Supplementary Information

Streptomyces natalensis programmed cell death and morphological differentiation are dependent on oxidative stress

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Table S1. *S. natalensis* homologues of known *S. coelicolor* development related proteins.

Protein name	SNA_code	Identity	Coverage	e-value	*S. coelicolor* RefSeq
BldA	SNA_04225	93%	100%	4.00E-28	Y00209.1
BldB	SNA_08815	68%	93%	1.00E-23	NP_629849.1
BldC	SNA_03650	100%	100%	6.00E-44	NP_628272.1
BldD	SNA_13365	98%	100%	4.00E-113	NP_625769.1
BldG	SNA_00365	96%	100%	1.00E-73	NP_627747.1
BldH (AdpA)	SNA_06025	92%	79%	0	NP_627022.1
BldKA	SNA_34770	60%	99%	8.00E-146	NP_629262.1
BldKB	SNA_34775	49%	97%	0	NP_629263.1
BldKC	SNA_34780	70%	99%	5.00E-166	NP_629264.1
BldKD	SNA_34785	78%	99%	0	NP_629265.1
BldKE	SNA_34790	80%	93%	0	NP_733655.1
BldM	SNA_39180	100%	100%	7.00E-142	NP_628926.1
BldN	SNA_38050	96%	67%	7.00E-123	NP_627533.1
WhiA	SNA_10605	92%	99%	0	NP_626214.1
WhiB	SNA_03895	95%	98%	7.00E-56	NP_627256.1
WhiD	SNA_39175	97%	84%	4.00E-64	NP_628925.1
WhiEI	SNA_26210	57%	96%	2.00E-138	NP_629462.1
WhiEII	SNA_26205	72%	91%	9.00E-65	NP_629461.1
WhiEIII	SNA_26200	76%	99%	0	NP_629460.1
WhiEIV	SNA_26195	74%	96%	0	NP_629459.1
WhiEV	SNA_26190	52%	98%	9.00E-23	NP_629458.1
WhiEVI	SNA_26185	68%	91%	7.00E-69	NP_629457.1
WhiEVII	SNA_26180	72%	95%	2.00E-52	NP_629456.1
WhiEVIII	SNA_26175	77%	96%	0	NP_629463.1
WhiG	SNA_32585	90%	99%	0	NP_629755.1
WhiH	SNA_31720	76%	99%	7.00E-162	NP_629942.1
WhiI	SNA_30685	95%	99%	9.00E-140	NP_630140.1
ChpA	SNA_06310	50%	56%	3.00E-37	NP_733581.1
ChpC	SNA_01235	46%	99%	5.00E-38	NP_625949.1
ChpD	SNA_00490	67%	97%	2.00E-23	NP_626950.1
ChpD2	SNA_12255	77%	60%	1.00E-20	NP_626950.1

Protein name	SNA_code	Identity	Coverage	e-value	*S. coelicolor* RefSeq
ChpE	SNA_11245	64%	97%	6.00E-20	NP_626070.1
ChpE2	SNA_11250	67%	64%	1.00E-17	NP_626070.1
ChpG	SNA_00485	67%	49%	2.00E-16	NP_626939.1
ChpG2	SNA_05975	73%	48%	3.00E-15	NP_626939.1
ChpH	SNA_12040	86%	98%	8.00E-24	NP_625950.1
RdlA	SNA_27905	53%	71%	2.00E-25	NP_626951.1
RamR	SNA_20600	50%	98%	1.00E-50	NP_733711.1
RamB	SNA_20605	56%	96%	1.00E-174	NP_630759.1
RamA	SNA_20610	56%	92%	8.00E-147	NP_630758.1
RamS	SNA_20615	76%	97%	3.00E-17	NP_630757.1
RamC	SNA_20620	66%	99%	0	NP_630756.1
DivIVA	SNA_09545	84 %	54 %	4E-99	NP_626336
FilP	SNA_33665	92%	100 %	0	NP_629535
FtsK	SNA_11150	61 %	88 %	1E-152	NP_733622
FtsW	SNA_09505	79 %	94%	0	NP_626344
FtsZ	SNA_09520	86 %	100 %	0	NP_626341
Mbl	SNA_06725	97 %	100 %	0	NP_626848
MreB	SNA_07640	71 %	98 %	4E-170	NP_626694
ParA	SNA_02365	89 %	100 %	4E-173	NP_628072
ParB	SNA_02360	74 %	99 %	1E-149	NP_628073
Scy	SNA_33660	60 %	100 %	0	NP_629536
SigF	SNA_01565	92 %	94 %	8E-171	NP_628217
Smc	SNA_32725	82 %	86 %	0	NP_629712
SsgA	SNA_26640	49 %	97 %	4E-40	NP_630795
SsgB	SNA_00325	88 %	92 %	2E-159	NP_627756
SspA	SNA_27035	44 %	61 %	3E-3	NP_631483

