Supplemental table 1.
Intergenic Variants for each Pedigree

Family	Chromosome	Start	End	Ref	Alt	CADD score
SSC_12605	chr18	56296796	56296801	CACACA	-	20.8
SSC_12605	chr1	22862796	22862796	T	C	22.4
SSC_12605	chr11	11228877	11228877	A	G	26.3
SSC_12605	chr20	37967464	37967464	C	G	25.7
SSC_12605	chr1	219547206	219547207	AA	-	23.4
SSC_12605	chr1	97159431	97159432	TT	-	21.6
SSC_12605	chr11	79222737	79222737	-	ACACACAT	25.5
SSC_12605	chr13	88766728	88766729	TC	-	20.8
SSC_12605	chr2	121269539	121269539	A	-	20.3
SSC_12605	chr7	145605410	145605410	A	-	21.4
SSC_12605	chr1	83889368	83889368	C	T	23
SSC_12605	chr14	97431801	97431801	A	T	21
SSC_12605	chr16	73924770	73924770	A	C	20.4
SSC_12605	chr17	25783776	25783776	G	A	21.1
SSC_12605	chr2	174526700	174526700	A	T	24.9
SSC_12605	chr3	18950958	18950958	G	A	21.4
SSC_12605	chr3	88859609	88859609	C	A	22.5
SSC_12605	chr5	121878403	121878403	A	T	20.9
SSC_12605	chr5	163435978	163435978	C	A	20.5
SSC_12605	chr5	170260699	170260699	C	T	20.3
SSC_12605	chr6	57564457	57564457	T	G	20.1
SSC_12605	chr8	106076378	106076378	T	G	21
SSC_12605	chr9	112286567	112286567	A	T	21.3
SSC_12605	chr9	132190884	132190884	C	T	20.5
SSC_12605	chr9	27670625	27670625	A	G	29.3
SSC_12605	chr11	115803295	115803300	CAATCA	T	24.9
SSC_12605	chr2	153153402	153153488	ATGTTTCTCTGTTGAAAGAAATGCTATGCCTTTGTGAAAATTGCCATTCTGTAAAAGTACTACTGAAGAATAGGACTCTG	-	23.8

				CTAAGGA		
SSC_12605	chr5	91090315	91090316	CA	T	20.1
SSC_12605	chr6	106357487	106357509	GTGCATGGCTGTGTTTCAATAAA	-	22
SSC_12605	chr8	132824962	132824975	GTGTGTGTGTGTGT	-	21.7
SSC_12605	chr1	88929834	88929834	A	T	23.3
SSC_12605	chr10	58879722	58879722	A	G	24
SSC_12605	chr10	60606856	60606856	T	A	23.9
SSC_12605	chr10	63403543	63403543	C	A	20.5
SSC_12605	chr10	71303491	71303491	A	G	23.7
SSC_12605	chr11	124716092	124716092	C	T	26.2
SSC_12605	chr11	15780647	15780647	G	A	20.3
SSC_12605	chr11	15861794	15861794	G	T	20.9
SSC_12605	chr11	81529166	81529166	A	G	24.8
SSC_12605	chr12	127097187	127097187	T	C	22
SSC_12605	chr13	112225526	112225526	C	T	27.5
SSC_12605	chr14	25971418	25971418	A	G	24.4
SSC_12605	chr14	28712495	28712495	C	G	23.8
SSC_12605	chr14	57207364	57207364	T	C	23.2
SSC_12605	chr14	59545027	59545027	G	A	21
SSC_12605	chr14	83287826	83287826	T	C	21.3
SSC_12605	chr14	83347284	83347284	T	A	23.4
SSC_12605	chr15	57619867	57619867	A	G	29
SSC_12605	chr15	62055088	62055088	G	T	20.1
SSC_12605	chr15	72892707	72892707	G	A	22.9
SSC_12605	chr17	14584777	14584777	G	T	20.7
SSC_12605	chr18	45326973	45326973	G	A	20.2
SSC_12605	chr18	67037686	67037686	G	C	20.9
SSC_12605	chr2	122728041	122728041	A	G	25.3
SSC_12605	chr2	126951391	126951391	T	C	24.6
SSC_12605	chr2	138864352	138864352	T	C	23.7
SSC_12605	chr2	147340830	147340830	A	T	24.5
SSC_12605	chr2	148113998	148113998	C	T	25.5
SSC_12605	chr2	156118240	156118240	A	G	22.7
SSC_12605	chr2	2832756	2832756	G	A	21.4
SSC_12605	chr20	11017899	11017899	G	A	25.4
SSC_12605	chr20	5279049	5279049	T	C	26.6
SSC_12605	chr20	5279051	5279051	T	C	27.4
SSC_12605	chr3	190806183	190806183	G	T	25.6

