

Table S2. Genes differentially expressed in the PDS phase in response to the *rph1-H235A* mutation.

Genetic contrast		<i>rph1-H235A</i> vs. WT		<i>rph1Δ</i> vs. WT		<i>gis1Δ rph1-H235A</i> vs. <i>gis1Δ</i>		<i>gis1Δ</i> vs. WT		<i>gis1Δ rph1-H235A</i> vs. WT		<i>gis1Δ rph1Δ</i> vs. WT	
Cluster	Gene	Fold	p-value	Fold	p-value	Fold	p-value	Fold	p-value	Fold	p-value	Fold	p-value
P1	<i>SUL2</i>	2.1	1.4E-03	1.3	0.27	1.4	0.11	2.1	1.1E-03	2.9	1.8E-05	1.8	5.6E-03
	<i>SNZ1</i>	0.5	3.8E-03	0.4	1.4E-04	0.6	0.04	0.8	0.42	0.5	6.0E-03	0.4	4.3E-05
	<i>SNO1</i>	0.4	4.5E-05	0.4	8.6E-05	0.4	1.8E-04	1.0	0.94	0.4	2.2E-04	0.5	1.8E-03
	<i>PAU24</i>	0.7	0.03	0.7	0.09	0.5	7.0E-04	1.0	0.83	0.5	1.2E-03	0.9	0.34
	<i>GTT2</i>	0.6	8.3E-06	0.7	2.1E-04	0.6	5.7E-06	1.0	0.72	0.6	2.4E-06	1.0	0.79
P2	<i>OSW2</i>	1.6	8.7E-03	2.0	1.1E-04	1.3	0.11	2.5	3.3E-06	3.3	7.1E-08	3.3	7.0E-08
	<i>PRM7</i>	1.7	1.4E-04	2.0	2.7E-06	1.1	0.37	2.6	2.1E-08	2.8	3.1E-09	3.5	1.1E-10
	<i>YOL131W</i>	2.1	1.5E-03	2.9	4.1E-05	0.9	0.80	6.5	5.5E-09	6.2	9.3E-09	10.2	9.5E-11
	<i>YNL034W</i>	0.6	4.2E-03	0.7	0.03	0.9	0.54	1.0	0.88	0.9	0.65	1.1	0.42
	<i>SET4</i>	1.9	2.3E-04	2.7	1.3E-06	0.9	0.36	3.2	7.5E-08	2.8	6.3E-07	4.1	3.3E-09
	<i>SPO22</i>	1.5	3.2E-03	2.5	4.7E-07	0.9	0.56	2.9	3.6E-08	2.7	1.3E-07	5.0	1.2E-11
	<i>ARP10</i>	1.9	6.7E-03	2.7	6.9E-05	1.0	0.91	2.4	3.7E-04	2.3	4.9E-04	3.4	4.7E-06
	<i>YDL241W</i>	1.5	3.1E-04	1.5	2.0E-04	1.1	0.60	1.5	3.4E-04	1.6	8.9E-05	2.0	1.7E-07
	<i>ADH7</i>	1.6	1.2E-04	1.6	1.6E-04	1.0	0.86	1.7	3.4E-05	1.7	2.1E-05	2.5	4.3E-09
	<i>YOL163W</i>	2.9	3.0E-03	3.8	3.8E-04	1.0	1.00	2.9	3.4E-03	2.9	3.6E-03	4.2	1.6E-04
	<i>YAL016C-B</i>	0.4	5.0E-03	0.8	0.37	0.7	0.15	0.6	0.08	0.4	3.0E-03	0.6	0.13
P3	<i>PGU1</i>	0.7	0.23	0.4	2.4E-03	0.5	6.2E-03	0.8	0.35	0.4	6.0E-04	0.3	5.1E-05
	<i>ECM10</i>	0.8	0.02	0.7	1.2E-04	0.5	2.4E-07	0.8	4.6E-03	0.4	3.7E-10	0.4	5.4E-09
	<i>YOR032W-A</i>	0.8	0.26	0.5	4.1E-03	0.4	6.3E-04	0.6	8.9E-03	0.2	5.8E-07	0.3	2.3E-06
	<i>YKL071W</i>	0.8	0.14	0.7	0.04	0.6	2.6E-03	0.8	0.10	0.4	3.6E-05	0.7	0.02
	<i>AAD10</i>	0.6	4.4E-04	0.9	0.44	0.6	4.9E-04	0.6	1.5E-04	0.4	1.2E-08	0.6	1.6E-04
	<i>YNR066C</i>	2.0	3.7E-03	2.1	2.6E-03	0.9	0.61	1.5	0.09	1.3	0.22	1.7	0.02
	<i>CAX4</i>	1.6	2.5E-03	1.4	0.02	1.1	0.32	1.0	0.93	1.1	0.36	1.2	0.21
	<i>DAL80</i>	1.6	2.1E-05	1.3	2.6E-03	1.0	0.65	0.9	0.40	1.0	0.70	1.1	0.57
	<i>GPM3</i>	1.6	1.4E-03	1.4	0.02	1.0	0.76	1.1	0.35	1.2	0.22	1.2	0.18
	<i>YHK8</i>	2.2	3.5E-03	1.3	0.30	1.1	0.63	0.6	0.02	0.6	0.07	0.6	0.08
	<i>PUG1</i>	1.6	2.5E-03	1.7	8.0E-04	1.1	0.72	1.2	0.27	1.2	0.15	1.3	0.11
	<i>YGL262W</i>	4.4	1.7E-09	7.7	3.0E-12	1.0	0.91	0.9	0.42	0.9	0.49	0.7	0.01
	<i>COS12</i>	2.4	1.5E-03	7.5	3.0E-08	0.9	0.60	0.8	0.42	0.7	0.19	0.7	0.15
	<i>YMR118C</i>	0.7	0.16	0.9	0.59	0.1	1.1E-10	0.01	5.6E-17	0.001	1.0E-20	0.003	5.0E-20
	<i>MSH4</i>	2.3	9.9E-04	2.1	1.8E-03	0.9	0.73	1.7	0.02	1.6	0.04	1.5	0.09
P4	<i>AGA2</i>	1.6	1.3E-03	1.5	6.2E-03	1.0	0.88	1.3	0.04	1.3	0.06	1.7	7.0E-04
	<i>SPS1</i>	1.9	3.2E-03	1.6	0.02	1.0	0.87	1.5	0.05	1.6	0.03	2.0	2.0E-03
	<i>ATF2</i>	1.7	7.5E-03	1.7	4.4E-03	1.2	0.21	1.4	0.08	1.7	5.1E-03	1.7	3.7E-03
	<i>YDL063C</i>	1.5	7.8E-03	1.4	0.03	1.3	0.06	1.0	0.76	1.4	0.03	1.2	0.32
	<i>NRP1</i>	1.7	9.9E-04	1.3	0.05	1.1	0.40	1.2	0.31	1.3	0.07	1.1	0.34
	<i>SLZ1</i>	1.5	4.1E-04	1.0	0.75	1.1	0.30	1.0	0.89	1.1	0.24	1.0	0.81

The clusters are those shown in figure 3. Significantly upregulated genes are shown in red, significantly downregulated genes in green.