

On-line Suppl. Tab. 1. List of primers used in RT-qPCR validation.

Name	Sequence
NRT-F	GGATAGCGTCAGGGAATAAG
NRT-R	AGGTGGTTGAAGACGATG
ARGG-F	GTCCGTCCTGGTGAAATGG
ARGG-R	CTACTCGATGGATGACAACC
CHLB-F	CGCCTCTTGGAGACGATTAT
CHLB-R	TTTCTTGAGAACCACGGG
ACSF-F	CTCCGTGACGATTTTCATCC
ACSF-R	CGCCATCTTGAACAACATCC
GAPDH-F	GAACCTTCTTGCCGTTGATG
GAPDH-R	GAAGTACGATTCCATCCTGG
VPPA-F	ATGCTTCCGTACTTCTTTGG
VPPA-R	GGGATGACCATCTCAATGAT
TLA-F	CATGACGCTTCTTTTCTGTG
TLA-R	GGCACTTGTAGCTGTGGTAA

On-line Suppl. Tab. 2. List of annotated differentially expressed transcripts. This list does not include transcripts with non-specific annotations such as “hypothetical protein” or “unknown function”. Expression difference of each transcript between Py500G and PyWT is indicated as log₂-fold change (logFC) along with its correspondent false discovery rate value (FDR).

	Transcript ID	Description	logFC	FDR
1	DN10049_c0_g1_i1	Transposable element Tc1 transposase	4.097839	0.000261
2	DN1163_c0_g1_i1	K(+) efflux antiporter 3, chloroplastic {ECO:0000303 PubMed:11500563}	-8.30901	0.000206
3	DN1325_c0_g1_i1	PREDICTED: sodium/potassium/calcium exchanger 1-like [Chaetura pelagica]	-3.94781	0.024075
4	DN1509_c0_g1_i1	60S ribosomal protein L27a	-7.47848	0.001469
5	DN1627_c0_g1_i1	HSD17B1; 17beta-estradiol 17-dehydrogenase [EC:1.1.1.62]	2.653471	7.45E-07
6	DN174_c0_g1_i1	E2.1.1.41, SMT1, ERG6; sterol 24-C-methyltransferase [EC:2.1.1.41]	-7.85023	0.000814
7	DN2418_c0_g1_i1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1	-2.20044	3.06E-08
8	DN2802_c0_g1_i1	thiC; phosphomethylpyrimidine synthase [EC:4.1.99.17]	1.024393	0.002712
9	DN284_c0_g1_i1	E5.1.3.15; glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	-8.08729	0.000163
10	DN2895_c0_g1_i2	metE; 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]	-2.65597	2.55E-13
11	DN3899_c0_g1_i2	protein kinase, PfEST homolog, putative [Eimeria brunetti]	8.799801	1.55E-07
12	DN3901_c0_g1_i1	E1.14.13.81, acsF, chlE; magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase [EC:1.14.13.81]	1.731197	0.001166
12	DN3901_c0_g1_i1	chlB; light-independent protochlorophyllide reductase subunit B [EC:1.3.7.7]	1.731197	0.001166
13	DN4061_c0_g1_i1	Serine/threonine-protein kinase	-2.0927	0.029542
14	DN4209_c0_g1_i1	Putative D-cysteine desulfhydrase 1, mitochondrial	-7.64926	0.038624
15	DN4482_c0_g1_i1	2-oxoglutarate dehydrogenase, E2 component, dihydroliipoamide succinyltransferase [Streptomyces fradiae]	9.949595	5.08E-42
16	DN4522_c0_g1_i1	NPLOC4, NPL4; nuclear protein localization protein 4 homolog	13.56994	4.48E-34
17	DN4792_c0_g1_i1	Sodium/proton antiporter 1 {ECO:0000303 PubMed:11500563}	1.636608	1.86E-05
