Supplementary Materials:

Table S1 Oligonucleotides used in this study

Purpose	Sequence
Internal deletion of 36bp in *atpD*	
NS1	5'-GATCGGTCTGCAGGAGATGATCTACCGCGT-3'
NS2	3'-TCCCGCCGTTCTAGCCAGACGTCCTCTACT-5'
Primers for RT-PCR (Figure 3)	
HrdB forward	5'-AAGGAAGACGGCGAGCTTCT-3'
HrdB reverse	5'-GCACCGGGATACGGATGGTG-3'
CpkA forward	5'-AGGTCGGTCTGGTCGAGTTGT-3'
CpkA reverse	5'-CGCACAAGAACTCCAGCATGA-3'
CdaR forward	5'-ACTCGCTCCGTTTCGAACAACT-3'
CdaR reverse	5'-GAGGTCGGTACCCAGTTCAAGA-3'
Cda PSI forward	5'-GGCTTCCTCTTCCTCAACCTGT-3'
Cda PSI reverse	5'-ACGTACAGCTCGGTCAGTTCCT-3'
RedD forward	5'-CAACATATTGGGACCCGTATCG-3'
RedD reverse	5'-ATCGCGCTGATGAGATCCTC-3'
RedL forward	5'-AGCCGAGATAGCACGGTTCATC-3'
RedL reverse	5'-AGATGCCGGTGGAGAAGATGTG-3'
ActII-ORF4 forward	5'-GTGTCCATGTAATCACCGATGC-3'
ActII-ORF4 reverse	5'-AATTACCAGGGACCGGAGTTCC-3'
ActII-ORF1 forward	5'-TGAAGCGCAGAGTCGTCATCAC-3'
ActII-ORF1 reverse	5'-ACCAGGTAGTCGAACATGTGCC-3'
Primer PCR (Figure S1)	
Within promoter *ErmE** upstream of *atpA*	
5'-GACGGT*ATCGAT*AAGCTTGC-3'	
atpA reverse	
5'-TCCTCGATGCCGCTGAACT--3'	
Primers for RT-PCR (Figure S2)	
NRPS/SCO6431 forward	5'-GGCGTTCATCTTCTACACCTCC-3'
NRPS/SCO6431 reverse	5'-AGTCCGTAGACGTTGAACAGCC-3'
EizA/SCO5222 forward	5'-ATATGCCGACGGTCTGTGCTAC-3'
EizA/SCO5222 reverse	5'-TGAGCAGAGGTCGTTGTACCAG-3'
CpkA/SCO6275 forward	5'-AGGTCGGTCTGGTCGAGTTGT-3'
CpkA/SCO6275 reverse	5'-CGCACAAGAACTCCAGCATGA-3'
CrtE/SCO0185 forward	5'-ACCTTGAAGAGCGCCCTGTA-3'
CrtE/SCO0185 reverse	5'-AGGCTCATGTCCGTCAGCTC-3'
CchH/SCO0492 forward	5'-CAGCTTCTCCACCTGACGGTAA-3'
CchH/SCO0492 reverse	5'-CGCTTCTCTCGTACGGCTTTCT--3'

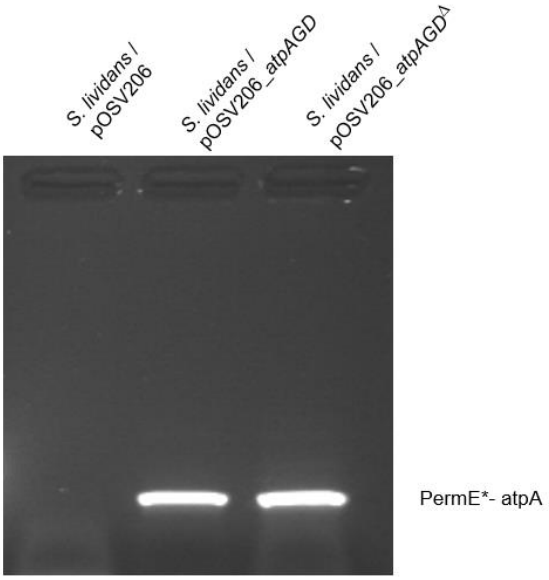

Figure S1: Determination by RT-PCR of the level of transcription of the *atpAGD* cluster present on the plasmid pOSV260 in S. lividans/pOSV206_*atpAGD* and S. lividans/pOSV206_*atpAGD*$^{\Delta}$, grown on solid HT medium for 48 h, with specific primers designed to amplify specifically the copy of the *atpAGD* cluster carried by the plasmid and not the genomic copy of this cluster (Table S1).

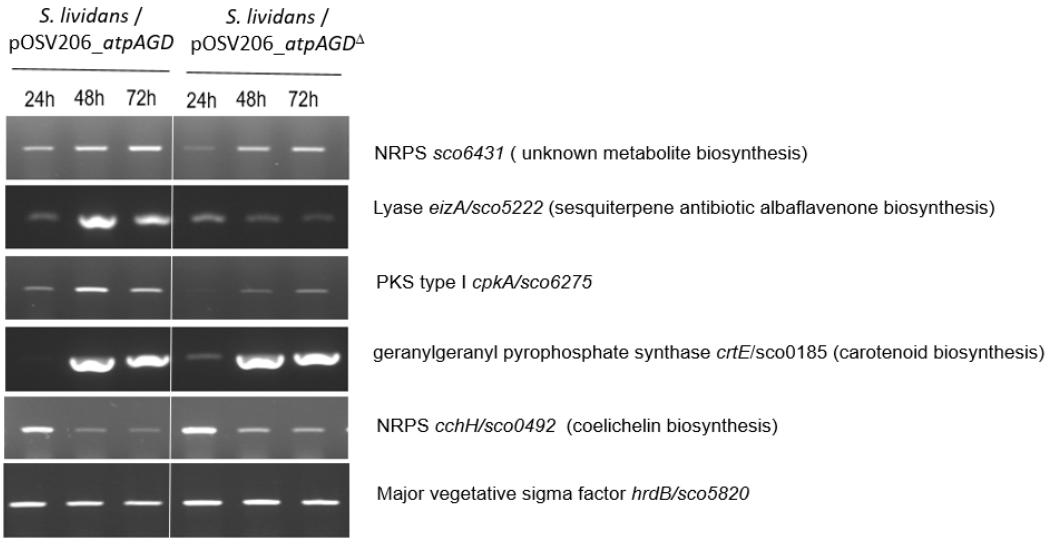

Figure S2: Determination by RT-PCR of the level of expression of genes belonging to various specialized metabolite biosynthetic pathways in S. lividans/pOSV206_*atpAGD* and S. lividans/pOSV206_*atpAGD*$^{\Delta}$, grown on solid HT medium for 48 h, using the primers specific to each gene listed in Table S1. These include the NRPS *sco6431*, *eizA*/*sco5222* involved in the biosynthesis of albaflavenone, *cpkA*/*sco6275* encoding a PKS of type I involved in the biosynthesis of a cryptic yellow polyketide, *crtE*/*sco0185* involved in carotenoid biosynthesis and that of the NRPS *cchH*/*sco0492* involved in coelichelin biosynthesis. *hrdB*/*sco5820* PCR amplification was used as internal control.