



Supplementary Figure 1. Scatterplot mapping SNV deltadeltaG stability score against deltadeltaG docking score for the purpose of observing covariance between the two variables. R-squared values were calculated using R Linear Model lm(). Adj R²= -0.0019368, P = 0.44395

Samples	Number of row reads (Exome)	Alignment rate	Total number of SNVs	Uniq. SNVs
CD91 ^{fl/fl} CD11c ^{Cre}	77,123,542	90.34%	9,210	1,478
CD91 ^{fl/fl} CD11c ^{Cre}	92,722,685	90.32%	10,207	2,206
CD91 ^{fl/fl} CD11c ^{Cre}	89,823,555	89.76%	9,913	1,885
CD91 ^{fl/fl} CD11c ^{Cre}	87,196,533	90.73%	12,206	1,649
CD91 ^{fl/fl} CD11c ^{Cre}	89,041,877	89.85%	13,239	2,646
CD91 ^{fl/fl} CD11c ^{Cre}	61,897,527	87.77%	12,335	4,276
CD91 ^{fl/fl}	89,569,026	91.04%	12,372	1,991
CD91 ^{fl/fl}	92,295,088	89.82%	8,706	669
CD91 ^{fl/fl}	91,336,559	90.59%	13,399	2,779
CD91 ^{fl/fl}	85,282,218	79.08%	13,132	2,876
CD91 ^{fl/fl}	79,766,039	85.63%	13,076	3,727
CD91 ^{fl/fl}	85,183,644	85.00%	9,688	1,183
CD91 ^{fl/fl}	77,448,013	87.71%	9,841	140

Supplementary Table 1. Single nucleotide variants from tumor lines harvested from CD91^{fl/fl}CD11c^{Cre} or CD91^{fl/fl} mice as deduced from transcriptome sequencing and bioinformatic analyses

Supplementary Table 2. Collection of all high impact SNVs filtered for predicted impact on CD91 function.

Data regarding the amino acid residue; the relative amino acid residue number within the domain; allele changes and residue changes caused by the SNV; SIFT and PolyPhen2 scores; qualitative iStable meta result; deltadeltaG value for stability from iMutant3.0 in iStable results; the deltadeltaG value for HSP binding energies; and the reference docking score for ligand binding domains I-IV

Energy Table

Domain 1

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
32	14	rs545853248	T or G	F -> L	(delet.) 0
42	24	rs372218876	C or T	S -> L	(delet.) 0.03
46	28	rs764409398	C or T	R -> W	(delet.) 0.03
49	31	rs375203123	G or A	G -> S	(delet.) 0.04
52	34	rs369927798	G or A	D -> N	(delet.) 0.03
55	37	rs143976462	C or A or T	D -> E	(delet.) 0
56	38	rs769357593	G or A	G -> R	(delet.) 0.03
105	87	rs373332583	G or A	G -> R	(delet.) 0.01
107	89	rs778563596	A or C	H -> P	(delet.) 0.02
158	140	rs759140255	G or A	G -> D	(delet.) 0.02
166	148	rs763952863	A or G	N -> S	(delet.) 0.03
166	148	rs2306691	A or G	N -> D	(delet.) 0
169	151	rs765594971	G or A	G -> S	(delet.) 0.01
169	151	rs201406588	G or A	G -> D	(delet.) 0.01
175	157	rs75821475	T or G	C -> W	(delet.) 0
175	157	rs758530079	G or A	C -> Y	(delet.) 0
196	178	rs773826305	G or C	D -> H	(delet.) 0
197	179	rs756708576	G or A	R -> Q	(delet.) 0.04
228	210	rs576800042	C or T	R -> W	(delet.) 0.01
254	236	rs756497827	C or T	T -> M	(delet.) 0.01
279	261	rs542050760	T or C	L -> P	(delet.) 0.01
286	268	rs750236140	G or A	A -> T	(delet.) 0.03
288	270	rs758269531	C or A	D -> E	(delet.) 0
293	275	rs768736912	A or G	N -> S	(delet.) 0.01
340	322	rs149677308	A or G	T -> A	(delet.) 0.01
340	322	rs757406803	C or G	T -> S	(delet.) 0.03
348	330	rs772498078	G or A	V -> M	(delet.) 0
354	336	rs780267759	G or A	D -> N	(delet.) 0.01
358	340	rs376832342	C or T	R -> C	(delet.) 0.01
379	361	rs540009385	G or A	R -> H	(delet.) 0.02
389	371	rs758647924	C or A	D -> E	(delet.) 0.01
394	376	rs747423446	G or A	V -> M	(delet.) 0
401	383	rs867247802	G or A	R -> H	(delet.) 0.01
401	383	rs551728223	C or T	R -> C	(delet.) 0
404	386	rs773827742	T or C	I -> T	(delet.) 0
444	426	rs750499142	C or T	R -> C	(delet.) 0
455	437	rs756622805	G or A	R -> Q	(delet.) 0.03
455	437	rs753045357	C or T	R -> W	(delet.) 0
467	449	rs757917239	G or C	Q -> H	(delet.) 0.03

477	459	rs746567808	C or T	A -> V	(delet.) 0.01
484	466	rs769491680	G or A	G -> R	(delet.) 0
486	468	rs749273635	C or G or T	P -> R	(delet.) 0.04
502	484	rs754240973	G or A	R -> Q	(delet.) 0.02
503	485	rs199896480	A or C or G	T -> P	(delet.) 0.01
505	487	rs41291995	C or G or T	R -> G	(delet.) 0.03
505	487	rs780842387	G or A	R -> H	(delet.) 0.04
507	489	rs752317686	C or T	R -> C	(delet.) 0
509	491	rs770978664	G or A	G -> S	(delet.) 0.01
510	492	rs779062839	T or G	F -> C	(delet.) 0
516	498	rs373613577	G or A	G -> R	(delet.) 0.01
530	512	rs774850713	T or C	Y -> H	(delet.) 0
534	516	rs760300449	G or A	R -> Q	(delet.) 0
539	521	rs753559627	G or C	R -> P	(delet.) 0
577	559	rs760047932	C or A	D -> E	(delet.) 0
585	567	rs763726478	C or T	R -> C	(delet.) 0
585	567	rs776319763	G or A	R -> H	(delet.) 0
593	575	rs765040892	C or T	R -> W	(delet.) 0
619	601	rs141139469	C or T	T -> M	(delet.) 0
621	603	rs369026283	G or A	D -> N	(delet.) 0
639	621	rs756192493	G or A	R -> H	(delet.) 0.02
639	621	rs752770422	C or T	R -> C	(delet.) 0
692	674	rs202220274	T or G	F -> C	(delet.) 0
694	676	rs775367641	A or C	T -> P	(delet.) 0.03
705	687	rs758792312	G or A	S -> N	(delet.) 0.03
714	696	rs778489217	A or T	Y -> F	(delet.) 0.03
714	696	rs756731467	T or C	Y -> H	(delet.) 0
716	698	rs147180309	G or A or C	V -> M	(delet.) 0.01
722	704	rs775250463	C or T	R -> C	(delet.) 0.01
724	706	rs776447046	G or C	E -> D	(delet.) 0.01
736	718	rs771211636	G or A	V -> M	(delet.) 0
761	743	rs764650029	C or T	R -> W	(delet.) 0.01
767	749	rs779629494	C or T	R -> C	(delet.) 0

