Supplemental Materials

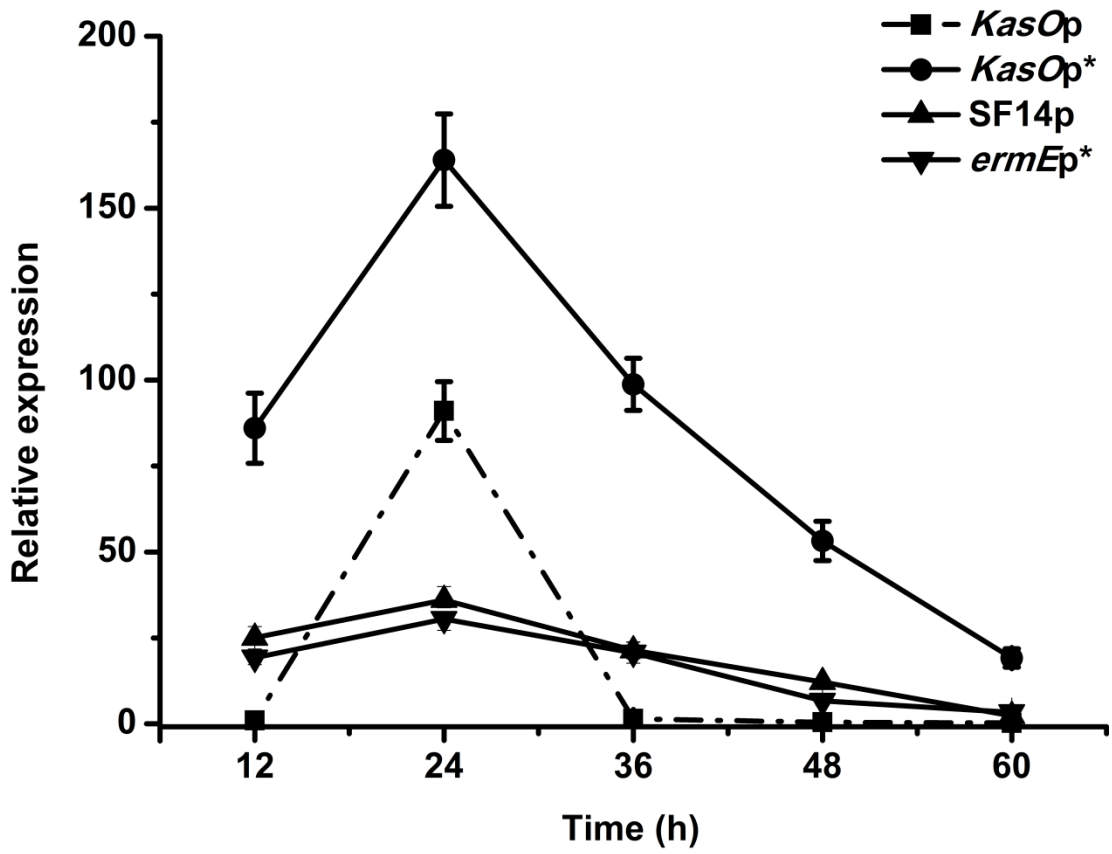

Fig. S1. The transcription profile of *neo* gene under the control of different promoters in *S. coelicolor* measured by real-time qPCR . The error bars indicate standard deviations (SD).

