Supplementary Material

Genomic analysis of *Sinorhizobium meliloti* LPU63, an acid-tolerant and symbiotically efficient alfalfa-nodulating rhizobia

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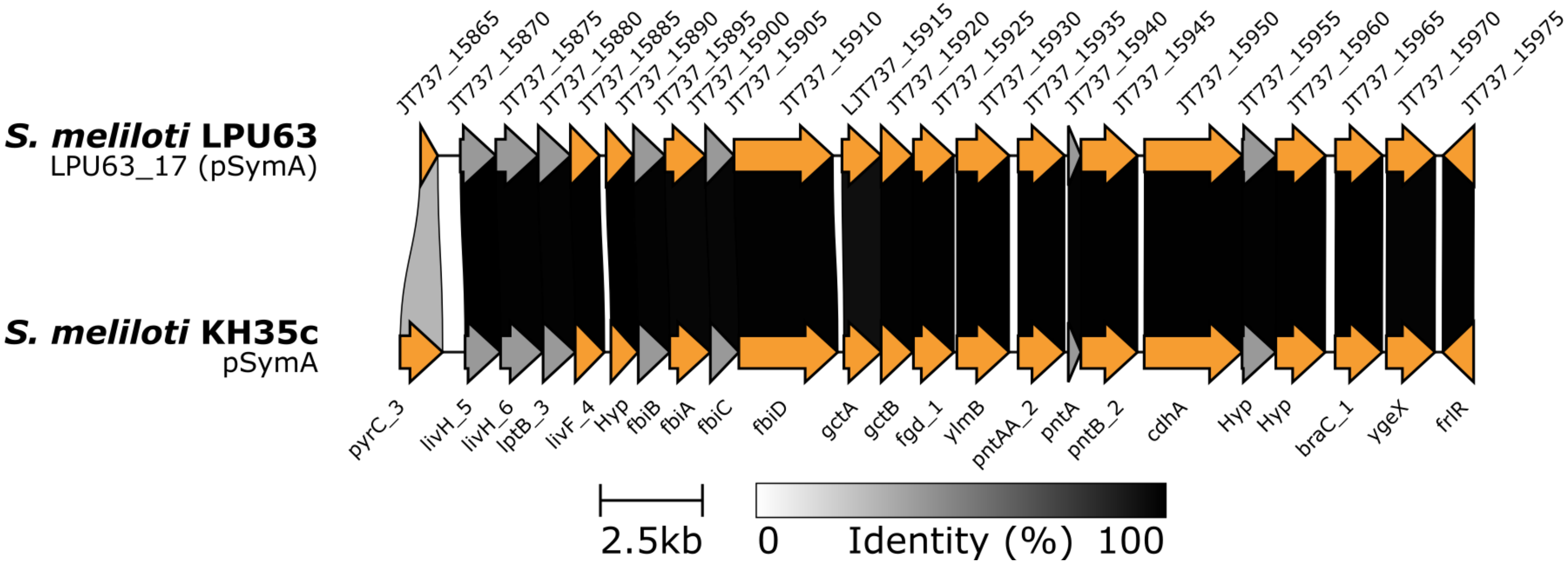
Supplementary material listing



Supplementary Figure 1. *S. meliloti* LPU63 has the competition gene cluster identified by GWAS in *S. meliloti* KH35c. Synteny plot performed with Clinker. The competition gene cluster includes genes involved in the synthesis of the redox cofactor F_{420} (*fbi* operon) and several Bra/Liv type of ABC transporters involved in uptake of branched-chain amino acids. Orange arrows depict genes associated by GWAS with higher nodule occupancy in competition experiments as reported by Bellabarba *et al* (2021).

Supplementary Table 1. Strains and genomes used for the phylogenetic analysis by EDGAR, pan-genome analysis.

Species	Strain	NCBI accession number	Used for
Sinorhizobium alkalisoli	YIC4027 ^{T}	GCA_008932245.1	EDGAR
Sinorhizobium americanum	CFNEI 156 ^{T}	GCA_001651855.1	EDGAR
Sinorhizobium arboris	LMG 14919 ^{T}	GCA_000427465.1	EDGAR
Sinorhizobium fredii	USDA 205 ^{T}	GCA_001461695.1	EDGAR
Sinorhizobium glycinis	CCBAU 23380	GCA_001651865.1	EDGAR
Sinorhizobium medicae	WSM419	GCA_000017145.1	EDGAR
Sinorhizobium meliloti	B399	GCA_002302375.1	EDGAR
Sinorhizobium meliloti	B401	GCA_002302355.1	EDGAR, pan-genome
Sinorhizobium meliloti	1021	GCA_000006965.1	EDGAR
Sinorhizobium meliloti	BL225c	GCA_000147775.3	EDGAR, pan-genome
Sinorhizobium meliloti	GR4	GCA_000320385.2	EDGAR, pan-genome
Sinorhizobium meliloti	Rm41	GCA_000304415.1	EDGAR
Sinorhizobium meliloti	AK83	GCA_000147795.3	EDGAR, pan-genome
Sinorhizobium meliloti	2011	GCA_000346065.1	EDGAR, pan-genome
Sinorhizobium meliloti	SM11	GCA_000218265.1	EDGAR, pan-genome
Sinorhizobium meliloti	KH35c	GCA_002197105.1	EDGAR, pan-genome
Sinorhizobium meliloti	USDA1002 ^{T}	GCA_009601385.1	EDGAR
Sinorhizobium meliloti	KH46	GCA_002197465.1	Pan-genome
Sinorhizobium meliloti	RMO17	GCA_000747295.1	Pan-genome
Sinorhizobium meliloti	HM006	GCA_002197165.1	Pan-genome
Sinorhizobium meliloti	WSM1022	GCA_013315775.1	Pan-genome
Sinorhizobium meliloti	CCMM_B554	GCA_002215195.1	Pan-genome
Sinorhizobium mexicanus	ITTG R7 ^{T}	GCA_013488225.1	EDGAR
Sinorhizobium psoraleae	CCBAU 65732	GCA_013283645.1	EDGAR

Sinorhizobium saheli	LMG 7837 ^{T}	GCA_001651875.1	EDGAR
Ensifer sesbaniae	CCBAU 65729	GCA_013283665.1	EDGAR
Sinorhizobium sojae	CCBAU 05684	GCA_002288525.1	EDGAR
Sinorhizobium terangae	USDA4894	GCA_009601505.1	EDGAR
Ensifer adhaerens	Casida A ^{T}	GCA_000697965.2	EDGAR
Sinorhizobium glycinis	CCBAU 23380	GCA_001651865.1	EDGAR

Supplementary Table 2. Statistical index for the genome assembly of *S. meliloti* LPU63.