Domain 2

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
811	18	rs778911320	A or C	N -> H	(delet.) 0.05
813	20	rs199752894	G or C	G -> R	(delet.) 0.01
828	35	rs775184509	G or A	A -> T	(delet.) 0.05
847	54	rs749676594	C or T	S -> F	(delet.) 0
894	101	rs755600829	A or C	T -> P	(delet.) 0.01
906	113	rs267603599	C or T	R -> W	(delet.) 0

916	123	rs760765530	G or A	G -> R	(delet.) 0.04
918	125	rs768585729	A or C or T	N -> H	(delet.) 0.03
928	135	rs537651271	A or G	N -> S	(delet.) 0.01
934	141	rs759947950	G or A	R -> H	(delet.) 0.04
938	145	rs574238888	C or A or G or P	-> H	(delet.) 0.01
940	147	rs779698934	G or T	Q -> H	(delet.) 0
947	154	rs746886209	G or A	R -> H	(delet.) 0.02
978	185	rs749453167	C or G	P -> R	(delet.) 0
1004	211	rs376320670	C or A or T	D -> E	(delet.) 0.04
1010	217	rs773782629	G or A	G -> S	(delet.) 0.05
1034	241	rs779033764	G or A	C -> Y	(delet.) 0
1034	241	rs757185200	T or C	C -> R	(delet.) 0
1072	279	rs771741064	G or C	D -> H	(delet.) 0
1073	280	rs775184428	G or A	G -> R	(delet.) 0
1073	280	rs746642500	G or A	G -> E	(delet.) 0
1079	286	rs768256707	C or T	R -> W	(delet.) 0.04
1080	287	rs776417449	T or C	W -> R	(delet.) 0.02
1081	288	rs761523540	C or T	R -> C	(delet.) 0
1105	312	rs779702143	G or A	D -> N	(delet.) 0
1117	324	rs769492677	G or A	R -> Q	(delet.) 0.02
1128	335	rs774179421	G or A	D -> N	(delet.) 0.01
1133	340	rs772015966	G or A	D -> N	(delet.) 0.01
1135	342	rs775690898	C or T	S -> L	(delet.) 0
1137	344	rs368351482	G or A	E -> K	(delet.) 0
1142	349	rs750861138	C or T	S -> F	(delet.) 0
1150	357	rs541735845	C or A or T	H -> N	(delet.) 0.02
1154	361	rs749034996	A or T	N -> I	(delet.) 0
1155	362	rs770745847	A or C	N -> T	(delet.) 0
1174	381	rs765494898	G or A	D -> N	(delet.) 0
1175	382	rs143746304	G or A	G -> S	(delet.) 0.05
1181	388	rs752090769	T or C	L -> P	(delet.) 0
1190	397	rs760065131	G or A	G -> D	(delet.) 0.03
1192	399	rs763544264	G or C	C -> S	(delet.) 0.01
1220	427	rs781356205	A or G	T -> A	(delet.) 0.02
1223	430	rs748306355	C or G	I -> M	(delet.) 0.04
1228	435	rs769895130	C or T	A -> V	(delet.) 0.02

Domain 3

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
2469	19	rs750633008	G or A	A -> T	(delet.) 0.04
2487	37	rs199726731	G or A	G -> S	(delet.) 0.02
2494	44	rs748042150	C or A	L -> M	(delet.) 0.03
2506	56	rs201669141	G or A	R -> Q	(delet.) 0.04

2507	57	rs759883573	G or A	G -> R	(delet.) 0
2514	64	rs758017835	C or G	D -> E	(delet.) 0.03
2564	114	rs35451280	G or A	R -> H	(delet.) 0
2571	121	rs778074768	C or T	R -> W	(delet.) 0.04
2575	125	rs771465981	A or G	N -> S	(delet.) 0.01
2577	127	rs775027515	G or A	R -> H	(delet.) 0.01
2587	137	rs140788492	G or A	G -> R	(delet.) 0.02
2611	161	rs377122314	C or T	R -> C	(delet.) 0
2613	163	rs367968116	C or T	R -> W	(delet.) 0.01
2614	164	rs769527712	G or C	D -> H	(delet.) 0.02
2614	164	rs574972738	C or A or T	D -> E	(delet.) 0.02
2615	165	rs372493625	G or A	G -> R	(delet.) 0.01
2623	173	rs868577215	C or T	R -> C	(delet.) 0.01
2632	182	rs149099223	C or A or T	D -> E	(delet.) 0
2633	183	rs757577718	G or A	A -> T	(delet.) 0
2652	202	rs373019949	G or A	V -> M	(delet.) 0.01
2665	215	rs142978324	C or T	L -> F	(delet.) 0.01
2702	252	rs200648115	G or A	A -> T	(delet.) 0.04
2715	265	rs76750685	G or C	C -> S	(delet.) 0
2720	270	rs772889897	A or G	D -> G	(delet.) 0
2734	284	rs557873392	G or T	C -> F	(delet.) 0
2739	289	rs770483111	T or C	F -> S	(delet.) 0
2745	295	rs773872972	G or A	R -> H	(delet.) 0.02
2747	297	rs759280898	A or G	I -> V	(delet.) 0.04
2755	305	rs149415384	G or A	G -> S	(delet.) 0.03
2764	314	rs200835075	C or G or T	D -> E	(delet.) 0
2791	341	rs755214895	C or T	R -> C	(delet.) 0.01
2796	346	rs148421667	G or A	G -> S	(delet.) 0.04
2799	349	rs747920082	C or G	D -> E	(delet.) 0
2810	360	rs150972965	G or T	A -> S	(delet.) 0.01
2811	361	rs767716437	G or A	G -> D	(delet.) 0.01
2811	361	rs759708060	G or A	G -> S	(delet.) 0.01
2848	398	rs769453950	T or G	D -> E	(delet.) 0
2864	414	rs748342380	C or G	R -> G	(delet.) 0.05
2874	424	rs148336699	C or T	R -> C	(delet.) 0.04
2915	465	rs746176099	G or A	G -> E	(delet.) 0.03
2932	482	rs763968301	G or A	D -> N	(delet.) 0
2934	484	rs201465531	C or G or T	S -> W	(delet.) 0
2950	500	rs776806696	A or G	S -> G	(delet.) 0.04
2954	504	rs770490623	A or C	Q -> P	(delet.) 0.02
2966	516	rs778272616	G or A	R -> H	(delet.) 0.01
2966	516	rs756570852	C or T	R -> C	(delet.) 0
2972	522	rs749876967	C or T	R -> W	(delet.) 0

2982	532	rs763064412	G or A	D -> N	(delet.) 0
2985	535	rs774606880	G or A	E -> K	(delet.) 0
3001	551	rs147829909	G or A	G -> S	(delet.) 0.02

