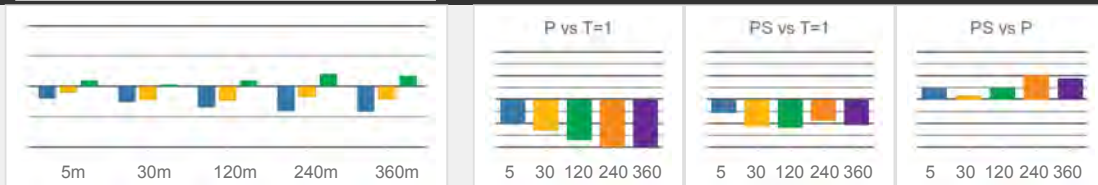
PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0001 *dnaA*	P vs T=1	-0.993	-1.280	-1.679	-1.982	-1.992
	PS vs T=1	-0.524	-1.110	-1.162	-0.863	-1.051
	PS vs P	0.468	0.155	0.475	1.031	0.888
	chromosomal replication initiator protein DnaA					
	DNA metabolism					
PGN_0002	P vs T=1	-1.196	-1.124	-1.125	-0.968	-0.738
	PS vs T=1	-0.560	-0.933	-0.657	-0.644	-0.786
	PS vs P	0.567	0.138	0.390	0.268	-0.055
	conserved hypothetical protein					
	unknown function					
PGN_0003	P vs T=1	-0.165	-0.328	-0.083	0.591	1.728
	PS vs T=1	0.203	0.178	0.489	1.107	1.034
	PS vs P	0.313	0.399	0.458	0.544	-0.556
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0004	P vs T=1	0.632	1.073	1.177	1.173	0.907
	PS vs T=1	0.252	0.567	1.036	1.393	1.388
	PS vs P	-0.392	-0.492	-0.134	0.222	0.470
	putative nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase					
	energy metabolism					
PGN_0005	P vs T=1	0.130	0.117	0.268	0.711	1.174
	PS vs T=1	-0.751	-0.899	-0.244	0.250	0.636
	PS vs P	-0.857	-0.988	-0.500	-0.391	-0.477
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0006	P vs T=1	-0.799	-0.651	-0.088	0.549	1.262
	PS vs T=1	-1.438	-1.186	-0.722	-0.274	0.230
	PS vs P	-0.659	-0.548	-0.607	-0.700	-0.928
	putative Na+driven multidrug efflux pump					
	transport and binding proteins					
PGN_0007	P vs T=1	-0.315	0.017	0.273	-0.648	0.678
	PS vs T=1	-1.721	-2.463	-1.462	-1.145	-1.228
	PS vs P	-1.088	-1.674	-1.053	-0.505	-1.089
	hypothetical protein					
	hypothetical proteins					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0008 *clpC*	P vs T=1	1.417	2.180	2.781	2.919	2.498
	PS vs T=1	-0.205	0.048	0.784	1.374	1.331
	PS vs P	-1.590	-2.030	-1.896	-1.445	-1.119
	ATP-dependent Clp protease ATP-binding subunit ClpC					
	protein fate					
PGN_0009	P vs T=1	-0.292	0.114	0.219	0.193	0.150
	PS vs T=1	-0.013	-0.119	-0.361	-0.127	-0.163
	PS vs P	0.258	-0.223	-0.566	-0.309	-0.308
	glycosyl hydrolase family 3					
	cell envelope					
PGN_0010 *CobC*	P vs T=1	-0.597	-0.502	-0.962	-1.122	-1.215
	PS vs T=1	-0.204	-0.185	-0.947	-1.421	-1.569
	PS vs P	0.387	0.326	-0.005	-0.328	-0.378
	probable L-threonine-O-3-phosphate decarboxylase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0011	P vs T=1	-0.008	0.107	-0.411	-0.703	-0.737
	PS vs T=1	0.655	0.467	-0.297	-0.690	-0.841
	PS vs P	0.652	0.372	0.085	-0.066	-0.148
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0012	P vs T=1	-0.617	-0.682	-0.649	-0.475	-0.271
	PS vs T=1	-0.350	-0.614	-0.962	-0.540	-0.611
	PS vs P	0.255	0.052	-0.329	-0.065	-0.328
	two-component system response regulator					
	signal transduction					
PGN_0013	P vs T=1	-1.061	-1.348	-1.247	-0.655	0.456
	PS vs T=1	-0.956	-1.287	-1.417	-1.149	-0.687
	PS vs P	0.099	0.004	-0.244	-0.417	-0.994
	putative two-component system sensor histidine kinase					
	signal transduction					
PGN_0014	P vs T=1	-1.166	-1.659	-1.638	-0.888	0.217
	PS vs T=1	-0.776	-1.354	-1.900	-1.696	-1.376
	PS vs P	0.393	0.259	-0.326	-0.732	-1.490
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

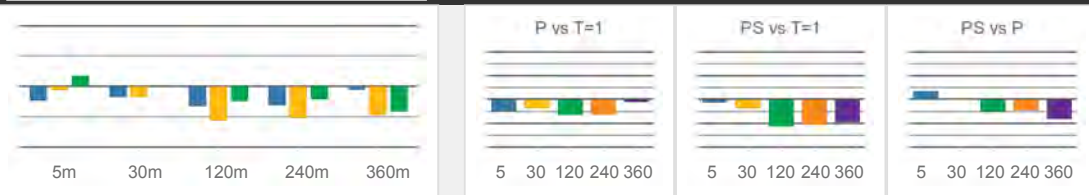
Locus		5m	30m	120m	240m	360m
PGN_0015	P vs T=1	-0.102	-0.741	-1.244	-1.297	-1.123
	PS vs T=1	-0.269	-0.785	-0.691	-0.354	-0.489
	PS vs P	-0.134	-0.059	0.481	0.845	0.593
	probable transcriptional regulator					
	regulatory functions					
PGN_0016	P vs T=1	-0.236	-0.628	-0.683	-0.260	0.574
	PS vs T=1	-0.641	-1.133	-0.681	-0.312	0.129
	PS vs P	-0.380	-0.526	-0.083	-0.056	-0.367
	putative TIM-barrel protein					
	unknown function					
PGN_0017	P vs T=1	0.223	0.110	0.180	0.625	1.281
	PS vs T=1	-0.079	-0.083	-0.042	0.460	0.386
	PS vs P	-0.293	-0.198	-0.239	-0.117	-0.820
	sulfate transporter permease					
	transport and binding proteins					
PGN_0018	P vs T=1	0.024	0.832	1.489	1.336	2.831
	PS vs T=1	-0.207	-0.188	0.648	1.240	1.104
	PS vs P	-0.437	-0.570	-0.256	0.140	-0.485
	hypothetical protein					
	hypothetical proteins					
PGN_0019	P vs T=1	0.165	0.238	1.396	2.102	3.247
	PS vs T=1	-0.387	0.262	1.618	1.838	1.976
	PS vs P	-0.665	-0.265	0.370	0.265	-0.257
	hypothetical protein					
	hypothetical proteins					
PGN_0020	P vs T=1	-0.864	-0.542	-0.614	-0.641	-0.701
	PS vs T=1	-0.595	-0.338	-0.163	-0.051	-0.084
	PS vs P	0.178	0.185	0.407	0.531	0.565
	probable DNA-binding protein					
	unknown function					
PGN_0021	P vs T=1	-0.886	-0.571	-0.217	-0.280	-0.622
	PS vs T=1	-0.755	-0.586	-0.566	-0.210	-0.179
	PS vs P	0.099	-0.022	-0.329	0.079	0.422
	probable hydrolase					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0022	P vs T=1	-0.469	-0.349	-0.626	-0.604	-0.099
porU	PS vs T=1	-0.119	-0.344	-1.111	-1.026	-0.919
	PS vs P	0.347	0.013	-0.489	-0.423	-0.798
	Por secretion system protein porU					
	hypothetical proteins					
PGN_0023	P vs T=1	1.319	1.642	1.137	0.437	0.046
porV	PS vs T=1	1.935	2.661	2.691	1.972	1.690
	PS vs P	0.597	1.024	1.534	1.454	1.576
	Por secretion system protein porV (pg27, lptO)					
	hypothetical proteins					
PGN_0024	P vs T=1	-0.074	-0.562	-1.097	-1.082	-0.910
	PS vs T=1	0.145	-0.039	-0.007	-0.377	-0.350
	PS vs P	0.235	0.499	0.993	0.595	0.517
	putative 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase					
	hypothetical proteins-Conserved					
PGN_0025	P vs T=1	-0.592	-1.772	-1.998	-1.689	-1.491
	PS vs T=1	-0.478	-0.957	-0.654	-0.693	-0.882
	PS vs P	0.157	0.716	1.204	0.908	0.571
	probable SpoU rRNA methylase family protein					
	transcription					
PGN_0026	P vs T=1	0.866	1.001	0.916	0.881	1.076
	PS vs T=1	0.531	0.984	1.782	2.050	2.116
	PS vs P	-0.357	-0.032	0.790	1.041	0.990
	putative cytidine deaminase					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0027	P vs T=1	0.299	0.265	0.357	0.490	0.133
	PS vs T=1	0.194	0.047	0.151	0.255	0.269
	PS vs P	-0.111	-0.228	-0.213	-0.229	0.112
	transposase in ISPg1					
PGN_0028	P vs T=1	0.496	0.349	0.855	0.681	0.837
	PS vs T=1	0.089	0.203	0.517	0.555	1.018
	PS vs P	-0.397	-0.193	-0.277	-0.154	0.190
	hypothetical protein					
	hypothetical proteins					



PgSg Time Course

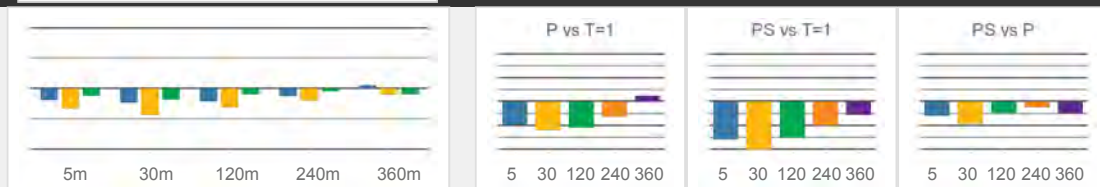
log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0029	P vs T=1	-0.092	-0.189	-0.144	0.152	0.335
	PS vs T=1	-0.237	-0.306	-0.156	0.199	0.100
	PS vs P	-0.146	-0.132	-0.042	0.069	-0.206
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0030	P vs T=1	-0.512	-0.345	-0.195	0.256	0.885
	PS vs T=1	-0.279	-0.647	-0.800	-0.157	0.046
	PS vs P	0.206	-0.307	-0.612	-0.367	-0.776
	beta-mannosidase					
	cell envelope					
PGN_0031	P vs T=1	0.158	0.015	-0.197	0.178	0.678
	PS vs T=1	-0.438	-0.280	0.187	0.697	0.501
	PS vs P	-0.576	-0.292	0.333	0.517	-0.140
	conserved hypothetical protein with RmuC domain					
	hypothetical proteins-Conserved					
PGN_0032	P vs T=1	0.307	0.204	0.848	1.256	2.379
	PS vs T=1	-0.626	0.117	0.212	0.332	1.069
	PS vs P	-0.799	-0.157	-0.404	-0.453	-0.591
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0033	P vs T=1	-0.872	-0.437	-0.124	-0.135	-0.715
	PS vs T=1	-1.447	-0.220	0.467	-0.053	-0.353
	PS vs P	-0.609	0.217	0.611	0.104	0.338
	thioredoxin					
	energy metabolism					
PGN_0034	P vs T=1	0.333	0.011	-0.780	-0.839	-0.910
	PS vs T=1	0.672	0.283	-0.091	-0.179	-0.472
	PS vs P	0.352	0.275	0.659	0.630	0.418
	DNA polymerase III alpha subunit					
	DNA metabolism					
PGN_0035	P vs T=1	-0.004	0.184	0.753	0.832	0.213
rplS	PS vs T=1	-1.083	-0.686	-0.242	-0.469	-0.509
	PS vs P	-1.049	-0.830	-0.926	-1.226	-0.702
	50S ribosomal protein L19					
	protein synthesis					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0036	P vs T=1	-0.935	-1.186	-1.069	-0.607	0.241
	PS vs T=1	-1.570	-2.122	-1.501	-0.980	-0.527
	PS vs P	-0.572	-0.897	-0.457	-0.215	-0.476
	hypothetical protein					
	hypothetical proteins					
PGN_0037	P vs T=1	-0.632	-1.113	-0.269	0.290	1.059
	PS vs T=1	-1.226	-1.344	-0.973	-0.117	0.298
	PS vs P	-0.525	-0.457	-0.517	-0.004	-0.206
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0038	P vs T=1	0.120	0.546	1.253	1.419	0.851
	PS vs T=1	0.004	0.356	0.683	1.170	1.144
	PS vs P	-0.146	-0.189	-0.527	-0.201	0.293
	serine hydroxymethyltransferase					
	central intermediary metabolism					
PGN_0039	P vs T=1	0.507	0.747	0.921	0.718	0.786
	PS vs T=1	0.924	0.793	0.379	0.150	0.381
	PS vs P	0.403	0.060	-0.501	-0.548	-0.383
	beta-hexosaminidase					
	cell envelope					
PGN_0040	P vs T=1	-0.063	0.271	0.631	0.411	0.943
	PS vs T=1	0.704	0.901	1.032	0.854	0.662
	PS vs P	0.569	0.525	0.429	0.303	-0.147
	hypothetical protein					
	hypothetical proteins					
PGN_0041	P vs T=1	2.230	2.692	2.793	2.663	2.119
htpG	PS vs T=1	0.367	0.555	0.460	0.624	0.719
	PS vs P	-1.762	-1.989	-2.212	-1.930	-1.354
	heat shock protein 90					
	protein fate					
PGN_0042	P vs T=1	0.501	1.072	1.400	1.549	1.231
	PS vs T=1	-0.019	0.540	2.026	2.525	2.427
	PS vs P	-0.555	-0.520	0.631	0.982	1.180
	probable phosphatidate cytidylyltransferase					
	regulatory functions					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0043	P vs T=1	0.816	1.601	1.826	1.806	1.407
	PS vs T=1	0.153	2.391	3.769	3.969	3.590
	PS vs P	-0.753	0.772	1.916	2.116	2.122
	putative transmembrane AAA-metalloprotease FtsH					
	cellular processes					
PGN_0044	P vs T=1	-0.758	-1.480	-2.259	-2.197	-1.558
	PS vs T=1	-1.063	-1.123	-1.540	-1.457	-1.742
	PS vs P	-0.243	0.342	0.612	0.642	-0.177
	GTP-binding protein					
	hypothetical proteins-Conserved					
PGN_0045	P vs T=1	1.470	0.900	0.219	0.292	1.696
	PS vs T=1	0.697	0.927	0.644	1.156	0.682
	PS vs P	-0.455	0.096	0.150	0.563	-0.555
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0046	P vs T=1	1.233	0.958	1.360	2.547	3.104
	PS vs T=1	0.776	0.369	1.629	1.873	1.920
	PS vs P	-0.356	-0.573	0.196	-0.100	-0.647
	hypothetical protein					
	hypothetical proteins					
PGN_0047	P vs T=1	-0.136	-0.937	0.328	0.638	2.569
	PS vs T=1	-1.025	-0.085	0.028	0.159	1.196
	PS vs P	-0.735	0.142	-0.116	-0.227	-0.381
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0048	P vs T=1	0.609	0.178	1.168	1.715	2.716
	PS vs T=1	-0.121	0.822	1.615	1.719	2.036
	PS vs P	-0.701	0.373	0.475	0.203	-0.380
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0049	P vs T=1	1.098	1.081	1.699	2.168	3.295
	PS vs T=1	0.519	1.427	2.239	2.158	2.015
	PS vs P	-0.581	0.271	0.549	0.111	-1.056
	probable anti-restriction protein					
	anti-restriction					

PgSg Time Course

log$_2$ (Fold Change)

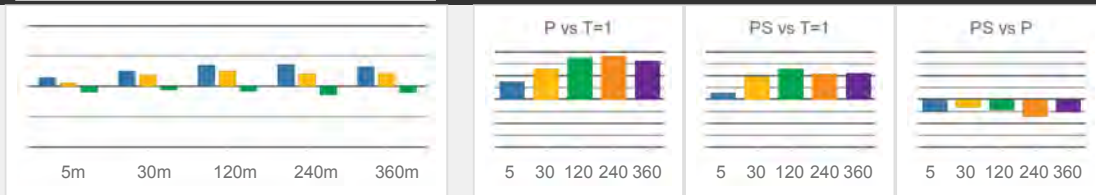
P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0050	P vs T=1	0.547	0.566	1.196	1.772	2.239
	PS vs T=1	-0.063	0.526	1.534	1.334	1.342
	PS vs P	-0.621	-0.081	0.353	-0.324	-0.784
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0051	P vs T=1	0.548	0.527	0.977	1.713	1.957
	PS vs T=1	-0.216	0.320	0.995	0.844	1.139
	PS vs P	-0.732	-0.234	0.038	-0.553	-0.588
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0052	P vs T=1	0.130	0.257	1.423	1.843	1.875
	PS vs T=1	-0.521	-0.103	0.682	1.105	1.439
	PS vs P	-0.685	-0.415	-0.578	-0.483	-0.292
	hypothetical protein					
	hypothetical proteins					
PGN_0053	P vs T=1	2.026	1.595	1.436	1.119	0.697
	PS vs T=1	-0.578	-0.182	0.006	-0.365	-0.739
	PS vs P	-2.258	-1.543	-1.261	-1.358	-1.380
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0054	P vs T=1	1.733	2.139	2.667	2.601	1.995
	PS vs T=1	-0.915	-0.335	0.169	0.047	-0.179
	PS vs P	-2.501	-2.291	-2.315	-2.382	-2.090
	hypothetical protein					
	hypothetical proteins					
PGN_0055	P vs T=1	1.426	1.543	1.690	1.467	1.074
	PS vs T=1	-0.628	-0.331	0.143	0.145	0.095
	PS vs P	-1.977	-1.790	-1.471	-1.253	-0.950
	probable lysozyme					
	cellular processes					
PGN_0056	P vs T=1	1.614	2.164	2.928	3.027	2.753
	PS vs T=1	0.886	1.471	2.424	2.421	2.629
	PS vs P	-0.739	-0.648	-0.409	-0.506	-0.080
	probable conserved protein found in conjugate transposon					
	other categories					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0057 *traP*	P vs T=1	0.746	1.290	1.758	1.828	1.636
	PS vs T=1	0.277	0.961	1.289	1.066	1.104
	PS vs P	-0.486	-0.305	-0.419	-0.701	-0.503
	probable conserved protein found in conjugate transposon TraP					
	other categories					
PGN_0058	P vs T=1	1.313	2.220	2.849	2.847	2.511
	PS vs T=1	0.422	0.984	1.645	1.626	1.946
	PS vs P	-0.911	-1.111	-1.049	-1.070	-0.498
	probable conserved protein found in conjugate transposon					
	other categories					
PGN_0059 *traN*	P vs T=1	0.872	1.554	2.311	2.432	2.093
	PS vs T=1	0.292	0.904	1.490	1.655	1.898
	PS vs P	-0.608	-0.623	-0.757	-0.709	-0.172
	conserved protein found in conjugate transposon TraN					
	other categories					
PGN_0060 *traM*	P vs T=1	0.809	1.580	2.731	3.167	3.013
	PS vs T=1	0.253	0.889	1.576	2.023	2.422
	PS vs P	-0.613	-0.675	-1.066	-1.029	-0.531
	conserved protein found in conjugate transposon TraM					
	other categories					
PGN_0061	P vs T=1	1.250	1.960	3.197	3.664	3.670
	PS vs T=1	0.368	1.202	2.098	3.013	3.544
	PS vs P	-0.940	-0.711	-0.914	-0.423	0.009
	hypothetical protein					
	hypothetical proteins					
PGN_0062 *traK*	P vs T=1	1.181	1.676	2.613	3.067	3.146
	PS vs T=1	0.223	0.818	1.286	2.099	2.460
	PS vs P	-0.966	-0.811	-1.196	-0.794	-0.572
	putative conserved protein found in conjugate transposon TraK					
	other categories					
PGN_0063 *traJ*	P vs T=1	1.167	1.898	2.851	3.128	3.016
	PS vs T=1	0.501	0.901	1.620	2.136	2.351
	PS vs P	-0.705	-0.942	-1.112	-0.861	-0.588
	conserved transmembrane protein found in conjugate transposon TraJ					
	other categories					

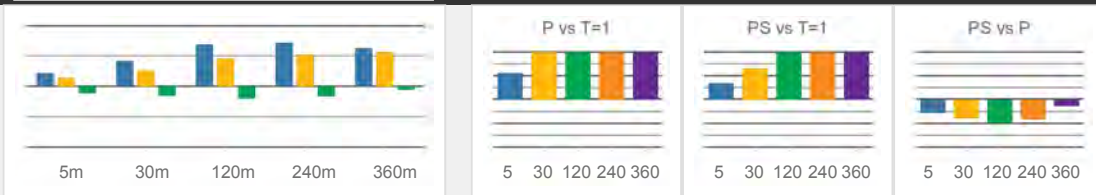


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0064 *traI*	P vs T=1	1.102	2.130	3.455	3.616	3.182
	PS vs T=1	0.685	1.309	2.293	2.627	2.848
	PS vs P	-0.533	-0.765	-0.975	-0.811	-0.257
	putative conserved protein found in conjugate transposon TraI					
	other categories					
PGN_0065 *traG*	P vs T=1	0.493	1.145	1.851	2.081	1.961
	PS vs T=1	-0.273	0.150	0.615	0.705	0.914
	PS vs P	-0.797	-0.919	-1.108	-1.231	-0.961
	conserved protein found in conjugate transposon TraG					
	other categories					
PGN_0066 *traF*	P vs T=1	0.854	1.683	2.598	2.972	2.558
	PS vs T=1	0.092	0.575	1.201	1.691	1.936
	PS vs P	-0.839	-0.962	-1.141	-0.978	-0.484
	probable conserved transmembrane protein found in conjugate transposon TraF					
	other categories					
PGN_0067 *traF*	P vs T=1	1.262	1.928	2.769	2.991	2.698
	PS vs T=1	0.697	1.190	1.656	2.020	2.220
	PS vs P	-0.589	-0.694	-1.011	-0.849	-0.422
	probable conserved transmembrane protein found in conjugate transposon TraE					
	other categories					
PGN_0068	P vs T=1	-0.826	-0.337	-0.127	-0.236	-0.924
	PS vs T=1	-0.644	-0.205	-0.117	-0.356	-0.580
	PS vs P	0.107	0.131	0.033	-0.108	0.289
	hypothetical protein					
	hypothetical proteins					
PGN_0069 *traA*	P vs T=1	0.942	1.676	2.848	3.187	3.299
	PS vs T=1	0.906	1.242	2.105	2.498	2.703
	PS vs P	-0.160	-0.440	-0.622	-0.541	-0.492
	probable conserved protein found in conjugate transposon TraA					
	other categories					
PGN_0070	P vs T=1	0.946	1.692	2.376	2.698	2.626
	PS vs T=1	0.889	1.079	1.754	2.005	1.888
	PS vs P	-0.128	-0.575	-0.532	-0.544	-0.646
	hypothetical protein					
	hypothetical proteins					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0071	P vs T=1	1.545	2.220	3.106	3.239	3.157
	PS vs T=1	1.343	1.779	2.544	2.630	2.573
	PS vs P	-0.252	-0.414	-0.459	-0.483	-0.503
	hypothetical protein					
	hypothetical proteins					
PGN_0072	P vs T=1	0.335	1.288	2.199	2.350	2.405
	PS vs T=1	0.134	0.572	1.589	1.719	1.691
	PS vs P	-0.308	-0.682	-0.509	-0.519	-0.634
	hypothetical protein					
	hypothetical proteins					
PGN_0073	P vs T=1	2.409	3.110	4.007	4.329	4.492
traA	PS vs T=1	1.940	2.344	3.196	3.651	3.562
	PS vs P	-0.500	-0.711	-0.698	-0.538	-0.817
	putative conserved protein found in conjugate transposon TraA					
	other categories					
PGN_0074	P vs T=1	0.855	0.650	0.515	0.791	1.571
	PS vs T=1	-0.379	-0.334	-0.027	-0.159	0.277
	PS vs P	-1.110	-0.888	-0.510	-0.812	-1.091
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0075	P vs T=1	0.307	0.007	-0.146	0.614	1.686
	PS vs T=1	-0.433	-0.569	0.212	0.333	0.536
	PS vs P	-0.705	-0.572	0.283	-0.217	-1.044
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0076	P vs T=1	0.244	0.145	0.463	1.118	1.814
	PS vs T=1	-0.116	-0.406	-0.141	0.003	0.327
	PS vs P	-0.351	-0.549	-0.592	-1.033	-1.411
	putative mobilization protein TraG family					
	other categories					
PGN_0077	P vs T=1	-0.075	-0.864	-1.411	-1.631	-1.613
	PS vs T=1	-0.904	-1.408	-1.601	-1.853	-2.025
	PS vs P	-0.681	-0.517	-0.234	-0.296	-0.454
	hypothetical protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0078	P vs T=1	0.272	-0.817	-1.401	-1.403	-1.713
	PS vs T=1	-0.736	-1.058	-1.185	-1.359	-1.555
	PS vs P	-0.869	-0.249	0.148	-0.007	0.087
	hypothetical protein					
	hypothetical proteins					
PGN_0079	P vs T=1	0.447	-0.130	-0.457	-0.536	-0.732
	PS vs T=1	-0.191	-0.234	-0.298	-0.482	-0.586
	PS vs P	-0.571	-0.106	0.132	0.030	0.116
	conserved hypothetical protein with DUF1016 domain					
	hypothetical proteins-Conserved					
PGN_0080	P vs T=1	-0.501	-0.563	-0.238	-0.178	-0.641
	PS vs T=1	-0.712	-0.342	-0.052	-0.088	-0.021
	PS vs P	-0.222	0.192	0.192	0.100	0.587
	probable tetracycline resistance element mobilization regulatory protein RteC					
	mobile and extrachromosomal element functions					
PGN_0081	P vs T=1	0.126	-0.429	-0.970	-1.094	-1.095
	PS vs T=1	-0.247	-0.739	-0.924	-1.129	-1.008
	PS vs P	-0.338	-0.300	0.032	-0.053	0.076
	putative Na driven multidrug efflux pump					
	transport and binding proteins					
PGN_0082	P vs T=1	0.662	-0.801	-1.707	-1.492	-1.207
	PS vs T=1	0.224	-0.621	-0.975	-1.092	-1.211
	PS vs P	-0.351	0.162	0.652	0.353	-0.016
	probable transcriptional regulator AraC family					
	regulatory functions					
PGN_0083	P vs T=1	0.915	1.835	3.060	3.378	3.133
	PS vs T=1	0.686	1.195	2.015	2.334	2.507
	PS vs P	-0.338	-0.605	-0.895	-0.880	-0.538
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0084	P vs T=1	0.977	1.750	2.848	3.335	3.080
	PS vs T=1	0.432	0.893	1.566	2.096	2.292
	PS vs P	-0.604	-0.823	-1.173	-1.099	-0.716
	DNA topoisomerase I					
	DNA metabolism					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0085	P vs T=1	0.563	0.956	1.685	2.578	2.717
	PS vs T=1	-0.017	0.282	0.609	1.165	1.607
	PS vs P	-0.611	-0.618	-0.912	-1.005	-0.845
	hypothetical protein					
	hypothetical proteins					
PGN_0086	P vs T=1	0.768	1.141	1.796	2.351	2.781
	PS vs T=1	0.366	0.494	0.704	1.143	1.333
	PS vs P	-0.407	-0.638	-1.067	-1.163	-1.411
	putative DNA methylase					
	DNA metabolism					
PGN_0087	P vs T=1	-0.032	-0.564	-0.186	0.195	0.227
	PS vs T=1	-0.153	0.189	0.705	0.764	0.740
	PS vs P	-0.131	0.610	0.822	0.559	0.500
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0088	P vs T=1	0.138	-0.085	0.171	0.753	0.845
	PS vs T=1	-0.124	-0.050	0.645	0.840	0.713
	PS vs P	-0.269	-0.005	0.424	0.121	-0.113
	putative transcriptional regulator					
	regulatory functions					
PGN_0089	P vs T=1	-0.294	-0.532	0.105	0.999	1.241
	PS vs T=1	-0.632	-0.246	0.029	-0.049	0.084
	PS vs P	-0.350	0.200	-0.077	-0.862	-1.030
	hypothetical protein					
	hypothetical proteins					
PGN_0090	P vs T=1	0.486	0.596	1.119	1.738	1.932
	PS vs T=1	0.194	0.540	1.257	0.873	0.791
	PS vs P	-0.307	-0.072	0.184	-0.681	-0.992
	hypothetical protein					
	hypothetical proteins					
PGN_0091	P vs T=1	1.207	1.507	2.116	2.324	2.074
	PS vs T=1	0.452	1.211	2.468	2.734	2.692
	PS vs P	-0.762	-0.293	0.379	0.446	0.627
	hypothetical protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0092	P vs T=1	0.375	0.728	1.336	1.624	1.377
	PS vs T=1	-0.503	0.293	1.554	1.660	1.662
	PS vs P	-0.898	-0.430	0.251	0.091	0.300
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0093	P vs T=1	0.400	0.681	1.162	1.362	1.090
	PS vs T=1	0.218	0.558	1.026	0.790	1.010
	PS vs P	-0.209	-0.120	-0.088	-0.495	-0.058
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0094	P vs T=1	0.493	0.318	0.229	0.348	0.369
	PS vs T=1	0.039	0.256	0.420	0.158	-0.103
	PS vs P	-0.415	-0.053	0.187	-0.171	-0.455
	putative bacteriophage integrase					
	mobile and extrachromosomal element functions					
PGN_0095	P vs T=1	0.349	0.064	-0.341	-0.486	-0.210
	PS vs T=1	0.353	0.274	0.086	-0.214	-0.371
	PS vs P	0.064	0.212	0.344	0.133	-0.164
	hypothetical protein					
	hypothetical proteins					
PGN_0096	P vs T=1	0.323	0.046	-0.586	-0.932	-0.885
	PS vs T=1	0.266	0.099	-0.362	-0.678	-0.688
	PS vs P	-0.044	0.060	0.208	0.208	0.177
	aspartate kinase					
	amino acid biosynthesis					
PGN_0097	P vs T=1	0.997	0.843	0.255	-0.220	-0.593
	PS vs T=1	0.868	0.890	0.571	0.463	0.152
	PS vs P	-0.099	0.066	0.300	0.617	0.681
	putative cell-division ATP-binding protein					
	cellular processes					
PGN_0098	P vs T=1	3.920	2.666	2.001	2.975	3.595
	PS vs T=1	2.137	2.051	2.262	2.553	2.403
	PS vs P	-1.379	-0.480	0.019	-0.073	-0.726
	hypothetical protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0099	P vs T=1	0.167	0.165	0.082	-0.505	-1.396
	PS vs T=1	-1.266	-1.143	-1.206	-1.282	-1.297
	PS vs P	-1.265	-1.141	-1.148	-0.733	0.033
	probable peptidase					
	protein fate					
PGN_0100	P vs T=1	-0.164	-0.334	-0.789	-0.965	-1.154
	PS vs T=1	-0.837	-0.743	-1.008	-0.833	-0.907
	PS vs P	-0.645	-0.389	-0.228	0.104	0.216
	diaminopimelate decarboxylase					
	amino acid biosynthesis					
PGN_0101	P vs T=1	0.338	0.152	0.080	0.174	0.317
MenA	PS vs T=1	-0.820	-0.283	-0.392	-0.427	-0.013
	PS vs P	-1.111	-0.411	-0.456	-0.557	-0.295
	putative 1,4-dihydroxy-2-naphthoate octaprenyltransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0102	P vs T=1	0.155	0.302	0.618	0.607	0.392
	PS vs T=1	-0.521	0.024	0.501	0.773	0.457
	PS vs P	-0.685	-0.283	-0.095	0.173	0.039
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0103	P vs T=1	1.133	1.845	2.558	2.555	2.114
	PS vs T=1	1.036	1.621	2.243	2.345	2.123
	PS vs P	-0.156	-0.213	-0.258	-0.164	0.013
	putative TonB					
	transport and binding proteins					
PGN_0104	P vs T=1	0.329	0.266	0.322	0.498	0.158
	PS vs T=1	0.135	-0.019	0.106	0.177	0.236
	PS vs P	-0.195	-0.293	-0.226	-0.313	0.058
	transposase in ISPg1					
PGN_0105	P vs T=1	-0.126	-0.008	0.510	1.340	2.611
	PS vs T=1	0.545	0.439	0.049	1.121	0.635
	PS vs P	0.392	0.187	-0.482	0.142	-1.143
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0106	P vs T=1	0.428	-0.179	-0.185	0.309	1.357
	PS vs T=1	0.104	-0.030	0.581	0.327	0.786
	PS vs P	-0.282	0.046	0.597	-0.016	-0.441
	partial transposase in ISPg3					
PGN_0107	P vs T=1	0.183	-0.148	-0.159	-0.005	0.620
	PS vs T=1	-0.123	0.113	0.240	0.422	0.259
	PS vs P	-0.302	0.173	0.242	0.272	-0.306
	partial transposase in ISPg3					
PGN_0108	P vs T=1	-0.357	-0.431	-0.578	-0.346	-0.581
	PS vs T=1	-0.550	-0.847	-0.581	-0.467	-0.302
	PS vs P	-0.196	-0.422	-0.038	-0.131	0.247
	partial transposase in ISPg1					
PGN_0109	P vs T=1	-1.026	-1.379	-1.620	-1.422	-1.152
	PS vs T=1	-1.472	-1.614	-1.383	-1.220	-1.037
	PS vs P	-0.392	-0.251	0.134	0.157	0.127
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0110	P vs T=1	0.160	0.067	-0.260	-0.975	-0.722
	PS vs T=1	-0.478	-0.605	-1.324	-1.242	-1.190
	PS vs P	-0.423	-0.441	-0.808	-0.414	-0.394
	hypothetical protein					
	hypothetical proteins					
PGN_0111	P vs T=1	0.687	-0.098	-0.106	0.254	0.395
	PS vs T=1	-0.763	-0.338	-0.210	0.504	-0.267
	PS vs P	-1.067	-0.258	-0.159	0.395	-0.380
	partial transposase in ISPg6					
PGN_0112	P vs T=1	0.147	0.423	0.669	0.677	0.623
	PS vs T=1	-0.280	-0.013	0.373	1.101	1.101
	PS vs P	-0.448	-0.411	-0.253	0.432	0.465
	partial transposase Orf1 in ISPg5					

