

Supplementary Table 1. Details of 371 Predicted Target Genes of *B. japonicum* having SinR Binding Sites in their Upstream Sequences

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
bll4327	R	-279	-271	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_770967.1	putative methyl-accepting chemotaxis protein	chemotaxis
mcpK	D	-352	-344	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_768985.1	probable methyl-accepting chemotaxis protein	chemotaxis
mcpK	D	-73	-65	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_768985.1	probable methyl-accepting chemotaxis protein	chemotaxis
blr0576	R	-339	-331	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767216.1	putative methyl-accepting chemotaxis protein	chemotaxis
bll1471	R	-234	-226	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_768111.1	putative methyl accepting chemotaxis protein	chemotaxis
bll0894	R	-164	-156	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_767534.1	putative cytochrome P450	cytochrome
soxA	R	-363	-355	CAGCTCGTC	8.88	-10.72	26.39	97.27%	NP_770154.1	probable diheme cytochrome C	cytochrome
bll0026	D	-89	-81	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_766666.1	probable dehydrogenase	enzyme
coxG	D	-142	-134	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_767814.1	cytochrome C oxidase assembly protein	enzyme
bll1794	D	-376	-368	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_768434.1	similar to protease	enzyme
bll3254	D	-198	-190	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_769894.1	oxidoreductase	enzyme
bll6224	R	-64	-56	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_772864.1	putative oxidoreductase protein	enzyme
hisC	D	-172	-164	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_772865.1	histidinol-phosphate aminotransferase	enzyme
blr3894	R	-57	-49	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_770534.1	putative transposase	enzyme
blr1543	R	-57	-49	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_768183.1	RSbeta putative transposase	enzyme
bll6631	D	-220	-212	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_773271.1	probable phosphatidylserine decarboxylase proenzyme	enzyme
blr6570	D	-101	-93	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_773210.1	probable dehydrogenase	enzyme
blr2576	R	-20	-12	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_769216.1	N-carbamyl-D-amino acid amidohydrolase	enzyme
thrB	R	-64	-56	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_767955.1	homoserine kinase	enzyme
bll0843	R	-129	-121	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_767483.1	putative crotonobetaine/carnitine-CoA ligase	enzyme
fixO	D	-269	-261	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_769404.1	cytochrome-c oxidase	enzyme
nadB	R	-96	-88	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_769181.1	L-aspartate oxidase	enzyme
nadC	R	-106	-98	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_769180.1	nicotinate-mononucleotide pyrophosphorylase	enzyme
blr0463	R	-216	-208	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_767103.1	acetyltransferase	enzyme
nuoE	R	-12	-4	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_769778.1	formate dehydrogenase subunit gamma	enzyme
dnaE	R	-387	-379	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_771506.1	DNA polymerase III subunit alpha	enzyme
dnaE	R	-376	-368	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_771506.1	DNA polymerase III subunit alpha	enzyme

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
lipA	R	-179	-171	AGCCCCTGA	9.24	-11.2	26.75	98.60%	NP_770357.1	lipoyl synthase	enzyme
blr6770	R	-258	-250	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_773410.1	alpha-amylase	enzyme
blr6965	D	-226	-218	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_773605.1	putative dehalogenase	enzyme
blr5423	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772063.1	probable dTDP-glucose-4,6 dehydratase	enzyme
bll5413	D	-269	-261	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772053.1	2-hydroxyacid dehydrogenase	enzyme
fdhF	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_769776.1	formate dehydrogenase alpha subunit	enzyme
blr7443	D	-369	-361	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774083.1	putative hydrolase	enzyme
blr0110	D	-377	-369	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_766750.1	gentisate 1,2-dioxygenase	enzyme
blr6795	D	-206	-198	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_773435.1	putative recemase	enzyme
fabG	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_770804.1	3-ketoacyl-(acyl-carrier-protein) reductase	enzyme
blr7566	D	-371	-363	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774206.1	oxidoreductase	enzyme
bsl5728	R	-62	-54	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772368.1	phosphoribosylformylglycinamide synthase subunit PurS	enzyme
bll8293	D	-134	-126	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774933.1	putative transposase	enzyme
bll5009	D	-379	-371	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_771649.1	putative deoxycytidine triphosphate deaminase	enzyme
hyfB	R	-39	-31	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_772979.1	hydrogenase 4 subunit B	enzyme
blr7602	D	-81	-73	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_774242.1	putative monooxygenase	enzyme
bll7798	R	-22	-14	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_774438.1	putative nitroreductase	enzyme
blr1253	D	-146	-138	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767893.1	dehydrogenase	enzyme
bll4779	R	-369	-361	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_771419.1	branched-chain alpha-keto acid dehydrogenase subunit E2	enzyme
bll6263	R	-237	-229	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772903.1	putative enoyl-CoA hydratase	enzyme
pcaF	R	-11	-3	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767565.1	beta-ketoacyl CoA thiolase	enzyme
apt	R	-391	-383	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_769130.1	adenine phosphoribosyltransferase	enzyme
glmS	D	-216	-208	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_771247.1	D-fructose-6-phosphate amidotransferase	enzyme
cobN	R	-306	-298	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769903.1	cobaltochelate	enzyme
blr6416	R	-10	-2	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_773056.1	benzoylformate decarboxylase	enzyme
idnD	D	-247	-239	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_773471.1	L-idonate 5-dehydrogenase	enzyme
bll3935	D	-364	-356	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770575.1	putative glutaminase	enzyme
bll2517	D	-198	-190	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769157.1	putative acetate kinase (acetate kinase) protein	enzyme
celB	R	-298	-290	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769029.1	phosphoglucosyltransferase	enzyme
blr0937	D	-105	-97	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_767577.1	putative dioxygenase	enzyme
blr2578	D	-28	-20	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_769218.1	MFS permease	enzyme

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
ahpC	D	-134	-126	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_768417.1	alkyl hydroperoxide reductase	enzyme
norB	R	-84	-76	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769855.1	nitric oxide reductase subunit B	enzyme
blr6721	D	-296	-288	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_773361.1	putative reductase	enzyme
bl18205	D	-235	-227	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_774845.1	probable maturase; reverse transcriptase	enzyme
cblP	D	-136	-128	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769899.1	cobyrinic acid synthase	enzyme
blr3930	D	-124	-116	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770570.1	aminotransferase	enzyme
blr3095	D	-320	-312	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_769735.1	probable aminotransferase	enzyme
lpxD	D	-75	-67	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771492.1	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	enzyme
pcal	R	-110	-102	GCTCCGCGG	8.54	-10.38	26.05	96.02%	NP_770102.1	3-oxoadipate CoA-transferase subunit A	enzyme
secF	D	-330	-322	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771374.1	preprotein translocase subunit SecF	enzyme
bl18192	R	-340	-332	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_774832.1	putative transposase	enzyme
blr7028	R	-50	-42	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773668.1	acetoacetate decarboxylase	enzyme
bl14907	D	-220	-212	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_771547.1	NADH dehydrogenase subunit K	enzyme
bl15420	R	-389	-381	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_772060.1	putative phosphoheptose isomerase	enzyme
blr0257	R	-91	-83	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_766897.1	two-component sensor histidine kinase	enzyme
ligD	R	-183	-175	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773413.1	ATP-dependent DNA ligase	enzyme
mpp	D	-196	-188	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767822.1	mitochondrial processing peptidase-like protein	enzyme
papS	D	-237	-229	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_769109.1	poly(A) polymerase	enzyme
ftsH	D	-127	-119	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773786.1	metalloprotease	enzyme
bl12949	R	-265	-257	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_769589.1	hypothetical oxidoreductase	enzyme
bl10593	R	-93	-85	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767233.1	putative oxidoreductase protein	enzyme
blr1248	R	-150	-142	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767888.1	putative thioredoxin reductase	enzyme
blr1958	D	-266	-258	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768598.1	probable reverse transcriptase/maturase family protein	enzyme
glgA	D	-252	-244	CTCGTGCG	8.17	-10.17	25.68	94.66%	NP_769418.1	glycogen synthase	enzyme
ribH	D	-387	-379	CGACCTTCT	8.17	-10.17	25.68	94.66%	NP_771669.1	riboflavin synthase subunit beta	enzyme
blr4974	D	-362	-354	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_771614.1	polysaccharide biosynthesis glycosyltransferase	enzyme
bl11129	R	-305	-297	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_767769.1	putative FAD-binding dehydrogenase	enzyme
blr0367	R	-30	-22	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_767007.1	putative glucose dehydrogenase (acceptor)	enzyme

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
intA	D	-300	-292	TTGTTCCCA	8.16	-10.03	25.67	94.62%	NP_771166.1	probable site-specific integrase	enzyme
ctpA	D	-169	-161	CACGGCGGT	8.16	-10.03	25.67	94.62%	NP_767074.1	carboxy-terminal protease	enzyme
ispH	R	-261	-253	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_769647.1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	enzyme
blr2084	D	-145	-137	TTGTTCCCA	8.16	-10.03	25.67	94.62%	NP_768724.1	putative glutamine synthetase	enzyme
upp	R	-189	-181	CTCTCCAC	8.16	-10.03	25.67	94.62%	NP_773428.1	probable uracil phosphoribosyltransferase	enzyme
prmA	R	-43	-35	TTGTTCCCA	8.16	-10.03	25.67	94.62%	NP_773228.1	ribosomal protein L11 methyltransferase	enzyme
blr1873	R	-178	-170	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_768513.1	putative transposase	enzyme
rbcL	D	-117	-109	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_769225.1	ribulose biphosphate carboxylase	enzyme
pheC	D	-356	-348	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771201.1	probable cyclohexadienyl dehydratase precursor	enzyme
blr6960	D	-286	-278	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_773600.1	arylesterase	enzyme
blt2706	D	-33	-25	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_769346.1	probable transglycosylase	enzyme
nthA	D	-258	-250	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771138.1	nitrile hydratase subunit alpha	enzyme
mtnK	R	-390	-382	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_771538.1	methylthioribose kinase	enzyme
blt6402	D	-40	-32	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_773042.1	nitrilase	enzyme
blr0960	D	-84	-76	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_767600.1	5'-methylthioadenosine phosphorylase	enzyme
blr3044	D	-347	-339	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_769684.1	probable extracellular protease	enzyme
recA	R	-13	-5	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772395.1	recombinase A	enzyme
nrdF	R	-297	-289	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_766646.1	ribonucleotide-diphosphate reductase subunit beta	enzyme
purC	R	-238	-230	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772369.1	phosphoribosylaminoimidazole-succinocarboxamide synthase	enzyme
proS	D	-397	-389	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771517.1	prolyl-tRNA synthetase	enzyme
blr2054	R	-185	-177	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_768694.1	putative transposase	enzyme
bsr0027	R	-327	-319	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_766667.1	hypothetical protein	hypothetical
blt0998	D	-159	-151	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_767639.1	hypothetical protein	hypothetical
bsr1831	D	-311	-303	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_768471.1	hypothetical protein	hypothetical
blr2368	D	-230	-222	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_769008.1	hypothetical protein	hypothetical
blt8223	D	-134	-126	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_774863.1	hypothetical protein	hypothetical
blr8224	R	-48	-40	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_774864.1	hypothetical protein	hypothetical
blr1269	R	-339	-331	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_767909.1	hypothetical protein	hypothetical
blt1796	D	-237	-229	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_768436.1	hypothetical protein	hypothetical
bsl2575	D	-192	-184	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_769215.1	hypothetical protein	hypothetical
blt5157	R	-297	-289	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_771797.1	hypothetical protein	hypothetical

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
bl16279	R	-372	-364	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_772919.1	hypothetical protein	hypothetical
bl16613	D	-278	-270	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_773253.1	hypothetical protein	hypothetical
bl18274	D	-183	-175	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_774914.1	hypothetical protein	hypothetical
bl10636	R	-400	-392	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_767276.1	hypothetical protein	hypothetical
bl10637	D	-128	-120	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_767277.1	hypothetical protein	hypothetical
bs11683	R	-182	-174	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_768323.1	hypothetical protein	hypothetical
bl13139	D	-221	-213	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_769779.1	hypothetical protein	hypothetical
bl13169	D	-162	-154	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_769809.1	hypothetical protein	hypothetical
bs13718	D	-39	-31	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_770358.1	hypothetical protein	hypothetical
bl13719	D	-370	-362	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_770359.1	hypothetical protein	hypothetical
bl14996	D	-127	-119	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_771636.1	hypothetical protein	hypothetical
bl15017	R	-299	-291	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_771657.1	hypothetical protein	hypothetical
bs18278	R	-183	-175	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_774918.1	hypothetical protein	hypothetical
bl10475	D	-105	-97	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_767115.1	hypothetical protein	hypothetical
bl10818	R	-281	-273	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_767458.1	hypothetical protein	hypothetical
bl11430	R	-266	-258	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_768070.1	hypothetical protein	hypothetical
bl12041	R	-142	-134	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_768681.1	hypothetical protein	hypothetical
bl12284	R	-164	-156	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_768924.1	hypothetical protein	hypothetical
bl12750	R	-273	-265	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_769390.1	hypothetical protein	hypothetical
bl12857	D	-167	-159	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_769497.1	hypothetical protein	hypothetical
bl13081	D	-350	-342	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_769721.1	hypothetical protein	hypothetical
bl13083	R	-216	-208	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_769723.1	hypothetical protein	hypothetical
bl13381	R	-304	-296	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_770021.1	hypothetical protein	hypothetical
bl13890	R	-93	-85	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_770530.1	hypothetical protein	hypothetical
bl14503	R	-123	-115	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_771143.1	hypothetical protein	hypothetical
bl15202	R	-86	-78	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_771842.1	hypothetical protein	hypothetical
bl15259	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_771899.1	hypothetical protein	hypothetical
bl15289	D	-207	-199	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_771929.1	hypothetical protein	hypothetical
bl15435	R	-131	-123	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772075.1	hypothetical protein	hypothetical
bl15514	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772154.1	hypothetical protein	hypothetical
bl15515	D	-245	-237	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772155.2	hypothetical protein	hypothetical
bs15585	R	-363	-355	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772225.1	hypothetical protein	hypothetical
bl15787	D	-14	-6	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772427.1	hypothetical protein	hypothetical
bl15788	R	-140	-132	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772428.1	hypothetical protein	hypothetical
bl16433	R	-336	-328	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_773073.1	hypothetical protein	hypothetical
bl16531	D	-101	-93	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_773171.1	hypothetical protein	hypothetical
bl17463	D	-107	-99	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774103.1	hypothetical protein	hypothetical

