

A					
ORF	SEED Rank3	Log2 fold change	base mean	lfcSE	padj
k99_74160	[Protein-PII]uridylyltransferase(EC2.7.7.59)	-5.7	4	1.70	5.3E-03
k99_90735	[Protein-PII]uridylyltransferase(EC2.7.7.59)	-6.0	5	1.61	1.9E-03
k99_78664	6-phosphofructokinase(EC2.7.1.11)	3.5	101	0.57	3.3E-08
k99_40746	6-phosphofructokinase(EC2.7.1.11)	2.3	25	0.58	1.0E-03
k99_106596	6-phosphofructokinase(EC2.7.1.11)	-2.3	48	0.43	2.7E-06
k99_119667	6-phosphofructokinase(EC2.7.1.11)	-7.8	16	1.36	3.8E-07
k99_98626	Alkalinephosphatase(EC3.1.3.1)	3.4	14	0.89	1.0E-03
k99_91249	Alkalinephosphatase(EC3.1.3.1)	2.3	20	0.62	1.9E-03
k99_5133	Alkalinephosphatase(EC3.1.3.1)	-1.4	4724	0.29	4.5E-05
k99_37031	Alkalinephosphatase(EC3.1.3.1)	-1.7	148	0.45	1.5E-03
k99_70372	Alkalinephosphatase(EC3.1.3.1)	-2.2	12064	0.31	4.7E-10
k99_112543	Alkalinephosphatase(EC3.1.3.1)	-4.8	8	1.33	2.5E-03
k99_41619	Alkalinephosphatase(EC3.1.3.1)	-5.0	8	1.33	1.6E-03
k99_107071	Alkalinephosphatase(EC3.1.3.1)	-5.5	3	1.74	9.6E-03
k99_125798	Alkalinephosphatase(EC3.1.3.1)	-5.5	3	1.73	8.4E-03
k99_40946	Alkalinephosphatase(EC3.1.3.1)	-5.6	4	1.76	9.2E-03
k99_137106	Alkalinephosphatase(EC3.1.3.1)	-5.7	4	1.78	8.0E-03
k99_123111	Alkalinephosphatase(EC3.1.3.1)	-5.8	4	1.68	4.0E-03
k99_124107	Alkalinephosphatase(EC3.1.3.1)	-5.9	4	1.72	4.7E-03
k99_135863	Alkalinephosphatase(EC3.1.3.1)	-6.1	5	1.62	1.6E-03
k99_112715	Alkalinephosphatase(EC3.1.3.1)	-6.3	21	1.18	2.8E-06
k99_120266	Alkalinephosphatase(EC3.1.3.1)	-6.4	6	1.62	7.6E-04
k99_103319	Alkalinephosphatase(EC3.1.3.1)	-7.2	11	1.42	7.4E-06
k99_90812	Alkalinephosphatase(EC3.1.3.1)	-10.5	107	1.25	7.0E-15
k99_2232	Allantoicase(EC3.5.3.4)	-3.3	53	0.51	3.9E-09
k99_68238	Ammoniumtransporter	4.6	9	1.29	3.1E-03
k99_102453	Ammoniumtransporter	4.3	47	0.60	1.1E-10
k99_99418	Ammoniumtransporter	3.4	31	0.70	2.1E-05
k99_78121	Ammoniumtransporter	2.9	104	0.36	3.9E-14
k99_40197	Ammoniumtransporter	2.9	112	0.37	6.5E-13
k99_44476	Ammoniumtransporter	2.4	41	0.53	6.6E-05
k99_12752	Ammoniumtransporter	2.4	346	0.28	1.3E-15
k99_37236	Ammoniumtransporter	2.3	112	0.46	1.0E-05
k99_9566	Ammoniumtransporter	2.1	122	0.37	4.6E-07
k99_79607	Ammoniumtransporter	2.1	84	0.41	1.3E-05
k99_45003	Ammoniumtransporter	-1.9	23	0.54	3.9E-03
k99_135476	Ammoniumtransporter	-5.0	9	1.38	2.3E-03
k99_59870	Arginase(EC3.5.3.1)	-6.5	7	1.52	2.5E-04
k99_132005	Argininosuccinatelyase(EC4.3.2.1)	-6.0	5	1.75	4.4E-03
k99_41597	Argininosuccinatelyase(EC4.3.2.1)	-6.2	6	1.70	2.1E-03
k99_133943	Argininosuccinatelyase(EC4.3.2.1)	-8.4	25	1.32	9.9E-09
k99_49979	Argininosuccinatesynthase(EC6.3.4.5)	5.5	5	1.58	3.8E-03
k99_20256	Argininosuccinatesynthase(EC6.3.4.5)	2.3	28	0.68	5.7E-03
k99_109825	Argininosuccinatesynthase(EC6.3.4.5)	-3.4	16	0.93	1.9E-03
k99_10167	Argininosuccinatesynthase(EC6.3.4.5)	-5.7	4	1.72	6.5E-03
k99_557	Argininosuccinatesynthase(EC6.3.4.5)	-5.8	4	1.67	3.4E-03
k99_45731	Argininosuccinatesynthase(EC6.3.4.5)	-6.1	5	1.59	1.2E-03
k99_89448	Argininosuccinatesynthase(EC6.3.4.5)	-6.6	25	1.16	4.0E-07
k99_9010	ATPsynthasebetachain(EC3.6.3.14)	6.7	41	1.16	2.2E-07
k99_38987	ATPsynthasebetachain(EC3.6.3.14)	6.1	7	1.52	6.6E-04
k99_59114	ATPsynthasebetachain(EC3.6.3.14)	5.3	4	1.69	9.8E-03
k99_128204	ATPsynthasebetachain(EC3.6.3.14)	5.2	4	1.65	9.1E-03
k99_78576	ATPsynthasebetachain(EC3.6.3.14)	4.2	8	1.33	9.4E-03
k99_112296	ATPsynthasebetachain(EC3.6.3.14)	3.4	18	0.82	3.8E-04
k99_93510	ATPsynthasebetachain(EC3.6.3.14)	3.4	73	0.52	3.9E-09
k99_56943	ATPsynthasebetachain(EC3.6.3.14)	2.7	26	0.64	3.4E-04
k99_32351	ATPsynthasebetachain(EC3.6.3.14)	2.5	85	0.39	2.7E-09
k99_77567	ATPsynthasebetachain(EC3.6.3.14)	2.5	18	0.71	3.7E-03
