**Table S3. SIB Carbon sources metabolism subsystem composition into Janthinobacterium sp. SLB01 and Flavobacterium sp. SLB02 genomes**

|  |  |  |  |
| --- | --- | --- | --- |
| Carbon source group | Subsystem | *Subsystem gene loci for*  *Janthinobacterium* sp. SLB01 | *Subsystem gene loci for*  *Flavobacterium* sp. SLB02 |
| Central carbohydrate metabolism  (74/54) | TCA Cycle (15/0) | F3B38\_21755\*  Citrate synthase (si)  F3B38\_21805  Aconitate hydratase  F3B38\_21730  2-oxoglutarate dehydrogenase E1 component  F3B38\_21725  Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex  F3B38\_21715  Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase  F3B38\_00435  Dihydrolipoamide dehydrogenase  **F3B38\_26675**  Succinyl-CoA ligase [ADP-forming] alpha chain  F3B38\_26680  Succinyl-CoA ligase [ADP-forming] beta chain  F3B38\_06840  Fumarate hydratase class I, aerobic  F3B38\_07520  Fumarate hydratase class II  F3B38\_21790  Malate dehydrogenase  F3B38\_25650  Malate:quinone oxidoreductase  F3B38\_08570  Isocitrate dehydrogenase  F3B38\_17225  Isocitrate dehydrogenase [NADP]  F3B38\_23935  Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex |  |
| Pentose phosphate pathway (0/9) |  | GIY83\_17730\*  Ribulose-phosphate 3-epimerase  GIY83\_19305  Transketolase  GIY83\_24600  Transketolase, C-terminal section  GIY83\_24605  Transketolase, N-terminal section  GIY83\_19300  Transaldolase  GIY83\_03155  Transaldolase  GIY83\_07110  Transaldolase  GIY83\_19205  Ribose-phosphate pyrophosphokinase  GIY83\_21110  Ribose-phosphate pyrophosphokinase |
| Di- and oligosaccharides (3/14) | Sucrose utilization (0/2) |  | GIY83\_05790  Fructokinase  GIY83\_10050  Sucrose-6-phosphate hydrolase |
| Organic acids (19/3) | Methylcitrate cycle (7/0) | F3B38\_08615  Propionate catabolism operon regulatory protein PrpR  F3B38\_15375  2-methylcitrate synthase  F3B38\_18875  Propionate--CoA ligase  F3B38\_18890  2-methylaconitate isomerase  F3B38\_18900  2-methylcitrate synthase  F3B38\_18905  Methylisocitrate lyase  F3B38\_21805  Aconitate hydratase |  |
| Propionate-CoA to Succinate Module (7/0) | Same except F3B38\_08615 |  |
| Lactose and Galactose Uptake and Utilization (0/8) |  | GIY83\_09355  Aldose 1-epimerase  GIY83\_10655  Aldose 1-epimerase  GIY83\_19225  Aldose 1-epimerase  GIY83\_19315  Aldose 1-epimerase  GIY83\_19320  Galactokinase  GIY83\_19325  Galactose-1-phosphate uridylyltransferase  GIY83\_16220  UDP-glucose 4-epimerase  GIY83\_23050  UDP-glucose 4-epimerase |
| Fermentation (37/24) | Mixed acid (0/7) |  | GIY83\_17280  pyruvate formate lyase-activating protein  GIY83\_17285  formate C-acetyltransferase  GIY83\_11695  phosphate acetyltransferase  GIY83\_11690  acetate/propionate family kinase  GIY83\_10940  Cinnamyl alcohol dehydrogenase/reductase  GIY83\_07850 phosphoenolpyruvate carboxylase  GIY83\_15085  D-lactate dehydrogenase |
| Polysaccharides (0/4) | Glycogen metabolism (0/4) |  | GIY83\_07355  glucose-1-phosphate adenylyltransferase  GIY83\_07350  Glycogen synthase, ADP-glucose transglucosylase  GIY83\_07360  1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type  GIY83\_07365  DUF4968 domain-containing protein |
| Monosaccharides (37/35) | 2-Ketogluconate Utilization (4/0) | F3B38\_18135  2-ketogluconate utilization repressor PtxS  F3B38\_18110  Epimerase KguE  F3B38\_18105  2-ketogluconate kinase  F3B38\_18100  2-ketogluconate 6-phosphate reductase |  |
| L-Arabinose utilization (0/9) |  | GIY83\_19255  family 43 glycosylhydrolase  GIY83\_19265  family 43 glycosylhydrolase  GIY83\_19270  family 43 glycosylhydrolase  GIY83\_19280  family 43 glycosylhydrolase  GIY83\_19240  Ribulokinase  GIY83\_19230  L-arabinose isomerase  GIY83\_19235  L-ribulose-5-phosphate 4-epimerase AraD  GIY83\_07080  MFS transporter  GIY83\_23865  Protein AraJ precursor |