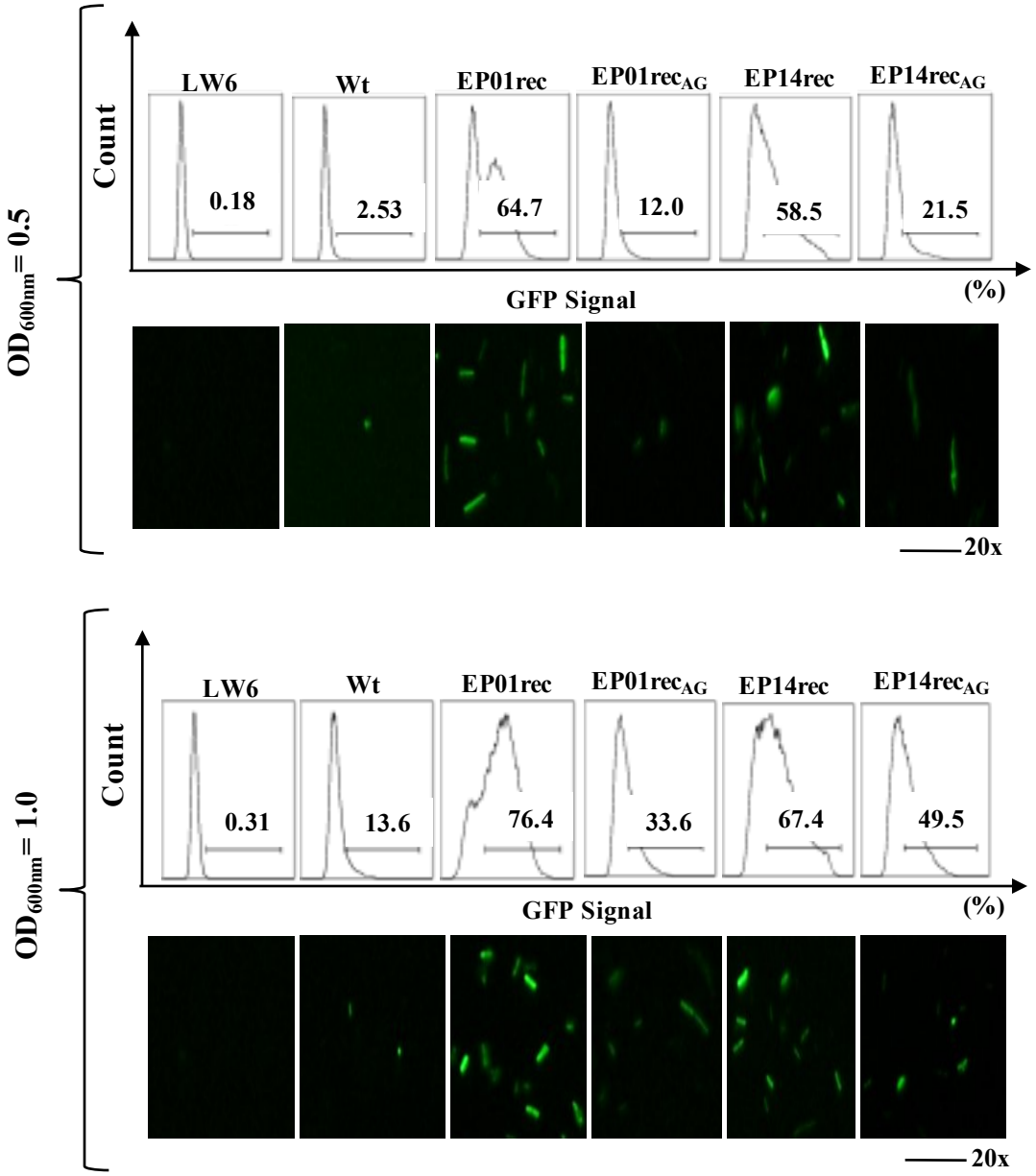
Supplementary Figure S1.



FACS histogram and microscopy fluorescence of GFP expression at OD_{600nm}: 0.5 and 1.0.

Supplementary Table S1 - Strains and plasmids used in this study.

***E. coli* strains**	**Relevant genotype and property**	**Reference or source**
NEB turbo electrocompetent	DNA library constructions	New England labs
DH5α	Used for cloning	New England labs
LW6	W3110 Δ*lsr*R::Kan	Wang *et al*., 2005
LW7	W3110 Δ*lacU169 tna-2* Δ*lux*S::Kan	Wang *et al*., 2005
Plasmids		
pTS40	pTS1 plasmid backone, containing *tet* (A) and *gfp* reporter genes, Cm^r	Sohka *et al*., 2009
pLSR	pTS40 plasmid backbone, containing *lsr*ACDBFG promoter region, Cm^r	This study
pFZY1	*galK'-lacZYA* transcriptional fusion vector, Ap^r	Koop *et al.*, 1987
pLW11	pFZY1 derivative, containing *lsr*ACDBFG promoter region, Ap^r	Wang *et al*., 2005
pPH01	pFZY1 derivative, containing EP01rec promoter region, Ap^r	This study
pPH14	pFZY1 derivative, containing EP14rec promoter region, Ap^r	This study

Supplementary Table S2 – Primers used in this study.