PgSg Time Course

log$_2$ (Fold Change)

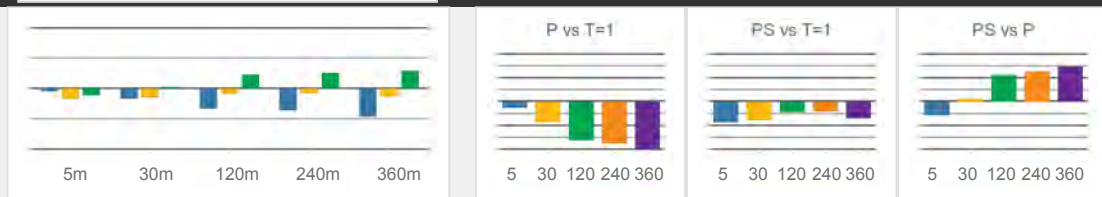
P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0113	P vs T=1	0.063	-0.231	-0.235	-1.143	-0.099
	PS vs T=1	-0.626	-0.863	-0.749	-0.494	-0.032
	PS vs P	-0.523	-0.545	-0.434	-0.113	0.121
	hypothetical protein					
	hypothetical proteins					
PGN_0114	P vs T=1	-0.808	-0.524	-0.513	-0.519	-0.663
	PS vs T=1	-0.971	-0.553	-0.307	0.109	-0.112
	PS vs P	-0.182	-0.031	0.198	0.613	0.532
	Na translocating NADH-quinone reductase subunit A					
	energy metabolism					
PGN_0115	P vs T=1	-1.543	-1.419	-1.759	-1.878	-2.125
	PS vs T=1	-0.625	-1.073	-1.624	-1.435	-1.630
	PS vs P	0.854	0.324	0.077	0.364	0.404
	Na translocating NADH-quinone reductase subunit B					
	energy metabolism					
PGN_0116	P vs T=1	-0.192	0.079	-0.153	-0.796	-0.646
	PS vs T=1	0.354	0.115	-0.087	-0.212	-0.383
	PS vs P	0.530	0.048	0.070	0.474	0.227
	probable Na translocating NADH-quinone reductase subunit C					
	energy metabolism					
PGN_0117	P vs T=1	-0.967	-0.532	-0.498	-1.060	-1.418
	PS vs T=1	-0.633	-0.663	-0.729	-0.888	-1.138
	PS vs P	0.294	-0.113	-0.200	0.122	0.215
	putative Na translocating NADH-quinone reductase subunit D					
	transport and binding proteins					
PGN_0118	P vs T=1	-0.333	-0.095	-0.531	-1.109	-1.387
	PS vs T=1	0.133	0.101	-0.304	-0.677	-0.922
	PS vs P	0.457	0.215	0.224	0.344	0.390
	putative Na translocating NADH-quinone reductase subunit E					
	transport and binding proteins					
PGN_0119	P vs T=1	-0.093	-0.040	-0.233	-0.830	-1.260
	PS vs T=1	0.528	0.354	-0.156	-0.678	-1.053
	PS vs P	0.616	0.399	0.087	0.113	0.160
	Na translocating NADH-quinone reductase subunit F					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

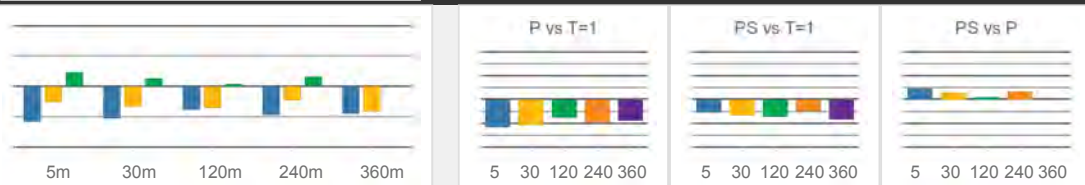
Locus		5m	30m	120m	240m	360m
PGN_0120	P vs T=1	-0.235	-0.834	-1.612	-1.742	-2.253
	PS vs T=1	-0.850	-0.745	-0.417	-0.379	-0.670
	PS vs P	-0.545	0.096	1.114	1.264	1.456
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0121	P vs T=1	-0.611	-0.712	-1.190	-1.530	-1.823
	PS vs T=1	-0.415	-0.418	-0.466	-0.537	-0.843
	PS vs P	0.196	0.291	0.696	0.937	0.930
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0122	P vs T=1	0.660	0.418	-0.108	-0.930	-1.893
	PS vs T=1	0.869	1.043	0.588	-0.483	-1.287
	PS vs P	0.273	0.653	0.701	0.358	0.454
	28 kDa outer membrane protein Omp28					
	cell envelope					
PGN_0123	P vs T=1	0.743	0.672	0.586	0.266	-0.514
	PS vs T=1	0.189	0.497	0.409	-0.034	-0.097
	PS vs P	-0.487	-0.129	-0.136	-0.292	0.351
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0124	P vs T=1	1.329	1.243	1.259	0.768	-0.153
	PS vs T=1	1.153	1.360	1.217	0.622	0.534
	PS vs P	-0.088	0.165	0.045	-0.158	0.500
	hypothetical protein					
	hypothetical proteins					
PGN_0125	P vs T=1	-0.526	-0.394	-0.501	-0.849	-1.293
	PS vs T=1	-0.284	-0.354	-0.878	-1.278	-1.461
	PS vs P	0.237	0.044	-0.371	-0.438	-0.193
	D-isomer specific 2-hydroxyacid dehydrogenase family protein					
	unknown function					
PGN_0126	P vs T=1	-0.568	-0.342	0.069	-0.080	-0.384
	PS vs T=1	-0.139	0.026	0.024	0.327	0.395
	PS vs P	0.387	0.344	-0.032	0.399	0.755
	putative transmembrane glucose/galactose transporter					
	transport and binding proteins					



log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0127	P vs T=1	-1.141	-1.042	-0.741	-0.917	-0.873
	PS vs T=1	-0.509	-0.635	-0.689	-0.460	-0.801
	PS vs P	0.464	0.269	0.076	0.317	-0.010
	hypothetical protein					
	hypothetical proteins					
PGN_0128	P vs T=1	-0.867	-0.822	-0.967	-1.476	-2.253
	PS vs T=1	-1.532	-1.214	-1.271	-1.884	-2.167
	PS vs P	-0.637	-0.360	-0.278	-0.413	0.046
	immunoreactive 53 kDa antigen					
	cell envelope					
PGN_0129	P vs T=1	-1.013	-0.989	-1.388	-2.189	-3.103
	PS vs T=1	-1.730	-1.210	-1.226	-2.070	-2.624
	PS vs P	-0.663	-0.164	0.188	0.059	0.359
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0130	P vs T=1	0.649	0.523	0.626	0.776	0.490
	PS vs T=1	0.488	0.294	0.476	0.481	0.436
	PS vs P	-0.156	-0.238	-0.156	-0.283	-0.069
	partial transposase in ISPg1					
PGN_0131	P vs T=1	-0.375	-0.527	-0.595	-0.437	-0.618
	PS vs T=1	-0.568	-0.947	-0.702	-0.632	-0.436
	PS vs P	-0.193	-0.432	-0.140	-0.207	0.149
	partial transposase in ISPg1					
PGN_0132	P vs T=1	-0.075	0.750	1.428	1.752	2.153
	PS vs T=1	0.508	0.719	1.036	1.630	1.700
	PS vs P	0.328	-0.043	-0.277	0.053	-0.268
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0133	P vs T=1	-1.562	-1.426	-0.887	-0.421	0.413
BioA	PS vs T=1	-0.786	-0.981	-1.075	-0.522	-0.594
	PS vs P	0.625	0.302	-0.225	-0.024	-0.837
	adenosylmethionine--8-amino-7-oxononanoate aminotransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0134	P vs T=1	-0.664	-0.991	-1.004	-0.736	0.172
BioB	PS vs T=1	-0.221	-0.751	-0.519	-0.299	-0.234
	PS vs P	0.428	0.167	0.369	0.365	-0.312
	putative biotin synthetase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0135	P vs T=1	-1.696	-1.969	-2.162	-2.577	-3.063
	PS vs T=1	-1.648	-1.604	-2.068	-2.603	-2.690
	PS vs P	0.066	0.353	0.091	-0.064	0.311
	putative H+/peptide symporter					
	transport and binding proteins					
PGN_0136	P vs T=1	-0.500	-1.111	-1.939	-1.958	-1.458
	PS vs T=1	-0.352	-0.755	-0.753	-0.558	-0.715
	PS vs P	0.174	0.337	1.069	1.258	0.711
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0137	P vs T=1	-0.454	-0.475	-0.855	-1.460	-1.996
	PS vs T=1	-0.754	-0.558	-0.385	-0.287	-0.610
	PS vs P	-0.282	-0.064	0.464	1.090	1.287
	putative tryptophanyl-tRNA synthetase					
	protein synthesis					
PGN_0138	P vs T=1	0.099	0.636	0.975	0.749	0.190
	PS vs T=1	0.059	0.216	0.252	0.153	0.051
	PS vs P	-0.052	-0.400	-0.685	-0.569	-0.145
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0139	P vs T=1	-0.298	-0.108	-0.039	-0.317	-0.679
	PS vs T=1	-0.124	-0.454	-0.621	-0.682	-0.902
	PS vs P	0.169	-0.333	-0.553	-0.361	-0.251
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0140	P vs T=1	-0.292	-0.283	-0.762	-1.200	-0.930
	PS vs T=1	0.079	-0.360	-0.761	-0.752	-0.867
	PS vs P	0.376	-0.062	-0.007	0.365	0.049
	peptide methionine sulfoxide reductase					
	protein fate					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

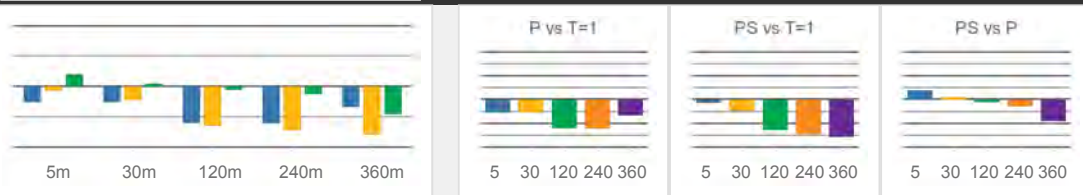
Locus		5m	30m	120m	240m	360m
PGN_0141	P vs T=1	0.077	-0.002	-0.329	-0.463	-0.392
	PS vs T=1	0.474	-0.051	-0.363	-0.345	-0.384
	PS vs P	0.402	-0.041	-0.046	0.089	-0.001
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0142	P vs T=1	-0.664	-1.123	-1.670	-1.954	-1.411
	PS vs T=1	-1.392	-1.589	-1.847	-1.763	-1.650
	PS vs P	-0.658	-0.433	-0.205	0.078	-0.222
	putative cation efflux protein					
	transport and binding proteins					
PGN_0143	P vs T=1	-0.888	-0.728	-0.739	-0.827	-0.908
	PS vs T=1	-1.410	-1.054	-1.076	-0.855	-0.924
	PS vs P	-0.519	-0.295	-0.308	-0.030	-0.038
	probable dihydroneopterin aldolase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0144	P vs T=1	-0.506	-0.732	-1.140	-1.033	-0.723
	PS vs T=1	-0.293	-0.388	-0.218	0.012	-0.096
	PS vs P	0.203	0.310	0.814	0.936	0.594
	hypothetical protein					
	hypothetical proteins					
PGN_0145	P vs T=1	-0.720	-0.955	-1.197	-1.083	-0.171
	PS vs T=1	-0.706	-1.149	-1.690	-1.409	-1.288
	PS vs P	0.027	-0.193	-0.511	-0.336	-1.067
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0146	P vs T=1	0.171	-0.214	0.041	0.626	1.877
	PS vs T=1	0.682	-0.101	0.771	0.409	0.427
	PS vs P	0.442	-0.141	0.479	-0.017	-0.502
	hypothetical protein					
	hypothetical proteins					
PGN_0147	P vs T=1	-0.641	-0.551	-0.740	-0.514	0.072
	PS vs T=1	0.331	-0.039	-0.632	-0.956	-0.920
	PS vs P	0.942	0.495	0.072	-0.443	-0.952
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

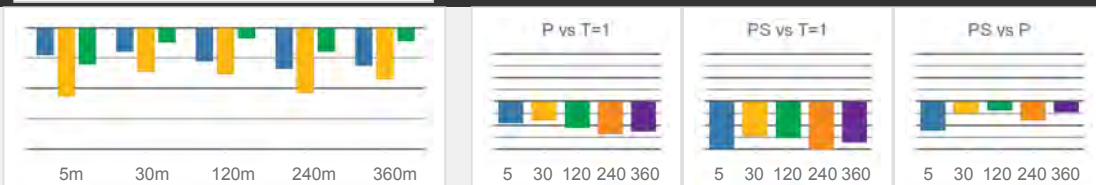
Locus		5m	30m	120m	240m	360m
PGN_0148	P vs T=1	-0.518	-0.511	-1.185	-1.196	-0.650
	PS vs T=1	-0.132	-0.431	-1.264	-1.415	-1.556
	PS vs P	0.388	0.090	-0.107	-0.244	-0.892
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0149	P vs T=1	0.321	-0.036	-0.336	-0.914	-1.368
	PS vs T=1	-0.043	-0.377	-0.591	-0.592	-0.773
	PS vs P	-0.315	-0.316	-0.239	0.286	0.546
	ribose-phosphate pyrophosphokinase					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0150	P vs T=1	-0.794	-0.474	-0.083	0.233	0.046
	PS vs T=1	-0.782	-0.779	-0.647	-0.399	-0.164
	PS vs P	-0.034	-0.310	-0.538	-0.567	-0.192
	putative ATP-dependent RNA helicase					
	transcription					
PGN_0151	P vs T=1	0.368	0.905	1.288	0.904	0.122
	PS vs T=1	0.319	0.035	-0.364	-0.906	-0.994
	PS vs P	-0.043	-0.738	-1.461	-1.675	-1.108
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0152	P vs T=1	0.765	1.212	1.851	1.741	1.030
	PS vs T=1	-0.196	-0.110	-0.090	-0.614	-0.698
	PS vs P	-0.933	-1.259	-1.848	-2.270	-1.699
	immunoreactive 61 kDa antigen					
	cell envelope					
PGN_0153	P vs T=1	2.020	1.959	1.965	2.086	2.072
	PS vs T=1	0.506	0.587	0.582	0.605	1.271
	PS vs P	-1.233	-1.085	-1.103	-1.049	-0.530
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0154	P vs T=1	-1.243	-1.084	-0.622	-0.616	-1.180
	PS vs T=1	-1.081	-0.549	-0.367	-0.554	-0.469
	PS vs P	0.108	0.491	0.273	0.080	0.673
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0155	P vs T=1	-0.891	-0.779	-1.094	-1.349	-1.234
	PS vs T=1	-2.262	-1.429	-1.521	-2.143	-1.695
	PS vs P	-1.201	-0.468	-0.338	-0.775	-0.424
	hypothetical protein					
	hypothetical proteins					
PGN_0156	P vs T=1	0.355	0.477	0.626	0.177	-0.852
	PS vs T=1	-0.474	0.094	0.171	0.090	-0.025
	PS vs P	-0.786	-0.335	-0.392	-0.070	0.766
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0157 *ThiH*	P vs T=1	0.662	0.899	2.010	2.604	3.449
	PS vs T=1	0.321	0.407	1.584	2.355	2.653
	PS vs P	-0.429	-0.546	-0.294	-0.009	-0.544
	putative thiamine biosynthesis protein ThiH					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0158 *ThiG*	P vs T=1	-0.124	-0.143	1.066	2.111	2.982
	PS vs T=1	-0.316	0.070	0.717	1.774	1.739
	PS vs P	-0.429	-0.166	-0.269	0.148	-0.666
	putative thiazole biosynthesis protein ThiG					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0159 *ThiD/E*	P vs T=1	-0.586	-0.274	0.822	1.757	2.646
	PS vs T=1	-0.389	-0.054	0.588	1.118	1.467
	PS vs P	-0.072	0.000	-0.184	-0.319	-0.859
	probable thiamin-phosphate pyrophosphorylase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0160 *ThiC*	P vs T=1	-0.503	-0.351	0.632	1.567	2.420
	PS vs T=1	-0.232	-0.176	0.305	1.096	1.418
	PS vs P	0.061	-0.037	-0.316	-0.209	-0.736
	thiamine biosynthesis protein					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0161 *ThiS*	P vs T=1	-0.993	-2.650	-2.400	-1.196	-0.413
	PS vs T=1	-1.511	-2.126	-1.918	-1.495	-1.424
	PS vs P	-0.344	-0.001	0.002	-0.061	-0.664
	putative thiamine biosynthesis protein ThiS					
	biosynthesis of cofactors, prosthetic groups, and carriers					



PgSg Time Course

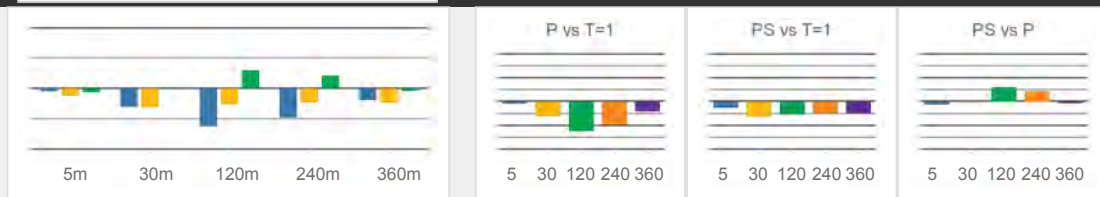
log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0162	P vs T=1	-0.317	-0.459	0.127	0.499	0.955
	PS vs T=1	-0.829	-0.895	-0.234	-0.076	0.358
	PS vs P	-0.502	-0.470	-0.299	-0.417	-0.450
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0163	P vs T=1	0.046	0.192	0.484	0.390	-0.218
	PS vs T=1	-0.221	0.397	1.085	0.658	0.586
	PS vs P	-0.279	0.199	0.635	0.291	0.742
	hypothetical protein					
	hypothetical proteins					
PGN_0164	P vs T=1	0.563	0.243	-0.045	1.746	2.682
	PS vs T=1	-0.074	-0.309	0.231	0.992	0.823
	PS vs P	-0.441	-0.479	-0.184	0.024	-0.894
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0165	P vs T=1	0.835	0.123	0.352	0.086	1.248
	PS vs T=1	-0.818	-0.712	-0.837	0.078	-0.176
	PS vs P	-0.932	-0.571	-0.726	-0.002	-0.476
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0166	P vs T=1	0.525	-0.068	0.774	1.382	2.573
	PS vs T=1	-0.806	-0.560	-1.231	0.823	0.970
	PS vs P	-0.991	-0.516	-1.422	0.004	-0.819
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0167	P vs T=1	0.291	0.497	0.899	0.781	-0.001
rpsP	PS vs T=1	-1.387	-1.042	-0.667	-0.714	-0.669
	PS vs P	-1.624	-1.473	-1.491	-1.428	-0.659
	30S ribosomal protein S16					
	protein synthesis					
PGN_0168	P vs T=1	0.245	-0.314	-1.001	-0.642	-0.438
wbpB	PS vs T=1	0.280	-0.281	-0.607	-0.555	-0.789
	PS vs P	0.091	0.030	0.274	0.060	-0.345
	lipopolysaccharide biosynthesis protein WbpB					
	unknown function					

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0169	P vs T=1	-0.083	-0.587	-1.222	-0.933	-0.373
	PS vs T=1	-0.239	-0.601	-0.519	-0.448	-0.466
	PS vs P	-0.122	-0.019	0.594	0.428	-0.073
	probable metallo-beta-lactamase superfamily protein					
	unknown function					
PGN_0170	P vs T=1	-0.039	-0.538	-1.641	-1.653	-1.374
	PS vs T=1	-0.416	-0.664	-0.632	-0.582	-1.107
	PS vs P	-0.320	-0.104	0.911	0.970	0.238
	L-asparaginase					
	energy metabolism					
PGN_0171	P vs T=1	0.824	-0.173	-0.589	-0.667	0.219
	PS vs T=1	0.614	0.246	0.831	0.520	0.158
	PS vs P	-0.029	0.310	1.151	0.826	0.032
	partial transposase in ISPg2					
PGN_0172	P vs T=1	1.712	1.878	1.263	0.379	-0.174
	PS vs T=1	1.289	1.707	2.270	2.346	1.668
	PS vs P	-0.318	-0.030	1.020	1.742	1.615
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0173	P vs T=1	0.466	0.859	0.888	0.509	-0.256
	PS vs T=1	0.090	0.480	0.939	1.025	0.873
	PS vs P	-0.375	-0.336	0.084	0.509	1.079
	glyceraldehyde 3-phosphate dehydrogenase type I					
	energy metabolism					
PGN_0174	P vs T=1	-0.166	-0.267	-0.468	-0.167	0.440
	PS vs T=1	0.082	-0.090	0.049	0.270	0.187
	PS vs P	0.241	0.159	0.432	0.406	-0.202
	probable transcriptional regulator AraC family					
	regulatory functions					
PGN_0175	P vs T=1	-0.075	-0.123	-0.226	-0.394	-0.296
	PS vs T=1	0.475	0.048	-0.665	-0.397	-0.520
	PS vs P	0.544	0.168	-0.435	-0.037	-0.227
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

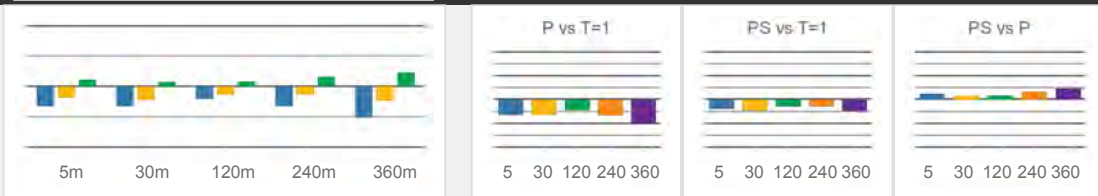


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0176	P vs T=1	-0.629	-0.629	-0.412	-0.635	-1.003
	PS vs T=1	-0.366	-0.443	-0.269	-0.267	-0.450
	PS vs P	0.224	0.146	0.163	0.323	0.450
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0177	P vs T=1	-0.580	-0.239	0.062	0.257	1.598
	PS vs T=1	-1.443	-0.672	0.177	0.391	-0.035
	PS vs P	-0.899	-0.387	0.152	0.180	-0.891
	hypothetical protein					
	hypothetical proteins					
PGN_0178	P vs T=1	-2.200	-2.216	-2.200	-2.696	-3.538
	PS vs T=1	-1.695	-2.063	-1.772	-1.554	-1.748
	PS vs P	0.452	0.110	0.404	1.038	1.621
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0179	P vs T=1	-0.762	-0.326	-0.451	-1.325	-2.159
	PS vs T=1	0.355	0.263	-0.110	-0.448	-1.076
	PS vs P	1.052	0.584	0.347	0.795	0.974
	60 kDa protein					
	unknown function					
PGN_0180	P vs T=1	0.134	0.751	1.097	0.552	-0.407
fimA	PS vs T=1	1.471	1.993	2.035	1.276	0.779
	PS vs P	1.231	1.202	0.950	0.688	1.108
	FimA type I fimbrilin					
	cellular processes					
PGN_0181	P vs T=1	-0.427	-0.127	0.419	0.253	-0.252
	PS vs T=1	1.047	0.699	0.308	0.270	0.036
	PS vs P	1.314	0.729	-0.085	0.007	0.210
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0182	P vs T=1	0.024	0.010	-0.308	-0.229	-0.772
	PS vs T=1	1.591	1.237	0.205	-0.254	-0.657
	PS vs P	1.412	1.091	0.364	-0.087	-0.085
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