Table S2. Primers used in PCR and RT-qPCR.

Primer	Sequence	T.A. (ºC)	Amplicon (bp)
D_catR_F	ATTCCGGGGATCCGTCGACCGTACCCTGGGCTGTATCTGACTGATAGGTGATTGGCATG	60	1462
D_catR_R	TGTAGGCTGGAGCTGCTTCCCTGGGGGCGGGCCGGACGCGGGACGCCGACCGCGGTCA		
C_catR_F	GTGCGCCTCCTGAAGTGATC	60	584
C_catR_R	TCAGGCGTGGTGGCCGCT		
adpA_S	CCCGCGACCACCCATTGGA	65	105
adpA_AS	GGTGAGCACATCGCCGTCGTC		
bldD_S	CTGGAAGGCCGTGGTGGTGG	65	105
bldD_AS	AGCTCCTGGACCGGCACCC		
bldN_S	CACGGCCGAGGACCTCACCA	65	102
bldN_AS	ATGGTCACCAGCCAGGCGC		
chpC_S	CACCAGGGCGGGTCGGA	60	109
chpC_AS	TGGCCGGTACCGCGTAGC		
ramC_S	ATCCATATCTCGGCCTGCCTGG	60	102
ramC_AS	CCGGCTCGGCATGCATTTG		
ramS_S	TCGACCTGCAGACGATGGAAAC	60	99
ramS_AS	TCAGACTGCTGTCGCCGCA		
rdlA_S	GAGTAACCGCCACGCCAGCA	60	103
rdlA_AS	CCCTGCGGGCTCATGTCG		
bfrA_S	CGGCTGGCCGAAGCTTGC	60	103
bfrA_AS	CGGCAGCCCTTCGAGGAAGA		
catR_S	CAACGCCCACCACGACCA	65	75
catR_AS	TCGCCCTGGAGATGGACG		
cpx_S	GAGCGGCTCCAGCAGGACT	60	106

Primer	Sequence	T.A. (ºC)	Amplicon (bp)
cpx_AS	TCGCGGCTTGTTCGACG		
dpsA_S	CACTGGAACGTCGTCGGCC	60	150
dps_AS	CTTGGCGACCGTCGAGGC		
katA1_S	CCTGGTCGGTCTTGAAGTGGTA	60	80
katA1_AS	CTACGGCTCGCACACCTTC		
katA3_S	CACACCAAGGACGACGACTT	60	81
katA3_AS	CTCCACCAGACGCTTCTTCTC		
16S_S	CAGGCTAGAGTTCGGTAGG	65	117
16S_AS	CTCCTCAGCGTCAGTATCG		