k99_15669	ATPsynthasebetachain(EC3.6.3.14)	2.4	46	0.52	4.3E-05
k99_19625	ATPsynthasebetachain(EC3.6.3.14)	2.4	24	0.64	1.9E-03
k99_66608	ATPsynthasebetachain(EC3.6.3.14)	2.3	16	0.69	5.9E-03
k99_97684	ATPsynthasebetachain(EC3.6.3.14)	2.3	170	0.30	3.2E-12
k99_19470	ATPsynthasebetachain(EC3.6.3.14)	2.2	47	0.46	3.4E-05
k99_24352	ATPsynthasebetachain(EC3.6.3.14)	2.2	20	0.63	3.7E-03
k99_86307	ATPsynthasebetachain(EC3.6.3.14)	1.9	37	0.58	6.4E-03
k99_48952	ATPsynthasebetachain(EC3.6.3.14)	1.9	56	0.47	4.7E-04
k99_84733	ATPsynthasebetachain(EC3.6.3.14)	1.8	48	0.44	4.1E-04
k99_140504	ATPsynthasebetachain(EC3.6.3.14)	1.6	39	0.49	8.2E-03
k99_94862	ATPsynthasebetachain(EC3.6.3.14)	-1.3	280	0.26	1.4E-05
k99_100738	ATPsynthasebetachain(EC3.6.3.14)	-1.4	56	0.41	4.2E-03

k99_35046	ATPSynthasebetachain(EC3.6.3.14)	-1.4	198	0.39	2.0E-03
k99_25335	ATPSynthasebetachain(EC3.6.3.14)	-1.8	405	0.30	1.6E-07
k99_20385	ATPSynthasebetachain(EC3.6.3.14)	-1.8	157	0.31	5.7E-07
k99_108473	ATPSynthasebetachain(EC3.6.3.14)	-1.9	44	0.43	9.1E-05
k99_4519	ATPSynthasebetachain(EC3.6.3.14)	-1.9	40	0.51	1.3E-03
k99_130313	ATPSynthasebetachain(EC3.6.3.14)	-2.4	28	0.53	1.0E-04
k99_29496	ATPSynthasebetachain(EC3.6.3.14)	-2.5	63	0.50	1.2E-05
k99_6434	ATPSynthasebetachain(EC3.6.3.14)	-2.7	32	0.67	6.2E-04
k99_14606	ATPSynthasebetachain(EC3.6.3.14)	-2.7	108	0.44	2.4E-08
k99_87460	ATPSynthasebetachain(EC3.6.3.14)	-2.9	53	0.44	1.8E-09
k99_27380	ATPSynthasebetachain(EC3.6.3.14)	-3.1	116	0.36	4.6E-15
k99_96996	ATPSynthasebetachain(EC3.6.3.14)	-3.1	295	0.35	2.3E-16
k99_733	ATPSynthasebetachain(EC3.6.3.14)	-3.3	22	0.74	9.6E-05
k99_91622	ATPSynthasebetachain(EC3.6.3.14)	-3.4	67	0.49	3.1E-10
k99_56202	ATPSynthasebetachain(EC3.6.3.14)	-3.6	34	0.58	4.2E-08
k99_45704	ATPSynthasebetachain(EC3.6.3.14)	-3.7	29	0.63	2.2E-07
k99_738	ATPSynthasebetachain(EC3.6.3.14)	-3.7	13	0.90	5.5E-04
k99_103258	ATPSynthasebetachain(EC3.6.3.14)	-3.8	25	0.80	5.0E-05
k99_41626	ATPSynthasebetachain(EC3.6.3.14)	-3.8	116	0.38	3.0E-21
k99_87306	ATPSynthasebetachain(EC3.6.3.14)	-3.9	55	0.54	3.1E-11
k99_43455	ATPSynthasebetachain(EC3.6.3.14)	-4.0	11	0.97	4.3E-04
k99_12672	ATPSynthasebetachain(EC3.6.3.14)	-4.1	28	0.68	9.0E-08
k99_103337	ATPSynthasebetachain(EC3.6.3.14)	-4.1	9	1.23	5.9E-03
k99_125426	ATPSynthasebetachain(EC3.6.3.14)	-4.3	33	0.63	6.7E-10
k99_71693	ATPSynthasebetachain(EC3.6.3.14)	-4.5	48	0.68	2.5E-09
k99_13848	ATPSynthasebetachain(EC3.6.3.14)	-4.8	16	1.01	3.0E-05
k99_90551	ATPSynthasebetachain(EC3.6.3.14)	-5.2	112	0.49	2.3E-23
k99_52575	ATPSynthasebetachain(EC3.6.3.14)	-5.7	29	0.92	2.6E-08
k99_111892	ATPSynthasebetachain(EC3.6.3.14)	-5.8	4	1.76	7.1E-03
k99_130035	ATPSynthasebetachain(EC3.6.3.14)	-5.8	4	1.74	5.6E-03
k99_42810	ATPSynthasebetachain(EC3.6.3.14)	-6.0	5	1.73	4.2E-03
k99_16876	ATPSynthasebetachain(EC3.6.3.14)	-6.0	5	1.60	1.5E-03
k99_21059	ATPSynthasebetachain(EC3.6.3.14)	-6.1	5	1.61	1.6E-03
k99_49959	ATPSynthasebetachain(EC3.6.3.14)	-6.3	64	0.82	1.4E-12
k99_120071	ATPSynthasebetachain(EC3.6.3.14)	-6.7	54	0.89	7.2E-12
k99_113207	ATPSynthasebetachain(EC3.6.3.14)	-6.9	9	1.44	2.7E-05
k99_66732	ATPSynthasebetachain(EC3.6.3.14)	-7.2	11	1.40	6.2E-06
k99_13273	ATPSynthasebetachain(EC3.6.3.14)	-7.3	12	1.39	3.5E-06
k99_93328	ATPSynthasebetachain(EC3.6.3.14)	-7.5	48	1.13	2.2E-09
k99_14080	ATPSynthasebetachain(EC3.6.3.14)	-7.6	52	1.13	9.9E-10
k99_27937	ATPSynthasebetachain(EC3.6.3.14)	-7.6	109	0.88	9.2E-16
k99_102519	ATPSynthasebetachain(EC3.6.3.14)	-7.8	17	1.37	3.2E-07
k99_16115	ATPSynthasebetachain(EC3.6.3.14)	-8.3	23	1.31	9.8E-09
