+
4	81121524	81121524	+
X	23685964	23685964	+
X	23689636	23689636	+
X	23689637	23689637	+
6	105850712	105850712	+
8	69002965	69002965	+
11	57156438	57156438	+
4	185578248	185578248	+
3	53220569	53220569	+
3	53223287	53223291	+
1	2076055	2076055	+
14	23394327	23394327	+
19	5783713	5783713	+
22	45126638	45126638	+
22	45243780	45243780	+
16	31152697	31152698	+

9	79234158	79234159	+
19	43579815	43579815	+
19	43430945	43430945	+
19	43762316	43762316	+
17	65341976	65341976	+
21	40549289	40549289	+
18	12703067	12703067	+
9	114348513	114348513	+
10	129870510	129870510	+
1	44064623	44064623	+
3	61734539	61734539	+
6	128307118	128307118	+
7	157396697	157396697	+
16	1536677	1536677	+
1	31414769	31414769	+
1	31440212	31440212	+
1	31406228	31406228	+
1	31409473	31409474	+
15	55841281	55841281	+
12	21590621	21590621	+
17	29844658	29844658	+
2	238494742	238494742	+
11	87908563	87908563	+
X	69502479	69502479	+
17	5249998	5249998	+
14	24736027	24736027	+
17	79990418	79990419	+
14	68290372	68290372	+
7	4845312	4845312	+
3	12626516	12626516	+
5	34687135	34687135	+
1	21932530	21932530	+
12	48134214	48134214	+
11	47463484	47463484	+
3	50378154	50378154	+
X	47045138	47045138	+
13	79929326	79929326	+
5	145647151	145647151	+
8	30242747	30242747	+
9	36105264	36105264	+
19	45513147	45513152	+
6	139264930	139264930	+
3	108475993	108475994	+
22	29834766	29834766	+
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3	53126143	53126143	+
3	16450872	16450872	+
19	11529958	11529958	+
1	240975213	240975213	+
22	45809698	45809698	+
21	43161022	43161022	+
2	86992337	86992338	+
2	86947783	86947783	+
19	12917761	12917761	+
1	182555819	182555819	+

17	41180772	41180772	+
4	154633581	154633581	+
1	33414040	33414040	+
17	8296080	8296080	+
3	78711350	78711350	+
3	78737962	78737962	+
2	11359120	11359120	+
1	64608423	64608423	+
6	117714346	117714346	+
22	30682404	30682404	+
13	76210742	76210742	+
10	97748040	97748040	+
12	31267744	31267744	+
1	15671483	15671483	+
12	48081637	48081637	+
17	181479	181479	+
19	17973862	17973862	+
17	27047015	27047016	+
17	27047016	27047017	+
22	39714490	39714490	+
X	71493691	71493691	+
6	166862431	166862431	+
17	78897547	78897547	+
17	78896529	78896529	+
21	45089877	45089877	+
21	45096206	45096206	+
17	48559559	48559559	+
10	16806545	16806545	+
11	63487386	63487386	+
5	178986987	178986987	+
5	179036457	179036457	+
10	70167004	70167004	+
9	137328286	137328286	+
19	38959680	38959680	+
19	38933120	38933120	+
19	38985101	38985101	+
19	38993118	38993118	+
1	237551376	237551376	+
1	237765470	237765470	+
15	33795775	33795775	+
13	21720868	21720868	+
9	136584264	136584264	+
7	66459145	66459145	+
22	50885775	50885775	+
11	9830595	9830595	+
19	50150105	50150105	+
1	155230131	155230131	+
22	20784217	20784217	+
13	78130924	78130924	+
7	12610594	12610594	+
4	129878342	129878342	+
4	129805716	129805716	+
6	108026402	108026402	+
2	166012203	166012203	+
2	167099158	167099158	+

2	167060449	167060449	+
1	226187129	226187129	+
7	4002204	4002204	+
3	10353538	10353538	+
22	30934886	30934886	+
1	177917479	177917479	+
20	18523002	18523002	+
4	119726949	119726949	+
10	102265446	102265448	+
10	102275780	102275780	+
10	102269206	102269206	+
10	102258439	102258439	+
9	91943884	91943884	+
17	80280054	80280054	+
1	169700961	169700961	+
1	169563062	169563062	+
7	83739762	83739762	+
7	83764309	83764309	+
3	50219991	50219991	+
22	42392811	42392811	+
14	95088626	95088626	+
19	40929553	40929553	+
12	122255910	122255910	+
12	122248775	122248775	+
3	9484025	9484025	+
22	26688388	26688388	+
16	70601254	70601254	+
6	144416685	144416685	+
10	72635144	72635145	+
17	2268681	2268681	+
17	2268139	2268139	+
22	40802739	40802739	+
1	87208953	87208953	+
10	105363289	105363289	+
19	51207508	51207508	+
19	51207775	51207775	+
7	155599300	155599300	+
X	9900279	9900279	+
19	52004469	52004469	+
21	44845436	44845437	+
21	38118089	38118089	+
1	232601241	232601241	+
1	160720074	160720074	+
4	48485674	48485674	+
4	87769929	87769929	+
5	1089037	1089037	+
7	122808528	122808528	+
X	73641569	73641569	+
19	15065171	15065171	+
19	15079104	15079104	+
5	131705949	131705949	+
5	138714817	138714817	+
14	92909073	92909073	+
7	95906737	95906738	+
17	42399754	42399754	+

17	42399223	42399223	+
17	78225035	78225035	+
15	85451852	85451852	+
15	45560655	45560655	+
9	130167338	130167338	+
7	133984878	133984878	+
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11	124954282	124954282	+
3	50254624	50254624	+
16	58709777	58709777	+
8	142225990	142225990	+
7	150765236	150765236	+
19	18001839	18001839	+
X	115586700	115586700	+
19	49812403	49812403	+
17	28549898	28549898	+
1	44463170	44463170	+
14	23607271	23607271	+
14	23598976	23598976	+
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X	128614827	128614827	+
4	144449251	144449252	+
22	45779553	45779553	+
14	70418881	70418881	+
22	31493125	31493125	+
1	246078824	246078824	+
10	97099169	97099169	+
4	7731310	7731310	+
1	118644430	118644430	+
1	118629599	118629599	+
X	142795438	142795438	+
8	145086924	145086924	+
2	220353104	220353104	+
2	220349351	220349351	+
19	38782485	38782485	+
10	73848075	73848075	+
15	42155816	42155816	+
15	42166333	42166333	+
16	30735348	30735348	+
7	149517978	149517978	+
7	149507964	149507964	+
7	149518961	149518961	+
3	8668094	8668094	+
16	70415567	70415567	+
17	74570707	74570707	+
17	74570408	74570408	+
9	130672600	130672600	+
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2	74058260	74058260	+
4	68447040	68447040	+
15	42986979	42986979	+
2	191937738	191937738	+
17	40354497	40354497	+

8	74585325	74585325	+
15	74277795	74277795	+
17	79980756	79980756	+
7	134943328	134943328	+
9	125932153	125932156	+
1	110581780	110581780	+
7	129102743	129102743	+
6	147695051	147695051	+
12	10782115	10782115	+
7	75623954	75623954	+
3	151599379	151599379	+
21	46233863	46233863	+
6	149721690	149721690	+
19	39964247	39964247	+
19	39949764	39949764	+
9	95840077	95840077	+
11	9734945	9734945	+
19	46319415	46319415	+
3	12224712	12224712	+
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6	158502527	158502527	+
15	99670265	99670265	+
4	119947985	119947985	+
6	149700491	149700491	+
6	149718650	149718650	+
4	1732978	1732978	+
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6	159461931	159461931	+
6	159463221	159463221	+
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13	76055397	76055397	+
3	17208267	17208267	+
4	107153024	107153024	+
11	67402744	67402744	+
X	101382005	101382005	+
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5	145834529	145834529	+
22	31022590	31022590	+
14	104436931	104436931	+
X	123538803	123538810	+
5	167652999	167652999	+
16	69395434	69395434	+
2	74307792	74307793	+
17	56692800	56692800	+
17	62232165	62232165	+
13	31531009	31531009	+
6	155606325	155606325	+
X	132351861	132351861	+
19	54613420	54613420	+
1	92200593	92200593	+

X	89177673	89177673	+
15	43579566	43579566	+
6	169622263	169622263	+
19	373619	373619	+
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14	24029340	24029340	+
2	39996767	39996767	+
21	32525542	32525542	+
6	155571135	155571135	+
19	4816719	4816719	+
18	71825731	71825731	+
3	53268965	53268965	+
3	53260716	53260716	+
17	27053148	27053148	+
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15	70349744	70349744	+
17	60558610	60558610	+
4	167020644	167020644	+
10	98133282	98133282	+
10	98146654	98146654	+
10	98133483	98133483	+
15	63092993	63092993	+
2	74741767	74741767	+
16	69385641	69385641	+
2	98382886	98382886	+
7	134849213	134849213	+
4	83411197	83411197	+
X	148685623	148685623	+
11	61161532	61161545	+
17	10618880	10618880	+
4	68777054	68777054	+
6	138197331	138197331	+
9	117668142	117668142	+
7	5399044	5399044	+
17	38644752	38644752	+
17	38640744	38640744	+
15	43767774	43767774	+
15	43724646	43724646	+
15	43730486	43730486	+
18	34398914	34398914	+
19	16187132	16187133	+
5	666323	666323	+
5	665280	665280	+
3	188925391	188925391	+
19	45668327	45668327	+
14	39627695	39627695	+
14	39623533	39623533	+
6	42224546	42224546	+
X	152728003	152728003	+
6	30138662	30138662	+
6	28876509	28876509	+
1	155148781	155148781	+
1	33625275	33625275	+
1	231344908	231344908	+
14	51475794	51475794	+

14	51492135	51492136	+
5	14397238	14397238	+
7	100465171	100465171	+
19	13218417	13218417	+
X	100265713	100265713	+
20	33600740	33600740	+
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9	135786904	135786904	+
9	135781563	135781563	+
16	2115697	2115697	+
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X	99890204	99890204	+
X	38535174	38535174	+
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6	43230970	43230970	+
10	75101070	75101070	+
17	15930087	15930087	+
22	29025743	29025743	+
10	134672798	134672798	+
10	134756013	134756013	+
10	134726470	134726470	+
10	134722022	134722022	+
10	134650440	134650440	+
22	43455531	43455531	+
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12	44191434	44191434	+
22	50964657	50964657	+
21	43846729	43846729	+
11	122653689	122653689	+
7	157000176	157000176	+
1	19401296	19401296	+
8	59345705	59345705	+
11	73715666	73715666	+
19	4954454	4954454	+
9	6475319	6475319	+
3	41957466	41957466	+
21	43539523	43539523	+
21	43547873	43547873	+
21	43541342	43541342	+
17	33491278	33491278	+
16	1451533	1451533	+
10	124436375	124436375	+
22	24919627	24919627	+
X	74519534	74519534	+
1	216144049	216144049	+
19	17366278	17366278	+

16	84793822	84793823	+
X	47099242	47099242	+
22	18649922	18649922	+
9	132632653	132632653	+
17	20906272	20906273	+
2	61570855	61570855	+
5	72872766	72872766	+
12	101705433	101705433	+
12	101715202	101715202	+
Y	15448300	15448300	+
10	17278467	17278467	+
7	158823375	158823375	+
2	58276115	58276115	+
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7	73115314	73115314	+
7	73101137	73101137	+
7	73249165	73249165	+
10	49929491	49929491	+
10	122646113	122646113	+
10	122624679	122624679	+
10	122659490	122659490	+
10	122663585	122663585	+
10	122664967	122664967	+
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7	134878237	134878237	+
7	5262385	5262385	+
12	863152	863152	+
1	113063125	113063125	+
10	102222957	102222957	+
6	2768905	2768905	+
12	118476079	118476079	+
5	167868950	167868950	+
16	69973297	69973297	+
19	7686282	7686282	+
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10	111648006	111648006	+
22	41282558	41282558	+
6	43496662	43496662	+
19	44057227	44057227	+
19	44055898	44055898	+
17	7192756	7192756	+
1	155630752	155630752	+
1	155658085	155658085	+
6	151686905	151686905	+
6	144224312	144224312	+
6	149773721	149773721	+
6	149772645	149772645	+
6	149795692	149795692	+
8	144590112	144590112	+
22	41739647	41739647	+

X	103359423	103359423	+
10	99211653	99211653	+
10	114200355	114200355	+
16	85023855	85023855	+
7	1195264	1195264	+
14	23994517	23994517	+
8	106646683	106646683	+
15	41106485	41106485	+
7	99103607	99103607	+
3	50378946	50378946	+
3	50380661	50380661	+
X	152089039	152089039	+
X	152613112	152613112	+
19	57867599	57867599	+
19	58982044	58982044	+
10	64415031	64415031	+
19	8576307	8576307	+
19	37617933	37617933	+
19	52537576	52537576	+
19	11878095	11878095	+
X	134493747	134493747	+
19	21588692	21588692	+
20	62594160	62594160	+
15	85341859	85341859	+
16	2050192	2050192	+
19	52521296	52521296	+
19	20844340	20844341	+
19	22375868	22375868	+
1	120166681	120166681	+
19	21477431	21477431	+
3	75790972	75790972	+
X	134421168	134421168	+
16	30594521	30594521	+
19	53453777	53453777	+
14	102808330	102808330	+
11	60637164	60637164	+
15	85149927	85149927	+
19	13940959	13940959	+
17	3961489	3961489	+

Variant_Classification	Variant_Type	Reference_Allele	Tumor_Seq_Allele1
Intron	INS	-	-
Intron	SNP	T	T
Intron	SNP	G	G
Silent	SNP	A	A
3'UTR	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	A	A
Silent	SNP	T	T
Intron	DEL	C	C
Silent	SNP	C	C
5'UTR	INS	-	-
Splice_Region	SNP	G	G
5'Flank	SNP	T	T
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
5'UTR	SNP	G	G
Intron	SNP	G	G
Splice_Region	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Splice_Region	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	INS	-	-
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
Intron	DEL	A	A
Intron	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Intron	DEL	TCTGTCCTCCCCCTA	TCTGTCCTCCCCCTA
5'Flank	SNP	C	C
Silent	SNP	T	T
Intron	SNP	T	T
Intron	SNP	G	G
Intron	INS	-	-
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Silent	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
Missense_Mutation	SNP	C	C
Silent	SNP	C	C
Intron	SNP	T	T
Splice_Region	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C

Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
5'UTR	SNP	A	A
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Silent	SNP	C	C
Intron	SNP	T	T
Intron	DEL	TTTTT	TTTTT
Intron	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	T	T
Splice_Region	SNP	A	A
Silent	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
5'UTR	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	T	T
5'UTR	SNP	A	A
Intron	SNP	A	A
Missense_Mutation	SNP	G	G
Intron	DEL	GG	GG
Missense_Mutation	SNP	A	A
Intron	SNP	A	A
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
5'Flank	SNP	C	C
Missense_Mutation	SNP	A	A
Silent	SNP	T	T
Intron	SNP	A	A
Splice_Region	SNP	G	G
Intron	SNP	C	C
5'UTR	SNP	C	C
Missense_Mutation	SNP	A	A
5'Flank	SNP	G	G
Silent	SNP	C	C
Intron	SNP	A	A
Intron	SNP	C	C
Splice_Region	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	A	A
Intron	DEL	T	T

5'UTR	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	G	G
3'UTR	SNP	G	G
Silent	SNP	G	G
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	C	C
Intron	SNP	C	C
Splice_Region	SNP	A	A
Missense_Mutation	SNP	A	A
Intron	INS	-	-
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
5'UTR	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Splice_Site	SNP	T	T
Intron	SNP	G	G
Missense_Mutation	SNP	A	A
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	A	A

5'Flank	INS	-	-
Silent	SNP	T	T
Intron	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	C	C
Frame_Shift_Del	DEL	TA	TA
Intron	DEL	GAGA	GAGA
3'Flank	SNP	G	G
3'UTR	SNP	T	T
Missense_Mutation	SNP	T	T
5'UTR	SNP	T	T
Missense_Mutation	SNP	A	A
Silent	SNP	A	A
Intron	DEL	TAAT	TAAT
Intron	SNP	T	T
Splice_Region	SNP	G	G
Intron	SNP	T	T
3'UTR	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	A	A
Intron	SNP	G	G
5'UTR	SNP	T	T
Intron	SNP	C	C
Intron	SNP	A	A
Silent	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	DEL	ACACAC	ACACAC
Splice_Region	SNP	A	A
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	C	C
5'UTR	SNP	G	G
3'UTR	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
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3'UTR	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	C	C
Silent	SNP	C	C
Intron	DEL	ATATGAATAC	ATATGAATAC
Missense_Mutation	SNP	G	G

Intron	SNP	T	T
3'UTR	SNP	G	G
3'UTR	SNP	A	A
Intron	SNP	T	T
Silent	SNP	A	A
Missense_Mutation	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Silent	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	A	A
Frame_Shift_Del	DEL	T	T
Intron	SNP	A	A
Intron	DEL	T	T
Missense_Mutation	SNP	A	A
Intron	SNP	A	A
In_Frame_Del	DEL	GGGCAGAGGCTGCTG	GGGCAGAGGCTGCTG
5'Flank	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	A	A
Silent	SNP	A	A
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
5'UTR	SNP	A	A
Intron	SNP	G	G
Intron	INS	-	-
Intron	SNP	C	C
Intron	SNP	A	A
Missense_Mutation	SNP	G	G
Intron	SNP	T	T
Silent	SNP	T	T
Intron	DEL	A	A
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	T	T
Missense_Mutation	SNP	C	C
Silent	SNP	G	G
5'UTR	SNP	T	T
Silent	SNP	G	G
Intron	SNP	G	G

Intron	SNP	T	T
Missense_Mutation	SNP	C	C
3'UTR	SNP	T	T
3'UTR	SNP	G	G
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
3'UTR	SNP	C	C
5'UTR	SNP	T	T
3'UTR	SNP	T	T
Splice_Site	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Silent	SNP	G	G
Intron	SNP	A	A
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	A	A
Splice_Region	SNP	A	A
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Intron	INS	-	-
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	T	T
Missense_Mutation	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	T	T
Intron	DEL	TTG	TTG
Silent	SNP	C	C
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C
3'UTR	SNP	C	C
Missense_Mutation	SNP	A	A
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	G	G
Intron	INS	-	-
Intron	SNP	A	A
Intron	SNP	A	A
5'UTR	SNP	C	C
5'UTR	SNP	C	C
Intron	SNP	A	A

Silent	SNP	A	A
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	T	T
Silent	SNP	C	C
Silent	SNP	G	G
Intron	SNP	A	A
Missense_Mutation	SNP	A	A
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	A	A
Silent	SNP	C	C
Missense_Mutation	SNP	G	G
5'UTR	SNP	C	C
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Intron	DEL	AA	AA
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	A	A
Silent	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	G	G
5'UTR	SNP	C	C
Silent	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Missense_Mutation	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	INS	-	-
Intron	SNP	C	C
3'Flank	SNP	T	T
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
3'UTR	DEL	TCAC	TCAC
3'UTR	SNP	A	A
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C

Intron	SNP	C	C
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	T	T
Splice_Region	SNP	T	T
Intron	SNP	G	G
Intron	DEL	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Silent	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	A	A
Intron	SNP	C	C
Splice_Region	SNP	C	C
Splice_Region	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	DEL	TATT	TATT
Silent	SNP	C	C
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	T	T
Silent	SNP	G	G
5'UTR	SNP	G	G
Missense_Mutation	SNP	A	A
Intron	SNP	G	G
Intron	SNP	T	T
5'UTR	SNP	A	A
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	T	T
Intron	INS	-	-
Intron	SNP	A	A
Intron	DEL	TCTC	TCTC
Intron	SNP	C	C

Silent	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	C	C
Silent	SNP	C	C
Silent	SNP	G	G
Silent	SNP	G	G
Silent	SNP	A	A
Intron	SNP	C	C
Splice_Region	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Missense_Mutation	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	C	C
Intron	SNP	A	A
Intron	SNP	C	C
Intron	SNP	T	T
3'Flank	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	A	A
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	A	A
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	G	G
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	A	A
Silent	SNP	C	C
Intron	SNP	T	T
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Missense_Mutation	SNP	G	G
Intron	INS	-	-
Intron	INS	-	-
3'UTR	SNP	G	G
3'UTR	SNP	G	G
Intron	SNP	T	T
Silent	SNP	G	G
Intron	SNP	G	G

3'UTR	SNP	C	C
Intron	SNP	T	T
Intron	SNP	C	C
5'Flank	SNP	A	A
Intron	SNP	C	C
5'UTR	SNP	C	C
Intron	SNP	G	G
Silent	SNP	A	A
Missense_Mutation	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	A	A
Silent	SNP	A	A
3'UTR	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
5'Flank	SNP	C	C
Missense_Mutation	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
RNA	SNP	G	G
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	G	G
Missense_Mutation	SNP	G	G
3'UTR	SNP	G	G
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	INS	-	-
Silent	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	A	A
Intron	INS	-	-
Intron	SNP	T	T
Intron	SNP	G	G
Silent	SNP	C	C
In_Frame_Del	DEL	GGTGGT	GGTGGT
Intron	SNP	C	C
Intron	SNP	C	C
Silent	SNP	C	C
Silent	SNP	T	T
Intron	SNP	G	G
3'UTR	SNP	T	T
Silent	SNP	T	T
Intron	SNP	C	C

Silent	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	G	G
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	T	T
Splice_Region	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
Intron	DEL	G	G
Intron	SNP	G	G
5'Flank	SNP	A	A
Intron	SNP	C	C
Intron	SNP	A	A
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	T	T
Missense_Mutation	SNP	G	G
Silent	SNP	T	T
Missense_Mutation	SNP	G	G
3'UTR	INS	-	-
5'UTR	SNP	G	G
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	G	G
Silent	SNP	C	C
Intron	SNP	A	A
Splice_Region	SNP	A	A
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	C	C
Missense_Mutation	SNP	C	C
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Silent	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
5'UTR	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	A	A
Silent	SNP	C	C
Missense_Mutation	SNP	C	C
Silent	SNP	G	G
Silent	SNP	G	G

Splice_Region	SNP	T	T
Silent	SNP	G	G
Intron	SNP	A	A
Intron	DEL	CG	CG
Silent	SNP	G	G
Missense_Mutation	SNP	C	C
Missense_Mutation	SNP	G	G
5'UTR	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
5'Flank	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
5'UTR	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
3'UTR	SNP	G	G
Intron	SNP	G	G
3'UTR	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Silent	SNP	C	C
Missense_Mutation	SNP	T	T
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
Missense_Mutation	SNP	C	C
Silent	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	C	C
3'UTR	SNP	C	C
Intron	SNP	C	C

Silent	SNP	G	G
Intron	DEL	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Intron	DEL	TTT	TTT
Silent	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Silent	SNP	C	C
Intron	INS	-	-
Silent	SNP	G	G
Splice_Region	SNP	G	G
Silent	SNP	T	T
Silent	SNP	T	T
Missense_Mutation	SNP	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
3'UTR	SNP	A	A
Intron	SNP	G	G
Intron	SNP	A	A
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Splice_Region	SNP	T	T
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	T	T
Silent	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
Splice_Region	SNP	T	T
Intron	DEL	GCCT	GCCT
Silent	SNP	C	C
Intron	DEL	GG	GG
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
3'UTR	SNP	C	C
3'UTR	SNP	A	A
3'UTR	SNP	G	G
Intron	SNP	A	A
Silent	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Intron	DEL	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Silent	SNP	G	G

Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	INS	-	-
Splice_Region	SNP	C	C
Silent	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	C	C
3'UTR	DEL	TT	TT
3'UTR	SNP	C	C
Intron	SNP	A	A
Silent	SNP	G	G
Silent	SNP	G	G
Silent	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
5'UTR	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Silent	SNP	T	T
Missense_Mutation	SNP	G	G
Silent	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	T	T
Intron	DEL	ACACACAC	ACACACAC
Silent	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	C	C
Intron	INS	-	-
Intron	SNP	C	C
Intron	DEL	CT	CT
Intron	SNP	A	A
Intron	SNP	T	T

Silent	SNP	T	T
Splice_Region	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Splice_Region	SNP	A	A
Silent	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
3'UTR	SNP	T	T
3'UTR	SNP	T	T
3'UTR	SNP	T	T
Silent	SNP	A	A
Intron	SNP	C	C
Intron	DEL	C	C
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
5'UTR	SNP	C	C
Silent	SNP	A	A
5'UTR	SNP	G	G
Intron	INS	-	-
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	T	T
Intron	DEL	T	T
Silent	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	A	A
Missense_Mutation	SNP	C	C
3'UTR	SNP	A	A
Intron	SNP	T	T
Missense_Mutation	SNP	A	A
Missense_Mutation	SNP	G	G
3'UTR	SNP	A	A

Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
5'UTR	SNP	C	C
3'Flank	SNP	T	T
5'UTR	SNP	C	C
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Silent	SNP	T	T
5'UTR	SNP	C	C
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	C	C
Silent	SNP	T	T
Missense_Mutation	SNP	A	A
Missense_Mutation	SNP	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Silent	SNP	A	A
Intron	SNP	A	A
Intron	DEL	GGG	GGG
Intron	SNP	T	T
Splice_Region	SNP	T	T
5'UTR	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	C	C
5'UTR	SNP	T	T
Intron	SNP	T	T
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
3'UTR	INS	-	-
Intron	SNP	C	C
Silent	SNP	C	C
Intron	SNP	G	G
Silent	SNP	G	G
Intron	SNP	G	G
Silent	SNP	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	C	C

Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	A	A
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	T	T
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	T	T
Missense_Mutation	SNP	A	A
Missense_Mutation	SNP	T	T
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Splice_Region	SNP	C	C
Intron	DEL	TT	TT
Intron	SNP	C	C
Silent	SNP	C	C
Silent	SNP	A	A
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	DEL	TGTG	TGTG
Splice_Region	INS	-	-
Silent	SNP	T	T
5'UTR	SNP	G	G
Intron	SNP	G	G
Silent	SNP	T	T
Intron	SNP	G	G
Silent	SNP	A	A
Silent	SNP	G	G
Intron	DEL	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	T	T
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	C	C
Silent	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
5'UTR	SNP	A	A
Silent	SNP	C	C
Intron	SNP	A	A
Intron	SNP	C	C

Intron	SNP	T	T
Silent	SNP	C	C
5'Flank	SNP	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Missense_Mutation	SNP	A	A
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Silent	SNP	C	C
Silent	SNP	T	T
Intron	SNP	C	C
Missense_Mutation	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	A	A
Silent	SNP	A	A
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	C	C
Missense_Mutation	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Intron	DEL	TTTT	TTTT
Intron	SNP	T	T
Splice_Region	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
3'UTR	SNP	C	C
Intron	SNP	C	C
Missense_Mutation	SNP	T	T
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	C	C
Silent	SNP	A	A
Missense_Mutation	SNP	T	T
Missense_Mutation	SNP	C	C

Intron	INS	-	-
5'UTR	SNP	C	C
5'Flank	DEL	AGAG	AGAG
Intron	SNP	C	C
Silent	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
3'Flank	SNP	T	T
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Silent	SNP	A	A
Intron	SNP	A	A
Intron	SNP	G	G
5'UTR	SNP	A	A
3'UTR	DEL	TTAAAG	TTAAAG
Intron	DEL	TCTAA	TCTAA
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	A	A
Silent	SNP	G	G
3'UTR	SNP	G	G
Intron	SNP	C	C
3'UTR	SNP	T	T
Missense_Mutation	SNP	C	C
Silent	SNP	G	G
Missense_Mutation	SNP	A	A
3'Flank	SNP	C	C
Silent	SNP	G	G
Silent	SNP	A	A
Missense_Mutation	SNP	T	T
Silent	SNP	C	C
Silent	SNP	G	G
5'UTR	SNP	A	A
Intron	SNP	C	C
Splice_Region	SNP	A	A
Silent	SNP	A	A
Intron	DEL	AA	AA
Intron	SNP	C	C
In_Frame_Ins	INS	-	-
Missense_Mutation	SNP	T	T
Silent	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Silent	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	T	T

Missense_Mutation	SNP	C	C
Silent	SNP	C	C
Splice_Region	SNP	C	C
Intron	SNP	A	A
Missense_Mutation	SNP	A	A
Intron	SNP	A	A
Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
5'Flank	SNP	A	A
Silent	SNP	G	G
Silent	SNP	G	G
Intron	SNP	C	C
Silent	SNP	T	T
Splice_Region	SNP	T	T
Intron	SNP	A	A
Intron	SNP	A	A
3'Flank	SNP	A	A
3'Flank	DEL	T	T
Missense_Mutation	SNP	C	C
Intron	SNP	T	T
Silent	SNP	G	G
Silent	SNP	T	T
Missense_Mutation	SNP	G	G
3'UTR	SNP	A	A
Intron	SNP	A	A
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
Missense_Mutation	SNP	C	C
5'UTR	SNP	A	A
Splice_Region	SNP	C	C
Intron	INS	-	-
Intron	DEL	T	T
Intron	SNP	C	C
Silent	SNP	C	C
3'UTR	SNP	A	A
Intron	SNP	T	T
Silent	SNP	A	A
Missense_Mutation	SNP	A	A
Intron	SNP	A	A
Intron	SNP	C	C
Silent	SNP	C	C
Intron	SNP	A	A
Silent	SNP	G	G
RNA	SNP	G	G
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C

Intron	INS	-	-
Missense_Mutation	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	T	T
Missense_Mutation	SNP	T	T
Silent	SNP	A	A
3'UTR	SNP	G	G
Silent	SNP	G	G
Silent	SNP	A	A
Silent	SNP	A	A
Intron	SNP	C	C
Intron	SNP	C	C
Splice_Region	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	INS	-	-
Intron	SNP	G	G
Intron	SNP	G	G
Intron	INS	-	-
Missense_Mutation	SNP	C	C
Intron	SNP	T	T
Silent	SNP	G	G
Intron	DEL	CC	CC
Intron	SNP	C	C
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	G	G
Missense_Mutation	SNP	A	A
Missense_Mutation	SNP	C	C
Silent	SNP	C	C
Intron	SNP	T	T
In_Frame_Ins	INS	-	-
Intron	SNP	C	C
Intron	SNP	G	G
3'UTR	SNP	G	G
Intron	INS	-	-
Splice_Region	SNP	C	C
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	A	A
Intron	SNP	A	A
5'UTR	SNP	G	G
Intron	SNP	G	G
Intron	DEL	CTGGT	CTGGT
Intron	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	INS	-	-

Intron	DEL	AA	AA
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	A	A
Splice_Region	SNP	A	A
Intron	SNP	G	G
5'UTR	SNP	A	A
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	C	C
Intron	SNP	T	T
Intron	SNP	T	T
Silent	SNP	G	G
Intron	SNP	C	C
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Intron	INS	-	-
Intron	SNP	T	T
5'UTR	SNP	T	T
Intron	SNP	C	C
Missense_Mutation	SNP	A	A
5'UTR	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Silent	SNP	G	G
Intron	INS	-	-
Intron	SNP	T	T
Silent	SNP	T	T
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	DEL	G	G
Missense_Mutation	SNP	C	C
Silent	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Silent	SNP	A	A
Intron	DEL	GCCTTC	GCCTTC
Intron	SNP	T	T
Nonsense_Mutation	INS	-	-
5'UTR	SNP	A	A
Silent	SNP	T	T
Intron	SNP	G	G
Intron	SNP	T	T
5'UTR	SNP	C	C
Splice_Region	SNP	T	T
5'UTR	SNP	G	G
Silent	SNP	C	C
Intron	INS	-	-
5'UTR	SNP	C	C
Intron	SNP	A	A
Silent	SNP	G	G

3'UTR	SNP	C	C
Intron	DEL	A	A
Intron	SNP	G	G
3'UTR	SNP	G	G
Intron	SNP	T	T
Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
3'Flank	SNP	A	A
3'Flank	SNP	G	G
Intron	SNP	A	A
5'Flank	SNP	G	G
Intron	SNP	C	C
Intron	SNP	C	C
Intron	SNP	G	G
5'UTR	INS	-	-
5'UTR	INS	-	-
Silent	SNP	C	C
Silent	SNP	C	C
Intron	SNP	A	A
Intron	SNP	C	C
Silent	SNP	C	C
Intron	SNP	G	G
Silent	SNP	G	G
Silent	SNP	A	A
Intron	SNP	A	A
Missense_Mutation	SNP	T	T
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Silent	SNP	G	G
5'Flank	SNP	T	T
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	G	G
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Silent	SNP	C	C
Intron	SNP	C	C
Intron	SNP	T	T
Missense_Mutation	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
3'Flank	SNP	A	A
Intron	SNP	C	C
Missense_Mutation	SNP	A	A

Intron	SNP	A	A
5'Flank	SNP	C	C
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Missense_Mutation	SNP	C	C
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Missense_Mutation	SNP	A	A
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Intron	SNP	C	C
Missense_Mutation	SNP	A	A
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Intron	SNP	T	T
Intron	SNP	C	C
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Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	T	T
Silent	SNP	A	A
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Intron	DEL	TT	TT
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Intron	SNP	G	G
Intron	SNP	G	G
3'Flank	SNP	T	T
Silent	SNP	T	T
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Splice_Region	SNP	C	C
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Missense_Mutation	SNP	G	G
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Silent	SNP	G	G
Missense_Mutation	SNP	T	T
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Intron	SNP	A	A
Missense_Mutation	SNP	T	T
Intron	SNP	G	G
Intron	SNP	G	G
Silent	SNP	T	T
Intron	SNP	G	G
Silent	SNP	T	T
Intron	INS	-	-
Intron	SNP	C	C

Intron	SNP	C	C
Intron	SNP	C	C
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Intron	SNP	G	G
Splice_Region	SNP	C	C
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Silent	SNP	G	G
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Missense_Mutation	SNP	G	G
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Missense_Mutation	SNP	G	G
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Silent	SNP	G	G
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Missense_Mutation	SNP	T	T
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Intron	SNP	G	G
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	T	T
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3'UTR	SNP	C	C
Silent	SNP	C	C
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Splice_Site	SNP	G	G
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Missense_Mutation	SNP	C	C
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Intron	SNP	A	A

Missense_Mutation	SNP	G	G
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Intron	SNP	G	G
Intron	DEL	C	C
Silent	SNP	T	T
3'UTR	SNP	T	T
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Silent	SNP	G	G
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Silent	SNP	C	C
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Intron	SNP	T	T
Missense_Mutation	SNP	A	A
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Intron	SNP	C	C
Silent	SNP	G	G
Intron	DEL	T	T
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Intron	SNP	G	G
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Silent	SNP	C	C
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Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	T	T
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Silent	SNP	C	C
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Splice_Region	SNP	T	T
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Missense_Mutation	SNP	A	A
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Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	G	G
Intron	SNP	C	C
Missense_Mutation	SNP	A	A
Splice_Region	SNP	A	A

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Silent	SNP	T	T
Intron	SNP	T	T
Intron	SNP	C	C
Intron	SNP	T	T
Missense_Mutation	SNP	C	C
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Missense_Mutation	SNP	A	A
Intron	SNP	G	G
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Intron	SNP	A	A
Missense_Mutation	SNP	C	C
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Intron	SNP	G	G
Missense_Mutation	SNP	C	C
Intron	SNP	G	G
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Splice_Region	SNP	C	C
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Intron	SNP	A	A
3'UTR	SNP	A	A
Intron	SNP	C	C
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Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	C	C
Silent	SNP	T	T
3'UTR	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
RNA	SNP	C	C
Intron	SNP	G	G
Splice_Region	SNP	T	T
Intron	SNP	C	C
Missense_Mutation	SNP	G	G
Splice_Region	SNP	C	C
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Intron	SNP	C	C
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Intron	SNP	C	C
Missense_Mutation	SNP	C	C
Silent	SNP	T	T

Nonsense_Mutation	INS	-	-
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3'UTR	INS	-	-
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Intron	SNP	C	C
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Missense_Mutation	SNP	C	C
Intron	SNP	C	C
Silent	SNP	C	C
3'Flank	DEL	C	C
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Missense_Mutation	SNP	T	T
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Missense_Mutation	SNP	G	G
Silent	SNP	A	A
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Intron	SNP	C	C
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Silent	SNP	C	C
Intron	SNP	A	A
3'UTR	SNP	G	G
Intron	SNP	G	G
Intron	SNP	G	G
Splice_Region	SNP	A	A
Silent	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Silent	SNP	T	T
Silent	SNP	C	C
Intron	SNP	T	T
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Intron	SNP	A	A
5'UTR	SNP	G	G
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Intron	SNP	C	C

Silent	SNP	C	C
Missense_Mutation	SNP	A	A
Silent	SNP	G	G
Intron	SNP	C	C
Intron	SNP	T	T
Missense_Mutation	SNP	A	A
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3'UTR	SNP	A	A
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Intron	SNP	G	G
Splice_Region	SNP	C	C
Missense_Mutation	SNP	T	T
Intron	SNP	C	C
Intron	SNP	G	G
Intron	SNP	A	A
Intron	SNP	G	G
Silent	SNP	T	T
Intron	SNP	T	T
Intron	SNP	A	A
Intron	SNP	T	T
Intron	SNP	T	T
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	G	G
Missense_Mutation	SNP	G	G
5'UTR	INS	-	-
Missense_Mutation	SNP	C	C
Silent	SNP	G	G
Missense_Mutation	SNP	T	T
Intron	SNP	C	C
Silent	SNP	C	C
Missense_Mutation	SNP	A	A
Silent	SNP	C	C
Silent	SNP	C	C
Missense_Mutation	SNP	C	C
Intron	SNP	T	T
Intron	SNP	G	G
Intron	SNP	C	C

Tumor_Seq_Allele2	dbSNP_RS	dbSNP_Val_Status	Tumor_Sample_Barcode
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NORMAL	C	C

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NORMAL	C	C
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NORMAL	TCTAA	TCTAA
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NORMAL	T	T
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NORMAL	C	C
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NORMAL	T	T
NORMAL	G	G
NORMAL	C	C

umor_Validation_Allelech_Norm_Validation_Allch_Norm_Validation_All	Verification_Status

Validation_Status	Mutation_Status	Sequencing_Phase	Sequence_Source

Validation_Method	Score	BAM_File	Sequencer

Tumor_Sample_UUID	tched_Norm_Sample_U	HGVSc	HGVSp
		c.361+98_361+99insAA	
		c.553+23A>G	
		c.687+71C>G	
		c.783T>C	p.=
		c.*35G>A	
		c.301+85A>C	
		c.2741-20T>C	
		c.1791+26T>C	
		c.4038T>A	p.=
		c.1868-85delG	
		c.3819G>A	p.=
		c.-61_-52dupTCGCCCGCTC	
		c.2342+5C>T	
		c.340G>A	p.Ala114Thr
		c.1093-50C>A	
		c.30+67C>G	
		c.1229-84C>T	
		c.1376-83A>G	
		c.-42C>T	
		c.639+94C>T	
		c.239-6G>A	
		c.1072-31C>T	
		c.666+73C>T	
		c.201+89C>T	
		c.810+5G>A	
		c.2305C>T	p.Pro769Ser
		c.1192-91_1192-90insTTAT	
		c.2818C>A	p.Leu940Met
		c.2291-43T>C	
		c.868-9delT	
		c.1549-17G>A	
		c.1223+39T>C	
		c.2217+23A>G	
		c.342-14456_342-14442delTCCTCCCCCTATCTG	
		c.621A>G	p.=
		c.2965-16T>C	
		c.1359+29G>A	
		c.478+77dupG	
		c.64-43T>C	
		c.573C>T	p.=
		c.2623+85A>G	
		c.-4-71G>A	
		c.48T>C	p.=
		c.1449+55G>A	
		c.1417-43G>A	
		c.286G>A	p.Val96Ile
		c.588C>T	p.=
		c.879+156T>C	
		c.6945+8C>T	
		c.4149-59C>G	
		c.909-11C>T	
		c.1058+47C>A	

c.321-35G>A	
c.1392-42T>A	
c.1451+82C>T	
c.-74A>C	
c.4735+37C>T	
c.911+92A>G	
c.772+26T>C	
c.4341G>A	p.=
c.426+42A>C	
c.3031+23_3031+27delTTTTT	
c.480+24G>A	
c.2616-97C>T	
c.3025T>C	p.Phe1009Leu
c.2376-16A>G	
c.1874-7T>C	
c.804G>A	p.=
c.463-41G>A	
c.483+60G>A	
c.2480+90T>A	
c.-462C>T	
c.1537-74A>G	
c.1455+52G>C	
c.703-36C>T	
c.1066G>A	p.Gly356Arg
c.1-99C>T	
c.395-30G>T	
c.83T>G	p.Leu28Arg
c.-64A>G	
c.447+90T>C	
c.1918G>T	p.Val640Phe
c.148+91_148+92delCC	
c.2050A>G	p.Met684Val
c.403+11T>C	
c.1104+13T>C	
c.1806G>A	p.=
c.1283-89G>A	
c.635-67G>A	
c.1099T>G	p.Leu367Val
c.543T>C	p.=
c.865+84T>C	
c.492G>A	p.=
c.795+68C>T	
c.-196C>T	
c.250A>G	p.Arg84Gly
c.6009C>T	p.=
c.843-27A>G	
c.341+92C>A	
c.274+6G>A	
c.585G>T	p.Trp195Cys
c.1698+53A>C	
c.317-15G>A	
c.716-93T>C	
c.187+30delT	

c.-69C>A	
c.963+97G>A	
c.1354-50C>T	
c.456-50C>T	
c.638-60T>C	
c.2654-35158C>G	
c.716-49G>A	
c.1161+86T>A	
c.76+47A>G	
c.574-24G>C	
c.*350G>A	
c.1005C>T	p.=
c.2259C>T	p.=
c.2970-39C>G	
c.986+17C>G	
c.*30+81G>T	
c.2782-29C>A	
c.-22-28A>T	
c.1294-60C>T	
c.2637-41C>T	
c.1882+22A>G	
c.2172+52C>T	
c.833-41C>T	
c.848-6T>C	
c.1564A>C	p.Ile522Leu
c.2463-85dupG	
c.983G>A	p.Arg328His
c.352-63C>T	
c.1491+61G>A	
c.1157G>A	p.Arg386Gln
c.-34T>G	
c.93-66A>G	
c.4853+21C>T	
c.457-72G>T	
c.2764+2T>A	
c.205-56C>T	
c.308A>G	p.Asn103Ser
c.99+1475T>C	
c.1258+96G>A	
c.6477+33G>T	
c.5215+66G>A	
c.5137+65G>A	
c.4548-63C>G	
c.681+56C>T	
c.1423-50G>A	
c.864C>T	p.=
c.1312-37T>C	
c.68-14T>C	
c.656-71C>T	
c.1453-105G>T	
c.992G>A	p.Gly331Asp
c.544+78T>A	
c.148+59G>A	
c.993G>T	p.=
c.4984-45T>C	

c.4272T>C	p.=
c.1244-68C>T	
c.822-71G>A	
c.164A>G	p.Gln55Arg
c.1540-23C>T	
c.550_551delAT	p.Met184AspfsTer14
c.434+86_434+89delGAGA	
c.*49T>C	
c.1112A>G	p.His371Arg
c.-7T>C	
c.393T>A	p.Asp131Glu
c.1734A>G	p.=
c.347-7128_347-7125delATTA	
c.1228-73A>G	
c.1000+6C>G	
c.296-46T>C	
c.*10C>G	
c.28-83A>T	
c.2441-24C>A	
c.177+94C>A	
c.3391-35T>C	
c.4017+17C>G	
c.-333T>C	
c.567+71C>T	
c.790-34T>C	
c.645C>T	p.=
c.2446C>T	p.Leu816Phe
c.5941-93_5941-88delGTGTGT	
c.1974+8A>C	
c.2663+79C>T	
c.1152+78G>T	
c.3312+10G>C	
c.334-89T>C	
c.2478+95C>G	
c.1795-85C>T	
c.-71G>A	
c.*41G>A	
c.517+95C>T	
c.437+38C>T	
c.849C>T	p.=
c.1237+63C>T	
c.283+96C>T	
c.262-13C>T	
c.1383+22A>G	
c.772+16C>T	
c.*97C>T	
c.365-88G>C	
c.3868+98C>T	
c.1316-57C>G	
c.27C>T	p.=
c.1293G>A	p.=
c.640+37_640+46delTGAATACATA	
c.733G>A	p.Val245Met

c.778-12A>T	
c.*67G>A	
c.*23A>G	
c.497+65T>C	
c.570A>G	p.=
c.2024A>T	p.Glu675Val
c.280-12528G>A	
c.3356+21G>A	
c.156C>T	p.=
c.303+38C>A	
c.298+18G>A	
c.50-61G>A	
c.941+103G>A	
c.2390A>G	p.Asn797Ser
c.608delA	p.His203ProfsTer5
c.975+39T>C	
c.774+59delT	
c.776A>C	p.Lys259Thr
c.673+58A>G	
c.515_541delACCCGCCAGCAGCCTCT(	p.Asp172_Pro180del
c.1953+62A>G	
c.*1+24G>T	
c.1574A>G	p.Gln525Arg
c.229-51G>A	
c.1111-80C>G	
c.116+17C>A	
c.528-74A>T	
c.1227A>G	p.=
c.2980+57C>A	
c.57+14C>A	
c.86-34C>T	
c.-6T>C	
c.65-57G>A	
c.425-1789_425-1788insGAA	
c.1081+78G>A	
c.1306-78A>C	
c.755G>A	p.Arg252His
c.935+62A>G	
c.552A>G	p.=
c.592-20delA	
c.83G>T	p.Arg28Leu
c.1050+86C>T	
c.3167+99T>A	
c.-25-96T>C	
c.222+31C>T	
c.404G>A	p.Ser135Asn
c.590-64A>T	
c.1070+88A>G	
c.1474+97T>A	
c.1204C>T	p.His402Tyr
c.4389G>A	p.=
c.-35A>G	
c.39G>C	p.=
c.343+56C>T	

c.403+68A>G	
c.545C>T	p.Ala182Val
c.*68T>C	
c.*6G>A	
c.2888+34C>T	
c.633C>T	p.=
c.5702+64C>A	
c.366C>G	p.His122Gln
c.1141-15T>C	
c.1372+20C>A	
c.1227+83G>A	
c.*93G>A	
c.-25A>G	
c.*19A>C	
c.309-1G>T	
c.1006-50G>A	
c.1534+41G>A	
c.1977-95G>C	
c.2340+88G>A	
c.4716C>T	p.=
c.1036-93A>G	
c.1359G>A	p.=
c.1486+67C>A	
c.3381+17A>C	
c.3248-4A>G	
c.5656-81T>G	
c.3525G>A	p.=
c.1482-25T>C	
c.1120-43T>C	
c.3278-76_3278-75insTTTCAACATTGTCTCCATTCGG	
c.703-67G>T	
c.2463+60A>G	
c.2257-71A>T	
c.1240G>A	p.Ala414Thr
c.2519-46A>G	
c.4098+57C>A	
c.1399-32T>C	
c.1897+66_1897+68delCAA	
c.408C>G	p.=
c.157+13A>G	
c.2285+72C>G	
c.191-159G>A	
c.*54C>A	
c.3154A>G	p.Ile1052Val
c.1054+1196G>A	
c.396+45T>C	
c.505+91G>A	
c.749-88C>A	
c.777C>A	p.=
c.2029-61_2029-60insACAGACAATGCCCAA	
c.700-28A>T	
c.1730+79A>C	
c.-33C>T	
c.-15C>A	
c.621+43T>A	

c.3912T>C	p.=
c.-11-33C>T	
c.4488G>A	p.=
c.292+13A>G	
c.423G>A	p.=
c.1911C>T	p.=
c.35+143T>C	
c.4715T>C	p.Leu1572Pro
c.64-93C>G	
c.2932G>A	p.Gly978Arg
c.1919+24T>A	
c.2403G>A	p.=
c.1327C>T	p.His443Tyr
c.-55G>A	
c.756+26G>T	
c.152-57C>T	
c.1304-56T>G	
c.1162-64C>T	
c.798+50_798+51delTT	
c.38C>T	p.Pro13Leu
c.292-52G>T	
c.63G>A	p.=
c.124+67A>G	
c.715-52T>C	
c.366+61A>C	
c.234T>C	p.=
c.133-78G>A	
c.2053+13A>G	
c.1017C>T	p.=
c.-80G>C	
c.348T>C	p.=
c.1290-93T>C	
c.881-95T>C	
c.1596+34C>A	
c.1488+88T>G	
c.670G>C	p.Glu224Gln
c.48+53C>G	
c.625+80C>T	
c.591+44C>T	
c.460-34G>A	
c.1544-193_1544-192dupCA	
c.738+13G>A	
c.1728+91A>G	
c.3264-32G>A	
c.1281-26A>G	
c.2325+47G>A	
c.*78_*81delCTCA	
c.*68A>G	
c.1981+609C>T	
c.112-100C>T	
c.1825+96T>C	
c.358-300A>G	
c.4189-28C>A	
c.-55-80G>A	

c.1191+71G>A	
c.2466+38T>C	
c.9945+96T>C	
c.4477-37T>C	
c.8726+54C>T	
c.8190+9T>G	
c.8545-65A>G	
c.11340+76T>G	
c.9445-23A>G	
c.346-80C>A	
c.3537+71T>C	
c.12298-36T>C	
c.463+6T>C	
c.386-20G>A	
c.4548+22delC	
c.3877-55C>G	
c.4250-63C>T	
c.3438G>A	p.=
c.1051G>C	p.Glu351Gln
c.676+40T>G	
c.531-100G>C	
c.1900+3G>A	
c.847+5C>A	
c.2247-9C>T	
c.1698+48G>C	
c.2629-52G>A	
c.2362+43C>T	
c.84+83_84+86delTTTA	
c.3123C>A	p.=
c.30C>T	p.=
c.273+10C>T	
c.2195-66A>C	
c.181+73C>T	
c.110+52T>G	
c.219-51A>G	
c.279G>A	p.=
c.-39C>G	
c.430T>G	p.Ser144Ala
c.795-38G>A	
c.11955+73T>C	
c.-93T>C	
c.77G>T	p.Arg26Leu
c.1022C>T	p.Thr341Ile
c.1507-30G>C	
c.1428+31C>A	
c.66+81C>T	
c.205-75G>T	
c.233+30G>T	
c.1071+35T>A	
c.2339+67C>A	
c.324+88A>G	
c.87+306_87+307insGGTGATTCCCACCCC	
c.806-69A>G	
c.307+63_307+66delCTCT	
c.762+25G>T	

c.372G>A	p.=
c.160-72C>A	
c.1059-31T>C	
c.99C>T	p.=
c.1509G>A	p.=
c.417C>T	p.=
c.1509C>A	p.=
c.1218T>C	p.=
c.1150+70C>T	
c.631-4C>T	
c.1034G>C	p.Ser345Thr
c.807+60A>T	
c.592-74A>G	
c.1723T>C	p.Ser575Pro
c.884+40G>C	
c.884+41A>G	
c.489G>A	p.=
c.1742-72T>C	
c.208+60G>A	
c.53-26T>C	
c.1435+68C>A	
c.1747+31G>A	
c.416A>G	p.His139Arg
c.1236C>T	p.=
c.581-52G>T	
c.2225-56A>G	
c.1768G>A	p.Gly590Arg
c.512C>T	p.Thr171Ile
c.734C>T	p.Thr245Met
c.6G>A	p.=
c.1479+89G>A	
c.327+9C>T	
c.988-53C>T	
c.1012-85T>A	
c.3150G>A	p.=
c.590+99T>A	
c.1765G>A	p.Glu589Lys
c.2533-71G>T	
c.96+37A>G	
c.3780C>G	p.Asp1260Glu
c.1010-27G>A	
c.1120G>A	p.Val374Ile
c.193-24T>A	
c.744+47C>G	
c.747+17G>C	
c.364+85T>G	
c.716G>A	p.Arg239His
c.189+6969_189+6970insCG	
c.189+6970_189+6971insCCTAGATGCAGGAG	
c.*27C>G	
c.*244C>A	
c.297+12A>G	
c.348C>T	p.=
c.70+24C>T	

c.*74G>A	
c.2346+27A>C	
c.7034+89G>T	
c.282+100G>T	
c.-42C>G	
c.655+39C>T	
c.3000T>C	p.=
c.560C>T	p.Ala187Val
c.827-10C>T	
c.249-35A>G	
c.855+58A>G	
c.387A>C	p.=
c.*18T>C	
c.1032-19T>C	
c.1893+1626C>T	
c.3651C>T	p.=
c.3732+52C>T	
c.3224-18C>T	
c.464C>T	p.Pro155Leu
c.5896C>G	p.His1966Asp
c.579+53G>A	
n.926G>A	
c.2697-16C>T	
c.1570-87T>C	
c.557+98C>T	
c.406-84G>T	
c.675+37C>A	
c.314-95G>A	
c.1152G>A	p.=
c.1162G>A	p.Gly388Arg
c.*16C>T	
c.1197-5086T>C	
c.2952C>T	p.=
c.1197-4807C>T	
c.26-12C>A	
c.923+74_923+75insCCTTTTAAACAACCAG	
c.594G>A	p.=
c.222-13C>T	
c.1286C>T	p.Thr429Met
c.1748-61A>G	
c.3001+69_3001+70insTAGGGTAACC	
c.4765+69T>C	
c.4307+76G>A	
c.441C>T	p.=
c.172_177delACCACC	p.Thr58_Thr59del
c.314-67G>A	
c.5175-16C>T	
c.2091C>G	p.=
c.1284T>C	p.=
c.301-78G>A	
c.*192T>C	
c.1947T>C	p.=
c.7682+85C>G	

c.8439C>T	p.=
c.1820-26G>A	
c.8604+28A>T	
c.3987C>A	p.=
c.1898+85G>A	
c.559+49A>T	
c.1458+59C>T	
c.1587C>T	p.=
c.-2-33A>T	
c.-11T>G	
c.65-60A>G	
c.3057+67A>G	
c.1393-41G>T	
c.1662-27G>A	
c.382+60delC	
c.1671-15C>T	
c.611+34G>A	
c.1057-77A>G	
c.1420C>A	p.Gln474Lys
c.157T>G	p.Tyr53Asp
c.1543G>T	p.Val515Phe
c.1056A>G	p.=
c.1469C>T	p.Ala490Val
c.*94dupA	
c.-148G>C	
c.-19-57C>T	
c.1647+33T>A	
c.660C>T	p.=
c.1095C>T	p.=
c.926-34528A>G	
c.988+7A>G	
c.548-61C>G	
c.347-28A>G	
c.345+56A>G	
c.1380+73A>G	
c.44-32G>A	
c.1438G>C	p.Ala480Pro
c.1550C>T	p.Ala517Val
c.1405C>T	p.Arg469Cys
c.278-42G>A	
c.289G>A	p.Val97Ile
c.2652C>T	p.=
c.2318+23A>T	
c.776-81G>T	
c.-7C>T	
c.253A>G	p.Ile85Val
c.494+41A>C	
c.880+32C>T	
c.186+61A>G	
c.934+80A>T	
c.309C>T	p.=
c.110G>A	p.Arg37His
c.453C>T	p.=
c.3042C>T	p.=

c.-5T>C	
c.1248G>A	p.=
c.822-32T>C	
c.771+76_771+77delCG	
c.21G>T	p.=
c.370G>T	p.Val124Leu
c.652G>C	p.Ala218Pro
c.-161C>T	
c.131+24G>A	
c.401+20G>A	
c.172+25G>C	
c.1425T>C	p.=
c.540+82T>A	
c.930+100C>A	
c.1478+100G>T	
c.809+56G>A	
c.3322+81T>A	
c.721-50G>A	
c.268+18363T>A	
c.1789C>T	p.=
c.227-87G>C	
c.1847C>T	p.Thr616Met
c.-64C>T	
c.445-16C>T	
c.15+318C>T	
c.1191+80C>T	
c.*2239G>T	
c.2957-68C>T	
c.*40C>A	
c.716-35A>G	
c.91-98G>T	
c.350-60T>G	
c.2355+50A>G	
c.3170+76C>T	
c.379-22C>T	
c.525G>A	p.=
c.5355+28C>T	
c.2242-15C>T	
c.1842G>A	p.=
c.1895T>C	p.Val632Ala
c.2155+84A>T	
c.141-59A>T	
c.1229+57A>C	
c.31+20T>C	
c.867-45C>T	
c.1027-97G>T	
c.187C>G	p.His63Asp
c.1008G>A	p.=
c.288+32C>G	
c.1730+666G>A	
c.39C>T	p.=
c.216+289G>T	
c.*89C>T	
c.-20+107G>A	

c.48C>T	p.=
c.591+34delC	
c.619C>A	p.Leu207Met
c.1681-30G>A	
c.1375+57_1375+59delAAA	
c.606G>T	p.=
c.1297+59G>A	
c.494G>T	p.Gly165Val
c.527-51T>A	
c.1519-78G>A	
c.1386G>A	p.=
c.455-21dupC	
c.516G>A	p.=
c.198+4C>A	
c.12T>A	p.=
c.2109A>G	p.=
c.5987G>A	p.Arg1996His
c.382G>A	p.Val128Ile
c.407-74T>A	
c.*5909T>C	
c.207+94C>G	
c.780-92A>G	
c.536G>C	p.Ser179Thr
c.28T>G	p.Phe10Val
c.2956+72A>G	
c.1765+64T>G	
c.6996-5T>A	
c.2899-56G>A	
c.80-80C>T	
c.1347A>G	p.=
c.2571T>C	p.=
c.952+76C>T	
c.581-66C>T	
c.999G>T	p.Glu333Asp
c.425-15T>C	
c.696+3A>G	
c.967+68_967+71delAGGC	
c.3069G>C	p.=
c.1090+31_1090+32delGG	
c.530C>A	p.Ser177Tyr
c.177-55G>A	
c.*70G>A	
c.*57A>C	
c.*9C>T	
c.408-73T>C	
c.1650G>A	p.=
c.1610+28A>C	
c.1425+27C>T	
c.6347+50A>T	
c.1275+98C>T	
c.1521+57A>G	
c.3423-40delG	
c.3114+22C>A	
c.1299+93C>A	
c.957G>C	p.=

c.2835-60A>G	
c.2089+20T>C	
c.1385+39T>C	
c.1840-13G>A	
c.1540-83A>G	
c.390G>A	p.=
c.2297-63A>G	
c.552+28T>C	
c.1933-26A>G	
c.526-58G>A	
c.6946-99_6946-98insCAGCTTC	
c.1714-4C>A	
c.729C>T	p.=
c.4174-47G>A	
c.3784-69G>C	
c.297-67C>T	
c.285-76G>A	
c.1948-20A>G	
c.181+50G>A	
c.906+9C>G	
c.1206C>T	p.=
c.*49_*50delTT	
c.*54C>T	
c.2884-81T>C	
c.1578C>T	p.=
c.2781C>T	p.=
c.234G>A	p.=
c.566C>G	p.Pro189Arg
c.866-63C>A	
c.378-33G>T	
n.1143+41G>A	
c.217+12C>G	
c.-57C>T	
c.4239+18G>A	
c.1734+61G>A	
c.2086-13C>T	
c.228+40C>A	
c.2177C>A	p.Thr726Lys
c.1052-25G>C	
c.1612A>C	p.=
c.1930C>A	p.Arg644Ser
c.33C>T	p.=
c.901+120C>A	
c.2065T>G	p.Ser689Ala
c.3879+55_3879+62delGTGTGTGT	
c.3486C>T	p.=
c.28-79T>A	
c.1554+39G>T	
c.270C>T	p.=
c.456+70C>T	
c.799-96_799-95insAAGGCCCCGGGCCCTGGCTGGGGAGGCCCATGATTAACTCTTAAGAA	
c.1336-73C>A	
c.3976+101_3976+102delTC	
c.842-25T>A	
c.799-20A>G	

c.648A>C	p.=
c.39A>G	p.=
c.1378-59A>T	
c.357+42T>A	
c.14461-53A>G	
c.3387+25C>A	
c.4884+8A>G	
c.936G>A	p.=
c.1416+42G>A	
c.632-55C>T	
c.1749-80C>A	
c.709-38C>G	
c.*67A>T	
c.*4T>C	
c.*33T>C	
c.330T>C	p.=
c.1251+20C>T	
c.4717+61delC	
c.284-85A>G	
c.1077+64C>T	
c.967-34C>A	
c.3486+17G>A	
c.1021+64T>C	
c.3999+69G>A	
c.-6C>A	
c.1446T>C	p.=
c.-46G>T	
c.448-257_448-256insCCAGGTCACCTGCACCT	
c.805+60G>A	
c.1695+100G>A	
c.736-51C>A	
c.656-19G>A	
c.1152+74G>A	
c.1277G>A	p.Arg426His
c.1082+179G>A	
c.1509-35G>A	
c.2219+55T>A	
c.722-46delA	
c.42T>C	p.=
c.1060-2463A>G	
c.1212-24T>C	
c.1240+75A>G	
c.607-59T>C	
c.13659+18G>T	
c.2503+37C>T	
c.562C>T	p.Arg188Trp
c.656-54C>T	
c.350-19A>T	
c.282+96A>T	
c.20G>T	p.Gly7Val
c.*52A>G	
c.4541+85T>A	
c.275T>C	p.Leu92Pro
c.713G>A	p.Arg238Gln
c.*83A>G	

c.1194+52G>A	
c.4359-72C>T	
c.597+75T>C	
c.68-57C>A	
c.-59G>C	
c.-40C>T	
c.1074-9C>G	
c.221-9A>G	
c.-65-13C>G	
c.888A>G	p.=
c.-36C>T	
c.5-45T>C	
c.909G>A	p.=
c.46-28C>A	
c.2464+85G>A	
c.2193C>T	p.=
c.1547-43G>C	
c.1245T>A	p.=
c.728A>C	p.Gln243Pro
c.2594C>T	p.Pro865Leu
c.574G>A	p.Ala192Thr
c.1746-53C>T	
c.945T>G	p.=
c.418-73A>G	
c.360-93_360-91delGGG	
c.489-66T>C	
c.1011T>C	p.=
c.-36C>G	
c.490C>A	p.Arg164Ser
c.1594+39T>C	
c.4136+31C>T	
c.429G>A	p.=
c.15661+81G>A	
c.15661+80G>A	
c.978C>T	p.=
c.4098+65G>A	
c.-4A>G	
c.1375-55T>C	
c.419G>C	p.Cys140Ser
c.-282+72G>T	
c.3094+45C>G	
c.2092-75A>G	
c.*85dupT	
c.724-46G>A	
c.666G>A	p.=
c.1195-19C>T	
c.1704G>A	p.=
c.1190+78G>A	
c.1356C>T	p.=
c.343C>T	p.Leu115Phe
c.1207-33A>T	
c.2241+96C>T	
c.1695-24T>C	
c.1142-88G>A	

c.124-30A>C	
c.2401-73T>C	
c.414+28C>T	
c.1924+89A>G	
c.194-34G>A	
c.979+34C>T	
c.691+693G>C	
c.460A>C	p.Lys154Gln
c.937-61G>A	
c.1418C>T	p.Thr473Ile
c.115+9C>T	
c.241-28C>T	
c.20+141G>A	
c.916T>G	p.Tyr306Asp
c.1853A>G	p.His618Arg
c.1526T>C	p.Val509Ala
c.418-16T>C	
c.-9+19G>A	
c.238+18C>T	
c.522+52G>A	
c.226-5G>A	
c.366+84_366+85delTT	
c.404+72C>T	
c.6909G>A	p.=
c.3144A>G	p.=
c.3711+15G>T	
c.1515+27A>G	
c.3205-49G>A	
c.758+95_758+98delTGTG	
c.41011-10_41011-5dupTCTCCC	
c.7599A>G	p.=
c.-461G>C	
c.*7027+91G>A	
c.7662T>C	p.=
c.1013+88C>T	
c.7353T>C	p.=
c.123C>T	p.=
c.506-12delC	
c.3721G>A	p.Ala1241Thr
c.2322+46A>G	
c.1095G>A	p.=
c.2044+93G>A	
c.3973-30A>G	
c.3485+25G>A	
c.3558C>T	p.=
c.8225-53G>T	
c.3369-73T>C	
c.1354-88G>A	
c.2855-69A>G	
c.4240-1197T>A	
c.1936-77T>C	
c.-12T>C	
c.1134C>T	p.=
c.3300+70A>C	
c.1662-82G>C	

c.2037+93T>A	
c.912G>A	p.=
c.928G>A	p.Ala310Thr
c.190+21T>C	
c.4797+29T>A	
c.2768A>G	p.His923Arg
c.2468+18C>T	
c.165+9T>C	
c.184+31G>A	
c.274C>T	p.Pro92Ser
c.445-50C>T	
c.3684+88C>A	
c.1882-14T>A	
c.1675+48C>T	
c.6679+67C>T	
c.1290C>T	p.=
c.11077-94A>T	
c.1674+30T>G	
c.402+101A>G	
c.1062G>A	p.=
c.510T>C	p.=
c.342+45C>G	
c.995A>C	p.Glu332Ala
c.1637+25G>T	
c.21+99C>A	
c.430-32A>G	
c.312T>C	p.=
c.203-2816T>C	
c.2404+88C>A	
c.4951-65A>T	
c.773+84C>A	
c.637A>G	p.Arg213Gly
c.8049+84T>A	
c.272+68G>A	
c.1528+218G>A	
c.185G>C	p.Ser62Thr
c.914-36C>G	
c.2783-41_2783-38delAAAA	
c.3299+89T>C	
c.2955G>T	p.=
c.443-29G>A	
c.2330+27C>T	
c.1074-40A>G	
c.727+70C>T	
c.2200-46C>T	
c.*42C>G	
c.940-142C>T	
c.894T>G	p.Asp298Glu
c.1820+93T>C	
c.5168-43T>C	
c.2587+74G>A	
c.3888T>C	p.=
c.433A>C	p.Ile145Leu
c.723C>G	p.Ser241Arg

c.888+82_888+83insTGATCCGCCTGCCTTGA	
c.-87C>G	
c.3297+79G>A	
c.3705T>C	p.=
c.1602-11G>T	
c.1413-21G>A	
c.703C>T	p.Arg235Cys
c.735-65C>T	
c.417T>A	p.=
c.1083+59A>C	
c.6074+41G>A	
c.-44T>C	
c.*59_*64delAAGTTA	
c.1057-81_1057-77delTTAGA	
c.1395+10G>A	
c.2163-87G>A	
c.1836-38G>T	
c.197+37A>G	
c.1083-363A>G	
c.1083-242T>A	
c.1083-243A>G	
c.821-44A>G	
c.244-78T>C	
c.1884C>T	p.=
c.*120C>T	
c.143-23906G>A	
c.*61A>C	
c.374G>A	p.Arg125Gln
c.546G>A	p.=
c.43T>A	p.Phe15Ile
c.657C>T	p.=
c.570T>C	p.=
c.895A>G	p.Ile299Val
c.759C>A	p.=
c.630C>T	p.=
c.-59A>G	
c.259-95C>T	
c.489-5A>G	
c.855A>G	p.=
c.1586-53_1586-52delAA	
c.551-51G>C	
c.1445_1447dupGCA	p.Ser482dup
c.533A>C	p.Asn178Thr
c.714C>T	p.=
c.685A>G	p.Lys229Glu
c.1294-34G>T	
c.250+12G>A	
c.57+11G>A	
c.1310+66G>T	
c.612G>C	p.=
c.1640C>T	p.Ala547Val
c.1989+16T>A	

c.84G>T	p.Arg28Ser
c.726C>T	p.=
c.874-8C>G	
c.389+83T>C	
c.218T>C	p.Ile73Thr
c.2220+47T>C	
c.3362G>T	p.Gly1121Val
c.11113-93G>T	
c.532G>A	p.Val178Ile
c.8065-19G>A	
c.67C>T	p.Arg23Trp
c.2205C>T	p.=
c.252G>A	p.=
c.1365-66C>T	
c.3252A>G	p.=
c.3137+4A>G	
c.228-65A>C	
c.2107+49A>G	
c.4625G>C	p.Ser1542Thr
c.207-79T>G	
c.9G>A	p.=
c.1320T>C	p.=
c.1303C>T	p.Leu435Phe
c.*52T>C	
c.1154+56A>G	
c.1090-75C>T	
c.1553-92G>T	
c.937-64G>C	
c.1181G>A	p.Arg394Gln
c.-38T>C	
c.789+6C>T	
c.4829-87_4829-86insCATCCCATCAGAGATGAAGT	
c.919-95delA	
c.3771+20C>A	
c.381C>A	p.=
c.*9A>G	
c.987-87A>G	
c.2010T>C	p.=
c.376A>G	p.Asn126Asp
c.2383-27T>C	
c.614-89C>A	
c.132C>A	p.=
c.102+39T>C	
c.1170C>T	p.=
n.161C>G	
c.8107+81T>A	
c.2145+72A>G	
c.110-92G>T	
c.1223-46G>A	
c.1008+56T>A	
c.5036-26T>A	
c.3398-28C>G	

c.6720+49dupT	
c.5330C>T	p.Thr1777Ile
c.194-92A>C	
c.44-23A>G	
c.1155-56T>C	
c.4376A>G	p.His1459Arg
c.789T>C	p.=
c.*10C>T	
c.8664C>T	p.=
c.13872T>C	p.=
c.11538T>C	p.=
c.829-85G>A	
c.3183+9C>T	
c.2088+4G>C	
c.3933+335A>G	
c.1294-57G>A	
c.201+34_201+47dupGTGGGGTCCCTGGC	
c.1186+55C>T	
c.1763-17C>A	
c.-31-35_-31-34insAACATAGTTTAAAAATTATAGTT	
c.1469C>T	p.Thr490Met
c.1218-48T>C	
c.2121G>A	p.=
c.15+26_15+27delGG	
c.122+84C>A	
c.181-95A>T	
c.874-24A>G	
c.1530-61C>T	
c.545A>C	p.Lys182Thr
c.34C>G	p.Pro12Ala
c.1431C>T	p.=
c.477+17T>C	
c.126_131dupACCCGA	p.Pro43_Glu44dup
c.88-47C>G	
c.342-64C>T	
c.*15G>C	
c.1996-3594_1996-3585dupTTTTGTTTTG	
c.180-3C>T	
c.744-38C>T	
c.219+71T>A	
c.241+36T>C	
c.242-10A>T	
c.242-9T>C	
c.45+10T>C	
c.2250+15A>G	
c.366+45T>C	
c.-47G>C	
c.1261-51G>A	
c.1743+29_1743+33delTCTGG	
c.552+275G>A	
c.778-78G>T	
c.545C>T	p.Pro182Leu
c.392-972G>T	
c.1301-73G>A	
c.1901+85_1901+92dupGTTTGTTT	

c.9236+97_9236+98delTT	
c.431-31C>T	
c.710-77C>T	
c.1243+38T>G	
c.796-3T>C	
c.792+72C>G	
c.-40A>G	
c.210-68C>T	
c.1464+32A>G	
c.2313+39C>A	
c.86-13T>C	
c.3115-98A>C	
c.2415C>T	p.=
c.782-97G>T	
c.3120+76T>C	
c.1646-55A>T	
c.3436-39A>G	
c.3435+15_3435+16dupGC	
c.50-88A>T	
c.-44T>C	
c.337-11C>G	
c.56T>C	p.Val19Ala
c.-11C>T	
c.180+38A>G	
c.649-87G>A	
c.1422C>T	p.=
c.107+86_107+92dupTCCACGT	
c.84+28T>G	
c.2175A>C	p.=
c.1669-36C>T	
c.-137+75G>A	
c.1620+29G>T	
c.2232-36C>G	
c.691-11delC	
c.83G>A	p.Arg28His
c.2379A>C	p.=
c.1854+29C>T	
c.2332-61C>T	
c.66+73G>C	
c.1560A>G	p.=
c.163+67_163+72delGCCTTC	
c.916+60A>C	
c.32_39dupTAATCCCC	p.Leu14Ter
c.-15A>G	
c.1623A>G	p.=
c.1459-57C>T	
c.441+10A>G	
c.-4G>A	
c.1082+5A>G	
c.-85G>A	
c.2331G>A	p.=
c.688+22_688+23insAA	
c.-8C>T	
c.128-61A>T	
c.123C>A	p.=

c.*75C>T	
c.866+46delT	
c.842-73C>T	
c.*37C>A	
c.1967-86A>G	
c.1046-40C>T	
c.1292C>A	p.Thr431Asn
c.1174+90G>A	
c.1262+41G>C	
c.1197-317G>A	
n.4098+27T>G	
c.864+22G>A	
c.-37+2071G>T	
c.438+26G>C	
c.-9_-8insCC	
c.-8_-7insACTTCCCTAAATGAGCAGGGATTTAGGAGTGG	
c.111G>A	p.=
c.492G>A	p.=
c.1231-94T>C	
c.2808+74C>T	
c.2526C>T	p.=
c.213+30G>A	
c.603G>A	p.=
c.582A>G	p.=
c.161-36T>G	
c.1412T>C	p.Val471Ala
c.311-39C>T	
c.2064G>C	p.=
c.1242-27G>A	
c.3456C>T	p.=
c.270+27G>A	
c.6384C>T	p.=
c.7615-29G>A	
c.677-11T>A	
c.4683+59A>T	
c.172-57G>A	
c.240-76C>G	
c.916-100C>T	
c.258+54T>G	
c.5559T>C	p.=
c.4156-46C>T	
c.478+18G>T	
c.378G>A	p.=
c.1203-97G>A	
c.161+76T>C	
c.182A>G	p.His61Arg
c.1048-63C>T	
c.2005-22C>T	
c.1173+69G>A	
c.3448T>C	p.Trp1150Arg

c.4741+16T>A	
c.1235-85G>C	
c.450+111G>A	
c.58C>T	p.Arg20Trp
c.1546-402C>T	
c.1467C>G	p.His489Gln
c.913+49C>T	
c.1045-196_1045-194delGTC	
c.203+73T>C	
c.266T>C	p.Val89Ala
c.1684+23G>A	
c.801+83C>T	
c.730T>G	p.Tyr244Asp
c.529+15T>C	
c.2288-100C>T	
c.453+24A>G	
c.113-42G>C	
c.764-86C>G	
c.1012-95G>A	
c.918-52G>C	
c.1-100C>G	
c.3289+100G>A	
c.1890+34G>A	
c.1077+96T>A	
c.111A>C	p.=
c.2827-60G>A	
c.-51C>T	
c.1299-10_1299-9delTT	
c.1288+46T>C	
c.1001-52G>C	
c.1185+73G>A	
c.1602A>G	p.=
c.1156-65G>A	
c.1078-4G>A	
c.301-49G>A	
c.2956G>A	p.Ala986Thr
c.427+92G>A	
c.157-34_157-33insACTTTGATATAGTT	
c.1576+652G>C	
c.2244-79A>G	
c.650-20C>T	
c.96G>A	p.=
c.340A>G	p.Ile114Val
c.489+60G>T	
c.611+30T>C	
c.97T>C	p.Ser33Pro
c.1170-30C>A	
c.548+11C>T	
c.285T>C	p.=
c.1085+79C>A	
c.495T>C	p.=
c.70-88_70-87insGACAACATCAT	
c.324+33G>A	

c.325-88G>A	
c.1657-93C>T	
c.718-97T>C	
c.1368+80delC	
c.1150+68C>T	
c.597+26C>T	
c.349+15G>A	
c.1238-86G>A	
c.1125+67A>G	
n.702-46A>G	
c.883+67C>A	
c.1656C>T	p.=
c.1147+95G>A	
c.1767+29A>G	
c.1614+68A>G	
c.988-29C>A	
c.-123-799C>A	
c.913-38G>A	
c.1146C>T	p.=
c.144G>C	p.=
c.725-21_725-13delCACTCTTCG	
c.2329-36A>T	
c.957+76_957+77delTT	
c.1912-60G>A	
c.126G>A	p.=
c.2089+79G>A	
c.813+8G>A	
c.2671-85G>T	
c.2983-4G>A	
c.567T>C	p.=
c.1392C>T	p.=
c.240C>A	p.=
c.211+30G>A	
c.7858+72A>G	
c.7166A>G	p.Glu2389Gly
c.598G>C	p.Val200Leu
c.12G>A	p.=
c.7149+86C>A	
c.4690-90G>T	
c.4603C>G	p.Pro1535Ala
n.12321G>T	
n.9397-39C>T	
n.12765T>C	
c.675-87delC	
c.*25G>A	
c.187-86C>T	
c.361+39T>C	
c.612-263delG	
c.3705T>C	p.=
c.203+75delC	
c.381C>T	p.=
c.12962+56G>A	
c.465+86T>C	
c.2130-32delG	

c.410+17T>C	
c.654A>G	p.=
c.-19G>T	
c.535+25_535+28delATAT	
c.326-14T>G	
c.1477-64A>G	
c.3193+73G>C	
c.610A>G	p.Ser204Gly
c.*43C>A	
c.150+28C>G	
c.163G>A	p.Val55Met
c.2492+86G>A	
c.458+51C>T	
c.278-51A>G	
c.241-68A>G	
c.3381C>G	p.=
n.1481-100A>T	
c.399G>C	p.=
c.6880-24T>C	
c.2850C>T	p.=
c.1697C>T	p.Pro566Leu
c.461G>C	p.Gly154Ala
c.1440G>A	p.=
c.1604-90C>T	
c.1541G>A	p.Gly514Glu
c.835+52A>G	
c.478-67G>A	
c.204C>T	p.=
c.2260+939G>A	
c.1967+35A>G	
c.766G>A	p.Val256Ile
c.1961+59dupT	
c.338C>T	p.Thr113Met
c.498+9G>A	
c.2152A>G	p.Ile718Val
c.1640-88G>C	
c.8-10C>T	
c.203G>C	p.Gly68Ala
c.1487T>C	p.Leu496Ser
c.60-90C>T	
c.*82C>T	
c.819C>T	p.=
c.5391+71_5391+78delGTTTGTTT	
c.5109-94C>T	
c.1215-42T>C	
c.2274+74_2274+75insGACATGCCCAC	
c.786-94C>A	
c.2951+37A>G	
c.313-1G>A	
c.633G>A	p.=
c.427G>A	p.Ala143Thr
c.353+14C>T	
c.385-77T>C	

c.589G>A	p.Val197Ile
c.777T>C	p.=
c.3273+29C>T	
c.504-88delG	
c.1734A>G	p.=
c.*1291T>C	
c.672+83delC	
c.3172-90A>T	
c.3951+32G>A	
c.1671C>T	p.=
c.*16G>C	
c.653+34A>G	
c.1720+56G>A	
c.-33C>T	
c.1689G>A	p.=
c.1260+54A>G	
c.81+43T>A	
c.2872A>G	p.Thr958Ala
c.2662+71C>G	
c.1852+56G>C	
c.2532C>T	p.=
c.6477+26delT	
c.-167G>T	
c.16T>C	p.Phe6Leu
c.4573+55C>T	
c.20G>A	p.Arg7Gln
c.541+17A>G	
c.507+30C>G	
c.229+87_229+100delGTTGACTATCATAG	
c.373T>C	p.=
c.*6G>A	
c.805+28A>C	
c.276G>A	p.=
c.4818G>C	p.=
c.863+46C>T	
c.1493G>A	p.Ser498Asn
c.1074C>G	p.Asp358Glu
c.3421A>C	p.Lys1141Gln
c.3191+36T>C	
c.108G>A	p.=
c.240+150_240+151insTTGGAAGTACCCAGGGTAGGG	
c.312-85T>C	
c.597A>G	p.=
c.210+8T>A	
c.194+58G>A	
c.150-89G>A	
c.268-35A>G	
c.2500T>A	p.Cys834Ser
c.-1168+65A>G	
c.848-91C>T	
c.919+76C>T	
c.669+74G>A	
c.761+14G>A	
c.2035A>G	p.Met679Val
c.1306+4T>A	

c.823-58_823-57insAAAACACCTGTGTG	
c.4398T>C	p.=
c.52C>T	p.Pro18Ser
c.1554A>G	p.=
c.1389-17A>G	
c.1409+71G>A	
c.54+53A>G	
c.1003G>T	p.Val335Leu
c.123-49T>C	
c.713-67C>T	
c.965T>C	p.Met322Thr
c.1439-37C>T	
c.1716+61C>A	
c.-142+746A>G	
c.322G>A	p.Ala108Thr
c.597+60A>G	
c.1026G>A	p.=
c.331-42T>C	
c.1868G>C	p.Gly623Ala
c.792+87C>A	
c.994+71G>A	
c.178G>A	p.Glu60Lys
c.5199-47C>A	
c.-25A>G	
c.2333+80A>G	
c.2874T>C	p.=
c.6439-22A>G	
c.750G>A	p.=
c.603T>C	p.=
c.1380+80A>G	
c.*77A>G	
c.4315+56G>A	
c.597A>G	p.=
c.859+76T>C	
c.630+77G>C	
c.1159+18C>A	
c.1047-77A>G	
c.602-72C>A	
c.1503T>C	p.=
c.*30C>T	
c.340-14G>C	
c.542-36C>T	
n.2487C>T	
c.864-72G>A	
c.803+3A>C	
c.3073+89C>T	
c.4006G>A	p.Asp1336Asn
c.3211+8C>T	
c.1151+93T>A	
c.598+36G>C	
c.957G>A	p.=
c.563-36C>T	
c.6875G>A	p.Arg2292His
c.1608A>G	p.=

c.1495_1496insAGCTCAGT	p.Phe499Ter
c.600G>T	p.=
c.401-100A>G	
c.1566-79A>G	
c.*71_*72insA	
c.2500+95T>A	
c.810-11C>T	
c.2232-64T>C	
c.2916-80C>A	
c.1771-85T>A	
c.1359+89G>A	
c.1249G>A	p.Gly417Ser
c.136+13C>G	
c.669G>A	p.=
c.183-11A>G	
c.646A>T	p.Arg216Trp
c.456+79A>C	
c.1974-88C>T	
c.834G>A	p.=
c.2516-51C>T	
c.2958G>A	p.=
c.3291+39C>T	
c.3220-21T>G	
c.1961-42C>T	
c.1438-32C>T	
c.48+74G>A	
c.2258-73T>C	
c.6785_6802delTAAGGGAGGAGG	p.Val2262_Glu2267del
c.1491-86C>G	
c.740+82G>A	
c.421G>A	p.Ala141Thr
c.1170A>G	p.=
c.32G>C	p.Cys11Ser
c.823-20A>G	
c.660+14G>A	
c.2433+111G>C	
c.2494C>T	p.=
c.1618-99T>A	
c.*7G>A	
c.509-56C>G	
c.792+39G>A	
c.2679T>G	p.=
c.618A>G	p.=
c.1083-59G>A	
c.1044+93C>A	
c.1411-48T>C	
c.171A>G	p.=
c.1296G>A	p.=
c.598+23T>G	
c.787+31G>C	
c.788-30T>C	
c.-13C>T	
c.1562-43G>A	
c.1459+67C>T	

c.621C>G	p.=
c.221A>T	p.Asn74Ile
c.618C>T	p.=
c.315+55G>A	
c.151-44A>G	
c.4634T>C	p.Val1545Ala
c.532+98A>T	
c.*61A>C	
c.-40-21G>T	
c.1248-30T>C	
c.511-24C>T	
c.614+84G>A	
c.969C>T	p.=
c.362T>C	p.Leu121Pro
c.239-54C>T	
c.1130-1125G>A	
c.925+63T>C	
c.137-97G>T	
c.1356A>C	p.=
c.3+84T>G	
c.560-70A>T	
c.253+34T>C	
c.1969-26A>G	
c.2777G>A	p.Ser926Asn
c.1358C>A	p.Ser453Tyr
c.203C>T	p.Thr68Ile
c.-89_-88insACTT	
c.80G>A	p.Gly27Glu
c.285C>T	p.=
c.337A>G	p.Lys113Glu
c.58-85G>A	
c.1434G>A	p.=
c.578T>G	p.Val193Gly
c.1251G>A	p.=
c.2598C>T	p.=
c.473C>T	p.Thr158Ile
c.406+2363T>A	
c.2111-46G>C	
c.5004-40G>A	

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	ENST00000284425		5
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	ENST00000340001		20
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	ENST00000205557		18
p.R1273R	ENST00000389817	31/39	180
	ENST00000289119	1/9	15
	ENST00000302538		34
	ENST00000436594		82
p.A114T	ENST00000600805	1/1	66
	ENST00000281182		28
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	ENST00000256997		29
	ENST00000286353		66
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	ENST00000317447		24
	ENST00000399422		67
	ENST00000352511		82
p.P769S	ENST00000356955	20/23	94
	ENST00000310823		68
p.L940M	ENST00000373208	19/22	132
	ENST00000251582		58
	ENST00000389420		54
	ENST00000367996		157
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p.V96I	ENST00000381129	3/6	86
p.S196S	ENST00000291582	5/14	227
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p.V640F	ENST00000357872	12/20	46
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p.M684V	ENST00000336498	21/23	139
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p.E602E	ENST00000370028	16/23	21
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p.A753A	ENST00000361216	16/23	68
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p.I522L	ENST00000367618	16/26	87
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p.R328H	ENST00000318683	3/3	246
	ENST00000321300		84
	ENST00000324385		3
p.R386Q	ENST00000542236	3/3	75
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	ENST00000223368		38
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p.G331D	ENST00000260723	11/16	58
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p.T331T	ENST00000327705	11/11	35
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p.D1424D	ENST00000374144	3/3	102
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p.Q55R	ENST00000261318	2/5	30
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p.M184Dfs*14	ENST00000330828	2/2	58
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p.H371R	ENST00000590083	9/9	76
	ENST00000301246	1/4	138
p.D131E	ENST00000304661	2/2	74
p.T578T	ENST00000366534	11/22	90
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p.F215F	ENST00000309893	6/7	113
p.L816F	ENST00000398319	17/37	68
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	ENST00000371372		56
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	ENST00000378847	11/11	27
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p.C283C	ENST00000446248	8/19	117
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p.Q431Q	ENST00000258214	7/9	153
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p.V245M	ENST00000292574	3/7	35

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p.E675V	ENST00000388914	13/24	28
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p.C52C	ENST00000392343	3/15	202
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	ENST00000311925		11
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p.N797S	ENST00000287097	21/33	67
p.H203Pfs*5	ENST00000398214	4/6	91
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p.K259T	ENST00000309424	3/3	120
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p.D172_P180del	ENST00000312648	3/4	45
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p.Q525R	ENST00000296129	6/9	98
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p.R252H	ENST00000262608	7/18	78
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p.R184R	ENST00000331437	1/1	39
	ENST00000372927		33
p.R28L	ENST00000368328	1/3	62
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p.S135N	ENST00000264982	6/18	47
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p.H402Y	ENST00000367429	9/22	62
p.Q1463Q	ENST00000003084	27/27	73
	ENST00000597853	3/5	78
p.A13A	ENST00000369258	1/23	37
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p.A182V	ENST00000445067	8/13	71
	ENST00000306071	11/11	42
	ENST00000306243	1/1	134
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p.S211S	ENST00000536961	5/5	40
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p.H122Q	ENST00000453707	5/5	68
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p.T453T	ENST00000537554	2/2	148
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p.P1496P	ENST00000598234	31/50	53
	ENST00000433211		81
p.V141V	ENST00000325551	3/19	100
p.L637L	ENST00000377833	15/67	64
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p.L1572P	ENST00000535468	24/26	92
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p.G978R	ENST00000360264	18/24	32
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p.P21P	ENST00000257215	2/20	110
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p.E351Q	ENST00000393092	10/11	133
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	ENST00000344537		86
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p.R93R	ENST00000324432	5/12	73
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p.S144A	ENST00000279488	2/3	110
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p.R26L	ENST00000495186	2/5	29
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	ENST00000257934		76
p.G590R	ENST00000389567	18/23	45
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p.T245M	ENST00000354232	4/5	127
p.A2A	ENST00000292147	1/7	42
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p.E589K	ENST00000366548	13/16	117
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	ENST00000367075		15
p.D1260E	ENST00000360256	14/26	37
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p.V374I	ENST00000218099	8/8	33
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p.L116L	ENST00000368557	3/4	78
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	ENST00000374362	1/30	33
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p.A1000A	ENST00000259698	21/23	50
p.A187V	ENST00000283357	5/10	47
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	ENST00000229769		27
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p.P129P	ENST00000229769	2/10	73
	ENST00000536681	12/12	37
	ENST00000264042		58
	ENST00000264042		159
p.G1217G	ENST00000306749	22/43	81
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p.P155L	ENST00000404922	2/18	126
p.H1966D	ENST00000600128	47/64	90
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p.A384A	ENST00000594202	16/29	85
p.G388R	ENST00000292408	9/18	106
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p.N984N	ENST00000257209	17/25	115
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p.T429M	ENST00000369850	9/48	30
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p.T58_T59del	ENST00000263773	1/17	30
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p.Y428Y	ENST00000259806	2/2	104
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p.H649H	ENST00000264895	17/74	63
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p.D2813D	ENST00000264895	56/74	14
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p.I1329I	ENST00000329798	1/8	147
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	ENST00000350221		17
	ENST00000306100		60
p.H529H	ENST00000319725	18/19	127
	ENST00000310160		47
	ENST00000318336	3/3	89
	ENST00000292079		175
	ENST00000296137		19
	ENST00000282538		18
	ENST00000314167		35
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	ENST00000588479		143
	ENST00000297107		94
p.Q474K	ENST00000324589	15/16	152
p.Y53D	ENST00000252318	1/11	40
p.V515F	ENST00000252318	9/11	101
p.E352E	ENST00000269209	4/6	164
p.A490V	ENST00000269209	4/6	109
	ENST00000269209	6/6	56
	ENST00000373387	1/28	8
	ENST00000343435		23
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p.P220P	ENST00000343435	7/12	79
p.F365F	ENST00000400723	12/14	141
	ENST00000379597		71
	ENST00000238018		67
	ENST00000342560		41
	ENST00000249598		37
	ENST00000308317		29
	ENST00000486715		47
	ENST00000233838		45
p.A480P	ENST00000334928	3/4	38
p.A517V	ENST00000334928	3/4	144
p.R469C	ENST00000301671	9/9	33
	ENST00000367419		30
p.V97I	ENST00000262460	4/7	82
p.C884C	ENST00000205061	19/27	68
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	ENST00000262366		25
	ENST00000373365	1/6	83
p.I85V	ENST00000372617	3/9	41
	ENST00000372617		132
	ENST00000360814		31
	ENST00000287275		36
	ENST00000282570		56
p.D103D	ENST00000248996	2/3	292
p.R37H	ENST00000329517	3/8	51
p.S151S	ENST00000226413	1/3	72
p.L1014L	ENST00000204726	15/24	153

	ENST00000329125	2/2	38
p.T416T	ENST00000377047	7/9	83
	ENST00000230036		82
	ENST00000316715		17
p.R7R	ENST00000264718	1/14	25
p.V124L	ENST00000298110	1/1	63
p.A218P	ENST00000607359	3/16	81
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p.H475H	ENST00000529750	13/20	89
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	ENST00000381486		15
	ENST00000518783		23
	ENST00000296526		23
	ENST00000264357		32
p.L597L	ENST00000357716	8/10	119
	ENST00000253458		26
p.T616M	ENST00000373818	13/17	101
	ENST00000340438	1/1	28
	ENST00000398606		203
	ENST00000216465		101
	ENST00000360803		18
	ENST00000360803	17/17	42
	ENST00000218006		41
	ENST00000389617	7/7	122
	ENST00000261208		59
	ENST00000598398		11
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	ENST00000441542		23
	ENST00000398153		79
p.P175P	ENST00000424830	4/5	27
	ENST00000366582		115
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p.T614T	ENST00000366582	15/45	59
p.V632A	ENST00000297440	9/13	178
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	ENST00000348459		22
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	ENST00000232854		84
	ENST00000443617		9
p.H63D	ENST00000357618	2/6	82
p.E336E	ENST00000222390	8/18	74
	ENST00000441594		105
	ENST00000330710		75
p.D13D	ENST00000253410	1/3	70
	ENST00000304043		14
	ENST00000359985	1/1	44
	ENST00000377831		25

p.A16A	ENST00000377364	1/1	101
	ENST00000354624		22
p.L207M	ENST00000418931	3/6	92
	ENST00000399120		58
	ENST00000310053		39
p.V202V	ENST00000278715	9/14	78
	ENST00000216106		32
p.G165V	ENST00000216106	5/11	35
	ENST00000257555		38
	ENST00000392006		49
p.L462L	ENST00000397668	15/23	46
	ENST00000262626		133
p.G172G	ENST00000299238	1/1	122
	ENST00000592984		13
p.P4P	ENST00000287907	1/2	209
p.S703S	ENST00000342160	22/83	32
p.R1996H	ENST00000342160	44/83	41
p.V128I	ENST00000407780	3/7	72
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	ENST00000330062		26
	ENST00000299518		62
p.S179T	ENST00000368131	4/11	87
p.F10V	ENST00000342136	2/9	72
	ENST00000268035		16
	ENST00000356956		25
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	ENST00000270642		42
p.E449E	ENST00000370903	8/20	85
p.Y857Y	ENST00000370903	14/20	77
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	ENST00000393775		33
p.E333D	ENST00000393775	7/7	97
	ENST00000393775		27
	ENST00000513874		61
	ENST00000533871		10
p.L1023L	ENST00000374647	28/37	87
	ENST00000295981		72
p.S177Y	ENST00000316649	4/7	88
	ENST00000270800		116
	ENST00000379959	8/8	91
	ENST00000563197	7/7	64
	ENST00000397262	2/2	114
	ENST00000397270		27
p.A550A	ENST00000302850	8/22	89
	ENST00000302850		12
	ENST00000404767		29
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	ENST00000311234		5
	ENST00000274364		32
	ENST00000361170		18
	ENST00000538872		86
	ENST00000357234		66
p.V319V	ENST00000244314	2/2	156

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p.V130V	ENST00000266041	4/24	110
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	ENST00000373298		23
	ENST00000429204		132
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p.I243I	ENST00000278071	3/3	72
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	ENST00000226319		20
	ENST00000218343		19
	ENST00000298622		84
	ENST00000341776		24
	ENST00000341776		98
p.P402P	ENST00000341776	7/18	97
	ENST00000458427	1/1	20
	ENST00000382303	16/16	110
	ENST00000371153		57
p.S526S	ENST00000371153	3/10	150
p.H927H	ENST00000371153	9/10	99
p.L78L	ENST00000367411	3/11	71
p.P189R	ENST00000221444	2/2	51
	ENST00000490337		30
	ENST00000399881		49
	ENST00000476647		44
	ENST00000228495		45
	ENST00000405872	2/2	30
	ENST00000314358		14
	ENST00000372396		16
	ENST00000159111		53
	ENST00000317961		15
p.T726K	ENST00000377967	17/29	55
	ENST00000397560		69
p.R538R	ENST00000397560	12/20	55
p.R644S	ENST00000397560	15/20	49
p.N11N	ENST00000251993	1/10	100
	ENST00000264501		13
p.S689A	ENST00000251691	12/34	150
	ENST00000297591		13
p.A1162A	ENST00000392413	4/4	109
	ENST00000368847		21
	ENST00000367350		38
p.Y90Y	ENST00000247986	2/15	61
	ENST00000389916		29
ATGTTGTTAACAT	ENST00000498729		22
	ENST00000320785		29
	ENST00000260753		14
	ENST00000361580		33
	ENST00000379562		54

p.T216T	ENST00000285407	3/4	78
p.V13V	ENST00000514860	2/15	39
	ENST00000273963		23
	ENST00000356986		23
	ENST00000262189		86
	ENST00000304613		141
	ENST00000333479		108
p.T312T	ENST00000327442	7/10	129
	ENST00000290158		27
	ENST00000327813		45
	ENST00000269576		27
	ENST00000225899		148
	ENST00000328119	7/7	10
	ENST00000397911	1/1	115
	ENST00000397907	1/1	22
p.T110T	ENST00000391618	1/1	75
	ENST00000216237		103
	ENST00000421865		19
	ENST00000421865		48
	ENST00000230538		52
	ENST00000230538		71
	ENST00000258341		31
	ENST00000258341		11
	ENST00000258341		43
	ENST00000264144	1/23	20
p.S482S	ENST00000543571	4/8	83
	ENST00000333881	1/1	19
	ENST00000371688		2
	ENST00000344642		50
	ENST00000308330		18
	ENST00000222725		93
	ENST00000291759		73
	ENST00000336180		26
p.R426H	ENST00000585527	1/1	158
	ENST00000267102		15
	ENST00000465261		67
	ENST00000231368		21
	ENST00000398246		16
p.A14A	ENST00000371628	1/11	54
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	ENST00000261921		122
	ENST00000312675		31
	ENST00000354454		26
	ENST00000389484		132
	ENST00000294304		53
p.R188W	ENST00000402859	5/6	149
	ENST00000402859		32
	ENST00000500728		78
	ENST00000298288		30
p.G7V	ENST00000374160	1/2	106
	ENST00000360375	19/19	38
	ENST00000393217		23
p.L92P	ENST00000265245	3/14	34
p.R238Q	ENST00000544216	5/10	84
	ENST00000502781	4/4	34

	ENST00000397728		44
	ENST00000389194		20
	ENST00000336930		27
	ENST00000330743		59
	ENST00000368908	1/3	23
	ENST00000370220		221
	ENST00000370220	1/4	39
	ENST00000406869		36
	ENST00000296509		68
	ENST00000356661		59
p.G296G	ENST00000393900	3/3	137
	ENST00000378982	1/1	22
	ENST00000285879		54
p.P303P	ENST00000247452	3/3	40
	ENST00000375068		25
	ENST00000317446		18
p.C731C	ENST00000432680	5/5	75
	ENST00000368468		73
p.R415R	ENST00000261483	8/22	82
p.Q243P	ENST00000285599	6/19	179
p.P865L	ENST00000324096	5/7	193
p.A192T	ENST00000338883	4/29	82
	ENST00000361357		38
p.P315P	ENST00000591517	13/32	61
	ENST00000347699		25
	ENST00000446044		47
	ENST00000251472		157
p.D337D	ENST00000251472	10/26	92
	ENST00000403625	1/29	70
p.R164S	ENST00000537548	4/11	97
	ENST00000265594		9
	ENST00000397708		68
p.V143V	ENST00000434837	4/17	88
	ENST00000369393		13
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p.I326I	ENST00000453960	3/3	105
	ENST00000324817		35
	ENST00000491289	2/5	72
	ENST00000312865		46
p.C140S	ENST00000315588	3/4	62
	ENST00000162023		17
	ENST00000356575		27
	ENST00000269202		71
	ENST00000295408	19/19	51
	ENST00000298717		72
p.P222P	ENST00000375258	6/10	40
	ENST00000398558		149
p.P568P	ENST00000428789	12/16	285
	ENST00000428789		56
p.F452F	ENST00000428789	10/16	228
p.L115F	ENST00000306010	3/5	86
	ENST00000441493		36
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	ENST00000441493		75
	ENST00000317552		37

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	ENST00000228506		22
	ENST00000366624		50
	ENST00000252674		154
	ENST00000368808		73
	ENST00000252971		37
p.K154Q	ENST00000357066	4/5	151
	ENST00000355610		32
p.T473I	ENST00000355610	12/17	44
	ENST00000379535		29
	ENST00000278949		48
	ENST00000323929		25
p.Y306D	ENST00000421030	3/24	102
p.H618R	ENST00000421030	10/24	91
p.V509A	ENST00000421030	7/24	145
	ENST00000290208		150
	ENST00000371443		17
	ENST00000342071		193
	ENST00000053468		59
	ENST00000423302		68
	ENST00000233146		16
	ENST00000261507		37
p.L2303L	ENST00000361445	49/58	65
p.A1048A	ENST00000366577	29/33	76
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	ENST00000366577		53
	ENST00000366577		77
	ENST00000457717		15
	ENST00000397910		47
p.A2533A	ENST00000397910	1/84	114
	ENST00000454784	4/84	54
	ENST00000454784		74
p.P2554P	ENST00000441003	42/49	132
	ENST00000301012		34
p.T2451T	ENST00000217939	7/7	60
p.A41A	ENST00000409745	3/3	155
	ENST00000545968		84
p.A1241T	ENST00000396324	29/42	160
	ENST00000273353		76
p.K365K	ENST00000355349	12/40	38
	ENST00000355349		10
	ENST00000355349		65
	ENST00000216181		21
p.T1186T	ENST00000360304	19/34	46
	ENST00000205890		22
	ENST00000335473		50
	ENST00000431794		18
	ENST00000338257		55
	ENST00000399231		25
	ENST00000595618		59
	ENST00000241651	1/3	140
p.I378I	ENST00000358913	5/20	62
	ENST00000278836		55
	ENST00000472487		21

