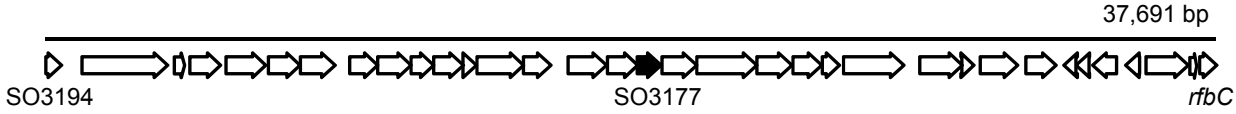
TABLE S1. Primers used in this study.

Primer	Sequence (5' to 3')	Modification, for use
T7kan-2-SacI-F	GAGCTCCCTATAGTGAGTCGTATTACCATCA TCGATGAATTGTG	*Sac*I, Km^r gene amplification
T7kan-2-SacI-R	GAGCTCTGAGGCCGGTCTCCCTATAG	*Sac*I, Km^r gene amplification
KAN-2 FP-1	ACCTACAACAAAGCTCTCATCAACC	Inverse PCR
KAN-2 RP-1	GCAATGTAACATCAGAGATTTTGAG	Inverse PCR
3177_F-O	CATTTGTCAGCGAATTTACC	SO3177 disruption
3177_5-O_SpeI	ATGACTAGTCGGACATTAATCTATCTCCC	*Spe*I, SO3177 disruption
3177_5-I	CTGATCGGTGCAAAAGTTCTGACTGTTACC ACAAAG	Linker sequence, SO3177 disruption
3177_3-I	AACTTTTGCACCGATCAGAACCGGATGATT AAAGGT	Linker sequence, SO3177 disruption
3177_3-O-SpeI	ACGACTAGTTCATTATTGCACTCTCGACC	*Spe*I, SO3177 disruption
3177_R-O	TTCGCCAAGGAGGATAAC	SO3177 disruption
SO3177-F-HindIII	ACGGAAGCTTGGAAGAATTAAGTTTTTTGG	*Hin*dIII, SO3177 complementation
SO3177-R-XbaI	ACCGTCTAGAGTTATTTAACACCTTTAATC	*Xba*I, SO3177 complementation



Locus tag	Putative function
SO3194	Transcriptional activator RfaH
SO3193	Polysaccharide export protein
SO3192	Hypothetical protein
SO3191	Chain length determinant protein
SO3190	UDP-N-acetyl-D-galactosamine dehydrogenase
SO3189	Nucleoside-diphosphate-sugar epimerase
SO3188	*rfbB*, dTDP-glucose 4,6 dehydratase
SO3186	*rfbA*, glucose-1-phosphate-thymidylyltransferas
SO3185	Sugar transamine/perosamine synthetase
SO3184	Hypothetical protein
SO3183	Perosamine synthetase-related protein
SO3182	Acetyltransferase
SO3181	Polysaccharide biosynthesis domain-containing protein
SO3180	Glycosyl transferase, group 2 family protein
SO3179	Lipopolysaccharide biosynthesis polymerase
SO3178	Hypothetical protein
SO3177	Formyl transferase domain-containing protein
SO3176	Glycosyl transferase, group 1 family protein
SO3175	*asnB*-2, asparagine synthetase, glutamine-hydrolyzing
SO3174	Glycosyl transferase, group 1 family protein
SO3173	UDP-galactose 4-epimerase
SO3172	Galactosyl transferase
SO3171	Polysaccharide biosynthesis protein
SO3170	Hypothetical protein
SO3169	Cro/CI family transcriptional regulator
SO3168	DnaJ domain-containing protein
SO3167	dTDP-glucose 4,6-dehydratase
SO3166	Conserved hypothetical protein
SO3165	Conserved hypothetical protein
SO3164	Conserved hypothetical protein
SO3163	Lipoprotein
SO3162	Sensor histidine kinase
SO3161	Glucose-1-phosphate thymidylyltransferase
SO3160	*rfbC*, dTDP-4-dehydrorhamnose 3,5-epimerase

FIG. S1. Putative polysaccharide biosynthesis gene cluster, including SO3177, in the genome of *S. oneidensis* MR-1. ORFs are indicated in order of locus tag from the left.

FIG. S2. Silver-stained SDS-PAGE gel, showing sizes of LPSs extracted from the wild-type MR-1 (lane 1), 4A (lane 2), and ΔSO3177 (lane 3). The arrow indicates the positions of LPSs from S. *oneidensis*.