

Table S3: Gene distribution in the central region *versus* the extremities (defined by the first and last rRNA operons) of *Streptomyces ambofaciens* ATCC23877 chromosome depending on features of interest

Features	Number of genes of interest	% of genes of interest present within the extremities	% of genes within the central region presenting the feature of interest	% of genes within the extremities presenting the feature of interest	Odds ratio ^a	<i>p</i> value ^b
Chromosomal genes	7128	46.5				
Genome features related to the level of conservation						
CDSs of the actinobacterial signature	72	16.7	1.6	0.4	0.23	1.4.10 ⁻⁷
Core CDSs	1020	11.3	23.7	3.5	0.12	<2.2.10 ⁻¹⁶
CDSs with a high level of persistence (>0.95)	2186	17.6	47.2	11.6	0.15	<2.2.10 ⁻¹⁶
GIs	1207	80.4	6.2	29.3	6.27	<2.2.10 ⁻¹⁶
Strain-specific CDSs ^c	158	85.4	0.6	4.1	6.99	<2.2.10 ⁻¹⁶
Genome features related to functional annotation						
Functional RNA (excluding rRNA)	75	13.3	1.7	0.3	0.17	1.3.10 ⁻⁹
CDSs encoding functions involved in translation	175	13.7	4.0	0.7	0.18	<2.2.10 ⁻¹⁶
NAP genes	49	26.5	0.9	0.4	0.41	0.005798
SMBGCs	385	76.4	2.4	8.9	3.98	<2.2.10 ⁻¹⁶
Features related to the level of expression						
Genes always expressed at very high level (CAT_4) ^d	332	11.7	7.7	1.2	0.14	<2.2.10 ⁻¹⁶
Genes always expressed at very low level (CAT_0) ^d	849	72.3	6.2	18.5	3.46	<2.2.10 ⁻¹⁶

^aThe odds ratio represents the odds than an outcome will occur within the extremities compared to the odds of the outcome occurring in the central region. Genes which distribution is statistically enriched in the central region or within the extremities are written in blue or in red, respectively. The genetic information of each TIR was taken into consideration for the calculations.

^bThe statistical significance of the odd ratios was assessed by a Fisher's exact test for count data.

^cFor this calculation, only the chromosomal strain-specific CDSs were taken into account (excluding the 44 strain-specific CDSs present on pSAM1 non-integrative plasmid).

^d'always' refers to all the conditions investigated in this study (i.e. C1 to C7). Only chromosomal genes were considered in the calculation.