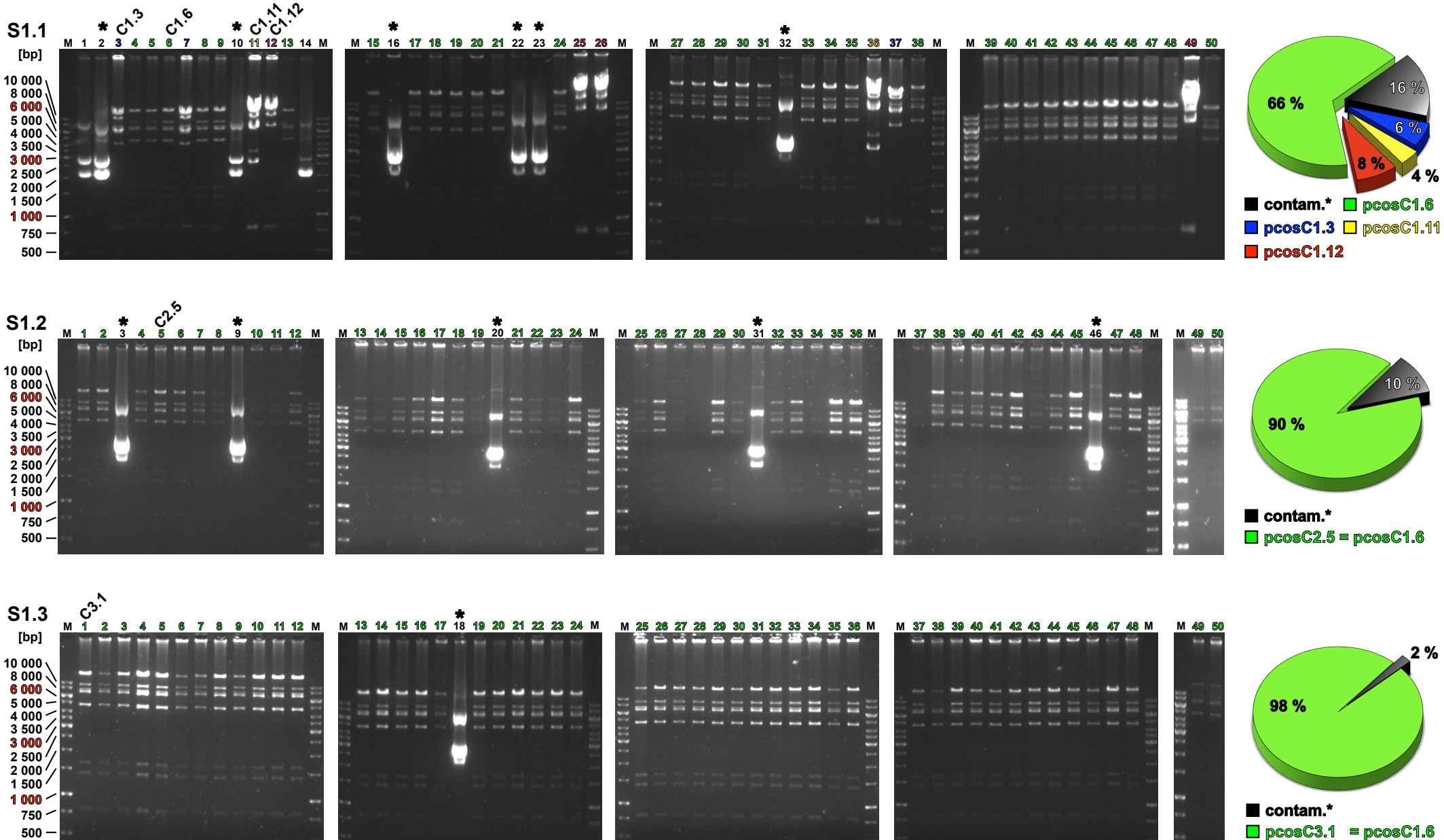
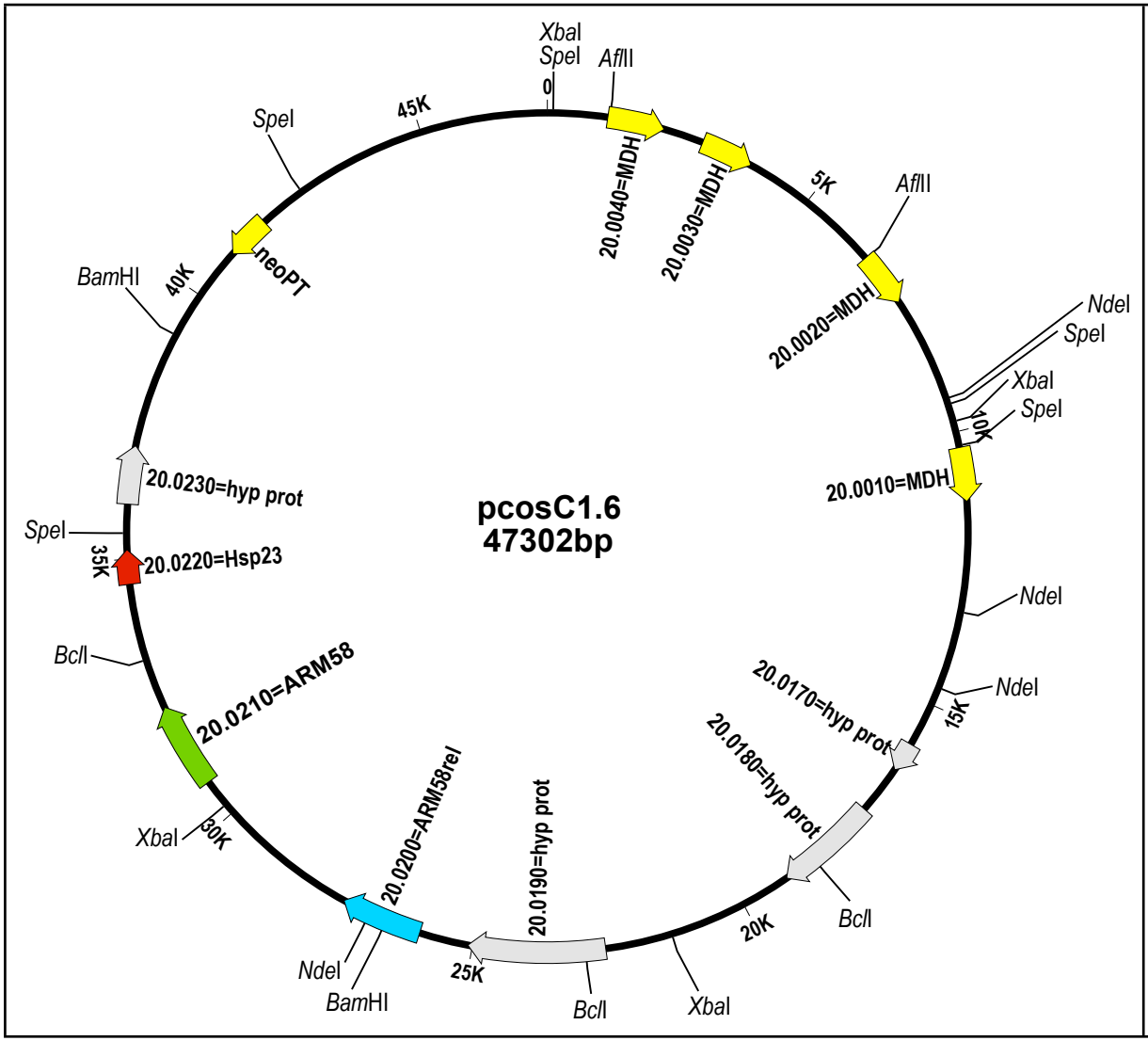
**Supplementary data 1:** Restriction fragment length analysis of selected cosmids.