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
blr7465	R	-313	-305	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774105.1	hypothetical protein	hypothetical
blr7595	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774235.1	hypothetical protein	hypothetical
blr7741	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774381.1	hypothetical protein	hypothetical
bl17875	D	-220	-212	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774515.1	hypothetical protein	hypothetical
blr1588	R	-105	-97	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_768228.1	hypothetical protein	hypothetical
bl12627	R	-353	-345	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_769267.1	hypothetical protein	hypothetical
bsl4407	R	-331	-323	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_771047.1	hypothetical protein	hypothetical
bsr4408	D	-243	-235	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_771048.1	hypothetical protein	hypothetical
bsl5321	R	-239	-231	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_771961.1	hypothetical protein	hypothetical
blr5743	R	-14	-6	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_772383.1	hypothetical protein	hypothetical
bl17601	R	-110	-102	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_774241.1	hypothetical protein	hypothetical
bl10809	D	-39	-31	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767449.1	hypothetical protein	hypothetical
blr1085	D	-341	-333	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767725.1	hypothetical protein	hypothetical
bl11313	R	-242	-234	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767953.1	hypothetical protein	hypothetical
bl12796	R	-10	-2	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_769436.1	hypothetical protein	hypothetical
bsr2797	D	-137	-129	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_769437.1	hypothetical protein	hypothetical
bl13105	R	-98	-90	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_769745.1	hypothetical protein	hypothetical
bl15492	D	-397	-389	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772132.1	hypothetical protein	hypothetical
bl15640	R	-10	-2	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772280.1	hypothetical protein	hypothetical
blr5641	D	-105	-97	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772281.1	hypothetical protein	hypothetical
bl15882	R	-332	-324	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772522.1	hypothetical protein	hypothetical
blr7453	D	-206	-198	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_774093.1	hypothetical protein	hypothetical
blr7534	R	-285	-277	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_774174.1	hypothetical protein	hypothetical
bl10203	D	-134	-126	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_766843.1	hypothetical protein	hypothetical
blr0355	R	-161	-153	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_766995.1	hypothetical protein	hypothetical
bsl0728	R	-64	-56	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767368.1	hypothetical protein	hypothetical
blr1265	D	-299	-291	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767905.1	hypothetical protein	hypothetical
blr1282	R	-66	-58	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767922.1	hypothetical protein	hypothetical
bl11797	R	-385	-377	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_768437.1	hypothetical protein	hypothetical
bl12128	R	-223	-215	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_768768.1	hypothetical protein	hypothetical
bsr2129	D	-210	-202	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_768769.1	hypothetical protein	hypothetical
bsl2206	R	-102	-94	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_768846.1	hypothetical protein	hypothetical
bsl2596	D	-254	-246	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769236.1	hypothetical protein	hypothetical
blr2597	R	-65	-57	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769237.1	hypothetical protein	hypothetical
bl12699	D	-301	-293	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769339.1	hypothetical protein	hypothetical
bl12700	R	-385	-377	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_769340.1	hypothetical protein	hypothetical
bl13359	R	-92	-84	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769999.1	hypothetical protein	hypothetical

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
blr3531	D	-306	-298	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770171.1	hypothetical protein	hypothetical
bsr3674	R	-292	-284	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770314.1	hypothetical protein	hypothetical
bl14123	R	-114	-106	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770763.1	hypothetical protein	hypothetical
blr4344	D	-83	-75	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770984.1	hypothetical protein	hypothetical
bsr4434	D	-126	-118	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771074.1	hypothetical protein	hypothetical
bsl4625	R	-89	-81	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771265.1	hypothetical protein	hypothetical
bl14947	R	-205	-197	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771587.1	hypothetical protein	hypothetical
blr5270	D	-295	-287	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771910.1	hypothetical protein	hypothetical
blr5406	R	-131	-123	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_772046.1	hypothetical protein	hypothetical
blr6107	R	-397	-389	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_772747.1	hypothetical protein	hypothetical
bl16309	R	-225	-217	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_772949.1	hypothetical protein	hypothetical
bsr7045	R	-331	-323	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_773685.1	hypothetical protein	hypothetical
bl17668	D	-198	-190	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_774308.1	hypothetical protein	hypothetical
blr7724	R	-111	-103	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_774364.1	hypothetical protein	hypothetical
bl10505	D	-203	-195	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767145.1	hypothetical protein	hypothetical
bl10523	D	-305	-297	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_767163.1	hypothetical protein	hypothetical
blr0855	D	-54	-46	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767495.1	hypothetical protein	hypothetical
bl10955	D	-372	-364	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767595.1	hypothetical protein	hypothetical
bl11127	D	-305	-297	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767767.1	hypothetical protein	hypothetical
blr1247	R	-320	-312	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_767887.1	hypothetical protein	hypothetical
blr1303	D	-31	-23	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_767943.1	hypothetical protein	hypothetical
bl11368	D	-328	-320	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_768008.1	hypothetical protein	hypothetical
bl11489	D	-334	-326	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_768129.1	hypothetical protein	hypothetical
bl11565	R	-12	-4	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_768205.1	hypothetical protein	hypothetical
blr1753	R	-174	-166	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768393.1	hypothetical protein	hypothetical
bl11786	R	-55	-47	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768426.1	hypothetical protein	hypothetical
bsl1884	R	-285	-277	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768524.1	hypothetical protein	hypothetical
bsr1886	D	-61	-53	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768526.1	hypothetical protein	hypothetical
blr2001	D	-385	-377	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768641.1	hypothetical protein	hypothetical
blr2614	R	-83	-75	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_769254.1	hypothetical protein	hypothetical
bl13417	R	-51	-43	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_770057.1	hypothetical protein	hypothetical
blr3478	D	-232	-224	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_770118.1	hypothetical protein	hypothetical
bl13583	D	-194	-186	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_770223.1	hypothetical protein	hypothetical
bl14901	D	-22	-14	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_771541.1	hypothetical protein	hypothetical
bl14941	R	-14	-6	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_771581.1	hypothetical protein	hypothetical
bl15043	R	-379	-371	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_771683.1	hypothetical protein	hypothetical
bl15437	R	-279	-271	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_772077.1	hypothetical protein	hypothetical

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
blr5439	D	-375	-367	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_772079.1	hypothetical protein	hypothetical
bll5622	R	-176	-168	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_772262.1	hypothetical protein	hypothetical
blr5939	R	-202	-194	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_772579.1	hypothetical protein	hypothetical
bsl6289	D	-57	-49	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_772929.1	hypothetical protein	hypothetical
bll6909	D	-249	-241	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773549.1	hypothetical protein	hypothetical
blr6973	R	-381	-373	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773613.1	hypothetical protein	hypothetical
blr7061	R	-15	-7	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773701.1	hypothetical protein	hypothetical
bll7279	R	-136	-128	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773919.1	hypothetical protein	hypothetical
bsl7546	R	-124	-116	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_774186.1	hypothetical protein	hypothetical
bll8014	D	-357	-349	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_774654.1	hypothetical protein	hypothetical
blr8015	R	-327	-319	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_774655.1	hypothetical protein	hypothetical
bll8091	D	-327	-319	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_774731.1	hypothetical protein	hypothetical
bsl8092	D	-35	-27	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_774732.1	hypothetical protein	hypothetical
bsl0049	D	-217	-209	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_766689.1	hypothetical protein	hypothetical
bll0546	D	-276	-268	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_767186.1	hypothetical protein	hypothetical
blr0709	D	-118	-110	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_767349.1	hypothetical protein	hypothetical
bll1872	D	-213	-205	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_768512.1	hypothetical protein	hypothetical
blr3008	D	-199	-191	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_769648.1	hypothetical protein	hypothetical
bsr4179	D	-333	-325	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_770819.1	hypothetical protein	hypothetical
bsl4527	D	-10	-2	TTGTCCCA	8.16	-10.03	25.67	94.62%	NP_771167.1	hypothetical protein	hypothetical
blr4567	R	-385	-377	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_771207.1	hypothetical protein	hypothetical
bsl5225	D	-300	-292	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_771865.1	hypothetical protein	hypothetical
blr5245	D	-279	-271	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_771885.1	hypothetical protein	hypothetical
bll5835	R	-83	-75	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_772475.1	hypothetical protein	hypothetical
bll8136	R	-103	-95	TTGTCCCA	8.16	-10.03	25.67	94.62%	NP_774776.1	hypothetical protein	hypothetical
bll0438	R	-256	-248	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_767078.1	hypothetical protein	hypothetical
blr1104	R	-196	-188	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_767744.1	hypothetical protein	hypothetical
blr1246	R	-223	-215	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_767886.1	hypothetical protein	hypothetical
bsl1639	D	-139	-131	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_768279.1	hypothetical protein	hypothetical
blr2135	R	-173	-165	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_768775.1	hypothetical protein	hypothetical
bll2208	R	-155	-147	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_768848.1	hypothetical protein	hypothetical
blr3882	D	-360	-352	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_770522.1	hypothetical protein	hypothetical
bll3891	R	-338	-330	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_770531.1	hypothetical protein	hypothetical
bll3990	R	-132	-124	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_770630.1	hypothetical protein	hypothetical
blr4003	R	-144	-136	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_770643.1	hypothetical protein	hypothetical
blr4562	R	-61	-53	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771202.1	hypothetical protein	hypothetical
bll4697	D	-391	-383	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771337.1	hypothetical protein	hypothetical

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
bll4899	R	-9	-1	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_771539.1	hypothetical protein	hypothetical
bsl5083	R	-37	-29	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_771723.1	hypothetical protein	hypothetical
bsr5084	D	-40	-32	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_771724.1	hypothetical protein	hypothetical
blr5173	R	-246	-238	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771813.1	hypothetical protein	hypothetical
blr5341	R	-376	-368	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_771981.1	hypothetical protein	hypothetical
bll5661	D	-289	-281	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772301.1	hypothetical protein	hypothetical
blr5730	D	-80	-72	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772370.1	hypothetical protein	hypothetical
bsr5794	D	-159	-151	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772434.1	hypothetical protein	hypothetical
blr5815	D	-230	-222	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_772455.1	hypothetical protein	hypothetical
bsl6030	D	-149	-141	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772670.1	hypothetical protein	hypothetical
bll6870	D	-216	-208	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_773510.1	hypothetical protein	hypothetical
bll7171	R	-339	-331	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_773811.1	hypothetical protein	hypothetical
blr7450	D	-102	-94	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_774090.1	hypothetical protein	hypothetical
blr7567	D	-339	-331	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_774207.1	hypothetical protein	hypothetical
bll7670	R	-88	-80	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_774310.1	hypothetical protein	hypothetical
bll8179	D	-309	-301	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_774819.1	hypothetical protein	hypothetical
bll8309	R	-157	-149	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_774949.1	hypothetical protein	hypothetical
blr2272	R	-160	-152	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_768912.1	putative porin precursor	others
bll5925	D	-260	-252	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_772565.1	putative capsular polysaccharide biosynthesis protein	others
grpE	R	-275	-267	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767316.1	heat shock protein	others
blr4937	R	-182	-174	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_771577.1	probable cation efflux system protein	others
bll6257	D	-95	-87	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772897.1	putative efflux pump protein	others
mutS	D	-213	-205	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767564.1	DNA mismatch repair protein	others
fliN	R	-183	-175	GGCGAGCCG	8.54	-10.38	26.05	96.02%	NP_773519.1	probable flagellar motor switch protein	others
tdlD	D	-385	-377	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767808.1	TldD protein	others
ureF	R	-65	-57	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_768099.1	urease accessory protein	others
ftsZ	D	-368	-360	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773236.1	cell division protein FtsZ	others
bcpB	R	-342	-334	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_771709.1	BcpB protein	others
bsr1739	D	-237	-229	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_768379.1	ferredoxin	others
blr0153	D	-286	-278	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_766793.1	probable surfeit locus protein 1	others
rhcT	D	-246	-238	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_768461.1	RhcT protein	others
trxA	D	-284	-276	CAAAAGCGC	8.17	-10.17	25.68	94.66%	NP_767234.1	thioredoxin	others
blr5623	D	-50	-42	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_772263.1	TPR domain protein	others
groEL	R	-51	-43	TGCGTCTTG	8.16	-10.03	25.67	94.62%	NP_771867.1	chaperonin GroEL	others
blr0277	R	-333	-325	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_766917.1	AcrB/AcrD/AcrF family protein	others

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
pilA	D	-130	-122	TTGTTCCCA	8.16	-10.03	25.67	94.62%	NP_773227.1	components of type IV pilus pilin subunit	others
bsr8137	D	-54	-46	TTGTTCCCA	8.16	-10.03	25.67	94.62%	NP_774777.1	similar to sigma-70 subunit	others
flgB	R	-130	-122	CGGCGACG G	7.93	-9.95	25.44	93.77%	NP_772454.1	flagellar basal body rod protein FlgB	others
blr4504	D	-229	-221	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_771144.1	TonB-dependent receptor	receptor
bll6026	R	-152	-144	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_772666.1	probable outer membrane protein B	receptor
bll4321	R	-124	-116	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770961.1	putative outer membrane channel lipoprotein	receptor
blr0690	D	-294	-286	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767330.1	putative multidrug resistance protein	receptor
bll3903	D	-236	-228	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_770543.1	putative multidrug resistance protein	receptor
blr6804	R	-11	-3	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773444.1	probable substrate-binding protein	receptor
minC	R	-17	-9	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_770851.1	septum formation inhibitor	receptor
bll6948	D	-69	-61	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773588.1	putative outer membrane receptor signal peptide protein	receptor
bll7923	R	-330	-322	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_774563.1	putative adenylate/guanylate cyclase transmembrane protein	receptor
blr7816	D	-42	-34	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_774456.1	probable mannitol-binding protein	receptor
bll3524	R	-159	-151	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_770164.1	transcriptional regulatory protein	regulatory
bll3578	R	-139	-131	TTGTTCTCA	9.24	-11.2	26.75	98.60%	NP_770218.1	two-component response regulator	regulatory
bll2223	R	-391	-383	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_768863.1	probable transcriptional regulator	regulatory
blr5260	D	-111	-103	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_771900.1	transcriptional regulatory protein	regulatory
blr6291	R	-83	-75	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_772931.1	transcriptional regulatory protein	regulatory
bll1252	R	-78	-70	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767892.1	transcriptional regulatory protein	regulatory
glnB	D	-148	-140	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771588.1	nitrogen regulatory protein PII	regulatory
blr0609	R	-140	-132	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767249.1	transcriptional regulatory protein	regulatory
blr2391	D	-300	-292	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_769031.1	transcriptional regulatory protein	regulatory
blr4322	D	-52	-44	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770962.1	transcriptional regulatory protein	regulatory
bll6415	D	-94	-86	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_773055.1	transcriptional regulatory protein	regulatory

