

Table S1 The information about 45 DEGs (FDR \leq 0.5 & FC \geq 2)

PG3-1 vs. PG3-2

Name	Gene ID	PG3-1_1	PG3-1_2	PG3-2_1	PG3-2_2	PG3-2_3	logFC	type	pvalue	qvalue	function
holB	EXU60063	469.0319468	727.1235971	197.9659261	163.0565015	157.4546434	-1.190276482	down	4.29E-05	0.000280903	DNA polymerase III delta subunit
tmk	EXU60064	1066.85847	1578.269985	419.1881724	365.7385259	331.8195815	-1.231532666	down	2.27E-05	0.000164374	Thymidylate kinase
pncA	EXU60157	3.202532962	15.73466824	1.377341761	1.366387538	0.832571053	-1.972725468	down	5.18E-08	1.68E-06	Pyrazinamidase/nicotinamidase
fbxA	EXU60212	3.244279971	15.17473312	3.344752755	2.680045355	2.599489583	-1.013168688	down	0.001828494	0.006656059	Fructose-bisphosphate aldolase class II
gltX	EXU60218	23.16263013	44.94798657	11.62357399	10.77623229	9.603073087	-1.050285106	down	0.000389455	0.001861259	Glutamyl-tRNA synthetase
cdsA	EXU60242	67.40760902	151.5255273	36.71539375	25.42271857	22.06330629	-1.069799395	down	7.30E-05	0.00078981	Phosphatidate cytidyltransferase
nadK	EXU60281	58.92642128	46.17639526	85.03100484	77.63495508	74.97074294	1.134361978	up	0.000260311	0.001342926	Hypothetical protein, predicted NAD kinase
glpK	EXU60321	498.6017142	253.4939086	528.9763601	517.060024	603.2235843	1.059749759	up	0.000554537	0.002482668	Glycerol kinase
pepA	EXU60345	3.140128261	10.47777031	2.099151119	1.442393924	1.494101909	-1.066188493	down	0.000489724	0.003973907	Leucyl aminopeptidase
pts	EXU60380	345.3036733	89.21922817	1425.844086	1139.62967	1331.732288	1.331010033	up	7.59E-07	1.56E-05	Phosphotransferase system PTS, IIA component
pfs	EXU60400	63.5803572	56.45643875	5.401892649	6.075100955	5.687974059	-2.343803961	down	1.50E-15	1.46E-13	5-methylthioadenosinenucleosidase/S-adenosylhomocystein nucleosidase
cmk	EXU60432	100.802874	331.4682631	59.54224543	59.44359902	65.52016661	-1.133728591	down	0.000106988	0.000612821	Cytidylate kinase
pgi	EXU60445	153.8433176	213.0607368	55.98132645	53.80971857	48.49670807	-1.201582788	down	3.77E-05	0.000251031	Glucose-6-phosphate isomerase
nifS	EXU60449	620.83896	160.46677	18.40221416	15.58868107	17.12141621	-3.509595766	down	3.45E-33	6.71E-31	Nitrogen fixation protein NifS
metK	EXU60457	58.26432218	45.63492332	87.46637869	83.09155556	66.6528919	1.144070385	up	0.0002216	0.00116899	S-adenosylmethionine synthetase
ldh	EXU60488	4435.858369	4635.476625	1144.822689	1128.160043	1230.495275	-1.021032822	down	0.000129289	0.001325217	L-lactate dehydrogenase
dctD	EXU60529	1.679193107	7.274888142	1.238748698	0.665267402	0.675604305	-1.463620447	down	0.000637843	0.004919598	Deoxycytidylate deaminase (dCMP deaminase)
udk	EXU60547	2.1756853	1.322071018	3.732231972	3.369515422	1.62339919	1.330383339	up	0.001792575	0.006618085	Uridine kinase
atpA	EXU60577	1400.123254	1697.256781	440.492669	445.6021653	497.570001	-1.15409945	down	7.05E-05	0.00042929	ATP synthase alpha chain
atpD	EXU60578	803.6654715	1353.366419	266.6436337	250.1550054	246.0392257	-1.106191155	down	3.52E-05	0.000434764	ATP synthase beta chain
pncB	EXU60614	26.20655966	8.027037594	54.87789338	42.17494641	58.46610947	1.150353074	up	2.54E-05	0.00032966	Nicotinic phosphoribosyltransferase
dnaE	EXU60616	110.2833018	12.75682561	300.3149308	257.8813468	329.6857376	1.341716951	up	6.09E-07	1.32E-05	DNA polymerase III alpha subunit
polA	EXU60617	122.5184953	16.90214965	328.1680355	296.4926116	378.1330625	1.367061215	up	3.78E-07	8.93E-06	DNA polymerase I
gatC	EXU60650	41.76356796	19.13516033	50.24341013	47.25078521	42.53440919	1.127524543	up	0.000515959	0.002336813	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C
dhaK	EXU60661	44.59946978	19.63564403	145.7747016	134.6507215	137.9657028	1.328082471	up	9.53E-07	1.86E-05	Glycerone kinase
nagB	EXU60750	0.671677243	3.67901486	0.1955919	0.199580221	0.648580132	-1.941283924	down	0.000219289	0.001986349	Glucosamine-6-phosphate deaminase
rpiB	EXU60762	7.088350633	23.84492052	4.921515099	4.295020286	4.026236464	-1.161679918	down	0.000469457	0.002189862	Ribose 5-phosphate isomerase
atpE	EXU60767	1.210006798	10.48439762	0.657725702	0.958767726	0.389466011	-2.146126729	down	2.00E-05	0.000282674	ATP synthase C chain
atpF	EXU60768	4.746949745	25.35018714	3.896792464	1.701549316	1.85531336	-1.51640128	down	1.45E-06	2.76E-05	ATP synthase B chain
atpH	EXU60769	4.746949745	26.27353833	3.422858246	1.88065977	1.96444944	-1.641400772	down	2.74E-07	7.35E-06	ATP synthase delta chain