18	DN4952_c0_g2_i1	add, ADA; adenosine deaminase [EC:3.5.4.4]	1.303975	0.00503
19	DN4967_c0_g2_i1	Tigger transposable element-derived protein 4	6.277311	1.25E-15
20	DN4995_c0_g1_i2	Stress-induced-phosphoprotein 1	2.372867	0.03389
21	DN5006_c0_g1_i1	Serine/threonine-protein phosphatase 6 catalytic subunit	-7.56206	0.000713
22	DN5075_c0_g1_i1	ALOX12; arachidonate 12-lipoxygenase [EC:1.13.11.31]	-1.09693	0.048941
23	DN5245_c0_g1_i1	argH, ASL; argininosuccinate lyase [EC:4.3.2.1]	1.681926	0.000133
23	DN5245_c0_g1_i1	ppnK, NADK; NAD+ kinase [EC:2.7.1.23]	1.681926	0.000133
24	DN5266_c0_g2_i1	mRNA-capping enzyme subunit beta	-1.4451	0.000286

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	Transcript ID	Description	logFC	FDR
25	DN5408_c0_g1_i9	Ankyrin-3	-7.45583	0.004075
26	DN5421_c0_g1_i1	Putative transposon Ty5-1 protein YCL074W	4.348569	2.79E-05
27	DN5449_c0_g1_i2	Intersectin-2	1.769322	0.000119
28	DN5456_c1_g2_i2	amt, AMT, MEP; ammonium transporter, Amt family	1.290219	0.017711
29	DN5459_c0_g1_i1	Beta-glucuronosyltransferase GlcAT14A {ECO:0000305}	-1.08006	0.006473
30	DN5497_c0_g1_i2	PREDICTED: LOW QUALITY PROTEIN: mucin-2 [Ursus maritimus]	-3.27525	0.000771
31	DN5516_c0_g3_i1	Probable myosin light chain kinase	2.26289	0.038624
32	DN5535_c1_g1_i1	Tigger transposable element-derived protein 2	3.165459	0.004952
33	DN5733_c1_g1_i1	ddl; D-alanine-D-alanine ligase [EC:6.3.2.4]	2.393714	0.00503
34	DN5746_c1_g4_i2	Vacuolar iron transporter 1	-7.71791	0.002533
35	DN5747_c0_g1_i2	Kunitz-type serine protease inhibitor cvp2	-1.35062	0.011818
36	DN5769_c0_g1_i1	Arginine deiminase	-10.0324	1.24E-08
37	DN5772_c5_g4_i3	SPT; serine palmitoyltransferase [EC:2.3.1.50]	1.550679	0.0022
38	DN5792_c2_g2_i1	Glycerol uptake facilitator protein	-3.04504	6.33E-13
39	DN5792_c2_g2_i5	major intrinsic protein AQP1	-1.91228	0.000434
40	DN5796_c0_g1_i1	Translocator protein	-9.14016	2.90E-07
41	DN5800_c6_g6_i1	rocD, OAT; ornithine--oxo-acid transaminase [EC:2.6.1.13]	-10.5643	0.00191
42	DN5829_c0_g1_i2	Transposable element Tcb2 transposase	10.14786	2.23E-13
43	DN5850_c2_g4_i2	PyKPA2; ATP1A; sodium/potassium-transporting ATPase subunit alpha [EC:3.6.3.9]	1.101731	0.036709
44	DN5861_c0_g1_i4	Tubulin beta chain	8.450625	4.82E-07
45	DN5863_c0_g1_i1	High-affinity nitrate transporter 2.2	1.776852	2.04E-05
46	DN5897_c0_g4_i1	SLC30A1, ZNT1; solute carrier family 30 (zinc transporter), member 1	1.045204	0.038297
47	DN5917_c1_g1_i2	Heme-binding-like protein At3g10130, chloroplastic	1.668741	0.04111
48	DN5923_c14_g2_i1	ABC transporter G family member 7	2.755925	0.007972
49	DN5956_c0_g1_i1	Krueppel-like factor 5	-2.36508	3.47E-13
