

Additional File 3. Non coding RNAs

Table S3A Codon and tRNA gene usage in *A.adeninivorans* and *Y. lipolytica*.

Genes encoding tRNAs were searched with tRNAScan-SE¹ and sequences were analyzed for possible exceptions to the eukaryotic cloverleaf model, as described in². Initiator Met tRNA genes were distinguished from the elongator sequences thanks to the "GGG" sequence in positions 29 -31.

Table S3B Genes encoding snRNAs and snoRNAs.

Blast³ and Infernal⁴ searches were performed on *A. adeninivorans* genome for snRNAs and snoRNAs detection. For the Blast search, ncRNA sequences from the Genolevures database⁵ were used as queries. All hits with an e-value lower than 0.1 were retained for validation. For the Infernal search, covariance models found in the RFam⁶ database were used. All hits with an e-value lower than 0.5 were retained for validation. All retained hits were aligned and manually checked. Hits were accepted as candidates if: i) the sequence agrees with known structural features, guiding sequences (for snoRNAs) and conserved sequence motifs for homologous molecules and ii) known synteny was verified.

