	-4 (strong)
	-3
	-2 (moderate)
	-1 (supporting)
	0 (indeterminate)
	+1 (supporting)
	+2 (moderate)
	+3
	+4 (strong)

cDNA (NM_177559.3)	HGVSp (NP_808227.1)	Comment	Curation/precuration	Curation/precuration_group	Domain	Total_ACMG	PM1	PM5	PS1	PS2	PM2_Supp	PS4/PP5	PS3	BS2	Existing_variation	PubMed	clinvar_clnsig	clinvar_clnsig_group
c.593A>G	p.Lys198Arg	Established pathogenic	P	P/LP	p+1 loop	15	2	0	0	8	1	2	1	-1	rs869312840,CM167589	27048600 (n =1, dn)	likely_pathogenic,pa	Pathogenic/Likely_pathoger
c.79G>A	p.Glu27Lys	36368308 and 3598215	LP	P/LP	non-kinase	10	0	0	0	4	1	4	1	0	rs2018650479	29240241 (n=1, dn)	pathogenic,likely_pa	Pathogenic/Likely_pathoger
c.473A>G	p.Lys158Arg	Although the scores do	LP	P/LP	nonspecific kinase doma	4	0	0	0	2	1	1	0	0	rs2122531973	-	pathogenic	Pathogenic
c.934C>T	p.Arg312Trp	Established pathogenic	P	P/LP	nonspecific kinase doma	8	0	0	0	2	1	4	1	0	rs2018124491,COSV104	29383814 (n=1, dn)	pathogenic,likely_pa	Pathogenic/Likely_pathoger
c.935G>A	p.Arg312Gln	No further comment	LP	P/LP	nonspecific kinase doma	6	0	0	0	2	1	2	1	0	rs2122506319,COSV539	29249241 (n=1, dn)	pathogenic/likely_pa	Pathogenic/Likely_pathoger
c.137G>T	p.Gly46Val	Only one clinvar entry is	LP	P/LP	ATP/GTP binding loop	7	2	0	0	0	1	4	0	0	rs2122559628	39497417 (n = 2, mo	likely_pathogenic, u	Conflicting_classifications_
c.139C>G	p.Arg47Gly	There is at least 1 indiv	LP	P/LP	ATP/GTP binding loop	7	2	2	0	2	1	0	0	0	rs886041956,COSV5393	-	pathogenic	Pathogenic
c.140G>A	p.Arg47Gln	Established pathogenic	P	P/LP	ATP/GTP binding loop	12	2	0	0	8	1	0	1	0	rs869312845,CM167592	27048600 (n =1, dn)	pathogenic,likely_pa	Pathogenic/Likely_pathoger
c.142G>A	p.Gly48Ser	PMID:37195306 patient	LP	P/LP	ATP/GTP binding loop	6	2	0	0	2	1	1	0	0	rs2122559586	37195306 (n = 1, dn)	pathogenic	Pathogenic
c.143G>A	p.Gly48Asp	The cited article by 3bill	LP	P/LP	ATP/GTP binding loop	6	2	0	0	2	1	1	0	0	rs868337994	39829082 (n = 1, dn)	likely_pathogenic	Likely_pathogenic
c.149A>C	p.Tyr50Ser	ClinVar entries from the	LP	P/LP	ATP/GTP binding loop	7	2	2	0	2	1	0	0	0	rs869312849,CM167591	27048600 (n =1, dn)	pathogenic	Pathogenic
c.149A>G	p.Tyr50Cys	Established pathogenic	P	P/LP	ATP/GTP binding loop	12	2	0	0	8	1	1	0	0	rs869312849,CM167591	31729156 (n=1, dn)	pathogenic/likely_pa	Pathogenic/Likely_pathoger
c.151A>C	p.Ser51Arg	PS1 is used at the supp	LP	P/LP	ATP/GTP binding loop	6	2	0	1	0	1	1	1	0	-	29240241 (n=1, dn)	Pathogenic	Pathogenic
c.152G>A	p.Ser51Asn	Large-scale cohort stud	P	P/LP	ATP/GTP binding loop	11	2	2	0	2	1	4	0	0	-	29383814 (n=1, dn)	Pathogenic/Likely pa	Likely_pathogenic
c.152G>T	p.Ser51Ile	No further comment	LP	P/LP	ATP/GTP binding loop	6	2	2	0	0	1	1	0	0	-	33004838 (n=1, unkn	-	-
c.153T>A	p.Ser51Arg	PS1 is used at the supp	LP	P/LP	ATP/GTP binding loop	9	2	0	1	4	1	0	1	0	rs1555764992	33258288 (n=1, dn)	likely_pathogenic	Likely_pathogenic
c.154G>A	p.Glu52Lys	Although the scoring do	LP	P/LP	ATP/GTP binding loop	5	2	0	0	2	1	0	0	0	rs2018549058,COSV994	39039281 (n=1, dn)	likely_pathogenic	Likely_pathogenic
c.218T>A	p.Val73Glu	The two individuals in F	LP	P/LP	Basic cluster	6	2	0	0	2	1	0	1	0	-	29240241 (n=1, dn)	-	-
c.238C>T	p.Arg80Cys	34038195 and 3876402	LP	P/LP	Basic cluster	7	2	2	0	2	1	0	0	0	rs777370152,COSV1060	34038195 (n=1, dn)	-	-
c.239G>A	p.Arg80His	Established pathogenic	P	P/LP	Basic cluster	12	2	0	0	4	1	4	1	0	rs1057518092,COSV539	29383814 (n=1, dn)	pathogenic/likely_pa	Conflicting_classifications_
c.466G>C	p.Asp156His	PMID:37120078 include	LP	P/LP	Active site	8	2	2	0	2	1	1	0	0	rs1568512728	28725024 (n=1, dn)	pathogenic	Pathogenic
c.466G>T	p.Asp156Tyr	No clinical paper but Cl	LP	P/LP	Active site	7	2	2	0	2	1	0	0	0	rs1568512728	-	likely_pathogenic	Likely_pathogenic
c.467A>G	p.Asp156Gly		LP	P/LP	Active site	6	2	2	0	0	1	1	0	0	-	-	Pathogenic	Pathogenic
c.468T>A	p.Asp156Glu	35982159 and 3305719	P	P/LP	Active site	11	2	0	0	6	1	1	1	0	rs1064795110	32371413 (n=1, dn)	pathogenic,likely_pa	Pathogenic/Likely_pathoger
c.479A>G	p.His160Arg	34038195 and 3876402	LP	P/LP	nonspecific kinase doma	7	0	0	0	4	1	2	0	0	rs2018334830,COSV539	32651551 (n=1, dn)	likely_pathogenic,pa	Pathogenic/Likely_pathoger
c.523G>A	p.Asp175Asn	No further comment	LP	P/LP	Activation segment	8	2	2	0	2	1	1	0	0	COSV53937708	33278787 (n=1, dn)	Pathogenic	Pathogenic
c.524A>C	p.Asp175Ala		LP	P/LP	Activation segment	6	2	2	0	0	1	1	0	0	CM167590	-	Pathogenic	Pathogenic
c.524A>G	p.Asp175Gly	35982159 is reporting t	P	P/LP	Activation segment	12	2	0	0	8	1	0	1	0	rs869312848,CM167590	27048600 (n=1, dn)	pathogenic	Pathogenic
c.524A>T	p.Asp175Val		LP	P/LP	Activation segment	6	2	2	0	0	1	1	0	0	CM167590	-	likely_pathogenic	Likely_pathogenic
c.525C>A	p.Asp175Glu	Although not published	LP	P/LP	Activation segment	6	2	2	0	0	1	1	0	0	rs2018253563	-	uncertain_significan	Uncertain_significance
c.529G>A	p.Gly177Ser	35982159 patient is Ge	P	P/LP	Activation segment	12	2	0	0	8	1	1	0	0	rs1555762734,COSV539	35982159 (n=1, dn)	pathogenic,likely_pa	Pathogenic/Likely_pathoger
c.530G>A	p.Gly177Asp		LP	P/LP	Activation segment	6	2	2	0	0	1	1	0	0	rs2122521881	-	likely_pathogenic	Likely_pathogenic
c.572G>A	p.Arg191Gln	No further comment	P	P/LP	p+1 loop	9	2	0	0	4	1	1	1	0	COSV53935120	29383814 (n=1, dn)	Pathogenic	Pathogenic
c.580T>C	p.Ser194Pro	Although the scores do	LP	P/LP	p+1 loop	5	2	0	0	2	1	0	0	0	-	36474027 (n=1, dn)	likely_pathogenic	Likely_pathogenic
c.581C>A	p.Ser194Tyr	No further comment	LP	P/LP	p+1 loop	6	2	1	0	2	1	0	0	0	COSV53937543	34356170 (n=1, dn)	-	-
c.581C>T	p.Ser194Phe		LP	P/LP	p+1 loop	6	2	1	0	2	1	0	0	0	COSV53937543	40290421 (n=1, dn)	-	-
c.584G>A	p.Arg195Gln		LP	P/LP	p+1 loop	6	2	1	0	0	1	2	0	0	COSV107250836,COSV	-	Uncertain significan	Uncertain_significance
c.584G>C	p.Arg195Pro	Although the scores do	LP	P/LP	p+1 loop	5	2	0	0	2	1	0	0	0	rs2122521678,COSV107	-	likely_pathogenic	Likely_pathogenic
c.589T>A	p.Phe197Ile	It looks like there is onl	LP	P/LP	p+1 loop	6	2	0	0	2	1	0	1	0	COSV99424416	29383814 (n=1, dn)	-	-
c.589T>G	p.Phe197Val	Although the scores do	LP	P/LP	p+1 loop	5	2	1	0	0	1	1	0	0	COSV99424416	-	Pathogenic	Pathogenic
c.596G>A	p.Gly199Asp	Although the scores do	LP	P/LP	Activation segment	5	2	0	0	0	1	2	0	0	rs1555762709	-	uncertain_significan	Uncertain_significance
c.692C>G	p.Pro231Arg	No further comment	LP	P/LP	nonspecific kinase doma	6	0	0	0	4	1	0	1	0	-	29240241 (n=1, dn)	-	-

clinvar_id	clinvar_review	clinvar_dn	clinvar_affected	clinvar_entry_from_PMID	gnomAD4.1_joint_AC	AllofUs_AC	TOPMed_frz8_AC	v4.1+AoU+TOPMed	am_pathogenicity	am_PP3score	am_PP3_cat	MutPred2	MutPred2_PP3score	MutPred2_PP3cat
224790	criteria provided, multiple submitters, no conflicts	yes	yes	yes/no	2	4	0	6	0,9254	2	PP3_M	0,951667094	4	PP3_S
3375742	criteria provided, multiple submitters, no conflicts	unknown	yes	no	0	0	1	1	0,9983	4	PP3_S	0,912979066	3	PP3_MS
1172788	criteria provided, multiple submitters, no conflicts	yes	yes	no	1	0	0	1	0,9838	3	PP3_MS	0,890598454	2	PP3_M
984881	criteria provided, multiple submitters, no conflicts	unknown	yes	yes/no	1	0	0	1	0,9989	4	PP3_S	0,969724732	4	PP3_S
1328596	criteria provided, multiple submitters, no conflicts	unknown	yes	no	1	0	0	1	0,9987	4	PP3_S	0,973611341	4	PP3_S
1299317	criteria provided, conflicting classifications	unknown	yes	yes/no	0	0	0	0	0,9999	4	PP3_S	0,962792397	4	PP3_S
280816	criteria provided, single submitter	yes	yes	no	0	0	0	0	0,9967	4	PP3_S	0,876961522	2	PP3_M
224796	criteria provided, multiple submitters, no conflicts	yes	yes	yes/no	0	0	0	0	0,9978	4	PP3_S	0,922546911	3	PP3_MS
1675245	criteria provided, single submitter	unknown	yes	no	0	0	0	0	1	4	PP3_S	0,939117873	4	PP3_S
1687213	criteria provided, single submitter	unknown	yes	no	0	0	0	0	1	4	PP3_S	0,954038941	4	PP3_S
224800	no assertion criteria provided	yes	yes	yes	0	0	0	0	0,9993	4	PP3_S	0,966528064	4	PP3_S
432689	criteria provided, multiple submitters, no conflicts	unknown	yes	yes/no	0	0	0	0	1	4	PP3_S	0,964020771	4	PP3_S
3340574	criteria provided, single submitter	unknown	yes	no	0	0	0	0	0,9999	4	PP3_S	0,972045393	4	PP3_S
2506470	criteria provided, multiple submitters, no conflicts	yes	yes	no	0	0	0	0	0,9999	4	PP3_S	0,946103632	4	PP3_S
-	-				0	0	0	0	0,9999	4	PP3_S	0,97204664	4	PP3_S
559896	criteria provided, single submitter	yes	yes	no	0	0	0	0	0,9999	4	PP3_S	0,971828008	4	PP3_S
976763	criteria provided, single submitter	yes	yes	probably	0	0	0	0	0,9997	4	PP3_S	0,934663886	4	PP3_S
-	-				0	0	0	0	0,9996	4	PP3_S	0,867919212	2	PP3_M
-	-				0	0	0	0	0,9999	4	PP3_S	0,933063657	4	PP3_S
372946	criteria provided, conflicting classifications	yes	yes	yes/no	0	0	0	0	0,9997	4	PP3_S	0,941517184	4	PP3_S
619014	criteria provided, single submitter	yes	yes	yes/no	0	0	0	0	1	4	PP3_S	0,969214119	4	PP3_S
984880	no assertion criteria provided	yes	yes	no	0	0	0	0	0,9997	4	PP3_S	0,974772772	4	PP3_S
3774820	criteria provided, single submitter	unknown	yes	no	0	0	0	0	1	4	PP3_S	0,982065712	4	PP3_S
421395	criteria provided, multiple submitters, no conflicts	unknown	yes	yes/no	0	0	0	0	1	4	PP3_S	0,952652767	4	PP3_S
975528	criteria provided, multiple submitters, no conflicts	unknown	yes	no	0	0	0	0	0,9971	4	PP3_S	0,914121396	3	PP3_MS
2504560	criteria provided, single submitter	unknown	yes	no	0	0	0	0	0,9999	4	PP3_S	0,981982389	4	PP3_S
3391482	criteria provided, single submitter	unknown	yes	no	0	0	0	0	0,9999	4	PP3_S	#YOK	#YOK	NA
224799	no assertion criteria provided	yes	yes	yes	0	0	0	0	0,9998	4	PP3_S	0,982779257	4	PP3_S
3897634	criteria provided, single submitter	presumed	yes	no	0	0	0	0	1	4	PP3_S	#YOK	#YOK	NA
986044	criteria provided, single submitter	unknown	yes	no	0	0	0	0	0,9999	4	PP3_S	0,973444793	4	PP3_S
522077	criteria provided, multiple submitters, no conflicts	yes	yes	yes/no	0	0	0	0	0,9997	4	PP3_S	0,956301933	4	PP3_S
1685288	criteria provided, multiple submitters, no conflicts	unknown	yes	no	0	0	0	0	0,9999	4	PP3_S	#YOK	#YOK	NA
2663860	criteria provided, multiple submitters, no conflicts	unknown	yes	yes/no	0	0	0	0	0,9985	4	PP3_S	0,865204457	2	PP3_M
3255564	criteria provided, single submitter	yes	yes	yes	0	0	0	0	0,9999	4	PP3_S	0,974416699	4	PP3_S
-	-				0	0	0	0	0,9999	4	PP3_S	0,96964319	4	PP3_S
-	-				0	0	0	0	0,9999	4	PP3_S	0,98017548	4	PP3_S
2440584	criteria provided, multiple submitters, no conflicts	unknown	yes	no	0	0	0	0	0,9996	4	PP3_S	0,955652482	4	PP3_S
1700219	criteria provided, single submitter	yes	yes	no	0	0	0	0	0,9997	4	PP3_S	0,974510551	4	PP3_S
-	-				0	0	0	0	0,9998	4	PP3_S	0,956916204	4	PP3_S
3899537	criteria provided, single submitter	unknown	yes	no	0	0	0	0	0,9995	4	PP3_S	0,954309081	4	PP3_S
521897	criteria provided, multiple submitters, no conflicts	unknown	yes	no	0	0	0	0	0,9999	4	PP3_S	0,965528843	4	PP3_S
-	-				0	0	0	0	0,999	4	PP3_S	0,966799818	4	PP3_S

VARITY_R_score_MANE	VARITY_R_PP3score	VARITY_R_PP3cat	ESM1b_score_MANE	ESM1b_PP3score	ESMPP3b_PP3cat	REVEL	REVEL_PP3score	REVEL_PP3cat	VEST4	VEST4_PP3score	VEST4_PP3cat	BayesDel_noAF_score	BayesDel_PP3score	BayesDel_PP3cat	MutPred2_RankScore
0,9174192	3	PP3_MS	-9,07	0	NA	0,387	0	NA	0,902	2	PP3_M	-0,0797154	0	NA	0,90024
0,867668	2	PP3_M	-12,613	2	PP3_M	0,357	0	NA	0,761	0	NA	-0,117068	0	NA	0,96842
0,8732419	2	PP3_M	-16,008	3	PP3_MS	0,933	4	PP3_S	0,594	0	NA	0,405677	2	PP3_M	0,90841
0,94712484	3	PP3_MS	-14,32	3	PP3_MS	0,71	1	PP3	0,927	3	PP3_MS	0,319369	2	PP3_M	0,99093
0,9178626	3	PP3_MS	-14,39	3	PP3_MS	0,59	0	NA	0,971	4	PP3_S	0,361524	2	PP3_M	0,97947
0,97284985	4	PP3_S	-17,51	3	PP3_MS	0,93	3	PP3_MS	0,911	3	PP3_MS	0,418652	3	PP3_MS	0,99158
0,9869429	4	PP3_S	-13,58	2	PP3_M	0,552	0	NA	0,714	0	NA	0,149905	1	PP3	0,95019
0,9541987	3	PP3_MS	-14,47	3	PP3_MS	0,434	0	NA	0,921	3	PP3_MS	-0,0416269	0	NA	0,83031
0,88288915	2	PP3_M	-14,563	3	PP3_MS	0,977	4	PP3_S	0,654	0	NA	0,543434	4	PP3_S	0,96186
0,9615914	3	PP3_MS	-14,708	3	PP3_MS	0,981	4	PP3_S	0,657	0	NA	0,56896	4	PP3_S	0,9897
0,9866127	4	PP3_S	-15,345	3	PP3_MS	0,662	1	PP3	0,88	2	PP3_M	0,0787474	0	NA	0,97351
0,979115	4	PP3_S	-13,518	2	PP3_M	0,697	1	PP3	0,873	2	PP3_M	0,108325	0	NA	0,97226
0,97101134	4	PP3_S	-16,239	3	PP3_MS	0,721	1	PP3	0,947	3	PP3_MS	0,136583	1	PP3	0,97531
0,95114434	3	PP3_MS	-14,936	3	PP3_MS	0,401	0	NA	0,932	3	PP3_MS	-0,252803	-1	BP4	0,94021
0,96936125	4	PP3_S	-18,953	3	PP3_MS	0,667	1	PP3	0,985	4	PP3_S	0,132187	1	PP3	0,9846
0,96975523	4	PP3_S	-16,239	3	PP3_MS	0,508	0	NA	0,892	2	PP3_M	0,0808771	0	NA	0,97531
0,91326874	2	PP3_M	-16,035	3	PP3_MS	0,584	0	NA	0,909	3	PP3_MS	0,224509	1	PP3	0,92705
0,955256	3	PP3_MS	-14,581	3	PP3_MS	0,398	0	NA	0,584	0	NA	-0,223292	-1	BP4	0,98469
0,9518626	3	PP3_MS	-14,227	3	PP3_MS	0,407	0	NA	0,727	0	NA	-0,0680604	0	NA	0,97662
0,951048	3	PP3_MS	-13,96	2	PP3_M	0,373	0	NA	0,907	2	PP3_M	-0,113673	0	NA	0,95285
0,95703214	3	PP3_MS	-17,659	3	PP3_MS	0,945	4	PP3_S	0,952	3	PP3_MS	0,497667	3	PP3_MS	0,98821
0,971817	4	PP3_S	-15,227	3	PP3_MS	0,935	4	PP3_S	0,931	3	PP3_MS	0,497682	3	PP3_MS	0,99296
0,9665832	4	PP3_S	-15,704	3	PP3_MS	0,963	4	PP3_S	0,963	3	PP3_MS	0,491541	3	PP3_MS	0,97923
0,9140096	2	PP3_M	-16,822	3	PP3_MS	0,906	3	PP3_MS	0,844	1	PP3	0,441838	3	PP3_MS	0,9351
0,96266854	3	PP3_MS	-15,425	3	PP3_MS	0,533	0	NA	0,756	0	NA	0,0578342	0	NA	0,94631
0,8185283	1	PP3	-16,868	3	PP3_MS	0,797	2	PP3_M	0,977	4	PP3_S	0,03161	0	NA	0,95974
0,9496355	3	PP3_MS	-18,976	3	PP3_MS	0,953	4	PP3_S	0,121	-2	BP4_M	0,49053	3	PP3_MS	0,99292
0,8897876	2	PP3_M	-16,339	3	PP3_MS	0,902	3	PP3_MS	0,962	3	PP3_MS	0,412586	3	PP3_MS	0,98785
0,913994	2	PP3_M	-18,622	3	PP3_MS	0,937	4	PP3_S	0,427	-1	BP4	0,493954	3	PP3_MS	0,99316
0,86275506	2	PP3_M	-16,498	3	PP3_MS	0,845	2	PP3_M	0,904	2	PP3_M	0,429268	3	PP3_MS	0,94065
0,94946104	3	PP3_MS	-13,924	2	PP3_M	0,76	1	PP3	0,739	0	NA	0,354176	2	PP3_M	0,96633
0,9600197	3	PP3_MS	-15,777	3	PP3_MS	0,765	1	PP3	0,376	-1	BP4	0,388558	2	PP3_M	0,99456
0,9775623	4	PP3_S	-15,131	3	PP3_MS	0,415	0	NA	0,539	0	NA	0,0879396	0	NA	0,90499
0,9729647	4	PP3_S	-16,953	3	PP3_MS	0,678	1	PP3	0,95	3	PP3_MS	0,206809	1	PP3	0,99449
0,95799035	3	PP3_MS	-16,874	3	PP3_MS	0,682	1	PP3	0,956	3	PP3_MS	0,249498	1	PP3	0,98888
0,9575799	3	PP3_MS	-17,499	3	PP3_MS	0,671	1	PP3	0,826	1	PP3	0,241889	1	PP3	0,97982
0,9498538	3	PP3_MS	-13	2	PP3_M	0,487	0	NA	0,775	1	PP3	0,171742	1	PP3	0,9117
0,9830777	4	PP3_S	-14,564	3	PP3_MS	0,535	0	NA	0,92	3	PP3_MS	0,127385	0	NA	0,99463
0,93273133	3	PP3_MS	-16,571	3	PP3_MS	0,677	1	PP3	0,901	2	PP3_M	0,148515	1	PP3	0,96212
0,95573485	3	PP3_MS	-14,879	3	PP3_MS	0,674	1	PP3	0,765	1	PP3	0,175072	1	PP3	0,96045
0,9448411	3	PP3_MS	-13,799	2	PP3_M	0,466	0	NA	0,71	0	NA	0,0904813	0	NA	0,97978
0,950387	3	PP3_MS	-16,373	3	PP3_MS	0,703	1	PP3	0,881	2	PP3_M	0,354336	2	PP3_M	0,97923

