Table 2. The complete list of the 103 gene probes

Transcript	Control*	HU*	Control/HU†	*P* ‡	Functional category
CG4842	0.62120366	0.08597007	7.225813123	0.041903717	Metabolic enzyme
CG13244	0.88593566	0.12602329	7.029935975	0.026534949	Unknown function
CG13297	0.8580723	0.13925481	6.161886257	0.019176568	Unknown function
CG32473	1.116919	0.1985642	5.624976708	0.000945086	Proteolysis and peptidolysis
Rab10	0.9745181	0.18009323	5.41118675	0.002215184	Other function
CG12866	1.069942	0.21671154	4.93717132	0.001438827	Channel and transporter
CG5476	0.6407198	0.13052787	4.908681954	0.03582609	Unknown function
CG18266	0.7340551	0.16247323	4.518006443	0.018687103	Unknown function
Kif3C (CG17461)	0.642304	0.14294009	4.493518928	0.027082064	Cytoskeletal component
CG13312	0.7033072	0.16542795	4.251441186	0.004251386	Unknown function
CG2070	0.78866506	0.1883391	4.18747387	0.004086318	Metabolic enzyme
CG2196	0.5167162	0.12433376	4.155880109	0.043902138	Channel and transporter
CG13350	1.6129706	0.40935668	3.940257186	0.004890306	DNA/RNA binding
CG11164	0.54253936	0.13870656	3.911418177	0.027800502	Unknown function
CG14313	1.2044793	0.3086713	3.902142182	0.031750815	Unknown function
CG13566	1.0102236	0.26260048	3.846998299	0.003480984	Unknown function
CG32676	0.6017328	0.15967444	3.768497951	0.014603726	Metabolic enzyme
Hr46	0.7447138	0.21342456	3.489353803	0.022341466	Transcription
Dhod	1.2143683	0.34879887	3.481571772	0.047043204	Metabolic enzyme
CG14446	1.5227469	0.4586867	3.319797369	0.014390305	Unknown function
CG2267	0.6127484	0.19564371	3.131960644	0.004936265	Unknown function
CG3994	0.92971987	0.2980912	3.118910823	0.043875327	Channel and transporter
CG15185	1.032592	0.34153596	3.023377099	0.032572662	Unknown function
CG14350	0.97661704	0.3237962	3.016147317	0.047763205	Existence-uncertain gene

CG14014	1.3587749	0.45256904	3.002359375	0.019445448	Other function
CG14628	0.89648676	0.2992783	2.995495363	0.035018514	DNA/RNA binding
CG3371	1.2696533	0.4261838	2.979121449	0.038104515	DNA/RNA binding
CG3818	0.8604355	0.29154265	2.951319472	0.043480413	Other function
CG14911	0.75341684	0.26623556	2.829888089	0.021047885	Unknown function
CG4575	0.9942012	0.3559386	2.793181745	0.007799474	Transcription
CG14460	0.72721463	0.27166274	2.676902361	0.022337944	Unknown function
CG10205	1.2248445	0.45870465	2.67022473	0.020574162	Unknown function
fkh	0.8734546	0.32807544	2.662358999	0.049245175	Transcription
trio	0.67975944	0.2559854	2.655461757	0.018048142	Signaling
CG33143	0.6361374	0.2408915	2.640763165	0.020769898	Other function
CG13444	1.4296904	0.54238164	2.635949108	0.011454441	Channel and transporter
CG7945	1.343363	0.52288735	2.569125071	0.030503629	Other function
jing	1.6422457	0.6762096	2.428604533	0.007763174	Transcription
CG6974	0.65079576	0.28037432	2.321167502	0.02231156	Proteolysis and peptidolysis
CG7846	1.4918656	0.6512441	2.290793268	0.019468361	Cytoskeletal component
CG13716	0.6227518	0.2966155	2.09952548	0.032279552	Unknown function
CG12301	1.1438428	0.54607886	2.094647649	0.020210569	Other function
CG4940	1.334251	0.6372656	2.093712574	0.044957735	Unknown function
CG10505	0.7553747	0.36574423	2.06530859	0.004793401	Channel and transporter
CG31559	0.9356782	0.45937234	2.036862298	0.016356365	Channel and transporter
CG6372	0.543297	0.2681848	2.025830696	0.01817835	Proteolysis and peptidolysis
CG31530	0.56348175	0.28044647	2.009231031	0.03223217	Channel and transporter
Brf	1.2662749	0.6318126	2.004193807	0.044252611	Transcription
CG12744	1.1669402	0.58361876	1.999490558	0.048008803	Other function

