

SUPPLEMENTAL FIG S1

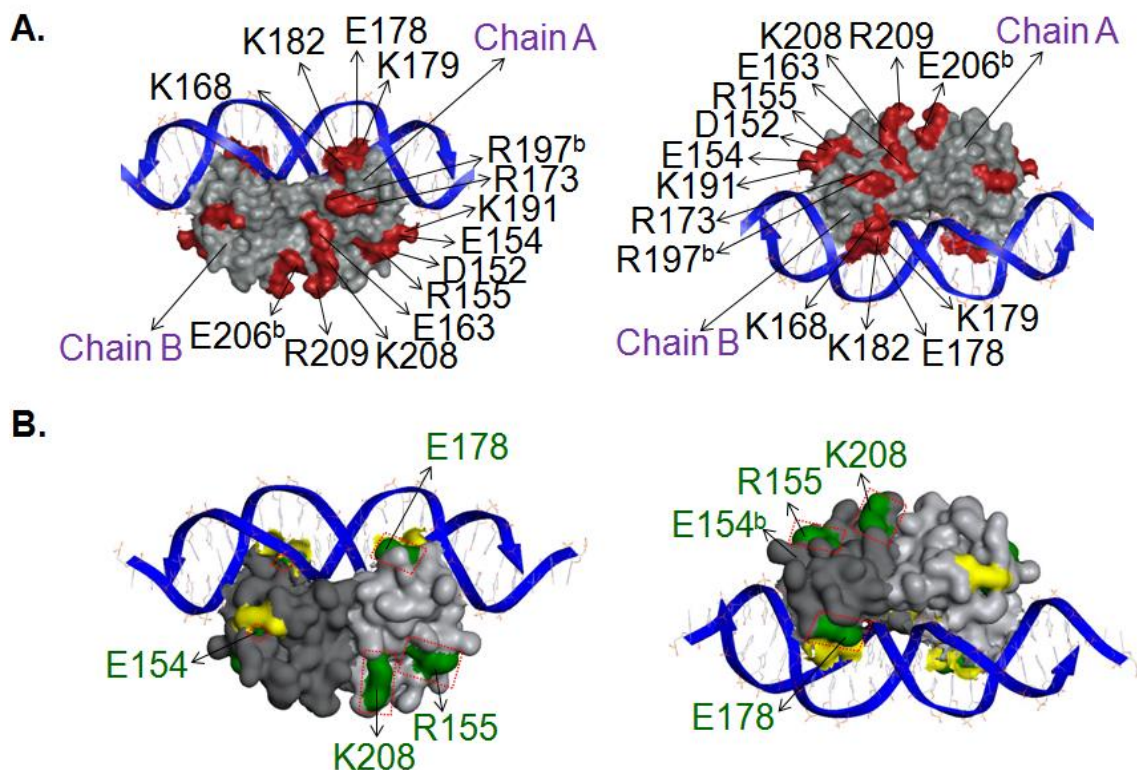
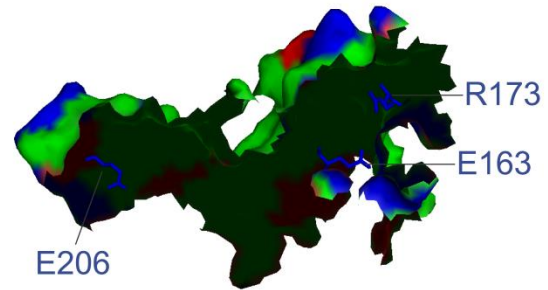
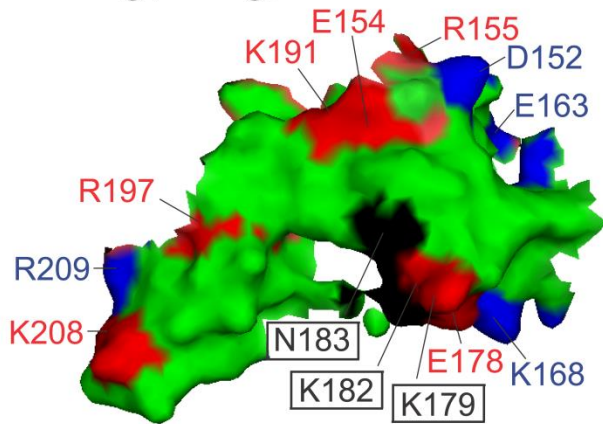


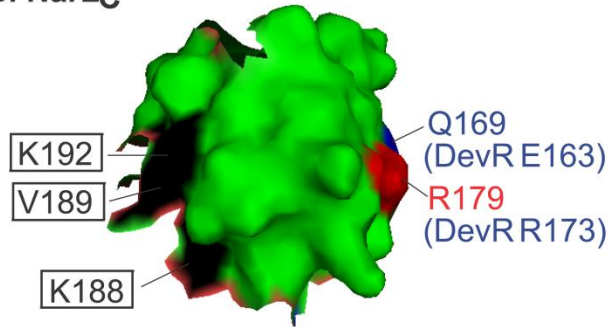
FIG S1 Location of amino acids important for DevR-mediated activation. A. All amino acids mutated in this study are colored in red. **B.** pc mutants (pc) are in dark green and boxed in red rectangles. Alanine substitution mutants defective in DNA binding are in yellow (K191, R197 and K179). The molecular surface representation of both chains of DevR_C (chains A and B in light grey and dark grey) was created from data in PDB file 3C3W (Wisedchaisri *et al.*, 2008) using a marching cubes algorithm of Discovery Studio 3.1 and probe radius of 1.4Å. Individual surfaces of amino acid atoms were depicted by custom colors to highlight the mutations studied. The blue arrows represent the backbone of double stranded DNA, ‘b’ suffix for some residues (e.g. E154^b) indicates that this residue is located at the back.

