



Table S1. Primers used in this study.

Name	Sequence (5'-3') (restriction site underlined)	Use
Lrp-F	AAACATATGATGGATGACGTTGATCGGAA (<i>NdeI</i>)	Expression of <i>SLCG_Lrp</i> in <i>E. coli</i>
Lrp-R	AAAAAGCTTCTACGCCGGCAGCGGGCGGT (<i>HindIII</i>)	
2185-P1	AAATCTAGACAGCTCCGGGTCCGCGACGT (<i>XbaI</i>)	Inactivation of <i>SLCG_2185</i>
2185-P2	AAAGAATTCGGGCCGACGAGGTTCTGGAG (<i>EcoRI</i>)	
2185-P3	AAAAAGCTTAGGTCACCGAACTCGCTGTGCG (<i>HindIII</i>)	
2185-P4	AAATCTAGACTGTCCGGGATCGTTTCGGCCG (<i>XbaI</i>)	
2185-P5	ATGGGGCGCGGTCAGTGCTCGCGC	Confirmation of Δ <i>SLCGL_2185</i> by PCR
2185-P6	CCGCCGCTCCGACACTCCGGTC	
2185-P7	AAACATATGGTGCTTTTCACCAAAGAC (<i>NdeI</i>)	Complementation and overexpression of <i>SLCG_2185</i>
2185-P8	AAATCTAGATCAGTGCTCGCGCGC(<i>XbaI</i>)	
apr-R	GTGCAATACGAATGGCGAAA	Confirmation of overexpressing strain by PCR
apr-F	CCGCTCGCCAGTCGATTGGC	
2388-P1	AAAGAATTCCGCTCCGAGCGGGTCAACACTCG (<i>EcoRI</i>)	Inactivation of <i>SLCG_2388</i>
2388-P2	AAATCTAGAGGCGGTGATGAGCTTCATGCG (<i>XbaI</i>)	
2388-P3	AAATCTAGACGCGGCCCGACGCGCTCTGA (<i>XbaI</i>)	
2388-P4	AAAAAGCTTGCGGTGGGCACGGCGTCCCCGG (<i>HindIII</i>)	
2388-P5	CCGGACAGCCAGTCGTCCGTCAG	Confirmation of Δ <i>SLCGL_2388</i> by PCR
2388-P6	CTCCGCGATCCTCGCCCTCATCC	
3009-P1	AAATCTAGACTCCAGTTGGCCGATGAACGAGC (<i>XbaI</i>)	Inactivation of <i>SLCG_3009</i>
3009-P2	AAAGAATTCCTCGCAACGGCTGCCGAT (<i>EcoRI</i>)	
3009-P3	AAAAAGCTTGCATCGGCCTCTCCGAACGC (<i>HindIII</i>)	
3009-P4	AAATCTAGATTGAGGGTGTGCGCACCCGG (<i>XbaI</i>)	
3009-P5	AGGTCGTACTIONCAGGGATGCTGCT	Confirmation of Δ <i>SLCGL_3009</i> by PCR
3009-P6	GCATGTTGAGCACACAGCGTGTC	
3141-P1	AAAGAATTCAGGCCTACAACGACTGGA (<i>EcoRI</i>)	Inactivation of <i>SLCG_3141</i>
3141-P2	AAATCTAGACCGGAAGGGCGGGGTCAGGC (<i>XbaI</i>)	
3141-P3	AAATCTAGACCGCGCAACGGCAGATCATG (<i>XbaI</i>)	
3141-P4	AAAAAGCTTGGTTGACCTCGACGATCCGC (<i>HindIII</i>)	
3141-P5	GCGGGCGTACTCCGCGATGGGCG	Confirmation of Δ <i>SLCGL_3141</i> by PCR
3141-P6	GCGCGCCCTCAGGTCCGAACCCGG	
7585-P1	AAATCTAGAGTCGAGCACCGCGGAACGCA (<i>XbaI</i>)	Inactivation of <i>SLCG_7585</i>
7585-P2	AAAGAATTCACGCGAGCTGAGGAGTGCGA (<i>EcoRI</i>)	
7585-P3	AAAAAGCTTCCGGATCGTCTCACCCCGGCG (<i>HindIII</i>)	
7585-P4	AAATCTAGAGCGGCCCATCGGGCACTGCAC (<i>XbaI</i>)	
7585-P5	ATGCGCTGGGTCGTCAGCGCGA	Confirmation of Δ <i>SLCGL_7585</i> by PCR
7585-P6	CGGGACGAGGCGGCTTCGCAAT	
0182-83-P1	TCCGGGTGATCTCCACGGCC	EMSA analysis of <i>SLCG_0182-0183-int</i>
0182-83-P2	CGACGGCGGTCTTGCCTTCC	
2247-48-P1	GTGCTCCGCCTGCCAATCCG	EMSA analysis of <i>SLCG_2274-2275-int</i>
2247-48-P2	GCGGCCGGTGAGGTCGTAC	
7060-61-P1	TAGCCGGTGTCCGCGTGCAG	EMSA analysis of <i>SLCG_7060-7061-int</i>
7060-61-P2	CGGTGACGACGGCGACCTTG	
0569-70-P1	TGGGCCATCTCCCTCTGAC	EMSA analysis of <i>SLCG_0569-0570-int</i>
0569-70-P2	CCACCGCTCCTCCTGACCTC	
0656-57-P1	GTCAGTGGGCGCTCCTTCCG	EMSA analysis of <i>SLCG_0656-0657-int</i>
0656-57-P2	CCGCTCCCCTCTCTCACCG	
3108-09-P1	ATCTCGTGGTCCGCAAGTGC	EMSA analysis of <i>SLCG_3108-3109-int</i>
3108-09-P2	CCACGAGGGCTCTCCTCTCAAC	
5773-74-P1	ACCAGGGTCGCCGTGAGCGC	EMSA analysis of <i>SLCG_5773-5774-int</i>
5773-74-P2	CGAAGCCCACCGCCTCGACG	
5545-46-P1	CGCCGATCACCACACACGCG	EMSA analysis of <i>SLCG_5545-5546-int</i>
5545-46-P2	TCCCGGAGCTGGTCTGTCGG	
3492-93-P1	CAGGCACCGGTGACCCTCAT	EMSA analysis of <i>SLCG_3492-3493-int</i>
3492-93-P2	GCTGTGCTCGGGGCTGTCATG	

