Supplemental Table 1. Differentially Expressed Genes as Assessed by RNA-Seq.

Upregulated Genes

Gene Name/Number	PA01 ortholog*	logFC*	PValue*	CPM WT*	CPM PS-CKOn*	Function/Predicted Function
Pyocin Related						
prtN	PA0610	1.026	0.032	85.915	175.008	transcriptional Activator of Pyocins
ptrB	PA0612	1.091	0.022	148.830	317.020	phage related DnaK suppressor protein
PA14_07980	PA0613	1.097	0.020	392.180	839.132	unknown function, phage related
PA14_07990	PA0614	1.096	0.021	278.963	596.191	predicted holin
PA14_08000	PA0615	1.072	0.023	331.639	697.443	R2 pyocin specific
PA14_08010	PA0616	1.099	0.020	664.020	1422.383	R2 pyocin specific
PA14_08020	PA0617	1.081	0.022	421.115	890.890	R2 pyocin specific
PA14_08030	PA0618	1.087	0.021	885.410	1880.767	R2 pyocin specific
PA14_08040	PA0619	1.094	0.020	596.208	1272.607	R2 pyocin specific
PA14_08050	PA0620	1.079	0.022	3328.855	7033.630	R2 pyocin specific
PA14_08060	PA0621	1.074	0.023	2334.086	4912.510	R2 pyocin specific
PA14_08070	PA0622	1.093	0.020	2240.010	4779.233	R2 pyocin specific
PA14_08090	PA0623	1.092	0.021	749.489	1598.038	R2 pyocin specific
PA14_08100	PA0624	1.094	0.021	383.870	819.722	R2 pyocin specific
PA14_08110	n/a	1.093	0.021	203.583	434.446	R2 pyocin specific
PA14_08120	PA0625	1.082	0.022	3751.602	7943.929	R2 pyocin specific
PA14_08130	PA0626	1.072	0.023	463.998	975.644	R2 pyocin specific
PA14_08140	PA0627	1.097	0.020	345.290	738.526	R2 pyocin specific
PA14_08150	PA0628	1.087	0.021	1421.522	3020.097	R2 pyocin specific
PA14_08160	PA0629	1.090	0.021	229.105	487.822	lytic enzyme
PA14_08180	PA0630	1.053	0.031	46.444	96.400	lysis control
PA14_08190	PA0631	1.110	0.020	102.830	221.914	lysis control
PA14_08200	PA0632	1.102	0.020	692.361	1486.434	F2 pyocin specific
PA14_08210	PA0633	1.078	0.022	798.753	1686.674	F2 pyocin specific

PA14_08220	PA0634	1.077	0.022	815.520	1720.640	F2 pyocin specific
PA14_08230	PA0635	1.097	0.021	187.409	400.803	F2 pyocin specific
PA14_08240	PA0636	1.093	0.020	2376.524	5068.432	F2 pyocin specific
PA14_08250	PA0637	1.107	0.019	268.576	578.723	F2 pyocin specific
PA14_08260	PA0638	1.092	0.021	370.367	789.638	F2 pyocin specific
PA14_08270	PA0639	1.093	0.020	1434.283	3059.886	F2 pyocin specific
PA14_08280	PA0640	1.096	0.020	1603.738	3427.694	F2 pyocin specific
PA14_08300	PA0641	1.088	0.021	3221.276	6847.300	F2 pyocin specific
PA14_08310	PA0646	1.038	0.027	2014.911	4136.459	F2 pyocin specific
PA14_08320	PA0647	1.043	0.027	814.482	1678.263	F2 pyocin specific
PA14_08330	PA0648	1.070	0.024	259.376	544.433	F2 pyocin specific
Phage related PA0906 operon						
PA14_52480	PA0911	1.099	0.021	137.256	294.052	unknown, phage related
PA14_52490	PA0910	1.090	0.022	125.682	267.526	unknown, phage related
PA14_52500	PA0909	1.103	0.027	30.567	65.668	unknown, phage related
PA14_52510	PA0908	1.113	0.029	20.329	43.995	unknown, phage related
PA14_52520	PA0907	1.062	0.027	92.147	192.476	unknown, phage related
Unknown group 1						
PA14_14540	n/a	1.103	0.019	2225.024	4779.556	mu-like prophage protein Com
PA14_14550	n/a	1.089	0.021	3998.959	8508.418	unknown
PA14_14560	n/a	1.069	0.025	113.662	238.412	predicted ABC transporter/OM receptor
Unknown group 2						
PA14_53540	PA0829	1.028	0.037	32.496	66.315	predicted alpha/beta hydrolase
PA14_53570	n/a	1.023	0.031	205.809	418.272	predicted phage like integrase

Unknown group 3						
PA14_53620	PA0826	1.056	0.028	61.431	127.778	unknown
PA14_53630	PA0825	1.090	0.023	81.760	174.037	predicted membrane protein
PA14_53640	PA0824	1.070	0.030	36.503	76.667	predicted membrane protein
Unknown group 4						
PA14_53740	PA0814	1.084	0.026	43.180	91.548	unknown, predicted type 5 amino transferase
PA14_53750	PA0813	1.076	0.024	117.669	248.116	unknown
PA14_53770	PA0812	1.076	0.023	306.562	646.332	unknown
PA14_53780	PA0811	1.025	0.030	586.712	1194.323	uncharacterized MFS family transporter
PA14_53790	PA0810	1.082	0.023	199.577	422.477	unknown, predicted haloacid dehalogenase
mntH2	PA0809	1.097	0.020	636.866	1361.890	manganese transporter
ampDh3	PA0807	1.082	0.022	1146.269	2426.171	N-acetyl-anhydromuramyl-L-alanine amidase
Miscellaneous						
PA14_52380	PA0918	1.066	0.026	101.347	212.209	cytochrome b561
nirS	PA0519	1.018	0.039	35.612	72.138	nitrite reductase
PA14_52300	PA0924	1.013	0.034	98.230	198.299	predicted hydrolase of alkaline phosphatase superfamily, predicted SOS regulated
PA14_46670	PA1362	1.032	0.035	43.328	88.636	unknown
PA14_52440	PA0914	1.091	0.037	13.651	29.114	uncharacterized

Downregulated Genes

Gene Name/Number	PA01 Ortholouge	logFC	PValue	CPM WT	CPM PS-CKOn	Function/Predicted Function
Miscellaneous						
aqpZ	PA4034	-1.949	0.011	13.800	4.852	aquaporin Z
PA14_11670	PA4033	-1.503	0.014	7.568	1.941	unknown, adjacent to aquaporin Z

PA14_36780	PA2148	-5.575	0.044	1.187	0.000	unknown, putative Mg2+ transporter
PA14_47450	PA1295	-1.065	0.042	37.244	17.792	unknown
PA14_02450	PA0195	-1.084	0.030	60.392	28.467	NAD(P) transhydrogenase subunit alpha part 1

***Legend**

PA01 ortholog	Homolog of the gene in *P. aeruginosa* PAO1
logFC	log2 fold change of PS-CKOn compared to WT
Pvalue	P value calculated with an exact test for the negative binomial distribution (see methods)
CPM WT	Specific reads of the transcript (counts per million) after edgeR normalization in the WT strain sequence
CPM PS-CKOn	Specific reads of the transcript (counts per million) after edgeR normalization in the PS-CKOn strain sequence
Function/Predicted Function	Assignment based on information from www.Pseudomonas.com