

**Table S1.** Transcripts detected by *de novo* assembly RNA-Seq data

ID	Non-redundant	Description	Organism	Non-redundant length	Fraction of Alignment nr covered by alignment	Alignment % identity	Alignment e-value
8	319794846	hypothetical protein Varpa_4205	Variovorax paradoxus EPS	90	0.89	63	1.00E-23
48	323139488	SEC-C motif domain protein	Methylocystis sp. ATCC 49242	169	0.20	55	0.0004
48	323139488	SEC-C motif domain protein	Methylocystis sp. ATCC 49242	169	0.41	63	4.00E-18
90	307110660	hypothetical protein CHLNCDRAFT_50435	Chlorella variabilis	1535	0.05	24	4.5
90	307110660	hypothetical protein CHLNCDRAFT_50435	Chlorella variabilis	1535	0.05	24	4.6
120	309365749	hypothetical protein CBG_01089	Caenorhabditis briggsae AF16	812	0.12	32	0.7
121	310821854	hypothetical protein STAUR_4605	Stigmatella aurantiaca DW4/3-1	728	0.08	38	3.5
125	197103309	hypothetical protein PHZ_p0169	Phenylobacterium zucineum HLK1	223	0.55	60	8.00E-34
142	78213547	glycosyltransferase	Synechococcus sp. CC9605	1003	0.31	31	5.00E-14
142	325116388	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA, related	Neospora caninum Liverpool	819	0.21	31	0.088
171	323136696	hypothetical protein Met49242DRAFT_1164	Methylocystis sp. ATCC 49242	92	0.64	53	6.00E-06
266	338532669	chloride channel	Myxococcus fulvus HW-1	628	0.72	63	3.00E-138
300	323136327	Patatin	Methylocystis sp. ATCC 49242	284	0.44	60	3.00E-38
303	227819692	transposase Y4ZB	Sinorhizobium fredii NGR234	493	0.35	42	8.00E-24
308	323449050	hypothetical protein AURANDRAFT_66784	Aureococcus anophagefferens	1445	0.48	25	3.00E-33
314	341615616	two-component response regulator	Citromicrobium sp. JLT1363	257	0.15	59	0.32
339	149918868	site-specific recombinase, phage integrase family protein	Plesiocystis pacifica SIR-1	120	0.53	36	7.9
360	46153	endo-glucanase	Ruminococcus flavefaciens	680	0.09	38	4.6
370	167901659	hypothetical protein BpseN_05228	Burkholderia pseudomallei NCTC 13177	474	0.32	29	4.9
381	203288753	BdrQ-like protein	Borrelia duttonii Ly	239	0.67	30	4.00E-05
401	323457221	hypothetical protein AURANDRAFT_70536	Aureococcus anophagefferens	1999	0.06	33	2.1
431	221486147	conserved hypothetical protein	Toxoplasma gondii GT1	702	0.16	30	5.9
469	16519794	transposase number 3 of uncharacterized insertion sequence	Sinorhizobium fredii NGR234	511	0.31	62	7.00E-51
518	323135994	2-oxoglutarate dehydrogenase, E2 subunit, dihydrolipoamide succinyltransferase	Methylocystis sp. ATCC 49242	410	0.10	68	0.0002