5871-72 -P1	GGGCCACATCCTTAGGGGGT	EMSA analysis of <i>SLCG_5871-5872-int</i>
5871-72-P2	GGTGAGGCCATCGGCGTAGG	
5557-58-P1	TGCCTCTCAGCGTGCTTCGG	EMSA analysis of <i>SLCG_5557-5558-int</i>
5557-58-P2	GCATGGCTGGGGGACCTCCTG	
Fluorescent primers-F	F-AACATTGCTTACTATGCTTA	Fluorescent labeling for fragments
Fluorescent primers-H	H-AACATTGCTTACTATGCTTA	
<i>rpoD</i> -1	TCAGCTTCACGCTCCTCCA	qRT-PCR analysis of <i>rpoD</i> as an internal control
<i>rpoD</i> -2	GTGACGCCGTACACCTTGC	
<i>lmrA</i> -1	ATTGCGTGCGGTGCTCTCG	qRT-PCR analysis of <i>lmrA</i>
<i>lmrA</i> -2	AAGGCGTTGAGCGTCTGGG	
<i>lmbA</i> -1	GCCAGCGGTATGTCGGTGAA	qRT-PCR analysis of <i>lmbA</i>
<i>lmbA</i> -2	CCCAAGGCCCGGTCTTTCT	
<i>lmbC</i> -1	TTCACCCACCGACCCACC	qRT-PCR analysis of <i>lmbC</i>
<i>lmbC</i> -2	CCGAGACCAACGGCTGTACG	
<i>lmbD</i> -1	GGTGTTTCGTCGCCGATGTCC	qRT-PCR analysis of <i>lmbD</i>
<i>lmbD</i> -2	GCCGTGGGCCGGTATCTGTT	
<i>lmbW</i> -1	ACGGCCTGTGCGTGATGAG	qRT-PCR analysis of <i>lmbW</i>
<i>lmbW</i> -2	GCTGCGTGAGGACGTGGATG	
<i>lmrB</i> -1	CCCGCTTGAGCACCGAGAA	qRT-PCR analysis of <i>lmrB</i>
<i>lmrB</i> -2	CGTCGGCGAGGACATTCTGC	
<i>lmbU</i> -1	ACCTCGGCGTGGTGCTGGAA	qRT-PCR analysis of <i>lmbU</i>
<i>lmbU</i> -2	CCTGGTGTCTGGGCGACTGGAT	
<i>lmrC</i> -1	CCTCATGGCACGTC AACACG	qRT-PCR analysis of <i>lmrC</i>
<i>lmrC</i> -2	TCAGCGACAGGCTCAGGAATC	
<i>lmbV</i> -1	CTCGCCTTCTCCCAGTACG	qRT-PCR analysis of <i>lmbV</i>
<i>lmbV</i> -2	GCTCACGGGTCAGTACGAGT	
<i>lmbR</i> -1	AGTCGGGAATCGAGGACTGG	qRT-PCR analysis of <i>lmbR</i>
<i>lmbR</i> -2	CGGCACCTTGATGACGATGTT	
<i>lmbK</i> -1	GGAGGCAGGTGAAGAAGGAC	qRT-PCR analysis of <i>lmbK</i>
<i>lmbK</i> -2	GCCGTTCGTCACCAATCAG	
<i>lmbJ</i> -1	CGGTGACAAGATCGCAG	qRT-PCR analysis of <i>lmbJ</i>
<i>lmbJ</i> -2	TACCCACGCCGAGTTCGAG	
<i>lmbE</i> -1	CGTCTACCACATCGCCTTCT	qRT-PCR analysis of <i>lmbE</i>
<i>lmbE</i> -2	GTGGTGATCCACTCGTCGT	
Lrp-P1	ATGGATGACGTTGATCGGAAAA	qRT-PCR analysis of <i>Lrp</i>
Lrp-P2	CGATGACACGGCGAGACG	
3127-P1	TGTGGCTGGGCTGGAGCGTG	qRT-PCR analysis of <i>SLCG_3127</i>
3127-P2	ACTGCGGCAGGACCGACAGG	
7585-P1	CTTCTACGAACTCCGCAACA	qRT-PCR analysis of <i>SLCG_7585</i>
7585-P2	CGTACCAGCGGTCCAGTT	
2388-P1	GCTCGACGAGATCAAGGAAG	qRT-PCR analysis of <i>SLCG_2388</i>
2388-P2	CACCAGGTCGACGGTGTACT	
3009-P1	TCGCTTACTTCGAGGGTGTG	qRT-PCR analysis of <i>SLCG_3009</i>
3009-P2	GCTGTGAGCAGCTCGTAGGT	
2185-P1	GCCGACAAAGGATCCGTGA	qRT-PCR analysis of <i>SLCG_2185</i>
2185 -P2	TAGGGGTAGCGGTGAGTT	
3141 -P1	ACCAAAGCCTTACGGGAGTT	qRT-PCR analysis of <i>SLCG_3141</i>
3141-P2	AGCATGCAGGTGCAGTAGTC	
7061-P1	GAAGATGACCGACGAGGACT	qRT-PCR analysis of <i>SLCG_7061</i>
7061-P2	TAGTTCGTCTGCCCAGGTT	
2248-P1	CTACGGGCCTCGAAGAGAC	qRT-PCR analysis of <i>SLCG_2248</i>
2248-P2	TAGAGGACGCCCTTGAAGTT	
0656-P1	GTC AACCACCTTCGTCG	qRT-PCR analysis of <i>SLCG_0656</i>
0656-P2	TAGTTCATCACCCAGCCGAG	
3493-P1	CATGGACAACATCGAGAACG	qRT-PCR analysis of <i>SLCG_3493</i>