Index / Prediction	Value
Quality-filtered reads	710,276
Contigs	178
N50	107,219
Largest conitg length	413,770
Total length	6,931,924
G+C content	62.00%
rRNA genes	1, 1, 1 (5S, 16S, 23S)
tRNA genes	50
Genes	6,702
CDS (total)	6,645
CDS (coding)	6,374

Supplementary Table 3. Mapping of contigs to putative replicons. Contigs with a query coverage below 5% were annotated as not determined (ND)

Contig	Putative replicon
LPU63_1	pSymB
LPU63_2	Chromosome
LPU63_3	pSymB
LPU63_4	Chromosome
LPU63_5	pSymB
LPU63_6	pSymB
LPU63_7	Chromosome
LPU63_8	Chromosome
LPU63_9	Chromosome
LPU63_10	pSymA
LPU63_11	Chromosome
LPU63_12	pSymA
LPU63_13	Chromosome
LPU63_14	Chromosome
LPU63_15	Chromosome
LPU63_16	pSymB
LPU63_17	pSymA
LPU63_18	Chromosome
LPU63_19	Chromosome
LPU63_20	Chromosome
LPU63_21	pSymB
LPU63_22	Chromosome
LPU63_23	Chromosome
LPU63_24	Chromosome
LPU63_25	pSymB
LPU63_26	pSymA
LPU63_27	Chromosome
LPU63_28	Chromosome
LPU63_29	pSymA
LPU63_30	Chromosome

LPU63_31	Chromosome
LPU63_32	pSymB
LPU63_33	Chromosome
LPU63_34	Chromosome
LPU63_35	Chromosome
LPU63_36	pSymA
LPU63_37	Chromosome
LPU63_38	pSymA
LPU63_39	pSymA
LPU63_40	Chromosome
LPU63_41	Chromosome
LPU63_42	Chromosome
LPU63_43	Chromosome
LPU63_44	Accessory plasmid A
LPU63_45	pSymA
LPU63_46	Chromosome
LPU63_47	Chromosome
LPU63_48	Chromosome
LPU63_49	Chromosome
LPU63_50	Chromosome
LPU63_51	pSymA
LPU63_52	Chromosome
LPU63_53	Chromosome
LPU63_54	pSymA
LPU63_55	pSymA
LPU63_56	Accessory plasmid A
LPU63_57	pSymB
LPU63_58	Chromosome
LPU63_59	pSymA
LPU63_60	pSymA
LPU63_61	Accessory plasmid A

LPU63_62	pSymA
LPU63_63	Chromosome
LPU63_64	ND
LPU63_65	Chromosome
LPU63_66	Chromosome
LPU63_67	Chromosome
LPU63_68	pSymA
LPU63_69	pSymA
LPU63_70	pSymA
LPU63_71	Chromosome
LPU63_72	Chromosome
LPU63_73	Chromosome
LPU63_74	Chromosome
LPU63_75	pSymA
LPU63_76	Chromosome
LPU63_77	pSymA
LPU63_78	pSymA
LPU63_79	Chromosome
LPU63_80	Chromosome
LPU63_81	ND
LPU63_82	Chromosome
LPU63_83	pSymA
LPU63_84	pSymA
LPU63_85	pSymA
LPU63_86	pSymA
LPU63_87	Chromosome
LPU63_88	pSymA
LPU63_89	Chromosome
LPU63_90	Chromosome
LPU63_91	Accessory plasmid A
LPU63_92	Chromosome

LPU63_93	ND
LPU63_94	pSymA
LPU63_95	pSymA
LPU63_96	pSymA
LPU63_97	pSymB
LPU63_98	pSymA
LPU63_99	pSymA
LPU63_100	pSymA
LPU63_101	pSymB
LPU63_102	Chromosome
LPU63_103	pSymA
LPU63_104	Chromosome
LPU63_105	pSymA
LPU63_106	pSymA
LPU63_107	pSymA
LPU63_108	pSymA
LPU63_109	Chromosome
LPU63_110	pSymA
LPU63_111	Chromosome
LPU63_112	pSymA
LPU63_113	pSymA
LPU63_114	Chromosome
LPU63_115	ND
LPU63_116	pSymA
LPU63_117	Chromosome
LPU63_118	Chromosome
LPU63_119	pSymA
LPU63_120	pSymA
LPU63_121	ND
LPU63_122	Accessory plasmid A
LPU63_123	pSymA

LPU63_124	pSymA
LPU63_125	Chromosome
LPU63_126	pSymA
LPU63_127	pSymA
LPU63_128	Chromosome
LPU63_129	pSymA
LPU63_130	pSymA
LPU63_131	pSymA
LPU63_132	pSymA
LPU63_133	Chromosome
LPU63_134	ND
LPU63_135	Chromosome
LPU63_136	pSymB
LPU63_137	ND
LPU63_138	pSymA
LPU63_139	pSymA
LPU63_140	pSymA
LPU63_141	pSymA
LPU63_142	Chromosome
LPU63_143	pSymA
LPU63_144	pSymA
LPU63_145	Accessory plasmid A
LPU63_146	Chromosome
LPU63_147	Chromosome
LPU63_148	pSymB
LPU63_149	pSymA
LPU63_150	pSymA
LPU63_151	ND
LPU63_152	pSymB
LPU63_153	pSymA
LPU63_154	ND

LPU63_155	Chromosome
LPU63_156	Chromosome
LPU63_157	pSymA
LPU63_158	pSymA
LPU63_159	Chromosome
LPU63_160	Chromosome
LPU63_161	pSymB
LPU63_162	pSymB
LPU63_163	pSymA
LPU63_164	Accessory plasmid A
LPU63_165	pSymA
LPU63_166	pSymA
LPU63_167	pSymB
LPU63_168	pSymA
LPU63_169	pSymA
LPU63_170	pSymA
LPU63_171	ND
LPU63_172	ND
LPU63_173	pSymA
LPU63_174	pSymA
LPU63_175	pSymB
LPU63_176	pSymA
LPU63_177	Chromosome
LPU63_178	Chromosome

Supplementary Table 4. Contigs mapped to the putative Accessory plasmid A of LPU63.

Contig	Length (kb)	GC %	CDS
LPU63_115	5,313	60.0	5
LPU63_56	32,024	57.2	36
LPU63_93	11,017	59.4	10
LPU63_61	27,532	60.0	13
LPU63_64	26,695	57.3	32
LPU63_81	13,534	57.1	12
LPU63_44	48,632	60.8	47

Supplementary Table 5. Genes involved in plasmid partitioning and replication identified in the Accessory plasmid A putative contigs.