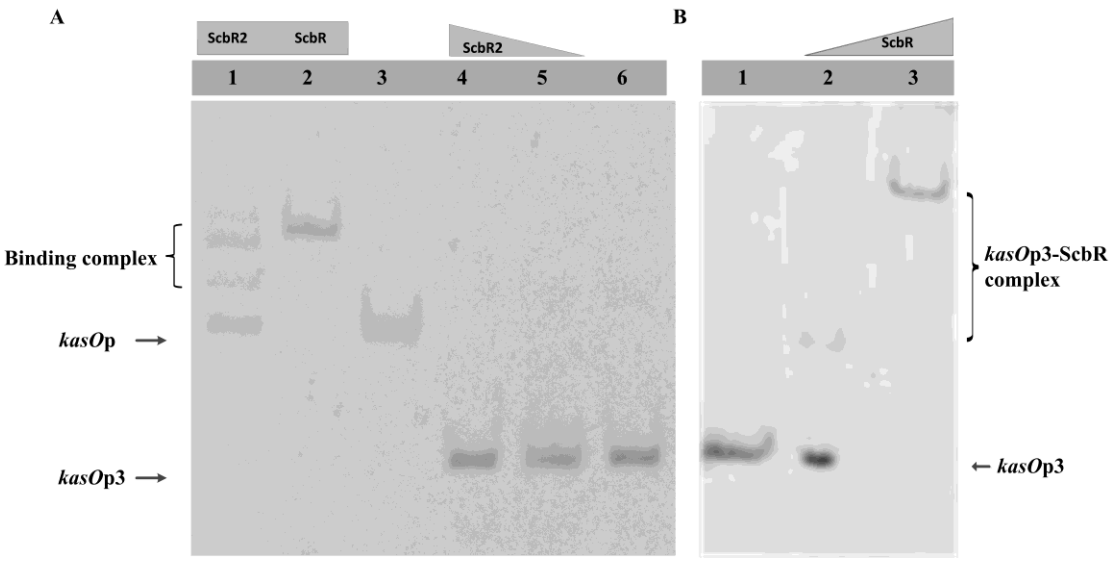

Fig. S2. Gel mobility shift assays (EMSA) of the interaction of *kasO*p3 with purified ScbR and ScbR2 protein. A. EMSA of the interaction of *kasO*p3 with ScbR2. Lane 1-3 as positive control, each contained 5 ng *kasO*p probe. Lane 4-6 each contained 5 ng *kasO*p3 probe. Lanes 1-6 contain 120 nM ScbR2, 120 nM ScbR, 0, 240 nM ScbR2, 120 nM ScbR2 and 0, respectively. B. EMSA of the interaction of *kasO*p3 with ScbR. Each lane contained 5 ng *kasO*p3 probe. Lane 1-3 contained 0, 120 nM ScbR and 240 nM ScbR, respectively.

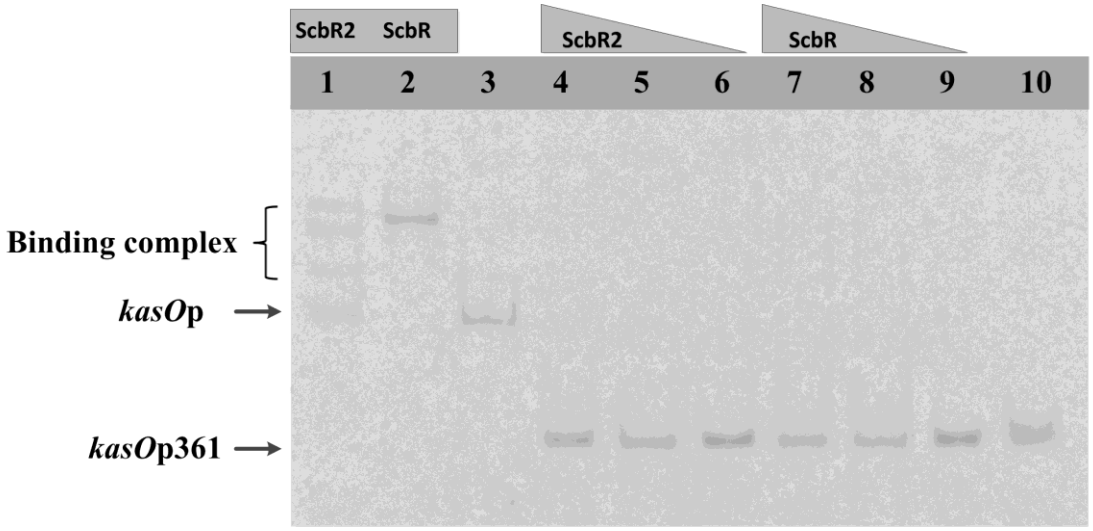

Fig. S3. EMSA of the interaction of *kasO*p361 (*kasO*p*) with purified ScbR and ScbR2 protein. Lane 1-3 each contained 5 ng *kasO*p probe and lane 4-10 each contained 5 ng *kasO*p361 probe. Lanes 1-10 contain 120 nM ScbR2, 120 nM ScbR, 0, 240 nM ScbR2, 120 nM ScbR2, 60 nM ScbR2, 240 nM ScbR, 120 nM ScbR, 60 nM ScbR and 0, respectively.