Cosmid DNA was recovered from populations after SbIII selection and used to transform *E. coli* DH5-alpha competent cells. For each selection 50 individual colonies were picked. The clones were grown and a cosmid DNA minipreparation was performed. Cosmid DNAs were then cleaved with *Eco*RV and *Xba*I. Restriction fragments were anaylsed on a 1% agarose gel in 0.5 X Tris-borate EDTA buffer by field inversion electrophoresis. The gels were then stained in 50 $\mu$g/ml ethidium bromide solution. Size marker mixes were run on both sides of the lanes, and the sizes [bp] are shown on the left. Samples with indistinguishable fragment patterns were assumed to be replicas of the same cosmid prototype. The distribution of the major cosmid prototypes (marked by designation) is represented in the pie charts to the right. Note that selection S1.1 was not stringent (25 $\mu$M SbIII) whilst S1.2 and S1.3 were performed at 90$\mu$M SbIII. Cosmid C1.6 and its replicas could be aligned with DNA sequences on *L. braziliensis* Chromosome 20. The "cosmid" marked with asterisks turned out to be a gene replacement plasmid constructed elsewhere in the lab, and thus a contamination.






**Supplementary data 2:** Physical map of cosmid pcosC1.6. The ruler shows the relative position in [kbp]. Gene identifiers refer to systematic numbers from the *L. braziliensis* genome project (LbrM.20.xxxx). MDH=malate dehydrogenase; ARM58=58 kD antimony resistance marker; ARM58rel=ARM58--related; Hsp23=23 kD heat shock protein; NeoPT=neomycin phosphotransferase. Restriction sites relevant for derivative construction (3.7) are marked.

**Supplementary data 3: Sequence of pcosC1.6**

Range: 1 to 473023

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42900

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