atpA	EXU60770	1.994440863	9.410330593	1.275437673	1.146511216	0.981809754	-1.400906335	down	7.31E-06		ATP synthase alpha chain
atpC	EXU60773	14.39908089	11.45794882	24.05584775	18.74390904	18.86962823	1.225009957	up	0.000354563	0.001737134	ATP synthase epsilon chain

PG3-2 vs. PG3-3

Name	Gene ID	PG3-2_1	PG3-2_2	PG3-2_3	PG3-3_1	PG3-3_2	PG3-3_3	logFC	type	pvalue	qvalue	function
holB	EXU60063	197.9659261	163.0565015	157.4546434	262.4684391	306.9893425	331.2673956	0.942494805	up	0.000416412	0.002718928	DNA polymerase III delta subunit
tmk	EXU60064	419.1881724	365.7385259	331.8195815	607.9756009	664.2334596	740.1329868	0.993459565	up	0.000197666	0.001409048	Thymidylate kinase
pncA	EXU60157	1.377341761	1.366387538	0.832571053	0.698833165	1.364258716	2.134429813	0.369755735	up	0.428064844	0.582100085	Pyrazinamidase/nicotinamidase
ribC/ribF	EXU60170	595.8500724	520.1410409	600.7893374	195.670966	204.8913015	186.8876131	-1.411850732	down	1.63E-07	2.82E-06	Riboflavin kinase / FAD synthetase
dpck	EXU60177	21.58922801	16.12748238	15.68113149	6.040002783	5.995558041	7.504205868	-1.299797144	down	8.19E-06	9.22E-05	Dephospho-CoA kinase
gltX	EXU60218	11.62357399	10.77623229	9.603073087	4.822526385	4.536083357	5.118442071	-1.003339318	down	0.0003508	0.002349757	Glutamyl-tRNA synthetase
nadE	EXU60403	33.50505144	30.41164458	24.94957263	99.94261185	82.67932146	85.20019102	1.733267113	up	2.69E-10	1.49E-08	NH(3)-dependent NAD(+) synthetase
pgi	EXU60445	55.98132645	53.80971857	48.49670807	26.72220461	24.29296202	27.1501467	-0.880555416	down	0.00106181	0.005914009	Glucose-6-phosphate isomerase
plsX	EXU60469	16.87928902	15.66655084	13.63712331	46.21755734	42.16577536	40.69911653	1.622716915	up	4.06E-09	1.09E-07	Fatty acid/phospholipid synthesis protein PlsX
pncB	EXU60614	54.87789338	42.17494641	58.46610947	15.27496634	15.38767516	15.10380418	-1.628612914	down	3.24E-09	9.32E-08	Nicotinic phosphoribosyltransferase
dnaE	EXU60616	300.3149308	257.8813468	329.6857376	72.76352766	70.64696014	69.6123328	-1.92764531	down	1.81E-12	2.81E-10	DNA polymerase III alpha subunit
poLA	EXU60617	328.1680355	296.4926116	378.1330625	122.3996327	119.2752683	118.5234599	-1.348167267	down	5.32E-07	7.65E-06	DNA polymerase I
dhaK	EXU60661	145.7747016	134.6507215	137.9657028	74.88287667	75.63274529	64.4927903	-0.824290189	down	0.002035788	0.009471899	Glycerone kinase
manB	EXU60743	47.37137841	43.76543124	43.9539217	19.52044803	21.82348025	19.73545734	-1.007352599	down	0.000184848	0.00132988	Phosphoglucomutase or phosphomannomutase