k99_104313	ATPSynthasebetachain(EC3.6.3.14)	-8.3	24	1.37	4.6E-08
k99_38141	Branched-chain aminoacidtransportsystemLivM(TC3.A.1.4.1)	-2.7	1456	0.61	1.8E-04
k99_38139	Branched-chain aminoacidtransportsystemLivM(TC3.A.1.4.1)	-3.9	65	0.48	3.5E-14
k99_126272	Branched-chain aminoacidtransportsystemLivM(TC3.A.1.4.1)	-4.9	16	0.98	1.2E-05
k99_10274	Branched-chain aminoacidtransportsystemLivM(TC3.A.1.4.1)	-9.4	49	1.26	8.9E-12
k99_847	Chitinase(EC3.2.1.14)	1.7	79	0.46	1.6E-03
k99_76684	Chitinase(EC3.2.1.14)	-6.4	6	1.55	4.0E-04
k99_68511	D-xylosetransportATP-bindingproteinXylG	-4.9	24	0.83	1.1E-07
k99_53371	GlutaminesynthetasetypeI(EC6.3.1.2)	6.0	7	1.48	5.3E-04
k99_25349	GlutaminesynthetasetypeI(EC6.3.1.2)	5.4	5	1.69	8.4E-03
k99_121314	GlutaminesynthetasetypeI(EC6.3.1.2)	5.3	4	1.63	7.0E-03
k99_106126	GlutaminesynthetasetypeI(EC6.3.1.2)	4.7	11	1.31	2.9E-03
k99_5110	GlutaminesynthetasetypeI(EC6.3.1.2)	3.6	15	0.83	2.2E-04
k99_93784	GlutaminesynthetasetypeI(EC6.3.1.2)	3.1	198	0.42	4.6E-12
k99_95363	GlutaminesynthetasetypeI(EC6.3.1.2)	2.7	42	0.65	4.0E-04
k99_118162	GlutaminesynthetasetypeI(EC6.3.1.2)	2.7	27	0.62	2.3E-04
k99_135343	GlutaminesynthetasetypeI(EC6.3.1.2)	2.4	69	0.45	1.7E-06
k99_45102	GlutaminesynthetasetypeI(EC6.3.1.2)	2.3	18	0.71	9.2E-03
k99_15839	GlutaminesynthetasetypeI(EC6.3.1.2)	2.1	60	0.42	1.2E-05
k99_121529	GlutaminesynthetasetypeI(EC6.3.1.2)	-2.5	22	0.63	5.5E-04
k99_58904	GlutaminesynthetasetypeI(EC6.3.1.2)	-2.8	31	0.60	3.7E-05
k99_101960	GlutaminesynthetasetypeI(EC6.3.1.2)	-3.5	10	0.99	3.2E-03
k99_106279	GlutaminesynthetasetypeI(EC6.3.1.2)	-3.8	12	0.86	1.4E-04
k99_125040	GlutaminesynthetasetypeI(EC6.3.1.2)	-7.2	11	1.39	4.5E-06
k99_109485	GlutaminesynthetasetypeI(EC6.3.1.2)	-8.3	24	1.34	2.0E-08
k99_15998	HistidineABCtransporter,permeaseproteinHisQ(TC3.A.1.3.1) □	1.46	47	0.48	1.3E-02
k99_34176	Manganesesuperoxidedismutase(EC1.15.1.1)	2.4	15	0.74	8.5E-03
k99_9914	Manganesesuperoxidedismutase(EC1.15.1.1)	-4.0	10	1.15	3.5E-03
k99_38359	Manganesesuperoxidedismutase(EC1.15.1.1)	-4.9	42	0.63	5.6E-13
k99_131797	Manganesesuperoxidedismutase(EC1.15.1.1)	-5.9	4	1.67	3.3E-03

k99_129162	Manganesesuperoxidedismutase(EC1.15.1.1)	-7.1	10	1.46	2.5E-05
k99_17186	Manganesesuperoxidedismutase(EC1.15.1.1)	-7.1	110	0.76	2.2E-18
k99_49884	Myo-inositol2-dehydrogenase1(EC1.1.1.18)	5.8	6	1.62	2.7E-03
k99_136972	NAD-specificglutamatedehydrogenase(EC1.4.1.2)	4.0	13	1.04	1.4E-03
k99_33501	NAD-specificglutamatedehydrogenase(EC1.4.1.2)	2.1	91	0.36	1.8E-07
k99_6952	NAD-specificglutamatedehydrogenase(EC1.4.1.2)	-5.7	4	1.78	8.7E-03
k99_57834	NAD-specificglutamatedehydrogenase(EC1.4.1.2)	-6.2	6	1.62	1.1E-03
k99_102083	NAD-specificglutamatedehydrogenase(EC1.4.1.2)	-9.8	65	1.27	1.2E-12
k99_59590	NitricoxidereductaseactivationproteinNorQ	-3.6	78	0.47	2.4E-12
k99_1664	OligopeptidettransportATP-bindingproteinOppD(TC3.A.1.5.1)	1.5	58	0.42	3.8E-03
k99_15812	OligopeptidettransportATP-bindingproteinOppD(TC3.A.1.5.1)	1.4	211	0.36	1.4E-03
k99_65033	OligopeptidettransportATP-bindingproteinOppF(TC3.A.1.5.1)	4.2	8	1.32	8.9E-03
k99_100343	Ornithinecarbamoyltransferase(EC2.1.3.3)	-6.6	7	1.56	2.8E-04
k99_93102	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	2.9	22	0.71	5.3E-04
k99_15416	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	1.8	72	0.49	2.2E-03
k99_61853	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	1.6	56	0.41	7.9E-04
k99_77599	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	1.5	46	0.45	4.8E-03
k99_139659	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-3.4	12	0.93	2.4E-03
k99_28769	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-3.8	16	0.84	9.2E-05