Primers	Sequence	Relevant description
pts40delampR_F	5'- CGATACGTAACTACTAGTTCTGA CGGGCCCGGACACCC-3	Primer for deletion *amp*C and *amp*R from pTS40
pts40delampR_R	5'- GCTAGGATTAGCCGATCGAAAA GGCCCGCCAATAGCGGGC-3	Primer for deletion ampC and ampR from pTS40
lsrpF_PvuI	5'- CGATCG GCGACCTGTTCTTCT TCACACATT -3	Primer for cloning *lsr* operon promoter into pTS40 backbone and to create pLSR
lsrpR_SpeI	5'- ACTAGTTCGATGCCTTTCAGGA CATTG-3	Primer for cloning *lsr* operon promoter into pTS40 backbone and to create pLSR
LsrpEP_F	5'- GGCGGGCCTTTTCGATCG -3'	Primer for Error-prone PCR
LsrpEP_R	5'- CCGGGCCCGTCAGAACTAGT -3'	Primer for Error-prone PCR
gfpmut2_F	5'-ACTACTTTCGCGTATGGTCTT C-3'	qPCR
gfpmut2_R	5'- TTCAGCACGTGTCTTGTAGTT-3'	pPCR
lsrpF_BamHI	5'- ATCCGCGGATCCGCGAC CTGTTCTTCTTCACACATT-3	Primer for cloning *lsr* operon promoter into pFZY1
lsrpR_HindIII	5' CTACCCAAGCTTTCGATGC CTTTCAGGACATTG-3	Primer for cloning *lsr* operon promoter into pFZY1

Supplementary Table S3 – Mutagenic primers used in this study.

Primers	Sequence	Relevant description
plsrR_F	5'-CACTTTGAACATATTTAAATCTTTAATGCAATTG TTCAGTT-3'	Mutagenic primer to restore p-*lsr*R-box sites
plsrR_R	5'- AACTGAACAATTGCATTAAAGATTTAAATATGT TCAAAGTG-3'	Mutagenic primer to restore p-*lsr*R-box sites
plsrR4_F	5'- CACATTGAACATATTTAAATCTTTAATGCAATTG TTCAGTT-3'	Mutagenic primer to restore p-*lsr*R-box sites in EP04 sequence
plsrR4_R	5'- AACTGAACAATTGCATTAAAGATTTAAATATGT TCAATGTG-3'	Mutagenic primer to restore p-*lsr*R-box sites in EP04 sequence
plsrR6/12_F	5'- CACTTTAAACATATTTAAATCTTTAATGCAATTGT TCAGTT-3	Mutagenic primer to restore p-*lsr*R-box sites in EP06 and EP12 sequence
plsrR6/12_R	5'- AACTGAACAATTGCATTAAAGATTTAAATATGT TTAAAGTG-3'	Mutagenic primer to restore p-*lsr*R-box sites in EP06 and EP12 sequence
mutAG1_F	5'- ATTCGTCAGAAATATGTGCAATGTCCACCTAAGG-3'	Mutagenic primer to restore G into putative CytR-binding site in EP01rec sequence
mutAG1_R	5'- CCTTAGGTGGACATTGCACATATTTCTGACGAAT-3'	Mutagenic primer to restore G into putative CytR-binding site in EP01rec sequence
mutAG14_F	5- ATTCGTCGGAAATATGTGCAATGTCCACCTAAGG-3'	Mutagenic primer to restore G into putative CytR-binding site in EP14rec sequence
mutAG14_R	5'- CCTTAGGTGGACATTGCACATATTTCCGACGAAT-3'	Mutagenic primer to restore G into putative CytR-binding site in EP14rec sequence

Supplementary Table S4 - Putative CytR-binding sites found in *E. coli lsrACDBFG* operon promoter.

	***lsrACDBFG* operon direction**			
	Left motif (highest to lowest score		**Highest motif (highest to lowest score**	
Rank	Sequence	Score	Sequence	Score
1	AATGCAAT	0.847	TGTGCAAT	0.741
2	AACGCAAC	0.845	TTTAAATC	0.737
3	CGTGAAAA	0.794	AATACATT	0.733
4	CCTGCAAA	0.788	AATGCAAT	0.723
5	TATTTAAA	0.766	ATAGCATA	0.715
6	TGTGCAAT	0.765	TTTGAACA	0.703
7	ATGGCAAC	0.754	GTTCAAAA	0.702
	***lsrRK* operon direction**			
1	AATGTATT	0.797	ATTGCATT	0.918
2	GATATAAA	0.770	GTTGCGTT	0.852
2 (tie)	GATTTAAA	0.770	GTTGCCAT	0.804
4	AGTCAAAC	0.758	TTTGCAGG	0.788
5	TGAGCAAG	0.748	ATTGCACA	0.787
6	AATGAATT	0.741	TTTTAATT	0.757
7	AAAGTGAA	0.724	TTTAAATA	0.743