	ENST00000361671		28
p.P304P	ENST00000371753	2/5	27
	ENST00000312251		23
p.A310T	ENST00000253719	7/9	66
	ENST00000357814		45
	ENST00000281513		101
p.H923R	ENST00000422280	21/21	64
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	ENST00000422280		25
	ENST00000422280		50
p.P92S	ENST00000252575	3/15	164
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	ENST00000534548		22
	ENST00000240423		50
	ENST00000374796		73
	ENST00000268712		15
p.A430A	ENST00000367993	13/15	71
	ENST00000397345		13
	ENST00000397345		69
	ENST00000397345		79
p.T354T	ENST00000382882	8/11	26
p.D170D	ENST00000366988	4/4	32
	ENST00000366988		52
p.E332A	ENST00000334785	9/13	17
	ENST00000226574		46
	ENST00000369966		20
	ENST00000326172		13
p.H104H	ENST00000340650	1/1	59
	ENST00000427025		31
	ENST00000264187		38
	ENST00000382041		19
	ENST00000374399		25
p.R213G	ENST00000311946	5/6	30
	ENST00000282516		30
	ENST00000216121		96
	ENST00000345716		76
p.S62T	ENST00000258829	2/2	87
	ENST00000358741		17
	ENST00000404025		25
	ENST00000390649		26
p.L985L	ENST00000390649	11/15	92
	ENST00000390649		52
	ENST00000332836		45
	ENST00000330579		77
	ENST00000297990		86
	ENST00000416614		197
	ENST00000329276	12/12	32
	ENST00000361897		35
p.D298E	ENST00000297494	8/27	224
	ENST00000297494		28
	ENST00000277541		15
	ENST00000277541		27
p.V1296V	ENST00000289547	20/20	37
p.I145L	ENST00000277942	4/4	61
p.S241R	ENST00000359791	6/9	154

	ENST00000265634		17
	ENST00000312521	1/8	24
	ENST00000367980		18
	ENST00000354366		28
p.N1235N	ENST00000439151	5/23	75
	ENST00000264670		60
	ENST00000422318		82
	ENST00000301411		78
p.R235C	ENST00000355451	4/6	74
	ENST00000379161		20
p.I139I	ENST00000413272	5/19	30
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	ENST00000359428		14
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	ENST00000347635	8/8	57
	ENST00000264883		18
	ENST00000264883		81
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	ENST00000573584		46
	ENST00000395065		44
	ENST00000537026		21
	ENST00000537026		71
	ENST00000537026		72
	ENST00000336868		44
	ENST00000479950		15
p.Y628Y	ENST00000404537	5/21	87
	ENST00000329197	10/10	136
	ENST00000323060		21
	ENST00000316368	1/1	13
p.R125Q	ENST00000323404	1/1	70
p.L182L	ENST00000314721	1/1	55
p.F15I	ENST00000319760	1/1	44
	ENST00000314634		24
p.L219L	ENST00000380224	1/1	82
p.S190S	ENST00000317078	1/1	69
p.I299V	ENST00000304418	1/1	80
p.G253G	ENST00000356526	1/1	62
p.I210I	ENST00000301532	1/1	66
	ENST00000313033	1/1	25
	ENST00000313733		59
	ENST00000361711		57
p.S285S	ENST00000361711	6/6	201
	ENST00000274276		16
	ENST00000307050		28
p.S482dup	ENST00000285848	10/10	59
p.N178T	ENST00000374519	1/1	107
p.I238I	ENST00000331483	5/11	83
p.K229E	ENST00000372858	5/16	53
	ENST00000320580		40
	ENST00000289619		36
	ENST00000338448		70
	ENST00000307534		25
p.L204L	ENST00000307534	1/7	38
p.A547V	ENST00000378466	13/19	163
	ENST00000238714		18

p.R28S	ENST00000371279	2/2	178
p.R242R	ENST00000334956	6/13	143
	ENST00000406477		75
	ENST00000429538		45
p.I73T	ENST00000527246	1/1	79
	ENST00000361849		17
p.G1121V	ENST00000544246	5/5	60
	ENST00000333891		25
p.V178I	ENST00000367384	5/8	67
	ENST00000359568		119
p.R23W	ENST00000311180	1/3	81
	ENST00000435564		36
p.I735I	ENST00000334456	26/31	53
p.L84L	ENST00000371447	1/22	99
	ENST00000257290		9
p.P1084P	ENST00000261799	23/23	27
	ENST00000261799		35
	ENST00000376215		70
	ENST00000396410		74
	ENST00000396410		39
	ENST00000370215		47
p.S1542T	ENST00000560626	7/7	96
	ENST00000338302		38
p.P3P	ENST00000338302	3/24	123
p.P440P	ENST00000338302	12/24	149
p.L435F	ENST00000244137	14/15	43
	ENST00000244137	15/15	48
	ENST00000381125		52
	ENST00000381125		48
	ENST00000354764		24
	ENST00000373316		32
p.R394Q	ENST00000340880	3/5	56
	ENST00000290722	1/7	38
	ENST00000359246		18
	ENST00000275034		16
	ENST00000373542		17
	ENST00000361417		58
p.A127A	ENST00000416188	4/18	82
	ENST00000369738	6/6	61
	ENST00000370812		20
p.T670T	ENST00000357637	22/31	47
p.N126D	ENST00000592983	2/2	88
	ENST00000447110		49
	ENST00000264380		13
p.A44A	ENST00000360612	2/6	130
	ENST00000332271		82
p.G390G	ENST00000361478	2/2	80
	ENST00000529079	1/2	26
	ENST00000371117		40
	ENST00000070846		18
	ENST00000274793		26
	ENST00000220809		65
	ENST00000327757		21
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p.T1777I	ENST00000371380	23/32	141
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	ENST00000449969		24
p.H1459R	ENST00000322810	30/32	173
p.A263A	ENST00000322810	5/32	193
	ENST00000322810	32/32	32
p.N2888N	ENST00000322810	32/32	179
p.A4624A	ENST00000322810	32/32	108
p.A3846A	ENST00000322810	32/32	157
	ENST00000537245		19
	ENST00000329153		12
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	ENST00000329153		71
	ENST00000379410		115
	ENST00000334770		27
	ENST00000315392		16
	ENST00000449103		33
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p.T490M	ENST00000394571	7/8	81
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p.P707P	ENST00000414982	19/34	209
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p.K182T	ENST00000465342	2/2	46
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p.H477H	ENST00000287820	7/7	80
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p.P43_E44dup	ENST00000308249	1/7	147
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p.P182L	ENST00000419421	3/3	114
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	ENST00000302000		26
	ENST00000240651	1/12	26
	ENST00000325874		76
p.V19A	ENST00000264601	2/6	59
	ENST00000243662	1/3	71
	ENST00000276066		47
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p.R474R	ENST00000399409	14/16	89
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p.A725A	ENST00000399583	10/15	106
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p.R793R	ENST00000377604	21/24	87
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p.P520P	ENST00000377966	13/21	68
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p.L14*	ENST00000295755	1/3	36
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p.V41V	ENST00000367559	2/7	108

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p.A201A	ENST00000340648	7/16	100
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p.V471A	ENST00000377819	3/9	85
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p.I1152I	ENST00000359596	26/106	126
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p.T1853T	ENST00000380817	40/41	162
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	ENST00000367569	1/1	59
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	ENST00000482504		41
p.A534A	ENST00000355946	14/14	214
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p.A48A	ENST00000328306	1/17	52
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p.S68S	ENST00000367066	5/10	89
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p.I718V	ENST00000446818	23/24	127
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p.T958A	ENST00000061240	20/21	124
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p.A844A	ENST00000357947	19/21	97
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p.E250E	ENST00000266254	8/11	141
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p.A536A	ENST00000252597	10/13	158

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p.V866V	ENST00000442396	8/8	143
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81	12	220	220
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37	5	115	115
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76	10	185	185
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25	3	60	60
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113	23	293	293
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214	26	286	285
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81	13	105	105
142	23	185	185
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0	ASTL,intron_variant,,ENS	G	ENSG00000188886
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1	ASXL3,intron_variant,,EN	A	ENSG00000141431
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0	ATG4C,intron_variant,,EI	G	ENSG00000125703
0	ATL1,intron_variant,,ENS	C	ENSG00000198513
0	ATP11A,3_prime_UTR_v	A	ENSG00000068650
0	ATP13A2,synonymous_v	A	ENSG00000159363
0	ATP1A2,synonymous_va	T	ENSG00000018625
0	ATP1A4,intron_variant,,E	G	ENSG00000132681
1	ATP2C2,intron_variant,,E	G	ENSG00000064270
0	ATP5C1,intron_variant,,E	T	ENSG00000165629
0	ATP7A,intron_variant,,EN	A	ENSG00000165240
0	ATP8B1,intron_variant,,E	A	ENSG00000081923
0	ATP9A,intron_variant,,EN	A	ENSG00000054793
0	ATP9A,intron_variant,,EN	A	ENSG00000054793
0	ATRIP,intron_variant,,EN	G	ENSG00000164053
0	ATXN2L,intron_variant,,E	T	ENSG00000168488
0	AWAT1,intron_variant,,E	T	ENSG00000204195
0	AWAT2,splice_region_va	G	ENSG00000147160
0	AXDND1,missense_varia	C	ENSG00000162779
0	AXIN1,intron_variant,,EN	C	ENSG00000103126
0	B3GNT3,missense_varia	A	ENSG00000179913
0	BAIAP2,intron_variant,,E	T	ENSG00000175866
0	BAIAP3,intron_variant,,E	A	ENSG00000007516
0	BBS12,missense_variant	A	ENSG00000181004
0	BCKDHA,5_prime_UTR_	G	ENSG00000248098
0	BCL7B,intron_variant,,EN	C	ENSG00000106635
0	BCORL1,intron_variant,,I	T	ENSG00000085185
0	BEST1,intron_variant,,EN	T	ENSG00000167995
0	BICD1,splice_donor_vari	A	ENSG00000151746
0	BLNK,intron_variant,,ENS	A	ENSG00000095585
0	BMP15,missense_varian	G	ENSG00000130385
1	BNC1,intron_variant,,ENS	G	ENSG00000169594
0	BPIFB2,intron_variant,,EI	A	ENSG00000078898
0	BPTF,intron_variant,,ENS	T	ENSG00000171634
1	BRCA1,intron_variant,,EI	T	ENSG00000012048
0	BRCA1,intron_variant,,EI	T	ENSG00000012048
0	BRCA1,intron_variant,,EI	C	ENSG00000012048
0	BRCA2,intron_variant,,EI	T	ENSG00000139618
0	BRD9,intron_variant,,ENS	T	ENSG00000028310
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0	BTBD16,intron_variant,,E	T	ENSG00000138152
0	BTBD16,missense_varia	A	ENSG00000138152
0	BTBD8,intron_variant,,EN	A	ENSG00000189195
0	BTG1,intron_variant,,ENS	T	ENSG00000133639
0	BTNL9,synonymous_vari	T	ENSG00000165810
0	BZRAP1,intron_variant,,E	G	ENSG00000005379

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0	C11orf49,3_prime_UTR_	A	ENSG00000149179
0	C12orf49,missense_varia	C	ENSG00000111412
0	C12orf55,intron_variant,,	T	ENSG00000188596
0	C12orf60,frameshift_vari	-	ENSG00000182993
0	C14orf164,intron_variant	-	ENSG00000215277
0	C17orf107,downstream_	A	ENSG00000205710
0	C17orf53,3_prime_UTR_	C	ENSG00000125319
0	C19orf26,missense_varia	C	ENSG00000099625
0	C19orf33,5_prime_UTR_	C	ENSG00000167644
0	C1GALT1C1,missense_v	T	ENSG00000171155
0	C1orf101,synonymous_v	G	ENSG00000179397
0	C1orf141,intron_variant,,	-	ENSG00000203963
0	C1orf168,intron_variant,,	C	ENSG00000187889
0	C1orf173,splice_region_v	C	ENSG00000178965
0	C1QTNF1,intron_variant,	C	ENSG00000173918
0	C2orf54,3_prime_UTR_v	C	ENSG00000172478
0	C2orf81,5_prime_UTR_v	A	ENSG00000159239
0	C3,intron_variant,,ENST0	T	ENSG00000125730
0	C4orf29,intron_variant,,E	A	ENSG00000164074
0	C5,intron_variant,,ENST0	G	ENSG00000106804
0	C5,intron_variant,,ENST0	C	ENSG00000106804
0	C6orf201,missense_varia	C	ENSG00000185689
0	C7,intron_variant,,ENST0	T	ENSG00000112936
0	CA10,intron_variant,,ENS	G	ENSG00000154975
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0	CACNA2D2,intron_varian	G	ENSG00000007402
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0	CAGE1,intron_variant,,EI	C	ENSG00000164304
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0	CALR,5_prime_UTR_var	A	ENSG00000179218
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0	CAMK2D,intron_variant,,	A	ENSG00000145349
0	CAMKMT,intron_variant,,	T	ENSG00000143919
0	CAMSAP3,synonymous_	T	ENSG00000076826
0	CAPN11,intron_variant,,E	T	ENSG00000137225
0	CAPN9,intron_variant,,EN	T	ENSG00000135773
0	CAPS,intron_variant,,EN	T	ENSG00000105519
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0	CARD8,intron_variant,,EI	A	ENSG00000105483
0	CASP14,3_prime_UTR_v	T	ENSG00000105141
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0	CASZ1,intron_variant,,EN	A	ENSG00000130940
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0	CCDC105,missense_var	A	ENSG00000160994

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0	CCDC132,3_prime_UTR	G	ENSG00000004766
0	CCDC137,intron_variant,	C	ENSG00000185298
0	CCDC147,synonymous_	G	ENSG00000120051
0	CCDC158,missense_var	A	ENSG00000163749
0	CCDC169-SOHLH2,intro	T	ENSG00000250709
0	CCDC18,intron_variant,,I	A	ENSG00000122483
0	CCDC57,synonymous_va	A	ENSG00000176155
0	CCDC6,intron_variant,,EI	T	ENSG00000108091
0	CCDC81,intron_variant,,I	A	ENSG00000149201
0	CCL19,intron_variant,,EN	T	ENSG00000172724
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0	CD200R1L,frameshift_va	-	ENSG00000206531
0	CD244,intron_variant,,EN	G	ENSG00000122223
0	CD300A,intron_variant,,E	-	ENSG00000167851
0	CD3EAP,missense_varia	C	ENSG00000117877
0	CD46,intron_variant,,ENS	G	ENSG00000117335
0	CD7,inframe_deletion,p.A	-	ENSG00000173762
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0	CDC42BPG,intron_varian	C	ENSG00000171219
0	CDC45,intron_variant,,EN	T	ENSG00000093009
0	CDCP1,missense_varian	C	ENSG00000163814
0	CDH18,intron_variant,,EN	T	ENSG00000145526
0	CDK19,intron_variant,,EN	C	ENSG00000155111
0	CDK3,intron_variant,,ENS	A	ENSG00000250506
0	CDK7,intron_variant,,ENS	T	ENSG00000134058
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0	CIT,intron_variant,,ENST	T	ENSG00000122966
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0	CLEC4E,5_prime_UTR_	C	ENSG00000166523
0	CLIC2,3_prime_UTR_var	G	ENSG00000155962
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0	DBR1,intron_variant,,ENS	G	ENSG00000138231
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0	DGKB,intron_variant,,EN	A	ENSG00000136267
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0	EXO1,missense_variant,	A	ENSG00000174371
0	EXOC1,intron_variant,,EI	T	ENSG00000090989
0	EZR,intron_variant,,ENS	C	ENSG00000092820
0	F8,missense_variant,p.A	C	ENSG00000185010
0	F8,intron_variant,,ENSTC	T	ENSG00000185010
0	F9,missense_variant,p.V	A	ENSG00000101981
0	FAAH2,intron_variant,,EN	A	ENSG00000165591
0	FADS2,intron_variant,,EN	G	ENSG00000134824
0	FADS3,intron_variant,,EN	G	ENSG00000221968
0	FAH,intron_variant,,ENS	G	ENSG00000103876
0	FAM118A,missense_vari	A	ENSG00000100376
0	FAM122C,3_prime_UTR_	CG	ENSG00000156500
0	FAM122C,3_prime_UTR_	CCTAGATGCAGGAG	ENSG00000156500
1	FAM127C,3_prime_UTR_	C	ENSG00000212747
0	FAM127C,3_prime_UTR_	T	ENSG00000212747
0	FAM135B,intron_variant,	C	ENSG00000147724
0	FAM162B,synonymous_v	A	ENSG00000183807
0	FAM168A,intron_variant,	A	ENSG00000054965

0	FAM181B,3_prime_UTR_	T	ENSG00000182103
0	FAM184B,intron_variant,	G	ENSG00000047662
0	FAM186A,intron_variant,	A	ENSG00000185958
0	FAM187B,upstream_gen	G	ENSG00000177558
0	FAM189B,intron_variant,	A	ENSG00000160767
0	FAM21C,5_prime_UTR_'	G	ENSG00000172661
0	FAM63A,intron_variant,,E	A	ENSG00000143409
0	FAM65B,synonymous_va	G	ENSG00000111913
0	FAM81B,missense_varia	T	ENSG00000153347
0	FANCA,intron_variant,,EI	A	ENSG00000187741
0	FANCE,intron_variant,,EI	G	ENSG00000112039
0	FANCE,intron_variant,,EI	G	ENSG00000112039
0	FANCE,synonymous_var	C	ENSG00000112039
0	FAR2,3_prime_UTR_var	C	ENSG00000064763
0	FARP2,intron_variant,,EN	C	ENSG00000006607
0	FARP2,3_prime_UTR_va	T	ENSG00000006607
0	FASN,synonymous_varia	A	ENSG00000169710
0	FASN,intron_variant,,ENS	A	ENSG00000169710
0	FASN,intron_variant,,ENS	A	ENSG00000169710
0	CCDC57,3_prime_UTR_	T	ENSG00000169710
0	FBLN2,missense_variant	T	ENSG00000163520
0	FBN3,missense_variant,I	C	ENSG00000142449
0	FBRSL1,intron_variant,,E	A	ENSG00000112787
0	LECT2,intron_variant,,EN	A	ENSG00000164616
0	FBXO10,intron_variant,,E	A	ENSG00000147912
0	FBXO10,intron_variant,,E	G	ENSG00000147912
0	FBXO17,intron_variant,,E	A	ENSG00000269190
0	FBXW12,intron_variant,,I	T	ENSG00000164049
0	FBXW4,intron_variant,,E	T	ENSG00000107829
0	FCAMR,intron_variant,,E	T	ENSG00000162897
0	FCHO1,synonymous_var	A	ENSG00000130475
1	FGFR4,missense_varian	A	ENSG00000160867
0	FGG,3_prime_UTR_varia	A	ENSG00000171557
0	FHOD3,intron_variant,,EI	C	ENSG00000134775
0	FHOD3,synonymous_var	T	ENSG00000134775
0	FHOD3,intron_variant,,EI	T	ENSG00000134775
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0	FKBP6,synonymous_vari	A	ENSG00000077800
0	FKBP7,intron_variant,,EN	A	ENSG00000079150
0	FLNA,missense_variant,I	A	ENSG00000196924
0	FLNB,intron_variant,,ENS	G	ENSG00000136068
0	FLT4,intron_variant,,ENS	GGTTACCCTA	ENSG00000037280
0	FMN2,intron_variant,,ENS	C	ENSG00000155816
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0	FMO3,synonymous_varia	T	ENSG00000007933
0	FNBP4,inframe_deletion,	-	ENSG00000109920
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0	FNDC1,synonymous_var	G	ENSG00000164694
0	FOXF2,synonymous_var	C	ENSG00000137273
0	FOXP4,intron_variant,,EN	A	ENSG00000137166
0	FPGS,3_prime_UTR_var	C	ENSG00000136877
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0	FRAS1,intron_variant,,EN	G	ENSG00000138759

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0	FSTL5,intron_variant,,EN	A	ENSG00000168843
0	FUBP3,synonymous_vari	T	ENSG00000107164
0	FUT1,intron_variant,,ENS	A	ENSG00000174951
0	FUT6,splice_region_varia	C	ENSG00000156413
1	FXYD2,intron_variant,,EN	C	ENSG00000137731
0	FYCO1,intron_variant,,EN	C	ENSG00000163820
0	GADL1,intron_variant,,EN	A	ENSG00000144644
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0	GAK,intron_variant,,ENST	-	ENSG00000178950
1	GALC,intron_variant,,EN	A	ENSG00000054983
0	GALC,intron_variant,,EN	G	ENSG00000054983
0	GALK1,intron_variant,,EN	T	ENSG00000108479
0	GALNT10,intron_variant,	G	ENSG00000164574
0	GALNT14,missense_vari	T	ENSG00000158089
0	GALNT8,missense_varia	G	ENSG00000130035
0	GALNT8,missense_varia	T	ENSG00000130035
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0	GAREM,missense_varia	A	ENSG00000141441
0	GAREM,3_prime_UTR_v	T	ENSG00000141441
0	GARNL3,5_prime_UTR_	C	ENSG00000136895
0	GBP5,5_prime_UTR_var	A	ENSG00000154451
0	GBP5,intron_variant,,EN	T	ENSG00000154451
0	GBP5,synonymous_varia	A	ENSG00000154451
0	GCGR,synonymous_vari	T	ENSG00000215644
1	GCNT2,synonymous_var	G	ENSG00000111846
0	GDA,splice_region_varia	G	ENSG00000119125
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0	GDF2,intron_variant,,EN	C	ENSG00000128802
0	GEMIN2,intron_variant,,E	G	ENSG00000092208
0	GFM1,intron_variant,,EN	G	ENSG00000168827
0	GGCX,intron_variant,,EN	T	ENSG00000115486
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0	GGN,missense_variant,p	A	ENSG00000179168
0	GHDC,missense_variant	A	ENSG00000167925
0	GINM1,intron_variant,,EN	A	ENSG00000055211
0	GINS1,missense_variant	A	ENSG00000101003
0	GLG1,synonymous_varia	A	ENSG00000090863
0	GLG1,intron_variant,,EN	A	ENSG00000090863
0	GLIS2,intron_variant,,EN	T	ENSG00000126603
0	GLO1,5_prime_UTR_var	A	ENSG00000124767
0	GLRA4,missense_varian	C	ENSG00000188828
0	GLRA4,intron_variant,,EN	G	ENSG00000188828
0	GLT8D2,intron_variant,,E	A	ENSG00000120820
0	GLYATL2,intron_variant,	C	ENSG00000156689
0	GMCL1,intron_variant,,EI	T	ENSG00000087338
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0	GNRHR,synonymous_va	A	ENSG00000109163
0	GOLGA3,synonymous_v	A	ENSG00000090615

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0	GPC6,synonymous_varia	A	ENSG00000183098
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0	GPM6B,intron_variant,,E	-	ENSG00000046653
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0	GPR101,missense_varia	A	ENSG00000165370
0	GPR123,missense_varia	C	ENSG00000197177
0	GPR123,5_prime_UTR_v	T	ENSG00000197177
1	GPR123,intron_variant,,E	A	ENSG00000197177
0	GPR123,intron_variant,,E	A	ENSG00000197177
0	GPR176,intron_variant,,E	G	ENSG00000166073
0	GRAMD1B,synonymous_	C	ENSG00000023171
0	GRAMD1C,intron_varian	A	ENSG00000178075
0	GRAMD4,intron_variant,,	A	ENSG00000075240
0	GRAMD4,intron_variant,,	T	ENSG00000075240
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0	GREB1,intron_variant,,EI	A	ENSG00000196208
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0	GRIA2,intron_variant,,EN	A	ENSG00000120251
1	GRIA3,intron_variant,,EN	A	ENSG00000125675
0	GRM7,synonymous_varia	T	ENSG00000196277
0	GSE1,intron_variant,,ENS	C	ENSG00000131149
0	GSN,missense_variant,p	T	ENSG00000148180
0	GSPT2,5_prime_UTR_va	T	ENSG00000189369
0	GSTP1,intron_variant,,EN	T	ENSG00000084207
0	GSTZ1,5_prime_UTR_va	T	ENSG00000100577
0	GTPBP4,intron_variant,,E	T	ENSG00000107937
0	GTPBP4,3_prime_UTR_	T	ENSG00000107937
0	GUCY2F,intron_variant,,I	A	ENSG00000101890
0	GXYLT2,3_prime_UTR_v	A	ENSG00000172986
0	HAL,intron_variant,,ENST	C	ENSG00000084110
0	HAMP,intron_variant,,EN	T	ENSG00000105697
0	HDAC7,intron_variant,,EI	C	ENSG00000061273
0	HDAC7,intron_variant,,EI	C	ENSG00000061273
0	HDAC9,intron_variant,,EI	T	ENSG00000048052
0	HDDC2,intron_variant,,EI	A	ENSG00000111906
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0	HELLS,intron_variant,,EN	C	ENSG00000119969
0	HEMK1,intron_variant,,EI	T	ENSG00000114735
0	HERC1,intron_variant,,EI	A	ENSG00000103657
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0	HGF,synonymous_varian	T	ENSG00000019991
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0	HIGD1B,synonymous_va	T	ENSG00000131097
0	HINT1,3_prime_UTR_va	A	ENSG00000169567
0	HIST1H2BF,3_prime_UT	T	ENSG00000197846
0	HIST1H3D,intron_variant	T	ENSG00000197409

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0	HLTF,intron_variant,,EN	-	ENSG00000071794
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0	HMGXB4,missense_varia	T	ENSG00000100281
0	HNF1A,intron_variant,,EN	A	ENSG00000135100
0	HNRNPUL1,intron_varian	A	ENSG00000105323
0	HOOK2,synonymous_va	T	ENSG00000095066
0	HPN,intron_variant,,ENS	C	ENSG00000105707
0	HPS6,synonymous_varia	A	ENSG00000166189
0	HSPB6,splice_region_va	T	ENSG00000004776
0	HTR5A,synonymous_var	A	ENSG00000157219
0	HUWE1,synonymous_va	C	ENSG00000086758
0	HUWE1,missense_varian	T	ENSG00000086758
0	ICOSLG,missense_varia	T	ENSG00000160223
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0	ICOSLG,3_prime_UTR_v	G	ENSG00000160223
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0	IDH3A,intron_variant,,EN	G	ENSG00000166411
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0	IGF2R,intron_variant,,EN	G	ENSG00000197081
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0	IGSF9B,intron_variant,,E	-	ENSG00000080854
0	IKBKAP,synonymous_va	G	ENSG00000070061
0	IL17RC,intron_variant,,EI	-	ENSG00000163702
0	IL20RA,missense_varian	T	ENSG00000016402
0	IL22RA1,intron_variant,,E	T	ENSG00000142677
0	IL2RA,3_prime_UTR_var	T	ENSG00000134460
0	INO80E,3_prime_UTR_v	C	ENSG00000169592
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0	IGF2,intron_variant,,ENS	G	ENSG00000129965
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0	IQSEC3,intron_variant,,E	A	ENSG00000120645
0	IRF5,intron_variant,,ENS	A	ENSG00000128604
0	IRGC,synonymous_varia	C	ENSG00000124449

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0	ITGA9,intron_variant,,EN	A	ENSG00000144668
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0	ITPKB,intron_variant,,EN	C	ENSG00000143772
0	ITPR2,intron_variant,,EN	T	ENSG00000123104
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0	JADE3,intron_variant,,EN	A	ENSG00000102221
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0	JARID2,synonymous_var	T	ENSG00000008083
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0	KCP,intron_variant,,ENS	T	ENSG00000135253
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0	KCTD4,5_prime_UTR_va	A	ENSG00000180332
0	KDM3B,intron_variant,,EI	A	ENSG00000120733
0	KDM4A,intron_variant,,EI	A	ENSG00000066135
0	KDM4B,intron_variant,,EI	T	ENSG00000127663
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0	KDM7A,missense_varian	T	ENSG00000006459
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0	KIAA1244,missense_vari	G	ENSG00000112379
0	KIAA1429,intron_variant,	-	ENSG00000164944
0	KIAA1683,synonymous_\	A	ENSG00000130518
0	KIAA1919,intron_variant,	A	ENSG00000173214
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0	KIFAP3,intron_variant,,EI	T	ENSG00000075945
0	KIN,intron_variant,,ENST	C	ENSG00000151657

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0	KLRG1,intron_variant,,EN	A	ENSG00000139187
0	KMT2C,intron_variant,,EI	C	ENSG00000055609
0	KNDC1,intron_variant,,EI	A	ENSG00000171798
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0	KRT32,intron_variant,,EN	C	ENSG00000108759
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0	KRTAP10-9,3_prime_UT	C	ENSG00000221837
0	KRTAP12-3,3_prime_UT	C	ENSG00000205439
0	KRTAP12-4,synonymous	G	ENSG00000212933
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0	LEMD3,intron_variant,,EN	A	ENSG00000174106
0	LFNG,intron_variant,,ENS	A	ENSG00000106003
0	LILRA4,intron_variant,,EN	T	ENSG00000239961
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0	LMBR1L,intron_variant,,E	T	ENSG00000139636
0	LMO7,intron_variant,,ENS	A	ENSG00000136153
0	LNPEP,intron_variant,,EN	A	ENSG00000113441
0	LONRF1,intron_variant,,E	-	ENSG00000154359
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0	LOXL1,intron_variant,,EN	C	ENSG00000129038
0	LPP,3_prime_UTR_varia	G	ENSG00000145012
0	LRMP,intron_variant,,EN	C	ENSG00000118308
0	LRP1B,intron_variant,,EN	A	ENSG00000168702
0	LRP5,intron_variant,,ENS	T	ENSG00000162337
0	LRP5L,missense_variant	A	ENSG00000100068
0	LRP5L,intron_variant,,EN	A	ENSG00000100068
0	LRPAP1,intron_variant,,E	A	ENSG00000163956
0	LRR1,intron_variant,,ENS	T	ENSG00000165501
0	LRRC18,missense_varia	A	ENSG00000165383
0	LRRCC1,3_prime_UTR_	G	ENSG00000133739
0	LRRIQ1,intron_variant,,E	A	ENSG00000133640
0	LSG1,missense_variant,p	G	ENSG00000041802
0	LSM14A,missense_varia	A	ENSG00000257103
0	LSM6,3_prime_UTR_var	G	ENSG00000164167

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0	LTN1,intron_variant,,ENS	A	ENSG00000198862
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0	LYPD4,intron_variant,,EN	T	ENSG00000183103
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0	LZTS2,downstream_gen	G	ENSG00000107816
0	LZTS2,splice_region_var	T	ENSG00000107816
0	MAD1L1,intron_variant,,E	C	ENSG00000002822
0	MAD2L1,intron_variant,,E	C	ENSG00000164109
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0	MAGEB4,5_prime_UTR_	T	ENSG00000120289
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0	MAP3K15,missense_vari	T	ENSG00000180815
0	MAP3K3,intron_variant,,E	T	ENSG00000198909
0	MAP4K1,synonymous_va	C	ENSG00000104814
0	MAP4K4,intron_variant,,E	G	ENSG00000071054
0	MAPKAPK3,intron_varian	-	ENSG00000114738
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0	MAST1,splice_region_va	C	ENSG00000105613
0	MAST4,5_prime_UTR_va	G	ENSG00000069020
0	MATN4,missense_varian	T	ENSG00000124159
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0	MED22,5_prime_UTR_va	C	ENSG00000148297
0	MED25,intron_variant,,EN	C	ENSG00000104973
0	MED29,missense_varian	C	ENSG00000063322
0	MEF2B,intron_variant,,EN	A	ENSG00000213999
0	MEGF6,intron_variant,,EN	C	ENSG00000162591
0	MEP1B,intron_variant,,EN	G	ENSG00000141434
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0	METTL3,intron_variant,,E	T	ENSG00000165819
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0	MFSD12,intron_variant,,E	A	ENSG00000161091
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0	MGAT5B,synonymous_v	T	ENSG00000167889
0	MGMT,missense_variant	T	ENSG00000170430
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0	MMP21,intron_variant,,EI	A	ENSG00000154485
0	MNX1,intron_variant,,EN	G	ENSG00000130675
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0	MRPL41,intron_variant,,E	A	ENSG00000182154
0	MRPL43,intron_variant,,E	A	ENSG00000055950
0	MRPS10,intron_variant,,E	T	ENSG00000048544
0	MRVI1,splice_acceptor_v	T	ENSG00000072952
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0	MYO18B,intron_variant,,I	C	ENSG00000133454
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0	RIBC2,5_prime_UTR_va	A	ENSG00000128408
0	RIPK4,synonymous_varia	T	ENSG00000183421
0	RMND5A,intron_variant,,	AA	ENSG00000153561
0	RMND5A,5_prime_UTR_	T	ENSG00000153561
0	RNASEH2A,intron_variar	T	ENSG00000104889
0	RNASEL,synonymous_va	T	ENSG00000135828

0	RND2,3_prime_UTR_var	T	ENSG00000108830
0	RNF175,intron_variant,,E	-	ENSG00000145428
0	RNF19B,intron_variant,,E	A	ENSG00000116514
0	RNF222,3_prime_UTR_v	T	ENSG00000189051
0	ROBO1,intron_variant,,E	C	ENSG00000169855
0	ROBO1,intron_variant,,E	A	ENSG00000169855
0	ROCK2,missense_varian	T	ENSG00000134318
0	ROR1,3_prime_UTR_var	A	ENSG00000185483
0	ROS1,intron_variant,,EN	G	ENSG00000047936
0	RP1-130H16.18,intron_v	T	ENSG00000248751
0	LMO7,5_prime_UTR_var	C	ENSG00000228444
0	CC2D2B,5_prime_UTR_	A	ENSG00000269948
0	RP11-551L14.1,intron_va	C	ENSG00000177359
0	FHAD1,intron_variant,,EN	A	ENSG00000233485
0	RPAP3,intron_variant,,EN	T	ENSG00000005175
0	RPH3AL,intron_variant,,E	A	ENSG00000181031
0	RPL18A,intron_variant,,E	C	ENSG00000105640
0	RPL23A,5_prime_UTR_v	CC	ENSG00000198242
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0	RPL3,synonymous_varia	T	ENSG00000100316
0	RPS4X,synonymous_var	T	ENSG00000198034
0	RPS6KA2,intron_variant,	G	ENSG00000071242
0	RPTOR,missense_variar	T	ENSG00000141564
0	RPTOR,synonymous_var	T	ENSG00000141564
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0	RRP1B,synonymous_var	A	ENSG00000160208
0	RSAD1,synonymous_var	G	ENSG00000136444
0	RSU1,intron_variant,,EN	C	ENSG00000148484
0	RTN3,missense_variant,p	C	ENSG00000133318
0	RUFY1,5_prime_UTR_va	T	ENSG00000176783
2	RUFY1,synonymous_var	C	ENSG00000176783
0	RUFY2,5_prime_UTR_va	C	ENSG00000204130
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0	RYR1,intron_variant,,EN	A	ENSG00000196218
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0	SCAF1,intron_variant,,EN	T	ENSG00000126461
0	SCAMP3,synonymous_va	T	ENSG00000116521
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0	SCEL,intron_variant,,EN	C	ENSG00000136155
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0	SCLT1,intron_variant,,EN	A	ENSG00000151466
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0	SCN9A,missense_varian	G	ENSG00000169432

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0	SEC16B,intron_variant,,E	A	ENSG00000120341
0	SEC23B,missense_varia	G	ENSG00000101310
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0	SELP,intron_variant,,ENS	A	ENSG00000174175
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0	SMARCA5,intron_variant	-	ENSG00000153147
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0	SMYD3,splice_region_va	T	ENSG00000185420
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0	SORCS2,splice_region_v	A	ENSG00000184985
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0	ST6GALNAC2,intron_var	G	ENSG00000070731
0	ST6GALNAC4,intron_var	-	ENSG00000136840
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0	STAT4,intron_variant,,EN	G	ENSG00000138378
0	STAT5B,intron_variant,,E	-	ENSG00000173757

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0	STRA8,downstream_gen	T	ENSG00000146857
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0	STRIP1,intron_variant,,E	G	ENSG00000143093
0	STRIP2,intron_variant,,E	G	ENSG00000128578
0	STXBP5,intron_variant,,E	C	ENSG00000164506
0	STYK1,missense_variant	C	ENSG00000060140
0	STYXL1,downstream_ge	A	ENSG00000127952
0	SUCNR1,3_prime_UTR_	A	ENSG00000198829
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0	SUMO4,missense_variar	A	ENSG00000177688
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0	TBC1D4,intron_variant,,E	T	ENSG00000136111
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0	WDR60,intron_variant,,E	C	ENSG00000126870
0	WDR87,inframe_deletion	-	ENSG00000171804
0	WDR91,intron_variant,,E	C	ENSG00000105875
0	WIPI2,intron_variant,,EN	A	ENSG00000157954
0	WNK1,missense_variant	A	ENSG00000060237
0	WNT2B,synonymous_va	G	ENSG00000134245
0	WNT8B,missense_variar	C	ENSG00000075290
0	WRNIP1,intron_variant,,E	G	ENSG00000124535
0	WSB2,intron_variant,,EN	T	ENSG00000176871
1	WWC1,intron_variant,,EN	C	ENSG00000113645
0	WWP2,synonymous_vari	T	ENSG00000198373
0	XAB2,intron_variant,,ENS	T	ENSG00000076924
0	XKR8,3_prime_UTR_var	A	ENSG00000158156
0	XPNPEP1,intron_variant,	C	ENSG00000108039
0	XPNPEP3,intron_variant,	A	ENSG00000196236
0	XPO5,splice_region_varia	C	ENSG00000124571
0	XRCC1,synonymous_var	C	ENSG00000073050
0	XRCC1,intron_variant,,EI	T	ENSG00000073050
0	YBX2,intron_variant,,ENS	T	ENSG00000006047
0	YY1AP1,3_prime_UTR_v	G	ENSG00000163374
0	YY1AP1,synonymous_va	C	ENSG00000163374
0	ZBTB2,synonymous_vari	T	ENSG00000181472
0	ZC2HC1B,intron_variant,	G	ENSG00000118491
0	ZC3H12D,3_prime_UTR_	G	ENSG00000178199
0	ZC3H12D,intron_variant,	G	ENSG00000178199
0	ZC3H12D,5_prime_UTR_	A	ENSG00000178199
0	ZC3H3,intron_variant,,EN	T	ENSG00000014164
0	ZC3H7B,intron_variant,,E	T	ENSG00000100403

0	ZCCHC18,synonymous_	G	ENSG00000166707
0	ZDHHC16,missense_var	T	ENSG00000171307
0	ZDHHC6,synonymous_va	A	ENSG00000023041
0	ZDHHC7,intron_variant,,I	T	ENSG00000153786
0	ZFAND2A,intron_variant,	C	ENSG00000178381
0	ZFHX2,missense_variant	G	ENSG00000136367
0	ZFPM2,intron_variant,,EN	T	ENSG00000169946
0	ZFYVE19,3_prime_UTR_	C	ENSG00000166140
0	ZKSCAN5,5_prime_UTR	T	ENSG00000196652
0	ZMYND10,intron_variant,	G	ENSG00000004838
0	ZMYND10,intron_variant,	A	ENSG00000004838
0	ZNF185,intron_variant,,E	A	ENSG00000147394
0	ZNF275,splice_region_va	T	ENSG00000063587
0	ZNF304,missense_varian	C	ENSG00000131845
0	ZNF324,intron_variant,,E	T	ENSG00000083812
0	ZNF365,intron_variant,,E	A	ENSG00000138311
0	ZNF414,3_prime_UTR_v	G	ENSG00000133250
0	ZNF420,intron_variant,,E	T	ENSG00000197050
0	ZNF432,synonymous_va	G	ENSG00000256087
0	ZNF441,intron_variant,,E	G	ENSG00000197044
0	ZNF449,intron_variant,,E	T	ENSG00000173275
0	ZNF493,intron_variant,,E	C	ENSG00000196268
0	ZNF512B,intron_variant,,	C	ENSG00000196700
1	ZNF592,missense_varian	A	ENSG00000166716
0	ZNF598,missense_varian	T	ENSG00000167962
0	ZNF614,missense_varian	A	ENSG00000142556
0	ZNF626,5_prime_UTR_v	AAGT	ENSG00000188171
2	ZNF676,missense_varian	T	ENSG00000196109
0	ZNF697,synonymous_va	A	ENSG00000143067
0	ZNF708,missense_varian	C	ENSG00000182141
0	ZNF717,5_prime_UTR_v	T	ENSG00000227124
0	ZNF75D,synonymous_va	T	ENSG00000186376
0	ZNF785,missense_varian	C	ENSG00000197162
0	ZNF816,synonymous_va	T	ENSG00000180257
0	ZNF839,synonymous_va	T	ENSG00000022976
1	ZP1,missense_variant,p.	T	ENSG00000149506
0	ZSCAN2,3_prime_UTR_	A	ENSG00000176371
0	ZSWIM4,intron_variant,,I	C	ENSG00000132003
0	ZZEF1,intron_variant,,EN	T	ENSG00000074755

Feature	Feature_type	Consequence	cDNA_position
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ENST00000375234	Transcript	intron_variant	-/2863
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ENST00000269081	Transcript	synonymous_variant	1693/6362
ENST00000301732	Transcript	3_prime_UTR_variant	5851/6609
ENST00000284425	Transcript	intron_variant	-/5300
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ENST00000340001	Transcript	intron_variant	-/6514
ENST00000399410	Transcript	synonymous_variant	4213/6552
ENST00000205557	Transcript	intron_variant	-/5747
ENST00000389817	Transcript	synonymous_variant	3888/4921
ENST00000289119	Transcript	5_prime_UTR_variant	89-90/2064
ENST00000302538	Transcript	e_region_variant,intron_va	-/5289
ENST00000436594	Transcript	upstream_gene_variant	-/588
ENST00000600805	Transcript	missense_variant	340/756
ENST00000281182	Transcript	intron_variant	-/2249
ENST00000420607	Transcript	intron_variant	-/1332
ENST00000358776	Transcript	intron_variant	-/5859
ENST00000366812	Transcript	intron_variant	-/3573
ENST00000301452	Transcript	5_prime_UTR_variant	37/1445
ENST00000256997	Transcript	intron_variant	-/2203
ENST00000286353	Transcript	e_region_variant,intron_va	-/3281
ENST00000258873	Transcript	intron_variant	-/6357
ENST00000317447	Transcript	intron_variant	-/3664
ENST00000399422	Transcript	intron_variant	-/2142
ENST00000352511	Transcript	e_region_variant,intron_va	-/11821
ENST00000356955	Transcript	missense_variant	2406/2949
ENST00000310823	Transcript	intron_variant	-/4349
ENST00000373208	Transcript	missense_variant	2818/5269
ENST00000251582	Transcript	intron_variant	-/6754
ENST00000389420	Transcript	intron_variant	-/6076
ENST00000367996	Transcript	intron_variant	-/9773
ENST00000381055	Transcript	intron_variant	-/7311
ENST00000380548	Transcript	intron_variant	-/8030
ENST00000367236	Transcript	intron_variant	-/3407
ENST00000369716	Transcript	upstream_gene_variant	-/1517
ENST00000304129	Transcript	synonymous_variant	651/3705
ENST00000395146	Transcript	intron_variant	-/9285
ENST00000370460	Transcript	intron_variant	-/13746
ENST00000397238	Transcript	intron_variant	-/3225
ENST00000436302	Transcript	intron_variant	-/3533
ENST00000542281	Transcript	synonymous_variant	1019/2412
ENST00000367800	Transcript	intron_variant	-/5921
ENST00000302312	Transcript	intron_variant	-/524
ENST00000357847	Transcript	synonymous_variant	98/1395
ENST00000527815	Transcript	intron_variant	-/2523
ENST00000527815	Transcript	intron_variant	-/2523
ENST00000381129	Transcript	missense_variant	367/2959
ENST00000291582	Transcript	synonymous_variant	715/2257
ENST00000291582	Transcript	intron_variant	-/2257
ENST00000356239	Transcript	e_region_variant,intron_va	-/12471
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ENST00000359579	Transcript	intron_variant	-/1590
ENST00000295897	Transcript	intron_variant	-/2263

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ENST00000329841	Transcript	intron_variant	-/3924
ENST00000374391	Transcript	intron_variant	-/2504
ENST00000258888	Transcript	5_prime_UTR_variant	94/10917
ENST00000258888	Transcript	intron_variant	-/10917
ENST00000356289	Transcript	intron_variant	-/1944
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ENST00000341068	Transcript	synonymous_variant	5114/8259
ENST00000265709	Transcript	intron_variant	-/6379
ENST00000520309	Transcript	intron_variant	-/4410
ENST00000303941	Transcript	intron_variant	-/2543
ENST00000357997	Transcript	intron_variant	-/4481
ENST00000290943	Transcript	missense_variant	3121/3773
ENST00000376087	Transcript	intron_variant	-/6591
ENST00000399451	Transcript	e_region_variant,intron_va	-/6564
ENST00000355594	Transcript	synonymous_variant	891/3342
ENST00000267116	Transcript	intron_variant	-/8688
ENST00000341048	Transcript	intron_variant	-/2500
ENST00000374700	Transcript	intron_variant	-/5070
ENST00000595053	Transcript	5_prime_UTR_variant	62/1130
ENST00000357586	Transcript	intron_variant	-/4176
ENST00000359032	Transcript	intron_variant	-/3286
ENST00000261842	Transcript	intron_variant	-/6758
ENST00000261842	Transcript	ıse_variant,splice_region_	1172/6758
ENST00000376236	Transcript	intron_variant	-/2771
ENST00000373173	Transcript	intron_variant	-/1279
ENST00000337801	Transcript	missense_variant	152/1084
ENST00000337801	Transcript	5_prime_UTR_variant	6/1084
ENST00000383168	Transcript	intron_variant	-/5274
ENST00000357872	Transcript	missense_variant	2042/4581
ENST00000256682	Transcript	intron_variant	-/4105
ENST00000336498	Transcript	missense_variant	2289/3299
ENST00000453547	Transcript	intron_variant	-/8956
ENST00000276211	Transcript	intron_variant	-/3083
ENST00000370028	Transcript	synonymous_variant	1864/3372
ENST00000368194	Transcript	intron_variant	-/6889
ENST00000378378	Transcript	intron_variant	-/3061
ENST00000361247	Transcript	upstream_gene_variant	-/4149
ENST00000338458	Transcript	missense_variant	1209/3639
ENST00000375741	Transcript	synonymous_variant	793/5525
ENST00000378909	Transcript	intron_variant	-/1411
ENST00000377275	Transcript	egion_variant,synonymous	725/7196
ENST00000481646	Transcript	intron_variant	-/3043
ENST00000423738	Transcript	5_prime_UTR_variant	7/7420
ENST00000423738	Transcript	missense_variant	452/7420
ENST00000423738	Transcript	upstream_gene_variant	-/7420
ENST00000423738	Transcript	synonymous_variant	6211/7420
ENST00000412477	Transcript	intron_variant	-/1779
ENST00000222250	Transcript	intron_variant	-/2503
ENST00000222250	Transcript	e_region_variant,intron_va	-/2503
ENST00000216124	Transcript	missense_variant	978/2050
ENST00000263207	Transcript	intron_variant	-/4041
ENST00000420175	Transcript	intron_variant	-/1694
ENST00000487349	Transcript	intron_variant	-/3179
ENST00000325885	Transcript	intron_variant	-/3825

ENST00000277458	Transcript	5_prime_UTR_variant	98/2330
ENST00000347842	Transcript	intron_variant	-/2684
ENST00000306729	Transcript	intron_variant	-/2123
ENST00000342380	Transcript	intron_variant	-/1296
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ENST00000361209	Transcript	intron_variant	-/4622
ENST00000269197	Transcript	intron_variant	-/11344
ENST00000284629	Transcript	intron_variant	-/1865
ENST00000317868	Transcript	intron_variant	-/2938
ENST00000358385	Transcript	intron_variant	-/2647
ENST00000487903	Transcript	3_prime_UTR_variant	3843/8858
ENST00000326735	Transcript	synonymous_variant	1039/3840
ENST00000361216	Transcript	synonymous_variant	2348/5421
ENST00000368081	Transcript	intron_variant	-/3839
ENST00000262429	Transcript	intron_variant	-/3376
ENST00000356708	Transcript	intron_variant	-/1163
ENST00000341514	Transcript	intron_variant	-/8483
ENST00000536015	Transcript	intron_variant	-/5935
ENST00000338821	Transcript	intron_variant	-/8106
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ENST00000320211	Transcript	intron_variant	-/2590
ENST00000395547	Transcript	intron_variant	-/3981
ENST00000374521	Transcript	intron_variant	-/1365
ENST00000276101	Transcript	e_region_variant,intron_va	-/2124
ENST00000367618	Transcript	ıse_variant,splice_region_	1951/3642
ENST00000262320	Transcript	intron_variant	-/3643
ENST00000318683	Transcript	missense_variant	1130/2226
ENST00000321300	Transcript	intron_variant	-/2879
ENST00000324385	Transcript	intron_variant	-/4678
ENST00000542236	Transcript	missense_variant	1538/3431
ENST00000269980	Transcript	5_prime_UTR_variant	335/2103
ENST00000223368	Transcript	intron_variant	-/1975
ENST00000540052	Transcript	intron_variant	-/7127
ENST00000449131	Transcript	intron_variant	-/4267
ENST00000281474	Transcript	splice_donor_variant	-/3281
ENST00000224337	Transcript	intron_variant	-/1784
ENST00000252677	Transcript	missense_variant	308/1179
ENST00000345382	Transcript	intron_variant	-/4610
ENST00000170150	Transcript	intron_variant	-/1898
ENST00000306378	Transcript	intron_variant	-/9688
ENST00000471181	Transcript	intron_variant	-/5936
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ENST00000544455	Transcript	intron_variant	-/10984
ENST00000467963	Transcript	intron_variant	-/2156
ENST00000333229	Transcript	synonymous_variant	1192/10141
ENST00000446293	Transcript	intron_variant	-/1505
ENST00000333511	Transcript	intron_variant	-/1974
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ENST00000260723	Transcript	intron_variant	-/1849
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ENST00000342818	Transcript	intron_variant	-/1408
ENST00000256015	Transcript	intron_variant	-/2448
ENST00000327705	Transcript	synonymous_variant	1224/3500
ENST00000343736	Transcript	intron_variant	-/5947

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ENST00000374144	Transcript	synonymous_variant	4560/5230
ENST00000284694	Transcript	intron_variant	-/3076
ENST00000378615	Transcript	intron_variant	-/1651
ENST00000261318	Transcript	missense_variant	325/2801
ENST00000524981	Transcript	intron_variant	-/9766
ENST00000330828	Transcript	frameshift_variant	753-754/1684
ENST00000399910	Transcript	intron_variant	-/1670
ENST00000381365	Transcript	downstream_gene_varian	-/3199
ENST00000319977	Transcript	3_prime_UTR_variant	2230/2725
ENST00000590083	Transcript	missense_variant	1405/4261
ENST00000301246	Transcript	5_prime_UTR_variant	95/467
ENST00000304661	Transcript	missense_variant	632/1613
ENST00000366534	Transcript	synonymous_variant	1788/3333
ENST00000371007	Transcript	intron_variant	-/2153
ENST00000343433	Transcript	intron_variant	-/3135
ENST00000326665	Transcript	e_region_variant,intron_v	-/7159
ENST00000339142	Transcript	intron_variant	-/3100
ENST00000388934	Transcript	3_prime_UTR_variant	1513/1911
ENST00000290390	Transcript	intron_variant	-/2227
ENST00000245907	Transcript	intron_variant	-/5263
ENST00000398965	Transcript	intron_variant	-/2177
ENST00000223642	Transcript	intron_variant	-/5462
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ENST00000380175	Transcript	5_prime_UTR_variant	433/1834
ENST00000313164	Transcript	intron_variant	-/4257
ENST00000451037	Transcript	intron_variant	-/3189
ENST00000309893	Transcript	synonymous_variant	711/1094
ENST00000398319	Transcript	missense_variant	2831/7480
ENST00000360228	Transcript	intron_variant	-/8392
ENST00000371372	Transcript	e_region_variant,intron_v	-/9790
ENST00000347598	Transcript	intron_variant	-/6655
ENST00000479441	Transcript	intron_variant	-/3453
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ENST00000324631	Transcript	intron_variant	-/3446
ENST00000502583	Transcript	intron_variant	-/3284
ENST00000361675	Transcript	intron_variant	-/3612
ENST00000316448	Transcript	5_prime_UTR_variant	3/1903
ENST00000378847	Transcript	3_prime_UTR_variant	1536/8154
ENST00000342666	Transcript	intron_variant	-/1940
ENST00000378494	Transcript	intron_variant	-/1495
ENST00000446248	Transcript	synonymous_variant	950/4179
ENST00000398776	Transcript	intron_variant	-/2728
ENST00000271971	Transcript	intron_variant	-/2362
ENST00000222125	Transcript	intron_variant	-/1221
ENST00000403299	Transcript	intron_variant	-/4113
ENST00000391898	Transcript	intron_variant	-/5263
ENST00000427043	Transcript	3_prime_UTR_variant	1134/3241
ENST00000368078	Transcript	intron_variant	-/1897
ENST00000377022	Transcript	intron_variant	-/7936
ENST00000409235	Transcript	intron_variant	-/3746
ENST00000343849	Transcript	synonymous_variant	104/1431
ENST00000258214	Transcript	synonymous_variant	1540/2463
ENST00000349456	Transcript	intron_variant	-/2048
ENST00000292574	Transcript	missense_variant	815/1732

ENST00000398545	Transcript	intron_variant	-/1851
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ENST00000305866	Transcript	3_prime_UTR_variant	3046/3613
ENST00000329214	Transcript	intron_variant	-/2468
ENST00000369704	Transcript	synonymous_variant	704/3313
ENST00000388914	Transcript	missense_variant	2177/3663
ENST00000511166	Transcript	intron_variant	-/2051
ENST00000370276	Transcript	intron_variant	-/4779
ENST00000392343	Transcript	synonymous_variant	511/2896
ENST00000263102	Transcript	intron_variant	-/5811
ENST00000445632	Transcript	intron_variant	-/2528
ENST00000311925	Transcript	intron_variant	-/687
ENST00000292301	Transcript	intron_variant	-/2671
ENST00000287097	Transcript	missense_variant	2502/9130
ENST00000398214	Transcript	frameshift_variant	834/1296
ENST00000368033	Transcript	intron_variant	-/1360
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ENST00000322875	Transcript	intron_variant	-/3278
ENST00000312648	Transcript	inframe_deletion	622-648/1281
ENST00000394886	Transcript	upstream_gene_variant	-/3153
ENST00000342711	Transcript	intron_variant	-/5742
ENST00000437685	Transcript	intron_variant	-/2007
ENST00000296129	Transcript	missense_variant	1709/6006
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ENST00000425876	Transcript	intron_variant	-/1582
ENST00000256443	Transcript	intron_variant	-/1432
ENST00000274695	Transcript	synonymous_variant	1394/3272
ENST00000379989	Transcript	intron_variant	-/3459
ENST00000460006	Transcript	intron_variant	-/9298
ENST00000376288	Transcript	intron_variant	-/2552
ENST00000376288	Transcript	5_prime_UTR_variant	22/2552
ENST00000401445	Transcript	intron_variant	-/1008
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ENST00000399839	Transcript	intron_variant	-/3986
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ENST00000336737	Transcript	intron_variant	-/1799
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ENST00000368328	Transcript	missense_variant	183/750
ENST00000397527	Transcript	intron_variant	-/8398
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ENST00000264982	Transcript	missense_variant	671/2732
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ENST00000597853	Transcript	5_prime_UTR_variant	2838/3386
ENST00000369258	Transcript	synonymous_variant	59/2967
ENST00000432561	Transcript	intron_variant	-/2648

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ENST00000445067	Transcript	missense_variant	1316/2169
ENST00000306071	Transcript	3_prime_UTR_variant	1641/2557
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ENST00000324288	Transcript	intron_variant	-/9438
ENST00000536961	Transcript	synonymous_variant	722/845
ENST00000392521	Transcript	intron_variant	-/8708
ENST00000453707	Transcript	missense_variant	619/998
ENST00000424301	Transcript	intron_variant	-/1637
ENST00000346436	Transcript	intron_variant	-/5583
ENST00000331433	Transcript	intron_variant	-/2475
ENST00000401528	Transcript	3_prime_UTR_variant	1906/2131
ENST00000299663	Transcript	5_prime_UTR_variant	142/2159
ENST00000369449	Transcript	3_prime_UTR_variant	982/2655
ENST00000374379	Transcript	splice_acceptor_variant	-/4346
ENST00000540338	Transcript	intron_variant	-/4400
ENST00000320081	Transcript	intron_variant	-/4293
ENST00000379510	Transcript	intron_variant	-/5315
ENST00000356713	Transcript	intron_variant	-/5959
ENST00000317147	Transcript	synonymous_variant	5049/8471
ENST00000289382	Transcript	intron_variant	-/2599
ENST00000537554	Transcript	synonymous_variant	4922/8974
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ENST00000361727	Transcript	intron_variant	-/9894
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ENST00000373855	Transcript	intron_variant	-/7660
ENST00000265136	Transcript	synonymous_variant	3691/5291
ENST00000323786	Transcript	intron_variant	-/2833
ENST00000297135	Transcript	intron_variant	-/4060
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ENST00000390654	Transcript	intron_variant	-/3061
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ENST00000372216	Transcript	intron_variant	-/6570
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ENST00000411948	Transcript	intron_variant	-/2631
ENST00000264613	Transcript	intron_variant	-/4676
ENST00000568128	Transcript	intron_variant	-/2112
ENST00000265085	Transcript	3_prime_UTR_variant	3698/9483
ENST00000367057	Transcript	missense_variant	3343/4240
ENST00000373631	Transcript	intron_variant	-/5550
ENST00000348438	Transcript	intron_variant	-/1600
ENST00000280527	Transcript	intron_variant	-/5912
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ENST00000433368	Transcript	synonymous_variant	847/2205
ENST00000377340	Transcript	intron_variant	-/4406
ENST00000268184	Transcript	intron_variant	-/2537
ENST00000182096	Transcript	intron_variant	-/4782
ENST00000419587	Transcript	5_prime_UTR_variant	135/4261
ENST00000370287	Transcript	5_prime_UTR_variant	314/875
ENST00000217244	Transcript	intron_variant	-/4416

ENST00000308508	Transcript	synonymous_variant	4005/8290
ENST00000423479	Transcript	intron_variant	-/2465
ENST00000598234	Transcript	synonymous_variant	4641/7627
ENST00000433211	Transcript	intron_variant	-/10675
ENST00000325551	Transcript	synonymous_variant	510/2490
ENST00000377833	Transcript	synonymous_variant	1977/11949
ENST00000537177	Transcript	intron_variant	-/2376
ENST00000535468	Transcript	missense_variant	4802/5504
ENST00000360264	Transcript	intron_variant	-/13762
ENST00000360264	Transcript	missense_variant	2952/13762
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ENST00000410053	Transcript	synonymous_variant	2703/3280
ENST00000282251	Transcript	missense_variant	1355/3278
ENST00000373691	Transcript	5_prime_UTR_variant	110/1861
ENST00000426130	Transcript	intron_variant	-/3205
ENST00000533558	Transcript	intron_variant	-/1658
ENST00000330436	Transcript	intron_variant	-/1739
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ENST00000336411	Transcript	intron_variant	-/2153
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ENST00000257215	Transcript	synonymous_variant	179/5757
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ENST00000260803	Transcript	intron_variant	-/2666
ENST00000254337	Transcript	intron_variant	-/2271
ENST00000254337	Transcript	synonymous_variant	255/2271
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ENST00000442544	Transcript	intron_variant	-/5721
ENST00000378454	Transcript	synonymous_variant	1319/4707
ENST00000339452	Transcript	5_prime_UTR_variant	282/5055
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ENST00000284690	Transcript	intron_variant	-/3070
ENST00000308736	Transcript	intron_variant	-/4548
ENST00000262415	Transcript	downstream_gene_varian	-/5558
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ENST00000220812	Transcript	intron_variant	-/894
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ENST00000374360	Transcript	intron_variant	-/5905
ENST00000372391	Transcript	intron_variant	-/7415
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ENST00000351747	Transcript	intron_variant	-/9542
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ENST00000324472	Transcript	e_region_variant,intron_va	-/4060
ENST00000294485	Transcript	e_region_variant,intron_va	-/7346
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ENST00000257189	Transcript	intron_variant	-/5525
ENST00000359747	Transcript	synonymous_variant	3152/4526
ENST00000359747	Transcript	synonymous_variant	59/4526
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ENST00000310850	Transcript	intron_variant	-/2717
ENST00000344537	Transcript	intron_variant	-/1403
ENST00000510708	Transcript	intron_variant	-/2307
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ENST00000334679	Transcript	5_prime_UTR_variant	468/2479
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ENST00000398093	Transcript	intron_variant	-/12945
ENST00000431635	Transcript	5_prime_UTR_variant	57/1503
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ENST00000318130	Transcript	intron_variant	-/6898
ENST00000379375	Transcript	intron_variant	-/2033
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ENST00000450662	Transcript	intron_variant	-/1691
ENST00000440314	Transcript	intron_variant	-/2697

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ENST00000268206	Transcript	intron_variant	-/3675
ENST00000426333	Transcript	intron_variant	-/4548
ENST00000253039	Transcript	synonymous_variant	352/2858
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ENST00000477853	Transcript	missense_variant	1077/6664
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ENST00000261488	Transcript	intron_variant	-/2982
ENST00000371207	Transcript	intron_variant	-/12515
ENST00000334696	Transcript	downstream_gene_varian	-/5842
ENST00000389561	Transcript	intron_variant	-/12268
ENST00000392957	Transcript	intron_variant	-/4043
ENST00000366837	Transcript	missense_variant	612/1776
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ENST00000257934	Transcript	intron_variant	-/6623
ENST00000389567	Transcript	missense_variant	1954/4407
ENST00000557943	Transcript	missense_variant	593/2287
ENST00000354232	Transcript	missense_variant	3202/3551
ENST00000292147	Transcript	synonymous_variant	73/963
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ENST00000409018	Transcript	intron_variant	-/3252
ENST00000366548	Transcript	missense_variant	2358/3473
ENST00000381295	Transcript	intron_variant	-/3551
ENST00000367075	Transcript	intron_variant	-/3096
ENST00000360256	Transcript	missense_variant	3981/9059
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ENST00000218099	Transcript	missense_variant	1127/2780
ENST00000374900	Transcript	intron_variant	-/1983
ENST00000278840	Transcript	intron_variant	-/3630
ENST00000278829	Transcript	intron_variant	-/1779
ENST00000407106	Transcript	intron_variant	-/2152
ENST00000216214	Transcript	missense_variant	1550/3458
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ENST00000391440	Transcript	3_prime_UTR_variant	656/2017
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ENST00000368557	Transcript	synonymous_variant	495/1033
ENST00000356467	Transcript	intron_variant	-/1767

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ENST00000327337	Transcript	intron_variant	-/7127
ENST00000324675	Transcript	upstream_gene_variant	-/1184
ENST00000361361	Transcript	intron_variant	-/3082
ENST00000374362	Transcript	5_prime_UTR_variant	58/4623
ENST00000361738	Transcript	intron_variant	-/1961
ENST00000259698	Transcript	synonymous_variant	3176/5471
ENST00000283357	Transcript	missense_variant	606/1560
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ENST00000536681	Transcript	3_prime_UTR_variant	1812/3616
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ENST00000600128	Transcript	missense_variant	6311/9362
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ENST00000324852	Transcript	intron_variant	-/2605
ENST00000594202	Transcript	synonymous_variant	1431/3214
ENST00000292408	Transcript	missense_variant	1407/3122
ENST00000336098	Transcript	3_prime_UTR_variant	1417/1659
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ENST00000257209	Transcript	synonymous_variant	3074/4967
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ENST00000337488	Transcript	intron_variant	-/2198
ENST00000252037	Transcript	synonymous_variant	663/1500
ENST00000424785	Transcript	intron_variant	-/2834
ENST00000369850	Transcript	missense_variant	1523/8382
ENST00000490882	Transcript	intron_variant	-/8079
ENST00000261937	Transcript	intron_variant	-/5857
ENST00000319653	Transcript	intron_variant	-/6434
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ENST00000263773	Transcript	intron_variant	-/3969
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ENST00000297267	Transcript	synonymous_variant	2291/6552
ENST00000259806	Transcript	synonymous_variant	1398/2187
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ENST00000373247	Transcript	3_prime_UTR_variant	2006/2274
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ENST00000350221	Transcript	intron_variant	-/2805
ENST00000306100	Transcript	intron_variant	-/4831
ENST00000319725	Transcript	synonymous_variant	1662/3124
ENST00000310160	Transcript	intron_variant	-/4246
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ENST00000292079	Transcript	intron_variant	-/571
ENST00000296137	Transcript	intron_variant	-/8504
ENST00000282538	Transcript	intron_variant	-/3759
ENST00000314167	Transcript	intron_variant	-/4442
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ENST00000261304	Transcript	intron_variant	-/3883
ENST00000261304	Transcript	upstream_gene_variant	-/3883
ENST00000588479	Transcript	intron_variant	-/1866
ENST00000297107	Transcript	intron_variant	-/5961
ENST00000324589	Transcript	missense_variant	1481/2169
ENST00000252318	Transcript	missense_variant	494/2380
ENST00000252318	Transcript	missense_variant	1880/2380
ENST00000269209	Transcript	synonymous_variant	1060/3006
ENST00000269209	Transcript	missense_variant	1473/3006
ENST00000269209	Transcript	3_prime_UTR_variant	2729-2730/3006
ENST00000373387	Transcript	5_prime_UTR_variant	205/3800
ENST00000343435	Transcript	intron_variant	-/4047
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ENST00000400723	Transcript	synonymous_variant	1388/2051
ENST00000379597	Transcript	intron_variant	-/4525
ENST00000238018	Transcript	e_region_variant,intron_v	-/1599
ENST00000342560	Transcript	intron_variant	-/2265
ENST00000249598	Transcript	intron_variant	-/1936
ENST00000308317	Transcript	intron_variant	-/1420
ENST00000486715	Transcript	intron_variant	-/3721
ENST00000233838	Transcript	intron_variant	-/7569
ENST00000334928	Transcript	missense_variant	1571/2239
ENST00000334928	Transcript	missense_variant	1683/2239
ENST00000301671	Transcript	missense_variant	1847/2650
ENST00000367419	Transcript	intron_variant	-/2024
ENST00000262460	Transcript	missense_variant	383/3249
ENST00000205061	Transcript	synonymous_variant	2672/3730
ENST00000205061	Transcript	intron_variant	-/3730
ENST00000262366	Transcript	intron_variant	-/4469
ENST00000373365	Transcript	5_prime_UTR_variant	81/2012
ENST00000372617	Transcript	missense_variant	674/1795
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ENST00000360814	Transcript	intron_variant	-/1880
ENST00000287275	Transcript	intron_variant	-/1636
ENST00000282570	Transcript	intron_variant	-/4191
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ENST00000329517	Transcript	missense_variant	347/6706
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ENST00000204726	Transcript	synonymous_variant	3601/9252

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ENST00000316715	Transcript	intron_variant	-/3275
ENST00000264718	Transcript	synonymous_variant	42/2496
ENST00000298110	Transcript	missense_variant	370/1527
ENST00000607359	Transcript	missense_variant	652/6004
ENST00000392607	Transcript	5_prime_UTR_variant	276/4283
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ENST00000264357	Transcript	intron_variant	-/5172
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ENST00000373818	Transcript	missense_variant	1916/2657
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ENST00000216465	Transcript	intron_variant	-/1338
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ENST00000261208	Transcript	intron_variant	-/3913
ENST00000598398	Transcript	intron_variant	-/652
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ENST00000441542	Transcript	intron_variant	-/3210
ENST00000398153	Transcript	intron_variant	-/918
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ENST00000366582	Transcript	intron_variant	-/8447
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ENST00000297440	Transcript	missense_variant	1915/3410
ENST00000399332	Transcript	intron_variant	-/9134
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ENST00000232854	Transcript	intron_variant	-/6087
ENST00000443617	Transcript	intron_variant	-/15137
ENST00000357618	Transcript	missense_variant	309/5286
ENST00000222390	Transcript	synonymous_variant	1235/5989
ENST00000441594	Transcript	intron_variant	-/1865
ENST00000330710	Transcript	intron_variant	-/7390
ENST00000253410	Transcript	synonymous_variant	290/635
ENST00000304043	Transcript	intron_variant	-/1081
ENST00000359985	Transcript	3_prime_UTR_variant	509/1195
ENST00000377831	Transcript	intron_variant	-/865

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ENST00000354624	Transcript	intron_variant	-/3689
ENST00000418931	Transcript	missense_variant	735/1560
ENST00000399120	Transcript	intron_variant	-/6466
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ENST00000278715	Transcript	synonymous_variant	757/1501
ENST00000216106	Transcript	intron_variant	-/4047
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ENST00000257555	Transcript	intron_variant	-/3442
ENST00000392006	Transcript	intron_variant	-/3555
ENST00000397668	Transcript	synonymous_variant	1460/2513
ENST00000262626	Transcript	intron_variant	-/2363
ENST00000299238	Transcript	synonymous_variant	601/2646
ENST00000592984	Transcript	ɛ_region_variant,intron_v	-/1634
ENST00000287907	Transcript	synonymous_variant	588/2912
ENST00000342160	Transcript	synonymous_variant	2567/14796
ENST00000342160	Transcript	missense_variant	6445/14796
ENST00000407780	Transcript	missense_variant	510/7080
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ENST00000407780	Transcript	3_prime_UTR_variant	6946/7080
ENST00000330062	Transcript	intron_variant	-/2694
ENST00000299518	Transcript	intron_variant	-/4128
ENST00000368131	Transcript	missense_variant	826/2734
ENST00000342136	Transcript	missense_variant	354/2899
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ENST00000356956	Transcript	intron_variant	-/9091
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ENST00000370903	Transcript	synonymous_variant	1630/4594
ENST00000370903	Transcript	synonymous_variant	2854/4594
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ENST00000393775	Transcript	intron_variant	-/3495
ENST00000393775	Transcript	missense_variant	1305/3495
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ENST00000513874	Transcript	ɛ_region_variant,intron_v	-/4284
ENST00000533871	Transcript	intron_variant	-/5050
ENST00000374647	Transcript	synonymous_variant	3377/5905
ENST00000295981	Transcript	intron_variant	-/2621
ENST00000316649	Transcript	missense_variant	766/3485
ENST00000270800	Transcript	intron_variant	-/2798
ENST00000379959	Transcript	3_prime_UTR_variant	1063/3176
ENST00000563197	Transcript	3_prime_UTR_variant	1809/2103
ENST00000397262	Transcript	3_prime_UTR_variant	575/639
ENST00000397270	Transcript	intron_variant	-/828
ENST00000302850	Transcript	synonymous_variant	1793/4721
ENST00000302850	Transcript	intron_variant	-/4721
ENST00000404767	Transcript	intron_variant	-/6959
ENST00000404767	Transcript	intron_variant	-/6959
ENST00000311234	Transcript	intron_variant	-/3662
ENST00000274364	Transcript	intron_variant	-/5844
ENST00000361170	Transcript	intron_variant	-/5988
ENST00000538872	Transcript	intron_variant	-/7094
ENST00000357234	Transcript	intron_variant	-/1680
ENST00000244314	Transcript	synonymous_variant	1156/1662

ENST00000369304	Transcript	intron_variant	-/5269
ENST00000369304	Transcript	intron_variant	-/5269
ENST00000397033	Transcript	intron_variant	-/4189
ENST00000264741	Transcript	intron_variant	-/7889
ENST00000266041	Transcript	intron_variant	-/3336
ENST00000266041	Transcript	synonymous_variant	487/3336
ENST00000266041	Transcript	intron_variant	-/3336
ENST00000373298	Transcript	intron_variant	-/1641
ENST00000429204	Transcript	intron_variant	-/6150
ENST00000381340	Transcript	intron_variant	-/10511
ENST00000381340	Transcript	intron_variant	-/10511
ENST00000374316	Transcript	e_region_variant,intron_v	-/9870
ENST00000278071	Transcript	synonymous_variant	1182/4362
ENST00000381318	Transcript	intron_variant	-/17015
ENST00000381318	Transcript	intron_variant	-/17015
ENST00000226319	Transcript	intron_variant	-/5771
ENST00000218343	Transcript	intron_variant	-/4931
ENST00000298622	Transcript	intron_variant	-/6626
ENST00000341776	Transcript	intron_variant	-/5755
ENST00000341776	Transcript	intron_variant	-/5755
ENST00000341776	Transcript	synonymous_variant	1450/5755
ENST00000458427	Transcript	3_prime_UTR_variant	2279-2280/3570
ENST00000382303	Transcript	3_prime_UTR_variant	4765/5581
ENST00000371153	Transcript	intron_variant	-/4665
ENST00000371153	Transcript	synonymous_variant	1957/4665
ENST00000371153	Transcript	synonymous_variant	3160/4665
ENST00000367411	Transcript	synonymous_variant	493/1894
ENST00000221444	Transcript	missense_variant	922/4372
ENST00000490337	Transcript	intron_variant	-/3122
ENST00000399881	Transcript	intron_variant	-/3695
ENST00000476647	Transcript	riant,non_coding_transcri	-/5108
ENST00000228495	Transcript	intron_variant	-/4163
ENST00000405872	Transcript	5_prime_UTR_variant	348/2115
ENST00000314358	Transcript	intron_variant	-/6813
ENST00000372396	Transcript	intron_variant	-/4474
ENST00000159111	Transcript	intron_variant	-/5593
ENST00000317961	Transcript	intron_variant	-/5472
ENST00000377967	Transcript	missense_variant	2218/5438
ENST00000397560	Transcript	intron_variant	-/9272
ENST00000397560	Transcript	synonymous_variant	1710/9272
ENST00000397560	Transcript	missense_variant	2028/9272
ENST00000251993	Transcript	synonymous_variant	178/2723
ENST00000264501	Transcript	intron_variant	-/15896
ENST00000251691	Transcript	missense_variant	2231/14877
ENST00000297591	Transcript	intron_variant	-/6528
ENST00000392413	Transcript	synonymous_variant	3702/4402
ENST00000368847	Transcript	intron_variant	-/5958
ENST00000367350	Transcript	intron_variant	-/7274
ENST00000247986	Transcript	synonymous_variant	581/3969
ENST00000389916	Transcript	intron_variant	-/3643
ENST00000498729	Transcript	intron_variant	-/9162
ENST00000320785	Transcript	intron_variant	-/7919
ENST00000260753	Transcript	intron_variant	-/6306
ENST00000361580	Transcript	intron_variant	-/2957
ENST00000379562	Transcript	intron_variant	-/6348

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ENST00000514860	Transcript	egion_variant,synonymous	289/2442
ENST00000273963	Transcript	intron_variant	-/5621
ENST00000356986	Transcript	intron_variant	-/1206
ENST00000262189	Transcript	intron_variant	-/16862
ENST00000304613	Transcript	intron_variant	-/6793
ENST00000333479	Transcript	e_region_variant,intron_va	-/6975
ENST00000327442	Transcript	synonymous_variant	976/1725
ENST00000290158	Transcript	intron_variant	-/6139
ENST00000327813	Transcript	intron_variant	-/2719
ENST00000269576	Transcript	intron_variant	-/2124
ENST00000225899	Transcript	intron_variant	-/1750
ENST00000328119	Transcript	3_prime_UTR_variant	1471/1644
ENST00000397911	Transcript	3_prime_UTR_variant	932/1255
ENST00000397907	Transcript	3_prime_UTR_variant	372/410
ENST00000391618	Transcript	synonymous_variant	375/447
ENST00000216237	Transcript	intron_variant	-/3296
ENST00000421865	Transcript	intron_variant	-/9640
ENST00000421865	Transcript	intron_variant	-/9640
ENST00000230538	Transcript	intron_variant	-/6547
ENST00000230538	Transcript	intron_variant	-/6547
ENST00000258341	Transcript	intron_variant	-/7889
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ENST00000264144	Transcript	5_prime_UTR_variant	60/5147
ENST00000543571	Transcript	synonymous_variant	1994/7517
ENST00000333881	Transcript	5_prime_UTR_variant	25/425
ENST00000371688	Transcript	intron_variant	-/867
ENST00000344642	Transcript	intron_variant	-/4012
ENST00000308330	Transcript	intron_variant	-/4764
ENST00000222725	Transcript	intron_variant	-/2377
ENST00000291759	Transcript	intron_variant	-/1944
ENST00000336180	Transcript	intron_variant	-/3219
ENST00000585527	Transcript	missense_variant	1525/2241
ENST00000267102	Transcript	intron_variant	-/2349
ENST00000465261	Transcript	intron_variant	-/5580
ENST00000231368	Transcript	intron_variant	-/12752
ENST00000398246	Transcript	intron_variant	-/3594
ENST00000371628	Transcript	synonymous_variant	73/2550
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ENST00000261921	Transcript	intron_variant	-/2351
ENST00000312675	Transcript	intron_variant	-/18278
ENST00000354454	Transcript	intron_variant	-/2504
ENST00000389484	Transcript	intron_variant	-/16535
ENST00000294304	Transcript	intron_variant	-/5159
ENST00000402859	Transcript	missense_variant	1086/1661
ENST00000402859	Transcript	intron_variant	-/1661
ENST00000500728	Transcript	intron_variant	-/7819
ENST00000298288	Transcript	intron_variant	-/1745
ENST00000374160	Transcript	missense_variant	97/1617
ENST00000360375	Transcript	3_prime_UTR_variant	3300/3813
ENST00000393217	Transcript	intron_variant	-/5394
ENST00000265245	Transcript	missense_variant	590/3572
ENST00000544216	Transcript	ıse_variant,splice_region_	790/3596
ENST00000502781	Transcript	3_prime_UTR_variant	1045/1352

ENST00000397728	Transcript	intron_variant	-/4936
ENST00000389194	Transcript	intron_variant	-/7749
ENST00000336930	Transcript	intron_variant	-/3553
ENST00000330743	Transcript	intron_variant	-/2022
ENST00000368908	Transcript	5_prime_UTR_variant	603/2479
ENST00000370220	Transcript	downstream_gene_varian	-/5741
ENST00000370220	Transcript	5_prime_UTR_variant	3024/5741
ENST00000406869	Transcript	intron_variant	-/2991
ENST00000296509	Transcript	intron_variant	-/5468
ENST00000356661	Transcript	intron_variant	-/1708
ENST00000393900	Transcript	synonymous_variant	1242/1853
ENST00000378982	Transcript	5_prime_UTR_variant	161/2237
ENST00000285879	Transcript	intron_variant	-/4270
ENST00000247452	Transcript	synonymous_variant	1257/1991
ENST00000375068	Transcript	intron_variant	-/2189
ENST00000317446	Transcript	intron_variant	-/3658
ENST00000432680	Transcript	synonymous_variant	2368/3224
ENST00000368468	Transcript	intron_variant	-/5014
ENST00000261483	Transcript	synonymous_variant	2297/4667
ENST00000285599	Transcript	missense_variant	764/5143
ENST00000324096	Transcript	missense_variant	2745/3419
ENST00000338883	Transcript	missense_variant	574/4635
ENST00000361357	Transcript	intron_variant	-/4818
ENST00000591517	Transcript	synonymous_variant	974/2700
ENST00000347699	Transcript	intron_variant	-/3792
ENST00000446044	Transcript	intron_variant	-/2988
ENST00000251472	Transcript	intron_variant	-/4833
ENST00000251472	Transcript	egion_variant,synonymous	1050/4833
ENST00000403625	Transcript	5_prime_UTR_variant	260/10711
ENST00000537548	Transcript	missense_variant	735/2282
ENST00000265594	Transcript	intron_variant	-/2545
ENST00000397708	Transcript	intron_variant	-/6333
ENST00000434837	Transcript	synonymous_variant	1608/8898
ENST00000369393	Transcript	intron_variant	-/18413
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ENST00000453960	Transcript	synonymous_variant	1033/1685
ENST00000324817	Transcript	intron_variant	-/7984
ENST00000491289	Transcript	5_prime_UTR_variant	579/4380
ENST00000312865	Transcript	intron_variant	-/2332
ENST00000315588	Transcript	missense_variant	468/3653
ENST00000162023	Transcript	intron_variant	-/1623
ENST00000356575	Transcript	intron_variant	-/5455
ENST00000269202	Transcript	intron_variant	-/2312
ENST00000295408	Transcript	3_prime_UTR_variant	3339-3340/3954
ENST00000298717	Transcript	intron_variant	-/2015
ENST00000375258	Transcript	synonymous_variant	882/8203
ENST00000398558	Transcript	intron_variant	-/2104
ENST00000428789	Transcript	synonymous_variant	1807/4053
ENST00000428789	Transcript	intron_variant	-/4053
ENST00000428789	Transcript	synonymous_variant	1459/4053
ENST00000306010	Transcript	missense_variant	375/1759
ENST00000441493	Transcript	intron_variant	-/9445
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ENST00000317552	Transcript	intron_variant	-/6463

ENST00000355280	Transcript	intron_variant	-/4961
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ENST00000366624	Transcript	intron_variant	-/5809
ENST00000252674	Transcript	intron_variant	-/1931
ENST00000368808	Transcript	intron_variant	-/1919
ENST00000252971	Transcript	intron_variant	-/2174
ENST00000357066	Transcript	missense_variant	840/3391
ENST00000355610	Transcript	intron_variant	-/3834
ENST00000355610	Transcript	missense_variant	1693/3834
ENST00000379535	Transcript	intron_variant	-/2274
ENST00000278949	Transcript	intron_variant	-/3964
ENST00000323929	Transcript	intron_variant	-/2746
ENST00000421030	Transcript	missense_variant	1201/4329
ENST00000421030	Transcript	missense_variant	2138/4329
ENST00000421030	Transcript	missense_variant	1811/4329
ENST00000290208	Transcript	intron_variant	-/2013
ENST00000371443	Transcript	intron_variant	-/1262
ENST00000342071	Transcript	intron_variant	-/894
ENST00000053468	Transcript	intron_variant	-/2110
ENST00000423302	Transcript	e_region_variant,intron_va	-/6126
ENST00000233146	Transcript	intron_variant	-/3307
ENST00000261507	Transcript	intron_variant	-/2269
ENST00000361445	Transcript	synonymous_variant	6986/8677
ENST00000366577	Transcript	synonymous_variant	3538/10529
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ENST00000457717	Transcript	intron_variant	-/4092
ENST00000397910	Transcript	e_region_variant,intron_va	-/43816
ENST00000397910	Transcript	synonymous_variant	7803/43816
ENST00000454784	Transcript	5_prime_UTR_variant	273/19628
ENST00000454784	Transcript	intron_variant	-/19628
ENST00000441003	Transcript	synonymous_variant	7689/8637
ENST00000301012	Transcript	intron_variant	-/1823
ENST00000217939	Transcript	synonymous_variant	7508/9793
ENST00000409745	Transcript	synonymous_variant	478/2452
ENST00000545968	Transcript	intron_variant	-/4217
ENST00000396324	Transcript	missense_variant	3809/6847
ENST00000273353	Transcript	intron_variant	-/7074
ENST00000355349	Transcript	synonymous_variant	1258/6087
ENST00000355349	Transcript	intron_variant	-/6087
ENST00000355349	Transcript	intron_variant	-/6087
ENST00000216181	Transcript	intron_variant	-/7501
ENST00000360304	Transcript	synonymous_variant	3840/7834
ENST00000205890	Transcript	intron_variant	-/11863
ENST00000335473	Transcript	intron_variant	-/8565
ENST00000431794	Transcript	intron_variant	-/4054
ENST00000338257	Transcript	intron_variant	-/4303
ENST00000399231	Transcript	intron_variant	-/12225
ENST00000595618	Transcript	intron_variant	-/7623
ENST00000241651	Transcript	5_prime_UTR_variant	64/1528
ENST00000358913	Transcript	synonymous_variant	1622/6013
ENST00000278836	Transcript	intron_variant	-/5927
ENST00000472487	Transcript	intron_variant	-/7785

ENST00000361671	Transcript	intron_variant	-/2649
ENST00000371753	Transcript	synonymous_variant	971/6802
ENST00000312251	Transcript	upstream_gene_variant	-/2202
ENST00000253719	Transcript	missense_variant	1137/1548
ENST00000357814	Transcript	intron_variant	-/1875
ENST00000281513	Transcript	intron_variant	-/7281
ENST00000422280	Transcript	missense_variant	3227/4973
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ENST00000252575	Transcript	missense_variant	373/6387
ENST00000315579	Transcript	intron_variant	-/5548
ENST00000534548	Transcript	intron_variant	-/5061
ENST00000240423	Transcript	intron_variant	-/2763
ENST00000374796	Transcript	intron_variant	-/9311
ENST00000268712	Transcript	intron_variant	-/10720
ENST00000367993	Transcript	synonymous_variant	1738/2042
ENST00000397345	Transcript	intron_variant	-/26202
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ENST00000382882	Transcript	synonymous_variant	2180/3343
ENST00000366988	Transcript	synonymous_variant	567/942
ENST00000366988	Transcript	intron_variant	-/942
ENST00000334785	Transcript	missense_variant	1179/2607
ENST00000226574	Transcript	intron_variant	-/4085
ENST00000369966	Transcript	intron_variant	-/3101
ENST00000326172	Transcript	intron_variant	-/3923
ENST00000340650	Transcript	synonymous_variant	326/2134
ENST00000427025	Transcript	intron_variant	-/7500
ENST00000264187	Transcript	intron_variant	-/5864
ENST00000382041	Transcript	intron_variant	-/6496
ENST00000374399	Transcript	intron_variant	-/1711
ENST00000311946	Transcript	missense_variant	753/3274
ENST00000282516	Transcript	intron_variant	-/10435
ENST00000216121	Transcript	intron_variant	-/2237
ENST00000345716	Transcript	intron_variant	-/5238
ENST00000258829	Transcript	missense_variant	403/1261
ENST00000358741	Transcript	intron_variant	-/3046
ENST00000404025	Transcript	intron_variant	-/3581
ENST00000390649	Transcript	intron_variant	-/3888
ENST00000390649	Transcript	egion_variant,synonymous	2955/3888
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ENST00000332836	Transcript	intron_variant	-/3484
ENST00000330579	Transcript	intron_variant	-/1632
ENST00000297990	Transcript	intron_variant	-/4741
ENST00000416614	Transcript	intron_variant	-/3538
ENST00000329276	Transcript	3_prime_UTR_variant	2343/2400
ENST00000361897	Transcript	intron_variant	-/4931
ENST00000297494	Transcript	missense_variant	1251/4388
ENST00000297494	Transcript	intron_variant	-/4388
ENST00000277541	Transcript	intron_variant	-/9371
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ENST00000289547	Transcript	synonymous_variant	3944/5048
ENST00000277942	Transcript	missense_variant	433/8921
ENST00000359791	Transcript	missense_variant	851/1410

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ENST00000312521	Transcript	5_prime_UTR_variant	233/5258
ENST00000367980	Transcript	upstream_gene_variant	-/1408
ENST00000354366	Transcript	intron_variant	-/5828
ENST00000439151	Transcript	synonymous_variant	3750/12892
ENST00000264670	Transcript	intron_variant	-/3303
ENST00000422318	Transcript	intron_variant	-/1795
ENST00000301411	Transcript	downstream_gene_varian	-/999
ENST00000355451	Transcript	missense_variant	983/8256
ENST00000379161	Transcript	intron_variant	-/3492
ENST00000413272	Transcript	synonymous_variant	560/3887
ENST00000229179	Transcript	intron_variant	-/3653
ENST00000359428	Transcript	intron_variant	-/7600
ENST00000340413	Transcript	5_prime_UTR_variant	34/3874
ENST00000347635	Transcript	3_prime_UTR_variant	1929-1934/5233
ENST00000264883	Transcript	intron_variant	-/2367
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ENST00000573584	Transcript	intron_variant	-/2916
ENST00000573584	Transcript	intron_variant	-/2916
ENST00000395065	Transcript	intron_variant	-/1938
ENST00000537026	Transcript	intron_variant	-/1613
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ENST00000336868	Transcript	intron_variant	-/3036
ENST00000479950	Transcript	intron_variant	-/3330
ENST00000404537	Transcript	synonymous_variant	1941/5841
ENST00000329197	Transcript	3_prime_UTR_variant	1207/1652
ENST00000323060	Transcript	intron_variant	-/2250
ENST00000316368	Transcript	3_prime_UTR_variant	1057/1071
ENST00000323404	Transcript	missense_variant	374/948
ENST00000314721	Transcript	synonymous_variant	596/1081
ENST00000319760	Transcript	missense_variant	96/1071
ENST00000314634	Transcript	downstream_gene_varian	-/933
ENST00000380224	Transcript	synonymous_variant	707/983
ENST00000317078	Transcript	synonymous_variant	570/963
ENST00000304418	Transcript	missense_variant	933/1197
ENST00000356526	Transcript	synonymous_variant	759/942
ENST00000301532	Transcript	synonymous_variant	630/945
ENST00000313033	Transcript	5_prime_UTR_variant	28/1118
ENST00000313733	Transcript	intron_variant	-/3970
ENST00000361711	Transcript	e_region_variant,intron_va	-/2230
ENST00000361711	Transcript	synonymous_variant	1327/2230
ENST00000274276	Transcript	intron_variant	-/5539
ENST00000307050	Transcript	intron_variant	-/3042
ENST00000285848	Transcript	inframe_insertion	1434-1435/1728
ENST00000374519	Transcript	missense_variant	713/1639
ENST00000331483	Transcript	synonymous_variant	937/2603
ENST00000372858	Transcript	missense_variant	1135/2753
ENST00000320580	Transcript	intron_variant	-/4392
ENST00000289619	Transcript	intron_variant	-/741
ENST00000338448	Transcript	intron_variant	-/2725
ENST00000307534	Transcript	intron_variant	-/3367
ENST00000307534	Transcript	synonymous_variant	768/3367
ENST00000378466	Transcript	missense_variant	1653/2649
ENST00000238714	Transcript	intron_variant	-/4263

ENST00000371279	Transcript	missense_variant	167/2347
ENST00000334956	Transcript	synonymous_variant	1069/4458
ENST00000406477	Transcript	e_region_variant,intron_va	-/1569
ENST00000429538	Transcript	intron_variant	-/4084
ENST00000527246	Transcript	missense_variant	313/2499
ENST00000361849	Transcript	intron_variant	-/6957
ENST00000544246	Transcript	missense_variant	4054/6226
ENST00000333891	Transcript	intron_variant	-/20329
ENST00000367384	Transcript	missense_variant	817/1938
ENST00000359568	Transcript	intron_variant	-/10560
ENST00000311180	Transcript	missense_variant	170/8773
ENST00000435564	Transcript	upstream_gene_variant	-/4885
ENST00000334456	Transcript	synonymous_variant	2451/4315
ENST00000371447	Transcript	synonymous_variant	390/3307
ENST00000257290	Transcript	intron_variant	-/6576
ENST00000261799	Transcript	synonymous_variant	3722/5717
ENST00000261799	Transcript	e_region_variant,intron_va	-/5717
ENST00000376215	Transcript	intron_variant	-/1626
ENST00000396410	Transcript	intron_variant	-/3884
ENST00000396410	Transcript	downstream_gene_varian	-/3884
ENST00000370215	Transcript	downstream_gene_varian	-/2032
ENST00000560626	Transcript	missense_variant	5101/11715
ENST00000338302	Transcript	intron_variant	-/4970
ENST00000338302	Transcript	synonymous_variant	234/4970
ENST00000338302	Transcript	synonymous_variant	1545/4970
ENST00000244137	Transcript	missense_variant	1337/1910
ENST00000244137	Transcript	3_prime_UTR_variant	1568/1910
ENST00000381125	Transcript	intron_variant	-/2645
ENST00000381125	Transcript	intron_variant	-/2645
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ENST00000340880	Transcript	missense_variant	1662/2230
ENST00000290722	Transcript	5_prime_UTR_variant	16/1173
ENST00000359246	Transcript	e_region_variant,intron_va	-/5565
ENST00000275034	Transcript	intron_variant	-/10460
ENST00000373542	Transcript	intron_variant	-/6020
ENST00000361417	Transcript	intron_variant	-/5753
ENST00000416188	Transcript	synonymous_variant	474/5227
ENST00000369738	Transcript	3_prime_UTR_variant	950/2627
ENST00000370812	Transcript	intron_variant	-/4596
ENST00000357637	Transcript	synonymous_variant	2426/5501
ENST00000592983	Transcript	missense_variant	956/2333
ENST00000447110	Transcript	intron_variant	-/4488
ENST00000264380	Transcript	intron_variant	-/9901
ENST00000360612	Transcript	synonymous_variant	567/2369
ENST00000332271	Transcript	intron_variant	-/3504
ENST00000361478	Transcript	synonymous_variant	1548/2755
ENST00000529079	Transcript	ot_exon_variant,non_codi	161/574
ENST00000371117	Transcript	intron_variant	-/16282
ENST00000070846	Transcript	intron_variant	-/4241
ENST00000274793	Transcript	intron_variant	-/1882
ENST00000220809	Transcript	intron_variant	-/2706
ENST00000327757	Transcript	intron_variant	-/5107
ENST00000371380	Transcript	intron_variant	-/12024
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ENST00000371380	Transcript	missense_variant	5565/12024
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ENST00000322810	Transcript	missense_variant	4546/15249
ENST00000322810	Transcript	synonymous_variant	959/15249
ENST00000322810	Transcript	3_prime_UTR_variant	14235/15249
ENST00000322810	Transcript	synonymous_variant	8834/15249
ENST00000322810	Transcript	synonymous_variant	14042/15249
ENST00000322810	Transcript	synonymous_variant	11708/15249
ENST00000537245	Transcript	intron_variant	-/3381
ENST00000329153	Transcript	intron_variant	-/6604
ENST00000329153	Transcript	e_region_variant,intron_va	-/6604
ENST00000329153	Transcript	intron_variant	-/6604
ENST00000379410	Transcript	intron_variant	-/2404
ENST00000334770	Transcript	intron_variant	-/2106
ENST00000315392	Transcript	intron_variant	-/6252
ENST00000449103	Transcript	intron_variant	-/6383
ENST00000369239	Transcript	intron_variant	-/5112
ENST00000394571	Transcript	ıse_variant,splice_region_	1469/2478
ENST00000216180	Transcript	intron_variant	-/2805
ENST00000414982	Transcript	synonymous_variant	2316/4522
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ENST00000301788	Transcript	intron_variant	-/827
ENST00000377603	Transcript	intron_variant	-/2416
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ENST00000379747	Transcript	intron_variant	-/3373
ENST00000465342	Transcript	missense_variant	1702/5357
ENST00000287820	Transcript	missense_variant	155/1850
ENST00000287820	Transcript	synonymous_variant	1552/1850
ENST00000412327	Transcript	intron_variant	-/2709
ENST00000308249	Transcript	inframe_insertion	228-229/2988
ENST00000367999	Transcript	intron_variant	-/1740
ENST00000330261	Transcript	intron_variant	-/782
ENST00000455566	Transcript	3_prime_UTR_variant	1284/5133
ENST00000264977	Transcript	intron_variant	-/6795
ENST00000218224	Transcript	e_region_variant,intron_va	-/1110
ENST00000264808	Transcript	intron_variant	-/5330
ENST00000339711	Transcript	intron_variant	-/4095
ENST00000379341	Transcript	intron_variant	-/1005
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ENST00000288368	Transcript	intron_variant	-/10750
ENST00000311862	Transcript	intron_variant	-/1424
ENST00000314970	Transcript	5_prime_UTR_variant	387/2289
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ENST00000394729	Transcript	intron_variant	-/2810
ENST00000378567	Transcript	intron_variant	-/2326
ENST00000324366	Transcript	intron_variant	-/2531
ENST00000419421	Transcript	missense_variant	650/1392
ENST00000403581	Transcript	intron_variant	-/2279
ENST00000352766	Transcript	intron_variant	-/2043
ENST00000268281	Transcript	intron_variant	-/2840

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ENST00000406070	Transcript	intron_variant	-/2025
ENST00000270077	Transcript	intron_variant	-/1705
ENST00000356126	Transcript	e_region_variant,intron_va	-/4406
ENST00000331573	Transcript	intron_variant	-/2154
ENST00000317615	Transcript	5_prime_UTR_variant	643/1686
ENST00000407693	Transcript	intron_variant	-/1407
ENST00000254667	Transcript	intron_variant	-/5331
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ENST00000474889	Transcript	intron_variant	-/9021
ENST00000368213	Transcript	intron_variant	-/5816
ENST00000389418	Transcript	synonymous_variant	2425/4706
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ENST00000302000	Transcript	intron_variant	-/8488
ENST00000240651	Transcript	5_prime_UTR_variant	11/3169
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ENST00000243662	Transcript	5_prime_UTR_variant	73/1465
ENST00000276066	Transcript	intron_variant	-/1071
ENST00000262477	Transcript	intron_variant	-/5387
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ENST00000487270	Transcript	intron_variant	-/2596
ENST00000399583	Transcript	synonymous_variant	2363/3689
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ENST00000515799	Transcript	intron_variant	-/3486
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ENST00000449771	Transcript	intron_variant	-/3370
ENST00000298854	Transcript	intron_variant	-/1671
ENST00000357043	Transcript	missense_variant	119/1864
ENST00000377604	Transcript	synonymous_variant	3121/3747
ENST00000267229	Transcript	intron_variant	-/3624
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ENST00000339877	Transcript	intron_variant	-/1341
ENST00000377966	Transcript	synonymous_variant	2126/4888
ENST00000221452	Transcript	intron_variant	-/2294
ENST00000258062	Transcript	intron_variant	-/3161
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ENST00000354373	Transcript	5_prime_UTR_variant	195/1496
ENST00000296292	Transcript	synonymous_variant	1685/5108
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ENST00000334133	Transcript	intron_variant	-/2982
ENST00000393423	Transcript	5_prime_UTR_variant	47/2278
ENST00000366565	Transcript	e_region_variant,intron_va	-/2494
ENST00000538017	Transcript	5_prime_UTR_variant	125/1394
ENST00000332512	Transcript	synonymous_variant	2396/3889
ENST00000283632	Transcript	intron_variant	-/6301
ENST00000283632	Transcript	5_prime_UTR_variant	488/6301
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ENST00000367559	Transcript	synonymous_variant	377/4238

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ENST00000368508	Transcript	intron_variant	-/7435
ENST00000434291	Transcript	intron_variant	-/1818
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ENST00000472454	Transcript	downstream_gene_varian	-/1615
ENST00000518559	Transcript	riant,non_coding_transcri	-/4427
ENST00000428747	Transcript	upstream_gene_variant	-/3105
ENST00000005386	Transcript	intron_variant	-/2332
ENST00000331302	Transcript	intron_variant	-/2606
ENST00000222247	Transcript	intron_variant	-/665
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ENST00000316084	Transcript	synonymous_variant	597/1526
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ENST00000306801	Transcript	intron_variant	-/6408
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ENST00000340648	Transcript	intron_variant	-/5088
ENST00000340648	Transcript	synonymous_variant	720/5088
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ENST00000377819	Transcript	missense_variant	1566/4937
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ENST00000360565	Transcript	intron_variant	-/4306
ENST00000302631	Transcript	synonymous_variant	486/1446
ENST00000266214	Transcript	intron_variant	-/3278
ENST00000349847	Transcript	intron_variant	-/2386
ENST00000297029	Transcript	missense_variant	283/3137
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ENST00000369020	Transcript	downstream_gene_varian	-/1491
ENST00000283254	Transcript	intron_variant	-/9091
ENST00000409672	Transcript	missense_variant	3795/9768