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
bll0535	R	-345	-337	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_767175.1	two-component response regulator	regulatory
blr3468	R	-183	-175	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_770108.1	two-component response regulator	regulatory
bll0256	D	-245	-237	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_766896.1	transcriptional regulatory protein	regulatory
blr1086	D	-109	-101	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_767726.1	transcriptional regulatory protein	regulatory
blr3685	R	-79	-71	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_770325.1	transcriptional regulatory protein	regulatory
bll6568	R	-212	-204	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773208.1	transcriptional regulatory protein	regulatory
blr7619	D	-330	-322	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_774259.1	two-component response regulator	regulatory
blr5836	D	-75	-67	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_772476.1	transcriptional regulatory protein PadR-	regulatory
bll3773	D	-197	-189	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_770413.1	transcriptional regulatory protein	regulatory
blr5735	D	-245	-237	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772375.1	transcriptional regulatory protein	regulatory
blr6320	R	-55	-47	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772960.1	transcriptional regulatory protein	regulatory
rplY	R	-313	-305	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_774081.1	50S ribosomal protein L25/general stress protein Ctc	ribosomal
rplI	R	-11	-3	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_770716.1	50S ribosomal protein L9	ribosomal
rpsL	D	-272	-264	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_772045.1	30S ribosomal protein S12	ribosomal
rplT	R	-364	-356	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_767347.1	50S ribosomal protein L20	ribosomal
rpmI	R	-83	-75	TTGTGCTCA	8.16	-10.03	25.67	94.62%	NP_767348.1	50S ribosomal protein L35	ribosomal
bll0989	D	-364	-356	TCGTTCTCA	9.62	-12.45	27.13	100.00%	NP_767629.1	peptide ABC transporter ATP-binding protein	transporter
bll0113	R	-34	-26	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_766753.1	ABC transporter substrate-binding protein	transporter
mtbA	D	-73	-65	TCGTTCTCT	9.25	-11.65	26.76	98.64%	NP_767833.1	integral inner membrane metabolite transport protein	transporter
blr3566	D	-104	-96	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_770206.1	ABC transporter substrate-binding protein	transporter
bll1002	D	-146	-138	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_767642.1	probable ABC transporter ATP-binding protein	transporter
blr1483	R	-395	-387	TCGTTCTCC	9.01	-11.02	26.52	97.75%	NP_768123.1	sulfate ABC transporter permease protein	transporter
blr6443	R	-231	-223	TTGTTCTCT	8.88	-10.72	26.39	97.27%	NP_773083.1	ABC transporter permease protein	transporter
bll5950	D	-173	-165	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_772590.1	ABC transporter ATP-binding protein	transporter

(Suppl Table 1). Contd.....

Gene name	Strand	Start	End	TFBS	Score	ln(P)	Obv.Score	MSSP*	Gene ID	Description	Category
blr1354	R	-294	-286	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_767994.1	peptide ABC transporter permease protein	transporter
rfbA	D	-51	-43	TTGTTCTCC	8.63	-10.56	26.14	96.35%	NP_770291.1	probable O-antigen export system ATP-binding protein	transporter
bll0885	D	-208	-200	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767525.1	ABC transporter ATP-binding protein	transporter
blr3828	D	-130	-122	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770468.1	ABC transporter ATP-binding protein	transporter
blr3795	D	-210	-202	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_770435.1	ABC transporter HlyB/MsbA family	transporter
bll0883	D	-358	-350	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_767523.1	ABC transporter permease protein	transporter
blr4886	D	-92	-84	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_771526.1	ABC transporter permease protein	transporter
bll6389	D	-268	-260	TCGTGCTCA	8.54	-10.38	26.05	96.02%	NP_773029.1	ABC transporter permease protein	transporter
bll6236	D	-245	-237	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_772876.1	ABC transporter substrate-binding protein	transporter
bll6327	R	-202	-194	TCGTTCCCA	8.54	-10.38	26.05	96.02%	NP_772967.1	ABC transporter substrate-binding protein	transporter
bll6411	R	-79	-71	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773051.1	ABC transporter permease protein	transporter
bll6823	D	-208	-200	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773463.1	ABC transporter permease protein	transporter
bll6914	R	-10	-2	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773554.1	ABC transporter permease protein	transporter
bll7008	D	-130	-122	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_773648.1	ABC transporter ATP-binding protein, aliphatic sulfonate	transporter
blr4555	D	-226	-218	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_771195.1	similar to ABC transporter permease protein	transporter
bll6803	D	-396	-388	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_773443.1	hypothetical metabolite transport protein	transporter
mntH	R	-351	-343	TCGTGCTCT	8.17	-10.17	25.68	94.66%	NP_771684.1	manganese transport protein MntH	transporter
gudP	D	-131	-123	TCGTTCCCT	8.17	-10.17	25.68	94.66%	NP_772509.1	probable glucarate transporter	transporter
blr6155	R	-153	-145	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_772795.1	ABC transporter ATP-binding protein	transporter
blr6445	D	-385	-377	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_773085.1	ABC transporter ATP-binding protein	transporter
bll6478	D	-47	-39	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_773118.1	ABC transporter ATP-binding protein	transporter
bll3425	R	-16	-8	TCGTTCCCC	7.93	-9.95	25.44	93.77%	NP_770065.1	ABC transporter permease protein	transporter
bll6550	R	-365	-357	TCGTGCTCC	7.93	-9.95	25.44	93.77%	NP_773190.1	probable ABC transporter permease protein	transporter

Note: * = MSSP (Motif Score Similarity Percentage) = Similarity of predicted motif score with known SinR-box consensus sequence score. Shaded rows indicate false positives, since predicted genes showed no similarity with known motifs.

Supplementary Table 2. Distribution of Predicted Target Genes According to Sin-box Like Nucleotide Level Conservation in *B. japonicum* and Comparison with Binding Patterns of *B. subtilis* SinR Regulated Genes

<i>B. japonicum</i>					<i>B. subtilis</i>	
Target Gene Functional Category	Predicted Motif Pattern	No. of Genes	Score	MSSP	Known Sin-Box Pattern	SinR Regulated Gene
Chemotaxis	<u>TCGTTCTCA</u>	1	9.62	100.00%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTGCTCA</u>	1	8.54	96.02%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCA</u>	2	8.54	96.02%	<u>GTTCCCA</u>	epr
	<u>TCGTGCTCT</u>	1	8.17	94.66%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
Cytochrome	<u>TCGTTCTCC</u>	1	9.01	97.75%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	CAGCTCGTC	1	8.88	97.27%	No match	
Enzymes	<u>TCGTTCTCA</u>	8	9.62	100.00%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCTCT</u>	9	9.25	98.64%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	AGCCCTGA	1	9.24	98.60%	No match	
	<u>TTGTTCTCA</u>	3	9.24	98.60%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCTCC</u>	12	9.01	97.75%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTTCTCT</u>	1	8.88	97.27%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTTCTCT</u>	3	8.88	97.27%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTTCTCC</u>	6	8.63	96.35%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	GCTCCGCGG	1	8.54	96.02%	No match	
	<u>TCGTGCTCA</u>	12	8.54	96.02%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCA</u>	6	8.54	96.02%	<u>GTTCCCA</u>	epr
	CGACCTTCT	1	8.17	94.66%	No match	
	CTCGCTGCG	1	8.17	94.66%	No match	
	<u>TCGTGCTCT</u>	8	8.17	94.66%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCT</u>	5	8.17	94.66%	<u>GTTCCCA</u>	epr
	CACGGCGGT	1	8.16	94.62%	No match	
	CTCTCCAC	1	8.16	94.62%	No match	
	<u>TTGTGCTCA</u>	7	8.16	94.62%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTGCTCC</u>	9	7.93	93.77%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCQC</u>	5	7.93	93.77%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK

(Suppl Table 2). Contd.....

<i>B. japonicum</i>					<i>B. subtilis</i>	
Target Gene Functional Category	Predicted Motif Pattern	No. of Genes	Score	MSSP	Known Sin-Box Pattern	SinR Regulated Gene
Hypothetical	TCGTTCTCA	6	9.62	100.00%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCTCT	7	9.25	98.64%	GTTCTCA GTTCTCT	aprE yveK
	TTGTTCTCA	10	9.24	98.60%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCTCC	28	9.01	97.75%	GTTCTCA GTTCTCT	aprE yveK
	TTGTTCTCT	7	8.88	97.27%	GTTCTCA GTTCTCT	aprE yveK
	TTGTTCTCC	12	8.63	96.35%	GTTCTCA GTTCTCT	aprE yveK
	TCGTGCTCA	21	8.54	96.02%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCCCA	7	8.54	96.02%	GTTCCCA	epr
	TCGTGCTCT	18	8.17	94.66%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCCCT	18	8.17	94.66%	GTTCCCA	epr
	TTGTGCTCA	10	8.16	94.62%	GTTCTCA GTTCTCT	aprE yveK
	TTGTTCCCA	2	8.16	94.62%	GTTCCCA	epr
	TCGTGCTCC	20	7.93	93.77%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCCCC	9	7.93	93.77%	GTTCCCA	epr
Others	TCGTTCTCA	1	9.62	100.00%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCTCT	1	9.25	98.64%	GTTCTCA GTTCTCT	aprE yveK
	TTGTTCTCC	4	8.63	96.35%	GTTCTCA GTTCTCT	aprE yveK
	GGCGAGCCG	1	8.54	96.02%	No match	
	TCGTGCTCA	2	8.54	96.02%	GTTCTCA GTTCTCT	aprE yveK
	CAAAAGCGC	1	8.17	94.66%	No match	
	TCGTGCTCT	4	8.17	94.66%	GTTCTCA GTTCTCT	aprE yveK
	TCGTTCCCT	2	8.17	94.66%	GTTCCCA	epr
	TGCGTCTTG	1	8.16	94.62%	No match	
	TTGTGCTCA	1	8.16	94.62%	GTTCTCA GTTCTCT	aprE yveK
	TTGTTCCCA	2	8.16	94.62%	GTTCCCA	epr
	CGGCGACGG	1	7.93	93.77%	No match	

(Suppl Table 2). Contd.....

<i>B. japonicum</i>					<i>B. subtilis</i>	
Target Gene Functional Category	Predicted Motif Pattern	No. of Genes	Score	MSSP	Known Sin-Box Pattern	SinR Regulated Gene
Receptor	<u>TCGTTCTCC</u>	1	9.01	97.75%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTGCTCA</u>	3	8.54	96.02%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCA</u>	1	8.54	96.02%	<u>GTTCCCA</u>	epr
	<u>TCGTGCTCT</u>	2	8.17	94.66%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCT</u>	2	8.17	94.66%	<u>GTTCCCA</u>	epr
	<u>TCGTTCCCC</u>	1	7.93	93.77%	<u>GTTCCCA</u>	epr
Regulatory	<u>TCGTTCTCA</u>	1	9.62	100.00%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCTCC</u>	3	9.01	97.75%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTTCTCC</u>	1	8.63	96.35%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTGCTCA</u>	4	8.54	96.02%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCA</u>	3	8.54	96.02%	<u>GTTCCCA</u>	epr
	<u>TCGTGCTCT</u>	3	8.17	94.66%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCCCT</u>	2	8.17	94.66%	<u>GTTCCCA</u>	epr
	<u>TTGTGCTCA</u>	2	8.16	94.62%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTGCTCC</u>	3	7.93	93.77%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
Ribosomal	<u>TCGTTCTCC</u>	2	9.01	97.75%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTTCTCT</u>	1	8.88	97.27%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTGCTCA</u>	2	8.16	94.62%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
Transporter	<u>TCGTTCTCA</u>	1	9.62	100.00%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCTCT</u>	2	9.25	98.64%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TCGTTCTCC</u>	3	9.01	97.75%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK
	<u>TTGTTCTCT</u>	1	8.88	97.27%	<u>GTTCTCA</u> <u>GTTCTCT</u>	aprE yveK

(Suppl Table 2). Contd.....

<i>B. japonicum</i>					<i>B. subtilis</i>	
Target Gene Functional Category	Predicted Motif Pattern	No. of Genes	Score	MSSP	Known Sin-Box Pattern	SinR Regulated Gene
	<u>TTG</u> TCTCC	3	8.63	96.35%	<u>GTT</u> CTCA <u>GTT</u> CTCT	aprE yveK
	TCG <u>TG</u> CTCA	6	8.54	96.02%	<u>GTT</u> CTCA <u>GTT</u> CTCT	aprE yveK
	TCG <u>TT</u> CCCA	2	8.54	96.02%	<u>GTT</u> CCCA	epr
	TCG <u>TG</u> CTCT	4	8.17	94.66%	<u>GTT</u> CTCA <u>GTT</u> CTCT	aprE yveK
	TCG <u>TT</u> CCCT	4	8.17	94.66%	<u>GTT</u> CCCA	epr
	TCG <u>TG</u> CTCC	3	7.93	93.77%	<u>GTT</u> CTCA <u>GTT</u> CTCT	aprE yveK
	TCG <u>TT</u> CCCC	2	7.93	93.77%	<u>GTT</u> CCCC	epr

Note: Underlined nucleotides refer identical nature of predicted patterns with known patterns.

Supplementary Table 3. Genes Distribution Details. (a) Distribution of 360 True Positive Genes of *B. japonicum* According to Known *Sin-box* like Binding Site. Additional 11 Genes were Assumed False Positives Since Showed no Similarity with Known Motifs of *B. subtilis*. (b) Details of Genes Under the Variable Pattern Set which had no Similarity with Known *sin-box* Motifs and thus Considered as False Positive Predictions

(a)

S. No.	Pattern Category	Total No. of Target Genes	Pattern Type	Predicted Motif Pattern	No. of Genes	Functional Category
1.	TCGTGCTCA	49	P2	TCGTGCTCA	1	Chemotaxis
			P1	TCGTGCTCA	12	Enzyme
			P2	TCGTGCTCA	21	Hypothetical
			P3	TCGTGCTCA	2	Others
			P1	TCGTGCTCA	3	Receptor
			P1	TCGTGCTCA	4	Regulatory
			P1	TCGTGCTCA	6	Transporter
2.	TCGTGCTCC	35	P3	TCGTGCTCC	9	Enzyme
			P3	TCGTGCTCC	20	Hypothetical
			P2	TCGTGCTCC	3	Regulatory
			P4	TCGTGCTCC	3	Transporter
3.	TCGTGCTCT	40	P3	TCGTGCTCT	1	Chemotaxis
			P5	TCGTGCTCT	8	Enzyme
			P4	TCGTGCTCT	18	Hypothetical
			P1	TCGTGCTCT	4	Others
			P2	TCGTGCTCT	2	Receptor
			P3	TCGTGCTCT	3	Regulatory
			P2	TCGTGCTCT	4	Transporter

(Suppl Table 3a). Contd.....