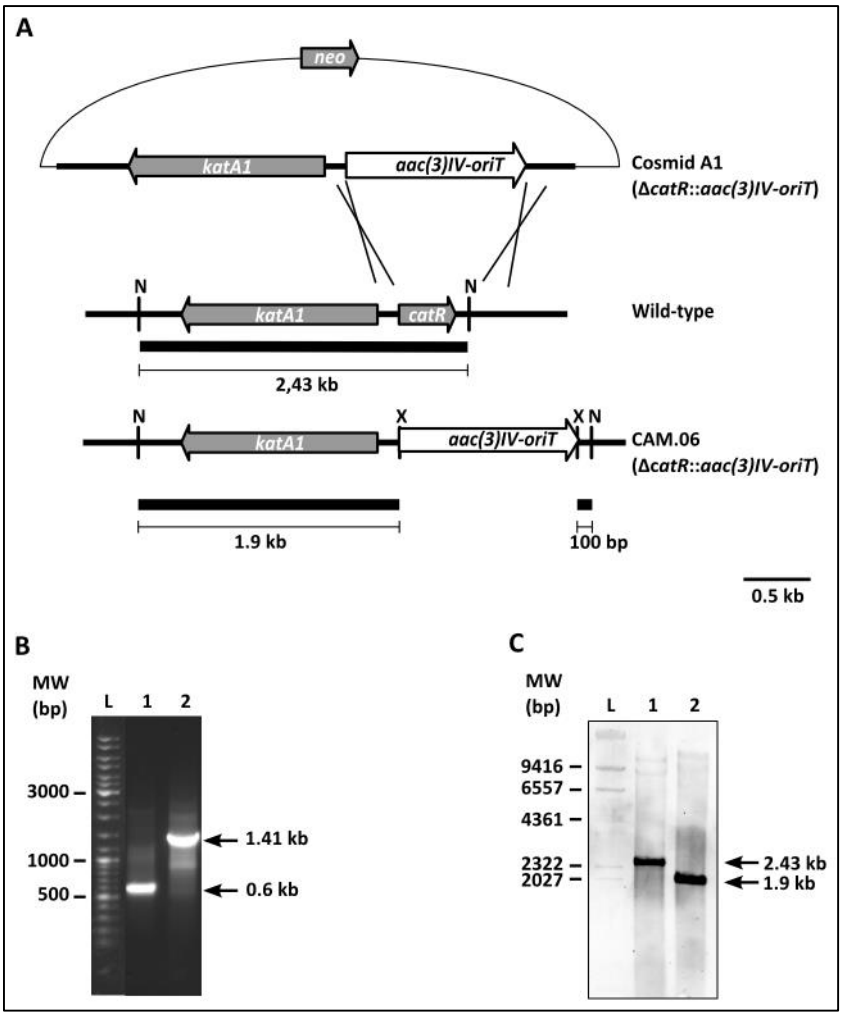

Fig. S1 - Construction of *S. natalensis* Δ*catR* strain by gene replacement.

(A) Predicted restriction enzyme polymorphism caused by gene replacement. The *Nco*I-*Xba*I restriction pattern before and after replacement is shown. The probe used for southern hybridization is indicated by thick lines. N, NcoI; X, XbaI. (B) Confirmation of gene disruption by PCR. A pair of primers, C_catR_F and C_catR_R, covering the deleted region in the chromosome were to identify double crossover mutants. Lane L, GeneRuler™ (Thermo Scientific).(C) Confirmation of gene disruption by Southern blot of the NcoI-XbaI digested chromosomal DNA of the wild type (lane 1), and Δ*catR* (lane 2) strains. Lane L, DIG-labelled DNA Molecular Weight Marker II (Roche).