Locus tag	Product	Contig
JT737_28370	Replication protein C	LPU63_56
JT737_28400	Plasmid partitioning protein RepA	LPU63_56
JT737_28405	Plasmid partitioning protein RepB	LPU63_56
JT737_28410	Replication initiation protein RepC	LPU63_56
JT737_25655	Plasmid mobilization relaxosome protein MobC	LPU63_44
JT737_25660	Conjugal transfer protein TraA	LPU63_44
JT737_25760	Type IV secretory system conjugative DNA transfer family protein	LPU63_44
JT737_25775	P-type conjugative transfer protein VirB9	LPU63_44
JT737_25795	Conjugal transfer protein	LPU63_44

Supplementary Table 6. Accession number and product of singletons genes present in the genome of *S. meliloti* LPU63.

LPU63- gene	Annotation
JT737_RS22840	2-hydroxyacid dehydrogenase
JT737_RS29315	3'-5' exonuclease
JT737_RS22810	ABC transporter ATP-binding protein
JT737_RS27890	ABC transporter ATP-binding protein
JT737_RS31760	ABC transporter ATP-binding protein
JT737_RS25705	ABC transporter permease
JT737_RS27895	ABC transporter permease
JT737_RS27900	ABC transporter permease
JT737_RS31750	ABC transporter permease
JT737_RS31755	ABC transporter permease
JT737_RS22825	ABC transporter substrate-binding protein
JT737_RS27905	ABC transporter substrate-binding protein
JT737_RS28225	ABC transporter substrate-binding protein
JT737_RS31745	ABC transporter substrate-binding protein
JT737_RS25635	acetyl-CoA C-acetyltransferase
JT737_RS22730	acetyl-CoA carboxylase biotin carboxylase subunit family protein
JT737_RS22760	acetyl-CoA carboxylase biotin carboxylase subunit family protein
JT737_RS32925	adenylate/guanylate cyclase domain-containing protein
JT737_RS19490	aldehyde dehydrogenase family protein
JT737_RS28265	aldehyde dehydrogenase family protein
JT737_RS25640	aldo/keto reductase
JT737_RS25660	alkene reductase
JT737_RS25675	alpha/beta fold hydrolase
JT737_RS25650	alpha/beta hydrolase
JT737_RS32255	amidohydrolase

JT737_RS28250	aminotransferase
JT737_RS30930	anti-phage dCTP deaminase
JT737_RS27645	Arc family DNA-binding protein
JT737_RS27650	Arc family DNA-binding protein
JT737_RS30630	aromatic ring-hydroxylating dioxygenase subunit alpha
JT737_RS27475	ASCH domain-containing protein
JT737_RS22870	aspartate kinase
JT737_RS32390	aspartate-semialdehyde dehydrogenase
JT737_RS25710	ATP-binding cassette domain-containing protein
JT737_RS28305	ATP-binding protein
JT737_RS32720	ATP-dependent DNA ligase
JT737_RS22710	autoinducer binding domain-containing protein
JT737_RS31965	autoinducer binding domain-containing protein
JT737_RS28275	CaiB/BaiF CoA-transferase family protein
JT737_RS31770	CapA family protein
JT737_RS22820	carbohydrate ABC transporter permease
JT737_RS27920	class I SAM-dependent methyltransferase
JT737_RS28005	class I SAM-dependent methyltransferase
JT737_RS33195	co-chaperone GroES
JT737_RS28270	CoA ester lyase
JT737_RS25630	conjugal transfer protein TraA
JT737_RS32345	cytochrome P450
JT737_RS08640	D-alanyl-D-alanine carboxypeptidase family protein
JT737_RS27995	DEAD/DEAH box helicase family protein
JT737_RS22875	DegT/DnrJ/EryC1/StrS family aminotransferase
JT737_RS22770	diaminobutyrate--2-oxoglutarate transaminase

JT737_RS28970	dienelactone hydrolase-related enzyme
JT737_RS31765	dipeptide ABC transporter ATP-binding protein
JT737_RS22850	DMT family transporter
JT737_RS27480	DNA polymerase III subunit beta
JT737_RS10995	DNA-binding protein
JT737_RS20965	DUF1254 domain-containing protein
JT737_RS20970	DUF1254 domain-containing protein
JT737_RS33080	DUF2163 domain-containing protein
JT737_RS28955	DUF2235 domain-containing protein
JT737_RS27485	DUF2303 family protein
JT737_RS08660	DUF3168 domain-containing protein
JT737_RS30925	DUF3606 domain-containing protein
JT737_RS27980	DUF4062 domain-containing protein
JT737_RS31930	DUF5372 family protein
JT737_RS32230	DUF5372 family protein
JT737_RS17820	DUF6065 family protein
JT737_RS33485	DUF6065 family protein
JT737_RS10980	DUF6074 family protein
JT737_RS27965	DUF982 domain-containing protein
JT737_RS28360	Fic family protein
JT737_RS11985	formate dehydrogenase
JT737_RS28260	fumarate hydratase
JT737_RS28220	gamma-glutamyl-gamma-aminobutyrate hydrolase family protein
JT737_RS23765	GcrA cell cycle regulator
JT737_RS08695	gene transfer agent family protein
JT737_RS25720	Gfo/Idh/MocA family oxidoreductase

JT737_RS19485	glutamine--fructose-6-phosphate transaminase (isomerizing)
JT737_RS22855	GMC family oxidoreductase
JT737_RS27580	gpW family head-tail joining protein
JT737_RS32780	group II intron reverse transcriptase/maturase
JT737_RS22835	HAD family phosphatase
JT737_RS32790	HAMP domain-containing sensor histidine kinase
JT737_RS30940	HD domain-containing protein
JT737_RS27600	head decoration protein
JT737_RS19180	head-tail adaptor protein
JT737_RS08670	head-tail connector protein
JT737_RS27515	helix-turn-helix domain-containing protein
JT737_RS31950	helix-turn-helix domain-containing protein
JT737_RS32225	helix-turn-helix domain-containing protein
JT737_RS10930	helix-turn-helix transcriptional regulator
JT737_RS19345	helix-turn-helix transcriptional regulator
JT737_RS32515	HEPN domain-containing protein
JT737_RS19155	HK97 family phage prohead protease
JT737_RS08665	HK97 gp10 family phage protein
JT737_RS19185	HK97 gp10 family phage protein
JT737_RS08680	HNH endonuclease signature motif containing protein
JT737_RS28020	homocysteine S-methyltransferase family protein
JT737_RS25685	HTH domain-containing protein
JT737_RS25715	hydroxypyruvate isomerase family protein
JT737_RS11005	integrase arm-type DNA-binding domain-containing protein
JT737_RS33245	IS110 family transposase
JT737_RS22795	IS3 family transposase