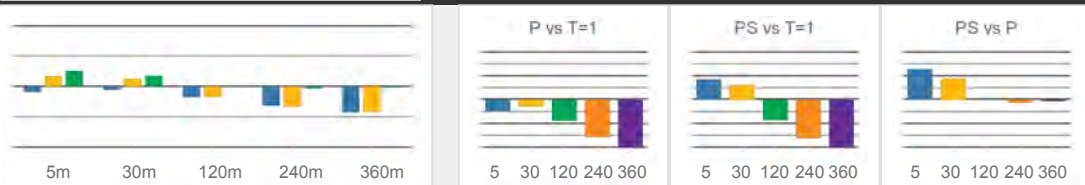


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0183 *fimC*	P vs T=1	-0.450	-0.264	-0.872	-1.545	-2.069
	PS vs T=1	0.846	0.608	-0.851	-1.600	-2.038
	PS vs P	1.270	0.885	0.014	-0.133	-0.064
	minor component FimC					
	cellular processes					
PGN_0184 *fimD*	P vs T=1	-1.317	-0.912	-1.420	-2.224	-2.747
	PS vs T=1	0.156	0.270	-0.699	-1.643	-1.927
	PS vs P	1.380	1.162	0.687	0.455	0.692
	minor component FimD					
	cellular processes					
PGN_0185 *fimE*	P vs T=1	-1.000	-0.906	-1.147	-1.702	-2.412
	PS vs T=1	0.288	0.366	-0.345	-1.347	-1.493
	PS vs P	1.237	1.236	0.778	0.291	0.830
	minor component FimE					
	cellular processes					
PGN_0186	P vs T=1	-1.348	-1.005	-0.822	-0.710	-0.956
	PS vs T=1	-0.655	-0.619	-0.462	-0.350	-0.433
	PS vs P	0.516	0.290	0.276	0.288	0.379
	hypothetical protein					
	hypothetical proteins					
PGN_0187	P vs T=1	0.018	-0.092	0.038	-0.077	-0.664
	PS vs T=1	-1.342	-1.013	-0.757	-1.042	-0.917
	PS vs P	-1.305	-0.879	-0.747	-0.916	-0.257
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0188 *rpmF*	P vs T=1	0.234	0.742	1.558	1.761	0.884
	PS vs T=1	-0.706	-0.361	-0.106	0.201	0.391
	PS vs P	-0.928	-1.030	-1.529	-1.411	-0.465
	50S ribosomal protein L32					
	protein synthesis					
PGN_0189	P vs T=1	0.158	0.288	0.624	0.699	0.164
	PS vs T=1	-0.538	-0.476	-0.028	0.129	0.070
	PS vs P	-0.685	-0.747	-0.628	-0.544	-0.093
	beta-ketoacyl-acyl-carrier-protein synthase III					
	fatty acid and phospholipid metabolism					



log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0190	P vs T=1	-0.649	-0.852	-1.285	-1.398	-1.216
	PS vs T=1	-0.460	-1.024	-1.279	-1.627	-1.488
	PS vs P	0.211	-0.157	-0.013	-0.259	-0.271
	putative GTP-binding protein					
	regulatory functions					
PGN_0191	P vs T=1	-0.617	-1.103	-1.699	-1.650	-1.456
	PS vs T=1	-0.694	-1.627	-2.189	-2.053	-2.246
	PS vs P	-0.046	-0.508	-0.513	-0.410	-0.778
	GTP-binding protein EngA					
	unknown function					
PGN_0192	P vs T=1	0.178	0.465	0.263	-0.379	-0.669
	PS vs T=1	0.343	0.241	-0.507	-1.094	-1.057
	PS vs P	0.174	-0.192	-0.737	-0.719	-0.399
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0193	P vs T=1	-0.477	-0.492	-0.518	-0.354	-0.038
	PS vs T=1	0.102	-0.284	-1.205	-0.910	-0.868
	PS vs P	0.563	0.197	-0.679	-0.492	-0.740
	putative polysaccharide deacetylase					
	energy metabolism					
PGN_0194	P vs T=1	-0.471	-0.367	-0.266	-0.438	0.238
	PS vs T=1	0.050	-0.114	-0.510	-0.368	-0.460
	PS vs P	0.494	0.244	-0.211	0.036	-0.596
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0195	P vs T=1	-0.097	0.027	0.112	-0.009	-0.291
	PS vs T=1	-0.236	-0.183	0.116	0.499	0.329
	PS vs P	-0.140	-0.196	0.023	0.502	0.588
	putative xanthine phosphoribosyltransferase					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0196	P vs T=1	0.305	0.236	0.285	0.452	0.886
	PS vs T=1	0.308	0.150	0.266	0.713	0.702
	PS vs P	0.004	-0.091	-0.029	0.264	-0.150
	xanthine/uracil permease					
	transport and binding proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0197	P vs T=1	-0.578	-0.381	-0.305	-0.548	-0.487
	PS vs T=1	-0.666	-0.992	-1.006	-0.881	-0.791
	PS vs P	-0.095	-0.583	-0.662	-0.341	-0.300
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0198	P vs T=1	0.068	0.171	-0.045	-0.161	-0.292
	PS vs T=1	-0.314	-0.382	-0.116	0.004	-0.176
	PS vs P	-0.372	-0.533	-0.069	0.156	0.106
	conserved hypothetical protein					
	unknown function					
PGN_0199	P vs T=1	0.314	0.975	1.639	1.829	1.458
	PS vs T=1	0.627	1.124	1.535	1.748	1.942
	PS vs P	0.222	0.136	-0.060	-0.023	0.485
	hypothetical protein					
	hypothetical proteins					
PGN_0200	P vs T=1	1.054	1.506	1.557	1.124	0.557
	PS vs T=1	1.344	1.731	1.669	1.286	0.999
	PS vs P	0.275	0.243	0.138	0.156	0.412
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0201	P vs T=1	0.623	0.776	0.672	0.379	0.215
	PS vs T=1	0.823	0.779	0.776	1.062	0.867
	PS vs P	0.194	0.011	0.105	0.640	0.617
	conserved hypothetical protein with DUF558 domain					
	hypothetical proteins-Conserved					
PGN_0202	P vs T=1	-0.305	-0.151	-0.179	-0.239	-0.094
	PS vs T=1	-0.416	-0.542	-0.496	-0.246	-0.357
	PS vs P	-0.108	-0.356	-0.288	0.007	-0.230
	probable leucine aminopeptidase precursor					
	unknown function					
PGN_0203	P vs T=1	-0.715	0.052	0.642	0.602	-0.151
	PS vs T=1	-0.395	-0.471	-0.482	-0.145	-0.100
	PS vs P	0.262	-0.496	-1.037	-0.648	0.029
	probable SufE Fe/S-cluster-related protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0204	P vs T=1	-0.966	-0.676	-0.469	-0.392	-0.375
HemY	PS vs T=1	-0.605	-0.791	-0.953	-0.986	-0.883
	PS vs P	0.309	-0.116	-0.455	-0.545	-0.479
	protoporphyrinogen oxidase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0205	P vs T=1	-0.791	-1.172	-1.077	-0.579	0.819
	PS vs T=1	-0.445	-0.769	-0.768	-0.608	-0.283
	PS vs P	0.332	0.297	0.183	-0.013	-0.898
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0206	P vs T=1	-0.834	-0.727	-0.470	-0.203	0.356
	PS vs T=1	0.038	-0.186	-0.450	-0.354	-0.436
	PS vs P	0.796	0.479	-0.000	-0.123	-0.713
	putative lipid A disaccharide synthase					
	cell envelope					
PGN_0207	P vs T=1	-0.665	-0.463	-0.060	-0.522	-0.434
	PS vs T=1	0.031	-0.470	-0.602	-0.458	-0.745
	PS vs P	0.638	-0.019	-0.465	0.029	-0.306
	probable stationary-phase survival protein					
	cellular processes					
PGN_0208	P vs T=1	0.371	0.927	0.942	0.457	-0.083
	PS vs T=1	0.636	0.625	0.645	0.629	0.303
	PS vs P	0.240	-0.247	-0.237	0.164	0.329
	conserved hypothetical protein					
	protein fate					
PGN_0209	P vs T=1	-0.290	-0.425	-0.845	-1.094	-1.228
	PS vs T=1	-0.205	-0.163	-0.002	0.271	-0.070
	PS vs P	0.088	0.259	0.814	1.301	1.114
	glycyl-tRNA synthetase					
	protein synthesis					
PGN_0210	P vs T=1	0.358	0.279	0.374	0.405	-0.077
	PS vs T=1	0.193	0.011	0.143	0.239	0.269
	PS vs P	-0.164	-0.272	-0.233	-0.165	0.320
	transposase in ISPg1					

PgSg Time Course

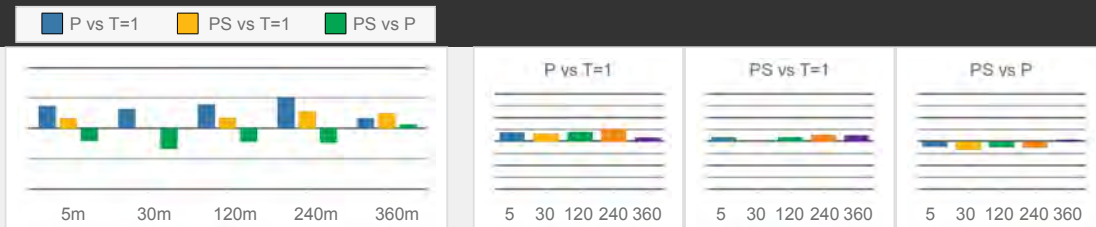
log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0211	P vs T=1	-0.299	-0.240	-0.088	-0.103	-0.386
	PS vs T=1	-0.148	-0.135	0.436	0.732	0.668
	PS vs P	0.126	0.082	0.506	0.805	1.013
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0212	P vs T=1	0.338	0.260	0.370	0.513	0.212
	PS vs T=1	0.194	0.013	0.178	0.271	0.219
	PS vs P	-0.146	-0.255	-0.198	-0.238	-0.007
	transposase in ISPg1					
PGN_0213	P vs T=1	-0.414	-0.327	0.729	1.899	3.153
	PS vs T=1	-0.240	-0.269	0.739	0.997	1.878
	PS vs P	-0.208	-0.344	-0.082	-0.355	-0.669
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0214	P vs T=1	-2.311	-1.658	-2.208	-2.200	-2.288
	PS vs T=1	-2.601	-2.352	-2.488	-2.330	-2.234
	PS vs P	-0.408	-0.505	-0.332	-0.163	-0.018
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0215	P vs T=1	1.806	2.244	3.037	3.119	2.116
	PS vs T=1	2.277	2.728	2.800	3.039	3.007
	PS vs P	0.383	0.479	-0.074	0.078	0.854
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0216	P vs T=1	-1.741	-1.018	-0.508	-0.864	-1.464
	PS vs T=1	-1.607	-1.175	-1.068	-0.864	-0.699
	PS vs P	-0.169	-0.158	-0.412	-0.011	0.585
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0217	P vs T=1	-0.988	-0.746	-1.239	-1.704	-2.522
	PS vs T=1	-1.325	-1.277	-1.976	-2.929	-2.900
	PS vs P	-0.243	-0.350	-0.639	-1.179	-0.478
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0218	P vs T=1	0.373	0.323	0.394	0.517	0.166
	PS vs T=1	0.171	-0.003	0.178	0.275	0.248
	PS vs P	-0.201	-0.330	-0.222	-0.236	0.062
	transposase in ISPg1					
PGN_0219	P vs T=1	0.525	0.443	-0.077	-0.266	-0.191
	PS vs T=1	-0.096	-0.623	-1.139	-0.822	-0.714
	PS vs P	-0.578	-1.015	-1.066	-0.589	-0.535
	partial transposase in ISPg1					
PGN_0220	P vs T=1	1.130	1.065	0.955	0.862	0.780
	PS vs T=1	0.504	0.240	0.262	0.256	0.293
	PS vs P	-0.594	-0.793	-0.678	-0.597	-0.485
	partial transposase in ISPg1					
PGN_0221	P vs T=1	0.446	0.597	0.836	0.911	0.585
	PS vs T=1	0.352	0.226	0.150	0.350	0.176
	PS vs P	-0.094	-0.358	-0.658	-0.527	-0.404
	DNA topoisomerase III					
	DNA metabolism					
PGN_0222	P vs T=1	0.304	0.330	0.269	1.892	3.059
	PS vs T=1	0.520	0.349	1.031	0.879	1.609
	PS vs P	0.058	-0.131	0.268	-0.451	-0.786
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0223	P vs T=1	-1.163	-2.571	-2.832	-2.361	-1.219
wecA	PS vs T=1	-1.889	-2.096	-1.793	-1.576	-1.860
	PS vs P	-0.582	0.310	0.804	0.676	-0.541
	glycosyl transferase family 4					
	cell envelope					
PGN_0224	P vs T=1	-1.629	-2.748	-3.497	-3.040	-2.599
cap50	PS vs T=1	-1.920	-2.767	-3.228	-3.563	-3.270
	PS vs P	-0.155	-0.061	0.099	-0.547	-0.644
	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase					
	cell envelope					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0225	P vs T=1	-1.441	-3.032	-3.128	-2.778	-1.746
	PS vs T=1	-1.300	-2.025	-2.282	-2.458	-2.216
	PS vs P	0.299	0.645	0.529	0.139	-0.366
	probable glycosyltransferase					
	cell envelope					
PGN_0226	P vs T=1	-1.080	-2.078	-2.114	-1.678	-0.669
	PS vs T=1	-0.514	-1.248	-1.698	-1.727	-1.698
	PS vs P	0.625	0.589	0.222	-0.085	-0.853
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0227	P vs T=1	-0.981	-1.524	-1.714	-1.411	-1.098
	PS vs T=1	-0.758	-1.319	-2.236	-2.149	-2.068
	PS vs P	0.292	0.162	-0.564	-0.674	-0.882
	probable glycosyl transferase family 1					
	cell envelope					
PGN_0228	P vs T=1	-1.062	-2.123	-2.537	-2.622	-1.715
	PS vs T=1	-0.856	-1.066	-2.143	-2.509	-2.394
	PS vs P	0.296	0.945	0.267	-0.041	-0.632
	probable coenzyme F390 synthetase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0229	P vs T=1	-1.033	-0.798	-0.347	-0.432	-1.175
	PS vs T=1	-0.823	-0.399	-0.059	-0.455	-0.640
	PS vs P	0.162	0.371	0.310	-0.006	0.483
	putative DNA-binding protein histone-like family					
	hypothetical proteins-Conserved					
PGN_0230	P vs T=1	-0.625	-1.232	-1.838	-1.809	-1.570
	PS vs T=1	-0.680	-0.783	-1.480	-1.952	-1.940
	PS vs P	0.026	0.424	0.238	-0.231	-0.384
	probable serine acetyltransferase					
	cellular processes					
PGN_0231	P vs T=1	-0.937	-1.358	-1.963	-1.893	-1.368
	PS vs T=1	-0.474	-0.619	-1.822	-2.231	-2.230
	PS vs P	0.485	0.712	0.042	-0.406	-0.831
	probable delta-aminolevulinic acid dehydratase					
	biosynthesis of cofactors, prosthetic groups, and carriers					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0232	P vs T=1	-0.916	-1.476	-1.919	-1.997	-1.544
	PS vs T=1	-0.447	-0.500	-1.128	-1.472	-1.456
	PS vs P	0.491	0.877	0.636	0.343	0.061
	probable glycosyl transferase family 2					
	cell envelope					
PGN_0233	P vs T=1	-0.782	-1.525	-2.078	-2.374	-2.260
	PS vs T=1	-0.323	-0.621	-1.110	-1.780	-2.154
	PS vs P	0.515	0.834	0.838	0.374	-0.004
	conserved hypothetical protein with glycosyl transferase WecB/TagA/CpsF family domain					
	cell envelope					
PGN_0234	P vs T=1	-0.997	-1.316	-1.599	-2.100	-2.411
	PS vs T=1	-0.673	-0.645	-1.219	-1.834	-2.173
	PS vs P	0.332	0.658	0.368	0.204	0.180
	UDP-N-acetylglucosamine 2-epimerase					
	cell envelope					
PGN_0235	P vs T=1	-0.814	-0.727	-0.166	-0.057	-0.833
	PS vs T=1	-0.983	-0.599	-0.348	-0.405	-0.367
	PS vs P	-0.199	0.098	-0.144	-0.298	0.431
	DNA-binding protein HU					
	DNA metabolism					
PGN_0236	P vs T=1	-0.362	-0.891	-1.274	-1.028	-0.506
	PS vs T=1	-0.045	-0.216	-0.732	-0.746	-0.926
	PS vs P	0.343	0.621	0.400	0.214	-0.371
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0237	P vs T=1	-0.837	-0.875	-0.916	-0.660	-0.336
	PS vs T=1	-0.339	-0.634	-0.910	-0.720	-0.674
	PS vs P	0.469	0.207	-0.051	-0.064	-0.305
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0238	P vs T=1	-0.126	0.306	0.828	1.032	1.054
	PS vs T=1	0.170	-0.015	0.113	0.315	0.406
	PS vs P	0.236	-0.310	-0.632	-0.583	-0.565
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0239	P vs T=1	-0.836	-0.809	-0.765	-0.521	-0.285
	PS vs T=1	-0.701	-0.802	-0.527	0.021	-0.012
	PS vs P	0.117	-0.011	0.203	0.528	0.279
	putative type I phosphodiesterase-nucleotide pyrophosphatase					
	central intermediary metabolism					
PGN_0240	P vs T=1	-0.330	-0.571	-0.418	-0.371	0.052
HemH	PS vs T=1	-0.247	-0.407	0.054	0.486	0.468
	PS vs P	0.065	0.098	0.413	0.768	0.421
	putative ferrochelatase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0241	P vs T=1	-0.630	-0.410	0.291	0.618	0.817
	PS vs T=1	-0.488	-0.355	-0.411	-0.129	0.156
	PS vs P	0.052	-0.002	-0.605	-0.568	-0.530
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0242	P vs T=1	-0.294	0.055	0.930	1.332	1.445
	PS vs T=1	0.251	0.186	0.370	0.829	0.804
	PS vs P	0.428	0.068	-0.493	-0.382	-0.555
	probable glycosyl transferase family 1					
	cell envelope					
PGN_0243	P vs T=1	1.556	1.788	1.595	1.010	0.547
	PS vs T=1	2.131	2.337	2.319	2.079	1.912
	PS vs P	0.566	0.571	0.738	1.001	1.288
	phosphoglycerate mutase					
	energy metabolism					
PGN_0244	P vs T=1	0.043	0.685	0.684	-0.052	2.349
	PS vs T=1	0.390	0.750	0.971	0.891	0.836
	PS vs P	0.092	0.132	0.306	0.228	-0.734
	hypothetical protein					
	hypothetical proteins					
PGN_0245	P vs T=1	-0.690	-0.606	-0.985	-1.214	-0.219
	PS vs T=1	-0.310	-0.596	-1.620	-1.642	-1.572
	PS vs P	0.376	0.030	-0.648	-0.513	-1.250
	hypothetical protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

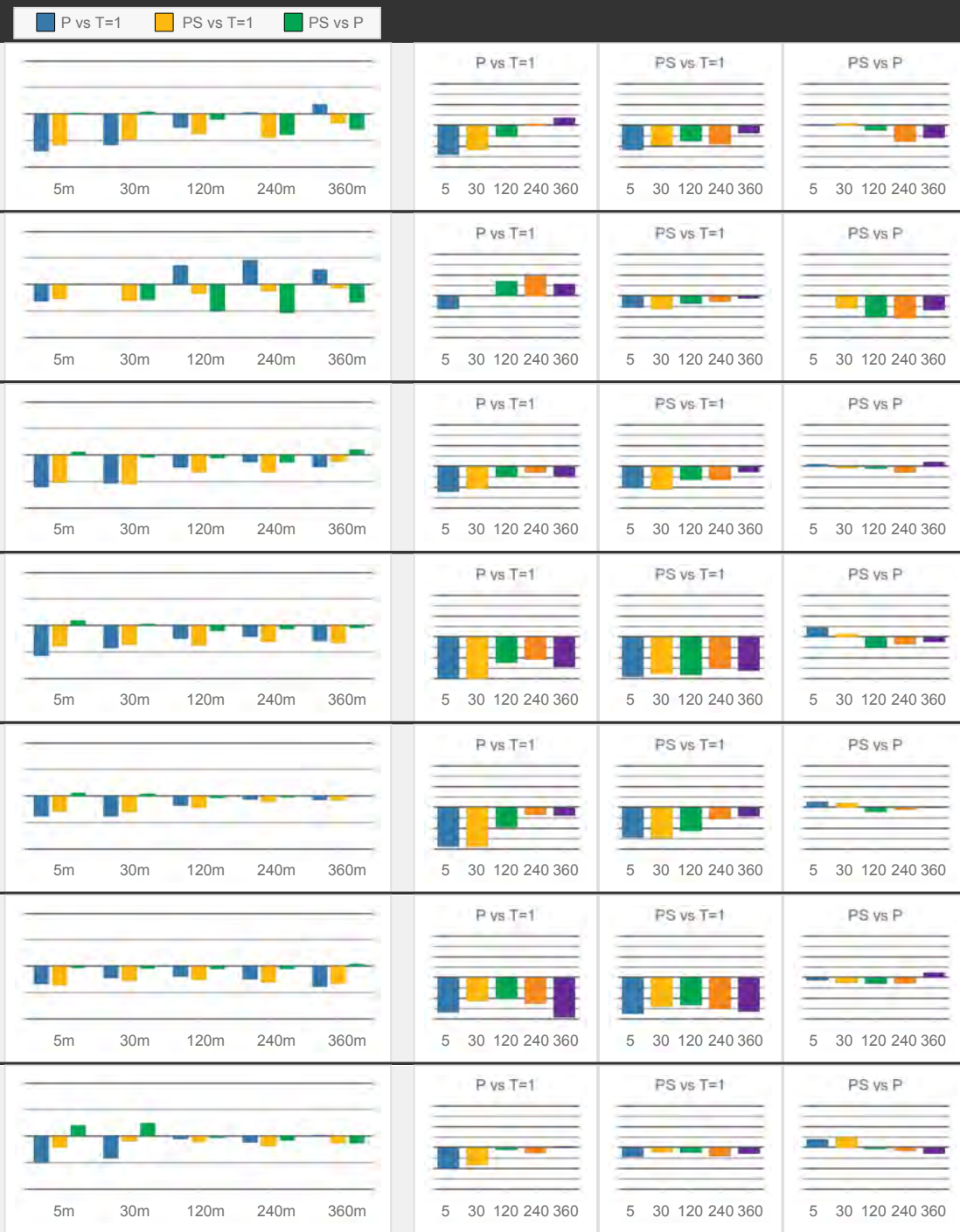
P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0246	P vs T=1	-0.220	-0.336	-0.517	-0.459	0.232
	PS vs T=1	-0.056	-0.539	-1.182	-1.102	-1.096
	PS vs P	0.180	-0.190	-0.664	-0.627	-1.238
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0247	P vs T=1	0.121	0.306	0.125	-0.160	-0.264
	PS vs T=1	0.382	-0.217	-0.867	-1.103	-0.707
	PS vs P	0.266	-0.501	-0.970	-0.935	-0.443
	putative magnesium transporter					
	transport and binding proteins					
PGN_0248	P vs T=1	0.225	-0.261	-0.762	-1.218	-1.125
	PS vs T=1	0.067	-0.962	-1.538	-1.172	-1.347
	PS vs P	-0.109	-0.672	-0.770	-0.015	-0.241
	putative dimethyladenosine transferase					
	protein synthesis					
PGN_0249	P vs T=1	-0.618	-0.951	-0.946	-1.202	-1.218
	PS vs T=1	-0.760	-0.809	-0.852	-0.700	-0.826
	PS vs P	-0.132	0.132	0.092	0.463	0.369
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0250	P vs T=1	0.016	0.586	0.999	0.595	-0.047
	PS vs T=1	0.593	0.646	0.434	0.196	-0.137
	PS vs P	0.539	0.077	-0.508	-0.376	-0.109
	aminoacyl-histidine dipeptidase					
	protein fate					
PGN_0251	P vs T=1	1.115	1.693	2.047	1.737	1.287
	PS vs T=1	2.182	2.520	2.280	1.872	1.494
	PS vs P	1.004	0.820	0.268	0.141	0.189
	malonyl CoA-acyl carrier protein transacylase					
	fatty acid and phospholipid metabolism					
PGN_0252	P vs T=1	0.159	0.032	-0.113	-0.203	0.037
	PS vs T=1	1.009	0.636	-0.007	-0.220	-0.254
	PS vs P	0.843	0.589	0.092	-0.042	-0.283
	putative membrane-bound lytic murein transglycosylase D					
	cell envelope					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0253	P vs T=1	-1.383	-1.154	-0.516	0.062	0.364
	PS vs T=1	-1.159	-0.934	-0.735	-0.882	-0.349
	PS vs P	0.049	0.088	-0.210	-0.755	-0.570
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0254	P vs T=1	-0.610	-0.013	0.723	0.935	0.563
	PS vs T=1	-0.533	-0.596	-0.349	-0.242	-0.130
	PS vs P	-0.009	-0.568	-0.980	-1.056	-0.656
	putative ParB chromosome partitioning protein					
	cellular processes					
PGN_0255	P vs T=1	-1.193	-1.045	-0.473	-0.267	-0.457
	PS vs T=1	-1.019	-1.081	-0.622	-0.622	-0.254
	PS vs P	0.111	-0.085	-0.111	-0.270	0.206
	putative ParA chromosome partitioning protein					
	regulatory functions					
PGN_0256	P vs T=1	-2.822	-2.086	-1.226	-1.066	-1.416
	PS vs T=1	-1.882	-1.765	-1.811	-1.503	-1.602
	PS vs P	0.463	0.146	-0.495	-0.328	-0.215
	hydrolase					
	unknown function					
PGN_0257	P vs T=1	-1.878	-1.877	-0.915	-0.323	-0.357
	PS vs T=1	-1.430	-1.453	-1.104	-0.533	-0.392
	PS vs P	0.278	0.220	-0.189	-0.095	0.004
	putative arginine deiminase					
	central intermediary metabolism					
PGN_0258	P vs T=1	-1.660	-1.129	-1.003	-1.245	-1.915
	PS vs T=1	-1.744	-1.386	-1.306	-1.498	-1.622
	PS vs P	-0.146	-0.231	-0.268	-0.248	0.230
	hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0259	P vs T=1	-0.959	-0.814	-0.104	-0.228	0.041
	PS vs T=1	-0.419	-0.187	-0.219	-0.379	-0.265
	PS vs P	0.404	0.497	-0.063	-0.165	-0.263
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0260	P vs T=1	-1.945	-1.349	-0.893	-0.716	-0.609
	PS vs T=1	-1.600	-1.435	-1.319	-1.294	-1.185
	PS vs P	0.196	-0.118	-0.393	-0.505	-0.530
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0261	P vs T=1	-1.261	-0.968	-0.428	-0.109	-0.214
	PS vs T=1	-1.023	-1.090	-1.141	-0.998	-0.972
	PS vs P	0.159	-0.150	-0.660	-0.775	-0.706
	sigma-54-dependent transcriptional regulator					
	regulatory functions					
PGN_0262	P vs T=1	-1.037	-0.945	-0.383	-0.386	-0.062
	PS vs T=1	-0.698	-0.917	-1.093	-1.158	-0.870
	PS vs P	0.301	-0.002	-0.667	-0.731	-0.759
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0263	P vs T=1	-0.387	-0.009	0.351	0.179	-0.147
	PS vs T=1	-0.548	-0.579	-1.028	-0.916	-0.863
	PS vs P	-0.175	-0.539	-1.307	-1.036	-0.706
	putative Fe-S oxidoreductase					
	hypothetical proteins-Conserved					
PGN_0264	P vs T=1	-0.112	0.438	1.304	1.349	0.727
	PS vs T=1	0.181	0.541	0.808	0.737	0.310
	PS vs P	0.220	0.084	-0.433	-0.542	-0.418
	signal recognition particle-docking protein					
	protein fate					
PGN_0265	P vs T=1	-0.580	-0.098	0.558	0.760	0.319
	PS vs T=1	-0.472	-0.320	-0.299	0.049	0.073
	PS vs P	0.041	-0.228	-0.794	-0.624	-0.236
	carboxynorspermidine decarboxylase					
	central intermediary metabolism					
PGN_0266	P vs T=1	-0.405	0.183	0.891	1.083	0.771
	PS vs T=1	-0.125	-0.087	0.061	0.562	0.526
	PS vs P	0.187	-0.275	-0.763	-0.440	-0.225
	aspartyl-tRNA synthetase					
	protein synthesis					

PgSg Time Course

log$_2$ (Fold Change)

