

Figure S3. Relative expression profiles of *M. nitratireducenticrescens* strain GP59 in Ref300N-23C and 900N-30C biofilm cultures

All the deduced amino acid sequences associated to the GP59 genome and plasmids in the Ref300N-23C and 900N-30C biofilm cultures were submitted to the BlastKOALA (genome annotation and KEGG mapping) at the Kyoto encyclopedia of genes and genomes (KEGG). Genes associated to specific metabolisms were sorted out and the corresponding ratio of the Biofilm TPM versus the pure culture TPM was derived. When the ratios were <1, the negative inverse value ($-1/\text{ratio}$) was calculated. Data are expressed as the percentage of genes in each category that are more expressed in the biofilm cultures (right, 2 to 5 times, and > 5 times) or in pure cultures (left, -2 to -5 times and > -5 times). Number within parentheses is the number of genes involved in the selected pathways. (see Supplemental document 8).

Figure S4. Relative expression profiles of *M. nitratireducenticrescens* strain GP59 and *H. nitrativorans* NI23 in the 0%NaCl biofilm cultures

All the deduced amino acid sequences associated to the GP59 genome and plasmids and the NL23 genome in the 0%NaCl biofilm cultures were analyzed as described in Figure legend S3 (see Supplemental document 8).

Relative expression profiles of *M. nitratireducenticrescens* strain JAM1 are detailed in the Supplemental documents 8 and 11.

Figure S3

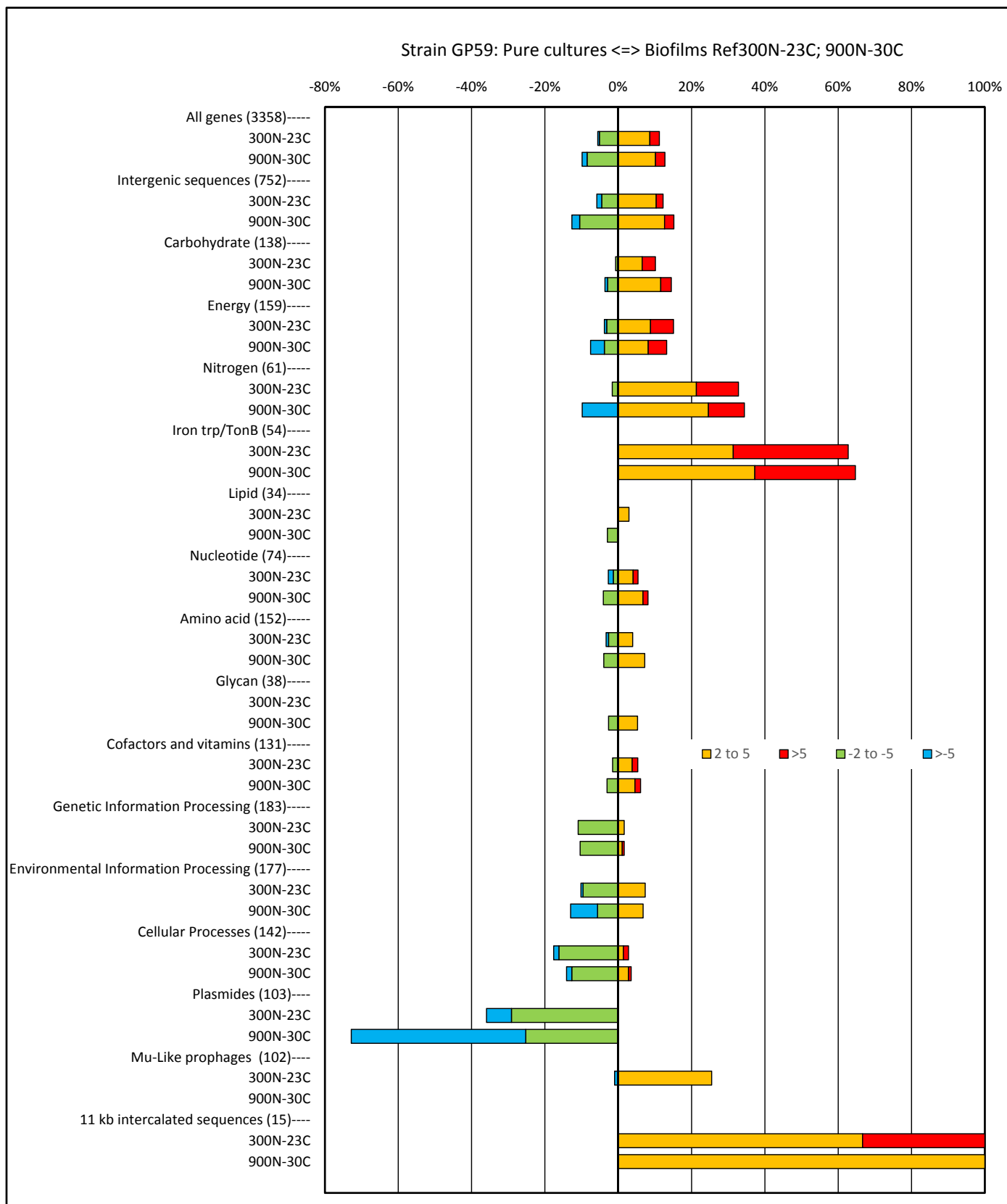


Figure S4