JT737_RS33410	IS630-like element ISRm10 family transposase
JT737_RS32805	IS66 family insertion sequence element accessory protein TnpB
JT737_RS22885	IS701 family transposase
JT737_RS33260	ISNCY family transposase
JT737_RS25695	LacI family DNA-binding transcriptional regulator
JT737_RS31615	lipopolysaccharide biosynthesis protein
JT737_RS28255	Lrp/AsnC family transcriptional regulator
JT737_RS33450	LuxR C-terminal-related transcriptional regulator
JT737_RS32395	LuxR family transcriptional regulator
JT737_RS28285	LysR family transcriptional regulator
JT737_RS28295	LysR family transcriptional regulator
JT737_RS28300	LysR substrate-binding domain-containing protein
JT737_RS25790	lytic transglycosylase domain-containing protein
JT737_RS27605	major capsid protein
JT737_RS22750	MATE family efflux transporter
JT737_RS28280	methylaspartate ammonia-lyase
JT737_RS32350	multicopper oxidase family protein
JT737_RS22805	MurR/RpiR family transcriptional regulator
JT737_RS25725	MurR/RpiR family transcriptional regulator
JT737_RS25690	myo-inosose-2 dehydratase
JT737_RS30950	N-6 DNA methylase
JT737_RS25980	NAD(P)-binding domain-containing protein
JT737_RS25990	NAD(P)-binding domain-containing protein
JT737_RS25655	NADP-dependent oxidoreductase
JT737_RS32760	nodulation protein NodN
JT737_RS19315	non-homologous end-joining DNA ligase

JT737_RS25595	non-homologous end-joining DNA ligase
JT737_RS22865	nucleoside-diphosphate kinase
JT737_RS28990	ornithine cyclodeaminase family protein
JT737_RS28000	PAN domain-containing protein
JT737_RS19960	PAS domain S-box protein
JT737_RS23735	PBSX family phage terminase large subunit
JT737_RS08655	phage head closure protein
JT737_RS19170	phage head-tail connector protein
JT737_RS08690	phage major capsid protein
JT737_RS19160	phage major capsid protein
JT737_RS08700	phage portal protein
JT737_RS19150	phage portal protein
JT737_RS27585	phage portal protein
JT737_RS23635	phage tail length tape measure family protein
JT737_RS19195	phage tail tube protein
JT737_RS27575	phage terminase large subunit family protein
JT737_RS08650	phage terminase small subunit P27 family
JT737_RS19140	phage terminase small subunit P27 family
JT737_RS27555	phage/plasmid primase%2C P4 family
JT737_RS22830	phosphodiesterase
JT737_RS33335	phosphopantetheine-binding protein
JT737_RS25625	plasmid mobilization relaxosome protein MobC
JT737_RS28380	plasmid replication protein RepC
JT737_RS27190	potassium transporter Kup
JT737_RS28320	PTS sugar transporter subunit IIA
JT737_RS28325	PTS sugar transporter subunit IIA

JT737_RS19290	Rap1a/Tai family immunity protein
JT737_RS29415	recombinase family protein
JT737_RS32215	recombinase family protein
JT737_RS33200	recombinase zinc beta ribbon domain-containing protein
JT737_RS22900	redoxin domain-containing protein
JT737_RS32480	response regulator
JT737_RS22895	response regulator transcription factor
JT737_RS32795	response regulator transcription factor
JT737_RS27660	Rha family transcriptional regulator
JT737_RS27590	S49 family peptidase
JT737_RS17645	SDR family oxidoreductase
JT737_RS25665	SDR family oxidoreductase
JT737_RS32475	sensor histidine kinase
JT737_RS27495	single-stranded DNA-binding protein
JT737_RS27530	site-specific DNA-methyltransferase
JT737_RS08705	site-specific integrase
JT737_RS22815	sugar ABC transporter permease
JT737_RS25700	sugar ABC transporter substrate-binding protein
JT737_RS33320	sulfatase-like hydrolase/transferase
JT737_RS27945	sulfate adenylyltransferase subunit CysD
JT737_RS27950	sulfate adenylyltransferase subunit CysN
JT737_RS27880	sulfotransferase family 2 domain-containing protein
JT737_RS25820	T6SS effector amidase Tae4 family protein
JT737_RS32825	tail fiber domain-containing protein
JT737_RS19215	tape measure protein
JT737_RS27910	TauD/TfdA family dioxygenase

JT737_RS08645	terminase large subunit
JT737_RS19145	terminase large subunit
JT737_RS23740	terminase small subunit
JT737_RS25670	TetR/AcrR family transcriptional regulator
JT737_RS01360	tetratricopeptide repeat protein
JT737_RS25805	thermonuclease family protein
JT737_RS32410	TlpA disulfide reductase family protein
JT737_RS27975	transcriptional regulator
JT737_RS28025	transposase
JT737_RS31330	transposase domain-containing protein
JT737_RS30965	type II toxin-antitoxin system VapB family antitoxin
JT737_RS30970	type II toxin-antitoxin system VapC family toxin
JT737_RS22745	tyrosine-type recombinase/integrase
JT737_RS27460	tyrosine-type recombinase/integrase
JT737_RS31735	tyrosine-type recombinase/integrase
JT737_RS32385	uridylate kinase
JT737_RS28545	VOC family protein
JT737_RS25600	WGR domain-containing protein
JT737_RS28215	Xaa-Pro peptidase family protein

Supplementary Table 6 - Continuation

LPU63- genes	Annotated as hypothetical protein

JT737_RS33445, JT737_RS33445, JT737_RS08600, JT737_RS08605, JT737_RS33470, JT737_RS08610, JT737_RS08615, JT737_RS08620, JT737_RS08625, JT737_RS08630, JT737_RS08635, JT737_RS08675, JT737_RS08685, JT737_RS08990, JT737_RS10915, JT737_RS10920, JT737_RS10925, JT737_RS10935, JT737_RS10940, JT737_RS10945, JT737_RS10950, JT737_RS10955, JT737_RS10960, JT737_RS10965, JT737_RS10970, JT737_RS10975, JT737_RS10985, JT737_RS10990, JT737_RS11000, JT737_RS33475, JT737_RS19090, JT737_RS19115, JT737_RS19130, JT737_RS19135, JT737_RS19165, JT737_RS19175, JT737_RS19210, JT737_RS19220, JT737_RS19225, JT737_RS19235,