SUPPLEMENTAL FIG S2

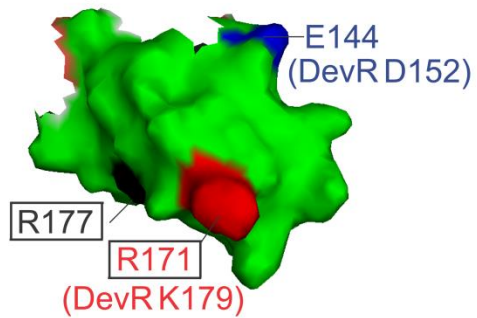
A. DevR_C (DosR_C)



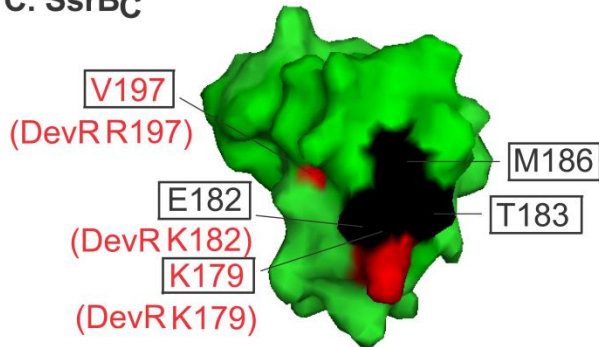
B. NarL_C



D. FixJ_C



C. SsrB_C



E.

		$\alpha 7$		
DevR	152	DQ ERT LLGLLS	162	
NarL	158	PR ERD ILKLI	168	
FixJ	144	ER ERQ VLSAVV	154	
SsrB	152	LR ERQ VLKLID	162	

		$\alpha 9$		
DevR	178	E K T V K N YVS R LL A K	191	
NarL	184	EST V K V H V K H ML K K	197	
FixJ	170	P R T V E V H R AN V MA K	183	
SsrB	178	I K T V E T H R M N MM R K	191	

FIG S2 Comparison of DevR_C/DosR_C with NarL family members. A. Left panel:

DevR_C/DosR_C structure was generated from PDB file 3C3W (Wisedchaisri *et al.*, 2008) using

PyMol. Amino acid mutations that are proficient (in blue) and defective (in red) in transcription

activation are indicated. Right panel: Back view of DevR_C/DosR_C. **B-D**. The amino acids in the DevR orthologs corresponding to amino acids with known phenotypes in DevR are indicated using the same color code as in panel A. The residues with probable or confirmed DNA binding function are boxed. PDB files 3C3W, 1RNL, 1X3U and 2JPC were used to generate protein structures for DosR/ DevR, NarL, FixJ and SsrB, respectively using PyMol. **E**. Protein sequence alignment of DevR and orthologs for α 7 and α 9 helices. Three residues that are conserved among all regulators and display a pc phenotype (E, R and K) in DevR are in bold. The residues implicated in binding to DNA are underlined.

RT16S f	ATGACGGCCTTCGGGTTGTAA	Real Time RT PCR (Gautam <i>et al.</i> , 2011b)
RT16S r	CGGCTGCTGGCACGTAGTTG	
RT3134c f	CTGGCTGGGTCGGCCTTA	Real Time RT PCR (Gautam <i>et al.</i> , 2011b)
RT3134c r	GCTGACCTGGGAGGTTGTGC	
devR f4	CCGATCTGCGCTGTCTGATC	Real Time RT PCR (Taneja <i>et al.</i> , 2010)
devR r3	GTCCAGCGCCCACATCTTT	
RTnarK2 f	CGGTTTGTACGGTGGTTCGGC'	Real Time RT PCR (Gautam <i>et al.</i> , 2011a)
RTnarK2 r	TCACGAAGCACGACCATGGCC	
RT1738 f	CGACGAACACGAAGGATTGA	Real Time RT PCR (Gautam <i>et al.</i> , 2011a)
RT1738 r	ACACCCACCAATTCCTTTTCC	
fdxA f	TGTCCGGTCGACTGTATCTATGA	Real Time RT PCR (Gupta <i>et al.</i> , 2011)
fdxA r	GGCAGG CCG GTTTGC	
RT2031c f	CGCACCGAGCAGAAGGA	Real Time RT PCR (Gautam <i>et al.</i> , 2011a)
RT2031c r	ACCGTGCGAACGAAGGAA	
RTTgs1 f	CAGTGATTTGCGTCGCTACAG	Real Time RT PCR (Gautam <i>et al.</i> , 2011b)
RTTgs1 r	ACATCATTGATGGTGACGTCG	

GCT, GCC, GCA, GCG codes for Alanine; SDM- site directed mutagenesis; BamHI sites are underlined; Bold and underline represents nucleotide substitution; Bold represents substituted codon.