S. No.	Pattern Category	Total No. of Target Genes	Pattern Type	Predicted Motif Pattern	No. of Genes	Functional Category
4.	TCGTTCCCA	21	P1	TCGTTCCCA	2	Chemotaxis
			P8	TCGTTCCCA	6	Enzyme
			P10	TCGTTCCCA	7	Hypothetical
			P4	TCGTTCCCA	1	Receptor
			P4	TCGTTCCCA	3	Regulatory
			P7	TCGTTCCCA	2	Transporter
5.	TCGTTCCCC	17	P10	TCGTTCCCC	5	Enzyme
			P9	TCGTTCCCC	9	Hypothetical
			P5	TCGTTCCCC	1	Receptor
			P8	TCGTTCCCC	2	Transporter
6.	TCGTTCCCT	33	P11	TCGTTCCCT	5	Enzyme
			P5	TCGTTCCCT	18	Hypothetical
			P4	TCGTTCCCT	2	Others
			P3	TCGTTCCCT	2	Receptor
			P6	TCGTTCCCT	2	Regulatory
			P3	TCGTTCCCT	4	Transporter
7.	TCGTTCTCA	18	P4	TCGTTCTCA	1	Chemotaxis
			P6	TCGTTCTCA	8	Enzyme
			P13	TCGTTCTCA	6	Hypothetical
			P9	TCGTTCTCA	1	Others
			P8	TCGTTCTCA	1	Regulatory
			P10	TCGTTCTCA	1	Transporter
8.	TCGTTCTCC	50	P2	TCGTTCTCC	1	Cytochrome
			P2	TCGTTCTCC	12	Enzyme
			P1	TCGTTCTCC	28	Hypothetical
			P6	TCGTTCTCC	1	Receptor
			P5	TCGTTCTCC	3	Regulatory
			P1	TCGTTCTCC	2	Ribosomal
			P5	TCGTTCTCC	3	Transporter
9.	TCGTTCTCT	19	P4	TCGTTCTCT	9	Enzyme
			P11	TCGTTCTCT	7	Hypothetical
			P10	TCGTTCTCT	1	Others
			P9	TCGTTCTCT	2	Transporter
10.	TTGTGCTCA	22	P7	TTGTGCTCA	7	Enzyme
			P7	TTGTGCTCA	10	Hypothetical
			P12	TTGTGCTCA	1	Others
			P7	TTGTGCTCA	2	Regulatory
			P2	TTGTGCTCA	2	Ribosomal

(Suppl Table 3a). Contd.....

S. No.	Pattern Category	Total No. of Target Genes	Pattern Type	Predicted Motif Pattern	No. of Genes	Functional Category
11.	TTGTTCCCA	17	P14	TTGTTCCCA	2	Hypothetical
			P5	TTGTTCCCA	2	Others
			P12	TTGTTCTCA	3	Enzyme
			P8	TTGTTCTCA	10	Hypothetical
12.	TTGTTCTCC	26	P9	TTGTTCTCC	6	Enzyme
			P6	TTGTTCTCC	12	Hypothetical
			P2	TTGTTCTCC	4	Others
			P9	TTGTTCTCC	1	Regulatory
			P6	TTGTTCTCC	3	Transporter
13.	TTGTTCTCT	13	P13	TTGTTCTCT	3	Enzyme
			P20	TTGTTCTCT	1	Enzyme
			P12	TTGTTCTCT	7	Hypothetical
			P3	TTGTTCTCT	1	Ribosomal
			P11	TTGTTCTCT	1	Transporter
14.	Variable patterns (False Positives)	11	P14	AGCCCCTGA	1	Enzyme
			P15	CACGGCGGT	1	Enzyme
			P16	CGACCTTCT	1	Enzyme
			P17	CTCGCTGCG	1	Enzyme
			P18	CTCTCCAC	1	Enzyme
			P19	GCTCCGCGG	1	Enzyme
			P8	GGCGAGCCG	1	Others
			P11	TGCGTCTTG	1	Others
			P6	CAAAAGCGC	1	Others
			P7	CGGCGACGG	1	Others
			P1	CAGCTCGTC	1	Cytochrome

(b)

S.No.	Gene name	Strand	Start	End	TFBS	Score	MSSP*	Gene ID	Description	Category
1.	lipA	R	-179	-171	AGCCCCTGA	9.24	98.60%	NP_770357.1	Lipoyl synthase	Enzyme
2.	ctpA	D	-169	-161	CACGGCGGT	8.16	94.62%	NP_767074.1	Carboxy-terminal protease	Enzyme
3.	ribH	D	-387	-379	CGACCTTCT	8.17	94.66%	NP_771669.1	Riboflavin synthase subunit beta	Enzyme
4.	glgA	D	-252	-244	CTCGCTGCG	8.17	94.66%	NP_769418.1	Glycogen synthase	Enzyme
5.	upp	R	-189	-181	CTCTCCAC	8.16	94.62%	NP_773428.1	Probable uracil phosphoribosyltransferase	Enzyme
6.	pcaI	R	-110	-102	GCTCCGCGG	8.54	96.02%	NP_770102.1	3-oxoadipate CoA-transferase subunit A	Enzyme
7.	fliN	R	-183	-175	GGCGAGCCG	8.54	96.02%	NP_773519.1	probable flagellar motor switch protein	Others
8.	groEL	R	-51	-43	TGCGTCTTG	8.16	94.62%	NP_771867.1	Chaperonin GroEL	Others
9.	trxA	D	-284	-276	CAAAAGCGC	8.17	94.66%	NP_767234.1	Thioredoxin	Others
10.	flgB	R	-130	-122	CGGCGACGG	7.93	93.77%	NP_772454.1	Flagellar basal body rod protein FlgB	Others
11.	soxA	R	-363	-355	CAGCTCGTC	8.88	97.27%	NP_770154.1	Probable diheme cytochrome C	Others

Supplementary Table 4. Details of Predicted Genes in Operons Found as Conserved Gene Pairs in *B. japonicum*.

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
Chemotaxis	NP_770967.1	bll4327	NP_770966 putative methyl-accepting chemotaxis protein	NP_770967 putative methyl-accepting chemotaxis protein	confidence=85 n=23
			NP_770967 putative methyl-accepting chemotaxis protein	NP_770969 hypothetical protein	confidence=85 n=39
	NP_768985.1	mcpK	NP_768983 chemotaxis two-component sensor histidine kinase	NP_768985 probable methyl-accepting chemotaxis protein	confidence=86 n=76
			NP_768984 probable chemotaxis protein	NP_768985 probable methyl-accepting chemotaxis protein	confidence=87 n=96
			NP_768985 probable methyl-accepting chemotaxis protein	NP_768986 probable chemotaxis protein	confidence=87 n=79
			NP_768985 probable methyl-accepting chemotaxis protein	NP_768987 putative sensory transducer protein	confidence=87 n=55
	NP_767216.1	blr0576	NP_767214 hypothetical protein	NP_767216 putative methyl-accepting chemotaxis protein	confidence=68 n=3
			NP_767216 putative methyl-accepting chemotaxis protein	NP_767217 hypothetical protein	confidence=64 n=1
	NP_768111.1	bll1471	NP_768110 putative methyl accepting chemotaxis protein	NP_768111 putative methyl accepting chemotaxis protein	confidence=64 n=4
Cytochrome	NP_767534.1	bll0894	NP_767532 hypothetical protein	NP_767534 putative cytochrome P450	confidence=64 n=2
			NP_767534 putative cytochrome P450	NP_767535 probable monooxygenase	confidence=61 n=2
			NP_767534 putative cytochrome P450	NP_767536 putative oxidoreductase	confidence=74 n=7
	NP_770154.1	soxA	NP_770152 sulfur oxidation protein SoxY	NP_770154 probable diheme cytochrome C	confidence=83 n=11
			NP_770153 probable sulfur oxidation protein	NP_770154 probable diheme cytochrome C	confidence=85 n=15
			NP_770154 probable diheme cytochrome C	NP_770155 probable Mn-dependent hydrolase	confidence=85 n=9
			NP_770154 probable diheme cytochrome C	NP_770156 probable sulfite oxidase molybdopterin subunit	confidence=74 n=2
Enzyme	NP_767814.1	coxG	NP_767812 protoheme IX farnesyltransferase	NP_767814 cytochrome C oxidase assembly protein	confidence=84 n=28
			NP_767813 CoxF protein	NP_767814 cytochrome C oxidase assembly protein	confidence=71 n=9
			NP_767814 cytochrome C oxidase assembly protein	NP_767815 cytochrome C oxidase subunit III	confidence=86 n=83
			NP_767814 cytochrome C oxidase assembly protein	NP_767816 hypothetical protein	confidence=74 n=17
	NP_769894.1	bll3254	NP_769894 oxidoreductase	NP_769896 cobinamide kinase/cobinamide phosphate guanylyl-transferase	confidence=59 n=2
	NP_772864.1	bll6224	NP_772863 3-hydroxybutyryl-CoA dehydrogenase	NP_772864 putative oxidoreductase protein	confidence=75 n=3
	NP_772865.1	hisC	NP_772865 histidinol-phosphate aminotransferase	NP_772866 probable ABC transporter permease protein	confidence=81 n=14
	NP_770534.1	blr3894	NP_770533 putative transposase	NP_770534 putative transposase	confidence=85 n=14

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
	NP_768183.1	blr1543	NP_768182 putative transposase	NP_768183 RSbeta putative transposase	confidence=85 n=14
	NP_773271.1	bll6631	NP_773271 probable phosphatidylserine decarboxylase proenzyme	NP_773273 hypothetical protein	confidence=64 n=1
	NP_773210.1	blr6570	NP_773209 MFS permease	NP_773210 probable dehydrogenase	confidence=73 n=7
	NP_769216.1	blr2576	NP_769216 N-carbamyl-D-amino acid amidohydrolase	NP_769218 MFS permease	confidence=71 n=6
	NP_767955.1	thrB	NP_767954 penicillin tolerance protein	NP_767955 homoserine kinase	confidence=87 n=26
			NP_767955 homoserine kinase	NP_767956 ribonuclease H	confidence=87 n=30
	NP_769404.1	fixO	NP_769403 cytochrome-c oxidase	NP_769404 cytochrome-c oxidase	confidence=88 n=86
			NP_769404 cytochrome-c oxidase	NP_769405 cbb3 oxidase subunit IV	confidence=64 n=5
			NP_769404 cytochrome-c oxidase	NP_769406 cbb3 oxidase subunit III	confidence=88 n=89
	NP_769181.1	nadB	NP_769180 nicotinate-mononucleotide pyrophosphorylase	NP_769181 L-aspartate oxidase	confidence=91 n=72
			NP_769181 L-aspartate oxidase	NP_769182 quinolinate synthetase	confidence=91 n=61
	NP_769180.1	nadC	NP_769180 nicotinate-mononucleotide pyrophosphorylase	NP_769181 L-aspartate oxidase	confidence=91 n=72
			NP_769180 nicotinate-mononucleotide pyrophosphorylase	NP_769182 quinolinate synthetase	confidence=91 n=81
	NP_767103.1	blr0463	NP_767101 probable ABC transporter permease protein	NP_767103 acetyltransferase	confidence=74 n=11
			NP_767102 probable ABC transporter permease protein	NP_767103 acetyltransferase	confidence=74 n=11
	NP_769778.1	nuoE	NP_769776 formate dehydrogenase alpha subunit	NP_769778 ATP synthase subunit E	confidence=85 n=89
			NP_769777 NADH dehydrogenase I chain F	NP_769778 ATP synthase subunit E	confidence=98 n=154
	NP_773410.1	blr6770	NP_773408 glycogen branching enzyme	NP_773410 alpha-amylase	confidence=82 n=38
			NP_773409 glycogen debranching enzyme	NP_773410 alpha-amylase	confidence=81 n=39
			NP_773410 alpha-amylase	NP_773411 probable glycosyl hydrolase	confidence=85 n=58
	NP_773605.1	blr6965	NP_773603 transcriptional regulatory protein	NP_773605 putative dehalogenase	confidence=82 n=36
			NP_773605 putative dehalogenase	NP_773606 hypothetical protein	confidence=57 n=1
			NP_773605 putative dehalogenase	NP_773607 MFS permease	confidence=77 n=39
	NP_772063.1	blr5423	NP_772061 dehydratase-like protein	NP_772063 probable dTDP-glucose-4,6 dehydratase	confidence=84 n=16
			NP_772062 hypothetical protein	NP_772063 probable dTDP-glucose-4,6 dehydratase	confidence=89 n=13
			NP_772063 probable dTDP-glucose-4,6 dehydratase	NP_772064 hypothetical protein	confidence=83 n=3