50	DN5991_c2_g8_i1	MRPL43; large subunit ribosomal protein L43	11.23215	1.39E-13
50	DN5991_c2_g8_i1	SSRP1; structure-specific recognition protein 1	11.23215	1.39E-13
51	DN6028_c1_g1_i1	Phycobilisome 31.8 kDa linker polypeptide, phycoerythrin-associated, rod	-1.92291	0.006047
52	DN6049_c2_g4_i3	Aldehyde dehydrogenase 22A1	-1.28542	0.022452
52	DN6049_c2_g4_i3	Putative aldehyde dehydrogenase-like protein YHR039C	-1.28542	0.022452
53	DN6091_c6_g4_i1	NPC1; Niemann-Pick C1 protein	1.415302	0.001496
54	DN6097_c4_g1_i1	SMC1; structural maintenance of chromosome 1	-1.46248	0.000925
55	DN6102_c1_g1_i1	NRT, narK, nrtP, nasA; MFS transporter, NNP family, nitrate/nitrite transporter	1.483347	1.08E-05
56	DN6133_c3_g13_i3	L2HGDH; 2-hydroxyglutarate dehydrogenase [EC:1.1.99.2]	7.927365	9.31E-06
57	DN6142_c5_g2_i1	Sodium/hydrogen exchanger 7	-8.11166	0.029537
58	DN6147_c0_g1_i1	Gluconolactonase	-3.53284	8.78E-06
59	DN6149_c3_g1_i1	Putative polysaccharide-binding protein	-2.14	0.006758
60	DN6151_c0_g2_i1	HMGB2; high mobility group protein B2	-3.4989	7.57E-09
61	DN6168_c0_g3_i1	SNF1-related protein kinase regulatory subunit beta-2	1.014229	0.018158
62	DN6196_c5_g2_i2	RNA helicase Mov10l1 {ECO:0000305}	7.526225	4.60E-05
63	DN6206_c2_g1_i1	DRG5 [Pyropia tenera]	1.405633	0.001353
64	DN6229_c1_g1_i9	charged multivesicular body protein 1 [Strigomonas culicis]	2.074216	0.002178
65	DN6235_c0_g2_i1	basic proline-rich protein-like [Oncorhynchus kisutch]	-10.1811	0.001927
66	DN6244_c1_g1_i1	E1.6.99.1; NADPH2 dehydrogenase [EC:1.6.99.1]	1.761453	2.87E-05
67	DN6250_c0_g2_i1	PyKPA2	4.337301	0.006701
68	DN6254_c6_g1_i1	Carboxypeptidase A2	-1.52873	6.86E-07
69	DN6255_c2_g2_i1	Ankyrin repeat and MYND domain-containing protein 2	-4.80417	4.14E-05

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	Transcript ID	Description	logFC	FDR
70	DN6277_c0_g1_i2	TOP2; DNA topoisomerase II [EC:5.99.1.3]	-2.70388	2.83E-07
71	DN6277_c8_g1_i1	Serine/threonine-protein kinase	1.36869	0.007944
72	DN6304_c0_g1_i2	valine--tRNA ligase [Archangium sp. Cb G35]	-3.59891	0.017714
73	DN6305_c1_g2_i1	Beta-glucuronosyltransferase GlcAT14B {ECO:0000305}	-1.56602	1.53E-05
74	DN6308_c0_g2_i7	PREDICTED: LOW QUALITY PROTEIN: mucin-2 [Alligator sinensis]	9.273107	9.28E-10
75	DN6320_c0_g1_i1	predicted protein [Streptomyces sp. C]	-4.94863	0.014183
76	DN6320_c4_g1_i1	accB, bccP; acetyl-CoA carboxylase biotin carboxyl carrier protein	12.36948	2.22E-28
76	DN6320_c4_g1_i1	hisD; histidinol dehydrogenase [EC:1.1.1.23]	12.36948	2.22E-28
77	DN6320_c4_g2_i1	ECM29; proteasome component ECM29	5.20639	0.002187
78	DN6348_c5_g1_i5	ACADSB; short/branched chain acyl-CoA dehydrogenase [EC:1.3.99.12]	9.464283	1.85E-71