3493-P2	GAAGTGGTTGGTCAGCACCT	
5557-P1	GTGCCTACGAACTCCTGGAC	qRT-PCR analysis of <i>SLCG_5557</i>
5557-P2	GACAGCACGACGTCACACAC	
5774-P1	GAGGGCTTCGACTACGTCTT	qRT-PCR analysis of <i>SLCG_5774</i>
5774-P2	GTCGAAGAACAGCTCGAACA	
5871-P1	CTCGACCACGTCAAGCACTA	qRT-PCR analysis of <i>SLCG_5871</i>
5871-P2	GGTTGGAGACACCGTAGGAG	
0235-P1	ATGACGAACGTGAACCTGCT	qRT-PCR analysis of <i>SLCG_0235</i>
0235-P2	TCGATGGAGAAGGAGTGGTT	

Table S2. Quality statistics of sequencing raw and clean data.

Sample	reads	bases	Q20 (%)	Q30 (%)	GC (%)
Raw data					
LCGL	52050880	7807632000	97.30	92.96	62.07
Δ <i>SLCG_Lrp</i>	51559302	7733895300	97.15	92.61	63.27
Clean data					
LCGL	51850164	7664588366	97.61	93.39	62.27
Δ <i>SLCG_Lrp</i>	51345164	7598036980	97.48	93.06	63.46

Table S3. qRT-PCR tests verify the selection of genes.