Domain 4

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
3271	12	rs149120364	C or T	T -> M	(delet.) 0
3308	49	rs746509315	C or T	S -> F	(delet.) 0
3309	50	rs768297468	C or T	P -> S	(delet.) 0.01
3310	51	rs142253456	G or A or C	G -> R	(delet.) 0.01
3310	51	rs369454885	G or A	G -> E	(delet.) 0.04
3360	101	rs754487074	G or A	G -> R	(delet.) 0
3366	107	rs747687591	C or G	P -> A	(delet.) 0.01
3392	133	rs747081898	A or G	I -> V	(delet.) 0.04
3425	166	rs369992341	G or A	R -> H	(delet.) 0.01
3432	173	rs200178766	G or A	R -> H	(delet.) 0
3440	181	rs777824091	G or A	G -> R	(delet.) 0.01
3443	184	rs749571391	G or A	E -> K	(delet.) 0
3455	196	rs762564374	C or T	P -> L	(delet.) 0.01
3465	206	rs752456669	G or A	R -> Q	(delet.) 0.03
3465	206	rs375520801	C or T	R -> W	(delet.) 0
3475	216	rs759490492	C or T	R -> W	(delet.) 0.01
3500	241	rs755361380	G or A or C	R -> H	(delet.) 0.02
3504	245	rs142721778	C or T	S -> L	(delet.) 0
3516	257	rs768385613	G or A	G -> R	(delet.) 0.03
3522	263	rs761702371	A or G	D -> G	(delet.) 0
3534	275	rs766415186	C or T	R -> C	(delet.) 0.01
3542	283	rs762152236	G or A	R -> H	(delet.) 0.04
3546	287	rs756616082	C or A	N -> K	(delet.) 0.01
3546	287	rs753051105	A or T	N -> I	(delet.) 0
3549	290	rs879057829	G or A	V -> M	(delet.) 0
3560	301	rs780883543	G or A	D -> N	(delet.) 0.04
3562	303	rs747929960	G or A	G -> S	(delet.) 0.04
3581	322	rs867669203	C or T	S -> F	(delet.) 0.04
3586	327	rs772329528	C or T	R -> C	(delet.) 0
3603	344	rs745752639	G or T	G -> V	(delet.) 0
3616	357	rs868740565	A or C	D -> A	(delet.) 0.04
3617	358	rs748349980	A or T	Q -> L	(delet.) 0
3631	372	rs753321543	C or T	R -> C	(delet.) 0.04
3634	375	rs146774492	G or A	A -> T	(delet.) 0.01
3658	399	rs772620629	G or A	E -> K	(delet.) 0.01
3699	440	rs755480423	G or A	R -> Q	(delet.) 0.05
3702	443	rs141307381	G or A	R -> H	(delet.) 0.02

3707	448	rs745462082	C or T	R -> C	(delet.) 0
3709	450	rs775090032	G or T	C -> F	(delet.) 0
3750	491	rs769600453	C or T	R -> W	(delet.) 0.01
3753	494	rs771090395	C or T	R -> C	(delet.) 0
3760	501	rs548508591	C or T	R -> C	(delet.) 0.03
3768	509	rs762252932	G or A	G -> R	(delet.) 0.01
3770	511	rs571678726	G or A	G -> S	(delet.) 0.01
3772	513	rs553846743	C or A or T	D -> E	(delet.) 0
3773	514	rs150481288	G or C	E -> Q	(delet.) 0
3811	552	rs142687241	C or G or T	S -> W	(delet.) 0
3832	573	rs773131700	G or A or C	G -> S	(delet.) 0.01
3832	573	rs149488896	G or C	G -> A	(delet.) 0
3851	592	rs375922181	C or T	R -> W	(delet.) 0

INTERDOMAIN REGIONS

Domain 2-3

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
1257	13	rs530078568	G or A	D -> N	(delet.) 0.03
1280	36	rs772776317	G or A	R -> Q	(delet.) 0.03
1280	36	rs769050147	C or T	R -> W	(delet.) 0
1284	40	rs748808744	C or A	L -> I	(delet.) 0
1297	53	rs775159677	G or T	R -> L	(delet.) 0
1321	77	rs755499025	T or C	I -> T	(delet.) 0
1323	79	rs781599125	C or T	R -> C	(delet.) 0
1332	88	rs544821808	T or A	L -> Q	(delet.) 0
1339	95	rs776501958	A or T	I -> F	(delet.) 0
1356	112	rs763071789	G or A	G -> D	(delet.) 0.03
1359	115	rs878890519	A or C	Y -> S	(delet.) 0
1382	138	rs749929105	C or A or G	L -> M	(delet.) 0
1394	150	rs780963506	C or A or T	L -> M	(delet.) 0
1413	169	rs752298286	A or G	I -> V	(delet.) 0.02
1423	179	rs777476570	G or A	R -> H	(delet.) 0
1428	184	rs745902553	C or T	R -> W	(delet.) 0.04
1447	203	rs766956828	G or A	R -> H	(delet.) 0
1488	244	rs774878420	G or A	G -> R	(delet.) 0
1497	253	rs764859711	G or C	R -> P	(delet.) 0.02
1514	270	rs370442828	G or A	V -> M	(delet.) 0
1529	285	rs752787876	A or C	H -> P	(delet.) 0
1588	344	rs201999318	G or A	A -> T	(delet.) 0
1597	353	rs765334064	G or A	D -> N	(delet.) 0.04
1603	359	rs763253986	A or G	Y -> C	(delet.) 0
1608	364	rs766587273	C or G	S -> C	(delet.) 0.01

1612	368	rs185813305	C or T	P -> S	(delet.)	0
1617	373	rs371975627	G or A	V -> I	(delet.)	0.02
1626	382	rs761763756	G or A	E -> K	(delet.)	0.01
1628	384	rs769810027	C or T	R -> C	(delet.)	0
1628	384	rs773350053	G or A	R -> H	(delet.)	0
1646	402	rs549171552	G or A	G -> S	(delet.)	0
1648	404	rs753206313	G or T	G -> V	(delet.)	0.01
1649	405	rs756702192	G or A	V -> M	(delet.)	0.01
1667	423	rs762009228	G or T	W -> L	(delet.)	0
1669	425	rs866680003	C or T	S -> F	(delet.)	0
1670	426	rs751158586	G or A	R -> Q	(delet.)	0.02
1688	444	rs755983371	C or T	R -> W	(delet.)	0
1705	461	rs775980210	C or G	H -> D	(delet.)	0.02
1707	463	rs761146982	C or G	L -> V	(delet.)	0.05
1716	472	rs371203873	C or T	L -> F	(delet.)	0
1743	499	rs780297448	G or T	G -> V	(delet.)	0.04
1745	501	rs755226183	G or A	V -> M	(delet.)	0.04
1768	524	rs771491897	C or T	R -> C	(delet.)	0.01
1783	539	rs762970763	C or T	R -> W	(delet.)	0
1802	558	rs774111664	G or A	A -> T	(delet.)	0.02
1848	604	rs756835410	C or G	N -> K	(delet.)	0
1848	604	rs753442564	A or G	N -> S	(delet.)	0
1851	607	rs749454499	G or A	S -> N	(delet.)	0.03
1860	616	rs745534728	C or T	L -> F	(delet.)	0.02
1867	623	rs200163030	C or T	T -> M	(delet.)	0
1869	625	rs564564960	G or A	R -> H	(delet.)	0.01
1880	636	rs774925057	C or T	R -> W	(delet.)	0
1890	646	rs776013646	G or T	G -> V	(delet.)	0.04
1898	654	rs764738064	A or G	H -> R	(delet.)	0.04
1905	661	rs762580465	C or A	P -> T	(delet.)	0.01
1914	670	rs142834460	G or A	A -> T	(delet.)	0.03
1917	673	rs868675595	C or T	P -> S	(delet.)	0
1921	677	rs771244223	A or C	T -> P	(delet.)	0
1925	681	rs746110783	G or C	V -> L	(delet.)	0.01
1931	687	rs761240617	G or A	A -> T	(delet.)	0.03
1945	701	rs773920979	C or T	T -> M	(delet.)	0.04
1954	710	rs747084009	C or G or T	T -> R	(delet.)	0
1956	712	rs765402939	C or T	R -> C	(delet.)	0
1956	712	rs200890734	G or A	R -> H	(delet.)	0
1959	715	rs144804370	G or A or T	V -> M	(delet.)	0
1963	719	rs755242603	G or A	G -> S	(delet.)	0.04
1966	722	rs770347168	G or A	R -> H	(delet.)	0.01
1966	722	rs182778466	C or T	R -> C	(delet.)	0