SSC_12605	chr3	65290074	65290074	T	C	23.7
SSC_12605	chr4	112669550	112669550	T	C	32
SSC_12605	chr4	112736297	112736297	T	G	22.6
SSC_12605	chr4	118823288	118823288	T	C	21.8
SSC_12605	chr4	130168145	130168145	T	C	28.4
SSC_12605	chr4	130443766	130443766	G	A	24.8
SSC_12605	chr4	147575215	147575215	T	G	22.5
SSC_12605	chr4	149381748	149381748	A	C	21.3
SSC_12605	chr4	169969161	169969161	A	C	20.4
SSC_12605	chr4	17252272	17252272	C	T	22
SSC_12605	chr4	18180348	18180348	G	A	21.9
SSC_12605	chr4	22881303	22881303	T	C	27.6
SSC_12605	chr4	67841685	67841685	T	C	21.5
SSC_12605	chr5	124316013	124316013	G	C	22
SSC_12605	chr5	30453417	30453417	A	G	20.5
SSC_12605	chr5	86837724	86837724	A	G	21.3
SSC_12605	chr5	86870158	86870158	G	A	21.9
SSC_12605	chr5	87009307	87009307	C	T	21
SSC_12605	chr5	87296764	87296764	C	T	25.3
SSC_12605	chr5	87343056	87343056	A	C	22.7
SSC_12605	chr5	94682116	94682116	A	C	26.1
SSC_12605	chr6	122419624	122419624	C	T	21.2
SSC_12605	chr6	143740082	143740082	A	G	28
SSC_12605	chr6	148282813	148282813	G	T	25
SSC_12605	chr6	40574804	40574804	C	T	29.2
SSC_12605	chr6	67067895	67067895	T	C	25.6
SSC_12605	chr7	14101770	14101770	C	T	21.4
SSC_12605	chr7	155665998	155665998	T	G	20.2
SSC_12605	chr7	156821142	156821142	G	A	28.4
SSC_12605	chr8	122228750	122228750	G	T	20.1
SSC_12605	chr8	124174622	124174622	C	G	20.6
SSC_12605	chr8	23844495	23844495	G	A	23.4
SSC_12605	chr8	37211547	37211547	G	A	28.7
SSC_12605	chr8	37478445	37478445	G	A	23.3
SSC_12605	chr8	64544103	64544103	G	A	25.4
SSC_12605	chr8	82285517	82285517	C	T	25.4
SSC_12605	chr9	116552467	116552467	C	G	34
SSC_12605	chr9	118422612	118422612	G	A	21.7
K21	chr22	27687672	27687672	C	T	20.4
K21	chr3	61335581	61335581	A	C	25.4
K21	chr3	61335633	61335633	G	C	20.1