cDNA (NM_177559.3)	HGVSp (NP_808227.1)	Comment	Curation/precuration	Curation/precuration_group	Domain	Total_ACMG	PM1	PM5	PS1	PS2	PM2_Supp	PS4/PP5	PS3	BS2	Existing_variation	PubMed	clinvar_clnsig	clinvar_clnsig_group	clinvar_id	clinvar_review	clinvar_dn	clinvar_affected	clinvar_entry_from_PMID	VAR_SYNONYMS
c.1159G>A	p.Ala387Thr		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs199715	-	benign,likely_benign	Benign/Likely	1261752	criteria provi	unknown	yes	no	ClinVar::R
c.401G>A	p.Arg134Gln		B	B/LB	nonspecific kin	-4	0	0	0	0	0	0	0	-4	rs200528	-	Likely benign	Likely_benign	3911441	criteria provi	unknown	yes	no	-
c.1045G>A	p.Ala349Thr		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs199556	-	Likely benign	Likely_benign	3497841	criteria provi	unknown	unknown	no	-
c.809A>G	p.Asn270Ser		B	B/LB	nonspecific kin	-4	0	0	0	0	0	0	0	-4	rs375633	-	uncertain_significanc	Uncertain_sig	2440583	criteria provi	unknown	unknown	no	ClinVar::R
c.1087C>T	p.Pro363Ser		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs373111	-	likely_benign	Likely_benign	3078293	criteria provi	unknown	unknown	no	ClinVar::V
c.1036G>A	p.Val346Ile		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs617458	-	uncertain_significanc	Conflicting_cl	809211	criteria provi	unknown	yes	no	ClinVar::R
c.1165G>A	p.Ala389Thr		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs781253	-	likely_benign	Likely_benign	2367767	criteria provi	unknown	unknown	no	ClinVar::R
c.289C>A	p.Leu97Met		B	B/LB	nonspecific kin	-4	0	0	0	0	0	0	0	-4	rs138635	-	-	-	-	-				-
c.409A>G	p.Met137Val		LB	B/LB	nonspecific kin	-4	0	0	0	0	0	0	0	-4	rs757192	-	-	-	-	-				-
c.1049A>G	p.Asn350Ser		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs754815	-	-	-	-	-				-
c.13G>A	p.Val5Met		LB	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs748335	-	likely_benign	Likely_benign	3269894	criteria provi	unknown	unknown	no	ClinVar::V
c.1017G>A	p.Met339Ile		LB	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs201538	-	-	-	-	-				-
c.1006T>C	p.Ser336Pro		LB	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs761935	-	-	-	-	-				-
c.1166C>T	p.Ala389Val		B	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs758405	-	-	-	-	-				-
c.1103C>T	p.Ala368Val		LB	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs148928	-	Uncertain significance	Uncertain_sig	3389256	criteria provi	unknown	yes	no	-
c.1078A>G	p.Thr360Ala		LB	B/LB	non-kinase	-4	0	0	0	0	0	0	0	-4	rs577076	-	Likely benign	Likely_benign	3911440	criteria provi	unknown	yes	no	-
c.346G>A	p.Val116Ile		LB	B/LB	nonspecific kin	-3	0	0	0	0	0	0	0	-3	rs124057	-	-	-	-	-				COSMIC:
c.998G>A	p.Arg333Gln		LB	B/LB	non-kinase	-3	0	0	0	0	0	0	0	-3	rs150985	-	-	-	-	-				COSMIC:
c.1040G>A	p.Ser347Asn		LB	B/LB	non-kinase	-3	0	0	0	0	0	0	0	-3	rs771672	-	-	-	-	-				-
c.62G>A	p.Arg21Gln	ClinVar e	LB	B/LB	non-kinase	-2	0	0	0	1	0	0	0	-3	rs140273	36588763 (n= 1, dn)	uncertain_significanc	Uncertain_sig	1048801	no assertion	yes	yes	yes	ClinVar::R
c.328G>A	p.Ala110Thr		LB	B/LB	nonspecific kin	-3	0	0	0	0	0	0	0	-3	rs132813	-	-	-	-	-				COSMIC:
c.955A>G	p.Met319Val		LB	B/LB	nonspecific kin	-3	0	0	0	0	0	0	0	-3	rs105695	-	uncertain_significanc	Uncertain_sig	2440582	criteria provi	unknown	unknown	no	ClinVar::R
c.1031C>T	p.Thr344Met		LB	B/LB	non-kinase	-3	0	0	0	0	0	0	0	-3	rs146587	-	-	-	-	-				COSMIC:
c.413A>T	p.Tyr138Phe		LB	B/LB	nonspecific kin	-3	0	0	0	0	0	0	0	-3	rs970324	-	-	-	-	-				-
c.1013G>C	p.Ser338Thr		LB	B/LB	non-kinase	-3	0	0	0	0	0	0	0	-3	rs191244	-	uncertain_significanc	Uncertain_sig	3242179	criteria provi	unknown	yes	no	ClinVar::V
c.1055T>C	p.Met352Thr		LB	B/LB	non-kinase	-2	0	0	0	0	0	0	0	-2	rs121313	-	-	-	-	-				-
c.391T>G	p.Tyr131Asp		LB	B/LB	nonspecific kin	-2	0	0	0	0	0	0	0	-2	rs201837	-	-	-	-	-				-
c.1013G>A	p.Ser338Asn		LB	B/LB	non-kinase	-2	0	0	0	0	0	0	0	-2	rs191244	-	likely_benign	Likely_benign	3269895	criteria provi	unknown	unknown	no	ClinVar::V
c.1025G>A	p.Gly342Asp		LB	B/LB	non-kinase	-2	0	0	0	0	0	0	0	-2	rs201877	-	uncertain_significanc	Uncertain_sig	2494434	criteria provi	unknown	unknown	no	ClinVar::R
c.1053G>A	p.Met351Ile		LB	B/LB	non-kinase	-2	0	0	0	0	0	0	0	-2	rs136335	-	-	-	-	-				-
c.52C>T	p.His18Tyr		LB	B/LB	non-kinase	-2	0	0	0	0	0	0	0	-2	rs116711	-	uncertain_significanc	Uncertain_sig	2572873	criteria provi	unknown	yes	no	ClinVar::R
c.272G>T	p.Gly91Val		LB	B/LB	nonspecific kin	-2	0	0	0	0	0	0	0	-2	-	-	-	-	-	-				-
c.815T>C	p.Ile272Thr		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	rs755588	-	-	-	-	-				COSMIC:
c.256G>C	p.Glu86Gln		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	rs992671	-	-	-	-	-				-
c.380C>T	p.Thr127Met		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	rs769568	-	-	-	-	-				-
c.224A>G	p.Lys75Arg	Given bot	LB	B/LB	Basic cluster	-1	0	0	0	0	0	0	0	-1	rs129957	-	-	-	-	-				-
c.338T>C	p.Phe113Ser		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	rs201840	-	uncertain_significanc	Uncertain_sig	3269896	criteria provi	unknown	unknown	no	ClinVar::V
c.411G>A	p.Met137Ile		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	rs201837	-	-	-	-	-				-
c.610G>A	p.Val204Ile		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	-	-	-	-	-	-				-
c.652T>A	p.Leu218Met		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	-	-	-	-	-	-				-
c.905A>G	p.Asp302Gly		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	rs116043	-	-	-	-	-				-
c.956T>C	p.Met319Thr		LB	B/LB	nonspecific kin	-1	0	0	0	0	0	0	0	-1	-	-	-	-	-	-				-
c.980T>C	p.Val327Ala		LB	B/LB	non-kinase	-1	0	0	0	0	0	0	0	-1	-	-	-	-	-	-				-
c.1003G>A	p.Gly335Ser		LB	B/LB	non-kinase	-1	0	0	0	0	0	1	0	-1	rs201810	-	uncertain_significanc	Uncertain_sig	1304215	criteria provi	unknown	yes	no	ClinVar::R
c.1054A>T	p.Met352Leu		LB	B/LB	non-kinase	-1	0	0	0	0	0	0	0	-1	-	-	-	-	-	-				-
c.1088C>A	p.Pro363His		LB	B/LB	non-kinase	-1	0	0	0	0	0	0	0	-1	rs119328	-	uncertain_significanc	Uncertain_sig	1029545	criteria provi	unknown	yes	no	ClinVar::R
c.1126G>A	p.Ala376Thr		LB	B/LB	non-kinase	-1	0	0	0	0	0	0	0	-1	rs101494	-	-	-	-	-				-

v4.1+AoU+TOPMed	gnomAD4.1_joint_AC	gnomAD4.1_joint_nhomalt	AllofUs_Web	AllofUs_AC	TOPMed_frz8_AC	TOPMed_frz8_AN	1000Gp3_AC	ALFA_Total_AC	ALFA_Total_AN	SpliceAI_pred_DS_AG	SpliceAI_pred_DS_AL	SpliceAI_pred_DS_DG	SpliceAI_pred_DS_DL	SpliceAI (at least 1 with >0.2)	VariantID	am_pathogenicity	am_PP3score	am_PP3_cat	REVEL	REVEL_PP3score
809	288	0	395	395	126	264690	0	33	44756	0	0	0	0	No	20-483978-C-T	0,0786	-2	BP4_M	0,075	-2
241	102	0	119	119	20	264690	0	13	189528	0	0	0	0,03	No	20-497746-C-T	0,6817	0	NA	0,484	0
167	133	0	26	26	8	264690	0	20	205986	0	0	0	0	No	20-486391-C-T	0,0734	-2	BP4_M	0,104	-2
148	78	0	60	60	10	264690	1	6	56256	0	0	0	0	No	20-488693-T-C	0,0653	-3	BP4_MS	0,068	-2
137	46	0	76	76	15	264690	0	1	14050	0,03	0	0	0	No	20-484050-G-A	0,0591	-3	BP4_MS	0,058	-2
104	56	0	34	34	14	264690	0	2	14050	0	0	0	0	No	20-486400-C-T	0,085	-2	BP4_M	0,131	-2
88	62	0	21	21	5	264690	0	4	48844	0	0	0	0	No	20-483972-C-T	0,0722	-2	BP4_M	0,143	-2
55	44	0	10	10	1	264690	0	1	35430	0	0	0	0	No	20-499859-G-T	0,7981	1	PP3	0,417	0
55	13	0	35	35	7	264690	0	1	14050	0	0	0	0	No	20-497738-T-C	0,1843	0	NA	0,359	0
52	29	0	16	16	7	264690	0	2	30358	0	0	0,03	0	No	20-486387-T-C	0,0468	-3	BP4_MS	0,178	-2
48	32	0	15	15	1	264690	0	0	10680	0	0	0	0	No	20-508539-C-T	0,1139	-1	BP4	0,135	-2
47	28	0	17	17	2	264690	2	0	14050	0	0	0	0	No	20-486419-C-T	0,1067	-1	BP4	0,046	-3
44	26	0	14	14	4	264690	0	2	35432	0	0	0	0	No	20-486430-A-G	0,0958	-2	BP4_M	0,157	-2
38	36	0	0	6	2	264690	0	0	14050	0	0	0	0	No	20-483971-G-A	0,0833	-2	BP4_M	0,181	-2
28	23	0	4	1	1	264690	0	0	14050	0	0	0	0	No	20-484034-G-A	0,1116	-1	BP4	0,072	-2
25	7	0	11	11	7	264690	1	0	14050	0	0	0	0	No	20-484059-T-C	0,0566	-3	BP4_MS	0,051	-3
16	9	0	5	5	2	264690	0	1	35426	0	0	0	0	No	20-499275-C-T	0,1692	-1	BP4	0,116	-2
16	6	0	8	8	2	264690	1	2	35432	0	0	0	0	No	20-486438-C-T	0,147	-1	BP4	0,106	-2
14	10	0	4	2	0	0	0	0	14050	0	0	0	0	No	20-486396-C-T	0,1769	0	NA	0,069	-2
13	7	0	4	4	2	264690	0	0	14050	0	0	0	0	No	20-508490-C-T	0,6417	0	NA	0,203	-1
13	9	0	3	1	1	264690	0	0	10680	0	0,01	0	0	No	20-499293-C-T	0,9864	3	PP3_MS	0,322	0
13	7	0	4	2	2	264690	0	0	14050	0	0	0	0	No	20-487445-T-C	0,4933	0	NA	0,584	0
13	10	0	3	1	0	0	0	0	10680	0	0	0,01	0	No	20-486405-G-A	0,0848	-2	BP4_M	0,182	-2
11	9	0	1	0	1	264690	0	0	10680	0	0	0	0	No	20-497734-T-A	0,0782	-2	BP4_M	0,109	-2
11	9	0	2	0	0	0	0	1	23038	0	0	0	0	No	20-486423-C-G	0,0602	-3	BP4_MS	0,05	-3
9	2	0	0	0	7	264690	0	0	14050	0	0	0,12	0	No	20-486381-A-G	0,2042	0	NA	0,192	-1
8	2	0	5	5	1	264690	0	0	10680	0	0	0,01	0	No	20-497756-A-C	0,4239	0	NA	0,368	0
8	7	0	1	1	0	0	1	0	23038	0	0	0	0	No	20-486423-C-T	0,0822	-2	BP4_M	0,066	-2
8	5	0	3	0	0	0	1	1	23698	0	0	0	0	No	20-486411-C-T	0,3703	0	NA	0,048	-3
8	3	0	4	1	1	264690	0	1	14050	0	0	0	0	No	20-486383-C-T	0,2249	0	NA	0,203	-1
7	1	0	2	1	4	264690	0	0	14050	0	0	0	0,01	No	20-508500-G-A	0,1571	-1	BP4	0,183	-2
7	7	0	0	0	0	0	0	0	0	0	0	0	0	No	20-499876-C-A	0,9915	4	PP3_S	0,567	0
7	3	0	2	0	2	264690	0	0	14050	0	0	0	0	No	20-488687-A-G	0,9819	3	PP3_MS	0,316	0
6	5	0	0	0	1	264690	0	0	14050	0	0	0	0	No	20-499892-C-G	0,5233	0	NA	0,16	-2
6	6	0	0	5	0	0	0	0	10680	0	0	0	0	No	20-497767-G-A	0,2125	0	NA	0,385	0
5	1	0	3	0	1	264690	0	0	14050	0,01	0	0	0	No	20-499924-T-C	0,5299	0	NA	0,224	-1
5	2	0	0	0	3	264690	0	0	10680	0	0	0	0	No	20-499283-A-G	0,9949	4	PP3_S	0,618	0
5	3	0	1	1	1	264690	0	0	10680	0	0	0	0	No	20-497736-C-T	0,5907	0	NA	0,249	-1
5	2	0	3	1	0	0	0	0	0	0	0	0	0	No	20-492265-C-T	0,1921	0	NA	0,136	-2
5	5	0	0	0	0	0	0	0	0	0	0	0	0	No	20-489851-A-T	0,5662	0	NA	0,264	-1
5	2	0	1	0	2	264690	0	0	14050	0	0	0	0	No	20-487495-T-C	0,8761	1	PP3	0,703	1
5	4	0	1	0	0	0	0	0	0	0	0	0	0	No	20-487444-A-G	0,8886	1	PP3	0,702	1
5	3	0	2	0	0	0	0	0	0	0	0	0	0	No	20-486456-A-G	0,5005	0	NA	0,288	-1
5	0	0	2	1	3	264690	0	0	10680	0	0	0	0	No	20-486433-C-T	0,0764	-2	BP4_M	0,074	-2
5	5	0	0	0	0	0	0	0	0	0	0	0	0	No	20-486382-T-A	0,077	-2	BP4_M	0,12	-2
5	5	0	0	0	0	0	0	0	0	0,01	0	0	0	No	20-484049-G-T	0,1294	-1	BP4	0,189	-1
5	2	0	0	0	3	264690	0	0	14050	0	0	0	0	No	20-484011-C-T	0,0675	-3	BP4_MS	0,071	-2