79	DN6361_c0_g2_i2	APY1_2; apyrase [EC:3.6.1.5]	-9.52142	1.44E-07
80	DN6374_c0_g1_i10	Kinesin light chain	2.380781	1.11E-05
81	DN6374_c0_g1_i9	Regulatory protein AfsR	1.149916	6.13E-05
82	DN6375_c0_g1_i10	dnaK; molecular chaperone DnaK	1.136642	0.004743
82	DN6375_c0_g1_i10	psbB; photosystem II CP47 chlorophyll apoprotein	1.136642	0.004743
83	DN6375_c0_g9_i1	ATPF1A, atpA; F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]	1.956919	7.27E-07
84	DN6377_c1_g1_i1	TUBA; tubulin alpha	9.715899	4.53E-12
85	DN6377_c1_g2_i2	TUBA; tubulin alpha	7.172275	2.93E-14
86	DN6401_c2_g1_i2	formin-like protein 20 [Arachis ipaensis]	4.026649	0.001007
87	DN6416_c4_g3_i1	Kinesin light chain 2	2.198658	2.47E-05
88	DN6416_c4_g3_i2	NPHP3; nephrocystin-3	2.130343	1.42E-08
89	DN6424_c5_g1_i1	ASPO2608 [Pyropia yezoensis]	4.953745	0.021281
90	DN6460_c2_g1_i2	Transposable element Tcb1 transposase	3.315518	0.014183
90	DN6460_c2_g1_i2	paired box protein and transposase domain containing protein [Lasius niger]	3.315518	0.014183
91	DN6465_c2_g1_i1	GLO1, gloA; lactoylglutathione lyase [EC:4.4.1.5]	11.61747	1.90E-12
91	DN6465_c2_g1_i1	PRKCSH; protein kinase C substrate 80K-H	11.61747	1.90E-12
92	DN6471_c4_g2_i4	Retrovirus-related Pol polyprotein from transposon TNT 1-94	5.732638	1.86E-06
93	DN6471_c4_g2_i8	Retrovirus-related Pol polyprotein from transposon TNT 1-94	13.1111	1.04E-49
94	DN6478_c0_g1_i4	Protein BOLA4, chloroplastic/mitochondrial {ECO:0000303}[PubMed:24203231]	-3.09513	0.036119
95	DN6479_c1_g1_i5	ATP-dependent DNA helicase thl1	2.001475	2.35E-06
96	DN6484_c0_g5_i1	Protein cbbX homolog, chloroplastic	1.204794	0.00328
96	DN6484_c0_g5_i1	COPS4, CSN4; COP9 signalosome complex subunit 4	1.204794	0.00328
97	DN6497_c5_g5_i1	sugar transferase [Streptomyces sp. NRRL F-4489]	1.076861	0.022452
98	DN6504_c3_g1_i14	PREDICTED: splicing factor U2AF 35 kDa subunit-like [Notothenia coriiceps]	2.373906	0.006887
99	DN6505_c0_g3_i3	putative protein transport protein Sec31 [Trypanosoma vivax Y486]	8.950323	5.83E-08
100	DN6537_c3_g2_i1	SELENBP1; selenium-binding protein 1	-2.5547	0.006614
101	DN6614_c1_g3_i2	Heat shock protein 83	-10.8397	7.03E-16
102	DN6614_c1_g5_i1	Heat shock protein 83	-10.1051	1.59E-10
103	DN6652_c0_g2_i1	E2.7.1.20, ADK; adenosine kinase [EC:2.7.1.20]	-2.98125	0.000642
104	DN6680_c6_g4_i1	NRT, narK, nrtP, nasA; MFS transporter, NNP family, nitrate/nitrite transporter	1.186616	0.003007
105	DN6704_c0_g1_i2	Retrotransposable element SLACS 132 kDa protein	3.31226	0.015422
106	DN6711_c0_g2_i2	cah; carbonic anhydrase [EC:4.2.1.1]	-2.49598	8.29E-05
107	DN6746_c0_g4_i1	ATP synthase CF1 beta subunit (chloroplast)	-10.4513	2.54E-13