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ENST00000350697	Transcript	intron_variant	-/1425
ENST00000402034	Transcript	missense_variant	58/3392
ENST00000308284	Transcript	intron_variant	-/3985
ENST00000336714	Transcript	missense_variant	1899/3411
ENST00000280551	Transcript	intron_variant	-/4030
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ENST00000370345	Transcript	intron_variant	-/4612
ENST00000375807	Transcript	intron_variant	-/3454
ENST00000269389	Transcript	missense_variant	1081/2235
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ENST00000263686	Transcript	intron_variant	-/3142
ENST00000265362	Transcript	intron_variant	-/8225
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ENST00000357949	Transcript	intron_variant	-/2114
ENST00000267197	Transcript	intron_variant	-/8195
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ENST00000402198	Transcript	intron_variant	-/6827
ENST00000248933	Transcript	synonymous_variant	206/3248
ENST00000302516	Transcript	intron_variant	-/6969
ENST00000367569	Transcript	5_prime_UTR_variant	70/737
ENST00000373202	Transcript	intron_variant	-/5745
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ENST00000293441	Transcript	intron_variant	-/6643
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ENST00000380913	Transcript	missense_variant	3046/7447
ENST00000291707	Transcript	intron_variant	-/2121
ENST00000270162	Transcript	intron_variant	-/4712
ENST00000290399	Transcript	intron_variant	-/4442
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ENST00000368043	Transcript	intron_variant	-/2689
ENST00000273861	Transcript	synonymous_variant	315/1790
ENST00000273905	Transcript	missense_variant	488/1502
ENST00000264930	Transcript	intron_variant	-/5272
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ENST00000587091	Transcript	missense_variant	274/4161
ENST00000221742	Transcript	intron_variant	-/1719
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ENST00000245407	Transcript	synonymous_variant	506/3237
ENST00000353963	Transcript	intron_variant	-/2303
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ENST00000366618	Transcript	intron_variant	-/2891
ENST00000308074	Transcript	intron_variant	-/2696
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ENST00000570101	Transcript	intron_variant	-/4549
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ENST00000485713	Transcript	intron_variant	-/4925
ENST00000222248	Transcript	intron_variant	-/3576
ENST00000371900	Transcript	intron_variant	-/4521
ENST00000335875	Transcript	intron_variant	-/2938
ENST00000401766	Transcript	intron_variant	-/6543
ENST00000360584	Transcript	downstream_gene_varian	-/2330
ENST00000316902	Transcript	intron_variant	-/4216
ENST00000316902	Transcript	synonymous_variant	1872/4216
ENST00000328306	Transcript	synonymous_variant	170/3838
ENST00000310926	Transcript	intron_variant	-/4223
ENST00000371122	Transcript	intron_variant	-/4099
ENST00000283131	Transcript	intron_variant	-/7923
ENST00000357450	Transcript	intron_variant	-/4201
ENST00000361956	Transcript	synonymous_variant	389/2040
ENST00000358743	Transcript	intron_variant	-/3198
ENST00000388985	Transcript	e_region_variant,intron_v	-/1287
ENST00000371247	Transcript	intron_variant	-/7354
ENST00000507866	Transcript	e_region_variant,intron_v	-/6152
ENST00000336338	Transcript	synonymous_variant	633/6924
ENST00000336338	Transcript	synonymous_variant	1458/6924
ENST00000370498	Transcript	synonymous_variant	994/1377
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ENST00000312358	Transcript	intron_variant	-/10782
ENST00000312358	Transcript	missense_variant	7298/10782
ENST00000301244	Transcript	missense_variant	1033/1802
ENST00000373109	Transcript	synonymous_variant	457/5445
ENST00000320955	Transcript	intron_variant	-/11722
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ENST00000262518	Transcript	missense_variant	4988/10474
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ENST00000394070	Transcript	intron_variant	-/6691
ENST00000265404	Transcript	synonymous_variant	463/1511
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ENST00000392320	Transcript	intron_variant	-/2822
ENST00000293328	Transcript	intron_variant	-/5103

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ENST00000392359	Transcript	5_prime_UTR_variant	39/805
ENST00000275764	Transcript	downstream_gene_varian	-/993
ENST00000447404	Transcript	intron_variant	-/6290
ENST00000369795	Transcript	intron_variant	-/3265
ENST00000249344	Transcript	intron_variant	-/5115
ENST00000321680	Transcript	intron_variant	-/3456
ENST00000075503	Transcript	missense_variant	1131/2995
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ENST00000362032	Transcript	3_prime_UTR_variant	1153/4179
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ENST00000318950	Transcript	intron_variant	-/4882
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ENST00000358025	Transcript	synonymous_variant	629/21875
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ENST00000336292	Transcript	missense_variant	1817/7322
ENST00000307142	Transcript	missense_variant	657/7295
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ENST00000377636	Transcript	intron_variant	-/6364
ENST00000446818	Transcript	missense_variant	2416/3124
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ENST00000335385	Transcript	intron_variant	-/1548
ENST00000372780	Transcript	missense_variant	422/1100
ENST00000418390	Transcript	missense_variant	1758/5154
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ENST00000215838	Transcript	3_prime_UTR_variant	1860/2535
ENST00000409874	Transcript	synonymous_variant	867/4782
ENST00000422452	Transcript	intron_variant	-/12891
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ENST00000603068	Transcript	intron_variant	-/2894
ENST00000409262	Transcript	intron_variant	-/10983
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ENST00000367166	Transcript	synonymous_variant	689/1424
ENST00000310125	Transcript	missense_variant	516/1680
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ENST00000212355	Transcript	intron_variant	-/6416

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ENST00000423059	Transcript	synonymous_variant	1986/10663
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ENST00000286827	Transcript	intron_variant	-/7200
ENST00000461783	Transcript	intron_variant	-/6981
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ENST00000561311	Transcript	intron_variant	-/11880
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ENST00000288025	Transcript	missense_variant	72/938
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ENST00000275767	Transcript	missense_variant	243/1997
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ENST00000341871	Transcript	synonymous_variant	838/3106
ENST00000334830	Transcript	3_prime_UTR_variant	2019/3054
ENST00000237289	Transcript	intron_variant	-/4432
ENST00000223795	Transcript	synonymous_variant	390/1906
ENST00000430969	Transcript	synonymous_variant	5167/10562
ENST00000254051	Transcript	intron_variant	-/4067
ENST00000254051	Transcript	missense_variant	1652/4067
ENST00000382044	Transcript	missense_variant	1202/6231
ENST00000382044	Transcript	missense_variant	3549/6231
ENST00000382044	Transcript	intron_variant	-/6231
ENST00000334295	Transcript	synonymous_variant	536/4030
ENST00000538887	Transcript	intron_variant	-/1542
ENST00000360578	Transcript	intron_variant	-/5116
ENST00000360578	Transcript	synonymous_variant	719/5116
ENST00000345063	Transcript	e_region_variant,intron_va	-/5479
ENST00000006275	Transcript	intron_variant	-/805
ENST00000330149	Transcript	intron_variant	-/3242
ENST00000330149	Transcript	intron_variant	-/3242
ENST00000372922	Transcript	missense_variant	3063/7286
ENST00000330912	Transcript	intron_variant	-/2262
ENST00000376694	Transcript	intron_variant	-/2214
ENST00000377199	Transcript	intron_variant	-/2967
ENST00000334634	Transcript	intron_variant	-/3061
ENST00000291416	Transcript	intron_variant	-/3437
ENST00000366653	Transcript	missense_variant	2035/3936
ENST00000298355	Transcript	e_region_variant,intron_va	-/5284

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ENST00000344204	Transcript	synonymous_variant	4422/11100
ENST00000200457	Transcript	missense_variant	412/1942
ENST00000592062	Transcript	synonymous_variant	2125/2579
ENST00000372936	Transcript	intron_variant	-/3327
ENST00000252015	Transcript	intron_variant	-/3226
ENST00000542188	Transcript	intron_variant	-/5715
ENST00000155858	Transcript	missense_variant	1012/3929
ENST00000313478	Transcript	intron_variant	-/7263
ENST00000418703	Transcript	intron_variant	-/3247
ENST00000298552	Transcript	missense_variant	1187/8604
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ENST00000219476	Transcript	intron_variant	-/6156
ENST00000372003	Transcript	intron_variant	-/1615
ENST00000373020	Transcript	missense_variant	434/2206
ENST00000378482	Transcript	intron_variant	-/1909
ENST00000399635	Transcript	synonymous_variant	1618/1814
ENST00000259750	Transcript	intron_variant	-/6932
ENST00000259750	Transcript	missense_variant	1951/6932
ENST00000310715	Transcript	intron_variant	-/3703
ENST00000261647	Transcript	intron_variant	-/3002
ENST00000397906	Transcript	missense_variant	320/11793
ENST00000368586	Transcript	intron_variant	-/8278
ENST00000368586	Transcript	5_prime_UTR_variant	77/8278
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ENST00000368586	Transcript	synonymous_variant	2975/8278
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ENST00000266254	Transcript	egion_variant,synonymous	991/1645
ENST00000393382	Transcript	synonymous_variant	745/3551
ENST00000305253	Transcript	intron_variant	-/6420
ENST00000283645	Transcript	3_prime_UTR_variant	3282/3849
ENST00000248846	Transcript	intron_variant	-/5612
ENST00000367097	Transcript	synonymous_variant	1954/11123
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ENST00000548315	Transcript	intron_variant	-/1170
ENST00000395681	Transcript	intron_variant	-/1604
ENST00000319294	Transcript	intron_variant	-/2504
ENST00000284273	Transcript	intron_variant	-/6912
ENST00000348165	Transcript	synonymous_variant	1863/5229
ENST00000375254	Transcript	3_prime_UTR_variant	15610/15906
ENST00000399598	Transcript	intron_variant	-/5068
ENST00000314032	Transcript	intron_variant	-/2623
ENST00000592666	Transcript	ot_exon_variant,non_codi	2487/4308
ENST00000276893	Transcript	intron_variant	-/3452
ENST00000301831	Transcript	e_region_variant,intron_va	-/4613
ENST00000408989	Transcript	intron_variant	-/5262
ENST00000408989	Transcript	missense_variant	4006/5262
ENST00000408989	Transcript	e_region_variant,intron_va	-/5262
ENST00000268876	Transcript	intron_variant	-/5679
ENST00000389221	Transcript	intron_variant intergenic_variant	-/5078
ENST00000326010	Transcript	synonymous_variant	1301/2290
ENST00000373383	Transcript	intron_variant	-/2186
ENST00000307340	Transcript	missense_variant	7262/18883
ENST00000252597	Transcript	synonymous_variant	1782/3335

ENST00000219473	Transcript	›p_gained,frameshift_vari	1608-1609/3009
ENST00000218348	Transcript	synonymous_variant	600/3289
ENST00000215794	Transcript	intron_variant	-/2129
ENST00000315480	Transcript	intron_variant	-/4458
ENST00000261497	Transcript	3_prime_UTR_variant	1853-1854/5216
ENST00000398571	Transcript	intron_variant	-/11357
ENST00000296792	Transcript	intron_variant	-/3687
ENST00000261637	Transcript	intron_variant	-/9025
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ENST00000331397	Transcript	intron_variant	-/6529
ENST00000544301	Transcript	intron_variant	-/2128
ENST00000262178	Transcript	missense_variant	1435/3944
ENST00000435505	Transcript	intron_variant	-/2446
ENST00000554659	Transcript	synonymous_variant	1011/5351
ENST00000423497	Transcript	downstream_gene_varian	-/1219
ENST00000423497	Transcript	intron_variant	-/1219
ENST00000297873	Transcript	missense_variant	696/941
ENST00000325239	Transcript	intron_variant	-/9962
ENST00000263461	Transcript	intron_variant	-/4732
ENST00000263461	Transcript	synonymous_variant	1080/4732
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ENST00000263461	Transcript	synonymous_variant	3204/4732
ENST00000263461	Transcript	intron_variant	-/4732
ENST00000280190	Transcript	intron_variant	-/4705
ENST00000414423	Transcript	intron_variant	-/6872
ENST00000407426	Transcript	intron_variant	-/3533
ENST00000302313	Transcript	intron_variant	-/3707
ENST00000407559	Transcript	intron_variant	-/3769
ENST00000303868	Transcript	inframe_deletion	7010-7027/8847
ENST00000354475	Transcript	intron_variant	-/4588
ENST00000288828	Transcript	intron_variant	-/4476
ENST00000315939	Transcript	missense_variant	1064/10452
ENST00000369684	Transcript	synonymous_variant	1655/3818
ENST00000343737	Transcript	missense_variant	160/2112
ENST00000380773	Transcript	intron_variant	-/2670
ENST00000315436	Transcript	intron_variant	-/2646
ENST00000521089	Transcript	intron_variant	-/3562
ENST00000359154	Transcript	synonymous_variant	2595/4515
ENST00000358368	Transcript	intron_variant	-/2667
ENST00000373884	Transcript	3_prime_UTR_variant	1803/2692
ENST00000502935	Transcript	intron_variant	-/2539
ENST00000357137	Transcript	intron_variant	-/7988
ENST00000265351	Transcript	egion_variant,synonymous	2890/5360
ENST00000262887	Transcript	synonymous_variant	1166/2802
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ENST00000007699	Transcript	intron_variant	-/1590
ENST00000368339	Transcript	intron_variant	-/2874
ENST00000368339	Transcript	synonymous_variant	176/2874
ENST00000325144	Transcript	synonymous_variant	1437/3090
ENST00000237275	Transcript	intron_variant	-/992
ENST00000409806	Transcript	intron_variant	-/1930
ENST00000409806	Transcript	intron_variant	-/1930
ENST00000409806	Transcript	5_prime_UTR_variant	307/1930
ENST00000262577	Transcript	intron_variant	-/3280
ENST00000352645	Transcript	intron_variant	-/5909

ENST00000537356	Transcript	synonymous_variant	2035/2907
ENST00000393760	Transcript	missense_variant	570/1959
ENST00000369405	Transcript	synonymous_variant	1042/2170
ENST00000564466	Transcript	intron_variant	-/1488
ENST00000316495	Transcript	intron_variant	-/860
ENST00000419474	Transcript	missense_variant	4990/9180
ENST00000407775	Transcript	intron_variant	-/4700
ENST00000355341	Transcript	3_prime_UTR_variant	1978/2260
ENST00000394170	Transcript	intron_variant	-/4344
ENST00000231749	Transcript	intron_variant	-/2896
ENST00000231749	Transcript	intron_variant	-/2896
ENST00000535861	Transcript	intron_variant	-/4421
ENST00000370251	Transcript	egion_variant,synonymous	1146/6320
ENST00000391705	Transcript	missense_variant	646/4313
ENST00000536459	Transcript	intron_variant	-/3795
ENST00000410046	Transcript	intron_variant	-/3379
ENST00000393927	Transcript	intron_variant	-/1400
ENST00000337995	Transcript	intron_variant	-/3535
ENST00000594154	Transcript	synonymous_variant	1569/4513
ENST00000357901	Transcript	intron_variant	-/4356
ENST00000339249	Transcript	intron_variant	-/3773
ENST00000392288	Transcript	intron_variant	-/5023
ENST00000450537	Transcript	intron_variant	-/5926
ENST00000299927	Transcript	missense_variant	2799/7861
ENST00000431526	Transcript	missense_variant	1373/3195
ENST00000270649	Transcript	missense_variant	748/4818
ENST00000601440	Transcript	5_prime_UTR_variant	59-60/5963
ENST00000397121	Transcript	missense_variant	398/2944
ENST00000421812	Transcript	synonymous_variant	405/5041
ENST00000356929	Transcript	missense_variant	535/4004
ENST00000422325	Transcript	intron_variant	-/3068
ENST00000370766	Transcript	synonymous_variant	4144/5592
ENST00000395216	Transcript	missense_variant	738/3282
ENST00000357666	Transcript	synonymous_variant	1552/2697
ENST00000442396	Transcript	synonymous_variant	2613/2987
ENST00000278853	Transcript	missense_variant	473/1954
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ENST00000254323	Transcript	intron_variant	-/4339
ENST00000381638	Transcript	intron_variant	-/11456

CDS_position	Protein_position	Amino_acids	Codons	
-/1206	-/401			
-/681	-/226			
-/2781	-/926			
783/4632	261/1543	Y	taT/taC	
-/5115	-/1704			
-/4854	-/1617			
-/4854	-/1617			
-/4875	-/1624			
4038/4596	1346/1531	S	tcT/tcA	
-/4512	-/1503			
3819/4746	1273/1581	R	agG/agA	
-/1230	-/409			
-/2580	-/859			
340/756	114/251	A/T	Gcc/Acc	
-/1248	-/415			
-/1278	-/425			
-/1299	-/432			
-/1587	-/528			
-/795	-/264			
-/1272	-/423			
-/1443	-/480			
-/2175	-/724			
-/1731	-/576			
-/1743	-/580			
-/1539	-/512			
2305/2592	769/863	P/S	Ccc/Tcc	
-/2475	-/824			
2818/3681	940/1226	L/M	Ctg/Atg	
-/3636	-/1211			
-/5733	-/1910			TMP_
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-/3354	-/1117			
-/5289	-/1762			
-/981	-/326			
-/1044	-/347			
621/2457	207/818	K	aaA/aaG	
-/3657	-/1218			
-/3936	-/1311			
-/2736	-/911			
-/2763	-/920			
573/1080	191/359	L	ctC/ctT	
-/3591	-/1196			
-/309	-/102			
48/717	16/238	S	tcT/tcC	
-/2364	-/787			
-/2364	-/787			
286/1155	96/384	V/I	Gtc/Atc	
588/1638	196/545	S	tcC/tcT	
-/1638	-/545			
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-/11724	-/3907			
-/951	-/316			
-/1830	-/609			

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4341/5835	1447/1944	P	ccG/ccA
-/5694	-/1897		
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-/2817	-/938		
3025/3036	1009/1011	F/L	Ttt/Ctt
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804/3006	268/1001	Q	caG/caA
-/3231	-/1076		
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-/3414	-/1137		
1066/3414	356/1137	G/R	Gga/Aga
-/2001	-/666		
-/807	-/268		
83/888	28/295	L/R	cTg/cGg
-/888	-/295		
-/972	-/323		
1918/2973	640/990	V/F	Gtt/Ttt
-/546	-/181		
2050/2361	684/786	M/V	Atg/Gtg
-/1554	-/517		
-/1644	-/547		
1806/2961	602/986	E	gaG/gaA
-/4689	-/1562		
-/2130	-/709		
-/2961	-/986		
1099/1677	367/558	L/V	Ttg/Gtg
543/2412	181/803	D	gaT/gaC
-/1239	-/412		
492/540	164/179	G	ggG/ggA
-/1980	-/659		
-/6873	-/2290		
250/6873	84/2290	R/G	Agg/Ggg
-/6873	-/2290		
6009/6873	2003/2290	H	caC/caT
-/1293	-/430		
-/1224	-/407		
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585/1530	195/509	W/C	tgG/tgT
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-/1764	-/587		
-/1281	-/426		

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-/1377	-/458			
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-/3405	-/1134			rs
1005/3543	335/1180	A	gcC/gcT	
2259/3063	753/1020	A	gcC/gcT	
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-/2841	-/946			
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-/2376	-/791			
-/3294	-/1097			
-/987	-/328			
-/1002	-/333			
1564/3039	522/1012	I/L	Atc/Ctc	
-/2589	-/862			
983/1119	328/372	R/H	cGc/cAc	
-/1659	-/552			
-/3564	-/1187			
1157/2133	386/710	R/Q	cGg/cAg	
-/1338	-/445			
-/609	-/202			
-/5136	-/1711			
-/1815	-/604			
2764/2928	922/975			
-/1371	-/456			
308/1179	103/392	N/S	aAt/aGt	
-/2985	-/994			
-/1377	-/458			
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-/5655	-/1884			
-/5655	-/1884			
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-/1794	-/597			
864/6963	288/2320	Y	taC/taT	
-/1344	-/447			
-/1158	-/385			
-/1158	-/385			
-/1521	-/506			
992/1521	331/506	G/D	gGc/gAc	
-/1137	-/378			
-/516	-/171			
993/1608	331/535	T	acG/acT	
-/5574	-/1857			

-/402	-/133		
4272/4308	1424/1435	D	gaT/gaC
-/2100	-/699		
-/1014	-/337		
164/618	55/205	Q/R	cAg/cGg
-/9291	-/3096		
549-550/738	183-184/245	TM/TX	acTAtg/actg
-/903	-/300		
-/573	-/190		
-/1944	-/647		
1112/1362	371/453	H/R	cAc/cGc
-/321	-/106		
393/957	131/318	D/E	gaT/gaA
1734/2856	578/951	T	acA/acG
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-/2187	-/728		
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645/918	215/305	F	ttC/ttT
2446/6663	816/2220	L/F	Ctt/Ttt
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-/1158	-/385		
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-/972	-/323		
849/3831	283/1276	C	tgC/tgT
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-/3480	-/1159		
27/456	9/151	L	ctC/ctT
1293/1653	431/550	Q	caG/caA
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733/1500	245/499	V/M	Gtg/Atg

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-/2895	-/964		
-/870	-/289		
570/2619	190/872	K	aaA/aaG
2024/3342	675/1113	E/V	gAg/gTg
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-/4527	-/1508		
156/2256	52/751	C	tgC/tgT
-/1425	-/474		
-/1959	-/652		
-/297	-/98		
-/1125	-/374		
2390/4338	797/1445	N/S	aAt/aGt
608/816	203/271	H/X	cAc/cc
-/1113	-/370		
-/900	-/299		
776/1533	259/510	K/T	aAa/aCa
-/1200	-/399		
515-541/723	172-181/240	DPPAASALPA/A	AGCAGCCTCTGCCCTC
-/1794	-/597		
-/4656	-/1551		
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1574/2511	525/836	Q/R	cAa/cGa
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-/918	-/305		
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1227/1740	409/579	P	ccA/ccG
-/3093	-/1030		
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-/759	-/252		
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755/4332	252/1443	R/H	cGt/cAt
-/1272	-/423		
552/1737	184/578	R	agA/agG
-/2271	-/756		
83/267	28/88	R/L	cGa/cTa
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404/1794	135/597	S/N	aGt/aAt
-/2466	-/821		
-/1788	-/595		
-/1872	-/623		
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-/498	-/165		
39/2694	13/897	A	gcG/gcC
-/1995	-/664		

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545/1173	182/390	A/V	gCg/gTg
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-/1131	-/376		
-/3393	-/1130		
633/684	211/227	S	agC/agT
-/6210	-/2069		
366/660	122/219	H/Q	caC/caG
-/1260	-/419		
-/2610	-/869		
-/2064	-/687		
-/687	-/228		
-/660	-/219		
-/744	-/247		
309/762	103/253		
-/4317	-/1438		
-/2118	-/705		
-/3105	-/1034		
-/2856	-/951		
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-/5238	-/1745		
-/3087	-/1028		
-/9534	-/3177		
408/816	136/271	L	ctC/ctG
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-/3198	-/1065		
-/1686	-/561		
-/2190	-/729		
3154/3279	1052/1092	I/V	Att/Gtt
-/3858	-/1285		
-/1317	-/438		
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777/807	259/268	A	gcC/gcA
-/2547	-/848		
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-/3069	-/1022		
-/4094	-/1364		
-/237	-/78		
-/1176	-/391		

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-/2103	-/700		
4488/7474	1496/2491	P	ccG/ccA
-/2688	-/895		
423/2205	141/734	V	gtG/gtA
1911/10872	637/3623	L	ctC/ctT
-/2295	-/764		
4715/5349	1572/1782	L/P	cTg/cCg
-/4551	-/1516		
2932/4551	978/1516	G/R	Ggg/Agg
-/2727	-/908		
2403/2727	801/908	A	gcG/gcA
1327/2685	443/894	H/Y	Cac/Tac
-/1248	-/415		
-/780	-/259		
-/831	-/276		
-/1485	-/494		
-/1485	-/494		
-/1512	-/503		
38/1575	13/524	P/L	cCg/cTg
-/1530	-/509		
63/3129	21/1042	P	ccG/ccA
-/1506	-/501		
-/1635	-/544		
-/1803	-/600		
234/1803	78/600	H	caT/caC
-/1803	-/600		
-/4344	-/1447		
1017/1431	339/476	V	gtC/gtT
-/4110	-/1369		
348/570	116/189	V	gtT/gtC
-/2913	-/970		
-/2913	-/970		
-/1860	-/619		
-/3030	-/1009		
670/3864	224/1287	E/Q	Gag/Cag
-/1590	-/529		
-/1653	-/550		
-/2415	-/804		
-/909	-/302		
-/2232	-/743		
-/3474	-/1157		
-/3663	-/1220		
-/3663	-/1220		
-/3663	-/1220		
-/3819	-/1272		
-/4731	-/1576		
-/3165	-/1054		
-/2037	-/678		
-/2268	-/755		
-/675	-/224		
-/2928	-/975		
-/2454	-/817		r
-/5760	-/1919		
-/1152	-/383		

-/1431	-/476		
-/3441	-/1146		
-/13572	-/4523		
-/9279	-/3092		
-/13548	-/4515		
-/13548	-/4515		
-/13548	-/4515		
-/13548	-/4515		
-/13548	-/4515		
-/13458	-/4485		
-/13473	-/4490		
-/13461	-/4486		
-/843	-/280		
-/1086	-/361		
-/4734	-/1577		
-/5493	-/1830		
-/6093	-/2030		
3438/4614	1146/1537	P	ccG/ccA
1051/1236	351/411	E/Q	Gag/Cag
-/1245	-/414		
-/858	-/285		
-/2277	-/758		
-/1050	-/349		
-/2874	-/957		
-/2874	-/957		
-/2874	-/957		
-/6342	-/2113		
-/3000	-/999		
3123/3180	1041/1059	P	ccC/ccA
30/3180	10/1059	C	tgC/tgT
-/8616	-/2871		
-/15516	-/5171		
-/507	-/168		
-/1056	-/351		
-/897	-/298		
279/1869	93/622	R	cgG/cgA
-/567	-/188		
430/1146	144/381	S/A	Tcc/Gcc
-/1938	-/645		
-/12945	-/4314		
-/1086	-/361		
77/693	26/230	R/L	cGc/cTc
1022/2313	341/770	T/I	aCc/aTc
-/2328	-/775		
-/2745	-/914		
-/2715	-/904		
-/2799	-/932		
-/639	-/212		
-/1599	-/532		
-/4236	-/1411		
-/1392	-/463		
-/525	-/174		
-/2922	-/973		
-/1473	-/490		
-/2196	-/731		

372/2502	124/833	R	cgG/cgA
-/3363	-/1120		
-/2919	-/972		
99/1419	33/472	H	caC/caT
1509/1992	503/663	T	acG/acA
417/2463	139/820	I	atC/atT
1509/2463	503/820	I	atC/atA
1218/2463	406/820	F	ttT/ttC
-/2175	-/724		
-/891	-/296		
1034/2982	345/993	S/T	aGt/aCt
-/894	-/297		
-/894	-/297		
1723/2505	575/834	S/P	Tct/Cct
-/2505	-/834		
-/2505	-/834		
489/1179	163/392	A	gcG/gcA
-/1977	-/658		
-/1932	-/643		
-/1569	-/522		
-/1287	-/428		
-/9372	-/3123		
-/3066	-/1021		
416/1368	139/455	H/R	cAt/cGt
1236/1668	412/555	S	agC/agT
-/2934	-/977		
-/6363	-/2120		
1768/2661	590/886	G/R	Ggg/Agg
512/1002	171/333	T/I	aCa/aTa
734/1041	245/346	T/M	aCg/aTg
6/765	2/254	A	gcG/gcA
-/2433	-/810		
-/2418	-/805		
-/2418	-/805		
-/6102	-/2033		
3150/6102	1050/2033	S	tcG/tcA
-/1866	-/621		
1765/2541	589/846	E/K	Gag/Aag
-/2685	-/894		
-/1761	-/586		
3780/7056	1260/2351	D/E	gaC/gaG
-/7056	-/2351		
1120/1386	374/461	V/I	Gtt/Att
-/1599	-/532		
-/1335	-/444		
-/1338	-/445		
-/1260	-/419		
716/1074	239/357	R/H	cGt/cAt
-/588	-/195		
-/588	-/195		
-/342	-/113		
-/342	-/113		
-/4221	-/1406		
348/489	116/162	L	ctC/ctT
-/708	-/235		

-/1281	-/426			
-/3183	-/1060			
-/7056	-/2351			
-/1110	-/369			
-/2007	-/668			
-/3963	-/1320			
-/1554	-/517			
3000/3207	1000/1068	A	gcT/gcC	
560/1359	187/452	A/V	gCt/gTt	
-/4368	-/1455			
-/1611	-/536			
-/1611	-/536			rs38
387/1611	129/536	P	ccA/ccC	
-/1548	-/515			
-/3165	-/1054			
-/3165	-/1054			
3651/7536	1217/2511	G	ggC/ggT	
-/7536	-/2511			
-/7536	-/2511			
-/7536	-/2511			
464/3696	155/1231	P/L	cCg/cTg	
5896/8430	1966/2809	H/D	Cac/Gac	
-/3138	-/1045			
-/2871	-/956			
-/2871	-/956			
-/837	-/278			
-/1395	-/464			
-/1239	-/412			
-/1734	-/577			
1152/2676	384/891	A	gcG/gcA	
1162/2409	388/802	G/R	Ggg/Agg	
-/1362	-/453			
-/4320	-/1439			
2952/4320	984/1439	N	aaC/aaT	
-/4320	-/1439			
-/2280	-/759			
-/1785	-/594			
594/984	198/327	L	ctG/ctA	
-/669	-/222			
1286/7944	429/2647	T/M	aCg/aTg	
-/7902	-/2633			
-/4092	-/1363			
-/5169	-/1722			
-/5169	-/1722			
441/1599	147/532	S	tcC/tcT	
172-177/3054	58-59/1017	TT/-	ACCACC/-	
-/3054	-/1017			
-/5685	-/1894			
2091/5685	697/1894	A	gcC/gcG	
1284/1335	428/444	Y	taT/taC	
-/2043	-/680			
-/1764	-/587			
1947/12039	649/4012	H	caT/caC	
-/12039	-/4012			

8439/12039	2813/4012	D	gaC/gaT
-/12039	-/4012		
-/12039	-/4012		
3987/6420	1329/2139	I	atC/atA
-/3120	-/1039		
-/1746	-/581		
-/2544	-/847		
1587/1719	529/572	H	caC/caT
-/1098	-/365		
-/1080	-/359		
-/201	-/66		
-/4437	-/1478		
-/1566	-/521		
-/3936	-/1311		
-/3936	-/1311		
-/2058	-/685		
-/2058	-/685		
-/1179	-/392		
-/1812	-/603		
1420/1674	474/557	Q/K	Cag/Aag
157/1914	53/637	Y/D	Tac/Gac
1543/1914	515/637	V/F	Gtt/Ttt
1056/2631	352/876	E	gaA/gaG
1469/2631	490/876	A/V	gCg/gTg
-/2631	-/876		
-/3042	-/1013		
-/1761	-/586		
-/1761	-/586		
660/1761	220/586	P	ccC/ccT
1095/1434	365/477	F	ttC/ttT
-/1209	-/402		r
-/1416	-/471		rs170575
-/1104	-/367		
-/1290	-/429		
-/843	-/280		
-/2256	-/751		
-/2277	-/758		
1438/1959	480/652	A/P	Gca/Cca
1550/1959	517/652	A/V	gCg/gTg
1405/1593	469/530	R/C	Cgc/Tgc
-/993	-/330		
289/591	97/196	V/I	Gtc/Atc
2652/3612	884/1203	C	tgC/tgT
-/3612	-/1203		
-/1575	-/524		
-/555	-/184		
253/1254	85/417	I/V	Atc/Gtc
-/1254	-/417		
-/1050	-/349		
-/885	-/294		
-/1548	-/515		
309/1068	103/355	D	gaC/gaT
110/984	37/327	R/H	cGc/cAc
453/987	151/328	S	agC/agT
3042/4497	1014/1498	L	ctC/ctT

-/1959	-/652		
1248/1668	416/555	T	acG/acA
-/2523	-/840		
-/987	-/328		
21/1167	7/388	R	cgG/cgT
370/1527	124/508	V/L	Gtg/Ttg
652/3840	218/1279	A/P	Gcc/Ccc
-/1683	-/560		
-/1683	-/560		
-/1683	-/560		
-/1548	-/515		
1425/2217	475/738	H	caT/caC
-/1989	-/662		
-/1737	-/578		
-/1737	-/578		
-/1737	-/578		
-/5850	-/1949		
-/2751	-/916		
-/2652	-/883		
-/2685	-/894		
1789/2748	597/915	L	Ctg/Ttg
-/3654	-/1217		
1847/2349	616/782	T/M	aCg/aTg
-/1887	-/628		
-/633	-/210		
-/651	-/216		
-/1905	-/634		
-/1905	-/634		
-/3327	-/1108		
-/1332	-/443		
-/1974	-/657		
-/255	-/84		
-/2976	-/991		
-/2976	-/991		
-/3210	-/1069		
-/615	-/204		
525/756	175/251	P	ccG/ccA
-/6435	-/2144		
-/6435	-/2144		
1842/6435	614/2144	T	acG/acA
1895/2568	632/855	V/A	gTg/gCg
-/7833	-/2610		
-/7833	-/2610		
-/2517	-/838		
-/2517	-/838		
-/1017	-/338		
-/14586	-/4861		
187/1047	63/348	H/D	Cat/Gat
1008/2187	336/728	E	gaG/gaA
-/1515	-/504		
-/2349	-/782		
39/300	13/99	D	gaC/gaT
-/381	-/126		
-/381	-/126		
-/411	-/136		

48/312	16/103	A	gcC/gcT
-/2754	-/917		
619/777	207/258	L/M	Ctg/Atg
-/2181	-/726		
-/3030	-/1009		
606/1086	202/361	V	gtG/gtT
-/1806	-/601		
494/1806	165/601	G/V	gGc/gTc
-/1896	-/631		
-/2571	-/856		
1386/2160	462/719	L	ctG/ctA
-/1254	-/417		
516/2328	172/775	G	ggG/ggA
-/483	-/160		
12/1074	4/357	P	ccT/ccA
2109/13125	703/4374	S	tcA/tcG
5987/13125	1996/4374	R/H	cGt/cAt
382/909	128/302	V/I	Gtt/Att
-/909	-/302		
-/909	-/302		
-/1359	-/452		
-/1101	-/366		
536/2190	179/729	S/T	aGt/aCt
28/1548	10/515	F/V	Ttc/Gtc
-/4104	-/1367		
-/7476	-/2491		
-/7476	-/2491		
-/7476	-/2491		
-/1011	-/336		
1347/4026	449/1341	E	gaA/gaG
2571/4026	857/1341	Y	taT/taC
-/4026	-/1341		
-/1296	-/431		
999/1296	333/431	E/D	gaG/gaT
-/1296	-/431		
-/3981	-/1326		
-/4314	-/1437		
3069/3999	1023/1332	L	ctG/ctC
-/2376	-/791		
530/1662	177/553	S/Y	tCc/tAc
-/1725	-/574		
-/819	-/272		
-/735	-/244		
-/333	-/110		
-/603	-/200		
1650/4149	550/1382	A	gcG/gcA
-/4149	-/1382		
-/6573	-/2190		
-/6573	-/2190		
-/2664	-/887		
-/4728	-/1575		
-/4896	-/1631		
-/3549	-/1182		
-/1545	-/514		
957/1392	319/463	V	gtG/gtC

-/3504	-/1167		
-/3504	-/1167		
-/3099	-/1032		
-/3108	-/1035		
-/2793	-/930		
390/2793	130/930	V	gtG/gtA
-/2793	-/930		
-/792	-/263		
-/2841	-/946		
-/8106	-/2701		
-/8106	-/2701		
-/8016	-/2671		
729/1644	243/547	I	atC/atT
-/5166	-/1721		
-/5166	-/1721		
-/2529	-/842		
-/2472	-/823		
-/2535	-/844		
-/3741	-/1246		
-/3741	-/1246		
1206/3741	402/1246	P	ccC/ccT
-/1575	-/524		
-/4059	-/1352		
-/2988	-/995		
1578/2988	526/995	S	agC/agT
2781/2988	927/995	H	caC/caT
234/1476	78/491	L	ctG/ctA
566/1371	189/456	P/R	cCg/cGg
-/1260	-/419		
-/3450	-/1149		
-/942	-/313		
-/780	-/259		
-/5286	-/1761		
-/3195	-/1064		
-/3291	-/1096		
-/4620	-/1539		
2177/4206	726/1401	T/K	aCg/aAg
-/2826	-/941		
1612/2826	538/941	R	Aga/Cga
1930/2826	644/941	R/S	Cgt/Agt
33/1230	11/409	N	aaC/aaT
-/15018	-/5005		
2065/6534	689/2177	S/A	Tct/Gct
-/5439	-/1812		
3486/4104	1162/1367	A	gcC/gcT
-/1557	-/518		
-/4947	-/1648		
270/3090	90/1029	Y	taC/taT
-/2997	-/998		
-/5376	-/1791		
-/3312	-/1103		
-/5343	-/1780		
-/2379	-/792		
-/1182	-/393		

648/1443	216/480	T	acA/acC	
39/1794	13/597	V	gtA/gtG	
-/1863	-/620			
-/570	-/189			
-/14736	-/4911			
-/5250	-/1749			
-/6630	-/2209			
936/1551	312/516	T	acG/acA	
-/2631	-/876			
-/1479	-/492			
-/1755	-/584			
-/1347	-/448			
-/1404	-/467			
-/879	-/292			
-/291	-/96			
330/339	110/112	T	acT/acC	
-/2118	-/705			
-/9369	-/3122			
-/9369	-/3122			rs7493
-/5472	-/1823			
-/5472	-/1823			
-/4830	-/1609			
-/4830	-/1609			
-/4830	-/1609			
-/3582	-/1193			
1446/3393	482/1130	S	tcT/tcC	
-/285	-/94			
-/459	-/152			
-/819	-/272			
-/2736	-/911			
-/1140	-/379			
-/1500	-/499			
-/1944	-/647			
1277/1779	426/592	R/H	cGc/cAc	
-/1470	-/489			
-/4158	-/1385			
-/3078	-/1025			
-/2322	-/773			
42/2280	14/759	A	gcT/gcC	
-/2280	-/759			
-/1725	-/574			
-/1839	-/612			
-/1500	-/499			
-/13800	-/4599			
-/4848	-/1615			
562/759	188/252	R/W	Cgg/Tgg	
-/759	-/252			
-/1074	-/357			
-/1245	-/414			
20/786	7/261	G/V	gGc/gTc	
-/3099	-/1032			
-/5169	-/1722			
275/1977	92/658	L/P	cTg/cCg	
713/1392	238/463	R/Q	cGa/cAa	
-/243	-/80			

-/2199	-/732		
-/5439	-/1812		
-/1041	-/346		
-/741	-/246		
-/684	-/227		
-/2010	-/669		
-/2010	-/669		
-/2157	-/718		
-/618	-/205		
-/930	-/309		
888/945	296/314	G	ggA/ggG
-/1041	-/346		
-/3429	-/1142		
909/1122	303/373	P	ccG/ccA
-/1821	-/606		
-/3414	-/1137		
2193/2997	731/998	C	tgC/tgT
-/1962	-/653		
1245/3435	415/1144	R	cgT/cgA
728/3030	243/1009	Q/P	cAa/cCa
2594/3180	865/1059	P/L	cCc/cTc
574/3942	192/1313	A/T	Gct/Act
-/1974	-/657		
945/2502	315/833	P	ccT/ccG
-/3720	-/1239		
-/1149	-/382		
-/4713	-/1570		
1011/4713	337/1570	D	gaT/gaC
-/7872	-/2623		
490/1746	164/581	R/S	Cgc/Agc
-/2178	-/725		
-/5943	-/1980		
429/2868	143/955	V	gtG/gtA
-/16791	-/5596		
-/16791	-/5596		
978/1497	326/498	I	atC/atT
-/4365	-/1454		
-/603	-/200		
-/2244	-/747		
419/666	140/221	C/S	tGc/tCc
-/1107	-/368		
-/4626	-/1541		
-/2106	-/701		
-/3000	-/999		
-/1743	-/580		
666/1137	222/378	P	ccG/ccA
-/1617	-/538		
1704/2406	568/801	P	ccG/ccA
-/2406	-/801		
1356/2406	452/801	F	ttC/ttT
343/717	115/238	L/F	Ctt/Ttt
-/6009	-/2002		
-/6009	-/2002		
-/6009	-/2002		
-/2004	-/667		

-/3999	-/1332			
-/3999	-/1332			
-/879	-/292			
-/3111	-/1036			
-/1680	-/559			
-/1710	-/569			
-/1206	-/401			
460/654	154/217	K/Q	Aag/Cag	
-/2814	-/937			
1418/2814	473/937	T/I	aCt/aTt	
-/1047	-/348			
-/708	-/235			
-/2127	-/708			
916/3972	306/1323	Y/D	Tat/Gat	
1853/3972	618/1323	H/R	cAc/cGc	
1526/3972	509/1323	V/A	gTg/gCg	
-/816	-/271			
-/414	-/137			
-/708	-/235			
-/606	-/201			
-/2739	-/912			
-/2805	-/934			
-/882	-/293			
6909/7650	2303/2549	L	ctG/ctA	
3144/3798	1048/1265	A	gcA/gcG	
-/3798	-/1265			
-/3798	-/1265			
-/3798	-/1265			
-/2685	-/894			
-/43524	-/14507			
7599/43524	2533/14507	A	gcA/gcG	
-/10893	-/3630			rs
-/10893	-/3630			
7662/8454	2554/2817	P	ccT/ccC	
-/1203	-/400			
7353/8487	2451/2828	T	acT/acC	
123/924	41/307	A	gcC/gcT	
-/3825	-/1274			
3721/5940	1241/1979	A/T	Gca/Aca	
-/5841	-/1946			
1095/5808	365/1935	K	aaG/aaA	
-/5808	-/1935			
-/5808	-/1935			
-/5883	-/1960			
3558/5745	1186/1914	T	acC/acT	
-/10593	-/3530			
-/7704	-/2567			
-/2913	-/970			
-/3297	-/1098			
-/5568	-/1855			
-/6069	-/2022			
-/675	-/224			
1134/3963	378/1320	I	atC/atT	
-/3456	-/1151			
-/2487	-/828			

-/2178	-/725		
912/1764	304/587	P	ccG/ccA
-/1548	-/515		
928/1263	310/420	A/T	Gct/Act
-/624	-/207		
-/7116	-/2371		
2768/2901	923/966	H/R	cAt/cGt
-/2901	-/966		
-/2901	-/966		
-/2901	-/966		
274/3966	92/1321	P/S	Ccc/Tcc
-/4206	-/1401		
-/4497	-/1498		
-/2226	-/741		
-/6192	-/2063		
-/7323	-/2440		
1290/1392	430/463	A	gcC/gcT
-/25578	-/8525		
-/25578	-/8525		
-/25578	-/8525		
1062/1620	354/539	T	acG/acA
510/519	170/172	D	gaT/gaC
-/519	-/172		
995/2028	332/675	E/A	gAa/gCa
-/2910	-/969		
-/2703	-/900		
-/2157	-/718		
312/1188	104/395	H	caT/caC
-/4833	-/1610		
-/3744	-/1247		
-/6273	-/2090		
-/1221	-/406		
637/1401	213/466	R/G	Agg/Ggg
-/8415	-/2804		
-/855	-/284		
-/4515	-/1504		
185/720	62/239	S/T	aGc/aCc
-/2547	-/848		
-/3075	-/1024		
-/3603	-/1200		
2955/3603	985/1200	L	ctG/ctT
-/3603	-/1200		
-/2976	-/991		
-/1551	-/516		
-/3441	-/1146		
-/2574	-/857		
-/1785	-/594		
-/1521	-/506		
894/3612	298/1203	D/E	gaT/gaG
-/3612	-/1203		
-/7668	-/2555		
-/7668	-/2555		
3888/4080	1296/1359	V	gtT/gtC
433/1293	145/430	I/L	Atc/Ctc
723/1134	241/377	S/R	agC/agG

r

-/1296	-/431			
-/1740	-/579			
-/1074	-/357			
-/3495	-/1164			
3705/8091	1235/2696	N	aaT/aaC	
-/2304	-/767			
-/1674	-/557			
-/633	-/210			
703/1086	235/361	R/C	Cgc/Tgc	
-/1488	-/495			
417/2391	139/796	I	atT/atA	
-/2778	-/925			
-/6273	-/2090			
-/1143	-/380			rs
-/1407	-/468			
-/1524	-/507			
-/1524	-/507			r
-/2226	-/741			
-/2226	-/741			
-/1596	-/531			
-/1098	-/365			
-/1098	-/365			
-/1098	-/365			
-/1308	-/435			
-/459	-/152			
1884/5691	628/1896	Y	taC/taT	
-/996	-/331			
-/543	-/180			
-/972	-/323			
374/948	125/315	R/Q	cGa/cAa	
546/987	182/328	L	ttG/ttA	
43/948	15/315	F/I	Ttt/Att	
-/933	-/310			
657/933	219/310	L	ctC/ctT	
570/963	190/320	S	tcT/tcC	
895/1089	299/362	I/V	Atc/Gtc	
759/942	253/313	G	ggC/ggA	
630/945	210/314	I	atC/atT	
-/981	-/326			
-/1443	-/480			
-/1434	-/477			
855/1434	285/477	S	tcA/tcG	
-/2940	-/979			
-/2781	-/926			
1434-1435/1488	478-479/495	-/S	-/AGC	
533/1098	178/365	N/T	aAc/aCc	
714/1527	238/508	I	atC/atT	
685/1983	229/660	K/E	Aaa/Gaa	
-/2892	-/963			
-/393	-/130			
-/1164	-/387			
-/1797	-/598			
612/1797	204/598	L	ctG/ctC	
1640/2322	547/773	A/V	gCg/gTg	
-/2211	-/736			

84/1428	28/475	R/S	agG/agT
726/1239	242/412	R	cgC/cgT
-/1194	-/397		
-/1353	-/450		
218/408	73/135	I/T	aTa/aCa
-/5874	-/1957		
3362/3714	1121/1237	G/V	gGa/gTa
-/15429	-/5142		
532/861	178/286	V/I	Gta/Ata
-/10011	-/3336		
67/1830	23/609	R/W	Cgg/Tgg
-/1638	-/545		
2205/2826	735/941	I	atC/atT
252/2577	84/858	L	ctG/ctA
-/3270	-/1089		
3252/3321	1084/1106	P	ccA/ccG
-/3321	-/1106		
-/1248	-/415		
-/2367	-/788		
-/2367	-/788		
-/1554	-/517		
4625/5241	1542/1746	S/T	aGc/aCc
-/3114	-/1037		
9/3114	3/1037	P	ccG/ccA
1320/3114	440/1037	P	ccT/ccC
1303/1482	435/493	L/F	Ctt/Ttt
-/1482	-/493		
-/2355	-/784		
-/2355	-/784		
-/2769	-/922		
-/1254	-/417		
1181/1731	394/576	R/Q	cGg/cAg
-/1026	-/341		
-/3291	-/1096		
-/5466	-/1821		
-/3672	-/1223		
-/4134	-/1377		
381/4947	127/1648	A	gcC/gcA
-/576	-/191		
-/1188	-/395		
2010/2796	670/931	T	acT/acC
376/1515	126/504	N/D	Aat/Gat
-/2643	-/880		
-/6297	-/2098		
132/981	44/326	A	gcC/gcA
-/2649	-/882		
1170/1932	390/643	G	ggC/ggT
-/12225	-/4074		
-/2646	-/881		
-/1326	-/441		
-/1689	-/562		
-/4377	-/1458		
-/6909	-/2302		
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5330/6909	1777/2302	T/I	aCc/aTc
-/3798	-/1265		
-/3390	-/1129		
-/3390	-/1129		
4376/14055	1459/4684	H/R	cAc/cGc
789/14055	263/4684	A	gcT/gcC
-/14055	-/4684		
8664/14055	2888/4684	N	aaC/aaT
13872/14055	4624/4684	A	gcT/gcC
11538/14055	3846/4684	A	gcT/gcC
-/3258	-/1085		
-/4095	-/1364		
-/4095	-/1364		
-/4095	-/1364		
-/1836	-/611		
-/1011	-/336		
-/1503	-/500		
-/5517	-/1838		
-/2418	-/805		
1469/1599	490/532	T/M	aCg/aTg
-/1446	-/481		
2121/4128	707/1375	P	ccG/ccA
-/1728	-/575		TMP_ESP_
-/519	-/172		
-/951	-/316		
-/951	-/316		
-/2511	-/836		
545/1080	182/359	K/T	aAg/aCg
34/1518	12/505	P/A	Cca/Gca
1431/1518	477/505	H	caC/caT
-/1584	-/527		
99-100/2268	33-34/755	-/EP	-/GAACCC
-/1434	-/477		
-/465	-/154		
-/1269	-/422		
-/3453	-/1150		
-/798	-/265		
-/1893	-/630		
-/2070	-/689		
-/816	-/271		
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-/2133	-/710		
-/4821	-/1606		
-/669	-/222		
-/1683	-/560		
-/2031	-/676		
-/2031	-/676		
-/1779	-/592		
-/1914	-/637		
545/1269	182/422	P/L	cCg/cTg
-/1236	-/411		
-/1932	-/643		
-/2568	-/855		

-/9267	-/3088		
-/1008	-/335		
-/1260	-/419		
-/1281	-/426		
-/1371	-/456		
-/867	-/288		
-/795	-/264		
-/990	-/329		
-/2103	-/700		
-/5724	-/1907		
-/4338	-/1445		
-/4341	-/1446		
2415/3048	805/1015	P	ccC/ccT
-/1422	-/473		
-/3567	-/1188		
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-/3567	-/1188		
-/3567	-/1188		
-/1260	-/419		
-/1503	-/500		
-/1914	-/637		
56/639	19/212	V/A	gTg/gCg
-/636	-/211		
-/666	-/221		
-/2589	-/862		
1422/1704	474/567	R	cgC/cgT
-/579	-/192		
-/1155	-/384		
2175/3228	725/1075	A	gcA/gcC
-/1947	-/648		
-/2952	-/983		
-/2184	-/727		
-/2772	-/923		
-/1239	-/412		
83/1035	28/344	R/H	cGt/cAt
2379/2793	793/930	R	cgA/cgC
-/2943	-/980		
-/3183	-/1060		
-/660	-/219		
1560/2916	520/971	P	ccA/ccG
-/1740	-/579		
-/2388	-/795		
39-40/336	13-14/111	-/*SX	-/TAATCCCC
-/954	-/317		
1623/1626	541/541	T	acA/acG
-/1626	-/541		
-/1737	-/578		
-/2151	-/716		
-/1464	-/487		
-/1134	-/377		
2331/2355	777/784	T	acG/acA
-/1176	-/391		
-/1176	-/391		
-/900	-/299		
123/2226	41/741	V	gtC/gtA

-/684	-/227			
-/987	-/328			
-/2199	-/732			
-/663	-/220			
-/4956	-/1651			
-/4956	-/1651			
1292/4167	431/1388	T/N	aCt/aAt	
-/2814	-/937			
-/7044	-/2347			
-/1443	-/480			
-/1326	-/441			
-/1998	-/665			
-/948	-/315			
-/531	-/176			
-/471	-/156			
-/471	-/156			
111/1212	37/403	P	ccG/ccA	
492/792	164/263	L	ttG/ttA	
-/2226	-/741			
-/4008	-/1335			
2526/4008	842/1335	T	acC/acT	
-/2277	-/758			
603/2277	201/758	A	gcG/gcA	
582/1329	194/442	V	gtA/gtG	
-/834	-/277			
1412/3099	471/1032	V/A	gTt/gCt	
-/2127	-/708			
2064/2127	688/708	P	ccG/ccC	
-/1926	-/641			
-/1389	-/462			
3456/15117	1152/5038	I	atC/atT	
-/15117	-/5038			rs3
6384/15117	2128/5038	Y	taC/taT	
-/15117	-/5038			
-/14904	-/4967			
-/14904	-/4967			
-/14613	-/4870			
-/519	-/172			
-/2757	-/918			
-/753	-/250			
5559/5682	1853/1893	T	acT/acC	
-/5550	-/1849			
-/3939	-/1312			
378/1044	126/347	G	ggG/ggA	
-/2613	-/870			
-/2067	-/688			
182/2148	61/715	H/R	cAc/cGc	
-/2067	-/688			
-/2067	-/688			
-/1245	-/414			
-/6003	-/2000			
3448/5934	1150/1977	W/R	Tgg/Cgg	

-/5934	-/1977		
-/1356	-/451		
-/6642	-/2213		
-/969	-/322		
58/1194	20/397	R/W	Cgg/Tgg
-/3183	-/1060		
1467/2304	489/767	H/Q	caC/caG
-/3099	-/1032		
-/3540	-/1179		
-/3540	-/1179		
266/3540	89/1179	V/A	gTt/gCt
-/3540	-/1179		
-/2565	-/854		
730/747	244/248	Y/D	Tat/Gat
-/1833	-/610		
-/2493	-/830		
-/2316	-/771		
-/2316	-/771		
-/2358	-/785		
-/1077	-/358		
-/1272	-/423		
-/711	-/236		
-/5772	-/1923		
-/5772	-/1923		
-/4329	-/1442		
111/3075	37/1024	G	ggA/ggC
-/3654	-/1217		
-/261	-/86		
-/1707	-/568		
-/3156	-/1051		
-/3156	-/1051		
-/2250	-/749		
-/1161	-/386		
1602/3318	534/1105	A	gcA/gcG
-/6486	-/2161		
-/6486	-/2161		
-/1389	-/462		
2956/4851	986/1616	A/T	Gca/Aca
-/1788	-/595		
-/2352	-/783		
-/2004	-/667		
-/5169	-/1722		
-/1008	-/335		
96/1314	32/437	T	acG/acA
340/1134	114/377	I/V	Att/Gtt
-/3252	-/1083		
-/1788	-/595		
97/1620	33/539	S/P	Tct/Cct
-/1695	-/564		
-/1695	-/564		
285/1674	95/557	L	ctT/ctC
-/1809	-/602		
495/1869	165/622	H	caT/caC
-/2031	-/676		
-/1080	-/359		

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-/1821	-/606		
-/1950	-/649		
-/1977	-/658		
-/1434	-/477		
-/996	-/331		
-/1227	-/408		
-/1473	-/490		
-/1518	-/505		
-/1389	-/462		
1656/2397	552/798	V	gtC/gtT
-/3726	-/1241		
-/1932	-/643		
-/1929	-/642		
-/2211	-/736		
-/1893	-/630		
-/2121	-/706		
-/1608	-/535		
1146/1608	382/535	S	agC/agT
144/2178	48/725	A	gcG/gcC
-/1932	-/643		
-/3165	-/1054		
-/3159	-/1052		
-/3708	-/1235		
126/1308	42/435	Q	caG/caA
-/2823	-/940		
-/1287	-/428		
-/3879	-/1292		
-/3480	-/1159		
567/6672	189/2223	N	aaT/aaC
1392/6672	464/2223	P	ccC/ccT
240/543	80/180	P	ccC/ccA
-/1776	-/591		
-/9804	-/3267		
7166/9804	2389/3267	E/G	gAg/gGg
598/759	200/252	V/L	Gtt/Ctt
12/1275	4/424	P	ccG/ccA
-/11025	-/3674		
-/11025	-/3674		
4603/9693	1535/3230	P/A	Cca/Gca
-/1128	-/375		
-/1053	-/350		
-/1125	-/374		
-/1125	-/374		
-/909	-/302		
3705/7656	1235/2551	H	caT/caC
-/1275	-/424		
381/888	127/295	N	aaC/aaT
-/14103	-/4700		
-/2247	-/748		
-/2364	-/787		

-/1713	-/570			
654/1197	218/398	A	gcA/gcG	
-/246	-/81			
-/993	-/330			
-/2019	-/672			rs746073071
-/2514	-/837			
-/2505	-/834			
-/3456	-/1151			
610/1269	204/422	S/G	Agc/Ggc	
-/942	-/313			
-/1005	-/334			
-/312	-/103			rs
163/288	55/95	V/M	Gtg/Atg	
-/3264	-/1087			
-/3264	-/1087			
-/768	-/255			
-/1758	-/585			
3381/3825	1127/1274	A	gcC/gcG	
399/20724	133/6907	L	ctG/ctC	
-/20724	-/6907			
2850/4491	950/1496	D	gaC/gaT	
1697/4695	566/1564	P/L	cCg/cTg	
461/3786	154/1261	G/A	gGc/gCc	
1440/2082	480/693	V	gtG/gtA	
-/2082	-/693			
1541/2517	514/838	G/E	gGg/gAg	
-/1389	-/462			
-/2196	-/731			
204/2196	68/731	S	tcC/tcT	
-/2409	-/802			
-/2409	-/802			
766/2286	256/761	V/I	Gtc/Atc	
-/2286	-/761			
338/1554	113/517	T/M	aCg/aTg	
-/3897	-/1298			
2152/2454	718/817	I/V	Att/Gtt	
-/2682	-/893			
-/1158	-/385			
203/684	68/227	G/A	gGa/gCa	
1487/2397	496/798	L/S	tTa/tCa	
-/3297	-/1098			
-/1284	-/427			
819/4149	273/1382	L	ctC/ctT	
-/8199	-/2732			
-/8325	-/2774			
-/1503	-/500			
-/4983	-/1660			
-/4494	-/1497			
-/3405	-/1134			
313/870	105/289			rs
633/1041	211/346	T	acG/acA	
427/1218	143/405	A/T	Gct/Act	
-/762	-/253			
-/2556	-/851			

589/726	197/241	V/I	Gtc/Atc
777/2133	259/710	S	agT/agC
-/3519	-/1172		
-/1140	-/379		
1734/4974	578/1657	A	gcA/gcG
-/693	-/230		
-/1512	-/503		
-/4776	-/1591		
-/5106	-/1701		
1671/2139	557/712	D	gaC/gaT
-/747	-/248		
-/1896	-/631		
-/1896	-/631		
-/744	-/247		
1689/2319	563/772	S	tcG/tcA
-/2319	-/772		
-/2253	-/750		
2872/3042	958/1013	T/A	Aca/Gca
-/3048	-/1015		
-/3048	-/1015		
2532/3048	844/1015	A	gcC/gcT
-/7629	-/2542		
-/855	-/284		
16/723	6/240	F/L	Ttt/Ctt
-/5652	-/1883		
20/558	7/185	R/Q	cGg/cAg
-/750	-/249		
-/1053	-/350		
-/438	-/145		
373/483	125/160	L	Ttg/Ctg
-/1266	-/421		
-/2373	-/790		
276/705	92/234	R	agG/agA
4818/8907	1606/2968	S	tcG/tcC
-/2148	-/715		
1493/2148	498/715	S/N	aGt/aAt
1074/5934	358/1977	D/E	gaC/gaG
3421/5934	1141/1977	K/Q	Aag/Cag
-/5934	-/1977		
108/903	36/300	E	gaG/gaA
-/855	-/284		
-/660	-/219		
597/660	199/219	S	tcA/tcG
-/828	-/275		
-/522	-/173		
-/477	-/158		
-/477	-/158		
2500/3603	834/1200	C/S	Tgt/Agt
-/711	-/236		
-/1398	-/465		
-/1542	-/513		
-/2280	-/759		
-/1428	-/475		
2035/2352	679/783	M/V	Atg/Gtg
-/2133	-/710		

-/2133	-/710		
4398/9294	1466/3097	D	gaT/gaC
52/1431	18/476	P/S	Cct/Tct
1554/1980	518/659	P	ccA/ccG
-/1515	-/504		
-/2394	-/797		
-/4929	-/1642		
1003/3498	335/1165	V/L	Gtg/Ttg
-/5598	-/1865		
-/2616	-/871		
965/3495	322/1164	M/T	aTg/aCg
-/3495	-/1164		
-/5424	-/1807		
-/726	-/241		
322/738	108/245	A/T	Gcc/Acc
-/750	-/249		
1026/1077	342/358	R	agG/agA
-/3966	-/1321		
1868/3966	623/1321	G/A	gGc/gCc
-/3366	-/1121		
-/1143	-/380		
178/7446	60/2481	E/K	Gag/Aag
-/8148	-/2715		
-/8148	-/2715		
-/8148	-/2715		
2874/8148	958/2715	C	tgT/tgC
-/8148	-/2715		
750/1272	250/423	E	gaG/gaA
603/2676	201/891	L	ctT/ctC
-/1686	-/561		
-/3075	-/1024		
-/5460	-/1819		
597/4632	199/1543	R	agA/agG
-/4632	-/1543		
-/1074	-/357		
-/1464	-/487		
-/1986	-/661		
-/1950	-/649		
1503/3252	501/1083	Y	taT/taC
-/15552	-/5183		
-/996	-/331		
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2679/3615	893/1204	R	cgT/cgG
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221/1134	74/377	N/I	aAc/aTc
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CAMK2D	HGNC	1462	protein_coding
CAMKMT	HGNC	26276	protein_coding
CAMSAP3	HGNC	29307	protein_coding
CAPN11	HGNC	1478	protein_coding
CAPN9	HGNC	1486	protein_coding
CAPS	HGNC	1487	protein_coding
CARD10	HGNC	16422	protein_coding
CARD8	HGNC	17057	protein_coding
CASP14	HGNC	1502	protein_coding
CASQ1	HGNC	1512	protein_coding
CASZ1	HGNC	26002	protein_coding
CATSPERG	HGNC	25243	protein_coding
CAV3	HGNC	1529	protein_coding
CCDC102A	HGNC	28097	protein_coding
CCDC104	HGNC	30540	protein_coding
CCDC105	HGNC	26866	protein_coding

CCDC11	HGNC	26530	protein_coding
CCDC120	HGNC	28910	protein_coding
CCDC132	HGNC	25956	protein_coding
CCDC137	HGNC	33451	protein_coding
CCDC147	HGNC	26676	protein_coding
CCDC158	HGNC	26374	protein_coding
CCDC169-SOHLH2	HGNC	38866	protein_coding
CCDC18	HGNC	30370	protein_coding
CCDC57	HGNC	27564	protein_coding
CCDC6	HGNC	18782	protein_coding
CCDC81	HGNC	26281	protein_coding
CCL19	HGNC	10617	protein_coding
CCR2	HGNC	1603	protein_coding
CD109	HGNC	21685	protein_coding
CD200R1L	HGNC	24665	protein_coding
CD244	HGNC	18171	protein_coding
CD300A	HGNC	19319	protein_coding
CD3EAP	HGNC	24219	protein_coding
CD46	HGNC	6953	protein_coding
CD7	HGNC	1695	protein_coding
CDC23	HGNC	1724	protein_coding
CDC42BPG	HGNC	29829	protein_coding
CDC45	HGNC	1739	protein_coding
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CDK7	HGNC	1778	protein_coding
CDKAL1	HGNC	21050	protein_coding
CDKL5	HGNC	11411	protein_coding
CDS2	HGNC	1801	protein_coding
CDSN	HGNC	1802	protein_coding
CDSN	HGNC	1802	protein_coding
CEACAM21	HGNC	28834	protein_coding
CEACAM3	HGNC	1815	protein_coding
CECR1	HGNC	1839	protein_coding
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CECR5	HGNC	1843	protein_coding
CECR6	HGNC	1844	protein_coding
CENPI	HGNC	3968	protein_coding
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CFH	HGNC	4883	protein_coding
CFTR	HGNC	1884	protein_coding
CGB7	HGNC	16451	protein_coding
CHD1L	HGNC	1916	protein_coding
CHFR	HGNC	20455	protein_coding

CHFR	HGNC	20455	protein_coding
CHI3L2	HGNC	1933	protein_coding
CHRNB1	HGNC	1961	protein_coding
CHST14	HGNC	24464	protein_coding
CIITA	HGNC	7067	protein_coding
CINP	HGNC	23789	protein_coding
CIT	HGNC	1985	protein_coding
CITED1	HGNC	1986	protein_coding
CKMT2	HGNC	1996	protein_coding
CLCN6	HGNC	2024	protein_coding
CLCNKA	HGNC	2026	protein_coding
CLDN15	HGNC	2036	protein_coding
CLEC4E	HGNC	14555	protein_coding
CLIC2	HGNC	2063	protein_coding
CLIC4	HGNC	13518	protein_coding
CLIP1	HGNC	10461	protein_coding
CLIP4	HGNC	26108	protein_coding
CNKSR2	HGNC	19701	protein_coding
CNNM1	HGNC	102	protein_coding
CNOT1	HGNC	7877	protein_coding
CNOT11	HGNC	25217	protein_coding
CNR1	HGNC	2159	protein_coding
CNTN4	HGNC	2174	protein_coding
CNTNAP2	HGNC	13830	protein_coding
CNTNAP2	HGNC	13830	protein_coding
CNTRL	HGNC	1858	protein_coding
COBL	HGNC	22199	protein_coding
COG4	HGNC	18620	protein_coding
COG5	HGNC	14857	protein_coding
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COL24A1	HGNC	20821	protein_coding
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COL26A1	HGNC	18038	protein_coding
COL4A6	HGNC	2208	protein_coding
COL5A3	HGNC	14864	protein_coding
COL6A1	HGNC	2211	protein_coding
COL6A3	HGNC	2213	protein_coding
COMT	HGNC	2228	protein_coding
COX20	HGNC	26970	protein_coding
CP	HGNC	2295	protein_coding
CPEB1	HGNC	21744	protein_coding
CPEB4	HGNC	21747	protein_coding
CR2	HGNC	2336	protein_coding
CRB2	HGNC	18688	protein_coding
CRHR2	HGNC	2358	protein_coding
CRIM1	HGNC	2359	protein_coding
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CRISP3	HGNC	16904	protein_coding
CRNKL1	HGNC	15762	protein_coding
CRTC3	HGNC	26148	protein_coding
CRYBG3	HGNC	34427	protein_coding
CRYBG3	Uniprot_gn	34427	protein_coding
CSAG1	HGNC	24294	protein_coding
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CSPG4	HGNC	2466	protein_coding
CTCFL	HGNC	16234	protein_coding
CTD-3088G3.8	Clone_based_vega_gene		protein_coding
CTNNA3	HGNC	2511	protein_coding
CTNNAL1	HGNC	2512	protein_coding
CUBN	HGNC	2548	protein_coding
CUL2	HGNC	2552	protein_coding
CUL7	HGNC	21024	protein_coding
CUX1	HGNC	2557	protein_coding
CUX1	HGNC	2557	protein_coding
CWC22	HGNC	29322	protein_coding
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CWF19L2	HGNC	26508	protein_coding
CXCR3	HGNC	4540	protein_coding
CYB561A3	HGNC	23014	protein_coding
CYB5R2	HGNC	24376	protein_coding
CYP2A13	HGNC	2608	protein_coding
CYP2A13	HGNC	2608	protein_coding
CYP3A4	HGNC	2637	protein_coding
CYP4F12	HGNC	18857	protein_coding
CYP51A1	HGNC	2649	protein_coding
DAGLA	HGNC	1165	protein_coding
DARS	HGNC	2678	protein_coding
DBR1	HGNC	15594	protein_coding
DCAF15	HGNC	25095	protein_coding
DCAF15	HGNC	25095	protein_coding
DCAF15	HGNC	25095	protein_coding
DCC	HGNC	2701	protein_coding
DCDC2	HGNC	18141	protein_coding
DCHS2	HGNC	23111	protein_coding
DCTD	HGNC	2710	protein_coding
DDX11	HGNC	2736	protein_coding
DDX11	HGNC	2736	protein_coding
DDX59	HGNC	25360	protein_coding
DENND1A	HGNC	29324	protein_coding
DENND5A	HGNC	19344	protein_coding
DEPDC1B	HGNC	24902	protein_coding
DGCR2	HGNC	2845	protein_coding
DGKB	HGNC	2850	protein_coding
DHRS3	HGNC	17693	protein_coding
DHX32	HGNC	16717	protein_coding
DHX37	HGNC	17210	protein_coding
DHX8	HGNC	2749	protein_coding
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DIAPH1	HGNC	2876	protein_coding
DIP2B	HGNC	29284	protein_coding
DIS3L	HGNC	28698	protein_coding
DISC1	HGNC	2888	protein_coding
DISC1	HGNC	2888	protein_coding
DKK4	HGNC	2894	protein_coding
DLG2	HGNC	2901	protein_coding
DLG3	HGNC	2902	protein_coding
DLG5	HGNC	2904	protein_coding
DLK2	HGNC	21113	protein_coding

DMKN	HGNC	25063	protein_coding
DNA2	HGNC	2939	protein_coding
DNAH11	HGNC	2942	protein_coding
DNAH12	HGNC	2943	protein_coding
DNAH14	HGNC	2945	protein_coding
DNAH14	HGNC	2945	protein_coding
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DNAH17	HGNC	2946	protein_coding
DNAH8	HGNC	2952	protein_coding
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DNALI1	HGNC	14353	protein_coding
DNASE2B	HGNC	28875	protein_coding
DNMBP	HGNC	30373	protein_coding
DOCK2	HGNC	2988	protein_coding
DOCK3	HGNC	2989	protein_coding
DOT1L	HGNC	24948	protein_coding
DPEP1	HGNC	3002	protein_coding
DPF1	HGNC	20225	protein_coding
DPH5	HGNC	24270	protein_coding
DPY19L2	HGNC	19414	protein_coding
DRAXIN	HGNC	25054	protein_coding
DRP2	HGNC	3032	protein_coding
DRP2	HGNC	3032	protein_coding
DRP2	HGNC	3032	protein_coding
DSCAML1	HGNC	14656	protein_coding
DSG3	HGNC	3050	protein_coding
DSG4	HGNC	21307	protein_coding
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DSP	HGNC	3052	protein_coding
DST	HGNC	1090	protein_coding
DTD2	HGNC	20277	protein_coding
DTNBP1	HGNC	17328	protein_coding
DTWD2	HGNC	19334	protein_coding
DTX2	HGNC	15973	protein_coding
DUSP18	HGNC	18484	protein_coding
DUSP6	HGNC	3072	protein_coding
DYNC1I1	HGNC	2963	protein_coding
DYNC2H1	HGNC	2962	protein_coding
EBNA1BP2	HGNC	15531	protein_coding
EBP	HGNC	3133	protein_coding
ECE1	HGNC	3146	protein_coding
ECEL1	HGNC	3147	protein_coding
ECT2	HGNC	3155	protein_coding
ECT2L	HGNC	21118	protein_coding
EDEM3	HGNC	16787	protein_coding
EDN1	HGNC	3176	protein_coding
EDNRB	HGNC	3180	protein_coding
EEA1	HGNC	3185	protein_coding
EEF1A2	HGNC	3192	protein_coding
EEF1E1	HGNC	3212	protein_coding
EFCAB13	HGNC	26864	protein_coding
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EFHB	HGNC	26330	protein_coding
EFTUD1	HGNC	25789	protein_coding
EFTUD2	HGNC	30858	protein_coding
EIF2S3	HGNC	3267	protein_coding
ELF4	HGNC	3319	protein_coding
ELFN2	HGNC	29396	protein_coding
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ELN	HGNC	3327	protein_coding
ELOVL2	HGNC	14416	protein_coding
EMC1	HGNC	28957	protein_coding
EMC2	HGNC	28963	protein_coding
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EML1	HGNC	3330	protein_coding
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EN1	HGNC	3342	protein_coding
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ENOX1	HGNC	25474	protein_coding
ENTPD1	HGNC	3363	protein_coding
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EP400	HGNC	11958	protein_coding
EPHB6	HGNC	3396	protein_coding
EPHX1	HGNC	3401	protein_coding
EPHX2	HGNC	3402	protein_coding
ERN1	HGNC	3449	protein_coding
ESPL1	HGNC	16856	protein_coding
ESYT3	HGNC	24295	protein_coding
ETFA	HGNC	3481	protein_coding
ETFB	HGNC	3482	protein_coding
ETHE1	HGNC	23287	protein_coding
EVI5	HGNC	3501	protein_coding
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EVPL	HGNC	3503	protein_coding
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EXD2	HGNC	20217	protein_coding
EXO1	HGNC	3511	protein_coding
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EZR	HGNC	12691	protein_coding
F8	HGNC	3546	protein_coding
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F9	HGNC	3551	protein_coding
FAAH2	HGNC	26440	protein_coding
FADS2	HGNC	3575	protein_coding
FADS3	HGNC	3576	protein_coding
FAH	HGNC	3579	protein_coding
FAM118A	HGNC	1313	protein_coding
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FAM127C	HGNC	33156	protein_coding
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FAM162B	HGNC	21549	protein_coding
FAM168A	HGNC	28999	protein_coding

FAM181B	HGNC	28512	protein_coding
FAM184B	HGNC	29235	protein_coding
FAM186A	HGNC	26980	protein_coding
FAM187B	HGNC	26366	protein_coding
FAM189B	HGNC	1233	protein_coding
FAM21C	HGNC	23414	protein_coding
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FAM65B	HGNC	13872	protein_coding
FAM81B	HGNC	26335	protein_coding
FANCA	HGNC	3582	protein_coding
FANCE	HGNC	3586	protein_coding
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FBRSL1	HGNC	29308	protein_coding
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FBXW4	HGNC	10847	protein_coding
FCAMR	HGNC	24692	protein_coding
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FGFR4	HGNC	3691	protein_coding
FGG	HGNC	3694	protein_coding
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FKBP6	HGNC	3722	protein_coding
FKBP7	HGNC	3723	protein_coding
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FLT4	HGNC	3767	protein_coding
FMN2	HGNC	14074	protein_coding
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FMO3	HGNC	3771	protein_coding
FNBP4	HGNC	19752	protein_coding
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FNDC1	HGNC	21184	protein_coding
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FOXF2	HGNC	3810	protein_coding
FOXP4	HGNC	20842	protein_coding
FPGS	HGNC	3824	protein_coding
FRAS1	HGNC	19185	protein_coding
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FSIP1	HGNC	21674	protein_coding
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FUBP3	HGNC	4005	protein_coding
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FXYD2	HGNC	4026	protein_coding
FYCO1	HGNC	14673	protein_coding
GADL1	HGNC	27949	protein_coding
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GALK1	HGNC	4118	protein_coding
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GALNT14	HGNC	22946	protein_coding
GALNT8	HGNC	4130	protein_coding
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GAREM	HGNC	26136	protein_coding
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GDA	HGNC	4212	protein_coding
GDAP1L1	HGNC	4213	protein_coding
GDF2	HGNC	4217	protein_coding
GEMIN2	HGNC	10884	protein_coding
GFM1	HGNC	13780	protein_coding
GGCX	HGNC	4247	protein_coding
GGN	HGNC	18869	protein_coding
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GINM1	HGNC	21074	protein_coding
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GLG1	HGNC	4316	protein_coding
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GLO1	HGNC	4323	protein_coding
GLRA4	HGNC	31715	protein_coding
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GLT8D2	HGNC	24890	protein_coding
GLYATL2	HGNC	24178	protein_coding
GMCL1	HGNC	23843	protein_coding
GNAZ	HGNC	4395	protein_coding
GNB1L	HGNC	4397	protein_coding
GNRHR	HGNC	4421	protein_coding
GOLGA3	HGNC	4426	protein_coding

GP1BA	HGNC	4439	protein_coding
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GPLD1	HGNC	4459	protein_coding
GPM6B	HGNC	4461	protein_coding
GPN1	HGNC	17030	protein_coding
GPR101	HGNC	14963	protein_coding
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GPR176	HGNC	32370	protein_coding
GRAMD1B	HGNC	29214	protein_coding
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GRAMD4	HGNC	29113	protein_coding
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GREB1	HGNC	24885	protein_coding
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GRIA3	HGNC	4573	protein_coding
GRM7	HGNC	4599	protein_coding
GSE1	HGNC	28979	protein_coding
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GSPT2	HGNC	4622	protein_coding
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GSTZ1	HGNC	4643	protein_coding
GTPBP4	HGNC	21535	protein_coding
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GXYLT2	HGNC	33383	protein_coding
HAL	HGNC	4806	protein_coding
HAMP	HGNC	15598	protein_coding
HDAC7	HGNC	14067	protein_coding
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HDAC9	HGNC	14065	protein_coding
HDDC2	HGNC	21078	protein_coding
HDHD1	HGNC	16818	protein_coding
HEATR1	HGNC	25517	protein_coding
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HELLS	HGNC	4861	protein_coding
HELLS	HGNC	4861	protein_coding
HEMK1	HGNC	24923	protein_coding
HERC1	HGNC	4867	protein_coding
HFE	HGNC	4886	protein_coding
HGF	HGNC	4893	protein_coding
HHATL	HGNC	13242	protein_coding
HHIPL1	HGNC	19710	protein_coding
HIGD1B	HGNC	24318	protein_coding
HINT1	HGNC	4912	protein_coding
HIST1H2BF	HGNC	4752	protein_coding
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HIST1H4B	HGNC	4789	protein_coding
HKDC1	HGNC	23302	protein_coding
HLA-DPB1	HGNC	4940	protein_coding
HLCS	HGNC	4976	protein_coding
HLTF	HGNC	11099	protein_coding
HMBS	HGNC	4982	protein_coding
HMGXB4	HGNC	5003	protein_coding
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HNF1A	HGNC	11621	protein_coding
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HOOK2	HGNC	19885	protein_coding
HPN	HGNC	5155	protein_coding
HPS6	HGNC	18817	protein_coding
HSPB6	HGNC	26511	protein_coding
HTR5A	HGNC	5300	protein_coding
HUWE1	HGNC	30892	protein_coding
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ICOSLG	HGNC	17087	protein_coding
ICOSLG	HGNC	17087	protein_coding
ICOSLG	HGNC	17087	protein_coding
IDH2	HGNC	5383	protein_coding
IDH3A	HGNC	5384	protein_coding
IFI16	HGNC	5395	protein_coding
IFNAR2	HGNC	5433	protein_coding
IGF1R	HGNC	5465	protein_coding
IGF2R	HGNC	5467	protein_coding
IGF2R	HGNC	5467	protein_coding
IGF2R	HGNC	5467	protein_coding
IGLON5	HGNC	34550	protein_coding
IGSF1	HGNC	5948	protein_coding
IGSF1	HGNC	5948	protein_coding
IGSF1	HGNC	5948	protein_coding
IGSF11	HGNC	16669	protein_coding
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IKBKAP	HGNC	5959	protein_coding
IL17RC	HGNC	18358	protein_coding
IL20RA	HGNC	6003	protein_coding
IL22RA1	HGNC	13700	protein_coding
IL2RA	HGNC	6008	protein_coding
INO80E	HGNC	26905	protein_coding
INS	HGNC	6081	protein_coding
INS-IGF2	HGNC	33527	protein_coding
INSR	HGNC	6091	protein_coding
INSR	HGNC	6091	protein_coding
INTS1	HGNC	24555	protein_coding
INTS1	HGNC	24555	protein_coding
INTS6	HGNC	14879	protein_coding
IQGAP2	HGNC	6111	protein_coding
IQGAP3	HGNC	20669	protein_coding
IQSEC3	HGNC	29193	protein_coding
IRF5	HGNC	6120	protein_coding
IRGC	HGNC	28835	protein_coding

ITGA10	HGNC	6135	protein_coding
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ITGA4	HGNC	6140	protein_coding
ITGA9	HGNC	6145	protein_coding
ITIH4	HGNC	6169	protein_coding
ITIH4	HGNC	6169	protein_coding
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ITM2A	HGNC	6173	protein_coding
ITPKB	HGNC	6179	protein_coding
ITPR2	HGNC	6181	protein_coding
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ITPR3	HGNC	6182	protein_coding
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JADE1	HGNC	30027	protein_coding
JADE3	HGNC	22982	protein_coding
JAKMIP3	HGNC	23523	protein_coding
JARID2	HGNC	6196	protein_coding
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JRKL	HGNC	6200	protein_coding
KANK1	HGNC	19309	protein_coding
KANK4	HGNC	27263	protein_coding
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KANK4	HGNC	27263	protein_coding
KATNA1	HGNC	6216	protein_coding
KCNA7	HGNC	6226	protein_coding
KCNAB1	HGNC	6228	protein_coding
KCNU1	HGNC	18867	protein_coding
KCP	HGNC	17585	processed_transcript
KCTD10	HGNC	23236	protein_coding
KCTD4	HGNC	23227	protein_coding
KDM3B	HGNC	1337	protein_coding
KDM4A	HGNC	22978	protein_coding
KDM4B	HGNC	29136	protein_coding
KDM5D	HGNC	11115	protein_coding
KDM6A	HGNC	12637	protein_coding
KDM7A	HGNC	22224	protein_coding
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KDM7A	HGNC	22224	protein_coding
KIAA0930	HGNC	1314	protein_coding
KIAA1109	HGNC	26953	protein_coding
KIAA1244	HGNC	21213	protein_coding
KIAA1429	HGNC	24500	protein_coding
KIAA1683	HGNC	29350	protein_coding
KIAA1919	HGNC	21053	protein_coding
KIF14	HGNC	19181	protein_coding
KIF17	HGNC	19167	protein_coding
KIF19	HGNC	26735	protein_coding
KIF1A	HGNC	888	protein_coding
KIF1C	HGNC	6317	protein_coding
KIF20B	HGNC	7212	protein_coding
KIFAP3	HGNC	17060	protein_coding
KIN	HGNC	6327	protein_coding

KLF10	HGNC	11810	protein_coding
KLHL2	HGNC	6353	protein_coding
KLHL8	HGNC	18644	protein_coding
KLRG1	HGNC	6380	protein_coding
KMT2C	HGNC	13726	protein_coding
KNDC1	HGNC	29374	protein_coding
KNTC1	HGNC	17255	protein_coding
KPNA7	HGNC	21839	protein_coding
KPNB1	HGNC	6400	protein_coding
KREMEN1	HGNC	17550	protein_coding
KRT10	HGNC	6413	protein_coding
KRT32	HGNC	6449	protein_coding
KRT36	HGNC	6454	protein_coding
KRTAP10-9	HGNC	22971	protein_coding
KRTAP12-3	HGNC	20531	protein_coding
KRTAP12-4	HGNC	20532	protein_coding
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LAMA2	HGNC	6482	protein_coding
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LAMC1	HGNC	6492	protein_coding
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LATS1	HGNC	6514	protein_coding
LCE3C	HGNC	16612	protein_coding
LCN8	HGNC	27038	protein_coding
LDLRAD2	HGNC	32071	protein_coding
LEMD3	HGNC	28887	protein_coding
LFNG	HGNC	6560	protein_coding
LILRA4	HGNC	15503	protein_coding
LIMK1	HGNC	6613	protein_coding
LINGO3	HGNC	21206	protein_coding
LMBR1L	HGNC	18268	protein_coding
LMO7	HGNC	6646	protein_coding
LNPEP	HGNC	6656	protein_coding
LONRF1	HGNC	26302	protein_coding
LONRF3	HGNC	21152	protein_coding
LONRF3	HGNC	21152	protein_coding
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LRP5L	HGNC	25323	protein_coding
LRP5L	HGNC	25323	protein_coding
LRPAP1	HGNC	6701	protein_coding
LRR1	HGNC	19742	protein_coding
LRRC18	HGNC	23199	protein_coding
LRRCC1	HGNC	29373	protein_coding
LRRIQ1	HGNC	25708	protein_coding
LSG1	HGNC	25652	protein_coding
LSM14A	HGNC	24489	protein_coding
LSM6	HGNC	17017	protein_coding

LSS	HGNC	6708	protein_coding
LTN1	HGNC	13082	protein_coding
LUZP2	HGNC	23206	protein_coding
LYPD4	HGNC	28659	protein_coding
LYSMD1	HGNC	32070	protein_coding
LZTS2	HGNC	29381	protein_coding
LZTS2	HGNC	29381	protein_coding
MAD1L1	HGNC	6762	protein_coding
MAD2L1	HGNC	6763	protein_coding
MAGEA1	HGNC	6796	protein_coding
MAGEA12	HGNC	6799	protein_coding
MAGEB4	HGNC	6811	protein_coding
MAGEC1	HGNC	6812	protein_coding
MAGEC2	HGNC	13574	protein_coding
MAGED2	HGNC	16353	protein_coding
MAMDC4	HGNC	24083	protein_coding
MAMLD1	HGNC	2568	protein_coding
MAN1A1	HGNC	6821	protein_coding
MAN2A1	HGNC	6824	protein_coding
MAN2B2	HGNC	29623	protein_coding
MAP1S	HGNC	15715	protein_coding
MAP3K15	HGNC	31689	protein_coding
MAP3K3	HGNC	6855	protein_coding
MAP4K1	HGNC	6863	protein_coding
MAP4K4	HGNC	6866	protein_coding
MAPKAPK3	HGNC	6888	protein_coding
MAST1	HGNC	19034	protein_coding
MAST1	HGNC	19034	protein_coding
MAST4	HGNC	19037	protein_coding
MATN4	HGNC	6910	protein_coding
MCCC1	HGNC	6936	protein_coding
MCM3AP	HGNC	6946	protein_coding
MDGA1	HGNC	19267	protein_coding
MDN1	HGNC	18302	protein_coding
MDN1	HGNC	18302	protein_coding
MECP2	HGNC	6990	protein_coding
MED14	HGNC	2370	protein_coding
MED22	HGNC	11477	protein_coding
MED25	HGNC	28845	protein_coding
MED29	HGNC	23074	protein_coding
MEF2B	HGNC	6995	protein_coding
MEGF6	HGNC	3232	protein_coding
MEP1B	HGNC	7020	protein_coding
MERTK	HGNC	7027	protein_coding
METTL3	HGNC	17563	protein_coding
METTL8	HGNC	25856	protein_coding
MFSD12	HGNC	28299	protein_coding
MGAT5B	HGNC	24140	protein_coding
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MGMT	HGNC	7059	protein_coding
MICAL3	HGNC	24694	protein_coding
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MICAL3	HGNC	24694	protein_coding
MID1	HGNC	7095	protein_coding

MINK1	HGNC	17565	protein_coding
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MLEC	HGNC	28973	protein_coding
MLK4	Uniprot_gn		protein_coding
MLLT1	HGNC	7134	protein_coding
MMP21	HGNC	14357	protein_coding
MNX1	HGNC	4979	protein_coding
MOB3A	HGNC	29802	protein_coding
MORC4	HGNC	23485	protein_coding
MORC4	HGNC	23485	protein_coding
MORF4L1	HGNC	16989	protein_coding
MPZL3	HGNC	27279	protein_coding
MRE11A	HGNC	7230	protein_coding
MROH7	HGNC	24802	protein_coding
MROH7	HGNC	24802	protein_coding
MROH7	HGNC	24802	protein_coding
MRPL10	HGNC	14055	protein_coding
MRPL41	HGNC	14492	protein_coding
MRPL43	HGNC	14517	protein_coding
MRPS10	HGNC	14502	protein_coding
MRVI1	HGNC	7237	protein_coding
MSH2	HGNC	7325	protein_coding
MSMO1	HGNC	10545	protein_coding
MTOR	HGNC	3942	protein_coding
MTR	HGNC	7468	protein_coding
MTR	HGNC	7468	protein_coding
MTR	HGNC	7468	protein_coding
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MYO15A	HGNC	7594	protein_coding
MYO18B	HGNC	18150	protein_coding
MYO19	HGNC	26234	protein_coding
MYO1F	HGNC	7600	protein_coding
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MYO9B	HGNC	7609	protein_coding
MYOG	HGNC	7612	protein_coding
MYPN	HGNC	23246	protein_coding
MYRF	HGNC	1181	protein_coding
MYSM1	HGNC	29401	protein_coding

NAA35	HGNC	24340	protein_coding
NACC2	HGNC	23846	protein_coding
NAGPA	HGNC	17378	protein_coding
NAPSA	HGNC	13395	protein_coding
NAT9	HGNC	23133	protein_coding
NBAS	HGNC	15625	protein_coding
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NCAN	HGNC	2465	protein_coding
NCAPD2	HGNC	24305	protein_coding
NCAPD3	HGNC	28952	protein_coding
NCAPH	HGNC	1112	protein_coding
NCOA6	HGNC	15936	protein_coding
NCOR1	HGNC	7672	protein_coding
NDUFS2	HGNC	7708	protein_coding
NEB	HGNC	7720	protein_coding
NEB	HGNC	7720	protein_coding
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NENF	HGNC	30384	protein_coding
NEXN	HGNC	29557	protein_coding
NFKB1	HGNC	7794	protein_coding
NFKB2	HGNC	7795	protein_coding
NFKBIZ	HGNC	29805	protein_coding
NHLRC1	HGNC	21576	protein_coding
NHSL1	HGNC	21021	protein_coding
NID1	HGNC	7821	protein_coding
NIN	HGNC	14906	protein_coding
NIPAL3	HGNC	25233	protein_coding
NIPAL4	HGNC	28018	protein_coding
NIPBL	HGNC	28862	protein_coding
NIPSNAP1	HGNC	7827	protein_coding
NISCH	HGNC	18006	protein_coding
NKX2-8	HGNC	16364	protein_coding
NLGN3	HGNC	14289	protein_coding
NLRC4	HGNC	16412	protein_coding
NLRP5	HGNC	21269	protein_coding
NLRP5	HGNC	21269	protein_coding
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NLRP9	HGNC	22941	protein_coding
NOC4L	HGNC	28461	protein_coding
NOL6	HGNC	19910	protein_coding
NOP14	HGNC	16821	protein_coding
NOP56	HGNC	15911	protein_coding
NOS1AP	HGNC	16859	protein_coding
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NOTCH1	HGNC	7881	protein_coding
NOTCH1	HGNC	7881	protein_coding
NPC1L1	HGNC	7898	protein_coding
NPFFR1	HGNC	17425	protein_coding
NPSR1	HGNC	23631	protein_coding

NPTX2	HGNC	7953	protein_coding
NR1D2	HGNC	7963	protein_coding
NR1I3	HGNC	7969	protein_coding
NRDE2	HGNC	20186	protein_coding
NSD1	HGNC	14234	protein_coding
NSUN2	HGNC	25994	protein_coding
NT5DC2	HGNC	25717	protein_coding
NTF4	HGNC	8024	protein_coding
NUDCD3	HGNC	22208	protein_coding
NUFIP1	HGNC	8057	protein_coding
NUGGC	HGNC	33550	protein_coding
NUP107	HGNC	29914	protein_coding
NUP214	HGNC	8064	protein_coding
NUP43	HGNC	21182	protein_coding
NUP50	HGNC	8065	protein_coding
NUP54	HGNC	17359	protein_coding
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NUP88	HGNC	8067	protein_coding
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NXF3	HGNC	8073	protein_coding
NXF5	HGNC	8075	protein_coding
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NXF5	HGNC	8075	protein_coding
NXN	HGNC	18008	protein_coding
OARD1	HGNC	21257	protein_coding
OBSL1	HGNC	29092	protein_coding
OGFOD3	HGNC	26174	protein_coding
OPA3	HGNC	8142	protein_coding
OR2AE1	HGNC	15087	protein_coding
OR3A1	HGNC	8282	protein_coding
OR4A16	HGNC	15153	protein_coding
OR4A5	HGNC	15162	protein_coding
OR4C16	HGNC	15172	protein_coding
OR51B4	HGNC	14708	protein_coding
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OSBPL2	HGNC	15761	protein_coding
OSGIN1	HGNC	30093	protein_coding
OSGIN1	HGNC	30093	protein_coding
OSMR	HGNC	8507	protein_coding
OTUD7A	HGNC	20718	protein_coding
OXA1L	HGNC	8526	protein_coding
P2RY4	HGNC	8542	protein_coding
P4HB	HGNC	8548	protein_coding
PABPC4	HGNC	8557	protein_coding
PACS1	HGNC	30032	protein_coding
PAGE5	HGNC	29992	protein_coding
PALM	HGNC	8594	protein_coding
PANK1	HGNC	8598	protein_coding
PANK1	HGNC	8598	protein_coding
PANK4	HGNC	19366	protein_coding
PAPOLG	HGNC	14982	protein_coding

PARS2	HGNC	30563	protein_coding
PARVA	HGNC	14652	protein_coding
PARVB	HGNC	14653	protein_coding
PAX8	HGNC	8622	protein_coding
PBOV1	HGNC	21079	protein_coding
PCDH15	HGNC	14674	protein_coding
PCDH9	HGNC	8661	protein_coding
PCLO	HGNC	13406	protein_coding
PCMT1	HGNC	8728	protein_coding
PCNT	HGNC	16068	protein_coding
PDE12	HGNC	25386	protein_coding
PDE1A	HGNC	8774	protein_coding
PDE2A	HGNC	8777	protein_coding
PDE6C	HGNC	8787	protein_coding
PDGFRA	HGNC	8803	protein_coding
PDGFRB	HGNC	8804	protein_coding
PDGFRB	HGNC	8804	protein_coding
PDSS1	HGNC	17759	protein_coding
PDXDC1	HGNC	28995	protein_coding
PDXDC1	HGNC	28995	protein_coding
PDZD7	HGNC	26257	protein_coding
PEAK1	HGNC	29431	protein_coding
PEAR1	HGNC	33631	protein_coding
PEAR1	HGNC	33631	protein_coding
PEAR1	HGNC	33631	protein_coding
PEPD	HGNC	8840	protein_coding
PEPD	HGNC	8840	protein_coding
PFKP	HGNC	8878	protein_coding
PFKP	HGNC	8878	protein_coding
PGAP1	HGNC	25712	protein_coding
PGK1	HGNC	8896	protein_coding
PGLYRP2	HGNC	30013	protein_coding
PGLYRP3	HGNC	30014	protein_coding
PHF2	HGNC	8920	protein_coding
PHIP	HGNC	15673	protein_coding
PHKA1	HGNC	8925	protein_coding
PHLDB1	HGNC	23697	protein_coding
PHRF1	HGNC	24351	protein_coding
PIFO	HGNC	27009	protein_coding
PIGK	HGNC	8965	protein_coding
PIGN	HGNC	8967	protein_coding
PIGW	HGNC	23213	protein_coding
PIK3R5	HGNC	30035	protein_coding
PIKFYVE	HGNC	23785	protein_coding
PIM3	HGNC	19310	protein_coding
PIWIL3	HGNC	18443	protein_coding
PJA1	HGNC	16648	protein_coding
PKD1L2	HGNC	21715	retained_intron
PKHD1	HGNC	9016	protein_coding
PKP2	HGNC	9024	protein_coding
PLA2G7	HGNC	9040	protein_coding
PLAT	HGNC	9051	protein_coding
PLB1	HGNC	30041	protein_coding
PLCE1	HGNC	17175	protein_coding
PLCE1	HGNC	17175	protein_coding

PLCE1	HGNC	17175	protein_coding
PLCE1	HGNC	17175	protein_coding
PLCG2	HGNC	9066	protein_coding
PLCH2	HGNC	29037	protein_coding
PLCH2	HGNC	29037	protein_coding
PLEC	HGNC	9069	protein_coding
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PLEKHG5	HGNC	29105	protein_coding
PLEKHH1	HGNC	17733	protein_coding
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PLEKHN1	HGNC	25284	protein_coding
PLK5	HGNC	27001	protein_coding
PLXDC1	HGNC	20945	protein_coding
PLXNB2	HGNC	9104	protein_coding
PNISR	HGNC	21222	protein_coding
PNPLA1	HGNC	21246	protein_coding
PNPLA3	HGNC	18590	protein_coding
PNPLA6	HGNC	16268	protein_coding
POC1B-GALNT4	HGNC	42957	protein_coding
POLR2G	HGNC	9194	protein_coding
POLR3F	HGNC	15763	protein_coding
POLR3F	HGNC	15763	protein_coding
POSTN	HGNC	16953	protein_coding
POU5F1B	HGNC	9223	protein_coding
PPARG	HGNC	9236	protein_coding
PPARG	HGNC	9236	protein_coding
PPIL2	HGNC	9261	protein_coding
PPM1E	HGNC	19322	protein_coding
PPOX	HGNC	9280	protein_coding
PPP1R27	HGNC	16813	protein_coding
PPP2R2D	HGNC	23732	protein_coding
PPP2R3A	HGNC	9307	protein_coding
PQBP1	HGNC	9330	protein_coding
PRDM5	HGNC	9349	protein_coding
PRDM8	HGNC	13993	protein_coding
PRDX4	HGNC	17169	protein_coding
PRDX4	HGNC	17169	protein_coding
PRDX4	HGNC	17169	protein_coding
PREP	HGNC	9358	protein_coding
PREX2	HGNC	22950	protein_coding
PRG2	HGNC	9362	protein_coding
PRIMPOL	HGNC	26575	protein_coding
PRKCD	HGNC	9399	protein_coding
PRKCD	HGNC	9399	protein_coding
PRKCZ	HGNC	9412	protein_coding
PRMT5	HGNC	10894	protein_coding
PRR22	HGNC	28354	protein_coding
PRR5	HGNC	31682	protein_coding
PRR5-ARHGAP8	HGNC	34512	protein_coding
PRSS36	HGNC	26906	protein_coding

PRUNE2	HGNC	25209	protein_coding
PSG2	HGNC	9519	protein_coding
PSG7	HGNC	9524	polymorphic_pseudogene
PSG9	HGNC	9526	protein_coding
PSMD12	HGNC	9557	protein_coding
PSMG1	HGNC	3043	protein_coding
PSMG2	HGNC	24929	protein_coding
PTGR1	HGNC	18429	protein_coding
PTPRE	HGNC	9669	protein_coding
PTPRF	HGNC	9670	protein_coding
PTPRG	HGNC	9671	protein_coding
PTPRK	HGNC	9674	protein_coding
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PUM1	HGNC	14957	protein_coding
PYGO1	HGNC	30256	protein_coding
PYROXD1	HGNC	26162	protein_coding
RAB11FIP4	HGNC	30267	protein_coding
RAB17	HGNC	16523	protein_coding
RAB38	HGNC	9776	protein_coding
RAB41	HGNC	18293	protein_coding
RABEP1	HGNC	17677	protein_coding
RABGGTA	HGNC	9795	protein_coding
RAC3	HGNC	9803	protein_coding
RAD51B	HGNC	9822	protein_coding
RADIL	HGNC	22226	protein_coding
RAF1	HGNC	9829	protein_coding
RAI14	HGNC	14873	protein_coding
RAP1GAP	HGNC	9858	protein_coding
RAPGEF3	HGNC	16629	protein_coding
RAPSN	HGNC	9863	protein_coding
RASSF1	HGNC	9882	protein_coding
RBM10	HGNC	9896	protein_coding
RBM26	HGNC	20327	protein_coding
RBM27	HGNC	29243	protein_coding
RBPMS	HGNC	19097	protein_coding
RECK	HGNC	11345	protein_coding
RELB	HGNC	9956	protein_coding
REPS1	HGNC	15578	protein_coding
RETNLB	HGNC	20388	protein_coding
RFPL1	HGNC	9977	protein_coding
RFT1	HGNC	30220	protein_coding
RFT1	HGNC	30220	protein_coding
RFTN1	HGNC	30278	protein_coding
RGL3	HGNC	30282	protein_coding
RGS7	HGNC	10003	protein_coding
RIBC2	HGNC	13241	protein_coding
RIPK4	HGNC	496	protein_coding
RMND5A	HGNC	25850	protein_coding
RMND5A	HGNC	25850	protein_coding
RNASEH2A	HGNC	18518	protein_coding
RNASEL	HGNC	10050	protein_coding

RND2	HGNC	18315	protein_coding
RNF175	HGNC	27735	protein_coding
RNF19B	HGNC	26886	protein_coding
RNF222	HGNC	34517	protein_coding
ROBO1	HGNC	10249	protein_coding
ROBO1	HGNC	10249	protein_coding
ROCK2	HGNC	10252	protein_coding
ROR1	HGNC	10256	protein_coding
ROS1	HGNC	10261	protein_coding
RP1-130H16.18	Clone_based_vega_gene		protein_coding
RP11-173B14.4	Clone_based_vega_gene		sense_intronic
RP11-248J23.6	Clone_based_vega_gene		protein_coding
RP11-551L14.1	Clone_based_vega_gene		transcribed_unprocessed_pseuc
RP3-467K16.2	Clone_based_vega_gene		antisense
RPAP3	HGNC	26151	protein_coding
RPH3AL	HGNC	10296	protein_coding
RPL18A	HGNC	10311	protein_coding
RPL23A	HGNC	10317	protein_coding
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RPL3	HGNC	10332	protein_coding
RPS4X	HGNC	10424	protein_coding
RPS6KA2	HGNC	10431	protein_coding
RPTOR	HGNC	30287	protein_coding
RPTOR	HGNC	30287	protein_coding
RRP1B	HGNC	23818	protein_coding
RRP1B	HGNC	23818	protein_coding
RSAD1	HGNC	25634	protein_coding
RSU1	HGNC	10464	protein_coding
RTN3	HGNC	10469	protein_coding
RUFY1	HGNC	19760	protein_coding
RUFY1	HGNC	19760	protein_coding
RUFY2	HGNC	19761	protein_coding
RXRA	HGNC	10477	protein_coding
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RYR2	HGNC	10484	protein_coding
RYR2	HGNC	10484	protein_coding
RYR3	HGNC	10485	protein_coding
SAP18	HGNC	10530	protein_coding
SARDH	HGNC	10536	protein_coding
SBDS	HGNC	19440	protein_coding
SBF1	HGNC	10542	protein_coding
SBF2	HGNC	2135	protein_coding
SCAF1	HGNC	30403	protein_coding
SCAMP3	HGNC	10565	protein_coding
SCARF2	HGNC	19869	protein_coding
SCEL	HGNC	10573	protein_coding
SCIN	HGNC	21695	protein_coding
SCLT1	HGNC	26406	protein_coding
SCLT1	HGNC	26406	protein_coding
SCML4	HGNC	21397	protein_coding
SCN3A	HGNC	10590	protein_coding
SCN9A	HGNC	10597	protein_coding