REVEL_PP3cat	BayesDel_noAF_score	BayesDel_PP3score	BayesDel_PP3cat	ESM1b_score_MANE	ESM1b_PP3score	ESMPP3b_PP3cat	VARITY_R_score_MANE	VARITY_R_PP3score	VARITY_R_PP3cat	MutPred2	MutPred2_PP3score	MutPred2_PP3cat	VEST4	VEST4_PP3score	VEST4_PP3cat	MutPred2_RankScore	gnomAD2.1.1_exomes_controls_AC	gnomAD2.1.1_exomes_controls_AF	gnomAD2.1.1_exomes_controls_AFR_AC
BP4_M	-0,350756	-1	BP4	-4,496	-1	BP4	0,07991795	-2	BP4_M	0,303768239	-1	BP4	0,371	-1	BP4	0,64189	13	1,19E-04	0
NA	0,0338911	0	NA	-9,931	0	NA	0,88209456	2	PP3_M	0,954578504	4	PP3_S	0,73	0	NA	0,90661	5	4,59E-05	0
BP4_M	-0,406446	-2	BP4_M	-3,841	-1	BP4	0,43898875	0	NA	0,718443716	0	NA	0,634	0	NA	0,49879	16	1,46E-04	0
BP4_M	-0,459098	-2	BP4_M	-9,17	0	NA	0,47932065	0	NA	0,798069785	1	PP3	0,536	0	NA	0,72148	4	3,66E-05	0
BP4_M	-0,427678	-2	BP4_M	-2,951	-2	BP4_M	0,0893418	-2	BP4_M	0,355298108	-1	BP4	0,347	-1	BP4	0,48025	3	2,78E-05	0
BP4_M	-0,283832	-1	BP4	-3,84	-1	BP4	0,22802696	-1	BP4	0,83637707	2	PP3_M	0,654	0	NA	0,3015	2	1,83E-05	0
BP4_M	-0,281782	-1	BP4	-3,982	-1	BP4	0,09386622	-2	BP4_M	0,58508569	0	NA	0,694	0	NA	0,53316	4	3,67E-05	0
NA	-0,180435	-1	BP4	-10,836	1	PP3	0,73739576	1	PP3	0,851849452	2	PP3_M	0,622	0	NA	0,89255	0	0,00E+00	0
NA	0,0896827	0	NA	-6,777	0	NA	0,64501566	0	NA	0,959404069	4	PP3_S	0,941	3	PP3_MS	0,91339	0	0,00E+00	0
BP4_M	-0,627425	-3	BP4_MS	-1,44	-2	BP4_M	0,2523523	0	NA	0,139831552	-2	BP4_M	0,15	-2	BP4_M	0,34802	7	6,40E-05	2
BP4_M	-0,310936	-1	BP4	-6,434	0	NA	0,5033799	0	NA	0,221561393	-1	BP4	0,194	-2	BP4_M	0,84639	5	4,59E-05	0
BP4_MS	-0,375175	-2	BP4_M	-3,409	-1	BP4	0,22100721	-1	BP4	0,697423591	0	NA	0,392	-1	BP4	0,24759	3	2,74E-05	0
BP4_M	-0,323971	-1	BP4	-4,421	-1	BP4	0,33898008	0	NA	0,343644988	-1	BP4	0,425	-1	BP4	0,46689	2	1,83E-05	0
BP4_M	-0,209561	-1	BP4	-3,99	-1	BP4	0,12597543	-1	BP4	0,393979798	0	NA	0,247	-2	BP4_M	0,55658	-	-	-
BP4_M	-0,344653	-1	BP4	-4,399	-1	BP4	0,08351923	-2	BP4_M	0,195706015	-2	BP4_M	0,405	-1	BP4	0,39723	1	9,20E-06	0
BP4_MS	-0,465339	-2	BP4_M	-2,902	-2	BP4_M	0,05354672	-3	BP4_MS	0,118659022	-2	BP4_M	0,278	-2	BP4_M	0,32168	-	-	-
BP4_M	-0,372614	-2	BP4_M	-6,806	0	NA	0,42731312	0	NA	0,234376816	-1	BP4	0,509	0	NA	0,63643	-	-	-
BP4_M	-0,222166	-1	BP4	-5,174	-1	BP4	0,71967757	1	PP3	0,910581658	3	PP3_MS	0,868	2	PP3_M	0,52386	1	9,14E-06	1
BP4_M	-0,451329	-2	BP4_M	-4,837	-1	BP4	0,4679835	0	NA	0,468851598	0	NA	0,251	-2	BP4_M	0,49307	1	9,14E-06	0
BP4	-0,224801	-1	BP4	-9,302	0	NA	0,7959958	1	PP3	0,803422875	1	PP3	0,693	0	NA	0,69743	-	-	-
NA	-0,0636629	0	NA	-11,196	1	PP3	0,907018	2	PP3_M	0,860784642	2	PP3_M	0,676	0	NA	0,90266	-	-	-
NA	0,025674	0	NA	-11,403	1	PP3	0,8823091	2	PP3_M	0,915781759	3	PP3_MS	0,805	1	PP3	0,93722	1	9,14E-06	1
BP4_M	-0,193682	-1	BP4	-4,46	-1	BP4	0,23708557	-1	BP4	0,829125081	2	PP3_M	0,799	1	PP3	0,46706	1	9,14E-06	0
BP4_M	-0,340073	-1	BP4	-6,572	0	NA	0,62824726	0	NA	0,890254971	2	PP3_M	0,769	1	PP3	0,79699	-	-	-
BP4_MS	-0,570824	-3	BP4_MS	-4,44	-1	BP4	0,0441216	-3	BP4_MS	0,25138076	-1	BP4	0,198	-2	BP4_M	0,19726	0	0,00E+00	0
BP4	-0,188289	-1	BP4	-2,643	-2	BP4_M	0,44746268	0	NA	0,889266328	2	PP3_M	0,772	1	PP3	0,67898	-	-	-
NA	-0,118346	0	NA	-13	2	PP3_M	0,89461786	2	PP3_M	0,87852868	2	PP3_M	0,634	0	NA	0,88464	-	-	-
BP4_M	-0,625318	-3	BP4_MS	-4,598	-1	BP4	0,03288327	-4	BP4_S	0,191764422	-2	BP4_M	0,113	-2	BP4_M	0,17363	4	3,66E-05	0
BP4_MS	-0,365535	-2	BP4_M	-5,394	-1	BP4	0,15660518	-1	BP4	0,510900557	0	NA	0,638	0	NA	0,15506	0	0,00E+00	0
BP4	-0,0908233	0	NA	-3,809	-1	BP4	0,44756982	0	NA	0,881368365	2	PP3_M	0,631	0	NA	0,64324	-	-	-
BP4_M	-0,36596	-2	BP4_M	-8,583	0	NA	0,73597014	1	PP3	0,574303378	0	NA	0,416	-1	BP4	0,6236	-	-	-
NA	0,210035	1	PP3	-14,497	3	PP3_MS	0,9643528	3	PP3_MS	0,924116907	3	PP3_MS	0,652	0	NA	0,93754	-	-	-
NA	-0,0301078	0	NA	-10,991	1	PP3	0,7421755	1	PP3	0,891915175	2	PP3_M	0,528	0	NA	0,89556	1	9,16E-06	0
BP4_M	-0,327448	-1	BP4	-4,958	-1	BP4	0,6348187	0	NA	0,360628046	-1	BP4	0,367	-1	BP4	0,81255	-	-	-
NA	-0,188518	-1	BP4	-10,366	0	NA	0,66563743	0	NA	0,876851354	2	PP3_M	0,597	0	NA	0,79562	3	2,75E-05	1
BP4	-0,250284	-1	BP4	-12,103	1	PP3	0,5135445	0	NA	#YOK	#YOK	NA	0,453	0	NA	0,70918	-	-	-
NA	0,135043	1	PP3	-14,494	3	PP3_MS	0,9842131	4	PP3_S	0,956082103	4	PP3_S	0,749	0	NA	0,94266	-	-	-
BP4	0,0186664	0	NA	-4,322	-1	BP4	0,6035945	0	NA	0,942262408	4	PP3_S	0,816	1	PP3	0,92796	-	-	-
BP4_M	-0,252841	-1	BP4	-10,57	0	NA	0,37982404	0	NA	0,63452082	0	NA	0,768	1	PP3	0,67374	-	-	-
BP4	0,017528	0	NA	-7,766	0	NA	0,623611	0	NA	0,776425834	1	PP3	0,509	0	NA	0,78994	-	-	-
PP3	0,228193	1	PP3	-12,774	2	PP3_M	0,9105888	2	PP3_M	0,929995028	3	PP3_MS	0,659	0	NA	0,93917	1	9,14E-06	1
PP3	0,13501	1	PP3	-10,707	1	PP3	0,8979273	2	PP3_M	0,941864825	4	PP3_S	0,842	1	PP3	0,98389	-	-	-
BP4	-0,27088	-1	BP4	-7,99	0	NA	0,7395653	1	PP3	0,740135144	1	PP3	0,396	-1	BP4	0,67787	-	-	-
BP4_M	-0,49432	-2	BP4_M	-2,973	-2	BP4_M	0,4388177	0	NA	0,307897924	-1	BP4	0,471	0	NA	0,29067	-	-	-
BP4_M	-0,290388	-1	BP4	-2,503	-2	BP4_M	0,48926535	0	NA	0,566034559	0	NA	0,417	-1	BP4	0,48291	-	-	-
BP4	-0,3149	-1	BP4	-4,231	-1	BP4	0,28210828	0	NA	0,503548243	0	NA	0,69	0	NA	0,49318	-	-	-
BP4_M	-0,463043	-2	BP4_M	-4,034	-1	BP4	0,03124167	-4	BP4_S	0,083462586	-2	BP4_M	0,469	0	NA	0,3164	-	-	-

gnomAD2.1.1_exomes_controls_AFR_AF	gnomAD2.1.1_exomes_controls_AFR_AN	gnomAD2.1.1_exomes_controls_AFR_nhomalt	gnomAD2.1.1_exomes_controls_AMR_AC	gnomAD2.1.1_exomes_controls_AMR_AF	gnomAD2.1.1_exomes_controls_AMR_AN	gnomAD2.1.1_exomes_controls_AMR_nhomalt	gnomAD2.1.1_exomes_controls_AN	gnomAD2.1.1_exomes_controls_ASJ_AC	gnomAD2.1.1_exomes_controls_ASJ_AF	gnomAD2.1.1_exomes_controls_ASJ_AN	gnomAD2.1.1_exomes_controls_ASJ_nhomalt	gnomAD2.1.1_exomes_controls_EAS_AC	gnomAD2.1.1_exomes_controls_EAS_AF	gnomAD2.1.1_exomes_controls_EAS_AN	gnomAD2.1.1_exomes_controls_EAS_nhomalt	gnomAD2.1.1_exomes_controls_FIN_AC	gnomAD2.1.1_exomes_controls_FIN_AF	gnomAD2.1.1_exomes_controls_FIN_AN	gnomAD2.1.1_exomes_controls_FIN_nhomalt	gnomAD2.1.1_exomes_controls_NFE_AC	gnomAD2.1.1_exomes_controls_NFE_AF
0,00E+00	7096	0	2	1,18E-04	16988	0	108964	8	3,48E-03	2300	0	0	0,00E+00	9018	0	0	0,00E+00	13390	0	3	7,04E-05
0,00E+00	7160	0	1	5,87E-05	17026	0	109006	2	8,62E-04	2320	0	0	0,00E+00	9044	0	0	0,00E+00	13134	0	2	4,68E-05
0,00E+00	7164	0	0	0,00E+00	17108	0	109396	0	0,00E+00	2320	0	0	0,00E+00	9046	0	8	5,97E-04	13390	0	8	1,87E-04
0,00E+00	7154	0	1	5,88E-05	16996	0	109192	0	0,00E+00	2318	0	1	1,11E-04	9046	0	0	0,00E+00	13390	0	2	4,68E-05
0,00E+00	6982	0	0	0,00E+00	16792	0	108068	0	0,00E+00	2302	0	3	3,37E-04	8892	0	0	0,00E+00	13382	0	0	0,00E+00
0,00E+00	7162	0	0	0,00E+00	17110	0	109398	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13390	0	2	4,68E-05
0,00E+00	7104	0	0	0,00E+00	17002	0	108926	0	0,00E+00	2310	0	0	0,00E+00	9012	0	0	0,00E+00	13388	0	1	2,35E-05
0,00E+00	7164	0	0	0,00E+00	17106	0	109402	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	0	0,00E+00
0,00E+00	7160	0	0	0,00E+00	17026	0	108968	0	0,00E+00	2320	0	0	0,00E+00	9044	0	0	0,00E+00	13108	0	0	0,00E+00
2,79E-04	7164	0	1	5,85E-05	17104	0	109400	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	4	9,35E-05
0,00E+00	7144	0	0	0,00E+00	16958	0	108998	0	0,00E+00	2304	0	0	0,00E+00	9022	0	0	0,00E+00	13388	0	1	2,35E-05
0,00E+00	7162	0	0	0,00E+00	17112	0	109402	0	0,00E+00	2320	0	3	3,32E-04	9046	0	0	0,00E+00	13394	0	0	0,00E+00
0,00E+00	7164	0	2	1,17E-04	17112	0	109404	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0,00E+00	7066	0	0	0,00E+00	16946	0	108734	0	0,00E+00	2312	0	0	0,00E+00	8978	0	0	0,00E+00	13386	0	1	2,35E-05
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1,40E-04	7162	0	0	0,00E+00	17110	0	109398	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	0	0,00E+00
0,00E+00	7164	0	1	5,85E-05	17108	0	109398	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1,40E-04	7164	0	0	0,00E+00	17112	0	109408	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	0	0,00E+00
0,00E+00	7164	0	1	5,85E-05	17104	0	109388	0	0,00E+00	2320	0	0	0,00E+00	9044	0	0	0,00E+00	13394	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0,00E+00	7162	0	0	0,00E+00	17108	0	109394	0	0,00E+00	2320	0	0	0,00E+00	9044	0	0	0,00E+00	13394	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0,00E+00	7162	0	0	0,00E+00	17108	0	109394	0	0,00E+00	2320	0	4	4,42E-04	9044	0	0	0,00E+00	13394	0	0	0,00E+00
0,00E+00	7158	0	0	0,00E+00	17092	0	109358	0	0,00E+00	2320	0	0	0,00E+00	9032	0	0	0,00E+00	13394	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0,00E+00	7156	0	0	0,00E+00	16974	0	109164	0	0,00E+00	2318	0	1	1,11E-04	9044	0	0	0,00E+00	13384	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1,40E-04	7156	0	0	0,00E+00	17032	0	109120	0	0,00E+00	2318	0	1	1,11E-04	9046	0	0	0,00E+00	13236	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
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-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1,40E-04	7164	0	0	0,00E+00	17112	0	109406	0	0,00E+00	2320	0	0	0,00E+00	9046	0	0	0,00E+00	13394	0	0	0,00E+00
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
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-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

gnomAD2.1.1_exomes_controls_NFE_AN	gnomAD2.1.1_exomes_controls_NFE_nhomalt	gnomAD2.1.1_exomes_controls_POPMAX_AC	gnomAD2.1.1_exomes_controls_POPMAX_AF	gnomAD2.1.1_exomes_controls_POPMAX_AN	gnomAD2.1.1_exomes_controls_POPMAX_nhomalt	gnomAD2.1.1_exomes_controls_SAS_AC	gnomAD2.1.1_exomes_controls_SAS_AF	gnomAD2.1.1_exomes_controls_SAS_AN	gnomAD2.1.1_exomes_controls_SAS_nhomalt	gnomAD2.1.1_exomes_controls_nhomalt	gnomAD2.1.1_exomes_flag	gnomAD2.1.1_exomes_non_cancer_AC	gnomAD2.1.1_exomes_non_cancer_AF	gnomAD2.1.1_exomes_non_cancer_AFR_AC	gnomAD2.1.1_exomes_non_cancer_AFR_AF	gnomAD2.1.1_exomes_non_cancer_AFR_AN	gnomAD2.1.1_exomes_non_cancer_AFR_nhomalt	gnomAD2.1.1_exomes_non_cancer_AMR_AC	gnomAD2.1.1_exomes_non_cancer_AMR_AF	gnomAD2.1.1_exomes_non_cancer_AMR_AN	gnomAD2.1.1_exomes_non_cancer_AMR_nhomalt
42632	0	2	1,18E-04	16988	0	0	0,00E+00	15634	0	0	segdup	57	2,43E-04	1	6,95E-05	14394	0	5	1,47E-04	34042	0
42736	0	1	5,87E-05	17026	0	0	0,00E+00	15676	0	0	segdup	18	7,62E-05	0	0,00E+00	14860	0	3	8,79E-05	34120	0
42764	0	8	1,87E-04	42764	0	0	0,00E+00	15690	0	0	segdup	29	1,22E-04	0	0,00E+00	14902	0	0	0,00E+00	34250	0
42740	0	1	1,11E-04	9046	0	0	0,00E+00	15638	0	0	segdup	9	3,81E-05	0	0,00E+00	14890	0	1	2,94E-05	34052	0
42406	0	3	3,37E-04	8892	0	0	0,00E+00	15436	0	0	segdup	5	2,14E-05	0	0,00E+00	14448	0	0	0,00E+00	33644	0
42768	0	2	4,68E-05	42768	0	0	0,00E+00	15688	0	0	segdup	9	3,80E-05	0	0,00E+00	14900	0	0	0,00E+00	34256	0
42606	0	3	1,92E-04	15604	0	3	1,92E-04	15604	0	0	segdup	12	5,12E-05	1	6,92E-05	14450	0	0	0,00E+00	34048	0
42768	0	-	-	-	-	0	0,00E+00	15690	0	0	segdup	1	4,22E-06	0	0,00E+00	14902	0	0	0,00E+00	34254	0
42738	0	-	-	-	-	0	0,00E+00	15664	0	0	segdup	0	0,00E+00	0	0,00E+00	14860	0	0	0,00E+00	34126	0
42768	0	2	2,79E-04	7164	0	0	0,00E+00	15690	0	0	segdup	10	4,22E-05	2	1,34E-04	14902	0	1	2,92E-05	34248	0
42640	0	4	2,56E-04	15646	0	4	2,56E-04	15646	0	0	segdup	7	2,97E-05	1	6,74E-05	14832	0	0	0,00E+00	33960	0
42764	0	3	3,32E-04	9046	0	0	0,00E+00	15690	0	0	segdup	7	2,96E-05	0	0,00E+00	14896	0	0	0,00E+00	34260	0
42766	0	2	1,17E-04	17112	0	0	0,00E+00	15688	0	0	segdup	2	8,44E-06	0	0,00E+00	14902	0	2	5,84E-05	34260	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
42576	0	1	2,35E-05	42576	0	0	0,00E+00	15570	0	0	segdup	1	4,26E-06	0	0,00E+00	14642	0	0	0,00E+00	33930	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
42764	0	1	1,40E-04	7162	0	0	0,00E+00	15688	0	0	segdup	2	8,44E-06	1	6,71E-05	14898	0	0	0,00E+00	34250	0
42766	0	1	5,85E-05	17108	0	0	0,00E+00	15686	0	0	segdup	3	1,27E-05	0	0,00E+00	14900	0	1	2,92E-05	34254	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
42768	0	1	1,40E-04	7164	0	0	0,00E+00	15690	0	0	segdup	2	8,44E-06	1	6,71E-05	14902	0	1	2,92E-05	34260	0
42764	0	1	5,85E-05	17104	0	0	0,00E+00	15686	0	0	segdup	1	4,22E-06	0	0,00E+00	14900	0	1	2,92E-05	34246	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
42762	0	-	-	-	-	0	0,00E+00	15690	0	0	segdup	2	8,44E-06	0	0,00E+00	14900	0	0	0,00E+00	34240	0
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42762	0	4	4,42E-04	9044	0	0	0,00E+00	15690	0	0	segdup	4	1,69E-05	0	0,00E+00	14900	0	0	0,00E+00	34240	0
42764	0	-	-	-	-	0	0,00E+00	15684	0	0	segdup	2	8,45E-06	0	0,00E+00	14892	0	0	0,00E+00	34226	0
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42742	0	1	1,11E-04	9044	0	0	0,00E+00	15636	0	0	segdup	3	1,27E-05	0	0,00E+00	14892	0	0	0,00E+00	34038	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
42742	0	1	1,40E-04	7156	0	1	6,38E-05	15678	0	0	segdup	3	1,27E-05	1	6,73E-05	14858	0	0	0,00E+00	34128	0
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42766	0	1	1,40E-04	7164	0	0	0,00E+00	15690	0	0	segdup	1	4,22E-06	1	6,71E-05	14902	0	0	0,00E+00	34258	0
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gnomAD2.1.1_exomes_non_cancer_AN	gnomAD2.1.1_exomes_non_cancer_ASJ_AC	gnomAD2.1.1_exomes_non_cancer_ASJ_AF	gnomAD2.1.1_exomes_non_cancer_ASJ_AN	gnomAD2.1.1_exomes_non_cancer_ASJ_nhomalt	gnomAD2.1.1_exomes_non_cancer_EAS_AC	gnomAD2.1.1_exomes_non_cancer_EAS_AF	gnomAD2.1.1_exomes_non_cancer_EAS_AN	gnomAD2.1.1_exomes_non_cancer_EAS_nhomalt	gnomAD2.1.1_exomes_non_cancer_FIN_AC	gnomAD2.1.1_exomes_non_cancer_FIN_AF	gnomAD2.1.1_exomes_non_cancer_FIN_AN	gnomAD2.1.1_exomes_non_cancer_FIN_nhomalt	gnomAD2.1.1_exomes_non_cancer_NFE_AC	gnomAD2.1.1_exomes_non_cancer_NFE_AF	gnomAD2.1.1_exomes_non_cancer_NFE_AN	gnomAD2.1.1_exomes_non_cancer_NFE_nhomalt	gnomAD2.1.1_exomes_non_cancer_POPMAX_AC	gnomAD2.1.1_exomes_non_cancer_POPMAX_AF	gnomAD2.1.1_exomes_non_cancer_POPMAX_AN	gnomAD2.1.1_exomes_non_cancer_POPMAX_nhomalt	gnomAD2.1.1_exomes_non_cancer_SAS_AC
234724	35	3,70E-03	9472	0	0	0,00E+00	17634	0	0	0,00E+00	21596	0	13	1,28E-04	101610	0	5	1,47E-04	34042	0	0
236312	12	1,25E-03	9566	0	0	0,00E+00	17684	0	0	0,00E+00	21368	0	3	2,92E-05	102606	0	3	8,79E-05	34120	0	0
236830	0	0,00E+00	9568	0	0	0,00E+00	17692	0	11	5,09E-04	21626	0	18	1,75E-04	102660	0	18	1,75E-04	102660	0	0
236402	0	0,00E+00	9566	0	2	1,13E-04	17676	0	0	0,00E+00	21624	0	6	5,85E-05	102572	0	2	1,13E-04	17676	0	0
233294	0	0,00E+00	9480	0	4	2,30E-04	17390	0	0	0,00E+00	21562	0	0	0,00E+00	101212	0	4	2,30E-04	17390	0	0
236852	0	0,00E+00	9568	0	1	5,65E-05	17692	0	0	0,00E+00	21626	0	7	6,82E-05	102678	0	7	6,82E-05	102678	0	1
234592	0	0,00E+00	9504	0	2	1,14E-04	17618	0	0	0,00E+00	21566	0	4	3,94E-05	101510	0	5	1,65E-04	30344	0	5
236952	0	0,00E+00	9572	0	0	0,00E+00	17692	0	0	0,00E+00	21632	0	1	9,73E-06	102754	0	1	9,73E-06	102754	0	0
236252	0	0,00E+00	9566	0	0	0,00E+00	17680	0	0	0,00E+00	21344	0	0	0,00E+00	102596	0	-	-	-	-	0
236860	0	0,00E+00	9568	0	0	0,00E+00	17692	0	0	0,00E+00	21628	0	7	6,82E-05	102684	0	2	1,34E-04	14902	0	0
235638	0	0,00E+00	9518	0	0	0,00E+00	17626	0	0	0,00E+00	21588	0	2	1,96E-05	102152	0	4	1,32E-04	30394	0	4
236866	0	0,00E+00	9568	0	7	3,96E-04	17692	0	0	0,00E+00	21630	0	0	0,00E+00	102684	0	7	3,96E-04	17692	0	0
236852	0	0,00E+00	9564	0	0	0,00E+00	17692	0	0	0,00E+00	21632	0	0	0,00E+00	102670	0	2	5,84E-05	34260	0	0
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234900	0	0,00E+00	9530	0	0	0,00E+00	17528	0	0	0,00E+00	21600	0	1	9,82E-06	101824	0	1	9,82E-06	101824	0	0
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236836	0	0,00E+00	9564	0	0	0,00E+00	17690	0	0	0,00E+00	21622	0	1	9,74E-06	102682	0	1	6,71E-05	14898	0	0
236852	0	0,00E+00	9568	0	0	0,00E+00	17692	0	0	0,00E+00	21630	0	1	9,74E-06	102678	0	1	2,92E-05	34254	0	0
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236914	0	0,00E+00	9572	0	0	0,00E+00	17692	0	0	0,00E+00	21632	0	0	0,00E+00	102718	0	1	6,71E-05	14902	0	0
236828	0	0,00E+00	9568	0	0	0,00E+00	17688	0	0	0,00E+00	21630	0	0	0,00E+00	102668	0	1	2,92E-05	34246	0	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
236846	0	0,00E+00	9568	0	0	0,00E+00	17688	0	0	0,00E+00	21630	0	0	0,00E+00	102682	0	2	6,55E-05	30526	0	2
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236846	0	0,00E+00	9568	0	4	2,26E-04	17688	0	0	0,00E+00	21630	0	0	0,00E+00	102682	0	4	2,26E-04	17688	0	0
236770	1	1,05E-04	9568	0	0	0,00E+00	17672	0	0	0,00E+00	21630	0	1	9,74E-06	102654	0	1	9,74E-06	102654	0	0
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236378	0	0,00E+00	9560	0	3	1,70E-04	17674	0	0	0,00E+00	21618	0	0	0,00E+00	102582	0	3	1,70E-04	17674	0	0
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236422	0	0,00E+00	9568	0	1	5,65E-05	17686	0	0	0,00E+00	21472	0	0	0,00E+00	102602	0	1	6,73E-05	14858	0	1
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236910	0	0,00E+00	9570	0	0	0,00E+00	17692	0	0	0,00E+00	21632	0	0	0,00E+00	102718	0	1	6,71E-05	14902	0	0
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gnomAD2.1.1_exomes_non_cancer_SAS_AF	gnomAD2.1.1_exomes_non_cancer_SAS_AN	gnomAD2.1.1_exomes_non_cancer_SAS_nhomalt	gnomAD2.1.1_exomes_non_cancer_nhomalt	gnomAD2.1.1_exomes_non_neuro_AC	gnomAD2.1.1_exomes_non_neuro_AF	gnomAD2.1.1_exomes_non_neuro_AFR_AC	gnomAD2.1.1_exomes_non_neuro_AFR_AF	gnomAD2.1.1_exomes_non_neuro_AFR_AN	gnomAD2.1.1_exomes_non_neuro_AFR_nhomalt	gnomAD2.1.1_exomes_non_neuro_AMR_AC	gnomAD2.1.1_exomes_non_neuro_AMR_AF	gnomAD2.1.1_exomes_non_neuro_AMR_AN	gnomAD2.1.1_exomes_non_neuro_AMR_nhomalt	gnomAD2.1.1_exomes_non_neuro_AN	gnomAD2.1.1_exomes_non_neuro_ASJ_AC	gnomAD2.1.1_exomes_non_neuro_ASJ_AF	gnomAD2.1.1_exomes_non_neuro_ASJ_AN	gnomAD2.1.1_exomes_non_neuro_ASJ_nhomalt	gnomAD2.1.1_exomes_non_neuro_EAS_AC	gnomAD2.1.1_exomes_non_neuro_EAS_AF	gnomAD2.1.1_exomes_non_neuro_EAS_AN
0,00E+00	30416	0	0	39	1,89E-04	1	6,37E-05	15690	0	4	1,32E-04	30320	0	206302	20	3,25E-03	6146	0	0	0,00E+00	13346
0,00E+00	30504	0	0	15	7,23E-05	0	0,00E+00	16176	0	2	6,58E-05	30390	0	207544	8	1,29E-03	6212	0	0	0,00E+00	13412
0,00E+00	30522	0	0	19	9,13E-05	0	0,00E+00	16218	0	0	0,00E+00	30514	0	208090	0	0,00E+00	6210	0	0	0,00E+00	13416
0,00E+00	30428	0	0	9	4,33E-05	0	0,00E+00	16206	0	1	3,30E-05	30328	0	207664	0	0,00E+00	6208	0	3	2,24E-04	13406
0,00E+00	30052	0	0	0	0,00E+00	0	0,00E+00	15738	0	0	0,00E+00	29932	0	204918	0	0,00E+00	6146	0	0	0,00E+00	13108
3,28E-05	30524	0	0	6	2,88E-05	0	0,00E+00	16216	0	0	0,00E+00	30520	0	208092	0	0,00E+00	6210	0	1	7,45E-05	13416
1,65E-04	30344	0	0	13	6,30E-05	1	6,35E-05	15740	0	0	0,00E+00	30342	0	206238	0	0,00E+00	6164	0	2	1,50E-04	13336
0,00E+00	30526	0	0	1	4,80E-06	0	0,00E+00	16218	0	0	0,00E+00	30518	0	208130	0	0,00E+00	6212	0	0	0,00E+00	13416
0,00E+00	30482	0	0	1	4,82E-06	1	6,18E-05	16176	0	0	0,00E+00	30400	0	207486	0	0,00E+00	6212	0	0	0,00E+00	13412
0,00E+00	30526	0	0	7	3,36E-05	2	1,23E-04	16218	0	1	3,28E-05	30512	0	208098	0	0,00E+00	6210	0	0	0,00E+00	13416
1,32E-04	30394	0	0	8	3,86E-05	1	6,19E-05	16146	0	0	0,00E+00	30242	0	207194	0	0,00E+00	6180	0	0	0,00E+00	13356
0,00E+00	30524	0	0	6	2,88E-05	0	0,00E+00	16212	0	0	0,00E+00	30524	0	208104	0	0,00E+00	6210	0	6	4,47E-04	13416
0,00E+00	30520	0	0	2	9,61E-06	0	0,00E+00	16218	0	2	6,55E-05	30524	0	208114	0	0,00E+00	6210	0	0	0,00E+00	13416
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0,00E+00	30292	0	0	1	4,84E-06	0	0,00E+00	15950	0	0	0,00E+00	30212	0	206408	0	0,00E+00	6192	0	0	0,00E+00	13234
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0,00E+00	30522	0	0	1	4,81E-06	1	6,17E-05	16214	0	0	0,00E+00	30514	0	208084	0	0,00E+00	6210	0	0	0,00E+00	13414
0,00E+00	30518	0	0	3	1,44E-05	0	0,00E+00	16216	0	1	3,28E-05	30518	0	208092	0	0,00E+00	6210	0	0	0,00E+00	13416
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0,00E+00	30526	0	0	2	9,61E-06	1	6,17E-05	16218	0	1	3,28E-05	30524	0	208128	0	0,00E+00	6212	0	0	0,00E+00	13416
0,00E+00	30520	0	0	1	4,81E-06	0	0,00E+00	16216	0	1	3,28E-05	30510	0	208074	0	0,00E+00	6210	0	0	0,00E+00	13412
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6,55E-05	30526	0	0	2	9,61E-06	0	0,00E+00	16216	0	0	0,00E+00	30508	0	208092	0	0,00E+00	6210	0	0	0,00E+00	13412
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0,00E+00	30526	0	0	3	1,44E-05	0	0,00E+00	16216	0	0	0,00E+00	30508	0	208092	0	0,00E+00	6210	0	3	2,24E-04	13412
0,00E+00	30514	0	0	2	9,61E-06	0	0,00E+00	16210	0	0	0,00E+00	30492	0	208024	1	1,61E-04	6210	0	0	0,00E+00	13396
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0,00E+00	30416	0	0	1	4,82E-06	0	0,00E+00	16208	0	0	0,00E+00	30308	0	207642	0	0,00E+00	6206	0	1	7,46E-05	13406
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3,28E-05	30502	0	0	3	1,44E-05	1	6,18E-05	16174	0	0	0,00E+00	30402	0	207640	0	0,00E+00	6210	0	1	7,46E-05	13412
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0,00E+00	30526	0	0	1	4,80E-06	1	6,17E-05	16218	0	0	0,00E+00	30522	0	208126	0	0,00E+00	6210	0	0	0,00E+00	13416
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-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