108	DN6834_c1_g7_i4	Probable mRNA-splicing protein ubp10	-6.12873	0.039281
109	DN6836_c1_g2_i1	Heat shock 70 kDa protein	-11.7522	8.50E-23

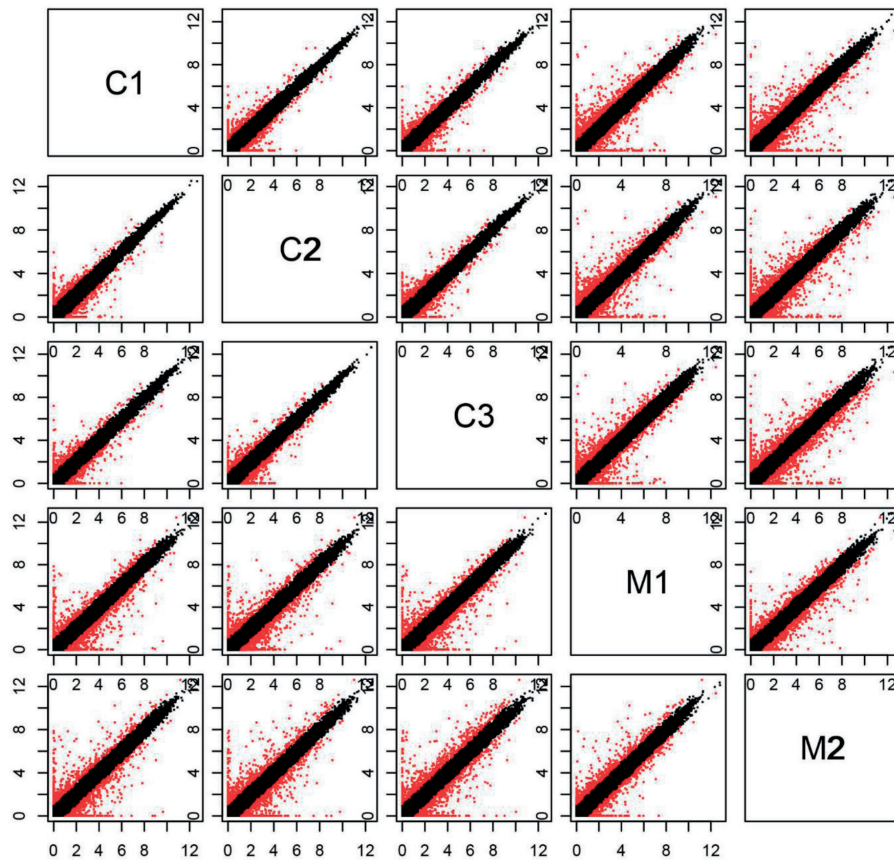
On-line Suppl. Tab. 2. Continued

	Transcript ID	Description	logFC	FDR
110	DN6882_c6_g1_i2	proteophosphoglycan ppg4 [Leishmania major strain Friedlin]	-1.28114	0.008866
111	DN6911_c3_g1_i1	DYNLL; dynein light chain LC8-type	-5.04756	5.38E-05
112	DN6913_c4_g4_i4	Stress-induced-phosphoprotein 1 {ECO:0000303 PubMed:19467242, ECO:0000312 EMBL:CCD63252.1}	-3.65345	7.16E-05
113	DN6913_c5_g2_i1	DRG5 [Pyropia tenera]	-4.17717	3.23E-33
114	DN6921_c2_g1_i4	Ubiquitin-60S ribosomal protein L40	-8.69081	1.38E-06
115	DN6921_c2_g1_i6	Ubiquitin-60S ribosomal protein L40	-5.56612	1.29E-05
116	DN6922_c8_g2_i3	ASPO2608 [Pyropia yezoensis]	-4.81499	0.00106
117	DN6925_c1_g2_i13	Hkr1p [Sugiyamaella lignohabitans]	-10.2469	1.90E-12
118	DN6953_c7_g1_i2	ppa; inorganic pyrophosphatase [EC:3.6.1.1]	1.548605	1.99E-08
119	DN6960_c1_g3_i5	Myb-like protein H	1.969395	0.030512
120	DN6972_c7_g8_i1	CA; carbonic anhydrase [EC:4.2.1.1]	-11.1548	1.42E-17
121	DN6977_c3_g1_i2	Beta-porphyrinase A	-1.72794	0.014183
122	DN6987_c4_g13_i1	MRS2, MFM1; magnesium transporter	-9.27312	0.006758
123	DN7005_c4_g4_i1	LOW QUALITY PROTEIN: hypothetical protein BU14_0490s0020 [Porphyra umbilicalis]	-11.913	1.05E-17
124	DN7006_c3_g21_i1	Tetracycline resistance protein, class C	-8.43435	9.41E-06
125	DN7016_c3_g2_i1	LigA [Anaeromyxobacter dehalogenans 2CP-C]	-8.71048	6.24E-05
126	DN7022_c7_g1_i3	KRAB; KRAB domain-containing zinc finger protein	-3.97341	0.000149
127	DN7046_c1_g1_i10	R-phycoerythrin gamma chain, chloroplastic	-1.42957	0.001069
128	DN7074_c0_g2_i1	RP-L11e, RPL11; large subunit ribosomal protein L11e	-8.47058	8.27E-06
129	DN7087_c3_g2_i2	MSI60-related protein [Pinctada fucata]	-7.82215	0.03265
130	DN7091_c10_g2_i2	translation initiation factor IF-2 [Streptomyces sp. NRRL WC-3626]	-7.99819	1.76E-17
131	DN7094_c5_g3_i1	Nitrate reductase [NADH]	1.185227	0.038693
132	DN7095_c1_g5_i2	High affinity nitrate transporter 2.6	1.438567	1.31E-05
133	DN7097_c7_g4_i1	E3.5.1.49; formamidase [EC:3.5.1.49]	1.264569	0.000434
134	DN7105_c6_g1_i2	Serine/threonine-protein phosphatase 4 regulatory subunit 4	-4.48809	0.014648
135	DN7106_c1_g4_i1	Germin-like protein subfamily 1 member 10	-1.71704	8.35E-06
136	DN7116_c0_g3_i1	Ubiquitin-60S ribosomal protein L40	-8.89442	3.96E-07
137	DN7122_c3_g1_i7	Nephrocystin-3	2.969283	1.23E-06
138	DN7142_c4_g2_i1	DNA excision repair protein CSB {ECO:0000305}	-8.14773	5.91E-05
139	DN7167_c8_g3_i2	PREDICTED: fibroin heavy chain-like, partial [Capra hircus]	-9.91775	3.22E-08
