POSITION	POSITION SORT	GENE	FALSE POSITIVE SCORE	TYPE	SUBTYPE	SIZE	SIZE SORT	POLYMORPH SUMMARY	NCM4139	NCM4287	NCM4299	NCM4300	NCM4370	NCM4384	NCM4401	10_NT_ALIGN	ANNOTATION	(STRAND)CODON	GEVO_LINK	COGE_ALIGN_LINK	HOMOPOLYMER FALSE POSITIVE SCORE	MULTI-HIT FALSE POSITIVE SCORE
46,171	46171	-	0	contig join	-	-	-	-						N		show	-	-	GEvo Link GEvo_Link_20k	-	0	0
48,332	48332	araB, b0063	6	insertion	Frameshift	1	1	--T----	-	-	T	-	-	-	-	show	L-ribulokinase	show	GEvo Link GEvo_Link_20k	CoGeAlign Link	6	0
57,023	57023	b0070, setA	8	indel	Frameshift	1	1	TT-TTT-	T	T	-	T	T	T	-	! TACCTGCTGGTTTTTTTTATT TACCTGCTGGTTTTTTTTATT TACCTGCTGG-TTTTTTTATT TACCTGCTGGTTTTTTTTATT TACCTGCTGGTTTTTTTTATT TACCTGCTGGTTTTTTTTATT TACCTGCTGG-TTTTTTTATT hide	broad specificity sugar efflux system	show	GEvo Link GEvo_Link_20k	CoGeAlign Link	8	0
63,009	63009		8	insertion		1	1	-----A-	-	-	-	-	-	A	-	show	INTERGENIC		GEvo Link GEvo_Link_20k		8	0
63,714	63714		5	insertion		1	1	-----T-	-	-	-	-	-	T	-	show	INTERGENIC		GEvo Link GEvo_Link_20k		5	0
70,349	70349	b0082, mraW	7	insertion	Frameshift	1	1	---A---	-	-	-	A	-	-	-	show	S-adenosyl-dependent methyltransferase activity on membrane-located substrates, putative apolipoprotein	show	GEvo Link GEvo_Link_20k	CoGeAlign Link	7	0
105,354	105354	-	0	contig join	-	-	-	-							N	show	-	-	GEvo Link GEvo_Link_20k	-	0	0
105,593	105593	aceF, b0115	31	SNP	Synonymous	1	1	CCCCCCT	C	C	C	C	C	C	T	show	pyruvate dehydrogenase (dihydrolipoyltransacetylase component), pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	show	GEvo Link GEvo_Link_20k	CoGeAlign Link	0	31
105,597	105597	aceF, b0115	31	SNP	Nonsynonymous Amino acids: I V	1	1	AAAAAAG	A	A	A	A	A	A	G	show	pyruvate dehydrogenase (dihydrolipoyltransacetylase component), pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	! (1):ATC CTG GTG AAA GTT (1):ATC CTG GTG aAA GTT (1):ATC CTG GTG AAa GTT (1):GTG ATG GTG aaa GTg hide	GEvo Link GEvo_Link_20k	CoGeAlign Link	0	31
105,599	105599	aceF, b0115	31	SNP	Nonsynonymous Amino acids: I V	1	1	CCCCCCG	C	C	C	C	C	C	G	show	pyruvate dehydrogenase (dihydrolipoyltransacetylase component), pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	show	GEvo Link GEvo_Link_20k	CoGeAlign Link	0	31
105,600	105600	aceF, b0115	31	SNP	Nonsynonymous Amino acids: L M	1	1	CCCCCCA	C	C	C	C	C	C	A	! GACCGAAATCCTGGTGAAAGT GACCGAAATCCTGGTGAAAGT GACCGAAATCCTGGTGAAAGT GACCGAAATCCTGGTGAAAGT GACCGAAATCCTGGTGAAAGT GACCGAAATCCTGGTGAAAGT GACTGAAGTGATGGTGAAAGT hide	pyruvate dehydrogenase (dihydrolipoyltransacetylase component), pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	! (1):CTG GTG AAA GTT GGC (1):CTG GTG aAA GTT gGC (1):CTG GTG AAa GTT GGC (1):ATG GTG aaa GTg ggC hide	GEvo Link GEvo_Link_20k	CoGeAlign Link	0	31
105,611	105611	aceF, b0115	31	SNP	Synonymous	1	1	TTTTTTG	T	T	T	T	T	T	G	show	pyruvate dehydrogenase (dihydrolipoyltransacetylase component), pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2	show	GEvo Link GEvo_Link_20k	CoGeAlign Link	0	31
105,682	105682	-	0	contig join	-	-	-	-			N	N		N		show	-	-	GEvo Link GEvo_Link_20k	-	0	0