gnomAD2.1.1_exomes_non_neuro_EAS_nhomalt	gnomAD2.1.1_exomes_non_neuro_FIN_AC	gnomAD2.1.1_exomes_non_neuro_FIN_AF	gnomAD2.1.1_exomes_non_neuro_FIN_AN	gnomAD2.1.1_exomes_non_neuro_FIN_nhomalt	gnomAD2.1.1_exomes_non_neuro_NFE_AC	gnomAD2.1.1_exomes_non_neuro_NFE_AF	gnomAD2.1.1_exomes_non_neuro_NFE_AN	gnomAD2.1.1_exomes_non_neuro_NFE_nhomalt	gnomAD2.1.1_exomes_non_neuro_POPMAX_AC	gnomAD2.1.1_exomes_non_neuro_POPMAX_AF	gnomAD2.1.1_exomes_non_neuro_POPMAX_AN	gnomAD2.1.1_exomes_non_neuro_POPMAX_nhomalt	gnomAD2.1.1_exomes_non_neuro_SAS_AC	gnomAD2.1.1_exomes_non_neuro_SAS_AF	gnomAD2.1.1_exomes_non_neuro_SAS_AN	gnomAD2.1.1_exomes_non_neuro_SAS_nhomalt	gnomAD2.1.1_exomes_non_neuro_nhomalt	gnomAD4.1_joint_AF	gnomAD4.1_joint_AFR_AC	gnomAD4.1_joint_AFR_AF	gnomAD4.1_joint_AFR_AN
0	0	0,00E+00	16716	0	11	1,24E-04	88782	0	4	1,32E-04	30320	0	0	0,00E+00	30496	0	0	1,79E-04	4	5,35E-05	74772
0	0	0,00E+00	16474	0	5	5,59E-05	89442	0	2	6,58E-05	30390	0	0	0,00E+00	30586	0	0	6,33E-05	2	2,67E-05	74864
0	8	4,78E-04	16728	0	11	1,23E-04	89538	0	11	1,23E-04	89538	0	0	0,00E+00	30604	0	0	8,24E-05	0	0,00E+00	74692
0	0	0,00E+00	16726	0	5	5,59E-05	89430	0	3	2,24E-04	13406	0	0	0,00E+00	30510	0	0	4,83E-05	2	2,66E-05	75054
0	0	0,00E+00	16668	0	0	0,00E+00	88442	0	-	-	-	-	0	0,00E+00	30128	0	0	2,86E-05	0	0,00E+00	74696
0	0	0,00E+00	16728	0	4	4,47E-05	89536	0	1	7,45E-05	13416	0	1	3,27E-05	30606	0	0	3,47E-05	3	4,01E-05	74724
0	0	0,00E+00	16704	0	5	5,64E-05	88726	0	5	1,64E-04	30424	0	5	1,64E-04	30424	0	0	-	-	-	-
0	0	0,00E+00	16734	0	1	1,12E-05	89558	0	1	1,12E-05	89558	0	0	0,00E+00	30608	0	0	2,73E-05	0	0,00E+00	74870
0	0	0,00E+00	16448	0	0	0,00E+00	89426	0	1	6,18E-05	16176	0	0	0,00E+00	30564	0	0	8,07E-06	9	1,20E-04	74900
0	0	0,00E+00	16730	0	4	4,47E-05	89542	0	2	1,23E-04	16218	0	0	0,00E+00	30608	0	0	1,80E-05	1	1,34E-05	74794
0	0	0,00E+00	16726	0	3	3,36E-05	89244	0	4	1,31E-04	30476	0	4	1,31E-04	30476	0	0	1,98E-05	1	1,34E-05	74886
0	0	0,00E+00	16732	0	0	0,00E+00	89538	0	6	4,47E-04	13416	0	0	0,00E+00	30606	0	0	1,74E-05	0	0,00E+00	74856
0	0	0,00E+00	16734	0	0	0,00E+00	89546	0	2	6,55E-05	30524	0	0	0,00E+00	30602	0	0	1,61E-05	1	1,34E-05	74766
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0,00E+00	16704	0	1	1,12E-05	88930	0	1	1,12E-05	88930	0	0	0,00E+00	30374	0	0	1,43E-05	0	0,00E+00	74666
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4,36E-06	5	6,73E-05	74324
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5,60E-06	0	0,00E+00	74738
0	0	0,00E+00	16728	0	0	0,00E+00	89540	0	1	6,17E-05	16214	0	0	0,00E+00	30604	0	0	3,72E-06	2	2,67E-05	74842
0	0	0,00E+00	16732	0	1	1,12E-05	89538	0	1	3,28E-05	30518	0	0	0,00E+00	30600	0	0	6,20E-06	0	0,00E+00	74764
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5,60E-06	0	0,00E+00	74782
0	0	0,00E+00	16734	0	0	0,00E+00	89552	0	1	6,17E-05	16218	0	0	0,00E+00	30608	0	0	4,34E-06	1	1,33E-05	74918
0	0	0,00E+00	16732	0	0	0,00E+00	89534	0	1	3,28E-05	30510	0	0	0,00E+00	30602	0	0	6,20E-06	1	1,34E-05	74694
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5,59E-06	0	0,00E+00	74900
0	0	0,00E+00	16732	0	0	0,00E+00	89540	0	2	6,53E-05	30608	0	2	6,53E-05	30608	0	0	5,58E-06	0	0,00E+00	74846
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,24E-06	0	0,00E+00	74818
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,24E-06	0	0,00E+00	74918
0	0	0,00E+00	16732	0	0	0,00E+00	89540	0	3	2,24E-04	13412	0	0	0,00E+00	30608	0	0	4,34E-06	0	0,00E+00	74846
0	0	0,00E+00	16732	0	1	1,12E-05	89522	0	1	1,12E-05	89522	0	0	0,00E+00	30596	0	0	3,10E-06	0	0,00E+00	74828
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,86E-06	0	0,00E+00	74906
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6,20E-07	0	0,00E+00	74924
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4,34E-06	0	0,00E+00	74800
0	0	0,00E+00	16720	0	0	0,00E+00	89442	0	1	7,46E-05	13406	0	0	0,00E+00	30498	0	0	1,86E-06	0	0,00E+00	75042
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3,10E-06	0	0,00E+00	74768
0	0	0,00E+00	16576	0	0	0,00E+00	89428	0	1	7,46E-05	13412	0	1	3,27E-05	30584	0	0	3,72E-06	1	1,33E-05	74980
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6,20E-07	0	0,00E+00	74400
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,24E-06	0	0,00E+00	74796
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,86E-06	0	0,00E+00	74866
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,24E-06	0	0,00E+00	74906
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3,10E-06	0	0,00E+00	75020
0	0	0,00E+00	16734	0	0	0,00E+00	89554	0	1	6,17E-05	16218	0	0	0,00E+00	30608	0	0	1,24E-06	2	2,67E-05	74926
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2,48E-06	0	0,00E+00	75032
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1,86E-06	0	0,00E+00	74850
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3,10E-06	0	0,00E+00	74886
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3,10E-06	0	0,00E+00	74682
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

gnomAD4.1_joint_AFR_nhomalt	gnomAD4.1_joint_AMI_AC	gnomAD4.1_joint_AMI_AF	gnomAD4.1_joint_AMI_AN	gnomAD4.1_joint_AMI_nhomalt	gnomAD4.1_joint_AMR_AC	gnomAD4.1_joint_AMR_AF	gnomAD4.1_joint_AMR_AN	gnomAD4.1_joint_AMR_nhomalt	gnomAD4.1_joint_AN	gnomAD4.1_joint_ASJ_AC	gnomAD4.1_joint_ASJ_AF	gnomAD4.1_joint_ASJ_AN	gnomAD4.1_joint_ASJ_nhomalt	gnomAD4.1_joint_EAS_AC	gnomAD4.1_joint_EAS_AF	gnomAD4.1_joint_EAS_AN	gnomAD4.1_joint_EAS_nhomalt	gnomAD4.1_joint_FIN_AC	gnomAD4.1_joint_FIN_AF	gnomAD4.1_joint_FIN_AN	gnomAD4.1_joint_FIN_nhomalt
0	0	0,00E+00	912	0	27	4,52E-04	59766	0	1611458	119	4,04E-03	29474	0	0	0,00E+00	44592	0	0	0,00E+00	64004	0
0	0	0,00E+00	912	0	8	1,34E-04	59908	0	1611918	41	1,39E-03	29572	0	0	0,00E+00	44822	0	0	0,00E+00	63672	0
0	0	0,00E+00	912	0	1	1,67E-05	59894	0	1613352	0	0,00E+00	29596	0	0	0,00E+00	44904	0	44	6,88E-04	63918	0
0	0	0,00E+00	912	0	3	5,00E-05	59946	0	1613886	0	0,00E+00	29596	0	3	6,69E-05	44870	0	2	3,12E-05	64028	0
0	0	0,00E+00	912	0	0	0,00E+00	59688	0	1610868	0	0,00E+00	29542	0	10	2,25E-04	44390	0	0	0,00E+00	63988	0
0	0	0,00E+00	912	0	0	0,00E+00	59908	0	1613472	0	0,00E+00	29602	0	1	2,23E-05	44898	0	0	0,00E+00	63912	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0,00E+00	912	0	0	0,00E+00	59982	0	1613588	0	0,00E+00	29596	0	0	0,00E+00	44862	0	0	0,00E+00	63886	0
0	0	0,00E+00	912	0	0	0,00E+00	59926	0	1611584	0	0,00E+00	29574	0	1	2,23E-05	44832	0	0	0,00E+00	63662	0
0	0	0,00E+00	910	0	1	1,67E-05	59938	0	1613628	0	0,00E+00	29602	0	0	0,00E+00	44890	0	0	0,00E+00	63962	0
0	0	0,00E+00	912	0	0	0,00E+00	59880	0	1613280	0	0,00E+00	29562	0	3	6,69E-05	44842	0	0	0,00E+00	64020	0
0	0	0,00E+00	910	0	0	0,00E+00	59928	0	1613582	0	0,00E+00	29602	0	22	4,90E-04	44878	0	0	0,00E+00	63904	0
0	0	0,00E+00	912	0	2	3,34E-05	59926	0	1613538	0	0,00E+00	29600	0	0	0,00E+00	44894	0	0	0,00E+00	63940	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0,00E+00	912	0	1	1,67E-05	59796	0	1611846	0	0,00E+00	29564	0	0	0,00E+00	44572	0	0	0,00E+00	64022	0
0	0	0,00E+00	910	0	1	1,69E-05	59148	0	1606830	0	0,00E+00	29386	0	0	0,00E+00	44030	0	0	0,00E+00	63864	0
0	0	0,00E+00	912	0	0	0,00E+00	59500	0	1607808	3	1,02E-04	29540	0	0	0,00E+00	44626	0	0	0,00E+00	63930	0
0	0	0,00E+00	912	0	0	0,00E+00	59928	0	1613412	0	0,00E+00	29606	0	0	0,00E+00	44872	0	0	0,00E+00	63868	0
0	0	0,00E+00	912	0	1	1,67E-05	59906	0	1613544	0	0,00E+00	29602	0	0	0,00E+00	44902	0	0	0,00E+00	63928	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0,00E+00	912	0	1	1,69E-05	59304	0	1606892	0	0,00E+00	29518	0	0	0,00E+00	44544	0	0	0,00E+00	63928	0
0	0	0,00E+00	912	0	1	1,67E-05	60006	0	1613950	0	0,00E+00	29606	0	0	0,00E+00	44898	0	0	0,00E+00	64048	0
0	0	0,00E+00	912	0	2	3,34E-05	59872	0	1613092	0	0,00E+00	29592	0	0	0,00E+00	44880	0	0	0,00E+00	63848	0
0	0	0,00E+00	912	0	0	0,00E+00	59896	0	1611156	0	0,00E+00	29560	0	0	0,00E+00	44824	0	0	0,00E+00	63626	0
0	0	0,00E+00	904	0	0	0,00E+00	59918	0	1613358	0	0,00E+00	29594	0	0	0,00E+00	44868	0	0	0,00E+00	63902	0
0	0	0,00E+00	910	0	2	3,34E-05	59942	0	1613676	0	0,00E+00	29600	0	0	0,00E+00	44898	0	0	0,00E+00	63970	0
0	0	0,00E+00	912	0	0	0,00E+00	59964	0	1612606	0	0,00E+00	29566	0	0	0,00E+00	44828	0	0	0,00E+00	63782	0
0	0	0,00E+00	904	0	0	0,00E+00	59918	0	1613358	0	0,00E+00	29594	0	7	1,56E-04	44868	0	0	0,00E+00	63902	0
0	0	0,00E+00	912	0	3	5,01E-05	59862	0	1613070	1	3,38E-05	29596	0	0	0,00E+00	44850	0	0	0,00E+00	63882	0
0	0	0,00E+00	910	0	0	0,00E+00	59940	0	1613664	0	0,00E+00	29604	0	0	0,00E+00	44882	0	0	0,00E+00	63956	0
0	0	0,00E+00	912	0	1	1,67E-05	59992	0	1614042	0	0,00E+00	29604	0	0	0,00E+00	44900	0	0	0,00E+00	64034	0
0	0	0,00E+00	912	0	0	0,00E+00	59976	0	1613582	0	0,00E+00	29604	0	0	0,00E+00	44862	0	0	0,00E+00	63892	0
0	0	0,00E+00	912	0	0	0,00E+00	59938	0	1613796	0	0,00E+00	29590	0	3	6,69E-05	44866	0	0	0,00E+00	64030	0
0	0	0,00E+00	910	0	0	0,00E+00	59942	0	1613506	0	0,00E+00	29604	0	0	0,00E+00	44862	0	0	0,00E+00	63864	0
0	0	0,00E+00	912	0	1	1,67E-05	59942	0	1612388	0	0,00E+00	29558	0	1	2,23E-05	44804	0	0	0,00E+00	63756	0
0	0	0,00E+00	908	0	0	0,00E+00	59852	0	1612394	0	0,00E+00	29604	0	0	0,00E+00	44816	0	0	0,00E+00	63850	0
0	0	0,00E+00	912	0	1	1,68E-05	59548	0	1608728	1	3,38E-05	29562	0	0	0,00E+00	44656	0	0	0,00E+00	63988	0
0	0	0,00E+00	912	0	0	0,00E+00	59912	0	1611174	0	0,00E+00	29560	0	0	0,00E+00	44816	0	0	0,00E+00	63592	0
0	0	0,00E+00	910	0	0	0,00E+00	60006	0	1613536	0	0,00E+00	29598	0	0	0,00E+00	44866	0	0	0,00E+00	63968	0
0	0	0,00E+00	912	0	0	0,00E+00	60008	0	1613154	0	0,00E+00	29586	0	0	0,00E+00	44864	0	0	0,00E+00	63946	0
0	0	0,00E+00	912	0	0	0,00E+00	60004	0	1614074	0	0,00E+00	29604	0	0	0,00E+00	44894	0	0	0,00E+00	64040	0
0	0	0,00E+00	912	0	0	0,00E+00	60020	0	1614054	0	0,00E+00	29604	0	0	0,00E+00	44880	0	0	0,00E+00	64044	0
0	0	0,00E+00	910	0	0	0,00E+00	59916	0	1613576	0	0,00E+00	29602	0	0	0,00E+00	44876	0	0	0,00E+00	63940	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0,00E+00	910	0	0	0,00E+00	59936	0	1613594	0	0,00E+00	29602	0	0	0,00E+00	44878	0	0	0,00E+00	63946	0
0	0	0,00E+00	912	0	0	0,00E+00	59694	0	1610778	0	0,00E+00	29546	0	0	0,00E+00	44392	0	0	0,00E+00	63992	0
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