140	DN7169_c3_g1_i2	Poly(A)-specific ribonuclease PARN	-3.32071	0.024405
141	DN7169_c3_g15_i1	DEPDC5; DEP domain-containing protein 5	-12.744	4.64E-14
142	DN7177_c3_g2_i1	Chlorophyll a-b binding protein 7, chloroplastic	2.55647	0.004748
143	DN7183_c0_g1_i2	GH12646 [Drosophila grimshawi]	-8.54948	3.14E-06
144	DN7183_c2_g1_i1	ABC transporter G family member 16	-7.63038	0.040887
145	DN7183_c2_g4_i3	Putative polysaccharide-binding protein	-11.5786	2.02E-16
146	DN7184_c0_g2_i1	60S ribosomal protein L10a	-7.52728	0.000763
147	DN7190_c2_g4_i3	ACTB_G1; actin beta/gamma 1	-6.39746	7.92E-17
148	DN7202_c1_g2_i4	Polyubiquitin	-7.76034	0.000259
149	DN7207_c1_g4_i1	A49-like RNA polymerase I associated factor	-10.2735	4.53E-09
149	DN7207_c1_g4_i1	Protein spinster homolog 1	-10.2735	4.53E-09
150	DN7215_c0_g2_i1	RecName: Full=Vegetative cell wall protein gp1; AltName: Full=Hydroxyproline-rich glycoprotein 1; Flags: Precursor	-2.68391	0.000979
151	DN7221_c6_g5_i1	TBC1 domain family member 23	-1.62837	0.000335
152	DN7258_c5_g2_i1	RAB1A; Ras-related protein Rab-1A	-8.29761	3.30E-05
153	DN7265_c3_g2_i1	argG, ASS1; argininosuccinate synthase [EC:6.3.4.5]	-3.22415	0.000752
154	DN7268_c0_g4_i1	DRG5 [Pyropia tenera]	1.516952	1.08E-05

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	Transcript ID	Description	logFC	FDR
155	DN7282_c1_g4_i2	Ankyrin-3	-5.77882	3.58E-07
156	DN7282_c1_g6_i1	Ankyrin-3 {ECO:0000303 PubMed:7836469}	-5.69853	1.22E-11
157	DN7288_c4_g2_i1	Pre-rRNA-processing protein esf1	-4.05797	0.008844
158	DN7295_c1_g1_i1	TRM11, TRMT11; tRNA (guanine10-N2)-methyltransferase [EC:2.1.1.214]	-6.99375	1.29E-06
159	DN7301_c1_g1_i1	ATP1A; sodium/potassium-transporting ATPase subunit alpha [EC:3.6.3.9]	-9.6944	5.55E-06
160	DN7304_c3_g2_i1	Mucin-like protein {ECO:0000303 PubMed:23765379}	-10.7451	3.88E-13
161	DN7325_c3_g1_i1	Protein sey1 {ECO:0000255 HAMAP-Rule:MF_03109}	-10.0646	0.008126
162	DN7331_c1_g1_i1	TUBA; tubulin alpha	-12.4366	9.10E-99
163	DN7336_c6_g2_i2	PREDICTED: neural Wiskott-Aldrich syndrome protein isoform X1 [Pygocentrus nattereri]	-7.95188	0.029375
164	DN7338_c0_g2_i1	hornerin-like, partial [Zea mays]	-1.38062	0.028755
165	DN7338_c0_g3_i2	Nudix hydrolase 18, mitochondrial	-9.55488	5.51E-09
166	DN7348_c4_g1_i10	GBE1, glgB; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	-2.46688	0.004952
167	DN7350_c6_g10_i2	RNA pseudouridylate synthase domain-containing protein 1	-8.77812	0.011614
168	DN7380_c8_g4_i2	Putative polysaccharide-binding protein	1.020065	0.018369
169	DN7390_c2_g2_i2	DNAJB11; DnaJ homolog subfamily B member 11	-4.67741	0.000133