CG13604	1.2823262	0.66222966	1.936376876	0.005377419	Unknown function
klg	1.4166996	0.74138844	1.910873604	0.007996672	Cell adhesion
CG15057	1.3013203	0.6921264	1.880177234	0.026333796	Unknown function
RluA-1	1.3239578	0.70624053	1.87465565	0.006681915	DNA/RNA binding
CG13159	1.4359236	0.775147	1.852453277	0.044429414	Unknown function
ey	1.326726	0.72115475	1.839724414	0.000640844	Transcription
CG17319	1.3354533	0.72651273	1.838169167	0.002320462	Unknown function
CG11178	1.3806639	0.75597507	1.826335226	0.029038908	Unknown function
Kif3C (CG17459)	0.80010986	0.43961567	1.820021247	0.026527212	Cytoskeletal component
CG8412	1.3024764	0.7240048	1.798988625	0.002113087	Metabolic enzyme
CG17221	1.3830123	0.77424556	1.786270883	0.010107509	Metabolic enzyme
CG13176	1.2768408	0.71816385	1.777924077	0.035108495	Transcription
CG9296	1.3009821	0.73469734	1.770772846	0.008231768	Signaling
Hrb87F	1.3284181	0.75198746	1.766542889	0.035787748	DNA/RNA binding
CG12253	1.2745266	0.72188824	1.765545592	0.005403967	Unknown function
CG15579	1.3062333	0.74874055	1.744574005	0.008359675	Unknown function
CG13879	0.6955133	0.40191934	1.730479802	0.048178831	Unknown function
CG1234	1.2869878	0.7448268	1.727902111	0.002233795	Unknown function
Itp-r83A	1.2440314	0.7322822	1.698841512	0.028087255	Signaling
CG3983	1.1087883	0.6560402	1.690122496	0.03552447	Signaling
CG6083	1.2994611	0.7707109	1.686055173	0.045103515	Metabolic enzyme
PP2A-B'	1.161467	0.690583	1.681864454	0.044209208	Signaling
Sema-1a	1.3625939	0.81081873	1.680516063	0.024452729	Signaling
elk	1.2432847	0.7452786	1.668214678	0.049328179	Channel and transporter
Atg5	1.3488524	0.8106	1.664017271	0.027621725	Other function

CG4853	1.286643	0.77333194	1.663765498	0.020183216	Signaling
RN-tre	0.7963538	0.47925064	1.661664552	0.012891125	Cell adhesion
Pkn	0.9298963	0.56370634	1.649611214	0.027029908	Signaling
CG10948	1.256458	0.773693	1.623974884	0.035747802	DNA/RNA binding
Nep1	1.2786309	0.78752583	1.623605031	0.016998033	Proteolysis and peptidolysis
CG5669	1.2916471	0.80355585	1.60741422	0.044701357	DNA/RNA binding
CG10880	1.2182193	0.75835884	1.606389002	0.007009798	Unknown function
CG13213	1.1837968	0.73825985	1.603496113	0.045421652	Metabolic enzyme
CG16803	1.3160511	0.8213089	1.602382611	0.022331094	Existence-uncertain gene
CG10083	1.1961869	0.7485394	1.598027973	0.027550075	Cytoskeletal component
CG14483	1.3165572	0.8308509	1.584589004	0.011896991	Unknown function
Rpb11	1.2870793	0.8130244	1.583075858	0.035099475	DNA/RNA binding
Dp1	1.1898068	0.7525036	1.58113104	0.045426871	DNA/RNA binding
mod(mdg4)	1.2520987	0.79475975	1.575443019	0.001930805	Transcription
CG5384	1.2303114	0.7811922	1.574915111	0.037242924	Proteolysis and peptidolysis
tra2	1.2459004	0.79328823	1.57055198	0.026421175	DNA/RNA binding
usp	1.2848113	0.8264749	1.55456784	0.018507156	Transcription
fra	1.2037536	0.77479035	1.553650739	0.023309958	Cell adhesion
CG7328	1.2617912	0.8200672	1.538643662	0.008263914	Metabolic enzyme
CG3305	1.2219881	0.7958872	1.535378506	0.021659607	Other function
CG13004	1.2544899	0.81922567	1.531311757	0.007160437	Unknown function
CG2915	1.1752964	0.7677926	1.530747236	0.047374181	Proteolysis and peptidolysis
CG9839	1.1967986	0.7829864	1.528504965	0.009522896	Unknown function
CG4287	1.2098343	0.79151803	1.528498725	0.018154626	Unknown function
apt	1.2301352	0.8140435	1.511141849	0.010257268	Transcription

PHDP	1.2285808	0.8130407	1.511093848	0.022832258	Transcription
CG12252	1.2362815	0.8186447	1.51015636	0.0095676	Transcription
CG9248	1.166326	0.7727544	1.509310073	0.045361564	Metabolic enzyme
Sara	1.1719639	0.78052014	1.50151654	0.041912054	Signaling

The microarray probes that exhibited Control/HU fold change > 1.5 with p < 0.05 by Welch *t* test are listed on the descending order of the Control/HU value. Note that Kif3C is represented twice by two independent oligonucleotide probes on the microarray. The existence of CG14351 and CG16803 are uncertain and eliminated in the recent genome annotation.

***Microarray signals of the non-ablated control and HU-treated samples after MAS 5.0 normalization.**

†Ratios of the Control signal to the HU signal.

‡Welch *t* test.