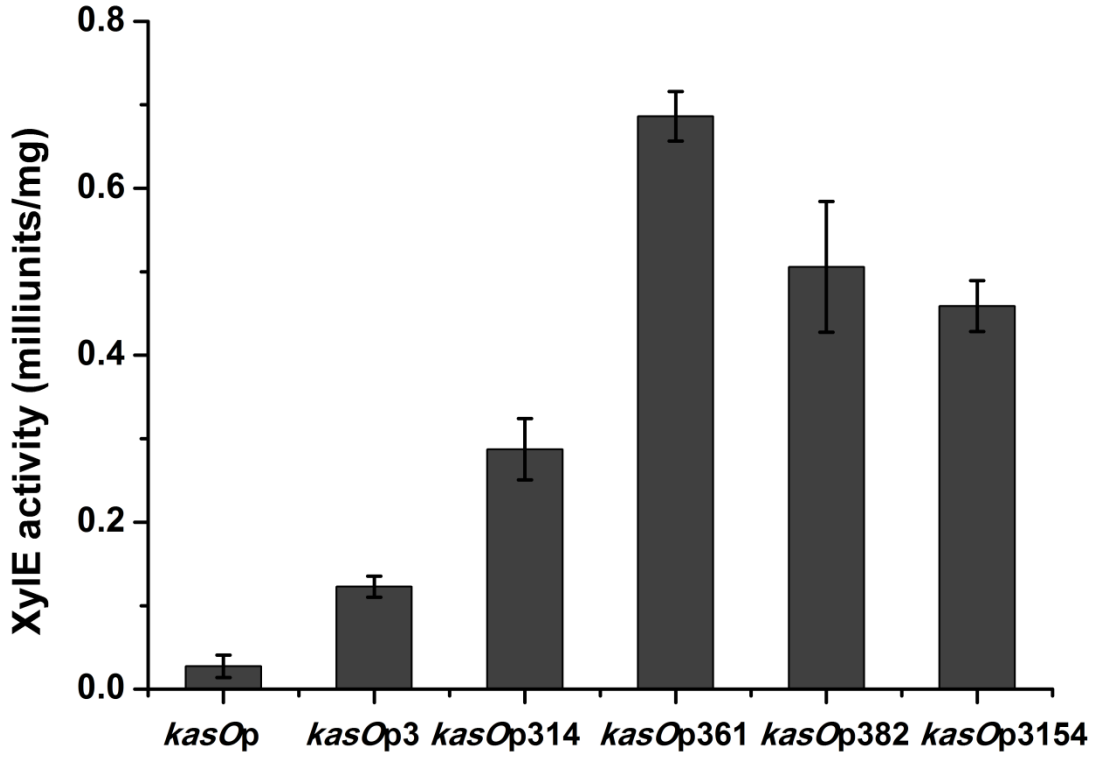

Fig. S4. The relative activities of XylE under the native *kasO*p, *kasO*p3 and the four ScbR-derepressed mutants in *S. coelicolor* M145. Samples were harvested at 36 h in SMM liquid medium. XylE activity was represented as the average of at least three independent readings and error bars indicate the means ± SDs.