k99_2362	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-4.2	104	0.53	1.7E-13
k99_37437	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-4.4	41	0.63	1.5E-10
k99_74519	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-4.5	153	0.43	2.2E-23
k99_131385	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-4.7	7	1.38	4.7E-03
k99_116808	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-5.2	11	1.35	9.6E-04
k99_67662	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-5.6	4	1.76	9.3E-03
k99_68465	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-5.7	4	1.70	5.4E-03
k99_43817	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-5.8	4	1.66	3.8E-03
k99_49359	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-5.8	4	1.65	3.1E-03
k99_30972	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-6.1	5	1.59	1.2E-03
k99_79978	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-6.3	6	1.54	5.4E-04
k99_24748	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-6.3	6	1.53	4.7E-04
k99_117578	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-6.4	6	1.56	4.3E-04
k99_8318	PhosphateABCtransporter.PstS(TC3.A.1.7.1)	-7.4	12	1.44	7.3E-06
k99_48312	PhosphatetransportsystemregulatoryproteinPhoU	1.1	186	0.29	2.5E-03
k99_138630	PhosphatetransportsystemregulatoryproteinPhoU	-3.5	20	0.72	1.7E-05
k99_49682	PhosphatetransportsystemregulatoryproteinPhoU	-4.6	7	1.40	6.5E-03
k99_91508	PhosphatetransportsystemregulatoryproteinPhoU	-5.6	4	1.73	8.3E-03
k99_104778	PhosphatetransportsystemregulatoryproteinPhoU	-5.9	17	1.21	1.9E-05
k99_106506	PhosphatetransportsystemregulatoryproteinPhoU	-6.0	5	1.65	2.4E-03
k99_54157	PhosphonateABCtransporterphosphate-bindingperiplasmiccomponent(TC3.A.1.9.1)	1.0	215	0.28	4.3E-03
k99_135398	PredictederythritolABCtransporter1	4.9	83	0.55	1.5E-16
k99_96118	Sucrose-6-phosphatehydrolase(EC3.2.1.B3)	2.8	28	0.80	3.6E-03
k99_100752	Sucrose-6-phosphatehydrolase(EC3.2.1.B3)	-6.0	5	1.63	2.2E-03
k99_17505	Sucrosephosphorylase(EC2.4.1.7)	-4.1	14	1.09	1.7E-03
k99_27403	Sucrosephosphorylase(EC2.4.1.7)	-5.7	4	1.70	5.9E-03
k99_50382	Sucrosephosphorylase(EC2.4.1.7)	-5.7	4	1.74	6.5E-03
k99_29387	Sucrosephosphorylase(EC2.4.1.7)	-7.0	10	1.64	2.4E-04
k99_135348	Trehalase(EC3.2.1.28)	-3.3	83	0.49	8.9E-10
k99_98326	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	5.9	7	1.51	8.7E-04
k99_47169	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	5.3	16	1.22	1.7E-04
k99_80755	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	3.7	21	0.84	1.7E-04
k99_123766	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	3.1	19	0.72	2.0E-04
k99_6906	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	1.5	79	0.41	2.5E-03
k99_101136	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-2.7	50	0.53	1.1E-05
k99_55618	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-3.1	27	0.64	3.0E-05
k99_100819	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-3.1	25	0.63	1.4E-05
k99_13072	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-5.6	4	1.76	9.2E-03
k99_27908	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-5.9	5	1.66	2.7E-03
k99_51170	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-6.1	5	1.60	1.2E-03
k99_91794	Ubiquinol-cytochromeCredutaseiron-sulfursubunit(EC1.10.2.2)	-6.4	6	1.55	4.0E-04
K99_82950	UreaABCtransporter,ureabindingprotein □	1	47	0.42	5.3E-02
k99_60413	XyloseABCtransporter.periplasmicxylose-bindingproteinXylF	6.0	7	1.48	5.2E-04
k99_99023	XyloseABCtransporter.periplasmicxylose-bindingproteinXylF	3.0	27	0.85	3.4E-03
k99_90382	XyloseABCtransporter.periplasmicxylose-bindingproteinXylF	2.7	18	0.85	9.8E-03