JT737_RS19245, JT737_RS19250, JT737_RS19255, JT737_RS19260, JT737_RS19265, JT737_RS19270, JT737_RS19280, JT737_RS19285, JT737_RS19295, JT737_RS19300, JT737_RS19305, JT737_RS19320, JT737_RS19325, JT737_RS19335, JT737_RS19340, JT737_RS19360, JT737_RS19365, JT737_RS19370, JT737_RS19375, JT737_RS20960, JT737_RS21150, JT737_RS22735, JT737_RS22740, JT737_RS22755, JT737_RS22765, JT737_RS22845, JT737_RS22860, JT737_RS22890, JT737_RS23650, JT737_RS23725, JT737_RS23745, JT737_RS23750, JT737_RS23785, JT737_RS33495, JT737_RS25610, JT737_RS25680, JT737_RS25810, JT737_RS25815, JT737_RS25825, JT737_RS25875, JT737_RS25925, JT737_RS25930, JT737_RS33520, JT737_RS27150, JT737_RS27160, JT737_RS27170, JT737_RS27180, JT737_RS27185, JT737_RS27465, JT737_RS27470, JT737_RS27490, JT737_RS27500, JT737_RS27505, JT737_RS27510, JT737_RS27520, JT737_RS27525, JT737_RS27535, JT737_RS27540, JT737_RS27545, JT737_RS27550, JT737_RS27560, JT737_RS27565, JT737_RS27570, JT737_RS27595, JT737_RS27610, JT737_RS27620, JT737_RS27625, JT737_RS27655, JT737_RS33530, JT737_RS27665, JT737_RS33535, JT737_RS27875, JT737_RS27915, JT737_RS27930, JT737_RS27970, JT737_RS27985, JT737_RS28230, JT737_RS28310, JT737_RS28330, JT737_RS28335, JT737_RS28940, JT737_RS28945, JT737_RS28950, JT737_RS28960, JT737_RS28965, JT737_RS28975, JT737_RS28980, JT737_RS29350, JT737_RS29410, JT737_RS30920, JT737_RS30935, JT737_RS30945, JT737_RS30955, JT737_RS31140, JT737_RS33545, JT737_RS31265, JT737_RS31625, JT737_RS31640, JT737_RS31645, JT737_RS31945, JT737_RS31970, JT737_RS32220, JT737_RS32250, JT737_RS32340, JT737_RS33560, JT737_RS32505, JT737_RS32510, JT737_RS32575, JT737_RS32580, JT737_RS32680, JT737_RS33210, JT737_RS33220, JT737_RS33280, JT737_RS33360

Supplementary Table 7. BLASTp analysis of nodulation proteins identified in the genome of *S. meliloti* LPU63.

Gene	Locus tag LPU63	Locus tag 1021	Query cover	E-value	Percent identity	Contig	Putative Replicon
*nod*D2	JT737_33300	SMa0757	100%	0	99.40%	LPU63_144	pSymA
*nod*L	JT737_30570	SMa0772	100%	9.00E-133	98.40%	LPU63_75	pSymA
*noe*A	JT737_30580	SMa0773	100%	0	99.20%	LPU63_75	pSymA
*noe*B	JT737_30585	SMa0774	100%	0	98.70%	LPU63_75	pSymA
*nod*D3	JT737_30020	SMa0840	100%	0	99.40%	LPU63_69	pSymA
*nod*H	JT737_30035	SMa0841	100%	0	97.60%	LPU63_69	pSymA
syrM	JT737_30030	SMa0849	100%	0	99.10%	LPU63_69	pSymA
*nod*F	JT737_30040	SMa0852	100%	9.00E-61	100.00%	LPU63_69	pSymA
*nod*E	JT737_30045	SMa0853	100%	0	99.30%	LPU63_69	pSymA
*nod*G	JT737_30050	SMa0854	100%	0	99.60%	LPU63_69	pSymA

*nod*P1	JT737_30055	SMa0855	100%	0	99.70%	LPU63_69	pSymA
*nod*Q1	JT737_30060	SMa0857	98%	0	99.10%	LPU63_69	pSymA
*nod*J	JT737_32185	SMa0863	100%	0	99.60%	LPU63_100	pSymA
*nod*I	JT737_32180	SMa0864	100%	0	96.60%	LPU63_100	pSymA
*nod*C	JT737_32175	SMa0866	100%	0	96.00%	LPU63_100	pSymA
*nod*B	JT737_32170	SMa0868	100%	2.00E-158	97.70%	LPU63_100	pSymA
*nod*A	JT737_32165	SMa0869	100%	2.00E-144	98.50%	LPU63_100	pSymA
*nod*D1	JT737_32160	SMa0870	100%	0	97.70%	LPU63_100	pSymA
*nol*G	JT737_32830	SMa0875	100%	0	99.90%	LPU63_119	pSymA
*nol*F	JT737_32835	SMa0876	100%	0	100.00%	LPU63_119	pSymA
*nod*M	JT737_19495	SMa0878	95%	0	99.10%	LPU63_24	Chromosome
*nfe*D	JT737_07840	SMb20990	96%	0	99.80%	LPU63_6	pSymB
*nod*Q2	JT737_27975	SMb21224	94%	0	57.40%	LPU63_54	pSymA
*nod*N2	JT737_05490	SMc03927	100%	3.00E-120	98.80%	LPU63_4	Chromosome

Supplementary Table 8. BLASTp analysis of nitrogen fixation proteins identified in the genome of *S. meliloti* LPU63.

Gene	Locus tag LPU63	Locus tag 1021	Query cover	E-value	Percent identity	Contig	Putative Replicon
*fix*N3	JT737_21245	SMa0612	100%	0	98.40%	LPU63_29	pSymA
*fix*O3	JT737_21250	SMa0615	100%	0	98.40%	LPU63_29	pSymA
*fix*Q3	JT737_21255	SMa0616	100%	7.00E-37	92.90%	LPU63_29	pSymA
*fix*P3	JT737_21260	SMa0617	100%	0	96.30%	LPU63_29	pSymA
*fix*I2	JT737_21275	SMa0621	100%	0	97.20%	LPU63_29	pSymA
*fix*S2	JT737_21280	SMa0622	100%	1.00E-59	100.00%	LPU63_29	pSymA
*fix*T2	JT737_30535	SMa0760	100%	5.00E-58	76.50%	LPU63_75	pSymA
*fix*K2	JT737_30540	SMa0762	100%	3.00E-149	94.80%	LPU63_75	pSymA
*fix*N2	JT737_30545	SMa0765	100%	0	98.50%	LPU63_75	pSymA
*fix*O2	JT737_30550	SMa0766	100%	0	98.40%	LPU63_75	pSymA