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_772063 probable dTDP-glucose-4,6 dehydratase	NP_772065 hypothetical protein	confidence=83 n=3
	NP_772053.1	bll5413	NP_772051 50S ribosomal protein L7/L12	NP_772053 2-hydroxyacid dehydrogenase	confidence=62 n=2
			NP_772052 50S ribosomal Protein L10	NP_772053 2-hydroxyacid dehydrogenase	confidence=62 n=2
			NP_772053 2-hydroxyacid dehydrogenase	NP_772054 50S ribosomal protein L1	confidence=64 n=5
			NP_772053 2-hydroxyacid dehydrogenase	NP_772055 50S ribosomal Protein L11	confidence=64 n=5
	NP_769776.1	fdhF	NP_769774 putative NAD-dependent formate dehydrogenase	NP_769776 formate dehydrogenase alpha subunit	confidence=85 n=27
			NP_769775 formate dehydrogenase accessory protein	NP_769776 formate dehydrogenase alpha subunit	confidence=87 n=39
			NP_769776 formate dehydrogenase alpha subunit	NP_769777 NADH dehydrogenase I chain F	confidence=85 n=97
			NP_769776 formate dehydrogenase alpha subunit	NP_769778 ATP synthase subunit E	confidence=85 n=89
	NP_774083.1	blr7443	NP_774083 putative hydrolase	NP_774084 prolipoprotein diacylglyceryl transferase	confidence=62 n=2
			NP_774083 putative hydrolase	NP_774085 hypothetical protein	confidence=62 n=2
	NP_773435.1	blr6795	NP_773435 putative recemase	NP_773436 probable acyl dehydratase	confidence=67 n=10
			NP_773435 putative recemase	NP_773437 putative Citrate lyase	confidence=76 n=27
	NP_770804.1	fabG	NP_770803 hypothetical protein	NP_770804 short chain dehydrogenase	confidence=66 n=2
			NP_770804 short chain dehydrogenase	NP_770805 hypothetical protein	confidence=80 n=1
	NP_774206.1	blr7566	NP_774206 oxidoreductase	NP_774207 hypothetical protein	confidence=65 n=4
			NP_774206 oxidoreductase	NP_774208 TrpR binding protein WrbA	confidence=69 n=1
	NP_772368.1	bsl5728	NP_772368 phosphoribosylformylglycinamide synthase	NP_772369 phosphoribosylaminoimidazole-succinocarboxamidesynthase	confidence=90 n=85
	NP_774933.1	bll8293	NP_774933 putative transposase	NP_774935 probable ATP-binding protein	confidence=80 n=1
	NP_772979.1	hyfB	NP_772979 NADH dehydrogenase subunit N	NP_772980 probable hydrogenlyase component	confidence=87 n=57
			NP_772979 NADH dehydrogenase subunit N	NP_772981 hypothetical protein	confidence=85 n=36
	NP_774438.1	bll7798	NP_774438 putative nitroreductase	NP_774439 putative acyl-CoA dehydrogenase	confidence=64 n=6
			NP_774438 putative nitroreductase	NP_774440 putative acyl-CoA dehydrogenase	confidence=64 n=6
	NP_767893.1	blr1253	NP_767891 non-heme haloperoxidase	NP_767893 dehydrogenase	confidence=79 n=43
			NP_767893 dehydrogenase	NP_767894 hypothetical protein	confidence=64 n=1
	NP_771419.1	bll4779	NP_771417 threonine synthase	NP_771419 dihydroliipoamide acetyltransferase	confidence=64 n=1

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_771418 dihydrolipoamide dehydrogenase	NP_771419 dihydrolipoamide acetyltransferase	confidence=99 n=225
			NP_771419 dihydrolipoamide acetyltransferase	NP_771421 hypothetical protein	confidence=64 n=5
	NP_772903.1	bll6263	NP_772901 hypothetical protein	NP_772903 putative enoyl-CoA hydratase	confidence=64 n=1
	NP_767565.1	pcaF	NP_767563 probable chemotaxis protein	NP_767565 acetyl-CoA acetyltransferase	confidence=79 n=8
			NP_767565 acetyl-CoA acetyltransferase	NP_767567 protocatechuate 3,4-dioxygenase beta chain	confidence=76 n=11
	NP_769130.1	apt	NP_769129 anthranilate synthase component I and II	NP_769130 adenine phosphoribosyltransferase	confidence=66 n=5
	NP_771247.1	glmS	NP_771246 hypothetical protein	NP_771247 D-fructose-6-phosphate amidotransferase	confidence=71 n=13
			NP_771247 D-fructose-6-phosphate amidotransferase	NP_771248 UDP-N-acetylglucosamine pyrophosphorylase	confidence=98 n=117
	NP_769903.1	cobN	NP_769901 hypothetical protein	NP_769903 cobaltochelatase	confidence=77 n=12
			NP_769902 cobalamin synthesis protein	NP_769903 cobaltochelatase	confidence=82 n=41
			NP_769903 cobaltochelatase	NP_769904 hypothetical protein	confidence=82 n=9
			NP_769903 cobaltochelatase	NP_769905 precorrin-8X methylmutase	confidence=82 n=15
	NP_773056.1	blr6416	NP_773056 benzoylformate decarboxylase	NP_773057 vanillin: NAD oxidoreductase	confidence=78 n=41
			NP_773056 benzoylformate decarboxylase	NP_773058 hypothetical protein	confidence=69 n=12
	NP_773471.1	idnD	NP_773470 mannonate dehydratase	NP_773471 L-idonate 5-dehydrogenase	confidence=74 n=8
			NP_773471 L-idonate 5-dehydrogenase	NP_773472 probable ABC transporter permease protein	confidence=77 n=11
			NP_773471 L-idonate 5-dehydrogenase	NP_773473 probable ABC transporter permease protein	confidence=77 n=7
	NP_769157.1	bll2517	NP_769155 similar to pyruvate phosphate dikinase	NP_769157 putative acetate kinase (acetokinase) protein	confidence=64 n=1
			NP_769157 putative acetate kinase (acetokinase) protein	NP_769158 putative phosphoketolase	confidence=84 n=9
	NP_767577.1	blr0937	NP_767575 hypothetical protein	NP_767577 putative dioxygenase	confidence=59 n=1
	NP_769218.1	blr2578	NP_769216 N-carbamyl-D-amino acid amidohydrolase	NP_769218 MFS permease	confidence=71 n=6
			NP_769217 transcriptional regulatory protein	NP_769218 MFS permease	confidence=80 n=27
			NP_769218 MFS permease	NP_769219 hypothetical protein	confidence=64 n=1
	NP_768417.1	ahpC	NP_768416 alkyl hydroperoxide reductase	NP_768417 alkyl hydroperoxide reductase	confidence=84 n=43
	NP_769855.1	norB	NP_769853 hypothetical protein	NP_769855 nitric oxide reductase subunit B	confidence=65 n=4

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_769854 nitric oxide reductase subunit C	NP_769855 nitric oxide reductase subunit B	confidence=86 n=30
			NP_769855 nitric oxide reductase subunit B	NP_769856 NorQ protein	confidence=86 n=24
			NP_769855 nitric oxide reductase subunit B	NP_769857 NorD protein	confidence=86 n=25
	NP_769899.1	cbiP	NP_769899 cobyric acid synthase	NP_769900 cob(I)yrinic acid a,c-diamide adenosyltransferase	confidence=82 n=34
	NP_770570.1	blr3930	NP_770570 hypothetical protein	NP_770571 probable substrate-binding protein	confidence=70 n=8
	NP_769735.1	blr3095	NP_769733 hypothetical protein	NP_769735 probable aminotransferase	confidence=74 n=9
			NP_769735 probable aminotransferase	NP_769736 ABC transporter substrate-binding protein	confidence=79 n=2
			NP_769735 probable aminotransferase	NP_769737 ABC transporter permease protein	confidence=82 n=9
	NP_771492.1	lpxD	NP_771491 (3R)-hydroxymyristoyl ACP dehydrase	NP_771492 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	confidence=93 n=147
			NP_771492 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	NP_771493 putative outer membrane protein	confidence=93 n=155
			NP_771492 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	NP_771494 zinc metallopeptidase	confidence=93 n=130
	NP_770102.1	pcaI	NP_770100 nodulation protein N	NP_770102 3-oxoadipate CoA-transferase subunit A	confidence=68 n=1
			NP_770101 3-oxoadipate CoA-transferase subunit B	NP_770102 3-oxoadipate CoA-transferase subunit A	confidence=92 n=124
	NP_771374.1	secF	NP_771372 putative phytoene synthase	NP_771374 protein-export membrane protein	confidence=76 n=17
			NP_771373 hypothetical protein	NP_771374 protein-export membrane protein	confidence=77 n=25
			NP_771374 protein-export membrane protein	NP_771375 protein-export membrane protein	confidence=93 n=187
			NP_771374 protein-export membrane protein	NP_771376 preprotein translocase protein	confidence=92 n=143
	NP_773668.1	blr7028	NP_773667 hypothetical protein	NP_773668 acetoacetate decarboxylase	confidence=77 n=4
			NP_773668 acetoacetate decarboxylase	NP_773669 d-beta-hydroxybutyrate dehydrogenase	confidence=68 n=10
	NP_771547.1	blh4907	NP_771545 NADH dehydrogenase subunit M	NP_771547 NADH dehydrogenase kappa subunit	confidence=98 n=213
			NP_771546 NADH dehydrogenase subunit L	NP_771547 NADH dehydrogenase kappa subunit	confidence=98 n=211
			NP_771547 NADH dehydrogenase kappa subunit	NP_771548 NADH dehydrogenase subunit J	confidence=98 n=225

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_771547 NADH dehydrogenase kappa subunit	NP_771549 NADH dehydrogenase subunit I	confidence=98 n=172
	NP_766897.1	blr0257	NP_766897 two-component sensor histidine kinase	NP_766898 two-component response regulator	confidence=76 n=29
			NP_766897 two-component sensor histidine kinase	NP_766899 two-component response regulator	confidence=76 n=28
	NP_773413.1	ligD	NP_773413 DNA ligase	NP_773415 two-component response regulator	confidence=64 n=5
	NP_767822.1	mpp	NP_767820 two-component response regulator	NP_767822 mitochondrial processing peptidase-like protein	confidence=79 n=7
			NP_767821 threonine synthase	NP_767822 mitochondrial processing peptidase-like protein	confidence=87 n=30
			NP_767822 mitochondrial processing peptidase-like protein	NP_767823 ribosomal-protein-alanine N-acetyltransferase	confidence=77 n=23
			NP_767822 mitochondrial processing peptidase-like protein	NP_767824 hypothetical protein	confidence=66 n=6
	NP_769109.1	papS	NP_769107 hypothetical protein	NP_769109 poly(A) polymerase	confidence=82 n=32
			NP_769108 hypothetical protein	NP_769109 poly(A) polymerase	confidence=66 n=6
	NP_773786.1	ftsH	NP_773786 metalloprotease	NP_773787 hypothetical protein	confidence=97 n=45
			NP_773786 metalloprotease	NP_773788 hypothetical protein	confidence=77 n=21
	NP_769589.1	bll2949	NP_769588 acyl-CoA synthase	NP_769589 hypothetical oxidoreductase	confidence=90 n=104
	NP_767888.1	blr1248	NP_767888 putative thioredoxin reductase	NP_767889 hypothetical protein	confidence=64 n=1
			NP_767888 putative thioredoxin reductase	NP_767890 hypothetical protein	confidence=64 n=2
	NP_771669.1	ribH	NP_771667 putative thiamine-monophosphate kinase	NP_771669 riboflavin synthase subunit beta	confidence=98 n=100
			NP_771668 transcription antitermination protein NusB	NP_771669 riboflavin synthase subunit beta	confidence=97 n=160
			NP_771669 riboflavin synthase subunit beta	NP_771670 riboflavin synthase subunit alpha	confidence=92 n=158
			NP_771669 riboflavin synthase subunit beta	NP_771671 riboflavin biosynthesis protein	confidence=93 n=178
	NP_771614.1	blr4974	NP_771613 probable glycosyl transferase	NP_771614 polysaccharide biosynthesis glycosyltransferase	confidence=78 n=14
			NP_771614 polysaccharide biosynthesis glycosyltransferase	NP_771615 hypothetical protein	confidence=71 n=8
	NP_767007.1	blr0367	NP_767007 putative glucose dehydrogenase (acceptor)	NP_767008 hypothetical protein	confidence=64 n=1
	NP_767074.1	ctpA	NP_767072 hypothetical protein	NP_767074 carboxy-terminal protease	confidence=87 n=28
			NP_767073 hypothetical protein	NP_767074 carboxy-terminal protease	confidence=91 n=96
			NP_767074 carboxy-terminal protease	NP_767075 hypothetical protein	confidence=69 n=10
			NP_767074 carboxy-terminal protease	NP_767076 dinucleoside polyphosphate hydrolase	confidence=87 n=28

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
	NP_769647.1	ispH	NP_769646 hypothetical protein	NP_769647 4-hydroxy-3-methylbut-2-enyl diphosphate reductase	confidence=80 n=21
			NP_769647 4-hydroxy-3-methylbut-2-enyl diphosphate reductase	NP_769649 hypothetical protein	confidence=66 n=3
	NP_773228.1	prmA	NP_773226 probable phytoene dehydrogenase	NP_773228 ribosomal protein L11 methyltransferase	confidence=66 n=7
			NP_773228 ribosomal protein L11 methyltransferase	NP_773229 aminopeptidase P	confidence=76 n=21
			NP_773228 ribosomal protein L11 methyltransferase	NP_773230 major facilitator superfamily transporter	confidence=87 n=6
	NP_768513.1	blr1873	NP_768513 putative transposase	NP_768514 putative transposase	confidence=84 n=32
	NP_769225.1	rbcL	NP_769223 transketolase	NP_769225 methionine sulfoxide reductase A	confidence=77 n=7
			NP_769224 fructose-bisphosphate aldolase	NP_769225 methionine sulfoxide reductase A	confidence=77 n=8
			NP_769225 methionine sulfoxide reductase A	NP_769226 ribulose 1,5-bisphosphate carboxylase/oxygenase small subunit	confidence=86 n=24
			NP_769225 methionine sulfoxide reductase A	NP_769227 probable CbbX protein	confidence=81 n=10
	NP_771201.1	pheC	NP_771201 probable cyclohexadienyl dehydratase precursor	NP_771202 hypothetical protein	confidence=64 n=6
	NP_773600.1	blr6960	NP_773600 arylesterase	NP_773601 putative hydrolase	confidence=68 n=7
	NP_771138.1	nthA	NP_771136 hypothetical protein	NP_771138 nitrile hydratase subunit alpha	confidence=74 n=9
			NP_771137 nitrile hydratase subunit beta	NP_771138 nitrile hydratase subunit alpha	confidence=74 n=14
	NP_773042.1	bll6402	NP_773042 nitrilase	NP_773043 ABC transporter permease protein	confidence=68 n=8
			NP_773042 nitrilase	NP_773044 ABC transporter permease protein	confidence=68 n=8
	NP_767600.1	blr0960	NP_767600 5'-methylthioadenosine phosphorylase	NP_767601 translation initiation factor IF-2B subunit alpha	confidence=82 n=11
	NP_769684.1	blr3044	NP_769682 RNA polymerase sigma-70 factor	NP_769684 probable extracellular protease	confidence=66 n=3
			NP_769683 hypothetical protein	NP_769684 probable extracellular protease	confidence=66 n=3
	NP_766646.1	nrdF	NP_766646 ribonucleotide-diphosphate reductase beta subunit	NP_766647 ribonucleotide-diphosphate reductase alpha subunit	confidence=92 n=135
	NP_772369.1	purC	NP_772368 phosphoribosylformylglycinamide synthase	NP_772369 phosphoribosylaminoimidazole-succinocarboxamidesynthase	confidence=90 n=85
			NP_772369 phosphoribosylaminoimidazole-succinocarboxamidesynthase	NP_772371 cyanate hydratase	confidence=66 n=2
	NP_771517.1	proS	NP_771515 probable ABC transporter ATP-binding protein	NP_771517 prolyl-tRNA synthetase	confidence=91 n=44
			NP_771516 probable ABC transporter permease protein	NP_771517 prolyl-tRNA synthetase	confidence=87 n=31