SCN9A	HGNC	10597	protein_coding
SDE2	HGNC	26643	protein_coding
SDK1	HGNC	19307	protein_coding
SEC13	HGNC	10697	protein_coding
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SEC16B	HGNC	30301	protein_coding
SEC23B	HGNC	10702	protein_coding
SEC24D	HGNC	10706	protein_coding
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SELE	HGNC	10718	protein_coding
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SEMA3A	HGNC	10723	protein_coding
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SEMA3F	HGNC	10728	protein_coding
SEPT3	HGNC	10750	protein_coding
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SERTAD1	HGNC	17932	protein_coding
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SEZ6L	HGNC	10763	protein_coding
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SGPL1	HGNC	10817	protein_coding
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SH3GLB1	HGNC	10833	protein_coding
SH3PXD2A	HGNC	23664	protein_coding
SHANK1	HGNC	15474	protein_coding
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SHH	HGNC	10848	protein_coding
SHROOM2	HGNC	630	protein_coding
SIGLEC12	HGNC	15482	protein_coding
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SIM2	HGNC	10883	protein_coding
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WWP2	HGNC	16804	protein_coding
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CANONICAL	CCDS	ENSP	SWISSPROT
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YES	CCDS5783.1	ENSP00000377040	Q9UDR5
YES	CCDS11684.1	ENSP00000269081	Q8WWZ4
YES	CCDS10466.1	ENSP00000301732	Q99758
YES	CCDS11683.1	ENSP00000284425	Q8N139
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YES	CCDS10568.1	ENSP00000205557	O95255
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YES	CCDS46769.1	ENSP00000382379	O15084
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YES	CCDS46854.1	ENSP00000341071	Q9NR81
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YES	CCDS35006.1	ENSP00000368189	A6NKF2
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YES	CCDS47750.2	ENSP00000391137	Q8WXI3
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	UPI0000163938	NM_138340.4	
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B4DQ51	UPI00001251DF	NM_001609.3	
	UPI000006F1E1	NM_022735.3	
	UPI000003FD52	NM_133492.2	
F5GWV7	UPI0000131FE1	NM_001610.2	
D6RE60,D6RDP0,D6R92	UPI0000048EC7	NM_001037172.1	
H0YNX0,F5H4U6	UPI000006E955	_001199377.1,NM_015162.4	
755,F5H5A1,F5H3B2,F5H	UPI00001AF19E	1127214.2,NM_001243279.1,NM_001284316.1	
	UPI0000DD812A	NM_001080454.1	
Q71UM3,Q4VAU9	UPI00001AF0AE	NM_001106.3	
	UPI000035CC78	NM_207197.2	tolerated(0.13)
540,Q53RS1,Q53RF5,B2F	UPI00001254D4	NM_003183.4	
	UPI000013E57B	NM_139155.2	deleterious(0.01)
	UPI00001AE729	NM_014244.4	
	UPI00004565F4	NM_025003.3	
	UPI000014194C	NM_005099.4	
Q5IR90	UPI000050D3F1	NM_197941.2	
H7BYE3	UPI000004FD83	NM_001040272.5	
	UPI00000503E1	NM_001048230.1	
	UPI000004C602	NM_020683.6	
	UPI0000071FAF	NM_001287824.1	
2L1,F5GXF9,D6RIZ5,D6F	UPI000013EC52	NM_001166693.1	
	UPI000049E130	_002025.3,NM_001169123.1	
Q96T14,D3DX07	UPI0000DAC777	NM_031946.5	
	UPI000192952B	NM_178563.3	
Q53YY0,D3DNG8	UPI0000039D66	NM_031850.3	
	UPI00000701FB	NM_001134830.1	
Q549J4,H3BSK6	UPI0000001C48	NM_016633.2	
Q5THU2,Q5T2H0	UPI000006F22E	_016108.2,NM_001286587.1	
E9PIR9	UPI0001F7836C	NM_001039775.3	
E9PIR9	UPI0001F7836C	NM_001039775.3	
F1T0C0,F1T0B6	UPI0000125741	_014336.3,NM_0010330[illegible]	tolerated(0.08)
	UPI0000030FA6	NM_000383.3	
	UPI0000030FA6	NM_000383.3	
Q8IW64	UPI000002A38D	M_147185.2,NM_005751.4	
Q8IW64	UPI000002A38D	M_147185.2,NM_005751.4	
	UPI00000362E9	NM_020299.4	
	UPI000002C1AC	NM_000477.5	

F8WBH3	UPI000013E0FF	NM_153329.3	
	UPI00001AFAF8	NM_000693.2	
E5FPY7	UPI0000043F84	_000698.3,NM_001256153.1	
	UPI000013D013	NM_020778.4	
	UPI000013D013	NM_020778.4	
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	UPI000006EC6E	NM_022662.3	
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	UPI0000EE047B	NM_001244752.1	erated_low_confidence(0.
	UPI000006FC41	_014915.2,NM_001256053.1	
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	UPI000013E1CE	NM_144698.4	
	UPI0000237861	NM_173595.3	
	UPI00004572EF	NM_024669.2	
C9J244,B4DNI5	UPI0000071863	NM_001159.3	
Q8NEQ1	UPI000006F684		
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	UPI00001D89D8	_001252127.1,NM_007347.4	
	UPI00001D89D8	_001252127.1,NM_0073	deleterious(0)
	UPI00001AF165	NM_019043.3	
	UPI00001D6936	NM_198450.5	
	UPI00000743B9	NM_198998.2	deleterious(0)
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	UPI0000457329	NM_173800.4	deleterious(0.01)
F5H6T5,F5H1V1,F5H0C7	UPI00000012C8	NM_001659.2	
Q8ND72,Q3KQX3	UPI000013EA63	NM_024605.3	tolerated(0.59)
	UPI0000D60FAD		
	UPI0000041347	NM_144967.3	
Q6PJ34,C9JLA8,C9J5M2	UPI000019275E	NM_001164741.1	
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	UPI000045892C	)01162384.1,NM_001162383.1	
C9J609,C9J5K8	UPI00001B3D98	NM_001128615.1	tolerated(0.07)
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	UPI0000509F06	NM_001017363.1	
B0YIW9	UPI000006F7A5	NM_178815.3	
C9J8P8,C9J625,B7Z979	UPI000007471D	NM_015396.4	
F8W8Y7	UPI0002466A58	NM_001256155.1	
F8W8Y7	UPI0002466A58	NM_001256155.1	
F8W8Y7	UPI0002466A58	NM_001256155.1	
F8W8Y7	UPI0002466A58	NM_001256155.1	
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	UPI000003F083	_015683.1,NM_001286826.1	
	UPI000013C6C4	NM_000487.5	deleterious(0.05)
	UPI00001260C8	NM_001670.2	
	UPI000020F32F		
	UPI0000E5A753	_001142733.2,NM_130387.5	
	UPI00001260E8	NM_016116.2	

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	UPI000007263D	NM_001251888.1	
	UPI0000161978	NM_001002036.3	
	UPI0000161978	NM_001002036.3	
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	UPI00001FCB27		
Q8N4D4	UPI0000049724		
Q58I22	UPI0000124FC1	NM_000702.3	
Q13818	UPI0000124FC5	NM_144699.3	
	UPI0000252110	NM_014861.2	
Q8TAS0,B4DL14,B4DFE6	UPI0000126574	NM_001001973.1	
	UPI000013E478	NM_000052.5	
K7ERI0,K7EQC4	UPI000013DD54	NM_005603.4	
Q2NLD0,B4DR18	UPI000004D334	NM_006045.1	
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C9IZM8	UPI0000070A6A	NM_130384.2	
H3BSQ5	UPI000016783F	NM_148414.2	
	UPI00002122D8	NM_001013579.2	
	UPI00001D7BE0	NM_001002254.1	
D6RDY4,D6RCN1,D6RB8	UPI000022AC91	NM_144696.5	tolerated(0.19)
	UPI000012669E	NM_003502.3	
M0R199,M0QX58	UPI000007021E	NM_014256.3	tolerated(0.12)
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	UPI0000071E58	NM_003933.4	
C9J8H7	UPI0000231CAC	NM_001178007.1	tolerated(0.35)
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F2Z3H6	UPI000006FE5A	NM_001707.3	
Q9HAM3	UPI00001B4EFB	NM_021946.4	
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	UPI00001AEA67	NM_001714.2	
Q2MD56	UPI000006FDD6	NM_013314.3	
	UPI000013CD7C	NM_005448.2	tolerated(0.3)
	UPI0000126796	NM_001717.3	
	UPI00000377B0	NM_025227.2	
	UPI00002263BF	NM_182641.3	
',K4K7V3,K4JXS7,K4JUB	UPI0000E0360B	NM_007300.3	
',K4K7V3,K4JXS7,K4JUB	UPI0000E0360B	NM_007300.3	
',K4K7V3,K4JXS7,K4JUB	UPI0000E0360B	NM_007300.3	
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	UPI000020BEBE	NM_023924.4	
	UPI0000163C12	NM_018963.4	
	UPI00017A7DA9		
R4GN83,R4GMX5	UPI0000051E38	NM_001728.3	
R4GN83,R4GMX5	UPI0000051E38	NM_001728.3	
	UPI00003CEFB9	NM_144587.2	
	UPI00003CEFB9	NM_144587.2	deleterious(0.01)
	UPI000014114A	NM_183242.3	
Q6IBC8,F8W0U7	UPI00000246C2	NM_001731.2	
Q8N324	UPI000004C620	NM_152547.4	
	UPI000013D7E3		

B1AVV1	UPI00001F8E63	NM_001164375.2	
	UPI0000161572		
S4R3N7,Q5T025	UPI00001D808F	NM_001004298.2	
E9PI28	UPI0000070A8D		
F8VVN2	UPI000004A078	NM_024738.1	tolerated(0.36)
R4GNI2,E9PJL5	UPI0001F77A4D		
	UPI00001608A3	NM_175874.3	
	UPI00001FD205		
	UPI00001C0FE1	NM_001145536.1	
	UPI0000073E49	_024032.3,NM_001171251.1	
K7EJP2	UPI000059D617		tolerated_low_confidence(0.
	UPI000006DC1A	NM_033520.1	
	UPI000004C659	NM_001011551.2	tolerated(1)
	UPI00004701CD	NM_001130957.1	
	UPI0000470AFA		
	UPI000022AE5B	NM_001004303.4	
	UPI0000237200	NM_001002912.4	
	UPI0000035539	NM_198593.3	
C9JP86,C9JEK0	UPI000049DF42	NM_001085437.1	
G3XAA6	UPI0000EE2496	NM_001145054.1	
Q6LDJ0,M0R1Q1	UPI000013EC9B	NM_000064.2	
D6RGX5	UPI00006C511D	NM_001039717.1	
	UPI000013C838	NM_001735.2	
	UPI000013C838	NM_001735.2	
	UPI00004573AE	NM_001085401.2	
	UPI000020CA08	NM_000587.2	
I3L375,B4DGL6	UPI000000167C	NM_020178.4	
	UPI0000126DF3	NM_001739.1	
	UPI0000126D6C	NM_001199281.1	deleterious(0)
Q9UN69,Q9UHM9	UPI0000141565	M_001174080.1,NM_023035.2,NM_000068.3	
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	UPI0001C0B380	NM_001170692.1	
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	UPI000013FFDA		
D6W5A4	UPI0000070B33	NM_024766.4	
Q8WZ12,D6W648	UPI0000161861	NM_001080429.2	
	UPI00000383D5	NM_007058.3	
	UPI000006E882	NM_006615.2	
Q96ET4,K7ES72	UPI00001270F7	NM_004058.3	
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B2CIS9	UPI0000044176	NM_012114.2	
C9JAC8	UPI0000204B81		
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Q32MQ2	UPI000022A813	NM_021185.4	
	UPI00001270F2	M_001234.4,NM_033337.2	
	UPI000013CFBA	NM_033212.3	
	UPI000013E20A		
	UPI0000073091	NM_173482.2	tolerated(0.11)

	UPI000014C50D	NM_145020.3	
	UPI0001AFF95B	2.2,NM_001163321.2,NM_001163323.2	
A7MD03	UPI000015F998	NM_017667.3	
H6QX63	UPI00001983C7	NM_199287.2	
B4DK97	UPI0000160405	NM_001008723.1	
	UPI00004DF23B	NM_001042784.1	deleterious(0.03)
	UPI00017A803A	NM_001198910.1	
	UPI0001F78148		
	UPI000022A20F		
	UPI000035B25A	NM_005436.4	
B4DQN0	UPI0000E5BE97	NM_001156474.1	
Q6IBD6	UPI00001362DB	NM_006274.2	
L7REX9,E9PH76,B4XH6	UPI0000043585	NM_001123041.2	
N1,Q5XUM8,Q5XUM6,F	UPI000013DE92		tolerated(0.27)
	UPI000042263C	NM_001008784.2	
	UPI0000367808		
J3QKQ4	UPI0000073EA9	_007261.3,NM_001256841.1	
K7EQC8	UPI0000070847	NM_012099.1	tolerated(0.53)
Q06C42	UPI000015FF6E	NM_172359.2	
Q29VG3,Q29VG2,J3QLC	UPI00000359A4	NM_006137.6	
	UPI000020C69D	NM_004661.3	
	UPI000047C9E2	NM_017525.2	
C9K087	UPI000042153E	NM_001178010.2	
	UPI000013E304	NM_022842.4	tolerated(0.37)
	UPI0000126DBD		
Q5JQZ9	UPI0000070643	NM_015076.3	
K7ELV5,K7EJ83	UPI0000113587		
D6REC6,D6R9G1	UPI0000127431	NM_001799.3	
	UPI000013DA21	NM_017774.3	
	UPI0000136103	NM_001037343.1	
	UPI0000001293	NM_003818.3	
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	UPI0000D617B1		
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7J3,C9IZA8,B4E3Q4,B4D	UPI000013D2E8	NM_001282228.1	
	UPI0001AE62C8	NM_031413.3	
	UPI0001AE62C8	NM_031413.3	deleterious(0.02)
	UPI000000D9E5	NM_033070.2	
	UPI0000127513	NM_031890.3	
Q5JX02,Q5JX01	UPI000004A007	NM_006733.2	
	UPI000013FCDF		tolerated(0.07)
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Q5JWS6,Q5JWS5,G1UI4	UPI000006FE8F	NM_007186.3	
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C9JZ04,C9J0F4	UPI000013D5A3	NM_024491.2	tolerated(0.69)
K7ENV0,B4DMD2	UPI000006F4B3	NM_138363.1	
B7ZBT0,B7ZBS9,B7ZBS8	UPI000046FF85	NM_016174.4	
J3QLP1,J3QKN7	UPI0000074733	NM_003869.5	
	UPI000013C4D1	NM_000186.3	tolerated(1)
,Q6KEF5,Q6KEE7,Q6KE	UPI000013C4D4	NM_000492.3	
J3KP00	UPI00001619C1		
B5MDZ7	UPI000020566F	6336.1,NM_024568.2,NM_004284.4	
U3KQ08,F5H829,F5H7R8	UPI000006FA02		

U3KQ08,F5H829,F5H7R8	UPI000006FA02		
RL9,E9PR52,E9PPX4,E9	UPI0000126C1A		deleterious(0.03)
I3L535,B7Z5H1,B7Z2M6	UPI0000125257	NM_000747.2	
	UPI000004616D	NM_130468.3	
I3L2E5	UPI0000456914	_000246.3,NM_001286402.1	
	UPI0001D0C47E		
	UPI0000683C41	NM_001206999.1	
RD8,C9J7P8,C9J300,C9J	UPI0000212358		tolerated(1)
D6R998,B3KVA7	UPI000013CE0D	NM_001825.2	
	UPI000013F2D3	NM_001286.3	
	UPI0000127993		
	UPI0000127AB6	NM_001185080.1	
	UPI0000037798	NM_014358.2	
	UPI0000169FC8	NM_001289.4	
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	UPI0000070D72	NM_014927.3	
F2YHU6,B3KPD2	UPI0000E19A44	NM_020348.2	
H3BT18,H3BPF1,B7Z6X2	UPI00001FF2F6	_016284.4,NM_001265612.1	
B3KNB0	UPI00000715FD	NM_017546.4	
S5TLS4,Q9BYY6,F8W187	UPI00000008AA	)01160258.1,NM_001160226.1	
G3XAD4,C9JMQ2,C9JGK	UPI000007446C	NM_001206955.1	
II8,Q75MQ9,Q75MF8,Q75	UPI00001285FA	NM_014141.5	
II8,Q75MQ9,Q75MF8,Q75	UPI00001285FA	NM_014141.5	
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C9J9X1	UPI00001A9480	NM_015198.3	
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U3KQU7,B3KMW0	UPI0000246D05	NM_006348.3	
	UPI000006DB58	NM_000494.3	
	UPI0000062274	NM_173465.3	
E9PNK8	UPI000013E81F	NM_152890.5	
E9PNK8	UPI000013E81F	NM_152890.5	
C9JPW4	UPI00004575C9	_001278563.1,NM_13345	tolerated(0.09)
B4DU54	UPI000049E122	NM_001847.2	
	UPI00002032A3	NM_015719.3	
Q05BT9	UPI000019B179	NM_001848.2	
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B3KM21	UPI000006D3AA	NM_198076.4	
	UPI000045718B	NM_000096.3	
H3BPD6,H3BNX1,G8JLI7	UPI000018CEBD	NM_030594.3	
	UPI000020C179	NM_030627.2	
	UPI0000366600	NM_001006658.2	tolerated(1)
	UPI000022D9DE	NM_173689.5	
	UPI000002A720	)01202475.1,NM_001202481.1	
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	UPI00004A39A7	NM_016652.5	
	UPI00001FEB98		
	UPI00006E232D	NM_153605.3	
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	UPI0001BE8116	_014780.4,NM_00116837	deleterious(0)
	UPI00001AEB98	NM_001202543.1	
	UPI00001AEB98	NM_001202543.1	deleterious(0)
B7WP74	UPI00001C1DAE	NM_020943.2	
B7WP74	UPI00001C1DAE	NM_020943.2	
Q6PIV4	UPI00005A81B4	NM_152434.2	tolerated(1)
	UPI00001A92CE	NM_001142797.1	
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E9PRM4,E9PMI2,E9PIV9	UPI000013E5AB		
	UPI000013E07A	NM_000766.4	
	UPI000013E07A	NM_000766.4	
M0,Q7Z448,Q6GRK0,B4	UPI000013E0B7	_001202855.2,NM_017460.5	
	UPI000013D3F9	NM_023944.3	tolerated(0.1)
	UPI000013C4D5	NM_000786.3	
	UPI00001678B3	NM_006133.2	
Q53R85,D3DP78,C9JQM	UPI000013639B	NM_001349.2	
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	UPI0000203531	NM_138353.2	
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	UPI000013DA24	_001195610.1,NM_016356.4	
	UPI00002372F1	NM_001142552.1	
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F5GXJ8	UPI000006F88F	M_030653.3,NM_152438.1	
F5GXJ8	UPI000006F88F	M_030653.3,NM_152438.1	
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B3KWN5	UPI00001C1F29	_015213.3,NM_0012432	tolerated(0.58)
	UPI000020C7D4	NM_018369.2	
B7Z8B7,B7Z3C4	UPI0000001613	_001184781.1,NM_005137.2	
C9JA18,B7Z3B3	UPI0000033B9B		
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	UPI00000467F4	NM_018180.2	
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J7,Q6UUU0,E5RJ79,B4D	UPI0000EA87E6	NM_005219.4	
Q96IB4	UPI0000406CA1	NM_173602.2	
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C4P0C8	UPI0000458AE1	NM_001012959.1	
C4P0C8	UPI0001A61692	NM_001164539.1	
	UPI0000051057	NM_014420.2	
F8W750,E9PQT9	UPI0000E59399	NM_001142699.1	
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	UPI0000470041	NM_004747.3	
Q5T3U0	UPI0000051E36	NM_206539.1	

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O15436	UPI00017AA3A8	NM_178504.4	
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	UPI0001A5EE11		
	UPI00003677EB		
Q92865	UPI0000141BA2	NM_001372.3	
	UPI00001D6A0B	NM_003462.3	
Q66K39	UPI000006DA43	NM_021233.2	
B4E0Q3	UPI000013D6C9	NM_015221.2	
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	UPI000007412C	NM_004947.4	
	UPI000002A839	NM_032482.2	
H3BQS5,H3BP43	UPI000006DF95	NM_004413.3	tolerated(0.23)
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Q96DC6,B3KWP1	UPI000003B000	395.1,NM_001077394.1,NM_015958.2	
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	UPI000013D388	NM_001939.2	
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	UPI000013CF4B	NM_001944.2	
	UPI000035DB4E	NM_001134453.1	
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G1UI31,B4DKX6	UPI000013C67F	NM_004415.2	
Q86T18	UPI00001C1577	NM_015548.4	
	UPI000006F286	NM_080664.2	
D6RAR7	UPI000006F968	667.1,NM_001271668.1,NM_032122.4	
	UPI00000738F2	NM_173666.2	
JY61,C9JVC8,C9JS11,C	UPI00001413A2	NM_020892.2	
F8VX42	UPI0000037B0A	NM_152511.3	
F8VZA4	UPI000013ED2F	NM_001946.2	tolerated(0.1)
Q75MI9,Q75LS9,A4D1I7	UPI0000129A01	NM_004411.4	
	UPI0000481AC7		
Q6IB29,H7C2Q8	UPI0000204E6D	NM_001159936.1	
C9JJ78,C9J719	UPI000000DB82	NM_006579.2	tolerated(0.67)
E9PN99,E9PJG1	UPI0000129B5E	NM_001397.2	tolerated(0.15)
	UPI000013E997	NM_004826.2	
SJ9,Q96J05,C9JTI2,C9J	UPI00003DFD0A	NM_001258315.1	
B7ZBI6	UPI0000E86804		
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Q6FH53	UPI000012A217	_001955.4,NM_001168319.1	
	UPI0000046D5C	NM_001201397.1	
	UPI000013C754	NM_003566.3	
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	UPI000012ED5C	NM_004280.4	
E5RI18,E5RFW6	UPI00001AFEA2	NM_152347.4	
E5RJB7,E5RHB1	UPI0001929531	NM_001144933.1	
	UPI00017A8807	NM_001144958.1	

	UPI0000209A4C	NM_144715.3	
H0YNW8	UPI00001FEA35	NM_024580.5	
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	UPI0000163BD6	NM_001415.3	
B1AL80	UPI0000072B32	NM_001421.3	
	UPI000004E87D	NM_052906.3	
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Q9UMK5	UPI0000D4A0DC	3,NM_001081755.2,NM_001278915.1	
	UPI0000051C66	NM_017770.3	
	UPI0000070A23	427.1,NM_001271428.1,N	tolerated(0.32)
	UPI000013927E	NM_014673.3	
	UPI000013927E	NM_014673.3	
G3V4U5,F8W717	UPI00004A074E	NM_001008707.1	tolerated(0.82)
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	UPI000013E21D	NM_001426.3	
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	UPI0000071D6F	_017993.3,NM_001242863.1	
	UPI0000EE3B3A	NM_001164178.1	
G3V450	UPI0000052B69	NM_001249.2	
	UPI00004566BC	NM_015409.4	
	UPI00006635A8	_004445.4,NM_001280794.1	
R4SBI6,B1AQP9,B1AQP8	UPI000012CFF2	NM_000120.3	tolerated(1)
E5RI53	UPI0000073FE5	NM_001979.5	
	UPI0000201263	NM_001433.3	
H3BRX7	UPI00003668C3	NM_012291.4	
	UPI0000251E45	NM_031913.3	tolerated(0.4)
H0YL83	UPI0000001BC8	NM_000126.3	deleterious(0)
	UPI00001A8223	NM_001014763.1	terious_low_confidence(0
B2RCZ7	UPI0000073C7C	NM_014297.3	
	UPI0000470AFE	NM_005665.4	
	UPI00019145BF	NM_001159944.1	
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K7EQ87	UPI000013E730	NM_001988.2	
K7EQ87	UPI000013E730	NM_001988.2	
C9JLF4	UPI0000577ED7	NM_001193361.1	
Q5T399	UPI000013DDA8	NM_130398.3	tolerated(0.68)
	UPI000013574F	NM_001024924.1	
B7Z9R6	UPI0000167BA1	NM_001111077.1	
Q2VF45,Q003V9,Q003V5	UPI000012A416	NM_000132.3	tolerated(1)
Q2VF45,Q003V9,Q003V5	UPI000012A416	NM_000132.3	
Q19UK5,Q19UK4,Q19UK	UPI000002BA13	NM_000133.3	deleterious(0.05)
B2C6G4	UPI000004CC6F	NM_174912.3	
22,E5RGZ5,E5RGD8,B3I	UPI000003405E	NM_004265.3	
E9PQC2,E9PPZ4	UPI000003405F	NM_021727.3	
Q53XA7,H0YLC7	UPI000012A422		
B4DY02,B0QY28	UPI000022B897	NM_001104595.1	tolerated(0.18)
	UPI0000227E33	NM_001170779.1	
	UPI0000227E33	NM_001170779.1	
	UPI00001613F2	NM_001078173.1	
	UPI00001613F2	NM_001078173.1	
J3QSR3	UPI000057A0DB	NM_015912.3	
	UPI00000373BF	NM_001085480.2	
	UPI00000EB9DB	NM_015159.1	

	UPI000015FCC7	NM_175885.3	
	UPI000020BD7C	NM_015688.1	
	UPI00001D7978	NM_001145475.1	
	UPI0000049306	NM_152481.1	
	UPI00000710DE	NM_006589.2	
	UPI0000551BE9		
	UPI0001AE7915	NM_001163258.1	
H3BP45	UPI0000EE554D	NM_014722.2	
	UPI000045731A	NM_152548.2	tolerated(0.57)
H3BT53	UPI0000520A1A	NM_000135.2	
	UPI000000DB76	NM_021922.2	
	UPI000000DB76	NM_021922.2	
	UPI000000DB76	NM_021922.2	
F8VV73,F8VPF2	UPI0000041260	NM_001271783.1	
C9JWM9,C9JVQ5	UPI0000073D5B	NM_014808.2	
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	UPI000013EB82	NM_004104.4	
	UPI000013EB82	NM_004104.4	
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	UPI000013EB82	NM_004104.4	
Q9Y3V7,C9JQS6	UPI000042B0C1	NM_001004019.1	deleterious(0.03)
	UPI000013D88F		tolerated(0.16)
	UPI00018830C3	NM_001142641.1	
Q08AL4,F5GXN9	UPI00001C1EC6	NM_012166.2	
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	UPI000012ADC1	NM_024907.6	
C9JK86	UPI00004123F1	NM_207102.2	
	UPI000012A581	NM_022039.3	
	UPI0000EE5E27	NM_001170631.1	
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E7EWF4,D6RJD4,D6RG0	UPI000012A72D	M_213647.1,NM_002011	tolerated(0.2)
C9JU00,C9JPQ9	UPI000012A78D	NM_021870.2	
	UPI0000251DB7	NM_025135.2	
	UPI0000251DB7	NM_025135.2	
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	UPI000022BD13	NM_018086.2	
	UPI0000035FBF	NM_030917.3	
	UPI000000165F	NM_003602.4	
	UPI000002A9BC	_001135212.1,NM_181342.2	
C61,Q86TQ3,Q6NXF2,Q6	UPI000013C596	NM_001110556.1	deleterious(0.01)
	UPI0001765F91	NM_001164317.1	
D6RFF2	UPI00001488E7	NM_182925.4	
Q96L17,B4DN09	UPI00015FA087	NM_020066.4	
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	UPI000016A103	NM_001002294.2	
	UPI0000DBEF37	NM_015308.2	
	UPI0000DBEF37	NM_015308.2	
	UPI0000579B80	NM_032532.2	
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	UPI000012ADD6	NM_001452.1	
Q8N4A5,Q69YN9	UPI000007462D	)01012426.1,NM_001012427.1	
	UPI000012AB4D	NM_004957.4	
Q69YV4,Q4W596	UPI000021D4C2	NM_025074.6	
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	UPI0000D615C2	NM_001168235.1	
F8WAN4	UPI0000366665	NM_018027.3	
	UPI000006F96D	NM_152597.4	
4W5Q0,Q4W5K3,Q4W5F	UPI000020B66B	_001128427.2,NM_020116.4	
	UPI00001C1EAA	NM_003934.1	
I68,Q5U805,E3UTT6,A7X	UPI00000338F8	NM_000148.3	
,E9PP56,E9PJB4,E9PJ18	UPI000012ADAC	NM_000150.2	
	UPI00001262A8	NM_001680.4	
C9J2W6	UPI000013E307	NM_024513.3	
	UPI000022BF90	NM_207359.2	
Q59HA5,D6RF16,D6RC24	UPI000012B04A	NM_005255.2	
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	UPI00001FD982	_000153.3,NM_001201401.1	
	UPI00001FD982	_000153.3,NM_001201401.1	
Q71UH7,C8CHJ6	UPI000012B056		
Q4G0E1,D3DQI7	UPI0000041292	NM_198321.3	
	UPI0000073A6F	NM_001253826.1	tolerated(0.52)
Q68VJ3	UPI0000070DEC	NM_017417.1	olerated_low_confidence(0
Q68VJ3	UPI0000070DEC	NM_017417.1	tolerated(0.07)
	UPI00005A72DA		
	UPI00005A72DA		tolerated(0.15)
	UPI00005A72DA		
B4DH81	UPI0000EE56F2	NM_032293.4	
E7ETN8	UPI000004B6D7	_001134486.2,NM_052942.3	
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I3L1L8	UPI000004EDF9	NM_000160.3	
Q8N7N7,Q08M29	UPI000006E705		
Q5SZC3,B4DIP8,B3KUM3	UPI000015828B		
H0UIB3,B7Z4H3	UPI0000038D5C	_024034.4,NM_001256737.1	
	UPI000012B394	NM_016204.1	
	UPI000012B3B7	NM_003616.2	
E5KND5,C9JA25	UPI000006232D	NM_024996.5	
	UPI0000000DD6	NM_000821.5	
K7ENT5,K7EJI6	UPI0000073CAB	NM_152657.3	olerated_low_confidence(0
K7ENT5,K7EJI6	UPI0000073CAB	NM_152657.3	erated_low_confidence(0
K7EQ41,K7EL54	UPI000006E533		tolerated(0.18)
	UPI0000049E0C	NM_138785.3	
	UPI00001393F9	NM_021067.3	tolerated(0.82)
Q6ZMF1,H3BQT1	UPI00001FFBD9	NM_012201.5	
Q6ZMF1,H3BQT1	UPI00001FFBD9	NM_012201.5	
B3KTH4	UPI000013D29C		
	UPI0000169DF9	NM_006708.2	
	UPI000188140C	NM_001024452.2	tolerated(0.4)
	UPI000188140C	NM_001024452.2	
F8VZP2	UPI000004B633	NM_031302.3	
	UPI000003FFB7	NM_145016.3	
Q53SE7	UPI00000704BE	NM_178439.3	
	UPI0000001249	NM_002073.2	
	UPI00000474FA	NM_053004.2	tolerated(0.54)
	UPI000004EEC8	NM_000406.2	
	UPI0000190979	NM_005895.3	

E7ES66,E5FY30,E0D854	UPI0001CB792B	NM_000173.5	
	UPI0000032F5B	NM_005708.3	
	UPI000013C91C	NM_001503.3	
C9JZE8,C9J8H8,B7Z613	UPI00000721CA	NM_001001995.1	
Q53RZ9,B4DQM4	UPI00017A77BC		
	UPI000003BCCD	NM_054021.1	tolerated(0.06)
	UPI0000366736		tolerated_low_confidence(:
	UPI00003D41AD	NM_001083909.1	
	UPI00003D41AD	NM_001083909.1	
	UPI00003D41AD	NM_001083909.1	
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	UPI00005C3025	NM_020716.1	
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	UPI0000161A59		
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	UPI0000163937	NM_014668.3	
	UPI0001E8F433	NM_001258021.1	
EK8,D6RDX5,D6RBV7,D6	UPI000002AA8D	NM_000826.3	
Q9UHA9	UPI000013D503	NM_000828.4	
C9JU97	UPI000004A7E3	NM_000844.3	
C9JLW9	UPI0000185F04	NM_014615.3	
Q5T0I0	UPI000012B3B4	_000177.4,NM_0012580:	deleterious(0.04)
	UPI0000073899	NM_018094.4	
C7DJS1,B2C310	UPI000011028B	NM_000852.3	
G3V5U6,G3V5G8	UPI000013C6F0	NM_145870.2	
3R7,D2CFK9,B7Z7A3,B4I	UPI000000D960	NM_012341.2	
3R7,D2CFK9,B7Z7A3,B4I	UPI000000D960	NM_012341.2	
	UPI000013C740	NM_001522.2	
C9J3Q6	UPI00001D7E8F	NM_001080393.1	
Q2PH61,Q2PH60,Q2PH5(	UPI000012CE8E	NM_002108.3	
B6EU04	UPI00000389A3	NM_021175.2	
IS90,C9JNI4,C9JH46,C9J	UPI00001D9A86	NM_015401.3	
IS90,C9JNI4,C9JH46,C9J	UPI00001D9A86	NM_015401.3	
N14,Q75N10,C9JLX1,C9	UPI000019AB75	NM_178425.2	
H0UI53,H0UI52	UPI0000070B81	NM_016063.2	
	UPI0001818C59	NM_001135565.1	
Q6P664	UPI000013D4D4	NM_018072.5	
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Q6P664	UPI000013D4D4	NM_018072.5	
	UPI0000D61BE2	NM_017802.3	deleterious(0.02)
G3V4V5	UPI0000E8AC98	NM_015382.2	
G3V4V5	UPI0000E8AC98	NM_015382.2	
B1ALG6	UPI000006F63A	NM_018063.3	
B1ALG6	UPI000006F63A	NM_018063.3	
	UPI000012C594	NM_016173.3	
H0YL74,H0YL07,H0YKW7	UPI0000212760	NM_003922.3	
63,I1VA60,I1VA56,I1VA5	UPI0000001700	M_000410.3,NM_139006	tolerated(0.74)
C9JS80,C9JDP4	UPI000000D92B	NM_000601.4	
C9JL39,C9JHL0,C9JEF1	UPI000012DC51	NM_020707.3	
F1T0G3	UPI000022988D	NM_001127258.1	
	UPI0000073F44	NM_016438.3	
	UPI000004F5CC	NM_005340.6	
B2R4S9	UPI0000000C24	NM_003522.3	
	UPI00000003C7	NM_003530.4	

Q6B823,B2R4R0	UPI000000003C	NM_003544.2	
	UPI00003666D2	NM_025130.3	
7AP3,Q67AP1,Q49U72,Q	UPI000004494C	NM_002121.5	deleterious(0.03)
C9JD75,C9JCQ9	UPI0000126A8C	NM_001242784.1	
	UPI0000161FA7	M_003071.3,NM_139048.2	
Y91,Q0G847,F5GY90,B5U	UPI000012C47A	NM_000190.3	
Q7Z641,B0QXZ9,B0QXZ8	UPI00003765B4	NM_001003681.2	
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IJ2,E0YMJ1,B8YNW1,B8	UPI000013CF6C		
)K8,M0QZV6,M0QYZ0,M0	UPI000013D3F4	NM_007040.3	
K7ENU5,K7EMR5,K7EJ48	UPI00003D0BC0	NM_013312.2	
M0R244,B2ZDQ2	UPI000003FE67	NM_182983.2	
	UPI000000D7EB	NM_024747.5	
	UPI000012CCD5		
Q86UN1,Q75LH0,A4D2N2	UPI000004477E	NM_024012.3	
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Q5H963	UPI00004A0DAC		
B7Z1W8,A0N0L8	UPI0000049DCB	NM_001283052.1	tolerated(0.11)
B7Z1W8,A0N0L8	UPI0000049DCB	NM_001283052.1	
B7Z1W8,A0N0L8	UPI0000049DCB	NM_001283052.1	
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,H0YLI6,H0YKD0,B7Z9J8	UPI000012D1AC	NM_005530.2	
VE6,H3BR88,H3BR65,H3I	UPI00001412C9	NM_005531.2	tolerated(1)
C9JCU0	UPI000012D69B		tolerated(0.36)
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A0N9R7,A0N9R6	UPI0000072478	NM_000876.2	
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G5EA26	UPI0002C439DB	NM_001277285.1	
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	UPI0000071143	NM_021258.3	
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B7ZBC9,B7ZBC8	UPI0000071D68	NM_007044.3	
	UPI000004F638	NM_031886.2	tolerated(0.72)
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	UPI000045761B	NM_030647.1	
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	UPI000012DDA3	NM_014875.2	
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	UPI000013D842	NM_000421.3	
	UPI000013C883	NM_002278.3	
	UPI000012DAFA	NM_003771.4	
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	UPI00003D4D71	NM_198697.2	
	UPI000021C443	NM_198698.1	
	UPI000012E77E	NM_031488.4	
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	UPI000012E5D5	NM_001040167.1	
	UPI0000202BCD	NM_012276.3	
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	UPI000013C94B	NM_005575.2	
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	UPI0000211E03	NM_001031855.1	
	UPI000013D224	NM_005576.2	
C9J5C8,C9J4E3,C9J3U9	UPI000002E034	_005578.3,NM_001167672.1	
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E9PHY1	UPI0000073246	NM_002335.2	
	UPI000006DF62	NM_001135772.1	deleterious(0)
	UPI000006DF62	NM_001135772.1	
	UPI00000354C2	NM_002337.3	
	UPI000013E4BC	NM_152329.3	
	UPI00001F98A9	NM_001006939.3	deleterious(0.04)
	UPI000021002F	NM_033402.4	
A8MY60	UPI0000ED4E82	NM_001079910.1	
	UPI0000DBEEC1	NM_018385.2	tolerated(0.11)
	UPI000006E20E	NM_015578.2	tolerated(0.38)
	UPI000000412A		

	UPI000012A14D	_002340.5,NM_001145436.1	
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	UPI0000000A29	NM_002358.3	
A8IF97	UPI0000035FCB	NM_004988.4	
Q6FHH8	UPI0000000C51	NM_001166386.1	
	UPI000012F055	NM_002367.3	
A0PK03	UPI000006F2FD	NM_005462.4	
	UPI000012F059	NM_016249.3	
	UPI000000123B		
	UPI0000237828	NM_206920.2	
Q6ZUZ1	UPI00017A6EBC	NM_001177465.2	
	UPI000013D632	NM_005907.3	
Q49A69	UPI000013D193	NM_002372.2	
Q05BN7,B3KQN1	UPI000004BF05	NM_015274.1	tolerated(0.37)
	UPI00002036F9	NM_018174.4	deleterious(0.02)
E7EWI5	UPI0000E444D0	NM_001001671.3	deleterious(0.02)
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	UPI00000747ED	NM_007181.4	
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	UPI000004A042	NM_014975.2	
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	UPI000016054E	NM_003833.4	
F5GYT8,F2Z3E2,E9PHF7	UPI000013D646	NM_020166.3	
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	UPI0000253F1B	NM_001110792.1	
	UPI00001414B1	NM_004229.3	
T8,Q5T8T6,E9PGW7,E7	UPI000013623C		
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	UPI000020380F		
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	UPI000013D922	NM_032435.2	
	UPI000006F7B3	NM_005934.3	
	UPI000006FDF6	NM_147191.1	
	UPI000020E726	NM_005515.3	
K7ESA9,K7EPX7,K7ELS3	UPI000006E000	NM_130807.2	tolerated(0.38)
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	UPI00003E75D3	_001085354.2,NM_0246[illegible]	tolerated(0.22)
NI8,H0YMT8,H0YM21,H0	UPI00001FE9BB		
	UPI000003617B		
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	UPI000007437B	NM_032477.2	
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96QW8,B1AKQ2,B1AKP	UPI000012ABD3	NM_004958.3	
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	UPI000012A0C6	NM_002461.1	
	UPI000013C73B	NM_015419.3	
	UPI0000EE5F22	NM_001145113.2	
B6D426	UPI000006EEAA	NM_000256.3	
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K7EQV1,G3V4G3	UPI0000E59E6E	NM_016239.3	
Q8N903	UPI0000207402	NM_032608.5	
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Q14779,M0QXU2	UPI00001678F0	NM_012335.3	
Q9UES4	UPI0000E445E1	NM_000259.3	
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	UPI000012FBA4	NM_002479.5	
A5PKT7	UPI00002288CF	_032578.3,NM_001256267.1	
	UPI0000D45F7B	NM_001127392.1	
	UPI0000204444	NM_001085487.2	

	UPI000004FA2B	NM_024635.3	
	UPI0000073EEB		
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,Q3LRJ5,Q3LRI9,Q3LRI6	UPI0000161BF3	NM_031858.2	
,Q3LRJ5,Q3LRI9,Q3LRI6	UPI0000161BF3	NM_031858.2	
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F5GZK7	UPI000013C8CA	NM_014865.3	
Q96FA6,E9PLE0,E9PL84	UPI00001C1EFE	NM_015261.2	
E9PHA2,B4E189	UPI0000163F72	711.1,NM_001281710.1,NM_015341.4	
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	UPI000013D4D9	NM_002508.2	
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	UPI000006FFD0	NM_020448.4	
	UPI00001D7EEA	NM_001099287.1	tolerated(0.81)
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C9JDV8	UPI00001303FF	_001202502.1,NM_003634.3	
	UPI000036715D	NM_007184.3	
	UPI0000074709	NM_014360.2	tolerated(0.11)
	UPI000006FCBB	NM_181303.1	
	UPI0000126FAD		
	UPI00001AEEBD	NM_153447.4	
	UPI00001AEEBD	NM_153447.4	
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	UPI00001B6B39	NM_176820.2	
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	UPI0000353D0F	NM_207173.1	deleterious(0.01)

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	UPI0000237454	NM_001010906.1	
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	UPI00001AF029		
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	UPI0000041D58	NM_001005272.3	terious_low_confidence(0
	UPI000013F8A8	NM_001004701.2	
A4FU14	UPI0000041B31	NM_033179.2	
	UPI0000041BDD	NM_001001913.1	
	UPI000015F240	NM_001004731.1	tolerated(1)
	UPI00001606CE	NM_001005515.1	
	UPI00000405D5	NM_006637.1	
	UPI000004B22E	NM_001004745.1	
H0Y7X4	UPI0000130E96	NM_144498.2	
J3KRK7,H3BTF9	UPI000006CF29		
J3KRK7,H3BTF9	UPI000006CF29		
	UPI000004CAC3	NM_003999.2	
H0YN66	UPI0000073AA5	NM_130901.1	
S4R3Q9,J3KNA0,C9JC63	UPI000013DE11	NM_005015.3	
C6G7W3	UPI000002E776	NM_002565.3	tolerated(0.7)
B3KTQ9	UPI0000000CAA	NM_000918.3	
B1ANR1	UPI00002057C5	NM_001135653.1	deleterious(0.04)
E9PSG7,E9PSE1,E9PNZ	UPI0000190973	NM_018026.3	
	UPI0000071A52	NM_130467.3	
B7Z6Y8	UPI0000001616	NM_002579.2	
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	UPI0000131D49	NM_148977.2	
	UPI000000DA54	NM_018216.1	deleterious(0.03)
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	UPI00000492D2	NM_152268.3	terious_low_confidence(0
J3KNQ4	UPI0000EE3866	NM_018222.4	
	UPI000041A256	NM_001003828.2	
R9W7C9	UPI0000071DEC	NM_003466.3	
	UPI0000073D97	NM_021635.2	erated_low_confidence(0
A2A3E7,A2A3D9	UPI0000EE048B	001142765.1,NM_001142764.1,NM_001142763.1	
	UPI00001FCE90	NM_203487.2	tolerated(0.12)
	UPI0001573469	NM_033026.5	
H7BY58,C9J0F2	UPI0001B7942B		tolerated(0.87)
	UPI00001AEB88	NM_006031.5	
	UPI000049DFA7	NM_177966.5	tolerated(0.06)
246,Q9UNL9,Q53TB0,Q5	UPI0000001072	_001258312.1,NM_005019.4	
F5GXX2,C9JPD5	UPI000003B340	NM_002599.4	
	UPI000013C84A	NM_006204.3	
D6RIG5,D6RG11,D6RDX(	UPI0000131793	NM_006206.4	
E5RJ14,E5RII0	UPI0000131791	NM_002609.3	
E5RJ14,E5RII0	UPI0000131791	NM_002609.3	
	UPI000013DB22	NM_014317.3	
K7,H3BU11,H3BQS3,H3I	UPI000004A864	_015027.2,NM_001285447.1	
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S4R3X4	UPI0000072FD2	NM_024895.4	
H3BUZ5,H3BUE6	UPI00002378D0		tolerated(0.34)
A6PVP2	UPI000045889A		
A6PVP2	UPI000045889A		
A6PVP2	UPI000045889A		
K7EQ51	UPI000006F8BF	NM_000285.3	tolerated(0.79)
K7EQ51	UPI000006F8BF	NM_000285.3	
SR6,Q5VSR5,B1APP8,B1	UPI00000012D2	NM_002627.4	
SR6,Q5VSR5,B1APP8,B1	UPI00000012D2	NM_002627.4	
	UPI000035154F	NM_024989.3	
B7Z7A9,B4DHM5	UPI00000727EE	NM_000291.3	
M0R2W8,M0QYW3	UPI000004EEA6	NM_052890.3	tolerated(0.18)
	UPI000006F12B	NM_052891.1	
	UPI0000211A97	NM_005392.3	
	UPI000013DA40	NM_017934.5	
	UPI000013D340	NM_002637.3	
	UPI0000192101	NM_015157.3	
	UPI000189A834		
	UPI000019790E	NM_181643.4	
	UPI000012B9D1	NM_005482.2	
PN0,K7ENC3,K7EMD7,K7	UPI0000070A47	NM_176787.4	
C9JLC8	UPI00001984EA		deleterious(0)
L7RT34,J3KT66,J3KRE9	UPI0000071DB4	3.2,NM_001251852.1,NM_001251853.1,NM_0012	
	UPI0000366FD6	NM_015040.3	
	UPI00001582C4	NM_001001852.3	
	UPI00002073D6	001255975.1,NM_001008496.3	
K7EPI8,B4DDN5	UPI000006D00A	9.3,NM_001032396.2,NM_022368.4	
	UPI000013C4C0	NM_138694.3	
	UPI000013C576	NM_004572.3	
	UPI000002FED1	NM_005084.3	
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	UPI0000D6117C	NM_153021.4	
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B7ZM61	UPI00001F93EE		

B7ZM61	UPI00001F93EE		
B7ZM61	UPI00001F93EE		tolerated(1)
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	UPI00006C0134		
	UPI00006C0134		
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Q96IE3,E9PQ28	UPI0000233FCD	NM_201380.2	
Q96IE3,E9PQ28	UPI0000233FCD	NM_201380.2	
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B3KR92	UPI000206539E	NM_001265592.1	
B3KWD2	UPI00001C1F64	NM_020715.2	
B3KWD2	UPI00001C1F64	NM_020715.2	
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J3KSM5	UPI00001416D8	NM_032129.2	
	UPI000015FEF2		
I3QR40,C9JWQ3,C9JCL2	UPI0000049814	NM_020405.4	
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B8XXQ3	UPI000189560E	NM_001145717.1	erated_low_confidence(0
U3N901	UPI000006CED5	NM_025225.2	
	UPI0001AE63FF	NM_001166111.1	
F8VUJ3	UPI0000228FE1	)01199781.1,NM_001199782.1	
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Q05DB8	UPI0000134605	NM_006466.2	
	UPI000013CEB8	NM_006475.2	
D5K9T1	UPI000013F18B		tolerated(1)
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)M1,E9PFJ1,E7EUD1,E7I	UPI0000055911	NM_015869.4	
	UPI000002A7A2	L76.2,NM_148175.2,NM_014337.3	
A7E2X1	UPI000013ECF6	NM_014906.4	
Q96TC9,Q96SE3	UPI0000000C3C	NM_001122764.1	
I3L267	UPI0000061E1A	NM_001007533.3	
Q6IN90,B3KMA9	UPI000013EC98	NM_018461.3	
	UPI0000124EAC	_001190447.1,NM_002718.4	
C9JQA1	UPI0000073DB7	NM_005710.2	
	UPI000013D572	NM_018699.2	
Q05CA1,E9PEH0	UPI0000422A1D	NM_020226.3	
	UPI00001314E8	NM_006406.1	
	UPI00001314E8	NM_006406.1	
	UPI00001314E8	NM_006406.1	
	UPI000006E28E	NM_002726.4	
Q56UR8	UPI0000375435	M_024870.2,NM_025170.4	
	UPI000013CF50	_002728.4,NM_001243245.1	
D6RAH5,D6R971	UPI000013E37F	NM_152683.2	
C9JZU8,C9J9P1,B4DFV1	UPI000000DA36	NM_212539.1	
C9JZU8,C9J9P1,B4DFV1	UPI000000DA36	NM_212539.1	
Z8,D6RDM0,D6RD31,D6I	UPI0000169EB7	NM_002744.4	
G3V5T6,G3V5L5,B4DV0(	UPI000006F09F	NM_006109.3	
	UPI00017E10D9	NM_001134316.1	tolerated(0.19)
B1AHG4,B1AHG3	UPI00002327F8	NM_001198721.1	
B1AHC4,Q52M44	UPI000002B27B		
B4DNP1	UPI00001FFF6A	_173502.4,NM_001258290.1	

	UPI0001612CC0	NM_015225.2	
	UPI000013CCF5	NM_031246.3	
		NM_002783.2	
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	UPI0000132792	NM_002816.3	
	UPI000012990A	_003720.3,NM_001261824.1	
	UPI0000039F04	NM_020232.4	
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31,Q69YS2,Q5VWH6,Q5'	UPI0000132991	NM_006504.4	
G1UI20	UPI0000470154	NM_002840.3	
O60420	UPI00001AEBFB	NM_002841.3	
	UPI0001747A04	NM_001135648.1	
Q9NSR5	UPI000002E7C7	NM_002847.3	
	UPI000007334C	NM_001013658.1	
E9PL65	UPI0000203D8E		
E9PL65	UPI0000203D8E		
E9PL65	UPI0000203D8E		
E9PL65	UPI0000203D8E		
	UPI00000510D0	NM_015617.2	
B5MDP1,B3KWN8	UPI000006CE59	NM_024854.3	
K7EL58	UPI000000D857	NM_032932.3	
Q6PJZ0,F8WAG1	UPI000006FCEB	NM_022449.3	tolerated(0.18)
	UPI000003F780	NM_022337.2	
D6REW8	UPI0000DA58DE	NM_001032726.2	
	UPI00000745A5	NM_004703.4	
H0YLG7,D3DS70	UPI000013188E	NM_004581.5	
J3QLK0,J3KSC4	UPI00000041DA	NM_005052.2	
G3V4W9,C9J5S9	UPI0000073AB0	NM_133509.3	
F5H6X3,C9J7G0	UPI0000E0A787	NM_018059.4	
L7RRS6	UPI0000049CFC	NM_002880.3	
B3KMZ9	UPI00001B296B	NM_001145525.1	
Q5T3T1,Q5T3T0,Q5T3S6	UPI0000EE7109	NM_001145658.1	
F8W0N0,F8VXK1,B3KP15	UPI0000406B36		
	UPI0000071D46	NM_005055.4	
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	UPI0000070DF1	468.1,NM_001204467.1,NM_005676.4	
	UPI00001A95DC	NM_022118.3	
	UPI00001D7F03	NM_018989.1	
E5RJD7,E5RFP4	UPI000002B229	NM_001008712.2	
	UPI0000133587	NM_021111.2	
	UPI00000012B7	NM_006509.3	
	UPI000020E30A	NM_031922.3	
	UPI00000015BE	NM_032579.2	
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	UPI0001A5C4AD		
	UPI000040E182	NM_002924.4	
F5GZV2	UPI0002065232	NM_015653.4	
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	UPI00001343E6	NM_006397.2	
	UPI000005339F	NM_021133.3	

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	UPI0001AE7525	NM_173662.2	
	UPI00015D777B	NM_153341.2	
	UPI00006C175E	NM_001146684.2	
	UPI00000713D9	NM_002941.3	
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	UPI00001AF82C	NM_005012.3	
	UPI000013D467	NM_002944.2	
H7C1Q1	UPI0001610F54		
R4GNH7,R4GMS1	UPI0002B83260		
	UPI0000035DAB	NM_024604.2	
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I54,M0R3D6,M0R1A7,B4I	UPI0000133CD9	NM_000980.3	
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K7EMA7	UPI0000028D48	NM_000984.5	
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	UPI0000198EE6	NM_015056.2	
	UPI0000198EE6	NM_015056.2	
K7EKD3	UPI0000070E2E	NM_018346.1	
	UPI0000000C72		
	UPI00004546A2	NM_001265589.1	tolerated(0.6)
	UPI0000D74C3F	NM_025158.4	
	UPI0000D74C3F	NM_025158.4	
	UPI000046FD20	NM_017987.4	
Q6P3U7,F1D8Q5,B3KY8:	UPI0000042A9A	NM_002957.4	
O75591,B4DET7	UPI0000D7E62F		
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O75591,B4DET7	UPI0000D7E62F		
O75591,B4DET7	UPI0000D7E62F		
L9,D7UNU4,D7UNU3,D7	UPI0000DD0308	NM_001035.2	
L9,D7UNU4,D7UNU3,D7	UPI0000DD0308	NM_001035.2	
	UPI0000E5B01A	NM_001036.3	
U3KPY7	UPI000187B6C9	NM_005870.4	
Q5SYV1,B4DPI2	UPI000006F076	NM_007101.3	
	UPI000013559C	NM_016038.2	
Q86TK5	UPI00001D69ED	NM_002972.2	
H0YDZ1	UPI00000622D5	NM_030962.3	
M0R3G4,M0R2L3	UPI0000071891	NM_021228.2	
	UPI000013E800	NM_005698.3	
	UPI0000135F1C	NM_153334.4	
	UPI000013CFF1	NM_144777.2	
Q8NBV9,Q75MG0	UPI000013C4DF	NM_001112706.2	tolerated(0.13)
	UPI000013DC5F	NM_144643.2	
	UPI000013DC5F	NM_144643.2	
	UPI0000EE1E57	NM_198081.3	
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	UPI0000DBEEC4	NM_152744.3	
A4UCS7	UPI0000072378	NM_183352.2	
	UPI0001662AB0	NM_001193336.2	deleterious(0.03)
	UPI0000203C4D	NM_033127.2	
Q5QPE2,B4DS04	UPI0000135455	985.4,NM_032986.3,NM_	deleterious(0.02)
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	UPI0000070A8E	NM_015490.3	
	UPI0000070A8E	NM_015490.3	
	UPI0000070A8E	NM_015490.3	tolerated(0.75)
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948,Q7L1Z0,Q6AW84,F8\	UPI00001AEA0A	_024077.3,NM_001282688.1	
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	UPI000012E44A	NM_000450.2	
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	UPI0000135A69	NM_004186.3	
B1AHR2	UPI000067DA91	NM_145733.2	
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	UPI00006C12ED	NM_015048.1	
	UPI00006C12ED	NM_015048.1	
C9JLM1,C9JLA7,A8K0G4	UPI0000411FEE	NM_001080517.1	
	UPI0000136779		
J3QL37,I3L4G7,H3BMB0	UPI0000167878	NM_012426.4	
	UPI0000135473	NM_031287.2	
	UPI0000032F1A	NM_003901.3	
I3L1Y7	UPI0000160300	NM_014853.2	
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B9A6J5,B0QY80	UPI0000035D8C	NM_015705.4	
	UPI0000073DAA	NM_001206652.1	
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	UPI000013E109	NM_016148.2	
	UPI000013E109	NM_016148.2	
D9ZGF9	UPI0000135942	NM_000193.2	
F5H3B6,C9IZC6	UPI0000125D05	NM_001649.2	tolerated(0.41)
	UPI0000135992	NM_053003.2	
	UPI0000206F2B	NM_173354.3	
	UPI000013599A	NM_005069.3	
	UPI00001D7D6A		
	UPI00000389DC	_021181.3,NM_001282595.1	
	UPI000006E8DB	NM_152679.3	
	UPI00001977FD	NM_197965.2	tolerated(0.2)
	UPI0000141815	NM_006598.2	
Q75MH3,Q75LT0,A4D0X1	UPI0000049F9D	NM_022444.3	
	UPI000019C3D5	NM_006517.4	tolerated(0.29)
753,M0R1V3,M0R106,M0	UPI0000129B1A	NM_005071.2	
753,M0R1V3,M0R106,M0	UPI0000129B1A	NM_005071.2	
	UPI0000130BB6	NM_003060.3	
	UPI000020C6FE	NM_152685.3	
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	UPI000013DE67	NM_004213.3		
	UPI000013D0D5	NM_004212.3		
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B4DJ02,B3KY53	UPI00001609C1	NM_001029858.3		
	UPI000006DD13	NM_173508.2		
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RZ0,H3BPV9,H3BPK8,H3	UPI000004EC72			
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VC2,C9J9M9,C9J722,C9	UPI000013EFE9	NM_001199692.1		
Q9UEU3	UPI00001359F6	NM_000453.2		
	UPI0000072E3C	NM_007231.3		
M0QYK3	UPI00001305CE	NM_014037.2		
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B7Z589	UPI000053030B	NM_201649.3		
E9PQT4,E9PIC3,B3KSX4	UPI000012E235	NM_012244.3		
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	UPI0000071389	_001257291.1,NM_032591.2		
Q4LEJ9	UPI000013F0AD	NM_005630.2		
F6TQG2	UPI0000161FA6	NM_003069.3		
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	UPI000042146E	NM_148674.3		
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C9JP19,C9JGQ0	UPI00001B0272	NM_134270.2		
I46,B0QZA0,B0QZ99,A8M	UPI000022AFDA			
	UPI000013D6B7			
	UPI0000EE6E4F	NM_020777.2		
A7LBF9	UPI00001601FD	NM_206996.2		
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	UPI000049D98C	NM_001009615.1		
	UPI00001D8243	NM_198572.2		
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B9A038	UPI000066D99E	NM_005876.4		p
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	UPI0000E59BE4	NM_016642.3		
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G1UI29,C9J4U4	UPI000059D368	NM_006662.2		p
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	UPI0000001C5C			
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H0YIF3	UPI00001ADDF4	NM_017564.9		
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	UPI0000073E6C	NM_012108.2		
B4DMS6	UPI0001BE8155	NM_020759.2		
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C9J4I3	UPI000006F059	NM_012448.3		

E5RJN7	UPI000013D271	)01164381.1,NM_001164380.1	
H3BVF2	UPI00000377B6	_001256677.1,NM_001256672.1,NM_004809.4	
	UPI000015D192	NM_001271006.1	
	UPI00001A36D9	NM_182489.1	
H0YD00,H0YC91,E9PKQ(	UPI00000467FD		
	UPI0000160E65	NM_033088.3	
A4D1K4	UPI00001C1E68	NM_020704.2	
	UPI0000199FE0	NM_001127715.2	
F5H4G3,F5H366,F5H2I9	UPI000013C57C	NM_018423.2	tolerated(0.07)
	UPI000012F694	NM_016086.2	
	UPI0000072507	NM_033050.4	
	UPI0000135A5D	NM_006936.2	
	UPI0000072D67	NM_001002255.1	tolerated(1)
2M5,M0R105,B4E0Q4,B4	UPI000006D81A		
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	UPI0000070B4A	NM_145006.2	
E9PJM7	UPI0000073652	NM_015055.2	
C2,M0R180,M0R039,M0(	UPI00002026C0	NM_004819.2	
Q6MZP0,G3V5D3,G3V40:	UPI00003677E5	NM_182914.2	
Q6MZP0,G3V5D3,G3V40:	UPI00003677E5	NM_182914.2	
B4DLC4	UPI000006E2F8	_001178088.1,NM_003898.3	
	UPI00001B03B3	NM_145728.2	tolerated(0.47)
	UPI00001D75EB	_133477.2,NM_0012867[	tolerated(0.49)
U3KQR0	UPI0000073C75		
U3KQR0	UPI0000073C75		
E7EMT0,C9JA91	UPI0000136869	NM_006342.2	tolerated(0.35)
	UPI0000212176	NM_024885.3	
	UPI0000071CD5	_054114.4,NM_001278733.1	
	UPI0000071CD5	_054114.4,NM_001278733.1	
	UPI00001FE055	NM_152334.2	
	UPI00001FE055	NM_152334.2	
H7BZJ2	UPI000013DEC1	NM_014760.3	tolerated(0.26)
H7BZJ2	UPI000013DEC1	NM_014760.3	
B9A6M3,B0QYI3	UPI0000128722	_014346.2,NM_0012843(	tolerated(0.12)
	UPI00001AE7B3	NM_014832.2	
W04,C9JNM0,C9JMP7,C[	UPI00017E10F6	NM_001134381.1	erated_low_confidence(0.[
)Y5,D6RDG2,D6RC61,D6	UPI000013EF70		
	UPI000017DA69	NM_005995.4	
	UPI00000709E1	NM_080390.3	tolerated(0.24)
	UPI000181BA17	NM_003198.2	tolerated(0.95)
	UPI000013E374	NM_006706.3	
	UPI0000167BDB		
	UPI0001642306	NM_153046.2	
G3CAS6,B7ZMH4	UPI0000211B6A	)01163279.1,NM_001163278.1	
G8BLJ6,G3CAS7	UPI0001C48FC2	NM_001122679.1	
	UPI0000137364		
K9JJH7	UPI0000DD79F5	_144993.1,NM_001287491.1	
	UPI0000DAC9CA		
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	UPI0000070D41	NM_152325.1	
E5KTM5	UPI000003B01A	NM_016020.3	
	UPI0000212570	NM_016521.2	tolerated(0.58)
G5E9B5	UPI000006CFD4	NM_013342.3	
E9PAW7	UPI000049D997	_001195683.1,NM_003243.4	

	UPI0000074793		tolerated(0.25)
	UPI0000049F68	NM_052955.2	
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	UPI000006E5C6	NM_016585.4	
	UPI00006C0B74	NM_015204.2	
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	UPI000000D72E	NM_182919.3	
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K7ELX5	UPI000006DF3D	NM_138463.3	
H0YNT2	UPI000013703A	NM_001282979.1	
H0YNT2	UPI000013703A	NM_001282979.1	
573,J3QQN4,J3QLK5,J3K	UPI00001B6B0F	NM_006852.3	
D6RCE0	UPI0000072EED	NM_012464.4	tolerated(0.11)
	UPI0000073AEE	NM_012465.3	
	UPI0000073AEE	NM_012465.3	
	UPI0000073AEE	NM_012465.3	
	UPI00001FE5FC		
	UPI0000137060	NM_016170.4	
	UPI0000039E20	NM_144676.3	tolerated(0.93)
C9J6W0	UPI00006C0498	NM_015348.1	
	UPI000045760C	NM_018295.4	tolerated(0.16)
D6RDW6	UPI000020B0D7		
	UPI0001AE6FF9	NM_032508.2	
J3QT25	UPI0001915109		
	UPI00001D79BC	NM_001004313.1	
	UPI0000457217		
Q5VXQ8,Q5PY18,D3TTZ	UPI000000D92D	507.1,NM_001270508.1,NM_006290.3	
Q52M88	UPI0000048FDE	NM_001244.3	
H7C3U5,C9J9K1	UPI00016632FD	NM_001080495.2	
	UPI000013CE0F	NM_032865.5	
	UPI000013CE0F	NM_032865.5	tolerated(0.9)
B3KVT9	UPI0000D720ED	001141980.1,NM_001141	tolerated(1)
B3KVT9	UPI0000D720ED	001141980.1,NM_001141	tolerated(1)
B3KVT9	UPI0000D720ED	001141980.1,NM_001141979.1	
	UPI0000201C11	949.1,NM_015476.3,NM_001271950.1	
K7EPV9,K7EMU5,K7ELP(	UPI000002B5B9		
Q4L233	UPI0000130FB2	NM_007030.2	
Q4L233	UPI0000130FB2	NM_007030.2	
C9JDW1	UPI00001C08BF	NM_198485.3	
	UPI0000052E20	NM_024108.2	
G3V4C3,B0AZV9	UPI000000CC28	NM_001079537.1	
G3V4C3,B0AZV9	UPI000000CC28	NM_001079537.1	
	UPI0000052952	NM_033502.2	deleterious(0.04)
	UPI000006F0D9		
Q5SRL0	UPI0000137066	NM_033229.2	
Q9NZT8	UPI0000000DCE	NM_006510.4	
F5GYK0	UPI000022B316	001282378.1,NM_001256601.1	
	UPI000004E050	NM_018207.2	
	UPI0000418F23		tolerated(1)
	UPI000006D630	NM_015163.5	

	UPI000006D630	NM_015163.5	
	UPI000034ECE6	NM_007118.2	
Q71V88	UPI00000012CD	NM_003302.2	tolerated(0.09)
QY6,K7EJX9,B4E3A3,B4D	UPI0000000A02		
	UPI0000070468	NM_024917.5	
	UPI000004FADD		
H0YKU7	UPI0001DBB3A9	NM_001252020.1	
	UPI000003B069	NM_014555.3	tolerated(0.06)
	UPI0000071CBA	NM_017672.4	
F5H6Q4	UPI000003BB44	NM_001177431.1	
	UPI000013773E	426.1,NM_001162427.1,N	tolerated(0.48)
	UPI000013773E	426.1,NM_001162427.1,NM_000368.4	
	UPI000013C781	NM_000548.3	
	UPI0000038C95	NM_005727.3	
	UPI0000049052	3,NM_001278741.1,NM_	deleterious(0)
Q7Z2J5,Q7Z2I5,Q7Z2E9	UPI000013683C	NM_004615.3	
A0ZT99	UPI000004FD58	NM_053006.4	
	UPI000041512B	NM_032538.1	
	UPI000041512B	NM_032538.1	
	UPI00001AEF7A	NM_145170.3	
	UPI0000042226	_001271420.1,NM_017775.3	
	UPI00003E58F8	NM_001145418.1	deleterious(0)
	UPI0001B79116	NM_001200049.2	
	UPI0001B79116	NM_001200049.2	
	UPI0001B79116	NM_001200049.2	
	UPI0001B79116	NM_001200049.2	
	UPI0001B79116	NM_001200049.2	
	UPI00001377A7	NM_012263.4	
D3DTW0,C9JMG1	UPI00017BCE80	NM_001130918.1	
Q9H4D2	UPI000013EA27	NM_003320.4	
	UPI000012B2EE	NM_052903.4	
	UPI000013CC55		
	UPI000013CD76	NM_020245.4	
	UPI000013CD76	NM_020245.4	
	UPI00006E2264		
	UPI000155D5D9		
	UPI0000137941	NM_018961.3	
	UPI0000047471	NM_032873.4	
	UPI000020E72A	NM_014671.2	
Q96HY5	UPI000021276F	NM_020765.2	
	UPI000013F1FC	NM_001077619.1	
F5H3N5	UPI000003021D	NM_003356.3	
	UPI000006E524	NM_152896.2	
B3KSE5	UPI0000E8267C	NM_017886.2	
Q6L9N9	UPI0000D6254B	NM_173568.3	
Q6L9N9	UPI0000D6254B	NM_173568.3	tolerated(1)
Q6L9N9	UPI0000D6254B	NM_173568.3	
	UPI0000074455	NM_173167.2	
D6RA68	UPI0001AE676E	NM_001193388.3	
A4QPH4	UPI0000126B4C	NM_016327.2	
E9PSD7,A8KAF9	UPI000004B62E	NM_145052.3	
	UPI000034E5B6	NM_206933.2	
M0R3B1,M0R172	UPI000006F7A8	NM_031941.3	

Q6P2I0	UPI00001379EB	NM_005153.2	
Q5JXD3,G5E9A6,B4DGK3	UPI0000161434	NM_004651.3	
Q53Y90	UPI000003772C	NM_017414.3	
Q9UQN9	UPI000013D050		
Q9NSJ7,K7ESK0,K7ERX6	UPI00001C1FC6	NM_015276.1	
	UPI0000410E09	NM_014709.3	
D6RF65,B4DU75	UPI000020CADC	NM_032175.2	
	UPI00001FB38B	NM_014503.2	
	UPI00001FB38B	NM_014503.2	
L08,Q86UB8,Q590G7,F4N	UPI00001B3DBF	_001258267.1,NM_007125.4	
	UPI00000012EB	NM_003380.3	
Q71V81	UPI0000055A9A	NM_003382.4	tolerated(0.58)
	UPI000013D498	NM_001288837.1	
	UPI0000070723	NM_006370.2	
C9K060	UPI0000423E27	NM_001202560.2	
C9K060	UPI0000423E27	NM_001202560.2	
	UPI000013E466	NM_152559.2	terious_low_confidence(0
Q6PIM1	UPI000176ADB8	NM_020945.1	
S4R3Z0,Q9NWV7,Q659C	UPI0000138ED1	NM_018117.11	
S4R3Z0,Q9NWV7,Q659C	UPI0000138ED1	NM_018117.11	
S4R3Z0,Q9NWV7,Q659C	UPI0000138ED1	NM_018117.11	
S4R3Z0,Q9NWV7,Q659C	UPI0000138ED1	NM_018117.11	
S4R3Z0,Q9NWV7,Q659C	UPI0000138ED1	NM_018117.11	
Q0QD35,E7EP77	UPI000019C575		
C9JCS7	UPI0000203FB7	_001115113.2,NM_025160.6	
C9JH61,C9JEE7,C9IZK7	UPI00001C1DCD	NM_015131.1	
F8W7Y5,C9JC24	UPI000006FF8C	NM_020839.2	
H7C1E8,A4D230	UPI000020E761	NM_018051.4	
B4DXE9	UPI0001662BC1	NM_031951.3	
	UPI000006F2DE	NM_014149.3	
	UPI0000073E34	299.1,NM_001033518.1,NM_015610.3	
Q96CZ6	UPI000013CD65	NM_018979.3	tolerated(0.16)
Q5TEH9,Q5TEH8	UPI0000138F23	NM_024494.2	
	UPI000013D6C5	NM_003393.3	tolerated(0.39)
	UPI000004A506	NM_020135.2	
B4DPV6,B4DFS1	UPI0000031565	NM_018639.4	
	UPI00017A7149		
H3BRX8,H3BPJ8,B4DHF6	UPI000006CD16	_001270454.1,NM_007014.4	
Q68CN2,F5H315	UPI0000001BDE	NM_020196.2	
Q9NW55	UPI000006F5DC	NM_018053.2	
Q5T6H7,Q5T6H2,B4E2P4	UPI00003D2EAD		
B7ZBB4	UPI00000401E0	NM_022098.3	
E2QRM3	UPI000006CC97	NM_020750.2	
M4WFF9	UPI000013D351		
M4WFF9	UPI000013D351		
	UPI000006E761	NM_015982.3	
A3KFK2,A3KFK1	UPI0001AE792F	NM_001198903.1	
A3KFK2,A3KFK1	UPI0001AE792F	NM_001198903.1	
Q658W5	UPI00000728EE	NM_020861.1	
B7ZW40	UPI000020E358	NM_001013623.2	
	UPI00002377F7		
	UPI00002377F7		
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	UPI0000160D96	NM_015117.2	
	UPI000002B2AD	NM_017590.5	

	UPI0000072244	NM_001143978.2		
B4DNL2,B1AMU5	UPI0000073C8D	NM_198046.1	tolerated(0.35)	
	UPI00000373E8	NM_022494.1		
H3BNQ9,H3BMI0	UPI000013EA61	NM_001145548.1		
	UPI000013FDD5	NM_182491.2		
G3V3N5,C9JSX6	UPI000198D01B	NM_033400.2		
PQ0,F5H542,E7ET52,E5I	UPI000057A0B4	NM_012082.3		
H3BUW6	UPI0000E5924A	NM_001077268.1		
Q75MV2,J7M2L3,J7M2K9	UPI000013C3AC	NM_014569.3		
C9JUQ8	UPI0000126A0E	NM_015896.2		
C9JUQ8	UPI0000126A0E	NM_015896.2		
H7BZT5,B3KPM4	UPI0001D27F7E	NM_001178106.1		
A6NFS0	UPI000059DBB5	NM_001080485.3		
M0QZ59	UPI000013CAB8	NM_020657.2	tolerated(0.46)	
F5H1K2	UPI000013C359			
C9J1G1	UPI00002323B9	NM_199451.2		
	UPI000059D659	NM_001146175.1		
K7ERS3,K7EQC9,K7ELF6	UPI000007049F	NM_144689.3		
M0R258,M0R0H8,M0R0E3	UPI0000139CDC			
J3KQM6	UPI000059D677	NM_152355.2		
Q7Z3P1	UPI000013F1DE	NM_152695.5		
	UPI000022ABBF	NM_001076678.2		
	UPI000013A290			
	UPI000013E5FC		tolerated(0.38)	
H3BQQ2	UPI0001AE67A3			P
M0QYG4	UPI0000202ADA	NM_025040.3	tolerated(0.68)	
M0QY39,I0CMK8	UPI000035E843	NM_001076675.2		
	UPI00002376EC	NM_001001411.2	tolerated(0.42)	
Q8N508	UPI0000DD78D7	NM_001080470.1		
M0R1G3,M0QYN4	UPI000041F9DE	NM_021269.2	tolerated(0.45)	
KB3,C9JVC3,C9JSV9,C9	UPI000176161D	NM_001128223.1		
	UPI000022DD3A	NM_007131.3		
	UPI0000074535	NM_152458.6	deleterious(0.01)	
I3L0H5	UPI0000251D78	NM_001031665.2		
H0YKY1,B3KWS2	UPI0001596890			
	UPI0000351AA0	NM_207341.2	tolerated(0.09)	
6Y9,F5H789,F5H2D8,F5I	UPI000021D4BC	NM_181877.3		
Q9HA55	UPI00001C2005	NM_023072.2		
	UPI00004569F7	NM_015113.3		

PolyPhen	EXON	INTRON	DOMAINS
		2/4	
		5/5	
		5/22	
	9/40	lices:TMhelix,hmmpanther:PTHR19229:SF120,hmr	
	33/33		
		3/38	
		20/38	
		13/38	
	28/31	PTHR24223,Gene3D:3.40.50.300,TIGRFAM_dom	
		14/30	
	31/39	ROSITE_profiles:PS50929,hmmpanther:PTHR242	
	1/9		
		21/22	
ossibly_damaging(0.691	1/1		Low_complexity_(Seg):se
		9/10	
		1/11	
		10/10	
		7/7	
	1/6		
		6/10	
		3/5	
		8/13	
		3/10	
		1/12	
		6/10	
ossibly_damaging(0.839	20/23	panther:PTHR11905,hmmpanther:PTHR11905:SF	
		10/18	
robably_damaging(0.934	19/22	ofiles:PS50092,hmmpanther:PTHR13723,hmmpan	
		15/21	
		4/38	
		5/8	
		9/24	
		16/28	
		2/2	
	7/19	4,hmmpanther:PTHR14338,Gene3D:2.30.29.30,Pf	
		16/20	
		8/20	
		3/17	
		2/16	
	4/4	1,PROSITE_profiles:PS50262,hmmpanther:PTHR2	
		17/26	
		1/2	
	1/6	elices:TMhelix,Pfam_domain:PF04750,hmmpanther	
		12/18	
		11/18	
benign(0.05)	3/6	hmmpanther:PTHR11242,hmmpanther:P	
	5/14	nmpanther:PTHR24102:SF15,Pfam_domain:PF013	
		7/13	
		30/49	
		14/49	
		9/9	
		8/14	

	3/16	
	11/12	
	10/13	
	1/14	
	9/13	
	7/9	
	6/9	
	35/48	hmmpanther:PTHR12827
	4/42	
	14/22	
	2/7	
	12/12	
ɔossibly_damaging(0.494	16/16	hmmpanther:PTHR24147:SF22,hmmpant
	21/33	
	18/27	
	10/14	hmmpanther:PTHR24161,hmmpanther:P
	5/27	
	6/11	
	22/34	
	1/1	
	12/22	
	11/23	
	6/20	
probably_damaging(1)	9/21	:PTHR22780,Gene3D:1.25.10.10,Pfam_domain:PF
	2/14	
	5/8	
ɔrobably_damaging(0.968	1/4	RSF017529,Prints_domain:PR02025,hmmpanther:
	1/4	
	2/4	
benign(0.288)	12/20	hmmpanther:PTHR11533:SF31,hmmpant
	2/4	
benign(0.015)	21/23	hmmpanther:PTHR12552,hmmpanther:P
	3/46	
	8/11	
	16/23	ofiles:PS50238,hmmpanther:PTHR14166,hmmpan
	15/40	
	3/14	
benign(0.086)	11/13	IR22825:SF12,hmmpanther:PTHR22825,Gene3D:2
	6/20	Gene3D:2.30.30.40,hmmpanther:PTHR22826:SF94
	4/6	
	6/6	,hmmpanther:PTHR11711,hmmpanther:PTHR1171
	11/22	
	1/2	
benign(0)	2/2	hmmpanther:PTHR15712:SF21,hmmpant
	2/2	hmmpanther:PTHR15712:SF21,hmmpant
	10/14	
	2/7	
	1/7	
ɔossibly_damaging(0.886	3/8	main:PF00884,hmmpanther:PTHR10342,hmmpant
	8/19	
	1/5	
	6/10	
	1/4	

	1/6	
		1/8
		12/16
		5/8
		6/8
		15/21
		7/11
		11/12
		2/10
		5/13
	30/30	
	11/29	omain:PF00122,hmmpanther:PTHR24093,hmmpar
	16/23	mmpanther:PTHR24093:SF229,Superfamily_domai
		20/21
		11/26
		9/9
		13/22
		1/27
		13/27
		24/27
		9/12
		16/23
		6/6
		6/7
benign(0)	16/26	hmmpanther:PTHR23052
		10/10
benign(0.003)	3/3	hmmpanther:PTHR11214,hmmpanther:P
		5/14
		15/33
benign(0.003)	3/3	ain:PF00118,hmmpanther:PTHR11353,hmmpanth
	1/9	
		1/5
		11/11
		4/8
		8/9
		4/16
benign(0.004)	1/2	hmmpanther:PTHR11848,hmmpanther:P
		1/4
		14/15
		19/27
		18/23
		17/23
		14/23
		8/27
		13/15
	9/42	,PROSITE_profiles:PS50294,hmmpanther:PTHR1
		10/10
		1/8
		4/8
		15/15
possibly_damaging(0.736	11/16	hmmpanther:PTHR23231,hmmpanther:P
		3/8
		1/1
	11/11	profiles:PS50188,hmmpanther:PTHR24100,hmmpa
		24/31

	3/3	
		3/8
		8/8
benign(0.002)	2/5	hmmpanther:PTHR13481
		10/67
	2/2	Pfam_domain:PF15047
		8/15
	10/10	
benign(0.089)	9/9	
	1/4	
benign(0.003)	2/2	hmmpanther:PTHR23033,hmmpanther:P
	11/22	Pfam_domain:PF15020
		5/7
		8/19
		8/14
		4/4
	5/5	
		1/3
		19/40
		3/10
		26/40
		30/40
	1/6	
		6/17
		7/8
	6/7	ofiles:PS51144,hmmpanther:PTHR18952,hmmpan
probably_damaging(0.972	17/37	hmmpanther:PTHR15502,hmmpanther:P
		40/46
		15/46
		19/48
		11/38
		38/38
		3/13
		13/13
		8/14
	1/9	
	11/11	
		7/18
		4/10
	8/19	1971,hmmpanther:PTHR21595,hmmpanther:PTHR
		11/22
		2/19
		3/4
		8/20
		6/10
	7/7	
		2/10
		18/20
		11/28
	1/2	ım_domain:PF01146,hmmpanther:PTHR10844,hm
	7/9	ed-coils_(Ncoils):Coil,hmmpanther:PTHR13140,hm
		7/9
probably_damaging(0.959	3/7	Pfam_domain:PF03148

		4/7
	11/11	
	28/28	
		3/5
	4/18	led-coils_(Ncoils):Coil,hmmpanther:PTHR32083,hm
benign(0.033)	13/24	ed-coils_(Ncoils):Coil,hmmpanther:PTHR13140:SF3
		6/15
		23/28
	3/15	iled-coils_(Ncoils):Coil,hmmpanther:PTHR23161,hr
		1/8
		3/14
		1/3
		2/2
benign(0.014)	21/33	hmmpanther:PTHR11412,hmmpanther:PT
	4/6	,PROSITE_profiles:PS50835,hmmpanther:PTHR2
		7/8
		6/6
benign(0)	3/3	_complexity_(Seg):seg,hmmpanther:PTHR15484:S
		5/12
	3/4	5343,hmmpanther:PTHR15343:SF0,Low_complexit
		16/36
		19/19
benign(0.002)	6/9	hmmpanther:PTHR14477,hmmpanther:P
		5/14
		11/12
		1/6
		7/11
	12/16	RFAM_domain:TIGR00089,Gene3D:2qgqB01,TIGR
		21/21
		1/12
		1/1
	1/2	
		1/6
		2/6
		7/9
		11/17
benign(0.006)	7/18	hmmpanther:PTHR22880,hmmpanther:PT
		7/7
	1/1	_complexity_(Seg):seg,hmmpanther:PTHR22146,h
		5/20
benign(0.007)	1/3	Gene3D:1.10.20.10,Pfam_domain:PF15510,Superf
		11/34
		24/34
		1/14
		3/14
benign(0.001)	6/18	hmmpanther:PTHR14594:SF1,hmmpantl
		6/19
		8/12
		9/11
benign(0)	9/22	files:PS50923,hmmpanther:PTHR19325,hmmpanth
	27/27	TIGRFAM_domain:TIGR012
	3/5	
	1/23	
		4/17

		5/17
possibly_damaging(0.87)	8/13	,hmmpanther:PTHR11177,hmmpanther:PTHR1117
	11/11	
	1/1	
		13/19
	5/5	Prints_domain:PR02040,hmmpanther
		45/47
benign(0.001)	5/5	am_domain:PF04487,hmmpanther:PTHR17045,hm
		10/10
		14/22
		12/19
	6/6	
	1/6	
	6/6	
		3/5
		4/24
		12/15
		17/21
		7/10
	34/49	hmmpanther:PTHR13162:SF8,hmmpantl
		4/6
	2/2	anther:PTHR22750,hmmpanther:PTHR22750:SF1
		13/23
		20/23
		19/23
		36/43
	12/13	am_domain:PF02205,hmmpanther:PTHR21557,hm
		11/18
		10/21
		47/55
		11/28
		22/59
		18/59
benign(0.036)	14/14	
		27/44
		56/66
		20/34
		5/43
	4/6	npanther:PTHR10509:SF2,Pfam_domain:PF01596,
		2/3
		12/18
		2/11
	10/10	
benign(0.001)	18/20	Low_complexity_(Seg):seg,Transmembran
		6/12
		4/12
		2/16
		3/16
	8/8	fam_domain:PF08562,hmmpanther:PTHR10334,h
		12/14
		8/14
		8/18
	1/4	
	3/5	
		9/13

	4/10	hmmpanther:PTHR15036,hmmpanther:P
		1/11
	31/50	Low_complexity_(Seg):se
		3/17
	3/19	omain:PF01044,hmmpanther:PTHR18914,hmmpa
	15/67	omain:PF00431,PROSITE_profiles:PS01180,SMA
		1/20
ɔossibly_damaging(0.713	24/26	Pfam_domain:PF00888,hmmpanther:PTHR22771:
		1/23
unknown(0)	18/24	ΓHR14043:SF4,hmmpanther:PTHR14043,Gene3D:
		18/19
	20/20	
benign(0)	8/18	hmmpanther:PTHR12072:SF5,hmmpant
	2/2	
		7/7
		3/8
		8/8
		7/8
		8/12
benign(0.021)	2/13	hmmpanther:PTHR24290,hmmpanther:P
		2/9
	2/20	nther:PTHR21493,hmmpanther:PTHR21493:SF87,
		2/15
		5/7
		3/12
	3/13	Pfam_domain:PF14939
		1/12
		13/28
	8/10	_complexity_(Seg):seg,hmmpanther:PTHR23004:S
	1/8	
	4/6	s:PS00903,Gene3D:3.40.140.10,Pfam_domain:PF
		11/26
		8/26
		7/7
		19/21
benign(0.014)	4/23	TE_profiles:PS50211,hmmpanther:PTHR10877,hm
		1/10
		5/9
		8/25
		3/5
		7/10
		4/26
		12/22
		21/22
		12/27
		19/37
	17/17	
	10/10	
		9/9
		1/3
		18/27
		1/18
		21/31
		1/5

		10/15
		14/20
		61/82
		29/58
		56/83
		53/83
		55/83
		71/83
		62/83
		2/80
		28/90
		64/68
		3/5
		3/5
		16/16
		38/51
		41/52
	25/28	F_domain:PIRSF037123,hmmpanther:PTHR21451
benign(0.05)	10/11	HR10443:SF17,hmmpanther:PTHR10443,Gene3D
		6/11
		6/7
		19/21
		5/6
		20/23
		15/23
		22/23
		10/32
		2/15
	15/15	hmmpanther:PTHR24025,hmmpanther:P
	1/15	site_(Signalp):SignalP-noTM,hmmpanther:PTHR24
		2/23
		14/83
		2/2
		2/9
		1/5
	5/12	ains:SM00678,Pfam_domain:PF02825,hmmpanther
	2/2	
benign(0.001)	2/3	anther:PTHR10159:SF45,Gene3D:3.40.250.10,PIR
		8/16
		82/89
	1/10	
benign(0.001)	2/5	hmmpanther:PTHR14207:SF0,hmmpanth
benign(0.093)	9/19	549,hmmpanther:PTHR11733,hmmpanther:PTHR1
		8/17
		13/24
		2/20
		2/19
		2/4
		4/7
		18/28
		3/7
		1/3
		10/24
		5/11
		8/19

	1/13	hmmpanther:PTHR12086:SF10,hmmpant
		3/19
		12/27
	2/12	R23115,hmmpanther:PTHR23115:SF94,Gene3D:3
	9/9	complexity_(Seg):seg,hmmpanther:PTHR11849,hn
	3/3	48,hmmpanther:PTHR24367,Pfam_domain:PF138
	3/3	hmmpanther:PTHR24367:SF248,hmmpan
	3/3	es:TMhelix,PROSITE_profiles:PS50847,hmmpanth
		19/32
		6/7
benign(0.008)	10/23	npanther:PTHR21573,hmmpanther:PTHR21573:SF
		10/10
		8/10
benign(0)	16/23	THR13720,hmmpanther:PTHR13720:SF22,Pfam_d
		8/22
		8/22
	1/2	hmmpanther:PTHR24341,hmmpanther:P
		13/14
		5/16
		1/9
		3/52
		11/19
benign(0)	4/9	21661:SF10,Gene3D:3.40.50.1820,Pfam_domain:P
	13/19	8,hmmpanther:PTHR10992,Pfam_domain:PF0056
		7/21
		10/30
possibly_damaging(0.669	18/23	nther:PTHR10774,hmmpanther:PTHR10774:SF27
probably_damaging(1)	6/12	620,Pfam_domain:PF01012,PIRSF_domain:PIRSF
probably_damaging(0.926	4/5	domain:PF01012,hmmpanther:PTHR21294,SMART
	1/7	
		12/17
		2/18
		7/18
		9/21
	22/22	hmmpanther:PTHR23169,hmmpanther:P
		3/8
benign(0.002)	13/16	hmmpanther:PTHR11081,hmmpanther:P
		18/18
		3/13
benign(0)	14/26	anther:PTHR10127:SF50,hmmpanther:PTHR1012
		7/25
benign(0.217)	8/8	3,PROSITE_profiles:PS50240,hmmpanther:PTHR2
		1/10
		5/11
		5/11
		5/14
probably_damaging(0.987	7/10	Pfam_domain:PF13289
		2/6
		2/6
	1/1	
	1/1	
		4/19
	3/4	elices:TMhelix,hmmpanther:PTHR13674:SF3,hmm
		2/7

	1/1	
		12/17
		7/7
		2/11
	1/30	
		4/10
	21/23	perfamily_domains:SSF48371,Gene3D:1.25.10.10,I
benign(0.014)	5/10	iled-coils_(Ncoils):Coil,hmmpanther:PTHR22420,hr
		9/42
		1/9
		2/9
	2/10	hmmpanther:PTHR32094
	12/12	
		10/26
		17/26
	22/43	nther:PTHR11712,hmmpanther:PTHR11712:SF227
		22/42
		20/42
possibly_damaging(0.723	2/18	hmmpanther:PTHR24048,hmmpanther:P
benign(0.158)	47/64	36,PROSITE_profiles:PS50026,hmmpanther:PTHR
		3/16
	3/3	
		10/10
		4/10
		4/5
		5/10
		4/8
		4/7
	16/29	hmmpanther:PTHR23065,hmmpanther:P
possibly_damaging(0.742	9/18	SF000628,hmmpanther:PTHR24416,hmmpanther:F
	9/9	
		10/24
	17/25	3213:SF213,hmmpanther:PTHR23213,Pfam_doma
		10/24
		2/2
		11/17
	6/9	,hmmpanther:PTHR10516:SF10,Low_complexity_(
		1/3
possibly_damaging(0.779	9/48	files:PS50194,hmmpanther:PTHR11915,hmmpanth
		11/46
		21/29
		13/17
		9/17
	4/9	ain:PIRSF000332,Prints_domain:PR00370,hmmpar
	1/17	panther:PTHR23213,hmmpanther:PTHR23213:SF
		2/16
		18/22
	11/23	hmmpanther:PTHR23197:SF8,hmmpantl
	2/2	hmmpanther:PTHR25042,hmmpanther:P
		3/16
	15/15	
	17/74	HR11878,Gene3D:2.10.220.10,SMART_domains:SI
		53/73

	56/74	nmpanther:PTHR11878,Pfam_domain:PF03160,SM
		16/73
		57/73
	1/8	hmmpanther:PTHR11878,hmmpanther:P
		20/24
		5/11
		12/15
	18/19	hmmpanther:PTHR10288:SF100,hmmpan
		3/3
	3/3	
		2/5
		8/17
		14/14
		15/27
		4/27
		14/16
		4/7
		7/11
ossibly_damaging(0.889	15/16	ofiles:PS50231,hmmpanther:PTHR11675,hmmpan
benign(0)	1/11	hmmpanther:PTHR11675,hmmpanther:P
benign(0.067)	9/11	mpanther:PTHR11675:SF13,Gene3D:2.80.10.50,P
	4/6	hmmpanther:PTHR14454,hmmpanther:P
benign(0.001)	4/6	hmmpanther:PTHR14454,hmmpanther:P
	6/6	
	1/28	
		2/11
		11/11
	7/12	,PROSITE_profiles:PS51715,hmmpanther:PTHR1
	12/14	mmpanther:PTHR12011:SF245,hmmpanther:PTHF
		1/2
		10/14
		3/5
		1/1
		3/9
		11/17
		1/14
unknown(0)	3/4	panther:PTHR22979,hmmpanther:PTHR22979:SF
unknown(0)	3/4	panther:PTHR22979,hmmpanther:PTHR22979:SF
benign(0.015)	9/9	am_domain:PF03321,hmmpanther:PTHR31901,hm
		3/7
benign(0.015)	4/7	nther:PTHR12914:SF2,hmmpanther:PTHR12914,S
	19/27	s:PS51289,hmmpanther:PTHR11884,hmmpanthe
		16/26
		7/7
	1/6	
benign(0.002)	3/9	:PTHR18945,Gene3D:2.70.170.10,Pfam_domain:F
		4/8
		10/10
		3/5
		8/13
	2/3	mains:SM00275,Pfam_domain:PF00503,Gene3D:
benign(0)	3/8	domains:SM00320,Pfam_domain:PF00400,Gene3D
	1/3	1,PROSITE_profiles:PS50262,hmmpanther:PTHR2
	15/24	(Seg):seg,Coiled-coils_(Ncoils):Coil,hmmpanther:P

	2/2	
	7/9	mpanther:PTHR10822:SF26,hmmpanther:PTHR1(
		10/24
		6/7
	1/14	hmmpanther:PTHR21231,hmmpanther:P
probably_damaging(0.923	1/1	21,Pfam_domain:PF00001,Gene3D:1.20.1070.10,F
benign(0)	3/16	
	2/7	
		3/6
		5/6
		1/2
	13/20	hmmpanther:PTHR23319,hmmpanther:P
		6/17
		11/18
		16/18
		9/18
		20/32
		5/15
		2/15
	8/10	es:TMhelix,PROSITE_profiles:PS50259,hmmpanth
		2/15
benign(0.404)	13/17	,hmmpanther:PTHR11977,hmmpanther:PTHR1197
	1/1	
		6/6
		1/8
		11/16
	17/17	
		15/19
	7/7	
		9/20
		2/3
		4/25
		20/25
		24/24
		4/5
	4/5	8901:SF10,Pfam_domain:PF13419,TIGRFAM_dor
		37/44
		17/44
	15/45	anther:PTHR13457,hmmpanther:PTHR13457:SF1,S
benign(0.006)	9/13	HR16216:SF2,hmmpanther:PTHR16216,Gene3D:1
		13/42
		2/42
		11/21
		1/21
		9/10
		3/77
probably_damaging(0.974	2/6	main:PF00129,hmmpanther:PTHR16675,hmmpantl
	8/18	am_domain:PF00051,Gene3D:2.40.20.10,PIRSF_(
		4/11
		7/8
	1/3	OSITE_profiles:PS51503,hmmpanther:PTHR12297,I
		2/2
	1/1	
		1/1

	1/1	OSITE_patterns:PS00047,Gene3D:1.10.20.10,SM/
		5/17
ɔossibly_damaging(0.576	3/6	46,hmmpanther:PTHR19944,Pfam_domain:PF076
		9/11
		13/24
	9/14	F001438,Pfam_domain:PF01379,Gene3D:3.40.190
		6/10
benign(0.16)	5/11	m_domain:PF13775,hmmpanther:PTHR13711,hm
		2/9
		10/14
	15/23	Pfam_domain:PF05622,hmmpanther:PTHR18947,L
		7/12
	1/1	ɔanther:PTHR14696:SF1,hmmpanther:PTHR14696
		2/3
	1/2	nts_domain:PR00518,hmmpanther:PTHR24247,hm
	22/83	mpanther:PTHR11254:SF67,hmmpanther:PTHR11
ɔossibly_damaging(0.729	44/83	hmmpanther:PTHR11254:SF67,hmmpant
possibly_damaging(0.73)	3/7	IR24100,hmmpanther:PTHR24100:SF55,Gene3D:2
		3/6
	7/7	
		2/10
		8/10
benign(0.006)	4/11	hmmpanther:PTHR12200,hmmpanther:P
benign(0)	2/9	nther:PTHR20859,hmmpanther:PTHR20859:SF23,
		15/20
		13/47
		46/47
		21/47
		1/7
	8/20	40.10,Pfam_domain:PF13927,SMART_domains:SM
	14/20	IR11738:SF95,Gene3D:2.60.40.10,Pfam_domain:P
		6/19
		4/6
benign(0.003)	7/7	hmmpanther:PTHR12231:SF74,hmmpant
		3/6
		7/22
		7/19
	28/37	hmmpanther:PTHR12747,PIRSF_domai
		10/18
ɔossibly_damaging(0.851	4/7	THR20859:SF21,hmmpanther:PTHR20859,Gene3D
		2/6
	8/8	
	7/7	
	2/2	
		3/4
	8/22	20,hmmpanther:PTHR24416,hmmpanther:PTHR24
		7/21
		10/47
		46/47
		10/17
		13/35
		27/37
		13/13
		8/8
	2/2	am_domain:PF05049,hmmpanther:PTHR32341,hm

		23/29	
		16/29	
		13/27	
		16/27	
		11/23	
	4/24	TE_profiles:PS51468,hmmpanther:PTHR10338,hm	
		20/23	
		4/5	
		2/7	
		5/56	
		49/56	
		16/58	
	3/3	hmmpanther:PTHR10656:SF8,hmmpantl	
		33/39	
		30/39	
442.1		4/10	
		4/10	
		14/23	
		2/17	
		6/17	
	7/18	hmmpanther:PTHR10694	
	1/1		
	16/16		
		9/9	
	3/10	hmmpanther:PTHR24168,hmmpanther:P	
	9/10	ımmpanther:PTHR24168,hmmpanther:PTHR24168	
	3/11	HAMAP:MF_03023,hmmpanther:PTHR23074,hmm	
benign(0)	2/2	_(Seg):seg,hmmpanther:PTHR11537:SF19,hmmpa	
		10/13	
		3/26	
		11/39	
		2/6	
	2/2		
		16/23	
		11/21	
		14/22	
		3/26	
benign(0.008)	17/29	hmmpanther:PTHR14017:SF9,hmmpantl	
		7/19	
	12/20	hmmpanther:PTHR23123,hmmpanther:P	
benign(0.001)	15/20	hmmpanther:PTHR23123,hmmpanther:P	
	1/10		
		10/85	
benign(0.001)	12/34	Seg):seg,SMART_domains:SM00222,hmmpanther:I	
		15/23	
	4/4	E_profiles:PS50096,hmmpanther:PTHR22590,hmm	
		1/3	
		5/29	
	2/15	ROSITE_profiles:PS50067,hmmpanther:PTHR241	
		5/19	
		8/49	
		14/22	
		23/32	
		8/19	
		8/12	

	3/4	hmmpanther:PTHR23223,hmmpanther:P
	2/15	_domain:PIRSF037037,hmmpanther:PTHR24412:S
		7/9
		3/4
		56/58
		17/29
		47/63
	7/10	_profiles:PS50176,hmmpanther:PTHR23316,hmmp
		11/21
		5/9
		7/7
		3/6
	7/7	
	1/1	
	1/1	
	1/1	hmmpanther:PTHR23262,hmmpanther:P
		10/16
		32/64
		2/64
		9/38
		8/38
		19/27
		4/27
		23/27
	1/23	
	4/8	hmmpanther:PTHR24356,hmmpanther:PT
	1/1	
		6/6
		4/4
		4/12
		4/7
		4/7
		9/15
benign(0.001)	1/1	r:PTHR24371,Gene3D:2.60.40.10,Pfam_domain:P
		13/16
		10/26
		12/17
		1/11
	1/11	
		3/10
		2/6
		7/10
		13/20
		90/90
		11/22
probably_damaging(0.996	5/6	20,hmmpanther:PTHR10529,hmmpanther:PTHR10
		5/5
		2/7
		2/3
benign(0.082)	1/2	
	19/19	
		21/26
benign(0.013)	3/14	hmmpanther:PTHR11089,hmmpanther:P
benign(0.077)	5/10	hmmpanther:PTHR13586,hmmpanther:P
	4/4	

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	23/29	
	8/11	
	2/4	
	1/3	
	1/4	
	11/18	
	2/4	
	2/2	
	3/3	SITE_profiles:PS50838,hmmpanther:PTHR11736,h
	1/1	
	3/3	
	3/3	01454,PROSITE_profiles:PS50838,hmmpanther:P
	2/12	
	19/26	
	5/5	hmmpanther:PTHR15275,hmmpanther:P
	10/12	
	8/22	npanther:PTHR11607:SF20,Gene3D:3.20.110.10,F
benign(0)	6/19	omain:PF01074,hmmpanther:PTHR11607,hmmpar
benign(0.002)	5/7	hmmpanther:PTHR13843
possibly_damaging(0.687	4/29	m_domain:PF13281,hmmpanther:PTHR11584,hmr
	16/16	
	13/32	anther:PTHR24361:SF88,hmmpanther:PTHR2436
	5/29	
	5/12	
	5/25	
	10/26	hmmpanther:PTHR24356,hmmpanther:PT
	1/29	
benign(0.023)	4/11	mains:SM00327,Pfam_domain:PF00092,Gene3D:3
	13/18	
	20/28	
	4/17	MART_domains:SM00409,hmmpanther:PTHR23282
	93/101	
	93/101	
	3/3	F_domain:PIRSF038006,hmmpanther:PTHR15074
	29/30	
	2/5	
	12/17	
benign(0.149)	3/4	Pfam_domain:PF11568
	2/12	
	24/36	
	14/14	
	19/19	
	3/10	
	6/10	ain:PIRSF037755,Gene3D:3.40.50.150,Pfam_dom
	7/10	
	12/16	mpanther:PTHR15075:SF4,hmmpanther:PTHR15
	8/15	
	10/16	mpanther:PTHR15075:SF4,hmmpanther:PTHR15
benign(0.089)	3/5	3155,Gene3D:3l00A01,Pfam_domain:PF02870,hm
	8/31	
	16/31	
	12/31	
	6/9	

