

Table 5. List of genes down regulated ≥ 3 fold upon GK gene silencing.

Gene ID	Expression level		Fold change	Gene Name	q_value
	pSAP2G	GK			
EHI_144490	124.22	1.05	118.5	hypothetical protein, conserved	4.77E-04
EHI_074090	69.91	2.68	26.1	40S ribosomal protein S14, putative	4.77E-04
EHI_190460	15.36	0.72	21.4	amino acid transporter, putative	4.77E-04
EHI_152650	6.71	0.35	19.4	type A flavoprotein, putative	4.77E-04
EHI_041465	14.86	0.91	16.3	AIG family protein	4.77E-04
EHI_119040	4.27	0.28	15.5	AIG1 family protein, putative	4.77E-04
EHI_072850	2.63	0.17	15.4	AIG1 family protein, putative	2.79E-02
EHI_072740	1.73	0.13	13.1	hypothetical protein	4.77E-04
EHI_073060	4.38	0.35	12.4	hypothetical protein, conserved	4.77E-04
EHI_180390	55.06	5.73	9.6	AIG1 family protein, putative	4.77E-04
EHI_176590	16.46	1.78	9.2	AIG1 family protein, putative	4.77E-04
EHI_174230	2.91	0.33	8.9	hypothetical protein	4.77E-04
EHI_180400	0.42	0.05	7.8	hypothetical protein	3.76E-02
EHI_176700	48.37	6.57	7.4	AIG1 family protein, putative	4.77E-04
EHI_001290	1.24	0.18	6.9	P-glycoprotein-2, putative	4.75E-02
EHI_142120	0.79	0.11	6.9	heat shock transcription factor, putative	4.76E-02
EHI_069090	2.59	0.39	6.7	hypothetical protein	8.10E-03
EHI_178050	0.76	0.13	5.8	ATP-binding cassette protein, putative	4.77E-04
EHI_176960	15.13	2.65	5.7	hypothetical protein	4.77E-04
EHI_154310	59.67	10.56	5.6	hypothetical protein	4.77E-04
EHI_077000	4.11	0.73	5.6	pre-mRNA cleavage factor I 25 kDa subunit, putative	4.77E-04
EHI_109010	2.10	0.38	5.5	hypothetical protein	4.77E-04
EHI_005260	3.33	0.61	5.5	surface antigen ariel1, putative	4.77E-04
EHI_096710	1.73	0.34	5.1	type A flavoprotein, putative	4.77E-04
EHI_182150	1.62	0.34	4.8	hypothetical protein	4.77E-04
EHI_114950	15.50	3.28	4.7	hypothetical protein, conserved	4.77E-04
EHI_051440	13.97	3.01	4.6	hypothetical protein	4.77E-04
EHI_201610	69.68	15.23	4.6	hypothetical protein, conserved	4.77E-04
EHI_167010	4.90	1.07	4.6	tubulin family protein	4.77E-04
EHI_188860	22.12	5.03	4.4	hypothetical protein	4.77E-04
EHI_180140	1.09	0.25	4.4	hypothetical protein	3.51E-03
EHI_109020	3.31	0.76	4.3	ABC transporter, pseudogene, putative	4.77E-04
EHI_151450	3.84	0.96	4.0	hypothetical protein	4.77E-04
EHI_187400	0.99	0.25	4.0	hypothetical protein	2.20E-02
EHI_192410	5.96	1.51	3.9	hypothetical protein	4.77E-04
EHI_158340	1.29	0.34	3.9	hypothetical protein	1.33E-02
EHI_082260	0.71	0.18	3.8	CXXC-rich protein	4.77E-04
EHI_062990	2.64	0.70	3.8	hypothetical protein	4.77E-04
EHI_150410	1.00	0.27	3.7	hypothetical protein	2.46E-02
EHI_187020	0.85	0.23	3.6	glyceraldehyde-3-phosphate dehydrogenase, putative	8.10E-03
EHI_117470	128.97	35.82	3.6	calmodulin, putative	4.77E-04
EHI_176580	15.86	4.48	3.5	AIG1 family protein, putative	4.77E-04
EHI_142670	6.78	1.92	3.5	hypothetical protein, conserved	4.77E-04
EHI_054820	1.71	0.51	3.3	FAD dependent oxidoreductase, pseudogene, putative	4.77E-04
EHI_067220	9.48	2.85	3.3	Rho family GTPase	4.77E-04
EHI_054720	23.08	6.98	3.3	CDP-alcohol phosphatidyltransferase family protein	4.77E-04
EHI_029500	4.53	1.37	3.3	hypothetical protein	4.77E-04
EHI_103640	1.15	0.36	3.2	protein kinase domain containing protein	4.77E-04
EHI_127670	8.29	2.56	3.2	hypothetical protein	4.77E-04
EHI_186600	1.54	0.47	3.2	P-glycoprotein-2, putative	8.84E-04
EHI_038150	4.82	1.51	3.2	hypothetical protein	4.77E-04
EHI_070690	4.46	1.40	3.2	hypothetical protein	4.77E-04
EHI_138070	10.51	3.31	3.2	hypothetical protein	8.84E-04
EHI_005930	3.90	1.23	3.2	hypothetical protein	4.77E-04
EHI_015430	14.28	4.62	3.1	hypothetical protein	4.77E-04
EHI_164850	2.38	0.77	3.1	glycerol kinase, putative	4.31E-04
EHI_192550	2.12	0.69	3.1	hypothetical protein	2.54E-02
EHI_142750	1.45	0.48	3.1	hypothetical protein	4.77E-04
EHI_046630	5.35	1.76	3.0	Rho family GTPase	4.77E-04
EHI_081625	0.58	0.19	3.0	hypothetical protein	3.90E-02
EHI_194180	15.26	5.02	3.0	hypothetical protein	4.77E-04
EHI_058470	73.85	24.28	3.0	N-acetylmuramidase pseudogene	4.77E-04
EHI_114650	8.12	2.67	3.0	hypothetical protein	4.77E-04
EHI_045340	59.30	19.58	3.0	glutamate synthase beta subunit, putative	4.77E-04
EHI_186940	1.85	0.61	3.0	hypothetical protein	2.42E-02
EHI_193520	1.86	0.61	3.0	regulator of nonsense transcripts, putative	4.77E-04
EHI_120260	1.67	0.56	3.0	hypothetical protein	1.26E-03
EHI_187080	10.56	3.56	3.0	hypothetical protein	4.77E-04
EHI_174280	4.09	1.38	3.0	phospholipid-translocating P-type ATPase, putative	4.77E-04