Supplementary table e-1. List of all protein-altering variants identified in genes located within RLS-associated loci.

Loci	Gene	CHR:POS (bp)	NT	AA	Family 1	Family 2	Family 3	Family 4	Family 5	Family 6	Family 7	ExAC MAF	Depth of coverage
rs12046503	NTNG1	-	-	-	-	-	-	-	-	-	-	-	67
	PRMT6	1:107599918	C/T	A194V	2/5	-	1/5	2/4	7/8	4/5	6/6	0.2063	70
rs10208712	DCDC2C	2:3816957	G/A	V304I	2/5	-	-	-	3/8	2/5	-	**0.04286**	72
		2:3751606	C/T	R89C	-	1/5	-	-	1/8	-	-	0.1212	
	ALLC	2:3729254	C/T	T110I	1/5	4/5	1/5	2/4	5/8	-	2/6	0.1915	92
		2:3726083	A/C	H37P	1/5	-	-	-	-	-	-	**0.004153**	
rs113851554	MEIS1	-	-	-	-	-	-	-	-	-	-	-	47
rs1820989	APLF	2:68753240	T/A	S224T	2/5	1/5	3/5	-	6/8	-	1/6	0.131	70
		2:68765205	C/T	L336F	2/5	1/5	3/5	-	2/8	-	1/6	0.08274	
		2:68729992	A/G	I100V	-	-	-	-	4/8	-	-	**0.04759**	
		2:68794483	C/A	Q433K	-	-	-	-	4/8	-	-	**0.03505**	
		2:68805142	A/-	K509fs	-	-	-	-	2/8	-	-	-	
		2:68794471	A/G	c.1287-2A >G	-	1/5	-	-	-	-	-	**0.000278**	
	ETAA1	2:67631831	G/A	E673K	4/5	4/5	4/5	4/4	3/8	5/5	3/6	0.4563	120
		2:67631129	G/A	G439R	1/5	-	1/5	-	-	-	-	0.0977	
		2:67630476	T/C	M221T	1/5	-	1/5	-	-	-	-	0.09877	
		2:67624665	G/A	V29M	-	-	-	-	1/8	-	-	**0.000896**	
	PNO1	-	-	-	-	-	-	-	-	-	-	-	89
	WDR92	2:68364478	T/C	M241V	-	4/5	2/5	¼	6/8	-	4/6	0.2446	89
		2:68361859	C/T	A281T	-	-	-	-	-	3/5	-	**0.01605**	
rs80319144	CCDC148	-	-	-	-	-	-	-	-	-	-	-	98
	TANC1	2:160086299	T/A	F1454L	-	-	-	¼	-	-	-	**0.001259**	122
		2:160086300	C/T	H1455Y	-	-	-	¾	-	-	-	**0.001259**	
		2:160028693	T/G	S471R	-	-	-	-	-	-	1/6	**0.008348**	
		2:160035542	A/G	Q793R	1/5	-	-	-	-	-	-	**0.00033**	
	PKP4	-	-	-	-	-	-	-	-	-	-	-	30
	DAPL1	-	-	-	-	-	-	-	-	-	-	-	37

