AAGGAGG	AAAAAACATATG	RBS (actinobacteria)
AAGGAGG		RBS (*Streptomyces*)
AAGGACC	GACCTGGCCATG	*kshB*
AAGGACG	GACGACAGTG	*kshA1*
GAGGACA	ATG	*kshA2*
AAGGAAA	GTGAGGGGACG ATG	*kshA3*
TAGGA GA	GAATTCAATG	*cyp450*
AAGGCTT	CGAGC ATG	*kstD1*
AAGGAGC	AGATCG ATG	*kstD2*

$A_{71}AGGAC_{42}A_{42}$

Figure S1. RBS comparison of some steroid *Rhodococcus ruber* genes. The Figure 41. or actinobacteria [42]. The rest lines are ORFs from *R. ruber* related with the steroid catabolism. The nucleotides before the initial codon are also indicated. The proposed consensus takes into account only the *R. ruber* putative RBS.

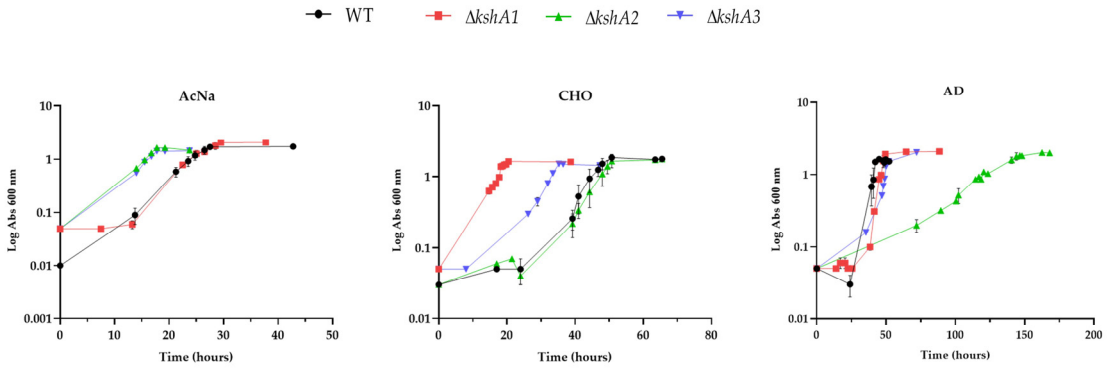

Figure S2. Growth curves of WT and *ksh* single mutants *Rhodococcus ruber* strains in minimal medium with different steroids as carbon source. A representative experiment of 3–6 replicates is shown.

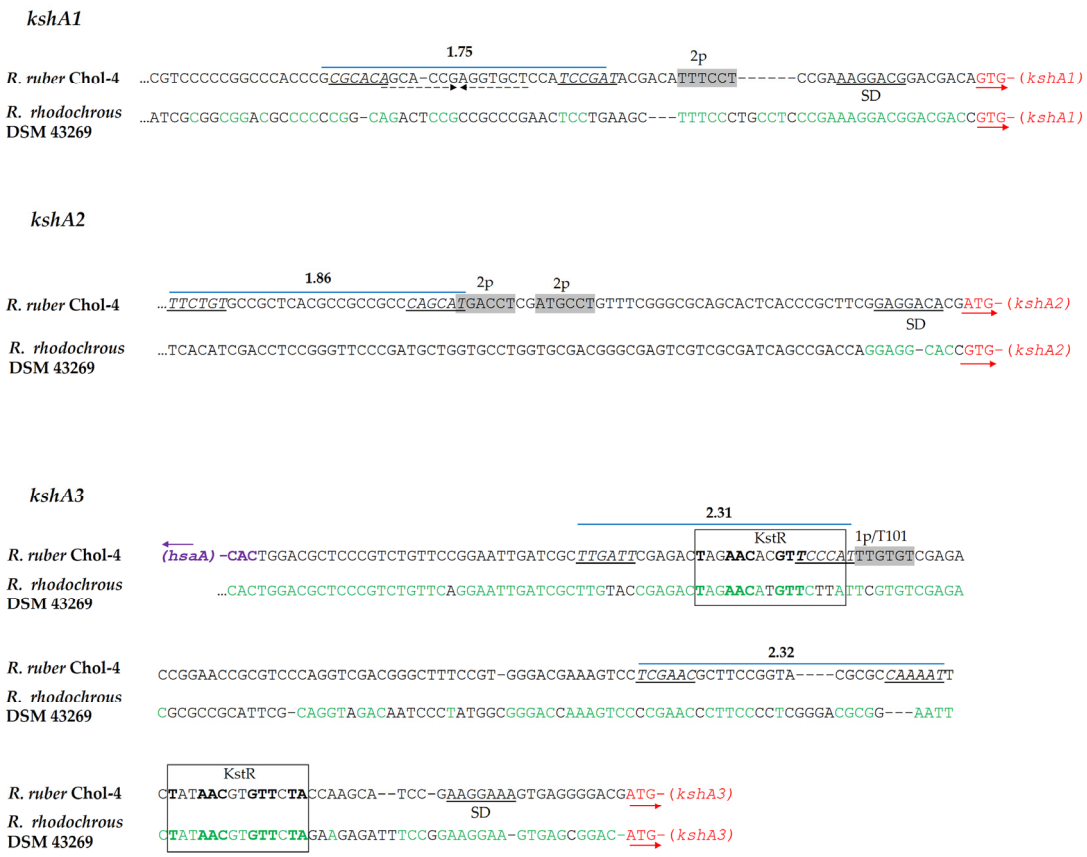

Figure S3. Comparison of upstream regions of *ksh* ORFs. Data accession: *R. ruber* (NCIB::ANGC00000000.2), HQ425873 (*kshA1*), HQ425874 (*kshA2*), HQ425875 (*kshA3*), HQ425876 (*kshA4*), and HQ425877 (*kshA5*).