1967	723	rs773833027	G or T	V -> L	(delet.)	0.05
1972	728	rs760386438	G or C	V -> L	(delet.)	0.01
1978	734	rs34398639	C or G or T	N -> K	(delet.)	0
1992	748	rs769741036	G or A	A -> T	(delet.)	0
1993	749	rs141826184	C or T	R -> W	(delet.)	0
1999	755	rs766366256	G or A	R -> H	(delet.)	0
2001	757	rs759735693	G or A	V -> M	(delet.)	0
2015	771	rs150485916	G or A	V -> I	(delet.)	0.03
2035	791	rs768348334	G or A	R -> Q	(delet.)	0.02
2037	793	rs193167795	C or G or T	R -> G	(delet.)	0.02
2037	793	rs145430854	G or A	R -> Q	(delet.)	0.05
2039	795	rs61734594	G or A	D -> N	(delet.)	0.03
2041	797	rs148823753	C or T	T -> M	(delet.)	0
2043	799	rs143462197	G or A	R -> H	(delet.)	0
2043	799	rs772068454	C or T	R -> C	(delet.)	0
2072	828	rs758299413	C or T	R -> W	(delet.)	0
2073	829	rs779924766	C or A	T -> K	(delet.)	0.01
2078	834	rs746942324	G or A	R -> Q	(delet.)	0.01
2081	837	rs571661266	T or C	L -> P	(delet.)	0
2087	843	rs773682342	G or T	R -> L	(delet.)	0
2122	878	rs772793077	C or T	R -> C	(delet.)	0
2122	878	rs762598842	G or A	R -> H	(delet.)	0
2126	882	rs754913793	A or G	D -> G	(delet.)	0.03
2132	888	rs778009174	G or A	V -> M	(delet.)	0.02
2135	891	rs375238409	G or A	R -> Q	(delet.)	0.02
2137	893	rs746255785	G or A	G -> S	(delet.)	0.01
2150	906	rs36003223	C or T	R -> W	(delet.)	0
2152	908	rs764383027	C or T	R -> W	(delet.)	0
2157	913	rs759234211	A or G	N -> S	(delet.)	0.01
2165	921	rs750545266	G or A	G -> R	(delet.)	0
2166	922	rs758714864	T or G	C -> G	(delet.)	0.01
2166	922	rs780269315	C or G	C -> W	(delet.)	0
2170	926	rs755366650	T or A	C -> S	(delet.)	0
2173	929	rs781626726	C or T	R -> W	(delet.)	0
2178	934	rs745489911	C or T	R -> W	(delet.)	0.01
2178	934	rs561234397	G or A	R -> Q	(delet.)	0.02
2181	937	rs377241209	G or A	A -> T	(delet.)	0.02
2195	951	rs755275163	C or T	R -> C	(delet.)	0.01
2220	976	rs773054498	C or T	L -> F	(delet.)	0.03
2244	1000	rs746656868	C or T	R -> W	(delet.)	0
2292	1048	rs200877384	G or A	R -> H	(delet.)	0.01
2292	1048	rs370171921	C or T	R -> C	(delet.)	0
2295	1051	rs757071051	A or G	D -> G	(delet.)	0.01

2297	1053	rs745822469	C or G	L -> V	(delet.)	0.02
2301	1057	rs780067120	G or C	S -> T	(delet.)	0.01
2304	1060	rs768811006	A or G	T -> A	(delet.)	0.04
2306	1062	rs777022730	A or G	T -> A	(delet.)	0
2308	1064	rs149869924	C or T	T -> M	(delet.)	0.03
2316	1072	rs374795916	G or A	R -> H	(delet.)	0.01
2322	1078	rs753507004	G or A	R -> H	(delet.)	0
2333	1089	rs375517607	C or G	H -> D	(delet.)	0
2411	1167	rs746349793	C or A	R -> S	(delet.)	0

Domain 3-4

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
3046	43	rs757090554	G or A	G -> R	(delet.) 0
3086	83	rs764819006	T or C	M -> T	(delet.) 0
3090	87	rs767671426	G or A	G -> R	(delet.) 0
3108	105	rs779470559	G or A or T	A -> T	(delet.) 0.02
3108	105	rs758897534	C or T	A -> V	(delet.) 0
3120	117	rs769243987	A or G	D -> G	(delet.) 0
3120	117	rs747634592	G or A	D -> N	(delet.) 0
3123	120	rs772910246	C or T	R -> W	(delet.) 0
3132	129	rs770686787	A or G	N -> S	(delet.) 0.03
3135	132	rs376337159	A or G	Y -> C	(delet.) 0
3137	134	rs553927301	C or T	T -> M	(delet.) 0.03
3145	142	rs370217380	G or A	R -> H	(delet.) 0.01
3174	171	rs148384329	G or A	G -> S	(delet.) 0.01
3174	171	rs368482360	G or C	G -> A	(delet.) 0.01
3180	177	rs773535117	C or T	R -> C	(delet.) 0.01
3180	177	rs763130531	G or A	R -> H	(delet.) 0.04
3184	181	rs768002005	G or A	V -> M	(delet.) 0.01
3195	192	rs554223507	A or G	T -> A	(delet.) 0.04
3198	195	rs749972945	A or G	Y -> C	(delet.) 0
3202	199	rs757948752	G or A	R -> H	(delet.) 0.01
3207	204	rs140370979	G or A	D -> N	(delet.) 0
3209	206	rs781268993	G or A	R -> H	(delet.) 0.01
3210	207	rs769969579	G or C	E -> Q	(delet.) 0.05
3223	220	rs369789736	G or A or C	R -> H	(delet.) 0.01
3223	220	rs770987853	C or T	R -> C	(delet.) 0