rs1848460	CNTN4	3:3095492	T/G	V938G	5/5	5/5	3/5	2/4	-	5/5	5/6	0.3207	71
	COL6A6	3:130361856	G/A	R1739Q	1/5	-	3/5	-	-	2/5	1/6	0.1018	121
		3:130346185	A/G	Y1655C	-	-	-	-	-	4/5	-	**0.01781**	
		3:130311398	C/T	A1429V	2/5	-	-	-	-	2/5	-	0.1256	
		3:130360527	C/T	S1708F	-	-	-	-	-	-	1/6	0.08165	
		3:130290007	T/C	I916T	-	1/5	-	-	-	-	-	**0.02929**	
	CRBN	3:3195658	C/G	D313H	-	-	2/5	-	-	-	-	**0**	118
	IL5RA	3:3139957	T/C	I129V	-	1/5	4/5	4/4	-	2/5	5/6	0.3618	52
	LRRN1	3:3886878	C/T	R185C	-	-	-	-	-	-	1/6	**0.000495**	172
		3:3886665	G/A	G114R	-	-	-	-	-	-	-	**0.006421**	
	ASTE1	3:130744039	G/A	R38C	-	-	-	-	-	-	1/6	**0**	115
	ATP2C1	-	-	-	-	-	-	-	-	-	-	-	67
rs35987657	NEK11	3:130992385	T/C	V562A	-	-	-	-	2/8	-	1/6	0.05898	55
		3:130962298	T/A	L527M	1/5	-	-	-	-	-	-	**0**	
	PIK3R4	3:130447530	T/TA	c.1586-2->TT	-	-	-	¼	-	-	4/6	0.1513	61
		3:130452431	C/A	A471S	-	-	-	¾	-	-	-	**0.002733**	
	TRNT1	-	-	-	-	-	-	-	-	-	-	-	55
rs17636328	CCDC167	-	-	-	-	-	-	-	-	-	-	-	93
	CMTR1	-	-	-	-	-	-	-	-	-	-	-	95
	MDGA1	6:37631768	A/G	L61P	-	-	-	2/4	2/8	-	4/6	0.2325	40
		6:37617926	T/C	N523S	1/5	-	-	-	-	-	-	**4.62E-05**	
	RNF8	-	-	-	-	-	-	-	-	-	-	-	54
	PIM1	-	-	-	-	-	-	-	-	-	-	-	68
	TBC1D22B	-	-	-	-	-	-	-	-	-	-	-	25
	TMEM217	-	-	-	-	-	-	-	-	-	-	-	153
	CMTR2	-	-	-	-	-	-	-	-	-	-	-	107
	ZFAND3	-	-	-	-	-	-	-	-	-	-	-	25

	BTBD9	-	-	-	-	-	-	-	-	-	-	-	53
	GLO1	6:38650628	T/G	E111A	4/5	3/5	5/5	4/4	8/8	5/5	5/6	0.4278	71
rs61192259	DNAH8	6:38773293	G/A	G1024E	-	5/5	4/5	-	8/8	-	1/6	0.4216	69
		6:38951998	C/T	T4323M	-	-	4/5	2/4	5/8	5/5	-	0.1443	
		6:38980081	A/G	I4488V	2/5	4/5	1/5	2/4	3/8	2/5	1/6	0.1783	
		6:38746176	G/A	A659T	1/5	1/5	-	-	5/8	5/5	1/6	0.1429	
		6:38747770	G/A	G690R	1/5	-	-	2/4	3/8	2/5	1/6	**0.04473**	
		6:38750888	A/G	I790V	4/5	-	4/5	-	-	-	1/6	0.1317	
		6:38757615	G/A	**V874M**	**-**	**-**	**-**	**4/4**	**4/8**	**-**	**-**	**0.03071**	
		6:38800164	G/A	E1419K	1/5	-	4/5	-	-	-	1/6	0.129	
		6:38759379	G/A	A944T	-	-	-	-	1/8	2/5	1/6	**0.03182**	
		6:38704943	A/G	N288S	-	3/5	-	-	-	-	-	**0.04324**	
		6:6:38854646	T/C	I2780T	-	-	-	-	-	-	2/6	**0.006819**	
		6:38850809	C/A	T2661N	-	-	-	-	-	2/5	-	**3.00E-05**	
		6:6:38897291	C/T	T3799I	-	-	-	-	-	-	1/6	**1.51E-05**	
		6:6:38905957	C/T	T3924M		-	-	-	-	-	1/6	**0.006307**	
rs10952927	ADAM22	7:87704999	G/A	E128K	-	-	-	¼	3/8	1/5	-	**0.02408**	30
		7:87822534	G/A	V894M	-	-	-	-	-	-	1/6	**0.000302**	
	STEAP4	7:87913221	C/T	A122T	3/5	3/5	3/5	2/4	-	-	1/6	0.1934	112
	ZNF804B	7:88964196	T/A	F634I	4/5	-	-	-	1/8	4/5	3/6	0.2301	88
		7:88965609	A/G	M1105V	2/5	-	-	-	-	-	3/6	0.05339	
		7:88965141	A/G	N949D	2/5	-	-	-	-	-	3/6	0.05304	
		7:88964227	C/G	P644R	2/5	-	-	-	-	-	3/6	0.05259	
		7:88964226	C/A	P644T	2/5	-	-	-	-	-	3/6	0.05259	
		7:88965021	G/A	E909K	2/5	-	-	-	1/8	-	-	0.1033	
	C7ORF62	-	-	-	-	-	-	-	-	-	-	-	62
rs1836229 **rs62535767**	PTPRD	9:8518052	G/C	Q447E	3/5	-	-	-	5/8	-	-	**0.04232**	77
		9:8497250	T/C	T781A	-	-	-	-	6/8	-	-	**0.03467**	
		9:8485834	G/A	R995C	1/5	1/5	-	¼	-	-	1/6	0.09301	
rs340561	DACH1	-	-	-	-	-	-	-	-	-	-	-	25

