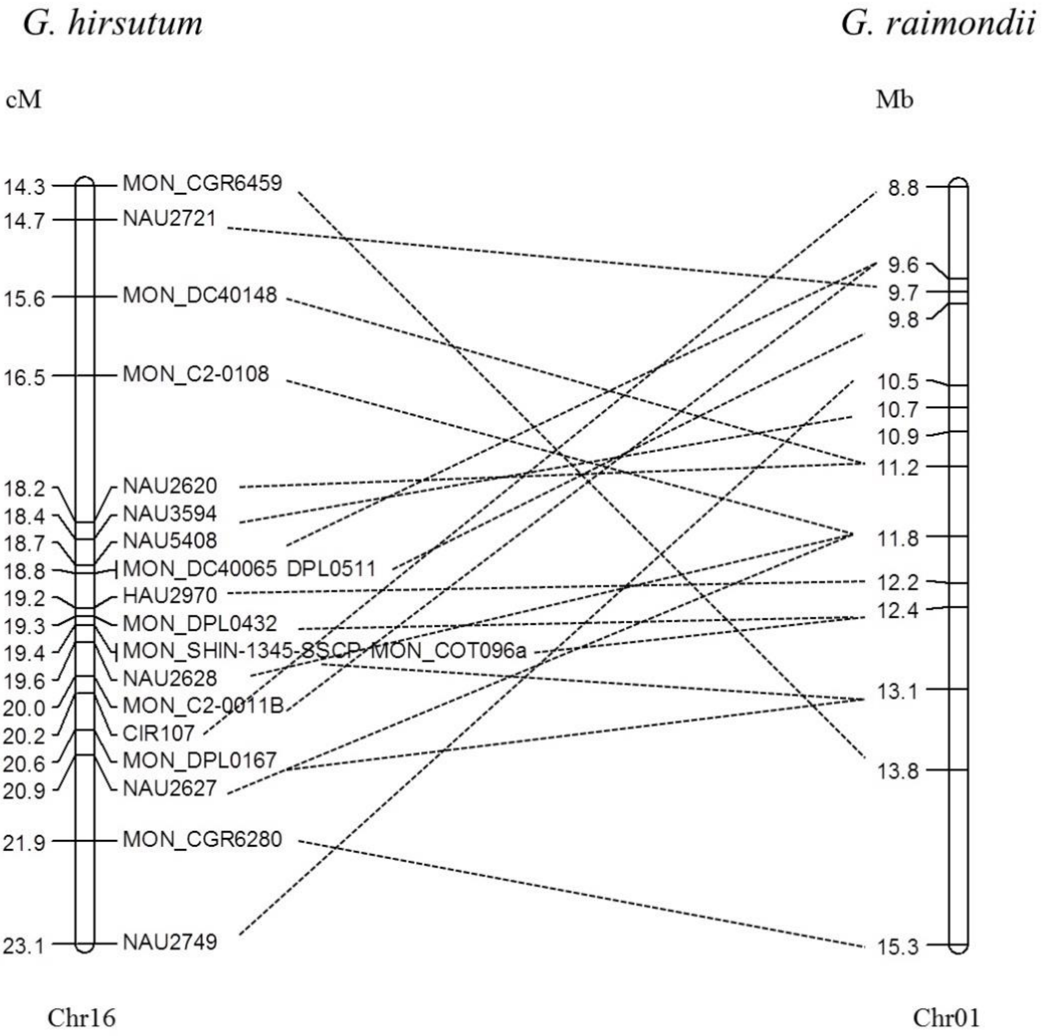
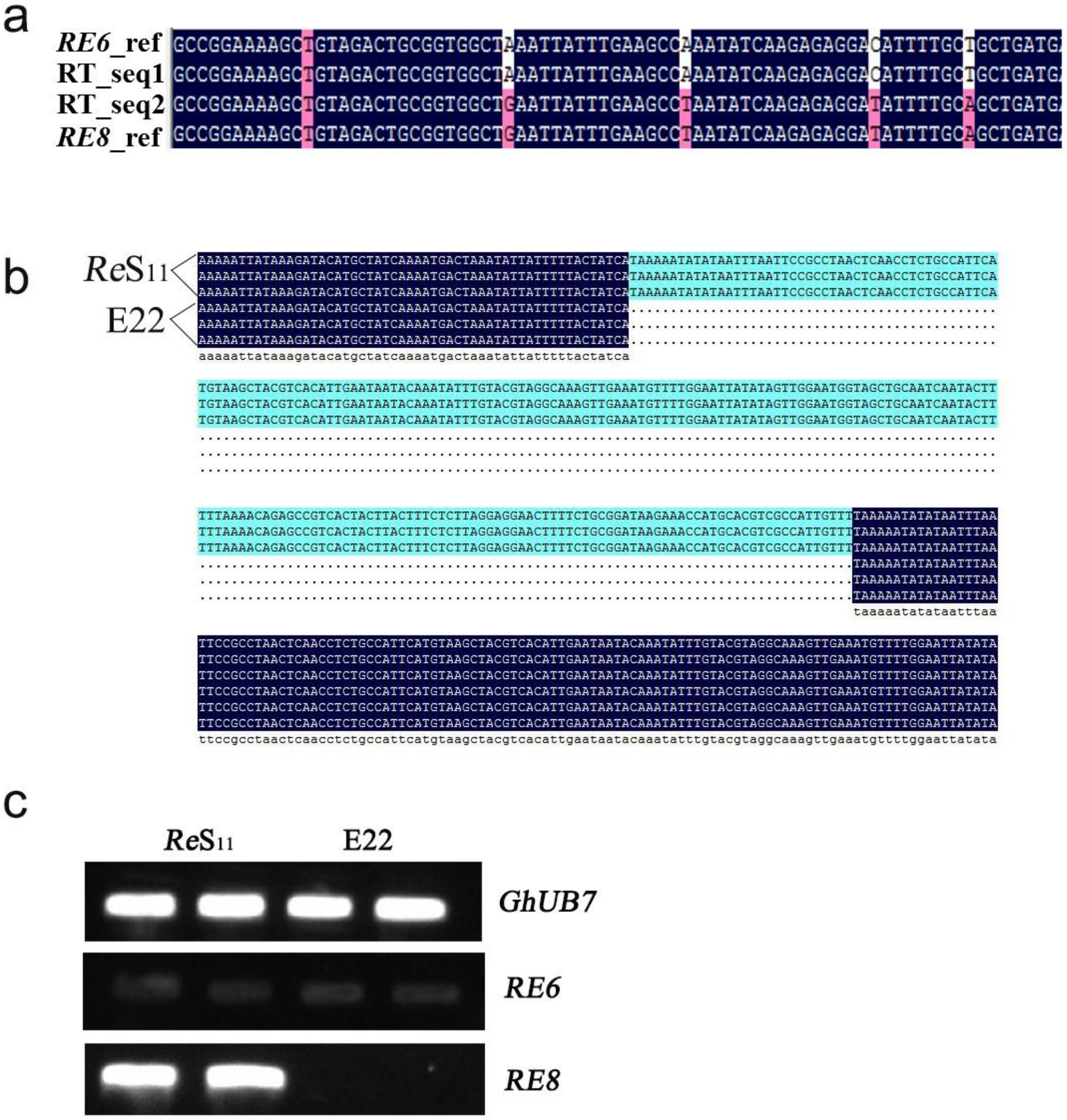
Supplemental Figures

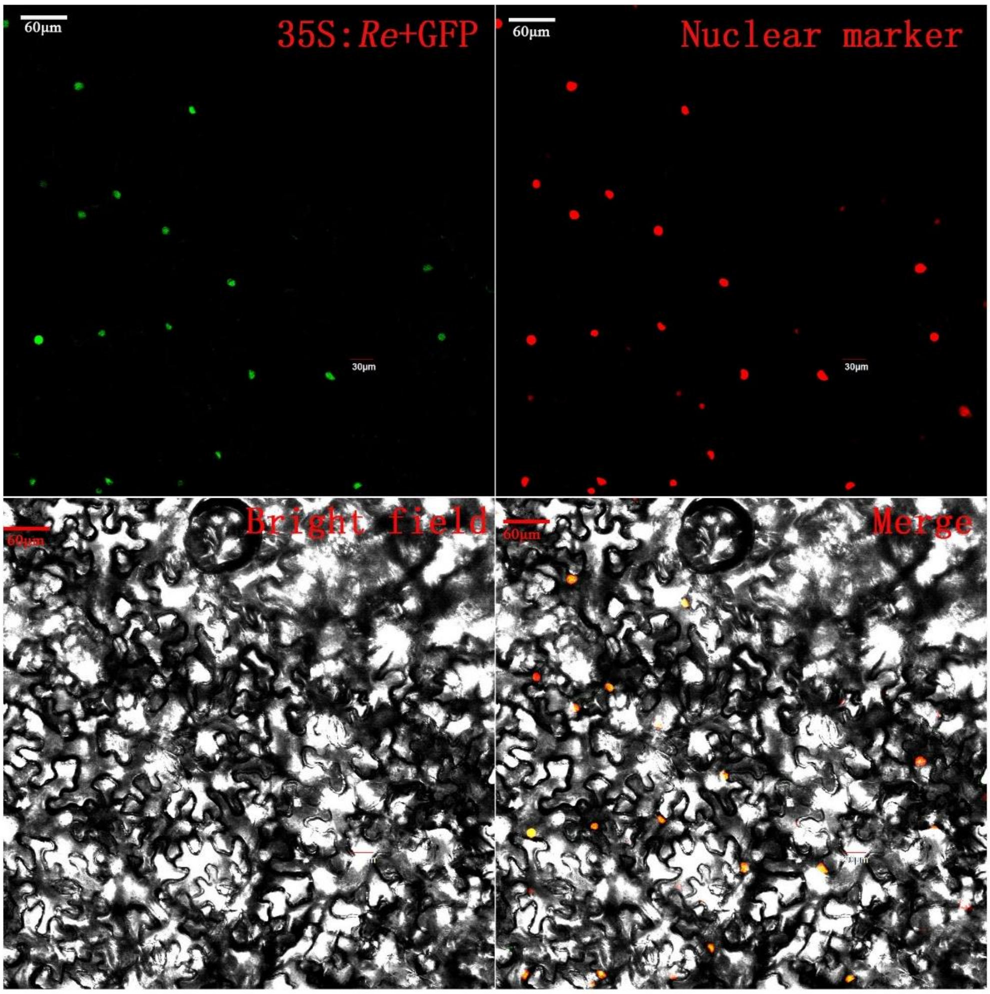
Supplemental Figure S1. A single red foliated cotton mutant appeared in the hybrid population of E22 and 3-79. a-b. Field phenotype of red