*fix*Q2	JT737_30555	SMa0767	100%	2.00E-30	94.00%	LPU63_75	pSymA
*fix*P2	JT737_30560	SMa0769	100%	0	97.90%	LPU63_75	pSymA
*nif*T	JT737_31340	SMa0810	100%	4.00E-46	100.00%	LPU63_86	pSymA
*nif*B	JT737_31330	SMa0814	100%	0	99.60%	LPU63_86	pSymA
*nif*A	JT737_31325	SMa0815	100%	0	96.30%	LPU63_86	pSymA
*fix*X	JT737_31320	SMa0816	100%	2.00E-71	99.00%	LPU63_86	pSymA
*fix*C	JT737_31315	SMa0817	100%	0	99.80%	LPU63_86	pSymA
*fix*B	JT737_31310	SMa0819	100%	0	99.20%	LPU63_86	pSymA
*fix*A	JT737_31305	SMa0822	80%	2.00E-166	97.50%	LPU63_86	pSymA
*nif*H	JT737_29975	SMa0825	100%	0	100.00%	LPU63_69	pSymA
*nif*D	JT737_29980	SMa0827	100%	0	100.00%	LPU63_69	pSymA
*nif*K	JT737_29985	SMa0829	100%	0	99.60%	LPU63_69	pSymA
*nif*E	JT737_29990	SMa0830	100%	0	98.30%	LPU63_69	pSymA
*nif*X	JT737_29995	SMa0831	98%	3.00E-117	97.00%	LPU63_69	pSymA
*nif*N	JT737_32155	SMa0873	100%	0	100.00%	LPU63_100	pSymA
*fix*S1	JT737_12995	SMa1208	100%	2.00E-34	100.00%	LPU63_12	pSymA
*fix*I1	JT737_12990	SMa1209	100%	0	99.90%	LPU63_12	pSymA
*fix*H	JT737_12985	SMa1210	100%	5.00E-124	100.00%	LPU63_12	pSymA
*fix*G	JT737_12980	SMa1211	100%	0	99.80%	LPU63_12	pSymA
*fix*P1	JT737_12975	SMa1213	100%	0	99.70%	LPU63_12	pSymA
*fix*Q1	JT737_12970	SMa1214	100%	5.00E-33	100.00%	LPU63_12	pSymA
*fix*O1	JT737_12965	SMa1216	100%	0	100.00%	LPU63_12	pSymA
*fix*N1	JT737_12960	SMa1220	100%	0	100.00%	LPU63_12	pSymA
*fix*M	JT737_12955	SMa1223	100%	5.00E-115	100.00%	LPU63_12	pSymA
*fix*K1	JT737_12950	SMa1225	100%	4.00E-157	99.50%	LPU63_12	pSymA
*fix*T1	JT737_12945	SMa1226	100%	2.00E-78	98.30%	LPU63_12	pSymA
*fix*J	JT737_12940	SMa1227	100%	2.00E-149	100.00%	LPU63_12	pSymA
*fix*L	JT737_12935	SMa1229	100%	0	99.80%	LPU63_12	pSymA
*nif*S	JT737_23295	SMc00529	100%	0	99.20%	LPU63_35	Chromosome
*nif*U	JT737_16335	SMc01119	100%	5.00E-144	99.50%	LPU63_18	Chromosome

Supplementary Table 9. Predicted Secretion Systems by TXSScan.

Locus tag	Predicted Gene	Predicted System	Contig	Putative Replicon
JT737_12685	T4SS_T_virB1	T4SS_typeT	LPU63_12	pSymA
JT737_12690	T4SS_T_virB2	T4SS_typeT	LPU63_12	pSymA
JT737_12695	T4SS_T_virB3	T4SS_typeT	LPU63_12	pSymA
JT737_12705	T4SS_T_virB5	T4SS_typeT	LPU63_12	pSymA
JT737_12715	T4SS_T_virB6	T4SS_typeT	LPU63_12	pSymA
JT737_12725	T4SS_T_virB8	T4SS_typeT	LPU63_12	pSymA
JT737_12730	T4SS_T_virB9	T4SS_typeT	LPU63_12	pSymA
JT737_12735	T4SS_T_virB10	T4SS_typeT	LPU63_12	pSymA
JT737_14565	T1SS_omf	T1SS	LPU63_15	Chromosome
JT737_14910	T1SS_mfp	T1SS	LPU63_15	Chromosome
JT737_14915	T1SS_abc	T1SS	LPU63_15	Chromosome
JT737_20780	T4SS_T_virB1	T4SS_typeT	LPU63_28	Chromosome
JT737_03350	T5aSS_PF03797	T5aSS	LPU63_2	Chromosome
JT737_03630	T1SS_abc	T1SS	LPU63_2	Chromosome
JT737_22530	Flg_sctN_FLG	Flagellum	LPU63_33	Chromosome
JT737_22540	Flg_sctN_FLG	Flagellum	LPU63_33	Chromosome
JT737_27040	T6SSi_tssH	T6SSi	LPU63_50	Chromosome
JT737_27105	Tad_flp	Tad	LPU63_50	Chromosome
JT737_21120	T5aSS_PF03797	T5aSS	LPU63_29	pSymA
JT737_26675	T1SS_abc	T1SS	LPU63_48	Chromosome
JT737_00055	T1SS_abc	T1SS	LPU63_1	pSymB
JT737_00935	T1SS_mfp	T1SS	LPU63_1	pSymB
JT737_20510	T3SS_sctN	T3SS	LPU63_28	Chromosome
JT737_19920	T1SS_mfp	T1SS	LPU63_25	pSymB
JT737_19925	T1SS_abc	T1SS	LPU63_25	pSymB
JT737_05000	T1SS_mfp	T1SS	LPU63_4	Chromosome