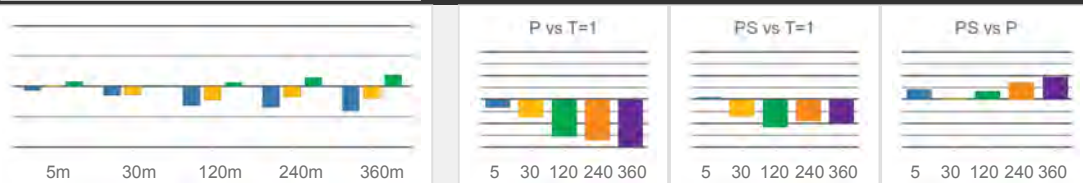
Locus		5m	30m	120m	240m	360m
PGN_0267 *RibD*	P vs T=1	-0.929	-0.886	-0.623	-0.226	0.272
	PS vs T=1	-0.782	-1.121	-0.682	-0.361	-0.357
	PS vs P	0.102	-0.272	-0.082	-0.071	-0.534
	putative riboflavin biosynthesis protein					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0268	P vs T=1	-0.648	-0.922	-0.719	-0.597	-0.287
	PS vs T=1	-0.313	-0.700	-1.034	-0.572	-0.779
	PS vs P	0.327	0.177	-0.326	0.026	-0.456
	protoporphyrinogen oxidase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0269	P vs T=1	-0.152	-0.283	0.348	0.676	0.696
	PS vs T=1	0.307	-0.052	-0.229	0.047	0.535
	PS vs P	0.391	0.110	-0.531	-0.490	-0.095
	putative transcriptional regulatory protein					
	regulatory functions					
PGN_0270	P vs T=1	0.270	0.372	1.053	1.270	1.334
	PS vs T=1	0.530	0.405	0.248	0.660	0.581
	PS vs P	0.228	0.005	-0.735	-0.505	-0.679
	probable amidophosphoribosyl-transferase					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0271	P vs T=1	0.562	0.778	0.539	-0.128	-1.053
	PS vs T=1	0.889	0.883	-0.091	-0.837	-0.995
	PS vs P	0.342	0.142	-0.593	-0.709	0.018
	endopeptidase PepO					
	protein fate					
PGN_0272	P vs T=1	0.692	1.071	0.839	0.109	-0.551
	PS vs T=1	1.102	1.140	0.610	0.298	-0.073
	PS vs P	0.409	0.108	-0.193	0.155	0.412
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0273	P vs T=1	0.911	0.508	0.441	0.309	-0.384
	PS vs T=1	2.493	2.745	2.746	1.856	1.589
	PS vs P	1.500	2.042	2.178	1.419	1.782
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0274	P vs T=1	-0.310	-0.713	-1.533	-1.681	-1.986
	PS vs T=1	0.090	-0.687	-1.143	-0.886	-0.981
	PS vs P	0.419	0.027	0.336	0.725	0.938
	putative RNA polymerase sigma-70 factor ECF subfamily					
	transcription					
PGN_0275	P vs T=1	-0.338	-0.321	-0.615	-0.517	-0.214
	PS vs T=1	-0.047	-0.167	-0.641	-0.586	-0.521
	PS vs P	0.284	0.154	-0.057	-0.086	-0.291
	phosphofructokinase					
	energy metabolism					
PGN_0276	P vs T=1	-1.425	-1.136	-1.231	-0.046	0.341
	PS vs T=1	-1.385	-1.529	-1.554	-1.105	-1.083
	PS vs P	-0.103	-0.399	-0.529	-0.579	-1.012
	hypothetical protein					
	hypothetical proteins					
PGN_0277	P vs T=1	-0.526	-0.235	-0.041	-0.089	0.692
hslR	PS vs T=1	-0.558	-0.992	-0.730	-0.342	-0.121
	PS vs P	-0.075	-0.691	-0.600	-0.228	-0.614
	putative heat shock protein 15					
	protein fate					
PGN_0278	P vs T=1	-0.274	-0.204	-0.233	0.597	0.823
	PS vs T=1	-0.789	-1.096	-0.999	-0.834	0.017
	PS vs P	-0.486	-0.826	-0.763	-1.162	-0.654
	putative peptidyl-tRNA hydrolase					
	protein synthesis					
PGN_0279	P vs T=1	0.554	0.373	0.682	0.663	0.149
rplY	PS vs T=1	-1.435	-1.292	-1.260	-1.265	-0.926
	PS vs P	-1.893	-1.588	-1.853	-1.830	-1.041
	putative 50S ribosomal protein L25					
	protein synthesis					
PGN_0280	P vs T=1	0.540	0.602	1.411	1.805	3.271
	PS vs T=1	-1.339	-0.814	0.940	1.354	1.711
	PS vs P	-1.466	-1.084	-0.219	-0.092	-0.796
	hypothetical protein					
	hypothetical proteins					



log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0281	P vs T=1	-0.478	-0.094	-0.087	-0.443	-0.421
	PS vs T=1	-0.218	-0.320	-0.452	-0.479	-0.606
	PS vs P	0.246	-0.207	-0.342	-0.047	-0.186
	methionyl-tRNA synthetase					
	protein synthesis					
PGN_0282	P vs T=1	-0.631	-0.388	0.034	0.135	0.144
	PS vs T=1	-0.050	-0.272	-0.490	-0.421	-0.172
	PS vs P	0.536	0.096	-0.502	-0.523	-0.300
	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0283	P vs T=1	-0.929	-0.625	-0.099	0.293	-0.194
	PS vs T=1	-0.402	-0.204	-0.183	-0.244	-0.076
	PS vs P	0.418	0.361	-0.063	-0.446	0.110
	probable exonuclease					
	DNA metabolism					
PGN_0284	P vs T=1	0.393	1.013	1.297	0.952	0.134
	PS vs T=1	0.071	0.313	0.372	0.414	0.362
	PS vs P	-0.331	-0.605	-0.809	-0.475	0.188
	probable transcriptional regulator					
	regulatory functions					
PGN_0285	P vs T=1	2.280	2.731	3.006	2.758	2.273
	PS vs T=1	1.922	1.673	1.317	1.311	1.143
	PS vs P	-0.299	-0.926	-1.538	-1.325	-1.075
	pyridine nucleotide-disulphide oxidoreductase					
	hypothetical proteins-Conserved					
PGN_0286	P vs T=1	0.463	-0.003	1.610	2.197	3.753
	PS vs T=1	-0.517	-0.121	1.231	1.454	1.795
	PS vs P	-0.742	-0.447	0.074	-0.000	-0.561
	hypothetical protein frame-shifted with PGN0285					
	hypothetical proteins					
PGN_0287	P vs T=1	-0.886	-0.544	-0.624	-1.194	-1.942
mfa1	PS vs T=1	-0.531	-0.154	-0.680	-1.378	-1.506
	PS vs P	0.314	0.400	-0.033	-0.217	0.357
	Mfa1fimbrilin					
	cellular processes					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

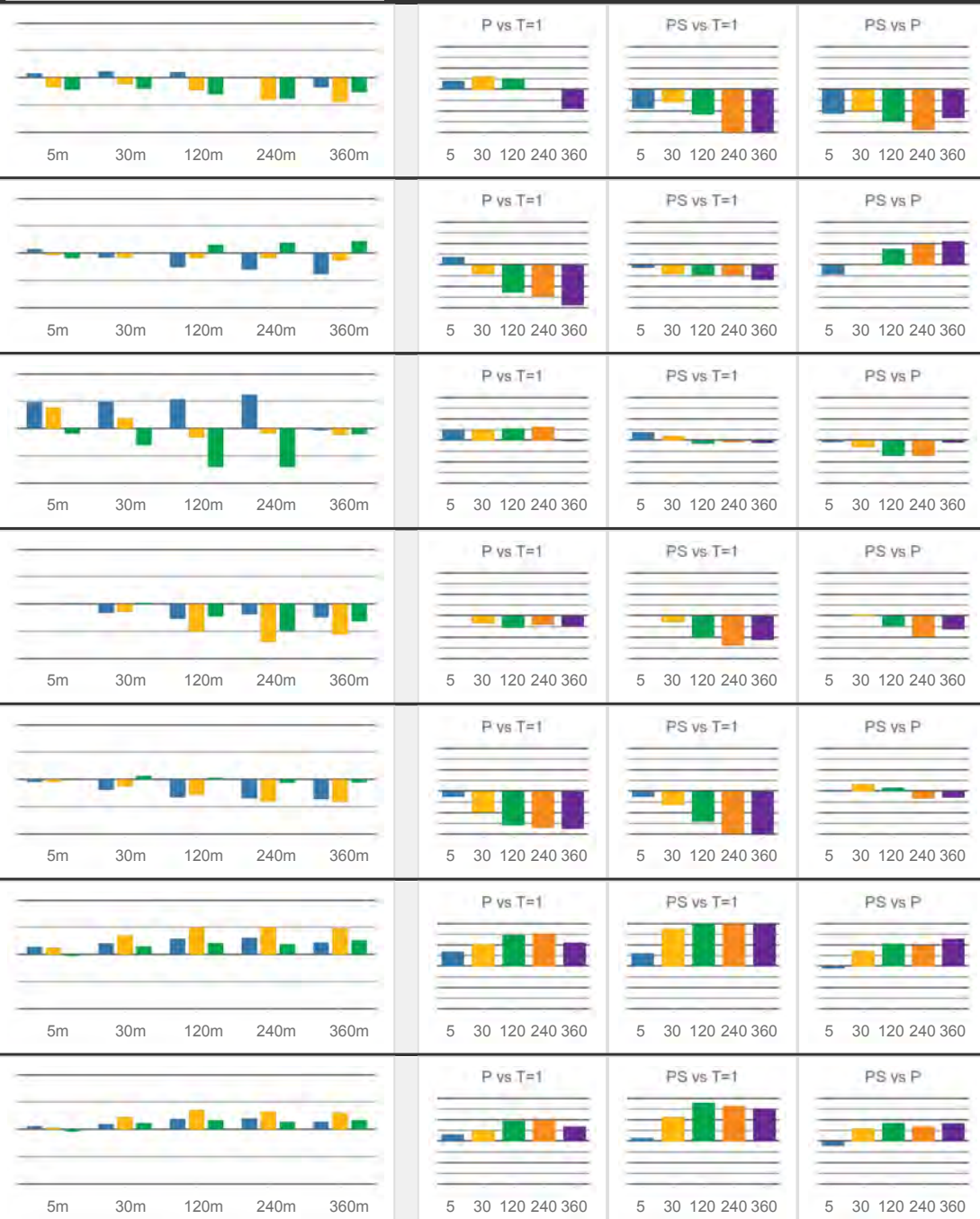
Locus		5m	30m	120m	240m	360m
PGN_0288	P vs T=1	-0.705	-0.802	-1.632	-2.363	-2.737
	PS vs T=1	-0.495	-0.385	-1.395	-2.263	-2.271
	PS vs P	0.238	0.443	0.201	-0.018	0.355
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0289	P vs T=1	-1.041	-1.098	-2.079	-2.490	-2.393
	PS vs T=1	-0.420	-0.124	-1.312	-2.320	-2.320
	PS vs P	0.619	0.974	0.715	0.083	0.030
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0290	P vs T=1	-0.560	-0.469	-1.132	-1.503	-1.773
	PS vs T=1	0.252	0.438	-0.378	-1.250	-1.428
	PS vs P	0.794	0.903	0.715	0.180	0.281
	immunoreactive 32 kDa antigen					
	cell envelope					
PGN_0291	P vs T=1	-1.354	-1.209	-1.396	-1.598	-1.897
	PS vs T=1	-0.329	-0.416	-0.865	-1.387	-1.635
	PS vs P	0.984	0.770	0.509	0.182	0.228
	conserved hypothetical protein					
	unknown function					
PGN_0292	P vs T=1	1.300	1.481	1.978	2.327	2.228
	PS vs T=1	-0.580	-0.207	0.117	0.408	0.745
	PS vs P	-1.522	-1.286	-1.386	-1.232	-1.011
	hypothetical protein					
	hypothetical proteins					
PGN_0293	P vs T=1	1.012	1.269	0.808	-0.326	-1.504
ragA	PS vs T=1	0.615	0.827	-0.303	-1.581	-1.670
	PS vs P	-0.281	-0.274	-0.973	-1.254	-0.269
	receptor antigen A					
	cell envelope					
PGN_0294	P vs T=1	1.460	1.935	2.271	1.984	1.303
ragB	PS vs T=1	1.170	1.525	0.959	0.136	0.176
	PS vs P	-0.266	-0.325	-1.187	-1.749	-1.108
	receptor antigen B					
	cell envelope					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

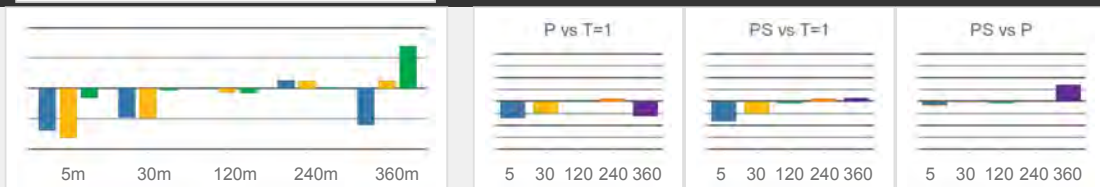
Locus		5m	30m	120m	240m	360m
PGN_0295	P vs T=1	0.395	0.602	0.500	0.014	-0.879
	PS vs T=1	-0.862	-0.573	-1.149	-1.983	-2.194
	PS vs P	-1.098	-0.977	-1.473	-1.876	-1.319
	C-terminal domain of Arg- and Lys-gingipain proteinase					
	hypothetical proteins-Conserved					
PGN_0296	P vs T=1	0.368	-0.397	-1.274	-1.465	-1.870
	PS vs T=1	-0.141	-0.399	-0.449	-0.429	-0.673
	PS vs P	-0.423	0.007	0.756	0.954	1.109
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0297	P vs T=1	0.482	0.486	0.541	0.628	-0.026
	PS vs T=1	0.387	0.187	-0.164	-0.086	-0.116
	PS vs P	-0.087	-0.289	-0.691	-0.691	-0.099
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0298	P vs T=1	-0.005	-0.322	-0.539	-0.382	-0.484
	PS vs T=1	-0.015	-0.279	-0.996	-1.372	-1.100
	PS vs P	0.015	0.048	-0.458	-0.961	-0.607
	putative undecaprenyl diphosphate synthase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0299	P vs T=1	-0.231	-0.956	-1.577	-1.678	-1.747
	PS vs T=1	-0.229	-0.630	-1.402	-1.961	-2.005
	PS vs P	0.041	0.324	0.153	-0.301	-0.272
	putative outer membrane protein					
	cell envelope					
PGN_0300	P vs T=1	0.676	1.025	1.453	1.538	1.103
	PS vs T=1	0.610	1.767	2.497	2.501	2.423
	PS vs P	-0.110	0.715	1.044	0.965	1.297
	conserved hypothetical protein					
	cell envelope					
PGN_0301	P vs T=1	0.304	0.492	0.940	0.976	0.677
	PS vs T=1	0.142	1.116	1.787	1.654	1.518
	PS vs P	-0.197	0.592	0.856	0.684	0.827
	conserved hypothetical protein					
	cell envelope					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0302	P vs T=1	-0.685	-0.464	0.017	0.128	-0.593
	PS vs T=1	-0.808	-0.474	-0.068	0.124	0.135
	PS vs P	-0.154	-0.027	-0.074	0.011	0.701
	rubrerythrin					
	energy metabolism					
PGN_0303	P vs T=1	1.341	1.589	1.399	1.076	0.531
	PS vs T=1	1.164	1.264	1.607	1.635	1.286
	PS vs P	-0.168	-0.293	0.219	0.545	0.723
	putative zinc protease					
	protein fate					
PGN_0304	P vs T=1	-0.099	-0.096	1.848	2.253	3.235
	PS vs T=1	-0.432	-0.269	0.959	2.161	2.057
	PS vs P	-0.485	-0.442	-0.091	0.597	0.105
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0305	P vs T=1	-0.020	-0.087	1.710	2.132	3.327
	PS vs T=1	-0.734	0.226	1.181	2.148	2.172
	PS vs P	-0.807	-0.185	-0.007	0.524	-0.108
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0306	P vs T=1	-0.113	-0.239	0.190	0.605	0.836
	PS vs T=1	-0.853	-0.225	0.549	0.989	0.873
	PS vs P	-0.737	-0.019	0.352	0.427	0.076
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0307	P vs T=1	-0.902	-1.036	-0.857	-0.560	-0.124
	PS vs T=1	-1.668	-1.170	-0.563	-0.325	-0.282
	PS vs P	-0.761	-0.157	0.268	0.253	-0.112
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0308	P vs T=1	-0.126	-0.305	-0.089	0.649	1.071
	PS vs T=1	-0.570	-0.847	-0.700	-0.299	0.724
	PS vs P	-0.385	-0.530	-0.600	-0.554	-0.050
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

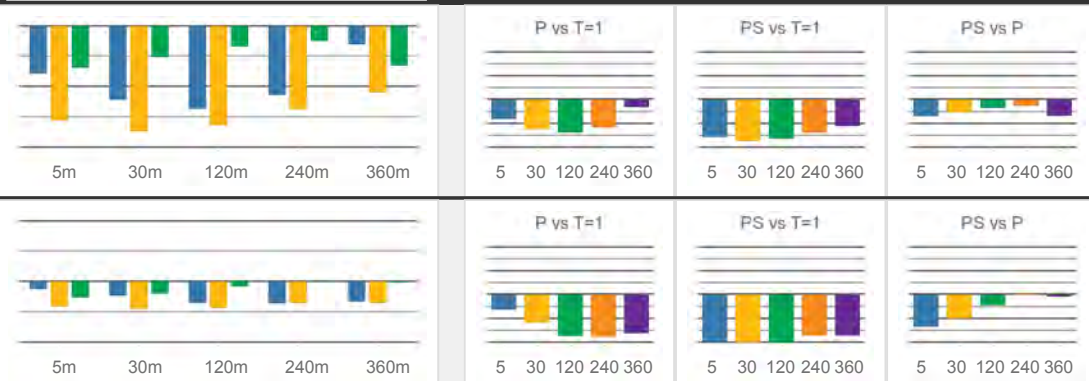


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0309	P vs T=1	-0.782	-1.216	-1.359	-1.136	-0.296
	PS vs T=1	-1.546	-1.729	-1.629	-1.367	-1.094
	PS vs P	-0.685	-0.513	-0.335	-0.240	-0.652
	probable ribonuclease P protein component					
	transcription					
PGN_0310 *HemD*	P vs T=1	-0.611	-1.163	-1.725	-1.766	-1.615
	PS vs T=1	-2.014	-2.178	-2.118	-1.707	-1.698
	PS vs P	-1.322	-0.975	-0.417	0.027	-0.090
	putative uroporphyrinogen-III synthase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0311	P vs T=1	-0.021	-0.864	-1.000	-0.319	0.283
	PS vs T=1	-0.414	-0.642	-0.069	0.141	0.045
	PS vs P	-0.320	0.090	0.695	0.443	-0.161
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0312	P vs T=1	0.537	-0.118	-0.623	-0.030	-0.139
	PS vs T=1	-0.059	-0.220	0.002	0.310	-0.097
	PS vs P	-0.487	-0.125	0.381	0.358	0.009
	hypothetical protein					
	hypothetical proteins					
PGN_0313	P vs T=1	-0.245	-0.427	-0.764	-0.550	-0.147
	PS vs T=1	-0.524	-0.822	-1.136	-1.051	-0.896
	PS vs P	-0.255	-0.376	-0.388	-0.475	-0.704
	peptide chain release factor 3					
	protein synthesis					
PGN_0314	P vs T=1	0.437	0.146	0.226	0.671	1.676
	PS vs T=1	0.205	0.671	1.414	1.144	0.654
	PS vs P	-0.221	0.433	1.061	0.483	-0.817
	probable formate/nitrite transporter					
	transport and binding proteins					
PGN_0315 *CbiD*	P vs T=1	-0.893	-0.659	-0.420	-0.239	0.212
	PS vs T=1	-0.063	-0.104	-0.563	-0.523	-0.388
	PS vs P	0.756	0.513	-0.145	-0.256	-0.536
	precorrin-6x reductase/cobalamin biosynthetic protein CbiD					
	biosynthesis of cofactors, prosthetic groups, and carriers					

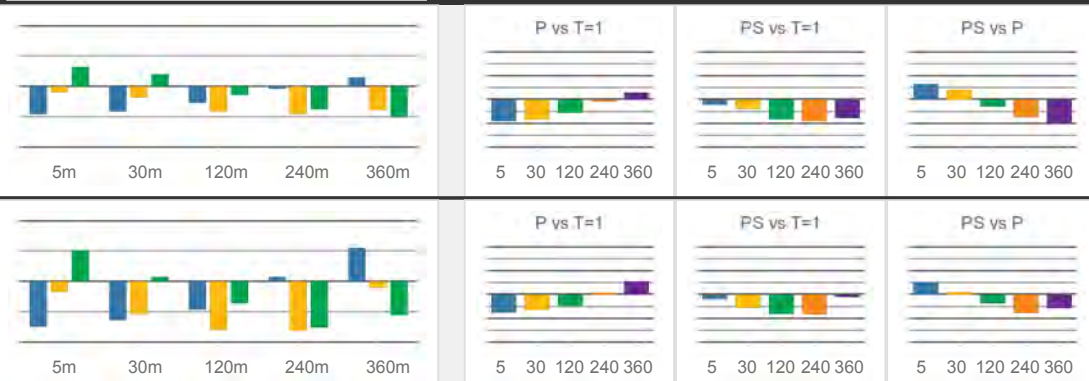


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0316 *CbiG*	P vs T=1	-0.888	-0.800	-0.539	-0.076	0.297
	PS vs T=1	-0.195	-0.369	-0.805	-0.884	-0.759
	PS vs P	0.647	0.392	-0.274	-0.724	-0.979
	precorrin-4 C11-methyltransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0317 *CobL*	P vs T=1	-0.739	-0.631	-0.453	0.072	0.556
	PS vs T=1	-0.170	-0.523	-0.788	-0.801	-0.105
	PS vs P	0.514	0.076	-0.350	-0.748	-0.550
	decarboxylating precorrin-6Y C5,15-methyltransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0318 *CobH/C*	P vs T=1	-1.025	-0.613	-0.223	-0.014	-0.145
	PS vs T=1	-0.534	-0.743	-0.766	-0.220	-0.188
	PS vs P	0.410	-0.146	-0.518	-0.157	-0.034
	precorrin-3B C17-methyltransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0319	P vs T=1	0.175	0.547	1.134	1.883	1.776
	PS vs T=1	-0.208	0.565	1.504	1.926	2.147
	PS vs P	-0.475	-0.031	0.365	0.177	0.426
	probable RNA polymerase sigma-70 factor ECF subfamily					
	transcription					
PGN_0320	P vs T=1	-0.434	-0.099	0.477	1.189	1.421
	PS vs T=1	-0.776	0.000	0.862	1.282	1.496
	PS vs P	-0.439	0.030	0.357	0.229	0.162
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0321	P vs T=1	0.319	0.470	1.256	1.902	1.854
	PS vs T=1	-0.264	0.401	2.014	2.245	2.009
	PS vs P	-0.629	-0.133	0.765	0.463	0.214
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0322	P vs T=1	0.628	1.058	1.606	1.884	1.837
	PS vs T=1	-0.023	0.241	1.081	1.650	1.816
	PS vs P	-0.663	-0.783	-0.470	-0.161	0.020
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

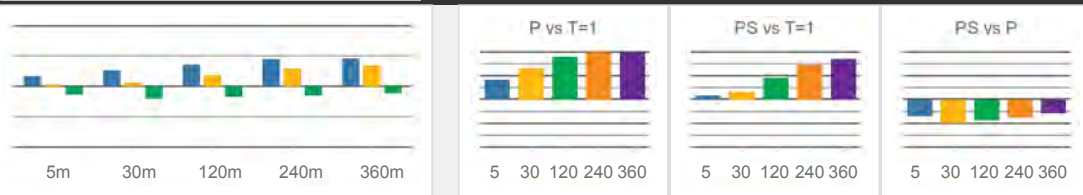


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0323	P vs T=1	0.836	1.318	1.793	2.255	2.300
	PS vs T=1	0.164	0.306	0.902	1.450	1.709
	PS vs P	-0.675	-0.980	-0.852	-0.735	-0.548
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0324	P vs T=1	0.281	0.206	0.237	0.310	-0.035
	PS vs T=1	0.089	-0.131	0.043	0.179	0.180
	PS vs P	-0.190	-0.341	-0.202	-0.132	0.190
	transposase in ISPg1					
PGN_0325	P vs T=1	-0.712	-1.492	-0.971	-1.144	0.117
	PS vs T=1	-0.630	-0.545	0.043	0.216	0.257
	PS vs P	0.071	0.514	0.844	0.901	0.347
	hypothetical protein					
	hypothetical proteins					
PGN_0326	P vs T=1	-0.835	-0.554	-0.022	0.170	0.518
	PS vs T=1	-1.277	-0.975	-0.070	0.067	0.412
	PS vs P	-0.505	-0.430	0.024	0.004	0.012
	DNA-binding protein histone-like family					
	DNA metabolism					
PGN_0327	P vs T=1	-0.740	-0.884	-0.867	-0.519	-0.484
	PS vs T=1	-1.022	-0.900	-0.627	-0.476	-0.456
	PS vs P	-0.286	-0.071	0.153	0.080	0.038
	putative DNA polymerase III epsilon chain					
	DNA metabolism					
PGN_0328	P vs T=1	0.293	0.392	0.483	0.388	0.212
	PS vs T=1	0.142	0.506	0.869	0.917	0.809
	PS vs P	-0.158	0.109	0.385	0.505	0.566
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0329	P vs T=1	-0.279	0.298	1.087	1.325	0.960
	PS vs T=1	-0.411	-0.245	-0.118	0.011	0.094
	PS vs P	-0.187	-0.523	-1.116	-1.206	-0.824
	conserved hypothetical protein					
	unknown function					

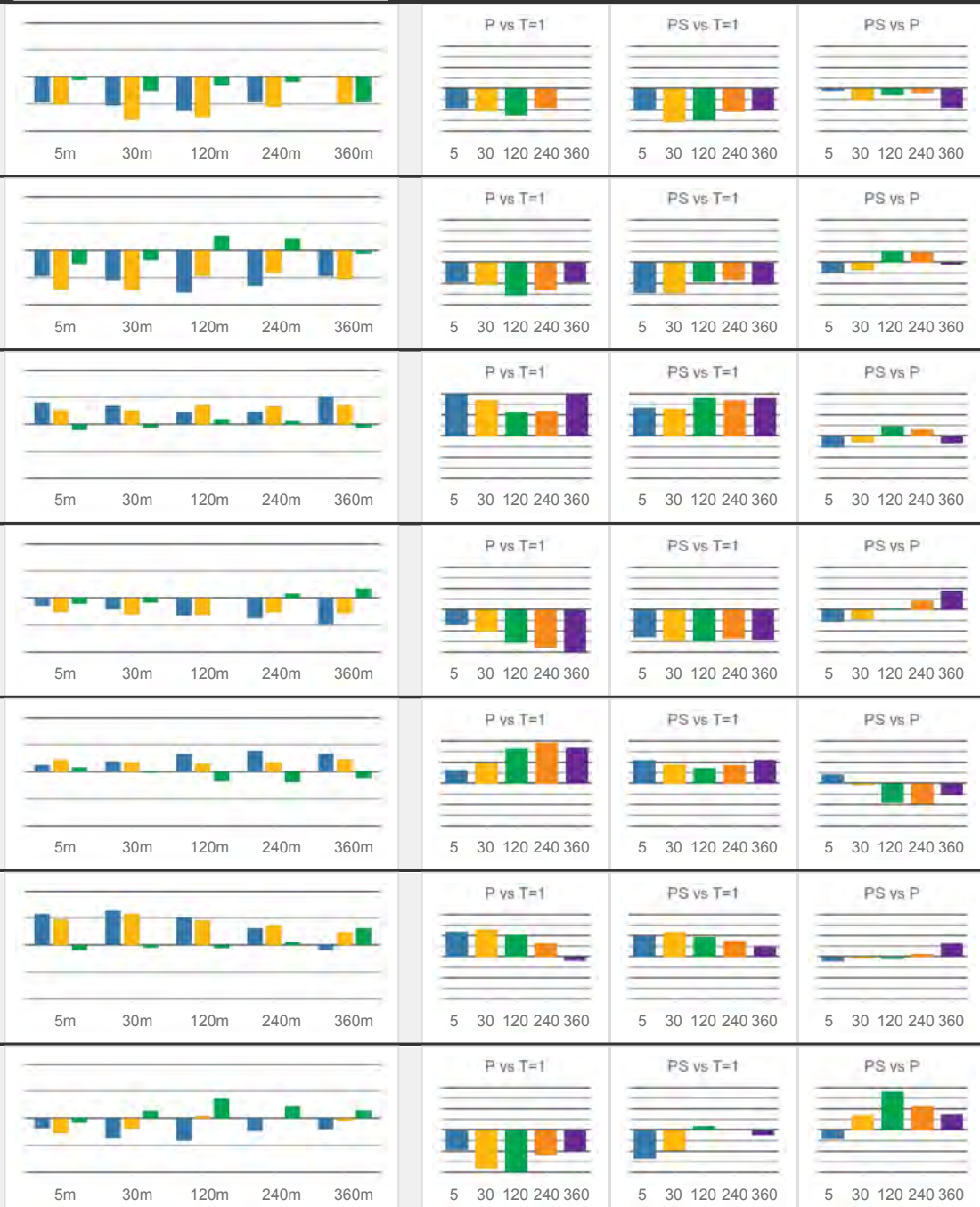


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0330	P vs T=1	-0.898	-1.042	-1.244	-0.887	0.011
	PS vs T=1	-1.012	-1.558	-1.473	-1.078	-0.972
	PS vs P	-0.106	-0.512	-0.290	-0.180	-0.887
	DNA repair protein					
	DNA metabolism					
PGN_0331	P vs T=1	-0.913	-1.059	-1.538	-1.283	-0.923
	PS vs T=1	-1.415	-1.426	-0.911	-0.798	-1.041
	PS vs P	-0.478	-0.353	0.536	0.448	-0.099
	conserved hypothetical protein					
	unknown function					
PGN_0332	P vs T=1	2.047	1.704	1.131	1.174	2.526
	PS vs T=1	1.328	1.294	1.801	1.682	1.789
	PS vs P	-0.510	-0.277	0.461	0.285	-0.308
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0333	P vs T=1	-0.699	-1.023	-1.530	-1.779	-2.361
	PS vs T=1	-1.268	-1.461	-1.483	-1.331	-1.402
	PS vs P	-0.522	-0.413	0.034	0.414	0.892
	putative transaldolase					
	energy metabolism					
PGN_0334	P vs T=1	0.628	0.947	1.645	1.917	1.690
	PS vs T=1	1.086	0.880	0.716	0.867	1.115
	PS vs P	0.418	-0.072	-0.865	-0.960	-0.534
	conserved hypothetical protein with DUF1343 domain					
	hypothetical proteins-Conserved					
PGN_0335	P vs T=1	1.172	1.288	1.042	0.622	-0.181
	PS vs T=1	0.955	1.164	0.919	0.745	0.480
	PS vs P	-0.194	-0.091	-0.104	0.118	0.624
	conserved hypothetical protein with Zinc carboxypeptidase domain					
	protein fate					
PGN_0336	P vs T=1	-0.915	-1.791	-1.990	-1.186	-0.970
	PS vs T=1	-1.339	-0.934	0.169	-0.017	-0.221
	PS vs P	-0.399	0.683	1.819	1.105	0.721
	immunoreactive 23 kDa antigen					
	cell envelope					

