Differential gene expression and alternative splicing between diploid and tetraploid watermelon. *T Saminathan, P Nimmakayala, S Manohar, S Malkaram, A Almeida, R Cantrell, Y Tomason, L Abburi, MA Rahman, VG Vajja, A Khachane, B Kumar, HK Rajasimha, A Levi, T Wehner, and UK Reddy*

SUPPLEMENTARY DATA

Supplementary Table S4. List of top 20 genes upregulated in tetraploid compared to Sugar Baby diploid.

Fold change (log2)	*p*_value	ICuGI Ref. ID	Gene name
10.2012	2.83E-12	*Cla018600*	Chlorophyll A-B binding protein
8.63253	2.52E-05	*Cla001931*	MLP-like protein 28
8.21858	1.41E-10	*Cla017463*	MYB transcription factor
8.18404	1.51E-14	*Cla022611*	Gibberellin-regulated family protein
8.05051	1.73E-09	*Cla005776*	Cellulose synthase 3
7.96636	0.005667	*Cla009350*	Membrane transporter D1
7.82779	0	*Cla019105*	Chlorophyll a-b binding protein P4, chloroplastic
7.5895	2.99E-07	*Cla007294*	Chalcone isomerase-like protein
7.08381	0.002006	*Cla021048*	Peroxidase 46
6.98685	3.77E-15	*Cla001440*	Phloem filament protein; PP1
6.87715	6.66E-16	*Cla012670*	Photosystem I reaction center subunit VI, chloroplastic
6.8493	7.32E-05	*Cla015457*	Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB
6.76786	1.74E-11	*Cla022418*	Tubulin beta-1 chain
6.67217	4.58E-10	*Cla014313*	Peroxidase
6.66647	3.11E-15	*Cla004746*	Chlorophyll a-b binding protein 6A, chloroplastic
6.65144	2.53E-10	*Cla020143*	Patatin-like protein 3
6.63136	6.13E-10	*Cla002155*	Pollen Ole e 1 allergen and extensin family protein
6.47261	5.79E-07	*Cla018935*	Uncharacterized GPI-anchored protein
6.46172	0.005806	*Cla005431*	Amine oxidase family protein
6.43315	1.26E-10	*Cla016148*	Two-component response regulator ARR11; SHAQKYF class

Supplementary Table S5. List of top 20 genes downregulated in tetraploid compared to Sugar Baby diploid.

Fold change (log2)	*p*_value	ICuGI Ref. ID	Gene name
-11.6429	1.50E-07	*Cla004097*	Nucleoside phosphorylase
-10.2893	3.11E-07	*Cla022835*	Choline dehydrogenase
-10.1997	0	*Cla006009*	Proteinase inhibitor I
-9.19615	0	*Cla019802*	Pathogenesis-related protein 4B
-9.0058	0	*Cla019124*	ABC transporter ATP-binding protein
-8.68444	0	*Cla004673*	CASP-like protein; trans-membrane plant subgroup
-8.51435	4.46E-08	*Cla019633*	Protein of unknown function DUF1264
-8.45729	0	*Cla013048*	Blue copper protein
-8.34065	0	*Cla019870*	Kunitz trypsin inhibitor 4
-8.07614	0.000374	*Cla008742*	Aquaporin 2
-8.06636	0	*Cla011719*	Phosphoglucosamine mutase
-7.98939	0.001618	*Cla020292*	Rhodanese-like domain-containing protein
-7.91976	0	*Cla013631*	Unknown Protein
-7.82536	0.001832	*Cla004567*	Methionine s-methyltransferase
-7.61228	5.49E-09	*Cla008813*	Glycine-rich protein-2
-7.56909	0	*Cla020593*	Serine carboxypeptidase-like 13
-7.43321	3.13E-05	*Cla013579*	Protein of unknown function DUF789
-7.31318	0	*Cla021554*	Proteinase inhibitor I-B
-6.72089	4.18E-13	*Cla009952*	Serine carboxypeptidase-like 13
-6.38885	0	*Cla022834*	Glucose-methanol-choline oxidoreductase

Supplementary Table S6. List of pathways that are altered in tetraploid compared to diploids (CLD1 and WM)