JT737_05005	T1SS_abc	T1SS	LPU63_4	Chromosome
JT737_05915	T1SS_abc	T1SS	LPU63_4	Chromosome
JT737_31835	T4SS_T_virB1	T4SS_typeT	LPU63_94	pSymA
JT737_31840	T4SS_T_virB2	T4SS_typeT	LPU63_94	pSymA
JT737_31845	T4SS_T_virB3	T4SS_typeT	LPU63_94	pSymA
JT737_31860	T4SS_T_virB6	T4SS_typeT	LPU63_94	pSymA
JT737_31870	T4SS_T_virB8	T4SS_typeT	LPU63_94	pSymA
JT737_31875	T4SS_T_virB9	T4SS_typeT	LPU63_94	pSymA
JT737_31880	T4SS_T_virB10	T4SS_typeT	LPU63_94	pSymA
JT737_22285	Tad_tadZ	Tad	LPU63_32	pSymB
JT737_24490	Tad_tadV	Tad	LPU63_39	pSymA
JT737_24500	Tad_tadZ	Tad	LPU63_39	pSymA
JT737_24510	Tad_flp	Tad	LPU63_39	pSymA
JT737_24515	Tad_tadA	Tad	LPU63_39	pSymA
JT737_24520	Tad_tadB	Tad	LPU63_39	pSymA
JT737_24525	Tad_tadC	Tad	LPU63_39	pSymA
JT737_09135	Flg_sctT_FLG	Flagellum	LPU63_7	Chromosome
JT737_09140	Flg_sctV_FLG	Flagellum	LPU63_7	Chromosome
JT737_09145	Flg_sctS_FLG	Flagellum	LPU63_7	Chromosome
JT737_09185	T4SS_T_virB1	T4SS_typeT	LPU63_7	Chromosome
JT737_09225	Flg_sctR_FLG	Flagellum	LPU63_7	Chromosome
JT737_09260	Flg_fliE	Flagellum	LPU63_7	Chromosome
JT737_09265	Flg_flgC	Flagellum	LPU63_7	Chromosome
JT737_09270	Flg_flgB	Flagellum	LPU63_7	Chromosome
JT737_09280	Flg_sctN_FLG	Flagellum	LPU63_7	Chromosome
JT737_09305	Flg_sctQ_FLG	Flagellum	LPU63_7	Chromosome
JT737_09315	Flg_sctU_FLG	Flagellum	LPU63_7	Chromosome
JT737_09335	Flg_sctJ_FLG	Flagellum	LPU63_7	Chromosome
JT737_11780	Tad_rcpA	Tad	LPU63_10	pSymA
JT737_15215	T1SS_mfp	T1SS	LPU63_16	pSymB

JT737_14260	T1SS_abc	T1SS	LPU63_14	Chromosome
JT737_14325	Tad_tadC	Tad	LPU63_14	Chromosome
JT737_14330	Tad_tadB	Tad	LPU63_14	Chromosome
JT737_14335	Tad_tadA	Tad	LPU63_14	Chromosome
JT737_14340	Tad_tadZ	Tad	LPU63_14	Chromosome
JT737_14350	Tad_rcpA	Tad	LPU63_14	Chromosome
JT737_14360	Tad_tadV	Tad	LPU63_14	Chromosome
JT737_14365	Tad_flp	Tad	LPU63_14	Chromosome
JT737_14375	Tad_flp	Tad	LPU63_14	Chromosome
JT737_17380	Tad_tadE	Tad	LPU63_20	Chromosome
JT737_17525	T1SS_abc	T1SS	LPU63_20	Chromosome
JT737_17530	T1SS_abc	T1SS	LPU63_20	Chromosome
JT737_25765	Tad_tadA	Tad	LPU63_44	Acc. plasmid A
JT737_25770	T4SS_T_virB10	T4SS_typeT	LPU63_44	Acc. plasmid A
JT737_25775	T4SS_T_virB9	T4SS_typeT	LPU63_44	Acc. plasmid A
JT737_25780	T4SS_T_virB8	T4SS_typeT	LPU63_44	Acc. plasmid A
JT737_25785	T4SS_T_virB6	T4SS_typeT	LPU63_44	Acc. plasmid A
JT737_25810	T4SS_T_virB3	T4SS_typeT	LPU63_44	Acc. plasmid A
JT737_25815	T4SS_T_virB2	T4SS_typeT	LPU63_44	Acc. plasmid A
JT737_24940	T1SS_mfp	T1SS	LPU63_41	Chromosome
JT737_03840	T1SS_abc	T1SS	LPU63_3	pSymB
JT737_04255	T1SS_abc	T1SS	LPU63_3	pSymB
JT737_04410	T1SS_mfp	T1SS	LPU63_3	pSymB
JT737_04415	T1SS_abc	T1SS	LPU63_3	pSymB
JT737_08080	T1SS_abc	T1SS	LPU63_6	pSymB
JT737_10515	T1SS_omf	T1SS	LPU63_9	Chromosome
JT737_30355	T1SS_abc	T1SS	LPU63_73	Chromosome

Table S10. Rhizobial genes involved in acid tolerance or upregulated in acidic conditions.

Gene	Function	Organism	Reference	LPU63 locus tag	Query Cover	Per. Ident
*phr*R	Stress response (low pH, and high concentrations of Zn^{2+}, Cu^{+}, H_2O_2 or ethanol)	*S. medicae*	(Reeve et al., 1998)	JT737_16380	100%	100.00%
*gsh*B	Glutathione synthetase, essential to grow in extreme conditions (acid, osmotic or oxidative stress)	*R. tropici*	(Riccillo et al., 2000)	JT737_21300	100%	86.03%
*exo*H	Synthesis of exopolysaccharides (succinylation of EPS), essential to grow in acidity and in the presence of Zn^{2+}	*S. medicae*	(Glenn et al., 1999)	JT737_08015	99%	94.05%
*exo*R	EPS synthesis regulator	*R. leguminosarun* bv. viciae	(Reeve et al., 1997)	JT737_14585	100%	70.04%
*act*A	Internal pH control in relation to Ca^{2+} concentrations	*S. meliloti*	(Tiwari et al., 1996a)	JT737_16375	100%	99.81%
*act*P	Control of Cu^{+} homeostasis and essential to grow in acidic conditions	*R. leguminosarum* bv. viciae	(Reeve et al., 2002)	No hit		
*act*S	Response to acidic pH	*S. medicae*	(Tiwari et al., 1996b)	JT737_29700	100%	94.92%
*act*R	Response to acidic pH	*S. medicae*	(Tiwari et al., 1996b)	JT737_29695	100%	97.94%
*lpi*A	Sulfate permease that is induced at low pH	*S. medicae*	(Glenn et al., 1999)	JT737_18400	99%	83.20%
*deg*P1	Protease	*S. medicae*	(Reeve et al., 2004)	JT737_03145	100%	99.60%
*clp*P2	Protease	*S. medicae*	(Reeve et al., 2004)	JT737_26575	100%	100%
*gro*ES1	Chaperone	*S. medicae*	(Reeve et al., 2004)	JT737_33265	100%	100%
SMb21377	ABC transport system	*S. medicae*	(Reeve et al., 2004)	JT737_04710	100%	100%
mdh	Malate dehydrogenase	*S. medicae*	(Reeve et al., 2004)	JT737_22640	100%	100%
*wrb*A1	NAD(P)H dehydrogenase	*S. medicae*	(Reeve et al., 2004)	JT737_24675	100%	100%