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_771517 prolyl-tRNA synthetase	NP_771518 possible Copper export protein	confidence=66 n=4
			NP_771517 prolyl-tRNA synthetase	NP_771519 hypothetical protein	confidence=66 n=5
	NP_768694.1	blr2054	NP_768692 probable maturase; reverse transcriptase	NP_768694 putative transposase	confidence=77 n=2
			NP_768693 putative transposase	NP_768694 putative transposase	confidence=84 n=43
			NP_768694 putative transposase	NP_768696 putative transposase	confidence=80 n=3
Hypothetical	NP_767639.1	bll0998	NP_767639 hypothetical protein	NP_767640 hypothetical protein	confidence=64 n=5
			NP_767639 hypothetical protein	NP_767641 probable ABC transporter permease protein	confidence=64 n=5
	NP_769008.1	blr2368	NP_769008 hypothetical protein	NP_769009 probable exopolysaccharide production protein	confidence=68 n=3
	NP_771797.1	bll5157	NP_771795 hypothetical protein	NP_771797 hypothetical protein	confidence=66 n=4
			NP_771797 hypothetical protein	NP_771799 hypothetical protein	confidence=80 n=10
	NP_773253.1	bll6613	NP_773252 hypothetical protein	NP_773253 hypothetical protein	confidence=73 n=41
			NP_773253 hypothetical protein	NP_773254 putative esterase	confidence=55 n=1
	NP_774914.1	bll8274	NP_774914 hypothetical protein	NP_774915 hypothetical protein	confidence=75 n=6
	NP_767276.1	bll0636	NP_767274 tRNA modification GTPase	NP_767276 hypothetical protein	confidence=84 n=21
			NP_767275 transcription termination factor Rho	NP_767276 hypothetical protein	confidence=84 n=31
	NP_767277.1	blr0637	NP_767277 hypothetical protein	NP_767278 Maf-like protein	confidence=87 n=30
			NP_767277 hypothetical protein	NP_767279 dephospho-CoA kinase	confidence=87 n=29
	NP_770359.1	blr3719	NP_770359 hypothetical protein	NP_770361 dihydrolipoamide S-acetyltransferase	confidence=98 n=118
	NP_774918.1	bsl8278	NP_774918 hypothetical protein	NP_774919 probable conjugal transfer protein	confidence=82 n=10
			NP_774918 hypothetical protein	NP_774920 probable conjugal transfer protein	confidence=82 n=8
	NP_768070.1	bll1430	NP_768070 hypothetical protein	NP_768071 aminopeptidase	confidence=87 n=26
	NP_769390.1	blr2750	NP_769389 probable C4-dicarboxylate-binding protein	NP_769390 hypothetical protein	confidence=87 n=27
	NP_769497.1	blr2857	NP_769497 hypothetical protein	NP_769498 probable sulfolipoamide decarboxylase	confidence=86 n=9
	NP_770021.1	bll3381	NP_770019 hypothetical protein	NP_770021 hypothetical protein	confidence=67 n=7
	NP_771842.1	bll5202	NP_771840 hypothetical protein	NP_771842 hypothetical protein	confidence=66 n=1
			NP_771841 hypothetical protein	NP_771842 hypothetical protein	confidence=66 n=1
	NP_771929.1	blr5289	NP_771928 transcriptional regulatory protein	NP_771929 hypothetical protein	confidence=67 n=6
	NP_772225.1	bsl5585	NP_772225 hypothetical protein	NP_772226 serine acetyltransferase	confidence=76 n=18
	NP_772427.1	bll5787	NP_772425 xylulokinase	NP_772427 hypothetical protein	confidence=62 n=1
			NP_772427 hypothetical protein	NP_772429 transcriptional regulatory protein	confidence=64 n=2

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
	NP_772428.1	blr5788	NP_772426 putative integral membrane protein	NP_772428 hypothetical protein	confidence=61 n=1
	NP_773073.1	bll6433	NP_773073 hypothetical protein	NP_773075 2-isopropylmalate synthase	confidence=66 n=2
	NP_774103.1	bll7463	NP_774103 hypothetical protein	NP_774104 hypothetical protein	confidence=66 n=7
	NP_774105.1	blr7465	NP_774105 hypothetical protein	NP_774106 ribonuclease	confidence=66 n=7
			NP_774105 hypothetical protein	NP_774107 hypothetical protein	confidence=66 n=2
	NP_774235.1	blr7595	NP_774233 multidrug resistance efflux pump	NP_774235 hypothetical protein	confidence=73 n=1
			NP_774234 putative multidrug resistance protein	NP_774235 hypothetical protein	confidence=82 n=8
	NP_769267.1	bll2627	NP_769267 hypothetical protein	NP_769268 ECF family sigma factor	confidence=80 n=40
	NP_771048.1	bsr4408	NP_771048 hypothetical protein	NP_771050 cold shock protein	confidence=66 n=2
	NP_774241.1	bll7601	NP_774239 amino acid ABC transporter permease protein	NP_774241 hypothetical protein	confidence=92 n=6
			NP_774240 ABC transporter amino-acid-binding protein	NP_774241 hypothetical protein	confidence=92 n=8
	NP_767725.1	blr1085	NP_767724 hypothetical protein	NP_767725 hypothetical protein	confidence=66 n=7
	NP_772281.1	blr5641	NP_772281 hypothetical protein	NP_772282 hypothetical protein	confidence=64 n=4
	NP_774093.1	blr7453	NP_774093 hypothetical protein	NP_774094 pyrroline-5-carboxylate reductase	confidence=82 n=26
	NP_774174.1	blr7534	NP_774172 co-chaperonin GroES	NP_774174 hypothetical protein	confidence=64 n=3
			NP_774173 chaperonin GroEL	NP_774174 hypothetical protein	confidence=66 n=7
	NP_766995.1	blr0355	NP_766993 hypothetical protein	NP_766995 hypothetical protein	confidence=64 n=8
			NP_766994 hypothetical protein	NP_766995 hypothetical protein	confidence=64 n=5
			NP_766995 hypothetical protein	NP_766996 Acr family transport protein	confidence=89 n=57
	NP_767368.1	bsl0728	NP_767368 hypothetical protein	NP_767369 small heat shock protein	confidence=87 n=21
			NP_767368 hypothetical protein	NP_767370 glycerol-3-phosphate ABC transporter ATP-binding protein	confidence=64 n=5
	NP_768846.1	bsl2206	NP_768846 hypothetical protein	NP_768847 flagellar biosynthesis protein	confidence=66 n=7
	NP_769339.1	bll2699	NP_769338 putative amidohydrolase	NP_769339 hypothetical protein	confidence=74 n=2
			NP_769339 hypothetical protein	NP_769340 hypothetical protein	confidence=64 n=1
	NP_769340.1	bll2700	NP_769338 putative amidohydrolase	NP_769340 hypothetical protein	confidence=84 n=17
			NP_769339 hypothetical protein	NP_769340 hypothetical protein	confidence=64 n=1
	NP_770171.1	blr3531	NP_770170 probable aromatic acid decarboxylase	NP_770171 hypothetical protein	confidence=87 n=16
			NP_770171 hypothetical protein	NP_770173 putative carbon monoxide dehydrogenase large chain	confidence=64 n=3
	NP_770763.1	bll4123	NP_770761 hypothetical protein	NP_770763 hypothetical protein	confidence=77 n=24
			NP_770762 polyphosphate kinase	NP_770763 hypothetical protein	confidence=82 n=23

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_770763 hypothetical protein	NP_770764 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	confidence=82 n=16
	NP_771587.1	bll4947	NP_771585 trigger factor	NP_771587 hypothetical protein	confidence=82 n=10
	NP_771910.1	blr5270	NP_771909 two-component hybrid sensor and regulator	NP_771910 hypothetical protein	confidence=81 n=5
			NP_771910 hypothetical protein	NP_771911 major facilitator superfamily transporter	confidence=69 n=4
	NP_772747.1	blr6107	NP_772746 hypothetical protein	NP_772747 hypothetical protein	confidence=62 n=1
	NP_773685.1	bsr7045	NP_773683 methionine sulfoxide reductase A	NP_773685 hypothetical protein	confidence=62 n=2
			NP_773684 methionine sulfoxide reductase B	NP_773685 hypothetical protein	confidence=62 n=2
	NP_774364.1	blr7724	NP_774363 hypothetical protein	NP_774364 hypothetical protein	confidence=66 n=1
	NP_767145.1	bll0505	NP_767143 3-isopropylmalate dehydrogenase	NP_767145 hypothetical protein	confidence=66 n=6
			NP_767145 hypothetical protein	NP_767146 hypothetical protein	confidence=80 n=38
			NP_767145 hypothetical protein	NP_767147 hypothetical protein	confidence=64 n=5
	NP_767163.1	bll0523	NP_767162 argininosuccinate synthase	NP_767163 hypothetical protein	confidence=66 n=7
			NP_767163 hypothetical protein	NP_767164 hypothetical protein	confidence=66 n=7
			NP_767163 hypothetical protein	NP_767165 hypothetical protein	confidence=66 n=7
	NP_767595.1	bll0955	NP_767594 hypothetical protein	NP_767595 hypothetical protein	confidence=68 n=1
	NP_767943.1	blr1303	NP_767941 immunogenic protein precursor	NP_767943 hypothetical protein	confidence=77 n=11
			NP_767942 hypothetical protein	NP_767943 hypothetical protein	confidence=77 n=16
			NP_767943 hypothetical protein	NP_767944 dehydrogenase	confidence=64 n=4
	NP_769254.1	blr2614	NP_769254 hypothetical protein	NP_769255 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	confidence=66 n=2
			NP_769254 hypothetical protein	NP_769256 glutaryl-CoA dehydrogenase	confidence=66 n=2
	NP_770057.1	bll3417	NP_770056 hypothetical protein	NP_770057 hypothetical protein	confidence=61 n=3
	NP_771541.1	bll4901	NP_771540 hypothetical protein	NP_771541 hypothetical protein	confidence=77 n=17
			NP_771541 hypothetical protein	NP_771542 hypothetical protein	confidence=76 n=19
			NP_771541 hypothetical protein	NP_771543 biotin--protein ligase	confidence=76 n=19
	NP_771581.1	bll4941	NP_771579 methyltransferase	NP_771581 hypothetical protein	confidence=65 n=1
	NP_771683.1	bll5043	NP_771681 hypothetical protein	NP_771683 hypothetical protein	confidence=64 n=1
			NP_771682 hypothetical protein	NP_771683 hypothetical protein	confidence=64 n=1
	NP_772579.1	blr5939	NP_772577 gluconate 5-dehydrogenase	NP_772579 hypothetical protein	confidence=81 n=81
			NP_772578 hypothetical protein	NP_772579 hypothetical protein	confidence=64 n=1
	NP_773549.1	bll6909	NP_773548 hypothetical protein	NP_773549 hypothetical protein	confidence=84 n=5

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
	NP_773701.1	blr7061	NP_773700 hypothetical protein	NP_773701 hypothetical protein	confidence=87 n=5
			NP_773701 hypothetical protein	NP_773703 probable 2-ketogluconate reductase	confidence=79 n=7
	NP_773919.1	bll7279	NP_773917 two-component hybrid sensor and regulator	NP_773919 hypothetical protein	confidence=62 n=2
			NP_773918 two-component response regulator	NP_773919 hypothetical protein	confidence=69 n=5
			NP_773919 hypothetical protein	NP_773920 hypothetical protein	confidence=66 n=1
	NP_766689.1	bsl0049	NP_766687 conjugal transfer protein precursor	NP_766689 hypothetical protein	confidence=71 n=3
			NP_766688 hypothetical protein	NP_766689 hypothetical protein	confidence=71 n=3
			NP_766689 hypothetical protein	NP_766690 putative partition protein	confidence=71 n=3
			NP_766689 hypothetical protein	NP_766691 replication protein A	confidence=71 n=1
	NP_767349.1	blr0709	NP_767349 hypothetical protein	NP_767351 hypothetical protein	confidence=62 n=1
	NP_769648.1	blr3008	NP_769648 hypothetical protein	NP_769650 probable ornithine aminotransferase	confidence=84 n=8
	NP_771207.1	blr4567	NP_771206 hypothetical protein	NP_771207 hypothetical protein	confidence=90 n=133
			NP_771207 hypothetical protein	NP_771208 hypothetical protein	confidence=84 n=71
	NP_772475.1	bll5835	NP_772474 dnaK deletion suppressor protein	NP_772475 hypothetical protein	confidence=65 n=1
	NP_767744.1	blr1104	NP_767742 hypothetical protein	NP_767744 hypothetical protein	confidence=82 n=8
			NP_767743 hypothetical protein	NP_767744 hypothetical protein	confidence=66 n=7
			NP_767744 hypothetical protein	NP_767746 2'-deoxycytidine 5'-triphosphate deaminase	confidence=66 n=6
	NP_767886.1	blr1246	NP_767885 hypothetical protein	NP_767886 hypothetical protein	confidence=61 n=1
	NP_768775.1	blr2135	NP_768773 hypothetical protein	NP_768775 hypothetical protein	confidence=65 n=1
			NP_768774 hypothetical protein	NP_768775 hypothetical protein	confidence=54 n=1
	NP_768848.1	bll2208	NP_768848 hypothetical protein	NP_768849 copper tolerance protein	confidence=69 n=5
			NP_768848 hypothetical protein	NP_768850 multicopper oxidase	confidence=80 n=14
	NP_770522.1	blr3882	NP_770522 hypothetical protein	NP_770524 putative dihydrodipicolinate synthase	confidence=69 n=2
	NP_770531.1	bll3891	NP_770531 hypothetical protein	NP_770532 hypothetical protein	confidence=61 n=1
	NP_770630.1	bll3990	NP_770630 hypothetical protein	NP_770631 putative oxidoreductase	confidence=65 n=6
	NP_770643.1	blr4003	NP_770643 hypothetical protein	NP_770644 transcriptional regulatory protein	confidence=71 n=2
	NP_771202.1	blr4562	NP_771201 probable cyclohexadienyl dehydratase precursor	NP_771202 hypothetical protein	confidence=64 n=6
	NP_771723.1	bsl5083	NP_771721 putative multidrug resistance protein	NP_771723 hypothetical protein	confidence=68 n=1
	NP_772301.1	bll5661	NP_772299 hypothetical protein	NP_772301 hypothetical protein	confidence=82 n=13
			NP_772300 hypothetical protein	NP_772301 hypothetical protein	confidence=81 n=14
			NP_772301 hypothetical protein	NP_772302 hypothetical protein	confidence=81 n=21