gnomAD4.1_joint_MID_AC	gnomAD4.1_joint_MID_AF	gnomAD4.1_joint_MID_AN	gnomAD4.1_joint_MID_nhomalt	gnomAD4.1_joint_NFE_AC	gnomAD4.1_joint_NFE_AF	gnomAD4.1_joint_NFE_AN	gnomAD4.1_joint_NFE_nhomalt	gnomAD4.1_joint_POPMAX_AC	gnomAD4.1_joint_POPMAX_AF	gnomAD4.1_joint_POPMAX_AN	gnomAD4.1_joint_POPMAX_nhomalt	gnomAD4.1_joint_SAS_AC	gnomAD4.1_joint_SAS_AF	gnomAD4.1_joint_SAS_AN	gnomAD4.1_joint_SAS_nhomalt	gnomAD4.1_joint_flag	AllOfUs	AllOfUs_gvs_all_af	AllOfUs_gvs_max_af	AllOfUs_gvs_afr_af	AllOfUs_gvs_amr_af
0	0,00E+00	6006	0	112	9,50E-05	1178778	0	119	4,04E-03	29474	0	2	2,20E-05	90768	0	-	chr20:48397	0,000473	0,003817	9,30E-05	0,00055
0	0,00E+00	6078	0	40	3,39E-05	1178720	0	41	1,39E-03	29572	0	0	0,00E+00	90970	0	-	chr20:49774	0,000167	0,000735	0	0,000225
0	0,00E+00	6084	0	77	6,53E-05	1179844	0	44	6,88E-04	63918	0	0	0,00E+00	91044	0	-	chr20:48639	3,90E-05	9,30E-05	9,30E-05	1,30E-05
0	0,00E+00	6062	0	66	5,59E-05	1179908	0	3	6,69E-05	44870	0	1	1,10E-05	91010	0	-	chr20:48869	7,30E-05	0,000134	8,30E-05	0,000125
0	0,00E+00	6050	0	1	8,48E-07	1178602	0	10	2,25E-04	44390	0	0	0,00E+00	90622	0	-	chr20:48405	9,60E-05	0,002883	0	3,80E-05
0	0,00E+00	6084	0	49	4,15E-05	1179914	0	49	4,15E-05	1179914	0	2	2,20E-05	91052	0	-	chr20:48640	3,70E-05	5,00E-05	2,80E-05	5,00E-05
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	chr20:48397	2,00E-05	2,80E-05	2,80E-05	0
0	0,00E+00	5970	0	43	3,64E-05	1179934	0	43	3,64E-05	1179934	0	0	0,00E+00	91072	0	-	chr20:49985	1,00E-05	1,90E-05	0	0
0	0,00E+00	6076	0	2	1,70E-06	1178308	0	9	1,20E-04	74900	0	0	0,00E+00	90998	0	-	chr20:49773	3,90E-05	0,000158	0,000158	0
0	0,00E+00	6084	0	26	2,20E-05	1179914	0	26	2,20E-05	1179914	0	0	0,00E+00	91064	0	-	chr20:48638	2,40E-05	5,60E-05	5,60E-05	0
0	0,00E+00	6082	0	15	1,27E-05	1179640	0	11	1,21E-04	91010	0	11	1,21E-04	91010	0	-	chr20:50853	2,20E-05	0,000186	1,90E-05	1,30E-05
0	0,00E+00	6062	0	6	5,09E-06	1179902	0	22	4,90E-04	44878	0	0	0,00E+00	91048	0	-	chr20:48641	1,20E-05	0,000279	0	1,30E-05
0	0,00E+00	6084	0	22	1,86E-05	1179882	0	2	3,34E-05	59926	0	0	0,00E+00	91060	0	-	chr20:48643	2,60E-05	6,30E-05	0	6,30E-05
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	chr20:48397	4,00E-06	8,00E-06	0	0
0	0,00E+00	6070	0	20	1,70E-05	1179062	0	20	1,70E-05	1179062	0	1	1,10E-05	90784	0	-	chr20:48403	6,00E-06	1,20E-05	0	0
0	0,00E+00	6034	0	1	8,50E-07	1176890	0	5	6,73E-05	74324	0	0	0,00E+00	90036	0	-	chr20:48405	1,40E-05	4,60E-05	4,60E-05	1,30E-05
0	0,00E+00	6074	0	2	1,70E-06	1176950	0	3	1,02E-04	29540	0	0	0,00E+00	89262	0	-	chr20:49927	1,00E-05	6,70E-05	0	0
0	0,00E+00	6062	0	4	3,39E-06	1179812	0	2	2,67E-05	74842	0	0	0,00E+00	91030	0	-	chr20:48643	1,40E-05	3,30E-05	9,00E-06	0
0	0,00E+00	6084	0	8	6,78E-06	1179936	0	1	1,67E-05	59906	0	0	0,00E+00	91050	0	-	chr20:48639	8,00E-06	1,30E-05	0	1,30E-05
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	chr20:50849	6,00E-06	1,30E-05	0	1,30E-05
0	0,00E+00	6048	0	7	5,95E-06	1176580	0	1	1,69E-05	59304	0	1	1,12E-05	89050	0	-	chr20:49929	4,00E-06	9,00E-06	9,00E-06	0
0	0,00E+00	5978	0	3	2,54E-06	1180032	0	1	1,67E-05	60006	0	1	1,10E-05	91078	0	-	chr20:48744	6,00E-06	9,30E-05	9,00E-06	0
0	0,00E+00	6080	0	6	5,09E-06	1179744	0	2	3,34E-05	59872	0	1	1,10E-05	91026	0	-	chr20:48640	2,00E-06	4,00E-06	0	0
0	0,00E+00	6076	0	9	7,64E-06	1177994	0	9	7,64E-06	1177994	0	0	0,00E+00	90982	0	-	-	-	-	-	-
0	0,00E+00	6062	0	0	0,00E+00	1179768	0	9	9,89E-05	91020	0	9	9,89E-05	91020	0	-	-	-	-	-	-
0	0,00E+00	6084	0	0	0,00E+00	1179916	0	2	3,34E-05	59942	0	0	0,00E+00	91066	0	-	-	-	-	-	-
0	0,00E+00	6076	0	2	1,70E-06	1179104	0	2	1,70E-06	1179104	0	0	0,00E+00	91040	0	-	chr20:49775	6,00E-06	9,00E-06	9,00E-06	0
0	0,00E+00	6062	0	0	0,00E+00	1179768	0	7	1,56E-04	44868	0	0	0,00E+00	91020	0	-	chr20:48642	2,00E-06	9,30E-05	0	0
0	0,00E+00	6062	0	1	8,48E-07	1179618	0	3	5,01E-05	59862	0	0	0,00E+00	90994	0	-	chr20:48641	2,00E-06	1,30E-05	0	1,30E-05
0	0,00E+00	6062	0	3	2,54E-06	1179862	0	3	2,54E-06	1179862	0	0	0,00E+00	91052	0	-	chr20:48638	6,00E-06	1,20E-05	0	0
0	0,00E+00	6084	0	0	0,00E+00	1180034	0	1	1,67E-05	59992	0	0	0,00E+00	91076	0	-	chr20:50850	4,00E-06	2,50E-05	0	2,50E-05
0	0,00E+00	6014	0	7	5,93E-06	1179956	0	7	5,93E-06	1179956	0	0	0,00E+00	91068	0	-	-	-	-	-	-
0	0,00E+00	6060	0	0	0,00E+00	1179864	0	3	6,69E-05	44866	0	0	0,00E+00	91004	0	-	chr20:48868	2,00E-06	9,30E-05	0	0
0	0,00E+00	6018	0	5	4,24E-06	1179982	0	5	4,24E-06	1179982	0	0	0,00E+00	91056	0	-	-	-	-	-	-
0	0,00E+00	6054	0	1	8,48E-07	1178966	0	1	2,23E-05	44804	0	1	1,10E-05	91012	0	-	chr20:49776	4,00E-06	9,00E-06	9,00E-06	0
0	0,00E+00	6038	0	1	8,48E-07	1179544	0	1	8,48E-07	1179544	0	0	0,00E+00	90926	0	-	chr20:49992	4,00E-06	8,00E-06	0	0
0	0,00E+00	6076	0	0	0,00E+00	1177556	0	1	3,38E-05	29562	0	0	0,00E+00	89336	0	-	-	-	-	-	-
0	0,00E+00	6078	0	3	2,55E-06	1178080	0	3	2,55E-06	1178080	0	0	0,00E+00	90986	0	-	chr20:49773	2,00E-06	4,00E-06	0	0
0	0,00E+00	6060	0	1	8,48E-07	1179684	0	1	8,48E-07	1179684	0	0	0,00E+00	91056	0	-	chr20:49226	6,00E-06	1,20E-05	0	0
0	0,00E+00	6060	0	5	4,24E-06	1179346	0	5	4,24E-06	1179346	0	0	0,00E+00	90978	0	-	-	-	-	-	-
0	0,00E+00	6082	0	0	0,00E+00	1180036	0	2	2,67E-05	74926	0	0	0,00E+00	91086	0	-	chr20:48749	2,00E-06	9,00E-06	9,00E-06	0
0	0,00E+00	5958	0	4	3,39E-06	1180034	0	4	3,39E-06	1180034	0	0	0,00E+00	91078	0	-	-	-	-	-	-
0	0,00E+00	6062	0	1	8,48E-07	1179884	0	1	8,48E-07	1179884	0	0	0,00E+00	91050	0	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	chr20:48643	2,00E-06	1,30E-05	0	1,30E-05
0	0,00E+00	6062	0	5	4,24E-06	1179842	0	5	4,24E-06	1179842	0	0	0,00E+00	91052	0	-	chr20:48638	4,00E-06	8,00E-06	0	0
0	0,00E+00	6046	0	5	4,24E-06	1178516	0	5	4,24E-06	1178516	0	0	0,00E+00	90622	0	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	chr20:48401	2,00E-06	4,00E-06	0	0

AllOfUs_gvs_eas_af	AllOfUs_gvs_eur_af	AllOfUs_gvs_mid_af	AllOfUs_gvs_oth_af	AllOfUs_gvs_sas_af	1000Gp3_AFR_AC	1000Gp3_AMR_AC	1000Gp3_EAS_AC	1000Gp3_EUR_AC	1000Gp3_SAS_AC	ALFA_African_AC	ALFA_African_AN	ALFA_African_American_AC	ALFA_African_American_AN	ALFA_African_Others_AC	ALFA_African_Others_AN	ALFA_Asian_AC	ALFA_Asian_AN	ALFA_East_Asian_AC	ALFA_East_Asian_AN	ALFA_European_AC	ALFA_European_AN
9,30E-05	0,000475	0,003817	0,001705	0,000215	-	-	-	-	-	0	3560	0	3438	0	122	0	168	0	112	25	32760
0	0,000164	0	0,000735	0	-	-	-	-	-	0	4920	0	4744	0	176	0	3392	0	2710	11	165382
9,30E-05	2,70E-05	0	0	0	-	-	-	-	-	2	9140	2	8788	0	352	0	3338	0	2686	18	178326
0	5,10E-05	0	0,000134	0	0	0	1	0	0	0	7756	0	7458	0	298	0	112	0	86	5	41132
0,002883	0	0	0,000435	0	-	-	-	-	-	0	2898	0	2784	0	114	1	112	0	86	0	9690
0	4,30E-05	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	2	9690
0	2,70E-05	0	0	0	-	-	-	-	-	0	3512	0	3390	0	122	0	168	0	112	3	37076
0	1,90E-05	0	0	0	-	-	-	-	-	0	2918	0	2804	0	114	0	112	0	86	1	26586
0	4,00E-06	0	3,30E-05	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	1	9690
0	1,90E-05	0	3,30E-05	0	-	-	-	-	-	1	7728	1	7430	0	298	0	112	0	86	1	19740
0,000186	1,60E-05	0	6,70E-05	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
0,000279	4,00E-06	0	3,30E-05	0	0	0	2	0	0	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	2,70E-05	0	3,30E-05	0	-	-	-	-	-	0	2918	0	2804	0	114	0	112	0	86	2	26588
0	8,00E-06	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	1,20E-05	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	0	0	3,30E-05	0	1	0	0	0	0	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	1,20E-05	0	6,70E-05	0	-	-	-	-	-	0	2918	0	2804	0	114	0	112	0	86	1	26586
0	1,90E-05	0	3,30E-05	0	1	0	0	0	0	1	2918	1	2804	0	114	0	112	0	86	1	26588
0	1,20E-05	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	8,00E-06	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	4,00E-06	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
0	8,00E-06	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	4,00E-06	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
9,30E-05	4,00E-06	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	4,00E-06	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
-	-	-	-	-	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
-	-	-	-	-	-	-	-	-	-	0	3492	0	3370	0	122	0	168	0	112	1	15752
-	-	-	-	-	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	8,00E-06	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
9,30E-05	0	0	0	0	0	0	1	0	0	0	3492	0	3370	0	122	0	168	0	112	0	15752
0	0	0	0	0	0	1	0	0	0	0	3926	0	3804	0	122	0	202	0	146	0	15830
0	1,20E-05	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	1	9690
0	0	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9,30E-05	0	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
-	-	-	-	-	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
0	4,00E-06	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
0	8,00E-06	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
-	-	-	-	-	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
0	4,00E-06	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
0	1,20E-05	0	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	0	0	0	0	-	-	-	-	-	0	2294	0	2210	0	84	0	108	0	84	0	6962
0	8,00E-06	0	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
0	4,00E-06	0	0	0	-	-	-	-	-	0	2898	0	2784	0	114	0	112	0	86	0	9690