foliated mutants photographed using a Motorola V3 camera. The whole plant is red. **c.** Phenotype of F_2 segregating population on seedbed. **d.** Field pictures of three phenotypes in the segregating population- red foliated plant, the intermediate type and the green plant.



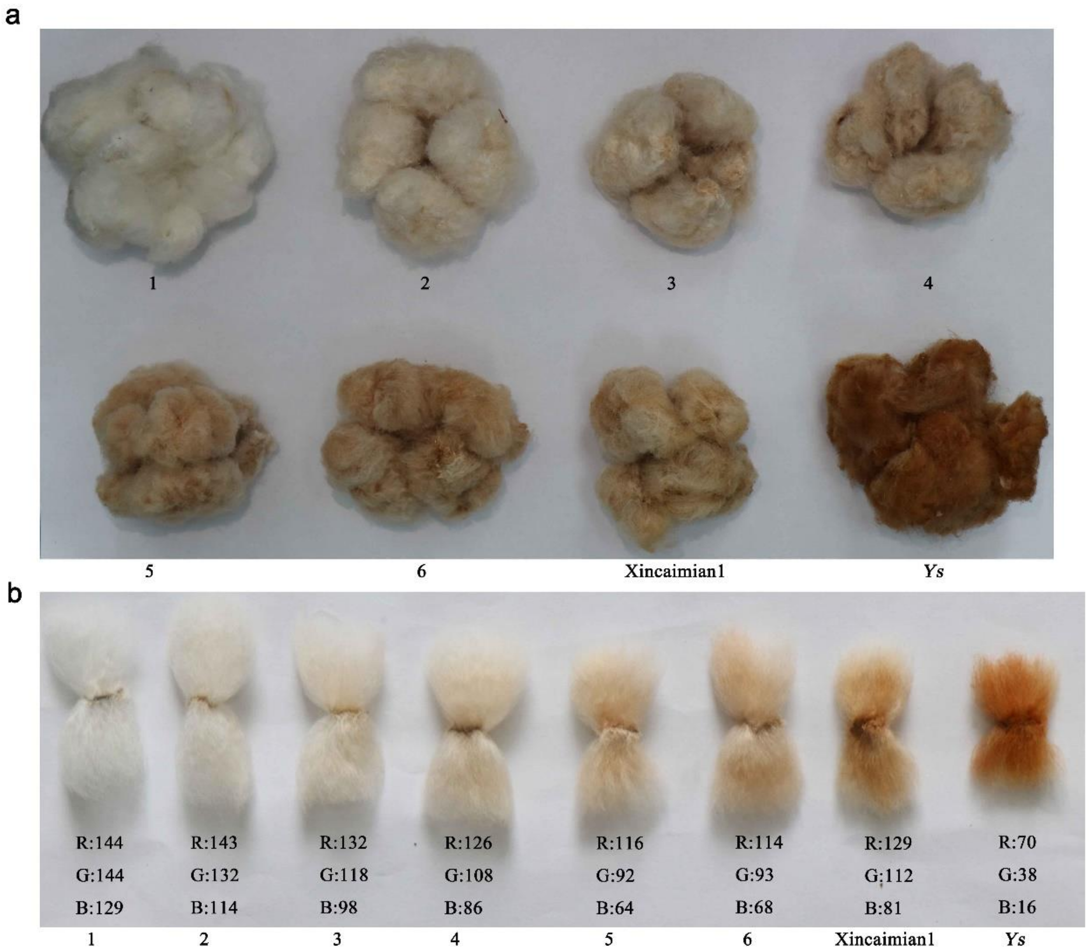
Supplemental Figure S2. Alignment relationship of markers linked to *Re* between *G. hirsutum* and *G. raimondii*. The left side is the *G. hirsutum* genetic linkage map, and the right side is the corresponding marker alignment in the *G. raimondii* genome.