gene	logFC	Regulation	Product
<i>SLCG_Lrp</i>	1.66332841	Ups	Lrp/AsnC family transcriptional regulator
<i>SLCG_3127</i>	-1.809704619	Down	LysE family translocator
<i>SLCG_0253</i>	-1.365224971	Down	LmbU
<i>SLCG_0248</i>	-2.070501673	Down	LmbV
<i>SLCG_0235</i>	-1.361518231	Down	LmbIH
<i>SLCG_2185</i>	1.703019535	Ups	FadR family transcriptional regulator
<i>SLCG_2388</i>	-2.34573907	Down	P-II family nitrogen regulator
<i>SLCG_3009</i>	1.66332841	Ups	XRE family transcriptional regulator
<i>SLCG_3141</i>	8.500799657	Ups	Two-component system response regulator
<i>SLCG_7585</i>	-2.606460781	Down	GntR family transcriptional regulator
<i>SLCG_0656</i>	3.674505639	Ups	acyl-CoA synthetase
<i>SLCG_7061</i>	1.598013559	Ups	SDR family oxidoreductase
<i>SLCG_3493</i>	-2.425978078	Down	NarK family nitrate/nitrite MFS transporter
<i>SLCG_5871</i>	-1.606763731	Down	glutamine synthetase
<i>SLCG_2248</i>	2.97780822	Ups	SDR family oxidoreductase

Table S4. KEGG enriched genes related to nitrogen metabolism pathway.

Gene	KEGG	Regulation	Product
Nitrogen metabolism			
<i>SLCG_3493</i>	K02575	down	NarK family nitrate/nitrite MFS transporter
<i>SLCG_5543</i>	K00363	down	nitrite reductase (NAD(P)H) small subunit
<i>SLCG_5544</i>	K00362	down	nitrite reductase large subunit
<i>SLCG_5545</i>	K00360	down	NAD(P)/FAD-dependent oxidoreductase
<i>SLCG_5557</i>	K00372	down	nitrite reductase
<i>SLCG_5871</i>	K01915	down	glutamine synthetase

Table S5. KEGG enriched genes related to fatty acid metabolism pathway.

Gene	KEGG	Regulation	Product
Fatty acid metabolism			
<i>SLCG_0183</i>	K00059	up	SDR family oxidoreductase
<i>SLCG_2248</i>	K00059	up	SDR family oxidoreductase
<i>SLCG_7061</i>	K00059	up	SDR family oxidoreductase
<i>SLCG_0656</i>	K01897	up	acyl-CoA synthetase
<i>SLCG_0566</i>	K00626	up	thiolase domain-containing protein
<i>SLCG_0569</i>	K01692	up	crotonase/enoyl-CoA hydratase family protein
<i>SLCG_3110</i>	K00121	up	Zn-dependent alcohol dehydrogenase
<i>SLCG_5774</i>	K00121	up	Zn-dependent alcohol dehydrogenase

Table S6. Transcriptional regulators in DEGs.

Gene name	logFC	Regulation	Product
<i>SLCG_7585</i>	-2.60646	Down	GntR family transcriptional regulator
<i>SLCG_2388</i>	-2.34574	Down	P _{II} family nitrogen regulator
<i>SLCG_3009</i>	1.663328	Ups	XRE family transcriptional regulator
<i>SLCG_Lrp</i>	1.663328	Ups	Lrp/AsnC family transcriptional regulator
<i>SLCG_2185</i>	1.70302	Ups	FadR family transcriptional regulator
<i>SLCG_3141</i>	8.5008	Ups	Two-component system response regulator