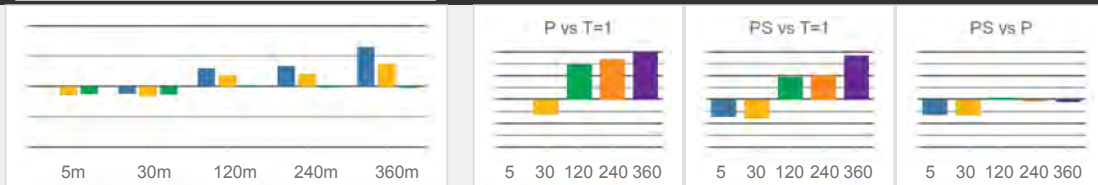


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0337	P vs T=1	-0.012	-0.598	1.487	1.685	3.253
	PS vs T=1	-0.706	-0.774	0.931	1.026	1.859
	PS vs P	-0.618	-0.650	0.073	-0.068	-0.101
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0338	P vs T=1	0.196	0.059	1.682	1.591	3.822
	PS vs T=1	-0.779	0.508	2.051	1.647	1.697
	PS vs P	-0.890	-0.050	0.762	0.201	-0.770
	hypothetical protein					
	hypothetical proteins					
PGN_0339	P vs T=1	-0.169	-1.121	-0.391	0.940	3.042
	PS vs T=1	-0.350	0.042	0.916	2.391	2.005
	PS vs P	-0.307	-0.007	0.421	1.287	0.336
	hypothetical protein					
	hypothetical proteins					
PGN_0340	P vs T=1	-0.577	-0.675	-0.907	-0.694	0.123
	PS vs T=1	-1.420	-1.147	-0.581	-0.522	-0.566
	PS vs P	-0.812	-0.452	0.289	0.167	-0.613
	carboxyl-terminal processing protease					
	protein fate					
PGN_0341	P vs T=1	-0.536	-0.725	-0.557	-0.440	-0.281
	PS vs T=1	0.392	-0.095	-0.502	-0.309	-0.445
	PS vs P	0.911	0.599	0.042	0.126	-0.157
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0342	P vs T=1	-0.076	-0.095	0.021	0.585	1.426
	PS vs T=1	0.813	0.653	0.523	0.861	0.872
	PS vs P	0.806	0.645	0.374	0.304	-0.419
	putative uracil-DNA glycosylase					
	DNA metabolism					
PGN_0343	P vs T=1	-0.582	-1.025	-1.712	-1.108	-1.054
	PS vs T=1	-1.348	-2.215	-2.418	-2.324	-1.277
	PS vs P	-0.513	-0.938	-0.839	-0.825	-0.051
	hypothetical protein					
	hypothetical proteins					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0344	P vs T=1	0.187	-0.319	-1.089	-1.427	-1.041
	PS vs T=1	-0.512	-1.178	-1.728	-1.503	-1.815
	PS vs P	-0.559	-0.763	-0.640	-0.153	-0.739
	probable haloacid dehalogenase-like hydrolase					
	unknown function					
PGN_0345	P vs T=1	0.605	1.321	1.924	1.941	1.261
	PS vs T=1	0.362	0.833	1.013	0.464	0.235
	PS vs P	-0.263	-0.440	-0.829	-1.393	-1.002
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0346	P vs T=1	1.046	1.502	1.330	0.679	-0.072
	PS vs T=1	0.713	0.874	0.601	0.113	-0.304
	PS vs P	-0.313	-0.569	-0.682	-0.559	-0.257
	putative methyltransferase					
	hypothetical proteins-Conserved					
PGN_0347	P vs T=1	0.447	0.299	-0.478	-1.337	-1.880
	PS vs T=1	-0.177	-0.408	-0.634	-0.920	-1.120
	PS vs P	-0.573	-0.658	-0.149	0.359	0.697
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0348	P vs T=1	1.049	1.281	1.219	0.638	-0.258
uspA	PS vs T=1	1.024	1.500	1.624	1.172	0.955
	PS vs P	-0.041	0.231	0.416	0.469	1.087
	putative universal stress protein UspA					
	cellular processes					
PGN_0349	P vs T=1	-0.726	-0.566	-0.449	-0.660	-1.473
ustA	PS vs T=1	-0.821	-0.569	-0.781	-1.036	-0.955
	PS vs P	-0.132	-0.010	-0.306	-0.379	0.400
	upregulated in stationary phase protein A					
	hypothetical proteins					
PGN_0350	P vs T=1	1.135	1.355	1.638	1.481	1.215
	PS vs T=1	0.854	1.135	1.460	1.555	1.448
	PS vs P	-0.284	-0.194	-0.115	0.095	0.211
	probable translation initation factor SUI1					
	protein synthesis					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0351	P vs T=1	0.721	1.145	1.380	0.998	0.165
	PS vs T=1	0.694	0.768	0.445	0.237	0.143
	PS vs P	-0.029	-0.349	-0.894	-0.742	-0.039
	pyruvate carboxylase subunit B					
	energy metabolism					
PGN_0352	P vs T=1	-0.395	-0.996	-0.566	0.618	1.660
	PS vs T=1	-0.810	-0.780	-0.571	0.663	1.023
	PS vs P	-0.421	-0.250	-0.381	0.336	-0.026
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0353	P vs T=1	0.331	-0.274	-0.868	-1.058	-0.987
	PS vs T=1	-0.357	-0.558	-0.981	-1.040	-0.923
	PS vs P	-0.628	-0.261	-0.137	-0.039	0.042
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0354	P vs T=1	0.380	0.287	-0.337	-0.692	-0.648
	PS vs T=1	-0.064	-0.230	-0.999	-1.039	-0.732
	PS vs P	-0.400	-0.472	-0.655	-0.375	-0.094
	putative nitrogen utilization substance protein A					
	transcription					
PGN_0355	P vs T=1	0.224	0.602	0.468	-0.023	-0.387
	PS vs T=1	-0.238	-0.419	-1.040	-1.142	-1.045
	PS vs P	-0.446	-0.983	-1.475	-1.104	-0.659
	translation initiation factor IF-2					
	protein synthesis					
PGN_0356	P vs T=1	-0.099	-0.046	0.310	0.003	-0.357
	PS vs T=1	-0.403	-0.469	-0.178	0.061	-0.267
	PS vs P	-0.292	-0.403	-0.404	0.069	0.046
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0357	P vs T=1	0.149	0.369	0.524	0.502	0.130
	PS vs T=1	-0.874	1.319	3.183	3.042	2.570
	PS vs P	-1.052	0.911	2.616	2.485	2.382
	ABC transporter membrane protein					
	transport and binding proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

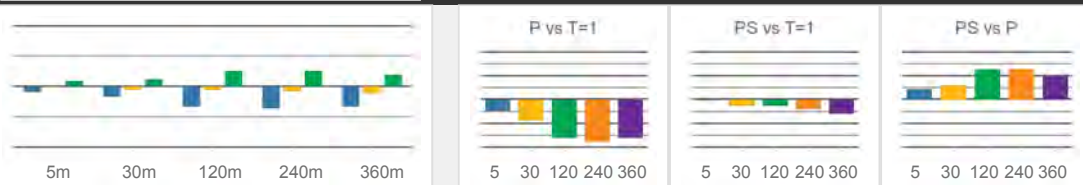
Locus		5m	30m	120m	240m	360m
PGN_0358	P vs T=1	0.865	1.157	1.532	1.573	1.282
	PS vs T=1	0.704	1.702	3.646	3.460	3.087
	PS vs P	-0.193	0.521	2.098	1.864	1.777
	putative ABC transporter ATP-binding protein					
	transport and binding proteins					
PGN_0359	P vs T=1	0.518	0.690	0.839	1.082	0.974
	PS vs T=1	0.873	1.041	2.560	2.713	2.405
	PS vs P	0.312	0.319	1.681	1.606	1.408
	putative ABC transporter permease protein					
	transport and binding proteins					
PGN_0360	P vs T=1	-0.031	-0.027	-0.250	-0.675	-0.731
	PS vs T=1	0.837	0.431	-0.026	-0.144	-0.269
	PS vs P	0.858	0.452	0.216	0.486	0.436
	tyrosyl-tRNA synthetase					
	protein synthesis					
PGN_0361	P vs T=1	0.004	-0.480	-1.543	-1.487	-1.067
wbbL	PS vs T=1	0.676	-0.038	-0.722	-1.016	-1.138
	PS vs P	0.697	0.442	0.696	0.355	-0.086
	putative glycosyl transferase family 2					
	cell envelope					
PGN_0362	P vs T=1	0.615	-0.695	0.261	-0.478	1.989
	PS vs T=1	0.098	-0.084	0.825	2.008	1.074
	PS vs P	-0.222	-0.134	0.436	1.281	0.053
	hypothetical protein					
	hypothetical proteins					
PGN_0363	P vs T=1	0.135	0.202	1.526	2.588	3.434
	PS vs T=1	-0.214	-0.014	1.330	1.979	1.643
	PS vs P	-0.504	-0.426	0.111	0.216	-0.626
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0364	P vs T=1	-0.372	-0.963	0.467	1.722	2.931
	PS vs T=1	-0.295	-0.581	1.025	1.007	1.738
	PS vs P	-0.198	-0.382	0.480	0.035	-0.121
	hypothetical protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0365	P vs T=1	-0.447	-0.848	-1.595	-1.767	-1.590
	PS vs T=1	-0.031	-0.240	-0.241	-0.366	-0.564
	PS vs P	0.420	0.580	1.260	1.278	0.967
	arginyl-tRNA synthetase					
	protein synthesis					
PGN_0366	P vs T=1	-0.393	-0.722	-1.459	-1.540	-1.404
	PS vs T=1	0.618	0.092	-0.327	-0.514	-0.803
	PS vs P	1.006	0.795	1.045	0.908	0.549
	putative tRNA 5-methylaminomethyl-2-thiouridylate 5-methyltransferase					
	protein synthesis					
PGN_0367	P vs T=1	-0.142	-0.725	-1.954	-1.818	-1.542
	PS vs T=1	0.560	0.085	-0.788	-1.142	-1.082
	PS vs P	0.738	0.786	0.911	0.464	0.377
	exodeoxyribonuclease III					
	DNA metabolism					
PGN_0368	P vs T=1	0.692	0.241	-0.490	-0.821	-0.411
oxyR	PS vs T=1	1.228	0.801	-0.089	-0.710	-1.032
	PS vs P	0.567	0.563	0.348	-0.009	-0.621
	redox-sensitive transcriptional activator OxyR					
	regulatory functions					
PGN_0369	P vs T=1	0.285	-0.628	-1.414	-1.460	-1.369
	PS vs T=1	0.163	-0.123	-0.278	-0.104	-0.323
	PS vs P	-0.036	0.467	0.949	1.133	0.928
	probable single-stranded binding protein					
	DNA metabolism					
PGN_0370	P vs T=1	-0.196	-1.180	-1.903	-1.617	-1.294
	PS vs T=1	-0.220	-0.602	-0.918	-0.896	-1.068
	PS vs P	0.041	0.538	0.851	0.646	0.211
	conserved hypothetical protein					
	cellular processes					
PGN_0371	P vs T=1	-0.244	-0.746	-0.724	-0.317	-0.390
	PS vs T=1	-0.679	-0.707	0.001	-0.172	-0.032
	PS vs P	-0.420	0.010	0.673	0.154	0.347
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

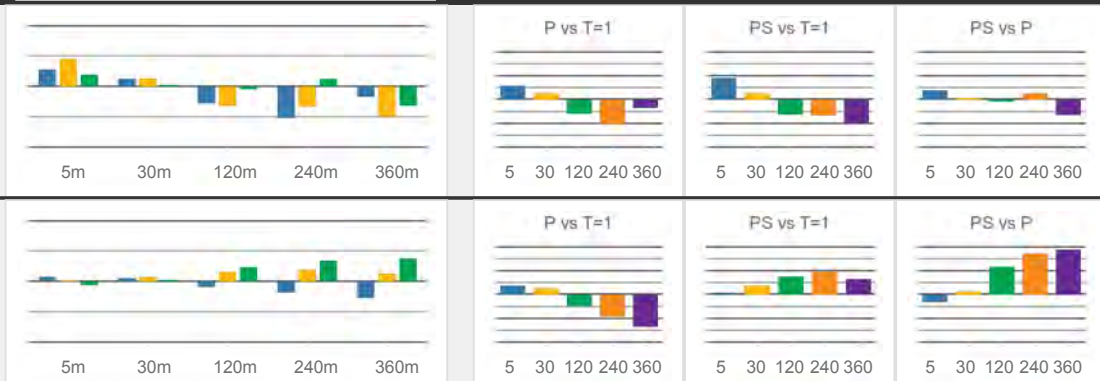
Locus		5m	30m	120m	240m	360m
PGN_0372	P vs T=1	0.627	-0.094	0.486	1.093	0.549
	PS vs T=1	-0.424	0.156	1.386	1.231	1.393
	PS vs P	-0.949	0.104	0.866	0.340	0.801
	hypothetical protein					
	hypothetical proteins					
PGN_0373	P vs T=1	0.674	1.519	1.692	1.492	0.836
	PS vs T=1	-0.674	1.681	3.317	2.851	2.580
	PS vs P	-1.389	0.226	1.656	1.349	1.673
	putative thioredoxin					
	energy metabolism					
PGN_0374	P vs T=1	0.849	0.329	-0.236	-0.494	-1.108
	PS vs T=1	0.544	0.451	0.351	0.184	-0.103
	PS vs P	-0.238	0.131	0.554	0.628	0.928
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0375	P vs T=1	0.675	0.844	0.915	0.773	0.154
	PS vs T=1	0.788	0.474	0.430	0.639	0.424
	PS vs P	0.113	-0.356	-0.469	-0.126	0.251
	phosphoribulose/uridine kinase					
	unknown function					
PGN_0376	P vs T=1	-0.625	-0.167	-0.127	-0.103	-0.121
	PS vs T=1	-0.583	-0.328	0.023	0.544	0.547
	PS vs P	-0.002	-0.157	0.140	0.626	0.651
	2-dehydro-3-deoxyphosphooctonate aldolase					
	cell envelope					
PGN_0377	P vs T=1	0.662	0.834	0.854	0.716	0.202
	PS vs T=1	0.926	0.817	0.589	0.900	0.603
	PS vs P	0.261	0.000	-0.243	0.191	0.376
	aspartate ammonia-lyase					
	energy metabolism					
PGN_0378	P vs T=1	0.324	0.037	-0.590	-0.700	-0.728
	PS vs T=1	0.628	0.027	-0.263	-0.223	-0.634
	PS vs P	0.331	0.005	0.284	0.419	0.062
	putative exopolyphosphatase					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0379	P vs T=1	0.561	0.245	-0.560	-1.023	-0.331
	PS vs T=1	0.905	0.260	-0.612	-0.636	-0.974
	PS vs P	0.375	0.039	-0.083	0.242	-0.618
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0380	P vs T=1	0.371	0.259	-0.452	-0.894	-1.338
GlcK	PS vs T=1	0.056	0.361	0.762	0.936	0.649
	PS vs P	-0.292	0.117	1.171	1.729	1.891
	partial ROK family transcriptional repressor with glucose kinase domain					
	energy metabolism					
PGN_0381	P vs T=1	0.919	1.261	1.193	0.898	0.415
	PS vs T=1	0.742	1.015	1.473	1.667	1.502
	PS vs P	-0.181	-0.226	0.289	0.740	1.032
	partial ROK family transcriptional repressor with glucose kinase domain					
	regulatory functions					
PGN_0382	P vs T=1	-0.701	-0.328	-0.369	-0.230	0.336
	PS vs T=1	-0.499	-0.623	0.032	0.612	0.482
	PS vs P	0.108	-0.301	0.301	0.726	0.198
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0383	P vs T=1	0.502	0.305	0.167	0.973	1.741
	PS vs T=1	0.629	0.439	0.663	1.150	0.942
	PS vs P	0.127	0.103	0.362	0.260	-0.672
	probable transporter					
	transport and binding proteins					
PGN_0384	P vs T=1	-0.815	-1.134	-1.316	-1.232	-0.749
	PS vs T=1	-0.492	-0.721	-0.798	-0.609	-1.089
	PS vs P	0.318	0.354	0.396	0.497	-0.309
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0385	P vs T=1	-0.458	-0.760	-1.220	-1.051	-0.401
	PS vs T=1	-0.241	-0.141	0.678	0.725	0.385
	PS vs P	0.197	0.547	1.685	1.567	0.764
	putative integrase/recombinase XerD					
	cellular processes					

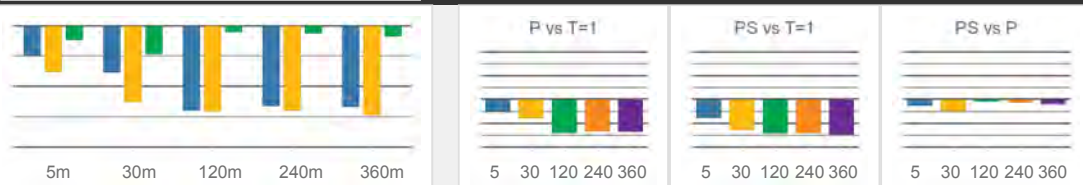


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0386	P vs T=1	-0.491	-0.764	-1.385	-1.313	-1.329
	PS vs T=1	-0.759	-1.259	-1.400	-1.384	-1.458
	PS vs P	-0.225	-0.462	-0.092	-0.118	-0.169
	probable 3-dehydroquinate dehydratase type II					
	amino acid biosynthesis					
PGN_0387	P vs T=1	0.267	0.074	-0.185	-0.086	0.284
	PS vs T=1	0.327	0.359	0.305	0.125	0.131
	PS vs P	0.066	0.272	0.425	0.155	-0.136
	putative O-methyltransferase					
	unknown function					
PGN_0388	P vs T=1	-0.406	0.294	0.661	0.634	-0.042
	PS vs T=1	-1.742	0.447	2.065	2.375	2.293
	PS vs P	-1.385	0.157	1.407	1.726	2.278
	putative thiol peroxidase					
	cellular processes					
PGN_0389	P vs T=1	-1.072	-1.265	-1.219	-1.015	-1.129
	PS vs T=1	-0.931	-1.321	-0.935	-0.901	-0.839
	PS vs P	0.135	-0.086	0.251	0.126	0.268
	putative cytidine/deoxycytidylate deaminase					
	unknown function					
PGN_0390	P vs T=1	-0.289	-0.448	-0.538	-0.495	-0.384
	PS vs T=1	0.001	-0.558	-0.905	-0.778	-0.624
	PS vs P	0.297	-0.110	-0.372	-0.276	-0.227
	conserved hypothetical protein					
	unknown function					
PGN_0391	P vs T=1	0.159	0.354	0.360	0.028	-0.563
	PS vs T=1	-0.022	0.026	0.198	0.302	0.184
	PS vs P	-0.178	-0.310	-0.144	0.268	0.715
	conserved hypothetical protein					
	unknown function					
PGN_0392	P vs T=1	-0.291	-0.529	-0.317	-0.326	0.524
	PS vs T=1	-0.489	-0.422	-0.271	0.314	0.236
	PS vs P	-0.193	0.043	0.020	0.538	-0.162
	conserved hypothetical protein with competence-damaged protein domain					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

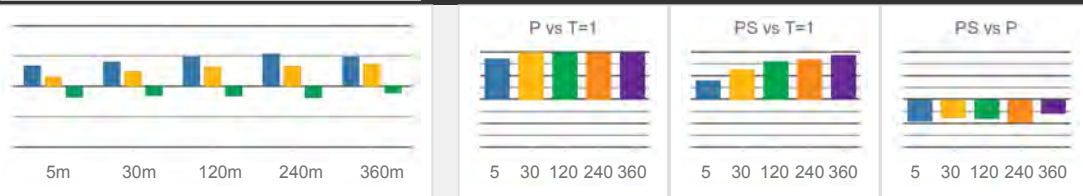
Locus		5m	30m	120m	240m	360m
PGN_0393	P vs T=1	-0.226	-0.381	-0.639	-0.036	0.098
	PS vs T=1	-0.648	-0.693	-0.214	0.484	0.547
	PS vs P	-0.415	-0.319	0.339	0.531	0.455
	putative O-sialoglycoprotein endopeptidase					
	protein fate					
PGN_0394	P vs T=1	-0.189	-0.559	-0.900	-0.874	-1.389
rpsT	PS vs T=1	-1.772	-1.406	-0.857	-0.597	-0.533
	PS vs P	-1.442	-0.779	0.025	0.271	0.759
	probable 30S ribosomal protein S20					
	protein synthesis					
PGN_0395	P vs T=1	0.073	-0.175	-0.248	0.309	1.411
	PS vs T=1	0.066	-0.221	-0.840	0.176	0.269
	PS vs P	0.026	-0.075	-0.674	-0.017	-0.825
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0396	P vs T=1	0.444	0.593	0.405	0.066	0.194
	PS vs T=1	0.831	0.541	-0.131	-0.150	-0.200
	PS vs P	0.389	-0.034	-0.519	-0.227	-0.387
	ribonuclease R					
	transcription					
PGN_0397	P vs T=1	-0.726	-0.721	-1.174	-1.340	-1.172
	PS vs T=1	-0.530	-0.693	-1.061	-0.811	-1.052
	PS vs P	0.195	0.033	0.088	0.478	0.104
	putative auxin-regulated protein					
	hypothetical proteins-Conserved					
PGN_0398	P vs T=1	-0.012	0.022	-0.378	-0.557	-0.349
	PS vs T=1	-0.248	-0.606	-1.177	-1.190	-1.079
	PS vs P	-0.220	-0.602	-0.785	-0.630	-0.710
	ABC transporter ATP-binding protein MsbA family					
	transport and binding proteins					
PGN_0399	P vs T=1	1.385	0.918	0.529	2.031	3.120
	PS vs T=1	0.437	0.384	0.872	1.631	1.071
	PS vs P	-0.561	-0.389	-0.081	0.242	-0.882
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0400	P vs T=1	1.721	2.052	2.444	2.707	2.461
	PS vs T=1	0.792	1.253	1.601	1.685	1.864
	PS vs P	-0.903	-0.751	-0.788	-0.953	-0.562
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0401	P vs T=1	0.204	0.231	1.711	2.507	3.646
	PS vs T=1	-0.646	-0.164	1.010	2.316	2.321
	PS vs P	-0.775	-0.510	-0.177	0.522	-0.096
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0402	P vs T=1	1.186	0.725	1.501	2.378	3.504
	PS vs T=1	-0.126	0.317	0.905	1.438	2.152
	PS vs P	-0.929	-0.423	-0.353	-0.235	-0.533
	hypothetical protein					
	hypothetical proteins					
PGN_0403	P vs T=1	-0.641	-0.718	-1.014	-0.907	-0.680
	PS vs T=1	-1.494	-1.262	-0.487	-0.267	-0.357
	PS vs P	-0.830	-0.526	0.480	0.598	0.322
	putative pyridoxamine-phosphate oxidase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0404	P vs T=1	-0.463	-0.526	-0.889	-0.647	-0.246
	PS vs T=1	-0.849	-0.922	-1.210	-1.030	-0.700
	PS vs P	-0.351	-0.355	-0.361	-0.336	-0.368
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0405	P vs T=1	-0.116	-0.350	-0.278	0.180	0.828
	PS vs T=1	-0.205	-0.662	-1.003	-0.758	-0.399
	PS vs P	-0.078	-0.311	-0.722	-0.877	-1.167
	alpha-1,2-mannosidase family protein					
	cell envelope					
PGN_0406	P vs T=1	0.002	-0.048	-0.078	-0.026	0.346
	PS vs T=1	0.356	-0.180	-1.002	-0.902	-0.779
	PS vs P	0.358	-0.126	-0.910	-0.849	-1.090
	conserved hypothetical protein with glycosyl hydrolase family 92 domain					
	cell envelope					



PgSg Time Course

log$_2$ (Fold Change)

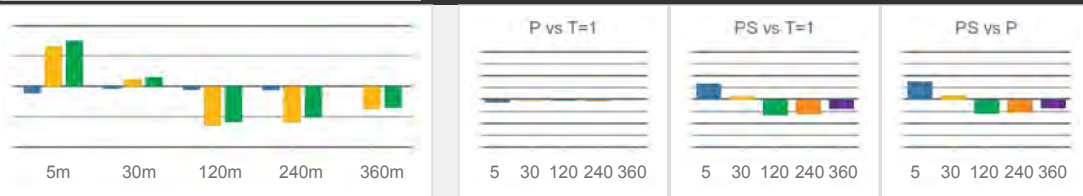
Locus		5m	30m	120m	240m	360m
PGN_0407	P vs T=1	0.482	0.329	-0.173	0.242	0.768
	PS vs T=1	0.675	0.751	-0.483	-0.315	-0.017
	PS vs P	0.247	0.446	-0.438	-0.405	-0.508
	hypothetical protein					
	hypothetical proteins					
PGN_0408	P vs T=1	0.484	-0.646	-1.328	-1.371	-1.673
	PS vs T=1	-0.558	-1.017	-1.255	-1.387	-1.379
	PS vs P	-0.899	-0.352	0.023	-0.055	0.230
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0409	P vs T=1	-0.215	-1.092	-1.817	-1.667	-0.979
	PS vs T=1	-1.071	-1.653	-1.999	-1.677	-1.359
	PS vs P	-0.724	-0.541	-0.345	-0.135	-0.327
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0410	P vs T=1	-0.400	-0.867	-1.281	-1.296	-1.352
	PS vs T=1	-0.836	-1.258	-1.698	-1.857	-1.465
	PS vs P	-0.399	-0.378	-0.430	-0.565	-0.126
	probable RNA pseudouridylate synthase					
	transcription					
PGN_0411	P vs T=1	0.481	0.872	0.777	0.315	-0.176
	PS vs T=1	1.263	1.196	0.765	0.535	0.525
	PS vs P	0.758	0.340	0.007	0.203	0.666
	thiol-disulfide interchange protein					
	protein fate					
PGN_0412	P vs T=1	-0.010	0.269	0.059	-0.598	-1.044
	PS vs T=1	1.194	1.159	0.480	-0.073	-0.349
	PS vs P	1.179	0.887	0.425	0.465	0.632
	conserved hypothetical protein					
	unknown function					
PGN_0413	P vs T=1	0.072	0.254	0.023	-0.505	-1.303
gyrB	PS vs T=1	0.436	0.444	-0.128	-0.573	-0.817
	PS vs P	0.364	0.204	-0.139	-0.078	0.451
	DNA gyrase B subunit					
	DNA metabolism					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0414	P vs T=1	-0.113	-0.040	-0.053	-0.062	-0.007
	PS vs T=1	0.661	0.116	-0.637	-0.581	-0.361
	PS vs P	0.760	0.155	-0.575	-0.506	-0.344
	probable membrane-bound dipeptidase					
	protein fate					
PGN_0415	P vs T=1	-0.072	-0.058	-0.772	-0.773	-0.456
	PS vs T=1	0.355	0.474	-0.095	-0.162	-0.297
	PS vs P	0.423	0.532	0.639	0.570	0.151
	restriction endonuclease					
	DNA metabolism					
PGN_0416	P vs T=1	-0.547	-1.208	-1.615	-1.515	-1.516
	PS vs T=1	0.074	-0.119	0.098	0.174	-0.218
	PS vs P	0.611	0.970	1.544	1.536	1.195
	putative type II DNA modification methyltransferase					
	DNA metabolism					
PGN_0417	P vs T=1	-0.447	-1.431	-1.067	-0.606	0.212
	PS vs T=1	-0.486	-1.117	-0.550	-0.470	0.039
	PS vs P	0.059	-0.019	0.327	0.129	0.036
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0418	P vs T=1	-0.687	-0.260	0.069	0.180	-0.001
	PS vs T=1	-0.516	-0.313	-0.271	-0.045	-0.155
	PS vs P	0.125	-0.058	-0.323	-0.200	-0.153
	conserved hypothetical protein with aminodeoxychorismate lyase domain					
	hypothetical proteins-Conserved					
PGN_0419	P vs T=1	-1.152	-0.866	-0.854	-0.837	-0.985
	PS vs T=1	-0.889	-0.999	-0.856	-0.635	-0.749
	PS vs P	0.213	-0.140	-0.020	0.178	0.191
	putative dinucleotide-utilizing enzyme involved in molybdopterin and thiamine biosynthesis					
	unknown function					
PGN_0420	P vs T=1	-0.922	-0.795	-0.972	-0.833	-0.613
	PS vs T=1	-0.664	-0.981	-1.485	-1.244	-1.409
	PS vs P	0.243	-0.169	-0.520	-0.374	-0.738
	putative lipoprotein releasing system ATP-binding protein					
	transport and binding proteins					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0421	P vs T=1	-0.037	-0.054	0.038	0.233	0.714
	PS vs T=1	0.545	0.228	-0.015	0.017	0.199
	PS vs P	0.538	0.233	-0.085	-0.188	-0.401
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0422	P vs T=1	-0.390	0.049	0.221	0.150	0.042
	PS vs T=1	0.678	0.819	0.767	0.590	0.433
	PS vs P	1.002	0.746	0.541	0.417	0.368
	conserved hypothetical protein					
	unknown function					
PGN_0423	P vs T=1	-0.407	-0.518	-0.787	-1.137	-1.826
	PS vs T=1	-0.695	-0.066	0.392	0.456	0.380
	PS vs P	-0.279	0.443	1.147	1.511	2.086
	putative transcription elongation factor					
	transcription					
PGN_0424	P vs T=1	-0.758	-0.676	-0.590	-0.553	-0.979
	PS vs T=1	-1.276	-0.616	-0.119	0.250	0.236
	PS vs P	-0.525	0.053	0.463	0.793	1.167
	putative HIT family protein					
	unknown function					
PGN_0425	P vs T=1	0.314	0.158	0.508	-0.043	-0.050
	PS vs T=1	-0.227	0.065	0.375	0.367	0.536
	PS vs P	-0.469	-0.099	-0.001	0.255	0.491
	partial transposase in ISPg3					
PGN_0426	P vs T=1	0.608	1.307	1.634	1.120	0.162
	PS vs T=1	0.534	1.286	1.771	1.754	1.588
	PS vs P	-0.148	0.008	0.195	0.608	1.316
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0427	P vs T=1	1.321	1.705	1.628	1.045	0.200
	PS vs T=1	1.989	2.523	2.550	2.295	2.102
	PS vs P	0.620	0.808	0.916	1.182	1.797
	putative glycosyl hydrolase					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0428	P vs T=1	1.292	1.739	1.235	0.713	0.466
	PS vs T=1	2.031	1.916	1.567	1.255	0.937
	PS vs P	0.712	0.203	0.319	0.467	0.413
	putative glycosyl transferase family 1					
	cell envelope					
PGN_0429	P vs T=1	-0.086	0.195	0.201	0.260	-0.118
	PS vs T=1	-0.039	-0.148	-0.126	0.105	0.172
	PS vs P	0.037	-0.342	-0.330	-0.156	0.277
	putative 4-alpha-glucanotransferase					
	unknown function					
PGN_0430	P vs T=1	0.989	1.125	1.229	1.586	2.194
	PS vs T=1	1.648	1.798	1.935	2.071	1.934
	PS vs P	0.585	0.613	0.634	0.511	-0.126
	putative ATP-binding component of ABC transporter protein					
	transport and binding proteins					
PGN_0431	P vs T=1	-0.174	-0.348	0.097	1.081	1.947
	PS vs T=1	-0.221	-0.574	-0.064	0.174	0.432
	PS vs P	-0.061	-0.286	-0.189	-0.652	-1.287
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0432	P vs T=1	-0.719	-0.111	-0.098	1.076	1.971
	PS vs T=1	-0.566	-0.958	-0.677	0.534	0.040
	PS vs P	-0.227	-0.548	-0.568	0.147	-0.573
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0433	P vs T=1	-0.032	0.355	1.026	1.097	0.542
	PS vs T=1	0.499	0.437	0.955	1.647	1.245
	PS vs P	0.474	0.063	-0.039	0.577	0.685
	phosphoglycerate kinase					
	energy metabolism					
PGN_0434	P vs T=1	-0.132	0.168	0.914	0.881	0.334
	PS vs T=1	0.472	0.628	0.842	1.233	1.154
	PS vs P	0.514	0.410	-0.020	0.382	0.788
	phosphoenolpyruvate carboxykinase					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0435	P vs T=1	-0.017	0.230	1.096	2.377	2.898
	PS vs T=1	-0.316	-0.053	0.542	1.002	1.607
	PS vs P	-0.489	-0.369	-0.342	-0.280	-0.279
	probable partial hemagglutinin-related protein					
	unknown function					
PGN_0436	P vs T=1	1.176	1.077	2.327	3.351	3.773
	PS vs T=1	0.254	0.556	1.926	2.278	3.113
	PS vs P	-0.798	-0.578	-0.147	-0.299	-0.108
	probable partial hemagglutinin-related protein					
	unknown function					
PGN_0437	P vs T=1	-2.293	-1.626	-2.023	-2.083	-2.271
	PS vs T=1	-2.426	-2.206	-2.308	-2.189	-2.132
	PS vs P	-0.295	-0.414	-0.303	-0.136	0.038
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0438	P vs T=1	1.802	2.238	3.032	3.104	2.129
	PS vs T=1	2.274	2.722	2.798	3.033	2.991
	PS vs P	0.384	0.479	-0.071	0.085	0.828
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0439	P vs T=1	-1.761	-1.035	-0.542	-0.840	-1.474
	PS vs T=1	-1.614	-1.195	-1.093	-0.823	-0.705
	PS vs P	-0.158	-0.163	-0.414	0.016	0.588
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0440	P vs T=1	-0.994	-0.747	-1.248	-1.709	-2.543
	PS vs T=1	-1.312	-1.283	-1.986	-2.896	-2.870
	PS vs P	-0.227	-0.353	-0.641	-1.142	-0.433
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0441	P vs T=1	0.647	0.876	1.853	2.513	3.164
	PS vs T=1	0.353	0.923	2.092	2.375	2.424
	PS vs P	-0.414	-0.079	0.349	0.198	-0.380
	hypothetical protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0442	P vs T=1	0.413	-0.176	0.055	0.527	1.647
	PS vs T=1	-0.121	0.062	0.509	0.521	1.022
	PS vs P	-0.490	0.121	0.345	-0.009	-0.480
	transposase in ISPg3					
PGN_0443	P vs T=1	-0.338	-0.742	-0.460	0.632	1.064
	PS vs T=1	-0.971	-0.887	-0.500	-0.236	0.221
	PS vs P	-0.541	-0.325	-0.217	-0.273	-0.279
	hypothetical protein					
	hypothetical proteins					
PGN_0444	P vs T=1	0.999	1.471	2.109	2.775	2.775
	PS vs T=1	1.043	1.236	1.525	2.050	2.449
	PS vs P	-0.013	-0.235	-0.539	-0.611	-0.260
	probable outer membrane efflux protein					
	transport and binding proteins					
PGN_0445	P vs T=1	0.762	1.050	1.420	1.805	1.648
	PS vs T=1	0.666	0.829	0.937	1.383	1.670
	PS vs P	-0.111	-0.216	-0.462	-0.370	0.041
	membrane fusion efflux protein					
	transport and binding proteins					
PGN_0446	P vs T=1	0.740	0.823	1.248	1.837	2.192
	PS vs T=1	0.712	0.802	1.363	1.921	2.417
	PS vs P	-0.045	-0.040	0.105	0.116	0.251
	putative ABC transporter ATP-binding protein					
	transport and binding proteins					
PGN_0447	P vs T=1	0.597	0.744	1.189	1.697	1.848
	PS vs T=1	0.752	0.934	1.381	2.043	2.570
	PS vs P	0.129	0.167	0.183	0.364	0.733
	putative ABC transporter permease protein					
	transport and binding proteins					
PGN_0448	P vs T=1	0.665	0.983	1.406	1.868	1.704
	PS vs T=1	0.707	0.874	1.367	1.904	2.227
	PS vs P	-0.016	-0.126	-0.031	0.098	0.538
	putative ABC transporter ATP-binding protein					
	transport and binding proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0449	P vs T=1	0.785	1.355	1.850	2.051	1.637
	PS vs T=1	0.841	1.235	1.908	2.251	2.599
	PS vs P	0.012	-0.119	0.080	0.233	0.951
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0450	P vs T=1	-0.276	0.042	0.428	0.571	0.638
	PS vs T=1	-0.098	-0.068	0.357	0.924	1.342
	PS vs P	0.099	-0.138	-0.065	0.358	0.704
	putative RNA polymerase sigma-70 factor ECF subfamily					
	transcription					
PGN_0451	P vs T=1	0.946	1.081	1.367	1.732	1.749
	PS vs T=1	0.973	1.193	1.635	2.093	2.506
	PS vs P	-0.005	0.085	0.248	0.384	0.763
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0452	P vs T=1	1.010	1.188	1.371	1.755	1.753
	PS vs T=1	0.514	0.826	1.327	1.276	2.338
	PS vs P	-0.482	-0.319	-0.035	-0.289	0.651
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0453	P vs T=1	1.424	1.468	1.974	2.582	2.471
	PS vs T=1	1.007	1.424	2.050	2.263	2.945
	PS vs P	-0.416	-0.076	0.102	-0.107	0.558
	partial transposase Orf1 in ISPg5					
PGN_0454	P vs T=1	0.440	-0.028	0.138	0.857	1.800
	PS vs T=1	0.058	0.101	0.667	0.742	1.003
	PS vs P	-0.358	0.037	0.408	-0.056	-0.655
	transposase in ISPg3					
PGN_0455	P vs T=1	-0.581	-0.950	-0.323	-0.285	0.281
	PS vs T=1	-0.886	-0.926	-0.386	-0.492	-0.065
	PS vs P	-0.292	-0.141	0.025	-0.151	-0.123
	partial transposase Orf1 in ISPg5					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