k99_60008	XyloseABCtransporter.periplasmicxylose-bindingproteinXylF	-4.0	9	1.27	9.0E-03
k99_32481	XyloseABCtransporter.periplasmicxylose-bindingproteinXylF	-8.7	114	1.10	1.9E-13

B					
ORF	SEED Rank3	log2 fold change	base mean	lfcSE	padj
k99_78664	6-phosphofructokinase(EC2.7.1.11)	3.5	101	0.57	3.3E-08
k99_40746	6-phosphofructokinase(EC2.7.1.11)	2.3	25	0.58	1.0E-03
k99_106596	6-phosphofructokinase(EC2.7.1.11)	-2.3	48	0.43	2.7E-06
k99_119667	6-phosphofructokinase(EC2.7.1.11)	-7.8	16	1.36	3.8E-07
k99_105355	Aconitatehydratase(EC4.2.1.3)	6.3	8	1.45	2.2E-04
k99_63359	Aconitatehydratase(EC4.2.1.3)	3.6	30	0.65	1.1E-06
k99_10280	Aconitatehydratase(EC4.2.1.3)	2.6	70	0.45	1.4E-07
k99_119437	Aconitatehydratase(EC4.2.1.3)	1.1	101	0.34	7.5E-03
k99_60749	Aconitatehydratase(EC4.2.1.3)	-1.3	361	0.31	4.6E-04
k99_35195	Aconitatehydratase(EC4.2.1.3)	-1.5	240	0.28	4.1E-06
k99_39473	Aconitatehydratase(EC4.2.1.3)	-1.6	34	0.49	8.7E-03
k99_61594	Aconitatehydratase(EC4.2.1.3)	-2.4	791	0.37	1.1E-08
k99_28348	Aconitatehydratase(EC4.2.1.3)	-2.5	19	0.79	8.9E-03
k99_12075	Aconitatehydratase(EC4.2.1.3)	-3.4	47	0.52	3.2E-09
k99_90324	Aconitatehydratase(EC4.2.1.3)	-3.6	13	0.89	6.4E-04
k99_133074	Aconitatehydratase(EC4.2.1.3)	-3.6	15	0.93	9.4E-04
k99_3937	Aconitatehydratase(EC4.2.1.3)	-6.1	20	1.22	9.3E-06
k99_36570	Aconitatehydratase(EC4.2.1.3)	-6.2	5	1.63	1.3E-03
k99_97954	Aconitatehydratase(EC4.2.1.3)	-6.6	7	1.52	2.2E-04
k99_194	Aconitatehydratase(EC4.2.1.3)	-6.9	9	1.45	4.0E-05
k99_107685	Aconitatehydratase(EC4.2.1.3)	-9.1	40	1.27	7.5E-11
k99_65768	Aldehydehydrogenase(EC1.2.1.3)	5.7	6	1.53	1.7E-03
k99_135857	Aldehydehydrogenase(EC1.2.1.3)	5.3	4	1.63	7.3E-03
k99_65964	Aldehydehydrogenase(EC1.2.1.3)	2.9	17	0.80	2.1E-03
k99_75941	Aldehydehydrogenase(EC1.2.1.3)	2.4	22	0.63	1.1E-03
k99_57335	Aldehydehydrogenase(EC1.2.1.3)	-4.0	9	1.05	1.3E-03
k99_128511	Aldehydehydrogenase(EC1.2.1.3)	-4.5	26	0.78	2.4E-07
k99_130613	Aldehydehydrogenase(EC1.2.1.3)	-5.9	15	1.28	7.5E-05
k99_93779	Aldehydehydrogenase(EC1.2.1.3)	-5.9	4	1.76	5.8E-03
k99_57029	Aldehydehydrogenase(EC1.2.1.3)	-6.0	5	1.71	3.7E-03
k99_123866	Aldehydehydrogenase(EC1.2.1.3)	-6.1	56	0.83	1.7E-11
k99_4952	Aldehydehydrogenase(EC1.2.1.3)	-6.6	26	1.20	1.1E-06
k99_57552	Aldehydehydrogenase(EC1.2.1.3)	-7.5	14	1.57	2.8E-05
k99_85656	Aldehydehydrogenase(EC1.2.1.3)	-7.6	15	1.40	1.2E-06
k99_14884	Aldehydehydrogenase(EC1.2.1.3)	-7.9	18	1.47	1.6E-06
k99_134650	Aldehydehydrogenase(EC1.2.1.3)	-9.1	42	1.43	8.0E-09
k99_110820	Fructose-1,6-bisphosphatase.GlpXtype(EC3.1.3.11)	-4.1	263	0.62	1.1E-09
k99_16838	Fructose-bisphosphatealdolaseclassI(EC4.1.2.13)	7.4	18	1.36	1.6E-06
k99_81024	Fructose-bisphosphatealdolaseclassI(EC4.1.2.13)	5.5	5	1.61	4.5E-03
k99_106085	Fructose-bisphosphatealdolaseclassI(EC4.1.2.13)	2.4	19	0.66	2.5E-03
k99_3510	Fructose-bisphosphatealdolaseclassI(EC4.1.2.13)	-10.5	104	1.25	7.6E-15
k99_66485	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	6.5	10	1.41	7.3E-05
k99_40833	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	5.2	4	1.65	9.1E-03
k99_74171	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	2.5	35	0.70	2.7E-03
k99_11376	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	1.3	129	0.33	7.7E-04
k99_54525	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-1.7	4700	0.37	5.4E-05
k99_81113	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-2.5	17	0.78	7.1E-03
k99_42885	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-3.5	139	0.36	1.4E-20
k99_8940	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-4.1	10	1.04	7.5E-04