Domain 4-END

Residue	RelativeRes	Variation ID	Alleles	Residues	SIFT Score
3964	25	rs147095966	G or A	A -> T	(delet.) 0.05
3976	37	rs768055016	G or A	D -> N	(delet.) 0
3977	38	rs142650905	C or T	S -> L	(delet.) 0.02

3985	46	rs769174000	C or T	A -> V	(delet.)	0.01
3986	47	rs200607506	G or T	Q -> H	(delet.)	0.04
3994	55	rs199660560	C or T	T -> M	(delet.)	0.04
4005	66	rs779077274	G or A	A -> T	(delet.)	0.02
4010	71	rs201514351	C or G	P -> A	(delet.)	0.04
4025	86	rs202069155	A or C	K -> T	(delet.)	0.03
4036	97	rs765243290	C or T	R -> W	(delet.)	0
4052	113	rs548671555	G or A or C	V -> M	(delet.)	0
4054	115	rs79435985	A or T	Y -> F	(delet.)	0.04
4058	119	rs764436555	G or A	R -> Q	(delet.)	0.02
4058	119	rs138103421	C or T	R -> W	(delet.)	0
4071	132	rs780786245	A or T	S -> C	(delet.)	0
4073	134	rs747715315	C or T	R -> W	(delet.)	0.02
4076	137	rs770714386	G or A	G -> D	(delet.)	0.03
4076	137	rs749017125	G or T	G -> C	(delet.)	0
4092	153	rs375257456	C or A	P -> T	(delet.)	0
4102	163	rs776577505	C or G	I -> M	(delet.)	0.04
4136	197	rs746896607	G or A or C	V -> M	(delet.)	0
4150	211	rs778032975	C or G	P -> R	(delet.)	0
4153	214	rs150845737	C or T	R -> C	(delet.)	0.01
4213	274	rs770309179	T or G	N -> K	(delet.)	0.03
4215	276	rs748740550	C or T	R -> W	(delet.)	0
4262	323	rs767798756	T or C	F -> S	(delet.)	0
4262	323	rs759744173	T or C	F -> L	(delet.)	0
4263	324	rs868280822	C or T	T -> M	(delet.)	0.01
4301	362	rs143041547	G or A	D -> N	(delet.)	0
4302	363	rs867675246	C or T	R -> C	(delet.)	0
4346	407	rs377314133	C or T	R -> C	(delet.)	0.04
4447	508	rs758629883	G or A	R -> Q	(delet.)	0.01
4458	519	rs753180993	C or T	R -> W	(delet.)	0.02
4461	522	rs778556244	A or G	N -> D	(delet.)	0.02
4466	527	rs530070761	G or T	V -> L	(delet.)	0.03
4468	529	rs768428192	T or C	I -> T	(delet.)	0
4496	557	rs765988432	C or T	P -> S	(delet.)	0.03
4502	563	rs750769667	T or A	F -> I	(delet.)	0
4506	567	rs574472742	G or A	V -> M	(delet.)	0.04
4515	576	rs777208086	C or T	H -> Y	(delet.)	0.03
4518	579	rs34630693	C or A or T	R -> S	(delet.)	0.01
4518	579	rs751094440	G or A	R -> H	(delet.)	0
4524	585	rs373559379	C or T	T -> M	(delet.)	0.04

D1 Reference Score: -78.6

PolyPhen Score	iStable	deltadeltaGiMutant3.0	deltadeltaGDocking
(prob. dam.) 0.973	decrease	0.51	-78.8
(prob. dam.) 0.987	decrease	0.06	-71.3
(prob. dam.) 0.996	increase	0.06	-80.6
(poss. dam.) 0.686	decrease	1.03	-74.4
(prob. dam.) 0.994	decrease	0.55	-74.8
(prob. dam.) 0.993	increase	0.21	-75.8
(prob. dam.) 1	decrease	0.23	-68.7
(prob. dam.) 1	decrease	0.03	-72.4
(poss. dam.) 0.501	increase	0.39	-78.9
(prob. dam.) 0.999	decrease	1.1	-79.4
(prob. dam.) 0.983	increase	0.04	-80.5
(prob. dam.) 0.989	increase	0.02	-80.5
(prob. dam.) 0.999	decrease	0.82	-80.1
(prob. dam.) 0.999	decrease	0.77	-78.8
(prob. dam.) 0.997	neutral	0	-76.2
(prob. dam.) 0.996	increase	0.08	-76.9
(prob. dam.) 0.995	decrease	0.82	-78.4
(prob. dam.) 0.968	decrease	0.57	-75.6
(poss. dam.) 0.644	increase	0.06	-76.8
(poss. dam.) 0.63	increase	0.14	-77.2
(poss. dam.) 0.69	decrease	1.47	-56.8
(prob. dam.) 0.977	increase	0.69	-78
(prob. dam.) 0.952	increase	0.07	-80.2
(prob. dam.) 0.935	decrease	0.43	-78.7
(prob. dam.) 0.935	decrease	0.78	-75.7
(prob. dam.) 0.935	decrease	0.41	-75.3
(prob. dam.) 0.987	decrease	0.63	-78.8
(prob. dam.) 0.977	decrease	0.84	-70.9
(prob. dam.) 0.985	increase	0.98	-68.8
(poss. dam.) 0.477	decrease	1.46	-76.8
(prob. dam.) 0.952	decrease	0.09	-89.1
(prob. dam.) 0.987	decrease	1.11	-78.9
(prob. dam.) 0.98	decrease	0.86	-78.5
(prob. dam.) 0.985	decrease	0.5	-81.7
(prob. dam.) 0.95	decrease	1.81	-74.5
(prob. dam.) 0.985	increase	0.85	-73.3
(prob. dam.) 0.953	decrease	0.34	-75.5
(prob. dam.) 0.985	decrease	0.06	-79.5
(prob. dam.) 0.969	increase	0.67	-77.3

(prob. dam.) 0.968	increase	0.29	-81.4
(poss. dam.) 0.457	decrease	0.29	-86.5
(poss. dam.) 0.519	increase	0.71	-76.8
(prob. dam.) 0.953	decrease	0.51	-79.6
(prob. dam.) 0.981	decrease	0.84	-79.2
(prob. dam.) 0.972	decrease	1.72	-74.7
(prob. dam.) 0.98	decrease	1.24	-76.2
(prob. dam.) 0.985	decrease	0.95	-79.7
(prob. dam.) 0.997	decrease	1.16	-77.8
(prob. dam.) 0.984	decrease	1.42	-77.5
(prob. dam.) 0.998	increase	0.46	-79.5
(prob. dam.) 0.987	decrease	1.24	-72
(prob. dam.) 0.953	decrease	0.78	-85.9
(prob. dam.) 0.989	decrease	0.78	-84
(prob. dam.) 0.952	increase	0.48	-76.7
(prob. dam.) 0.985	decrease	0.4	-82.4
(prob. dam.) 0.98	decrease	0.89	-82.9
(prob. dam.) 0.985	decrease	0.03	-79.6
(prob. dam.) 0.998	increase	0.18	-73.2
(prob. dam.) 0.996	decrease	0.74	-76.8
(prob. dam.) 0.997	decrease	0.68	-82.2
(prob. dam.) 0.998	increase	0.09	-84.7
(poss. dam.) 0.905	decrease	1.82	-81.6
(poss. dam.) 0.761	decrease	1.17	-78.4
(prob. dam.) 0.988	increase	0.3	-77.5
(prob. dam.) 0.956	decrease	0.65	-79.2
(prob. dam.) 0.991	decrease	1.64	-78.6
(poss. dam.) 0.691	decrease	1.17	-77.3
(poss. dam.) 0.719	decrease	0.82	-81.6
(prob. dam.) 0.956	decrease	0.65	-79.6
(prob. dam.) 0.987	decrease	1.44	-78.2
(prob. dam.) 0.924	increase	0.58	-84.3
(poss. dam.) 0.446	decrease	1.02	-81.7