		2/31
		20/31
		2/4
		8/9
		2/11
		4/6
		1/2
benign(0.035)	4/5	)93,Gene3D:1pi1A00,Pfam_domain:PF03637,hmm
		7/16
benign(0)	12/17	hmmpanther:PTHR23336,hmmpanther:P
		2/12
		2/5
		2/19
benign(0)	3/24	
benign(0)	10/24	anther:PTHR23120,hmmpanther:PTHR23120:SF9,:
possibly_damaging(0.641	7/24	anther:PTHR23120,hmmpanther:PTHR23120:SF9,:
		3/4
		1/1
		2/5
		6/6
		2/20
		2/15
		3/5
	49/58	panther:PTHR11139:SF63,Pfam_domain:PF00454
	29/33	o2kA01,TIGRFAM_domain:TIGR02082,Pfam_dom
		32/32
		15/32
		29/32
		7/18
		59/83
	1/84	
	4/84	
		73/83
	42/49	hmmpanther:PTHR11339,hmmpanther:PT
		8/9
	7/7	mmpanther:PTHR10489,hmmpanther:PTHR10489
	3/3	s:PS51225,hmmpanther:PTHR17068:SF5,hmmpa
		4/34
benign(0.419)	29/42	oils):Coil,Pfam_domain:PF01576,hmmpanther:PTH
		21/41
	12/40	456,hmmpanther:PTHR13140,hmmpanther:PTHR1
		18/39
		29/39
		26/40
	19/34	mpanther:PTHR22964:SF44,Pfam_domain:PF0767
		45/65
		18/43
		15/25
		25/27
		32/40
		12/39
	1/3	
	5/20	hmmpanther:PTHR19897
		25/26
		12/19

		21/22
	2/5	hmmpanther:PTHR23228:SF7,hmmpantl
benign(0.038)	7/9	ıain:PF00026,hmmpanther:PTHR13683,hmmpanth
		3/6
		40/51
possibly_damaging(0.67)	21/21	ımpanther:PTHR20930,hmmpanther:PTHR20930:
		17/20
		3/20
		4/20
ɔrobably_damaging(0.999	3/15	mpanther:PTHR22804:SF24,Pfam_domain:PF076
		5/31
		28/34
		14/17
		9/15
		42/45
	13/15	PF00346,hmmpanther:PTHR11993,hmmpanther:P
		74/181
		18/181
		6/181
	8/11	hmmpanther:PTHR13328,Low_comple
	4/4	hmmpanther:PTHR10281
		3/3
benign(0.003)	9/13	:oiled-coils_(Ncoils):Coil,hmmpanther:PTHR22964,
		15/23
		2/22
		2/11
	1/1	Low_complexity_(Seg):seg,hmmpanthe
		1/6
		11/19
		21/29
		8/11
benign(0)	5/6	R12570,hmmpanther:PTHR12570:SF7,Pfam_dom
		46/46
		3/9
		13/20
benign(0.002)	2/2	L0.60,hmmpanther:PTHR24340,hmmpanther:PTHF
		6/7
		9/9
		13/14
	11/15	,hmmpanther:PTHR24106,Gene3D:3.80.10.10,SM/
		2/14
		5/8
		11/14
		5/25
		15/17
	12/12	
		8/9
benign(0.001)	8/27	9384,hmmpanther:PTHR19384:SF66,Pfam_domair
		15/26
		27/33
		16/33
	20/20	hmmpanther:PTHR10796,hmmpanther:P
ɔrobably_damaging(0.922	4/4	1,PROSITE_patterns:PS00237,Pfam_domain:PF0(
ɔossibly_damaging(0.856	6/9	nain:PR00896,PROSITE_profiles:PS50262,hmmpa

	3/4	
	1/8	
M_001077482.2		
	12/13	
	5/23	hmmpanther:PTHR22884,hmmpanther:PT
	14/18	
	13/13	
benign(0.124)	4/6	HR12356:SF16,hmmpanther:PTHR12356,Pfam_d
	5/9	
	5/19	9331,hmmpanther:PTHR19331:SF254,Pfam_dom
	12/27	
	33/35	
	1/8	
	8/8	
	8/11	
	11/11	
	16/16	
	13/16	
	2/19	
	15/15	
	15/15	
	15/15	
	5/7	
	4/5	
	5/21	THR19900,hmmpanther:PTHR19900:SF1,Gene3D
	10/10	
	1/1	
	1/1	
benign(0.094)	1/1	PROSITE_profiles:PS50262,hmmpanther:PTHR26
	1/1	ain:PR00245,PROSITE_profiles:PS50262,hmmpan
benign(0.15)	1/1	10,hmmpanther:PTHR26451,hmmpanther:PTHR26
	1/1	r:PTHR26450:SF28,hmmpanther:PTHR26450,Pfam
	1/1	ain:PR00245,PROSITE_profiles:PS50262,hmmpan
benign(0)	1/1	es:PS50262,hmmpanther:PTHR26452,hmmpanthe
	1/1	es:PS50262,hmmpanther:PTHR26452,hmmpanthe
	1/1	mmpanther:PTHR26452,hmmpanther:PTHR2645
	1/1	
	4/13	
	5/5	
	6/6	main:PF13738,hmmpanther:PTHR15192,hmmpantl
	11/17	
	3/10	
	10/10	Low_complexity_(Seg):seg
benign(0)	1/1	ain:PR01066,PROSITE_profiles:PS50262,hmmpa
	5/11	m_domain:PF13848,Gene3D:3.40.30.10,TIGRFAM
possibly_damaging(0.794	5/16	THR24011,hmmpanther:PTHR24011:SF265,SMAR
	10/23	
	3/4	
	2/8	
	3/6	
	1/7	_complexity_(Seg):seg,hmmpanther:PTHR12280,h
benign(0.057)	13/19	12280,Pfam_domain:PF01937,PIRSF_domain:PIR
	19/21	

benign(0.007)	2/2	
	6/13	.10,hmmpanther:PTHR12114,hmmpanther:PTHR1
		10/13
		4/11
unknown(0)	1/1	
		18/33
benign(0.23)	5/5	hmmpanther:PTHR24027:SF25,hmmpant
		6/24
benign(0)	5/8	THR11579,Pfam_domain:PF01135,Gene3D:3.40.5
		37/46
benign(0)	1/3	hmmpanther:PTHR12121,hmmpanther:P
	26/31	,Pfam_domain:PF00233,Gene3D:1.10.1300.10,SM
	1/22	:PTHR11347,hmmpanther:PTHR11347:SF23,Low_
		9/22
	23/23	nther:PTHR24416:SF53,hmmpanther:PTHR24416,
		22/22
		3/11
		22/22
benign(0.01)	7/7	rofiles:PS50011,hmmpanther:PTHR22972,hmmpar
		4/23
	3/24	52,hmmpanther:PTHR24052:SF9,Low_complexity_
	12/24	A03,hmmpanther:PTHR24052,hmmpanther:PTHR
benign(0.029)	14/15	main:PF00557,hmmpanther:PTHR10804,hmmpant
	15/15	
		11/21
		10/21
		16/26
		8/10
benign(0.027)	3/5	ains:SM00701,SMART_domains:SM00644,Gene3
	1/7	
		6/21
		39/39
		9/31
		20/23
	4/18	:PTHR15242,PROSITE_patterns:PS00518,Pfam_d
	6/6	
		9/10
	22/31	Pfam_domain:PF04987,hmmpanther:
benign(0.007)	2/2	hmmpanther:PTHR20661,PIRSF_domai
51851.1		17/18
		5/41
	2/6	PTHR22984,Pfam_domain:PF00069,Gene3D:3.30.
		2/20
	2/2	hmmpanther:PTHR15710,hmmpanther:P
	1/2	
		50/66
		10/13
		2/11
		11/13
		15/57
		21/31
		9/31

		30/31
benign(0)	23/32	49,Gene3D:3.20.20.190,Pfam_domain:PF00387,h
		2/32
		1/21
		8/21
unknown(0)	30/32	915,hmmpanther:PTHR11915:SF247,SMART_dom
	5/32	),PROSITE_profiles:PS50021,hmmpanther:PTHR1
	32/32	
	32/32	,hmmpanther:PTHR11915,hmmpanther:PTHR119
	32/32	panther:PTHR11915,hmmpanther:PTHR11915:SF
	32/32	,hmmpanther:PTHR11915,hmmpanther:PTHR119
		8/21
		22/28
		14/28
		28/28
		12/15
		6/12
		11/13
		8/36
		2/11
benign(0)	7/8	hmmpanther:PTHR12406,hmmpanther:P
		8/8
	19/34	ofiles:PS50042,hmmpanther:PTHR14226,hmmpan
		1/2
		2/7
		2/8
		8/8
		11/22
benign(0.001)	2/2	,Gene3D:1.10.260.40,Pfam_domain:PF00157,PRO
benign(0)	1/7	
	7/7	04,Prints_domain:PR00398,hmmpanther:PTHR240
		8/20
	1/7	panther:PTHR13832,hmmpanther:PTHR13832:SF
		2/12
		2/2
	7/7	
		2/13
		2/5
		6/15
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	3/14	
		12/17
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possibly_damaging(0.852	3/3	Low_complexity_(Seg):se
		6/9
		13/16
		12/14

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	2/5	
	3/5	
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	16/23	PROSITE_profiles:PS50055,hmmpanther:PTHR19
	2/2	
	19/21	
	11/21	
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	21/21	
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	1/12	
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benign(0.003)	2/6	R24073,hmmpanther:PTHR24073:SF137,Gene3D:3
	1/3	
	2/7	
	5/18	
	14/16	omain:PF00560,PROSITE_profiles:PS51450,Low_c
	2/5	
	2/10	
	10/15	F01843,PROSITE_profiles:PS51126,hmmpanther:F
	15/16	
	3/19	
	18/24	
	21/27	
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probably_damaging(0.972	1/6	hmmpanther:PTHR22738,hmmpanther:P
	21/24	iled-coils_(Ncoils):Coil,hmmpanther:PTHR13948:SF
	12/20	
	14/20	
	1/6	
	13/21	hmmpanther:PTHR13487
	3/11	
	6/19	
	1/3	1,hmmpanther:PTHR21101:SF13,Low_complexity_
	1/2	
	13/13	
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	4/9	
	1/19	
	14/17	
	1/7	
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	5/8	
	1/9	
	1/7	
	2/7	rofiles:PS50088,PROSITE_profiles:PS50297,hmm

	5/5	
		8/8
		2/8
	3/3	
		14/30
		8/30
benign(0)	10/33	anther:PTHR22988:SF24,hmmpanther:PTHR2298
		7/8
		11/42
		10/12
		30/33
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	1/5	
	1/5	
	2/10	hmmpanther:PTHR11363,Superfamily_do
	5/7	ain:PIRSF002116,Pfam_domain:PF00900,hmmpa
		14/21
		23/33
	22/34	hmmpanther:PTHR12848,Superfamily_do
		2/15
	7/16	mpanther:PTHR13026,hmmpanther:PTHR13026:
	4/9	IGRFAM_domain:TIGR00539,Gene3D:2qgqB01,Pf
		2/7
benign(0.003)	3/9	hmmpanther:PTHR10994,hmmpanther:P
		1/17
	18/18	THR22835:SF84,hmmpanther:PTHR22835,Pfam_d
		9/9
	26/106	0188,hmmpanther:PTHR13715,hmmpanther:PTHR
		3/105
	39/106	hmmpanther:PTHR13715,hmmpanther:P
		47/105
		9/104
		35/104
		2/103
		2/3
		6/20
		2/4
	40/41	mpanther:PTHR10807:SF43,Pfam_domain:PF001
		30/39
		6/10
	4/9	hmmpanther:PTHR10687,hmmpanther:P
		6/10
		3/32
benign(0.001)	1/16	,hmmpanther:PTHR11977,hmmpanther:PTHR1197
		12/20
		20/20
		10/27
benign(0)	19/27	mpanther:PTHR10037,hmmpanther:PTHR10037:S

		26/26
		8/44
		5/8
benign(0.156)	2/12	1,hmmpanther:PTHR23324,Gene3D:3.40.525.10,F
		12/25
ɔossibly_damaging(0.516	13/20	F3,hmmpanther:PTHR11141,Pfam_domain:PF080
		7/22
		9/25
		3/25
benign(0.001)	4/26	10,hmmpanther:PTHR13923,hmmpanther:PTHR1
		14/25
		5/16
benign(0)	5/5	
		4/13
		13/16
		4/16
		1/16
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		10/10
		3/4
		1/1
		10/16
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		10/22
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		20/25
	1/1	
		12/14
		11/23
		9/23
		10/21
	14/14	hmmpanther:PTHR15706,hmmpanther:P
		8/22
		7/22
		1/2
benign(0)	6/10	hmmpanther:PTHR15012,hmmpanther:P
		1/7
		2/13
		10/10
		7/21
		3/6
	1/3	hmmpanther:PTHR10361,hmmpanther:PT
benign(0.06)	1/6	er:PTHR10361,hmmpanther:PTHR10361:SF4,TIGI
		4/23
		5/14
unknown(0)	1/6	complexity_(Seg):seg,hmmpanther:PTHR11360,hr
		6/8
		3/8
	1/10	IGR00898,hmmpanther:PTHR24064,hmmpanther:
		9/14
	6/17	1699,hmmpanther:PTHR10846,hmmpanther:PTHF
		2/17
		5/11

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	7/15	
	7/10	
	6/8	nmpanther:PTHR19432:SF7,hmmpanther:PTHR19
	8/22	
	14/14	
	12/13	
	6/11	
	1/13	
	6/10	
	9/11	R11785:SF113,hmmpanther:PTHR11785,TIGRFAI
	1/17	(Seg):seg,hmmpanther:PTHR10110,hmmpanther:F
	5/13	
	18/24	
	7/23	
	11/24	
	2/12	PS51465,hmmpanther:PTHR12352:SF10,hmmpant
	15/20	
	8/11	
	28/32	
	22/26	
	5/49	hmmpanther:PTHR21963
	11/49	hmmpanther:PTHR21963
	2/2	mpanther:PTHR23425:SF5,hmmpanther:PTHR23
	1/4	
	32/40	
probably_damaging(0.993	30/41	hmmpanther:PTHR19897,hmmpanther:PT
benign(0.184)	7/7	embrane_helices:TMhelix,hmmpanther:PTHR10083
	1/11	_site_(Signalp):SignalP-noTM,hmmpanther:PTHR1
	41/67	
	24/67	
possibly_damaging(0.539	25/34	hmmpanther:PTHR10799,hmmpanther:PT
	87/109	
	65/108	
	90/109	
	8/11	
	6/6	
	2/8	
	3/8	
	4/5	
	34/69	),hmmpanther:PTHR24038,Pfam_domain:PF02469
	2/9	
	5/9	nther:PTHR16186,hmmpanther:PTHR16186:SF10,
	24/32	
	5/23	
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		6/14
	5/7	HR10264,hmmpanther:PTHR10264:SF70,Pfam_do
	1/5	
		5/17
		3/20
		13/20
		26/27
benign(0.209)	6/11	mpanther:PTHR24418:SF216,Gene3D:1.10.510.1(
	3/3	
		2/3
benign(0.004)	1/1	mpanther:PTHR10562:SF10,Pfam_domain:PF119
		26/30
		8/30
		2/4
		2/11
	26/27	_complexity_(Seg):seg,hmmpanther:PTHR15245,h
		10/10
	6/116	64,hmmpanther:PTHR11915,Gene3D:1.10.418.10,I
		44/115
	20/27	,PROSITE_profiles:PS50102,hmmpanther:PTHR1
benign(0.001)	5/5	hmmpanther:PTHR23239,hmmpanther:P
benign(0.015)	3/5	hmmpanther:PTHR24217:SF9,hmmpantl
	4/8	hmmpanther:PTHR10351:SF27,hmmpant
		4/7
benign(0.201)	6/16	hmmpanther:PTHR13924
		8/12
		6/9
	5/10	hmmpanther:PTHR23179,hmmpanther:P
		18/18
		15/18
benign(0.017)	3/8	hmmpanther:PTHR10060,hmmpanther:P
		5/7
benign(0.11)	3/13	hmmpanther:PTHR22957,hmmpanther:PT
		1/20
benign(0)	23/24	
		18/26
		1/7
probably_damaging(0.939	3/3	F04538,hmmpanther:PTHR14754,hmmpanther:PTH
benign(0)	4/11	hmmpanther:PTHR15141:SF37,hmmpant
		1/21
	9/9	
	6/36	ofiles:PS51192,hmmpanther:PTHR18934,hmmpan
		27/31
		23/28
		7/9
		3/8
		7/32
		9/11
		3/6
	5/7	11727,hmmpanther:PTHR11727:SF10,Gene3D:3.4(
probably_damaging(0.97)	1/1	R12548:SF13,Gene3D:1.10.10.10,Pfam_domain:PF
		3/5
		4/16

benign(0)	1/1	_complexity_(Seg):seg,hmmpanther:PTHR11850,h
	6/13	in:PIRSF000459,hmmpanther:PTHR11590,hmmpa
		20/22
		3/7
	6/28	hmmpanther:PTHR11311,hmmpanther:P
	2/2	
		3/9
		18/28
		23/28
	2/2	PIRSF_domain:PIRSF0377
	6/6	
		6/14
		14/14
	1/4	
	16/20	es:PS50294,hmmpanther:PTHR10814,Gene3D:2.1
		13/19
		2/21
benign(0.012)	20/21	9,PROSITE_profiles:PS01180,hmmpanther:PTHR
		19/20
		14/20
	19/21	0127:SF613,Pfam_domain:PF00431,Gene3D:2.60
		49/57
	1/3	
benign(0)	1/4	site_(Signalp):SignalP-noTM,hmmpanther:PTHR22
		34/40
benign(0.04)	2/2	am_domain:PF14985,hmmpanther:PTHR16103:SF
		7/7
		4/6
		3/4
	6/6	Transmembrane_helices:TMI
	10/10	
		5/8
	3/4	F_domain:PIRSF019548,hmmpanther:PTHR32163
	15/30	hmmpanther:PTHR12505:SF21,hmmpant
		3/12
benign(0.002)	6/13	ofiles:PS50001,hmmpanther:PTHR12583,hmmpan
benign(0.005)	9/28	hmmpanther:PTHR15321
benign(0)	17/28	hmmpanther:PTHR15321
		16/27
	2/7	hmmpanther:PTHR31854
		2/9
		2/3
	4/4	mpanther:PTHR12932,hmmpanther:PTHR12932:S
		2/5
		2/5
		2/5
		3/5
benign(0.415)	12/18	s:PS51156,hmmpanther:PTHR16089:SF19,hmmpa
		4/12
		5/6
		6/7
		3/9
		3/4
benign(0.306)	8/10	ns:SM00449,Pfam_domain:PF00622,hmmpanther:
		5/9

		1/9
	29/57	10,hmmpanther:PTHR22826,hmmpanther:PTHR22
benign(0.001)	1/9	hmmpanther:PTHR24212,hmmpanther:P
	15/18	hmmpanther:PTHR10631:SF3,hmmpantl
		13/13
		11/18
		1/26
possibly_damaging(0.61)	7/24	hmmpanther:PTHR13800,hmmpanther:P
		3/38
		3/14
benign(0.001)	10/23	Pfam_domain:PF04388,hmmpanther:
		14/22
		16/41
		1/8
ɔossibly_damaging(0.792	3/8	ʾTHR19282,hmmpanther:PTHR19282:SF169,Pfam
		5/7
	1/1	
		4/14
benign(0.001)	13/15	
		7/27
		9/9
possibly_damaging(0.81)	2/23	TE_profiles:PS50005,SMART_domains:SM00028,:
		37/57
	1/58	
		18/57
	22/58	hmmpanther:PTHR15977:SF13,hmmpant
		44/57
	8/11	s:PS51221,hmmpanther:PTHR12241:SF31,hmmpa
	5/16	_profiles:PS51221,hmmpanther:PTHR12241,hmm
		11/12
	23/23	
		18/24
	4/14	_profiles:PS50294,hmmpanther:PTHR16517,hmmp
		5/13
		7/9
		8/9
		7/14
		4/13
	12/23	ıpanther:PTHR11254,hmmpanther:PTHR11254:SF
	106/106	
		3/7
		4/6
	14/17	
		4/15
		8/36
		14/21
benign(0)	19/22	˙E_profiles:PS51034,hmmpanther:PTHR22962,hmı
		15/21
		9/19
		4/14
	9/10	7,Gene3D:3.60.110.10,hmmpanther:PTHR23088:S
		4/6
benign(0)	36/72	ains:SM00060,Gene3D:2.60.40.10,hmmpanther:PT
	10/13	hmmpanther:PTHR23347,hmmpanther:P

	8/14	panther:PTHR24006,hmmpanther:PTHR24006:SF6
	4/21	hmmpanther:PTHR24006,hmmpanther:PT
		4/10
		14/24
	13/13	
		16/79
		7/12
		19/61
		24/61
		15/27
		9/9
benign(0.004)	13/13	mpanther:PTHR12011,hmmpanther:PTHR12011:S
		5/15
	6/6	):seg,Transmembrane_helices:TMhelix,hmmpanth
		3/12
ossibly_damaging(0.711	6/6	nther:PTHR10108,hmmpanther:PTHR10108:SF693
		3/60
		15/28
	6/29	hmmpanther:PTHR14593
		19/28
	24/29	hmmpanther:PTHR14593
		26/28
		25/30
		13/13
		11/17
		1/18
		17/24
	6/6	Coiled-coils_(Ncoils):Coil,Low_complex
		10/14
		8/12
unknown(0)	1/28	_complexity_(Seg):seg,hmmpanther:PTHR13902,h
	5/5	
benign(0)	1/6	Cleavage_site_(Signalp):SignalP
		1/6
		5/8
		16/22
	23/24	_profiles:PS50237,hmmpanther:PTHR11254,hmm
		12/18
	3/3	
		6/20
		4/9
	24/32	anther:PTHR11223,hmmpanther:PTHR11223:SF3,S
	7/17	hmmpanther:PTHR11370,hmmpanther:P
		9/16
		7/8
		9/9
	1/10	
	3/3	hmmpanther:PTHR24399,hmmpanther:P
		6/7
		5/5
		5/5
	2/6	
		3/11
		13/22

	2/2	ım_domain:PF14893,hmmpanther:PTHR23095,hm
benign(0.194)	3/12	hmmpanther:PTHR12246,hmmpanther:P
	5/11	her:PTHR22883,hmmpanther:PTHR22883:SF35,L
		3/8
		3/4
benign(0)	9/10	hmmpanther:PTHR24208,hmmpanther:P
		5/7
	11/11	
		1/6
		11/11
		5/11
		8/23
	4/5	hmmpanther:PTHR24409,hmmpanther:P
benign(0.002)	4/4	_profiles:PS50157,hmmpanther:PTHR24387,hmm
		3/3
		5/7
		6/7
		4/4
	5/5	,PROSITE_profiles:PS50157,hmmpanther:PTHR24
		1/3
		3/4
		3/3
		12/16
probably_damaging(0.997	5/8	complexity_(Seg):seg,hmmpanther:PTHR24402,hm
possibly_damaging(0.865	11/14	_complexity_(Seg):seg,hmmpanther:PTHR22938,h
benign(0)	4/5	S50805,hmmpanther:PTHR24381,hmmpanther:PT
	1/4	
possibly_damaging(0.672	2/3	anther:PTHR24384,hmmpanther:PTHR24384:SF1
	3/3	hmmpanther:PTHR24402,hmmpanther:P
benign(0.008)	4/4	hmmpanther:PTHR24384:SF113,hmmpan
		2/4
	7/7	ofiles:PS50157,hmmpanther:PTHR23226,hmmpan
probably_damaging(0.981	3/3	,PROSITE_profiles:PS50157,hmmpanther:PTHR2
	5/5	,PROSITE_profiles:PS50157,hmmpanther:PTHR2
	8/8	hmmpanther:PTHR16116
benign(0.018)	3/12	hmmpanther:PTHR23343,hmmpanther:P
		2/2
		12/12
		31/54

GMAF	AFR_MAF	AMR_MAF	ASN_MAF
C:0.0196 G:0.3333 G:0.4714	C:0.0008 C:0.9334	C:0.049 C:0.5634	
T:0.3009 G:0.4309 A:0.3862	G:0.8737 G:0.1974 G:0.7526	G:0.7637 G:0.5346 G:0.6398	
ain:TIGR00957,Pfam_domain:PF00005,SMART_domains:SM00382,Superfamily_domains:SSF52540			
T:0.3910	T:0.77	T:0.4236	
A:0.1575 T:0.1536 T:0.0168	A:0.112 C:0.9244 T:0.0008	A:0.1758 C:0.7925 T:0.013	
G:0.3187 T:0.0198 C:0.0863	G:0.5998 T:0.0363 C:0.0356	G:0.3602 T:0.0101 C:0.1081	
A:0.0489 G:0.4329 A:0.2438 T:0.0399	A:0.0136 A:0.3964 A:0.2352 T:0.0136 T:0.2035	A:0.0072 A:0.6599 A:0.3199 T:0.0677 T:0.281	
T:0.1332 ATAA:0.3061 A:0.1601 G:0.4627	T:0.1921 ATAA:0.3427 A:0.0159 G:0.4047	T:0.1254 ATAA:0.3213 A:0.2046 G:0.5346	
C:0.2975 G:0.0591 G:0.2175 -:0.0361 G:0.0595 C:0.3544 T:0.4327 A:0.0172 G:0.0248 C:0.3728 T:0.4581 C:0.0136 A:0.2680 C:0.3083 C:0.3289 T:0.2103 T:0.0044 T:0.1332 C:0.1989 T:0.3624 G:0.3738 C:0.1781	T:0.5893 G:0.1225 G:0.2231 -:0.0023 G:0.062 C:0.7322 C:0.5378 A:0.0015 G:0.0053 C:0.3691 T:0.1566 C:0.0015 A:0.2973 C:0.2965 T:0.82 T:0.1331 T:0.0023,T:0.0023 T:0.0151 C:0.1067 T:0.466 G:0.5076 T:0.8245	T:0.7061 G:0.0259 G:0.2248 -:0.0202 G:0.0836 C:0.1671 C:0.6715 A:0.0202 G:0.049 C:0.2738 T:0.585 C:0.0259 A:0.2622 C:0.255 T:0.6354 T:0.2507 T:0,T:0 T:0.1916 C:0.2334 T:0.3559 G:0.3573 T:0.817	

A:0.1709	A:0.2163	A:0.2032
A:0.1947	A:0.0136	A:0.2349
T:0.1569	T:0.1619	T:0.1196
C:0.3782	C:0.2912	C:0.3905
T:0.0737	T:0.0507	T:0.0274
T:0.4569	C:0.3949	C:0.5014
A:0.1981	G:0.9244	G:0.7954
T:0.1450	T:0.0325	T:0.1643
G:0.1967	G:0.0787	G:0.3084
-:0.2610	-:0.4539	-:0.2507
A:0.2875	A:0.3048	A:0.2565
A:0.1096	A:0.1672	A:0.072
C:0.1941	C:0.1679	C:0.2104
T:0.1348	C:0.8684	C:0.7262
G:0.2756	G:0.2897	G:0.1715
A:0.0365	A:0.0023	A:0.0692
T:0.0317	T:0.0015	T:0.0519
T:0.0130	T:0.0008	T:0.0173
C:0.1492	C:0.1112	C:0.085
C:0.0018	C:0.0015	C:0.0058

:01602,PIRSF_domain:PIRSF037097,Superfamily_domains:SSF48371

T:0.0833	T:0.0431	T:0.0778
G:0.1999	G:0.1989	G:0.3242
G:0.2161	G:0.2549	G:0.3256
G:0.2061	G:0.034	G:0.1052
T:0.0260	T:0.0015	T:0.0836
G:0.0395	G:0.0068	G:0.0461
G:0.2821	G:0.4372	G:0.2781
C:0.2381	C:0.2799	C:0.2579
T:0.0204	T:0.0015	T:0.0202
T:0.0487	T:0.062	T:0.0259
G:0.3181	A:0.388	A:0.7536
G:0.0663	G:0.0552	G:0.0548
C:0.4147	C:0.5688	C:0.487
C:0.2488	C:0.025	C:0.1225
G:0.3686	G:0.5287	G:0.3415
A:0.0278	A:0.0015	A:0.0476
C:0.3419	T:0.7065	T:0.7046
C:0.3401	T:0.6558	T:0.4914
A:0.3807	G:0.5537	G:0.4798
A:0.4411	A:0.1604	A:0.4207
T:0.4411	T:0.1657	T:0.4121
G:0.0966	G:0.0446	G:0.1311
A:0.1667	A:0.2383	A:0.0994
A:0.1619	A:0.2163	A:0.0994
A:0.0190	A:0.003	A:0.0231
T:0.2262	T:0.2995	T:0.2896
G:0.1146	G:0.0136	G:0.1671
-:0.0272	-:0.0151	-:0.0187

A:0.4960	A:0.1551	A:0.5591
T:0.4079	T:0.3661	T:0.4654
A:0.3584	A:0.202	A:0.4625
G:0.3998	G:0.3162	G:0.4726
C:0.2157	C:0.0666	C:0.0793
G:0.2426	A:0.8071	A:0.7277
G:0.1867	G:0.3124	G:0.2565
C:0.0244	C:0.0325	C:0.0331
A:0.1464	A:0.0893	A:0.281
A:0.0347	A:0.084	A:0.0159
T:0.0631	T:0.0045	T:0.1182
G:0.3770	G:0.2436	G:0.3314
G:0.1060	G:0.174	G:0.1023
T:0.2001	T:0.0802	T:0.281
A:0.3144	A:0.2867	A:0.1916
A:0.1639	A:0.1808	A:0.1873
A:0.2135	A:0.177	A:0.3026
G:0.3888	G:0.472	G:0.3184
T:0.3027	T:0.2277	T:0.1888
C:0.0323	T:0.7337	T:0.7233
G:0.4003	G:0.1293	G:0.4179
C:0.2129	C:0.2882	C:0.2435
C:0.3894	C:0.6634	C:0.2939
G:0.2600	A:0.8941	A:0.7666
T:0.1715	T:0.2005	T:0.1354
G:0.4936	A:0.584	A:0.4726
G:0.0825	G:0.0265	G:0.0778
C:0.0363	C:0.053	C:0.0346
T:0.1648	T:0.1747	T:0.2867
T:0.0286	T:0.0038	T:0.049
A:0.2192	A:0.0893	A:0.415
G:0.0283	G:0.003	G:0.0202
A:0.1757	A:0.0469	A:0.1671
T:0.0004	T:0	T:0
T:0.3425	T:0.2179	T:0.2925
T:0.3069	T:0.1611	T:0.3084
C:0.3534	C:0.2194	C:0.3746
T:0.1859	T:0.2746	T:0.2176
T:0.0469	T:0.0136	T:0.0648
A:0.2151	A:0.3003	A:0.2176
G:0.0417	G:0.0401	G:0.0159
C:0.1947	C:0.2095	C:0.098
T:0.1889	T:0.2095	T:0.0908
T:0.1673	T:0.0151	T:0.1988
A:0.0958	A:0.0113	A:0.0764
G:0.3303	T:0.5431	T:0.781
G:0.2825	G:0.3064	G:0.2738

C:0.3037	C:0.1316	C:0.3818
A:0.4914	A:0.3215	A:0.4654
A:0.1330	A:0.0144	A:0.0836
C:0.0242	C:0.0023	C:0.049
T:0.3688	T:0.3707	T:0.3069
-:0.1901	-:0.323	-:0.0893
-:0.0681	-:0.1619	-:0.0259
A:0.0751	A:0.115	A:0.062
T:0.4659	C:0.767	C:0.4986
T:0.3486	C:0.5923	C:0.5389
C:0.3415	C:0.174	C:0.3934
T:0.1475	T:0.0068,T:0.0068	T:0.1138,T:0.1138
G:0.2720	G:0.4289	G:0.2464
-:0.1136	-:0.2526	-:0.0836
C:0.1538	C:0.3124	C:0.098
C:0.1719	C:0.0666	C:0.1787
C:0.3610	C:0.3419	C:0.3934
G:0.2680	T:0.7095	T:0.7695
G:0.0541	G:0.0159	G:0.036
C:0.3057	C:0.649	C:0.1383
C:0.4858	C:0.8404	C:0.3991
T:0.0000	T:0	T:0
G:0.2865	G:0.1944	G:0.2464
A:0.0074	A:0.0015	A:0.0231
T:0.0006	T:0.0008	T:0
C:0.4215	C:0.6263	C:0.134
T:0.0092	T:0.0008	T:0.0086
G:0.0723	G:0.0076	G:0.0821
C:0.0707	C:0.0666	C:0.1037
C:0.0004	C:0	C:0
T:0.1849	T:0.0378	T:0.4078
A:0.0054	A:0	A:0.013
A:0.3488	A:0.5439	A:0.3573
T:0.2402	T:0.4675	T:0.1729
T:0.0741	T:0.0862	T:0.0994
C:0.4814	T:0.5787	T:0.4135
T:0.3061	T:0.3245	T:0.4222
T:0.0032	T:0	T:0
C:0.2897	C:0.3767	C:0.2118
A:0.3139	A:0.18	A:0.268
T:0.2680	T:0.1044	T:0.255
C:0.1581	C:0.1036	C:0.1499
G:0.2806	G:0.0847	G:0.3761
T:0.0425	T:0.0053,T:0.0053	T:0.062,T:0.062
T:0.0060	T:0.0008	T:0.0029
-:0.3093	-:0.3094	-:0.4524
A:0.3143	A:0.0666	A:0.4496

A:0.2965	A:0.3752	A:0.2305
G:0.0004	G:0	G:0
C:0.0645	C:0.1944	C:0.0375
G:0.0002	G:0	G:0
361,hmmpanther:PTHR13140		
T:0.1472	T:0.1362	T:0.0922
A:0.1160	A:0.2156	A:0.1138
A:0.1110	A:0.0552	A:0.1268
A:0.1494	A:0.0908	A:0.1052
T:0.1326	T:0.0121	T:0.1859
A:0.0441	A:0.0053	A:0.098
G:0.3724	G:0.4675	G:0.4049
-:0.1679	-:0.0953	-:0.2133
A:0.4968	G:0.3449	G:0.598
-:0.2812	-:0.5983	-:0.2147
C:0.2867	C:0.3109	C:0.2233
G:0.1164	G:0.034	G:0.2666
ty_(Seg):seg,Transmembrane_helices:TMhelix		
T:0.0002	T:0	T:0
T:0.3716	C:0.6286	C:0.6138
T:0.2883	T:0.0197	T:0.3905
T:0.2680	C:0.5499	C:0.7594
C:0.3015	C:0.1967	C:0.3458
A:0.0092	A:0.0008	A:0.0159
G:0.1879	G:0.239	G:0.1369
G:0.0003	G:0.0008	G:0
A:0.0853	A:0.2905	A:0.0476
	A:0.1717	A:0.2565
	G:0.6172	G:0.4035
A:0.0098	A:0	A:0.013
-:0.4427	AAG:0.8873	AAG:0.4957
C:0.3251	T:0.5106	T:0.7161
C:0.2390	C:0.2186	C:0.2104
A:0.2039	A:0.152	A:0.2205
C:0.2478	C:0.0567	C:0.4409
C:0.2260	C:0.1596	C:0.2233
-:0.2771	-:0.1959	-:0.2061
T:0.0515	T:0.025	T:0.0735
T:0.0012	T:0	T:0
T:0.3177	C:0.5794	C:0.7795
C:0.2913	T:0.59	T:0.7882
C:0.3093	T:0.5923	T:0.7061
G:0.3852	G:0.7088	G:0.2233
C:0.2666	T:0.6377	T:0.7666
A:0.1861	A:0.2496	A:0.1513
G:0.2821		
A:0.1348	A:0.0817	A:0.1671

C:0.2530	C:0.1884	C:0.2767
T:0.0727	T:0.0303	T:0.0634
C:0.3057	C:0.0953	C:0.3501
A:0.1534	A:0.3011	A:0.0908
T:0.4217	T:0.3631	T:0.3761
A:0.2640	A:0.0666	A:0.2478
T:0.2003	T:0.2867	T:0.1974
G:0.1907	C:0.7504	C:0.5994
C:0.0118	C:0	C:0.013
A:0.0533	A:0.0809	A:0.0447
	C:0.4372	C:0.1268
G:0.3542	G:0.447	G:0.268
T:0.1823	T:0.0272	T:0.1095
G:0.1364	A:0.8048	A:0.9222
A:0.4704	A:0.1445	A:0.5432
A:0.4852	A:0.6687	A:0.2983
G:0.4028	G:0.3033	G:0.4409
T:0.1294	T:0.0287	T:0.147
A:0.4706	A:0.8411	A:0.3963
C:0.3602	C:0.413	C:0.304
G:0.2214	G:0.1399	G:0.2925
G:0.0653	G:0.0393	G:0.0461
T:0.0030	T:0.0045	T:0.0043
A:0.4333	G:0.621	G:0.4481
G:0.2027	G:0.0772	G:0.2622
A:0.4904	A:0.5159	A:0.5562
C:0.3117	C:0.2829	C:0.3991
A:0.1851	A:0.1808	A:0.072
A:0.3211	A:0.3404	A:0.3184
C:0.3955	C:0.1974	C:0.3847
T:0.4884	C:0.3321	C:0.6715
G:0.2969	G:0.1702	G:0.2954
G:0.2099	G:0.4455	G:0.1412
T:0.0080		
A:0.1230	A:0.0325	A:0.1715
G:0.0491	G:0.0643	G:0.0562
A:0.2774	A:0.0522	A:0.3199
G:0.0060	G:0.0008	G:0.0014
C:0.0002	C:0	C:0
A:0.2995	A:0.233	A:0.2867
T:0.1554	T:0.2413	T:0.0634
T:0.0028	T:0	T:0.0058
C:0.4744	C:0.2526	C:0.5043
T:0.4605	T:0.202	T:0.5

G:0.3944	G:0.2723	G:0.5303
A:0.3444	A:0.1097	A:0.3429
T:0.1392	T:0.0356	T:0.2277
T:0.4700	C:0.888	C:0.3818
T:0.1983	T:0.0166	T:0.3228
A:0.0643	A:0.0113	A:0.0274
G:0.3650	G:0.4228	G:0.3646
G:0.0034	G:0	G:0
G:0.2248	G:0.4728	G:0.1556
1.10.260.40,Pfam_domain:PF02376,Superfamily_domains:SSF47413		
A:0.3916	T:0.615	T:0.4222
C:0.3934	T:0.6142	T:0.4193
A:0.1146	A:0.1604	A:0.1369
A:0.0681	A:0.034	A:0.049
G:0.2027	G:0.3707	G:0.2622
T:0.2314	T:0.4743	T:0.2738
T:0.2057	T:0.3139	T:0.2161
C:0.3990	A:0.8359	A:0.4957
A:0.3001	A:0.2269	A:0.3213
T:0.3231	C:0.9183	C:0.6268
A:0.4177	G:0.4599	G:0.7017
A:0.4675	C:0.7474	C:0.513
C:0.1737	C:0.2587	C:0.1167
A:0.1262	A:0.1029	A:0.1052
G:0.1617	G:0.0431	G:0.2277
A:0.1164	A:0.1218	A:0.1182
G:0.3107	G:0.5182	G:0.1974
C:0.0004	C:0	C:0
T:0.3658	C:0.7103	C:0.6066
T:0.0449	T:0.0061	T:0.0735
A:0.4317	C:0.2965	C:0.6297
G:0.3752	G:0.2103	G:0.464
A:0.4301	A:0.5711	A:0.4063
T:0.3914	T:0.1036	T:0.4856
TG:0.3355	TG:0.2118	TG:0.2723
T:0.4073	T:0.562	T:0.2421
C:0.2931	C:0.388	C:0.2421
G:0.2254	G:0.1407	G:0.2363
A:0.2264	A:0.143	A:0.2363
C:0.0002	C:0	C:0
-:0.1394	-:0.0666	-:0.1297
G:0.3446	G:0.2057	G:0.3559
T:0.2312	T:0.23	T:0.3516
A:0.3450	A:0.8101	A:0.1354
G:0.0621	G:0.143	G:0.0259
A:0.4238	G:0.618	G:0.438
T:0.0012	T:0.0008	T:0.0014
T:0.0735	T:0.034	T:0.0648

T:0.3247	T:0.4092	T:0.281
G:0.1308	G:0.0068	G:0.2089
G:0.4900	G:0.4448	G:0.4841
T:0.3381	T:0.1581	T:0.3862
G:0.3385	G:0.1127	G:0.3948
G:0.3257	G:0.1142	G:0.3804
G:0.0290	G:0.003	G:0.0259
G:0.0292	G:0.003	G:0.0259
T:0.3255		
C:0.2109	C:0.0356	C:0.2594
C:0.0230	C:0.0023	C:0.0202
A:0.0116	A:0.0015	A:0.0144
G:0.4828	G:0.5537	G:0.4683
T:0.1418	T:0.0938	T:0.2392
A:0.1240	A:0.2337	A:0.0692
C:0.2418	C:0.0772	C:0.3343
A:0.1715	C:0.9766	C:0.7651
T:0.0942	T:0.0825	T:0.1326
A:0.0451	A:0.0038	A:0.0274
T:0.2808	T:0.2564	T:0.2104
C:0.2792	C:0.261	C:0.1916
A:0.4199	A:0.6082	A:0.2248
A:0.2099	A:0.1188	A:0.2089
-:0.0070	-:0	-:0.0101
C:0.2568	A:0.6672	A:0.696
T:0.1216	T:0.121	T:0.0821
T:0.0126	T:0.0008	T:0.0317
A:0.4758	A:0.4213	A:0.5331
C:0.0042	C:0.0008	C:0.0086
A:0.2256	A:0.1256	A:0.2767
C:0.4876	C:0.7943	C:0.487
C:0.2175	C:0.3873	C:0.2406
A:0.0525	A:0.0197	A:0.0793
C:0.4357	C:0.2655	C:0.6081
G:0.1424	G:0.1309	G:0.1513
ıer:PTHR14207		
A:0.0286	A:0.0038	A:0.0317
G:0.3141	G:0.1785	G:0.3761
A:0.0467	A:0.0091	A:0.0807
C:0.4457	T:0.5061	T:0.5418
T:0.3562	T:0.0401	T:0.5
T:0.1689	T:0.1876	T:0.1542
T:0.4908	C:0.7799	C:0.5072
G:0.0102	G:0	G:0.0288
-:0.1777	-:0.1838	-:0.1455
A:0.2420	A:0.0257	A:0.2248

T:0.1054	T:0.0076	T:0.1988
T:0.0078	T:0.0015	T:0.0187
A:0.3319	G:0.8502	G:0.5807
T:0.3632	T:0.0877	T:0.4625
T:0.2045	T:0.0348	T:0.317
A:0.4177	A:0.4289	A:0.6556
T:0.3990	T:0.4924	T:0.5403
G:0.4461	G:0.6135	G:0.6225
T:0.2163	T:0.1036	T:0.2421
C:0.4277	G:0.7315	G:0.5101
A:0.3033	T:0.8457	T:0.5432
A:0.3035	G:0.8449	G:0.5447
T:0.3359	C:0.9259	C:0.621
G:0.4445	C:0.6876	C:0.5548
A:0.4425	G:0.6921	G:0.5576
T:0.0631	T:0.028	T:0.183
G:0.4860	G:0.4259	G:0.4885
C:0.0092	C:0.0008	C:0.0086
T:0.1188	T:0.0045	T:0.0922
T:0.0020	T:0.0068	T:0.0014
A:0.1695	A:0.5091	A:0.0908
G:0.2155	G:0.3533	G:0.1427
T:0.0627	T:0.084	T:0.0807
A:0.2157	A:0.18	A:0.2723
A:0.3662	G:0.4032	G:0.6009
A:0.3780	A:0.0514	A:0.5447
A:0.0505	A:0.0015	A:0.0331
A:0.4197	A:0.472	A:0.451
T:0.1524	T:0.177	T:0.085
T:0.0577	T:0.0061	T:0.0807
T:0.4203	T:0.1672	T:0.5159
T:0.4293	T:0.2156	T:0.4971
T:0.1438	T:0.1505	T:0.1383
T:0.0092	T:0.0008	T:0.0159
A:0.3516	A:0.4781	A:0.3876
C:0.1024	C:0.1536	C:0.0735

7,PIRSF_domain:PIRSF000354

T:0.0774	T:0.09	T:0.0648

4265,hmmpanther:PTHR24265:SF23,SMART_domains:SM00020,Superfamily_domains:SSF50494

A:0.4344	A:0.4735	A:0.3184
G:0.1344	G:0.0174	G:0.3199
G:0.2320	G:0.0582	G:0.4597
G:0.4159	G:0.2821	G:0.2752
G:0.4744	A:0.8411	A:0.3905
G:0.3287	C:0.5666	C:0.4611
T:0.2803	T:0.2179	T:0.2594
C:0.0990	C:0.093	C:0.0937
A:0.0052	A:0.0008	A:0.0072
A:0.0531	A:0.0212	A:0.1239

C:0.3598	T:0.8949	T:0.5778
T:0.3502	G:0.5325	G:0.7003
G:0.0174	G:0	G:0.0115
A:0.4681	A:0.6218	A:0.3012
G:0.2400	G:0.1906	G:0.3285
G:0.1775	A:0.7254	A:0.8833
G:0.3902	G:0.1762	G:0.4121
T:0.0144	T:0.0015	T:0.036
A:0.2234	G:0.888	G:0.817
A:0.2809	G:0.8843,G:0.8843	G:0.7839,G:0.7839
A:0.2220	C:0.8911,C:0.8911	C:0.817,C:0.817
C:0.4435	C:0.3601	C:0.3545
C:0.2107	C:0.0946	C:0.1153
T:0.2280	T:0.1157	T:0.1398
A:0.0651	A:0.0098	A:0.0965
A:0.0837	A:0.0189	A:0.1081
A:0.0859	A:0.0272	A:0.1081
T:0.1767	T:0.2988	T:0.134
T:0.0002	T:0.0008	T:0
C:0.0541	C:0.0068	C:0.0663
A:0.4331	A:0.6377	A:0.4654
A:0.2490	A:0.1974	A:0.2262
A:0.3425	A:0.3116	A:0.3919
G:0.2356	G:0.5787	G:0.1254
A:0.0002	A:0	A:0
T:0.3367	T:0.2398	T:0.3631
T:0.3498	T:0.6868	T:0.3501
G:0.4261	A:0.5696	A:0.536
A:0.2995	A:0.1097	A:0.3098
G:0.2991	A:0.8101	A:0.5159
C:0.3125	C:0.2663	C:0.4452
T:0.3195	T:0.1505	T:0.4452
C:0.4289	T:0.7247	T:0.6066
T:0.0156	T:0.0038	T:0.0288
A:0.0477	A:0.003	A:0.1124
A:0.4339	A:0.5628	A:0.2392
A:0.0042	A:0	A:0.0058
G:0.2021	G:0.3222	G:0.2017
-:0.3598	GGTTACCCTA:0.5582	GGTTACCCTA:0.7853
C:0.2053	C:0.0673	C:0.3761
G:0.3758		
T:0.1416	T:0.0651	T:0.2334
-:0.3438	-:0.084	-:0.317
T:0.3446	T:0.0847	T:0.317
C:0.3578	T:0.5416	T:0.6816
G:0.4934	G:0.295	G:0.6542
C:0.2173	C:0.1649	C:0.2291
A:0.3271	A:0.5318	A:0.2637
C:0.4930	C:0.5045	C:0.4683
M00261,Superfamily_domains:SSF57184,Superfamily_domains:SSF57184		
G:0.2766	G:0.0651	G:0.438

T:0.2913	T:0.1422	T:0.4424
A:0.1563	A:0.1808	A:0.232
T:0.2666	T:0.0825	T:0.4294
T:0.2626	T:0.2769	T:0.353
T:0.1030	T:0.1891	T:0.0634
A:0.2448	A:0.1467	A:0.3055
T:0.0044	T:0.0008	T:0.0058
T:0.3427	A:0.9236	A:0.5576
C:0.3229	C:0.27	C:0.3213
C:0.4687	C:0.2443	C:0.5317
T:0.4671	C:0.2095	C:0.6427
T:0.2119	T:0.1725	T:0.1787
T:0.3522	T:0.3434	T:0.3084
-:0.1192	-:0.0885	-:0.0634
A:0.4888	A:0.1808	A:0.6052
G:0.0781	G:0.0174	G:0.1643
T:0.0092	T:0.0015	T:0.0187
G:0.2760	G:0.1899	G:0.2954
T:0.1983	T:0.1407	T:0.1844
G:0.3820	G:0.4977	G:0.415
T:0.3297	T:0.2466	T:0.4251
C:0.0972	C:0.2716	C:0.0476
A:0.0613	A:0.174	A:0.0346
T:0.0487	T:0.1286	T:0.0303
A:0.1308	A:0.0303	A:0.1282
T:0.1428	T:0.0371	T:0.1441
A:0.1436	A:0.0371	A:0.1441
T:0.1262	T:0.0825	T:0.2378
G:0.0511	G:0.0121	G:0.062
G:0.3091	G:0.1074	G:0.2781
G:0.3924	G:0.438	G:0.4899
C:0.1146	C:0.208	C:0.062
G:0.2069	G:0.0825	G:0.2061
G:0.0008	G:0	G:0.0014
T:0.1645	T:0.0129	T:0.1787
G:0.2294	G:0.1437	G:0.2522
A:0.1204	A:0.0068	A:0.1398
A:0.0212	A:0.0015	A:0.0591
A:0.0064	A:0	A:0.0072
A:0.2310	A:0.0908	A:0.4035
A:0.1118	A:0.0552	A:0.1643
A:0.2556	A:0.2474	A:0.3084
G:0.4353	A:0.6974	A:0.4769
T:0.0132	C:0.7579	C:0.745
G:0.0535	G:0.0204	G:0.0562
A:0.1208	A:0.0053	A:0.1153
C:0.3363	C:0.2958	C:0.3242
A:0.3185	T:0.9418	T:0.683
T:0.2440	T:0.1286	T:0.3516
T:0.1440	T:0.0197	T:0.1758
A:0.0665	A:0.087	A:0.0908
A:0.2939	A:0.2958	A:0.2839

C:0.1875	C:0.2262	C:0.2075
A:0.1595	A:0.1051	A:0.0908
A:0.4069	G:0.7549	G:0.4683
THR21231:SF7		
A:0.2321	A:0.0113	A:0.147
G:0.3806	C:0.8079	C:0.5072
T:0.0072	T:0.0008	T:0.0159
A:0.3816	A:0.2466	A:0.3357
A:0.3003	A:0.2496	A:0.3127
G:0.1170	G:0.1498	G:0.0749
C:0.2418	C:0.0719	C:0.2392
A:0.1803	A:0.2042	A:0.1571
C:0.4696	A:0.6846	A:0.5793
T:0.1791	T:0.2194	T:0.1499
A:0.0040	A:0.0008	A:0.0058
G:0.3407	A:0.4841	A:0.7522
A:0.1076	A:0.0129	A:0.0865
T:0.1703	T:0.0552	T:0.2565
C:0.0655	C:0.0136	C:0.1196
T:0.0555	T:0.1415	T:0.0303
C:0.2223	T:0.5378	T:0.6297
T:0.2482	T:0.2784	T:0.2133
T:0.0090	T:0.003	T:0.0058
T:0.0733	T:0.0121	T:0.1369
T:0.0727	T:0.0121	T:0.1354
A:0.3176	A:0.0061	A:0.3401
C:0.4453	A:0.5363	A:0.67
C:0.3658	C:0.2905	C:0.2579
C:0.2454	C:0.4523	C:0.1844
T:0.1565	C:0.8517	C:0.8012
A:0.0206	A:0.0023	A:0.0504
C:0.3370	T:0.559	T:0.5187
A:0.0144	A:0.0121	A:0.013
A:0.0883	A:0.0703	A:0.1052
T:0.0891	T:0.0703	T:0.1052
C:0.3914	C:0.3578	C:0.4395
C:0.4379	C:0.2519	C:0.2882
T:0.4383	C:0.5613	C:0.3314
T:0.0749	T:0.0257	T:0.1268
G:0.0731	G:0.0113	G:0.1153
T:0.0006	T:0	T:0.0014
C:0.0325	C:0.0651	C:0.0086
A:0.3243	A:0.2292	A:0.2767
C:0.3474	T:0.8215	T:0.5476
T:0.1735	T:0.2315	T:0.1138
T:0.0661	T:0.0053	T:0.0389

A:0.3944	A:0.1309	A:0.4524
A:0.0797	A:0.0076	A:0.2464
T:0.3830	T:0.2943	T:0.33
T:0.1843	T:0.1286	T:0.1931
G:0.3582	A:0.4508	A:0.6326
T:0.4525	T:0.0696	T:0.5951
A:0.2524	A:0.236	A:0.3775
A:0.0427	A:0.0182	A:0.0331
T:0.0549	T:0.1195	T:0.0576
C:0.1224	C:0.1657	C:0.098
A:0.0661	A:0.0076	A:0.0663
A:0.2570	A:0.211	A:0.2075
C:0.3897	C:0.0265	C:0.3689
her:PTHR11254		
T:0.2692	T:0.3427	T:0.3271
G:0.4609	G:0.652	G:0.3588
C:0.0154	C:0.003	C:0.0173
G:0.3736	G:0.4849	G:0.3991
G:0.3638	C:0.4123	C:0.8444
G:0.3918	G:0.171	G:0.4481
G:0.2304	G:0.1346	G:0.3429
T:0.3844		
A:0.2224	A:0.093	A:0.2738
A:0.2770	A:0.3328	A:0.2925
T:0.2109	T:0.3661	T:0.183
T:0.4972	C:0.4236	C:0.3357
G:0.2437	G:0.3253	G:0.2406
A:0.3804	A:0.6067	A:0.4092
A:0.2634	A:0.3775	A:0.317
G:0.3950	G:0.7057	G:0.402
C:0.0599	C:0.1505	C:0.0346
-:0.0264	-:0.003	-:0.0447
G:0.3155		
GG:0.3822	-:0.6952,-:0.6952	-:0.572,-:0.572
T:0.0018	T:0	T:0
T:0.1104	T:0.177	T:0.1023
T:0.0178	T:0.0098	T:0.0274
C:0.0048	C:0.0008	C:0.0029
A:0.1268	A:0.0938	A:0.1729
G:0.3231	G:0.4145	G:0.2622
T:0.2448	T:0.1793	T:0.2363
G:0.2478	G:0.2057	G:0.2435
A:0.0168	A:0.0015	A:0.0288
G:0.3976	G:0.4054	G:0.5303
A:0.2698	A:0.146	A:0.2522
A:0.0497	A:0.0129	A:0.0259
C:0.0036	C:0	C:0.0014

A:0.4143	G:0.7141	G:0.5922
T:0.4123	C:0.7141	C:0.5922
C:0.1406	C:0.0083	C:0.1657
A:0.2642	A:0.4236	A:0.1931
C:0.2590	C:0.2012	C:0.3934
T:0.2450	T:0.1989	T:0.379
T:0.4922	C:0.7042	C:0.5576
A:0.0776	G:0.6967	G:0.5994
C:0.0016	C:0	C:0.0014
T:0.3031	T:0.3154	T:0.2752
A:0.0030	A:0	A:0
A:0.0407	A:0.0038	A:0.0591
G:0.4283	A:0.7716	A:0.389
C:0.2532	C:0.0234	C:0.2536
T:0.1591	T:0.1233	T:0.1772
A:0.2388	G:0.7073	G:0.8012
A:0.0755	A:0.0197	A:0.0764
G:0.2019	G:0.1006	G:0.2205
T:0.1877	T:0.056	T:0.2147
-:0.3087	-:0.2776	-:0.3012
T:0.1142	T:0.1339	T:0.1974
G:0.2831	G:0.3343	G:0.3228
A:0.2506	A:0.1641	A:0.2291
A:0.3189	A:0.3026	A:0.3444
C:0.4385	T:0.6074	T:0.6398
C:0.3672	C:0.4818	C:0.3228
T:0.2887	T:0.4455	T:0.3919
T:0.1510	T:0.0545	T:0.2882
C:0.0266	C:0.0015	C:0.0288
A:0.1456	A:0.2194	A:0.1484
A:0.0595	A:0.0764	A:0.0187
T:0.0012	T:0.0008	T:0
A:0.1555	A:0.0204	A:0.0259
G:0.3600	G:0.4387	G:0.3213
G:0.3335	G:0.416	G:0.281
T:0.3275		
A:0.0495	A:0.0325	A:0.0072
A:0.2712	A:0.028	A:0.3055
G:0.2969	G:0.5749	G:0.2233

ıpanther:PTHR22590:SF1,SMART_domains:SM00015,Superfamily_domains:SSF52540

A:0.0162	A:0.0008	A:0.0202
A:0.2804	A:0.0741	A:0.1614
T:0.2438	T:0.0741	T:0.2867
T:0.0974	T:0.1233	T:0.0533
C:0.3556	C:0.2073	C:0.3732

G:0.1354	G:0.0151	G:0.2666
SF155,hmmpanther:PTHR24412		
C:0.0042	C:0.0008	C:0.0072
C:0.4367	A:0.5287	A:0.4942
A:0.1999	G:0.8775	G:0.647
T:0.4481	T:0.1044	T:0.5951
T:0.0978	T:0.0356	T:0.1009
A:0.0004	A:0	A:0
C:0.3083	C:0.3729	C:0.1816
A:0.1707	A:0.0635	A:0.1196
T:0.2143	C:0.8714	C:0.7493
T:0.2592	C:0.82	C:0.7104
A:0.2149	G:0.9191	G:0.7493
T:0.0174	T:0	T:0.0274
-:0.1168	-:0.1717	-:0.1715
G:0.2536	G:0.4002	G:0.17
A:0.4169	A:0.118	A:0.5346
G:0.0994	T:0.9887	T:0.8746
G:0.4683	A:0.3321	A:0.6254
T:0.4950	C:0.2398	C:0.6138
A:0.4299	A:0.3729	A:0.4063
A:0.2748	A:0.0666	A:0.3516
A:0.4477	G:0.5779	G:0.6369
A:0.2955	A:0.3283	A:0.2291
A:0.2530	A:0.1997	A:0.3862
C:0.4551	A:0.4917	A:0.6297
T:0.3297	T:0.4781	T:0.3862
A:0.0002	A:0	A:0.0014
T:0.2875	T:0.4017	T:0.2536
A:0.3347	A:0.5076	A:0.281
T:0.4972	C:0.2247	C:0.464
G:0.0016	G:0.0008	G:0.0014
C:0.3357	C:0.348	C:0.2305
G:0.1212	G:0.0265	G:0.1902
T:0.4067	C:0.1717	C:0.6801
A:0.4675	A:0.3245	A:0.5288
T:0.0491	T:0.0401	T:0.0504
A:0.0002	A:0	A:0
A:0.0132	A:0.0015	A:0.0173
A:0.4093	A:0.3699	A:0.5231
T:0.4016	T:0.4637	T:0.3631
A:0.3630	A:0.0772	A:0.2925
G:0.0068	G:0.0015	G:0.0159
G:0.0815	G:0.0938	G:0.0965
A:0.0084	A:0.0008	A:0.0101
G:0.1508	G:0.0182	G:0.2003

T:0.2809	T:0.118	T:0.4251
A:0.1983	A:0.0983	A:0.1902
C:0.0222	C:0	C:0.0144
G:0.4034	T:0.8759	T:0.5735
G:0.0032	G:0.0008	G:0
T:0.2270	G:0.7595	G:0.8429
T:0.2750	T:0.084	T:0.4928
C:0.0411	C:0.0015	C:0.1052
T:0.2019	C:0.8707	C:0.8127
C:0.1113	C:0.025	C:0.0519
C:0.4225	C:0.1793	C:0.1758
C:0.2591	C:0.3964	C:0.1225
C:0.2866	T:0.4365	T:0.5865
T:0.1158	T:0.0257	T:0.2003
G:0.2416	G:0.0393	G:0.2579
A:0.3361	A:0.5552	A:0.3314
C:0.4339	C:0.1762	C:0.4841
C:0.3205	T:0.1082	T:0.6412
T:0.0064	T:0.0008	T:0.0086
C:0.0036	C:0	C:0.0115
G:0.0108	G:0.0008	G:0.0144
-:0.0050	-:0	-:0.0058
T:0.4976	C:0.6679	C:0.3473
C:0.4469	C:0.4652	C:0.3343
G:0.2772	G:0.2368	G:0.3718
T:0.3958	T:0.1959	T:0.3444
G:0.1030	G:0.1437	G:0.1873
A:0.3638	A:0.2814	A:0.5029
T:0.1360	T:0.0454	T:0.1499
A:0.0008	A:0,A:0	A:0.0014,A:0.0014
T:0.3135	C:0.8767	C:0.6297
C:0.3053	C:0.0408	C:0.4308
C:0.0006	C:0	C:0
C:0.0002	C:0	C:0.0014
G:0.4916	G:0.8101	G:0.3746
T:0.1873	T:0.0303	T:0.3084
T:0.0725	T:0.0061	T:0.1988
T:0.1348	T:0.1369	T:0.134
A:0.0527	A:0.0061	A:0.0879
A:0.2650	A:0.2451	A:0.1744
A:0.3832	A:0.2511	A:0.2925
T:0.2105	T:0.1135	T:0.1441
T:0.1484	T:0.1619	T:0.1974
T:0.4764	A:0.7814	A:0.5389
A:0.2244	A:0.2549	A:0.2205
A:0.4962	G:0.7118	G:0.5346
T:0.0609	T:0.1392	T:0.0159

C:0.0495	C:0.0287	C:0.0591
C:0.3107	C:0.5333	C:0.3098
C:0.4373	T:0.848	T:0.5086
G:0.2125	G:0.0121	G:0.317
T:0.2943	T:0.497	T:0.3501
A:0.2544	A:0.1785	A:0.2824
G:0.0335	G:0.0461	G:0.036
G:0.0014	G:0	G:0
T:0.1483	T:0.0068	T:0.1138
G:0.2485	A:0.6589	A:0.5764
T:0.4778	T:0.3623	T:0.5202
G:0.2079	A:0.9236	A:0.7666
C:0.4471	T:0.643	T:0.5173
G:0.4255	G:0.4251	G:0.3833
A:0.0903	G:0.9259	G:0.8559
C:0.3790	C:0.267	C:0.4669
G:0.3347	G:0.0333	G:0.3357
A:0.0036	A:0	A:0.0072
T:0.0581	T:0.0045	T:0.1427
T:0.1745	T:0.1921	T:0.2104
T:0.3103	T:0.1558	T:0.4654
T:0.2206	T:0.4365	T:0.1542
G:0.3233	G:0.149	G:0.4323
G:0.2476	T:0.9115	T:0.6844
G:0.3277	G:0.1619	G:0.4481
G:0.4625	A:0.4365	A:0.6124
GGGAGA:0.3542	GGGAGA:0.3321	GGGAGA:0.2651
C:0.2264	C:0.27	C:0.2983
C:0.1120	C:0.0068	C:0.1066
A:0.1991	A:0.3585	A:0.1571
T:0.3027	C:0.6808	C:0.6196
G:0.4914	A:0.2126	A:0.6441
A:0.3889	G:0.357	G:0.4769
A:0.4271	A:0.3374	A:0.451
G:0.3892	-:0.3555	-:0.6643
T:0.2039	T:0.0575	T:0.2349
C:0.1056	C:0.0212	C:0.1888
T:0.0797	T:0.1362	T:0.0706
C:0.3512	C:0.7171	C:0.2378
A:0.3327	A:0.0643	A:0.4856
C:0.4201	C:0.2095	C:0.3963
T:0.0705	T:0.0038	T:0.0418
C:0.4704	C:0.6626	C:0.3199
C:0.0315	C:0.0106	C:0.0389
A:0.4796	G:0.5219	G:0.6196
T:0.0034	T:0	T:0.0115
C:0.3059	C:0.0257	C:0.5908

T:0.1965	T:0.3306	T:0.2219
T:0.0176	T:0.0015	T:0.0231
G:0.4601	G:0.4796	G:0.549
A:0.3317	T:0.7935	T:0.549
G:0.3570	G:0.2231	G:0.3775
T:0.3363	T:0.1566	T:0.3631
C:0.3361	C:0.1566	C:0.3631
A:0.3528	A:0.2133	A:0.3732
T:0.0439	T:0.0061	T:0.0231
T:0.0038	T:0.0008	T:0.0101
A:0.0038	A:0	A:0.0029
A:0.2889	A:0.2065	A:0.2378
A:0.3143	A:0.1823	A:0.4294
T:0.1581	T:0.0348	T:0.2291
C:0.4988	C:0.0991	C:0.8199
T:0.3381	C:0.4516	C:0.8934
T:0.2588	T:0.0076	T:0.1844
C:0.4792	C:0.4939	C:0.5605
G:0.2774	G:0.2852	G:0.2925
C:0.0032	C:0	C:0.0014
T:0.0048	T:0	T:0.0043
A:0.4916	G:0.3502	G:0.6859
G:0.1158	G:0.2277	G:0.1138
G:0.3049	G:0.093	G:0.3761
A:0.4954	G:0.4334	G:0.4726
C:0.2716	T:0.8971	T:0.7651
A:0.0030	A:0	A:0.0043
G:0.0060	G:0	G:0.0159
-:0.0450		
C:0.0048	C:0.0008	C:0.013
T:0.2246	T:0.0272	T:0.2262
A:0.0240	A:0.053	A:0.0216
A:0.0162	A:0.0212	A:0.0029
G:0.3594	G:0.4402	G:0.353
A:0.2073	A:0.1089	A:0.196
A:0.0757	A:0.0061	A:0.1499
G:0.0074	G:0	G:0.0115
T:0.3155	T:0.1036	T:0.3963
T:0.1763	G:0.9297	G:0.7853
G:0.1166	G:0.1437	G:0.0692
T:0.0206	T:0.0038	T:0.0317
G:0.1164	G:0.1483	G:0.1153
G:0.1392	G:0.295	G:0.0648
G:0.3177	G:0.2708	G:0.3516

G:0.2440	G:0.4017	G:0.2378
T:0.0032	T:0.0061	T:0.0029
C:0.1056	C:0.2534	C:0.0706
C:0.3247	A:0.739	A:0.6182
T:0.0134	T:0.0015	T:0.0303
C:0.1374	C:0.0658	C:0.1066
A:0.0717	A:0.0174	A:0.0807
A:0.1486	A:0.354	A:0.1441
T:0.1144	T:0.0855	T:0.232
A:0.1605	A:0.0166	A:0.1484
A:0.4579	G:0.5386	G:0.6369
-:0.1550	-:0.0567	-:0.1282
T:0.1550	T:0.0567	T:0.1282
C:0.4477	T:0.3979	T:0.4236
C:0.4475	A:0.3986	A:0.4236
T:0.1823	C:0.7443	C:0.621
C:0.1311	C:0.1626	C:0.0951
T:0.1391	T:0.1815	T:0.1009
C:0.1391	C:0.1815	C:0.1009
C:0.3025	C:0.3828	C:0.2032
G:0.3998	G:0.5711	G:0.3631
A:0.0148	A:0.0015	A:0.0115
A:0.3199	A:0.2118	A:0.4409
C:0.2893	T:0.6384	T:0.7853
T:0.4103	G:0.9342	G:0.4625
A:0.0030		
A:0.0437	A:0.0741	A:0.0317
T:0.0234	T:0.003	T:0.0274
T:0.0240	T:0.0023	T:0.0259
A:0.1969	A:0.1354	A:0.2651
G:0.3217	G:0.4576	G:0.2738
T:0.2768	C:0.851	C:0.696
A:0.0102	A:0.0008	A:0.0043
A:0.1683	A:0.2958	A:0.0893
G:0.0395	G:0.0121	G:0.0447
T:0.0899	T:0.0068	T:0.0677
G:0.2077	G:0.3638	G:0.1196
G:0.3289	G:0.7421	G:0.1715
G:0.0615	G:0.1142	G:0.0706
AGC:0.2111	AGC:0.1596	AGC:0.2133
G:0.4196	G:0.5318	G:0.1383
A:0.0976	A:0.0083	A:0.2277
:T_domains:SM00360,SMART_domains:SM00361,Superfamily_domains:SSF54928,TIGRFAM_domai		
T:0.0216	T:0.0045	T:0.0331
A:0.3335	A:0.1339	A:0.3545
A:0.0489	A:0.1641	A:0.0216
A:0.0693	A:0.0885	A:0.1023
G:0.3608	G:0.4766	G:0.2233
A:0.2256	A:0.0136	A:0.2983

A:0.1302	A:0.0552	A:0.1297
T:0.1408	T:0.1679	T:0.0778
G:0.0050	G:0	G:0.0086
G:0.0357	G:0.0121	G:0.0562
G:0.1560	G:0.1498	G:0.1556
G:0.1573	G:0.1808	G:0.232
her:PTHR24027		
A:0.0885	A:0.0204	A:0.0793
G:0.3327	A:0.9009	A:0.6715
A:0.0022		
T:0.3880	T:0.1437	T:0.451
G:0.0144	G:0.0023	G:0.0187
A:0.2855	A:0.2534	A:0.2406
T:0.0006		
C:0.2853	C:0.3041	C:0.3184
C:0.2989	C:0.3525	C:0.3228
C:0.4507	C:0.351	C:0.6297
G:0.4177	G:0.3313	G:0.6153
G:0.3399	G:0.1687	G:0.5331
-:0.2288	-:0.0961	-:0.3718
G:0.1975	G:0.0696	G:0.2536
T:0.4365	G:0.7103	G:0.4179
A:0.1945	A:0.146	A:0.1499
C:0.2234	C:0.2617	C:0.1585
A:0.2784	A:0.4932	A:0.2176
G:0.2584	G:0.4206	G:0.2133
G:0.4467	G:0.438	G:0.4597
T:0.2594	T:0.1354	T:0.2161
C:0.0874	C:0.0053	C:0.1873
T:0.2246	T:0.1581	T:0.2406
G:0.3255	G:0.3389	G:0.3689
T:0.3087	T:0.3169	T:0.3415
A:0.1641	A:0.2504	A:0.245
G:0.2949	G:0.2708	G:0.17
C:0.2378	C:0.1982	C:0.1902
G:0.0956	G:0.0144	G:0.1239
G:0.0753	G:0.0038	G:0.0634
G:0.2222	G:0.3472	G:0.2997
A:0.3718	A:0.3676	A:0.2867
G:0.4421	G:0.4312	G:0.3429
A:0.1367	A:0.053	A:0.2205
C:0.3532	C:0.1808	C:0.4683
A:0.4920	T:0.3411	T:0.5519
C:0.0353	C:0.0136	C:0.0634
T:0.1034	T:0.0166	T:0.0706
A:0.0883	A:0.0416	A:0.062
G:0.4852	G:0.59	G:0.3473

T:0.2131	T:0.2012	T:0.1729
T:0.3079	T:0.4561	T:0.2104
C:0.2378	C:0.1672	C:0.2983
A:0.2929	G:0.7352	G:0.6671
T:0.1312	C:0.916	C:0.8343
C:0.4667	C:0.8782	C:0.3674
G:0.2324	G:0.0613	G:0.2882
A:0.2382	A:0.0416	A:0.2983
A:0.2302	A:0.0272	A:0.2968
G:0.4770	G:0.8979	G:0.3746
G:0.4461	G:0.7844	G:0.3703
T:0.2111	T:0.093	T:0.1974
G:0.4677	C:0.5605	C:0.6023
G:0.3926	G:0.3691	G:0.3559
A:0.1400	A:0.0605	A:0.1671
A:0.4830	A:0.3321	A:0.6484
T:0.2432	T:0.3101	T:0.1614
T:0.2404	T:0.3238	T:0.1859
C:0.3754	C:0.3177	C:0.2666
A:0.2021	A:0.3419	A:0.1758
-:0.2081	-:0.1172,-:0.1172	-:0.17,-:0.17
G:0.1354	G:0.1899	G:0.1744
A:0.3614	A:0.4168	A:0.4496
C:0.2228	C:0.5083	C:0.1268
G:0.0703	G:0.0053	G:0.1167
T:0.1266	T:0.0484	T:0.1138
T:0.4718	C:0.4887	C:0.6023
GAACCC:0.3890	GAACCC:0.4493	GAACCC:0.2896
G:0.3534	G:0.2315	G:0.3761
A:0.0974	A:0.0083	A:0.2262
C:0.3147	C:0.2874	C:0.2622
TGTTT:0.1777	TGTTTTGTTT:0.1604	TGTTTTGTTT:0.1556
C:0.3746	T:0.3956	T:0.4049
A:0.3958	A:0.3555	A:0.4049
A:0.3486	A:0.1679	A:0.3372
T:0.3470	C:0.5113	C:0.513
A:0.3526	T:0.5	T:0.5115
T:0.3528	C:0.5	C:0.5101
G:0.3349	G:0.5174	G:0.1888
G:0.4968	G:0.5915	G:0.5072
G:0.2899	G:0.2481	G:0.2565
A:0.2823	A:0.3411	A:0.2925
A:0.0196	A:0.0023	A:0.0504
A:0.0102	A:0	A:0.0202
T:0.3998	T:0.59	T:0.3588
A:0.1813	A:0.0363	A:0.3386
AAACAAAC:0.3103		

-:0.0014	-:0	-:0.0014
A:0.0964	A:0.0643	A:0.2061
A:0.1076	A:0.0885	A:0.2176
G:0.0036		
G:0.1979	G:0.2685	G:0.1556
C:0.3662	C:0.3094	C:0.2911
G:0.3051	G:0.2882	G:0.2882
A:0.3586	A:0.5461	A:0.3429
G:0.1308	G:0.2352	G:0.0735
T:0.4040	C:0.5454	C:0.5418
G:0.1408	G:0.0333	G:0.232
A:0.1196	A:0.0129	A:0.1628
A:0.2027	A:0.0998	A:0.134
G:0.0118	G:0	G:0
A:0.0118	A:0	A:0
C:0.0136	C:0.0068	C:0
GC:0.0118	GC:0	GC:0
C:0.4866	C:0.4932	C:0.4841
C:0.4868	G:0.6301	G:0.4424
G:0.2967	G:0.553	G:0.2075
A:0.2075	A:0.177	A:0.2522
A:0.0305	G:0.7352	G:0.7262
A:0.4830	A:0.7118	A:0.3271
G:0.4141	A:0.7254	A:0.5461
TTCCACG:0.0152	TTCCACG:0.0008	TTCCACG:0.0231
G:0.2504	G:0.3192	G:0.2349
G:0.3309	G:0.708	G:0.183
A:0.3646	A:0.6475	A:0.4683
C:0.2037	A:0.7337	A:0.8487
C:0.2230	C:0.0802	C:0.2248
G:0.3892	-:0.2965	-:0.6844
T:0.0004	T:0	T:0
=4,hmmpanther:PTHR13948		
A:0.4625	A:0.5628	A:0.3674
T:0.2863	T:0.2708	T:0.1945
C:0.1504	C:0.0998	C:0.1859
G:0.2554	G:0.0469	G:0.2464
-:0.2496	-:0.025	-:0.2363
G:0.2402	G:0.4455	G:0.1297
GGGGATTA:0.0917	GGGGATTA:0.0893	GGGGATTA:0.1239
G:0.1028	G:0.0522	G:0.1383
C:0.4904	C:0.174	C:0.585
A:0.4902	A:0.174	A:0.585
T:0.3690	C:0.7988	C:0.5591
T:0.2135	T:0.0159	T:0.2795
C:0.4046	C:0.2148	C:0.428
A:0.1368	A:0.1225	A:0.1671
T:0.4455	T:0.2799	T:0.4654
-:0.2997	AA:0.6331	AA:0.7147
C:0.1743	T:0.9145	T:0.7839
T:0.0929	T:0.1694	T:0.0764
panther:PTHR24141,SMART_domains:SM00248,Superfamily_domains:SSF48403		

T:0.3423	T:0.2201	T:0.2911
-:0.3185	-:0.1876	-:0.4568
A:0.0048	A:0	A:0.0072
C:0.3353	C:0.1861	C:0.3977
A:0.2939	A:0.0363	A:0.3847
T:0.3998	T:0.2035	T:0.5634
A:0.1040	A:0.084	A:0.1153
C:0.4415	G:0.6762	G:0.5677
T:0.0036	T:0	T:0.0072
A:0.4730	C:0.4788	C:0.598
G:0.3788	A:0.6127	A:0.5663
A:0.3628	C:0.7133	C:0.6095
A:0.4687	A:0.2769	A:0.4308
T:0.2310	T:0.028	T:0.2406
A:0.2746	A:0.1407	A:0.4813
C:0.2025	C:0.0734	C:0.3055
T:0.2997	T:0.1884	T:0.4121
T:0.3030	T:0.0726	T:0.3718
G:0.1989	G:0.1884	G:0.2723
T:0.2492	T:0.1634	T:0.2925
T:0.2454	T:0.1536	T:0.2911
G:0.3592	A:0.4244	A:0.7219
G:0.3538	A:0.4251	A:0.7291
G:0.2853	G:0.4909	G:0.2723
C:0.1809	C:0.3434	C:0.1859
T:0.2630	C:0.4221	C:0.879
T:0.4964	T:0.4145	T:0.4769
A:0.0044		
C:0.1831	C:0.1914	C:0.2291
A:0.4830	A:0.1876	A:0.5735
T:0.4493	T:0.4826,T:0.4826	T:0.3357,T:0.3357
A:0.1867	A:0.1059,A:0.1059	A:0.1902,A:0.1902
T:0.0058	T:0.0182	T:0.0043
T:0.4435	A:0.4697	A:0.7421
T:0.2931	T:0.0507	T:0.5245
A:0.1378	A:0.0628	A:0.0735
G:0.0296	G:0.0076	G:0.0403
C:0.2628	C:0.0741	C:0.4553
A:0.4990	G:0.4909	G:0.5389
A:0.2548	A:0.1846	A:0.3055
T:0.4519	T:0.5416	T:0.3199
T:0.1044	T:0.0575	T:0.147
G:0.4030	G:0.5681	G:0.3934
A:0.2927	A:0.5719	A:0.2464
A:0.4509	A:0.6906	A:0.4193
A:0.1408	C:0.8306	C:0.915
C:0.2672	T:0.6891	T:0.6744
A:0.1128	G:0.8979	G:0.8804

A:0.0986	T:0.9539	T:0.8862
T:0.1134	T:0.1815	T:0.085
C:0.4211	C:0.7534	C:0.4006
T:0.0002	T:0	T:0.0014
A:0.0028	A:0	A:0.0029
A:0.1959	A:0.0893	A:0.2305
G:0.1154	G:0.1225	G:0.1628
A:0.2492	A:0.0144	A:0.3487
-:0.1835	-:0.1944	-:0.183
G:0.2009	G:0.2542	G:0.1902
G:0.1853	G:0.1997	G:0.1844
T:0.1937	T:0.23	T:0.1859
T:0.0082	T:0.0038	T:0.0086
C:0.0481	C:0.1097	C:0.0562
G:0.0549	G:0.0257	G:0.0634
A:0.0361	A:0.0053	A:0.036
C:0.4898	C:0.2519	C:0.5793
C:0.4952	G:0.3313	G:0.5706
G:0.1893	G:0.3457	G:0.134
A:0.2600	A:0.3472	A:0.3876
C:0.2496	C:0.3192	C:0.281
G:0.4581	C:0.8797	C:0.4914
C:0.0433	C:0.0129	C:0.0793
A:0.4714	A:0.2874	A:0.4135
A:0.0014	A:0	A:0.0014
-:0.3105	-:0.3026	-:0.3084
T:0.4355	C:0.5371	C:0.3458
G:0.3470	C:0.7995	C:0.3919
A:0.0146	A:0.0038	A:0.0187
A:0.3423	A:0.6929	A:0.2839
C:0.1356	C:0.0643	C:0.1628
T:0.1232	T:0.0136	T:0.3646
T:0.1248	T:0.0159	T:0.3646
T:0.4750	T:0.1195	T:0.6441
T:0.0003	T:0	T:0.0014
C:0.4355	T:0.5477	T:0.7219
C:0.1721	C:0.0522	C:0.1729
C:0.0933	C:0.0469	C:0.1657
T:0.0403	T:0.003	T:0.0562
ΓHR10361:SF20		
C:0.0988	C:0.118	C:0.1268
G:0.1414	G:0.0628	G:0.1297
T:0.3362	C:0.531	C:0.3084
T:0.1238	T:0.0106	T:0.1066
A:0.1254	A:0.0106	A:0.1052
C:0.4862	C:0.3434	C:0.3285
T:0.1430	C:0.8691	C:0.8184
T:0.0565	T:0.0893	T:0.0245

T:0.0331	T:0.0061	T:0.0144
T:0.0090	T:0.003	T:0.0144
C:0.3560	C:0.3616	C:0.3761
T:0.2833	T:0.2632	T:0.2349
A:0.3059	A:0.0908	A:0.5
G:0.2380	A:0.8464	A:0.8127
A:0.3858	A:0.2738	A:0.3516
A:0.3339	G:0.9486	G:0.5173
G:0.1028	G:0.0545	G:0.1066
A:0.2967	A:0.3464	A:0.1801
A:0.1266	A:0.0643	A:0.1153
G:0.1601	G:0.2163	G:0.1902
G:0.1391	G:0.0809	G:0.1787
T:0.3051	T:0.3396	T:0.2248
G:0.2037	T:0.6717	T:0.8602
A:0.1565	A:0.2761	A:0.1268
T:0.3938	T:0.1157	T:0.5533
A:0.1046	A:0.1331	A:0.0778
C:0.2331	G:0.7428	G:0.5101
C:0.4495	T:0.8472	T:0.3905
A:0.2171	A:0.0076	A:0.3718
A:0.0535	A:0.0091	A:0.1427
T:0.0214	T:0.0643	T:0.013
A:0.3343	A:0.1324	A:0.5144
A:0.4361	G:0.6906	G:0.5072
A:0.1318	A:0.0749	A:0.0461
T:0.2363		
G:0.4976	G:0.1112	G:0.5648
HR19897:SF156		
C:0.0178	C:0.0015	C:0.0288
T:0.1442	T:0.2201	T:0.1585
A:0.0725	A:0.0091	A:0.0821
G:0.0032	G:0.0008	G:0.0058
T:0.1452	T:0.1324	T:0.1383
T:0.3896	T:0.525	T:0.3703
C:0.4629	C:0.7481	C:0.3833
T:0.0080	T:0.0008	T:0.0216
A:0.2190	G:0.6657	G:0.8184
C:0.3538	C:0.4168	C:0.3804
T:0.1260	T:0.1135	T:0.1628
G:0.0004	G:0	G:0.0014

G:0.2404	G:0.2352	G:0.2032
T:0.3139	C:0.8449	C:0.598
A:0.4121	A:0.3843	A:0.4654
T:0.2690	T:0.3873	T:0.1902
G:0.2979	G:0.1921	G:0.3357
G:0.1148	G:0.025	G:0.1585
C:0.0637	C:0.1475	C:0.0591
T:0.4014	C:0.3457	C:0.7032
C:0.1460	C:0.0106	C:0.1239
G:0.3540	A:0.767	A:0.5965
A:0.4952	A:0.621	A:0.4006
T:0.4954	T:0.6218	T:0.4006
G:0.3860	G:0.8192	G:0.183
G:0.2538	G:0.3313	G:0.183
C:0.3580	C:0.2905	C:0.232
C:0.1090	C:0.2542	C:0.1138
C:0.0160	C:0.0015	C:0.0303
T:0.0663	T:0.0923	T:0.049
T:0.1344	T:0.1921	T:0.196
C:0.2572	C:0.0908	C:0.3876
A:0.2181	A:0.0552	A:0.2507
C:0.3512	T:0.7693	T:0.598
A:0.1699	A:0.1331	A:0.196
C:0.3139	C:0.3381	C:0.1888
T:0.2067	T:0.1543	T:0.2983
A:0.0094	A:0.0068	A:0.0086
T:0.2500	T:0.2163	T:0.2464
C:0.2538	C:0.2383	C:0.2464
G:0.4038	A:0.3737	A:0.4207
T:0.3233	T:0.3638	T:0.2233
T:0.0030	T:0.003	T:0.0043
T:0.1919	T:0.1165	T:0.2594
C:0.2678	C:0.2103	C:0.3112
A:0.0990	A:0.1097	A:0.0807
C:0.1036	C:0.1309	C:0.0951
her:PTHR15141		
T:0.3652	T:0.2617	T:0.2291
T:0.1136	T:0.1649	T:0.1945
T:0.3514	T:0.3631	T:0.3646
G:0.2416	G:0.0295	G:0.3343
T:0.1328	T:0.0386	T:0.1816
C:0.0082	C:0.0015	C:0.0072
A:0.2548	A:0.0469	A:0.3141
C:0.3281	T:0.6846	T:0.7104
T:0.0032	T:0	T:0
A:0.1807	A:0.1014	A:0.1988
A:0.3834	G:0.4077	G:0.67

G:0.2726	A:0.7012	A:0.5994
A:0.4651	G:0.9682	G:0.3429
A:0.1843	A:0.2927	A:0.1715
-:0.2590	-:0.3555	-:0.1527
C:0.4716	C:0.4902	C:0.3775
A:0.0048	A:0.0015	A:0.0043
A:0.2776	A:0.1573	A:0.33
C:0.0012	C:0	C:0.0029
T:0.4365	T:0.2133	T:0.4207
T:0.3626	T:0.2284	T:0.4726
C:0.3822	C:0.2995	C:0.4741
G:0.1647	G:0.1906	G:0.0591
C:0.1565	C:0.1755	C:0.1282
G:0.1673	G:0.1914	G:0.1427
A:0.1530	A:0.1611	A:0.1282
-:0.0102	-:0.0008	-:0.0086
G:0.0104	G:0.0015	G:0.0101
A:0.1404	A:0.0234	A:0.2017
A:0.4559	A:0.4009	A:0.4798
C:0.1683	C:0.2005	C:0.2046
C:0.3521	C:0.0197	C:0.2089
G:0.0004	G:0	G:0
T:0.2412	T:0.053	T:0.17
A:0.4665	C:0.1067	C:0.5706
T:0.3291	T:0.1974	T:0.5
G:0.2552	G:0.2489	G:0.2536
A:0.3450	A:0.3638	A:0.3228
T:0.2768	T:0.1248	T:0.2954
G:0.4742	C:0.9728	C:0.3285
T:0.4736	G:0.9584	G:0.3285
G:0.1368	G:0.1974	G:0.1052
T:0.1236	T:0.0091	T:0.2277
A:0.2819	G:0.9266	G:0.6988
T:0.2786	C:0.9266	C:0.6988
T:0.1008		
T:0.1869	T:0.0091	T:0.2017
C:0.1873	C:0.0091	C:0.2017
T:0.0505	T:0.003	T:0.0548
T:0.4448	C:0.5287	C:0.2781
T:0.1492	T:0.0204	T:0.2752
A:0.3119	A:0.2201	A:0.3112
A:0.4299	A:0.1611	A:0.5576
T:0.0178	T:0.0023	T:0.049
G:0.0060	G:0	G:0.0072
A:0.2945	T:0.7224	T:0.5865

-:0.1911	ACACAGGTGTTTT:0.92	CACACAGGTGTTTT:0.67	C
C:0.3934	C:0.6974	C:0.3761	
T:0.0008	T:0.0015	T:0	
C:0.0018	C:0	C:0.0043	
C:0.1611	C:0.1732	C:0.0562	
T:0.1743	T:0.1649	T:0.134	
C:0.3413	C:0.2179	C:0.3228	
A:0.0393	A:0.0061	A:0.0692	
G:0.3287	G:0.031	G:0.4669	
G:0.1352	G:0.2337	G:0.0937	
A:0.1388	A:0.2337	A:0.0965	
G:0.3183	G:0.2103	G:0.3184	
T:0.0532	T:0.003	T:0.0562	
A:0.2665	G:0.5741	G:0.5706	
A:0.2159	A:0.2867	A:0.1527	
C:0.2712	C:0.3275	C:0.1859	
C:0.3351	C:0.3646	C:0.2867	
A:0.4924	A:0.6853	A:0.5173	
T:0.0004	T:0	T:0.0014	
T:0.2554	T:0.0242	T:0.4669	
C:0.4970	C:0.6346	C:0.5821	
C:0.4295	C:0.3979	C:0.5836	
A:0.4189	G:0.8116	G:0.6599	
C:0.3067	C:0.0991	C:0.513	
T:0.1482	T:0.0772	T:0.2363	
G:0.0559	G:0.0295	G:0.0648	
G:0.0280	G:0.003	G:0.0274	
G:0.1789	G:0.1929	G:0.0447	
T:0.0018	T:0	T:0.0029	
A:0.3946	G:0.7844	G:0.5288	
C:0.4768	C:0.6974	C:0.3977	
G:0.1761	G:0.031	G:0.1369	
A:0.2831	A:0.3306	A:0.3199	
T:0.4904	C:0.8253	C:0.3934	
C:0.1691	C:0.239	C:0.1167	
A:0.2728	A:0.3631	A:0.366	
T:0.2873	T:0.0582	T:0.2176	
A:0.3311	A:0.6263	A:0.2853	
T:0.3187	G:0.2806	G:0.8098	
C:0.3966	T:0.6445	T:0.7003	
A:0.3578	A:0.3253	A:0.4236	
C:0.3810	T:0.5416	T:0.7133	
G:0.0004	G:0	G:0	
A:0.0242	A:0.003	A:0.0317	
A:0.0066	A:0.0008	A:0	
T:0.0090	T:0	T:0.0115	
T:0.2206	C:0.9766	C:0.7709	

69,Pfam_domain:PF00443,Superfamily_domains:SSF54001
HR24006:SF403

G:0.3618	G:0.6301	G:0.3184
G:0.0551	G:0.0492	G:0.0591
T:0.1542		
C:0.2328	T:0.7292	T:0.7752
A:0.2256	A:0.0961	A:0.2911

F27,Prints_domain:PR01155

G:0.0176	G:0.0635	G:0.0043
T:0.1386	T:0.1634	T:0.1671
G:0.2574	G:0.0764	G:0.3674
T:0.4189	A:0.4629	A:0.6124
C:0.4810	C:0.3306	C:0.5634
T:0.3954	T:0.4289	T:0.4366
A:0.3229	A:0.171	A:0.4063
T:0.3934	T:0.4297	T:0.4337
G:0.3235	A:0.8752	A:0.6657
C:0.3552	T:0.8427	T:0.6297
G:0.4625	G:0.3676	G:0.6239
A:0.0054	A:0	A:0.0086
T:0.0010	T:0	T:0.0014
A:0.0058	A:0.0008	A:0.0173
C:0.1164	C:0.0076	C:0.098

ity_(Seg):seg

C:0.2282	C:0.3041	C:0.1412
A:0.3560	A:0.3525	A:0.255
A:0.0745	A:0.0166	A:0.0533
G:0.4834	G:0.5371	G:0.4438
C:0.1863	C:0.2012	C:0.1873
G:0.1707	G:0.0408	G:0.2421
T:0.1562	T:0.1702	T:0.1772
C:0.3067	C:0.5038	C:0.2608
T:0.0863	T:0.0227	T:0.0144
T:0.0960	T:0.1551	T:0.098
A:0.0016	A:0	A:0
C:0.3562	C:0.3805	C:0.5259
A:0.0026	A:0.0015	A:0.0014
C:0.3906	C:0.6354	C:0.4222
C:0.3213	C:0.4047	C:0.255
C:0.2829	T:0.8147	T:0.6772
G:0.3385	G:0.1581	G:0.3026
T:0.4684	C:0.8041	C:0.3631
T:0.4239	T:0.3517	T:0.5447
G:0.0954	G:0.2943	G:0.0461
G:0.3299	G:0.1467	G:0.3847
A:0.2548	G:0.9713	G:0.6599
A:0.3091	A:0.0734	A:0.3775
T:0.0455	T:0.0045	T:0.0807

G:0.0101	G:0	G:0.0072
G:0.0002	G:0	G:0
G:0.4860	A:0.3684	A:0.5677
C:0.3057	T:0.8979	T:0.7435
C:0.1404	C:0.3192	C:0.0648
G:0.3838	G:0.7814	G:0.4035
T:0.1919	T:0.1475	T:0.1801
C:0.3442	C:0.0946	C:0.2939
G:0.3101	G:0.2564	G:0.3761
A:0.0705	A:0.0076	A:0.0807
G:0.3889	A:0.5772	A:0.451
C:0.2779	T:0.6604	T:0.5692
C:0.0813	C:0.0424	C:0.0951
T:0.1356	T:0.0106	T:0.1527
A:0.2518	A:0.2799	A:0.3818
A:0.3662	G:0.8585	G:0.4769
T:0.4395	G:0.7587	G:0.4697
G:0.2891	G:0.3835	G:0.3112
T:0.1468	T:0.0197	T:0.1801
T:0.4105	C:0.6589	C:0.5519
C:0.1460	C:0.1778	C:0.1153
A:0.3784	A:0.3775	A:0.3602
T:0.1270	T:0.0061	T:0.2176
G:0.4571	A:0.7587	A:0.4438
-:0.2244	AAGT:0.9319	AAGT:0.6772
T:0.4413	T:0.6331	T:0.3689
G:0.3277	A:0.7927	A:0.5893
T:0.3790	C:0.7436	C:0.562
T:0.4918	T:0.1377,T:0.1377	T:0.5692,T:0.5692
T:0.1481	T:0.0166	T:0.1772
C:0.0030	C:0.0008	C:0.0058
4377,hmmpanther:PTHR24377:SF236,SMART_domains:SM00355,Superfamily_domains:SSF57667		
T:0.2682	T:0.0734	T:0.2594
C:0.3067	T:0.8359	T:0.8213
C:0.3448	C:0.6445	C:0.2925
T:0.4647	T:0.7806	T:0.4078

EAS_MAF	EUR_MAF	SAS_MAF	AA_MAF
C:0.001	C:0.0517	C:0.0102	C:0.0075
C:0.6042	C:0.4811	C:0.635	
			G:0.4163
G:0.4692	G:0.6849	G:0.6687	
G:0.3185	G:0.6153	G:0.5992	G:0.2861
G:0.3403	G:0.6849	G:0.6166	G:0.7435
T:0.0873	T:0.2704	T:0.2924	T:0.6832
			GAGCGGGCGA:0.5586
A:0.1488	A:0.2237	A:0.1472	A:0.1083
C:0.87	C:0.832	C:0.7699	
T:0.001	T:0.0408	T:0.0327	T:0.0047
G:0.0228	G:0.325	G:0.2076	G:0.5419
T:0	T:0.0278	T:0.0164	
C:0.005	C:0.1163	C:0.1922	
A:0.0506	A:0.0378	A:0.136	
A:0.5357	A:0.6421	A:0.6871	A:0.4439
A:0.0258	A:0.4095	A:0.2556	A:0.2434
T:0.0099	T:0.0895	T:0.0358	
T:0.0754	T:0.5417	T:0.2035	
T:0.002	T:0.1928	T:0.1329	T:0.204
ATAA:0.0218	ATAA:0.5099	ATAA:0.3292	
A:0.1637	A:0.2614	A:0.2157	A:0.0602
G:0.4256	G:0.5109	G:0.4785	G:0.4133
T:0.8909	T:0.5875	T:0.7771	T:0.5962
G:0.0843	G:0.007	G:0.0245	G:0.1155
G:0.2827	G:0.1461	G:0.2106	G:0.2069
-:0.0327	-:0.0577	-:0.0746	
G:0.001	G:0.1402	G:0.0164	
C:0.1071	C:0.2097	C:0.3804	C:0.6332
C:0.6002	C:0.6083	C:0.4571	C:0.554
A:0	A:0.0408	A:0.0082	A:0.0052
G:0.002	G:0.0716	G:0.0092	
C:0.377	C:0.4205	C:0.3947	C:0.3988
T:0.6865	T:0.492	T:0.5051	T:0.2158
C:0	C:0.0467	C:0.001	
A:0.1508	A:0.338	A:0.2812	
C:0.499	C:0.1113	C:0.3681	C:0.2556
T:0.4464	T:0.833	T:0.5603	T:0.8201
T:0.2639	T:0.3022	T:0.136	T:0.1676
T:0,T:0	T:0.0189,T:0.0189	T:0,T:0	T:0.0068,T:0.0068
T:0.1002	T:0.2555	T:0.1595	T:0.0488
C:0.256	C:0.2724	C:0.1646	
T:0.1617	T:0.3857	T:0.41	T:0.4788
G:0.1617	G:0.3867	G:0.41	
T:0.9464	T:0.7137	T:0.8047	T:0.8266

A:0.005	A:0.3191	A:0.1053	A:0.2068
A:0.499	A:0.16	A:0.1329	A:0.0458
T:0.0992	T:0.1978	T:0.1943	
C:0.4851	C:0.2992	C:0.4581	
T:0.1101	T:0.0845	T:0.089	T:0.064
C:0.5665	C:0.5298	C:0.7628	
G:0.6736	G:0.7356	G:0.8415	G:0.9027
T:0.1587	T:0.2256	T:0.1861	
G:0.0784	G:0.2922	G:0.3006	G:0.1207
-:0.2173	-:0.1988	-:0.1166	-:0.4492
A:0.4841	A:0.1441	A:0.2311	A:0.2757
A:0.0089	A:0.1233	A:0.1483	
C:0.2103	C:0.2048	C:0.1902	
C:0.9891	C:0.8101	C:0.8885	C:0.8639
G:0.5645	G:0.0885	G:0.2249	G:0.2511
A:0	A:0.1133	A:0.0184	A:0.0261
T:0.0357	T:0.0656	T:0.0194	T:0.0096
T:0	T:0.0408	T:0.0112	T:0.0072
C:0.2976	C:0.173	C:0.0685	
C:0	C:0.003	C:0	C:0.0008
T:0.0813	T:0.172	T:0.0521	
G:0.0357	G:0.3519	G:0.1258	
G:0.0357	G:0.3559	G:0.1278	
G:0.3869	G:0.1918	G:0.3384	
T:0.001	T:0.0298	T:0.0399	T:0.0057
G:0.0605	G:0.0696	G:0.0266	G:0.0132
G:0.0982	G:0.2684	G:0.2791	G:0.4142
C:0.0903	C:0.0765	C:0.1861	C:0.3468
T:0	T:0.0586	T:0.002	T:0.0132
T:0.001	T:0.0517	T:0.093	
A:0.6657	A:0.8698	A:0.8517	
G:0.0208	G:0.1083	G:0.093	
C:0.4206	C:0.2863	C:0.2812	C:0.5241
C:0.6825	C:0.174	C:0.271	C:0.0506
G:0.1677	G:0.3141	G:0.4346	
A:0	A:0.0905	A:0.0133	A:0.0136
T:0.7837	T:0.5308	T:0.5613	T:0.6763
T:0.369	T:0.5437	T:0.3722	
G:0.3631	G:0.5417	G:0.3701	
A:0.3423	A:0.5179	A:0.3016	
T:0.3423	T:0.5179	T:0.3006	
G:0.003	G:0.2137	G:0.1186	G:0.0835
A:0.124	A:0.1799	A:0.1483	
A:0.124	A:0.1829	A:0.1503	A:0.1739
A:0	A:0.0626	A:0.0123	A:0.017
T:0.0853	T:0.2594	T:0.1933	T:0.2736
G:0.002	G:0.2913	G:0.1483	
-:0.002	-:0.0437	-:0.0583	-:0.0265