SMb20317	ABC transport system (carbohydrates)	*S. medicae*	(Tiwari et al., 2004)	JT737_01315	100%	99.61%
SMa0199	ABC transport system (carbohydrates)	*S. medicae*	(Tiwari et al., 2004)	JT737_11660	99%	98.77%
SMb21240	Surface polysaccharide export protein	*S. medicae*	(Tiwari et al., 2004)	JT737_03705	100%	99.09%
*kdp*B	K^+ importing ATPase	*S. medicae*	(Tiwari et al., 2004)	JT737_15835	100%	96.47%
*kdp*C	K^+ importing ATPase	*S. medicae*	(Tiwari et al., 2004)	JT737_15840	100%	91.53%
*fix*N2	Cytochrome cbb3 oxidase	*S. medicae*	(Tiwari et al., 2004)	JT737_30545	100%	98.52%
*fix*O2	Cytochrome cbb3 oxidase	*S. medicae*	(Tiwari et al., 2004)	JT737_30550	100%	98.35%
*act*J	Tolerance to acidic pH and ATR	*S. meliloti*	(Albicoro et al., 2021)	JT737_03150	98%	100.00%
*act*K	Tolerance to acidic pH and ATR	*S. meliloti*	(Albicoro et al., 2021)	JT737_03155	100%	99.57%

Supplementary Table 11. BLASTp analysis of denitrifying proteins identified in the genome of *S. meliloti* LPU63.

Gene	Locus tag LPU63	Locus tag 1021	Query cover	E-value	Percent identity	Contig	Putative Replicon
*nap*C	JT737_12925	SMa1232	100%	2.00E-177	99.60%	LPU63_12	pSymA
*nap*B	JT737_12920	SMa1233	94%	9.00E-119	100.00%	LPU63_12	pSymA
*nap*A	JT737_12915	SMa1236	100%	0	100.00%	LPU63_12	pSymA
*nap*D	JT737_12910	SMa1239	100%	1.00E-65	100.00%	LPU63_12	pSymA
*nap*F	JT737_12905	SMa1240	100%	2.00E-118	99.40%	LPU63_12	pSymA
*nap*E	JT737_12900	SMa1241	100%	5.00E-40	100.00%	LPU63_12	pSymA
*nir*K	JT737_12880	SMa1250	100%	0	100.00%	LPU63_12	pSymA
*nir*V	JT737_12885	SMa1247	100%	0	100.00%	LPU63_12	pSymA
*nor*D	JT737_12830	SMa1269	100%	0	99.80%	LPU63_12	pSymA
*nor*Q	JT737_12825	SMa1272	100%	0	100.00%	LPU63_12	pSymA
*nor*B	JT737_12820	SMa1273	100%	0	99.80%	LPU63_12	pSymA

*nor*C	JT737_12815	SMa1276	100%	1.00E-113	100.00%	LPU63_12	pSymA
*nor*E	JT737_12805	SMa1279	97%	5.00E-128	100.00%	LPU63_12	pSymA
*nos*R	JT737_13070	SMa1179	100%	0	99.50%	LPU63_12	pSymA
*nos*Z	JT737_13065	SMa1182	100%	0	100.00%	LPU63_12	pSymA
*nos*D	JT737_13060	SMa1183	100%	0	100.00%	LPU63_12	pSymA
*nos*F	JT737_13055	SMa1184	100%	0	99.30%	LPU63_12	pSymA
*nos*Y	JT737_13050	SMa1185	100%	0	99.30%	LPU63_12	pSymA
*nos*L	JT737_13045	SMa1186	100%	2.00E-136	99.50%	LPU63_12	pSymA
*nos*X	JT737_13040	SMa1188	100%	0	99.40%	LPU63_12	pSymA
*nnr*U	JT737_12795	SMa1283	100%	1.00E-161	100.00%	LPU63_12	pSymA

Supplementary Table 12. Accession number and product of the genes involved in phenylacetic acid (PAA) degradation present in the genome of *S. meliloti* LPU63 and related rhizobia.

	***S. meliloti* LPU63**			***S. meliloti* 1021**		***S. medicae* WSM419**	
Gene	**Locus tag**	**Contig**	**Putative Replicon**	**Locus tag**	**Replicon**	**Locus tag**	**Replicon**
*paa*X	JT737_07105	LPU63_5	pSymB	SM_b21641	pSymB	Smed_4146	pSMED01
*paa*A	JT737_07110	LPU63_5	pSymB	SM_b21640	pSymB	Smed_4147	pSMED01
*paa*B	JT737_07115	LPU63_5	pSymB	SM_b21639	pSymB	Smed_4148	pSMED01
*paa*C	JT737_07120	LPU63_5	pSymB	SM_b21638	pSymB	Smed_4149	pSMED01
*paa*D	JT737_07125	LPU63_5	pSymB	SM_b21637	pSymB	Smed_4150	pSMED01
*paa*E	JT737_07130	LPU63_5	pSymB	SM_b21636	pSymB	Smed_4151	pSMED01
*paa*Z	JT737_07135	LPU63_5	pSymB	SM_b21635	pSymB	Smed_4152	pSMED01
*paa*G	JT737_07145	LPU63_5	pSymB	SM_b21633	pSymB	Smed_4154	pSMED01
*paa*H	JT737_07150	LPU63_5	pSymB	SM_b21632	pSymB	Smed_4155	pSMED01

S. fredii NGR234	*S. americanum* CCGM7

Gene	Locus tag	Replicon	Locus tag	Replicon
*paa*A	NGR_c26190	Chromosome	SAMCCGM7_Ch2795	Chromosome
*paa*B	NGR_c26180	Chromosome	SAMCCGM7_Ch2794	Chromosome
*paa*C	NGR_c26170	Chromosome	SAMCCGM7_Ch2793	Chromosome
*paa*D	NGR_c26160	Chromosome	SAMCCGM7_Ch2792	Chromosome
*paa*E	NGR_c26150	Chromosome	SAMCCGM7_Ch2791	Chromosome
*paa*Z	NGR_c26130	Chromosome	SAMCCGM7_Ch2789	Chromosome
*paa*G	NGR_c26090	Chromosome	SAMCCGM7_Ch2785	Chromosome
*paa*H	NGR_c26080	Chromosome	SAMCCGM7_Ch2784	Chromosome
*paa*A2	NGR_c26140	Chromosome	SAMCCGM7_Ch2790	Chromosome
*paa*K	NGR_c26110	Chromosome	SAMCCGM7_Ch2787	Chromosome
*paa*I	NGR_c26100	Chromosome	SAMCCGM7_Ch2786	Chromosome

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