D2 Reference Score: -96.2

PolyPhen Score	iStable	deltadeltaGiMutant3.0	deltadeltaGDocking
(prob. dam.) 0.991	decrease	0.76	-98
(prob. dam.) 0.999	decrease	0.49	-97.5
(poss. dam.) 0.493	decrease	0.66	-96.1
(prob. dam.) 0.986	decrease	0.51	-96.4
(prob. dam.) 0.998	increase	0.47	-96.3
(prob. dam.) 0.998	increase	0.45	-96.1

(prob. dam.) 1	decrease	0.37	-99
(prob. dam.) 0.999	decrease	0.6	-97.4
(prob. dam.) 0.992	decrease	0.01	-96
(prob. dam.) 0.998	decrease	0.9	-95
(poss. dam.) 0.823	decrease	1.37	-96.3
(prob. dam.) 0.998	decrease	0.53	-96.1
(prob. dam.) 0.999	decrease	1.09	-94.6
(prob. dam.) 1	decrease	0.92	-103.9
(prob. dam.) 0.996	increase	0.06	-95.2
(prob. dam.) 0.994	decrease	0.83	-96.9
(prob. dam.) 0.996	decrease	0.04	-95.7
(prob. dam.) 0.985	decrease	0.04	-88.4
(prob. dam.) 0.999	increase	0.37	-87.1
(poss. dam.) 0.813	decrease	0.25	-95.9
(poss. dam.) 0.475	decrease	0.37	-94.7
(prob. dam.) 0.998	decrease	0.11	-96.4
(prob. dam.) 0.999	decrease	0.83	-92.9
(prob. dam.) 0.91	decrease	0.59	-102.3
(prob. dam.) 0.997	decrease	0.58	-96.9
(prob. dam.) 0.994	decrease	0.26	-96.3
(prob. dam.) 0.997	decrease	0.7	-96.7
(prob. dam.) 0.997	decrease	0.49	-96.1
(prob. dam.) 0.994	increase	0.12	-95.7
(prob. dam.) 0.995	decrease	0.92	-95.9
(poss. dam.) 0.564	increase	0.15	-97.9
(prob. dam.) 0.992	decrease	0.26	-96.7
(poss. dam.) 0.454	increase	0.97	-95.4
(poss. dam.) 0.596	increase	0.05	-95.8
(prob. dam.) 0.997	decrease	0.36	-96
(poss. dam.) 0.824	decrease	0.68	-96.3
(prob. dam.) 0.913	decrease	1.02	-95.6
(prob. dam.) 0.998	decrease	0.81	-96.4
(prob. dam.) 0.966	decrease	0.86	-98.1
(prob. dam.) 0.956	decrease	0.69	-94.6
(prob. dam.) 0.986	decrease	1.32	-96.7
(prob. dam.) 0.978	increase	0.06	-95.1

D3 Reference Score: -209.3

PolyPhen Score	iStable	deltadeltaGiMutant3.0	deltadeltaGDocking
(poss. dam.) 0.825	decrease	0.5	-208
(prob. dam.) 0.998	decrease	1.05	-209.7
(poss. dam.) 0.526	decrease	0.31	-208.9
(prob. dam.) 0.968	decrease	0.59	-211.1

(prob. dam.) 0.999	decrease	0.4	-204.4
(prob. dam.) 0.931	increase	0.36	-207.6
(prob. dam.) 0.997	decrease	1.3	-210.4
(poss. dam.) 0.664	decrease	0.45	-207.1
(prob. dam.) 0.989	decrease	0.4	-209
(prob. dam.) 0.997	decrease	1.24	-209.5
(poss. dam.) 0.518	decrease	0.3	-201.9
(poss. dam.) 0.828	decrease	0.51	-208
(prob. dam.) 0.913	decrease	0.12	-211.6
(prob. dam.) 0.947	decrease	0.87	-210.5
(poss. dam.) 0.76	decrease	0.6	-208
(prob. dam.) 1	decrease	0.47	-202.1
(poss. dam.) 0.88	decrease	0.68	-215.6
(prob. dam.) 0.995	increase	0.04	-204.2
(prob. dam.) 0.996	decrease	0.71	-206.9
(poss. dam.) 0.542	decrease	1.17	-207.3
(poss. dam.) 0.709	decrease	0.68	-208.1
(prob. dam.) 0.997	decrease	0.33	-204.7
(prob. dam.) 0.994	decrease	0.44	-209.2
(prob. dam.) 0.997	decrease	0.05	-215.5
(prob. dam.) 0.997	increase	0.3	-203.4
(prob. dam.) 0.998	decrease	1.19	-205.7
(prob. dam.) 0.996	decrease	0.99	-211
(poss. dam.) 0.899	decrease	0.83	-207.5
(prob. dam.) 1	decrease	0.89	-208
(prob. dam.) 0.998	increase	0.45	-213
(prob. dam.) 0.939	decrease	0.55	-204.5
(prob. dam.) 0.999	decrease	1.03	-212.4
(prob. dam.) 0.997	decrease	0.26	-213.2
(poss. dam.) 0.652	decrease	0.53	-207.5
(prob. dam.) 1	increase	1.44	-212.9
(prob. dam.) 1	decrease	1.25	-210.9
(prob. dam.) 0.996	increase	0.48	-212.9
(poss. dam.) 0.792	decrease	1.58	-198.9
(poss. dam.) 0.456	decrease	0.51	-200.1
(poss. dam.) 0.691	decrease	0.49	-205.8
(prob. dam.) 0.997	increase	0.73	-206.8
(prob. dam.) 0.999	increase	0.09	-196.8
(poss. dam.) 0.878	decrease	1.2	-209
(prob. dam.) 0.948	decrease	0.54	-208.3
(prob. dam.) 0.973	decrease	1.26	-211.6
(prob. dam.) 0.991	decrease	0.97	-216.5
(poss. dam.) 0.877	decrease	0.19	-211.5

(prob. dam.) 0.997	decrease	0.16	-203.2
(prob. dam.) 0.995	decrease	0.8	-194.6
(prob. dam.) 0.998	decrease	1.09	-203.8