CLT1_vs_CLD1

Classified pathways	List of genes
Abscisic_acid_biosynthesis	Cla003134 Cla023114
Adenosyl.L.methionine_cycle_I	Cla004096 Cla015190 Cla017148 Cla017324
Aerobic_respiration_cytochrome_c	Cla000034 Cla000840 Cla001181 Cla002352 Cla005369 Cla005925 Cla005926 Cla006136 Cla007631 Cla007728 Cla008664 Cla009926 Cla010909 Cla011643 Cla013134 Cla013368 Cla014035 Cla015141 Cla017191 Cla017414 Cla017692 Cla018400 Cla018505 Cla019532 Cla020888 Cla020955 Cla021355 Cla022111 Cla022635 Cla022868
Alpha.amyrin_biosynthesis	Cla004749 Cla019849
Arginine_biosynthesis_IV	Cla002609 Cla002611 Cla012627 Cla019569
Ascorbate_glutathione_cycle	Cla011751 Cla013224 Cla013927 Cla015833 Cla016538 Cla017711 Cla020113
Calvin.Benson.Bassham_cycle	Cla001076 Cla001753 Cla002691 Cla003384 Cla003902 Cla003920 Cla007150 Cla012175 Cla013455 Cla016609 Cla017722 Cla018136 Cla018371 Cla018594 Cla020400 Cla020445 Cla021318 Cla023464
Cholesterol_biosynthesis_I	Cla001251 Cla018902 Cla020920 Cla022651
Cholesterol_biosynthesis_II_via_24.25.dihydrolanosterol	Cla001251 Cla018902 Cla020920 Cla022651
Dolichyl.diphosphooligosaccharide_biosynthesis	Cla008829 Cla023443
Fatty_acid_beta.oxidation_V_unsaturated._odd_number._di.isomerase.dependent	Cla000633 Cla002393 Cla004686 Cla010879
Flavonoid_biosynthesis	Cla004708 Cla006682 Cla006818 Cla007458 Cla008896 Cla015296 Cla017799
Gibberellin_biosynthesis_I_non_C.3._non_C.13_hydroxylation	Cla002362 Cla013892
Glucoside_biosynthesis	Cla013516 Cla014414 Cla016287
Glucoside_degradation	Cla009226 Cla017417 Cla017418 Cla017499 Cla022015 Cla023406
Glutathione.mediated_detoxification_II	Cla005408 Cla005410 Cla007412 Cla007826 Cla011819 Cla014638 Cla014674 Cla018149 Cla018150 Cla018159 Cla018161 Cla018163 Cla018614 Cla021309 Cla021338 Cla021465 Cla022390
Glycolipid_biosynthesis	Cla008401 Cla016674
Heptadecane_biosynthesis	Cla006996 Cla021363 Cla021364
Homogalacturonan_degradation	Cla000006 Cla000060 Cla000802 Cla002569 Cla002954 Cla005855 Cla005856 Cla007803 Cla008440 Cla008598 Cla008599 Cla008601 Cla009218 Cla009288 Cla009870 Cla010077 Cla010310 Cla011144 Cla011256 Cla011376 Cla011585 Cla012554 Cla014466 Cla014927 Cla015081 Cla015103 Cla015379 Cla015505 Cla015663 Cla015665 Cla015729 Cla017515 Cla019426 Cla019978 Cla021325 Cla023049
Homoserine_biosynthesis	Cla005922 Cla011076 Cla012443 Cla012444 Cla012768

