

Gene	Functional Description	Position	Mutation	Mutation annotation	No. Observed mutations	
					NL	PL
<i>SynWH7803_0099</i> ←	hypothetical protein	101,693	C→T	D237N (<u>G</u> AC→ <u>A</u> AC)	0	1
<i>SynWH7803_0101</i> → → <i>SynWH7803_0102</i>	hypothetical protein/glucose-1-phosphate thymidyltransferase	102,841	G→A	intergenic (+21/-38)	2	0
<i>SynWH7803_0101</i> → → <i>SynWH7803_0102</i>	hypothetical protein/glucose-1-phosphate thymidyltransferase	102,850	C→T	intergenic (+30/-29)	0	1
<i>SynWH7803_0102</i> →	glucose-1-phosphate thymidyltransferase	103,283	C→A	F135L (TT <u>C</u> →TT <u>A</u>)	3	1
<i>SynWH7803_0102</i> →	glucose-1-phosphate thymidyltransferase	103,376	C→T	P166P (CC <u>C</u> →CC <u>T</u>)	0	1
<i>rfbC</i> →	dTDP-4-dehydrorhamnose 3,5-epimerase	103,845	A→T	Q12H (CA <u>A</u> →CA <u>I</u>)	0	1
<i>rfbC</i> →	dTDP-4-dehydrorhamnose 3,5-epimerase	103,909	G→A	E34K (<u>G</u> AG→ <u>A</u> AG)	0	1
<i>rfbC</i> →	dTDP-4-dehydrorhamnose 3,5-epimerase	104,094	C→T	A95A (GC <u>C</u> →GC <u>I</u>)	0	1
<i>rfbC</i> →	dTDP-4-dehydrorhamnose 3,5-epimerase	104,119	C→T	R104C (<u>C</u> GC→ <u>I</u> GC)	0	1
<i>rfbD</i> →	putative dTDP-4-dehydrorhamnose reductase	104,891	Δ1 bp	coding (468/888 nt)	0	1
<i>rfbD</i> →	putative dTDP-4-dehydrorhamnose reductase	104,894	C→T	G157G (GG <u>C</u> →GG <u>I</u>)	0	2
<i>rfbD</i> →	putative dTDP-4-dehydrorhamnose reductase	104,895	G→T	A158S (<u>G</u> CG→ <u>I</u> CG)	0	1
<i>rfbD</i> →	putative dTDP-4-dehydrorhamnose reductase	104,908	A→T	N162I (<u>A</u> AC→ <u>A</u> IC)	0	1
<i>SynWH7803_0105</i> →	sugar transferase	106,218	G→A	W305* (TG <u>G</u> →TG <u>A</u>)	1	0
<i>SynWH7803_0105</i> →	sugar transferase	106,237	G→A	V312I (<u>G</u> TC→ <u>A</u> TC)	0	1
<i>SynWH7803_0140</i> ←	glycosyl transferase family protein	157,239	2 bp→AC	coding (118-119/981 nt)	0	1
<i>miaA</i> ←	tRNA delta(2)-isopentenylpyrophosphate transferase	163,807	G→T	I305I (AT <u>C</u> →AT <u>A</u>)	1	0
<i>xylB</i> →	xylulose kinase	185,296	Δ1 bp	coding (882/1506 nt)	1	0
<i>SynWH7803_0219</i> ←	hypothetical protein	239,739	A→G	L340P (C <u>I</u> T→C <u>C</u> T)	1	0
<i>SynWH7803_0219</i> ←	hypothetical protein	239,935	G→T	H275N (<u>C</u> AC→ <u>A</u> AC)	1	0
<i>SynWH7803_0219</i> ←	hypothetical protein	240,454	C→A	E102* (<u>G</u> AA→ <u>I</u> AA)	1	0
<i>SynWH7803_0219</i> ←	hypothetical protein	240,719	G→C	Y13* (T <u>A</u> C→T <u>A</u> <u>G</u>)	1	0
<i>SynWH7803_0232</i> →	hypothetical protein	256,217	C→A	P58T (<u>C</u> CG→ <u>A</u> CG)	0	1
<i>SynWH7803_0260</i> ←	ABC transporter ATPase/permease	284,356	A→G	Y333H (TAT→ <u>C</u> AT)	0	1
<i>SynWH7803_0311</i> →	alpha-glucosidase	337,494	G→T	G15V (G <u>G</u> T→G <u>I</u> T)	0	1
<i>SynWH7803_0389</i> ← → <i>SynWH7803_0390</i>	hypothetical protein/hypothetical protein	414,594	Δ1 bp	intergenic (-85/-116)	0	1
<i>SynWH7803_0470</i> →	oxidoreductase	482,235	2 bp→CC	coding (737-738/960 nt)	0	1
<i>cpeY</i> →	bilin biosynthesis protein CpeY	498,871	G→A	A231T (<u>G</u> CT→ <u>A</u> CT)	0	1
<i>cpeS</i> ←	phycoerythrin linker gene region	504,192	G→A	I96I (AT <u>C</u> →AT <u>I</u>)	0	1
<i>SynWH7803_0558</i> ←	hypothetical protein	565,198	+C	coding (4/1719 nt)	1	0
<i>SynWH7803_0562</i> →	hypothetical protein	568,385	A→G	L150L (CT <u>A</u> →CT <u>G</u>)	0	1
<i>psbA</i> →	photosystem II protein D1	771,126	2 bp→TG	coding (855-856/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,129	2 bp→AC	coding (858-859/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,136	A→G	I289V (<u>A</u> TC→ <u>G</u> TA)	0	1
<i>psbA</i> →	photosystem II protein D1	771,138	C→A	I289V (AT <u>C</u> →GT <u>A</u>)	0	1
<i>psbA</i> →	photosystem II protein D1	771,150	G→A	A293A (GC <u>G</u> →GC <u>A</u>)	0	1

