

Suppl. Table 3. Multinucleotide Mutations

MA Lines	Chromosome	Position	Reference	Mutant	AD*	DP**	SAC***	Homozygous or Heterozygous	Genic Region****	Amino Acid Change	Gene*****	Protein	syn/nonsyn*****
Hv29	NC_013966.1	443876	G	A	0,51	51	0,0,20,31	Homozygous	Coding	Thr171Thr	HVO_RS03775	hypothetical	syn
Hv29	NC_013966.1	443893	G	A	0,39	39	0,0,13,26	Homozygous	Coding	Val165Ile	HVO_RS03775	hypothetical	nonsyn
Hv86	NC_013966.1	121338	G	A	444,269	713	179,265,87,182	Heterozygous	Coding	Phe41Phe	HVO_RS19795	β beta-propelle	syn
Hv86	NC_013966.1	121358	C	A	424,209	633	181,243,70,139	Heterozygous	Coding	Ala35Ser	HVO_RS19795	β beta-propelle	nonsyn
Hv86	NC_013966.1	121405	C	A	353,77	430	140,213,16,61	Heterozygous	Coding	Arg19Leu	HVO_RS19795	β beta-propelle	nonsyn
Hv86	NC_013966.1	121413	G	C	358,58	416	140,218,3,55	Heterozygous	Coding	Gly16Gly	HVO_RS19795	β beta-propelle	syn
Hv90	NC_013967.1	1048889	A	G	152,48	200	81,71,20,28	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048893	G	A	150,49	199	81,69,20,29	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048899	A	C	150,57	207	83,67,23,34	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048911	G	A	178,63	241	110,68,26,37	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048916	A	C	172,63	235	107,65,25,38	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048918	G	T	166,63	229	105,61,25,38	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048920	C	T	163,63	226	105,58,25,38	Heterozygous	NonCoding				
Hv90	NC_013967.1	1048933	A	G	162,72	234	103,59,30,42	Heterozygous	NonCoding				

*AD is the allelic depths for the reference and alternative alleles

**DP is the approximate read depth

***SAC is the number of reads on the forward and reverse strand supporting each allele (including reference)

****Noncoding - noncoding sequence, Coding - coding sequence.

***** Gene is the gene name or type of gene where the base substitution occurs.

***** syn - synonymous, nonsyn - nonsynonymous.