D4 Reference Score: -258.2

PolyPhen Score	iStable	deltadeltaGiMutant3.0	deltadeltaGDocking
(poss. dam.) 0.828	increase	0.26	-256.9
(prob. dam.) 0.991	decrease	0.15	-250.2
(prob. dam.) 0.996	decrease	0.89	-271.2
(poss. dam.) 0.739	increase	0.11	-235.1
(poss. dam.) 0.652	increase	0.16	-253
(prob. dam.) 1	decrease	0.18	-260.4
(prob. dam.) 0.998	decrease	0.76	-266.9
(poss. dam.) 0.799	decrease	0.69	-262.8
(prob. dam.) 0.997	increase	1.17	-260.4
(prob. dam.) 0.997	decrease	0.89	-262.2
(prob. dam.) 1	decrease	0.22	-264.1
(poss. dam.) 0.482	decrease	0.72	-261.3
(prob. dam.) 0.999	increase	0.17	-265.6
(prob. dam.) 0.994	decrease	0.61	-261.2
(prob. dam.) 0.998	decrease	0.14	-262.2
(prob. dam.) 0.998	decrease	0.19	-262
(prob. dam.) 0.993	decrease	1.23	-253.9
(poss. dam.) 0.908	decrease	0.08	-272.7
(prob. dam.) 0.995	decrease	0.38	-272.2
(prob. dam.) 0.963	decrease	0.51	-249.5
(prob. dam.) 0.91	decrease	0.38	-269.6
(prob. dam.) 0.998	decrease	1.25	-281.4
(prob. dam.) 0.997	decrease	0.63	-266
(prob. dam.) 0.999	decrease	0.98	-269.5
(prob. dam.) 0.999	decrease	0.17	-261.8
(prob. dam.) 0.998	increase	0.65	-253.3
(prob. dam.) 1	decrease	0.93	-266.7
(poss. dam.) 0.886	increase	0.02	-273.4
(prob. dam.) 0.999	decrease	0.6	-268.6
(prob. dam.) 1	decrease	0.72	-266.5
(prob. dam.) 0.999	decrease	0.05	-259.9
(poss. dam.) 0.597	increase	0.06	-262.2
(prob. dam.) 0.934	decrease	0.58	-280.4
(poss. dam.) 0.851	decrease	0.58	-262.1
(prob. dam.) 0.995	decrease	0.63	-264.1
(prob. dam.) 0.982	decrease	0.49	-264.7
(prob. dam.) 0.991	decrease	1.26	-259.2

(prob. dam.) 0.991	decrease	0.94	-262.4
(prob. dam.) 0.993	decrease	0.1	-254.7
(poss. dam.) 0.545	decrease	0.17	-258.6
(poss. dam.) 0.745	decrease	0.71	-269
(poss. dam.) 0.828	decrease	0.82	-273.5
(poss. dam.) 0.778	decrease	0.28	-264.9
(poss. dam.) 0.532	decrease	0.84	-256.2
(poss. dam.) 0.482	increase	0.03	-255.3
(poss. dam.) 0.733	decrease	0.8	-264.9
(poss. dam.) 0.537	increase	0.58	-271.5
(prob. dam.) 0.999	decrease	1.18	-265.1
(prob. dam.) 0.996	decrease	0.96	-264.4
(poss. dam.) 0.518	decrease	0.06	-271.4

PolyPhen Score	iStable	deltadeltaGiMutant3.0
(prob. dam.) 0.984	increase	0.91
(prob. dam.) 0.968	decrease	1.9
(prob. dam.) 0.99	decrease	1.29
(prob. dam.) 0.967	decrease	1.48
(prob. dam.) 0.982	increase	0.45
(prob. dam.) 0.966	decrease	1.96
(prob. dam.) 0.99	decrease	0.72
(prob. dam.) 0.995	decrease	2.06
(prob. dam.) 0.979	decrease	0.85
(prob. dam.) 0.993	increase	1.44
(prob. dam.) 0.977	decrease	1.24
(prob. dam.) 0.993	decrease	1.13
(prob. dam.) 0.998	decrease	1
(poss. dam.) 0.566	decrease	0.91
(prob. dam.) 0.991	decrease	0.91
(poss. dam.) 0.813	increase	0.15
(prob. dam.) 0.965	decrease	1.48
(prob. dam.) 0.999	increase	-0.03
(prob. dam.) 0.995	decrease	0.61
(prob. dam.) 0.994	decrease	1.13
(prob. dam.) 0.991	decrease	-0.03
(prob. dam.) 0.985	increase	0.46
(prob. dam.) 0.984	decrease	1.15
(prob. dam.) 0.994	decrease	1.12
(prob. dam.) 0.99	decrease	1.43

(prob. dam.)	0.994	decrease	1.42
(prob. dam.)	0.959	decrease	0.6
(prob. dam.)	0.981	decrease	1.03
(prob. dam.)	0.998	decrease	1.36
(prob. dam.)	0.998	decrease	1.47
(prob. dam.)	1	decrease	1.09
(prob. dam.)	1	decrease	0.58
(prob. dam.)	0.99	decrease	1.11
(prob. dam.)	0.995	decrease	0.28
(prob. dam.)	0.986	decrease	-0.11
(prob. dam.)	0.968	decrease	0.38
(prob. dam.)	0.99	decrease	0.61
(prob. dam.)	0.966	increase	0.51
(prob. dam.)	0.967	decrease	1.09
(prob. dam.)	0.991	decrease	1.22
(prob. dam.)	0.942	decrease	-0.21
(prob. dam.)	0.992	increase	0.5
(poss. dam.)	0.719	decrease	1.75
(poss. dam.)	0.523	decrease	0.27
(prob. dam.)	0.984	decrease	0.55
(prob. dam.)	0.979	decrease	1.33
(prob. dam.)	0.956	decrease	1.2
(prob. dam.)	0.954	decrease	1.33
(prob. dam.)	0.991	decrease	1.57
(poss. dam.)	0.828	increase	0.32
(prob. dam.)	0.987	decrease	0.79
(poss. dam.)	0.523	increase	1.11
(prob. dam.)	0.998	increase	0.61
(prob. dam.)	0.966	increase	0.67
(prob. dam.)	0.994	decrease	1.48
(prob. dam.)	0.984	decrease	1.05
(prob. dam.)	0.994	decrease	1.26
(prob. dam.)	0.987	increase	-0.85
(prob. dam.)	0.956	decrease	-0.52
(prob. dam.)	0.985	decrease	0.47
(prob. dam.)	0.994	increase	0.51
(prob. dam.)	0.995	decrease	-0.24
(prob. dam.)	0.99	decrease	1.13
(prob. dam.)	0.987	decrease	1.38
(poss. dam.)	0.636	decrease	1.54
(prob. dam.)	0.998	decrease	1.25
(prob. dam.)	0.987	decrease	1.12
(prob. dam.)	0.99	decrease	1.08