ALFA_Latin_American_1_AC	ALFA_Latin_American_1_AN	ALFA_Latin_American_2_AC	ALFA_Latin_American_2_AN	ALFA_Other_AC	ALFA_Other_AN	ALFA_Other_Asian_AC	ALFA_Other_Asian_AN	ALFA_South_Asian_AC	ALFA_South_Asian_AN	am_class	AlphaMissense_rankscore	AlphaMissense_pred	AlphaMissense_score	AltaiNeandertal	BayesDel_addAF_pred	BayesDel_addAF_rankscore	BayesDel_addAF_score	BayesDel_noAF_pred	BayesDel_noAF_rankscore	CADD_RAW
0	500	0	628	8	7042	0	56	0	98	likely_benign	0,07209	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.0741,.,.,0.0751,.,0.078	./.	T	0,39582	-0,078653	T	0,38765	2,681571
0	796	0	968	2	13790	0	682	0	280	likely_pathog	0,84242	.,.,.,.,LP,.,.,.LP	.,.,.,.,.,0.7387,.,.,0.8111,.,0.921,0	./.	T	0,58251	0,0515336	D	0,72325	5,703069
0	794	0	968	0	13140	0	652	0	280	likely_benign	0,12044	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0886,0.0742,.,.,0.0736,.,.	./.	T	0,09383	-0,290288	T	0,32273	3,718349
0	500	0	628	1	6030	0	26	0	98	likely_benign	0,29563	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.1076,0.0972,.,.,0.0867,.,.	./.	T	0,0744	-0,311204	T	0,26345	3,755534
0	146	0	610	0	496	1	26	0	98	likely_benign	0,01309	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.0617,.,.,0.0555,.,0.056	./.	T	0,05452	-0,336521	T	0,2984	3,191176
0	146	0	610	0	496	0	26	0	98	likely_benign	0,1844	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.1028,0.0857,.,.,0.0863,.,.	./.	T	0,26186	-0,161483	T	0,46072	3,679392
0	500	0	628	1	6862	0	56	0	98	likely_benign	0,07399	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.076,.,.,0.0745,.,0.079	./.	T	0,46991	-0,0306353	T	0,46284	4,30078
0	500	0	628	0	4588	0	26	0	98	likely_pathog	0,78937	.,.,.,.,LP,.,LP	.,.,.,.,.,0.6295,.,0.6249,.,0.6575,.,.	./.	T	0,56738	0,0399194	T	0,56182	3,620928
0	146	0	610	0	496	0	26	0	98	likely_benign	0,48671	.,.,.,.,LB,.,.,.L	.,.,.,.,.,0.2122,.,.,.,0.2376,.,0.233	./.	D	0,64212	0,101593	D	0,76046	4,535994
0	146	0	610	0	1924	0	26	0	98	likely_benign	0,00613	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0533,0.0504,.,.,0.0436,.,.	./.	T	0,01276	-0,436023	T	0,10367	1,585702
0	146	0	610	0	466	0	24	0	94	likely_benign	0,46547	.,.,.,.,LB,.,LB	.,.,.,.,.,0.1121,.,0.1338,.,0.1244,.,.	./.	T	0,18282	-0,215693	T	0,43213	3,949348
0	146	0	610	0	496	0	26	0	98	likely_benign	0,33959	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.1524,0.124,.,.,0.1202,.,0	./.	T	0,0683	-0,318434	T	0,35926	2,874662
0	500	0	628	0	4588	0	26	0	98	likely_benign	0,21945	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.1108,0.0898,.,.,0.0845,.,.	./.	T	0,23044	-0,182425	T	0,41791	2,788113
0	146	0	610	0	496	0	26	0	98	likely_benign	0,17169	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.0963,.,.,0.0998,.,0.098	./.	T	0,54021	0,0196428	T	0,53422	3,801548
0	146	0	610	0	496	0	26	0	98	likely_benign	0,29092	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.1037,.,.,0.1338,.,0.119	./.	T	0,40273	-0,0744042	T	0,39464	3,855431
0	146	0	610	0	496	0	26	0	98	likely_benign	0,00765	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.0555,.,.,0.0587,.,0.058	./.	T	0,26656	-0,158422	T	0,2567	2,740003
0	500	0	628	0	4584	0	26	0	98	likely_benign	0,41558	.,.,.,.,LB,.,LB	.,.,.,.,.,0.1944,.,0.1164,.,0.145,0.1	./.	T	0,37082	-0,0938699	T	0,36226	3,85744
0	500	0	628	0	4588	0	26	0	98	likely_benign	0,43876	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.2107,0.147,.,.,0.1327,.,0	./.	T	0,33501	-0,115507	T	0,5221	4,264273
0	146	0	610	0	496	0	26	0	98	likely_benign	0,49656	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.2466,0.1433,.,.,0.1617,.,.	./.	T	0,19584	-0,206357	T	0,27196	3,341603
0	146	0	610	0	496	0	26	0	98	likely_pathog	0,73659	.,.,.,.,A,.,A,.,A	.,.,.,.,.,0.4135,.,0.476,.,0.5488,.,0	./.	T	0,52576	0,00903313	T	0,51954	4,943028
0	146	0	610	0	466	0	24	0	94	likely_pathog	0,94839	.,.,.,.,LP,.,.,LP	.,.,.,.,.,0.9756,.,0.9774,.,0.993,0.9	./.	D	0,66253	0,121213	T	0,65832	5,620608
0	146	0	610	0	496	0	26	0	98	ambiguous	0,788	.,.,.,.,LP,LP,.,.,L	.,.,.,.,.,0.7571,0.6665,.,.,0.5596,.,.	./.	T	0,58953	0,057032	D	0,71789	4,869856
0	146	0	610	0	466	0	24	0	94	likely_benign	0,20964	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0983,0.0868,.,.,0.0845,.,.	./.	T	0,47521	-0,0269911	T	0,54937	4,243043
0	146	0	610	0	466	0	24	0	94	likely_benign	0,25722	.,.,.,.,LB,.,.,.L	.,.,.,.,.,0.0819,.,.,.,0.0756,.,0.0761	./.	T	0,40786	-0,0712158	T	0,39984	3,516406
0	146	0	610	0	2772	0	56	0	98	likely_benign	0,03206	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0678,0.0653,.,.,0.0644,.,.	./.	T	0,08512	-0,299285	T	0,15087	1,80349
0	146	0	610	0	496	0	26	0	98	likely_benign	0,55903	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.2231,0.1436,.,.,0.24,.,0.1	./.	T	0,56013	0,0344517	T	0,55445	3,230147
0	146	0	610	0	466	0	24	0	94	ambiguous	0,71486	.,.,.,.,A,.,.,.A,.,.L	.,.,.,.,.,0.4939,.,.,.0.4933,.,0.6653,	./.	D	0,62141	0,0831439	T	0,61668	5,185716
0	146	0	610	0	2772	0	56	0	98	likely_benign	0,2402	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0963,0.1006,.,.,0.0827,.,.	./.	T	0,00766	-0,47318	T	0,10527	1,673531
0	146	0	610	1	2880	0	56	0	104	ambiguous	0,64871	.,.,.,.,A,A,.,.,.L	.,.,.,.,.,0.4655,0.4011,.,.,0.3162,.,.	./.	T	0,37899	-0,0889417	T	0,37055	3,013359
0	146	0	610	0	496	0	26	0	98	likely_benign	0,57638	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.267,0.2278,.,.,0.252,.,0.3	./.	D	0,64289	0,102304	T	0,63846	3,944766
0	146	0	610	0	496	0	26	0	98	likely_benign	0,38793	.,.,.,.,LB,.,LB,.,.,L	.,.,.,.,.,0.1203,.,0.1108,.,0.122,.,0	./.	T	0,3785	-0,0892375	T	0,37004	4,663024
-	-	-	-	-	-	-	-	-	-	likely_pathog	0,95276	.,.,.,.,LP,.,.,LP	.,.,.,.,.,0.9816,.,0.9691,.,0.9867,.,.	./.	D	0,83758	0,311753	D	0,83547	5,116796
0	146	0	610	0	496	0	26	0	98	likely_pathog	0,98761	.,.,.,.,LP,LP,.,.,L	.,.,.,.,.,0.9974,0.9946,.,.,0.9717,.,.	./.	T	0,49581	-0,0125541	D	0,68132	5,142573
0	146	0	610	0	496	0	26	0	98	ambiguous	0,69417	.,.,.,.,LB,.,.,LB	.,.,.,.,.,0.2874,.,0.3187,.,0.3924,.,.	./.	T	0,42182	-0,0624266	T	0,41404	4,195885
0	146	0	610	0	466	0	24	0	94	likely_benign	0,51652	.,.,.,.,LB,.,.,.LB	.,.,.,.,.,0.1849,.,.,.0.1755,.,0.1772,.	./.	T	0,37376	-0,092082	T	0,55424	5,676858
0	146	0	610	0	496	0	26	0	98	ambiguous	0,72122	.,.,.,.,A,.,.A,.,.A	.,.,.,.,.,0.4655,.,0.4516,.,0.4274,.,.	./.	T	0,50123	-0,0087074	T	0,49461	4,303965
0	146	0	610	0	466	0	24	0	94	likely_pathog	0,97748	.,.,.,.,LP,.,.,LP	.,.,.,.,.,0.9887,.,0.9892,.,0.9984,0	./.	D	0,79336	0,259546	D	0,79068	5,351046
0	146	0	610	0	466	0	24	0	94	likely_pathog	0,75209	.,.,.,.,LP,.,.,.L	.,.,.,.,.,0.6319,.,.,.,0.676,.,0.7394,	./.	D	0,71699	0,178528	D	0,71333	4,23322
-	-	-	-	-	-	-	-	-	-	likely_benign	0,54119	.,.,.,.,LB,.,.,LB	.,.,.,.,.,0.2398,.,.,0.3151,.,0.1607,	./.	T	0,49872	-0,0104875	T	0,49209	4,495214
-	-	-	-	-	-	-	-	-	-	likely_pathog	0,76083	.,.,.,.,LP,.,.,.LP	.,.,.,.,.,0.7109,.,.,.0.7242,.,0.7334,	./.	D	0,71627	0,177735	D	0,7126	4,47381
0	146	0	610	0	496	0	26	0	98	likely_pathog	0,92718	.,.,.,.,LP,LP,.,.,L	.,.,.,.,.,0.9802,0.9491,.,.,0.942,.,0	./.	D	0,8467	0,324394	D	0,8447	5,511051
-	-	-	-	-	-	-	-	-	-	likely_pathog	0,92587	.,.,.,.,LP,LP,.,.,L	.,.,.,.,.,0.9672,0.9649,.,.,0.8967,.,.	./.	D	0,79334	0,259523	D	0,79067	5,12074
-	-	-	-	-	-	-	-	-	-	ambiguous	0,81841	.,.,.,.,LP,LP,.,.,L	.,.,.,.,.,0.6472,0.6948,.,.,0.4633,.,.	./.	T	0,48088	-0,0230457	T	0,47398	4,339595
0	146	0	610	0	466	0	24	0	94	likely_benign	0,15449	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0926,0.0862,.,.,0.0821,.,.	./.	T	0,2361	-0,178598	T	0,22601	2,713821
-	-	-	-	-	-	-	-	-	-	likely_benign	0,17384	.,.,.,.,LB,LB,.,.,L	.,.,.,.,.,0.0825,0.0823,.,.,0.0744,.,.	./.	T	0,46112	-0,0366266	T	0,45394	2,859162
-	-	-	-	-	-	-	-	-	-	likely_benign	0,33436	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.1322,.,.,0.1509,.,0.131	./.	T	0,43544	-0,0536911	T	0,42787	4,361195
0	146	0	610	0	496	0	26	0	98	likely_benign	0,03748	.,.,.,.,.,.,LB,.,.,L	.,.,.,.,.,.,.,0.0676,.,.,0.0669,.,0.069	./.	T	0,26902	-0,156824	T	0,25916	3,237365

ChagyrskayaNeandertal	DANN_rankscore	DANN_score	DEOGEN2_pred	DEOGEN2_rankscore	DEOGEN2_score	Denisova	ESM1b_rankscore	ESM1b_pred	Eigen-PC-phred_coding	Eigen-PC-raw_coding	Eigen-PC-raw_coding_rankscore	Eigen-phred_coding	Eigen-raw_coding	Eigen-raw_coding_rankscore	ESM1b_score	VARITY_R_score	VARITY_R_rankscore	GERP++_NR	GERP++_RS	GERP++_RS_rankscore	GERP_91_mammals
./.	0,45252	0,98716981	T,T,T,T,.,T,.,	0,69217	0.323011,0.3	./.	0,31443	T,T,T,T,T,T,	3,03132	0,16809444	0,47845	2,335867	-0,0506481	0,39305	-4.496,-4.496	0.07991795,(	0,18118	5,44	5,44	0,79319	3,44
./.	0,99997	0,99960592	T,T,T,T,T,T,	0,78598	0.444016,0.4	./.	0,73576	D,D,D,D,.,D,	9,104142	0,76254769	0,8702	7,724405	0,74046016	0,82186	-9.931,-9.931	0.88209456,(	0,89697	5,46	5,46	0,79994	4,36
./.	0,56762	0,99246001	T,T,T,T,T,T,	0,69031	0.320954,0.3	./.	0,22954	T,T,T,.,.,T,	2,602659	0,06687119	0,42611	2,053714	-0,1391685	0,35423	-3.841,-3.841	0.43898875,(	0,63018	4,94	4,94	0,646	5,24
./.	0,79796	0,99688873	T,T,T,T,T,T,	0,63559	0.265742,0.2	./.	0,70189	D,D,D,D,.,.,D	3,324107	0,22812289	0,51162	2,562104	0,01424019	0,4224	-9.17,-9.17,-	0.47932065,(	0,65547	5,44	5,44	0,79319	-
./.	0,25347	0,94573703	T,T,T,T,.,T,.,	0,67811	0.307786,0.3	./.	0,09674	T,T,T,T,T,T,	2,961729	0,15284944	0,47024	2,254501	-0,0752201	0,38211	-2.951,-2.951	0.0893418,0	0,20683	5,29	5,29	0,74394	5,24
./.	0,69446	0,99523247	T,T,T,T,T,T,	0,68665	0.31695,0.31	./.	0,21421	T,T,T,.,.,T,	3,324639	0,22822876	0,51168	2,59151	0,02236889	0,4261	-3.84,-3.84,-	0.22802696,(	0,45188	4,94	4,94	0,646	5,24
./.	0,77971	0,996613	T,T,T,T,.,T,.,	0,70389	0.336098,0.3	./.	0,25976	T,T,T,T,T,T,	3,924195	0,33451274	0,57355	3,465799	0,23589685	0,5271	-3.982,-3.982	0.09386622,(	0,21856	5,44	4,5	0,54328	3,44
./.	0,64619	0,9943713	T,T,T,T,T,T,	0,67917	0.308912,0.3	./.	0,7882	D,D,D,D,.,D,	3,640009	0,28665061	0,54522	4,208082	0,37770163	0,60008	-10.836,-10.8	0.73739576,(	0,79906	5,41	1,95	0,25063	1,55
./.	0,35104	0,97616774	T,T,T,T,T,.,T	0,57049	0.21176,0.21	./.	0,52455	T,T,T,.,.T,T	4,348295	0,39857232	0,61269	3,550001	0,25379079	0,53594	-6.777,-6.777	0.64501566,(	0,74826	5,46	5,46	0,79994	5,24
./.	0,16253	0,85627656	T,T,T,T,T,T,	0,68178	0.311702,0.3	./.	0,01948	T,T,T,.,.,T,	1,736497	-0,2209175	0,30471	1,242758	-0,466736	0,22912	-1.44,-1.44,-	0.2523523,0	0,4792	4,94	4,94	0,646	4,13
./.	0,86358	0,99776529	T,T,T,T,T,T,	0,74123	0.380434,0.3	./.	0,49838	T,T,T,T,.,T,.,	4,515685	0,42168788	0,62719	4,374662	0,40505637	0,61502	-6.434,-6.434	0.5033799,0	0,66986	4,52	4,52	0,54744	3,06
./.	0,3032	0,96521841	T,T,T,T,T,T,	0,6929	0.323805,0.3	./.	0,1519	T,T,T,T,.,.,T,	2,344252	-0,0043736	0,39222	1,877841	-0,1995034	0,32877	-3.409,-3.409	0.22100721,(	0,44343	5,15	4,21	0,48925	4,36
./.	0,67445	0,99490175	T,T,T,T,T,T,	0,78906	0.448942,0.4	./.	0,29872	T,T,T,T,.,.,T,	1,721636	-0,2273942	0,30243	1,350235	-0,4151006	0,24667	-4.421,-4.421	0.33898008,(	0,55868	5,15	2,69	0,30841	4
./.	0,94006	0,99861997	T,T,T,T,.,T,.,	0,76665	0.414891,0.4	./.	0,24751	T,T,T,T,T,T,	5,181978	0,5025299	0,67988	4,254516	0,38547317	0,6043	-3.99,-3.99,-	0.12597543,(	0,29261	5,44	5,44	0,79319	5,24
./.	0,20183	0,90678912	T,T,T,T,.,T,.,	0,67936	0.309103,0.3	./.	0,2967	T,T,T,T,T,T,	2,667724	0,08345963	0,43436	2,014312	-0,1523395	0,34858	-4.399,-4.399	0.08351923,(	0,19114	5,29	5,29	0,74394	-
./.	0,20575	0,91071266	T,T,T,T,.,T,.,	0,67222	0.301605,0.3	./.	0,09173	T,T,T,T,T,T,	2,454204	0,02708566	0,40688	1,886934	-0,1962732	0,33011	-2.902,-2.902	0.053546716	0,10054	5,29	5,29	0,74394	-
./.	0,43585	0,98597685	T,T,T,T,T,T,	0,56486	0.207375,0.2	./.	0,52671	T,T,T,T,.,T,.,	3,328853	0,22904948	0,51214	2,654546	0,03946814	0,434	-6.806,-6.806	0.42731312,(	0,62255	4,99	4,99	0,65898	4,35
./.	0,73191	0,9958336	T,T,T,T,T,T,	0,72512	0.360616,0.3	./.	0,38722	T,T,T,T,.,.,T,	3,394206	0,24165212	0,51927	2,612068	0,02798661	0,42869	-5.174,-5.174	0.71967757,(	0,78898	5,15	5,15	0,70247	5,24
./.	0,478	0,988737	T,T,T,T,T,T,	0,71361	0.347183,0.3	./.	0,36091	T,T,T,T,.,.,T,	2,661813	0,0819799	0,43362	2,072851	-0,132821	0,35695	-4.837,-4.837	0.4679835,0	0,64852	4,94	4,94	0,646	-
./.	0,96206	0,99887476	D,D,D,D,T,D	0,85255	0.562716,0.5	./.	0,69698	D,D,D,D,.,D,	4,349632	0,39875952	0,6128	3,798027	0,30362992	0,56113	-9.302,-9.302	0.7959958,0	0,83444	5,01	5,01	0,66433	4,87
./.	0,99661	0,99937359	T,T,T,T,T,T,	0,64666	0.27606,0.27	./.	0,80783	D,D,D,D,.,D,	6,980153	0,65452356	0,78833	5,972646	0,60480478	0,73336	-11.196,-11.1	0.907018,0.9	0,91902	4,99	4,99	0,65898	5,24
./.	0,67333	0,99487777	T,T,T,T,T,T,	0,76568	0.413515,0.4	./.	0,81878	D,D,D,D,.,.,D	8,567454	0,73981191	0,85312	7,949558	0,75418555	0,83084	-11.403,-11.4	0.8823091,0	0,89715	5,35	5,35	0,76261	5,24
./.	0,8776	0,99791651	T,T,T,T,T,T,	0,81656	0.495167,0.4	./.	0,30395	T,T,T,.,.,T,	5,303655	0,51559034	0,68868	4,37634	0,40532553	0,61517	-4.46,-4.46,-	0.23708557,(	0,46238	4,94	4,94	0,646	4,4
./.	0,28783	0,96053544	T,T,T,T,T,.,T	0,6617	0.290815,0.2	./.	0,50904	T,T,T,T,.,T,T	3,218536	0,20716331	0,49989	2,521015	0,00277753	0,41719	-6.572,-6.572	0.62824726,(	0,73928	5,46	5,46	0,79994	-
./.	0,21031	0,91504153	T,T,T,T,T,T,	0,71815	0.352435,0.3	./.	0,30128	T,T,T,T,.,.,T,	1,588067	-0,2884914	0,28158	1,231654	-0,4722388	0,22729	-4.44,-4.44,-	0.0441216,0	0,06931	5,15	2,21	0,2697	3,44
./.	0,11549	0,7617686	T,T,T,T,T,T,	0,64737	0.276745,0.2	./.	0,07891	T,T,T,T,.,.,T,	2,432671	0,02104191	0,40404	1,862898	-0,2048468	0,32657	-2.643,-2.643	0.44746268,(	0,63563	4,94	4,94	0,646	-
./.	0,49573	0,98968482	T,T,T,T,T,T,	0,78619	0.444339,0.4	./.	0,89387	D,D,D,D,.,D,	4,307411	0,3927412	0,60908	3,461107	0,23489085	0,52661	-13.0,-13.0,-	0.89461786,(	0,90777	5,46	5,46	0,79994	-
./.	0,1754	0,87527026	T,T,T,T,T,T,	0,70242	0.334452,0.3	./.	0,33187	T,T,T,.,.,T,	1,503467	-0,3300597	0,26815	1,107082	-0,5358074	0,20681	-4.598,-4.598	0.032883268	0,03367	5,15	2,21	0,2697	3,44
./.	0,3721	0,97944751	T,T,T,T,T,T,	0,7025	0.334535,0.3	./.	0,41372	T,T,T,T,.,.,T,	1,364316	-0,4043432	0,24551	1,053962	-0,5639709	0,19805	-5.394,-5.394	0.15660518,(	0,3504	5,15	1,97	0,2521	1,09
./.	0,49992	0,98989324	T,T,T,T,T,T,	0,67723	0.306856,0.3	./.	0,20957	T,T,T,T,.,.,T,	3,345682	0,23232246	0,51398	2,603717	0,02570269	0,42764	-3.809,-3.809	0.44756982,(	0,6357	4,94	4,94	0,646	-
./.	0,57795	0,99276192	D,D,D,D,T,D	0,8327	0.52425,0.52	./.	0,65053	D,D,D,D,.,D,	4,790332	0,45706353	0,64983	4,015999	0,34427012	0,58224	-8.583,-8.583	0.73597014,(	0,79824	5,01	5,01	0,66433	4,87
./.	0,82494	0,99727233	T,T,T,T,T,T,	0,79208	0.453851,0.4	./.	0,94571	D,D,D,D,.,D,	9,417589	0,77478232	0,87924	8,071289	0,76135619	0,83551	-14.497,-14.4	0.9643528,0	0,97678	5,41	5,41	0,78283	4,35
./.	0,74486	0,99605165	T,T,T,T,T,T,	0,77025	0.42008,0.42	./.	0,81135	D,D,D,D,.,.,D	4,073758	0,35806339	0,58774	3,179399	0,17147493	0,49588	-10.991,-10.9	0.7421755,0	0,80181	5,43	5,43	0,78977	-
./.	0,00246	0,13110983	T,T,T,T,T,T,	0,50492	0.162697,0.1	./.	0,36424	T,T,T,T,.,T,.,	2,764484	0,10727135	0,44643	2,160708	-0,10447	0,36924	-4.958,-4.958	0.6348187,0	0,7428	5,2	5,2	0,71681	5,24
./.	0,97428	0,99903035	T,T,T,T,T,T,	0,7614	0.407475,0.4	./.	0,76149	D,D,D,D,.,D,	10,43598	0,81030212	0,90448	8,399761	0,77991364	0,8475	-10.366,-10.3	0.66563743,(	0,75935	5,46	5,46	0,79994	4,4
./.	0,77155	0,99647987	T,T,T,T,T,T,	0,66632	0.295522,0.2	./.	0,8539	D,D,D,D,.,D,	3,113912	0,18566445	0,48801	2,350089	-0,0464355	0,39494	-12.103,-12.1	0.5135445,0	0,67581	5,2	5,2	0,71681	-
./.	0,95576	0,99879054	T,T,T,T,T,T,	0,79282	0.455068,0.4	./.	0,94562	D,D,D,D,.,D,	9,201128	0,76640756	0,87307	8,685891	0,79514849	0,85721	-14.494,-14.4	0.9842131,0	0,99404	4,99	4,99	0,65898	-
./.	0,16448	0,85933507	T,T,T,T,T,.,T	0,51328	0.168661,0.1	./.	0,40611	T,T,T,T,.,T,T	2,993402	0,1598467	0,47399	2,226481	-0,0838189	0,37829	-4.322,-4.322	0.6035945,0	0,726	5,46	5,46	0,79994	4,36
./.	0,68958	0,99516228	T,T,T,T,T,.,T	0,57608	0.216121,0.2	./.	0,77322	D,D,D,D,.,D,	3,612191	0,28172902	0,54233	2,793065	0,0761279	0,45094	-10.57,-10.57	0.37982404,(	0,58976	5,07	5,07	0,68064	5,24
./.	0,77781	0,99658286	T,T,T,T,T,.,T	0,74079	0.379873,0.3	./.	0,64206	D,D,D,D,.,D,	4,50978	0,42089291	0,62667	4,865086	0,4774416	0,65594	-7.766,-7.766	0.623611,0.6	0,73678	4,97	3,84	0,43355	5,24
./.	0,93915	0,99860919	T,T,T,T,T,T,	0,7861	0.444202,0.4	./.	0,88436	D,D,D,D,.,.,D	8,096674	0,71767414	0,83634	7,505421	0,72644944	0,81264	-12.774,-12.7	0.9105888,0	0,92237	5,24	5,24	0,72825	-
./.	0,5495	0,99188056	T,T,T,T,T,T,	0,79463	0.458023,0.4	./.	0,78098	D,D,D,D,.,.,D	10,46581	0,81126849	0,90515	9,70538	0,84412537	0,8871	-10.707,-10.7	0.8979273,0	0,91072	5,35	5,35	0,76261	-
./.	0,82991	0,99733652	D,D,D,D,T,T	0,85549	0.568647,0.5	./.	0,62579	D,D,D,D,.,.,D	3,296363	0,22269898	0,50855	2,496132	-0,0042272	0,414	-7.99,-7.99,-	0.7395653,0	0,8003	5,15	5,15	0,70247	4
./.	0,3606	0,97775518	T,T,T,T,T,T,	0,6684	0.29766,0.29	./.	0,09904	T,T,T,.,.,T,	1,78827	-0,1989411	0,31261	1,358709	-0,4111308	0,24804	-2.973,-2.973	0.4388177,0	0,63006	5,15	3,95	0,44887	4,36
./.	0,2524	0,94515603	T,T,T,T,T,T,	0,65316	0.282352,0.2	./.	0,05807	T,T,T,T,.,.,T	2,37954	0,00592821	0,39697	1,852872	-0,2084829	0,32507	-2.503,-2.503	0.48926535,(	0,66148	4,94	4,94	0,646	-
./.	0,41713	0,98447837	T,T,T,T,.,T,.,	0,72942	0.365784,0.3	./.	0,27282	T,T,T,T,T,T,	4,234545	0,38218181	0,60255	3,235932	0,18463875	0,50217	-4.231,-4.231	0.28210828,(	0,50918	5,29	5,29	0,74394	-
./.	0,17617	0,8763367	T,T,T,T,.,T,.,	0,67978	0.309558,0.3	./.	0,2552	T,T,T,T,T,T,	2,136274	-0,0694679	0,36357	1,531905	-0,3341416	0,2758	-4.034,-4.034	0.031241672	0,02902	5,44	5,44	0,79319	5,24

GERP_91_mammals_rankscore	Interpro_domain	LIST-S2_pred	LIST-S2_rankscore	LIST-S2_score	MPC_rankscore	MPC_score	MVP_rankscore	MVP_score	MetaLR_pred	MetaLR_rankscore	MetaLR_score	MetaRNN_pred	MetaRNN_rankscore	MetaRNN_score	MetaSVM_pred	MetaSVM_rankscore	MetaSVM_score	MutFormer_rankscore	MutFormer_score	MutationAssessor_pred	MutationAssessor_rankscore
0,62291	.,.,.,.