K21	chr5	123532440	123532440	G	T	24.1
K21	chr5	9965489	9965489	C	T	21.1
K21	chr6	50840399	50840399	A	G	21.9
K21	chr7	41117784	41117784	T	C	28.4
K21	chr1	83856628	83856629	TG	-	22.4
K21	chr3	101042787	101042794	CACACACC	-	27.7
K21	chr5	56260260	56260260	-	T	21.8
K21	chr15	56076095	56076095	C	T	22.2
K21	chr20	20860914	20860914	G	A	21
K21	chr6	923029	923029	G	A	21.2
K21	chr9	132190774	132190774	T	C	27.2
K21	chr9	132190776	132190776	C	T	21.9
K21	chr9	132190777	132190777	G	A	25
K21	chrX	40247640	40247640	A	C	23
K21	chr15	56076080	56076091	ACACACACACAC	-	20.1
K21	chr5	61072614	61072619	GGCTCC	-	20.2
K21	chr6	106357487	106357509	GTGCATGGCTGTGTTTCAATAAA	-	22
K21	chr6	106357512	106357540	TTTATTTGCAAAAATGGTAGGCCAGATCT	-	20.3
K21	chr1	4583312	4583312	G	A	24
K21	chr1	53871085	53871085	G	C	21.7
K21	chr1	73408392	73408392	G	A	21.5
K21	chr10	113688392	113688392	T	C	21.5
K21	chr11	133467379	133467379	C	A	21.5
K21	chr12	122086571	122086571	G	A	20.6
K21	chr13	40562721	40562721	G	A	23
K21	chr13	53586912	53586912	T	C	25.5
K21	chr13	53860192	53860192	A	G	23.7
K21	chr13	54739462	54739462	G	A	28.2
K21	chr14	101851050	101851050	G	A	20.8
K21	chr14	61096535	61096535	G	A	22.4
K21	chr14	98708466	98708466	C	A	21
K21	chr14	99090043	99090043	C	T	23
K21	chr15	36592921	36592921	T	C	26.8
K21	chr15	70690919	70690919	A	T	20.5
K21	chr18	19484595	19484595	A	G	29

K21	chr18	76008014	76008014	G	A	23.7
K21	chr19	32514015	32514015	T	C	31
K21	chr2	118464682	118464682	G	A	26.2
K21	chr2	191069238	191069238	T	C	22.7
K21	chr3	112693983	112693983	T	G	28.1
K21	chr3	118572351	118572351	C	T	23.8
K21	chr3	125705514	125705514	G	C	21.1
K21	chr3	160295077	160295077	C	T	23.8
K21	chr3	51702481	51702481	T	G	20.8
K21	chr4	14342075	14342075	T	C	21.4
K21	chr4	182824707	182824707	C	T	22.8
K21	chr4	19056340	19056340	C	T	21.9
K21	chr4	24378792	24378792	C	G	22.4
K21	chr4	26860116	26860116	G	A	23.9
K21	chr4	30374172	30374172	G	A	20.5
K21	chr5	103344498	103344498	C	A	22.1
K21	chr5	103553737	103553737	T	C	21
K21	chr5	107154028	107154028	T	C	21.4
K21	chr5	109260124	109260124	T	C	22.3
K21	chr5	114649524	114649524	G	A	21.8
K21	chr5	123276353	123276353	C	T	23.2
K21	chr5	166069017	166069017	C	T	20.9
K21	chr5	166587688	166587688	T	C	22.2
K21	chr5	171086955	171086955	C	G	26.9
K21	chr5	171712758	171712758	T	C	27.8
K21	chr5	3115792	3115792	G	T	32
K21	chr5	4778242	4778242	C	T	27
K21	chr5	50814113	50814113	C	T	34
K21	chr5	61035688	61035688	A	G	28.8
K21	chr5	73787644	73787644	T	A	22
K21	chr5	86942915	86942915	C	T	28.2
K21	chr5	92145245	92145245	A	C	21.9
K21	chr6	106957825	106957825	C	T	22.7
K21	chr6	22558596	22558596	A	G	23.3
K21	chr6	48060847	48060847	A	G	24.4
K21	chr6	57675003	57675003	A	G	21.1
K21	chr6	7631966	7631966	C	T	20.1
K21	chr6	77104723	77104723	G	A	20.4
K21	chr6	88688027	88688027	T	C	27.2
K21	chr7	41174953	41174953	A	G	25.6
K21	chr8	10427001	10427001	A	T	27.7