Ioi.diquinones_biosynthesis	Cla019479 Cla019481 Cla019482 Cla019483
Isoleucine_biosynthesis_I_from_threonine	Cla014059 Cla018353 Cla022656
L.ascorbate_degradation_V	Cla013927 Cla015833 Cla016538
L.dopachrome_biosynthesis	Cla019479 Cla019481 Cla019482 Cla019483
Leucine_degradation_I	Cla014059 Cla014787 Cla016017 Cla022656
Methionine_salvage_I_bacteria_and_plants	Cla007532 Cla015852 Cla021593
NADNADH_phosphorylation_and_dephosphorylation	Cla000034 Cla002352 Cla002446 Cla006136 Cla007631 Cla007728 Cla009926 Cla011643 Cla013134 Cla013368 Cla014035 Cla017191 Cla017414 Cla018505 Cla019532 Cla020888 Cla022635
Oxygenic_photosynthesis	Cla001076 Cla001753 Cla002691 Cla003384 Cla003902 Cla003920 Cla007150 Cla008898 Cla012175 Cla013455 Cla015978 Cla016609 Cla017722 Cla018136 Cla018371 Cla018594 Cla020400 Cla020445 Cla021318 Cla023464
Proline_degradation	Cla008345 Cla016474
Pyridine_nucleotide_cycling_plants	Cla004412 Cla005242 Cla011637 Cla012921 Cla015842 Cla020230 Cla020306
Pyrimidine_ribonucleotides_ide_novoi_biosynthesis	Cla001144 Cla002593 Cla004257 Cla005332 Cla006509 Cla008326 Cla008640 Cla009176 Cla009591 Cla012430 Cla012806 Cla012882 Cla012883 Cla013319 Cla013360 Cla013669 Cla015409 Cla015561 Cla018438 Cla019065 Cla019856 Cla020705 Cla021068 Cla021290 Cla021811 Cla023188
Pyrimidine_ribonucleotides_interconversion	Cla001144 Cla002593 Cla004257 Cla006509 Cla008326 Cla008640 Cla009176 Cla009591 Cla012430 Cla012806 Cla012882 Cla012883 Cla013319 Cla013360 Cla013669 Cla015409 Cla015561 Cla019065 Cla019856 Cla020705 Cla021068 Cla021290 Cla021811 Cla023188
Salvage_pathways_of_pyrimidine_ribonucleotides	Cla002593 Cla007102 Cla011217 Cla012806 Cla021068
Soybean_saponin_I_biosynthesis	Cla004749 Cla019849
Sucrose_degradation_I	Cla002444 Cla007015 Cla015574 Cla017674
Sulfite_oxidation_III	Cla007535 Cla014443 Cla021584
Superpathway_of_leucine._valine._and_isoleucine_biosynthesis	Cla013165 Cla014059 Cla018353 Cla022656
Tetrapyrrole_biosynthesis_I	Cla005137 Cla011998 Cla018703 Cla022180 Cla022543
Thiosulfate_disproportionation_III_rhodanese	Cla013049 Cla014327
Uridine.5.phosphate_biosynthesis	Cla005332 Cla018438
Valine_biosynthesis	Cla014059 Cla022656
Very_long_chain_fatty_acid_biosynthesis	Cla006236 Cla008263 Cla012291 Cla013264 Cla021116 Cla021577
Vitamin_E_biosynthesis	Cla006029 Cla006807 Cla023238
Wax_esters_biosynthesis_I	Cla008654 Cla011600 Cla016291 Cla016293
Xyloglucan_biosynthesis	Cla019094 Cla019095