<i>psbA</i> →	photosystem II protein D1	771,183	2 bp→TA	coding (912-913/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,186	2 bp→CG	coding (915-916/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,189	G→T	L306L (CT G →CT I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,193	3 bp→AGT	coding (922-924/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,201	4 bp→TAAA	coding (930-933/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,207	2 bp→TA	coding (936-937/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,210	G→C	L313L (CT G →CT C)	0	1
<i>psbA</i> →	photosystem II protein D1	771,222	T→A	A317A (GCT→GCA)	0	1
<i>psbA</i> →	photosystem II protein D1	771,225	T→C	D318D (GAT→GAC)	0	1
<i>psbA</i> →	photosystem II protein D1	771,228	G→T	V319V (GT G →GT I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,231	G→C	L320L (CT G →CT C)	0	1
<i>psbA</i> →	photosystem II protein D1	771,237	C→T	R322R (CG C →CG I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,240	4 bp→TGGT	coding (969-972/1077 nt)	0	1
<i>psbA</i> →	photosystem II protein D1	771,246	C→T	L325L (CT C →CT I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,249	A→C	G326G (GGA→GGC)	0	1
<i>psbA</i> →	photosystem II protein D1	771,273	C→T	N334N (AAC→AAI)	0	1
<i>psbA</i> →	photosystem II protein D1	771,288	C→T	P339P (CC C →CC I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,291	C→T	L340L (CT C →CT I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,297	G→T	L342L (CT G →CT I)	0	1
<i>psbA</i> →	photosystem II protein D1	771,303	2 bp→TG	coding (1032-1033/1077 nt)	0	1
<i>ggt</i> ←	gamma-glutamyltranspeptidase	821,170	G→A	R602W (CGG→IGG)	0	1
<i>hupE</i> ←	hydrogenase accessory membrane protein	917,144	G→T	H41N (CAC→AAC)	1	1
<i>SynWH7803_1018</i> →	hypothetical protein	934,026	C→G	L338V (CTC→GTC)	1	0
<i>ftsH</i> →	cell division protein FtsH	1,019,857	C→A	P37T (CCG→ACG)	0	1
<i>ftsH</i> →	cell division protein FtsH	1,020,535	G→T	G263C (GGC→IGC)	0	1
<i>pstA</i> ←	phosphate ABC transporter permease	1,135,395	G→T	S5Y (TCT→TAT)	1	0
<i>SynWH7803_1279</i> ←	hypothetical protein	1,175,012	G→A	S24S (TC C →TC I)	0	1
<i>SynWH7803_1381</i> ←	cation efflux family protein	1,268,916	C→T	S44N (AGT→AAT)	0	1
<i>SynWH7803_1381</i> ←	cation efflux family protein	1,268,922	C→G	R42P (C GG →C CG)	0	1
<i>SynWH7803_1386</i> ←	two-component system sensor histidine kinase	1,271,925	Δ1 bp	coding (1105/1161 nt)	1	0
<i>SynWH7803_1386</i> ←	two-component system sensor histidine kinase	1,272,000	C→A	G344* (GGA→IGA)	2	0
<i>SynWH7803_1386</i> ←	two-component system sensor histidine kinase	1,272,008	C→A	S341I (AGT→AIT)	2	0
<i>SynWH7803_1386</i> ←	two-component system sensor histidine kinase	1,272,988	Δ1 bp	coding (42/1161 nt)	0	1
<i>SynWH7803_1446</i> →	hypothetical protein	1,328,915	+T	coding (205/636 nt)	0	1
<i>SynWH7803_1498</i> ← / → <i>RNA_30</i>	hypothetical protein/tRNA-Ser	1,372,875	C→A	intergenic (-79/-38)	1	0
<i>recC</i> →	exodeoxyribonuclease V subunit gamma	1,379,294	A→C	R331R (CGA→CGC)	1	0
<i>ilvC</i> →	ketol-acid reductoisomerase	1,618,650	G→C	L150L (CT G →CT C)	1	0
<i>SynWH7803_1789</i> ←	hypothetical protein	1,640,030	G→T	P169T (CCG→ACG)	0	1

<i>SynWH7803_1859</i> →	glycosyltransferase family protein	1,703,838	G→A	G163S (<u>G</u> GT→ <u>A</u> GT)	1	0
<i>SynWH7803_1882</i> ←	hypothetical protein	1,723,445	C→A	V70L (<u>G</u> TG→ <u>I</u> TG)	1	0
<i>SynWH7803_2208</i> →	Fe-S oxidoreductase	2,034,338	G→A	G328D (<u>G</u> GT→ <u>G</u> AT)	0	1
<i>SynWH7803_2230</i> ←	Na ⁺ /H ⁺ antiporter	2,050,905	G→A	L414F (<u>Q</u> TT→ <u>I</u> TT)	2	0
<i>purE</i> ← / → <i>nagA</i>	phosphoribosylaminoimidazole carboxylase catalytic subunit/N-acetylglucosamine-6-phosphate deacetylase	2,125,808	G→T	intergenic (-72/-44)	1	0
<i>SynWH7803_2356</i> ←	hypothetical protein	2,176,220	*G→A	N633N (AA <u>C</u> →AA <u>I</u>)	2	3
<i>SynWH7803_2356</i> ←	hypothetical protein	2,176,310	*G→A	D603D (GA <u>C</u> →GA <u>I</u>)	4	3