(prob. dam.)	0.956	decrease	0.79
(prob. dam.)	0.956	decrease	-0.3
(prob. dam.)	0.995	decrease	1
(prob. dam.)	0.992	decrease	1.74
(prob. dam.)	0.996	decrease	1.23
(prob. dam.)	0.997	decrease	1.34
(prob. dam.)	0.997	decrease	1.59
(prob. dam.)	0.975	decrease	-0.14
(prob. dam.)	0.994	decrease	1.51
(prob. dam.)	0.994	decrease	1.52
(prob. dam.)	0.994	decrease	1.13
(prob. dam.)	0.997	decrease	2.14
(prob. dam.)	0.91	decrease	0.35
(prob. dam.)	0.998	decrease	1.61
(prob. dam.)	0.998	decrease	1.28
(prob. dam.)	0.993	decrease	1.02
(prob. dam.)	0.991	decrease	1.52
(prob. dam.)	0.978	decrease	1.71
(prob. dam.)	0.997	decrease	0.67
(prob. dam.)	0.987	increase	0.41
(prob. dam.)	0.993	decrease	1.45
(prob. dam.)	0.991	decrease	1.67
(poss. dam.)	0.516	decrease	0.95
(prob. dam.)	0.994	decrease	1.18
(prob. dam.)	0.978	decrease	2.07
(prob. dam.)	0.999	decrease	1.58
(poss. dam.)	0.803	decrease	1
(prob. dam.)	0.976	decrease	1.21
(prob. dam.)	0.956	decrease	0.56
(prob. dam.)	0.999	decrease	0.47
(poss. dam.)	0.715	decrease	1.65
(prob. dam.)	0.962	increase	0.41
(prob. dam.)	0.916	decrease	1.41
(prob. dam.)	0.982	decrease	0.18
(prob. dam.)	0.982	decrease	0.11
(prob. dam.)	0.964	decrease	0.32
(prob. dam.)	0.968	decrease	0.53
(prob. dam.)	0.982	decrease	0.68
(poss. dam.)	0.564	decrease	0.63
(poss. dam.)	0.727	decrease	0.33
(prob. dam.)	0.991	decrease	0.92
(prob. dam.)	0.993	decrease	0.78
(prob. dam.)	0.989	decrease	-0.1

(prob. dam.) 0.978	decrease	0.95
(prob. dam.) 0.952	increase	0.71
(prob. dam.) 0.97	decrease	0.94
(poss. dam.) 0.901	decrease	1.74
(poss. dam.) 0.877	decrease	0.88
(prob. dam.) 0.984	decrease	0.56
(prob. dam.) 0.991	decrease	0.72
(prob. dam.) 0.977	decrease	1.49
(prob. dam.) 0.997	decrease	1.68

PolyPhen Score	iStable	deltadeltaGiMutant3.0
(prob. dam.) 0.999	decrease	0.56
(prob. dam.) 0.968	decrease	1.71
(prob. dam.) 1	increase	0.46
(prob. dam.) 0.997	decrease	1.24
(prob. dam.) 0.996	increase	-0.44
(prob. dam.) 0.997	decrease	2.02
(prob. dam.) 0.997	decrease	1.7
(prob. dam.) 0.998	decrease	0.4
(prob. dam.) 0.992	decrease	-0.9
(prob. dam.) 0.999	decrease	-0.07
(prob. dam.) 0.966	increase	-0.13
(prob. dam.) 0.998	decrease	1.02
(prob. dam.) 1	decrease	1.85
(prob. dam.) 0.999	decrease	1.86
(prob. dam.) 0.998	decrease	1.57
(prob. dam.) 0.998	decrease	1.88
(prob. dam.) 0.911	decrease	2
(prob. dam.) 0.992	decrease	1.12
(poss. dam.) 0.87	decrease	0.99
(prob. dam.) 0.998	decrease	1.63
(prob. dam.) 0.997	decrease	1.43
(prob. dam.) 0.998	decrease	0.66
(prob. dam.) 0.998	decrease	1.15
(prob. dam.) 0.998	decrease	1.73
(prob. dam.) 0.998	decrease	1.4

PolyPhen Score	iStable	deltadeltaGiMutant3.0
(prob. dam.) 0.978	decrease	1.29
(prob. dam.) 0.988	increase	2.36
(prob. dam.) 0.992	increase	0.35

(poss. dam.)	0.82	increase	-0.2
(prob. dam.)	0.994	decrease	0.74
(prob. dam.)	0.999	decrease	0.87
(prob. dam.)	0.997	decrease	0.53
(prob. dam.)	0.998	decrease	2.34
(prob. dam.)	0.998	decrease	0.66
(prob. dam.)	0.998	decrease	0.16
(prob. dam.)	0.999	decrease	1.25
(prob. dam.)	0.992	decrease	0.56
(prob. dam.)	0.994	decrease	1.89
(prob. dam.)	0.998	decrease	1.08
(prob. dam.)	0.998	decrease	0.81
(prob. dam.)	0.971	decrease	0.07
(prob. dam.)	1	decrease	0.91
(prob. dam.)	1	decrease	0.95
(prob. dam.)	0.999	decrease	1.03
(poss. dam.)	0.618	decrease	1.38
(poss. dam.)	0.499	increase	1.44
(prob. dam.)	0.997	decrease	1.28
(poss. dam.)	0.732	decrease	0.44
(prob. dam.)	0.986	decrease	1.16
(poss. dam.)	0.642	decrease	0.68
(prob. dam.)	0.986	decrease	-0.5
(prob. dam.)	0.952	decrease	0.48
(prob. dam.)	0.996	increase	-0.2
(prob. dam.)	0.99	increase	0.68
(poss. dam.)	0.446	decrease	0.95
(poss. dam.)	0.543	decrease	0.26
(prob. dam.)	0.968	decrease	0.56
(prob. dam.)	0.948	increase	0.44
(poss. dam.)	0.76	increase	1.14
(prob. dam.)	0.976	increase	0.53
(prob. dam.)	0.966	decrease	1.04
(prob. dam.)	0.994	decrease	1.37
(prob. dam.)	0.966	decrease	0.3
(prob. dam.)	0.992	decrease	0.79
(prob. dam.)	0.954	increase	-0.27
(prob. dam.)	0.982	decrease	0.63
(prob. dam.)	0.987	decrease	0.83
(prob. dam.)	0.994	increase	-0.13

Supplementary Table 3. SNPs transcriptome from the NIH National Cancer Institute Genomic Data Commons Data Portal

Lung
SNP 105 UUID is 2837e256-e615-497a-b955-ab1ad89a7b4b
SNP 639 UUID is 8e93c97e-895b-4ce5-ad84-128a1b28a0c2
SNP 2623 UUID is f13e917f-e632-44e7-aa02-4e8baa07de8e
SNP 3504 UUID is d8b0542e-0af9-4db2-a533-479b525f21a6
Skin
SNP 539 UUID is 099776a1-3c91-457c-b180-2d93d8002ccc
SNP 978 UUID is 02858806-e4e0-499b-b96f-7b98cd08e369
SNP 3308 UUID is 98e29196-7380-4c38-b19f-7720f23ae4b2
SNP 3581 UUID is 0e77ae63-c12c-4ad2-a8ba-8cac17b1a935