CLT1_vs_WM

Classified pathways	List of genes
Aerobic_respiration_cytochrome_c	Cla001604 Cla002352 Cla005369 Cla006136 Cla006811 Cla007631 Cla008663 Cla008664 Cla010909 Cla011643 Cla011790 Cla012327 Cla012694 Cla013134 Cla013368 Cla014035 Cla015141 Cla015924 Cla016610 Cla016936 Cla017191 Cla018400 Cla018505 Cla019456 Cla020888 Cla020955 Cla022111 Cla022868
Arginine_biosynthesis_II_acetyl_cycle	Cla002611 Cla022154 Cla022915
Chlorophyllide_iai_biosynthesis_I	Cla002769 Cla005862 Cla006432 Cla006520 Cla009670 Cla012169 Cla019253 Cla023399
Flavonoid_biosynthesis	Cla002602 Cla002689 Cla006682 Cla006818 Cla007400 Cla008896 Cla015296 Cla015298 Cla017226 Cla017799 Cla018820 Cla022860
GDP.mannose_biosynthesis	Cla003612 Cla006550 Cla016948 Cla022170
Gluconeogenesis_I	Cla002259 Cla003902 Cla006486 Cla006920 Cla006921 Cla007150 Cla007587 Cla011268 Cla012154 Cla013455 Cla013611 Cla014068 Cla015968 Cla017722 Cla018136 Cla018371 Cla019014 Cla020526 Cla021103 Cla022170 Cla023334 Cla023464
Glucose_and_glucose.1.phosphate_degradation	Cla002361 Cla011719
Glutathione.mediated_detoxification_II	Cla005408 Cla005410 Cla007412 Cla007826 Cla014674 Cla018149 Cla018151 Cla018159 Cla018160 Cla018614 Cla018615 Cla018942 Cla021338 Cla021463 Cla021465 Cla022390
Itransi.cinnamoyl.CoA_biosynthesis	Cla008727 Cla012779 Cla013761 Cla018297 Cla018302
Jasmonic_acid_biosynthesis	Cla006236 Cla007649 Cla008520 Cla009118 Cla009402 Cla011168 Cla011742 Cla011979 Cla012872 Cla015969 Cla016453 Cla017066 Cla017068 Cla019897 Cla019899 Cla019900 Cla019905 Cla019907 Cla021116 Cla021577 Cla021777
L.ascorbate_degradation_V	Cla013927 Cla016538
Leucine_degradation_I	Cla008590 Cla014787 Cla016017
Methylerythritol_phosphate_pathway	Cla007929 Cla009346 Cla011088 Cla014654 Cla022299
Oleate_beta.oxidation	Cla004547 Cla016773 Cla021543 Cla021546
Oxygenic_photosynthesis	Cla001076 Cla001753 Cla002691 Cla003384 Cla003902 Cla003920 Cla004700 Cla006515 Cla007124 Cla007150 Cla012175 Cla013455 Cla013611 Cla015978 Cla017722 Cla018136 Cla018371 Cla019816 Cla020400 Cla020445 Cla021318 Cla023464
Phenylpropanoid_biosynthesis	Cla000214 Cla002602 Cla002689 Cla004553 Cla006818 Cla007400 Cla008122 Cla010234 Cla010408 Cla015296 Cla015298 Cla015324 Cla017226 Cla017799 Cla018764 Cla018820 Cla022860
Phenylpropanoid_biosynthesis._initial_reactions	Cla005785 Cla008727 Cla012779 Cla013420 Cla013761 Cla018297 Cla018302
Purine_nucleotides_ide_novoi_biosynthesis_II	Cla005483 Cla006493 Cla008058 Cla011995 Cla011996 Cla017506 Cla022128
Pyridine_nucleotide_cycling_plants	Cla005242 Cla012921 Cla012953 Cla014101 Cla020306
Salvage_pathways_of_pyrimidine_ribonucleotides	Cla011217 Cla012806 Cla021068
Starch_degradation_I	Cla002226 Cla002291 Cla002361 Cla005462 Cla011719 Cla016310 Cla020126 Cla020676

	Cla021470
Suberin_biosynthesis	Cla004452 Cla005785 Cla008727 Cla012779 Cla013420 Cla013761 Cla015633 Cla018297 Cla018302
Sulfite_oxidation_III	Cla014443 Cla021584
Superoxide_radicals_degradation	Cla001158 Cla008101 Cla008698 Cla009820 Cla010691 Cla011299 Cla017817 Cla023447
Thiosulfate_disproportionation_III_rhodanese	Cla013049 Cla014295 Cla014327 Cla020292
Threonine_biosynthesis_from_homoserine	Cla011183 Cla015737
Trehalose_biosynthesis_I	Cla002241 Cla008123 Cla019181 Cla022086
Trehalose_biosynthesis_II	Cla002241 Cla008123 Cla019181 Cla022086
Trehalose_biosynthesis_III	Cla002241 Cla008123 Cla019181 Cla022086
Triacylglycerol_degradation	Cla005001 Cla020664 Cla020665 Cla021076
Tyrosine_biosynthesis_II	Cla016538 Cla016672
Tyrosine_biosynthesis_III	Cla016538 Cla016672
UDP.D.xylose_and_UDP.D.glucuronate_biosynthesis	Cla008682 Cla017409
Urea_cycle	Cla002611 Cla006970 Cla022154 Cla022915
Valine_degradation_I	Cla000753 Cla004547 Cla014095 Cla016773
Wax_esters_biosynthesis_II	Cla008963 Cla016021

Supplementary Table S7. Primers used in this study.

