

### Supplemental Table S1.

Transcriptional profiling reveals gene expression differences in *hand2* mutants

Probe set	Gene	Fold change	p value
Dr.8328.1.S1_at	<i>hand2</i>	- 5.270	8.53E-04
Dr.16219.1.A1_at		- 2.764	0.011
Dr.642.1.S1_at	<i>myl7</i>	- 2.445	0.003
Dr.8379.1.S1_at	LOC573558	- 2.146	0.044
Dr.10607.1.A1_at	<i>vmhc</i>	- 2.133	0.017
Dr.7897.1.A1_at	wu:fe24c01	- 1.874	0.005
Dr.3113.2.A1_at	zgc:91844	- 1.712	0.008
Dr.8176.1.S1_at	<i>pax5</i>	- 1.590	0.042
Dr.20019.1.S1_at	<i>thy1</i>	- 1.506	0.019
Dr.3300.1.S1_at	LOC564312	+ 1.508	0.047
Dr.17711.1.S1_at	<i>retl</i>	+ 1.512	0.032
Dr.22498.1.A1_at	<i>itga5</i>	+ 1.513	0.038
Dr.21394.1.S1_at	LOC559746	+ 1.521	0.033
Dr.17582.1.A1_at		+ 1.548	0.028
Dr.12836.2.A1_at	<i>id2b</i>	+ 1.579	0.049
Dr.13902.1.S1_at	<i>nbcel</i>	+ 1.586	0.041
Dr.10475.1.A1_at		+ 1.601	0.017
Dr.12315.1.A1_at		+ 1.604	0.019
Dr.20398.1.A1_x_at	<i>acsll</i>	+ 1.624	0.020
Dr.11707.2.A1_at	<i>smox</i>	+ 1.631	0.011
Dr.5094.3.A1_at	<i>smu1</i>	+ 1.649	0.027
Dr.16088.2.S1_at	<i>kctd12.2</i>	+ 1.669	0.008
Dr.4925.1.S1_at	<i>cygb</i>	+ 1.684	0.045
Dr.16297.1.A1_at		+ 1.692	0.021
Dr.12942.1.S1_at	LOC402976	+ 1.730	0.046
Dr.14662.1.S2_at	<i>tcf2</i>	+ 1.748	0.030
Dr.20398.1.A1_at	<i>acsll</i>	+ 1.750	0.024
Dr.5842.1.A1_at		+ 1.888	0.049
Dr.19965.1.S1_at	<i>fn1</i>	+ 2.004	0.036
Dr.3609.1.S1_at	<i>cdh17</i>	+ 2.176	0.042
Dr.14035.2.A1_at	LOC567858	+ 2.394	0.010
Dr.10719.1.S1_at	<i>atplala.4</i>	+ 2.398	0.045
Dr.12596.1.S1_at	<i>cldnc</i>	+ 2.595	0.035
Dr.15418.1.S1_at	wu:fc23f06	+ 2.982	0.048
Dr.12000.1.S1_at	LOC565439	+ 3.094	0.029

For each of the 35 genes exhibiting a >1.5-fold difference in gene expression in *hand2* mutants relative to their wild-type siblings, the Affymetrix probe set, gene name (if assigned), fold change in *hand2* mutants, and statistical significance of our results from triplicate samples are provided.