k99_18040	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-4.3	21	0.80	2.8E-06
k99_139919	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-4.9	8	1.36	2.8E-03
k99_31886	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-4.9	16	1.02	2.8E-05
k99_107362	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-5.3	11	1.45	2.1E-03
k99_94818	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-6.5	7	1.55	3.4E-04
k99_104971	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-6.6	7	1.52	1.9E-04
k99_53623	Fructose-bisphosphatealdolaseclassII(EC4.1.2.13)	-6.8	8	1.45	5.4E-05
k99_68137	L-lactatedehydrogenase(EC1.1.2.3)	5.1	14	1.24	4.4E-04
k99_71546	L-lactatedehydrogenase(EC1.1.2.3)	-4.3	16	0.99	1.7E-04
k99_133235	L-lactatedehydrogenase(EC1.1.2.3)	-6.7	8	1.75	1.3E-03
k99_132270	Lactoylglutathionelyase(EC4.4.1.5)	-6.3	6	1.65	1.2E-03
k99_31582	Malatedehydrogenase(EC1.1.1.37)	5.7	6	1.56	2.3E-03
k99_117298	Malatedehydrogenase(EC1.1.1.37)	2.2	58	0.64	3.5E-03
k99_26579	Malatedehydrogenase(EC1.1.1.37)	2.2	23	0.67	6.2E-03
k99_10686	Malatedehydrogenase(EC1.1.1.37)	-3.9	52	0.52	1.1E-11
k99_114059	Malatedehydrogenase(EC1.1.1.37)	-3.9	21	0.74	4.6E-06
k99_67900	Malatedehydrogenase(EC1.1.1.37)	-3.9	9	1.06	1.9E-03
k99_111766	Malatedehydrogenase(EC1.1.1.37)	-5.6	4	1.73	8.0E-03
k99_114909	Malatedehydrogenase(EC1.1.1.37)	-5.7	4	1.76	7.9E-03
k99_34961	Malatedehydrogenase(EC1.1.1.37)	-6.2	5	1.57	8.3E-04
k99_79636	Malatedehydrogenase(EC1.1.1.37)	-6.3	6	1.54	4.7E-04

k99_34145	Malatedehydrogenase(EC1.1.1.37)	-6.4	6	1.52	3.4E-04
k99_29964	Malatedehydrogenase(EC1.1.1.37)	-6.8	8	1.63	4.0E-04
k99_31414	Malatedehydrogenase(EC1.1.1.37)	-7.0	10	1.52	6.1E-05
k99_2370	Malatedehydrogenase(EC1.1.1.37)	-7.9	18	1.35	1.4E-07
k99_83293	Malatedehydrogenase(EC1.1.1.37)	-8.4	25	1.32	8.6E-09
k99_122142	MalatesynthaseG(EC2.3.3.9)	-2.5	2982	0.27	2.3E-18
k99_71016	MalatesynthaseG(EC2.3.3.9)	-5.8	4	1.67	3.4E-03
k99_42849	MalatesynthaseG(EC2.3.3.9)	-6.3	6	1.60	7.8E-04
k99_15603	MalatesynthaseG(EC2.3.3.9)	-7.2	11	1.39	6.4E-06
k99_131620	Phosphoglyceratekinase(EC2.7.2.3)	6.8	12	1.53	1.5E-04
k99_72128	Phosphoglyceratekinase(EC2.7.2.3)	6.7	11	1.43	4.0E-05
k99_2917	Phosphoglyceratekinase(EC2.7.2.3)	-3.4	14683	0.72	5.0E-05
k99_39359	Phosphoglyceratekinase(EC2.7.2.3)	-3.5	71	0.45	2.1E-12
k99_23380	Phosphoglyceratekinase(EC2.7.2.3)	-6.1	5	1.58	1.1E-03
k99_11282	Phosphoglyceratekinase(EC2.7.2.3)	-6.2	19	1.19	5.0E-06
k99_80576	Phosphoglyceratekinase(EC2.7.2.3)	-6.5	7	1.76	1.9E-03
k99_140926	Phosphoglyceratekinase(EC2.7.2.3)	-7.3	12	1.41	5.2E-06
k99_73154	Phosphoglyceratekinase(EC2.7.2.3)	-7.4	13	1.36	1.4E-06
k99_39134	Phospholipid-lipopolysaccharideABCtransporter □	-5.3	3	2.23	6.3E-02
k99_108070	Phospholipid-lipopolysaccharideABCtransporter □	-5.3	3	2.20	5.7E-02
k99_89058	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	4.3	8	1.30	5.9E-03
k99_10683	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	2.5	81	0.44	3.3E-07
k99_97801	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	2.0	99	0.42	2.7E-05
k99_55699	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	1.5	129	0.32	2.9E-05
k99_60807	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	-1.4	134	0.32	2.0E-04
k99_56337	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	-3.4	66	0.50	5.3E-10
k99_140108	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	-5.6	4	1.76	9.3E-03
k99_42359	PyruvatedehydrogenaseE1componentalphasubunit(EC1.2.4.1)	-6.9	167	0.63	1.8E-25
k99_58887	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	1.9	79	0.38	1.3E-05
k99_80142	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	1.1	342	0.32	2.8E-03
