Table 2 | Continued

Gene ID	Predicted function	Gene	Replicate 1	Replicate 2
METTOv1_760012	FecI-family sigma factor	*fecI*	922	951
METTOv1_870003	Ferribactin synthase	*pvdL*	433	441
METTOv1_870004	Pyoverdine biosynthesis regulatory protein-TauD/TfdA family protein		932	1039
METTOv1_870005	Pyoverdine synthetase, thioesterase component	*pvdG*	1542	1473
METTOv1_870006	Integral components of bacterial non-ribosomal peptide synthetases	*MbtH*	4176	5481
METTOv1_1220001	Putative pyoverdine sidechain peptide synthetase IV, d-Asp-l-Ser component	*pvdI/J*	480	564
METTOv1_1220002	Putative non-ribosomal peptide synthase	*pvdJ/D*	379	396

Values represent reads per kilobase of coding sequence per million (reads) mapped (RPKM).

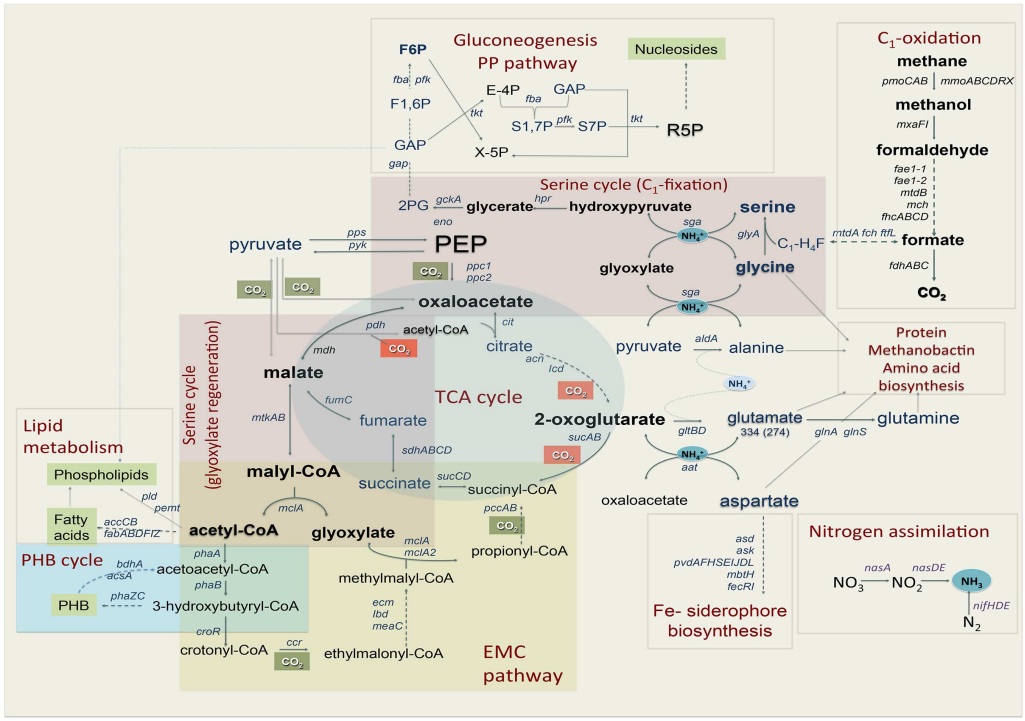

FIGURE 1 | Central metabolism of *Methylosinus trichosporium* OB3b grown on methane as sole source of energy and carbon as deduced from the genome sequences and transcriptomic studies. Font size of the gene name indicates the expression level.

published sequence as the scaffold (Holmes et al., 1995). For this sequence, two possible transcriptional start sites were identified. It is not known whether these reflect the same start sites of both operons, different start sites for each, or expression of only one operon with two start sites. The position −274nt (A) from the translational start of the *pmoC* gene was predicted as the most prominent start of transcription of the operon (Figure S1 in Supplementary Material). Putative σ^{70}-like -10 and -35 regions could be identified upstream of the predicted start (Table S3 in Supplementary Material). The structure of the putative promoter region from *M. trichosporium* OB3b shows significant similarity to a *pmoCAB* promoter region previously identified in *Methylocystis* sp. M (Gilbert et al., 2000). Another potential transcriptional start is at position −324 from the translational start of the *pmoC* gene. It should be noted that the region between the two predicted start sites was also covered with relatively high count (region between −324 and −274nt with respect to the translational start of *pmoC*). No putative promoter sequences were found upstream of position 324.

The genome predicts an additional copy of the *pmoC* gene by itself (*pmoC2, METTOv1_310040*), which can be distinguished from the other *pmoC* genes in the transcriptomics data due to sequence divergence. It has previously been demonstrated that additional copies of *pmoC* are essential for methanotrophic growth in other strains (Stolyar et al., 1999; Dam et al., 2012a). It has also been shown that the homologous *amoC* (additional lone copy of amoC in ammonia-oxidizing bacterium *Nitrosomonas europaea*) plays role in cell recovery from ammonium starvation (Berube and Stahl, 2012). However the functional role of PmoC is