MutationAssessor_score	MutationTaster_converted_rankscore	MutationTaster_model	MutationTaster_pred	MutationTaster_score	MutationTaster_trees_benign	MutationTaster_trees_deleterious	PolyPhen	PROVEAN_converted_rankscore	PROVEAN_pred	PROVEAN_score	PrimateAI_pred	PrimateAI_rankscore	PrimateAI_score	Reliability_index	SIFT	Uniprot_acc	Uniprot_entry	VARITY_ER_LOO_rankscore	VARITY_ER_LOO_score	VARITY_ER_rankscore	VARITY_ER_score
0.205,0.205,(	0,59775	simple_aae,.	N,.,.,.,N,.,.,.,.	0.16,.,.,.,.0.16	84.0,.,.,.,.84.0	16.0,.,.,.,.16.0	benign(0)	0,05888	N,.,.,.,.,.,.,.,.	0.09,.,.,.,.,.,.,.	T	0,63823	0,67730582	9	tolerated_low	P68400,P684	CSK21_HUM	0,35973	0.15358002,(	0,35974	0.15358002,(
1.665,1.665,(	0,91795	simple_aae,.	D,.,.,.,D,.,.,.,.	0.89,.,.,.,.0.89	11.0,.,.,.,.11.0	89.0,.,.,.,.89.0	probably_dar	0,71677	D,.,.,.,D,.,.,.,.	-3.79,.,.,.,.-3.7	D	0,97419	0,90948045	10	deleterious_l	P68400,P684	CSK21_HUM	0,7642	0.59815764,(	0,76419	0.59815764,(
0.55,0.55,0.5	0,65374	simple_aae,.	N,.,.,.,.,N,N,.	0.3,.,.,.,.,0.3,(	70.0,.,.,.,.,70	30.0,.,.,.,.,30	benign(0)	0,13346	N,.,.,.,.,N,.,.,.	-0.22,.,.,.,.,-0	T	0,58507	0,64004982	10	tolerated_low	P68400,P684	CSK21_HUM	0,51611	0.26045653,(	0,51611	0.26045653,(
0.875,0.875,(	0,75048	simple_aae,.	N,.,.,.,.,N,N,.	0.47,.,.,.,.,0.4	53.0,.,.,.,.,53	47.0,.,.,.,.,47	benign(0.013	0,40657	N,.,.,.,.,N,.,.,.	-1.71,.,.,.,.,-1	D	0,89917	0,85211468	10	tolerated_low	P68400,P684	CSK21_HUM	0,63775	0.3929183,0	0,63775	0.3929183,0
0.695,0.695,(	0,62259	simple_aae,.	N,.,.,.,N,.,.,.,.	0.23,.,.,.,.0.23	77.0,.,.,.,.77.0	23.0,.,.,.,.23.0	benign(0)	0,07691	N,.,.,.,.,.,.,.,.	-0.05,.,.,.,.,.,.	T	0,57049	0,62978554	10	tolerated_low	P68400,P684	CSK21_HUM	0,33515	0.14110166,(	0,33516	0.14110166,(
0.345,0.345,(	0,44282	simple_aae,.	N,.,.,.,.,N,N,.	0.18,.,.,.,.,0.1	82.0,.,.,.,.,82	18.0,.,.,.,.,18	benign(0)	0,10767	N,.,.,.,.,N,.,.,.	-0.24,.,.,.,.,-0	T	0,51738	0,59219378	10	tolerated_low	P68400,P684	CSK21_HUM	0,38634	0.16819979,(	0,38635	0.16819979,(
0.55,0.55,0.5	0,58037	simple_aae,.	N,.,.,.,.,N,.,.,.,.	0.23,.,.,.,.,0.23	77.0,.,.,.,.,77.0	23.0,.,.,.,.,23.0	benign(0.203	0,11659	N,.,.,.,.,.,.,.,.	-0.29,.,.,.,.,.,.	T	0,57752	0,63473916	9	deleterious_l	P68400,P684	CSK21_HUM	0,43527	0.19847679,(	0,43528	0.19847679,(
2.42,2.42,2.4	0,72539	simple_aae,.	D,.,.,.,.,D,.,.,.,.	0.53,.,.,.,.,0.53	47.0,.,.,.,.,47.0	53.0,.,.,.,.,53.0	probably_dar	0,43912	N,.,.,.,.N,.,.,.,.	-1.88,.,.,.,.-1.8	D	0,96906	0,90436929	10	deleterious_l	P68400,P684	CSK21_HUM	0,72595	0.5301312,0	0,72595	0.5301312,0
1.1,1.1,1.1,1	0,91553	simple_aae,.	D,.,.,.,.D,D,.,.,.	0.54,.,.,.,.0.54	46.0,.,.,.,.46.0	54.0,.,.,.,.54.0	possibly_dar	0,31344	N,.,.,.,.N,N,.,.,.	-1.24,.,.,.,.-1.2	D	0,95961	0,8958382	10	deleterious_l	P68400,P684	CSK21_HUM	0,79194	0.6481365,0	0,79193	0.6481365,0
-0.805,-0.805	0,28107	simple_aae,.	N,.,.,.,.,N,N,.	0.02,.,.,.,.,0.0	98.0,.,.,.,.,98	2.0,.,.,.,.,2.0,(	benign(0)	0,10245	N,.,.,.,.,N,.,.,.	-0.21,.,.,.,.,-0	T	0,43338	0,53259659	10	tolerated_low	P68400,P684	CSK21_HUM	0,26057	0.10840814,(	0,26058	0.10840814,(
2.215,2.215,(	0,7381	simple_aae,.	N,.,.,.,.,N,.,.,.,.	0.42,.,.,.,.,0.42	58.0,.,.,.,.,58.0	42.0,.,.,.,.,42.0	benign(0.25)	0,19869	N,.,.,.,.N,.,.,.,.	-0.69,.,.,.,.,-0.7	D	0,86146	0,82744002	10	tolerated_low	P68400,P684	CSK21_HUM	0,57473	0.31722614,(	0,57474	0.31722614,(
0.205,0.205,(	0,42965	simple_aae,.	N,.,.,.,.,.N,N,.	0.07,.,.,.,.,.0.0	93.0,.,.,.,.,.93	7.0,.,.,.,.,.7.0,(	benign(0.003	0,13154	N,.,.,.,.,N,.,.,.	-0.26,.,.,.,.,-0	T	0,44087	0,53790665	10	tolerated_low	P68400,P684	CSK21_HUM	0,3143	0.13122499,(	0,31431	0.13122499,(
0.345,0.345,(	0,53339	simple_aae,.	N,.,.,.,.,N,N,.	0.11,.,.,.,.,0.1	89.0,.,.,.,.,89	11.0,.,.,.,.,11	benign(0)	0,37748	N,.,.,.,.N,.,.,.,.	-1.36,.,.,.,.,-1	T	0,36699	0,4850156	10	tolerated_low	P68400,P684	CSK21_HUM	0,60363	0.34980932,(	0,60364	0.34980932,(
0.55,0.55,0.5	0,74433	simple_aae,.	N,.,.,.,.,N,.,.,.,.	0.41,.,.,.,.,0.41	59.0,.,.,.,.,59.0	41.0,.,.,.,.,41.0	benign(0.408	0,12963	N,.,.,.,.,.,.,.,.	-0.36,.,.,.,.,.,.	T	0,61205	0,65901202	9	tolerated_low	P68400,P684	CSK21_HUM	0,45505	0.21213652,(	0,45506	0.21213652,(
0.695,0.695,(	0,56225	simple_aae,.	N,.,.,.,.,N,.,.,.,.	0.15,.,.,.,.,0.15	85.0,.,.,.,.,85.0	15.0,.,.,.,.,15.0	benign(0.011	0,09401	N,.,.,.,.,.,.,.,.	-0.16,.,.,.,.,.,.	T	0,74053	0,74764246	10	tolerated_low	P68400,P684	CSK21_HUM	0,28868	0.11990823,(	0,28869	0.11990823,(
0.205,0.205,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0)	0,09735	N,.,.,.,.,.,.,.,.,.	-0.18,.,.,.,.,.,.	T	0,42094	0,5237509	10	tolerated_low	P68400,P684	CSK21_HUM	0,10598	0.057852533	0,10599	0.057852533
0.66,0.66,0.6	0,66863	simple_aae,.	N,.,.,.,.,N,.,.,.,.	0.44,.,.,.,.,0.44	56.0,.,.,.,.,56.0	44.0,.,.,.,.,44.0	benign(0.039	0,20082	N,.,.,.,.N,.,.,.,.	-0.71,.,.,.,.-0.7	D	0,92577	0,87015009	10	tolerated_low	P68400,P684	CSK21_HUM	0,60994	0.3573832,0	0,60995	0.3573832,0
0.895,0.895,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.013	0,18812	N,.,.,.,.,N,.,.,.,.	-0.65,.,.,.,.,-0	T	0,50454	0,58309209	10	tolerated_low	P68400,P684	CSK21_HUM	0,71794	0.51627916,(	0,71793	0.51627916,(
0.805,0.805,(	0,45549	simple_aae,.	N,.,.,.,.,N,N,.	0.18,.,.,.,.,0.1	82.0,.,.,.,.,82	18.0,.,.,.,.,18	benign(0)	0,14121	N,.,.,.,.,.N,.,.,.	-0.42,.,.,.,.,-0	T	0,68382	0,7089057	10	tolerated_low	P68400,P684	CSK21_HUM	0,51779	0.26193583,(	0,51779	0.26193583,(
1.255,1.255,(	0,73179	simple_aae,.	D,.,.,.,.D,.,.,.,.	0.53,.,.,.,.,0.54	47.0,.,.,.,.46.0	53.0,.,.,.,.,54.0	benign(0.081	0,41044	N,.,.,.,.N,.,.,.,.	-1.7,.,.,.,.-1.73	D	0,8707	0,83345711	10	deleterious_l	P68400,P684	CSK21_HUM	0,68504	0.46201974,(	0,68504	0.46201974,(
0.535,0.535,(	0,90354	simple_aae,.	D,.,.,.,.D,.,.,.,.	0.86,.,.,.,.,0.85	14.0,.,.,.,.,15.0	86.0,.,.,.,.,85.0	probably_dar	0,61315	N,.,.,.,.N,.,.,.,.	-1.91,.,.,.,.,-1.9	D	0,87308	0,83499455	10	deleterious_l	P68400,P684	CSK21_HUM	0,90614	0.83842415,(	0,90613	0.83842415,(
0.94,0.94,0.9	0,91311	simple_aae,.	D,.,.,.,.,D,D,.	0.88,.,.,.,.,0.8	12.0,.,.,.,.,13	88.0,.,.,.,.,87	probably_dar	0,66002	D,.,.,.,.,D,.,.,.,.	-3.31,.,.,.,.,-3	D	0,83475	0,81008387	10	deleterious_l	P68400,P684	CSK21_HUM	0,87934	0.7970379,0	0,87933	0.7970379,0
0.895,0.895,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.261	0,22237	N,.,.,.,.N,.,.,.,.	-0.7,.,.,.,.,-0.8	T	0,53058	0,60156071	10	tolerated_low	P68400,P684	CSK21_HUM	0,33876	0.14287823,(	0,33877	0.14287823,(
0.58,0.58,0.5	0,76257	simple_aae,.	D,.,.,.,.D,D,.,.,.	0.59,.,.,.,.,0.59	41.0,.,.,.,.,41.0	59.0,.,.,.,.,59.0	benign(0.065	0,47354	N,.,.,.,.N,.,.,.,.	-2.07,.,.,.,.,-2.0	D	0,98356	0,92044091	10	tolerated_low	P68400,P684	CSK21_HUM	0,64116	0.39753664,(	0,64116	0.39753664,(
-0.345,-0.345	0,26006	simple_aae,.	N,.,.,.,.,N,N,.	0.07,.,.,.,.,0.0	93.0,.,.,.,.,93	7.0,.,.,.,.,7.0,(	benign(0)	0,16934	N,.,.,.,.,N,.,.,.	-0.39,.,.,.,.,-0	T	0,25019	0,39985216	10	tolerated_low	P68400,P684	CSK21_HUM	0,07514	0.049283493	0,07515	0.049283493
0.695,0.695,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.003	0,06337	N,.,.,.,.,N,.,.,.,.	0.12,.,.,.,.,0.0	T	0,79365	0,78313708	10	tolerated_low	P68400,P684	CSK21_HUM	0,61823	0.367582,0.3	0,61823	0.367582,0.3
-0.295,-0.295	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	probably_dar	0,95062	D,.,.,.,.D,.,.,.,.	-7.5,.,.,.,.-7.5,(	D	0,97657	0,9120276	10	deleterious_l	P68400,P684	CSK21_HUM	0,93871	0.88557667,(	0,93871	0.88557667,(
-0.55,-0.55,-0	0,28107	simple_aae,.	N,.,.,.,.,.N,N,.	0.09,.,.,.,.,0.0	91.0,.,.,.,.,91	9.0,.,.,.,.,9.0,(	benign(0)	0,09401	N,.,.,.,.,N,.,.,.	-0.16,.,.,.,.,-0	T	0,29133	0,42970556	10	tolerated_low	P68400,P684	CSK21_HUM	0,04597	0.041071624	0,04598	0.041071624
0.345,0.345,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.017	0,19444	N,.,.,.,.,N,.,.,.,.	-0.66,.,.,.,.,-0	T	0,4536	0,54694557	10	deleterious_l	P68400,P684	CSK21_HUM	0,39877	0.17544483,(	0,39877	0.17544483,(
0.895,0.895,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.003	0,59257	N,.,.,.,.N,D,.,.,.	-0.35,.,.,.,.,-0	T	0,61428	0,66056347	10	deleterious_l	P68400,P684	CSK21_HUM	0,64185	0.39846805,(	0,64185	0.39846805,(
2.32,2.32,2.3	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.132	0,88795	N,.,.,.,.N,.,.,.,.	-1.93,.,.,.,.-1.9	D	0,86556	0,83010828	10	deleterious_l	P68400,P684	CSK21_HUM	0,61847	0.3678879,0	0,61847	0.3678879,0
1.525,1.525,(	0,933	simple_aae,.	D,.,.,.,D,.,.,.,.	0.92,.,.,.,.,0.92	8.0,.,.,.,.8.0,.,.	92.0,.,.,.,.92.0	possibly_dar	0,97004	D,.,.,.,D,.,.,.,.	-8.31,.,.,.,.-8.3	D	0,97688	0,9123702	10	deleterious_l	P68400,P684	CSK21_HUM	0,93639	0.8823125,0	0,93639	0.8823125,0
1.405,1.405,(	0,92286	simple_aae,.	D,.,.,.,.,D,D,.	0.87,.,.,.,.,0.8	13.0,.,.,.,.,13	87.0,.,.,.,.,87	possibly_dar	0,73719	D,.,.,.,.,D,.,.,.,.	-3.97,.,.,.,.,-3	D	0,9975	0,94997823	10	deleterious_l	P68400,P684	CSK21_HUM	0,80477	0.67100286,(	0,80476	0.67100286,(
-0.425,-0.425	0,84487	simple_aae,.	D,.,.,.,.D,.,.,.,.	0.74,.,.,.,.,0.74	26.0,.,.,.,.,26.0	74.0,.,.,.,.,74.0	benign(0.134	0,01747	N,.,.,.,.N,.,.,.,.	0.84,.,.,.,.,0.84	D	0,96481	0,90039688	10	deleterious_l	P68400,P684	CSK21_HUM	0,49878	0.24573722,(	0,49879	0.24573722,(
1.69,1.69,1.6	0,86984	simple_aae,.	D,.,.,.,.D,.,.,.,.	0.79,.,.,.,.,0.78	21.0,.,.,.,.,22.0	79.0,.,.,.,.,78.0	possibly_dar	0,69272	D,.,.,.,.D,.,.,.,.	-3.59,.,.,.,.-3.5	D	0,98368	0,92059106	10	deleterious_l	P68400,P684	CSK21_HUM	0,82367	0.7042716,0	0,82366	0.7042716,0
-0.285,-0.285	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.047	0,50847	N,.,.,.,.N,.,.,.,.	-2.28,.,.,.,.-2.2	D	0,89604	0,85003459	10	deleterious_l	P68400,P684	CSK21_HUM	0,62682	0.37851694,(	0,62682	0.37851694,(
2.08,2.08,2.0	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	probably_dar	0,89056	D,.,.,.,.D,.,.,.,.	-5.93,.,.,.,.-5.9	D	0,99733	0,94920015	10	deleterious_l	P68400,P684	CSK21_HUM	0,99834	0.98069316,(	0,99833	0.98069316,(
0.06,0.06,0.0	0,9204	simple_aae,.	D,.,.,.,.D,D,.,.,.	0.6,.,.,.,.0.6,0	40.0,.,.,.,.40.0	60.0,.,.,.,.60.0	benign(0.015	0,31344	N,.,.,.,.N,N,.,.,.	-0.7,.,.,.,.-0.7	D	0,9819	0,91829628	10	deleterious_l	P68400,P684	CSK21_HUM	0,73548	0.54680127,(	0,73547	0.54680127,(
-0.015,-0.015	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.006	0,22889	N,.,.,.,.N,.,.,.,.	-0.84,.,.,.,.-0.8	T	0,7626	0,76249492	10	deleterious_l	P68400,P684	CSK21_HUM	0,61293	0.36102226,(	0,61293	0.36102226,(
1.985,1.985,(	0,69764	simple_aae,.	N,.,.,.,.N,N,.,.,.	0.48,.,.,.,.,0.48	52.0,.,.,.,.52.0	48.0,.,.,.,.48.0	probably_dar	0,37165	N,.,.,.,.N,.,.,.,.	-1.53,.,.,.,.-1.5	T	0,7886	0,77980167	10	deleterious_l	P68400,P684	CSK21_HUM	0,56103	0.30290863,(	0,56104	0.30290863,(
1.65,1.65,1.6	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	probably_dar	0,90233	D,.,.,.,.D,.,.,.,.	-6.16,.,.,.,.-6	D	0,87224	0,8344534	10	deleterious_l	P68400,P684	CSK21_HUM	0,82121	0.70000815,(	0,8212	0.70000815,(
1.885,1.885,(	0,97016	simple_aae,.	D,.,.,.,.D,D,.,.,.	0.98,.,.,.,.,0.9	2.0,.,.,.,.,2.0,(	98.0,.,.,.,.,98	probably_dar	0,80627	D,.,.,.,.D,.,.,.,.	-4.79,.,.,.,.,-4	D	0,95567	0,89253128	10	deleterious_l	P68400,P684	CSK21_HUM	0,9	0.8291288,0	0,9	0.8291288,0
0.695,0.695,(	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0.211	0,54406	D,.,.,.,.N,.,.,.,.	-2.5,.,.,.,.,-2.4	T	0,68776	0,7116338	10	deleterious_l	P68400,P684	CSK21_HUM	0,68179	0.45691663,(	0,68179	0.45691663,(
0,0,0,0,.,.,.,.,0	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0)	0,88094	N,.,.,.,.,N,D,.,.	-0.06,.,.,.,.,0.	T	0,47139	0,55956113	10	tolerated_low	P68400,P684	CSK21_HUM	0,49655	0.24389765,(	0,49656	0.24389765,(
0.695,0.695,(	0,63842	simple_aae,.	N,.,.,.,.,N,N,.	0.27,.,.,.,.,0.27	73.0,.,.,.,.,73	27.0,.,.,.,.,27	benign(0)	0,10941	N,.,.,.,.,N,.,.,.	-0.21,.,.,.,.,-0	T	0,65965	0,69219691	10	tolerated_low	P68400,P684	CSK21_HUM	0,65064	0.4106112,0	0,65064	0.4106112,0
0.695,0.695,(	0,76851	simple_aae,.	D,.,.,.,.D,.,.,.,.	0.51,.,.,.,.,0.51	49.0,.,.,.,.,49.0	51.0,.,.,.,.,51.0	benign(0.073	0,11479	N,.,.,.,.,.,.,.,.	-0.28,.,.,.,.,.,.	T	0,64313	0,6807192	10	deleterious_l	P68400,P684	CSK21_HUM	0,56619	0.3082153,0	0,5662	0.3082153,0
-0.345,-0.345	-	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	.,.,.,.,.,.,.,.,.,.	benign(0)	0,06455	N,.,.,.,.,.,.,.,.	0.04,.,.,.,.,.,.	T	0,55696	0,62023759	10	tolerated_low	P68400,P684	CSK21_HUM	0,11659	0.060842786	0,11659	0.060842786