Gene ID	Primers	Sequence (5'→3')
Semiquantitative RT-PCR		
Cla015387	WMAS-418-1F	CAATCTCTTCTTCAGCCTTTTCAC
	WMAS-418-1R	GCTGTCAGACTATCAAGATC
	WMAS-418-2F	GATGATGGGAATGAGCTTACG
	WMAS-418-2R	CTTGTTCACGACCTTCATCC
	WMAS-418-3F	GAGGCTTACTTCTCCAACATG
	WMAS-418-3R	CTTGCAACTTGGGGAAATGG
	WMAS-418-4R	GTGAAGAATGAAACCACATAACG
Cla022427	WMAS-951-1F	GCCATCCTCTCCAAAGCTCTC
	WMAS-951-1R	GGTCATGGCGGCGTAGCAGG
	WMAS-951-2R	GTGGTCAACGGTCAACGGCA
Cla013951	WMAS-970-1F	CAGTGAAGAGATACCCAGCG
	WMAS-970-1R	CAAACGGATCATTAAGGACCG
	WMAS-970-2F	CTCGCCGAGAAGATTCATCT
	WMAS-970-2R	AAGTGCGATGATAATGGCTCC
	WMAS-970-3F	CGTGTATCGAAACACTATTGC
Cla010408	WMAS-875-1F	GATTTTCAGTGTACTCGGCGA
	WMAS-875-1R	GACCAGCAGGATCAATGGAG
	WMAS-875-2F	GGCGTCGTAATTCGTTCAGA
	WMAS-875-2R	CCAATCTGATGCGATAAAGAC
	WMAS-875-3R	ATCACATTCTCAGTGGTCCT
	WMAS-875-4R	CAATTTGGTCACATCCACG
Cla019245	WMAS-927-1F	CCTCCTAATCCACCCTCTTAC
	WMAS-927-1R	GGCAAGGTCAATACGTCACT
	WMAS-927-2R	TGCCCGTATCCAGAGTAATC
	WMAS-927-3R	CTACCCGGCACGGATTCTATC
Cla001640	WMAS-731-1F	GCTTCAACCAAGAGGCTCCA
	WMAS-731-1R	GAAGAATGACAAGTGGTTGGTC
	WMAS-731-2R	CTAGTCGAGGCAGGTCTAAA
	WMAS-731-3R	CCATTGCGAAGCCACCACA
Cla004401	WMAS-432-1F	CAGTTGTTGCTCCTCCAGAT
	WMAS-432-1R	CACAGCTATTACACAAGCCG
	WMAS-432-2F	AACAGTTGTTGCTCCTCCAG
	WMAS-432-2R	GCTACAATGGTCTATCTAAAG
Cla012247	WMAS-874-1F	GTGAGATAGGAGTTTGAAACTAG
	WMAS-874-1R	GAGGATACTAAATTGAAGGGC
	WMAS-874-2F	AGATGCTTTAGGAGTGGCAG
	WMAS-874-2R	GCATTTCACCTCCCACATTG
Cla011845	WMAS-012-1F	CAGTCGTGTGACCCATGTTG