K21	chr8	135352051	135352051	G	T	21
K21	chr8	20248897	20248897	C	T	22.9
K21	chr8	21481008	21481008	C	T	24.5
K21	chr9	108671886	108671886	G	C	21.7
K21	chr9	108978316	108978316	C	T	21.4
K21	chr9	118745741	118745741	G	A	25.2
K21	chr9	29591346	29591346	A	C	21.2
K21	chr9	34719492	34719492	C	A	20.7
K21	chr9	36809058	36809058	A	G	22
SSC_12596	chr5	148861846	148861846	T	C	21.4
SSC_12596	chr5	166473408	166473408	A	G	32
SSC_12596	chr6	105392777	105392777	G	A	26.1
SSC_12596	chr1	40157507	40157507	-	CCC	20.4
SSC_12596	chr6	99633447	99633447	-	AA	26.1
SSC_12596	chr7	41486661	41486661	A	-	20.2
SSC_12596	chr8	97126161	97126186	GAGAGAGAGAGAGTGTGTGTGTGTGT	-	25.7
SSC_12596	chr8	97126173	97126186	GTGTGTGTGTGTGT	-	26.7
SSC_12596	chr15	98525665	98525665	G	A	20
SSC_12596	chr16	73798270	73798270	G	T	20.9
SSC_12596	chr18	38192440	38192443	GACC	AACA	21.7
SSC_12596	chr2	143423002	143423002	T	C	20.2
SSC_12596	chr20	37967451	37967451	A	C	28.5
SSC_12596	chr20	52894853	52894853	G	T	24.7
SSC_12596	chr20	83275	83275	T	C	21.3
SSC_12596	chr3	75913410	75913410	C	G	24.7
SSC_12596	chr4	113424391	113424391	C	T	21.5
SSC_12596	chr4	150225458	150225458	A	T	31
SSC_12596	chr9	13447092	13447092	T	A	23.2
SSC_12596	chr11	114130425	114130428	ACTC	G	23.2
SSC_12596	chr16	54397489	54397489	-	AG	25.7
SSC_12596	chr17	68625736	68625742	ACACACA	-	22.7
SSC_12596	chr2	180748704	180748704	T	-	25.1
SSC_12596	chr22	27954051	27954051	-	TGTGTGTGTGTG	20.5
SSC_12596	chr3	16356392	16356396	TAAGA	-	21.9
SSC_12596	chr5	152622997	152622997	-	CT	25.6
SSC_12596	chr5	61050514	61050526	AGTCTAAGATTAC	-	21

SSC_12596	chr8	78870672	78870673	AG	-	24.5
SSC_12596	chr1	115944429	115944429	G	A	21.7
SSC_12596	chr1	209515989	209515989	G	A	25.2
SSC_12596	chr1	230059707	230059707	T	G	20.3
SSC_12596	chr1	26492528	26492528	G	A	21.8
SSC_12596	chr10	124858110	124858110	C	T	23
SSC_12596	chr10	128395835	128395835	C	T	21.2
SSC_12596	chr10	130983110	130983110	T	A	28.7
SSC_12596	chr10	131121537	131121537	A	T	29.1
SSC_12596	chr10	131191050	131191050	G	A	26.3
SSC_12596	chr10	131215926	131215926	A	C	23.5
SSC_12596	chr10	66344166	66344166	G	A	20.8
SSC_12596	chr11	115390478	115390478	G	T	20.7
SSC_12596	chr11	119663944	119663944	C	T	22.6
SSC_12596	chr11	13255161	13255161	C	T	23
SSC_12596	chr11	13846999	13846999	A	G	25.2
SSC_12596	chr11	75940022	75940023	AA	CC	21.5
SSC_12596	chr11	80129375	80129375	G	C	21.2
SSC_12596	chr12	113886945	113886945	G	A	29.6
SSC_12596	chr12	19562222	19562222	C	T	22.2
SSC_12596	chr12	26281499	26281499	T	A	22.7
SSC_12596	chr12	54699087	54699087	T	C	26
SSC_12596	chr12	88842526	88842526	C	T	20.2
SSC_12596	chr13	34578005	34578005	C	A	21.5
SSC_12596	chr13	53991175	53991175	T	C	21.1
SSC_12596	chr13	60050575	60050575	A	G	28
SSC_12596	chr13	74802722	74802722	A	G	24.6
SSC_12596	chr13	79580367	79580367	G	T	24.3
SSC_12596	chr13	82081219	82081219	A	G	20.4
SSC_12596	chr14	66339078	66339078	T	C	21.6
SSC_12596	chr15	47341462	47341462	A	G	20.3
SSC_12596	chr15	60055405	60055405	T	C	31
SSC_12596	chr15	93833334	93833334	C	T	23
SSC_12596	chr15	96548743	96548743	A	T	32
SSC_12596	chr16	51026783	51026783	G	A	26.5
SSC_12596	chr16	51279310	51279310	C	A	28.4
SSC_12596	chr16	59033833	59033833	A	G	24
SSC_12596	chr16	60300340	60300340	G	A	21.7
SSC_12596	chr18	51628566	51628566	A	T	25.4
SSC_12596	chr2	151619390	151619390	C	A	25.9
SSC_12596	chr2	164331585	164331585	C	G	24

