A

	A	B
1	C35E7.2	2
2	Y8A9A.2	2
3	Y16B4A.2	2

B

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1	Sample	# Chromo	Position	Reference	Change	Change_type	Homozygous	Quality	Coverage	Warnings	Gene_ID	Gene_name	Bio_type	Trancript_ID	Exon_ID	Exon_Rank	Effect	old_AA/new_AA	Old_codon/New_codon	Codon_Num	Codon_Dege	CDS_size
2	mutA	I	10841384	G	C	SNP	Hom	43.12	2		C35E7.2	C35E7.2	protein_coding	C35E7.2a	exon_I_10841103_10841965	1	NON_SYNONYMOUS_CODING	R/T	aGa/aCa	92	0	2124
3	mutB	I	10841434	A	C	SNP	Hom	80.72	3		C35E7.2	C35E7.2	protein_coding	C35E7.2a	exon_I_10841103_10841965	1	NON_SYNONYMOUS_CODING	I/L	Att/Ctt	109	0	2124
4	mutB	II	3796684	C	A	SNP	Hom	349.22	21		Y8A9A.2	Y8A9A.2	protein_coding	Y8A9A.2	exon_II_3796348_3797638	5	NON_SYNONYMOUS_CODING	P/Q	cCa/cAa	286	0	4083
5	mutC	II	3796759	A	T	SNP	Hom	1208.35	56		Y8A9A.2	Y8A9A.2	protein_coding	Y8A9A.2	exon_II_3796348_3797638	5	NON_SYNONYMOUS_CODING	N/I	aAt/aTt	311	0	4083
6	mutA	X	14766637	G	A	SNP	Hom	44.89	4		Y16B4A.2	Y16B4A.2	protein_coding	Y16B4A.2	exon_X_14766327_14766971	18	NON_SYNONYMOUS_CODING	S/F	tCc/tTc	1073	0	6504
7	mutB	X	14766625	*	—G	DEL	Hom	506.78	21		Y16B4A.2	Y16B4A.2	protein_coding	Y16B4A.2	exon_X_14766327_14766971	18	FRAME_SHIFT: Y16B4A.2					6504

Figure S1 CloudMap *in silico Complementation Test* tool. **A:** Summary output. CloudMap allows for large scale *in silico* comparison of annotated WGS variants (that have been filtered for quality and had common variants subtracted) between many samples. The summary output from this comparison shows the number of alleles of each gene sorted from most to fewest. **B:** Comprehensive output. For each in silico Complementation Test summary output file, CloudMap provides the corresponding detailed list of snpEff-annotated, allelic gene hits that is also sorted from most to fewest alleles.