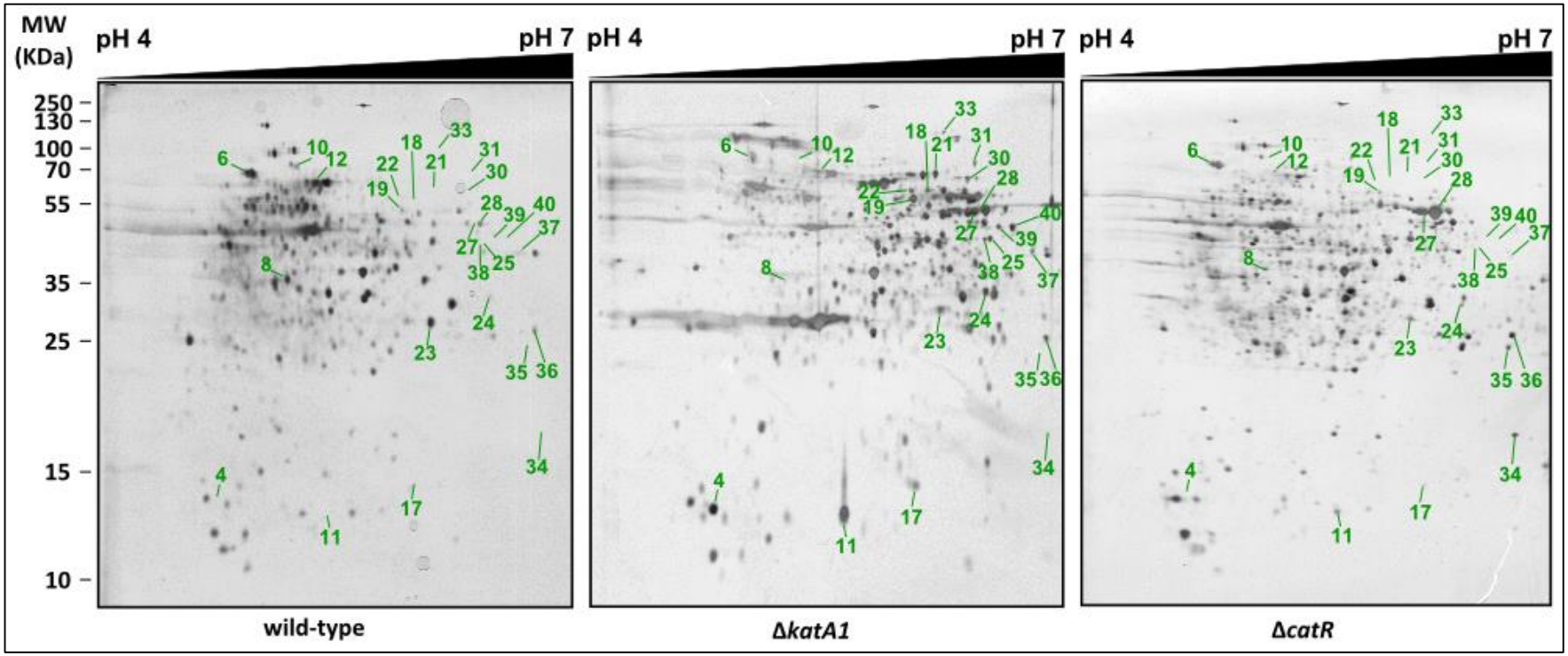

Fig. S2 - Proteome analysis by 2D-PAGE.

The presented 2D gels are representative of biological duplicates (100 μg of crude protein extracts per gel). The spots indicated in the figure correspond to the proteins identified by mass spectrometry (for SNA code correspondence to spot ID number see Table 1).

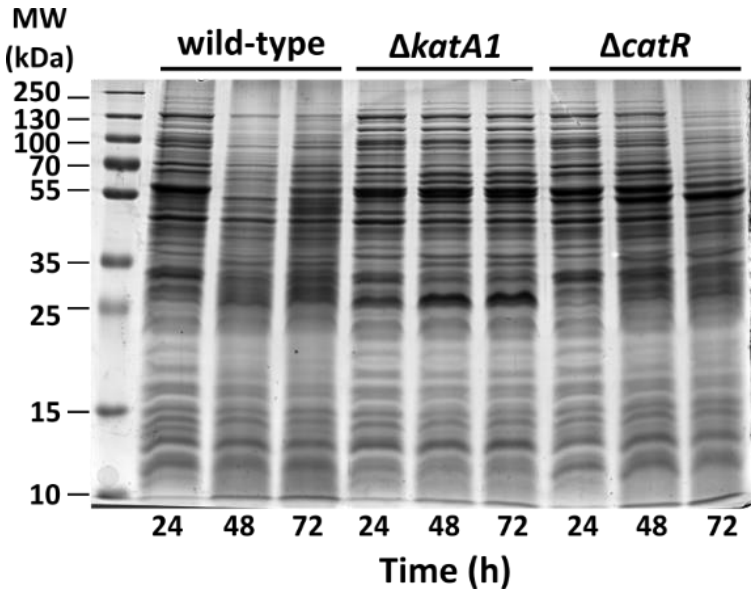

Fig. S3 - Coomassie coloration of SDS-PAGE with protein crude extracts (20 μg of protein per lane) used as loading control for the nuclease activity assay (Fig. 4B).