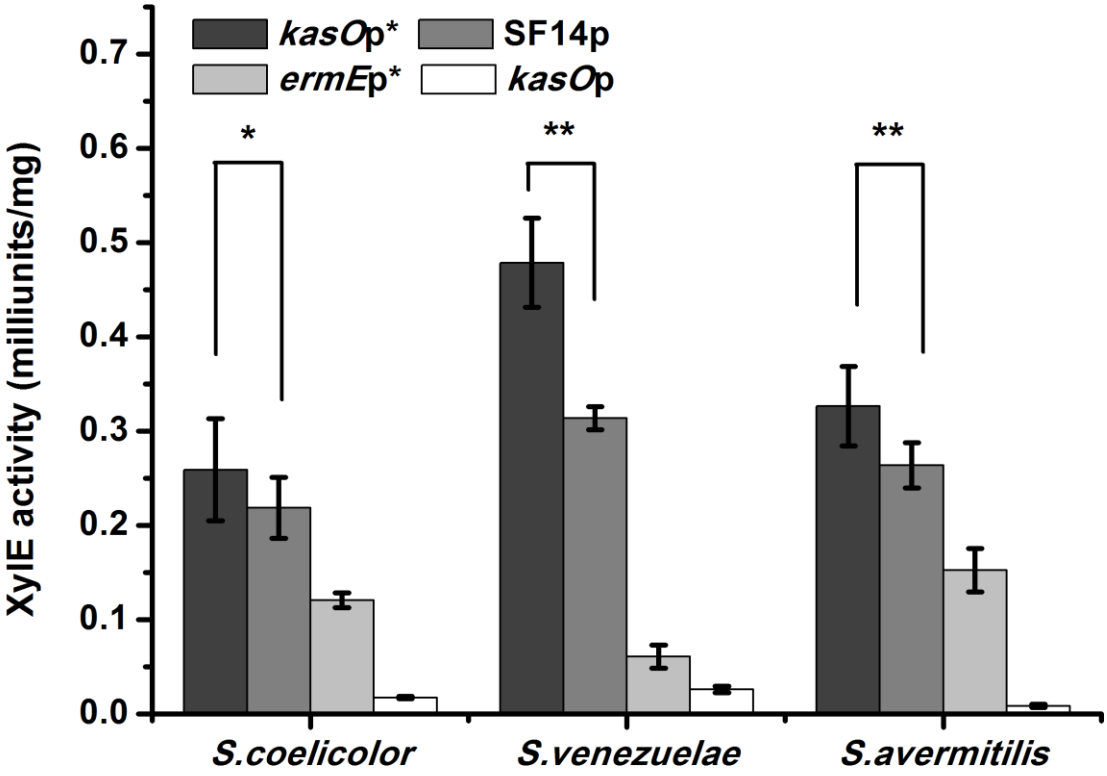

Fig. S5. The activities of XylE under *kasO*p*, SF14p and *ermE*p* in exponential phase of *S. coelicolor* M145, *S. venezuelae* ISP 5230 and *S. avermitilis* NRRL8165, respectively. Samples were harvested at 24 h from S. coelicolor; at 12 h from S. venezuelae; and at 48 h from S. avermilitis. Data were expressed as average values and standard deviations (SD) of three parallel studies. * indicates statistically significant results (0.05<P -value < 0.1). ** indicates highly statistically significant results (P -value < 0.05).

Table S1 Primers and synthetic oligonucleotides used in this study

Primers	Sequence (5′-3′)	Restriction enzymes
kasOpF	ACGTCTCGAGTGCGCGACGTGTGCGCGATCATC	*Xho*I
kasOpR	ACGTGGATCCAACTCCCCCAGTCCTGCACGCT	*BamH*I
HrdB-F	GATATACATATGTCGGCCAGCACATCCCGTACG	*Nde*I
HrdB-R	ATTGAGATCTGCGTACGCCGTTCCGCGCAC	*Bgl*II
KOF	ACGTGGATCCTGCGCGACGTGTGCGCGATCATC	*BamH*I
kasOp1F	ACGTCTCGAGAGTCTCGAAAACCGCTACACTGAGC	*Xho*I
kasOp2F	ACGTCTCGAGATCCCCCGTCCCAGGCCCTC	*Xho*I
kasOp3F	ACGTCTCGAGTGTTCACATTCGAACGGTCTCTG	*Xho*I
kasOp4F	ACGTCTCGAGCTGCTTTGACAAACCGGTGTGCT	*Xho*I
scbRF	TAAGAAGGAACGGAGCACGACATGGCCAAGCAGGACCGG	
scbRR	ACGTGGATCCGCTTCGGTACGCAGGGCAGA	*BamH*I
kasOp3nF	ACGTCTCGAGTGTTCACATTCGAACGGTCTCTGCTTTGACANNNNNNNNNNNNNNNNTGTAAAGTCGTGGCCAGGAG	*Xho*I
kasOp3nR	ACGTGGATCCAACTCCCCCAGTCCTGCACGCTGTCGTATTCTCCTGGCCACGACTTTA	*BamH*I
KF	AGTGGGATCCTTGTTCACATTCGAACGGTC	*BamH*I
KR	TGTACTAGTAACTCCCCCAGTCCTGCACGCT	*Spe*I
KMF	CTGCCGAGAAAGTATCCATC	
KMR	CCCCTGATGCTCTTCGTCC	
hrdBFv	GCCGAGTCCGAGTCTGTGA	
hrdBRv	CTGGGTTGGCGGAATCTGGT	
hrdBFc	GAGGACGGCGACAGCGAGTT	
hrdBRc	GACGCCGTACACCTTGCCGA	
MCS1	TCCGCGGGATCCTCGTGCGGCCGCAGCAAGATCTGTGTACTAGTA	
hygF	CTGTGTGCACGAACCCCCCGTTC	*ApaL*I
hygR	TCTAGCTAGCTCGCAGCAGCGGGCT	*Nhe*I
SF	ACGTGGATCCGCCTTGACCTTGATGAGGCGGCGTGAGCTACAATCAATAC	*BamH*I
SR	ACGTACTAGTCTAATCGAGTATTGATTGTAGCTCACGC	*Spe*I
EF	ACGTCCGCGGTCTGTGCACGCGGTCGATCTTGACGGCTGGCGAGAGGTGCGGGGAGGATCTGACCGACGCGGTCCACACGTGGCACCG	*Sac*II
ER	ACGTACTAGTTGGATCCTACCAACCGGCACGATTGTGCCCACAACAGCATCGCGGTGCCACGTGTGGACCGC	*Spe*I
ActF	ATGCACTAGTATCTGAGTTGAAGAGGTGACGTCAT	*Kpn*I

ActR	GAGATTCAACTTATTGGGACGTGTCCAT ATGCGGTACCCTACACGAGCACCTTCTCACCGTTG AGA	*Spe*I

The restriction enzyme sites of primers are underlined