VARITY_R_LOO_rankscore	VARITY_R_LOO_score	aapos	bStatistic	bStatistic_converted_rankscore	codon_degeneracy	fathmm-XF_coding_pred	fathmm-XF_coding_rankscore	fathmm-XF_coding_score	gMVP_rankscore	gMVP_score	phastCons100way_vertebrate	phastCons100way_vertebrate_rankscore	phastCons17way_primate	phastCons17way_primate_rankscore	phastCons470way_mammalian	phastCons470way_mammalian_rankscore	phyloP100way_vertebrate	phyloP100way_vertebrate_rankscore	phyloP17way_primate	phyloP17way_primate_rankscore	phyloP470way_mammalian
0,18117	0.07991795,(	##########	725	0,54878	0,0,0,0,0,0,0,	N	0,46609	0,388198	0,39043	0.393312835	1	0,71675	0,992	0,67791	1	0,68239	3,483	0,5305	0,599	0,40292	2,279
0,89699	0.88209456,(	##########	738	0,53328	0,0,0,0,0,0,0,	D	0,82321	0,889614	0,94203	0.942574717	1	0,71675	0,999	0,91597	1	0,68239	7,905	0,86513	0,549	0,27038	7,66
0,63019	0.43898875,(	349,349,349,	727	0,54643	0,0,0,0,0,0,0,	N	0,49122	0,430133	0,31202	0.314893899	1	0,71675	0,998	0,85369	1	0,68239	2,636	0,46311	0,547	0,25831	7,728
0,65547	0.47932065,(	270,270,270,	728	0,5455	0,0,0,0,0,0,0,	D	0,84998	0,902528	0,81219	0.813739322	1	0,71675	1	0,97202	1	0,68239	7,97	0,87634	0,665	0,62996	7,919
0,20682	0.0893418,0.	##########	725	0,54878	0,0,0,0,0,0,0,	D	0,59571	0,607016	0,65424	0.656533324	1	0,71675	0,998	0,85369	1	0,68239	5,237	0,65264	0,676	0,76753	10,024
0,45188	0.22802696,(	346,346,346,	727	0,54643	0,0,0,0,0,0,0,	D	0,73562	0,814346	0,12462	0.126931067	1	0,71675	0,946	0,49004	1	0,68239	5,636	0,67596	0,547	0,25831	7,728
0,21856	0.09386622,(	##########	725	0,54878	0,0,0,0,0,0,0,	D	0,56154	0,550716	0,56573	0.568319244	1	0,71675	0,986	0,61779	1	0,68239	5,214	0,65147	0,599	0,40292	4,944
0,79908	0.73739576,(	97,97,97,97,	740	0,53031	2,2,2,2,2,2,2,	D	0,61993	0,645368	0,70646	0.708536179	1	0,71675	0,997	0,79771	1	0,68239	4,877	0,62862	-0,244	0,07322	2,668
0,74827	0.64501566,(	137,137,137,	738	0,53328	0,0,0,0,0,0,0,	D	0,84351	0,899559	0,94623	0.946735497	1	0,71675	0,999	0,91597	1	0,68239	8,017	0,8876	0,609	0,47831	7,877
0,4792	0.2523523,0.	350,350,350,	727	0,54643	0,0,0,0,0,0,0,	N	0,24518	0,129237	0,13157	0.133932674	0,996	0,3946	0,997	0,79771	1	0,68239	1,089	0,30601	0,607	0,46558	2,427
0,66987	0.5033799,0.	5,5,5,5,5,5,5,	773	0,4875	0,0,0,0,0,0,0,	D	0,55981	0,547815	0,58332	0.585851438	1	0,71675	1	0,97202	1	0,68239	3,31	0,51715	0,599	0,40292	5,918
0,44343	0.22100721,(	339,339,339,	727	0,54643	0,0,0,0,0,0,0,	N	0,34484	0,22243	0,2556	0.258407553	1	0,71675	0,936	0,47515	1	0,68239	5,468	0,66549	0,547	0,25831	3,339
0,55868	0.33898008,(	336,336,336,	727	0,54643	0,0,0,0,0,0,0,	N	0,51282	0,467157	0,18647	0.189083725	0,99	0,37076	0,993	0,69292	1	0,68239	0,515	0,22588	0,688	0,8285	5,046
0,29261	0.12597543,(	##########	725	0,54878	0,0,0,0,0,0,0,	D	0,62476	0,65286	0,56136	0.563950590	1	0,71675	0,986	0,61779	1	0,68239	5,864	0,694	0,676	0,76753	11,916
0,19113	0.08351923,(	##########	725	0,54878	0,0,0,0,0,0,0,	D	0,54506	0,522782	0,62027	0.622681408	1	0,71675	1	0,97202	1	0,68239	5,624	0,67515	0,676	0,76753	9,863
0,10053	0.053546716	##########	725	0,54878	0,0,0,0,0,0,0,	N	0,2243	0,115082	0,41796	0.420810230	1	0,71675	0,997	0,79771	1	0,68239	5,086	0,64387	0,665	0,62996	7,947
0,62255	0.42731312,(	116,116,116,	739	0,53195	0,0,0,0,0,0,0,	D	0,55736	0,543696	0,69256	0.694697350	1	0,71675	1	0,97202	1	0,68239	4,083	0,57454	0,599	0,40292	7,65
0,789	0.71967757,(	333,333,333,	727	0,54643	0,0,0,0,0,0,0,	D	0,74598	0,827666	0,32475	0.327626419	1	0,71675	0,999	0,91597	1	0,68239	7,245	0,77734	0,547	0,25831	7,728
0,64853	0.4679835,0.	347,347,347,	727	0,54643	0,0,0,0,0,0,0,	D	0,59372	0,603831	0,42498	0.427823915	1	0,71675	0,99	0,65338	1	0,68239	4,51	0,6026	0,547	0,25831	7,728
0,83446	0.7959958,0.	21,21,21,21,	773	0,4875	0,0,0,0,0,0,0,	D	0,72506	0,799957	0,8192	0.820709641	1	0,71675	0,998	0,85369	1	0,68239	6,165	0,71798	0,599	0,40292	7,61
0,91903	0.907018,0.9	110,110,110,	739	0,53195	0,0,0,0,0,0,0,	D	0,78974	0,869816	0,88326	0.884305669	1	0,71675	0,993	0,69292	1	0,68239	7,741	0,83962	0,599	0,40292	7,65
0,89716	0.8823091,0.	319,319,319,	727	0,54643	0,0,0,0,0,0,0,	D	0,83458	0,895309	0,85311	0.854377039	1	0,71675	0,995	0,73271	1	0,68239	7,97	0,87634	0,609	0,47831	7,934
0,46238	0.23708557,(	344,344,344,	727	0,54643	0,0,0,0,0,0,0,	D	0,83683	0,896406	0,35003	0.352914885	1	0,71675	0,905	0,44105	1	0,68239	9,276	0,94969	0,616	0,49504	11,923
0,73929	0.62824726,(	138,138,138,	738	0,53328	0,0,0,0,0,0,0,	D	0,84351	0,899559	0,75598	0.757832833	1	0,71675	0,997	0,79771	1	0,68239	8,017	0,8876	0,609	0,47831	7,877
0,06931	0.0441216,0.	338,338,338,	727	0,54643	0,0,0,0,0,0,0,	N	0,32459	0,19994	0,16967	0.172210834	0,985	0,36067	0,98	0,58201	0,113	0,22887	0,128	0,15688	0,547	0,25831	-0,316
0,63563	0.44746268,(	352,352,352,	727	0,54643	0,0,0,0,0,0,0,	D	0,63761	0,672555	0,43695	0.439788300	1	0,71675	0,999	0,91597	1	0,68239	6,865	0,75357	0,688	0,8285	11,302
0,90779	0.89461786,(	131,131,131,	738	0,53328	0,0,0,0,0,0,0,	D	0,81596	0,885806	0,93775	0.938337920	1	0,71675	0,998	0,85369	1	0,68239	7,568	0,81592	0,691	0,84104	11,196
0,03366	0.032883268	338,338,338,	727	0,54643	0,0,0,0,0,0,0,	N	0,24582	0,129694	0,16269	0.165204049	0,985	0,36067	0,98	0,58201	0,113	0,22887	0,128	0,15688	0,547	0,25831	-0,316
0,3504	0.15660518,(	342,342,342,	727	0,54643	0,0,0,0,0,0,0,	N	0,35647	0,236024	0,3574	0.360284344	0,999	0,42732	0,863	0,40994	1	0,68239	1,828	0,38855	-0,309	0,06109	2,25
0,6357	0.44756982,(	351,351,351,	727	0,54643	0,0,0,0,0,0,0,	D	0,74828	0,830487	0,44621	0.449036568	1	0,71675	0,998	0,85369	1	0,68239	7,342	0,78601	0,547	0,25831	6,029
0,79825	0.7359701 4,(	18,18,18,18,	773	0,4875	0,0,0,0,0,0,0,	D	0,84978	0,902445	0,55817	0.560773929	1	0,71675	0,998	0,85369	1	0,68239	9,998	0,99327	0,676	0,76753	11,773
0,97678	0.9643528,0.	91,91,91,91,	740	0,53031	0,0,0,0,0,0,0,	D	0,89727	0,922525	0,93123	0.931872585	1	0,71675	0,998	0,85369	1	0,68239	7,83	0,84945	0,599	0,40292	7,655
0,80183	0.7421755,0.	272,272,272,	728	0,5455	0,0,0,0,0,0,0,	D	0,83393	0,894991	0,92732	0.927994662	1	0,71675	0,997	0,79771	1	0,68239	9,265	0,94812	0,754	0,88385	11,26
0,74281	0.6348187,0.	86,86,86,86,	740	0,53031	0,0,0,0,0,0,0,	D	0,68351	0,740403	0,75669	0.758546462	1	0,71675	0,999	0,91597	1	0,68239	4,839	0,62586	0,599	0,40292	7,657
0,75936	0.66563743,(	127,127,127,	738	0,53328	0,0,0,0,0,0,0,	D	0,84787	0,901572	0,73391	0.735878830	1	0,71675	0,994	0,71086	1	0,68239	8,15	0,89595	0,618	0,50684	11,811
0,67582	0.5135445,0.	75,75,75,75,	740	0,53031	0,0,0,0,0,0,0,	D	0,91214	0,928364	0,5836	0.586139858	1	0,71675	0,999	0,91597	1	0,68239	7,941	0,872	0,665	0,62996	7,873
0,99404	0.9842131,0.	113,113,113,	739	0,53195	0,0,0,0,0,0,0,	D	0,83746	0,896705	0,98442	0.984551901	1	0,71675	1	0,97202	1	0,68239	7,42	0,79443	0,756	0,943	11,184
0,72601	0.6035945,0.	137,137,137,	738	0,53328	0,0,0,0,0,0,0,	D	0,8358	0,895893	0,96149	0.961857071	1	0,71675	0,998	0,85369	1	0,68239	7,905	0,86513	0,549	0,27038	7,66
0,58976	0.37982404,(	204,204,204,	733	0,53927	0,0,0,0,0,0,0,	D	0,76088	0,844816	0,66229	0.664553285	1	0,71675	0,999	0,91597	1	0,68239	7,876	0,8566	0,599	0,40292	7,642
0,73679	0.623611,0.6	218,218,218,	730	0,54265	2,2,2,2,2,2,2,	N	0,45651	0,372869	0,89573	0.896671053	1	0,71675	0,997	0,79771	1	0,68239	2,996	0,49234	0,691	0,84104	7,991
0,92238	0.9105888,0.	302,302,302,	727	0,54643	0,0,0,0,0,0,0,	D	0,87283	0,912529	0,8151	0.816623128	1	0,71675	0,99	0,65338	1	0,68239	7,966	0,8754	0,609	0,47831	7,946
0,91073	0.8979273,0.	319,319,319,	727	0,54643	0,0,0,0,0,0,0,	D	0,82151	0,888743	0,93256	0.933196023	1	0,71675	0,995	0,73271	1	0,68239	9,268	0,94864	0,691	0,84104	11,28
0,80032	0.7395653,0.	327,327,327,	727	0,54643	0,0,0,0,0,0,0,	D	0,77687	0,859924	0,4003	0.403172469	1	0,71675	0,998	0,85369	1	0,68239	8,798	0,9153	0,688	0,8285	11,302
0,63007	0.4388177,0.	335,335,335,	727	0,54643	0,0,0,0,0,0,0,	D	0,55908	0,546595	0,21361	0.216317516	1	0,71675	0,997	0,79771	1	0,68239	3,658	0,54312	0,547	0,25831	2,749
0,66149	0.48926535,(	352,352,352,	727	0,54643	0,0,0,0,0,0,0,	D	0,56971	0,56444	0,30458	0.307452046	1	0,71675	0,999	0,91597	1	0,68239	4,543	0,6048	0,607	0,46558	7,948
0,50918	0.28210828,(	##########	725	0,54878	0,0,0,0,0,0,0,	D	0,8166	0,886142	0,6434	0.645737397	1	0,71675	0,998	0,85369	1	0,68239	9,025	0,93215	0,676	0,76753	9,984
0,02902	0.03124167 2	##########	725	0,54878	0,0,0,0,0,0,0,	N	0,13901	0,070871	0,39381	0.396690580	1	0,71675	0,996	0,76032	1	0,68239	1,927	0,39829	0,599	0,40292	4,945

phyloP470way_mammalian_rankscore	EVE_CLASS	EVE_SCORE	MaxEntScan_alt	MaxEntScan_diff	MaxEntScan_ref	ClinPred	ada_score	rf_score	AA	mutfunc_exp	mutfunc_int	mutfunc_mod	mutfunc_motif	Mastermind_MMID3	SpliceAI_pred_DP_AG	SpliceAI_pred_DP_AL	SpliceAI_pred_DP_DG	SpliceAI_pred_DP_DL	BLOSUM62
0,31967	-	-	-	-	-	0,02337506	-	-	C	-	-	-	-	-	-50	5	-50	-13	0
0,64235	-	-	-	-	-	0,75111079	-	-	C	0,38272	-	0,497348	-	CSNK2A1:R	22	34	-9	-25	1
0,677	-	-	-	-	-	0,10013016	-	-	C	0,249086	-	-	-	CSNK2A1:A	31	-27	-10	-27	0
0,74463	-	-	-	-	-	0,14966944	-	-	T	-0,34568	-0,1686	-0,47937	-	-	12	-16	-11	-15	1
0,83174	-	-	-	-	-	0,11356636	-	-	G	-	-	-	-	-	14	40	-3	14	-1
0,677	-	-	-	-	-	0,1246552	-	-	C	-0,05837	-	-	-	CSNK2A1:V	-24	48	-19	-36	3
0,46309	-	-	-	-	-	0,06233679	-	-	C	-	-	-	-	CSNK2A1:A	-44	50	-7	-44	0
0,34009	-	-	-	-	-	0,83909029	-	-	G	0,20506	-	0,735854	-	CSNK2A1:5	20	39	-35	-23	2
0,72327	-	-	-	-	-	0,36060604	-	-	T	2,88284	-	-1,88345	-	CSNK2A1:M	42	-2	-17	-1	1
0,32797	-	-	-	-	-	0,04980822	-	-	T	0,150122	-	-	-	-	-1	35	-23	-6	1
0,51195	-	-	-	-	-	0,13693373	-	-	C	-0,9134	-	-	-	-	-2	-11	11	-29	1
0,37772	-	-	-	-	-	0,08113902	-	-	C	-	-	-	-	CSNK2A1:M	3	43	-38	-43	1
0,47031	-	-	-	-	-	0,17780093	-	-	A	-	-	-	-	-	32	18	-49	32	-1
0,99706	-	-	-	-	-	0,3741266	-	-	G	-	-	-	-	-	12	-43	-6	-43	0
0,82099	-	-	-	-	-	0,25249339	-	-	G	-	-	-	-	-	-12	-3	2	30	0
0,75778	-	-	-	-	-	0,14359071	-	-	T	-	-	-	-	CSNK2A1:T	17	-28	5	-28	0
0,63706	-	-	-	-	-	0,42808137	-	-	C	-0,39268	-0,264	-0,07401	-	-	-13	30	30	-20	3
0,677	-	-	-	-	-	0,56910235	-	-	C	-	0,146399	-	-	-	44	24	24	5	1
0,677	-	-	-	-	-	0,21653591	-	-	C	0,005306	-	-	-	-	-4	46	-32	-23	1
0,61936	-	-	-	-	-	0,90256542	-	-	C	-0,13848	-	0,17277	-	CSNK2A1:5	-3	-28	-39	-28	1
0,63706	-	-	-	-	-	0,93188202	-	-	C	0,69136	-	0,017073	-	CSNK2A1:A	-31	12	12	-38	0
0,7521	-	-	-	-	-	0,91743666	-	-	T	3,44676	-	1,806306	-	CSNK2A1:M	-1	-29	-16	4	1
0,99841	-	-	-	-	-	0,7259199	-	-	G	-1,0371	-	-	-	CSNK2A1:T	-29	43	-41	-29	-1
0,72327	-	-	-	-	-	0,81566906	-	-	T	0,00254	0,209999	-0,5079	-	-	-5	34	-9	-13	3
0,10044	-	-	-	-	-	0,10426051	-	-	C	-	-	-	-	-	39	-1	-47	-50	1
0,92332	-	-	-	-	-	0,88455898	-	-	A	-0,19369	-	-	-	-	-5	41	-17	0	-1
0,88861	-	-	-	-	-	0,99540329	-	-	A	0,8733	-	0,428588	-	-	24	-27	-35	-39	-3
0,10044	-	-	-	-	-	0,06525275	-	-	C	-	-	-	-	-	39	-1	-47	-50	1
0,31764	-	-	-	-	-	0,18594153	-	-	C	1,979762	-	-	-	-	37	11	-35	-47	-1
0,52969	-	-	-	-	-	0,80228287	-	-	C	0,066209	-	-	-	-	24	-19	-10	-19	1
0,95915	-	-	-	-	-	0,82805949	-	-	G	0,018999	-0,79659	-0,68999	-	-	-5	-49	10	-49	2
0,63966	-	-	-	-	-	0,99119121	-	-	C	11,2782	10,69	5,575191	-	-	22	46	-43	1	-3
0,91057	-	-	-	-	-	0,77171761	-	-	A	1,38268	0,5566	0,999612	-	CSNK2A1:I2	-1	18	-13	-5	-1
0,64073	-	-	-	-	-	0,58687031	-	-	C	-0,34811	-	-0,44105	-	-	-3	38	38	13	2
0,9694	-	-	-	-	-	0,96041483	-	-	G	-1,06176	-	-0,7509	-	CSNK2A1:T	1	13	-30	-46	-1
0,72109	-	-	-	-	-	0,95086306	-	-	T	0,175399	0,2192	0,526442	-	-	-1	10	6	-2	2
0,88435	-	-	-	-	-	0,99864632	-	-	A	5,10634	-	5,24303	-	-	22	-8	-28	-7	-2
0,64235	-	-	-	-	-	0,63098496	-	-	C	1,56792	-	-2,678	-	-	-7	44	-14	-15	1
0,63305	-	-	-	-	-	0,92430013	-	-	C	0,19744	-1,8322	0,33837	-	-	14	16	-11	15	3
0,76147	-	-	-	-	-	0,84089418	-	-	A	0,311199	-	-0,08685	-	-	30	34	3	-18	2
0,75737	-	-	-	-	-	0,98721516	-	-	T	1,7253	-	1,39941	-	CSNK2A1:D	-43	44	-46	-12	-1
0,91714	-	-	-	-	-	0,99792504	-	-	A	1,50084	-	1,251574	-	-	25	5	-17	5	-1
0,92332	-	-	-	-	-	0,85727602	-	-	A	1,65948	-	0,902478	-	-	6	26	0	6	0
0,34602	-	-	-	-	-	0,5119195	-	-	C	-	-	-	-	-	29	49	4	-24	0
0,75811	-	-	-	-	-	0,66799235	-	-	T	0,043101	-	-	-	-	40	-18	-6	-18	2
0,8297	-	-	-	-	-	0,48362467	-	-	G	-	-	-	-	CSNK2A1:P	15	-18	2	15	-2
0,46317	-	-	-	-	-	0,26771128	-	-	C	-	-	-	-	-	-28	20	13	-46	0