

Figure S4: Schematic of selected metabolic pathways in *Methylophaga nitrireducens* JAM1 and GP59

- Pathways are based on functions deduced by gene annotations (see supplemental Data7)
- The arrow thickness is proportional to the level of transcript reads (TPM normalization)
- The red arrows represent GP59 genes with at least 2-fold lower TPM than those of strain JAM1
- The blue arrows represent GP59 genes with at least 2-fold higher TPM than those of strain JAM1