	WMAS-012-1R	CAGAAGCCCAAAGGGACACA
	WMAS-012-2F	CGAGTCCAGTTGATTTCAGC
	WMAS-012-2R	GATACCGAGACAAGCACTGA
	WMAS-012-3R	CTGAGCAGTTACATCAGCCTG
Cla015518	WMAS-932-1F	GTCTGAGGATCTGCATCCAG
	WMAS-932-1R	TAAGGCAACAGTCCAGATGG
	WMAS-932-2F	ACTCGTGGAATCCGAAACATC
	WMAS-932-2R	GACTAACATCAGTTCCAGAC
Cla012768	WMAS-092-1F	TGCTACCCTGAGAGGCTGGG
	WMAS-092-1R	GTCTTGGATTGGAACTAGCG
	WMAS-092-2F	GGAGAATGACCCGTGCGAAT
	WMAS-092-2R	CAATCTGCGAGCATGACATTC
Cla001006	WMAS-582-1F	TGACAACCACCTGCCCTCAC
	WMAS-582-1R	GGATTACTAAGGGCTCCTTGG
Cla006689	WMAS-633-1F	GGTGGCTGGTCAAACATGCTA
	WMAS-633-1R	CTTTCAGTCTTCCTCGTCGC
Cla002053	WMAS-151-1F	GAAGCTACGTCGTGGTCAAG
	WMAS-151-1R	ATGCCTCAGGATCAACCACC
	WMAS-151-2R	GAGGTTCTTCTAGCCCGTGG
Cla005769	WMAS-907-1F	GATCGAGAAGACAGAGTGAG
	WMAS-907-1R	GTTTAGCCAATAGAGATAGAGATAC
	WMAS-907-2F	GCCTTCCTACTCCGTTTAGC
	WMAS-907-2R	AACAGAAGCACAAGCACCAA
Cla009531	WMAS-444-1F	CAGCCAGTTCAGTCTTCAAG
	WMAS-444-1R	GAGCGGCGATTTGTTGCTGA
	WMAS-444-2R	CTCTCCAGGAACCCATTTCTC
Cla008232	WMAS-362-1F	CTCCAACCTTCAATCATCAC
	WMAS-362-1R	ATGCTGAACAGCCAAGTGCC
	WMAS-362-2F	TGGGTCTCTGATTGGCTAC
	WMAS-362-2R	TGCAAGCAAGATGAGGACTGG
Cla012250	WMAS-556-1F	CTATCTCACATACATCTTCTCC
	WMAS-556-1R	CTCACACTGTGATAGTATACG
	WMAS-556-2F	GAAGAAGCTAAGTTGGACGGT
	WMAS-556-2R	CTGTCTCGTCAAACTGGTCTG
Cla008071	WMAS-401-1F	CATTTGAAGAGTGACAAAATTC
	WMAS-401-1R	CAAATCCACAACAGTATGCAAAC
	WMAS-401-2R	AGTGAAATGACCAACCTGAC
	WMAS-401-3R	TCTACTGCAATAAAGCTACATC
Cla012755	WMAS-906-1F	GTCCGTATCCATGGAGATTC
	WMAS-906-1R	TATCACAACAGAACGAGACC
	WMAS-906-2R	CAAACCATCTTCCAGTTCAAG

	WMAS-906-3R	CACTTGGTCAACCAGTAGATG
Cla008582	WMAS-921-1F	AACTACGGTGGCGATAAGCAT
	WMAS-921-1R	TTCCTCACCCATCCAAGCAT
	WMAS-921-2F	GTGACATGTGTCCAGGTAC
	WMAS-921-2R	GGAGAAAAGGTAAAGGGTAG
Cla013509	WMAS-233-1F	CTCTATGGAGCTTCGTCTCCAG
	WMAS-233-1R	TCTTCACAATCTCTGGAGAGC
Cla004730	WM *EF1*-2F	TTGCTCTGTGGAAGTTCGAGA
	WM *EF1*-R	TGGGAAGTGAAATTGGCAGC
Quantitative RT-PCR (for cumulative expression)		
Cla012250	AS-556-QP-1F	CGTGCGTGTGAATTTAATGACATAA
	AS-556-QP-1R	CATATGAATCCATCACATGAGTGTTG
Cla015387	AS-418-QP-1F	ACATGGTGTTGGAGACAATGAAGT
	AS-418-QP-1R	TGCTGTGGTAGGTCCATGGA
Cla022427	AS-951-QP-1F	TGTGCTGGGAGGTGCAAGT
	AS-951-QP-1R	GCACGTCCCACACGCTCTAT
Cla013951	AS-970-QP-1F	CGCCGCAGCCAATCAG
	AS-970-QP-1R	ACACGCAGCCCAGAAGGAT
Cla010408	AS-875-QP-1F	CGGCGTTCAGAGGAGGAA
	AS-875-QP-1R	CCATCGGCTTAGATTTCAAGCT
Cla008071	AS-401-QP-1F	ACCCTCGTTCCCCCTTCTT
	AS-401-QP-1R	CCCATCGGCGCTTCTCTT
Cla012247	AS-874-QP-1F	AGATGCTTTAGGAGTGGCAGAAGT
	AS-874-QP-1R	CAAGTCCCCCTCCTTAAAATCA
Cla005769	AS-907-QP-1F	TTGCATGGCAGATAATAACCAAA
	AS-907-QP-1R	TCCATGCCCATCTTTTAGACATAG
Cla008232	AS-362-QP-1F	GGTTGGTGTTTCTGGCACTTG
	AS-362-QP-1R	AGTCAGCCGTGCAGATTAAAGG
Cla019245	AS-927-QP-1F	CCCCACCGCGAAAATGT
	AS-927-QP-1R	CGACAATCTCATTGCCTTTACG
Cla008582	AS-921-QP-1F	CCATCTGTGCTCCATTTTGCT
	AS-921-QP-1R	CAGAGAGGTTGGACGTGTTTGA
Cla011845	AS-012-QP-1F	GCCATCCATGCTAGCCTTTG
	AS-012-QP-1R	TCAATAAATGCCAATGCAGCTT
Cla015518	AS-932-QP-1F	CTGATTCCCCAAAAATTGATCTG
	AS-932-QP-1R	TCTCATAAGCCCGCATCAAAT
Cla001640	AS-731-QP-1F	GGCTGGAAGGTTGAAAGTTAACC
	AS-731-QP-1R	CACCGCCATTGCAATCAAT
Cla012755	AS-906-QP-1F	AACCTTGAATCCTGTCGTTTGAA
	AS-906-QP-1R	TCTTCGAATCACACACAACGAAA
Cla009531	AS-444-QP-1F	TGGCGTAACAAATGCTGAAAGTA