	DIS3	13:73349359	G/C	T326R	4/5	4/5	3/5	¾	2/8	-	5/6	0.4165	117
		13:73350079	T/C	N269S	-	3/5	2/5	¼	7/8	4/5	2/6	0.2862	
		13:73346905	C/T	D438N	-	-	-	¼	-	-	-	**0.01501**	
	BORA	-	-	-	-	-	-	-	-	-	-	-	213
rs996064	DPH6	15:35664373	G/C	S261C	-	2/5	-	-	-	-	-	**9.67E-05**	116
	MEIS2	-	-	-	-	-	-	-	-	-	-	-	48
rs111652004	SEMA6D	15:48058071	G/A	S478N	4/5	2/5	-	¾	8/8	-	2/6	0.3417	228
		15:48063914	G/A	V1052M	-	-	-	-	-	-	2/6	**6.07E-05**	
rs868036	MAP2K5	-	-	-	-	-	-	-	-	-	-	-	44
	SKOR1	15:68117300	T/A	W200R	1/5	1/5	3/5	-	1/8	-	1/6	0.2903	71
		15:68120472	C/T	A672V	1/5	-	-	-	-	-	-	**0.002419**	
	SMAD3	-	-	-	-	-	-	-	-	-	-	-	63
	CLN6	-	-	-	-	-	-	-	-	-	-	-	40
rs45544231	TOX3	-	-	-	-	-	-	-	-	-	-	-	33
rs12450895	HOXB1	17:46607958	T/A	Q103H	1/5	5/5	-	-	5/8	-	3/6	0.1984	117
	HOXB13	17:46804358	G/A	R217C	-	-	-	-	1/8	-	-	**0.00021**	116
	HOXB3	17:46629629	A/C	N70H	-	-	-	2/4	-	-	-	**0**	54
	HOXB7	17:46688135	G/A	A49V	-	-	-	2/4	-	-	-	**0.04438**	169
		17:46688107	C/G	L58F	-	-	-	-	-	1/5	-	**0.001733**	
	PRAC1	17	-	-	-	-	-	-	-	-	-	-	102
rs12962305	SETBP1	18:42529996	G/C	V231L	3/5	-	5/5	2/4	6/8	3/5	-	0.2077	381
		18:42532606	G/A	V1101I	2/5	3/5	3/5	-	1/8	4/5	-	0.1254	
		18:42532693	C/A	P1130T	-	-	-	2/4	-	1/5	2/6	0.1079	
		18:42618578	G/C	V1377L	-	-	-	-	-	1/5	1/6	**0.01142**	

rs365032	DNAJC5	-	-	-	-	-	-	-	-	-	-	-	50
	MYT1	20:62839435	G/A	E296K	-	-	-	¼	-	2/5	-	**0.002317**	154
	OPRL1	-	-	-	-	-	-	-	-	-	-	-	94
	PCMTD2	-	-	-	-	-	-	-	-	-	-	-	89
	PRPF6	-	-	-	-	-	-	-	-	-	-	-	74
	RGS19	-	-	-	-	-	-	-	-	-	-	-	87
	SAMD10	-	-	-	-	-	-	-	-	-	-	-	86
	TCEA2	20:62701627	G/A	V178I	-	1/5	-	-	-	-	-	**0.01153**	133
	UCKL1	-	-	-	-	-	-	-	-	-	-	-	170
	PTK6	-	-	-	-	-	-	-	-	-	-	-	144
	HELZ2	-	-	-	-	-	-	-	-	-	-	-	159
	RTEL1	-	-	-	-	-	-	-	-	-	-	-	90
	ZGPAT	-	-	-	-	-	-	-	-	-	-	-	59
	ZNF512B	-	-	-	-	-	-	-	-	-	-	-	155

Key: CHR, chromosome; POS, position (hg19; NT, nucleotide change; MAF, minor allele frequency; AA, amino acid change