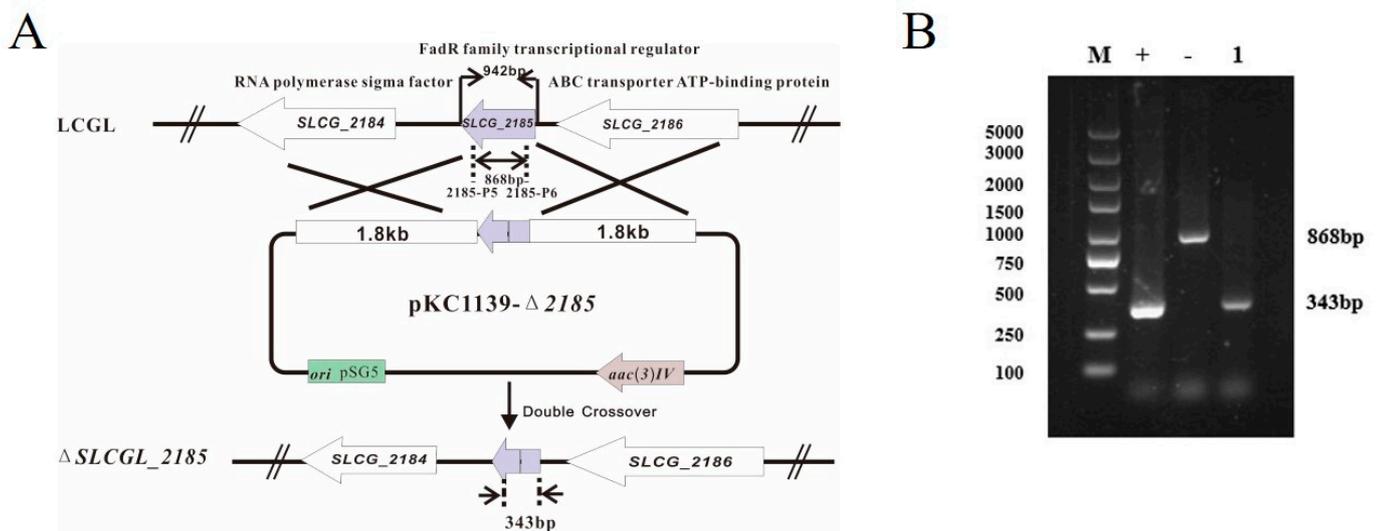


Figure S1. Inactivation of *SLCG_2185* in *S. lincolnensis* LCGL. **(A)** Schematic deletion of *SLCG_2185* by homologous recombination in *S. lincolnensis* LCGL. **(B)** PCR confirmation of the *SLCG_2185* deletion mutant. Lane M, 5,000-bp DNA ladder; lane 1, the positive control, 343bp amplified from pKC1139-Δ2185; lane 2, the negative control, 868 bp amplified from LCGL; lane 3, 343 bp amplified from the ΔSLCGL_2185 mutant.

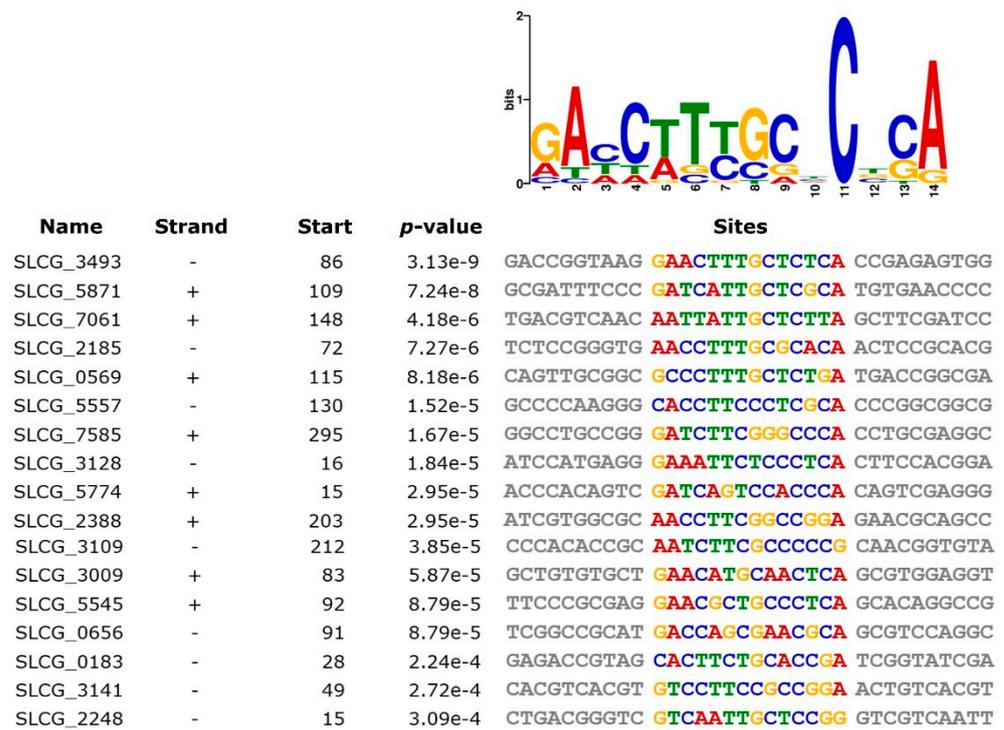


Figure S2. MEME analysis of the consensus SLCG_Lrp-binding motif within promoter regions of SLCG_Lrp, SLCG_3493, SLCG_5871, SLCG_37061, SLCG_2185, SLCG_0569, SLCG_5557, SLCG_7585, SLCG_2388, SLCG_3109, SLCG_3009, SLCG_5545, SLCG_0656, SLCG_0183, SLCG_3141, and SLCG_2248. The standard code of the WebLogo server is shown at the top.