A:0.7659	A:0.6342	A:0.4918	
T:0.255	T:0.5586	T:0.4264	T:0.3626
A:0.6081	A:0.3579	A:0.2393	A:0.2215
G:0.6429	G:0.3598	G:0.2515	G:0.3447
C:0.4018	C:0.0795	C:0.4622	
A:0.9861	A:0.5845	A:0.6534	A:0.781
G:0.0169	G:0.1372	G:0.1933	G:0.2964
C:0	C:0.0487	C:0.0072	C:0.0254
A:0.0357	A:0.2505	A:0.135	
A:0	A:0.0398	A:0.0123	A:0.0565
T:0.0615	T:0.0934	T:0.0736	T:0.0222
G:0.7054	G:0.3529	G:0.2761	G:0.2787
G:0.0863	G:0.0775	G:0.0665	G:0.1491
T:0.1984	T:0.2584	T:0.2464	
A:0.2431	A:0.1759	A:0.2587	A:0.357
A:0.004	A:0.2734	A:0.1769	
A:0.0972	A:0.3022	A:0.228	A:0.2047
G:0.3145	G:0.4821	G:0.3067	G:0.4678
T:0.3075	T:0.2624	T:0.5215	T:0.2139
T:0.7579	T:0.6958	T:0.7331	T:0.9664
G:0.38	G:0.2823	G:0.3916	G:0.1713
C:0.0526	C:0.2783	C:0.1871	C:0.2803
C:0.1597	C:0.3857	C:0.3272	
A:0.505	A:0.7783	A:0.7157	A:0.8772
T:0.122	T:0.2594	T:0.1186	
A:0.6597	A:0.3191	A:0.4601	A:0.5626
G:0.0466	G:0.1362	G:0.1431	G:0.0395
C:0	C:0.0736	C:0.0143	
T:0.001	T:0.1471	T:0.044	T:0.2276
T:0.001	T:0.0825	T:0.0204	
A:0.0377	A:0.4523	A:0.2035	
G:0	G:0.0507	G:0.0389	G:0.0113
A:0.1032	A:0.3221	A:0.2802	
T:0	T:0.002	T:0	T:0.0023
T:0.371	T:0.3598	T:0.499	
T:0.372	T:0.2744	T:0.4693	
C:0.371	C:0.3579	C:0.4969	
T:0.0794	T:0.1938	T:0.1452	
T:0.001	T:0.1491	T:0.0215	T:0.0361
A:0.0367	A:0.3171	A:0.1769	A:0.3034
G:0.0367	G:0.0447	G:0.0644	G:0.0484
C:0.2302	C:0.1153	C:0.2883	C:0.1359
T:0.2302	T:0.1103	T:0.2689	
T:0.2639	T:0.1541	T:0.2648	
A:0.1687	A:0.1044	A:0.1401	A:0.0263
T:0.7659	T:0.7376	T:0.593	T:0.5134
G:0.249	G:0.33	G:0.2423	G:0.3058

C:0.4127	C:0.333	C:0.3384	C:0.1727
A:0.5228	A:0.5378	A:0.6595	
A:0.0694	A:0.16	A:0.3661	
C:0.001	C:0.0746	C:0.0082	C:0.0104
T:0.248	T:0.4145	T:0.4877	
-:0.0823	-:0.1431	-:0.2413	-:0.2603
-:0.0188	-:0.0109	-:0.0808	
A:0.0585	A:0.0964	A:0.0256	A:0.1207
C:0.6944	C:0.3022	C:0.318	C:0.6825
C:0.9911	C:0.4911	C:0.6258	C:0.5869
C:0.5139	C:0.2803	C:0.4162	C:0.2009
T:0.0853,T:0.0853	T:0.1809,T:0.1809	T:0.2055,T:0.2055	
G:0.373	G:0.0785	G:0.1728	G:0.3842
-:0.0645	-:0.0507	-:0.0624	
C:0	C:0.1789	C:0.1115	
C:0.2659	C:0.1292	C:0.2566	C:0.0622
C:0.5724	C:0.174	C:0.3384	C:0.2953
T:0.8512	T:0.6272	T:0.7209	T:0.7047
G:0.0357	G:0.0875	G:0.1033	G:0.0338
C:0.2431	C:0.1899	C:0.1442	C:0.5738
C:0.3681	C:0.3519	C:0.3272	
T:0	T:0	T:0	
G:0.372	G:0.2266	G:0.4131	
A:0	A:0.0179	A:0.001	A:0.0025
T:0	T:0.002	T:0	T:0.0007
C:0.6538	C:0.1809	C:0.3569	C:0.5432
T:0	T:0.0278	T:0.0112	
G:0.0605	G:0.1203	G:0.1155	G:0.0222
C:0.0347	C:0.1064	C:0.0532	
C:0	C:0.002	C:0	
T:0.0724	T:0.16	T:0.3671	
A:0	A:0.0109	A:0.0072	A:0.0002
A:0.2956	A:0.332	A:0.1513	
T:0.0218	T:0.1849	T:0.2628	T:0.4076
T:0.002	T:0.161	T:0.0245	T:0.0751
T:0.6597	T:0.3698	T:0.5194	
T:0.1657	T:0.3966	T:0.2505	
T:0	T:0.0119	T:0.0041	T:0.0009
C:0.1458	C:0.3201	C:0.3446	C:0.3056
A:0.4851	A:0.34	A:0.3241	A:0.2089
T:0.3978	T:0.3579	T:0.272	
C:0.0893	C:0.1431	C:0.3241	
G:0.3998	G:0.2475	G:0.3885	G:0.1221
T:0.006,T:0.006	T:0.1302,T:0.1302	T:0.0266,T:0.0266	T:0.0266,T:0.0266
T:0	T:0.0258	T:0.001	T:0.0057
-:0.0933	-:0.5229	-:0.2106	-:0.3147
A:0.5367	A:0.2535	A:0.3865	A:0.111

A:0.2133	A:0.2883	A:0.3313	A:0.3586
G:0	G:0.002	G:0	G:0.0008
C:0	C:0.0199	C:0.0204	
G:0	G:0.001	G:0	G:0.0005
T:0.1389	T:0.1829	T:0.1728	
A:0	A:0.1909	A:0.0256	A:0.1748
A:0.0565	A:0.1998	A:0.1401	A:0.095
A:0.2371	A:0.1332	A:0.1861	A:0.1015
T:0.0685	T:0.2097	T:0.2444	
A:0	A:0.1332	A:0.0123	A:0.0282
G:0.4087	G:0.339	G:0.2178	G:0.4655
-:0.0625	-:0.3231	-:0.183	-:0.1313
G:0.4583	G:0.6044	G:0.592	G:0.3745
-:0.1706	-:0.1272	-:0.1718	
C:0.4613	C:0.1322	C:0.2781	C:0.2708
G:0.0099	G:0.2028	G:0.1421	
			-:0.0113
T:0	T:0.001	T:0	
C:0.9464	C:0.3857	C:0.5603	C:0.5809
T:0.3125	T:0.4314	T:0.407	T:0.086
C:0.9554	C:0.6292	C:0.8344	C:0.5676
			T:0.0002
C:0.3879	C:0.2445	C:0.3814	
A:0	A:0.0318	A:0.002	A:0.0052
G:0.1627	G:0.1998	G:0.1687	G:0.2186
G:0	G:0	G:0	
A:0	A:0.0099	A:0	A:0.2109
A:0.3393	A:0.2137	A:0.0695	A:0.1281
G:0.506	G:0.3519	G:0.3067	G:0.5321
A:0	A:0.0258	A:0.0143	
AAG:0.5367	AAG:0.3767	AAG:0.362	
T:0.87	T:0.7117	T:0.6288	
C:0.4256	C:0.165	C:0.1708	
A:0.4444	A:0.1193	A:0.1012	A:0.1244
C:0.4573	C:0.2237	C:0.1779	
C:0.2669	C:0.2833	C:0.2168	C:0.1011
-:0.2034	-:0.1849	-:0.2587	-:0.2486
T:0	T:0.1093	T:0.0654	T:0.0322
T:0	T:0.006	T:0	
C:0.8214	C:0.6899	C:0.6012	
T:0.8313	T:0.6918	T:0.7035	T:0.5849
T:0.9425	T:0.5338	T:0.7147	T:0.597
G:0.375	G:0.2058	G:0.2577	
T:0.9514	T:0.6382	T:0.7127	
A:0.0149	A:0.2525	A:0.2331	A:0.2444
			C:0.0272
A:0.2272	A:0.1223	A:0.1012	

C:0.1935	C:0.2783	C:0.3589	C:0.2074
T:0.0089	T:0.1223	T:0.1513	T:0.0415
C:0.6538	C:0.1839	C:0.3252	
A:0.0992	A:0.0765	A:0.1329	A:0.2705
T:0.3671	T:0.5696	T:0.4376	T:0.4037
A:0.4861	A:0.332	A:0.2434	A:0.1112
T:0.0099	T:0.2982	T:0.181	
C:0.3591	C:0.6551	C:0.6401	C:0.9742
C:0	C:0.0427	C:0.0072	C:0.0082
A:0.006	A:0.0755	A:0.0481	
C:0.0605	C:0.1759	C:0.0368	
G:0.2063	G:0.1481	G:0.2076	G:0.5544
T:0.4494	T:0.1044	T:0.2485	T:0.0372
A:0.876	A:0.9085	A:0.8425	A:0.8239
A:0.4405	A:0.7386	A:0.6145	
A:0.5704	A:0.3211	A:0.4509	A:0.6046
G:0.4048	G:0.4274	G:0.4826	
T:0.0764	T:0.2584	T:0.1748	T:0.0713
A:0.2827	A:0.3469	A:0.3436	
C:0.3085	C:0.4066	C:0.3344	C:0.4092
G:0.2907	G:0.1859	G:0.2464	G:0.1387
G:0.0337	G:0.1014	G:0.1094	
T:0	T:0.005	T:0.001	T:0.0032
G:0.5823	G:0.4215	G:0.7106	G:0.5639
G:0.3105	G:0.2734	G:0.1462	G:0.0924
A:0.4286	A:0.4841	A:0.4796	A:0.5036
C:0.4097	C:0.159	C:0.3446	C:0.2796
A:0.4405	A:0.0268	A:0.1708	A:0.1582
A:0.2401	A:0.3728	A:0.3272	A:0.3487
C:0.4821	C:0.1759	C:0.3088	C:0.2355
C:0.7083	C:0.5	C:0.4499	C:0.3858
G:0.3413	G:0.4026	G:0.3149	G:0.1961
G:0.0119	G:0.2058	G:0.1483	G:0.3992
A:0.0675	A:0.2873	A:0.0992	
G:0.002	G:0.0716	G:0.0491	G:0.0967
A:0.381	A:0.3877	A:0.3313	
G:0	G:0.003	G:0.0256	G:0.0009
C:0.001	C:0	C:0	
A:0.5685	A:0.1491	A:0.2761	
T:0.1875	T:0.1103	T:0.1176	T:0.1936
T:0	T:0.0089	T:0.001	T:0.0023
C:0.6776	C:0.5089	C:0.5082	
T:0.6766	T:0.5099	T:0.5082	
			A:0.3703

G:0.2728	G:0.5209	G:0.4581	G:0.2696
A:0.3988	A:0.499	A:0.4479	A:0.1568
T:0.1319	T:0.2247	T:0.136	
C:0.5149	C:0.2942	C:0.409	C:0.7819
T:0.3145	T:0.2674	T:0.1646	T:0.0579
A:0.0179	A:0.0527	A:0.2219	A:0.012
G:0.3274	G:0.3618	G:0.3292	
G:0	G:0.0139	G:0.0031	G:0.003
G:0.0159	G:0.1531	G:0.228	
T:0.5327	T:0.7137	T:0.7014	T:0.6212
T:0.5317	T:0.7117	T:0.6984	T:0.623
A:0.002	A:0.2227	A:0.0419	A:0.1751
A:0.1042	A:0.0835	A:0.0746	
G:0.0685	G:0.1103	G:0.1667	
T:0.0685	T:0.1093	T:0.1667	
T:0.0109	T:0.2584	T:0.1984	T:0.3442
A:0.5317	A:0.4781	A:0.5562	A:0.7579
A:0.4643	A:0.2416	A:0.2751	A:0.225
C:0.628	C:0.4145	C:0.7065	C:0.7948
G:0.5456	G:0.6819	G:0.5982	G:0.5004
C:0.4692	C:0.3946	C:0.4632	
C:0.131	C:0.1581	C:0.1595	C:0.2472
A:0.13	A:0.1511	A:0.1431	
G:0.0337	G:0.3996	G:0.1626	G:0.1123
A:0.0417	A:0.1451	A:0.1554	A:0.1434
G:0.2202	G:0.2913	G:0.2239	G:0.5116
C:0	C:0.002	C:0	
C:0.8125	C:0.4314	C:0.5757	
T:0	T:0.1431	T:0.0225	T:0.0311
C:0.6548	C:0.6839	C:0.684	
G:0.4573	G:0.2773	G:0.5511	G:0.221
A:0.3442	A:0.3539	A:0.4233	
			A:0
T:0.3591	T:0.5239	T:0.6104	T:0.1748
TG:0.5238	TG:0.3529	TG:0.3354	
T:0.4256	T:0.3241	T:0.3824	T:0.5225
C:0.3234	C:0.2316	C:0.2331	
G:0.3244	G:0.2256	G:0.2301	
A:0.3244	A:0.2276	A:0.2301	A:0.1437
C:0	C:0.001	C:0	
-:0.3204	-:0.0835	-:0.1155	
G:0.4226	G:0.3847	G:0.4029	G:0.2247
T:0.0337	T:0.336	T:0.2434	
A:0.1657	A:0.1243	A:0.2771	
G:0.0208	G:0.0249	G:0.0593	
G:0.2579	G:0.3847	G:0.4162	
T:0	T:0.003	T:0.001	T:0.0011
T:0.0744	T:0.1431	T:0.0603	

T:0.4355	T:0.2276	T:0.227	T:0.3743
G:0.125	G:0.1074	G:0.273	G:0.0208
G:0.4177	G:0.5517	G:0.5665	G:0.4508
T:0.4415	T:0.332	T:0.4468	
G:0.4484	G:0.3598	G:0.4683	G:0.1474
G:0.4415	G:0.332	G:0.4468	
G:0.0079	G:0.0557	G:0.0603	
G:0.0089	G:0.0557	G:0.0603	G:0.0079
C:0.1806	C:0.3429	C:0.3088	C:0.0842
C:0.0089	C:0.0547	C:0.0348	C:0.0177
A:0.0089	A:0.0328	A:0.0041	A:0.0051
G:0.5863	G:0.3897	G:0.3865	G:0.5079
T:0.3562	T:0.0199	T:0.0419	
A:0.122	A:0.0189	A:0.1247	A:0.2016
C:0.3562	C:0.2505	C:0.272	C:0.1102
C:0.9018	C:0.668	C:0.7628	C:0.9206
T:0.0129	T:0.1869	T:0.0716	T:0.0983
A:0.0833	A:0.0457	A:0.0736	A:0.0129
T:0.1855	T:0.2942	T:0.0941	T:0.3252
C:0.1806	C:0.2942	C:0.1002	C:0.3213
A:0.2083	A:0.3002	A:0.1155	A:0.732
A:0.2331	A:0.2127	A:0.3067	A:0.1336
-:0	-:0.0258	-:0.002	-:0.0032
A:0.8988	A:0.7485	A:0.7137	A:0.6947
T:0.1081	T:0.1382	T:0.1472	T:0.1369
T:0	T:0.0348	T:0.0051	T:0.0068
A:0.4107	A:0.5447	A:0.5051	
			C:0
C:0	C:0.0109	C:0.0031	C:0.0055
A:0.2302	A:0.2495	A:0.2955	A:0.1453
C:0.4385	C:0.2843	C:0.3333	C:0.7139
C:0.0248	C:0.2018	C:0.1861	C:0.3831
A:0.001	A:0.1024	A:0.0798	A:0.0354
C:0.4573	C:0.5209	C:0.4335	
G:0	G:0.2903	G:0.1462	
A:0	A:0.0785	A:0.0378	A:0.015
G:0.2698	G:0.4503	G:0.3589	G:0.2221
A:0	A:0.1252	A:0.0409	A:0.0302
T:0.6062	T:0.4682	T:0.6636	
T:0.5446	T:0.4672	T:0.3732	T:0.0969
T:0.0218	T:0.3141	T:0.1564	
C:0.2649	C:0.327	C:0.5838	
G:0	G:0.0268	G:0.0041	
-:0.119	-:0.1272	-:0.3047	-:0.1621
A:0.3948	A:0.2773	A:0.3528	A:0.0717

T:0.0149	T:0.2435	T:0.1227	T:0.0505
T:0	T:0.0189	T:0.0051	
G:0.5565	G:0.5895	G:0.68	G:0.8092
T:0.2698	T:0.5328	T:0.1288	T:0.1937
T:0.1002	T:0.2286	T:0.1789	T:0.0713
A:0.3522	A:0.4274	A:0.2914	A:0.4698
T:0.3502	T:0.3608	T:0.2618	T:0.5089
G:0.3492	G:0.3698	G:0.273	G:0.6158
T:0.1181	T:0.4235	T:0.2382	T:0.1395
G:0.7401	G:0.3469	G:0.4601	G:0.6836
T:0.5526	T:0.659	T:0.7914	
G:0.5526	G:0.659	G:0.7904	
C:0.5923	C:0.5795	C:0.502	C:0.8697
C:0.5903	C:0.4702	C:0.4294	C:0.0844
G:0.5913	G:0.4702	G:0.4305	G:0.1035
T:0.0397	T:0.0497	T:0.0634	T:0.0227
G:0.6905	G:0.4394	G:0.4029	
C:0	C:0.0149	C:0.0245	C:0.0041
T:0.1488	T:0.0775	T:0.3037	
T:0	T:0	T:0	
A:0.0278	A:0.0755	A:0.0092	A:0.4409
G:0.1181	G:0.164	G:0.2342	
T:0.001	T:0.0845	T:0.0624	T:0.0815
A:0.3333	A:0.1402	A:0.18	A:0.1707
G:0.8194	G:0.6382	G:0.773	
A:0.5347	A:0.4374	A:0.4785	A:0.1084
A:0.0585	A:0.0885	A:0.0818	A:0.0171
A:0.2887	A:0.5686	A:0.3088	A:0.5089
T:0.131	T:0.1998	T:0.1401	T:0.1417
T:0	T:0.1491	T:0.0767	
T:0.4583	T:0.3618	T:0.7157	T:0.2024
T:0.4732	T:0.3429	T:0.7137	
T:0.004	T:0.2177	T:0.2065	
T:0	T:0.0318	T:0.002	T:0.0052
A:0.2312	A:0.3688	A:0.2618	A:0.475
C:0.001	C:0.1412	C:0.1186	C:0.1432
			C:0.6498
T:0.0327	T:0.0706	T:0.0245	T:0.1484
A:0.2946	A:0.2147	A:0.2863	A:0.5849
G:0.1468	G:0.1968	G:0.0838	G:0.052
G:0.3046	G:0.1829	G:0.2812	G:0.0879
G:0.504	G:0.5199	G:0.499	
A:0.5218	A:0.2724	A:0.4591	A:0.7431
C:0.4504	C:0.5765	C:0.4407	C:0.7354
T:0.1855	T:0.332	T:0.0706	
C:0.0099	C:0.16	C:0.1401	C:0.1049
A:0	A:0.0199	A:0	A:0.0024
A:0.0278	A:0.0915	A:0.0327	A:0.0347

T:0.6319	T:0.3608	T:0.636	
G:0.8552	G:0.6382	G:0.5726	
G:0.001	G:0.0398	G:0.0389	
A:0.6974	A:0.2704	A:0.3456	
G:0.1081	G:0.338	G:0.2791	G:0.1685
A:0.8413	A:0.83	A:0.8834	A:0.7553
G:0.6944	G:0.3002	G:0.4427	G:0.198
T:0	T:0.0338	T:0.0112	T:0.004
G:0.7123	G:0.6779	G:0.7648	G:0.8568
G:0.5446,G:0.5446	G:0.6521,G:0.6521	G:0.6984,G:0.6984	
C:0.7133,C:0.7133	C:0.6779,C:0.6779	C:0.7669,C:0.7669	C:0.8604,C:0.8604
C:0.5754	C:0.4742	C:0.4519	C:0.3695
C:0.4157	C:0.1899	C:0.2454	C:0.1031
T:0.4137	T:0.2286	T:0.2505	
A:0.004	A:0.172	A:0.0706	A:0.0378
A:0.0506	A:0.1859	A:0.0828	A:0.0364
A:0.0506	A:0.1859	A:0.0828	A:0.0531
T:0.0565	T:0.1998	T:0.1421	
T:0	T:0	T:0	T:0.0002
C:0	C:0.1163	C:0.1012	C:0.0191
A:0.4067	A:0.2823	A:0.316	A:0.591
A:0.2589	A:0.2565	A:0.317	A:0.2132
A:0.4097	A:0.2942	A:0.3292	A:0.2908
G:0.0516	G:0.0944	G:0.1851	
A:0	A:0	A:0.001	
T:0.3373	T:0.4722	T:0.3088	
T:0.126	T:0.3022	T:0.1738	
A:0.7778	A:0.4006	A:0.5746	A:0.5499
A:0.4633	A:0.2942	A:0.3855	
A:0.8095	A:0.6769	A:0.5971	A:0.7501
C:0.1835	C:0.2833	C:0.4438	
T:0.3194	T:0.3161	T:0.4622	T:0.1886
T:0.4256	T:0.5139	T:0.547	
T:0.001	T:0.0179	T:0.0348	T:0.005
A:0.0784	A:0.0686	A:0.0092	A:0.016
A:0.6736	A:0.2147	A:0.3763	A:0.5356
A:0	A:0.0119	A:0	A:0.0025
G:0.0208	G:0.2913	G:0.135	
GGTTACCCTA:0.5665	GGTTACCCTA:0.7048	GGTTACCCTA:0.6575	
C:0.251	C:0.2237	C:0.2045	
T:0.1944	T:0.0636	T:0.2055	T:0.0806
-:0.4345	-:0.4304	-:0.5317	-:0.1024
T:0.4355	T:0.4304	T:0.5337	
T:0.6577	T:0.7495	T:0.6237	T:0.5589
G:0.2768	G:0.7724	G:0.5838	G:0.3657
C:0.2698	C:0.2336	C:0.2086	C:0.1484
A:0.122	A:0.3082	A:0.3262	
C:0.6905	C:0.3907	C:0.3967	
			C:0.8646
G:0.3214	G:0.3608	G:0.3149	

T:0.3284	T:0.3608	T:0.2761	T:0.1759
A:0.001	A:0.3181	A:0.0634	A:0.1897
T:0.2728	T:0.3489	T:0.3088	T:0.1131
T:0.0437	T:0.3469	T:0.318	T:0.2811
T:0.0526	T:0.0954	T:0.0746	
A:0.375	A:0.169	A:0.2781	
T:0	T:0.0169	T:0	T:0.0014
A:0.6776	A:0.3688	A:0.6442	A:0.8349
C:0.2927	C:0.4433	C:0.3027	C:0.2904
C:0.5546	C:0.5706	C:0.5337	C:0.3035
C:0.6667	C:0.5557	C:0.7311	
T:0.1954	T:0.3131	T:0.2014	T:0.2027
T:0.2817	T:0.3887	T:0.4305	T:0.36
-:0.1032	-:0.1213	-:0.2147	
A:0.6994	A:0.5119	A:0.5818	A:0.239
G:0.005	G:0.1551	G:0.0951	
T:0	T:0.0258	T:0.0051	T:0.0059
G:0.25	G:0.3549	G:0.3241	G:0.2268
T:0.1984	T:0.2614	T:0.2209	T:0.1639
G:0.3611	G:0.3777	G:0.228	G:0.4653
T:0.3611	T:0.4225	T:0.2464	T:0.2962
C:0.0397	C:0.0388	C:0.0164	C:0.2422
A:0	A:0.0388	A:0.0143	A:0.1625
T:0	T:0.0388	T:0.0143	
A:0.246	A:0.1223	A:0.1585	
T:0.2411	T:0.1581	T:0.1677	T:0.0556
A:0.245	A:0.1581	A:0.1677	A:0.0554
T:0.1379	T:0.1521	T:0.0675	T:0.0903
G:0.0079	G:0.1471	G:0.0419	G:0.0345
G:0.5397	G:0.2783	G:0.3978	G:0.1534
G:0.4246	G:0.2028	G:0.4233	
C:0.0079	C:0.0746	C:0.1769	C:0.1882
G:0.2331	G:0.2783	G:0.2751	G:0.1113
G:0	G:0.001	G:0.002	G:0.0007
T:0.1121	T:0.3121	T:0.2618	T:0.0615
G:0.4514	G:0.1074	G:0.226	G:0.0592
A:0.2649	A:0.0606	A:0.1728	A:0.0124
A:0.001	A:0.0586	A:0.0031	A:0.0114
A:0	A:0.0109	A:0.0164	A:0.0011
A:0.0069	A:0.4592	A:0.2945	A:0.1568
A:0.1548	A:0.1382	A:0.0798	A:0.0673
A:0.1687	A:0.3539	A:0.2178	A:0.2773
A:0.5833	A:0.4911	A:0.5041	A:0.6714
C:0.7579	C:0.7197	C:0.7342	C:0.992
G:0	G:0.1123	G:0.0235	G:0.0417
A:0.3234	A:0.0954	A:0.0982	A:0.0229
C:0.4841	C:0.2018	C:0.3855	
T:0.6706	T:0.4622	T:0.5654	
T:0.3601	T:0.2495	T:0.1984	T:0.1523
T:0.0913	T:0.1968	T:0.2894	T:0.054
A:0.0069	A:0.0815	A:0.0675	A:0.1058
A:0.1944	A:0.2883	A:0.407	A:0.3125

C:0.255 A:0.2897 G:0.5337	C:0.1252 A:0.0765 G:0.5507	C:0.1155 A:0.2331 G:0.5675	C:0.1953 A:0.1035
A:0.2619 C:0.6538 T:0	A:0.3678 C:0.4891 T:0.0189	A:0.1278 C:0.5429 T:0.0051	A:0.0767 C:0.745
A:0.5893	A:0.2674	A:0.5	A:0.2417
A:0.4911 G:0.244	A:0.163 G:0.0437	A:0.3047 G:0.047	A:0.2506 G:0.1263
C:0.1746 A:0.122	C:0.3141 A:0.2425	C:0.4683 A:0.1605	C:0.1009
A:0.4226 T:0.0169 A:0	A:0.4881 T:0.3042 A:0.0139	A:0.4417 T:0.184 A:0.001	A:0.0043
A:0.7897 A:0.003	A:0.6252 A:0.2346	A:0.7311 A:0.092	A:0.5111
T:0.1379 C:0.002	T:0.2932 C:0.16	T:0.1718 C:0.0654	T:0.0842
T:0 T:0.7044	T:0.0308 T:0.5199	T:0.0399 T:0.5675	T:0.1266
T:0.1468 T:0	T:0.333 T:0.0318	T:0.2495 T:0.0051	T:0.2719
T:0.001 T:0.001	T:0.2107 T:0.2087	T:0.044 T:0.044	T:0.0404
A:0.496 A:0.5268 C:0.4167	A:0.1382 A:0.5905 C:0.336	A:0.3231 A:0.4898 C:0.5225	A:0.5722 C:0.2819
C:0.0357 C:0.9534	C:0.2783 C:0.7117	C:0.1912 C:0.8845	C:0.8359
A:0 T:0.4524	A:0.0567 T:0.4185	A:0.0082 T:0.5389	A:0.0123 T:0.7402
A:0 A:0.1756 T:0.1766 C:0.3532	A:0.0388 A:0.0517 T:0.0557 C:0.4632	A:0.0082 A:0.0481 T:0.047 C:0.3681	A:0.0129 A:0.0613 T:0.0629 C:0.3561
C:0.7123 C:0.7927 T:0.0625	C:0.3966 C:0.4394 T:0.1133	C:0.5552 C:0.6135 T:0.0777	C:0.514 T:0.0481
G:0.0288 T:0 C:0.0337 A:0.2599 T:0.5446	G:0.172 T:0.002 C:0.0099 A:0.4254 T:0.5895	G:0.0706 T:0 C:0.0276 A:0.4489 T:0.6748	T:0.0002 C:0.0524 A:0.2421 T:0.7896
T:0.1161 T:0.0526	T:0.161 T:0.1143	T:0.2096 T:0.1319	

A:0.7123	A:0.3956	A:0.3804	A:0.1922
A:0.0367 T:0.2976	A:0.1163 T:0.4632	A:0.0654 T:0.546	A:0.0288 T:0.3411
T:0.1558 A:0.7837 T:0.5248 A:0.2728 A:0.001 T:0.0119 C:0.1508 A:0.1429	T:0.2952 A:0.7087 T:0.6571 A:0.2356 A:0.0676 T:0.0328 C:0.1083 A:0.1093	T:0.1687 A:0.6912 T:0.5838 A:0.182 A:0.1002 T:0.0327 C:0.0665 A:0.0215	T:0.1407 A:0.4754 T:0.1652 A:0.2499 T:0.0773 C:0.1545 A:0.0164
A:0.3492 C:0.3958	A:0.2734 C:0.4294	A:0.2423 C:0.3569	A:0.2093 C:0.0975
T:0.1438	T:0.2873	T:0.2393	T:0.3155
G:0.4345 C:0 G:0.1865 C:0.5933 G:0.5754 G:0.3909	G:0.3111 C:0.0308 G:0.4334 C:0.7853 G:0.333 G:0.1928	G:0.456 C:0.0307 G:0.3364 C:0.682 G:0.5215 G:0.1534	 C:0.4626 G:0.1879
A:0.3968 A:0.3373 T:0.0179 C:0.5 G:0.002	A:0.1918 A:0.1968 T:0.2823 C:0.3489 G:0.2525	A:0.2127 A:0.2106 T:0.1462 C:0.2556 G:0.0685	A:0.1012 C:0.5364 G:0.4368
A:0.2083 A:0.1319 G:0.2093 C:0 -:0	A:0.1938 A:0.1292 G:0.1412 C:0.0706 -:0.0785	A:0.4233 A:0.3446 G:0.4223 C:0.0061 -:0.0184	 A:0.3654 G:0.6142 C:0.122 G:0.1121
-:0.9236,-:0.9236 T:0 T:0.001 T:0 C:0 A:0.0486 G:0.3006 T:0.2798 G:0.2589 A:0	-:0.327,-:0.327 T:0.007 T:0.1382 T:0.0219 C:0.0189 A:0.2127 G:0.3549 T:0.2853 G:0.2883 A:0.0557	-:0.5297,-:0.5297 T:0.002 T:0.1104 T:0.0358 C:0.002 A:0.1309 G:0.2331 T:0.2618 G:0.2546 A:0.0061	 T:0.0009 T:0.0137 A:0.0942 T:0.1941 G:0.2077 A:0.0115
G:0.498	G:0.2475	G:0.3436	
A:0.3948 A:0.0933 C:0	A:0.2893 A:0.0557 C:0.0149	A:0.3006 A:0.0654 C:0.002	A:0.1811 C:0.0027

G:0.4415	G:0.6581	G:0.4816	
C:0.4454	C:0.6581	C:0.4877	C:0.6863
C:0.2361	C:0.1252	C:0.2188	C:0.0273
A:0.2212	A:0.2316	A:0.1769	A:0.3774
C:0.3175	C:0.3032	C:0.136	
T:0.3175	T:0.2584	T:0.1237	T:0.2152
C:0.37	C:0.4046	C:0.455	
G:0.7579	G:0.666	G:0.727	G:0.9207
C:0	C:0.005	C:0.002	C:0.0007
T:0.1944	T:0.5089	T:0.2065	
A:0	A:0.0119	A:0.0031	A:0.0023
A:0	A:0.1402	A:0.0174	A:0.0322
A:0.6141	A:0.5149	A:0.4458	A:0.7102
C:0.4782	C:0.2803	C:0.3037	
T:0.0933	T:0.1839	T:0.2372	
G:0.9375	G:0.7048	G:0.682	G:0.7255
A:0.0694	A:0.1103	A:0.1207	A:0.0256
G:0.3075	G:0.2555	G:0.1616	G:0.13
T:0.3056	T:0.2515	T:0.1595	T:0.0858
-:0.254	-:0.3996	-:0.319	-:0.2863
T:0.003	T:0.1869	T:0.0685	T:0.1423
G:0.1429	G:0.3748	G:0.2362	
A:0.1121	A:0.341	A:0.4325	A:0.1879
A:0.1429	A:0.4195	A:0.4008	A:0.3323
T:0.8224	T:0.3579	T:0.3845	T:0.5733
C:0.3323	C:0.328	C:0.32	C:0.4607
T:0.1716	T:0.168	T:0.2485	T:0.3963
T:0.0179	T:0.2803	T:0.1881	
C:0	C:0.0845	C:0.0266	C:0.015
A:0.0387	A:0.2058	A:0.092	
A:0.0198	A:0.0318	A:0.135	A:0.0563
T:0	T:0.005	T:0	T:0
A:0.3095	A:0.0775	A:0.1554	A:0.0485
G:0.245	G:0.4135	G:0.3446	G:0.4272
G:0.245	G:0.335	G:0.3487	G:0.3861
			T:0.3826
A:0.1815	A:0.008	A:0.0092	A:0.03
A:0.3601	A:0.2913	A:0.4632	
G:0.371	G:0.0895	G:0.1104	G:0.4893
			A:0
A:0	A:0.0368	A:0.0297	A:0.0055
A:0.7232	A:0.1451	A:0.3262	A:0.0837
T:0.3423	T:0.2714	T:0.3129	
T:0.0347	T:0.1074	T:0.1483	T:0.1135
C:0.4692	C:0.3718	C:0.41	C:0.2655

G:0.1458	G:0.1879	G:0.1401	G:0.0447
C:0	C:0.0139	C:0.001	C:0.0007
A:0.6181	A:0.5348	A:0.6319	A:0.629
G:0.8542	G:0.7336	G:0.817	G:0.8447
T:0.6746	T:0.6024	T:0.4162	T:0.1785
T:0.0456	T:0.1958	T:0.1329	
A:0.002	A:0	A:0	
C:0.4157	C:0.2515	C:0.2587	C:0.3509
A:0.2966	A:0.173	A:0.2198	
C:0.7103	C:0.7763	C:0.7832	C:0.8515
C:0.6627	C:0.6998	C:0.7781	C:0.8096
G:0.6458	G:0.7624	G:0.7965	G:0.895
T:0	T:0.0229	T:0.046	T:0.0045
-:0.0516	-:0.0706	-:0.1186	
G:0.1329	G:0.2694	G:0.2229	
A:0.5099	A:0.5129	A:0.5429	
T:0.9861	T:0.7396	T:0.8773	T:0.9446
A:0.628	A:0.5636	A:0.6033	A:0.3747
C:0.628	C:0.5596	C:0.6033	
A:0.5188	A:0.4573	A:0.4039	
A:0.4315	A:0.3052	A:0.3088	A:0.1053
G:0.8244	G:0.3579	G:0.3773	G:0.5411
A:0.1577	A:0.3012	A:0.4346	
A:0.13	A:0.3032	A:0.3057	
A:0.2976	A:0.7256	A:0.6258	A:0.5402
T:0.255	T:0.2505	T:0.2474	T:0.4514
A:0	A:0	A:0	
T:0.3363	T:0.1292	T:0.2699	
A:0.2788	A:0.2485	A:0.2853	A:0.4832
C:0.5923	C:0.327	C:0.3609	C:0.3161
G:0	G:0.004	G:0	
C:0.3621	C:0.2813	C:0.4223	C:0.111
G:0.001	G:0.2893	G:0.1513	
C:0.9107	C:0.6779	C:0.6871	
A:0.5069	A:0.5934	A:0.4468	A:0.4069
T:0.0575	T:0.0706	T:0.0297	T:0.0499
A:0	A:0.001	A:0	A:0
A:0	A:0.0398	A:0.0123	
A:0.4097	A:0.2843	A:0.5102	A:0.3293
T:0.1448	T:0.5288	T:0.4785	
A:0.7202	A:0.339	A:0.456	A:0.1133
G:0	G:0.0189	G:0.002	G:0.0049
G:0.0734	G:0.0507	G:0.0941	G:0.0767
A:0	A:0.0219	A:0.0123	A:0.0064
G:0.1101	G:0.335	G:0.1472	G:0.0672

T:0.3155	T:0.3181	T:0.3252	T:0.1649
A:0.121	A:0.3101	A:0.3037	
C:0.0923	C:0.006	C:0.002	
T:0.5248	T:0.4712	T:0.4387	
G:0	G:0.006	G:0.0092	
G:0.6647	G:0.833	G:0.7914	
T:0.0903	T:0.4891	T:0.3487	T:0.1382
C:0.0069	C:0.0308	C:0.0951	C:0.0073
C:0.8671	C:0.7207	C:0.6984	C:0.8495
C:0.1131	C:0.0865	C:0.1534	
C:0.4891	C:0.329	C:0.4213	C:0.2668
C:0.0903	C:0.1352	C:0.1452	C:0.4694
T:0.6657	T:0.5477	T:0.498	T:0.599
T:0.0397	T:0.1292	T:0.0961	
G:0.2034	G:0.4771	G:0.3006	G:0.1114
A:0.2609	A:0.3489	A:0.1074	A:0.559
C:0.6141	C:0.4543	C:0.5399	C:0.2306
T:0.6766	T:0.6948	T:0.6094	T:0.241
T:0	T:0.0209	T:0.0041	
C:0	C:0.0089	C:0.001	C:0.0035
G:0	G:0.0288	G:0.0143	
-:0.001	-:0.0169	-:0.0031	
C:0.621	C:0.2893	C:0.4857	
C:0.621	C:0.2893	C:0.4847	C:0.4351
G:0.3452	G:0.3032	G:0.1677	G:0.2136
T:0.755	T:0.2634	T:0.4683	T:0.1936
G:0.1042	G:0.0358	G:0.0562	G:0.1221
A:0.3274	A:0.4056	A:0.3712	A:0.32
T:0.1627	T:0.1988	T:0.1564	T:0.0687
A:0.002,A:0.002	A:0,A:0	A:0,A:0	A:0,A:0
C:0.7024	C:0.6064	C:0.5358	C:0.8318
C:0.4792	C:0.3748	C:0.3231	
C:0	C:0	C:0.0031	C:0
C:0	C:0	C:0	C:0
G:0.2589	G:0.4433	G:0.4335	G:0.7572
T:0.0863	T:0.2575	T:0.3456	
T:0.0833	T:0.0616	T:0.0726	T:0.0125
T:0	T:0.2376	T:0.1656	T:0.1642
A:0	A:0.1054	A:0.091	A:0.0194
A:0.371	A:0.2674	A:0.2444	A:0.2553
A:0.5873	A:0.3489	A:0.4509	
T:0.3631	T:0.1909	T:0.2515	T:0.1248
T:0.1062	T:0.1382	T:0.1493	T:0.1498
A:0.5119	A:0.3648	A:0.3395	A:0.6632
A:0.2738	A:0.2197	A:0.1401	
G:0.5099	G:0.3628	G:0.3395	G:0.6454
T:0.001	T:0.0129	T:0.0215	

C:0.0476	C:0.0954	C:0.0256	C:0.0325
C:0.1855	C:0.2594	C:0.1922	C:0.4332
T:0.5248	T:0.3559	T:0.4673	T:0.7642
G:0.3433	G:0.175	G:0.3129	
T:0.0278	T:0.2604	T:0.2904	T:0.4471
A:0.1667	A:0.3708	A:0.3078	A:0.2063
G:0	G:0.0577	G:0.0245	
G:0	G:0.006	G:0.001	G:0.0007
T:0.1597	T:0.1362	T:0.1779	
A:0.7063	A:0.3161	A:0.5481	A:0.8133
T:0.62	T:0.3857	T:0.5521	
A:0.6806	A:0.7117	A:0.8303	A:0.8923
T:0.501	T:0.4642	T:0.6012	
G:0.4157	G:0.328	G:0.5665	G:0.4019
G:0.998	G:0.8032	G:0.9448	G:0.9053
C:0.372	C:0.2863	C:0.5706	C:0.263
G:0.6419	G:0.3797	G:0.3783	G:0.094
A:0	A:0.0099	A:0.0031	A:0.0039
T:0.1101	T:0.0626	T:0.0123	T:0.0105
T:0.0308	T:0.2913	T:0.1534	T:0.1907
T:0.3462	T:0.2485	T:0.4356	
T:0.0565	T:0.2356	T:0.1299	T:0.4256
G:0.4276	G:0.3857	G:0.3098	G:0.1984
T:0.7778	T:0.5835	T:0.7331	T:0.8727
G:0.4266	G:0.3917	G:0.2986	G:0.2177
A:0.5218	A:0.5567	A:0.6176	A:0.4641
GGGAGA:0.4067	GGGAGA:0.2545	GGGAGA:0.4959	GGGAGA:0.2907
C:0.0228	C:0.3111	C:0.2393	C:0.2588
C:0.2262	C:0.164	C:0.0869	
A:0.1706	A:0.163	A:0.0798	
C:0.9931	C:0.5219	C:0.6503	C:0.6186
A:0.7639	A:0.6233	A:0.4315	
G:0.5575	G:0.4781	G:0.4714	G:0.4909
A:0.3135	A:0.5905	A:0.4806	A:0.3805
-:0.6607	-:0.7058	-:0.7689	-:0.4065
T:0.2728	T:0.2883	T:0.2219	T:0.0988
C:0	C:0.2992	C:0.0706	C:0.0649
T:0.001	T:0.1402	T:0.0286	T:0.1441
C:0.0952	C:0.3429	C:0.2096	C:0.6714
A:0.0685	A:0.7594	A:0.4202	A:0.1745
C:0.6667	C:0.3907	C:0.498	
T:0.1587	T:0.0835	T:0.0767	
C:0.6359	C:0.2724	C:0.3507	
C:0.003	C:0.0905	C:0.0235	
G:0.5308	G:0.5427	G:0.4141	G:0.5463
T:0	T:0.003	T:0.0061	T:0.0016
C:0.5675	C:0.3499	C:0.1677	

T:0.0883	T:0.1243	T:0.183	T:0.3044
T:0.001	T:0.0408	T:0.0286	T:0.01
G:0.2897	G:0.5417	G:0.4622	G:0.4703
T:0.8601	T:0.4334	T:0.6278	T:0.7301
G:0.373	G:0.3638	G:0.5	G:0.2478
T:0.371	T:0.3588	T:0.501	T:0.1856
C:0.371	C:0.3579	C:0.501	C:0.1876
A:0.371	A:0.3598	A:0.501	A:0.2293
T:0.0556	T:0.0676	T:0.0736	T:0.0138
T:0	T:0.0109	T:0	T:0.002
A:0	A:0.0139	A:0.0031	A:0.005
A:0.2639	A:0.3936	A:0.3548	A:0.2519
A:0.1518	A:0.5328	A:0.3538	
T:0.3562	T:0.1392	T:0.09	T:0.0506
C:0.378	C:0.8002	C:0.6258	C:0.2276
C:0.5149	C:0.8877	C:0.7014	
T:0.5952	T:0.1938	T:0.3712	T:0.0392
C:0.6746	C:0.3807	C:0.3016	C:0.4934
G:0.252	G:0.2873	G:0.272	G:0.2794
C:0	C:0.002	C:0.0133	C:0.0011
T:0	T:0.0199	T:0.001	T:0.002
G:0.4484	G:0.661	G:0.501	G:0.3978
G:0.0218	G:0.0905	G:0.089	G:0.1622
G:0.378	G:0.333	G:0.4366	G:0.1315
G:0.7232	G:0.4712	G:0.4325	G:0.4165
T:0.4177	T:0.7535	T:0.7689	T:0.8613
A:0	A:0.0109	A:0.001	
G:0	G:0.0169	G:0.002	G:0.0015
			G:0.0008
C:0	C:0.0099	C:0.0041	
T:0.4792	T:0.1252	T:0.3303	T:0.0429
A:0	A:0.0328	A:0.002	A:0.0561
A:0.001	A:0.0268	A:0.0235	A:0.0254
G:0.3244	G:0.2724	G:0.3804	G:0.4003
A:0.254	A:0.2694	A:0.2362	
A:0.0139	A:0.1103	A:0.1452	A:0.0254
G:0	G:0.0258	G:0.0031	G:0.0077
T:0.5437	T:0.3956	T:0.227	
G:0.87	G:0.6561	G:0.8323	
G:0.0089	G:0.1004	G:0.2413	G:0.0704
T:0	T:0.0596	T:0.0164	
G:0.005	G:0.1789	G:0.1247	G:0.1682
G:0.1052	G:0.0656	G:0.092	G:0.2312
G:0.3512	G:0.2177	G:0.4254	G:0.2676

G:0.0506	G:0.2525	G:0.226	
T:0	T:0.006	T:0	
C:0.0179	C:0.0537	C:0.0746	C:0.2394
A:0.6726	A:0.673	A:0.635	
T:0	T:0.0398	T:0.0041	T:0.0077
C:0.1567	C:0.2008	C:0.1708	
A:0.005	A:0.165	A:0.1115	A:0.0449
A:0.0069	A:0.0417	A:0.1299	
T:0.1448	T:0.0358	T:0.1196	T:0.0674
A:0.2272	A:0.2306	A:0.2229	A:0.0454
G:0.8234	G:0.3579	G:0.3793	G:0.4986
-:0.3512	-:0.1312	-:0.1288	
T:0.3512	T:0.1312	T:0.1288	T:0.0697
T:0.8244	T:0.4404	T:0.6871	
A:0.8244	A:0.4404	A:0.6871	A:0.4187
C:0.6468	C:0.5159	C:0.5123	C:0.9413
C:0.0427	C:0.1342	C:0.0368	
T:0.0427	T:0.1352	T:0.0368	
C:0.0427	C:0.1352	C:0.0368	
C:0.4375	C:0.165	C:0.2669	C:0.3301
G:0.2778	G:0.3201	G:0.4018	
A:0	A:0.0149	A:0.0501	A:0.0043
A:0.3581	A:0.2117	A:0.4519	A:0.2113
T:0.8532	T:0.6491	T:0.6718	
G:0.2927	G:0.5427	G:0.5685	
			T:0.308
A:0.001	A:0.0596	A:0.0389	A:0.0566
T:0.001	T:0.0606	T:0.0327	T:0.0095
T:0.001	T:0.0596	T:0.0389	T:0.0091
A:0.1458	A:0.2565	A:0.2229	A:0.1433
G:0.2004	G:0.332	G:0.2863	G:0.4309
C:0.496	C:0.7942	C:0.7311	C:0.818
A:0	A:0.0427	A:0.0041	A:0.007
A:0.0913	A:0.1849	A:0.1145	A:0.2494
G:0.001	G:0.0944	G:0.0562	
T:0.2123	T:0.0885	T:0.093	
G:0.0962	G:0.172	G:0.2106	G:0.2989
G:0.1052	G:0.1978	G:0.2474	G:0.6416
G:0.001	G:0.0706	G:0.0368	G:0.1068
AGC:0.1458	AGC:0.2396	AGC:0.317	AGC:0.201
G:0.4127	G:0.1093	G:0.2648	G:0.6407
A:0.0903	A:0.168	A:0.0613	A:0.0354
n:TIGR01628			
T:0.001	T:0.0696	T:0.0082	T:0.0141
A:0.3115	A:0.2416	A:0.2853	A:0.1732
A:0	A:0.0129	A:0	A:0.1419
A:0.0198	A:0.0736	A:0.0665	
G:0.2986	G:0.2604	G:0.4693	G:0.3757
A:0.3046	A:0.3867	A:0.2137	A:0.0717

A:0.1756	A:0.1471	A:0.1677	A:0.0649
T:0.1518	T:0.1133	T:0.1656	T:0.1419
G:0	G:0.0179	G:0.001	G:0.0039
G:0	G:0.0924	G:0.0317	
G:0.3581	G:0.0616	G:0.0532	G:0.1516
G:0.0585	G:0.2316	G:0.0982	G:0.2088
A:0.0159	A:0.2187	A:0.1278	
A:0.8343	A:0.3678	A:0.4847	A:0.796
			A:0.0025
T:0.4306	T:0.4722	T:0.5429	T:0.1827
G:0	G:0.0487	G:0.0072	
A:0.2798	A:0.2942	A:0.3579	A:0.2698
			A:0.2401
C:0.1071	C:0.3956	C:0.3067	C:0.3327
C:0.1071	C:0.3966	C:0.3067	C:0.3597
C:0.3988	C:0.6203	C:0.3374	
G:0.4425	G:0.335	G:0.454	G:0.3401
G:0.37	G:0.3062	G:0.4376	G:0.2069
-:0.0278	-:0.5437	-:0.1902	
G:0.2153	G:0.2873	G:0.2198	G:0.1094
G:0.7966	G:0.2038	G:0.5982	
A:0.3442	A:0.1113	A:0.2229	A:0.1448
C:0.3145	C:0.1243	C:0.226	C:0.2524
A:0.1915	A:0.2565	A:0.1431	A:0.3969
G:0.1925	G:0.2545	G:0.1431	G:0.387
G:0.4018	G:0.5646	G:0.3742	
T:0.3343	T:0.3668	T:0.2699	
C:0	C:0.1272	C:0.0665	
T:0.2966	T:0.2227	T:0.2311	T:0.154
G:0.1885	G:0.4672	G:0.272	G:0.3622
T:0.373	T:0.3767	T:0.138	T:0.3118
A:0.0198	A:0.2147	A:0.0869	A:0.254
G:0.3224	G:0.2863	G:0.3967	G:0.271
C:0.3938	C:0.1809	C:0.2229	
G:0.0069	G:0.2694	G:0.0982	G:0.057
G:0.1617	G:0.0845	G:0.0818	G:0.0104
G:0.002	G:0.3052	G:0.1401	G:0.3389
A:0.3383	A:0.2922	A:0.5542	A:0.3395
G:0.5466	G:0.4135	G:0.4489	G:0.4319
A:0.0774	A:0.1173	A:0.0992	A:0.1056
C:0.2579	C:0.495	C:0.4571	C:0.2077
T:0.8373	T:0.3201	T:0.5562	
C:0.0079	C:0.0666	C:0.0409	
T:0.1885	T:0.1143	T:0.1452	T:0.0311
A:0.2004	A:0.0984	A:0.044	A:0.043
G:0.5357	G:0.4573	G:0.4182	G:0.5466

T:0.2123	T:0.2753	T:0.1943	T:0.2088
T:0.2381	T:0.3091	T:0.2474	T:0.3935
C:0.0645	C:0.3419	C:0.362	
G:0.7897	G:0.6292	G:0.6922	G:0.7272
C:0.9871	C:0.7594	C:0.82	
C:0.1429	C:0.4344	C:0.3476	C:0.8228
G:0.1458	G:0.4066	G:0.3344	G:0.1049
A:0.1518	A:0.4314	A:0.3517	
A:0.1419	A:0.4284	A:0.3446	A:0.088
G:0.1508	G:0.4404	G:0.3548	G:0.8202
G:0.1448	G:0.4364	G:0.363	G:0.7332
T:0.246	T:0.2813	T:0.272	T:0.118
C:0.4563	C:0.5119	C:0.544	C:0.5625
G:0.4077	G:0.3996	G:0.4274	
A:0.0823	A:0.162	A:0.2648	
A:0.4107	A:0.5199	A:0.6063	
T:0.2887	T:0.2853	T:0.1207	T:0.2922
T:0.1032	T:0.2565	T:0.2914	T:0.318
C:0.4325	C:0.3509	C:0.4969	C:0.3193
A:0.0129	A:0.2386	A:0.1892	A:0.2716
-:0.1895,-:0.1895	-:0.2227,-:0.2227	-:0.362,-:0.362	
G:0.1627	G:0.1103	G:0.0317	G:0.1712
A:0.1349	A:0.4751	A:0.3405	
C:0.0585	C:0.1958	C:0.1022	
G:0.0258	G:0.1203	G:0.1196	
T:0.2113	T:0.1213	T:0.1595	
C:0.3849	C:0.6282	C:0.5736	C:0.5152
GAACCC:0.3323	GAACCC:0.4036	GAACCC:0.4213	
G:0.4474	G:0.4006	G:0.3569	G:0.2721
A:0.0863	A:0.17	A:0.0634	
C:0.4524	C:0.2644	C:0.2986	C:0.2738
TGTTTTGTTT:0.0268	TGTTTTGTTT:0.2416	TGTTTTGTTT:0.2505	
T:0.5724	T:0.4225	T:0.5675	T:0.5392
A:0.4881	A:0.3867	A:0.3579	A:0.3604
A:0.627	A:0.2724	A:0.3926	
C:0.5764	C:0.4463	C:0.4121	C:0.6384
T:0.5744	T:0.4463	T:0.409	T:0.3737
C:0.5744	C:0.4463	C:0.409	C:0.3786
G:0.2103	G:0.2704	G:0.3865	G:0.446
G:0.4722	G:0.4026	G:0.4836	G:0.5633
G:0.2341	G:0.4573	G:0.2556	G:0.2878
A:0.2202	A:0.2873	A:0.2546	A:0.3214
A:0	A:0.0527	A:0.0072	
A:0	A:0.0258	A:0.0112	A:0.0063
T:0.4375	T:0.2684	T:0.2679	
A:0.251	A:0.2624	A:0.1104	

-:0	-:0.005	-:0.001	
A:0.004	A:0.1103	A:0.1431	A:0.072
A:0.003	A:0.1431	A:0.1268	
			C:0.0094
G:0.1042	G:0.2256	G:0.2004	G:0.2767
C:0.4554	C:0.3986	C:0.3712	
G:0.3036	G:0.4334	G:0.2096	G:0.3367
A:0.1815	A:0.333	A:0.3252	
G:0.1538	G:0.1074	G:0.0307	G:0.1963
C:0.7302	C:0.5706	C:0.591	C:0.5506
G:0.0317	G:0.3111	G:0.1585	
A:0.006	A:0.334	A:0.1299	A:0.0681
A:0.4583	A:0.1451	A:0.1861	
G:0.0496	G:0.005	G:0.0041	
A:0.0496	A:0.005	A:0.0041	
C:0.0496	C:0.005	C:0.0041	C:0.002
GC:0.0496	GC:0.005	GC:0.0041	GC:0
C:0.5476	C:0.4483	C:0.456	C:0.4671
G:0.5615	G:0.2833	G:0.592	G:0.5498
G:0.1667	G:0.1561	G:0.2924	G:0.5082
A:0.1667	A:0.2674	A:0.1973	A:0.1899
G:0.7579	G:0.6998	G:0.7321	G:0.9671
A:0.4742	A:0.3936	A:0.3855	
A:0.6151	A:0.3628	A:0.6247	A:0.6578
TTCCACG:0	TTCCACG:0.0408	TTCCACG:0.0184	
G:0.0744	G:0.3757	G:0.2209	G:0.3484
G:0.0526	G:0.2117	G:0.3354	G:0.5512
A:0.0575	A:0.3767	A:0.2127	A:0.5931
A:0.9484	A:0.7455	A:0.7393	A:0.7486
C:0.2728	C:0.3042	C:0.2802	C:0.1092
-:0.6577	-:0.7048	-:0.8384	-:0.3888
T:0	T:0.002	T:0	T:0
			C:0
A:0.2698	A:0.506	A:0.5481	A:0.5572
T:0.2262	T:0.2883	T:0.4325	
C:0.0794	C:0.2704	C:0.1431	
G:0.3075	G:0.3907	G:0.3507	G:0.1019
-:0.2659	-:0.4443	-:0.3456	-:0.0747
G:0.2569	G:0.159	G:0.1074	
GGGGATTA:0	GGGGATTA:0.1909	GGGGATTA:0.0644	GGGGATTA:0.0985
G:0.0486	G:0.1481	G:0.1554	G:0.0679
C:0.746	C:0.5964	C:0.4785	C:0.2549
A:0.746	A:0.5964	A:0.4775	
C:0.5942	C:0.5517	C:0.5746	C:0.7483
T:0.252	T:0.328	T:0.2761	T:0.0717
C:0.4683	C:0.5557	C:0.4233	C:0.2724
A:0.1587	A:0.1402	A:0.1084	
T:0.5933	T:0.4851	T:0.4622	T:0.3071
AA:0.8968	AA:0.6869	AA:0.592	
T:0.9792	T:0.7992	T:0.6043	
T:0.0417	T:0.0775	T:0.0695	T:0.1308

T:0.371	T:0.3588	T:0.4969	
-:0.2202	-:0.3091	-:0.5082	-:0.2133
A:0	A:0.0189	A:0	
C:0.2262	C:0.496	C:0.4397	
A:0.2282	A:0.494	A:0.4397	A:0.1216
T:0.3889	T:0.5268	T:0.4294	T:0.2719
A:0.0437	A:0.169	A:0.1186	
G:0.5913	G:0.4066	G:0.5153	G:0.63
T:0	T:0.0089	T:0.0041	T:0.001
C:0.5625	C:0.5258	C:0.5061	
A:0.8075	A:0.5775	A:0.5245	
C:0.8294	C:0.4284	C:0.5706	
A:0.8938	A:0.3539	A:0.4346	
T:0.2708	T:0.3917	T:0.2924	T:0.081
A:0.2351	A:0.3549	A:0.2669	
C:0.25	C:0.2296	C:0.227	C:0.0993
T:0.119	T:0.493	T:0.3579	T:0.2217
T:0.0089	T:0.5636	T:0.2188	T:0.1627
G:0.0764	G:0.3072	G:0.1759	
T:0.1994	T:0.326	T:0.3067	
T:0.1964	T:0.3241	T:0.3067	T:0.1741
A:0.8353	A:0.6074	A:0.7096	A:0.466
A:0.8353	A:0.6252	A:0.7127	A:0.4687
G:0.0804	G:0.2594	G:0.2546	G:0.443
C:0.0228	C:0.1849	C:0.1166	C:0.2862
C:0.9921	C:0.8082	C:0.726	C:0.4798
T:0.7421	T:0.3519	T:0.5164	T:0.4149
			C:0.0483
C:0.125	C:0.1113	C:0.273	
A:0.6677	A:0.663	A:0.4427	A:0.2665
T:0.4683,T:0.4683	T:0.3419,T:0.3419	T:0.5757,T:0.5757	T:0.4385,T:0.4385
A:0.3115,A:0.3115	A:0.1034,A:0.1034	A:0.2505,A:0.2505	A:0.099,A:0.099
T:0	T:0.002	T:0	T:0.0154
A:0.6458	A:0.5716	A:0.4346	A:0.4582
T:0.2659	T:0.4771	T:0.2955	T:0.1337
A:0.2738	A:0.1014	A:0.182	
G:0.001	G:0.0646	G:0.045	
C:0.1369	C:0.3867	C:0.3834	
G:0.4673	G:0.5577	G:0.4642	G:0.4855
A:0.006	A:0.5368	A:0.2802	A:0.2567
T:0.6944	T:0.2753	T:0.3558	T:0.5354
T:0.001	T:0.2863	T:0.0573	
G:0.244	G:0.4066	G:0.3466	G:0.5282
A:0.2758	A:0.1889	A:0.0726	
A:0.3671	A:0.3748	A:0.3139	A:0.6117
C:0.7321	C:0.9105	C:0.9366	C:0.8338
T:0.8502	T:0.7097	T:0.7362	
G:0.9593	G:0.8738	G:0.817	G:0.8906

T:0.9563	T:0.8738	T:0.8129	T:0.9338
T:0.0446	T:0.1054	T:0.1207	
C:0.1915	C:0.2843	C:0.364	
T:0	T:0	T:0	
A:0	A:0.0089	A:0.0031	
A:0.2252	A:0.2485	A:0.2311	
G:0.1597	G:0.1113	G:0.0307	G:0.1205
A:0.3214	A:0.2783	A:0.3916	A:0.0608
-:0.1319	-:0.1909	-:0.2147	
G:0.131	G:0.1928	G:0.2168	
G:0.1319	G:0.1909	G:0.2157	G:0.1943
T:0.1319	T:0.1928	T:0.2147	T:0.2401
T:0	T:0.0249	T:0.0051	
C:0	C:0.0398	C:0.0174	C:0.1085
G:0.0119	G:0.0984	G:0.0879	G:0.0413
A:0.0109	A:0.1014	A:0.0368	
C:0.7024	C:0.5765	C:0.4397	C:0.3057
G:0.6835	G:0.5726	G:0.4387	G:0.3831
G:0.1369	G:0.1173	G:0.1452	
A:0.0585	A:0.2763	A:0.2423	
C:0.1528	C:0.2366	C:0.2464	C:0.2968
C:0.2411	C:0.503	C:0.4714	
C:0.001	C:0.1233	C:0.0204	C:0.0288
A:0.5813	A:0.4135	A:0.7076	
A:0	A:0.005	A:0.001	A:0.0007
-:0.2986	-:0.341	-:0.3037	
C:0.7629	C:0.4304	C:0.6902	C:0.51
C:0.7629	C:0.4781	C:0.7065	C:0.7471
A:0.001	A:0.0378	A:0.0164	
A:0.2133	A:0.2356	A:0.1524	A:0.6207
C:0.1548	C:0.1998	C:0.1268	C:0.0883
T:0.12	T:0.0964	T:0.1309	
T:0.122	T:0.0954	T:0.135	T:0.032
T:0.5853	T:0.5358	T:0.6595	T:0.2128
T:0	T:0	T:0	
T:0.37	T:0.6272	T:0.6115	
C:0.0417	C:0.3221	C:0.3139	
C:0.005	C:0.1879	C:0.0982	
T:0	T:0.1272	T:0.0317	T:0.03
C:0.001	C:0.1769	C:0.0736	C:0.1176
G:0.1716	G:0.2117	G:0.1524	G:0.0838
C:0.7361	C:0.333	C:0.5245	C:0.6243
T:0.1071	T:0.164	T:0.2648	T:0.0359
A:0.1052	A:0.164	A:0.2761	A:0.037
C:0.6736	C:0.4165	C:0.6697	C:0.3172
C:0.9871	C:0.7425	C:0.8517	C:0.8577
T:0.0159	T:0.0159	T:0.1186	T:0.0688

T:0.0159 T:0 C:0.3095	T:0.0159 T:0.0249 C:0.2376	T:0.1186 T:0.0061 C:0.5041	
T:0.1567 A:0.122 A:0.4762 A:0.5724 G:0.4643 G:0.124	T:0.3877 A:0.4374 A:0.7594 A:0.329 G:0.6233 G:0.1243	T:0.3681 A:0.5133 A:0.909 A:0.4274 G:0.6421 G:0.1217	A:0.1568 A:0.84 G:0.0561
A:0.4355 A:0.0149 G:0.0169 G:0.0347 T:0.3383 T:0.881 A:0.1548 T:0.4772 A:0.1438 G:0.6538	A:0.2604 A:0.1799 G:0.2744 G:0.159 T:0.1958 T:0.7873 A:0.0845 T:0.4871 A:0.0606 G:0.3549	A:0.2065 A:0.2791 G:0.093 G:0.1012 T:0.3937 T:0.8415 A:0.092 T:0.4744 A:0.09 G:0.5552	A:0.3457 G:0.2122 T:0.3046 A:0.214 T:0.1811 A:0.1357 G:0.9095
T:0.5278 A:0.375 A:0.0109 T:0.0099	T:0.3728 A:0.2634 A:0.1143 T:0.003	T:0.4693 A:0.18 A:0.0317 T:0	 A:0.0617 T:0.0606
A:0.3601 G:0.4534 A:0.2847	A:0.3698 G:0.5477 A:0.0596	A:0.4162 G:0.5634 A:0.1861	A:0.1751 G:0.6861 A:0.0769 T:0.4164
G:0.7679	G:0.6789	G:0.5072	
C:0 T:0.1438	C:0.0537 T:0.0437	C:0.0133 T:0.135	C:0.0052 T:0.1808
A:0.1905 G:0 T:0.2361 T:0.4097 C:0.4256	A:0.0517 G:0.0109 T:0.1372 T:0.2932 C:0.3091	A:0.0511 G:0 T:0.0818 T:0.2986 C:0.3303	 G:0.0018 T:0.1328 T:0.4882 C:0.6664
T:0	T:0.0219	T:0.002	T:0.0036
G:0.8869	G:0.8091	G:0.772	G:0.6893
C:0.37	C:0.3121	C:0.2761	C:0.3924
T:0.005	T:0.2475	T:0.1166	T:0.1416
G:0	G:0.001	G:0	

G:0.3542	G:0.1412	G:0.2587	G:0.2385
C:0.6379	C:0.6421	C:0.6288	C:0.8197
A:0.254	A:0.5567	A:0.4264	A:0.4172
T:0.0565	T:0.341	T:0.3098	
G:0.3403	G:0.1759	G:0.4959	G:0.1852
G:0.0139	G:0.2734	G:0.1462	
C:0.0129	C:0.0447	C:0.0256	
C:0.7917	C:0.6431	C:0.6217	C:0.3799
C:0.1002	C:0.2992	C:0.2342	C:0.0583
A:0.7361	A:0.4821	A:0.593	
A:0.4613	A:0.3887	A:0.5368	
T:0.4613	T:0.3887	T:0.5368	T:0.5808
G:0.2044	G:0.175	G:0.3487	G:0.7084
G:0.1488	G:0.3211	G:0.2382	
C:0.6409	C:0.3181	C:0.2883	
C:0.0466	C:0.0467	C:0.0378	C:0.2044
C:0	C:0.0388	C:0.0184	C:0.0112
T:0.001	T:0.1004	T:0.0757	T:0.1076
T:0.0496	T:0.1342	T:0.1002	T:0.1634
C:0.4196	C:0.2256	C:0.2546	C:0.1221
A:0.5496	A:0.0944	A:0.2004	A:0.0629
T:0.7361	T:0.4821	T:0.6033	
A:0.1478	A:0.2634	A:0.1278	A:0.1577
C:0.2024	C:0.2952	C:0.1084	C:0.4031
T:0.376	T:0.0755	T:0.1728	
A:0	A:0.0179	A:0.0143	A:0.0059
T:0.0536	T:0.4433	T:0.3016	
C:0.0446	C:0.4423	C:0.3016	C:0.2816
A:0.9643	A:0.4304	A:0.8129	A:0.3738
T:0.3046	T:0.3698	T:0.3108	
T:0	T:0.007	T:0.001	T:0.0014
T:0.2103	T:0.2922	T:0.1237	T:0.1406
C:0.0794	C:0.3936	C:0.3793	C:0.2338
A:0.0665	A:0.0915	A:0.1391	A:0.1059
C:0.001	C:0.1332	C:0.0174	C:0.1661
T:0.8403	T:0.1909	T:0.2914	
T:0.002	T:0.1054	T:0.1104	
T:0.3353	T:0.3688	T:0.3252	T:0.3728
G:0.3313	G:0.3022	G:0.3078	G:0.0737
T:0	T:0.3529	T:0.136	
C:0	C:0.0298	C:0.0041	C:0.0064
A:0.2946	A:0.3628	A:0.3415	A:0.0994
T:0.8333	T:0.5328	T:0.6043	T:0.6568
T:0	T:0.004	T:0.0082	T:0.0008
A:0.1944	A:0.2008	A:0.2403	A:0.1194
G:0.5784	G:0.6978	G:0.817	

A:0.5 G:0.4077 A:0.1032 -:0.5079 C:0.5387	A:0.496 G:0.34 A:0.2356 -:0.1133 C:0.4245	A:0.409 G:0.4172 A:0.0777 -:0.0971 C:0.4928	A:0.8986 G:0.8497 A:0.2796 C:0.4641
A:0.002 A:0.4345 C:0 T:0.6032 T:0.255 C:0.256 G:0.4325 C:0.0933 G:0.1012 A:0.0933 -:0.001 G:0 A:0.0119 A:0.2589 C:0.1389 C:0.498 G:0 T:0.5327 C:0.8492 T:0.245 G:0.2808 A:0.3571 T:0.3562 C:0.3869 G:0.3869 G:0.001 T:0.004 G:0.6925 C:0.6915 T:0.2321 C:0.2331 T:0.1042 C:0.5099 T:0.2103 A:0.504 A:0.7599 T:0 G:0 T:0.6567	A:0.0149 A:0.2694 C:0.004 T:0.4642 T:0.4781 C:0.4791 G:0.0368 C:0.1451 G:0.1531 A:0.1451 -:0.0219 G:0.0308 A:0.3986 A:0.4821 C:0.2028 C:0.1948 G:0.001 T:0.2028 C:0.6412 T:0.4016 G:0.2594 A:0.2654 T:0.2594 C:0.3032 G:0.3032 G:0.1948 T:0.2644 G:0.5964 C:0.6064 T:0.2783 C:0.2793 T:0.0815 C:0.2177 T:0.2286 A:0.2545 A:0.3529 T:0.0477 G:0.0229 T:0.7455	A:0.002 A:0.2495 C:0 T:0.5491 T:0.4581 C:0.4591 G:0.0603 C:0.228 G:0.2352 A:0.229 -:0.0215 G:0.0123 A:0.1217 A:0.6892 C:0.0941 C:0.4703 G:0.001 T:0.2853 C:0.6483 T:0.3978 G:0.2342 A:0.4049 T:0.4049 C:0.4335 G:0.456 G:0.1575 T:0.183 G:0.6012 C:0.6094 T:0.2761 C:0.2761 T:0.0245 C:0.4816 T:0.089 A:0.2975 A:0.4417 T:0.0041 G:0.002 T:0.7761	A:0.0048 A:0.1761 C:0 T:0.2736 G:0.1847 A:0.1527 -:0.0068 G:0.008 A:0.4387 C:0.1745 C:0.0644 G:0 T:0.0803 C:0.1766 T:0.246 G:0.249 A:0.3529 T:0.1659 C:0.8496 G:0.8351 G:0.1976 T:0.0608 C:0.8886 T:0.0845 C:0.0526 T:0.0118 C:0.6369 A:0.2001 T:0.01 G:0.0046 T:0.7326

ACACAGGTGTTTT:0.69(	ACACAGGTGTTTT:0.81(	ACACAGGTGTTTT:0.8712	
C:0.0982	C:0.334	C:0.3599	C:0.645
T:0	T:0.001	T:0.001	T:0
C:0	C:0.006	C:0	C:0.0009
C:0.0288	C:0.1461	C:0.1677	C:0.2065
T:0.1071	T:0.1948	T:0.2638	T:0.1777
C:0.5804	C:0.3121	C:0.3047	
A:0	A:0.1292	A:0.0112	A:0.021
G:0.4901	G:0.4245	G:0.3681	G:0.1014
G:0.0744	G:0.1312	G:0.0982	G:0.2195
A:0.0744	A:0.1441	A:0.1012	A:0.2036
G:0.3998	G:0.1909	G:0.5112	
T:0	T:0.1461	T:0.0112	T:0.0329
G:0.6369	G:0.4771	G:0.5031	
A:0.1448	A:0.1809	A:0.274	A:0.2458
C:0.3581	C:0.2197	C:0.2188	C:0.293
C:0.3631	C:0.3241	C:0.3119	C:0.3117
A:0.2242	A:0.5666	A:0.4141	
T:0	T:0.001	T:0	T:0
T:0.2659	T:0.3231	T:0.3374	
C:0.3433	C:0.4463	C:0.4611	C:0.4898
C:0.2738	C:0.4592	C:0.4928	
G:0.2927	G:0.495	G:0.5992	
C:0.2718	C:0.3917	C:0.3896	C:0.1437
T:0.001	T:0.2793	T:0.1984	T:0.1078
G:0.0446	G:0.1213	G:0.0297	G:0.0455
G:0	G:0.1074	G:0.0092	
G:0.4494	G:0.0934	G:0.0644	G:0.203
T:0	T:0.007	T:0	
G:0.3968	G:0.5895	G:0.6493	G:0.7651
C:0.3552	C:0.3141	C:0.5276	
G:0.1806	G:0.2565	G:0.3129	
A:0.3085	A:0.2416	A:0.2096	
C:0.4534	C:0.3648	C:0.3722	C:0.7567
C:0.1627	C:0.168	C:0.1196	C:0.2336
A:0.1637	A:0.2445	A:0.226	A:0.335
T:0.6736	T:0.2535	T:0.2832	T:0.0833
A:0.245	A:0.2087	A:0.1789	
G:0.8512	G:0.8091	G:0.8252	G:0.3391
T:0.5258	T:0.6004	T:0.5624	
A:0.369	A:0.3499	A:0.3517	A:0.3073
T:0.5962	T:0.6362	T:0.6626	T:0.5546
G:0	G:0.001	G:0.001	G:0.0005
A:0.001	A:0.0636	A:0.0307	
A:0.002	A:0.0109	A:0.0194	A:0.0018
T:0	T:0.0278	T:0.0092	T:0.0054
C:0.7996	C:0.5805	C:0.7025	C:0.919

G:0.1637 G:0.003	G:0.3101 G:0.0785	G:0.2873 G:0.09	
T:0.8442 A:0.374	T:0.7058 A:0.2078	T:0.7965 A:0.2198	T:0.7156
G:0 T:0.2312	G:0.001 T:0.0457	G:0 T:0.0849	G:0.0583 T:0.1468
G:0.1756 A:0.5813 C:0.7361 T:0.4177 A:0.4177 T:0.4177 A:0.5179 T:0.5149 G:0.3869 A:0 T:0 A:0 C:0.1696	G:0.3698 A:0.7256 C:0.3718 T:0.334 A:0.333 T:0.327 A:0.6511 T:0.5815 G:0.5427 A:0.0149 T:0.004 A:0.0159 C:0.0795	G:0.3926 A:0.5695 C:0.4755 T:0.3609 A:0.3609 T:0.3589 A:0.6053 T:0.5869 G:0.4714 A:0.0061 T:0 A:0 C:0.2597	G:0.1214 A:0.5197 A:0.1798 T:0.4167 A:0.8593 T:0.8182 G:0.3647 A:0.003 T:0 A:0.0029 -:0.529
C:0.1776 A:0.4117 A:0.0665 G:0.6151 C:0.129 G:0.3343 T:0.127 C:0.4008 T:0.2639 T:0.0149 A:0 C:0.4067 A:0 C:0.0565 C:0.1161 T:0.7569	C:0.2873 A:0.3668 A:0.1322 G:0.4612 C:0.2008 G:0.1402 T:0.1581 C:0.1571 T:0.0288 T:0.165 A:0.007 C:0.3111 A:0.0099 C:0.3917 C:0.4175 T:0.6362	C:0.1789 A:0.364 A:0.1166 G:0.3262 C:0.2096 G:0.1585 T:0.1503 C:0.1299 T:0.0992 T:0.0276 A:0.001 C:0.1973 A:0 C:0.3804 C:0.3681 T:0.6554	A:0.0255 G:0.5145 C:0.2029 G:0.069 T:0.1736 T:0.03 A:0.0011 A:0.0048 C:0.5918 C:0.4041
G:0.6806 C:0.6855 T:0.2778 G:0.0258 G:0.7589 G:0.881 A:0.752 T:0	G:0.2744 C:0.2972 T:0.6382 G:0.0169 G:0.1412 G:0.4821 A:0.1441 T:0.1233	G:0.3211 C:0.365 T:0.3661 G:0.0143 G:0.2904 G:0.6309 A:0.2924 T:0.0429	G:0.1541 T:0.3938 G:0.2464 G:0.1515 G:0.8963 A:0.062 T:0.0236

G:0	G:0.0219	G:0.0112	
G:0.001	G:0	G:0	
A:0.4802	A:0.6014	A:0.6176	A:0.3797
T:0.625	T:0.5388	T:0.6155	
C:0.1597	C:0.0616	C:0.0133	C:0.2758
G:0.251	G:0.2127	G:0.1452	
T:0.1696	T:0.2008	T:0.274	
C:0.6508	C:0.3718	C:0.3732	C:0.1402
G:0.6875	G:0.1292	G:0.1329	G:0.2528
A:0.0556	A:0.1153	A:0.1176	A:0.0207
A:0.4474	A:0.4443	A:0.3405	
T:0.5992	T:0.3827	T:0.4796	T:0.7938
C:0.1984	C:0.0348	C:0.0511	C:0.0325
T:0.3621	T:0.0686	T:0.1278	
A:0.2292	A:0.1421	A:0.2577	
G:0.7103	G:0.5129	G:0.4867	G:0.7791
G:0.5228	G:0.3131	G:0.6503	G:0.7131
G:0.1627	G:0.3608	G:0.2025	G:0.4075
T:0.0337	T:0.3211	T:0.047	
C:0.6359	C:0.503	C:0.5634	C:0.623
C:0.0377	C:0.1153	C:0.2679	C:0.158
A:0.4782	A:0.2326	A:0.4397	A:0.3282
T:0.0427	T:0.1869	T:0.2515	T:0.0317
A:0.5238	A:0.2813	A:0.6104	A:0.7074
AAGT:0.6349	AAGT:0.7763	AAGT:0.7781	AAGT:0.9064
T:0.3393	T:0.3459	T:0.4366	T:0.5675
A:0.7758	A:0.503	A:0.636	A:0.764
C:0.629	C:0.5089	C:0.6043	C:0.7059
T:0.6885,T:0.6885	T:0.6869,T:0.6869	T:0.5123,T:0.5123	
T:0.0367	T:0.3201	T:0.0562	T:0.0704
C:0	C:0.0099	C:0	C:0.0016
			T:0.8023
T:0.496	T:0.337	T:0.2321	T:0.1138
T:0.4038	T:0.8161	T:0.5818	T:0.8429
C:0.1875	C:0.2525	C:0.2342	C:0.6158
T:0.2431	T:0.4085	T:0.364	T:0.7275

EA_MAF	CLIN_SIG	SOMATIC	PUBMED
C:0.0365			
G:0.6569		0,1	
G:0.6216 G:0.6969			
			15459974
T:0.2695		0,0,1	
GAGCGGGCGA:0.12 A:0.2188			
T:0.0289		0,1	
G:0.3325			
			17357082
A:0.6387 A:0.4222			
T:0.2121		0,1	
A:0.2642 G:0.4873		0,1	16385451
T:0.5827 G:0.0156 G:0.1509			
C:0.1944 C:0.6126 A:0.0517		0,1,1,1	16385451
C:0.4233 T:0.4664		0,1	)8,21671168,21846682,19 18782849
C:0.1119 T:0.8297 T:0.3099		0,1,1	
T:0.0217,T:0.0217	not_provided,benign		22412862
T:0.2574	likely_benign	0,1	23320549 24419040
T:0.4004	benign		
T:0.7022			25887478

A:0.3323 A:0.17			
T:0.0869			
G:0.7585		0,1	
G:0.2784 -:0.1939 A:0.1349			24849541
		0,1	
C:0.8133 G:0.0828 A:0.1248 T:0.061 T:0.0377		0,1,1	
C:0.0059			
		0,1	
T:0.0317		0,1	18511455
G:0.0695 G:0.3177 C:0.1131 T:0.0784			
C:0.3036 C:0.1671		0,1,1,1,1,1,1,1,1 0,1,1,1	18499081,23103231
A:0.0779 T:0.5469			
G:0.2367			
A:0.1476 A:0.0771	benign		
T:0.2767			
-:0.0499			

T:0.5403 A:0.3617 G:0.3652			
A:0.5982			
G:0.1535 C:0.0464		0,1	
A:0.0324 T:0.1171 G:0.3253 G:0.0793	benign likely_benign		
A:0.2249			
A:0.3 G:0.4858 T:0.2577 T:0.9099 G:0.3805 C:0.3068		0,1	
A:0.755		0,0,1	17827388 19733838
A:0.3376 G:0.1419	benign benign	0,1	14740319,23559858 25260659
T:0.1784			
G:0.08	benign		18603647,18614612
T:0.0064	not_provided not_provided uncertain_significance,not_provided		12466288,17916242 21356067 19276285,19644020,17428325,213560
T:0.1522 A:0.3483 G:0.0333 C:0.0849		0,1,1,1,1	
A:0.1271		0,1	
T:0.682 G:0.302		0,1,1	

C:0.3199		0,1,1	
C:0.0699			
-:0.1544			
A:0.0918			17878953
C:0.3059			
C:0.4868		0,1,1,1,1	
C:0.232			
	pathogenic	0,0,1	18840896,19778426
G:0.089		0,1,1	
C:0.1142			
C:0.1707			
T:0.6173			16355111,18631248,214621
G:0.0907			
C:0.1949			18648537
		0,1	
A:0.0189			
T:0.0045			
C:0.1932		0,1	
G:0.1002			
A:0.0047			
T:0.1688			
T:0.136		0,1,1,1	
T:0.0037			
C:0.2924			
A:0.3329			
G:0.1983			
T:0.1248,T:0.1248	not_provided		17556197,24917393
T:0.0172			
-:0.4809			
A:0.2629		0,1	

A:0.3025			
G:0.0034			
G:0.0024			
A:0.155			
A:0.2224			
A:0.1453			
			23150742
A:0.1455			18172114
G:0.3555		0,1	
-:0.3166		0,0,1	
G:0.6117			
C:0.1349		0,1	37,24140460,20061190,20
			19680542,16621965,185986
-:0.044		0,1	
C:0.341			
T:0.4209			
C:0.6407			
T:0			
A:0.03			
G:0.1899		0,1	
A:0.0119			
A:0.1329			
G:0.3171			
A:0.1132		0,1	
C:0.1954		0,1	
-:0.2671			
T:0.0886			
T:0.6724			
T:0.5513			
	pathogenic,risk_factor	0,0,1	93,20689796,18081690,2
A:0.2164		0,0,1	728845,18992954,164366
C:0.0894			
		0,1	

C:0.318 T:0.1266		0,1	
			20736995
A:0.0814	benign		
T:0.5607			20211854,22461888,210722
A:0.3128			
			22140480
C:0.8793			
C:0.0414			
G:0.2359	benign		
T:0.1029			
A:0.9041			21750702
A:0.2926			
T:0.2709		0,0,1	567136,19016476,181793
C:0.4202	benign		
G:0.1733		0,1	
T:0.0102		0,1	
G:0.4255			
G:0.2389			
A:0.4849			
C:0.149			
A:0.0208			
A:0.3923		0,1	
C:0.2069			
C:0.5173	benign		12958705
G:0.3949		0,0,1	168589,21304959,168169
G:0.1749	benign		
G:0.0733		0,1	
G:0.007			
T:0.1117		0,1,1	
T:0.0101			
A:0.6012			

G:0.5134 A:0.4624	0,1	19675668
C:0.2893 T:0.283 A:0.0395	0,1	
G:0.0113		
T:0.7042 T:0.7045 A:0.2187	0,1 0,1,1	
T:0.2402 A:0.5022	0,1	
A:0.2534 C:0.321 G:0.6802	0,1	23420841
C:0.1627		
G:0.4265 A:0.1484		20068590
G:0.3065	0,1	25162786,22962485
T:0.1538 G:0.2801	0,1	24086769
A:0.0002 T:0.5429		
T:0.3231		
A:0.2556		
G:0.3501		18347602
T:0.0066	0,1	21559497

T:0.2162 G:0.0969			16385451
G:0.492			
G:0.358			
G:0.0534			
C:0.3358 C:0.0779 A:0.0247			
G:0.3624			
A:0.0167 C:0.2266 C:0.66		0,1	20031578
T:0.1937 A:0.0447 T:0.3563 C:0.3573 A:0.3737 A:0.2067 -:0.0151 A:0.7359 T:0.1435 T:0.0378	benign	0,1,1	
C:0.0003 C:0.0185 A:0.2313 C:0.2736 C:0.1984 A:0.1014		0,1	22155192
A:0.0755 G:0.4338 A:0.1398			21397065
T:0.4571		24886237,24633486,19593725,24123836,24	
-:0.1138 A:0.2872			

T:0.2337		0,1,1	
G:0.6197			
T:0.6748	likely_benign	0,1,1	
T:0.2581			
A:0.4344		0,1	
T:0.3686		0,1	
G:0.3806		0,1	
T:0.4199			17672902
G:0.3599			
C:0.6195		0,1	
C:0.0399			
G:0.0483			
T:0.0492		0,1	
			19299629,24447348
C:0.021			
A:0.0771			
	benign	0,0,1	35,17498780,18992263,17
T:0.1016		0,1	
A:0.143			
			21927923
A:0.446			
A:0.0857	benign		
A:0.5587	benign	0,1,1	
T:0.1525		0,1	
T:0.3457			
T:0.0298			
A:0.3748		0,0,1	515603,19846925,203371
C:0.128			
C:0.1736	benign	0,0,1,1	03,19552680,17209060,24
T:0.1488			17209060
	pathogenic		
A:0.2661			
G:0.1981			20565855,20427696,16893529,225633
G:0.1695			
A:0.271		0,1	18454203
C:0.7387			
C:0.1518			
A:0.0139			
A:0.0949			

G:0.2451 A:0.8503			
G:0.314 T:0.0285		0,1	
G:0.6713			
C:0.6717,C:0.6717			
C:0.4674 C:0.1844			
			20105321
A:0.1905 A:0.1796 A:0.2014		0,1	
			20679621,24511462,239891
T:0.0007 C:0.1073 A:0.292 A:0.2558 A:0.3119			
A:0.4093		0,1	
A:0.6895	pathogenic 23650146,17263791,19190816,18848323,18772067,18974842,200315	0,0,1	69,20691689,21412156,24
T:0.3427			17903299
T:0.0097			
A:0.0568 A:0.1977 A:0.0163	benign		
			19453265,19727905,241761
T:0.0565		0,0,1	15858076,23350966
-:0.3627		0,1	
T:0.7351 G:0.77		0,1	
C:0.2233		0,1	19276632
C:0.7656	benign	15922487,17119116,17286537,18842806,24 0,1,1,1,1	

T:0.3771 A:0.3261 T:0.3624 T:0.3325		0,1,1		
T:0.0096 A:0.356 C:0.4122 C:0.5239				17357072
T:0.3221 T:0.4092 A:0.5178	benign			20886637
T:0.0278 G:0.3833 T:0.242 G:0.3819 T:0.4197 C:0.0221 A:0.022		0,1 0,1		21819567
T:0.1752 A:0.1752 T:0.1741 G:0.1477 G:0.2788		0,1 0,1 0,1,1		
C:0.0717 G:0.2646 G:0.0028 T:0.3166 G:0.0517 A:0.0432 A:0.051 A:0.0068 A:0.4697 A:0.133 A:0.3533		0,1 0,1		16385451 19430760
A:0.4828 C:0.9503 G:0.1274 A:0.0992			23201419,24671236,25201284,18	
T:0.2625 T:0.2015 A:0.0992 A:0.3152		0,1 0,1,1 0,1,1,1		19640273

C:0.127 A:0.0928		0,1	18787502,18035074,18403734,25093390,17
A:0.5094 C:0.4393		0,1 0,1	
A:0.2477 A:0.1457 G:0.0322 C:0.3261		0,1,1	
A:0.0154			
A:0.6456			18484081 22669415
T:0.2787		0,1,1,1	18329248,19156168
T:0.0335			
T:0.3355			17601350,21320344,18559526,18709160,24
T:0.1897			
A:0.6153 C:0.331			
C:0.7166			
A:0.0587 T:0.5927 A:0.0407 A:0.0508 T:0.0519 C:0.4708		0,1,1,1 0,1	
C:0.4183 T:0.1267			
T:0.0031 C:0.0179 A:0.4142 T:0.6188	not_provided,likely_benign,pathogeni benign	0,0,1,1	566314,24467728,194014

A:0.4051		0,1	
A:0.1102 T:0.469		0,1,1,1	
T:0.2419 A:0.7018 T:0.6555 A:0.2386		0,1	19043567,19664584 18439552,20031592,219317
T:0.0339 C:0.121 A:0.0986	benign		19843503
A:0.2824 C:0.5378	likely_benign	0,1	17135278,18783506
T:0.2745		0,1,1	
C:0.778 G:0.317		0,0,1,1	22137500 26,18588853,21090563,20
A:0.2174			
C:0.4475 G:0.3472		0,1	
A:0.1497 G:0.1588 C:0.0668			
G:0.4551		0,1	
T:0.0065			
T:0.0239			
A:0.221			19434426,17348446,20226046,21
T:0.2416 G:0.2436 A:0.0549	benign	22666415,24824313,22395465,16750516,24895547,21 0,0,1,1	51,25622255,21082232,25 18411068,16473310
A:0.2957			
C:0.013			

C:0.6587			
C:0.125			18348195
A:0.2083			
			23871474,24174267,21926974,244616
T:0.233			25505091
G:0.8711			
C:0.008			
A:0.0156			
A:0.1512			
A:0.5249			
G:0.7113			
A:0.1194			
G:0.2597			25155265
T:0.2544		0,1	
-:0.3973			
T:0.2024			
A:0.3309			
A:0.4209		0,1	
T:0.3624		0,1	
C:0.3449			16175505
T:0.1647			
C:0.0807			
A:0.0324			
T:0.0016			
A:0.118	benign	0,1,1,1	24943594,20442750
G:0.4334			
G:0.3402		0,1	
T:0.3398		0,1	
A:0.0055		0,1	
G:0.086		0,1,1	
A:0.0005			
A:0.03			
A:0.1286			
T:0.0963			
C:0.3472			

G:0.1762		17931948
C:0.0148 A:0.6168 G:0.7303 T:0.6279	0,1	
C:0.2692		
C:0.7307 C:0.6618 G:0.7114 T:0.0298	0,1	
T:0.7115 A:0.5694		
A:0.2808 G:0.3644	0,1,1,1	
A:0.7221 T:0.2435		
A:0.2502		
C:0.4261		
C:0.0954		
A:0.5935 T:0.0699 A:0.0006		
A:0.3113		
A:0.3457 G:0.0347		20169177
G:0.0478 A:0.0274 G:0.3114	0,1	

T:0.3303			
	benign		16385451
T:0.4786			16385451
C:0.0356			
C:0.7187			
C:0.4156			
C:0.1881			
T:0.7001		0,1	
		0,1	
G:0.4559			
A:0.3388			
C:0.467		0,1	
T:0.8867		0,1	
C:0.015			
C:0.2672		0,1,1	
G:0.2501			
T:0.2681		0,1,1	16642431
G:0.0286			
A:0.4352			
T:0.1939		0,1,1	
A:0.0004,A:0.0004	benign		
C:0.622			
C:0.0003		0,1	
C:0.0019			
G:0.4594			
T:0.0595			
T:0.2456			
A:0.1234			
A:0.2506			
T:0.1694			
T:0.127		0,0,1,1,1,1	18,21787115,19536092,2(
A:0.3297			
G:0.3565			

C:0.0918 C:0.2381 T:0.3556			
T:0.2657 A:0.3531			16642439
G:0.0094			
A:0.4295			23946598
A:0.726			23148531
G:0.3305 G:0.7902 C:0.2852 G:0.3472		0,1,1,1 0,1,1,1 0,1,1,1	
A:0.0262 T:0.0685 T:0.3027			16400609
T:0.2388 G:0.4134 T:0.6317 G:0.4195 A:0.61	 benign benign	0,1 0,1	24996771 493349,18842806,219609 19493349
GGGAGA:0.2376 C:0.3273		0,1,1 0,1	
C:0.5171		0,1	
G:0.576 A:0.6147 -:0.7248 T:0.262 C:0.2881 T:0.1513	 benign benign benign	0,1,1 0,1 0,1,1 0,1	 23233322 20226094 20592870
C:0.3634 A:0.7626			
G:0.5355 T:0.0087	 benign		21829377

T:0.1059		0,1	
T:0.0529 G:0.509 T:0.4463 G:0.331 T:0.3296 C:0.3258 A:0.326 T:0.0741 T:0.0087		0,1,1 0,1 0,0,1,1	12466288 069270,24633158,181930
A:0.0176 A:0.391			
T:0.1343	likely_benign		17601350,20819849
C:0.8154			
T:0.1704 C:0.401 G:0.3001 C:0.0024 T:0.0165	likely_benign	0,1,1	
G:0.6663 G:0.0785 G:0.3611		0,1	
G:0.4653			
T:0.7766			
G:0.0081 G:0.0081			
T:0.1528 A:0.0358 A:0.0258 G:0.3043		0,1	
A:0.1049 G:0.0291			
	pathogenic,risk_factor	33443,23560644,24806096,19168583,20624112,2	20602773,15707951,162023
G:0.0627			16729972
			16729972
G:0.2015			24861377,19752398
G:0.064 G:0.2107		0,1,1	18340359,19732772,23565190,22

C:0.0498	benign		18001468
T:0.0364			
A:0.1863		0,1	
T:0.0383			
A:0.2287 G:0.363		0,1	
T:0.1509		0,1	
A:0.3941 C:0.6975			
C:0.1654			
A:0.0239 A:0.193		0,1,1	
T:0.5372 A:0.0616 T:0.061 T:0.058 A:0.2802 G:0.3073 C:0.7885 A:0.0247 A:0.1637		1,0 0,1 0,1 0,1 0,1	
G:0.1478 G:0.1741		0,1	
G:0.1012 AGC:0.2795 G:0.1507 A:0.1919		0,1	
T:0.0682 A:0.3151 A:0.0133			
G:0.2118 A:0.3748		0,1 0,1	 16038259,24223962

A:0.1429 T:0.1271 G:0.018		0,1,1,1	
G:0.0685 G:0.2398		0,1,1 0,1	19714462
A:0.3733 A:0.0112 T:0.4406		0,0,1,1 0,1	647835,23918616,162563
A:0.2973 A:0.1712	benign	0,1,1,1 0,1	
C:0.4329 C:0.4367		0,1 0,1	14574644
G:0.3359 G:0.3007			22504420,19148276
G:0.2854		0,1,1	
A:0.1133 C:0.1264 A:0.2398 G:0.2479		0,1 0,1	21247474
T:0.2057 G:0.4567 T:0.3897		0,1,1	23840689
A:0.2389 G:0.2955		0,1,1	
G:0.2492 G:0.0531 G:0.3302			
A:0.3131 G:0.4137 A:0.1686 C:0.4725		0,1	
T:0.1272			16828203
A:0.1071 G:0.4441			

T:0.2559			
T:0.2857	22865593,25139097,22001756,25992311,22359309,25687184,207298		
G:0.6267			
C:0.4294	likely_benign	0,1,1,1,1,1,1	
G:0.3868	likely_benign benign	0,1,1,1,1,1,1	
A:0.4082		0,1,1,1,1,1,1	
G:0.419		0,1,1,1,1,1,1	19052777
G:0.4404		0,1,1,1,1,1,1	
T:0.276 C:0.5238			
T:0.2664			
T:0.2865		0,1,1,1	19390624
C:0.3327			19390624
A:0.2118	likely_benign	0,1,1	
G:0.115			
			21474826
		0,1,1,1,1	
	likely_benign	377714,23334806,17187763,21178094,25043640,2	
	benign,likely_benign	0,0,1	347532,22410809,251972
C:0.607			
		0,1	
G:0.3776			23324528
C:0.2621			
T:0.5932			23127126
A:0.3756			
C:0.576			
T:0.346			
C:0.3518			
G:0.2255			
G:0.3915			
G:0.4582			19014520
A:0.2838			
A:0.0296			

A:0.1099			
C:0.0541 G:0.2124			
G:0.4454			
G:0.1052			
C:0.5576			
A:0.3384		0,1	
C:0.0056 GC:0.005			
C:0.4835 G:0.2551 G:0.1687 A:0.2748 G:0.9145		0,1	
A:0.3588			
G:0.3587 G:0.1945 A:0.3652	benign	0,1	25541970,21348951
A:0.7913 C:0.2937 -:0.7161 T:0.0021 C:0.0001 A:0.5145	benign		
G:0.4012 -:0.4397		0,1	21565829,22428065
GGGGATTA:0.1858 G:0.163 C:0.5579	benign	0,1	
C:0.5715 T:0.3393 C:0.5766		0,1	
T:0.4282		0,1,1	
T:0.0798		1	23592335

-:0.3277			
A:0.4972 T:0.5299		0,0,1	)0,18971541,25481646,22
G:0.4001 T:0.0067			
T:0.3698			
C:0.218			
T:0.4958		0,1	
T:0.7657		0,1	18389087
T:0.3228		0,1	
A:0.5865			
A:0.6031		0,1	
G:0.2501		0,1	
C:0.1878			16385451
C:0.8017			24934404,24942080
T:0.361 C:0.0859		0,1,1	
A:0.649			20145122,20558521,22265947,18
T:0.3544,T:0.3544	not_provided,benign	0,0,1	13,19513315,17033962,19
A:0.1262,A:0.1262	not_provided		16917943
T:0.0016	benign		
A:0.5597 T:0.4598	benign		24978818
G:0.5424 A:0.5483			24587951,21072201
T:0.262		0,1	141583,21812969,235988
G:0.4157		0,1,1	25374748,25374745
A:0.3666 C:0.8928			
G:0.8714	benign	7,25392755,22348792,22058430,22007172,224738	

T:0.865			
G:0.1177 A:0.3016	benign	0,1	25358694)4,20015893,23453696,21
G:0.2197 T:0.2207		0,1	16385451
C:0.0481 G:0.1058		0,1	
C:0.5748 G:0.5709			
C:0.2348			24528284,18854866
C:0.1197		0,1	
A:0.0048			
C:0.4417 C:0.5015			
A:0.2212 C:0.2235		0,1	
T:0.1049 T:0.5747		0,1	21204206,17476318
T:0.1366			
C:0.2007		0,1	
G:0.2103 C:0.3704 T:0.1676 A:0.1821	benign	0,1	23978482,18710470
C:0.366	not_provided,benign	0,1,1	
C:0.7327			
T:0.0166			

A:0.4406 A:0.7814			22544659
G:0.0987			
A:0.2484 G:0.2523			19491853
T:0.2129	19141529,19199283,19541292,20031642,20395645,23149035,15993855,17123473,166167		
A:0.0628 T:0.4884			16604304,16841561
A:0.0672 G:0.4458		0,1 0,1	
A:0.2515		0,1,1	
T:0.0023			
A:0.3963 G:0.5633 A:0.0569 T:0.1183			
C:0.0344 T:0.0514		0,1 0,1,1	19185281
G:0.0086 T:0.1438 T:0.301 C:0.3301	ıcertain_significance,benign		
T:0.0243			
G:0.7817			
C:0.2963			
T:0.2667		0,1	

G:0.1603 C:0.634 A:0.566			
G:0.1771			
C:0.589			18778477
C:0.3155	risk_factor	0,1 0,0,1	19,16380915,18657476,18
T:0.3517 G:0.1851			
C:0.072 C:0.0452 T:0.1057 T:0.1511 C:0.2594 A:0.1057	benign	0,1 0,1,1,1	
A:0.2477 C:0.3609		0,1	
A:0.0229			
C:0.4559 A:0.403			
T:0.0064 T:0.2672 C:0.4008	likely_benign		
A:0.105 C:0.1855		0,1	
T:0.3542		0,1	
G:0.2976			19285750,21116649,22363464,178489
C:0.0341 A:0.3703 T:0.4964 T:0.0071 A:0.187		0,1 0,1 0,1	15110318,18980857 20927379

A:0.6819 G:0.3279	0,1	
A:0.2512 C:0.4172		19880490
A:0.0181 A:0.24 C:0.0029	0,1	424379,19543401,235204
T:0.4702	0,1,1	
G:0.0449	0,1	
A:0.14 -:0.0265 G:0.0381		
A:0.5084 C:0.1986 C:0.2794 G:0.0027 T:0.1878 C:0.6415		24798189
T:0.4059	0,1	
G:0.2899	0,1,1,1	
A:0.2494 T:0.2455	0,1	
C:0.3029	0,0,1	646866,21212151,248205
G:0.3036	0,0,1	77,15987456,16741161,20
G:0.1901 T:0.2812		
C:0.606 T:0.0811	0,1	
C:0.2606 T:0.0793 C:0.3117 A:0.2219		
T:0.0405 G:0.0165 T:0.7434	0,1,1	

C:0.3381 T:0.0012 C:0.0087 C:0.2059 T:0.2027		0,1	
A:0.1194 G:0.3976			
G:0.1378 A:0.132	not_provided,benign not_provided	0,1	042,93284,10363127,206 16981987,10533067
T:0.1707		0,1	
A:0.1818 C:0.2037 C:0.317		0,1	20096481
T:0.0013			
C:0.3769			
		0,1,1	
C:0.3956 T:0.2966 G:0.1373		0,1	16400609
G:0.0996			
G:0.5824			
C:0.3528		0,1	
C:0.1951 A:0.2481 T:0.2184			
G:0.8242			20011102
A:0.3517 T:0.6362		0,1,1	
G:0.0009			
A:0.0094	not_provided		
T:0.0303 C:0.603	benign	0,1	18273898

T:0.6707			
G:0.0008 T:0.0403		0,1	
G:0.3776 A:0.7423		0,1	16385451
A:0.3356 T:0.3259		0,1	
A:0.6544 T:0.5819		0,1	
G:0.5523 A:0.015			
T:0.0007 A:0.0123			
-:0.4374		0,1	
A:0.1079 G:0.4559	benign	0,1,1	
C:0.2267 G:0.1527 T:0.1735		0,1	16385451
T:0.0535			
A:0.0073			
A:0.015 C:0.3856		0,1	
C:0.4286		0,1	76,22579466,20061190,23 18936436,19029194,216229
G:0.2397		0,1	
T:0.6369 G:0.0141 G:0.1384 G:0.4974 A:0.115 T:0.1313		0,1	

A:0.5801		0,1	20158892
C:0.0655			
C:0.3693			
G:0.1058 A:0.1003			
T:0.5039		0,1,1	
C:0.028		0,1	18682748
G:0.49			
G:0.3045		0,1	
G:0.395			
C:0.52			
C:0.1154			
A:0.2195	likely_benign	0,1	
T:0.1621			
A:0.2707		0,1	
AAGT:0.7549			
T:0.3511		0,1,1	
A:0.4852		0,1,1	
C:0.5216		0,1	
T:0.4238			21810217
C:0.0119			
T:0.3563		0,1	
T:0.3201		0,1	
T:0.8205			
C:0.2531 T:0.3976			