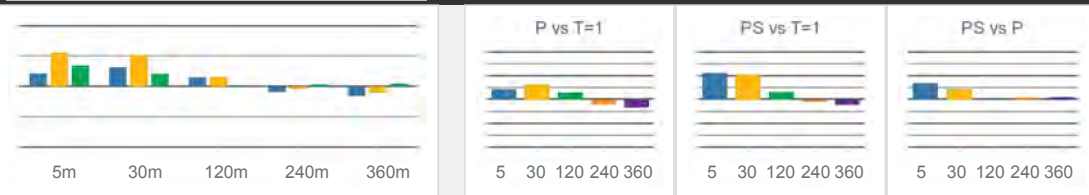
Locus		5m	30m	120m	240m	360m
PGN_0456	P vs T=1	0.503	1.008	1.475	1.431	1.085
	PS vs T=1	0.913	1.039	1.104	1.343	1.118
	PS vs P	0.372	0.032	-0.343	-0.069	0.030
	methylmalonyl-CoA mutase large subunit					
	energy metabolism					
PGN_0457	P vs T=1	0.003	0.243	0.305	0.072	-0.541
	PS vs T=1	-0.053	-0.311	-0.433	-0.098	-0.086
	PS vs P	-0.056	-0.542	-0.724	-0.167	0.436
	methylmalonyl-CoA mutase small subunit					
	energy metabolism					
PGN_0458	P vs T=1	0.179	0.567	0.864	0.825	0.642
	PS vs T=1	1.033	1.982	3.543	3.646	3.264
	PS vs P	0.766	1.349	2.627	2.750	2.568
	hypothetical protein					
	hypothetical proteins					
PGN_0459	P vs T=1	0.306	-0.280	0.066	0.753	1.625
	PS vs T=1	0.021	0.085	0.461	0.642	0.937
	PS vs P	-0.271	0.236	0.288	-0.059	-0.568
	transposase in ISPg3					
PGN_0460	P vs T=1	0.547	0.727	0.609	0.766	1.555
	PS vs T=1	-0.103	0.434	0.937	1.322	1.404
	PS vs P	-0.634	-0.254	0.268	0.503	-0.021
	DNA-binding protein histone-like family					
	DNA metabolism					
PGN_0461	P vs T=1	0.854	1.280	1.478	1.267	0.781
	PS vs T=1	1.620	1.751	1.479	0.989	0.663
	PS vs P	0.710	0.472	0.041	-0.256	-0.147
	probable D-alanyl-D-alanine dipeptidase					
	protein fate					
PGN_0462	P vs T=1	0.097	0.770	0.435	-0.249	-0.607
	PS vs T=1	0.991	1.013	0.272	-0.377	-0.737
	PS vs P	0.868	0.265	-0.149	-0.161	-0.164
	probable haloacid dehalogenase-like hydrolase					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0463	P vs T=1	0.423	0.625	0.295	-0.177	-0.313
	PS vs T=1	1.113	1.029	0.305	-0.078	-0.201
	PS vs P	0.681	0.410	0.009	0.061	0.087
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0464	P vs T=1	0.273	0.276	-0.062	-0.350	-0.514
	PS vs T=1	0.728	0.407	-0.224	-0.299	-0.176
	PS vs P	0.454	0.133	-0.168	0.027	0.318
	conserved hypothetical protein					
	unknown function					
PGN_0465	P vs T=1	-0.299	-0.035	-0.394	-0.652	-0.652
	PS vs T=1	0.199	-0.131	-0.567	-0.701	-0.882
	PS vs P	0.489	-0.086	-0.178	-0.079	-0.244
	GTP pyrophosphokinase					
	cellular processes					
PGN_0466	P vs T=1	-1.215	-1.022	-1.345	-1.069	-0.836
	PS vs T=1	-0.887	-0.905	-0.875	-0.849	-0.849
	PS vs P	0.300	0.108	0.404	0.191	-0.017
	putative cardiolipin synthetase					
	fatty acid and phospholipid metabolism					
PGN_0467	P vs T=1	-0.643	0.427	1.272	1.732	1.019
	PS vs T=1	-0.619	-0.472	0.101	0.419	0.178
	PS vs P	-0.343	-0.690	-0.731	-0.601	-0.561
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0468	P vs T=1	-0.121	-0.428	-0.718	-0.341	0.337
BioG	PS vs T=1	-0.127	-0.736	-1.357	-1.160	-0.852
	PS vs P	0.044	-0.286	-0.682	-0.714	-1.016
	conserved hypothetical protein with DUF452 domain					
	biosynthesis of cofactors, prosthetic groups, and carriers/ hypothetical					
PGN_0469	P vs T=1	0.019	-0.249	-0.219	0.061	1.105
BioC	PS vs T=1	0.533	0.353	-0.286	-0.138	0.059
	PS vs P	0.502	0.541	-0.136	-0.206	-0.909
	probable biotin synthesis protein					
	biosynthesis of cofactors, prosthetic groups, and carriers					

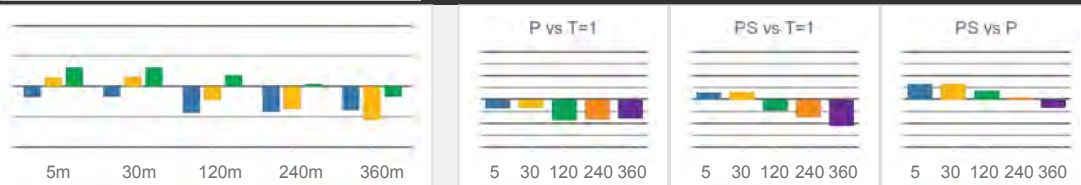


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0470	P vs T=1	-0.346	-0.332	-0.848	-0.814	-0.763
	PS vs T=1	0.296	0.305	-0.441	-0.709	-1.084
	PS vs P	0.634	0.634	0.362	0.070	-0.333
	conserved hypothetical protein					
	unknown function					
PGN_0471	P vs T=1	0.404	0.565	-0.130	-0.648	-0.661
	PS vs T=1	0.613	0.487	-0.557	-0.993	-1.015
	PS vs P	0.219	-0.053	-0.425	-0.411	-0.382
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0472	P vs T=1	-1.001	-0.561	-0.178	0.091	-0.112
	PS vs T=1	-0.759	-0.677	-0.458	-0.130	0.162
	PS vs P	0.176	-0.133	-0.276	-0.199	0.268
	DNA topoisomerase IV A subunit					
	DNA metabolism					
PGN_0473	P vs T=1	0.463	0.290	0.175	0.151	0.006
	PS vs T=1	0.425	0.297	0.467	0.692	0.656
	PS vs P	-0.032	0.001	0.276	0.518	0.627
	conserved hypothetical protein					
	regulatory functions					
PGN_0474	P vs T=1	-0.415	0.370	0.508	0.596	3.596
	PS vs T=1	-0.215	-0.129	0.730	0.895	1.159
	PS vs P	-0.245	-0.214	0.164	0.121	-0.172
	hypothetical protein					
	hypothetical proteins					
PGN_0475	P vs T=1	0.814	0.402	0.515	2.830	3.588
	PS vs T=1	0.921	1.223	0.968	1.768	2.410
	PS vs P	0.048	0.423	-0.163	-0.249	-0.568
	hypothetical protein					
	hypothetical proteins					
PGN_0476	P vs T=1	0.572	0.786	0.883	1.008	0.539
	PS vs T=1	0.522	1.122	1.423	1.538	1.359
	PS vs P	-0.074	0.322	0.528	0.527	0.793
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0477	P vs T=1	0.766	1.027	1.268	1.383	1.156
	PS vs T=1	0.743	1.222	1.637	1.839	1.723
	PS vs P	-0.040	0.190	0.369	0.459	0.561
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0478	P vs T=1	0.446	0.499	0.683	0.801	1.287
	PS vs T=1	-0.153	-0.171	-0.075	-0.276	-0.049
	PS vs P	-0.526	-0.573	-0.607	-0.830	-1.067
	partial transposase in ISPg4					
PGN_0479	P vs T=1	0.351	-0.235	0.098	0.250	1.707
	PS vs T=1	-0.430	-0.339	-0.340	0.034	-0.579
	PS vs P	-0.521	-0.222	-0.347	-0.126	-1.103
	hypothetical protein					
	hypothetical proteins					
PGN_0480	P vs T=1	2.327	2.197	2.372	2.633	2.868
	PS vs T=1	-0.477	-0.262	0.749	0.864	1.496
	PS vs P	-2.302	-1.970	-1.281	-1.261	-0.998
	partial transposase in ISPg4					
PGN_0481	P vs T=1	1.621	1.339	1.574	1.548	1.166
	PS vs T=1	-1.232	-0.887	-0.078	0.268	0.607
	PS vs P	-2.615	-2.050	-1.506	-1.144	-0.503
	hypothetical protein					
	hypothetical proteins					
PGN_0482	P vs T=1	0.408	0.358	0.849	0.920	0.645
	PS vs T=1	-2.134	-1.975	-1.234	-0.712	-0.233
	PS vs P	-2.454	-2.244	-1.992	-1.531	-0.833
	probable immunoreactive 23 kDa antigen					
	cell envelope					
PGN_0483	P vs T=1	-0.135	0.083	0.513	0.616	0.347
	PS vs T=1	0.064	-0.066	-0.006	0.214	0.133
	PS vs P	0.181	-0.152	-0.490	-0.359	-0.207
	putative aldose 1-epimerase					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0484	P vs T=1	-0.169	0.399	0.514	0.176	-0.291
	PS vs T=1	0.570	0.746	0.202	-0.317	-0.393
	PS vs P	0.707	0.356	-0.287	-0.486	-0.119
	putative galactokinase					
	energy metabolism					
PGN_0485	P vs T=1	0.263	0.580	0.986	1.291	1.116
	PS vs T=1	0.327	1.054	1.279	1.515	1.574
	PS vs P	0.004	0.444	0.302	0.262	0.467
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0486	P vs T=1	2.121	2.644	2.899	3.161	3.250
	PS vs T=1	2.020	2.903	3.242	3.458	3.522
	PS vs P	-0.154	0.278	0.368	0.350	0.320
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0487	P vs T=1	0.612	0.777	0.620	0.646	0.624
	PS vs T=1	0.552	0.639	0.475	0.772	0.810
	PS vs P	-0.055	-0.110	-0.140	0.132	0.189
	FtsK/SpoIIIE family cell division protein					
	unknown function					
PGN_0488	P vs T=1	0.930	1.421	2.073	2.205	2.184
	PS vs T=1	1.264	1.365	1.618	1.717	1.737
	PS vs P	0.272	-0.050	-0.381	-0.405	-0.391
	conserved hypothetical protein					
	energy metabolism					
PGN_0489	P vs T=1	-0.610	-0.392	0.756	1.428	1.265
	PS vs T=1	0.033	0.470	0.656	0.800	0.967
	PS vs P	0.269	0.495	0.049	-0.148	-0.050
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0490	P vs T=1	-0.678	-0.103	0.610	1.016	1.122
	PS vs T=1	-0.602	-0.375	-0.005	0.537	0.785
	PS vs P	-0.021	-0.293	-0.574	-0.395	-0.286
	putative DNA-damage-inducible protein F					
	transport and binding proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0491 *ltp1*	P vs T=1	-0.624	-0.025	0.528	0.667	0.786
	PS vs T=1	-0.577	-0.238	0.045	0.052	0.215
	PS vs P	-0.076	-0.211	-0.398	-0.501	-0.484
	probable phosphotyrosine protein phosphatase					
	regulatory functions					
PGN_0492	P vs T=1	0.320	1.011	1.409	1.380	0.829
	PS vs T=1	-0.139	0.391	0.992	1.167	1.070
	PS vs P	-0.482	-0.596	-0.387	-0.188	0.233
	cation-transporting ATPase					
	transport and binding proteins					
PGN_0493	P vs T=1	0.962	1.621	1.983	1.963	1.272
	PS vs T=1	-0.118	0.855	1.635	1.679	1.586
	PS vs P	-1.076	-0.696	-0.277	-0.220	0.310
	hypothetical protein					
	hypothetical proteins					
PGN_0494	P vs T=1	0.049	0.274	0.544	1.147	3.893
	PS vs T=1	0.017	0.174	1.011	1.311	1.190
	PS vs P	-0.204	-0.122	0.255	0.260	-0.338
	hypothetical protein					
	hypothetical proteins					
PGN_0495	P vs T=1	0.008	0.000	-0.585	0.609	0.954
	PS vs T=1	0.255	0.592	0.937	1.206	1.107
	PS vs P	0.171	0.492	0.961	0.707	0.290
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0496	P vs T=1	-0.352	-0.095	0.020	-0.300	-0.622
	PS vs T=1	-0.766	-0.351	0.074	0.281	0.391
	PS vs P	-0.422	-0.244	0.071	0.556	0.975
	putative cytochrome B subunit					
	energy metabolism					
PGN_0497	P vs T=1	1.043	1.237	1.297	0.926	0.338
	PS vs T=1	0.553	0.401	0.147	0.020	-0.072
	PS vs P	-0.452	-0.774	-1.086	-0.873	-0.420
	fumarate reductase flavoprotein subunit					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

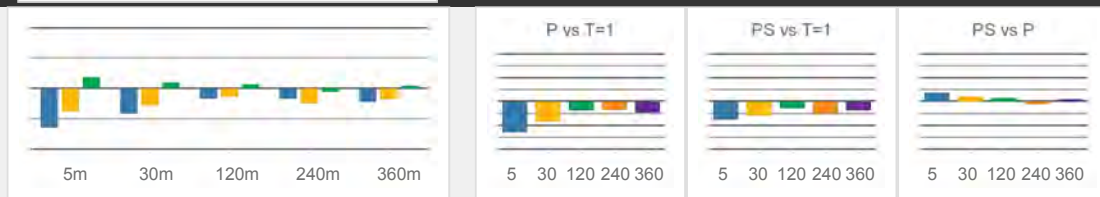
P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0498	P vs T=1	1.528	2.156	2.800	2.855	2.313
	PS vs T=1	0.717	1.113	1.200	1.192	1.271
	PS vs P	-0.810	-1.010	-1.549	-1.613	-1.025
	fumarate reductase iron-sulfur protein					
	energy metabolism					
PGN_0499	P vs T=1	-1.490	-1.515	-1.931	-2.314	-3.012
	PS vs T=1	-1.359	-1.012	-0.646	-0.616	-1.076
	PS vs P	0.108	0.478	1.211	1.554	1.742
	conserved hypothetical protein					
	unknown function					
PGN_0500	P vs T=1	0.624	0.945	0.528	-0.179	-0.824
	PS vs T=1	0.908	0.993	0.713	0.570	0.175
	PS vs P	0.285	0.084	0.197	0.705	0.941
	methylmalonyl-CoA decarboxylase alpha subunit					
	energy metabolism					
PGN_0501	P vs T=1	0.347	0.305	0.229	-0.134	-0.664
	PS vs T=1	0.545	0.450	0.128	-0.107	-0.149
	PS vs P	0.211	0.156	-0.082	0.008	0.460
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0502	P vs T=1	1.278	1.686	1.950	1.475	0.653
	PS vs T=1	1.995	2.391	2.372	1.833	1.567
	PS vs P	0.640	0.699	0.486	0.335	0.785
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0503	P vs T=1	0.874	1.403	1.412	0.825	0.120
	PS vs T=1	1.337	1.685	1.683	1.292	0.846
	PS vs P	0.426	0.305	0.302	0.431	0.648
	putative biotin carboxyl carrier protein					
	energy metabolism					
PGN_0504	P vs T=1	-0.191	0.146	0.463	0.209	-0.434
	PS vs T=1	0.240	0.468	0.532	0.523	0.366
	PS vs P	0.357	0.307	0.109	0.309	0.728
	methylmalonyl-CoA decarboxylase beta subunit					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0505	P vs T=1	-1.272	-0.806	-0.339	-0.331	-0.440
	PS vs T=1	-0.737	-0.560	-0.258	-0.487	-0.343
	PS vs P	0.371	0.188	0.137	-0.103	0.086
	hypothetical protein					
	hypothetical proteins					
PGN_0506	P vs T=1	-0.513	-0.680	-0.024	0.472	0.026
	PS vs T=1	-1.066	-1.048	-0.385	0.001	-0.120
	PS vs P	-0.499	-0.427	-0.156	0.012	-0.010
	hypothetical protein					
	hypothetical proteins					
PGN_0507	P vs T=1	-0.301	-1.064	-0.663	-0.200	0.420
	PS vs T=1	-0.933	-0.549	0.599	0.878	0.893
	PS vs P	-0.571	0.287	1.112	1.043	0.564
	putative ion transporter					
	transport and binding proteins					
PGN_0508	P vs T=1	1.473	1.611	1.493	1.184	0.647
	PS vs T=1	2.138	1.908	1.211	0.654	0.467
	PS vs P	0.679	0.335	-0.236	-0.504	-0.195
	putative aminopeptidase					
	protein fate					
PGN_0509	P vs T=1	-0.221	-0.423	-1.202	-1.558	-1.297
	PS vs T=1	-0.307	-0.769	-1.350	-1.505	-1.551
	PS vs P	-0.067	-0.327	-0.159	0.010	-0.260
	immunoreactive 84 kDa antigen					
	cell envelope					
PGN_0510	P vs T=1	0.135	-0.866	-1.986	-1.890	-1.388
	PS vs T=1	-0.559	-0.635	-0.609	-0.751	-1.246
	PS vs P	-0.584	0.226	1.162	0.944	0.115
	probable xanthosine triphosphate pyrophosphatase					
	unknown function					
PGN_0511	P vs T=1	0.092	-0.701	-1.037	-1.220	-1.462
	PS vs T=1	-0.227	-0.369	-0.317	-0.647	-0.743
	PS vs P	-0.218	0.287	0.640	0.449	0.592
	conserved hypothetical protein					
	unknown function					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0512	P vs T=1	0.298	-0.326	-0.684	-0.629	-0.587
	PS vs T=1	0.373	-0.141	-0.106	-0.315	-0.519
	PS vs P	0.110	0.172	0.524	0.272	0.050
	probable biotin--acetyl-CoA-carboxylase ligase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0513	P vs T=1	-0.383	-1.121	-1.734	-1.519	-0.899
	PS vs T=1	-0.027	-0.463	-0.723	-1.171	-1.330
	PS vs P	0.387	0.626	0.886	0.269	-0.405
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0514	P vs T=1	-0.714	-1.355	-1.998	-2.251	-2.122
	PS vs T=1	-0.249	-0.639	-1.650	-2.133	-2.204
	PS vs P	0.493	0.699	0.286	0.003	-0.130
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0515	P vs T=1	-0.804	-1.443	-2.055	-2.218	-2.371
	PS vs T=1	-0.509	-0.933	-1.856	-2.728	-2.614
	PS vs P	0.323	0.498	0.148	-0.577	-0.306
	probable lipoprotein signal peptidase					
	protein fate					
PGN_0516	P vs T=1	-0.478	-0.048	-0.114	-0.765	-1.839
	PS vs T=1	0.074	0.373	0.071	-0.601	-1.212
	PS vs P	0.529	0.431	0.204	0.138	0.531
	putative DnaK suppressor protein					
	DNA metabolism					
PGN_0517	P vs T=1	0.490	0.390	-0.356	-0.712	-1.035
	PS vs T=1	0.914	0.208	-0.718	-0.955	-0.924
	PS vs P	0.443	-0.159	-0.366	-0.262	0.088
	isoleucyl-tRNA synthetase					
	protein synthesis					
PGN_0518	P vs T=1	0.125	0.140	0.112	0.038	-0.121
	PS vs T=1	0.293	0.180	0.144	0.424	0.333
	PS vs P	0.153	0.029	0.014	0.344	0.404
	putative ribulose-phosphate 3-epimerase					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

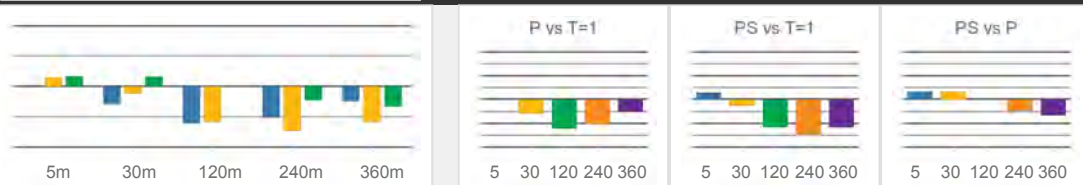
Locus		5m	30m	120m	240m	360m
PGN_0519	P vs T=1	-0.216	-0.703	-0.443	-0.127	0.785
	PS vs T=1	0.379	-0.181	-0.531	-0.403	-0.074
	PS vs P	0.587	0.431	-0.144	-0.267	-0.749
	probable competence protein					
	cellular processes					
PGN_0520	P vs T=1	-0.845	-1.174	-1.705	-1.702	-1.211
	PS vs T=1	-0.846	-1.370	-1.693	-2.222	-1.695
	PS vs P	0.042	-0.180	-0.097	-0.615	-0.432
	probable shikimate kinase					
	central intermediary metabolism					
PGN_0521	P vs T=1	-0.229	-0.641	-1.346	-1.344	-0.912
	PS vs T=1	-0.514	-0.955	-1.056	-1.251	-1.451
	PS vs P	-0.256	-0.300	0.253	0.057	-0.526
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0522	P vs T=1	0.934	1.027	0.983	1.567	1.662
	PS vs T=1	0.676	0.361	0.436	0.902	0.993
	PS vs P	-0.230	-0.611	-0.532	-0.521	-0.574
	putative dihydropteroate synthase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0523	P vs T=1	-0.481	-0.497	-0.372	-0.247	-0.336
	PS vs T=1	-0.072	-0.449	-0.708	-0.307	-0.418
	PS vs P	0.392	0.032	-0.329	-0.026	-0.078
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0524	P vs T=1	-0.780	-1.742	-1.894	-1.319	-0.995
	PS vs T=1	-0.289	-1.013	-1.579	-1.655	-1.404
	PS vs P	0.513	0.646	0.179	-0.329	-0.386
	lipid A 4'-phosphatase					
	unknown function					
PGN_0525	P vs T=1	-0.589	-1.202	-1.759	-1.601	-1.272
batE	PS vs T=1	-0.102	-0.701	-1.652	-2.131	-2.162
	PS vs P	0.512	0.486	0.037	-0.552	-0.867
	probable aerotolerance-related exported protein BatE					
	cellular processes					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0526 *batD*	P vs T=1	0.009	-0.564	-1.200	-1.013	-0.484
	PS vs T=1	0.297	-0.236	-1.151	-1.446	-1.149
	PS vs P	0.331	0.325	-0.002	-0.446	-0.636
	aerotolerance-related exported protein BatD					
	cellular processes					
PGN_0527 *batC*	P vs T=1	0.486	0.081	-0.340	-0.043	-0.084
	PS vs T=1	1.076	0.785	0.136	-0.505	-0.536
	PS vs P	0.605	0.694	0.442	-0.445	-0.444
	probable aerotolerance-related exported protein BatC					
	cellular processes					
PGN_0528 *batB*	P vs T=1	0.158	-0.264	-0.957	-0.975	-0.904
	PS vs T=1	0.128	-0.115	-0.908	-1.280	-1.063
	PS vs P	0.021	0.167	0.015	-0.325	-0.165
	putative aerotolerance-related exported protein BatB					
	cellular processes					
PGN_0529 *batA*	P vs T=1	0.225	-0.082	-0.504	-0.326	-0.392
	PS vs T=1	0.105	-0.209	-0.642	-0.947	-0.610
	PS vs P	-0.085	-0.113	-0.155	-0.606	-0.217
	aerotolerance-related membrane protein BatA					
	cellular processes					
PGN_0530	P vs T=1	0.377	0.112	-0.408	-0.284	-0.147
	PS vs T=1	0.288	0.030	-0.338	-0.673	-0.183
	PS vs P	-0.063	-0.069	0.048	-0.389	-0.031
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0531	P vs T=1	0.406	0.440	0.217	0.217	0.096
	PS vs T=1	0.399	0.505	0.353	0.098	0.193
	PS vs P	-0.000	0.073	0.134	-0.117	0.094
	putative von Willebrand factor type A					
	hypothetical proteins-Conserved					
PGN_0532	P vs T=1	1.499	1.668	1.348	1.361	1.274
	PS vs T=1	1.391	1.993	1.882	1.370	1.391
	PS vs P	-0.096	0.349	0.527	0.014	0.117
	magnesium chelatase subunit I					
	unknown function					