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_772301 hypothetical protein	NP_772303 hypothetical protein	confidence=81 n=21
	NP_772434.1	bsr5794	NP_772433 hypothetical protein	NP_772434 hypothetical protein	confidence=64 n=4
	NP_772455.1	blr5815	NP_772455 hypothetical protein	NP_772456 flagellar biosynthesis protein	confidence=68 n=10
	NP_773510.1	bll6870	NP_773508 flagellar protein	NP_773510 hypothetical protein	confidence=64 n=2
			NP_773509 flagellar L-ring protein precursor	NP_773510 hypothetical protein	confidence=77 n=12
			NP_773510 hypothetical protein	NP_773511 flagellar P-ring protein precursor	confidence=77 n=7
			NP_773510 hypothetical protein	NP_773512 flagellar basal body P-ring biosynthesis protein	confidence=64 n=2
	NP_773811.1	bll7171	NP_773809 hypothetical protein	NP_773811 hypothetical protein	confidence=67 n=5
			NP_773810 hypothetical protein	NP_773811 hypothetical protein	confidence=81 n=39
	NP_774090.1	blr7450	NP_774090 hypothetical protein	NP_774091 hypothetical protein	confidence=59 n=2
	NP_774207.1	blr7567	NP_774206 oxidoreductase	NP_774207 hypothetical protein	confidence=65 n=4
			NP_774207 hypothetical protein	NP_774208 TrpR binding protein WrbA	confidence=85 n=15
Others	NP_768912.1	blr2272	NP_768910 sugar ABC transporter ATP-binding protein	NP_768912 putative porin precursor	confidence=68 n=9
			NP_768911 sugar ABC transporter permease protein	NP_768912 putative porin precursor	confidence=67 n=1
	NP_772565.1	bll5925	NP_772563 putative UDP-glucose 4-epimerase	NP_772565 putative capsular polysaccharide biosynthesis protein	confidence=87 n=22
			NP_772564 probable glycosyl transferase	NP_772565 putative capsular polysaccharide biosynthesis protein	confidence=84 n=3
			NP_772565 putative capsular polysaccharide biosynthesis protein	NP_772567 probable ADP-heptose synthase	confidence=81 n=11
	NP_767316.1	grpE	NP_767315 heat-inducible transcription repressor	NP_767316 heat shock protein	confidence=92 n=140
	NP_771577.1	blr4937	NP_771575 putative divalent cation resistant determinant protein C	NP_771577 probable cation efflux system protein	confidence=87 n=69
			NP_771576 putative cation efflux system protein	NP_771577 probable cation efflux system protein	confidence=89 n=146
			NP_771577 probable cation efflux system protein	NP_771578 putative cation efflux system protein	confidence=83 n=6
	NP_772897.1	bll6257	NP_772896 probable dehydrogenase	NP_772897 putative efflux pump protein	confidence=79 n=39
			NP_772897 putative efflux pump protein	NP_772898 putative multidrug resistance protein	confidence=92 n=127
	NP_773519.1	fliN	NP_773517 flagellar biosynthesis protein	NP_773519 probable flagellar motor switch protein	confidence=76 n=8
			NP_773518 probable flagellar motor switch protein	NP_773519 probable flagellar motor switch protein	confidence=71 n=4
			NP_773519 probable flagellar motor switch protein	NP_773520 hypothetical protein	confidence=64 n=2
			NP_773519 probable flagellar motor switch protein	NP_773521 hypothetical protein	confidence=88 n=65

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
	NP_767808.1	tldD	NP_767807 signal peptidase	NP_767808 TldD protein	confidence=66 n=4
			NP_767808 TldD protein	NP_767809 hypothetical protein	confidence=87 n=10
	NP_768099.1	ureF	NP_768097 urease alpha subunit	NP_768099 urease accessory protein	confidence=93 n=83
			NP_768098 hypothetical protein	NP_768099 urease accessory protein	confidence=69 n=5
			NP_768099 urease accessory protein	NP_768100 urease accessory protein	confidence=93 n=114
	NP_773236.1	ftsZ	NP_773234 hypothetical protein	NP_773236 cell division protein FtsZ	confidence=87 n=29
			NP_773235 UDP-3-o-(3-hydroxymyristoyl) N-acetylglucosamine deacetylase	NP_773236 cell division protein FtsZ	confidence=87 n=30
			NP_773236 cell division protein FtsZ	NP_773237 cell division protein	confidence=87 n=33
			NP_773236 cell division protein FtsZ	NP_773238 putative cell division protein	confidence=87 n=26
	NP_771709.1	bcpB	NP_771709 BcpB protein	NP_771710 SsrA-binding protein	confidence=62 n=2
			NP_771709 BcpB protein	NP_771711 mechanosensitive channel homolog	confidence=62 n=2
	NP_766793.1	blr0153	NP_766791 cytochrome O ubiquinol oxidase subunit III	NP_766793 probable surfait locus protein 1	confidence=84 n=49
			NP_766792 cytochrome O ubiquinol oxidase subunit IV	NP_766793 probable surfait locus protein 1	confidence=72 n=13
			NP_766793 probable surfait locus protein 1	NP_766794 two-component sensor histidine kinase	confidence=72 n=7
			NP_766793 probable surfait locus protein 1	NP_766795 two-component response regulator	confidence=72 n=7
	NP_768461.1	rhcT	NP_768459 RhcR protein	NP_768461 RhcT protein	confidence=96 n=99
			NP_768460 RhcS protein	NP_768461 RhcT protein	confidence=96 n=96
			NP_768461 RhcT protein	NP_768462 RhcU protein	confidence=87 n=90
	NP_767234.1	trxA	NP_767234 thioredoxin	NP_767235 hypothetical protein	confidence=77 n=32
	NP_771867.1	groEL	NP_771866 co-chaperonin GroES	NP_771867 chaperonin GroEL	confidence=98 n=333
	NP_766917.1	blr0277	NP_766916 hypothetical protein	NP_766917 AcrB/AcrD/AcrF family protein	confidence=91 n=199
			NP_766917 AcrB/AcrD/AcrF family protein	NP_766919 two-component hybrid sensor and regulator	confidence=84 n=33
	NP_772454.1	flgB	NP_772452 flagellar basal body protein	NP_772454 flagellar basal body rod protein	confidence=85 n=32
			NP_772453 flagellar basal body rod protein	NP_772454 flagellar basal body rod protein	confidence=98 n=89
Receptor	NP_771144.1	blr4504	NP_771142 probable ABC transporter permease protein	NP_771144 TonB-dependent receptor	confidence=85 n=16
			NP_771144 TonB-dependent receptor	NP_771145 hypothetical protein	confidence=86 n=19
	NP_770961.1	bll4321	NP_770959 putative multidrug resistance protein	NP_770961 putative outer membrane channel lipoprotein	confidence=87 n=31
			NP_770960 probable RND efflux membrane fusion protein	NP_770961 putative outer membrane channel lipoprotein	confidence=92 n=117

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_770961 putative outer membrane channel lipoprotein	NP_770963 hypothetical protein	confidence=64 n=2
	NP_767330.1	blr0690	NP_767329 endonuclease III	NP_767330 putative multidrug resistance protein	confidence=64 n=1
			NP_767330 putative multidrug resistance protein	NP_767331 hypothetical protein	confidence=92 n=124
	NP_770543.1	bll3903	NP_770542 AcrB/AcrD/AcrF family protein	NP_770543 putative multidrug resistance protein	confidence=91 n=203
	NP_773444.1	blr6804	NP_773444 probable substrate-binding protein	NP_773446 transcriptional regulatory protein	confidence=64 n=2
	NP_770851.1	minC	NP_770851 septum formation inhibitor	NP_770852 putative cell division inhibitor protein	confidence=98 n=113
			NP_770851 septum formation inhibitor	NP_770853 cell division topological specificity factor MinE	confidence=98 n=110
	NP_773588.1	bll6948	NP_773586 putative methyl-accepting chemotaxis protein	NP_773588 putative outer membrane receptor signal peptide protein	confidence=64 n=1
			NP_773588 putative outer membrane receptor signal peptide protein	NP_773589 HupN protein	confidence=75 n=1
Regulatory	NP_771588.1	glnB	NP_771586 hypothetical protein	NP_771588 nitrogen regulatory protein PII	confidence=66 n=6
			NP_771588 nitrogen regulatory protein PII	NP_771589 glutamine synthetase I	confidence=87 n=43
	NP_767249.1	blr0609	NP_767249 transcriptional regulatory protein	NP_767250 hypothetical protein	confidence=70 n=4
			NP_767249 transcriptional regulatory protein	NP_767251 ATP-dependent Clp protease proteolytic subunit	confidence=71 n=4
	NP_769031.1	blr2391	NP_769030 vanillate O-demethylase oxygenase subunit	NP_769031 transcriptional regulatory protein	confidence=65 n=4
			NP_769031 transcriptional regulatory protein	NP_769032 putative dioxygenase subunit	confidence=65 n=3
	NP_773055.1	bll6415	NP_773053 indole acetamide hydrolase	NP_773055 transcriptional regulatory protein	confidence=73 n=7
			NP_773054 transcriptional regulatory protein	NP_773055 transcriptional regulatory protein	confidence=63 n=1
	NP_770108.1	blr3468	NP_770107 two-component response regulator	NP_770108 two-component response regulator	confidence=84 n=24
	NP_767726.1	blr1086	NP_767726 transcriptional regulatory protein	NP_767727 haloalkane dehalogenase	confidence=68 n=9
	NP_770325.1	blr3685	NP_770323 chaperonin GroEL	NP_770325 transcriptional regulatory protein	confidence=75 n=7
			NP_770324 hypothetical protein	NP_770325 transcriptional regulatory protein	confidence=77 n=1
			NP_770325 transcriptional regulatory protein	NP_770326 hypothetical protein	confidence=77 n=1
	NP_774259.1	blr7619	NP_774258 hypothetical protein	NP_774259 two-component response regulator	confidence=71 n=2

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_774259 two-component response regulator	NP_774260 two-component hybrid sensor and regulator	confidence=86 n=16
			NP_774259 two-component response regulator	NP_774261 hypothetical protein	confidence=77 n=2
Ribosomal	NP_774081.1	rplY	NP_774079 GTP-binding protein	NP_774081 50S ribosomal protein L25	confidence=92 n=57
			NP_774080 peptidyl-tRNA hydrolase	NP_774081 50S ribosomal protein L25	confidence=97 n=180
			NP_774081 50S ribosomal protein L25	NP_774082 hypothetical protein	confidence=64 n=4
	NP_770716.1	rplI	NP_770716 50S ribosomal protein L9	NP_770717 hypothetical protein	confidence=87 n=17
			NP_770716 50S ribosomal protein L9	NP_770718 30S ribosomal protein S18	confidence=97 n=232
	NP_772045.1	rpsL	NP_772043 elongation factor EF-2	NP_772045 30S ribosomal protein S12	confidence=99 n=349
			NP_772044 30S ribosomal protein S7	NP_772045 30S ribosomal protein S12	confidence=99 n=367
			NP_772045 30S ribosomal protein S12	NP_772047 ABC transporter	confidence=64 n=4
	NP_767347.1	rplT	NP_767345 phenylalanyl-tRNA synthetase beta subunit	NP_767347 50S ribosomal protein L20	confidence=98 n=143
			NP_767346 phenylalanyl-tRNA synthetase alpha chain	NP_767347 50S ribosomal protein L20	confidence=98 n=174
			NP_767347 50S ribosomal protein L20	NP_767348 50S ribosomal protein L35	confidence=99 n=251
	NP_767348.1	rpmI	NP_767347 50S ribosomal protein L20	NP_767348 50S ribosomal protein L35	confidence=99 n=251
			NP_767348 50S ribosomal protein L35	NP_767350 translation initiation factor IF-3	confidence=99 n=181
Transporter	NP_767629.1	bll0989	NP_767629 peptide ABC transporter ATP-binding protein	NP_767630 peptide ABC transporter ATP-binding protein	confidence=99 n=265
			NP_767629 peptide ABC transporter ATP-binding protein	NP_767631 peptide ABC transporter permease protein	confidence=99 n=262
	NP_766753.1	bll0113	NP_766751 ABC transporter permease protein	NP_766753 ABC transporter substrate-binding protein	confidence=86 n=16
			NP_766752 ABC transporter ATP-binding protein	NP_766753 ABC transporter substrate-binding protein	confidence=87 n=55
	NP_770206.1	blr3566	NP_770206 ABC transporter substrate-binding protein	NP_770207 ABC transporter permease protein	confidence=85 n=54
			NP_770206 ABC transporter substrate-binding protein	NP_770208 ABC transporter permease protein	confidence=85 n=54
	NP_767642.1	bll1002	NP_767640 hypothetical protein	NP_767642 probable ABC transporter ATP-binding protein	confidence=86 n=44
			NP_767641 probable ABC transporter permease protein	NP_767642 probable ABC transporter ATP-binding protein	confidence=86 n=68
			NP_767642 probable ABC transporter ATP-binding protein	NP_767644 hypothetical protein	confidence=68 n=1
	NP_768123.1	blr1483	NP_768121 phosphoadenosine phosphosulfate reductase	NP_768123 sulfate ABC transporter permease protein	confidence=66 n=7
			NP_768122 ABC transporter sulfate-binding protein	NP_768123 sulfate ABC transporter permease protein	confidence=93 n=121
			NP_768123 sulfate ABC transporter permease protein	NP_768124 sulfate ABC transporter permease protein	confidence=99 n=295