	AS-444-QP-1R	CCGTTGGAGGGAAGTTTGTTAG
Cla002053	AS-151-QP-1F	CAGCGAGCGTGCCATGT
	AS-151-QP-1R	CACCATCGCAAGCATCACA
Cla012768	AS-092-QP-1F	TGTGGAGGACAAAAAGCTGAGAT
	AS-092-QP-1R	TCAGGGAGCTGGCTCTCATC
Cla004401	AS-432-QP-1F	AAGAAAAAATGACATGCAGGTGAA
	AS-432-QP-1R	CCAACAAAAGCCCCTCCAT
Cla013509	AS-233-QP-1F	TCTGGATTGTGGAGTTCTTTGCT
	AS-233-QP-1R	CCATTCTGGAGCCAATCGTT
Cla001006	AS-582-QP-1F	GGAGCCCTTAGTAATCCCAGTTG
	AS-582-QP-1R	AACCGAGATGGATGGTCTTGA
Cla006689	AS-633-QP-1F	GAGGAGAATAACACTGGCTGACTTG
	AS-633-QP-1R	CCTTAAGTGCTTTTGCCACATCT
Quantitative RT-PCR (for spliced products)		
Cla008071	401-WMQP-1F	GGAAGTAACCGCCGACGAA
	401-WMQP-1R	AACTGTGCGGAATTCCACTTCT
Cla009531	444-WMQP-1F	AGGAGTCGGCAACCAATATGA
	444-WMQP-1R	TGTTGAACCGTAGCCAGAGAAA
Cla012250	556-WMQP-1F	GGTGACAGGAAACGATGGAGAA
	556-WMQP-1R	GAAGCAGTCAAGTCTGCCATAATTT
Cla010408	875-WMQP-1F	ATTTGCTTTAGAGCTACGATTGCTT
	875-WMQP-1R	AAGGACCAGATGGAGGTTGAAA
Cla001640	731-WMQP-1F	CCCGCCACGTGTCATTTT
	731-WMQP-1R	AGGGAAGTGGAGTGTCAAGCTT
Cla005769	907-WMQP-1F	GCTTTTCCCCATGTTGTTTCA
	907-WMQP-1R	CACAAGCACCAAAAGGCAACT
Cla015518	932-WMQP-1F	GCTTTGACCTGCTGAAGAGGAT
	932-WMQP-1R	ACAAATTTAAGCCCACCCGTTA
Cla019245	927-WMQP-1F	TCCTTTATGGTCAATCTGTTGGAA
	927-WMQP-1R	GGGCAAACGTGCAGCAA
Cla013951	970-WMQP-1F	CCTGTATTTGTGACGGCTTTCA
	970-WMQP-1R	CGGCGAGAACAATAGAGGAGAT