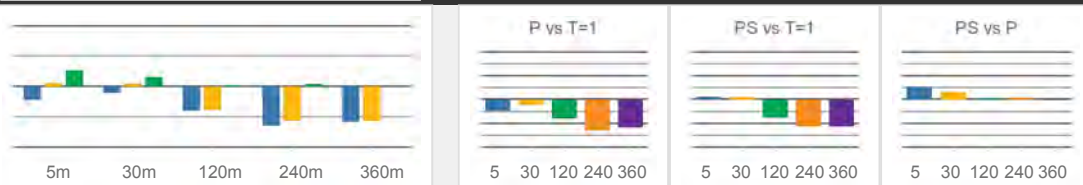


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0533	P vs T=1	-0.436	-0.199	-0.771	-1.268	-1.137
	PS vs T=1	0.096	0.083	-0.738	-1.113	-1.106
	PS vs P	0.526	0.306	0.025	0.070	0.003
	putative quinolinate synthetase complex subunit A					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0534	P vs T=1	-0.307	-0.135	-0.916	-1.411	-1.486
	PS vs T=1	0.082	-0.089	-0.929	-1.303	-1.222
	PS vs P	0.396	0.077	-0.030	-0.019	0.187
	putative nicotinate-nucleotide pyrophosphorylase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0535	P vs T=1	-1.035	-0.989	-1.043	-1.108	-1.254
	PS vs T=1	-0.788	-1.155	-1.717	-1.741	-1.627
	PS vs P	0.242	-0.157	-0.657	-0.616	-0.380
	L-aspartate oxidase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0536	P vs T=1	-0.541	-0.177	0.910	1.293	1.176
	PS vs T=1	-1.911	-1.857	-0.938	-0.538	-0.086
	PS vs P	-1.308	-1.470	-1.470	-1.309	-0.967
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0537	P vs T=1	-0.239	0.236	0.258	-0.378	-0.997
	PS vs T=1	-0.816	-0.392	-0.057	-0.165	-0.485
	PS vs P	-0.584	-0.539	-0.239	0.163	0.403
	probable transcriptional regulator Crp family					
	regulatory functions					
PGN_0538	P vs T=1	-0.490	-0.466	-0.186	0.556	1.221
	PS vs T=1	-0.368	-0.528	0.135	0.282	0.568
	PS vs P	0.069	-0.124	0.238	-0.142	-0.513
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0539	P vs T=1	0.593	0.861	1.174	1.857	2.601
	PS vs T=1	1.321	1.247	1.538	1.640	1.691
	PS vs P	0.636	0.334	0.323	-0.084	-0.744
	metallo-beta-lactamase superfamily protein					
	unknown function					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0540	P vs T=1	0.139	0.680	1.633	1.662	1.449
	PS vs T=1	0.188	0.594	1.119	0.969	0.994
	PS vs P	-0.069	-0.098	-0.334	-0.490	-0.353
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0541	P vs T=1	-0.903	-0.232	0.427	0.227	2.274
	PS vs T=1	-0.229	0.026	0.902	1.088	1.441
	PS vs P	-0.144	-0.064	0.390	0.345	0.135
	hypothetical protein					
	hypothetical proteins					
PGN_0542	P vs T=1	-0.330	-0.273	0.185	0.341	0.533
	PS vs T=1	-0.184	-0.119	0.762	0.814	0.933
	PS vs P	0.048	0.052	0.575	0.493	0.456
	partial transposase in ISPg2					
PGN_0543	P vs T=1	-0.122	-0.463	-1.236	-1.609	-1.452
	PS vs T=1	-0.362	-0.874	-0.882	-0.917	-1.182
	PS vs P	-0.215	-0.394	0.328	0.609	0.242
	glutamyl-tRNA synthetase					
	protein synthesis					
PGN_0544	P vs T=1	-0.634	-0.881	-1.318	-1.128	-0.534
	PS vs T=1	-0.297	-0.650	-0.959	-1.066	-0.969
	PS vs P	0.344	0.223	0.284	0.022	-0.395
	3-deoxy-D-manno-octulosonic-acid transferase					
	cell envelope					
PGN_0545	P vs T=1	-0.898	-1.757	-2.613	-2.230	-1.331
	PS vs T=1	-0.534	-1.423	-2.560	-2.776	-2.421
	PS vs P	0.402	0.323	-0.068	-0.579	-1.038
	putative sulfatase					
	cell envelope					
PGN_0546	P vs T=1	-0.550	-1.002	-1.303	-1.236	-1.390
	PS vs T=1	-0.350	-0.600	-0.547	-0.552	-0.719
	PS vs P	0.209	0.366	0.691	0.627	0.618
	glucose-1-phosphate thymidylyltransferase					
	cell envelope					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

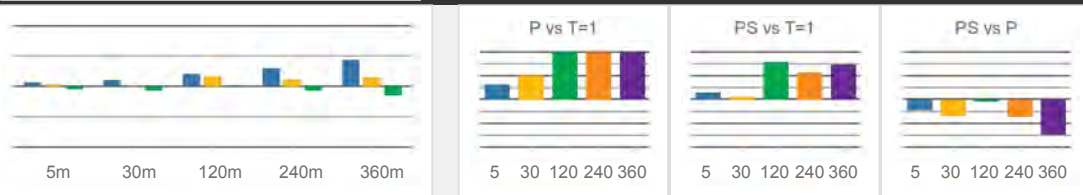
Locus		5m	30m	120m	240m	360m
PGN_0547	P vs T=1	-0.233	-1.129	-1.684	-1.813	-1.476
	PS vs T=1	0.236	-0.343	-0.631	-0.816	-1.089
	PS vs P	0.497	0.753	0.961	0.855	0.353
	dTDP-4-dehydrorhamnose 3,5-epimerase					
	cell envelope					
PGN_0548	P vs T=1	-1.195	-1.515	-2.249	-2.254	-1.906
	PS vs T=1	-0.201	-0.818	-1.597	-1.961	-1.675
	PS vs P	0.991	0.674	0.503	0.121	0.186
	putative dTDP-4-dehydrorhamnose reductase					
	cell envelope					
PGN_0549	P vs T=1	-0.651	-0.592	-1.024	-1.588	-1.573
	PS vs T=1	0.554	0.304	-0.587	-1.324	-1.519
	PS vs P	1.192	0.892	0.424	0.164	0.008
	dTDP-glucose 4,6-dehydratase					
	cell envelope					
PGN_0550	P vs T=1	0.508	0.945	1.277	1.271	0.606
	PS vs T=1	1.056	1.289	1.329	0.828	0.496
	PS vs P	0.522	0.344	0.071	-0.420	-0.118
	aminomethyltransferase					
	energy metabolism					
PGN_0551	P vs T=1	0.493	0.353	1.846	2.751	4.024
	PS vs T=1	-0.686	0.462	2.197	2.314	2.691
	PS vs P	-0.981	-0.241	0.619	0.284	-0.160
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0552	P vs T=1	0.154	-0.143	1.927	2.677	4.374
	PS vs T=1	-0.055	-0.048	2.120	2.707	2.722
	PS vs P	-0.368	-0.432	0.646	0.717	-0.102
	hypothetical protein					
	hypothetical proteins					
PGN_0553	P vs T=1	0.568	0.922	0.844	2.811	4.055
	PS vs T=1	-0.120	-0.384	0.269	1.948	1.371
	PS vs P	-0.582	-0.788	-0.662	0.176	-1.245
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0554	P vs T=1	0.627	1.016	2.057	3.028	4.350
	PS vs T=1	0.286	0.102	1.580	1.126	1.461
	PS vs P	-0.427	-0.667	-0.076	-0.692	-1.454
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0555	P vs T=1	0.197	0.566	1.319	2.768	4.223
	PS vs T=1	0.219	0.614	1.342	1.704	2.544
	PS vs P	-0.318	-0.157	-0.038	-0.259	-0.731
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0556	P vs T=1	0.785	0.433	0.708	1.446	2.566
CobNST	PS vs T=1	0.130	-0.321	0.349	0.929	1.390
	PS vs P	-0.624	-0.755	-0.376	-0.425	-1.069
	putative cobalamin biosynthesis-related protein					
	biosynthesis of cofactors, prosthetic groups, and carriers/ unknown					
PGN_0557	P vs T=1	0.537	0.556	1.241	1.653	2.469
hmuR	PS vs T=1	-0.425	-0.139	0.985	1.505	1.653
	PS vs P	-0.940	-0.695	-0.195	-0.032	-0.654
	TonB-dependent receptor HmuR					
	transport and binding proteins					
PGN_0558	P vs T=1	2.308	2.092	2.224	2.268	2.627
	PS vs T=1	-0.480	-0.191	0.389	0.292	0.760
	PS vs P	-2.516	-2.040	-1.627	-1.693	-1.638
	conserved hypothetical protein					
	transport and binding proteins					
PGN_0559	P vs T=1	-0.097	0.228	1.529	1.825	2.423
	PS vs T=1	-0.841	-0.423	0.502	1.262	1.731
	PS vs P	-0.781	-0.569	-0.380	0.091	0.084
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0560	P vs T=1	-0.602	-0.928	-0.189	0.032	0.467
	PS vs T=1	-0.575	-1.017	0.770	0.964	1.179
	PS vs P	-0.131	-0.437	0.846	0.822	0.821
	hypothetical protein					
	hypothetical proteins					

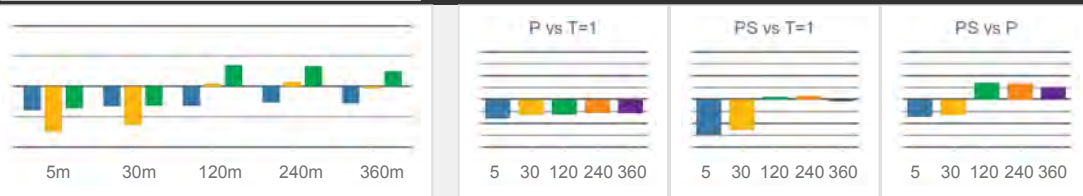


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

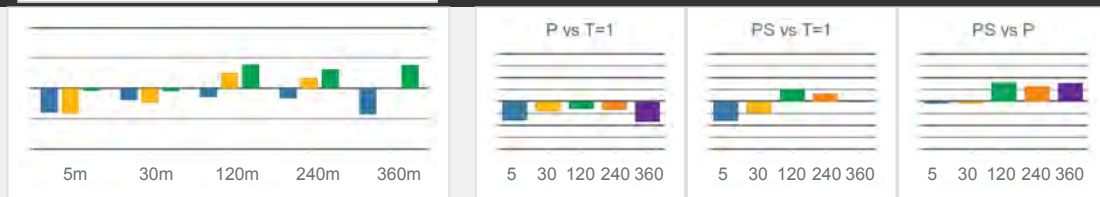
Locus		5m	30m	120m	240m	360m
PGN_0561 *prtT*	P vs T=1	-0.763	-0.628	-0.613	-0.521	-0.554
	PS vs T=1	-1.469	-1.257	0.094	0.147	-0.057
	PS vs P	-0.705	-0.619	0.702	0.666	0.493
	trypsin like proteinase PrtT					
	protein fate					
PGN_0562	P vs T=1	0.965	2.066	2.758	2.817	2.205
	PS vs T=1	-0.535	2.020	4.409	4.309	4.014
	PS vs P	-1.606	-0.006	1.711	1.532	1.754
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0563	P vs T=1	-0.285	0.528	1.526	1.601	0.952
	PS vs T=1	-1.601	0.364	2.294	2.374	2.355
	PS vs P	-1.403	-0.173	0.835	0.825	1.369
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0564 *sod*	P vs T=1	0.653	1.448	1.900	1.715	1.028
	PS vs T=1	-0.442	1.381	2.904	3.046	2.824
	PS vs P	-1.128	-0.044	1.033	1.333	1.763
	superoxide dismutase Fe-Mn					
	cellular processes					
PGN_0565	P vs T=1	0.640	0.636	0.114	0.329	1.148
	PS vs T=1	1.607	1.688	1.527	1.027	0.845
	PS vs P	0.931	1.014	1.233	0.562	-0.242
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0566	P vs T=1	-0.691	-0.597	-0.493	-0.456	-0.762
	PS vs T=1	0.088	0.371	0.624	0.317	0.168
	PS vs P	0.727	0.922	1.089	0.750	0.886
	probable thioesterase protein					
	hypothetical proteins-Conserved					
PGN_0567 *prtC*	P vs T=1	-0.070	-0.204	-0.254	-0.069	0.021
	PS vs T=1	0.795	0.744	0.678	0.470	0.159
	PS vs P	0.838	0.903	0.885	0.521	0.136
	collagenase					
	protein fate					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0568	P vs T=1	-0.770	-0.376	-0.283	-0.320	-0.833
	PS vs T=1	-0.798	-0.462	0.516	0.329	0.007
	PS vs P	-0.077	-0.087	0.790	0.633	0.774
	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0569	P vs T=1	0.736	1.370	1.498	1.334	0.641
	PS vs T=1	0.185	1.319	2.702	2.791	2.540
	PS vs P	-0.583	-0.031	1.209	1.439	1.846
	S-adenosylmethionine:tRNA ribosyltransferase-isomerase					
	protein synthesis					
PGN_0570	P vs T=1	0.716	0.612	0.528	0.168	0.490
	PS vs T=1	0.802	1.094	1.216	1.111	0.999
	PS vs P	0.088	0.463	0.665	0.818	0.490
	putative tRNA pseudouridine synthase B					
	protein synthesis					
PGN_0571	P vs T=1	-0.053	-0.294	-0.604	-0.369	0.368
	PS vs T=1	0.135	-0.159	-0.757	-0.699	-0.746
	PS vs P	0.216	0.133	-0.213	-0.313	-0.982
	putative undecaprenol kinase					
	cellular processes					
PGN_0572	P vs T=1	-0.624	-0.517	-0.944	-1.469	-1.076
	PS vs T=1	-0.742	-0.900	-1.459	-1.408	-1.457
	PS vs P	-0.090	-0.314	-0.490	-0.136	-0.378
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0573	P vs T=1	0.071	0.079	-0.468	-0.554	-0.323
	PS vs T=1	0.086	-0.109	-0.459	-0.694	-0.345
	PS vs P	0.023	-0.173	-0.014	-0.176	-0.022
	putative cell division protein FtsX					
	cellular processes					
PGN_0574	P vs T=1	-0.492	-0.402	0.295	1.075	1.646
	PS vs T=1	-0.029	0.767	1.861	2.011	2.149
	PS vs P	0.194	0.840	1.342	0.941	0.586
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

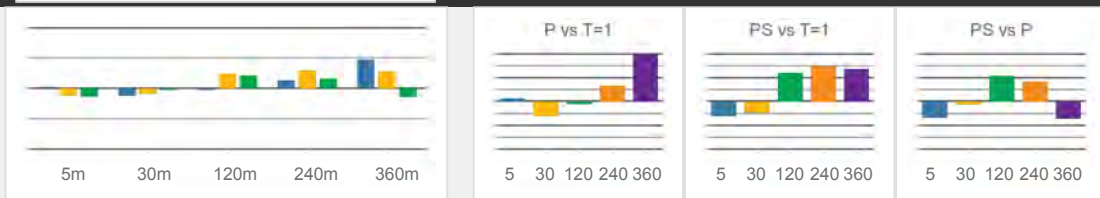
log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0575	P vs T=1	0.537	0.458	0.535	0.639	0.375
	PS vs T=1	0.329	0.162	0.374	0.345	0.327
	PS vs P	-0.206	-0.302	-0.167	-0.290	-0.062
	transposase in ISPg1					
PGN_0576	P vs T=1	0.244	-0.344	-0.005	0.712	1.735
	PS vs T=1	1.064	0.675	0.727	0.490	0.662
	PS vs P	0.672	0.417	0.369	0.004	-0.235
	hypothetical protein					
	hypothetical proteins					
PGN_0577	P vs T=1	0.337	0.302	0.311	0.459	0.117
	PS vs T=1	0.172	-0.042	0.069	0.187	0.206
	PS vs P	-0.164	-0.346	-0.249	-0.266	0.071
	transposase in ISPg1					
PGN_0578	P vs T=1	1.113	0.643	0.766	1.477	1.766
	PS vs T=1	0.927	0.496	1.238	1.125	1.408
	PS vs P	-0.149	-0.227	0.319	-0.229	-0.246
	conserved hypothetical protein found in conjugate transposon					
	hypothetical proteins-Conserved					
PGN_0579	P vs T=1	0.932	0.158	0.424	1.024	1.990
	PS vs T=1	0.961	0.848	1.264	1.227	1.236
	PS vs P	0.065	0.486	0.672	0.212	-0.583
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0580	P vs T=1	-0.557	-1.439	-1.712	-1.587	-0.341
	PS vs T=1	0.071	0.247	0.359	0.282	-0.107
	PS vs P	0.577	1.224	1.606	1.446	0.282
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0581	P vs T=1	-0.038	-0.735	0.041	0.984	2.797
	PS vs T=1	-0.896	-0.083	1.101	1.214	1.487
	PS vs P	-0.817	0.199	0.845	0.369	-0.773
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0582	P vs T=1	0.117	-0.592	-0.096	0.652	2.384
	PS vs T=1	-0.584	-0.435	1.198	1.483	1.369
	PS vs P	-0.656	-0.114	1.073	0.820	-0.691
	DNA topoisomerase I					
	DNA metabolism					
PGN_0583	P vs T=1	-1.173	-2.102	-2.818	-3.035	-1.914
	PS vs T=1	-0.820	-1.217	-1.789	-1.786	-1.821
	PS vs P	0.452	0.652	0.624	0.716	0.078
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0584	P vs T=1	-0.298	-1.217	-1.033	0.102	1.535
	PS vs T=1	-0.342	-0.547	-0.036	0.149	0.631
	PS vs P	-0.021	0.402	0.669	0.128	-0.678
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0585	P vs T=1	0.302	-0.340	-0.220	0.385	1.680
	PS vs T=1	-0.099	0.012	0.326	0.761	0.695
	PS vs P	-0.369	0.224	0.382	0.354	-0.828
	transposase in ISPg3					
PGN_0586	P vs T=1	0.518	-0.300	0.883	1.856	3.540
	PS vs T=1	-0.063	0.280	0.809	1.611	1.603
	PS vs P	-0.515	-0.004	-0.098	0.143	-1.163
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0587	P vs T=1	0.271	0.221	0.273	0.339	-0.004
	PS vs T=1	0.060	-0.123	-0.052	0.068	0.104
	PS vs P	-0.209	-0.346	-0.329	-0.268	0.085
	transposase in ISPg1					
PGN_0588	P vs T=1	1.868	1.746	1.498	1.552	1.976
	PS vs T=1	1.805	1.574	1.560	1.370	1.285
	PS vs P	-0.035	-0.154	0.039	-0.191	-0.635
	conserved hypothetical protein					
	hypothetical proteins-Conserved					

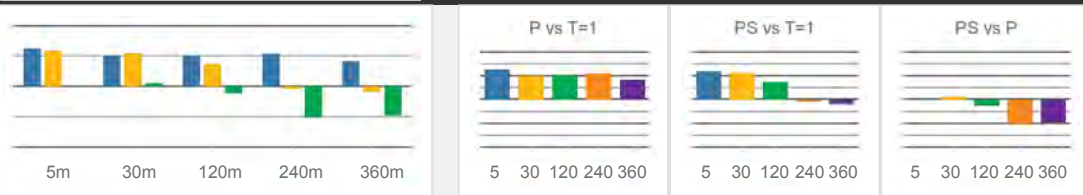


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

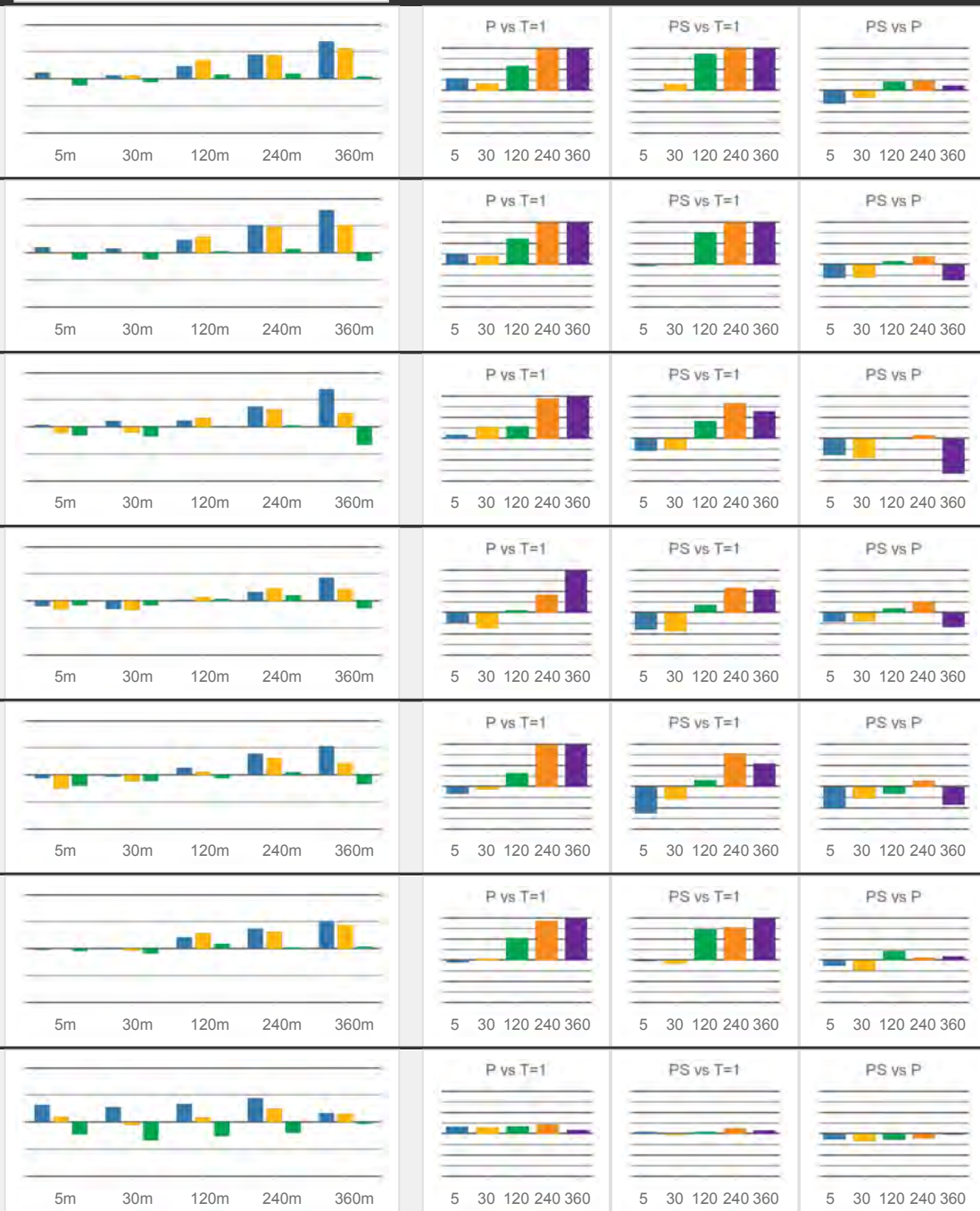
Locus		5m	30m	120m	240m	360m
PGN_0589	P vs T=1	1.258	1.002	1.005	1.080	0.830
	PS vs T=1	1.188	1.098	0.741	-0.078	-0.178
	PS vs P	-0.005	0.105	-0.224	-1.004	-0.933
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0590	P vs T=1	-0.255	-0.522	-0.364	-0.382	-0.963
	PS vs T=1	-0.544	-0.414	-0.250	-0.136	-0.299
	PS vs P	-0.281	0.093	0.111	0.243	0.635
	putative Fic family protein					
	unknown function					
PGN_0591	P vs T=1	-0.463	-0.947	-0.916	-0.997	-0.932
	PS vs T=1	-0.369	-0.019	0.470	0.718	0.636
	PS vs P	0.045	0.647	1.152	1.416	1.360
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0592 *traQ*	P vs T=1	-0.006	0.309	1.245	1.089	2.016
	PS vs T=1	0.574	1.108	1.463	1.815	1.557
	PS vs P	0.403	0.653	0.306	0.676	-0.290
	putative conserved protein found in conjugate transposon TraQ					
	mobile and extrachromosomal element functions					
PGN_0593 *traO*	P vs T=1	0.899	1.015	1.856	2.369	2.998
	PS vs T=1	1.314	1.792	2.392	2.537	2.573
	PS vs P	0.250	0.570	0.538	0.320	-0.203
	putative conserved protein found in conjugate transposon TraO					
	mobile and extrachromosomal element functions					
PGN_0594 *traN*	P vs T=1	0.506	0.870	1.840	2.384	3.176
	PS vs T=1	0.752	1.119	2.179	2.478	2.505
	PS vs P	0.061	0.114	0.388	0.271	-0.445
	conserved protein found in conjugate transposon TraN					
	other categories					
PGN_0595 *traM*	P vs T=1	0.412	0.477	1.301	2.473	3.394
	PS vs T=1	0.271	0.732	1.367	1.625	2.182
	PS vs P	-0.267	0.064	0.038	-0.448	-0.851
	putative conserved protein found in conjugate transposon TraM					
	mobile and extrachromosomal element functions					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0596	P vs T=1	0.570	0.318	1.162	2.254	3.449
	PS vs T=1	-0.050	0.311	1.740	2.229	2.829
	PS vs P	-0.577	-0.309	0.414	0.461	0.235
	conserved hypothetical protein found in conjugate transposon					
	hypothetical proteins-Conserved					
PGN_0597 *traK*	P vs T=1	0.497	0.397	1.210	2.557	3.992
	PS vs T=1	-0.060	-0.029	1.511	2.417	2.603
	PS vs P	-0.602	-0.580	0.160	0.379	-0.715
	putative conserved protein found in conjugate transposon TraK					
	mobile and extrachromosomal element functions					
PGN_0598 *traJ*	P vs T=1	0.171	0.546	0.569	1.883	3.495
	PS vs T=1	-0.554	-0.498	0.825	1.659	1.291
	PS vs P	-0.756	-0.890	0.029	0.159	-1.620
	conserved transmembrane protein found in conjugate transposon TraJ					
	other categories					
PGN_0599 *traI*	P vs T=1	-0.462	-0.718	0.107	0.842	2.153
	PS vs T=1	-0.771	-0.850	0.371	1.171	1.086
	PS vs P	-0.392	-0.387	0.200	0.518	-0.659
	putative conserved protein found in conjugate transposon TraI					
	mobile and extrachromosomal element functions					
PGN_0600	P vs T=1	-0.298	-0.137	0.640	1.983	2.662
	PS vs T=1	-1.229	-0.574	0.309	1.565	1.083
	PS vs P	-0.977	-0.531	-0.301	0.261	-0.824
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0601	P vs T=1	-0.110	0.071	1.044	1.874	2.545
	PS vs T=1	-0.037	-0.166	1.466	1.556	2.232
	PS vs P	-0.230	-0.449	0.436	0.126	0.173
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0602	P vs T=1	0.318	0.279	0.338	0.446	0.170
	PS vs T=1	0.092	-0.048	0.089	0.246	0.153
	PS vs P	-0.225	-0.331	-0.254	-0.197	-0.032
	transposase in ISPg1					



PgSg Time Course

log$_2$ (Fold Change)