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_768123 sulfate ABC transporter permease protein	NP_768125 sulfate ABC transporter ATP-binding protein	confidence=99 n=257
	NP_773083.1	blr6443	NP_773082 probable D-amino acid oxidase	NP_773083 ABC transporter permease protein	confidence=71 n=8
			NP_773083 ABC transporter permease protein	NP_773084 ABC transporter permease protein	confidence=92 n=198
			NP_773083 ABC transporter permease protein	NP_773085 ABC transporter ATP-binding protein	confidence=92 n=132
	NP_772590.1	bll5950	NP_772588 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	NP_772590 ABC transporter ATP-binding protein	confidence=64 n=4
			NP_772589 ABC transporter ATP-binding protein	NP_772590 ABC transporter ATP-binding protein	confidence=92 n=180
			NP_772590 ABC transporter ATP-binding protein	NP_772591 ABC transporter permease protein	confidence=92 n=179
			NP_772590 ABC transporter ATP-binding protein	NP_772592 ABC transporter permease protein	confidence=92 n=186
	NP_767994.1	blr1354	NP_767992 aminobenzoyl-glutamate utilization protein	NP_767994 peptide ABC transporter permease protein	confidence=76 n=3
			NP_767993 ABC transporter peptide-binding protein	NP_767994 peptide ABC transporter permease protein	confidence=90 n=197
			NP_767994 peptide ABC transporter permease protein	NP_767995 peptide ABC transporter permease protein	confidence=99 n=297
			NP_767994 peptide ABC transporter permease protein	NP_767996 peptide ABC transporter ATP-binding protein	confidence=99 n=253
	NP_770291.1	rfbA	NP_770291 probable O-antigen export system ATP-binding protein	NP_770292 probable O-antigen export system permease protein	confidence=91 n=96
	NP_767525.1	bll0885	NP_767523 ABC transporter permease protein	NP_767525 ABC transporter ATP-binding protein	confidence=89 n=135
			NP_767524 ABC transporter permease protein	NP_767525 ABC transporter ATP-binding protein	confidence=96 n=176
			NP_767525 ABC transporter ATP-binding protein	NP_767526 ABC transporter ATP-binding protein	confidence=96 n=179
			NP_767525 ABC transporter ATP-binding protein	NP_767527 ABC transporter substrate-binding protein	confidence=92 n=118
	NP_770468.1	blr3828	NP_770466 ABC transporter permease protein	NP_770468 ABC transporter ATP-binding protein	confidence=92 n=169
			NP_770467 ABC transporter ATP-binding protein	NP_770468 ABC transporter ATP-binding protein	confidence=92 n=181
			NP_770468 ABC transporter ATP-binding protein	NP_770469 transcriptional regulatory protein	confidence=72 n=12
	NP_770435.1	blr3795	NP_770433 putative lyase	NP_770435 ABC transporter HlyB/MsbA family	confidence=64 n=1
			NP_770435 ABC transporter HlyB/MsbA family	NP_770436 phosphatidylserine decarboxylase	confidence=87 n=18

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_770435 ABC transporter HlyB/MsbA family	NP_770437 phosphatidylserine synthase	confidence=87 n=17
	NP_767523.1	bll0883	NP_767522 hypothetical protein	NP_767523 ABC transporter permease protein	confidence=75 n=10
			NP_767523 ABC transporter permease protein	NP_767524 ABC transporter permease protein	confidence=92 n=183
			NP_767523 ABC transporter permease protein	NP_767525 ABC transporter ATP-binding protein	confidence=89 n=135
	NP_771526.1	bll4886	NP_771524 ABC transporter substrate-binding protein	NP_771526 ABC transporter permease protein	confidence=83 n=72
			NP_771525 ABC transporter ATP-binding protein	NP_771526 ABC transporter permease protein	confidence=93 n=174
	NP_773029.1	bll6389	NP_773027 ABC transporter ATP-binding protein	NP_773029 ABC transporter permease protein	confidence=92 n=251
			NP_773028 ABC transporter substrate-binding protein	NP_773029 ABC transporter permease protein	confidence=92 n=125
			NP_773029 ABC transporter permease protein	NP_773030 ABC transporter permease protein	confidence=92 n=230
	NP_772876.1	bll6236	NP_772874 ABC transporter permease protein	NP_772876 ABC transporter substrate-binding protein	confidence=92 n=92
			NP_772875 ABC transporter permease protein	NP_772876 ABC transporter substrate-binding protein	confidence=92 n=155
			NP_772876 ABC transporter substrate-binding protein	NP_772877 probable carbon monoxide dehydrogenase large chain	confidence=75 n=2
			NP_772876 ABC transporter substrate-binding protein	NP_772878 putative oxidoreductase protein	confidence=75 n=2
	NP_772967.1	bll6327	NP_772966 ABC transporter permease protein	NP_772967 ABC transporter substrate-binding protein	confidence=65 n=1
			NP_772967 ABC transporter substrate-binding protein	NP_772968 ABC transporter permease protein	confidence=87 n=79
	NP_773051.1	bll6411	NP_773049 ABC transporter ATP-binding protein	NP_773051 ABC transporter permease protein	confidence=92 n=172
			NP_773050 ABC transporter ATP-binding/permease protein	NP_773051 ABC transporter permease protein	confidence=86 n=47
			NP_773051 ABC transporter permease protein	NP_773052 putative nitrile hydratase regulator	confidence=91 n=123
			NP_773051 ABC transporter permease protein	NP_773053 indole acetamide hydrolase	confidence=69 n=11
	NP_773463.1	bll6823	NP_773461 hypothetical metabolite transport protein	NP_773463 ABC transporter permease protein	confidence=90 n=68
			NP_773463 ABC transporter permease protein	NP_773464 ABC transporter permease protein	confidence=90 n=143
			NP_773463 ABC transporter permease protein	NP_773465 ABC transporter substrate-binding protein	confidence=87 n=59
	NP_773554.1	bll6914	NP_773552 ABC transporter substrate-binding protein	NP_773554 ABC transporter permease protein	confidence=92 n=122

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
			NP_773553 ABC transporter permease protein	NP_773554 ABC transporter permease protein	confidence=92 n=231
			NP_773554 ABC transporter permease protein	NP_773555 putative oxidoreductase	confidence=79 n=10
			NP_773554 ABC transporter permease protein	NP_773556 hypothetical protein	confidence=68 n=1
	NP_773648.1	blt7008	NP_773647 putative oxidoreductase	NP_773648 aliphatic sulfonate ABC transporter ATP-binding protein	confidence=78 n=9
			NP_773648 aliphatic sulfonate ABC transporter ATP-binding protein	NP_773649 aliphatic sulfonate ABC transporter permease protein	confidence=92 n=221
			NP_773648 aliphatic sulfonate ABC transporter ATP-binding protein	NP_773650 alkanesulfonate monooxygenase	confidence=81 n=8
	NP_771195.1	blr4555	NP_771193 ABC transporter substrate-binding protein	NP_771195 similar to ABC transporter permease protein	confidence=76 n=12
			NP_771194 hypothetical protein	NP_771195 similar to ABC transporter permease protein	confidence=91 n=115
			NP_771195 similar to ABC transporter permease protein	NP_771196 ABC transporter permease protein	confidence=92 n=196
			NP_771195 similar to ABC transporter permease protein	NP_771197 ABC transporter ATP-binding protein	confidence=92 n=160
	NP_772509.1	gudP	NP_772507 hypothetical protein	NP_772509 probable glucarate transporter	confidence=64 n=1
			NP_772509 probable glucarate transporter	NP_772510 transcriptional regulatory protein	confidence=84 n=58
			NP_772509 probable glucarate transporter	NP_772511 putative 5-dehydro-4-deoxyglucarate dehydratase	confidence=77 n=15
	NP_772795.1	blr6155	NP_772793 hypothetical protein	NP_772795 ABC transporter ATP-binding protein	confidence=70 n=4
			NP_772795 ABC transporter ATP-binding protein	NP_772796 ABC transporter permease protein	confidence=99 n=184
			NP_772795 ABC transporter ATP-binding protein	NP_772797 ABC transporter permease protein	confidence=99 n=179
	NP_773085.1	blr6445	NP_773083 ABC transporter permease protein	NP_773085 ABC transporter ATP-binding protein	confidence=92 n=132
			NP_773084 ABC transporter permease protein	NP_773085 ABC transporter ATP-binding protein	confidence=92 n=187
			NP_773085 ABC transporter ATP-binding protein	NP_773086 ABC transporter substrate-binding protein	confidence=85 n=58
			NP_773085 ABC transporter ATP-binding protein	NP_773087 ABC transporter ATP-binding protein	confidence=81 n=39
	NP_773118.1	blr6478	NP_773116 ABC transporter permease protein	NP_773118 ABC transporter ATP-binding protein	confidence=99 n=164
			NP_773117 ABC transporter ATP-binding protein	NP_773118 ABC transporter ATP-binding protein	confidence=96 n=177
			NP_773118 ABC transporter ATP-binding protein	NP_773119 ABC transporter substrate-binding protein	confidence=87 n=63

(Suppl Table 4). Contd.....

Category	Gene ID	Gene	Paired Operon Gene 1	Paired Operon Gene 2	C-Value*
	NP_770065.1	bll3425	NP_770063 ABC transporter ATP-binding protein	NP_770065 ABC transporter permease protein	confidence=89 n=147
			NP_770064 ABC transporter ATP-binding/permease protein	NP_770065 ABC transporter permease protein	confidence=85 n=47
			NP_770065 ABC transporter permease protein	NP_770066 ABC transporter substrate-binding protein	confidence=87 n=78
	NP_773190.1	bll6550	NP_773189 hypothetical protein	NP_773190 probable ABC transporter permease protein	confidence=67 n=4
			NP_773190 probable ABC transporter permease protein	NP_773191 probable ABC transporter substrate-binding protein	confidence=87 n=37

Note: Shaded rows indicate false positive predictions.

* = C-value (confidence value) denotes frequency of co-occurrence of genes.

Supplementary Table 5. Comparison of SinR Transcription Factor of *B. subtilis* with Predicted SinR Ortholog of *B. japonicum*.

Organism	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	<i>Bradyrhizobium japonicum</i> USDA 110
Lineage	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium
Locus Tag	BSU24610	bll1669
Gene Name	sinR, sin, flaD	-
Gene type	protein coding	protein coding
Description	transcriptional regulator	hypothetical protein
Genomic Position	2551885 - 2552220 (chromosome-1)	1828320 - 1828646 (chromosome-1)
GI No.	16079517	27376780
Gene ID	NP_390341.1	NP_768309.1
Conserved Protein domain (PSSM ID)	cd00093: HTH_XRE; Helix-turn-helix XRE-family like proteins. Prokaryotic DNA binding proteins belonging to the xenobiotic response element family of transcriptional regulators. pfam08671: SinI; Anti-repressor SinI. SinR is a pleiotropic regulator of several late growth processes. It is a tetrameric DNA binding protein whose activity is down-regulated thorough the formation of a SinI:SinR protein complex.	cd00093: HTH_XRE, Helix-turn-helix XRE-family like proteins. Prokaryotic DNA binding proteins belonging to the xenobiotic response element family of transcriptional regulators.
Other DBs	BSORF: BG10754 Pasteur: BG10754 NCBI-GI: 16079517 NCBI-GeneID: 938544 UniProt: P06533	Kazusa: bll1669 TIGR: NTL01BJ1669 NCBI-GI: 27376780 NCBI-GeneID: 1054668 UniProt: Q89TV5
Structure	PDB: 1B0N	HSSP built from PDB template 1R69 based on UniProtKB P16117.
AA seq	111 aa	108 aa
Molecular weight	12989 Da	12223 Da
NT seq	336 nt	327 nt
Protein ID	CAB14392.1	gi_27376780

(Suppl Table 5). Contd.....

Organism	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	<i>Bradyrhizobium japonicum</i> USDA 110
Family and domain databases		
InterPro	IPR001387; HTH_3. IPR010981; SinR/SinI_dimer.	IPR001387; HTH_3.
Pfam	PF01381; HTH_3; 1. PF08671; SinI; 1.	PF01381; HTH_3; 1.
SMART	SM00530; HTH_XRE; 1.	SM00530; HTH_XRE; 1.
PROSITE	PS50943; HTH_CROC1; 1.	PS50943; HTH_CROC1; 1.
BLOCKS	P06533.	-
PRODOM	-	Q89TV5.
COG classification	Description: COG1396 [K] Predicted transcriptional regulators Category: INFORMATION STORAGE AND PROCESSING Group: Transcription	Description: COG1396 [K] Predicted transcriptional regulators Category: INFORMATION STORAGE AND PROCESSING Group: Transcription
GeneRIFs: Gene References Into Function	-SinR is a master regulator for biofilm formation and its principal biological function is to govern the assembly of complex multicellular communities. -Master regulator for biofilm formation by repressing transcription of exopolysaccharide operon	-

Supplementary Table 6. Upstream Sequences of Reference Data Set Genes Used for Sin-box Weight Matrix Construction

1. <i>aprE</i> upstream -350 to -250; size: 101; location: NC_000964.2 1105122 1105222 R <i>B.subtilis</i> CTTTGAAAAAATATCACGATAATATCCATTGTTCTCACGGAAGCACACGCAGGTC ATTTGAACGAATTTTTTCGACAGGAATTTGCCGGGACTCAGGAGCA
2. <i>epr</i> upstream -450 to -350; size: 101; location: NC_000964.2 3938440 3938540 D <i>B.subtilis</i> GATATCCGAGCTTATCGGCCCACTCGTTCCCAAACACACTCGCCATGAAATCAGC ATACCCCGGAATCGGCAAGCTCGTTAAATCAAGAAGACAGACCCG
3. <i>yqxM</i> upstream -145 to -30; size: 116; location: NC_000964.2 2554509 2554624 R <i>B.subtilis</i> TATGATGAAAACATTCTTTTAAACGAACAAAATGAGCGATTTCGGTGTTTTTAA TCTATAAATCGTTGATTATACTCTATTTGTGAAGTTCTTTAAAGAGAACGATTGTC ATATC
4. <i>yvek</i> upstream -225 to -100; size: 126; location: NC_000964.2 3528985 3529110 R <i>B.subtilis</i> TCCTGTCGTTATTTTCGTTTATTATAAGGAATTTTCGTTCTTTATAAAATTTAAAT AATAAGGGAAGTGCAGTAAATTAGAGGAAAATCATGATTTTGTCTCTAAAGAGA ACTTATTGGCTTAT
5. <i>rok</i> upstream -170 to -70; size: 101; location: NC_000964.2 1492924 1493024 D <i>B.subtilis</i> TCCCTTGAGAATAAAGGACTCTTTTGAAAAATAAAACATTTTCAGAAAATAAGGAA TTTTTCATAGAGTAAATATAATAGTAAATGCTAAAATAATAGTT
6. <i>blr3044</i> upstream -400 to -300; size: 101; location: NC_004463.1 3360281 3360381 D <i>B.japonicum</i> GAGCCTGTCGCCGCGGACCCTGGCTGGTCGCGCAGCCTCGGTGCAGTCGCGC TCGTGCTCCAGGCCGCGCATCATCGGCGCGGTGCTGATGAAGACCCAGC