k99_119863	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-1.2	98	0.36	4.8E-03
k99_91531	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-3.0	15	0.74	5.5E-04
k99_32773	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-4.8	7	1.37	3.6E-03
k99_43765	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-5.6	4	1.73	8.0E-03
k99_98042	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-5.7	4	1.69	5.2E-03
k99_136066	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-5.7	4	1.70	5.4E-03
k99_132454	PyruvatedehydrogenaseE1componentbetasubunit(EC1.2.4.1)	-6.8	62	0.89	1.9E-12
k99_69575	Pyruvatekinase(EC2.7.1.40)	5.5	5	1.60	4.1E-03
k99_4745	Pyruvatekinase(EC2.7.1.40)	5.3	4	1.62	6.5E-03
k99_133010	Pyruvatekinase(EC2.7.1.40)	4.7	11	1.33	3.0E-03
k99_10664	Pyruvatekinase(EC2.7.1.40)	3.5	20	0.86	4.9E-04
k99_33771	Pyruvatekinase(EC2.7.1.40)	3.1	21	0.69	9.8E-05
k99_8989	Pyruvatekinase(EC2.7.1.40)	1.9	3144	0.29	1.6E-09
k99_20189	Pyruvatekinase(EC2.7.1.40)	1.6	71	0.39	7.4E-04
k99_40888	Pyruvatekinase(EC2.7.1.40)	1.4	68	0.41	5.0E-03
k99_110851	Pyruvatekinase(EC2.7.1.40)	-2.1	39	0.61	5.1E-03
k99_22787	Pyruvatekinase(EC2.7.1.40)	-3.4	37	0.62	1.1E-06
k99_48095	Pyruvatekinase(EC2.7.1.40)	-4.4	18	0.87	8.0E-06
k99_114848	Pyruvatekinase(EC2.7.1.40)	-5.4	56	0.79	7.4E-10
k99_113884	Pyruvatekinase(EC2.7.1.40)	-7.9	65	1.13	1.9E-10
k99_53181	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	4.9	49	0.68	2.4E-11
k99_102233	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	1.9	49	0.44	2.7E-04
k99_8805	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	1.6	46	0.43	2.0E-03
k99_107887	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	1.6	67	0.43	2.2E-03
k99_141065	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-1.4	68	0.43	6.2E-03
k99_100030	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-2.9	29	0.57	9.0E-06
k99_48445	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-3.2	14	0.88	2.1E-03
k99_61226	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-3.4	9	1.02	6.4E-03
k99_9825	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-3.9	17	0.82	3.4E-05
k99_131909	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-4.6	7	1.40	7.3E-03
k99_140380	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-4.6	33	0.77	1.3E-07
k99_75948	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-5.3	11	1.32	7.2E-04
k99_26511	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-5.7	14	1.26	1.1E-04
k99_62436	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-5.7	4	1.70	5.4E-03
k99_20099	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-5.7	4	1.67	4.5E-03
k99_70899	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-6.2	6	1.63	1.2E-03
k99_6892	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-6.3	6	1.55	5.6E-04
k99_130494	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-6.3	22	1.17	1.4E-06
k99_74299	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-7.6	15	1.45	3.8E-06
k99_37228	Ribose-phosphatepyrophosphokinase(EC2.7.6.1)	-8.1	21	1.31	2.3E-08
k99_9159	Succinatedehydrogenaseflavoproteinsubunit(EC1.3.99.1)	5.8	22	1.16	1.3E-05
k99_23745	Succinatedehydrogenaseflavoproteinsubunit(EC1.3.99.1)	2.1	31	0.56	1.7E-03
k99_65158	Succinatedehydrogenaseflavoproteinsubunit(EC1.3.99.1)	2.1	103	0.39	3.3E-06

k99_91439	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	1.5	67	0.42	2.0E-03
k99_116248	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	1.4	74	0.35	9.5E-04
k99_48727	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	1.1	152	0.35	7.4E-03
k99_42797	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-1.5	176	0.34	8.9E-05