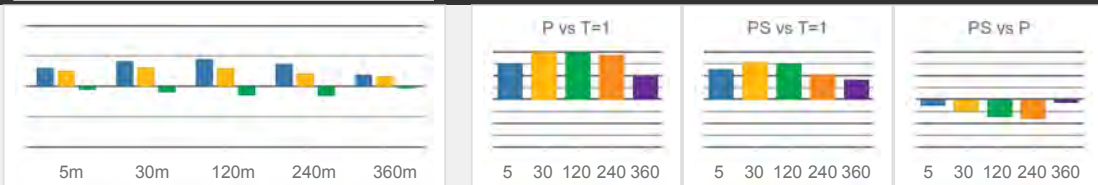
Locus		5m	30m	120m	240m	360m
PGN_0603	P vs T=1	-0.917	-0.237	0.159	0.727	0.040
	PS vs T=1	-1.019	-1.067	-0.998	-0.098	-0.692
	PS vs P	-0.349	-0.628	-0.836	-0.200	-0.548
	hypothetical protein					
	hypothetical proteins					
PGN_0604	P vs T=1	1.541	2.151	2.327	2.009	1.339
	PS vs T=1	0.947	2.085	2.891	2.466	2.071
	PS vs P	-0.599	-0.042	0.588	0.462	0.717
	ferritin					
	transport and binding proteins					
PGN_0605	P vs T=1	0.190	0.115	0.183	0.202	-0.065
	PS vs T=1	0.001	-0.189	-0.050	-0.010	0.005
	PS vs P	-0.188	-0.308	-0.236	-0.214	0.051
	transposase in ISPg1					
PGN_0606	P vs T=1	0.252	0.574	0.661	1.165	1.706
	PS vs T=1	0.594	0.582	0.338	0.145	0.551
	PS vs P	0.282	0.012	-0.326	-0.887	-1.012
	glucosamine-6-phosphate isomerase					
	central intermediary metabolism					
PGN_0607	P vs T=1	0.847	1.289	1.228	0.806	0.178
dpp11	PS vs T=1	1.111	0.902	0.531	0.224	-0.061
	PS vs P	0.263	-0.366	-0.675	-0.574	-0.252
	dipeptidyl peptidase 11					
	protein fate					
PGN_0608	P vs T=1	-0.064	0.224	0.666	0.551	0.303
	PS vs T=1	0.076	0.247	0.727	0.992	0.900
	PS vs P	0.100	0.008	0.089	0.439	0.568
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0609	P vs T=1	-0.583	-0.407	-0.341	-0.387	-0.436
	PS vs T=1	-0.681	-0.282	0.204	0.829	0.490
	PS vs P	-0.144	0.100	0.512	1.151	0.878
	probable DNA mismatch repair protein					
	hypothetical proteins					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0610	P vs T=1	1.526	2.079	2.281	1.862	0.949
	PS vs T=1	1.280	1.569	1.514	1.053	0.823
	PS vs P	-0.240	-0.468	-0.718	-0.783	-0.140
	conserved hypothetical protein with DUF1015 domain					
	hypothetical proteins-Conserved					
PGN_0611	P vs T=1	1.423	1.768	1.466	0.780	-0.145
	PS vs T=1	1.048	1.261	1.155	0.668	0.339
	PS vs P	-0.339	-0.439	-0.264	-0.112	0.438
	D-3-phosphoglycerate dehydrogenase					
	unknown function					
PGN_0612	P vs T=1	-0.500	-0.525	-0.394	-0.731	-1.441
	PS vs T=1	-1.023	-1.063	-1.169	-1.279	-1.251
	PS vs P	-0.490	-0.506	-0.730	-0.528	0.165
	phosphoserine aminotransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0613	P vs T=1	-0.749	-1.972	-2.679	-2.215	-1.770
ugdA	PS vs T=1	-1.585	-1.609	-1.313	-1.106	-1.285
	PS vs P	-0.732	0.297	1.171	1.014	0.468
	UDP-glucose 6-dehydrogenase					
	cell envelope					
PGN_0614	P vs T=1	0.156	0.678	1.458	1.946	1.947
	PS vs T=1	-0.079	0.077	0.344	0.623	0.728
	PS vs P	-0.275	-0.589	-1.053	-1.222	-1.155
	DNA-binding protein histone-like family					
	DNA metabolism					
PGN_0615	P vs T=1	1.897	2.235	2.756	3.188	3.441
	PS vs T=1	1.171	1.516	1.822	2.587	2.775
	PS vs P	-0.590	-0.489	-0.604	-0.138	-0.238
	hypothetical protein					
	hypothetical proteins					
PGN_0616	P vs T=1	0.652	0.882	0.900	0.821	0.298
	PS vs T=1	0.503	0.562	0.738	0.915	0.911
	PS vs P	-0.146	-0.287	-0.137	0.109	0.578
	probable elongation factor P					
	protein synthesis					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0617	P vs T=1	-1.373	-1.252	-0.832	-0.355	0.237
	PS vs T=1	-1.069	-1.148	-0.965	-0.890	-0.605
	PS vs P	0.226	0.039	-0.153	-0.476	-0.760
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0618	P vs T=1	0.987	1.038	0.877	0.499	0.116
	PS vs T=1	0.944	0.805	0.528	0.386	0.208
	PS vs P	-0.026	-0.208	-0.329	-0.122	0.067
	aspartate-semialdehyde dehydrogenase					
	amino acid biosynthesis					
PGN_0619	P vs T=1	0.301	0.170	0.178	-0.017	0.501
	PS vs T=1	-0.211	-0.079	-0.409	-0.307	-0.161
	PS vs P	-0.433	-0.220	-0.533	-0.365	-0.494
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0620	P vs T=1	0.003	-0.209	-0.628	-0.614	-0.432
	PS vs T=1	0.586	0.146	-0.203	-0.052	-0.306
	PS vs P	0.580	0.342	0.371	0.497	0.105
	putative S-adenosyl-methyltransferase MraW					
	hypothetical proteins-Conserved					
PGN_0621	P vs T=1	-0.525	-0.649	-0.519	-0.782	-0.478
	PS vs T=1	-0.096	-0.480	-0.439	-0.463	-0.566
	PS vs P	0.390	0.104	0.059	0.170	-0.106
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0622	P vs T=1	-0.791	-0.859	-0.852	-0.810	-0.420
	PS vs T=1	-0.384	-0.815	-1.330	-1.478	-1.470
	PS vs P	0.403	0.039	-0.476	-0.657	-1.023
	penicillin-binding protein					
	cell envelope					
PGN_0623	P vs T=1	-0.614	-0.910	-1.992	-2.299	-2.011
	PS vs T=1	-0.205	-0.603	-2.167	-2.763	-2.783
	PS vs P	0.434	0.324	-0.228	-0.560	-0.792
	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate ligase					
	cell envelope					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0624	P vs T=1	0.329	0.259	-0.154	-0.372	-0.128
	PS vs T=1	0.873	0.629	-0.581	-1.100	-0.817
	PS vs P	0.555	0.382	-0.433	-0.750	-0.677
	phospho-N-acetylmuramoyl-pentapeptide- transferase					
	cell envelope					
PGN_0625	P vs T=1	-0.597	-0.987	-1.668	-1.950	-2.099
	PS vs T=1	-0.205	-0.299	-1.523	-2.054	-2.101
	PS vs P	0.410	0.683	0.107	-0.175	-0.059
	UDP-N-acetylmuramoylalanine--D-glutamate ligase					
	cell envelope					
PGN_0626	P vs T=1	-0.124	-0.660	-1.548	-1.750	-1.092
	PS vs T=1	0.353	0.276	-0.836	-1.470	-1.452
	PS vs P	0.516	0.919	0.593	0.106	-0.359
	putative rod shape-determining protein RodA					
	cellular processes					
PGN_0627	P vs T=1	0.136	-0.055	-0.580	-0.646	0.057
	PS vs T=1	0.815	0.728	-0.158	-0.409	-0.415
	PS vs P	0.676	0.762	0.331	0.116	-0.438
	N-acetylglucosaminyl transferase					
	cell envelope					
PGN_0628	P vs T=1	-0.627	-0.769	-1.828	-1.455	-0.735
	PS vs T=1	-0.203	-0.393	-1.247	-1.675	-1.821
	PS vs P	0.431	0.384	0.410	-0.282	-1.031
	UDP-N-acetylmuramate-alanine ligase					
	cell envelope					
PGN_0629	P vs T=1	0.490	-0.024	-0.465	-0.241	0.139
	PS vs T=1	1.035	0.726	-0.210	-0.402	-0.240
	PS vs P	0.582	0.711	0.148	-0.189	-0.336
	putative cell division protein FtsQ					
	cellular processes					
PGN_0630	P vs T=1	-0.090	-0.235	-0.459	-0.896	-1.357
	PS vs T=1	0.532	0.159	-0.317	-0.760	-1.083
	PS vs P	0.623	0.389	0.140	0.101	0.227
	probable cell division protein FtsA					
	cellular processes					

log$_2$ (Fold Change)

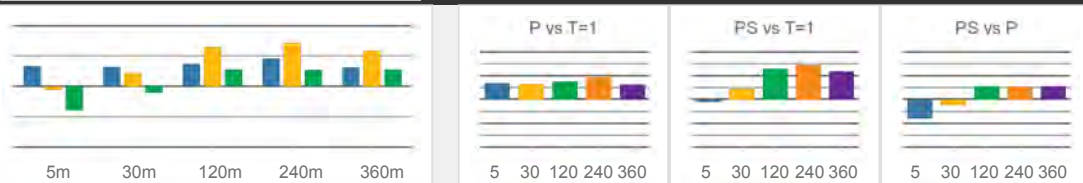
Locus		5m	30m	120m	240m	360m
PGN_0631	P vs T=1	-0.114	0.292	0.156	-0.460	-0.893
	PS vs T=1	0.748	0.858	0.297	-0.550	-0.966
	PS vs P	0.833	0.571	0.152	-0.123	-0.115
	putative cell division protein FtsZ					
	cellular processes					
PGN_0632	P vs T=1	0.212	0.879	1.154	0.934	0.284
	PS vs T=1	0.561	1.253	1.235	0.569	0.269
	PS vs P	0.303	0.380	0.109	-0.349	-0.037
	conserved hypothetical protein					
	unknown function					
PGN_0633	P vs T=1	-0.369	-0.666	-0.776	-0.822	0.073
	PS vs T=1	-0.121	-0.547	-0.728	-0.561	-0.267
	PS vs P	0.260	0.091	-0.003	0.154	-0.251
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0634	P vs T=1	-0.146	-0.007	0.007	0.001	0.377
	PS vs T=1	0.055	-0.281	-0.352	-0.453	-0.388
	PS vs P	0.189	-0.253	-0.336	-0.426	-0.690
	3-methyl-2-oxobutanoate hydroxymethyltransferase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0635	P vs T=1	-0.354	-0.214	-0.275	-0.475	-0.394
	PS vs T=1	-0.740	-1.004	-1.053	-0.515	-0.402
	PS vs P	-0.375	-0.761	-0.756	-0.044	-0.005
	glutamine-hydrolyzing GMP synthase					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0636	P vs T=1	-0.334	-0.742	-1.378	-1.623	-2.007
rpmE	PS vs T=1	-1.721	-1.536	-1.579	-1.549	-1.241
	PS vs P	-1.263	-0.723	-0.213	0.030	0.687
	50S ribosomal protein L31					
	protein synthesis					
PGN_0637	P vs T=1	1.518	2.221	2.723	2.943	2.673
	PS vs T=1	0.382	1.459	2.457	2.780	2.699
	PS vs P	-1.143	-0.699	-0.198	-0.088	0.060
	putative heat shock-related protease htrA protein					
	protein fate					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0638 *rpoD*	P vs T=1	0.670	0.647	0.747	0.913	0.621
	PS vs T=1	-0.103	0.436	1.297	1.442	1.184
	PS vs P	-0.763	-0.208	0.549	0.536	0.557
	RNA polymerase sigma factor RpoD					
	transcription					
PGN_0639 *rpsF*	P vs T=1	0.592	1.097	1.656	1.666	1.114
	PS vs T=1	0.054	0.823	1.715	1.869	1.787
	PS vs P	-0.568	-0.249	0.122	0.252	0.664
	30S ribosomal protein S6					
	protein synthesis					
PGN_0640 *rpsR*	P vs T=1	0.605	0.998	1.689	1.869	1.327
	PS vs T=1	0.023	0.724	1.814	1.939	1.822
	PS vs P	-0.602	-0.267	0.172	0.122	0.497
	30S ribosomal protein S18					
	protein synthesis					
PGN_0641 *rplI*	P vs T=1	0.290	0.645	1.376	1.656	1.188
	PS vs T=1	-0.240	0.332	1.180	1.228	1.283
	PS vs P	-0.547	-0.309	-0.154	-0.371	0.108
	50S ribosomal protein L9					
	protein synthesis					
PGN_0642	P vs T=1	-0.151	-0.021	0.096	0.134	0.297
	PS vs T=1	0.068	0.122	0.495	0.977	0.658
	PS vs P	0.202	0.132	0.387	0.824	0.358
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0643 *RibA*	P vs T=1	-0.106	0.546	1.325	1.550	1.137
	PS vs T=1	0.617	0.893	1.343	1.555	1.465
	PS vs P	0.676	0.332	0.033	0.026	0.327
	3,4-dihydroxy-2-butanone 4-phosphate synthase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0644	P vs T=1	0.443	0.362	0.456	0.624	0.244
	PS vs T=1	0.236	0.058	0.229	0.323	0.346
	PS vs P	-0.207	-0.310	-0.233	-0.293	0.085
	transposase in ISPg1					

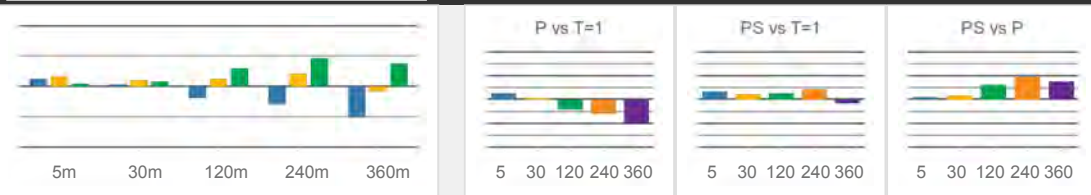


PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0645 *porQ*	P vs T=1	0.250	0.052	-0.387	-0.568	-0.990
	PS vs T=1	0.323	0.209	0.253	0.418	-0.162
	PS vs P	0.090	0.159	0.605	0.933	0.761
	Por secretion system protein porQ					
	hypothetical proteins					
PGN_0646	P vs T=1	-0.280	-0.227	-0.739	-1.057	-1.393
	PS vs T=1	-0.162	-0.260	-0.489	-0.692	-1.057
	PS vs P	0.127	-0.010	0.236	0.308	0.268
	probable cytidylate kinase					
	purines, pyrimidines, nucleosides and nucleotides					
PGN_0647	P vs T=1	-0.391	-0.473	-0.520	-0.490	-0.420
	PS vs T=1	0.023	-0.274	-0.689	-0.727	-0.602
	PS vs P	0.406	0.188	-0.182	-0.246	-0.185
	hydroxymethylbutenyl pyrophosphate reductase					
	cellular processes					
PGN_0648	P vs T=1	-0.666	-0.265	0.216	0.409	0.106
	PS vs T=1	-0.266	-0.343	-0.238	0.176	0.291
	PS vs P	0.315	-0.101	-0.424	-0.184	0.177
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0649	P vs T=1	0.205	-0.055	-0.084	-0.508	-1.408
	PS vs T=1	-1.083	-1.468	-2.009	-2.047	-1.808
	PS vs P	-1.082	-1.242	-1.743	-1.414	-0.474
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0650	P vs T=1	0.724	1.183	2.118	2.423	1.816
	PS vs T=1	-0.793	-0.609	-0.533	-0.188	-0.029
	PS vs P	-1.471	-1.704	-2.513	-2.456	-1.776
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0651	P vs T=1	1.140	1.383	1.192	1.182	1.505
	PS vs T=1	0.143	1.069	1.179	1.294	1.440
	PS vs P	-0.798	-0.110	0.049	0.155	0.151
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0652	P vs T=1	-0.214	-0.314	0.505	1.123	1.262
	PS vs T=1	-2.297	-1.519	-0.698	-0.348	0.259
	PS vs P	-1.874	-1.113	-0.983	-1.032	-0.743
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0653	P vs T=1	1.790	2.092	2.180	1.600	0.883
	PS vs T=1	1.343	1.751	1.653	1.114	1.025
	PS vs P	-0.387	-0.239	-0.401	-0.445	0.083
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0654	P vs T=1	0.903	1.427	1.367	0.532	-0.580
	PS vs T=1	0.743	1.157	1.094	0.363	-0.115
	PS vs P	-0.159	-0.205	-0.210	-0.188	0.376
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0655	P vs T=1	1.984	2.410	1.961	1.149	0.450
	PS vs T=1	1.874	2.264	1.871	0.946	0.619
	PS vs P	-0.093	-0.091	-0.057	-0.249	0.085
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0656	P vs T=1	1.415	1.889	1.663	0.926	0.178
	PS vs T=1	1.707	2.099	1.623	0.808	0.474
	PS vs P	0.282	0.265	0.006	-0.154	0.217
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0657	P vs T=1	-0.024	0.627	0.846	0.245	-0.734
	PS vs T=1	-0.055	0.325	0.179	-0.609	-0.931
	PS vs P	-0.055	-0.268	-0.615	-0.842	-0.238
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0658	P vs T=1	0.216	0.141	-0.095	0.133	0.393
	PS vs T=1	0.080	-0.280	-0.592	-0.445	-0.360
	PS vs P	-0.107	-0.390	-0.497	-0.534	-0.704
	GTP-binding elongation factor family protein TypA/BipA					
	unknown function					

PgSg Time Course

log$_2$ (Fold Change)

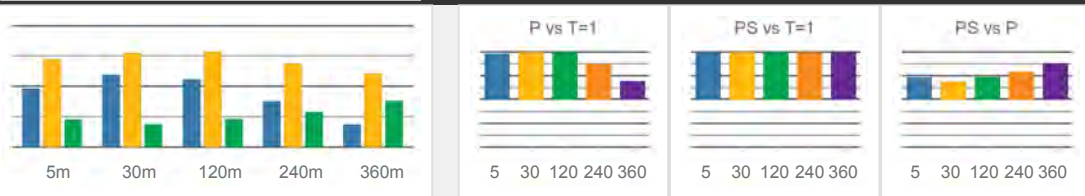
Locus		5m	30m	120m	240m	360m
PGN_0659	P vs T=1	-1.413	-1.818	-1.688	-2.032	-2.798
	PS vs T=1	-1.859	-1.770	-1.640	-1.643	-1.762
	PS vs P	-0.378	0.019	0.077	0.353	0.905
	35 kDa hemin binding protein					
	energy metabolism					
PGN_0660	P vs T=1	4.924	5.326	5.907	5.886	4.977
	PS vs T=1	3.733	4.696	4.483	4.020	3.802
	PS vs P	-1.119	-0.541	-1.303	-1.747	-1.136
	putative alkyl hydroperoxide reductase C subunit					
	cellular processes					
PGN_0661	P vs T=1	4.741	5.224	5.219	4.675	3.677
	PS vs T=1	4.033	4.848	3.910	3.207	2.849
	PS vs P	-0.560	-0.166	-1.096	-1.326	-0.816
	alkyl hydroperoxide reductase F subunit					
	cellular processes					
PGN_0662	P vs T=1	0.671	0.636	0.142	-0.211	-0.728
serB	PS vs T=1	0.686	0.354	-0.370	-0.634	-0.689
	PS vs P	0.031	-0.265	-0.505	-0.424	0.025
	HAD family serine phosphatase					
	cellular processes					
PGN_0663	P vs T=1	-0.497	-0.495	-1.121	-1.525	-1.936
	PS vs T=1	-0.572	-0.775	-1.478	-1.935	-2.019
	PS vs P	-0.040	-0.230	-0.355	-0.449	-0.151
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0664	P vs T=1	0.515	0.015	-1.329	-1.891	-1.764
	PS vs T=1	0.788	0.216	-1.115	-1.939	-2.018
	PS vs P	0.319	0.230	0.180	-0.140	-0.287
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0665	P vs T=1	0.622	0.957	0.644	-0.065	-0.890
	PS vs T=1	1.411	1.512	1.290	0.778	0.416
	PS vs P	0.774	0.564	0.649	0.797	1.232
	putative triosephosphate isomerase					
	energy metabolism					

PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0666	P vs T=1	1.934	2.375	2.229	1.498	0.764
	PS vs T=1	2.901	3.113	3.147	2.758	2.418
	PS vs P	0.914	0.754	0.934	1.162	1.519
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0667	P vs T=1	1.041	1.611	1.960	1.657	1.102
	PS vs T=1	1.900	2.253	2.411	2.298	2.260
	PS vs P	0.814	0.634	0.464	0.630	1.128
	putative GTP cyclohydrolase I					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0668	P vs T=1	0.317	0.313	0.261	0.268	-0.359
	PS vs T=1	-0.524	-0.202	-0.484	-0.491	-0.645
	PS vs P	-0.643	-0.336	-0.587	-0.578	-0.282
	RNA-binding protein					
	transcription					
PGN_0669	P vs T=1	0.034	0.380	0.377	0.169	0.551
	PS vs T=1	0.428	0.645	0.707	0.751	0.498
	PS vs P	0.338	0.264	0.327	0.500	-0.028
	ABC transporter ATP-binding protein					
	transport and binding proteins					
PGN_0670	P vs T=1	-0.542	-0.609	-0.528	0.218	0.139
	PS vs T=1	-0.642	-0.553	-0.334	0.194	0.105
	PS vs P	-0.125	0.010	0.113	0.067	-0.007
	probable inorganic polyphosphate/ATP-NAD kinase					
	hypothetical proteins-Conserved					
PGN_0671	P vs T=1	1.370	1.155	0.910	0.202	-0.053
	PS vs T=1	0.849	1.379	1.787	1.684	1.347
	PS vs P	-0.446	0.249	0.880	1.326	1.282
	putative pyridoxal phosphate biosynthetic protein					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0672	P vs T=1	0.482	0.974	1.164	0.795	0.535
	PS vs T=1	0.398	0.386	0.476	0.851	0.732
	PS vs P	-0.097	-0.535	-0.619	0.067	0.185
	probable biopolymer transport protein					
	transport and binding proteins					



PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0673	P vs T=1	0.723	1.371	2.114	2.318	2.033
	PS vs T=1	0.667	0.848	1.377	1.819	1.809
	PS vs P	-0.139	-0.476	-0.602	-0.342	-0.154
	probable biopolymer transport protein					
	transport and binding proteins					
PGN_0674	P vs T=1	0.388	0.658	1.513	1.687	1.221
	PS vs T=1	0.988	1.002	1.373	1.599	1.332
	PS vs P	0.485	0.275	-0.047	0.025	0.125
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0675	P vs T=1	-0.140	0.557	1.557	1.826	1.362
	PS vs T=1	0.165	0.543	1.000	1.141	1.149
	PS vs P	0.236	-0.022	-0.493	-0.601	-0.188
	conserved hypothetical protein					
	unknown function					
PGN_0676	P vs T=1	0.749	0.941	1.023	1.214	0.788
	PS vs T=1	0.990	1.094	1.064	1.043	0.705
	PS vs P	0.234	0.159	0.053	-0.129	-0.083
	putative ribosomal protein L11 methyltransferase					
	protein synthesis					
PGN_0677	P vs T=1	0.370	0.072	-0.303	-0.041	0.556
	PS vs T=1	0.867	0.439	-0.220	-0.665	-0.293
	PS vs P	0.510	0.360	0.030	-0.610	-0.786
	putative multi antimicrobial extrusion protein MatE					
	transport and binding proteins					
PGN_0678	P vs T=1	1.176	1.036	0.574	0.327	0.036
ThiL	PS vs T=1	1.475	1.174	0.312	0.310	-0.171
	PS vs P	0.327	0.161	-0.264	-0.046	-0.246
	thiamine monophosphate kinase					
	biosynthesis of cofactors, prosthetic groups, and carriers					
PGN_0679	P vs T=1	0.810	0.685	-0.117	-0.413	-0.372
	PS vs T=1	1.017	0.501	-0.109	0.072	-0.417
	PS vs P	0.249	-0.139	-0.032	0.392	-0.084
	putative tetraacyldisaccharide 4'-kinase					
	cell envelope					

PgSg Time Course

log$_2$ (Fold Change)

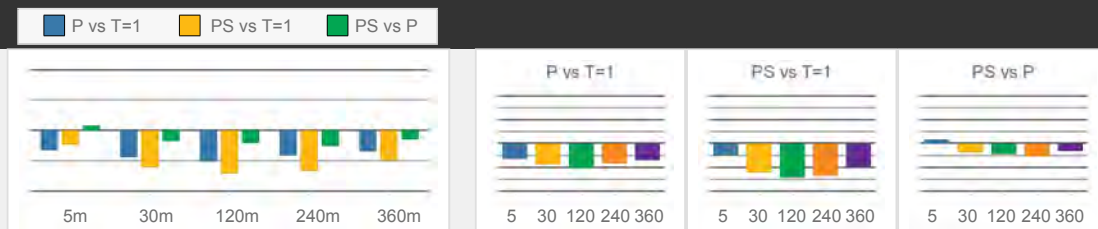
P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0680	P vs T=1	0.966	0.572	-0.302	-0.971	-1.473
	PS vs T=1	0.576	0.256	-0.205	-0.200	-0.693
	PS vs P	-0.323	-0.274	0.087	0.704	0.710
	signal peptide peptidase SppA 67K type					
	protein fate					
PGN_0681	P vs T=1	0.453	-1.732	-0.401	0.795	2.600
	PS vs T=1	0.308	0.431	1.046	0.330	0.621
	PS vs P	0.050	0.303	0.702	-0.086	-0.380
	hypothetical protein					
	hypothetical proteins					
PGN_0682	P vs T=1	-1.486	-0.488	0.564	0.924	0.802
	PS vs T=1	-1.467	-0.981	-0.267	-0.051	0.116
	PS vs P	-0.216	-0.516	-0.725	-0.810	-0.610
	hypothetical protein					
	hypothetical proteins					
PGN_0683	P vs T=1	1.278	1.901	2.683	2.621	2.090
	PS vs T=1	1.719	2.114	2.344	2.015	1.776
	PS vs P	0.321	0.212	-0.209	-0.498	-0.297
	TonB-linked receptor Tlr					
	transport and binding proteins					
PGN_0684	P vs T=1	-0.300	-0.234	-0.512	-0.389	-0.297
	PS vs T=1	-0.036	0.015	-0.111	-0.201	-0.391
	PS vs P	0.249	0.243	0.351	0.159	-0.102
	conserved hypothetical protein with adenosylcobinamide amidohydrolase domain					
	hypothetical proteins-Conserved					
PGN_0685	P vs T=1	-0.926	-1.029	-1.300	-1.088	-0.984
	PS vs T=1	-0.751	-0.917	-1.128	-1.514	-1.341
	PS vs P	0.172	0.103	0.118	-0.426	-0.354
	putative iron compound ABC transporter ATP-binding protein					
	transport and binding proteins					
PGN_0686	P vs T=1	-0.233	-0.243	-0.229	-0.226	0.222
	PS vs T=1	-0.363	-0.833	-1.226	-1.019	-0.483
	PS vs P	-0.121	-0.571	-0.971	-0.766	-0.647
	putative iron compound ABC transporter permease protein					
	transport and binding proteins					

PgSg Time Course

log$_2$ (Fold Change)

Locus		5m	30m	120m	240m	360m
PGN_0687	P vs T=1	-0.622	-0.855	-1.006	-0.805	-0.670
	PS vs T=1	-0.465	-1.199	-1.396	-1.321	-0.962
	PS vs P	0.163	-0.348	-0.412	-0.510	-0.287
	putative iron compound ABC transporter periplasmic iron compound-binding protein					
	transport and binding proteins					
PGN_0688	P vs T=1	-0.489	-0.642	-0.835	-0.048	0.326
	PS vs T=1	-0.980	-1.165	-0.553	0.058	0.419
	PS vs P	-0.467	-0.521	0.098	0.222	0.199
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0689	P vs T=1	-0.634	-1.302	-0.987	-0.267	0.609
	PS vs T=1	-1.615	-1.162	-0.399	-0.073	0.340
	PS vs P	-0.907	-0.033	0.425	0.297	-0.067
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0690	P vs T=1	-0.767	-1.484	-1.512	-1.251	-0.179
	PS vs T=1	-1.609	-1.407	-0.179	0.514	0.635
	PS vs P	-0.800	-0.083	1.040	1.464	0.863
	conserved hypothetical protein					
	unknown function					
PGN_0691	P vs T=1	-0.234	-0.009	-0.303	-0.991	-1.672
	PS vs T=1	-0.499	-0.445	-0.211	-0.346	-0.628
	PS vs P	-0.240	-0.370	0.131	0.561	0.892
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0692	P vs T=1	-0.159	-0.237	-0.871	-1.645	-2.106
	PS vs T=1	-0.731	-0.836	-0.824	-0.919	-1.158
	PS vs P	-0.517	-0.542	0.056	0.655	0.874
	phosphoserine phosphatase					
	amino acid biosynthesis					
PGN_0693	P vs T=1	0.153	-0.070	-0.304	-0.853	-1.712
	PS vs T=1	-0.835	-0.502	-0.026	-0.010	-0.249
	PS vs P	-0.907	-0.383	0.302	0.804	1.370
	conserved hypothetical protein					
	hypothetical proteins-Conserved					



PgSg Time Course

log$_2$ (Fold Change)

P vs T=1 | PS vs T=1 | PS vs P

Locus		5m	30m	120m	240m	360m
PGN_0694	P vs T=1	0.238	0.575	0.637	0.756	0.163
rpmH	PS vs T=1	-0.627	-0.168	-0.048	0.183	0.446
	PS vs P	-0.823	-0.640	-0.606	-0.465	0.263
	50S ribosomal protein L34					
	protein synthesis					
PGN_0695	P vs T=1	-0.125	0.014	0.262	0.154	0.288
	PS vs T=1	0.380	0.554	0.239	-0.044	-0.061
	PS vs P	0.460	0.507	-0.005	-0.202	-0.328
	probable septum formation protein Maf					
	cellular processes					
PGN_0696	P vs T=1	0.063	0.278	0.266	0.136	-0.066
	PS vs T=1	0.951	0.838	0.578	0.197	0.265
	PS vs P	0.842	0.542	0.301	0.027	0.284
	probable hydrolase					
	hypothetical proteins-Conserved					
PGN_0697	P vs T=1	-0.033	0.294	0.277	0.234	-0.119
	PS vs T=1	0.684	0.398	0.526	0.626	0.621
	PS vs P	0.692	0.100	0.236	0.369	0.698
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0698	P vs T=1	-0.311	-0.284	-0.623	-0.933	-1.264
	PS vs T=1	-0.230	-0.424	-0.435	-0.005	-0.250
	PS vs P	0.077	-0.134	0.159	0.841	0.925
	probable nitroreductase					
	unknown function					
PGN_0699	P vs T=1	0.286	-0.336	-0.363	0.861	1.491
	PS vs T=1	-0.129	-0.939	-0.128	0.623	1.061
	PS vs P	-0.232	-0.642	-0.114	0.198	0.088
	conserved hypothetical protein					
	hypothetical proteins-Conserved					
PGN_0700	P vs T=1	-0.259	-0.080	0.652	1.094	1.466
	PS vs T=1	0.163	0.121	0.740	1.325	1.218
	PS vs P	0.317	0.112	0.103	0.310	-0.162
	putative oxidoreductase Gfo/Idh/MocA family					
	unknown function					