MOTIF_NAME	MOTIF_POS	HIGH_INF_POS	MOTIF_SCORE_CHANGE

9716087,21935354,21688035,20594303,19327134

)67,18694767

36

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;42

0843825,23797962,25881145,24855199,23562679,23687431,23922956,24652518,18461138,171945
;43

201

891,24980155,25477898,24172113,24407958,18213623,20587580,21714860,19157983,25252306,18(

940,19605537,18983999,19693267,21423693,17994190,19699472,19900610,16848906,21462137,19

1069190,16466695

7363767,17548691,17686149,22928041,17885617,19017876,22655231,18191955,19111454,2569481

48,22573488,18559551,22146767

4086941

32,22591901

97

4340057,22271411,21504591,22313031,22696188,23524567,24239227,24248544,24381107,250128
577,25156046,16525568,17241179,21757653

11

4447348,22018726

7498578,18848323

4915237,22357570

l44,21138591,24659834,18795173,25071582,22074419,19165391,19879291,23996192,18194558,20(

'94

)112391,22123319,17540610

L708937
L078522,20639793,21422097
5927028,18411068

ɔ34,23967141

)206583,16857995,23720673,17482892,23852586,18708406,22655231,19124499,17569599,194388(

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)44,24531328,19802338,23804528,18852197,23594525,24966605,22617559,25018854,23394097

)94
4940036,24068186,24323870,17658478,18634977,25430627,23681449,19505917,25685286,227295

2216302

89,18582870

352,22740136,24884822,22960999,22323360

4059590,19466586,22535570,25784779,22328972,19587357,20929593,25516658,17141766,200431
274,18573313,18992148,18707223,22987045,22820754,16253648,18426866,18340007,23907334,25

2787471,23326532,22787467

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318

370,20212137,20033988,23102778,23129781,15302875,23006801

l203404

’19,17964050,15995945,15361494,17629953,19020798,19032574

3466472,18466513,18560894,19956095,19122825,16159953,16735488,17229939,17374705

)14,23300679

464

515,25532599,20805886,20686496,25937777,24603722
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3553206,20719408,19061777
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IMPACT	PICK	VARIANT_CLASS	TSL
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LOW	1	SNV	
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HGVS_OFFSET	PHENO	MINIMISED	ExAC_AF
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		1	0.03148
		1	
	0,1	1	0.5896
		1	
		1	
		1	0.5372
		1	0.6565
		1	0.00002832
		1	
	1,1,1	1	0.2943
		1	0.04186
		1	0.1952
		1	0.8436
	0,1	1	0.02675
		1	
		1	
		1	
		1	
		1	0.00001017
		1	0.04764
		1	0.6231
		1	0.3279
		1	
		1	
		1	
	0,1	1	0.1609
		1	
	0,1	1	0.2063
		1	0.4918
		1	0.0003527
		1	0.6522
		1	0.02838
		1	0.1771
4		1	0.04215
		1	
	0,1,1,1	1	0.2383
	1	1	0.5905
		1	0.03403
6		1	
		1	0.3969
	0,1	1	0.4859
		1	
		1	
	0,1,1	1	0.2049
		1	
		1	0.2525
	1,1,0	1	0.01398
	1,1	1	0.2044
		1	
	1	1	0.3711
		1	
		1	0.7586
		1	

	1	0.2411
	1	0.1891
	1	
	1	
	1	0.07678
	1	
	1	0.7742
0,1	1	0.1338
	1	0.2575
	1	0.2067
	1	0.1996
	1	
0,1	1	0.2086
	1	0.8381
0,1,1	1	0.1381
	1	0.08986
	1	0.04656
	1	
	1	
	1	
	1	
	1	
	1	0.00001883
	1	
	1	
	1	
0,1	1	0.2707
	1	0.2765
	1	
0,1	1	0.03878
	1	
	1	0.05899
	1	0.2946
	1	0.1807
	1	0.04946
	1	
	1	
	1	
0,1,1,1,1,1,1,1,1	1	0.3429
0,1,1,1	1	0.2193
	1	
	1	0.05041
	1	
	1	0.6179
	1	0.6092
	1	
	1	0.4945
	1	0.1662
	1	
	1	0.1418
1,1,1	1	0.05155
	1	
	1	0.2377
	1	
	1	0.04516

	1	
	1	
	1	0.4394
	1	0.3724
	1	
	1	
	1	0.6527
	1	
	1	0.1682
	1	0.03362
0,1	1	
1	1	0.02535
1	1	0.1074
	1	0.3557
	1	0.08105
	1	
	1	0.2591
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	1	
	1	0.2597
	1	0.4041
	1	0.27
	1	0.9352
	1	0.4145
0,1	1	0.2816
	1	0.3535
0,1,1	1	0.7634
	1	
	1	
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	1	0.1688
	1	
	1	
	1	
1	1	0.04792
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	1	0.004793
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1	1	
	1	0.1072
0,1,1,1,1	1	0.2671
	1	0.01512
	1	0.05177
	1	
1	1	
0,1	1	0.1092
	1	
	1	
0,1,1	1	0.6755
	1	0.279

		1	
	0,1,1	1	0.2485
	1	1	
		1	
		1	0.04318
		1	0.4009
1		1	0.1578
6		1	
		1	
	1	1	0.3923
	0,1,1,1,1	1	0.5446
		1	0.2958
	1,0,1	1	0.2026
	0,1,1	1	0.1701
		1	
		1	
		1	0.1606
		1	0.2612
		1	
		1	
		1	0.6596
		1	
		1	0.074
		1	0.2135
	0,1	1	0.2792
		1	
		1	0.263
		1	0.01044
		1	0.002674
		1	
	0,1	1	0.2681
		1	
		1	
		1	0.09573
		1	
		1	
		1	
		1	
		1	0.004711
		1	
		1	0.1852
	0,1,1,1	1	0.09765
		1	
		1	
		1	0.008002
		1	0.2481
		1	0.3299
		1	
		1	
		1	
		1	
	1,0	1	0.08206
		1	0.01244
3		1	0.4123
	0,1	1	0.3146

		1	0.2931
		1	
		1	0.001666
		1	
		1	0.00146
		1	
		1	
		1	0.1224
		1	0.1749
		1	
		1	0.1485
		1	
		1	0.0902
	0,1	1	0.3648
	0,0,1	1	0.2618
		1	0.5861
		1	
	0,1	1	0.2132
		1	
	0,1	1	0.01214
		1	
		1	
		1	0.3821
		1	0.7101
		1	0.00009422
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		1	0.0179
		1	
	0,1	1	0.1871
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		1	0.02002
		1	0.06587
	1	1	0.3054
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		1	
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		1	
	0,1	1	0.1664
		1	0.2565
		1	0.06684
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		1	0.7031
		1	0.6318
		1	
		1	
		1	
	1,1,1	1	0.6748
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		1	0.165
	0,1	1	0.5317
		1	

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	1	
1	1	0.1007
	1	0.4772
	1	0.29
	1	
	1	0.8317
	1	0.03131
	1	
	1	
	1	
	1	0.1529
1	1	0.2809
	1	
	1	0.1392
	1	0.8905
	1	
	1	
	1	0.373
	1	
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1	1	0.3698
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	1	
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	1	0.4818
	1	0.219
	1	
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	1	
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	1	0.3092
	1	
1	1	0.5382
	1	
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1	1	0.167
	1	
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	1	
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	1	0.007711
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	1	
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	1	0.007222
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	1	0.392
	1	0.5729
	1	

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	1	0.1521
	1	0.3814
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		1	
		1	
		1	0.0006501
		1	0.003633
		1	0.2077
	1,1	1	0.125
		1	0.3026
		1	
		1	
	0,1	1	0.2086
		1	0.2128
		1	
	0,1	1	0.04482
		1	0.083
		1	
		1	0.5252
		1	0.524
		1	
	1	1	
		1	
		1	
		1	
		1	
		1	
	0,1	1	0.08316
		1	
		1	0.002731
5		1	0.3184
		1	0.3669
		1	
		1	0.02612
		1	0.2453
	0,1	1	0.1826
		1	
		1	0.1228
		1	0.5826
	0,1	1	
		1	
		1	
		1	0.2683
		1	
		1	0.08478
		1	0.00009245
	0,1	1	0.1449
		1	
		1	0.1683
	1,1	1	0.4561
		1	0.1598
		1	0.1573
	1,1,1	1	0.3943
		1	
		1	0.7934
		1	
		1	0.03341

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		1	
		1	
1		1	
		1	
		1	0.3942
		1	0.7786
		1	
		1	
		1	0.08884
		1	
		1	0.2482
		1	
		1	0.1935
		1	
		1	0.2603
		1	
		1	0.1077
		1	0.4799
	0,1	1	0.08481
	0,1	1	0.5662
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		1	
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		1	0.008436
		1	
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		1	0.08542
		1	0.1663
		1	
		1	
		1	
	0,1	1	0.02811
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		1	
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		1	0.1406
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		1	
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		1	0.3137
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		1	
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		1	
		1	0.626
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		1	
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		1	0.4301
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		1	0.2828
		1	
	1,1	1	0.08281
		1	0.03084
		1	0.08721
		1	0.1475
	0,1,1,1	1	0.2795
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		1	
	0,1	1	0.2092
		1	
		1	
		1	0.02139
		1	0.2923
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		1	0.5139
1		1	
		1	0.007446
	1	1	0.2225
		1	0.333
		1	
		1	0.1042
	0,1	1	0.1294
		1	
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		1	
		1	0.3059
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		1	
		1	0.0236
	0,1	1	0.3417
	0,1	1	0.5778
	0,1	1	0.004557
		1	0.1913
		1	

	0,1	1	0.6886
		1	0.3925
		1	0.1922
		1	
	1	1	0.4256
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		1	
		1	
		1	0.01119
	0,1	1	0.2711
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		1	0.001686
		1	
		1	
	0,1,1	1	0.4173
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		1	
	0,1	1	0.09745
		1	
		1	
		1	0.1437
1		1	0.01739
		1	
		1	0.02399
		1	
		1	0.5064
		1	0.1935
		1	0.3416
3		1	
		1	0.002156
		1	0.2302
		1	0.6109
	0,1	1	0.3811
	0,1,1,1	1	0.2857
		1	0.2808
	0,1	1	0.2737
	1,0,1	1	0.3768
	1,0,1	1	0.3786
		1	0.164
		1	0.2199
		1	
		1	
	0,1	1	0.6331
		1	
		1	
		1	
		1	0.2438
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		1	0.02808
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		1	0.7207

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	1	0.0004854
	1	0.004879
	1	0.1785
	1	
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	1	0.07494
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	1	
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	1	
0,1	1	0.111
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	1	0.2252
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	1	
	1	0.001776
	1	0.2689
	1	0.2482
	1	
0,1,1	1	0.5111
	1	0.3933
0,1	1	0.244
	1	0.06265
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	1	
	1	
	1	0.5798
	1	
	1	
	1	0.00008032
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	1	
0,1	1	0.4033
	1	0.00005649
	1	0.1751
	1	0.2542
	1	0.2713
	1	
	1	0.7866
	1	
0,1,1	1	0.3653
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	1	
	1	0.0008345
	1	
1	1	0.01014
	1	
1	1	0.02211
0,1	1	0.6781

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	1	
	1	
	1	
	1	
	1	0.7352
	1	
	1	
	1	
	1	
	1	
	1	0.0058
0,1	1	0.08962
	1	
	1	0.3322
0,1	1	0.6581
	1	
	1	
0,1	1	0.344
	1	0.3546
0,1	1	0.6641
	1	0.6013
	1	0.5113
	1	0.01025
	1	0.001487
	1	
	1	
0,1	1	0.04712
	1	
	1	
1,1,1	1	0.1087
	1	0.4687
0,1	1	0.2118
	1	0.1689
	1	0.1642
	1	
	1	0.07038
	1	
	1	0.004317
	1	
	1	0.00731
0,1	1	0.3746
0,1	1	0.329
	1	
	1	
	1	0.3085
0,1	1	0.3415
0,1	1	0.5435
	1	0.04043
	1	0.2149
	1	0.5765
	1	0.2154
	1	0.08482
	1	

	1	0.02324
	1	0.000009415
0,1	1	0.5676
	1	
	1	0.08619
1	1	0.1421
	1	
	1	
	1	
	1	0.2152
	1	0.09412
	1	
0,1,1	1	0.5965
0,1	1	0.05295
	1	0.1201
	1	
	1	0.4803
	1	
0,1	1	0.4279
	1	
	1	
	1	0.5388
	1	0.1257
1,1	1	0.2979
	1	0.1779
0,1	1	0.4009
	1	
0,1,1	1	0.3875
0,1,1	1	0.5715
0,1	1	0.5574
	1	0.06103
	1	0.2859
	1	0.007843
0,1	1	0.3934
0,1	1	0.3011
	1	0.7523
	1	
	1	0.2741
	1	0.3903

ExAC_AF_AFR	ExAC_AF_AMR	ExAC_AF_EAS	ExAC_AF_FIN
0.005518	0.05396	0.0002543	0.04989
0.3205	0.5774	0.2962	0.6317
0.283	0.5403	0.2691	0.5682
0.7394	0.6357	0.3062	0.6405
0	0	0	0
0.7128	0.3869	0.08743	0.1535
0.2816	0.1429	0.05769	0.01307
0.114	0.28	0.1495	0.1951
0.9187	0.7993	0.8693	0.7889
0.01206	0.05562	0	0.0618
0	0	0	0
0.02538	0.01347	0.04009	0.0472
0.4397	0.6584	0.5211	0.6358
0.2429	0.2155	0.03117	0.3747
0.203	0.08012	0.005227	0.1727
0.07022	0.319	0.2173	0.4053
0.4207	0.6319	0.4396	0.5312
0	0	0	0
0.6018	0.7981	0.9054	0.5666
0.1224	0.01141	0.08502	0.005888
0.2535	0.3136	0.317	0.1323
0.0121	0.02817	0.02817	0
0.6516	0.1498	0.09091	0.1582
0.5557	0.7123	0.5801	0.531
0.005248	0.015	0	0.02983
0.406	0.3476	0.4178	0.3444
0.2016	0.5565	0.7035	0.5745
0.2538	0.3322	0.4329	0.152
0.2084	0.3152	0.3165	0.373
0.002992	0.002944	0	0.01092
0.04422	0.1825	0.1029	0.2593
0.4951	0.339	0.2118	0.4016
0.8157	0.8086	0.9534	0.7995

0.2194	0.1535	0.002575	0.2597
0.04101	0.2663	0.5322	0.1865
0.05543	0.02803	0.124	0.06819
0.9041	0.7806	0.6799	0.7489
0.1102	0.3415	0.3245	0.3223
0.1093	0.2993	0.06104	0.3316
0.482	0.2441	0.2557	0.2102
0.3004	0.2126	0.5063	0.2215
0.1627	0.243	0.2243	0.2283
0.8586	0.7329	0.9904	0.9086
0.3226	0.2922	0.586	0.1323
0.01812	0.04372	0	0.2248
0.008325	0.05328	0.02734	0.05397
0	0	0	0
0.214	0.2322	0.05783	0.3261
0.2645	0.2394	0.05893	0.3302
0.005927	0.1108	0.001273	0.07666
0.01125	0.04369	0.06217	0.1021
0.416	0.1971	0.1183	0.31
0.3537	0.3838	0.1258	0.1095
0.01825	0.01883	0	0.1625
0.528	0.5275	0.4233	0.2845
0.04555	0.2207	0.7087	0.2152
0.01325	0.02796	0	0.07357
0.8551	0.6134	0.4054	0.7117
0.7768	0.6095	0.4037	0.699
0.2857	0.5	0.4019	0.5
0.07938	0.09383	0.0003821	0.1782
0.2687	0.1372	0.1926	0.2578
0.01404	0.02806	0.0001277	0.07578
0.3084	0.21	0.0938	0.2528
0.02414	0.01897	0	0.08154

0.3743	0.403	0.2557	0.6351
0.2147	0.5242	0.6244	0.4998
0.7854	0.8263	0.9811	0.6289
0.2983	0.26	0.0242	0.141
0.02555	0.02506	0	0.03826
0.0724	0.01368	0.0001363	0.03082
0.02041	0.1366	0.05392	0.1622
0.2629	0.3678	0.7054	0.4289
0.1597	0.06786	0.07738	0.0443
0.3548	0.1631	0.2739	0.2442
0.1928	0.287	0.1058	0.3257
0.4728	0.2168	0.31	0.4205
0.2167	0.1329	0.3213	0.1338
0.9682	0.9696	0.9996	0.9439
0.1785	0.6118	0.5122	0.4427
0.3009	0.2635	0.04627	0.3807
0.6152	0.1997	0.2035	0.3462
0.8836	0.8035	0.4901	0.8349
0.5714	0.4959	0.6534	0.2859
0.03745	0.0609	0.05467	0.09811
0.2293	0.3171	0.001169	0.236
0.01343	0.04826	0	0.1815
0.001558	0.0002944	0	0.00157
0.03489	0.05358	0.0001493	0.2115
0.3026	0.1555	0.02998	0.2139
0.04308	0.009901	0.04124	0
0.2964	0.2097	0.3654	0.1667
0.02315	0.05386	0.1637	0.0904
0.5747	0.8325	0.7796	0.7962
0.3077	0.2172	0.2288	0.3286

0.1763	0.3651	0.3889	0.4858
0.008385	0.03768	0.0001271	0.03901
0.4243	0.4133	0.2239	0.2701
0.266	0.0838	0.07718	0.09739
0.6954	0.5044	0.7336	0.3147
0.6007	0.4585	0.9849	0.5146
0.1915	0.3904	0.4852	0.3242
0.03424	0.1569	0.1129	0.2267
0.3954	0.2931	0.4038	0.1062
0.06865	0.214	0.2446	0.1739
0.3197	0.4805	0.5752	0.1643
0.7053	0.8205	0.838	0.575
0.03184	0.06546	0.038	0.04459
0.5932	0.1244	0.2329	0.1544
0.732	0.3542	0.3786	0.3171
0.2044	0.2738	0.3774	0.2176
0.005032	0.02437	0	0.02849
0.0007723	0.0004462	0.0001272	0.004386
0.5717	0.1289	0.6625	0.1449
0.02478	0.06996	0.06261	0.15
0.0009434	0.01212	0	0.004202
0.4324	0.1529	0.01977	0.1788
0.0845	0.08688	0.0005101	0.1343
0.0003804	0.0004523	0	0.07027
0.2133	0.1413	0.1447	0.2509
0.1977	0.2497	0.4667	0.3788
0.02275	0.04339	0.001278	0.1121
0.003274	0.007191	0.000128	0.03172
0.3124	0.399	0.1037	0.5495
0.1076	0.5075	0.5375	0.3304

0.3679	0.2186	0.1989	0.3181
0.0005919	0.0002699	0	0.001211
0.0007766	0.00009051	0	0.0003031
0.2399	0.08713	0.0001894	0.1608
0.08733	0.08493	0.04643	0.217
0.09789	0.06446	0.2062	0.2312
0.0327	0.1501	0	0.1773
0.4704	0.5098	0.3973	0.2989
0.1239	0.2375	0.04336	0.3299
0.3672	0.686	0.5073	0.5975
0.2901	0.2894	0.4478	0.1509
0.007326	0.04896	0	0.04359
0.08011	0.3665	0.3068	0.4413
0.5651	0.843	0.978	0.6948
0	0	0	0
0.005213	0.01702	0.0001276	0.0193
0.2209	0.1052	0.1534	0.1686
0.3062	0.04545	0	0
0.1556	0.2102	0.2857	0.3158
0.5707	0.449	0.5108	0.3971
0.1297	0.2607	0.4926	0.1163
0.2037	0.3026	0.2471	0.2941
0.2868	0.381	0.3887	0.2768
0.02846	0.04191	0.0003815	0.05095
0.5945	0.8511	0.8305	0.7284
0.5942	0.8065	0.9524	0.6314
0.6325	0.8479	0.9511	0.5582
0.2423	0.1145	0.01915	0.3512
0.06099	0.07491	0.1427	0.2271
0.4422	0.5746	0.5517	0.5063

0.0359	0.05462	0.002543	0.1175
0.2784	0.07784	0.09557	0.0818
0.4068	0.3226	0.3857	0.5417
0.1155	0.2118	0.4945	0.4151
0.9803	0.7375	0.4979	0.8309
0.006184	0.007757	0.0001271	0.08074
0.4279	0.09727	0.09883	0.1532
0.5519	0.3741	0.2481	0.2287
0.03395	0.1375	0.4523	0.1113
0.8228	0.9414	0.8679	0.9244
0.6085	0.3103	0.5895	0.2612
0.05956	0.1317	0.06649	0.3044
0.4138	0.2643	0.3269	0.3961
0.1436	0.3687	0.3266	0.261
0.004006	0.006535	0	0.01141
0.5707	0.4669	0.5857	0.349
0.1133	0.255	0.3692	0.2886
0.3594	0.3797	0.2346	0.3863
0.242	0.6433	0.6114	0.1532
0.3783	0.7811	0.6701	0.5115
0.2003	0.1922	0.3239	0.3061
0.4157	0.09732	0.0102	0.108
0.08782	0.04428	0.0003819	0.06804
0.1095	0.3657	0.3551	0.75
0.001103	0.003927	0.0001272	0.0003025
0.2071	0.05773	0.1754	0.1471
0.001656	0.0034	0	0.003481
0.4545	0.4583	0.7292	0
0.3666	0.3341	0.6916	0.7104

0.3117	0.4147	0.2767	0.5251
0.1525	0.3248	0.3946	0.4423
0.06757	0.2344	0.1343	0.3571
0.8064	0.3844	0.5388	0.3173
0.04902	0.2903	0.3085	0.2864
0.01169	0.02554	0.02044	0.05049
0.4949	0.3889	0.3984	0
0.001894	0.002586	0	0.01104
0	0	0	0
0.636	0.3682	0.5737	0.7052
0.6182	0.3369	0.5447	0.6891
0.1696	0.1055	0.0008899	0.1464
0.3622	0.1964	0.0173	0.2732
0.7704	0.419	0.5713	0.4587
0.2186	0.3045	0.4416	0.251
0.4868	0.6114	0.5998	0.6718
0.2507	0.09823	0.1478	0.09433
0.09011	0.1625	0.03779	0.4062
0.1329	0.08659	0.05048	0.06879
0.5032	0.1262	0.2155	0.3462
0.6796	0.669	0.814	0.4418
0.02278	0.05837	0	0.1284
0.2197	0.591	0.4945	0.216
0	0	0	0
0.2016	0.4757	0.3797	0.5657
0.5485	0.2522	0.4861	0.4209
0.3384	0.2556	0.2578	0.5
0.1476	0.2294	0.3178	0.2748
0	0	0	0
0.7862	0.5174	0.3015	0.5824
0.001228	0.001966	0	0.001521

0.02603	0.3229	0.223	0.1814
0.4596	0.4795	0.4224	0.6176
0.1478	0.408	0.4467	0.4118
0.006667	0.02397	0.01887	0.07143
0.07271	0.1959	0.2005	0.3229
0.01515	0.01564	0.005544	0.09559
0.005647	0.009045	0.002307	0.04966
0.2249	0.06823	0.1495	0.02601
0.1177	0.4649	0.3484	0.3322
0.9306	0.7908	0.9149	0.6467
0.09204	0.08771	0.01263	0.1229
0.009828	0.01883	0.06779	0.03538
0.3287	0.2491	0.2629	0.411
0.3266	0.2328	0.268	0.4108
0.1384	0.2239	0.2304	0.2809
0.6946	0.6225	0.8858	0.7049
0.1295	0.06083	0.1303	0.1402
0.00445	0.0194	0.0001501	0.01369
0.003756	0.006109	0	0.03116
0.1469	0.3019	0.2572	0.2146
0.7401	0.5755	0.4601	0.374
0.4238	0.2996	0.04416	0.1967
0.03059	0.04947	0.0003818	0.08832
0.01324	0.01783	0	0.07789
0.2429	0.4521	0.3144	0.516
0.02276	0.06353	0.000647	0.08455
0.08722	0.5436	0.5538	0.5354
0.06194	0.1935	0.4324	0.2594

0.04062	0.1748	0.01006	0.2538
0.8292	0.6468	0.5792	0.623
0.1685	0.6174	0.4142	0.6833
0.06711	0.3573	0.1186	0.2633
0.4672	0.732	0.3514	0.4136
0.5133	0.5677	0.3434	0.3884
0.6194	0.7141	0.3475	0.4003
0.684	0.5666	0.7213	0.2572
0.8835	0.6527	0.5494	0.6478
0.6661	0.5832	0.5433	0.552
0.6669	0.5834	0.5438	0.5534
0.03821	0.2788	0.07024	0.1034
0.003756	0.004823	0.0001273	0.02165
0.4744	0.04611	0.02042	0.08057
0.3462	0.08035	0.1249	0.1576
0.08011	0.0443	0.001017	0.08119
0.1028	0.6072	0.5849	0.4716
0.01462	0.03103	0.05379	0.1339
0.5128	0.3173	0.2938	0.6386
0.25	0.1831	0.1947	0.6562
0.2207	0.5813	0.4575	0.5364
0.005296	0.01694	0.0001271	0.01935
0.4775	0.3642	0.1897	0.408
0.1616	0.06194	0.0009709	0.2164
0.6602	0.1878	0.05027	0.1616
0.1441	0.1512	0.05009	0.1367
0.5927	0.4747	0.3361	0.179
0.04445	0.3713	0.1324	0.1369
0.07708	0.5631	0.3081	0.124
0.3215	0.2353	0.5238	0.4756
0.7589	0.3612	0.4889	0.2411
0.7602	0.5961	0.5934	0.6955
0.3073	0.3261	0.2521	0.4877
0.1102	0.1289	0.009098	0.1414
0.00189	0.00437	0	0.02753
0.0327	0.1568	0.03221	0.137

0.5721	0.6379	0.8773	0.6987
0.2393	0.4602	0.1691	0.3646
0.7461	0.9068	0.7967	0.8254
0.1977	0.4172	0.7081	0.4153
0.004376	0.01716	0	0.00984
0.8667	0.8256	0.6866	0.6963
0.8722	0.8267	0.6868	0.6955
0.3705	0.3236	0.5605	0.4187
0.09869	0.1114	0.4075	0.2672
0.04012	0.09506	0.002697	0.2181
0.05273	0.09285	0.05103	0.2204
0.0005214	0	0.0002552	0.0003644
0.01616	0.07024	0.0002621	0.1629
0.2165	0.1649	0.2338	0.3127
0.31	0.4618	0.4293	0.396
0.549	0.6123	0.7638	0.3288
0.132	0.4344	0.4478	0.3358
0.7665	0.4751	0.8117	0.6195
0.1817	0.5035	0.3021	0.277
0.007444	0.01333	0.0002728	0.003579
0.01197	0.1779	0.08212	0.04215
0.5532	0.2329	0.6502	0.2066
0.003093	0.00333	0.0001664	0.06226
0.07732	0.2991	0.204	0.04354
0.2477	0.4205	0.3973	0.45
0.5568	0.6826	0.5907	0.7351
0.3452	0.6831	0.2406	0.7495
0.1577	0.2231	0.2365	0.1559
0.8536	0.7286	0.7026	0.7924

0.1825	0.5121	0.3461	0.4517
0.1899	0.2029	0.0006373	0.3019
0.1082	0.4678	0.2676	0.4145
0.2853	0.4212	0.05921	0.3382
0.001774	0.005534	0	0.001815
0.849	0.5932	0.6821	0.496
0.2919	0.3218	0.3027	0.4215
0.3304	0.5773	0.627	0.6126
0.3549	0.2509	0.2952	0.4341
0.2326	0.6902	0.7594	0.529
0.005982	0.01244	0	0.02654
0.2351	0.2521	0.2571	0.3857
0.1561	0.1691	0.2155	0.2792
0.4732	0.4316	0.3774	0.358
0.2846	0.4449	0.3796	0.3943
0.2544	0.0206	0.03992	0.06955
0.1689	0.01694	0.0002543	0.06955
0.0498	0.1871	0.2535	0.1943
0.05009	0.187	0.2604	0.1943
0.1065	0.1667	0.16	0.3571
0.02973	0.05145	0.01578	0.1538
0.1403	0.2837	0.527	0.3044
0.2075	0.05048	0.007459	0.06018
0.05182	0.2208	0.1349	0.3763
0.1346	0.2201	0.4184	0.2083
0.01072	0.1506	0.2874	0.06214
0.01724	0.2227	0.01929	0.203
0.001138	0.007825	0	0.001038
0.1446	0.3916	0.004577	0.4244
0.06541	0.1369	0.1677	0.1178
0.2697	0.224	0.1856	0.3131
0.6983	0.4558	0.6315	0.4135
0.9948	0.992	1	0.9212
0.04331	0.06043	0	0.1106
0.02037	0.1779	0.3194	0.1116
0.1505	0.3667	0.3718	0.2652
0.05422	0.1294	0.07949	0.2281
0.1065	0.0882	0.005962	0.02719
0.312	0.2583	0.1906	0.209

0.2222	0.2012	0.2671	0.1836
0.1053	0.06893	0.2733	0.07607
0.7113	0.3681	0.5698	0.5171
0.06202	0.1323	0.3642	0.5242
0.7718	0.5474	0.7116	0.5562
0.2467	0.4364	0.6085	0.3059
0.2612	0.3948	0.5097	0.1914
0.2325	0.2249	0.3356	0.1141
0.1003	0.2817	0.1751	0.2871
0.114	0.1667	0.1293	0
0.4982	0.8112	0.8198	0.644
0.05161	0.1622	0	0.3647
0.07712	0.2872	0.1572	0.433
0.1567	0.0288	0.0003377	0.01955
0.2828	0.1776	0.1517	0.2769
0.02083	0.01389	0	0.1667
0.03575	0.08213	0.0006593	0.1625
0.553	0.7518	0.5433	0.6805
0.2901	0.2793	0.4009	0.4193
0.8328	0.8633	0.9553	0.7545
0.009572	0.02695	0	0.04902
0.7543	0.6633	0.6459	0.5774
0.01238	0.01975	0.0004009	0.0114
0.06379	0.1173	0.1391	0.01391
0.0648	0.1167	0.1385	0.01378
0.3496	0.3846	0.3402	0.516
0.5887	0.4392	0.8209	0.4896
0.04405	0.06829	0.0748	0.1348
0.02713	0.09488	0.03407	0.1031
0.0005515	0.001427	0	0.0001512
0.06109	0.006957	0.02505	0.01119
0.259	0.3253	0.2742	0.4642
0.7976	0.5742	0.546	0.5634

0.1815	0.4683	0.7345	0.3979
0.02032	0.4214	0.03767	0.2132
0.3254	0.3208	0.3337	0.3824
0.1673	0.1926	0.1696	0.3529
0.1495	0.573	0.5377	0.5997
0.2446	0.4182	0.2359	0.1988
0.1723	0.05911	0.01809	0.08772
0.1569	0.05651	0.1823	0.115
0.02128	0.0781	0.1548	0.1389
0.209	0.2025	0.3931	0.2641
0.08813	0.515	0.5277	0.5777
0	0	0	0
0.3437	0.2428	0.1697	0.2871
0.6314	0.3241	0.4724	0.2335
0.445	0.8687	0.6546	0.7823
0.1908	0.4873	0.5809	0.3897
0.09712	0.3675	0.4094	0.2353
0.5414	0.4108	0.6953	0.5103
0.4343	0.2835	0.001492	0.3545
0.3599	0.3132	0.1374	0.07106
0.6322	0.3785	0.2108	0.07211
0.1336	0.03372	0	0.05745
0.09753	0.4123	0.4477	0.3969
0.6597	0.6554	0.9152	0.3593
0.0009929	0.000535	0	0.002874
0.1093	0.193	0.04063	0.1894
0.1899	0.2527	0.2455	0.3174
0.2092	0.2516	0.2397	0.3162
0.0105	0.02573	0.0001564	0.03411
0.1712	0.3096	0.4103	0.2977
0.002135	0.007006	0	0.021

0.6957	0.5535	0.447	0.5884
0.02139	0.2588	0.2707	0.09591
0.376	0.2158	0.2384	0.2597
0.2019	0.4894	0.3151	0.255
0.9308	0.768	1	0.898
0.0006711	0.001877	0	0.02756
0.001923	0.0008133	0	0.02245
0.02694	0.04263	0.0005148	0.2188
0.7267	0.4155	0.5698	0.6075
0.7183	0.8839	0.9449	0.7634
0.0234	0.06259	0.06041	0.07801
0.1422	0.2318	0.3316	0.2839
0.07748	0.2102	0.3016	0.2545
0.2994	0.3074	0.2805	0.401
0.1805	0.2058	0.1277	0.3414
0.3192	0.3176	0.165	0.4873
0.5847	0.7079	0.8006	0.3761
0.4729	0.3937	0.3486	0.3593
0.4299	0.5005	0.1749	0.1462
0.08855	0.2975	0.0146	0.4
0.0137	0.0288	0.0002545	0.06197
0.06448	0.01592	0.01032	0.03024
0.0002406	0.0009235	0	0.003239
0.04525	0.04307	0.3939	0.1627
0.4384	0.2674	0.2577	0.3528
0.3991	0.2292	0.2561	0.2579
0.397	0.23	0.2567	0.2576
0.03178	0.006107	0.1967	0.003028
0.5174	0.249	0.3855	0.1322
0.0001238	0.0001802	0	0
0.005765	0.01583	0	0.01063
0.08315	0.2671	0.749	0.08255
0.1298	0.04758	0.03378	0.06868
0.2413	0.3505	0.4903	0.418

0.03651	0.3044	0.18	0.2757
0.0002341	0.000279	0.0002693	0.0003086
0.6213	0.5533	0.7045	0.6923
0.8481	0.5933	0.8399	0.794
0.1734	0.5751	0.6975	0.6571
0.358	0.1364	0.3994	0.2045
0.8463	0.7759	0.7132	0.7807
0.8048	0.756	0.6592	0.71
0.8925	0.7763	0.6352	0.761
0.004977	0.00808	0	0.05593
0.9525	0.9088	0.9898	0.6475
0.3621	0.6914	0.6286	0.5998
0.143	0.4337	0.482	0.4952
0.5533	0.7027	0.8003	0.3761
0.5268	0.5949	0.3152	0.772
0.4687	0.394	0.2137	0.2596
0.5345	0.3148	0.381	0.3333
0.4886	0.2404	0.2797	0.1667
0.3448	0.7155	0.8236	0.5454
0	0.01124	0	0
0.2729	0.1639	0.2664	0.1784
0.05563	0.1414	0.0005137	0.2012
0.3939	0.5141	0.5261	0.6408
0.0523	0.04116	0.04439	0.04835
0.0003311	0.00008917	0	0
0.3431	0.6178	0.4214	0.2519
0.1022	0.2954	0.7232	0.342
0.004479	0.006712	0	0.01925
0.08036	0.1232	0.07488	0.0319
0.005094	0.01736	0	0.008085

0.8262	0.9059	0.6711	0.822
0.1322	0.5205	0.09566	0.5347
0.00785	0.1956	0.001186	0.0312
0.8512	0.7943	0.897	0.7818
0.2609	0.2711	0.6762	0.4744
0.4896	0.1291	0.1174	0.2261
0.597	0.7585	0.8755	0.6465
0.05357	0.1957	0.07692	0.25
0.09537	0.1817	0.1773	0.5241
0.5578	0.3272	0.2506	0.3182
0.227	0.5011	0.646	0.4083
0.2417	0.9147	0.8903	0.9589
0.00348	0.008224	0	0.005639
0.4448	0.3621	0.6342	0.3552
0.2794	0.4908	0.3856	0.3467
0.2434	0.488	0.7696	0.2881
0.1319	0.152	0.09377	0.05305
0.3118	0.5372	0.2852	0.4265
0.07447	0.1372	0.1358	0.1419
0.0001348	0.0001107	0.0009944	0.0004416
0.8356	0.6223	0.6822	0.5314
0.0001104	0.000446	0	0
0.0002255	0.0005371	0	0
0.01244	0.2447	0.1054	0.118
0.1947	0.1683	0.003085	0.3427
0.01899	0.05299	0	0.1768
0.2514	0.1432	0.3567	0.3078
0.1228	0.1145	0.3806	0.2224
0.1495	0.2369	0.09644	0.1103
0.7482	0.5466	0.5325	0.3824
0.6618	0.5934	0.5104	0.3635

0.02872	0.04762	0.04348	0.4333
0.7859	0.5342	0.4667	0.3454
0.4569	0.3366	0.04017	0.1558
0.2047	0.3644	0.1646	0.4416
0.04903	0.04206	0	0.08
0.0005863	0.0004689	0	0.001015
0.8183	0.8134	0.938	0.4027
0.3814	0.4333	0.5625	0.6667
0.8939	0.7382	0.6804	0.7173
0.6781	0.6284	0.6048	0.5626
0.421	0.4437	0.3953	0.3868
0.913	0.8984	0.9997	0.8471
0.2976	0.606	0.3626	0.4014
0.07759	0.3413	0.6189	0.4054
0.002618	0.005756	0	0.004958
0.2385	0.2041	0.03065	0.3809
0.4336	0.1099	0.05894	0.2267
0.1907	0.4507	0.4491	0.4486
0.8836	0.6887	0.8101	0.6538
0.2086	0.4579	0.4444	0.4501
0.4562	0.6385	0.5482	0.6373
0.3097	0.2393	0.3757	0.2565
0.274	0.2413	0.02192	0.2828
0.03015	0.09223	0.2033	0.2143
0.6252	0.6581	0.9925	0.5523
0.4847	0.6758	0.765	0.6253
0.4039	0.491	0.364	0.7809
0.4282	0.6001	0.6354	0.6219
0.08626	0.2575	0.3067	0.2647
0.06189	0.1154	0.0002552	0.2852
0.1428	0.05421	0.0001272	0.1049
0.6983	0.1672	0.08066	0.2834
0	0	0	0
0.1531	0.4295	0.04185	0.6327
0.5552	0.6337	0.5651	0.5409
0.001552	0.004471	0.0001276	0.001362

0.3122	0.2459	0.08661	0.1307
0.007673	0.0177	0.0001273	0.02398
0.4819	0.604	0.3157	0.5475
0.7479	0.5573	0.8596	0.3804
0.3121	0.4715	0.4411	0.4568
0.1802	0.3118	0.374	0.3956
0.205	0.3747	0.4049	0.4235
0.2367	0.3197	0.3739	0.3965
0.01193	0.01576	0.06634	0.06472
0.001338	0.001343	0	0.02152
0.003027	0.005621	0	0.009226
0.2425	0.1795	0.2411	0.4561
0.2336	0.3507	0.1483	0.5688
0.04776	0.2687	0.3305	0.1122
0.2027	0.857	0.427	0.8608
0.0469	0.3663	0.6434	0.3957
0.502	0.6497	0.681	0.2747
0.2917	0.3353	0.2689	0.1373
0.001303	0.001519	0.0002626	0.00711
0.001988	0.005894	0.0003815	0.00605
0.3899	0.7712	0.4913	0.5486
0.2243	0.113	0.01732	0.09444
0.1282	0.3986	0.3665	0.2965
0.4595	0.5508	0.7396	0.5261
0.005747	0	0	0
0.003136	0.0175	0	0.01624
0.001464	0.007722	0	0
0.4078	0.5707	0.4216	0.5607
0.04122	0.3525	0.5014	0.09631
0.08045	0.03665	0	0.0353
0.02284	0.008213	0.0005086	0.01785
0.4222	0.4356	0.3388	0.2519
0.02321	0.235	0.00928	0.08757
0.009091	0.01198	0	0.03143
0.8915	0.8324	0.8972	0.7079
0.1842	0.07787	0	0.075
0.1592	0.07403	0.002417	0.1953
0.2976	0.05836	0.1381	0.05715
0.2664	0.4317	0.3204	0.2291

0.2457	0.03984	0.0173	0.03462
0.735	0.5673	0.6576	0.5635
0.007484	0.01893	0	0.0267
0.117	0.1556	0.1406	0
0.03607	0.05957	0.002415	0.1898
0.09292	0.2514	0.162	0.0386
0.04071	0.1658	0.244	0.2383
0.5113	0.7004	0.8007	0.3759
0.07029	0.1424	0.3457	0.1252
0.4191	0.4324	0.8429	0.5712
0.9461	0.7884	0.8482	0.6662
0.3888	0.2884	0.4875	0.2999
0.003147	0.007274	0	0.01171
0.2483	0.4644	0.3544	0.2897
0.2859	0.6091	0.936	0.6227
0.05868	0.02704	0	0.0605
0.008933	0.0245	0	0.06258
0.01235	0.03393	0	0.07668
0.1447	0.3526	0.14	0.2237
0.4393	0.2584	0.2172	0.3092
0.8234	0.6307	0.453	0.7814
0.004986	0.01073	0	0.07754
0.2683	0.06832	0.1003	0.1899
0.3142	0.08178	0.1046	0.09846
0.6756	0.1143	0.1108	0.1548
0.1122	0.04277	0.001703	0.04087
0.193	0.2267	0.1157	0.2245
0.6722	0.1526	0.5122	0.09053
0.03191	0.2146	0.1107	0.1667
0.01128	0.0301	0	0.06923
0.2	0.5779	0.4296	0.3601
0.1536	0.01324	0.0001275	0.007023
0.5575	0.3488	0.3643	0.4247
0.06237	0.2239	0.3753	0.3522

0.06391	0.08873	0.1595	0.2157
0.1588	0.05241	0.1584	0.107
0.002868	0.003835	0	0.01648
0.1575	0.2277	0.364	0.1163
0.2052	0.2308	0.06529	0.2442
0	0	0	0
0.8209	0.7217	0.8167	0.3761
0.002635	0.001787	0	0.005443
0.2135	0.4517	0.4687	0.5152
0.2708	0.2383	0.2693	0.3277
0.2381	0.09817	0.1108	0.1052
0.3223	0.228	0.1148	0.2438
0.3525	0.2311	0.1169	0.2412
0.3655	0.6853	0.4842	0.3741
0.1992	0.5582	0.4058	0.3314
0.1439	0.3969	0.02431	0.5294
0.103	0.2769	0.2032	0.276
0.1411	0.1494	0.3874	0.124
0.2496	0.1798	0.3454	0.1445
0.5322	0.3048	0.2865	0.3953
0.1644	0.275	0.2906	0.2182
0.3551	0.2603	0.2132	0.4829
0.3122	0.3369	0.4035	0.3928
0.257	0.2848	0.02702	0.1492
0.2747	0.1598	0.3086	0.2154
0.046	0.1021	0.002316	0.2383
0.009045	0.0403	0.1772	0.1258
0.3562	0.2457	0.0006395	0.2393
0.4929	0.4826	0.4501	0.5197
0.438	0.259	0.5486	0.3962
0.1067	0.4919	0.09719	0.1656
0.2364	0.5977	0.3464	0.5536
0.02889	0.04387	0.194	0.1818
0.0437	0.05338	0.1829	0.03118
0.5575	0.344	0.5518	0.3322

0.207	0.1278	0.1912	0.1863
0.4235	0.1531	0.2312	0.1944
0.7327	0.6316	0.8095	0.6258
0.8329	0.2666	0.1512	0.412
0.1005	0.2237	0.1571	0.4008
0.1398	0.3729	0.1923	0.5
0.07581	0.2311	0.1502	0.4108
0.8531	0.2736	0.1629	0.4273
0.7456	0.2636	0.1517	0.4085
0.1248	0.2125	0.2627	0.44
0.5705	0.6182	0.4637	0.6333
0.4537	0.4444	0.3937	0.6667
0.2117	0.2917	0.6481	0.07895
0.3076	0.1299	0.3228	0.2825
0.3265	0.1638	0.07871	0.3056
0.3275	0.2096	0.4194	0.3565
0.386	0.1731	0.007576	0
0.2005	0.3481	0.3249	0.4444
0.2769	0.4131	0.4272	0.2438
0.4134	0.08154	0.06618	0.1833
0.0192	0.1286	0.04353	0.1637
0.06547	0.1153	0.2368	0.2024
0.5157	0.5633	0.4145	0.556
0.642	0.2595	0.4199	0.5671
0.2684	0.4141	0.4251	0.3317
0.3015	0.3018	0.475	0.2836
0.1555	0.1468	0.02875	0.2222
0.5367	0.5212	0.7521	0.5816
0.3571	0.5031	0.4856	0.4453
0.6536	0.7109	0.7506	0.5366
0.621	0.7011	0.742	0.5182
0.6213	0.7013	0.7423	0.5189
0.5057	0.3089	0.3372	0.2742
0.5718	0.5777	0.4646	0.5021
0.2821	0.1716	0.2582	0.4061
0.3323	0.2536	0.1996	0.2867
0.5431	0.6065	0.52	0.6602
0.01465	0.1593	0.003214	0.2047
0.6111	0.3385	0.462	0.2838

0.08284	0.2073	0.002303	0.08258
0.01287	0.2311	0.001045	0.07067
0.2747	0.1209	0.09477	0.1513
0.3585	0.2599	0.3246	0.5029
0.2084	0.05132	0.1516	0.1195
0.5581	0.6123	0.7331	0.4524
0.05317	0.1439	0.0007628	0.2465
0.0006974	0.001252	0.03737	0.006822
0.003861	0.002318	0.03715	0.006655
0.0007641	0.001456	0.04161	0.007681
0.4943	0.5019	0.5714	0.4524
0.6229	0.6286	0.6529	0.4638
0.5192	0.2698	0.1785	0.1227
0.1892	0.2296	0.1732	0.2299
0.9697	0.9741	0.9997	0.944
0.6896	0.5842	0.6011	0.3322
0.3539	0.1911	0.08048	0.2871
0.6396	0.1196	0.05712	0.1508
0.6105	0.4931	0.05517	0.3658
0.791	0.9098	0.9727	0.875
0.1079	0.1623	0.2948	0.2552
0.4279	0.6686	0.6486	0.6729
0.002674	0.001894	0	0.007937
0	0	0	0
0.5651	0.297	0.2575	0.4161
0.08802	0.2109	0.2441	0.3539
0.09993	0.07923	0	0.1474
0.0624	0.1417	0.04346	0.2652
0.242	0.6716	0.742	0.5838
0.7448	0.5127	0.6011	0.4518
0.06562	0.2659	0.2535	0.2765
0.2584	0.409	0.4511	0.6355
0.3209	0.4623	0.6097	0.4912
0.6657	0.7381	0.9135	0.6962
0.9129	0.8012	0.9867	0.8258

0.2332	0.5386	0.2323	0.346
0.1218	0.4984	0.25	0.4929
0.2513	0.5827	0.4258	0.5452
0.6472	0.5668	0.6049	0.4463
0.0009291	0.006223	0	0.02289
0.6667	0.6673	0.8363	0.4137
0.06632	0.1829	0.277	0.334
0.1895	0.2889	0.1719	0
0.09799	0.36	0.2752	0.2063
0.2178	0.3696	0.1042	0.4382
0.1525	0.5216	0.007558	0.7423
0.2123	0.3252	0.2303	0.4024
0.2391	0.3534	0.2822	0.4215
0.4626	0.816	0.8013	0.7044
0.4632	0.8221	0.798	0.704
0.4527	0.3382	0.08714	0.2169
0.3019	0.1001	0.02022	0.1211
0.4592	0.91	0.9889	0.8916
0.4228	0.6044	0.7545	0.3112
0.05145	0.04789	0.05228	0.09252
0.2516	0.5714	0.6456	0.647
0.4394	0.3217	0.4422	0.4107
0.09834	0.1793	0.3126	0.1177
0.01486	0.001789	0	0.0006107
0	0	0	0
0.4627	0.7863	0.6438	0.5519
0.4799	0.5431	0.4544	0.5138
0.2406	0.2689	0.002953	0.573
0.545	0.4258	0.7177	0.2891
0.5554	0.3986	0.2215	0.4061
0.6303	0.3996	0.357	0.3823
0.8331	0.8986	0.6883	0.8825
0.8836	0.867	0.9581	0.8948

0.94	0.9129	0.9454	0.8909
0.0004073	0.000612	0	0.002262
0	0.002688	0	0.0252
0.1132	0.2581	0.2451	0.2651
0.119	0.2022	0.1751	0.1344
0.0544	0.4027	0.3036	0.2895
0.1984	0.1651	0.1516	0.2349
0.2449	0.1657	0.1514	0.2355
0.1092	0.04488	0	0.04794
0.03946	0.04764	0.01286	0.0778
0.2896	0.5663	0.708	0.5275
0.3652	0.5553	0.6943	0.5244
0.03091	0.06329	0	0.1032
0.0007468	0.00114	0	0.002446
0.3025	0.2514	0.3533	0.4385
0.5197	0.3663	0.7886	0.5217
0.01589	0.07613	0.00134	0.08447
0.6374	0.2657	0.1887	0.1816
0.08915	0.151	0.1327	0.2458
0.03021	0.4155	0.08185	0.03932
0.1977	0.7116	0.6019	0.695
0.1019	0.2613	0.05128	0.4902
0.02208	0.03988	0.000509	0.09797
0	0	0	0
0.1294	0.0915	0.0006391	0.1541
0.08881	0.07965	0.1703	0.2658
0.689	0.3838	0.9695	0.6085
0.03457	0.1228	0.1088	0.1808
0.04571	0.185	0.1561	0.2466
0.3954	0.4118	0.6502	0.5484
0.863	0.8185	0.9823	0.7452
0.071	0.01237	0.02181	0.003634

0.1397	0.4786	0.1374	0.367
0.838	0.827	0.5062	0.7421
0.06193	0.1063	0.1467	0.1649
0.3576	0.15	0.4526	0.2679
0.2188	0.1213	0.008535	0.2655
0.3235	0.2087	0.34	0.1438
0.2387	0.1559	0.1461	0.1179
0.1645	0.6531	0.4672	0.531
0.1382	0.0979	0.1331	0.04445
0.9285	0.7193	0.8477	0.5002
0.05008	0.385	0.3819	0.2694
0.06509	0.00831	0.005472	0.0001512
0.2302	0.6364	0.4647	0.4836
0.6964	0.4325	0.4304	0.5758
0.08012	0.03839	0.2767	0.0378
0.4286	0.1675	0.1998	0.09382
0.004685	0.01803	0.0001286	0.08203
0.221	0.2563	0.1853	0.06749
0.001435	0.00616	0.0001271	0.001378
0.1464	0.1244	0.2609	0.1365
0.5158	0.3591	0.4218	0.2844
0.7376	0.514	0.5438	0.4958
0.003549	0.01254	0	0.02028
0.6897	0.8419	0.8825	0.8081
0.3973	0.3478	0.4022	0.2849
0.1348	0.1153	0.0007632	0.1752

0.2349	0.1981	0.3596	0.1539
0.8363	0.6535	0.7022	0.7682
0.444	0.4667	0.2931	0.6597
0.001634	0	0	0
0.1917	0.4192	0.3904	0.1668
0.3683	0.7745	0.8056	0.6883
0.05235	0.1255	0.09266	0.2776
0.7317	0.6322	0.715	0.533
0.5898	0.4483	0.4578	0.4819
0.7324	0.1303	0.1794	0.1306
0.4925	0.5167	0.7536	0.6131
0.2213	0.1682	0.04729	0.03982
0.008877	0.01512	0	0.04672
0.1035	0.0345	0.0003815	0.1057
0.1812	0.2528	0.03536	0.1394
0.1147	0.4096	0.4461	0.2611
0.0649	0.3438	0.5192	0.118
0.1445	0.2045	0.1645	0.2595
0.00662	0.008917	0.0002543	0.03493
0.2936	0.25	0.06818	0.5
0.2795	0.2068	0.05572	0.4511
0.3812	0.4157	0.9835	0.4421
0.003203	0.003709	0	0.0289
0.1662	0.1764	0.1939	0.1999
0.2298	0.2592	0.07479	0.3163
0.1089	0.09214	0.06993	0.09756
0.1751	0.08075	0	0.2222
0.374	0.305	0.3491	0.438
0.05716	0.4232	0.354	0.3837
0.005193	0.007744	0	0.04709
0.08878	0.3266	0.2966	0.3825
0.6615	0.7852	0.852	0.5389
0.0006907	0.001218	0	0.0002208
0.116	0.2305	0.1955	0.2241

0.9049	0.7866	0.6452	0.7136
0.8711	0.3243	0.4201	0.2455
0.2852	0.112	0.101	0.1626
0.4868	0.3694	0.4999	0.3436
0.003544	0.002769	0	0.00605
0.1701	0.3518	0.4236	0.354
0	0.0004495	0	0.0006057
0.2816	0.4055	0.2662	0.4085
0.1806	0.09749	0.4412	0.04325
0.1616	0.08156	0.09812	0.1382
0.005537	0.01425	0.0002082	0.01919
0.006751	0.006075	0	0.04433
0.423	0.4913	0.2484	0.4743
0.1916	0.277	0.1568	0.2152
0.06804	0.3371	0.6581	0.3935
0.0002279	0.0004529	0	0.0007634
0.06718	0.2579	0.5738	0.234
0.1688	0.5779	0.8495	0.6452
0.2379	0.4256	0.2656	0.4112
0.2557	0.343	0.2479	0.3355
0.3479	0.2393	0.3687	0.2526
0.1522	0.2308	0.3662	0.2641
0.8723	0.3121	0.4239	0.2039
0.8593	0.3133	0.4236	0.2039
0.2012	0.0946	0.001161	0.124
0.04492	0.2639	0.005339	0.2499
0.8893	0.7362	0.6609	0.5005
0.04593	0.1981	0.2435	0.2582
0.01136	0.03655	0.08437	0.05519
0.217	0.2559	0.5379	0.2096
0.009069	0.03709	0	0.0331
0.00335	0.006964	0	0.01757
0.7299	0.5603	0.6454	0.7781

0.666	0.4714	0.09321	0.3331
0	0	0	0
0.0012	0.004746	0	0.009078
0.2158	0.07858	0.02835	0.1478
0.02956	0.1146	0.0002644	0.2469
0.09026	0.548	0.4808	0.4141
0.2236	0.08188	0.08698	0.1024
0.2543	0.09914	0.09701	0.1355
0.03329	0.07641	0	0.223
0.2662	0.1275	0.1527	0.1642
0.3027	0.1574	0.3521	0.2487
0.4227	0.3824	0.4335	0.4393
0	0	0	0.01478
0.08148	0.4359	0.2832	0.3667
0.6089	0.6053	0.4	0.6667
0.7944	0.5991	0.2962	0.5614
0.1337	0.6463	0.2777	0.4501
0.1094	0.2796	0.0005552	0.2829
0.04079	0.05594	0.06211	0.2285
0.7712	0.4152	0.3886	0.6148
0	0	0	0
0.7745	0.4571	0.4483	0.3124
0.0001235	0	0	0
0.2259	0.08482	0.1758	0.1373
0.3448	0.3453	0.1533	0.2238
0.0843	0.2511	0.7052	0.4096
0.332	0.8722	0.8213	0.7708
0.3126	0.4501	0.3776	0.3545
0.5304	0.7435	0.5925	0.5649
0.0004078	0.0005624	0	0
0.001435	0.002319	0.003178	0.01906
0.004523	0.006032	0.0001273	0.04482
0.9306	0.7726	0.8214	0.6172

0.7272	0.8274	0.8346	0.7646
0.05832	0.004471	0	0
0.1454	0.214	0.2438	0.02511
0.1094	0.3519	0.1396	0.4537
0.5168	0.5897	0.6104	0.678
0.1831	0.5268	0.4226	0.2835
0.4183	0.5365	0.4209	0.2686
0.857	0.6865	0.526	0.666
0.8189	0.6677	0.5202	0.5076
0.3676	0.6452	0.4007	0.456
0.002278	0.003442	0	0.02536
0.0001215	0.0002785	0	0.009918
0.02778	0.0431	0.003125	0.03484
0.03354	0.09555	0.09871	0.3015
0.5345	0.4886	0.6522	0.5055
0.2096	0.1605	0.1334	0.2365
0.06115	0.2595	0.3246	0.1399
0.1838	0.1865	0.1251	0.147
0.03149	0.01972	0.3034	0.03645
0.001425	0.001171	0.0003871	0.0007569
0.003316	0.002807	0	0.001696
0.6331	0.3937	0.0631	0.3879
0.4417	0.2958	0.1509	0.5271
0.1787	0.4232	0.7055	0.2934
0.7488	0.4983	0.7318	0.4098
0.3881	0.5835	0.2936	0.6742
0.2596	0.04819	0.02795	0.001185
0.2322	0.5969	0.7539	0.2349
0.9162	0.7138	0.8743	0.5369
0.09983	0.5475	0.7457	0.2138
0.01986	0.06322	0.0002567	0.05593

0.003822	0.008525	0	0.03717
0	0	0	0
0.3821	0.6632	0.4365	0.5957
0.2986	0.07701	0.1869	0.07504
0.6917	0.2708	0.2535	0.1838
0.2606	0.5139	0.6695	0.1899
0.02211	0.07198	0.05049	0.1428
0.8236	0.8122	0.7874	0.5333
0.03497	0.08055	0.1966	0.03887
0.01761	0.214	0.391	0.1154
0.8055	0.4775	0.7236	0.4924
0.7186	0.5436	0.5206	0.2846
0.6256	0.5184	0.6328	0.4905
0.2116	0.1435	0.02476	0.1743
0.3511	0.4385	0.469	0.2352
0.03161	0.2189	0.03777	0.2203
0.7168	0.5277	0.5208	0.3017
0.5861	0.3931	0.3639	0.3424
0.7879	0.5879	0.8072	0.5402
0.7117	0.5256	0.6254	0.492
0.07937	0.4833	0.5	0.2727
0.05821	0.2807	0.04046	0.3739
0.001333	0.007321	0.0001274	0.001368
0.8072	0.2505	0.341	0.3058
0.1122	0.2026	0.4928	0.4111
0.8415	0.8134	0.3939	0.7242
0.6214	0.2354	0.1895	0.3266
0.7572	0.4616	0.287	0.3993

ExAC_AF_NFE	ExAC_AF_OTH	ExAC_AF_SAS	GENE_PHENO
0.03852	0.02639	0.01608	
			1
0.6659	0.611	0.6184	
			1
0.6329	0.5698	0.5932	
0.7088	0.6387	0.6374	
0.0000552	0	0	
			1
0.2554	0.283	0.2905	1
0.01094	0	0.05608	
0.2146	0.1988	0.145	
0.8635	0.822	0.7878	
0.07916	0.05825	0.04588	
			1
			1
			1
0	0	0	
0.03902	0.02915	0.1214	1
0.6369	0.6571	0.699	
0.4204	0.3598	0.2995	
			1
			1
0.2001	0.1652	0.1442	
			1
0.3808	0.3113	0.2435	
0.4892	0.4823	0.4759	1
0.0006711	0	0.001581	
0.584	0.6108	0.7575	
0.01294	0.02041	0.02643	
0.1976	0.2115	0.2364	
0.0482	0.05263	0.08418	
0.185	0.2229	0.3664	
0.6053	0.6225	0.5105	1
0.05142	0.03205	0.02327	1
0.4687	0.4023	0.4272	
0.4764	0.5362	0.4871	1
			1
0.1137	0.1441	0.3089	
0.3572	0.3172	0.1829	
0.02422	0.01156	0.001829	1
0.2516	0.2277	0.1777	1
			1
0.4315	0.4238	0.4052	1
			1
0.7068	0.6983	0.765	
			1

0.3358	0.271	0.1441	
0.1615	0.2139	0.1538	1
0.08443	0.07205	0.07811	
0.7525	0.7334	0.8279	
0.4136	0.3889	0.3771	
0.2844	0.2653	0.2924	1
0.2122	0.1977	0.1388	
0.1396	0.2042	0.2433	
0.209	0.2194	0.2111	
0.8221	0.8378	0.8787	1
0.1232	0.2056	0.2046	
0.128	0.07948	0.02529	
0.06035	0.04638	0.02365	
			1
0.00001848	0	0.00006118	1
			1
0.3484	0.2753	0.1445	
0.354	0.2807	0.1506	
0.03292	0.05217	0.02982	
0.07289	0.0634	0.03078	
0.3123	0.2741	0.3292	
0.1127	0.167	0.2466	
0.1164	0.05155	0.008339	
0.29	0.3055	0.2772	
0.1693	0.1835	0.2491	
0.07615	0.05347	0.01586	
0.7398	0.5664	0.5483	
0.7424	0.5641	0.542	
0.6942	0.5135	0.4613	
0.2307	0.1616	0.1598	
0.2177	0.2186	0.1657	
0.07687	0.05652	0.02271	1
			1
0.299	0.2751	0.2519	1
0.05088	0.07015	0.06787	

0.5904	0.5397	0.4367	1
0.3652	0.3381	0.2509	
0.5798	0.6393	0.6754	1
0.1601	0.1407	0.2091	
0.04818	0.02594	0.01041	1
			1
0.02991	0.0302	0.01866	1
0.1178	0.1297	0.104	1
0.3318	0.3516	0.2818	
0.08152	0.0913	0.06437	
0.2276	0.2196	0.3735	1
			1
0.2972	0.2551	0.2332	
0.4683	0.3775	0.3234	1
0.2386	0.2795	0.531	
0.9115	0.9428	0.9892	
0.3752	0.4245	0.5155	
0.325	0.2652	0.2235	
0.3899	0.3899	0.3175	1
0.7751	0.7579	0.7354	
0.341	0.415	0.4736	1
0.1364	0.1145	0.1627	1
0.1803	0.1488	0.07199	
			1
			1
0.1379	0.09677	0.06909	1
0.0091	0.001529	0.0009057	
			1
			1
			1
			1
0.1643	0.1377	0.03113	
0.3443	0.2847	0.2064	
0.03679	0	0.05928	
0.2109	0	0.3775	1
			1
0.1208	0.1199	0.1394	
0.7334	0.7457	0.6258	
0.3057	0.2738	0.2442	

0.3262	0.3793	0.3218	
0.06521	0.06196	0.01482	
0.4596	0.3736	0.48	
0.1474	0.1391	0.2509	
0.3095	0.3256	0.2955	
0.4958	0.5337	0.6212	
0.2375	0.3187	0.3886	
0.225	0.222	0.2873	1
0.086	0.1095	0.1567	
0.1242	0.1576	0.2928	
0.1841	0.2261	0.3026	
0.6066	0.6568	0.7102	1
0.09809	0.06575	0.07876	1
0.2014	0.1614	0.1215	1
0.3209	0.3906	0.3209	1
0.235	0.2232	0.3949	
0.03746	0.01869	0.002922	1
0.00416	0.004335	0.0007925	1
0.1851	0.2159	0.3442	1
0.1094	0.1171	0.1023	1
			1
0.01718	0.009434	0.01133	
0.1708	0.1733	0.2323	1
0.132	0.1485	0.04206	
0.005679	0.01757	0.006198	
0.2853	0.2799	0.3598	
0.3386	0.3299	0.349	
			1
0.1268	0.0791	0.02734	1
0.0181	0.01355	0.002328	
0.5129	0.4774	0.2559	
0.2655	0.2924	0.3541	

0.3035	0.2834	0.308	1
0.002958	0	0	
0.002619	0.001453	0.0001225	
0.1943	0.1512	0.03933	
0.2252	0.2	0.1631	
			1
0.1514	0.1612	0.1778	
0.1845	0.1644	0.02423	1
0.3456	0.3804	0.2847	1
0.3214	0.3012	0.2351	
0.6096	0.611	0.6013	
0.1442	0.1988	0.264	
			1
0.06086	0.04118	0.01094	
0.4199	0.4006	0.4468	
0.6438	0.6922	0.7989	
0	0	0.0007286	
0.0274	0.02985	0.003031	
0.2032	0.1902	0.1947	1
			1
0.02448	0.01613	0.005343	
0.1198	0.1393	0.06704	1
0.3756	0.3719	0.3371	1
			1
0.1202	0.187	0.1276	
0.3441	0.2407	0.2672	
0.3596	0.3387	0.4388	
0.08301	0.07061	0.08966	
			1
0.6833	0.698	0.6608	1
0.5445	0.6239	0.6695	
0.6154	0.6526	0.7008	1
0.2454	0.2349	0.2709	1
0.189	0.1749	0.1787	
0.5762	0.5263	0.5144	

0.1217	0.1239	0.1642	
			1
0.07601	0.08095	0.1452	1
0.5604	0.5635	0.4721	1
0.3267	0.3186	0.2452	
0.8916	0.8862	0.8991	
0.04607	0.03613	0.007591	
			1
0.207	0.1879	0.06418	
0.2323	0.2521	0.2726	1
0.102	0.1203	0.2072	1
0.9092	0.8948	0.8288	
			1
0.3129	0.3199	0.4294	
0.2714	0.2147	0.1784	
			1
0.4035	0.3458	0.3273	1
0.1764	0.1772	0.2125	1
0.01307	0.007267	0.001604	
0.4192	0.4638	0.6637	1
0.2617	0.2705	0.1563	1
			1
0.403	0.3801	0.3517	
0.2092	0.2353	0.406	1
0.523	0.4986	0.4624	1
			1
0.3952	0.3601	0.3152	1
0.1766	0.1792	0.1509	1
			1
0.0696	0.06541	0.06534	1
0.3722	0.4889	0.3626	1
0.006536	0.002924	0.02468	
0.1144	0.1326	0.1312	
0.01197	0.01153	0.002015	
0.6171	0.7308	0.5588	
0.6064	0.587	0.644	

0.5569	0.5306	0.4773	
0.4761	0.4607	0.4909	
0.2393	0.21	0.2099	
0.2907	0.3798	0.4286	1
0.2792	0.2637	0.2094	
0.04188	0.07493	0.1856	1
0.4039	0.3136	0.3492	
0.01278	0.01009	0.003108	1
0.00001899	0	0	
0.714	0.7015	0.723	
0.6995	0.6826	0.7131	
0.2219	0.1513	0.06517	
			1
0.2461	0.2536	0.2292	
0.4967	0.5017	0.5369	
0.2546	0.2522	0.2625	1
			1
0.6938	0.6647	0.6038	
0.1625	0.1686	0.1795	
0.4347	0.3545	0.2074	1
0.146	0.1369	0.1505	1
0.3097	0.281	0.2488	
			1
0.4358	0.5287	0.5706	1
0.1478	0.1159	0.03183	1
0.2796	0.3194	0.5179	
0.001222	0	0	
0.5816	0.5672	0.609	
0.3202	0.3661	0.3836	
0.2883	0.339	0.2641	
0.2536	0.2764	0.2761	
0.0001141	0	0	1
			1
			1
0.5029	0.5	0.5529	1
0.005304	0.005814	0.003396	

0.1581	0.1274	0.2755	1
			1
0.5572	0.4355	0.5588	
0.3842	0.5278	0.5122	
0.04878	0.05814	0.06951	
0.3386	0.3438	0.3298	
0.07746	0.04746	0.03767	
0.03472	0.05172	0.01305	
0.01783	0.05217	0.09526	
0.2503	0.2534	0.2362	
0.6697	0.7097	0.7559	
0.191	0.1949	0.1092	1
0.04908	0.04755	0.05967	
0.3655	0.3923	0.1804	
0.3711	0.4035	0.1692	
0.2126	0.2462	0.3127	
0.7359	0.7118	0.6869	1
0.1572	0.1529	0.1575	1
0.0371	0.02063	0.009311	1
			1
			1
0.01849	0.01208	0.003001	
0.2396	0.2303	0.3229	
0.3166	0.3665	0.3448	
0.2306	0.2199	0.199	1
0.1131	0.09157	0.09182	
			1
			1
0.07852	0.04467	0.03974	1
0.4941	0.4405	0.3718	1
0.1277	0.1083	0.0549	
0.4663	0.4798	0.4001	1
			1
			1
0.2789	0.3026	0.3195	

0.2397	0.2246	0.1342	
0.6519	0.6383	0.6927	1
0.6768	0.5952	0.2397	
0.2727	0.2403	0.2738	1
0.4349	0.4597	0.3211	
0.376	0.4035	0.289	
0.3853	0.4236	0.3012	
			1
0.3577	0.3501	0.4623	
0.6174	0.611	0.5487	
0.4968	0.4919	0.4889	
0.4975	0.4951	0.4865	
0.07481	0.09545	0.06971	
			1
0.01834	0.02017	0.01628	1
0.07542	0.06902	0.01243	
0.1961	0.1758	0.2333	1
0.09383	0.07493	0.06043	
0.4478	0.429	0.4427	
0.09367	0.1111	0.07048	1
0.5709	0.4833	0.3622	1
0.212	0.2049	0.1654	1
0.4326	0.471	0.6544	
0.0271	0.02882	0.002804	
0.3758	0.3497	0.2914	
0.154	0.1473	0.138	
0.163	0.1435	0.05425	1
0.1368	0.1075	0.05082	1
			1
0.2667	0.3348	0.4015	
0.1897	0.1715	0.1134	
0.169	0.1627	0.281	
0.5266	0.5	0.5328	1
0.28	0.3184	0.4225	
0.7562	0.7472	0.6436	
0.4344	0.3243	0.1682	
0.1533	0.1206	0.133	
0.01537	0.01014	0.003664	
0.1033	0.09012	0.04913	

0.6034	0.5662	0.6087	
0.3413	0.2971	0.2888	
0.8394	0.8242	0.8508	
0.3159	0.4222	0.4362	1
0.03241	0.02609	0.01256	
			1
0.6785	0.7248	0.7463	1
			1
0.679	0.7248	0.748	1
0.4615	0.4725	0.4134	
0.1869	0.1931	0.2479	
0.2287	0.1947	0.1221	
0.2193	0.1911	0.1247	
0.001078	0	0.00009126	
0.1112	0.1238	0.1257	
0.2665	0.2725	0.3118	
0.3112	0.3393	0.3432	
			1
0.4062	0.4193	0.5361	
0.3011	0.2994	0.3577	
0.6961	0.6551	0.6407	1
0.3199	0.3718	0.4486	
0.01829	0.01235	0.03342	
			1
0.06175	0.04348	0.01317	
0.2075	0.245	0.3686	
0.02064	0.01732	0.0002989	1
			1
			1
			1
			1
0.0542	0.08213	0.1872	1
0.4919	0.5347	0.5387	
0.7342	0.7391	0.6392	
0.7602	0.7152	0.6305	
0.2311	0.2161	0.2107	
0.7705	0.7333	0.5925	1
			1

0.4131	0.4099	0.3189	1
0.3284	0.2333	0.09024	1
0.3719	0.3681	0.2898	1
0.3419	0.3763	0.3647	
0.01008	0.005848	0	
0.3848	0.4905	0.6038	1
0.4316	0.3709	0.304	1
0.5836	0.5548	0.5377	1
			1
0.4024	0.4503	0.462	
0.5261	0.5712	0.5766	1
			1
0.0286	0.02035	0.003109	1
0.4032	0.3344	0.3347	
0.241	0.2536	0.2343	
0.3621	0.3473	0.2184	
0.4127	0.3761	0.2521	
0.02304	0.03026	0.01767	
0.023	0.02882	0.01585	
0.1764	0.1979	0.193	
0.1756	0.1974	0.184	
0.1548	0.1508	0.07631	
0.1484	0.1052	0.05589	1
0.2907	0.2695	0.3493	
0.07308	0.09422	0.1985	
			1
0.3118	0.2752	0.2732	1
0.1124	0.2097	0.2142	
0.04583	0.1007	0.1434	
0.1125	0.102	0.01515	
0.009382	0.009542	0.01516	
0.4698	0.4784	0.3201	
0.1322	0.1369	0.08772	
0.3527	0.3271	0.2359	
			1
0.5029	0.4966	0.5275	
0.9549	0.9757	0.9993	
0.1368	0.118	0.03272	
0.1136	0.09416	0.1032	
0.2697	0.2565	0.1986	
0.2236	0.2122	0.2808	
0.08864	0.05193	0.05357	1
0.3028	0.3333	0.4186	

0.1354	0.1667	0.1333	1
0.08871	0.0879	0.2153	1
0.5452	0.552	0.5764	
0.5062	0.3781	0.203	1
0.4904	0.5587	0.5557	
0.2436	0.4012	0.4504	
0.1468	0.2393	0.3096	
0.08294	0.1667	0.09878	
0.3208	0.328	0.4263	
0.2314	0.0625	0.1003	
0.6361	0.6455	0.7246	
0.2844	0.1942	0.1566	1
0.2844	0.2666	0.1765	
0.04099	0.05769	0.05127	1
			1
0.3261	0.2978	0.2745	
0.04739	0	0.02469	
0.1986	0.1475	0.0535	
0.6034	0.5928	0.4968	
0.336	0.4306	0.4967	1
			1
0.7296	0.7873	0.8698	
			1
0.06134	0.05523	0.0113	
0.6502	0.711	0.7751	
0.03855	0.03395	0.01676	
0.04733	0.05638	0.05684	
0.04712	0.05491	0.05192	
0.4705	0.4026	0.3603	1
0.4947	0.4452	0.5711	
0.1286	0.1239	0.08666	
0.1334	0.1254	0.07807	1
0.002797	0	0	1
0.01958	0.01012	0.03441	
0.4487	0.4113	0.4627	
0.6165	0.6153	0.6734	
			1

0.3915	0.3818	0.3736	
0.1232	0.1437	0.07568	1
0.4688	0.4321	0.5467	1
0.3196	0.2538	0.2089	1
0.6488	0.6138	0.5671	
0.2216	0.178	0.1678	1
0.06743	0.0538	0.04918	
0.1319	0.1283	0.08433	
0.1178	0.1036	0.02448	1
0.2701	0.2507	0.2478	
0.5419	0.5652	0.4887	1
0.0004025	0	0	1
0.2776	0.3062	0.2532	
0.3401	0.3353	0.3972	
			1
0.7682	0.7723	0.6681	
0.3374	0.4092	0.476	1
			1
0.2282	0.2205	0.2143	
0.4494	0.4397	0.3691	1
0.3465	0.3226	0.1448	1
			1
0.1438	0.1916	0.3236	
0.1529	0.2176	0.4139	
0.06755	0.06176	0.02281	
0.4447	0.3991	0.3086	1
0.3374	0.4249	0.4841	1
0.005834	0.007205	0.001889	
			1
0.2344	0.1919	0.1352	1
0.2616	0.2791	0.2624	1
0.2641	0.2876	0.2596	1
0.06454	0.04038	0.01392	
0.3089	0.2847	0.2732	
			1
0.0149	0.008798	0.003657	

0.6433	0.6311	0.5423	
0.125	0.1895	0.2134	
0.216	0.2277	0.1659	1
0.2338	0.245	0.1132	
0.8956	0.9247	0.9859	
0.01046	0.008671	0.004456	
0.02127	0.0177	0.004239	
0.1478	0.1515	0.03592	
0.5287	0.5394	0.4782	
0.7269	0.7621	0.7051	
0.1191	0.1177	0.1228	
0.285	0.2928	0.2275	
0.2584	0.2529	0.1886	
0.4052	0.4064	0.3537	
			1
0.3466	0.3112	0.4061	
0.4305	0.379	0.4054	
0.3634	0.4092	0.4089	
0.3674	0.3512	0.3434	
0.2155	0.2064	0.2409	
0.2703	0.2544	0.2137	
0.08661	0.06324	0.04185	
0.03568	0.04863	0.1188	
0.002887	0.003049	0.003019	
0.1225	0.1306	0.203	1
0.4334	0.3907	0.3105	
0.3472	0.3377	0.3007	
0.3466	0.3412	0.2968	
0.00829	0.01884	0.005463	
0.08345	0.1235	0.1173	
0.0008591	0.001488	0.00006289	
0.03971	0.01075	0.0303	
0.1229	0.1841	0.3056	
			1
			1
0.1065	0.1017	0.1514	
0.3624	0.3939	0.4156	

0.193	0.1931	0.1451	
0.0004438	0	0.002382	
0.6985	0.7	0.7323	
0.7362	0.7783	0.7908	
0.6229	0.5652	0.4685	1
			1
0.2689	0.2729	0.2534	
0.7415	0.7566	0.7646	
0.6777	0.7199	0.7495	
0.7263	0.7507	0.7696	
0.02825	0.03913	0.03645	
			1
			1
			1
0.7126	0.7795	0.8695	1
0.5567	0.6181	0.661	
0.3686	0.4065	0.3964	1
0.3635	0.4078	0.4037	
			1
0.721	0.7052	0.653	1
0.2592	0.2757	0.2861	
			1
0.3093	0.2833	0.3598	
0.2369	0.2581	0.3045	
0.4865	0.5215	0.5537	
0.01495	0	0.0002456	
0.2278	0.2228	0.3264	1
0.2698	0.2471	0.1645	
0.586	0.5411	0.5064	
0.07949	0.07854	0.04352	1
0.0005706	0	0	
0.3137	0.3783	0.51	1
0.3407	0.3627	0.4246	
0.03202	0.02193	0.003551	
0.04315	0.09654	0.09553	
0.02863	0.02344	0.01099	

0.8489	0.8176	0.7906	
0.4982	0.4789	0.3761	
0.03784	0.05992	0.1153	
0.7207	0.7486	0.6943	
0.4233	0.4243	0.5559	
0.1912	0.1789	0.2266	
0.6917	0.6874	0.6985	
0.3436	0.3333	0.2162	1
0.4613	0.4083	0.3609	
0.324	0.2486	0.1275	
0.4664	0.4856	0.5072	
0.9082	0.8989	0.8544	
0.01268	0.01228	0.002785	
0.2624	0.3098	0.4398	
0.3049	0.3221	0.2152	
0.3051	0.3485	0.4636	
0.03152	0.04899	0.05887	1
0.4233	0.4075	0.3741	
0.1995	0.1806	0.1845	
0.0005203	0	0.00009953	1
0.6232	0.6239	0.5447	
0.0003865	0.002882	0.006462	1
0.002137	0.002793	0	
0.06349	0.09644	0.08139	1
0.3143	0.2635	0.1866	
0.1301	0.1103	0.1005	
0.2632	0.2507	0.2485	
0.1766	0.1662	0.2193	
0.1296	0.1488	0.1502	1
0.3922	0.4425	0.3747	
0.3601	0.4305	0.3821	1

0.11	0.0625	0.04054	
0.3636	0.4288	0.4839	
0.2558	0.244	0.2939	
0.3558	0.3372	0.3372	
0.0678	0.0625	0.04144	1
0.006106	0.00463	0.004492	
0.4187	0.5107	0.7166	
0.3776	0.4831	0.5088	
0.7213	0.7133	0.8133	
0.5348	0.5566	0.63	1
0.3419	0.4026	0.5239	
0.7863	0.8464	0.9236	
0.3095	0.3962	0.5344	
0.3611	0.3916	0.3833	
0.02433	0.01765	0.006735	
0.3777	0.3454	0.1837	
			1
0.2354	0.2046	0.1624	1
0.4022	0.3833	0.3242	1
0.6129	0.6527	0.723	1
0.4108	0.3947	0.317	1
0.5902	0.5953	0.6318	1
			1
0.2589	0.3052	0.4507	
0.3335	0.3212	0.3045	
0.186	0.1325	0.1065	
0.5042	0.5493	0.6218	
0.5849	0.6094	0.6355	
0.6246	0.5385	0.4986	
0.7338	0.7225	0.7156	1
0.267	0.2277	0.2192	1
0.2939	0.2201	0.0962	
0.157	0.1167	0.04242	1
			1
0.3636	0.3207	0.2431	1
0.00002006	0	0	1
0.7575	0.6286	0.4769	1
			1
			1
			1
0.5509	0.5239	0.4708	
0.007339	0.01153	0.008899	1

0.104	0.1341	0.1738	
0.04701	0.05132	0.0418	
0.5213	0.4408	0.457	
0.442	0.487	0.5672	1
0.4246	0.4577	0.5411	
0.3299	0.3766	0.5271	
0.3847	0.3987	0.5268	
0.3318	0.381	0.5052	
0.08427	0.04848	0.05754	
0.01209	0.008955	0.0007433	
0.01839	0.007246	0.003951	
0.408	0.4072	0.3724	
0.5427	0.5418	0.4168	
0.1406	0.1369	0.1056	1
			1
0.8232	0.7726	0.6377	1
			1
0.2736	0.2647	0.3235	1
0.395	0.3714	0.2983	
0.3015	0.264	0.2849	
0.002535	0.008696	0.01256	1
0.01598	0.005848	0.004174	
			1
0.6613	0.5997	0.5327	
0.1048	0.09091	0.08621	1
0.3457	0.3427	0.4277	
			1
0.5357	0.5332	0.4577	1
			1
0.00354	0	0.003014	
0.02222	0.02907	0.002598	
0.03035	0.05814	0.0053	1
0.483	0.5206	0.3697	
0.1494	0.1988	0.3117	
0.06325	0.03247	0.01288	
0.02393	0.02762	0.02783	
0.3155	0.3387	0.3529	
0.1113	0.1113	0.1663	
0.0443	0.0177	0.002548	1
			1
0.6863	0.7118	0.8225	1
			1
0.1222	0.1667	0.3145	1
			1
0.2031	0.1623	0.1566	1
0.0832	0.09845	0.1123	
0.2242	0.2579	0.3989	1

0.05114	0.06772	0.0949	1
0.6831	0.6257	0.6365	1
0.03439	0.0218	0.008965	
0.1697	0.1441	0.1985	1
0.187	0.147	0.1401	
0.04325	0.07609	0.1261	
0.225	0.2222	0.2247	1
0.3626	0.4049	0.4025	
0.1544	0.1637	0.1096	
0.3893	0.5145	0.6391	
0.694	0.7291	0.7121	
0.1949	0.2912	0.2759	
0.02452	0.03254	0.05621	1
0.222	0.2945	0.4375	
			1
0.549	0.6297	0.5443	
0.06118	0.05764	0.0381	
0.06356	0.05752	0.03715	
0.08738	0.07396	0.05432	
0.2788	0.2565	0.2333	
0.3064	0.2861	0.2691	
0.7868	0.7847	0.7265	
0.02555	0.03324	0.01098	
0.1779	0.1636	0.1051	
			1
0.1533	0.1797	0.2329	
0.1891	0.2256	0.2663	
			1
0.08718	0.04574	0.03284	
0.2625	0.2954	0.3673	
0.1471	0.1816	0.3274	
0.1809	0.1758	0.09508	1
0.08253	0.05469	0.01633	1
0.3652	0.412	0.3853	
0.01452	0.01462	0.001596	
0.3465	0.3276	0.4625	
0.3713	0.353	0.2458	

0.1672	0.183	0.1906	
0.1366	0.1313	0.1688	
0.01785	0.01153	0.00317	
			1
0.06556	0.1037	0.0605	
0.2358	0.1778	0.1205	1
0.00001886	0	0	
			1
0.3723	0.4539	0.4851	
0.01296	0.00578	0	1
0.4829	0.4859	0.5661	
0.2954	0.2834	0.3666	
0.1863	0.1455	0.1322	1
			1
0.4148	0.3483	0.326	1
0.4221	0.3422	0.3446	1
			1
0.3717	0.431	0.4332	
0.3029	0.3466	0.3777	
0.4893	0.3375	0.2696	1
0.2846	0.2435	0.1925	
0.1103	0.1441	0.2175	
0.1271	0.1556	0.2212	
0.3677	0.3052	0.1875	1
			1
			1
			1
0.2053	0.2259	0.2278	
0.4679	0.3862	0.2837	
0.3918	0.3406	0.177	
			1
0.2146	0.1855	0.1031	
0.2933	0.3452	0.3982	
0.2373	0.1884	0.1115	1
0.05347	0.07781	0.07557	
0.3259	0.2681	0.1579	1
			1
0.4736	0.5	0.559	
0.4053	0.4099	0.4549	
0.1618	0.1794	0.1544	
0.5144	0.4703	0.5147	
			1
			1
			1
0.1306	0.164	0.1838	
0.1008	0.06812	0.03931	1
0.4304	0.4594	0.4249	1

0.2509	0.2602	0.208	1
0.2784	0.2971	0.2647	1
			1
0.622	0.6697	0.6551	
0.4233	0.4188	0.36	1
0.3937	0.3815	0.345	1
0.5112	0.41	0.4158	1
0.4163	0.3939	0.361	1
0.4349	0.4316	0.3677	1
0.4255	0.4196	0.3701	1
			1
0.3157	0.291	0.3011	
0.5672	0.6142	0.599	
0.4416	0.3644	0.4558	
0.177	0.234	0.3413	
0.2744	0.2434	0.1565	
0.2851	0.3038	0.2794	1
0.3343	0.3284	0.4851	1
0.2961	0.2034	0.1543	1
0.4263	0.4545	0.4873	
0.2558	0.1923	0.05758	
0.1823	0.1792	0.09664	
0.1207	0.1037	0.1199	1
0.1239	0.134	0.1439	1
0.6057	0.6058	0.5803	
0.5625	0.5708	0.552	
0.379	0.3598	0.3622	1
0.2919	0.2875	0.3178	
0.2024	0.1925	0.2151	
0.5971	0.6253	0.735	1
0.39	0.3728	0.3628	1
			1
0.5831	0.5745	0.617	
0.5739	0.5609	0.5823	
0.5742	0.5621	0.5823	
0.3033	0.3309	0.4017	
0.4001	0.4234	0.4611	
0.4557	0.3834	0.3026	
			1
0.2851	0.2907	0.2575	1
0.5913	0.5714	0.3803	1
0.07784	0.09524	0.02451	
0.2933	0.3333	0.2711	

0.1062	0.08824	0.1634	
0.0587	0.05977	0.04484	
0.2241	0.216	0.2102	
0.4774	0.4212	0.2554	
0.1039	0.07276	0.02976	
			1
0.5654	0.5515	0.5728	
0.3377	0.2116	0.1471	
0.007728	0.005797	0.002198	
0.007894	0.007205	0.002255	
0.008609	0.007353	0.003099	
0.4871	0.515	0.462	
0.4	0.4841	0.5789	
0.1591	0.2064	0.2977	
0.2632	0.239	0.2116	
0.9159	0.9537	0.9898	
0.3577	0.4377	0.5794	
0.3622	0.3163	0.2368	1
0.2076	0.2186	0.3252	
0.3591	0.3631	0.1989	1
0.8472	0.8095	0.743	
0.2922	0.2733	0.3142	
0.7442	0.7248	0.7775	1
0.00708	0	0.0001363	
0.0001777	0	0	1
0.5225	0.4709	0.5266	
0.3979	0.3602	0.3688	
0.1801	0.1243	0.07603	
0.1709	0.1661	0.2022	
0.5664	0.5783	0.4804	1
			1
0.5478	0.565	0.559	
0.3321	0.2818	0.2747	
0.5704	0.5101	0.4326	
0.4518	0.462	0.42	1
0.6678	0.6529	0.6012	
0.8113	0.7162	0.6472	
			1
			1

0.353	0.3627	0.4703	
0.5244	0.5148	0.4849	
0.5329	0.5333	0.4556	
0.3982	0.438	0.5015	
0.008121	0.01195	0.004727	
0.4155	0.4531	0.5416	
0.373	0.3444	0.3423	
0.3391	0.3559	0.2427	
0.2155	0.25	0.2383	
0.5007	0.4257	0.3745	
0.7705	0.6338	0.3814	
0.3996	0.4333	0.3406	
0.411	0.4375	0.3308	
0.6157	0.629	0.6732	
0.627	0.6412	0.6763	
0.2426	0.2837	0.2999	
0.1815	0.1667	0.1023	
0.8075	0.8084	0.7272	
0.3833	0.4075	0.5362	
0.08885	0.1036	0.1233	
0.6518	0.5901	0.4921	
0.3592	0.3991	0.5408	1
0.1311	0.1472	0.2225	1
0.002587	0	0.002685	1
0.00003446	0	0.00009084	1
0.5723	0.5542	0.4784	1
			1
			1
			1
0.5409	0.5	0.4602	1
0.5437	0.4321	0.3355	1
0.2401	0.2867	0.3296	
			1
0.4456	0.3819	0.3786	
0.3675	0.3957	0.342	
0.9082	0.8833	0.9298	
0.8807	0.875	0.8441	1

0.8793	0.8827	0.8477	1
0.001722	0.003205	0	
0.00686	0.005556	0.007846	
0.2692	0.247	0.2287	
0.1268	0.111	0.04279	1
0.3124	0.3157	0.3743	1
0.2199	0.2147	0.226	
0.2207	0.2174	0.2267	
			1
0.04831	0.04348	0.01863	
0.1072	0.1064	0.0894	
			1
0.5566	0.5058	0.4416	1
0.5509	0.497	0.4498	1
			1
			1
0.1304	0.112	0.03923	
0.004363	0.003145	0.001535	
0.3226	0.3496	0.3169	
0.4668	0.575	0.6489	
0.1131	0.03968	0.02621	
0.2166	0.2469	0.1966	
0.2204	0.217	0.1411	
			1
0.09113	0.1081	0.1332	1
0.5837	0.5887	0.661	1
			1
0.3555	0.3689	0.315	
0.1306	0.08746	0.03637	
0.0003519	0	0	
0.1966	0.2054	0.1225	
0.2069	0.2006	0.1605	
0.4654	0.5752	0.6223	1
0.1717	0.1569	0.2444	
0.2292	0.2168	0.2902	
0.4439	0.5677	0.6337	1
0.7394	0.8026	0.8459	1
			1
0.01547	0.01739	0.1054	

0.4348	0.3851	0.502	
0.7693	0.7882	0.893	
0.1156	0.1453	0.1148	
0.2421	0.2637	0.1711	
0.2434	0.2118	0.1253	1
0.2207	0.2616	0.4042	
			1
0.07191	0.1106	0.1076	
0.5018	0.4986	0.4649	
0.06902	0.1023	0.09126	
0.5246	0.6434	0.7197	
			1
			1
0.2496	0.232	0.2006	1
0.002805	0.01304	0.0004337	
0.4776	0.4819	0.4638	
0.5634	0.5245	0.5534	
0.05639	0.0806	0.1597	
0.1289	0.1407	0.1627	
			1
			1
0.03821	0.03583	0.01229	1
0.06906	0.08883	0.1527	
0.009799	0.004323	0.004145	1
0.1457	0.1683	0.1057	
0.3048	0.342	0.2999	
0.4469	0.4286	0.3708	
0.02398	0.02427	0.003442	
0.7798	0.7966	0.7727	
0.2892	0.2731	0.3016	
			1
0.2619	0.1739	0.1129	
			1
			1

0.1683	0.1794	0.2487	
0.6824	0.6707	0.6307	
0.6164	0.5594	0.4527	
0.002242	0.01064	0.001405	
0.1814	0.2363	0.4589	
0.6054	0.6633	0.6265	
0.305	0.2543	0.2568	
0.4922	0.5504	0.5825	1
0.3834	0.4333	0.4769	
0.1756	0.2198	0.3379	
0.5282	0.4568	0.389	
0.06844	0.04678	0.04106	1
0.04276	0.03655	0.02431	1
0.1037	0.07205	0.09452	
0.1471	0.1279	0.1224	
0.2619	0.2752	0.2678	
0.1085	0.1571	0.2122	1
			1
0.2437	0.2032	0.1366	1
0.02765	0.02023	0.02213	
0.4304	0.2881	0.2979	
0.4609	0.3882	0.3034	
0.4213	0.5144	0.768	
0.01193	0.01207	0.0005475	
0.2911	0.2736	0.151	
0.3833	0.3343	0.4076	
0.1002	0.09412	0.1465	
0.1995	0.1737	0.04742	
			1
0.3774	0.3764	0.3229	
0.3046	0.2977	0.318	
0.03704	0.0276	0.00515	
0.3782	0.3746	0.3754	
0.486	0.5318	0.5803	1
0.005668	0.004264	0.008765	
0.1879	0.2009	0.2028	
			1

0.6759	0.7263	0.5777	
0.3303	0.3143	0.4377	
0.2413	0.2131	0.1236	1
0.4123	0.4472	0.4761	
0.01873	0.00597	0.004952	
0.243	0.2939	0.2588	1
0.002967	0.001608	0.0008886	
0.4615	0.4851	0.4733	
0.04811	0.07205	0.07455	1
0.1339	0.134	0.2334	
0.02811	0.01842	0.03382	
0.0353	0.02017	0.01202	
0.5189	0.4481	0.6638	
0.2042	0.1959	0.1207	
0.356	0.3995	0.667	1
0.003689	0.002915	0.001108	
0.1985	0.2608	0.2427	
0.6393	0.6773	0.661	
0.4058	0.3862	0.3913	
0.2827	0.3	0.2707	
0.2581	0.2986	0.4149	
0.2532	0.2896	0.4018	
0.3045	0.3055	0.4377	
0.3051	0.3199	0.4526	
0.1881	0.175	0.2141	
0.2604	0.2536	0.2427	1
0.587	0.6282	0.614	
0.2862	0.3046	0.2915	
0.08272	0.0634	0.03236	
0.2299	0.2694	0.2917	1
0.04199	0.01741	0.007378	
0.01417	0.01324	0.002057	
0.7352	0.7572	0.7924	

0.3601	0.3517	0.3807	1
0.000484	0	0.00051	
0.01336	0.007426	0.0000844	
0.2056	0.2215	0.2554	
			1
0.2195	0.1424	0.02824	
0.4307	0.4333	0.4141	1
			1
0.1371	0.1225	0.1022	1
0.1673	0.1455	0.1114	1
			1
0.2421	0.1807	0.04665	
			1
0.181	0.1477	0.2814	
0.2065	0.2556	0.2459	
0.4215	0.366	0.3712	
			1
0.001197	0.005618	0.0002535	
0.3091	0.3934	0.3588	
0.462	0	0.5366	
0.4433	0.5882	0.5847	
0.3972	0.4104	0.3877	
0.3076	0.3344	0.2732	
0.1123	0.1164	0.03591	
			1
			1
0.5839	0.5997	0.6538	
0.001154	0	0	1
0.3432	0.4032	0.3769	
0.00001969	0	0.0002662	
0.2039	0.1652	0.1314	
0.2499	0.2317	0.2335	1
0.2312	0.2944	0.2679	
0.8258	0.7826	0.8246	
0.358	0.3783	0.359	
0.6302	0.6875	0.6855	
			1
0.002528	0	0.0006006	
0.01167	0.008646	0.01505	1
0.03124	0.0245	0.01396	1
0.5976	0.6614	0.699	

0.6882	0.7003	0.7754	
			1
0.000843	0.00436	0.0001859	
0.04059	0.05187	0.08978	
			1
0.3704	0.3473	0.3584	1
0.732	0.6185	0.5564	
			1
0.3373	0.3329	0.3183	1
0.3286	0.3348	0.3162	1
0.6702	0.6455	0.5912	1
0.5865	0.5882	0.5673	1
0.5333	0.5304	0.5102	
0.01397	0.01475	0.006543	
0.001653	0.001475	0	
			1
			1
0.07089	0.05405	0.1248	
0.1813	0.2238	0.1738	1
0.4727	0.4688	0.3407	
0.2264	0.2075	0.2286	
0.1541	0.1811	0.2403	
0.1799	0.203	0.2038	
0.05045	0.07781	0.09447	
0.007467	0	0.002549	
0.01236	0.0132	0.002613	1
0.3856	0.3869	0.415	
0.4932	0.4522	0.4158	
0.2566	0.2832	0.3092	
0.3658	0.43	0.3905	
0.6307	0.5533	0.3811	
0.02991	0.01087	0.01319	
0.2668	0.3951	0.4445	
0.5191	0.5794	0.6211	
0.2018	0.3115	0.3651	
0.1253	0.09194	0.06535	

0.03599	0.02083	0.01377	
0.00001864	0	0	
0.5833	0.5288	0.607	
0.06001	0.07391	0.01947	
0.185	0.2055	0.1307	
			1
0.1144	0.1835	0.1156	1
0.1085	0.1203	0.1027	1
0.5231	0.5813	0.6944	
0.03042	0.03026	0.05627	
0.07846	0.09448	0.1297	
			1
0.4934	0.5494	0.4745	
0.3082	0.4006	0.6003	
0.5221	0.5482	0.5762	
0.1613	0.1838	0.2698	
0.2146	0.2702	0.3936	1
0.186	0.1801	0.2714	
0.2761	0.354	0.5414	
0.3549	0.3858	0.4133	
0.4931	0.5612	0.6405	
0.5273	0.5504	0.5891	
0.3581	0.375	0.2727	
0.4048	0.2949	0.1035	
0.01213	0.00436	0.004278	
0.363	0.415	0.423	
0.3293	0.3187	0.2408	
0.8158	0.768	0.635	1
0.2536	0.2444	0.2392	
0.4115	0.4204	0.3977	

FILTER	flanking_bps	variant_id	variant_qual
PASS	TCT	.	.
common_variant	CTG	rs10978447	.
PASS	GGC	rs279677	.
common_variant	TAT	rs11077414	.
PASS	CCT	.	.
PASS	TTT	rs2041171	.
common_variant	GAG	rs2364315	.
common_variant	TAT	rs6501947	.
PASS	CTG	rs554012320	.
PASS	CGCC	rs55685226	.
common_variant	CCC	rs1799859	.
common_variant	GCG	.	.
common_variant	CGT	rs12600864	.
common_variant	GTT	rs740250	.
common_variant	GCC	rs144177905	.
PASS	GCT	.	.
PASS	CCT	rs1251075	.
PASS	GCG	rs41291346	.
PASS	TTT	rs41303309	.
PASS	AGA	rs747166030	.
common_variant	CGT	rs11039146	.
common_variant	CGC	rs13087169	.
common_variant	GGG	rs12915634	.
PASS	ACA	rs61729367	.
PASS	TCC	rs7485573	.
PASS	AGC	.	.
common_variant	CCC	rs41264285	.
PASS	CCT	rs35431407	.
common_variant	GCT	rs12774070	.
common_variant	GAG	rs2251105	.
common_variant	GTAA	rs752944731	.
common_variant	ACG	rs3813622	.
common_variant	GAG	rs75553188	.
common_variant	TAT	rs56778727	.
common_variant	CTCTGTCCTCCCCCTA	rs67418568	.
PASS	CCT	rs41282522	.
common_variant	ATT	rs621375	.
common_variant	ATG	rs342467	.
common_variant	GGA	rs34463921	.
PASS	GTG	rs200527701	.
common_variant	CTG	rs12671813	.
common_variant	TCC	rs5182	.
PASS	ATT	rs13218824	.
PASS	GGA	rs8050390	.
common_variant	CTT	rs1053192	.
PASS	CCG	rs7517559	.
common_variant	CCC	rs72649360	.
common_variant	ACC	rs62619924	.
common_variant	CCG	rs878081	.
PASS	TTT	rs1003854	.
common_variant	TCA	rs733957	.
PASS	GCA	rs17164315	.
common_variant	TCT	rs4732036	.
PASS	ACA	.	.

common_variant	CGT	rs62128062	.
common_variant	GTC	rs4646686	.
PASS	CCG	rs1051713	.
PASS	TAG	rs55736017	.
common_variant	ACC	rs2289140	.
PASS	ATA	rs1626649	.
common_variant	AAT	rs1793173	.
common_variant	ACG	rs56780932	.
common_variant	GTG	rs2304872	.
common_variant	TATTTTTA	rs3067424	.
common_variant	CGC	rs4938014	.
PASS	CGC	rs35235926	.
common_variant	CTT	rs7853994	.
common_variant	GTT	rs7096505	.
common_variant	AAG	rs7630642	.
common_variant	AGG	rs11578772	.
common_variant	TCG	rs871130	.
PASS	ACG	rs115250350	.
PASS	TTA	.	.
PASS	GCG	.	.
PASS	ATG	rs2301587	.
PASS	AGA	rs140072315	.
PASS	ACG	rs755049876	.
PASS	AGG	.	.
PASS	CCC	rs74869251	.
PASS	TGG	.	.
common_variant	CTG	rs71428454	.
common_variant	CAG	rs71428453	.
PASS	TAG	rs455671	.
common_variant	AGT	rs17138632	.
PASS	CTGGG	.	.
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common_variant	AAG	rs793524	.
common_variant	TTG	rs10521763	.
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PASS	GCT	rs16837847	.
PASS	CGG	rs7550948	.
PASS	CCG	rs74404550	.
common_variant	AAG	rs3772219	.
common_variant	ATA	rs2296354	.
PASS	AAT	rs10972173	.
common_variant	GGT	rs12359433	.
PASS	ACT	rs6778511	.
common_variant	ACT	rs963618	.
common_variant	TAG	rs5951332	.
PASS	AGG	rs2361298	.
common_variant	ACC	rs3174476	.
common_variant	CAT	rs28365160	.
PASS	CCA	rs2305738	.
common_variant	GGA	rs28597966	.
common_variant	GCC	rs6151415	.
PASS	CTG	.	.
common_variant	ACG	rs2257090	.
PASS	AAT	rs62251997	.
common_variant	ACTG	rs143019035	.