PG3-3 vs. PG3-4

Name	Gene ID	PG3-3_1	PG3-3_2	PG3-3_3	PG3-4_1	PG3-4_2	PG3-4_3	logFC	type	pvalue	qvalue	function
holB	EXU60063	262.4684391	306.9893425	331.2673956	230.7475697	242.1869339	213.0606438	-0.78285244	down	0.003292132	0.027770986	DNA polymerase III delta subunit
tmk	EXU60064	607.9756009	664.2334596	740.1329868	572.855986	548.4659629	512.1283599	-0.688240302	down	0.009562199	0.061324516	Thymidylate kinase
holB	EXU60112	21.35299064	21.16928896	21.19583069	16.37785974	18.53172202	15.23654324	-0.737311342	down	0.007238789	0.049993189	Hypothetical protein, putative DNA polymerase III, delta subunit, holA
pncA	EXU60157	0.698833165	1.364258716	2.134429813	4.244557015	6.720805374	5.930062893	1.585522724	up	1.69E-05	0.000408936	Pyrazinamidase/nicotinamidase
dpck	EXU60177	6.040002783	5.995558041	7.504205868	28.83762904	27.77656931	32.09626007	1.792446538	up	8.72E-10	8.45E-08	Dephospho-CoA kinase
gltX	EXU60218	4.822526385	4.536083357	5.118442071	14.88296985	17.66353394	16.40483072	1.363847586	up	1.27E-06	4.47E-05	Glutamyl-tRNA synthetase
pfk	EXU60319	12.49137568	9.057509702	8.338962714	6.678888872	8.179188217	7.119638791	-0.835547106	down	0.003233919	0.027770986	6-phosphofructokinase
pgi	EXU60445	26.72220461	24.29296202	27.1501467	61.05450577	61.93257567	56.74979765	0.812877344	up	0.002500361	0.023098569	Glucose-6-phosphate isomerase

plsX	EXU60469	46.21755734	42.16577536	40.69911653	21.10224582	28.94150816	31.63631877	-1.055177337	down	9.92E-05	0.001529605	Fatty acid/phospholipid synthesis protein PlsX
pdhD	EXU60553	35.98193748	36.12013895	30.92378875	21.10325576	25.77808131	14.34413339	-1.145574112	down	2.47E-05	0.000548023	Dihydrolipoyl dehydrogenase
dnaE	EXU60616	72.76352766	70.64696014	69.6123328	182.5426572	175.7426344	164.3675997	0.907620155	up	0.000662574	0.007910111	DNA polymerase III alpha subunit
polA	EXU60617	122.3996327	119.2752683	118.5234599	251.5520162	275.1734228	254.1144427	0.725689185	up	0.00630365	0.046586976	DNA polymerase I
gatB	EXU60652	8.509749683	7.206024873	7.834469095	14.48813574	17.8604807	18.64090128	0.721385164	up	0.008781386	0.057748779	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
dhaK	EXU60661	74.88287667	75.63274529	64.4927903	37.33770173	47.97575482	48.10471018	-1.082944353	down	5.89E-05	0.00106327	Glycerone kinase
aguA	EXU60707	286.5937146	268.006671	269.9252571	130.7458708	150.347805	111.8602827	-1.460868946	down	6.33E-08	4.46E-06	putative agmatine deiminase
deoA	EXU60742	4.129976363	2.317087811	3.173867893	7.391961782	8.886964105	8.925022559	0.996068059	up	0.000623948	0.007565368	Thymidine phosphorylase
manB	EXU60743	19.52044803	21.82348025	19.73545734	55.38302426	56.68903277	54.95046448	1.061763473	up	8.27E-05	0.001364893	Phosphoglucomutase or phosphomannomutase
gpmI	EXU60747	14.33220999	11.8353873	11.4238134	9.75898785	11.58105184	7.315386912	-0.785038101	down	0.004293423	0.034347381	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
arcB	EXU60776	4.628366437	4.117431426	3.435660518	10.04056804	12.22786879	12.29789253	1.112344797	up	0.000134449	0.001968541	Ornithine carbamoyltransferase
