Additional file 4

Table S1. Genes with an altered expression upon inactivation of spr0058 as determined by RNAseq.

R6_geneID	Function	FPKM[a] R6WT	FPKM[a] R6$^{\Delta spr0058}$	log2 (KO/WT)	*p* value	*q* value
Genes downregulated in R6$^{\Delta spr0058}$						
spr0081	ABC transporter permease	377.482	84.0558	-2.16699	0.000181602	0.00931757
spr0082	ABC transporter permease	341.228	57.1887	-2.57693	1.47E-05	0.00113125
spr0083	ABC transporter substrate-binding protein	259.203	30.1397	-3.10434	2.14E-07	3.05E-05
spr0127	hypothetical protein	5866.42	1367.38	-2.10107	0.000320174	0.015254
spr0128	hypothetical protein	2841.73	676.937	-2.06967	0.000470955	0.0204865
spr0440	endo-beta-N-acetylglucosaminidase	110.743	25.8047	-2.10151	0.000146839	0.0081618
spr1724	single-stranded DNA-binding protein	916.763	172.564	-2.40941	5.05E-05	0.00325931
spr1837	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	8237.01	1512.64	-2.44506	1.15E-07	1.91E-05
spr1856	hypothetical protein	139.4	19.6117	-2.82944	0.000188588	0.00943411
spr1858	hypothetical protein	571.991	83.9454	-2.76847	5.44E-06	0.000494609
spr1859	hypothetical protein	154.251	32.4824	-2.24755	0.00085038	0.0340322
spr1861	competence protein CglD	313.504	51.8821	-2.59518	3.56E-05	0.00245447
spr1862	competence protein CglC	714.751	134.909	-2.40545	9.97E-05	0.00586808
spr1863	competence protein CglB	380.283	56.4995	-2.75076	3.34E-06	0.000318369
spr1864	competence protein CglA	583.43	88.358	-2.72313	2.69E-06	0.000283159
spr1936	transketolase, C-terminal subunit	1426.9	273.37	-2.38396	9.15E-06	0.000796012
spr1937	transketolase n-terminal section	1232.83	238.558	-2.36955	1.08E-05	0.000904189
spr1938	PTS system ascorbate-specific transporter subunit IIC	808.009	164.622	-2.29522	1.92E-05	0.00140344
spr1939	PTS system IIB component	1402.61	285.359	-2.29726	0.000107708	0.00615784
spr1940	hypothetical protein	959.604	272.056	-1.81853	0.000947187	0.0371632
spr1949	glycosyl hydrolase-related protein	103.522	10.9756	-3.23756	1.27E-07	1.95E-05
spr1950	ROK family protein	99.2467	13.0581	-2.92608	1.28E-05	0.00102654
spr1951	hypothetical protein	98.0277	11.6118	-3.0776	3.28E-07	4.37E-05
spr1952	hypothetical protein	71.9572	12.4131	-2.53527	9.17E-05	0.00556239
spr1966	hypothetical protein	67.7091	13.9362	-2.28051	0.000177384	0.00931757
spr1967	PTS system IID component	193.493	26.2447	-2.88218	3.34E-06	0.000318369
spr1968	PTS system IIC component	180.5	28.3971	-2.66818	1.96E-05	0.00140344
spr1969	PTS system IIB component	649.476	151.453	-2.1004	0.000375416	0.01747
spr1970	PTS system IIA component	327.962	74.8861	-2.13076	0.000623509	0.0259925
spr1987	hypothetical protein	3327.55	314.128	-3.40504	5.13E-08	9.33E-06
spr1988	glycerol uptake facilitator protein	825.036	110.367	-2.90215	7.18E-07	8.45E-05
spr1989	glycerol-3-phosphate dehydrogenase	1521.66	236.257	-2.68722	2.07E-06	0.000230101

spr2013	helicase	17.531	2.65317	-2.72412	0.000734292	0.0299861
		Genes upregulated in R6$^{\Delta spr0058}$				
spr0059	Beta-galactosidase	263.543	4437.5	4.07364	6.98E-09	1.55E-06
spr0060	PTS system IIB component	104.66	1676.63	4.00179	2.37E-11	9.47E-09
spr0061	PTS system IIC component	235.929	2672.44	3.50174	2.57E-10	8.56E-08
spr0062	PTS system IID component	150.757	1645.83	3.44852	5.11E-10	1.28E-07
spr0063	PTS system IIA component	179.587	2353.97	3.71234	3.17E-10	9.08E-08
spr0064	tagatose-6-phosphate isomerase	102.829	1489.46	3.85647	5.29E-12	3.53E-09
spr0065	aldose 1-epimerase	57.9243	882.493	3.92934	2.16E-11	9.47E-09
spr0092	NAD-dependent epimerase/dehydratase family protein	340.426	1644.1	2.27189	7.16E-05	0.00447493
spr0310	glucan 1,6-alpha-glucosidase	177.718	824.112	2.21325	3.95E-05	0.00263421
spr0328	cell wall surface anchor family protein	32.4643	890.032	4.77693	1.40E-14	2.80E-11
spr0528	VncR, response regulator	167.727	646.49	1.94651	0.000599926	0.0255415
spr0529	VncS, histidine kinase	162.836	662.614	2.02475	0.00016685	0.00902344
spr0668	PTS system IIABC component	83.8985	316.363	1.91486	0.000410764	0.0186804
spr1324	thiamine biosynthesis protein	133.511	524.898	1.97508	0.000433737	0.0192868
spr1698	dextran glucosidase	45.9816	750.799	4.0293	2.47E-12	2.47E-09
spr1699	trehalose-specific PTS system IIBC component	33.3452	316.49	3.24661	2.22E-08	4.45E-06
spr1914	hypothetical protein	64.4146	445.444	2.78978	0.000283421	0.0138323
spr1915	hypothetical protein	272.417	1824.6	2.74369	5.77E-07	7.21E-05

[a]Fragments Per Kilobase of transcript per Million fragments mapped.