170	DN7390_c5_g1_i1	USP1; ubiquitin carboxyl-terminal hydrolase 1 [EC:3.4.19.12]	-9.95644	0.003194
171	DN7422_c3_g10_i1	Tubulin alpha-1/2/3 chain	-12.4087	4.31E-30
172	DN7445_c1_g4_i1	E2.2.1.2, talA, talB; transaldolase [EC:2.2.1.2]	1.207499	0.003483
173	DN7452_c8_g2_i1	RP-S2e, RPS2; small subunit ribosomal protein S2e	-14.1491	5.45E-35
174	DN7458_c1_g3_i2	flocculation protein FLO11-like [Monopterus albus]	-2.82922	0.001216
175	DN7476_c7_g4_i1	Putative uncharacterized protein YGL102C	-8.25982	2.37E-05
176	DN7482_c0_g1_i2	UBE2C, UBC11; ubiquitin-conjugating enzyme E2 C [EC:2.3.2.23]	-8.1743	0.000215
177	DN7492_c2_g2_i2	antifreeze glycoprotein precursor [Boreogadus saida]	-7.74332	0.03972
178	DN7503_c0_g4_i2	Aldehyde dehydrogenase 22A1	-1.07787	0.010845
179	DN7505_c2_g4_i6	ASPO1527 [Pyropia yezoensis]	3.759844	0.000458
180	DN7505_c2_g4_i7	ASPO1527 [Pyropia yezoensis]	3.321738	0.001245
181	DN7526_c5_g3_i5	Putative tyrosinase-like protein tyr-1	2.126669	0.025052
182	DN7534_c3_g2_i1	Heat shock 70 kDa protein	-8.79578	1.39E-06
183	DN7535_c3_g12_i1	MPV17; protein Mpv17	-2.20311	0.000763
184	DN7559_c2_g1_i1	Actin, cytoplasmic A3a	-8.41883	4.34E-05
185	DN7559_c2_g1_i2	Actin B	-8.37436	2.14E-05
186	DN7559_c2_g1_i4	Actin, nonmuscle	-2.31212	0.024227
187	DN7565_c1_g1_i1	Parallel beta-helix repeat protein [Oceanicola granulosus HTCC2516]	-4.65196	0.000464
188	DN7590_c3_g5_i1	SHIP1, INPP5D; phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 [EC:3.1.3.86]	-7.21337	0.002934
189	DN7593_c6_g1_i4	ABC transporter G family member 27	-8.14906	0.022452
190	DN7598_c5_g3_i2	typA, bipA; GTP-binding protein	1.087249	0.045568
191	DN8010_c0_g1_i1	predicted protein [Naegleria gruberi]	11.26473	1.32E-47
192	DN8191_c0_g1_i1	SARS, serS; seryl-tRNA synthetase [EC:6.1.1.11]	1.081104	0.049702
193	DN8445_c0_g2_i1	Zinc finger protein 42 homolog	-9.50527	1.52E-08
194	DN863_c0_g1_i1	Elongation factor 1-alpha {ECO:0000255 HAMAP-Rule:MF_00118}	-8.54583	6.55E-06
195	DN8782_c0_g1_i1	RP-S16e, RPS16; small subunit ribosomal protein S16e	6.842591	4.38E-06
196	DN8794_c0_g1_i1	Cofilin/tropomyosin-type actin-binding protein	7.843755	1.09E-05
197	DN904_c0_g1_i1	EEF1A; elongation factor 1-alpha	-8.14404	0.000149
198	DN958_c0_g1_i1	Werner Syndrome-like exonuclease	-8.67348	0.013306
199	DN9822_c0_g1_i1	psaO; photosystem I subunit PsalO	-10.6253	4.90E-117

Replicate Scatter: Py



On-line Suppl. Fig. 1. Scatter plot matrix of log₂-transformed CPM (counts per millions), which are counts scaled by the total number of reads, across all pair-wise comparisons. C1, C2, and C3 are the replicates of PyWT; M1 and M2 are the replicates of Py500G. The plot was generated with EdgeR software.