SSC_12596	chr2	172957618	172957618	C	T	24.9
SSC_12596	chr2	176130181	176130181	A	G	23.5
SSC_12596	chr2	191069238	191069238	T	C	22.7
SSC_12596	chr2	22153244	22153244	A	C	22.5
SSC_12596	chr2	227559824	227559824	T	C	27.2
SSC_12596	chr2	37975711	37975711	A	C	26.4
SSC_12596	chr2	38001226	38001226	C	T	20.8
SSC_12596	chr20	11020374	11020374	A	G	21.1
SSC_12596	chr20	7306898	7306898	C	T	22.2
SSC_12596	chr21	18115979	18115979	C	T	24.2
SSC_12596	chr3	115056229	115056229	T	A	29.1
SSC_12596	chr4	100608406	100608406	A	G	22.7
SSC_12596	chr4	111125850	111125850	C	A	24.2
SSC_12596	chr4	127008059	127008059	T	C	23.5
SSC_12596	chr4	24378792	24378792	C	G	22.4
SSC_12596	chr4	27726615	27726615	G	A	21.1
SSC_12596	chr4	27759790	27759790	G	T	21.8
SSC_12596	chr4	42222902	42222902	A	G	25.6
SSC_12596	chr4	96756053	96756053	T	C	20.9
SSC_12596	chr5	154973014	154973014	C	A	22.9
SSC_12596	chr5	155113061	155113061	A	C	25.7
SSC_12596	chr5	157541929	157541929	C	T	27.7
SSC_12596	chr5	165337596	165337596	T	C	24.1
SSC_12596	chr5	165525147	165525147	A	G	23.3
SSC_12596	chr5	166028177	166028177	T	G	24.3
SSC_12596	chr5	2848501	2848501	A	T	23.9
SSC_12596	chr5	3187598	3187598	T	C	24.8
SSC_12596	chr5	44441702	44441702	T	C	21.2
SSC_12596	chr5	57367474	57367474	C	T	27.3
SSC_12596	chr6	57731529	57731529	G	T	20.2
SSC_12596	chr6	63165651	63165651	G	A	24.9
SSC_12596	chr6	91956739	91956739	T	A	24
SSC_12596	chr6	99606759	99606759	A	G	23.5
SSC_12596	chr7	106684276	106684276	A	G	23.9
SSC_12596	chr7	11357015	11357015	T	C	20.9
SSC_12596	chr7	114990639	114990639	A	G	23.8
SSC_12596	chr7	115340835	115340835	C	T	25.7
SSC_12596	chr7	13842239	13842239	C	T	28
SSC_12596	chr7	13866759	13866759	T	C	21.7
SSC_12596	chr7	13874391	13874391	A	G	22.1
SSC_12596	chr7	13879370	13879370	T	G	25.7

SSC_12596	chr7	45499145	45499145	C	A	20.5
SSC_12596	chr8	124297256	124297256	A	G	22.6
SSC_12596	chr8	135046560	135046560	T	C	22.7
SSC_12596	chr8	136342563	136342563	T	C	21.5
SSC_12596	chr8	78361199	78361199	G	C	20.2
SSC_12596	chr9	16278494	16278494	G	C	36
SSC_12596	chr9	27763002	27763002	G	T	21.8
SSC_12596	chr9	30243440	30243440	T	C	24.7
SSC_12596	chr9	78473530	78473530	G	T	21.3
SSC_12596	chr9	83995471	83995471	A	C	23
SSC_12596	chrX	17351169	17351169	C	A	22.9
SSC_12596	chrX	97109589	97109589	A	C	34