k99_137091	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-1.6	45	0.46	5.2E-03
k99_126241	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-2.6	32	0.59	1.8E-04
k99_106479	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-2.6	13	0.76	3.8E-03
k99_43416	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-2.9	22	0.59	2.4E-05
k99_124612	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-3.2	19	0.87	1.9E-03
k99_94373	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-3.3	25467	0.30	1.4E-24
k99_19912	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-3.4	11	1.05	8.4E-03
k99_138913	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-3.7	15	0.80	4.4E-05
k99_122872	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-3.9	3559	0.62	1.5E-08
k99_95468	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-4.1	319	0.44	1.2E-18
k99_100266	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-4.5	7	1.38	7.1E-03
k99_88119	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-4.6	21	0.94	1.8E-05
k99_72287	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-4.6	13	1.08	2.6E-04
k99_135286	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-4.9	42	0.73	8.7E-10
k99_78057	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-5.1	10	1.27	6.2E-04
k99_59984	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-5.5	13	1.24	1.3E-04
k99_140342	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-5.7	4	1.69	5.0E-03
k99_69300	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-5.8	4	1.76	6.5E-03
k99_75870	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.0	5	1.65	2.4E-03
k99_101617	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.0	5	1.65	2.3E-03
k99_123744	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.1	5	1.58	1.1E-03
k99_62919	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.2	6	1.62	1.1E-03
k99_37518	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.3	22	1.17	1.5E-06
k99_50269	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.5	7	1.54	2.9E-04
k99_78897	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.6	7	1.47	9.0E-05
k99_3745	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.7	8	1.48	7.8E-05
k99_93892	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-6.9	9	1.46	4.3E-05
k99_131617	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-7.0	9	1.54	9.4E-05
k99_112356	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-7.5	14	1.44	4.2E-06
k99_119022	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-8.0	19	1.36	1.4E-07
k99_85559	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-8.6	28	1.29	1.9E-09
k99_21254	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-8.6	29	1.34	6.3E-09
k99_117485	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-8.9	36	1.34	1.3E-09
k99_130478	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-9.5	54	1.29	1.4E-11
k99_44258	Succinate dehydrogenase flavoprotein subunit (EC1.3.99.1)	-9.9	260	1.07	5.0E-18

Table 7

Differential expression of bacterial open reading frames (ORFs) using raw counts, normalized with internal standards (applying the *controlGenes* function (*estimatedSizeFactors*) in *DESeq2*, between timepoints (T2 vs T1) for distinct SEED Rank1/Rank3 annotations. Log2FoldChange – log2 fold changed between timepoints (in triplicates), base mean – mean transcription level at T1 & T2, lfcSE – log2 fold change standard error, padj – adjusted p-values, below threshold <0.01. A) Carbon, nitrogen and phosphorous uptake and assimilation, B) Carbon cycling. □ - indicate padj >0.01.