PASS	GGA	.	.
PASS	GGG	rs1872858	.
common_variant	CCG	rs9895872	.
common_variant	CGG	rs1168966	.
PASS	CAG	rs749457	.
PASS	AGA	rs11790014	.
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PASS	AAT	.	.
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common_variant	TGT	rs45570436	.
PASS	AGC	rs36048052	.
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common_variant	CCT	rs17846715	.
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common_variant	CCG	rs1891	.
PASS	AGA	rs2853759	.
common_variant	TCT	rs113968994	.
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PASS	GGA	rs6021355	.
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common_variant	GCG	rs35725751	.
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common_variant	GAT	rs11577579	.
common_variant	CAC	rs11374767	.
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PASS	GTT	rs73137012	.
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PASS	AGA	rs741886	.
PASS	GTA	.	.
PASS	CGT	rs34233512	.
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PASS	GAG	rs536159058	.
PASS	AGG	rs62207506	.
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PASS	ACG	rs3092994	.
PASS	CCG	rs8176235	.
PASS	TGC	rs273900734	.
PASS	CCT	rs2126042	.
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common_variant	GTG	rs2283569	.
PASS	GCC	rs28992474	.
PASS	AGA	rs11200559	.
common_variant	GGC	rs986178	.
PASS	TTC	.	.
PASS	GCC	.	.
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PASS	CGC	rs7079392	.
PASS	GGT	rs3740694	.
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PASS	CTGAGAG	rs112580616	.
PASS	TGT	rs2302315	.
common_variant	ATG	rs730228	.
common_variant	GTG	rs8110590	.
common_variant	TTA	rs2304176	.
common_variant	TAT	rs17261572	.
common_variant	CAA	rs10927267	.
PASS	AATAATT	rs148512971	.
PASS	GTT	rs6688703	.
common_variant	TGT	rs41289218	.
common_variant	CTA	rs11077410	.
PASS	GGT	.	.
PASS	CTC	.	.
common_variant	CGG	rs366510	.
PASS	ACA	.	.
common_variant	AAT	rs41260544	.
common_variant	AGA	rs2269067	.
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PASS	ACG	rs139255231	.
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common_variant	CCT	rs62231971	.
PASS	ATACACACA	.	.
common_variant	CAC	rs7034745	.
PASS	CCT	rs77802779	.
PASS	TCC	.	.
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PASS	GTT	rs11014511	.
PASS	GGA	rs187651793	.
PASS	CCA	rs7797991	.
PASS	CGT	.	.
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PASS	AGT	rs734348	.
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common_variant	GCT	rs62113420	.
PASS	ACG	rs6925778	.
PASS	ACG	rs2493145	.
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common_variant	CTC	rs738304	.
common_variant	CGC	rs2304134	.
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PASS	GGA	.	.
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common_variant	ACT	rs74901418	.
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common_variant	CGT	rs35352238	.

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common_variant	AAT	rs144266211	.
PASS	ATG	rs74002500	.
common_variant	AAG	rs146524252	.
PASS	CTC	.	.
PASS	TCC	rs3762117	.
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common_variant	GGC	rs11653797	.
PASS	GGA	.	.
common_variant	TGT	rs11234627	.
PASS	CCC	rs3136658	.
common_variant	CGC	rs3092960	.
common_variant	AAT	rs2351528	.
common_variant	TGTG	rs58161637	.
common_variant	CAT	rs11265493	.
PASS	CCTG	rs55682471	.
common_variant	AAA	rs735482	.
PASS	AAT	rs4844390	.
common_variant	AGGGCAGAGGCTGCTG	rs779696544	.
PASS	GCT	.	.
PASS	CTC	rs561895	.
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common_variant	TTG	rs3749191	.
PASS	ACA	rs368295466	.
PASS	GGC	rs2272211	.
common_variant	GCC	rs2069529	.
PASS	GAT	.	.
common_variant	CAG	rs56087852	.
PASS	CCG	.	.
common_variant	TCG	rs13043456	.
common_variant	AGG	rs1265045	.
common_variant	GAC	rs2302399	.
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PASS	CAA	rs5828129	.
PASS	ACC	rs2231496	.
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PASS	GTA	rs2244682	.
common_variant	CTC	rs75243280	.
common_variant	ATAT	rs56066672	.
common_variant	CGA	rs41285260	.
PASS	CCA	rs117156562	.
PASS	GTC	.	.
PASS	ATT	rs62269547	.
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PASS	TAG	.	.
PASS	CAG	rs2270202	.
PASS	TTA	.	.
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common_variant	TTA	rs111775228	.
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PASS	CGC	rs2291254	.

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PASS	CTA	rs2302764	.
common_variant	GGG	rs582736	.
common_variant	GCG	rs4781019	.
common_variant	TGC	rs7012	.
PASS	TGC	rs278126	.
common_variant	GGT	rs3012627	.
common_variant	TTC	rs34054011	.
PASS	GCC	.	.
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PASS	CCG	.	.
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PASS	GGA	rs3829211	.
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PASS	TAT	rs1660694	.
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PASS	CCG	rs13068264	.
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common_variant	TAT	rs3779031	.
PASS	CTT	rs72760251	.
common_variant	CCT	rs1129262	.
common_variant	GAA	rs2303793	.
common_variant	CAT	rs62482495	.
PASS	GGG	.	.
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PASS	ATT	rs7538391	.
PASS	ATA	rs17128726	.
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PASS	GGA	.	.
common_variant	GTG	rs2839077	.
PASS	TTTTGT	.	.
common_variant	TCA	rs4818	.
common_variant	TAT	rs10927335	.
PASS	TGT	.	.
PASS	ACG	rs117188117	.
PASS	TCA	rs1564823	.
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common_variant	TGG	rs10760282	.
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PASS	ACA	rs3821157	.
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PASS	CAA	.	.
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PASS	AAA	rs1506441	.
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PASS	AAA	.	.

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PASS	CGG	rs782154947	.
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common_variant	TCG	rs6433817	.
common_variant	TGT	rs659040	.
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PASS	CCT	.	.
PASS	AGG	rs35206429	.
PASS	GTT	rs1709082	.
PASS	CCC	rs1709081	.
PASS	CTAAA	.	.
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PASS	AAC	rs1056142	.
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common_variant	CGA	rs9467075	.
PASS	TCA	.	.
common_variant	CAA	rs4742	.
PASS	TTG	rs531346334	.
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PASS	GAA	rs10739633	.
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PASS	AGT	rs9942410	.
PASS	GGG	rs5993488	.
PASS	GGC	rs374861176	.
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PASS	TAT	rs55956367	.
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PASS	ATC	rs72792311	.
PASS	GGA	.	.
PASS	TGTCACT	rs3082917	.
PASS	AAC	rs3082	.
PASS	ACG	rs11588937	.
PASS	TGG	rs10096210	.
PASS	AAT	rs17146082	.
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PASS	GGT	rs12951733	.
PASS	CTT	.	.
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PASS	GCG	rs6884561	.
PASS	ACA	rs2306431	.
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common_variant	CGA	rs1126464	.
common_variant	CAC	rs2304175	.
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common_variant	ACC	rs3213505	.
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PASS	CGT	rs34278949	.
PASS	AAG	rs369225897	.
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PASS	ATG	rs313407	.
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PASS	ACA	rs1919691	.
PASS	TCA	.	.
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common_variant	CGA	rs2071857	.
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common_variant	CAA	rs7292751	.
PASS	CCT	rs2239691	.
PASS	GGG	.	.
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PASS	TAC	rs2252767	.
PASS	TAT	rs1871685	.
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common_variant	GAA	rs2273706	.
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PASS	CAT	rs10760503	.
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PASS	TAA	rs79643517	.
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PASS	GGC	.	.
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common_variant	CGT	rs1800291	.
common_variant	TCA	rs7058826	.
PASS	AGT	.	.
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common_variant	GCG	rs174589	.
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common_variant	CGT	rs6007594	.
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common_variant	GGC	rs62599865	.
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PASS	CCT	rs942482434	.
PASS	GAA	rs916668	.
PASS	GCA	rs2075566	.
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common_variant	AGC	rs771204	.
common_variant	GAG	rs9358802	.
common_variant	GCT	rs11555275	.
PASS	AGA	.	.
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PASS	CGC	rs553196851	.
PASS	GGC	rs7630741	.
PASS	GGA	.	.
PASS	TCA	rs11119925	.
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common_variant	CGG	rs351855	.
common_variant	AGT	rs1049636	.
PASS	GTT	rs1893433	.
common_variant	ACG	rs3744903	.
PASS	ACG	rs1893434	.
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PASS	ATA	.	.
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PASS	TGG	rs3214903	.
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common_variant	ATC	rs2293783	.
PASS	CGC	rs4714489	.
PASS	CTT	rs10106	.
common_variant	ATG	rs345514	.
PASS	TCT	rs35583270	.

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common_variant	CAA	rs34505482	.
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PASS	TTC	.	.
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common_variant	TAT	rs9807877	.
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PASS	ACA	.	.
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PASS	GAGG	rs3830208	.
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PASS	GAA	rs76999174	.
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common_variant	CGT	rs1468556	.
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PASS	GGA	.	.
PASS	AGG	rs3806338	.
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common_variant	TCG	rs5384	.
common_variant	TAC	rs71548508	.
common_variant	TAG	rs17057536	.
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common_variant	ATC	rs9971293	.
PASS	GAC	rs10136536	.
PASS	CAC	rs181881694	.
common_variant	GCG	rs1254898	.
common_variant	GCG	rs11083455	.
common_variant	CGC	rs56854837	.
common_variant	CGG	rs79309130	.
common_variant	TGG	rs147513433	.
common_variant	CGT	rs6076347	.
common_variant	TGC	rs2303275	.
common_variant	ATG	rs2303278	.
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common_variant	ATG	rs4907817	.
common_variant	TTC	rs12844618	.
common_variant	CGT	rs79806135	.
PASS	ATT	rs11229655	.
PASS	TAA	rs4852349	.
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common_variant	GCG	rs5748449	.
common_variant	TGC	rs4986942	.
common_variant	CGA	rs12823938	.

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common_variant	TAT	rs2793442	.
PASS	CTCGC	.	.
PASS	GGG	.	.
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common_variant	TGC	rs4838684	.
PASS	ACC	rs147825070	.
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PASS	TTC	rs62265406	.
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PASS	TGT	rs116870369	.
PASS	TTA	.	.
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common_variant	AGC	rs4475186	.
common_variant	CTC	rs41312596	.
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PASS	GGG	rs34108640	.
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PASS	GCG	rs974285	.
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common_variant	ACG	rs72681249	.
PASS	TCG	rs12356612	.
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PASS	TGC	rs616218	.
common_variant	ACC	rs1052278	.
common_variant	GTA	rs17676826	.
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common_variant	CCG	rs2379206	.
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common_variant	GTG	rs4720951	.
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PASS	TTA	.	.
PASS	AAT	rs12220588	.
common_variant	TTG	rs10882474	.
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PASS	CCA	.	.
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common_variant	GCT	rs148714837	.
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PASS	GCA	.	.
PASS	CCG	rs16891397	.
PASS	ACA	rs77463023	.

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PASS	CTCC	.	.
common_variant	CCT	rs14362	.
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PASS	AATTTT	rs546127026	.
common_variant	TGG	rs1131488	.
PASS	CGA	rs2272790	.
common_variant	GGC	rs1053593	.
common_variant	GTG	rs2071190	.
PASS	GGC	rs77856552	.
common_variant	GCA	rs35337531	.
common_variant	CGC	rs3830343	.
common_variant	GGG	rs3737243	.
PASS	GGC	.	.
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common_variant	ACG	rs200650762	.
common_variant	ACG	rs11558819	.
PASS	AAG	.	.
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PASS	GGT	rs540557518	.
PASS	TAG	rs12904700	.
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common_variant	CTT	rs1051393	.
PASS	AAT	rs33982004	.
PASS	ATC	rs609207	.
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PASS	TGT	rs2274849	.
PASS	GCG	rs34297802	.
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PASS	AGG	.	.
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common_variant	TTA	rs61886896	.
PASS	CAGCCTA	rs139927942	.
common_variant	TCA	rs1063110	.
common_variant	TTGGG	rs57179462	.
common_variant	GGA	rs146644651	.
PASS	GCC	rs41268137	.
PASS	TCA	rs12722600	.
PASS	CAC	rs143249661	.
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PASS	AAG	rs3741211	.
common_variant	ACG	rs2059806	.
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PASS	GTT	.	.
PASS	TGA	.	.
PASS	GAG	rs3797390	.
PASS	TGCC	.	.
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PASS	CCT	rs75282194	.
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PASS	TAT	rs1109216	.
common_variant	TTA	rs2274617	.
common_variant	GTT	rs2305586	.
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PASS	ATT	rs2239547	.
common_variant	ACA	rs2276817	.
PASS	ATG	rs2240917	.
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PASS	ATG	.	.
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PASS	GAG	rs41289438	.
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PASS	CCA	.	.
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common_variant	AGT	rs11913944	.
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PASS	ATACACACACA	rs147073742	.
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PASS	TTA	rs757731918	.
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common_variant	CGT	rs12046928	.
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PASS	AGT	.	.
PASS	CCA	.	.
PASS	AGCTC	.	.
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PASS	TTT	.	.
PASS	CTG	rs149140699	.
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PASS	GCG	rs34946378	.
PASS	AGG	.	.
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PASS	CTC	rs2071602	.
common_variant	GTC	rs463217	.
common_variant	CTG	rs9306112	.
common_variant	CAG	rs9984726	.
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PASS	TTCC	rs3841288	.
PASS	CAT	.	.
PASS	AGC	rs9374309	.
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PASS	ATG	rs6672093	.
PASS	TGA	rs2296299	.
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PASS	TGT	.	.
PASS	TCT	.	.
PASS	GGG	rs6695528	.
PASS	TGT	rs11610822	.
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PASS	CGG	rs575867042	.
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PASS	TATT	.	.
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PASS	GAG	rs2354444	.
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PASS	TCA	rs2839146	.
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common_variant	GTC	rs2233055	.
PASS	CCT	.	.
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PASS	GGA	.	.
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PASS	CCA	.	.
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PASS	GGG	rs2289718	.
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PASS	CCT	rs73492943	.

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PASS	GTG	rs2302320	.
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PASS	CAT	rs10489691	.
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PASS	CCG	rs12501541	.
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PASS	TTTGTGT	rs34883891	.
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PASS	CCA	.	.
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PASS	GGG	.	.
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PASS	CTG	rs56397652	.
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PASS	TCA	.	.

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PASS	ATTCTAAT	rs10567712	.
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PASS	ACA	rs1806222	.
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common_variant	CAG	rs173776	.
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common_variant	GCT	rs1867780	.
PASS	TTC	rs6676171	.
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common_variant	AGG	rs17570	.
PASS	GAA	rs1061338	.
PASS	CAG	rs2306304	.
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PASS	ATC	rs7967264	.
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PASS	GAG	rs4072830	.
common_variant	CAG	rs12727342	.
PASS	CTT	rs10752744	.
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PASS	TGG	rs3744078	.
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PASS	AGT	.	.
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PASS	TCG	.	.
PASS	AAA	.	.
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PASS	CGG	rs384726	.
PASS	CCT	.	.
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PASS	GGG	rs9626578	.
PASS	TTA	rs150305650	.

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PASS	GGC	rs59007873	.
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common_variant	TGG	rs17853260	.
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PASS	CTG	rs117568247	.
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common_variant	GTT	rs2058464	.
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common_variant	CAC	rs3751112	.
common_variant	CGG	rs3812730	.
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PASS	GCT	rs145796187	.
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common_variant	GTG	rs2306919	.
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common_variant	GGG	rs10875687	.
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common_variant	ACG	rs201983107	.
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PASS	TCT	rs2963925	.
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common_variant	CCG	rs1549168	.
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PASS	GGA	.	.

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PASS	AGT	rs144040326	.
PASS	AGG	.	.
PASS	ATA	rs9864412	.
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PASS	AAC	rs2224797	.
PASS	CGT	rs7900838	.
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common_variant	ACG	rs7136561	.
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common_variant	GGA	rs73020697	.
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PASS	TTT	.	.
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common_variant	CCA	rs7580	.
PASS	CAC	rs6932660	.
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common_variant	CGA	rs2155722	.
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common_variant	AAT	rs3765595	.
common_variant	GTT	rs542998	.
common_variant	TCA	rs12658664	.
common_variant	CGG	rs11541392	.
PASS	CTT	rs7098448	.
common_variant	CGG	rs1805343	.
common_variant	TCG	rs11083462	.
common_variant	GGG	rs3745843	.
common_variant	ACG	rs75181912	.
PASS	CGG	rs777579024	.
common_variant	TTA	rs10754602	.
PASS	GAT	rs791541	.
PASS	CGT	rs41279198	.
PASS	ACT	rs11147974	.
PASS	GGG	.	.
PASS	TAC	rs11763269	.
common_variant	CAG	rs1053744	.
common_variant	AGT	rs11042500	.
PASS	CGG	.	.
common_variant	CCC	rs1142287	.
PASS	TCC	rs882745	.
PASS	ATC	.	.
common_variant	CAC	rs2240572	.
PASS	TGA	rs35006492	.
common_variant	CGG	rs167618	.
common_variant	AAG	rs1546961	.
PASS	CCC	rs3731760	.
common_variant	CAT	rs6746030	.

common_variant	AAA	rs10180721	.
PASS	CCC	rs73100512	.
PASS	GGC	rs3801066	.
common_variant	CCC	rs530168313	.
common_variant	CGG	rs9608973	.
common_variant	AGC	rs6695715	.
common_variant	ACT	rs2273526	.
common_variant	CGG	rs2303513	.
PASS	AAGACT	rs3830973	.
PASS	TAA	rs3750630	.
common_variant	AAC	rs3763695	.
common_variant	CCC	rs9420792	.
PASS	GCT	rs117852708	.
common_variant	TAT	rs61738919	.
common_variant	CAA	rs5362	.
PASS	CGA	rs17522707	.
common_variant	ATA	rs1990044	.
common_variant	GCA	rs17241389	.
PASS	TCT	rs6446202	.
PASS	TGA	rs1062753	.
PASS	AGG	rs9323910	.
PASS	GGA	rs268686	.
PASS	TGT	.	.
PASS	GGT	.	.
PASS	GTA	.	.
common_variant	GAG	rs35377445	.
PASS	AGG	rs7197262	.
common_variant	CGC	rs147508693	.
common_variant	TATTT	rs3998628	.
common_variant	CTG	rs2429908	.
PASS	GGT	rs2447099	.
common_variant	CGC	rs143734853	.
common_variant	CTT	rs7805	.
common_variant	ATG	rs3740471	.
PASS	ACG	rs187882127	.
common_variant	GCG	rs41275786	.
common_variant	ACC	rs1233555	.
PASS	GGC	.	.
PASS	CCG	rs3810108	.
PASS	TGG	.	.
common_variant	GGT	rs9982519	.
PASS	ATA	rs12145798	.
common_variant	GCC	rs11581248	.
PASS	CGG	rs779111224	.
common_variant	ATG	rs13106574	.
PASS	GCC	.	.
common_variant	AAA	rs11976455	.
common_variant	GTC	rs6647476	.
common_variant	GGG	rs2269914	.
common_variant	AGG	rs11668879	.
common_variant	TTG	rs2631365	.
PASS	TGG	.	.
common_variant	ATG	rs941650	.
PASS	AAT	.	.
common_variant	CCG	rs12942600	.

PASS	ACG	rs112153156	.
PASS	CCG	rs145107782	.
PASS	GTC	rs4980349	.
PASS	AACC	.	.
PASS	TCC	rs41302651	.
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common_variant	AGC	rs205966	.
PASS	AGG	rs35870005	.
PASS	TAT	rs948270	.
common_variant	CAG	rs78020607	.
PASS	AGG	.	.
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PASS	AGC	rs12703112	.
common_variant	TAG	rs4808709	.
PASS	CAC	rs10521578	.
common_variant	GGT	rs2278405	.
PASS	AGA	rs6354	.
common_variant	CGG	rs2248253	.
common_variant	TCA	rs1569951	.
common_variant	CGC	rs17183863	.
common_variant	CCG	rs1056846	.
PASS	AACGAAGAGTGC	.	.
PASS	TTT	.	.
PASS	ACTTT	.	.
PASS	ACA	rs11090629	.
common_variant	AGT	rs3742909	.
PASS	CGT	rs917208	.
common_variant	ACT	rs12065652	.
PASS	GCA	.	.
common_variant	CGC	rs1544402	.
common_variant	CAT	rs10754367	.
common_variant	TGG	rs12142616	.
common_variant	CGG	rs5908761	.
PASS	GGA	.	.
PASS	TAG	rs875097	.
PASS	GAG	.	.
common_variant	GGT	rs11548457	.
common_variant	CCG	rs2306324	.
PASS	GGA	.	.
PASS	GCA	rs58090119	.
common_variant	TCC	rs117804715	.
common_variant	AGG	rs12536873	.
common_variant	CCA	rs55776327	.
common_variant	CTT	rs1008335	.
PASS	CTGG	.	.
common_variant	CCG	rs139731922	.
PASS	AGT	.	.
common_variant	TAA	.	.
PASS	AGCA	.	.
common_variant	ATA	rs697210	.
PASS	AACC	.	.
common_variant	ACG	rs11556615	.
PASS	TGG	.	.
PASS	CAT	rs557622174	.
PASS	TGCC	.	.

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common_variant	CTG	rs10851866	.
common_variant	GCG	rs3934983	.
PASS	GCC	rs58802664	.
PASS	ACATATA	rs746073071	.
common_variant	TTT	rs1834	.
PASS	CAA	rs34275118	.
PASS	CGT	rs41285881	.
common_variant	CTG	rs3759259	.
PASS	CCG	.	.
PASS	CCA	.	.
common_variant	AGG	rs13050872	.
common_variant	AGT	rs237025	.
PASS	TGG	rs4803244	.
common_variant	GCG	rs1529733	.
common_variant	AAG	rs4341217	.
PASS	TAT	rs1390679	.
common_variant	GGG	rs1132645	.
PASS	CAC	.	.
common_variant	TGC	rs33976862	.
common_variant	ATA	rs74413846	.
common_variant	ACG	rs1744177	.
common_variant	CCG	rs3743244	.
common_variant	GGC	rs12645298	.
common_variant	TGG	rs3734296	.
PASS	TCT	rs237028	.
common_variant	GGG	rs17680881	.
PASS	ATG	rs3788764	.
PASS	CCG	rs2073138	.
common_variant	GGG	rs35105682	.
common_variant	ACA	rs572705	.
common_variant	TTA	rs606511	.
common_variant	GGT	rs394558	.
PASS	GAT	rs3217211	.
common_variant	ACG	rs146025212	.
common_variant	CCT	rs9573565	.
common_variant	ATG	rs1138454	.
PASS	ACC	.	.
common_variant	AGA	rs59223436	.
common_variant	GGA	rs5944856	.
PASS	TTA	.	.
PASS	CCT	rs10044956	.
PASS	TCG	rs12169610	.
common_variant	TCT	rs11851097	.
PASS	TTAAACAAACA	rs530289129	.
PASS	CCA	.	.
common_variant	CAC	rs251796	.
PASS	GTT	.	.
PASS	GGT	rs302858	.
common_variant	CTG	rs118141221	.
common_variant	AGG	rs12857479	.
common_variant	TCG	rs324356	.
common_variant	GCT	rs199687528	.
common_variant	CGG	rs12609379	.
PASS	AAA	rs11165376	.

common_variant	TGT	rs2290380	.
common_variant	CAC	rs513970	.
common_variant	AGA	rs6605530	.
PASS	GGCC	rs3214576	.
common_variant	CTG	rs2074603	.
PASS	CTC	.	.
PASS	CTGG	.	.
PASS	ATA	.	.
common_variant	AGT	rs41284222	.
common_variant	CGT	rs2292151	.
PASS	TGG	.	.
common_variant	CTG	rs200152166	.
PASS	ACG	rs2279322	.
PASS	CGC	.	.
common_variant	GCG	rs2228178	.
PASS	CTG	rs8036209	.
PASS	TTA	.	.
common_variant	AAC	rs2291822	.
PASS	CGT	rs77173980	.
PASS	CCC	rs12252784	.
common_variant	GGG	rs61741039	.
common_variant	CCTT	rs144703742	.
PASS	CGG	.	.
common_variant	AAG	rs76116020	.
PASS	CGG	rs895438	.
common_variant	CGG	rs3800592	.
common_variant	TTC	rs2276884	.
common_variant	AGT	rs5936308	.
PASS	CCTAGGTTGACTATCAT	.	.
common_variant	AAT	rs147529920	.
common_variant	TCG	rs12646286	.
common_variant	TAT	rs661561	.
common_variant	CCC	rs3181195	.
common_variant	CCG	rs12531309	.
common_variant	CGT	rs34377860	.
common_variant	ACT	rs2290207	.
common_variant	TGT	rs560191	.
common_variant	TTA	rs2602141	.
common_variant	AAT	rs16957730	.
common_variant	CCT	rs1045781	.
PASS	GCA	.	.
PASS	CAG	rs1697964	.
common_variant	CTG	rs1697963	.
PASS	TTA	.	.
PASS	CCG	rs10410833	.
PASS	ACA	rs9322994	.
common_variant	ATG	rs12147991	.
common_variant	CAG	rs2295275	.
PASS	ATG	rs3020967	.
PASS	TCT	rs1029237	.
common_variant	CGT	rs2269553	.
PASS	TGG	rs4971059	.
common_variant	GCG	rs35622844	.
common_variant	CAT	rs114415891	.
common_variant	CAT	rs2297889	.

PASS	GCC	rs11268748	.
common_variant	ATG	rs30774	.
PASS	CCC	rs200889110	.
common_variant	CTG	rs148858467	.
common_variant	ATA	rs7885599	.
PASS	ACC	rs1885117	.
PASS	GTC	rs12906081	.
common_variant	ACC	rs34350821	.
common_variant	AAT	rs2063010	.
PASS	TGG	.	.
common_variant	CAT	rs1073123	.
common_variant	CGG	rs10901220	.
PASS	GCA	.	.
PASS	CAT	rs12030928	.
common_variant	GCA	rs1802288	.
PASS	TAT	rs4826996	.
common_variant	GGG	rs1052773	.
common_variant	ATG	rs12664472	.
common_variant	GGC	rs3800294	.
PASS	TGT	.	.
PASS	AGT	rs35168566	.
common_variant	TCA	rs182730993	.
common_variant	CGC	rs2001324	.
common_variant	CTC	rs7898115	.
PASS	GTG	rs12254171	.
common_variant	CAC	rs7075277	.
common_variant	ATC	rs3750580	.
common_variant	CCT	rs1132079	.
common_variant	GAA	rs17634167	.
PASS	GAT	rs12796222	.
PASS	AAA	rs1046860	.
PASS	ACG	rs56058201	.
common_variant	GAA	rs705956	.
PASS	CTC	rs827958	.
PASS	TCC	.	.
PASS	GGA	rs753582974	.
PASS	TAC	rs2839509	.
PASS	GCC	rs12575062	.
common_variant	ATC	rs2301914	.
PASS	CGT	rs781247113	.
common_variant	TGC	rs16923472	.
common_variant	GGT	rs2734828	.
common_variant	TCG	rs2247238	.
PASS	GGC	rs7852539	.
common_variant	CTA	rs1716698	.
PASS	TCG	rs220147	.
common_variant	CGA	rs220159	.
common_variant	TCG	rs220150	.
PASS	ATA	.	.
common_variant	CCC	rs373842487	.
PASS	GGG	rs72836153	.
common_variant	TGG	rs62231899	.
PASS	TCC	.	.
common_variant	ACG	rs41277210	.
common_variant	CTG	rs4430871	.

PASS	CTT	.	.
PASS	TGC	.	.
PASS	AAG	rs9605536	.
PASS	CAG	rs41279154	.
PASS	GGG	rs3214918	.
PASS	TAC	.	.
common_variant	CCT	rs1220622	.
PASS	TTC	rs17031260	.
PASS	TCT	rs55721648	.
PASS	AAA	.	.
PASS	TGG	.	.
PASS	CCC	rs939592692	.
common_variant	CCT	rs79238281	.
common_variant	CCA	rs15493	.
PASS	GGCC	.	.
common_variant	CAT	rs11769825	.
common_variant	CTC	rs13246460	.
PASS	CAT	rs10857625	.
PASS	GCG	rs7079527	.
common_variant	CGG	rs10886789	.
common_variant	ACT	rs2289336	.
common_variant	TGC	rs1652727	.
common_variant	TCG	rs1866516	.
common_variant	TTT	rs4538426	.
common_variant	GGA	rs41307688	.
common_variant	GCT	rs181113399	.
PASS	CGG	rs147562907	.
PASS	GTC	rs2527189	.
common_variant	CCTCCTCCTCCTCCCTT	rs763153590	.
PASS	AGG	rs2278128	.
PASS	AGA	rs4720537	.
common_variant	TGC	rs11554421	.
common_variant	AAA	rs910697	.
common_variant	TGT	rs3793771	.
common_variant	CAT	rs3734500	.
common_variant	ACG	rs11068780	.
PASS	GGG	rs3733979	.
common_variant	GCT	rs2270844	.
PASS	AAC	rs4134861	.
common_variant	CGG	rs114552728	.
PASS	AGG	rs2273739	.
common_variant	CGG	rs148023469	.
common_variant	CAC	rs1106841	.
common_variant	CTG	rs915927	.
PASS	ACG	rs25486	.
PASS	AGG	.	.
common_variant	GAA	rs3738590	.
common_variant	TTT	rs2666826	.
common_variant	CCT	rs11155787	.
common_variant	ATC	rs9484827	.
common_variant	ACA	rs1001242	.
common_variant	GAC	rs415434	.
common_variant	CGG	rs556775	.
common_variant	CCG	rs11774714	.
PASS	TCT	rs574606000	.

common_variant	CCA	rs139527148	.
PASS	AAC	rs537807113	.
common_variant	AGG	rs2306159	.
PASS	CCG	rs931713	.
common_variant	CTT	rs7781581	.
common_variant	AAC	rs4982766	.
PASS	AAT	rs4734883	.
PASS	CAG	rs7915	.
PASS	AGC	.	.
common_variant	AAT	rs1989839	.
common_variant	CGC	rs2301639	.
PASS	TGG	rs2071258	.
common_variant	GCG	rs7066295	.
common_variant	CTG	rs862708	.
common_variant	CCT	rs28444973	.
PASS	GGA	rs10822043	.
common_variant	CAG	rs2910443	.
PASS	TGT	.	.
common_variant	CTG	rs11666149	.
PASS	GTC	rs384148	.
PASS	AAA	rs4829778	.
common_variant	ATG	rs1055753	.
common_variant	CTA	rs7273242	.
common_variant	AGC	rs8182086	.
common_variant	GGA	rs11556528	.
common_variant	TGT	rs9636139	.
PASS	AGA	rs3217340	.
common_variant	TCC	rs8104929	.
common_variant	CGG	rs12067843	.
common_variant	TTA	rs1781873	.
common_variant	CCT	rs11710621	.
common_variant	ACG	rs1129093	.
common_variant	GAC	rs35215913	.
common_variant	TCT	rs8110062	.
common_variant	TCG	rs12590618	.
common_variant	ACC	rs489172	.
PASS	GTC	.	.
common_variant	TGT	rs10403445	.
common_variant	ACT	rs781839	.

ExAC_AF_Adj	ExAC_AC_AN_Adj	ExAC_AC_AN	ExAC_AC_AN_AFR
0.03174	3339/105188	3344/106210	50/9062
0.59	62613/106132	62619/106210	2897/9040
0.5578	50589/90694	56800/105742	2014/7116
0.6583	69519/105606	69713/106192	6668/9018
0.00002841	3/105586	3/105950	0/8478
0.2953	31211/105680	31254/106208	6444/9040
0.04284	299/6980	3248/77598	138/490
0.1961	20692/105522	20728/106200	1020/8948
0.8446	88054/104256	89278/105826	7524/8190
0.05888	1642/27886	2718/101626	18/1492
0	0/16528	1/98338	0/2218
0.04864	5055/103934	5060/106208	219/8630
0.6234	66165/106132	66176/106210	3985/9062
0.3329	34168/102638	34814/106182	2157/8880
0.1626	17030/104766	17089/106206	1800/8868
0.3122	16138/51688	21686/105112	290/4130
0.4952	51355/103714	52227/106198	3702/8800
0.000862	16/18562	33/93574	0/2336
0.6552	65788/100406	69137/106004	5393/8962
0.0291	2985/102584	3012/106146	1085/8866
0.2249	15921/70790	18666/105412	1432/5648
0.07192	772/10734	800/18980	3/248
0.2403	25294/105276	25312/106210	5901/9056
0.5914	62641/105912	62714/106210	5037/9064
0.03341	2529/75705	3614/106186	39/7432
0.4287	6683/15588	7053/17768	531/1308
0.4874	51507/105682	51594/106184	1750/8682
0.205	21746/106078	21762/106210	2297/9052
0.3108	24303/78184	26786/106100	1284/6162
0.014	1485/106072	1485/106210	27/9024
0.2046	21706/106108	21707/106206	398/9000
0.4068	36923/90774	39355/106038	3826/7728
0.76	79373/104444	80531/106162	7328/8984

0.2512	24777/98622	25581/106084	1949/8884
0.1905	19953/104764	20078/106192	367/8948
0.07686	8154/106094	8155/106210	502/9056
0.7744	82229/106190	82233/106210	8197/9066
0.3545	5064/14286	13462/100598	143/1298
0.2585	27200/105206	27350/106210	983/8992
0.2325	20973/90214	21904/105960	3827/7940
0.2084	20079/96346	21085/105646	2458/8182
0.2122	21458/101130	21678/103932	1199/7368
0.8428	86925/103136	88442/105530	7202/8388
0.2221	7272/32738	13991/101298	1291/4002
0.09028	9517/105414	9544/106208	158/8720
0.04679	4913/105004	4923/105730	70/8408
0.00001897	2/105444	2/106208	0/8682
0.2713	27361/100848	28168/104070	1754/8196
0.2818	27864/98882	28742/103936	2136/8076
0.03902	4117/105506	4117/106168	51/8604
0.059	6265/106190	6265/106210	102/9066
0.2969	31127/104838	31292/106208	3762/9044
0.1866	13882/74398	19195/106204	2624/7418
0.07413	3001/40481	5206/105250	74/4055
0.3431	36415/106132	36419/106210	4787/9066
0.2194	23289/106166	23293/106210	413/9066
0.05043	5350/106098	5354/106210	120/9056
0.6481	6084/9387	9772/15816	413/483
0.6328	5915/9347	9665/15866	268/345
0.5233	3653/6981	6228/12594	54/189
0.1714	17534/102292	17654/106204	716/9020
0.206	13690/66470	15028/105952	1465/5452
0.05208	5448/104600	5474/106194	120/8548
0.2647	23036/87034	25175/105904	2068/6706
0.0458	4722/103104	4796/106196	210/8698

0.511	19822/38790	43159/98228	1006/2688
0.384	37792/98420	39486/106038	1859/8658
0.6721	53970/80300	68601/105108	5675/7226
0.1784	15999/89694	17825/106002	2231/7478
0.03367	3566/105922	3571/106208	230/9002
0.02772	2646/95450	2691/106172	575/7942
0.1074	11408/106180	11410/106210	185/9066
0.3558	37774/106176	37777/106210	2383/9066
0.0811	8562/105576	8565/105678	1352/8468
0.2562	19449/75904	27518/106204	2622/7390
0.2649	26813/101226	27572/106180	1709/8866
0.4044	42860/105982	42915/106208	4269/9030
0.27	28551/105736	28673/106206	1963/9060
0.9431	57024/60464	98479/105300	6495/6708
0.4172	31240/74889	44028/106208	1322/7407
0.2833	29841/105338	29904/106194	2646/8794
0.3612	36376/100718	37501/106074	5276/8576
0.7639	81064/106122	81078/106210	8005/9060
0.4177	44292/106042	44328/106210	5170/9048
0.1157	12020/103854	12121/106208	326/8704
0.1814	12765/70357	17864/105844	1681/7332
0.0879	1649/18759	4874/101716	30/2233
0.005075	498/98130	509/106192	13/8346
0.1121	10487/93526	11378/106130	276/7910
0.2677	28319/105780	28365/106210	2733/9032
0.03945	160/4056	275/18182	56/1300
0.2879	296/1028	3116/60188	131/442
0.1095	11582/105748	11601/106210	209/9028
0.7193	43145/59980	67884/100490	2155/3750
0.2823	28745/101824	29556/105952	2486/8078

0.3291	5669/17228	7162/28820	268/1520
0.04319	4586/106176	4586/106210	76/9064
0.4415	5633/12758	6220/15516	157/370
0.1583	16717/105582	16764/106208	2387/8972
0.3927	41626/105986	41671/106210	6303/9064
0.5583	55089/98672	57055/104774	4496/7484
0.2973	31237/105070	31416/106202	1707/8914
0.1977	14912/75422	21517/106194	250/7302
0.1701	18057/106164	18061/106208	3585/9066
0.1652	16912/102392	17056/106200	611/8900
0.2736	25293/92440	25841/98930	2508/7844
0.6692	63706/95194	70007/106142	5559/7882
0.07791	7664/98370	7858/106196	262/8228
0.2135	22662/106156	22673/106210	5367/9048
0.3321	3684/11094	4571/16372	183/250
0.2697	27582/102288	27920/106162	1814/8876
0.01979	551/27846	1090/104406	14/2782
0.002675	284/106168	284/106210	7/9064
0.268	28282/105538	28352/105758	4841/8468
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3473/11192	4631/7856	1726/6608	17003/54344
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1087/11150	3431/7776	286/6612	2613/54316
914/11206	771/7858	914/6614	7273/54322
72/5052	1/4804	65/3388	927/32976
68/11194	0/7858	293/6610	1915/54246
5506/11208	1950/7850	3134/6608	28176/54296
3094/11170	1228/7830	1423/6612	11032/54028
2749/8154	3484/5294	1349/3428	10287/28900
5/11040	0/7844	5/6550	197/53406
2880/11168	4502/7846	1545/6602	10746/54140
6460/11178	6675/7858	4257/6598	34586/54104
4767/11200	2088/7862	2720/6614	22052/54342
3846/11212	1943/7838	2219/6614	15365/54344
2660/11118	2835/7690	1670/6612	13228/51250
2572/11144	2846/7772	1738/6582	13706/54136
3499/11212	3325/7844	1348/6610	16541/54326
3512/11208	3327/7854	1348/6612	16581/54340
1051/11110	9/7752	817/6590	10095/53660
2958/11210	42/7866	1653/6614	14136/54296
8241/11194	5180/7838	3293/6580	31869/54294
2006/10124	1804/7410	1583/6130	14028/49010
410/11216	663/7858	365/6614	4495/54342
2526/9872	3435/6386	1267/6046	10360/45058
404/10892	0/7716	202/6102	2133/50794
78/11200	0/7852	116/6602	764/53914
6270/11190	5057/7836	5145/6612	39892/54262

3896/8264	552/5922	1598/4798	16724/46442
0/132	0/138	0/0	1/2066
36/7586	0/5546	26/2864	397/29706
686/8730	166/5855	648/4385	7570/36818
480/4188	1/3782	361/1462	5122/23338
3925/7162	2355/4898	2354/5684	15188/35264
918/11212	684/7864	677/6614	7449/54344
713/7192	558/5752	656/4840	6366/38044
413/5405	0/2134	547/2453	4495/18567
1421/11148	1197/7838	1082/6590	9539/52716
1740/11052	2728/7748	1582/6362	10866/52628
933/2440	1233/2844	297/676	6425/15244
0/292	0/322	24/1624	6/5012
68/156	64/226	432/1178	685/2216
23/38	4/10	4/6	85/184
133/222	93/314	914/1628	1424/3212
7229/11186	2168/7806	2966/6590	21507/54148
2768/9900	4/7204	1579/5582	15708/51062
16/286	20/322	175/766	537/4780
4648/11194	3037/7816	4059/6602	31668/54232
0/626	0/892	0/166	6/5198
5119/11200	3519/7850	2064/6606	18646/54322
0/9940	0/7218	0/5628	1/50784
951/11212	1379/7842	908/6612	11069/54292
3814/11044	1196/7802	1469/6564	13407/53650
2771/11036	5503/7804	2676/6534	12381/53560
9777/11210	6434/7834	5095/6610	44789/54240
5045/11208	2954/7824	2342/6606	19447/54322
8336/11212	4642/7834	3734/6610	34193/54256
1/1778	0/1930	0/506	25/9888
26/11214	25/7866	126/6612	634/54330
67/11108	1/7858	296/6604	1696/54282
8659/11208	6451/7854	4080/6610	32404/54220

9275/11210	6548/7846	5057/6614	37332/54246
50/11184	0/7802	0/6600	45/53380
2399/11212	1917/7862	166/6612	2205/54318
3943/11206	1097/7856	2997/6606	20124/54334
6609/11208	4789/7846	4480/6608	39760/54318
5901/11202	3321/7858	1874/6610	18325/54330
5675/10578	2980/7080	1739/6474	16828/51218
7683/11192	4129/7850	4401/6608	36376/54278
7476/11196	4071/7826	3343/6586	31769/54168
7190/11144	3134/7822	3008/6596	28781/53968
38/11040	0/7690	166/6546	732/52408
3/10772	0/7370	65/6554	87/52622
10/232	1/320	57/1636	283/3992
361/3778	306/3100	682/2262	4603/25386
5297/10842	5030/7712	3227/6384	25028/52946
1790/11154	1049/7862	1562/6606	12295/54314
2787/10738	2461/7582	880/6292	7718/50100
1902/10200	916/7322	833/5668	9013/50108
221/11206	2382/7852	241/6612	2740/54310
13/11100	3/7750	5/6606	383/51290
30/10688	0/7288	11/6484	647/52334
4065/10324	450/7132	2470/6368	19924/51672
610/2062	407/2698	1013/1922	10765/21826
4653/10994	5496/7790	1920/6544	13745/53576
898/1802	1765/2412	1145/2794	5805/15870
6530/11192	2303/7844	4454/6606	34240/54292
16/332	9/322	2/1688	173/5784
2052/3438	2506/3324	521/2218	3446/12918
6190/8672	5583/6386	1875/3492	19938/38410
3517/6424	3651/4896	487/2278	4940/24474
703/11120	2/7792	369/6598	6572/52430

74/8680	0/5762	160/4305	1289/35815
0/11204	0/7858	0/6592	1/53640
7438/11216	3423/7842	3939/6612	31699/54342
863/11206	1467/7850	496/6610	3244/54058
39/144	36/142	222/1208	541/2924
5748/11186	5250/7842	1255/6608	6214/54334
803/11156	394/7804	935/6548	5873/54118
6500/8003	4048/5141	1780/3338	16181/30932
903/11210	1544/7852	257/6612	1652/54312
2379/11116	3041/7778	761/6592	4200/53532
2188/4582	3201/4424	1036/2104	13848/28064
6088/11200	4087/7850	1881/6610	16736/54308
5734/11062	4941/7808	3189/6502	27752/53150
687/4786	120/4846	454/2604	5296/32838
4910/11196	3676/7838	1555/6612	11649/54270
2433/11114	292/7732	1420/6446	9673/51994
5907/11194	4085/7844	1995/6612	14969/54210
4393/11176	2858/7854	2263/6610	19273/54302
6512/11076	6322/7832	3558/6586	26453/53646
5893/11212	4913/7856	3252/6610	28650/54336
29/60	2/4	60/220	53/148
2528/9006	244/6031	1691/4523	15566/38457
82/11200	1/7850	9/6578	656/54068
2810/11216	2678/7854	2022/6612	19721/54334
2252/11114	3815/7742	2705/6580	17774/53978
9118/11210	3086/7834	4765/6580	44315/54320
2613/11098	1474/7780	2148/6576	13299/52434
2744/5944	1267/4414	1821/4560	14498/35232

ExAC_AC_AN_OTH	ExAC_AC_AN_SAS	ExAC_FILTER	MAF
			0.117647059
18/682	253/15732	PASS	0.3125
			0.125
424/694	10145/16406	PASS	0.120879121
			0.107142857
			0.4
351/616	9047/15250	PASS	0.107142857
442/692	10446/16388	PASS	0.15
0/690	0/16408	PASS	0.115044248
			0.277777778
193/682	4754/16366	PASS	0.138888889
0/32	59/1052	PASS	0.266666667
136/684	2378/16396	PASS	0.117647059
554/674	12899/16374	PASS	0.146341463
12/206	426/9286	PASS	0.121212121
			0.107142857
			0.2
			0.173913043
			0.147058824
0/130	0/7470	AC_Adj0_Filter	0.12
20/686	1976/16276	PASS	0.103448276
456/694	11465/16402	PASS	0.151515152
236/656	4476/14946	PASS	0.1875
			0.125
			0.179104478
		PASS	0.109756098
111/672	2341/16230	PASS	0.14893617
			0.132352941
99/318	2501/10272	PASS	0.113636364
327/678	7704/16188	PASS	0.155172414
0/186	12/7592	PASS	0.12962963
386/632	9538/12592	PASS	0.114649682
14/686	423/16006	PASS	0.119565217
99/468	2792/11812	PASS	0.117647059
6/114	629/7472	;RTrancheINDEL97.00to9	0.12
			0.2
152/682	5808/15852	PASS	0.119318182
432/694	8291/16240	PASS	0.25
15/468	231/9928	PASS	0.185185185
			0.117647059
70/174	3309/7746	PASS	0.125
370/690	7986/16394	PASS	0.14084507
			0.125
			0.111111111
100/694	5067/16402	PASS	0.15
			0.15
151/476	2308/12622	PASS	0.133333333
8/692	30/16406	PASS	0.11627907
158/694	2915/16408	PASS	0.105726872
			0.235294118
267/630	6129/15126	PASS	0.107142857
			0.13559322
479/686	12419/16234	PASS	0.176470588
			0.272727273

168/620	1621/11250	PASS	0.227272727
145/678	2494/16212	PASS	0.107692308
			0.160493827
			0.128571429
50/694	1279/16374	PASS	0.107692308
			0.333333333
509/694	13583/16406	PASS	0.181818182
42/108	1461/3874	SRTrancheSNP99.60to9	0.206896552
182/686	4780/16346	PASS	0.108433735
119/602	1701/12254	PASS	0.12962963
125/612	2681/11020	PASS	0.137931034
			0.135135135
147/670	3435/16272	PASS	0.166666667
568/678	14338/16318	PASS	0.1
51/248	1823/8912	PASS	0.2
55/692	413/16330	PASS	0.128205128
32/690	386/16318	PASS	0.214285714
			0.1875
			0.15
			0.191489362
			0.145833333
			0.139534884
0/692	1/16346	PASS	0.125
			0.115384615
			0.23255814
			0.103448276
185/672	2312/16004	PASS	0.133333333
183/652	2207/14654	PASS	0.103448276
			0.173913043
36/690	489/16396	PASS	0.108695652
			0.222222222
44/694	505/16408	PASS	0.208633094
188/686	5318/16154	PASS	0.259259259
76/455	2171/8805	PASS	0.153846154
10/194	26/3118	PASS	0.19047619
			0.114285714
			0.15
			0.75
212/694	4541/16380	PASS	0.102564103
127/692	4085/16400	PASS	0.106382979
			0.197530864
37/692	260/16398	PASS	0.138888889
			0.161290323
64/113	2311/4215	PASS	0.353846154
66/117	2458/4535	PASS	0.211538462
			0.169491525
38/74	2085/4520	PASS	0.148148148
107/662	2179/13632	PASS	0.189655172
			0.202380952
94/430	2176/13136	PASS	0.138211382
39/690	372/16380	PASS	0.113821138
			0.135135135
148/538	2982/11840	PASS	0.134146341
			0.15
47/670	992/14616	PASS	0.166666667

			0.107142857
			0.192307692
136/252	2926/6700	PASS	0.14084507
215/636	3141/12520	PASS	0.125
			0.118644068
			0.333333333
335/524	7696/11394	PASS	0.142857143
			0.166666667
85/604	2828/13524	PASS	0.15625
18/694	170/16332	PASS	0.153846154
			0.106382979
18/596	276/14794	PASS	0.119205298
90/694	1706/16408	PASS	0.102941176
244/694	4622/16404	PASS	0.14516129
63/690	1056/16404	PASS	0.160714286
			0.296296296
103/469	3748/10035	PASS	0.185185185
			0.125
			0.118811881
174/682	3752/16088	PASS	0.111111111
262/694	5299/16386	PASS	0.192307692
194/694	8578/16154	PASS	0.122137405
346/367	6604/6676	PASS	0.35
194/457	4884/9475	PASS	0.166666667
183/690	3615/16178	PASS	0.103448276
262/672	5043/15882	PASS	0.325
526/694	12067/16408	PASS	0.113821138
			0.119047619
			0.666666667
288/694	7765/16394	PASS	0.16
76/664	2645/16254	PASS	0.103448276
			0.105263158
61/410	445/6181	PASS	0.166666667
			0.210526316
			0.103448276
			0.135416667
12/124	354/5124	PASS	0.166666667
			0.166666667
			0.117647059
1/654	14/15458	PASS	0.134615385
			0.16
			0.104166667
			0.121212121
			0.12
84/610	460/14776	PASS	0.1
197/692	3369/16320	PASS	0.12345679
0/8	23/388	PASS	0.173076923
0/0	77/204	PASS	0.173913043
			0.111111111
			0.428571429
83/692	2267/16264	PASS	0.103448276
			0.136363636
			0.214285714
261/350	6686/10684	PASS	0.342857143
184/672	3821/15644	PASS	0.120689655

			0.103448276
66/174	2502/7774	PASS	0.18627451
			0.1
			0.25
43/694	243/16402	PASS	0.166666667
65/174	3335/6948	PASS	0.14893617
96/690	4087/16290	PASS	0.103448276
			0.142857143
			0.109090909
226/694	4829/16344	PASS	0.140625
348/652	9363/15072	PASS	0.105263158
218/684	6314/16248	PASS	0.130434783
103/464	2854/9935	PASS	0.121621622
76/694	2570/16406	PASS	0.133333333
			0.117647059
			0.1875
104/660	4168/14234	PASS	0.245901639
128/566	2631/8696	PASS	0.142857143
		PASS	0.1
			0.2
398/606	10905/15354	PASS	0.136363636
			0.12
43/654	1220/15490	PASS	0.15625
112/694	1994/16406	PASS	0.111111111
50/128	2407/7500	PASS	0.121212121
			0.125
146/654	5954/15076	PASS	0.216216216
4/214	26/8898	PASS	0.14159292
3/692	13/16404	PASS	0.308823529
			0.142857143
149/690	5642/16390	PASS	0.142857143
			0.176470588
			0.1875
81/692	1677/16392	PASS	0.133333333
			0.136986301
			0.155555556
			0.142857143
			0.157894737
1/106	64/5650	PASS	0.185185185
			0.121212121
114/658	3645/15694	PASS	0.146341463
98/660	584/13884	PASS	0.230769231
			0.157894737
			0.214285714
11/626	81/13068	PASS	0.123076923
150/536	3314/9210	PASS	0.1875
227/688	5725/16402	PASS	0.125
			0.142857143
			0.166666667
			0.176470588
			0.121212121
53/670	436/15950	PASS	0.125
9/664	37/15892	PASS	0.104575163
317/664	3904/15256	PASS	0.153846154
200/684	5773/16302	PASS	0.171428571

195/688	5049/16392	PASS	0.12
			0.115384615
0/690	0/16154	PASS	0.137931034
			0.133333333
1/688	2/16330	PASS	0.121212121
			0.107142857
			0.155172414
85/562	552/14036	PASS	0.166666667
138/690	2668/16362	PASS	0.143564356
			0.172413793
109/676	2696/15164	PASS	0.153846154
			0.272727273
74/450	291/12012	PASS	0.110091743
264/694	4666/16390	PASS	0.149253731
209/694	3852/16382	PASS	0.164835165
424/694	9824/16338	PASS	0.111111111
			0.151515152
138/694	4327/16388	PASS	0.108333333
			0.151515152
7/170	93/8502	SRTrancheINDEL97.00to9	0.133333333
			0.136363636
			0.130434783
278/694	7329/16404	PASS	0.123287671
479/692	13105/16404	PASS	0.173469388
0/612	8/10980	PASS	0.136363636
			0.142857143
20/670	45/14846	PASS	0.115789474
			0.111111111
132/694	3193/16398	PASS	0.12195122
			0.111111111
2/124	41/7674	PASS	0.132075472
17/122	506/7548	PASS	0.125
90/242	3100/9196	PASS	0.116883117
			0.214285714
			0.151515152
			0.136363636
			0.235294118
129/690	2058/16128	PASS	0.153846154
			0.18
26/108	1701/6366	PASS	0.179487179
84/248	2537/5782	PASS	0.151515152
49/694	1471/16406	PASS	0.112903226
			0.157894737
			0.1
			0.175
483/692	10823/16378	PASS	0.157894737
433/694	10983/16406	PASS	0.106382979
			0.115384615
			0.173913043
			0.2
449/688	11475/16374	PASS	0.129032258
163/694	4439/16386	PASS	0.123287671
120/686	2863/16018	SRTrancheSNP99.80to9	0.179487179
40/76	930/1808	PASS	0.162162162
			0.208333333

			0.130952381
86/694	2692/16396	PASS	0.112676056
			0.119047619
51/630	1707/11758	PASS	0.179104478
355/630	7196/15244	PASS	0.120879121
202/634	3819/15572	PASS	0.1
			0.105263158
327/369	7630/8486	PASS	0.147058824
25/692	124/16336	PASS	0.133333333
			0.103448276
			0.115384615
			0.115384615
106/564	848/13212	PASS	0.148148148
118/468	2732/10021	PASS	0.230769231
			0.142857143
77/640	2954/14260	PASS	0.147058824
621/694	13507/16298	PASS	0.102564103
			0.5
			0.222222222
222/694	7045/16408	PASS	0.149253731
			0.333333333
149/694	2927/16406	PASS	0.108108108
			0.15
240/694	5349/16342	PASS	0.142857143
123/694	3475/16354	PASS	0.134328358
			0.107142857
5/688	26/16206	PASS	0.145454545
320/690	10857/16358	PASS	0.222222222
165/610	2326/14884	PASS	0.163265306
			0.285714286
			0.242857143
			0.146341463
			0.115384615
260/684	5741/16322	PASS	0.1
100/425	2843/7003	PASS	0.216216216
			0.142857143
345/692	7582/16396	PASS	0.133858268
			0.108108108
247/686	5166/16388	PASS	0.116666667
124/692	2470/16370	PASS	0.145454545
			0.5
			0.142857143
			0.2
45/688	1071/16392	PASS	0.14
44/90	2200/6068	PASS	0.130434783
2/684	401/16248	PASS	0.106382979
			0.176470588
			0.150793651
92/694	2151/16396	PASS	0.107692308
			0.142857143
8/694	33/16376	PASS	0.136363636
			0.263157895
19/26	1198/2144	PASS	0.136363636
270/460	6244/9696	PASS	0.352941176
			0.157894737

329/620	7457/15624	PASS	0.105263158
281/610	5377/10954	PASS	0.162790698
21/100	1389/6616	PASS	0.132075472
256/674	6574/15340	PASS	0.12345679
183/694	3427/16368	PASS	0.11
52/694	3045/16404	PASS	0.171875
37/118	2621/7506	PASS	0.16
7/694	51/16408	PASS	0.108695652
			0.159090909
0/648	0/12634	PASS	0.15625
456/650	11416/15790	PASS	0.134328358
471/690	11699/16406	PASS	0.101123596
105/694	1069/16404	PASS	0.120689655
			0.157894737
			0.107142857
			0.347826087
			0.3
			0.139534884
			0.285714286
175/690	3761/16408	PASS	0.8
296/590	6307/11748	PASS	0.146341463
175/694	4306/16406	PASS	0.145454545
			0.137931034
452/680	9701/16066	PASS	0.106382979
			0.148148148
117/694	2945/16406	PASS	0.140495868
			0.105263158
246/694	3403/16406	PASS	0.125
95/694	2447/16254	PASS	0.168421053
			0.15
195/694	4077/16384	PASS	0.147540984
			0.266666667
92/174	4655/8158	PASS	0.12
80/690	513/16116	PASS	0.176470588
			0.142857143
221/692	8493/16400	PASS	0.147058824
			0.186567164
			0.163636364
0/194	0/8008	PASS	0.119047619
329/580	9139/15006	PASS	0.125
			0.13253012
246/672	6278/16368	PASS	0.196969697
40/118	1982/7506	PASS	0.19047619
			0.142857143
183/662	4014/14540	PASS	0.135135135
0/674	0/16146	PASS	0.12962963
			0.115384615
			0.117647059
			0.222222222
			0.163636364
			0.1
			0.107142857
57/114	2509/4538	PASS	0.1
4/688	54/15902	PASS	0.169230769
			0.2

			0.222222222
27/212	1968/7144	PASS	0.107142857
			0.133333333
54/124	4409/7890	PASS	0.152173913
			0.189189189
38/72	2271/4434	PASS	0.172413793
			0.142857143
			0.13559322
10/172	532/7654	PASS	0.135135135
			0.222222222
			0.2
220/640	4049/12278	PASS	0.2
28/590	463/12290	PASS	0.151515152
27/522	166/12718	PASS	0.142857143
			0.12
			0.14084507
			0.222222222
36/690	1563/16408	PASS	0.147239264
149/588	3583/15168	PASS	0.135338346
484/682	12207/16150	PASS	0.147058824
			0.12
129/662	1572/14400	PASS	0.117647059
33/694	979/16406	PASS	0.104166667
162/413	1122/6221	PASS	0.166666667
140/347	843/4982	PASS	0.159090909
			0.14893617
161/654	4308/13776	PASS	0.1
			0.24
494/694	11270/16406	PASS	0.174603175
104/680	2564/16284	PASS	0.172727273
13/630	140/15036	PASS	0.327272727
			0.125
			0.155172414
			0.162790698
8/662	46/15326	PASS	0.113636364
152/660	4675/14480	PASS	0.109589041
140/382	3562/10332	PASS	0.16
106/482	2733/13734	PASS	0.118181818
63/688	1463/15934	PASS	0.125
			0.25
			0.107142857
		PASS	0.206896552
31/694	652/16408	PASS	0.138613861
148/336	4244/11416	PASS	0.149253731
73/674	864/15738	PASS	0.1
			0.115384615
			0.107142857
333/694	6561/16400	PASS	0.104477612
			0.130434783
			0.136363636
			0.111111111
			0.5
			0.125
			0.132352941
207/684	5188/16236	PASS	0.185185185

155/690	2201/16404	PASS	0.120879121
			0.133333333
120/188	5497/7936	PASS	0.112903226
275/462	2393/9984	PASS	0.153846154
105/437	2412/8808	PASS	0.103448276
319/694	5268/16406	PASS	0.15
280/694	4736/16386	PASS	0.14379085
294/694	4941/16406	PASS	0.108527132
			0.307692308
			0.115384615
243/694	7584/16406	PASS	0.123287671
			0.206896552
			0.2
424/694	8985/16376	PASS	0.125
305/620	6188/12658	PASS	0.111111111
305/616	6090/12518	PASS	0.111111111
42/440	897/12868	PASS	0.114754098
			0.14159292
			0.111111111
14/694	267/16404	PASS	0.134615385
			0.125
			0.19047619
45/652	194/15610	PASS	0.142857143
122/694	3828/16408	PASS	0.14516129
52/694	990/16382	PASS	0.111111111
			0.117647059
			0.118421053
296/690	7261/16402	PASS	0.244444444
74/666	1124/15948	PASS	0.107142857
319/660	5719/15788	PASS	0.133858268
25/122	1253/7574	PASS	0.214285714
			0.153846154
65/138	5269/8052	PASS	0.25
			0.183673469
			0.169230769
20/694	46/16408	PASS	0.121076233
			0.333333333
242/692	4781/16408	PASS	0.128205128
			0.142857143
86/584	1929/13974	PASS	0.2
67/467	543/10010	PASS	0.135135135
50/465	507/9976	PASS	0.133333333
			0.272727273
149/445	3369/8392	PASS	0.235294118
119/694	1854/16346	PASS	0.142857143
109/670	4176/14860	PASS	0.130434783
315/630	8360/15690	PASS	0.184615385
221/694	6933/16408	PASS	0.109375
			0.272727273
			0.272727273
331/443	6155/9564	PASS	0.131147541
24/74	601/3574	PASS	0.111111111
83/688	2168/16296	PASS	0.152173913
7/690	60/16374	PASS	0.192307692
62/688	799/16264	PASS	0.111111111

			0.142857143
77/136	4507/7404	PASS	0.1
			0.115384615
			0.444444444
			0.177419355
41/138	2336/8090	PASS	0.151515152
572/694	13951/16398	PASS	0.146341463
76/180	3421/7842	PASS	0.14
18/690	206/16398	PASS	0.106382979
			0.103448276
503/694	12246/16408	PASS	0.148148148
			0.125
503/694	12267/16400	PASS	0.123287671
327/692	6701/16210	PASS	0.108108108
134/694	4065/16400	PASS	0.155172414
			0.125786164
102/524	1635/13392	PASS	0.160493827
			0.153846154
94/492	1752/14048	PASS	0.140350877
			0.107142857
0/352	1/10958	PASS	0.126984127
80/646	1939/15430	PASS	0.155555556
			0.114285714
188/690	5114/16402	PASS	0.153061224
226/666	5095/14844	PASS	0.170731707
			0.115384615
			0.25
			0.3
			0.166666667
			0.111111111
291/694	8784/16386	PASS	0.258823529
203/678	5820/16272	PASS	0.103773585
452/690	10508/16400	PASS	0.182926829
			0.173469388
258/694	7360/16406	PASS	0.130434783
			0.103448276
8/648	488/14602	PASS	0.109375
			0.117647059
30/690	216/16400	PASS	0.115384615
170/694	6046/16402	PASS	0.111111111
8/462	3/10036	PASS	0.233333333
			0.183098592
			0.128440367
			0.375
			0.185714286
57/694	3071/16408	PASS	0.118644068
77/144	4272/7930	;RTrancheINDEL95.00to9	0.133333333
			0.121212121
510/690	10480/16396	PASS	0.155555556
472/660	9841/15608	PASS	0.103174603
150/694	3457/16408	PASS	0.105769231
			0.24
			0.15
506/690	9687/16348	PASS	0.158730159
			0.3

241/588	3193/10014	PASS	0.285714286
161/690	1480/16400	PASS	0.117647059
254/690	4753/16400	PASS	0.103448276
70/186	2864/7854	PASS	0.115646259
			0.174603175
			0.176470588
			0.116666667
4/684	0/16040	PASS	0.149606299
310/632	9490/15716	PASS	0.191489362
250/674	4963/16326	PASS	0.146067416
81/146	4434/8246	PASS	0.154285714
			0.210526316
		PASS	0.166666667
272/604	5279/11426	PASS	0.285714286
			0.125
393/688	9456/16400	PASS	0.159090909
			0.129411765
14/688	51/16404	PASS	0.104895105
204/610	5167/15440	PASS	0.117021277
176/694	3839/16384	PASS	0.118421053
241/694	3584/16408	PASS	0.175
261/694	4136/16406	PASS	0.128712871
21/694	290/16408	PASS	0.195121951
20/694	260/16408	PASS	0.128440367
			0.107142857
			0.25
			0.347826087
135/682	3000/15548	PASS	0.171428571
137/694	3019/16406	PASS	0.101265823
19/126	599/7850	PASS	0.156028369
73/694	917/16408	PASS	0.126760563
187/694	5731/16406	PASS	0.119402985
			0.219512195
62/658	2866/14440	PASS	0.108108108
			0.206896552
			0.106382979
191/694	4480/16396	PASS	0.155555556
26/124	1552/7244	PASS	0.131578947
59/586	2223/15500	PASS	0.111111111
10/98	69/4554	PASS	0.121212121
5/524	152/10024	PASS	0.2
332/694	5252/16406	PASS	0.12195122
95/694	1439/16404	PASS	0.132352941
227/694	3869/16404	PASS	0.128205128
			0.16
291/586	8393/15910	PASS	0.144578313
441/452	9737/9744	PASS	0.317073171
53/449	295/9015	PASS	0.166666667
58/616	1493/14464	PASS	0.129032258
			0.138888889
			0.125
178/694	3252/16378	PASS	0.126712329
146/688	4486/15976	PASS	0.117647059
35/674	858/16016	PASS	0.125
222/666	6780/16198	PASS	0.111111111

112/672	1997/14982	PASS	0.131578947
61/694	3533/16408	PASS	0.168674699
382/692	9447/16390	PASS	0.134146341
			0.117647059
			0.12
152/402	1549/7631	PASS	0.126984127
257/460	7017/12628	PASS	0.209876543
			0.1875
276/688	7374/16372	PASS	0.154411765
156/652	4807/15528	PASS	0.138888889
9/54	97/982	PASS	0.172413793
227/692	6993/16404	PASS	0.112359551
			0.16
			0.272727273
			0.230769231
			0.115942029
			0.266666667
4/64	348/3470	PASS	0.130434783
417/646	9972/13762	PASS	0.173913043
20/103	710/4534	PASS	0.21875
185/694	2895/16404	PASS	0.109243697
			0.153846154
27/468	684/13340	PASS	0.148514851
			0.25
193/648	3974/14476	PASS	0.147783251
0/28	36/1458	PASS	0.128712871
			0.222222222
54/366	342/6392	PASS	0.119047619
			0.146341463
377/636	6815/13718	PASS	0.106557377
298/692	8136/16380	PASS	0.101694915
			0.272727273
			0.256410256
507/644	11377/13080	PASS	0.189189189
			0.173913043
38/688	182/16100	PASS	0.215189873
246/346	5854/7553	PASS	0.37037037
22/648	251/14978	PASS	0.147826087
38/674	840/14778	PASS	0.111111111
38/692	851/16392	PASS	0.101694915
277/688	5907/16396	PASS	0.134831461
			0.375
			0.142857143
			0.136363636
65/146	4684/8202	PASS	0.117647059
86/694	1406/16224	PASS	0.142857143
			0.333333333
87/694	1281/16408	PASS	0.158536585
0/694	0/16408	PASS	0.108108108
7/692	562/16334	PASS	0.114285714
190/462	6358/13742	PASS	0.106666667
427/694	11048/16406	PASS	0.1
			0.214285714
			0.136363636
			0.36

265/694	6119/16380	PASS	0.158415842
			0.136363636
96/668	1169/15446	PASS	0.163043478
299/692	8967/16402	PASS	0.120689655
			0.128205128
33/130	1649/7894	PASS	0.128205128
			0.21875
426/694	9302/16402	PASS	0.142857143
115/646	2645/15766	PASS	0.105263158
			0.142857143
17/316	487/9902	PASS	0.108695652
87/678	1378/16340	PASS	0.165413534
58/560	354/14458	PASS	0.12295082
			0.230769231
170/678	3836/15482	PASS	0.119617225
260/460	4858/9941	PASS	0.25
0/452	0/9460	PASS	0.170731707
177/578	2350/9282	PASS	0.180555556
			0.176470588
57/170	3019/7600	PASS	0.153846154
			0.153846154
			0.161290323
536/694	10955/16398	PASS	0.114942529
284/694	7807/16400	PASS	0.166666667
			0.1875
			0.32
153/694	3515/16406	PASS	0.139784946
			0.12244898
			0.119047619
204/464	3695/10011	PASS	0.176470588
151/468	1449/10005	PASS	0.155844156
			0.12
			0.151515152
133/694	5310/16408	PASS	0.12371134
141/648	5738/13862	PASS	0.111111111
42/680	364/15960	PASS	0.131147541
			0.3
277/694	5058/16390	PASS	0.114942529
294/692	7915/16350	PASS	0.125
5/694	31/16408	PASS	0.113636364
			0.103448276
			0.164835165
			0.140625
109/568	1926/14248	PASS	0.149122807
			0.333333333
192/688	4299/16384	PASS	0.112359551
199/692	4259/16406	PASS	0.333333333
21/520	192/13796	PASS	0.137931034
			0.111111111
			0.4
			0.1875
			0.166666667
197/692	4482/16404	PASS	0.11627907
			0.136363636
6/682	59/16132	PASS	0.121794872

			0.315789474
438/694	8896/16404	PASS	0.105263158
130/686	3499/16394	PASS	0.173913043
158/694	2721/16404	PASS	0.136
			0.333333333
170/694	1858/16408	PASS	0.218181818
			0.214285714
405/438	8315/8434	PASS	0.260869565
6/692	73/16384	PASS	0.143939394
			0.222222222
			0.117647059
12/678	68/16040	PASS	0.113475177
90/594	353/9828	PASS	0.125
370/686	7817/16348	PASS	0.155172414
			0.111111111
			0.2
			0.210526316
471/618	10369/14706	PASS	0.154761905
81/688	1946/15848	PASS	0.333333333
171/584	2870/12614	PASS	0.204081633
175/692	3069/16274	PASS	0.103092784
178/438	1988/5620	PASS	0.15
			0.109090909
			0.192982456
216/694	6612/16282	PASS	0.153333333
263/694	6648/16400	PASS	0.121212121
284/694	6708/16404	PASS	0.112676056
229/652	5264/15328	PASS	0.117647059
			0.1
90/436	2794/11596	PASS	0.102040816
29/114	1609/7528	PASS	0.136363636
43/680	652/15580	PASS	0.133333333
			0.133333333
32/658	1677/14112	PASS	0.285714286
			0.1875
2/656	47/15568	PASS	0.150943396
			0.2
58/444	1938/9547	PASS	0.236363636
268/686	5061/16298	PASS	0.217391304
233/690	4933/16406	PASS	0.127272727
232/680	4819/16236	PASS	0.12244898
13/690	89/16292	PASS	0.1
			0.230769231
85/688	1908/16264	PASS	0.12
			0.153846154
1/672	1/15900	PASS	0.137614679
			0.142857143
6/558	415/13698	PASS	0.105263158
127/690	5012/16402	PASS	0.163934426
			0.103448276
			0.136363636
			0.103448276
			0.142857143
61/600	1906/12586	PASS	0.151515152
271/688	6780/16314	PASS	0.111111111

134/694	2381/16408	PASS	0.153846154
0/664	37/15530	SRTrancheSNP99.60to9	0.179487179
			0.130434783
			0.130434783
			0.104651163
42/60	2692/3676	PASS	0.163120567
537/690	12968/16398	PASS	0.148148148
104/184	3699/7896	PASS	0.186046512
			0.111111111
			0.155555556
			0.111111111
143/524	2142/8454	PASS	0.101351351
			0.3
513/678	12029/15732	PASS	0.113043478
478/664	11499/15342	PASS	0.136363636
509/678	12616/16392	PASS	0.173333333
27/690	595/16322	PASS	0.126213592
			0.210526316
			0.104166667
			0.134615385
541/694	14263/16404	PASS	0.126760563
424/686	10770/16294	PASS	0.193548387
			0.181818182
			0.139534884
174/428	5014/12650	PASS	0.2
283/694	6623/16406	PASS	0.13253012
			0.157894737
			1
			0.14
			0.166666667
457/648	10568/16184	PASS	0.11827957
177/642	4248/14846	PASS	0.109589041
			0.115384615
17/60	1452/4036	PASS	0.113924051
			0.2
143/554	2748/9026	PASS	0.149253731
			0.142857143
			0.1875
170/326	4050/7314	PASS	0.203703704
0/68	1/4072	PASS	0.125
123/552	4496/13776	PASS	0.139344262
170/688	2662/16180	PASS	0.129032258
			0.115384615
369/682	8215/16222	PASS	0.106060606
41/522	491/11282	PASS	0.150943396
0/694	0/16400	PASS	0.208053691
			0.15625
261/690	8292/16260	PASS	0.166666667
			0.166666667
251/692	6856/16146	PASS	0.122641509
15/684	58/16334	PASS	0.131578947
			0.130434783
67/694	1567/16404	PASS	0.176470588
12/512	137/12462	PASS	0.119047619
			0.117647059

			0.159090909
			0.15
			0.111111111
			0.13559322
			0.130434783
139/170	6015/7608	PASS	0.126696833
272/568	3313/8808	PASS	0.333333333
29/484	1159/10048	PASS	0.194444444
518/692	11297/16270	PASS	0.161764706
			0.169491525
199/469	5574/10027	PASS	0.102189781
			0.136363636
73/408	1441/6358	PASS	0.12962963
321/467	7013/10040	PASS	0.2
			0.12
			0.166666667
4/12	64/296	PASS	0.2
267/654	4991/13828	PASS	0.150684932
172/692	2080/16320	PASS	0.109756098
337/694	8321/16406	PASS	0.12849162
			0.129533679
400/445	8197/9594	PASS	0.134146341
			0.342105263
7/570	39/14004	PASS	0.147540984
			0.12
			0.106382979
			0.127388535
215/694	7217/16408	PASS	0.119565217
134/416	1529/7106	PASS	0.142857143
168/482	3917/8450	PASS	0.103092784
34/694	964/16374	PASS	0.222222222
282/692	6125/16374	PASS	0.102941176
117/648	2806/15210	PASS	0.147727273
			0.153846154
			0.153846154
0/469	1/10047	PASS	0.114285714
			0.114285714
428/686	8889/16320	PASS	0.152777778
			0.108695652
2/694	106/16404	PASS	0.112903226
			0.176470588
1/358	0/11250	PASS	0.148148148
			0.14084507
			0.137254902
65/674	1203/14780	PASS	0.166666667
107/406	2035/10904	PASS	0.225
73/662	1620/16118	PASS	0.147651007
174/694	4046/16280	PASS	0.157894737
			0.125
115/692	3598/16408	PASS	0.122807018
103/692	2446/16282	PASS	0.139534884
77/174	2952/7878	PASS	0.222222222
			0.151515152
291/676	5717/14962	PASS	0.106666667
			0.162162162

1/16	21/518	PASS	0.154761905
			0.125714286
295/688	7429/15352	PASS	0.318181818
			0.12
163/668	4698/15984	PASS	0.11038961
230/682	5404/16026	PASS	0.178082192
9/144	322/7770	PASS	0.108108108
3/648	71/15806	PASS	0.139072848
			0.3125
238/466	7162/9994	PASS	0.295454545
57/118	3809/7486	PASS	0.103448276
495/694	13341/16404	PASS	0.104166667
118/212	6382/10130	PASS	0.12
277/688	8596/16408	PASS	0.196078431
584/690	15154/16408	PASS	0.175824176
252/636	8457/15826	PASS	0.15862069
271/692	6249/16304	PASS	0.106666667
			0.176470588
12/680	110/16332	PASS	0.191709845
			0.13559322
172/498	2141/11652	PASS	0.205882353
			0.125
			0.135135135
142/694	2663/16394	PASS	0.184615385
266/694	5319/16408	PASS	0.184210526
453/694	11860/16404	PASS	0.126126126
270/684	5178/16336	PASS	0.150943396
406/682	10289/16286	PASS	0.116883117
			0.133333333
210/688	7376/16366	PASS	0.127659574
221/688	4994/16402	PASS	0.105263158
22/166	805/7558	PASS	0.148148148
			0.121621622
379/690	10202/16406	PASS	0.143939394
			0.117647059
273/448	6127/9641	PASS	0.133333333
70/130	3875/7772	PASS	0.116129032
263/364	8154/11394	PASS	0.19047619
158/694	3597/16408	PASS	0.1625
151/686	1576/16382	PASS	0.105263158
81/694	696/16408	PASS	0.105263158
			0.3
186/580	2877/11836	PASS	0.169230769
0/606	0/15370	PASS	0.142857143
435/692	7821/16400	PASS	0.217391304
			0.136363636
			0.1
			0.222222222
			0.109090909
			0.12
			0.118644068
285/544	4289/9110	PASS	0.15
8/694	146/16406	PASS	0.161290323
			0.127272727
			0.142857143

			0.107142857
92/686	2850/16402	PASS	0.111111111
			0.130434783
35/682	685/16386	PASS	0.136363636
305/692	7495/16400	PASS	0.133333333
338/694	9304/16402	PASS	0.118811881
227/496	7630/14102	PASS	0.171875
241/640	6542/12412	PASS	0.137931034
244/612	8035/15252	PASS	0.12
256/672	8182/16194	PASS	0.12
32/660	903/15694	PASS	0.12195122
6/670	11/14798	PASS	0.222222222
			0.136363636
5/690	63/15944	PASS	0.18
281/690	6063/16282	PASS	0.109589041
337/622	4856/11652	PASS	0.266666667
95/694	1733/16408	PASS	0.112676056
			0.230769231
513/664	9930/15572	PASS	0.130434783
			0.101265823
36/136	2557/7904	PASS	0.115384615
257/692	4891/16394	PASS	0.15625
160/606	3436/12062	PASS	0.115384615
6/690	206/16402	PASS	0.235294118
4/684	65/15572	PASS	0.108695652
			0.15
415/692	8430/15824	PASS	0.153846154
40/440	1222/14174	PASS	0.271186441
61/178	3161/7390	PASS	0.161290323
			0.131578947
			0.157894737
			0.12
305/572	6252/13660	PASS	0.2
			0.1
			0.135416667
0/56	10/3318	PASS	0.118421053
5/172	11/4234	PASS	0.183908046
5/86	25/4717	PASS	0.294117647
278/534	2800/7574	PASS	0.12
			0.269230769
136/684	5031/16142	PASS	0.184782609
10/308	124/9630	PASS	0.115384615
19/688	449/16134	PASS	0.133333333
231/682	5724/16222	PASS	0.103896104
			0.127906977
77/692	2720/16360	PASS	0.116751269
8/452	31/12168	PASS	0.125
			0.228571429
494/694	13496/16408	PASS	0.116071429
			0.107142857
3/18	217/690	PASS	0.266666667
			0.185185185
112/690	2569/16404	PASS	0.135135135
38/386	1348/12002	PASS	0.131147541
179/694	6545/16406	PASS	0.136363636

			0.117647059
			0.208333333
			0.166666667
			0.142857143
47/694	1557/16406	PASS	0.12
433/692	10430/16386	PASS	0.1
15/688	146/16286	PASS	0.12195122
17/118	1481/7460	PASS	0.128205128
102/694	2299/16406	PASS	0.189189189
			0.15
14/184	996/7898	PASS	0.1
			0.121212121
148/666	3625/16136	PASS	0.214285714
281/694	6603/16404	PASS	0.144144144
			0.105263158
			0.166666667
112/684	1771/16152	PASS	0.12345679
			0.275862069
356/692	10481/16400	PASS	0.152173913
323/443	5778/8114	PASS	0.136363636
			0.238095238
			0.14084507
			0.138888889
106/364	2383/8638	PASS	0.113636364
			0.266666667
22/676	893/15886	PASS	0.114942529
162/550	6508/14874	PASS	0.161764706
			0.285714286
			0.230769231
437/694	8929/16406	PASS	0.142857143
40/694	625/16406	PASS	0.109090909
39/678	586/15776	PASS	0.113636364
25/338	255/4694	PASS	0.125
178/694	3824/16392	PASS	0.109756098
198/692	4414/16402	PASS	0.188405797
543/692	11918/16404	PASS	0.175
23/692	180/16394	PASS	0.129032258
107/654	1630/15508	PASS	0.136363636
			0.12
			0.118644068
110/612	2609/11204	PASS	0.140350877
139/616	3118/11708	PASS	0.114427861
			0.125
29/634	494/15044	PASS	0.107142857
205/694	6026/16404	PASS	0.118644068
83/457	3257/9947	PASS	0.121495327
122/694	1560/16408	PASS	0.13253012
			0.113207547
35/640	237/14512	PASS	0.1
110/267	2534/6576	PASS	0.194444444
10/684	26/16292	PASS	0.128571429
			0.2
76/232	4265/9222	PASS	0.184210526
245/694	4011/16316	PASS	0.104294479
		PASS	0.166666667

123/672	3100/16264	PASS	0.112359551
89/678	2710/16056	PASS	0.153846154
8/694	52/16406	PASS	0.16
			0.133333333
72/694	992/16398	PASS	0.126582278
122/686	1954/16210	PASS	0.176470588
0/684	0/15890	PASS	0.133333333
			0.16
315/694	7924/16334	PASS	0.223880597
4/692	0/16370	PASS	0.159663866
310/638	9069/16020	PASS	0.172839506
			0.194444444
191/674	5650/15410	PASS	0.113207547
101/694	2168/16404	PASS	0.141414141
			0.333333333
232/666	5278/16190	PASS	0.222222222
232/678	5153/14952	PASS	0.142857143
			0.114285714
100/232	2890/6672	PASS	0.148648649
235/678	5880/15566	PASS	0.102564103
27/80	1429/5300	PASS	0.170212766
168/690	3157/16396	PASS	0.104166667
			0.157894737
100/694	3568/16406	PASS	0.113821138
108/694	3629/16408	PASS	0.100671141
94/308	1904/10154	PASS	0.139534884
			0.125
			0.269230769
			0.166666667
			0.125
			0.15625
150/664	3718/16320	PASS	0.107142857
268/694	4644/16372	PASS	0.105263158
235/690	2849/16094	PASS	0.222222222
			0.125
			0.176470588
			0.224137931
128/690	1692/16408	PASS	0.12195122
223/646	5248/13178	PASS	0.147540984
			0.15
130/690	1822/16338	PASS	0.127659574
54/694	1240/16408	PASS	0.102272727
185/690	2585/16372	PASS	0.102040816
			0.230769231
146/292	6010/10752	PASS	0.115384615
273/666	6255/13750	PASS	0.146341463
82/457	1545/10008	PASS	0.2375
190/404	4981/9678	PASS	0.115384615
			0.125
			0.166666667
			0.115384615
102/622	2244/12210	PASS	0.138461538
			0.142857143
47/690	645/16406	PASS	0.210526316
317/690	6971/16406	PASS	0.133333333

179/688	3398/16338	PASS	0.130434783
205/690	4343/16406	PASS	0.127659574
			0.210526316
438/654	10680/16304	PASS	0.136986301
			0.125
289/690	5906/16404	PASS	0.144508671
264/692	5660/16408	PASS	0.124352332
41/100	2596/6244	PASS	0.125
271/688	5890/16316	PASS	0.217877095
265/614	5832/15862	PASS	0.12962963
287/684	6048/16342	PASS	0.127388535
			0.157894737
110/378	3073/10206	PASS	0.25
199/324	4712/7866	PASS	0.157894737
43/118	3422/7508	PASS	0.126760563
			0.113043478
22/94	1876/5496	;RTrancheINDEL96.00to9	0.111111111
			0.3125
167/686	2562/16368	PASS	0.151515152
			0.142857143
209/688	4514/16156	PASS	0.12345679
222/676	7644/15756	PASS	0.149253731
24/118	1154/7478	PASS	0.100478469
10/22	308/632	PASS	0.25
			0.214285714
			0.136363636
40/208	528/9170	PASS	0.125
			0.25
95/530	1289/13338	PASS	0.130434783
72/694	1966/16400	PASS	0.12345679
93/694	2361/16406	PASS	0.175
395/652	9375/16156	PASS	0.166666667
266/466	7480/13550	PASS	0.183673469
249/692	5941/16404	PASS	0.125
			0.108695652
157/546	2873/9040	PASS	0.114285714
129/670	3383/15730	;RTrancheINDEL99.00to9	0.272727273
292/467	7328/9970	PASS	0.238095238
255/684	5917/16308	PASS	0.15
			0.103448276
239/416	5168/8376	PASS	0.272727273
258/460	5800/9961	PASS	0.228571429
258/459	5800/9961	PASS	0.228571429
45/136	3225/8028	PASS	0.208333333
293/692	7500/16266	PASS	0.162162162
240/626	3733/12338	PASS	0.161290323
			0.125
182/626	2984/11588	PASS	0.144927536
88/154	1865/4904	PASS	0.121212121
			0.128787879
			0.16
8/84	67/2734	PASS	0.122807018
2/6	45/166	PASS	0.173913043
			0.111111111
			0.142857143

			0.129032258
57/646	2176/13320	SRTrancheSNP99.60to9	0.127659574
			0.1625
41/686	728/16234	PASS	0.107438017
146/676	3381/16086	PASS	0.272727273
			0.114285714
230/546	3620/14172	PASS	0.111111111
			0.206896552
47/646	453/15222	PASS	0.104166667
			0.333333333
375/680	9326/16282	PASS	0.266666667
			0.166666667
146/690	2412/16402	PASS	0.114551084
			0.25
4/690	36/16376	PASS	0.333333333
			0.176470588
5/694	37/16408	PASS	0.158536585
4/544	33/10648	PASS	0.132352941
			0.115384615
172/334	5071/10976	PASS	0.153846154
152/314	6368/11000	PASS	0.118421053
142/688	4799/16118	PASS	0.203389831
163/682	3462/16362	PASS	0.126760563
433/454	9686/9786	PASS	0.212765957
			0.153846154
302/690	9505/16404	PASS	0.213483146
			0.147651007
217/686	3800/16046	PASS	0.12
146/668	5321/16364	PASS	0.179245283
252/694	3260/16394	PASS	0.151785714
			0.2
170/210	6916/9308	PASS	0.147058824
182/666	5076/16154	PASS	0.127118644
158/218	7349/9452	PASS	0.111111111
0/120	1/7338	PASS	0.125
0/377	0/8139	PASS	0.137931034
324/688	8452/16050	PASS	0.127272727
			0.15
			0.170212766
250/694	6049/16404	PASS	0.161764706
			0.109090909
			0.357142857
86/692	1242/16336	PASS	0.111111111
107/644	2750/13598	PASS	0.152173913
399/690	7875/16394	PASS	0.103448276
			0.186440678
391/692	9168/16402	PASS	0.107526882
195/692	4482/16314	PASS	0.115384615
354/694	7097/16406	PASS	0.162162162
			0.135416667
304/658	6372/15170	PASS	0.129032258
444/680	8979/14936	PASS	0.120689655
106/148	5342/8254	PASS	0.12
			0.108108108
			0.12037037

			0.125
111/306	4485/9536	PASS	0.178571429
			0.102564103
			0.157894737
			0.135135135
209/406	5275/10878	PASS	0.115384615
368/690	7255/15924	PASS	0.116883117
			0.104477612
304/694	8227/16404	PASS	0.135135135
7/586	69/14596	PASS	0.101694915
			0.117647059
			0.137254902
290/640	7731/14274	PASS	0.108108108
			0.115384615
239/694	5606/16378	PASS	0.153846154
42/118	1794/7392	PASS	0.169354839
161/644	3784/15876	PASS	0.25
			0.111111111
			0.111111111
292/686	6120/16342	PASS	0.166666667
289/456	3673/9631	PASS	0.142857143
			0.16
13/30	235/690	PASS	0.24
133/304	3336/10086	PASS	0.103174603
429/682	10795/16036	PASS	0.203389831
445/694	11076/16378	PASS	0.12
177/624	3511/11706	PASS	0.118181818
115/690	1652/16152	PASS	0.114285714
561/694	11930/16406	PASS	0.129411765
251/616	7459/13910	PASS	0.155555556
69/666	1999/16206	PASS	0.109375
			0.214285714
406/688	7864/15980	PASS	0.105882353
277/694	8872/16404	PASS	0.111111111
101/686	3625/16294	PASS	0.148148148
0/688	44/16390	PASS	0.123076923
0/344	1/11008	PASS	0.105263158
368/664	7441/15554	PASS	0.25
			0.151515152
			0.12987013
			0.5
			0.12
			0.106382979
345/690	7549/16404	PASS	0.111111111
299/692	5439/16214	PASS	0.108695652
		PASS	0.115384615
199/694	5408/16406	PASS	0.128571429
			0.152542373
			0.130434783
55/144	2912/7692	PASS	0.14516129
			0.137931034
273/690	5582/16322	PASS	0.130434783
159/180	7342/7896	PASS	0.18627451
			0.195652174
161/184	6685/7920	PASS	0.125

346/392	9247/10908	PASS	0.176470588
			0.157894737
			0.153846154
1/312	0/6520	PASS	0.134615385
1/180	62/7902	PASS	0.180851064
41/166	1683/7358	PASS	0.27027027
77/694	702/16406	PASS	0.101694915
209/662	5735/15320	PASS	0.102564103
			1
			0.230769231
149/694	3701/16378	PASS	0.146788991
150/690	3677/16222	PASS	0.130434783
			0.157894737
30/690	304/16318	PASS	0.102040816
73/686	1428/15974	PASS	0.155555556
			0.12195122
349/690	7231/16376	PASS	0.129032258
326/656	6000/13340	PASS	0.106382979
			0.2
			0.191489362
			0.129032258
			0.12195122
			0.133333333
			0.117647059
			0.142857143
69/616	575/14658	PASS	0.109947644
			0.12962963
2/636	24/15640	PASS	0.13559322
237/678	5067/15988	PASS	0.181818182
23/40	1682/2592	PASS	0.142857143
			0.111111111
5/126	163/6218	PASS	0.102564103
159/644	2552/12980	PASS	0.195121951
148/682	2166/15348	PASS	0.144859813
			0.257142857
75/694	2180/16370	PASS	0.126213592
405/688	10818/16366	PASS	0.111111111
		PASS	0.125786164
			0.162162162
			0.125
45/122	2395/7604	PASS	0.106761566
			0.428571429
60/686	576/15836	PASS	0.164383562
0/120	0/7090	PASS	0.126213592
129/628	1455/11876	PASS	0.244186047
			0.130434783
134/668	2556/15930	PASS	0.153846154
65/113	3307/5314	PASS	0.172413793
102/650	3971/16250	PASS	0.210526316
98/452	3732/12862	PASS	0.125
176/310	7302/11522	PASS	0.230769231
			0.166666667
557/694	13879/16408	PASS	0.132352941
			0.2
12/690	1723/16340	PASS	0.176470588

			0.111111111
			0.178571429
			0.183333333
			0.103448276
			0.131578947
258/670	7894/15726	PASS	0.173076923
547/694	14479/16214	PASS	0.275
			0.5
			0.101265823
50/344	1163/10130	PASS	0.125
			0.107142857
183/694	2805/16394	PASS	0.202614379
			0.222222222
147/694	2054/16396	PASS	0.138888889
			0.217391304
180/688	6630/16402	PASS	0.1875
			0.12
75/678	1755/16304	PASS	0.177777778
345/692	7544/16228	PASS	0.123287671
71/694	1497/16404	PASS	0.107142857
184/286	5385/7482	PASS	0.153846154
			0.4
			0.111111111
			0.375
			0.121212121
161/694	3292/16408	PASS	0.142857143
			0.113636364
9/690	7/16142	PASS	0.119047619
			0.25
133/276	4433/9558	PASS	0.129411765
364/694	9080/16408	PASS	0.150684932
54/670	2392/14974	PASS	0.1
66/469	1635/10047	PASS	0.15
			0.107142857
			0.2
			0.117647059
23/642	194/15780	PASS	0.102564103
35/394	1911/12514	PASS	0.142857143
			0.107142857
			0.105263158
3/694	68/16404	PASS	0.136363636
106/630	1590/15040	PASS	0.137931034
210/614	4652/15512	PASS	0.1375
120/280	3691/9954	PASS	0.104761905
			0.1875
15/618	52/15106	PASS	0.186046512
			0.176470588
513/644	10739/13898	PASS	0.109489051
			0.5
189/692	4883/16190	PASS	0.144
			0.130434783
120/690	1821/16126	PASS	0.15
			0.157894737
			0.136363636
			0.428571429

117/652	3617/14542	PASS	0.210526316
220/328	7126/11298	PASS	0.111111111
179/320	4978/10996	PASS	0.14893617
			0.103448276
1/94	7/4982	PASS	0.166666667
164/694	7484/16308	PASS	0.128
			0.127272727
			0.173913043
455/686	10264/16382	PASS	0.166666667
			0.125
			0.129032258
176/692	4210/16396	PASS	0.127272727
382/694	9558/16408	PASS	0.158415842
			0.454545455
299/690	7791/16338	PASS	0.131578947
149/678	5432/16074	PASS	0.128205128
			0.185185185
74/162	2515/6466	PASS	0.145833333
			0.230769231
32/684	669/16292	PASS	0.150943396
25/684	396/16292	PASS	0.118644068
50/694	1550/16398	PASS	0.107438017
88/688	1996/16302	PASS	0.103092784
191/694	4394/16406	PASS	0.2625
109/694	3482/16408	PASS	0.134615385
			0.1
141/694	2241/16404	PASS	0.207920792
			0.111111111
			0.179487179
14/692	363/16406	PASS	0.112359551
34/118	2236/7506	PASS	0.210084034
264/680	4831/15922	PASS	0.2
357/694	12596/16402	PASS	0.121621622
			0.12
7/580	8/14612	PASS	0.11965812
180/658	2403/15912	PASS	0.173913043
232/694	6653/16324	PASS	0.149606299
			0.166666667
64/680	2400/16378	PASS	0.133333333
62/357	368/7760	PASS	0.205128205
			0.233333333
			0.133333333
			0.1875
67/178	2543/7876	PASS	0.126760563
			0.115384615
			0.4
206/692	5210/16386	PASS	0.148148148
			0.117647059
			0.2
17/616	57/11068	PASS	0.12371134
260/694	6140/16354	PASS	0.142857143
368/692	9517/16400	PASS	0.139240506
2/469	88/10040	PASS	0.184210526
139/692	3327/16404	PASS	0.117647059
			0.133333333

337/464	5789/10021	PASS	0.166666667
215/684	7155/16348	PASS	0.192982456
127/596	1264/10224	PASS	0.227272727
			0.176470588
305/682	7806/16396	PASS	0.124087591
			0.285714286
			0.136363636
			0.176470588
4/670	72/14540	PASS	0.14893617
204/694	4245/16404	PASS	0.151111111
			0.1875
1/622	10/11254	PASS	0.238095238
			0.131578947
			0.15
326/672	7687/16242	PASS	0.229508197
			0.212121212
			0.1875
50/694	1222/16392	PASS	0.137096774
			0.210526316
			0.163265306
93/694	3829/16408	PASS	0.12371134
7/380	380/11236	PASS	0.103773585
			0.2
14/694	197/16396	PASS	0.147058824
			0.104166667
311/694	10842/16334	PASS	0.160714286
134/684	1881/15584	PASS	0.105263158
147/368	5401/8097	PASS	0.14516129
			0.166666667
2/686	18/16252	PASS	0.181818182
181/694	3956/16302	PASS	0.14
466/688	10718/16214	PASS	0.222222222
268/694	6421/16408	PASS	0.14
207/690	4440/16404	PASS	0.26
172/576	3690/8894	PASS	0.171428571
201/694	6566/16342	PASS	0.125
212/694	7182/16408	PASS	0.168831169
222/694	7425/16406	PASS	0.142857143
119/680	3334/15572	PASS	0.112676056
176/694	3977/16386	PASS	0.210526316
			0.222222222
			0.1875
436/694	10074/16406	PASS	0.12962963
			0.166666667
			0.107142857
			0.119402985
187/614	4533/15552	PASS	0.1
44/694	531/16408	PASS	0.1625
			0.461538462
			0.173913043
167/620	4318/14802	PASS	0.136363636
			0.129032258
11/632	107/14502	PASS	0.102564103
9/680	32/15560	PASS	0.1875
524/692	12986/16388	PASS	0.161764706

			0.102941176
185/526	4818/12656	PASS	0.137931034
0/94	3/5882	PASS	0.127272727
3/404	1/11848	PASS	0.157894737
97/438	2278/8918	PASS	0.135135135
			0.225806452
			0.126126126
41/288	267/9454	PASS	0.133333333
234/540	5776/13948	PASS	0.12
			0.125
85/694	1676/16406	PASS	0.137254902
71/488	1452/13034	PASS	0.166666667
			0.15
			0.193548387
45/249	251/5380	PASS	0.184210526
			0.133333333
101/684	4540/16132	PASS	0.146428571
159/622	3142/12780	PASS	0.235294118
71/194	3000/8082	PASS	0.140186916
			0.214285714
			0.230769231
1/178	2/7890	PASS	0.111111111
48/122	2000/5574	PASS	0.318181818
0/0	88/164	PASS	0.129032258
			0.115384615
100/170	4474/7652	PASS	0.109489051
284/692	6351/16382	PASS	0.102941176
208/622	4089/14968	PASS	0.170212766
17/146	283/7880	PASS	0.125
			0.109589041
			0.127272727
			0.14893617
415/692	10715/16388	PASS	0.195121951
			0.173913043
			0.272727273
0/104	0/5064	PASS	0.189873418
			0.145833333
			0.117647059
279/692	6180/16396	PASS	0.123188406
0/624	4/15026	PASS	0.25
114/690	2154/16388	PASS	0.133333333
158/682	3591/15380	PASS	0.116959064
199/676	4352/16242	PASS	0.130434783
			0.142857143
540/690	13524/16400	PASS	0.139240506
			0.333333333
261/690	5890/16406	PASS	0.137931034
473/688	11067/16144	PASS	0.109756098
			0.157894737
0/108	2/3330	PASS	0.172413793
			0.129032258
6/694	247/16408	PASS	0.186666667
			0.3
17/694	229/16408	PASS	0.119047619
459/694	11468/16406	PASS	0.101265823

			0.103448276
			0.181818182
			0.121621622
			0.11627907
			0.152173913
			0.230769231
486/694	12691/16366	PASS	0.1
			0.272727273
			0.19047619
			0.5
			0.125
			0.127272727
3/688	3/16140	PASS	0.25
36/694	1473/16406	PASS	0.220338983
			0.333333333
241/694	5881/16408	PASS	0.1625
428/692	9130/16408	PASS	0.134831461
			0.103448276
			0.176470588
231/694	5220/16402	PASS	0.142857143
223/666	5053/15978	PASS	0.125
448/694	9685/16382	PASS	0.120879121
407/692	9292/16380	PASS	0.101851852
366/690	8350/16366	PASS	0.146341463
10/678	106/16200	PASS	0.103448276
1/678	0/16170	PASS	0.176470588
			0.205128205
			0.285714286
8/148	608/4870	;RTrancheINDEL99.00to9	0.103448276
			0.106382979
			0.147540984
77/344	2134/12280	PASS	0.116666667
315/672	5471/16058	PASS	0.119047619
144/694	3749/16402	PASS	0.196078431
113/624	3068/12766	PASS	0.139534884
123/606	2904/14250	PASS	0.12
			0.5
54/694	1550/16408	PASS	0.14953271
			0.233333333
0/576	23/9022	PASS	0.14893617
			0.157894737
9/682	42/16074	PASS	0.225806452
253/654	6427/15486	PASS	0.142857143
123/272	4220/10148	PASS	0.244897959
			0.155555556
			0.103448276
192/678	5044/16312	PASS	0.178571429
129/300	4061/10400	PASS	0.145299145
384/694	6253/16408	PASS	0.114503817
2/184	104/7886	PASS	0.24
64/162	1122/2524	PASS	0.476190476
248/428	7353/11838	PASS	0.150684932
76/244	1434/3928	PASS	0.130434783
57/620	749/11462	PASS	0.112359551
			0.238095238

9/432	130/9440	PASS	0.228915663
0/672	0/14694	PASS	0.116959064
367/694	9960/16408	PASS	0.158415842
			0.166666667
51/690	310/15924	PASS	0.115942029
30/146	995/7612	PASS	0.106557377
			0.1
			0.159090909
			0.107142857
127/692	1897/16404	PASS	0.209302326
83/690	1681/16370	PASS	0.182692308
			0.318181818
211/363	5562/8010	PASS	0.184782609
21/694	923/16402	PASS	0.104
65/688	2126/16394	PASS	0.169117647
			0.157894737
178/324	5202/10964	PASS	0.119266055
			0.25
278/694	9843/16396	PASS	0.147540984
			0.133333333
			0.135135135
364/664	8409/14594	PASS	0.113636364
68/370	2696/9994	PASS	0.116666667
187/692	6455/16398	PASS	0.108333333
121/672	4304/15858	PASS	0.119047619
245/692	8872/16386	PASS	0.138297872
			0.139393939
267/692	6777/16398	PASS	0.147540984
385/686	10146/15840	PASS	0.19379845
382/694	9663/16404	PASS	0.128205128
3/8	36/132	PASS	0.263157895
138/468	1039/10041	PASS	0.14516129
3/688	70/16364	PASS	0.15
288/694	6938/16400	PASS	0.153846154
218/684	3947/16394	PASS	0.188811189
533/694	10411/16396	PASS	0.109243697
			0.230769231
153/626	2825/11810	PASS	0.145454545
190/452	4565/11478	PASS	0.333333333