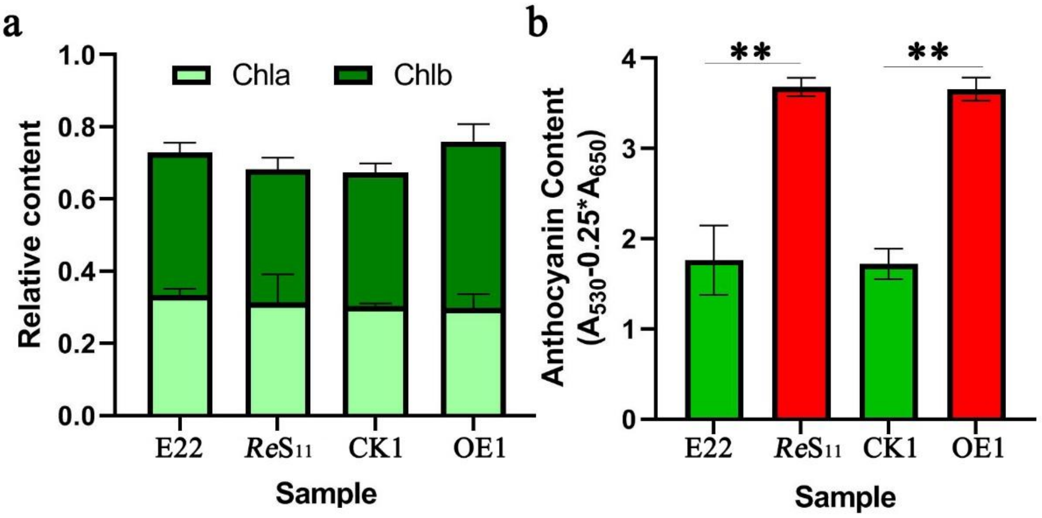
Supplemental Figure S3. Sequencing results of differentially expressed genes between E22 and *Re*S$_{11}$. a. Sequencing of RT-PCR products of *RE6* revealed the products were amplified from two different loci, based on 4 SNPs. RT_seq1 and RT_seq2 were the two sequencing results of RT-PCR products. *RE6*_ref and *RE8*_ref were matched genes in the reference genome. **b.** A 228 bp duplication was detected in the promoter region of *RE8* in *Re*S$_{11}$. Three replicates for each sequencing result are shown. **c.** The new RT-PCR results showed that the expression of *RE8* in *Re*S$_{11}$ was substantially higher than that of E22 and *RE6* showed no expression difference.



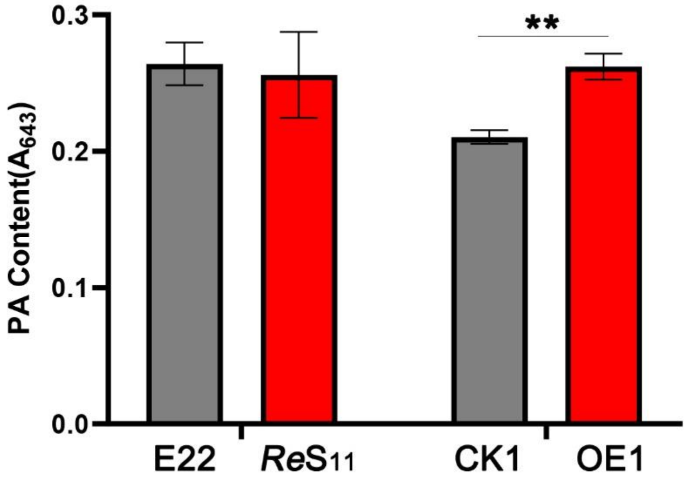
Supplemental Figure S4. Subcellular localization of *Re*. 35S: *Re+GFP* is an overexpression vector of *Re* fused with GFP. The nuclear marker is a red fluorescent protein (RFP) located in the nucleus. *Re* functions in the nucleus.



Supplemental Figure S5. The specific expression of *Re* in the fiber producing different shades of brown cotton. a. The color of cotton bolls. Numbers 1-6 represent different transgenic lines. Xincaimian1 and *Ys* are the existing light brown fiber cotton and dark brown fiber cotton used as control. **b.** The color of the unfolded fiber. The RGB value is obtained using color picker tool of Photoshop.

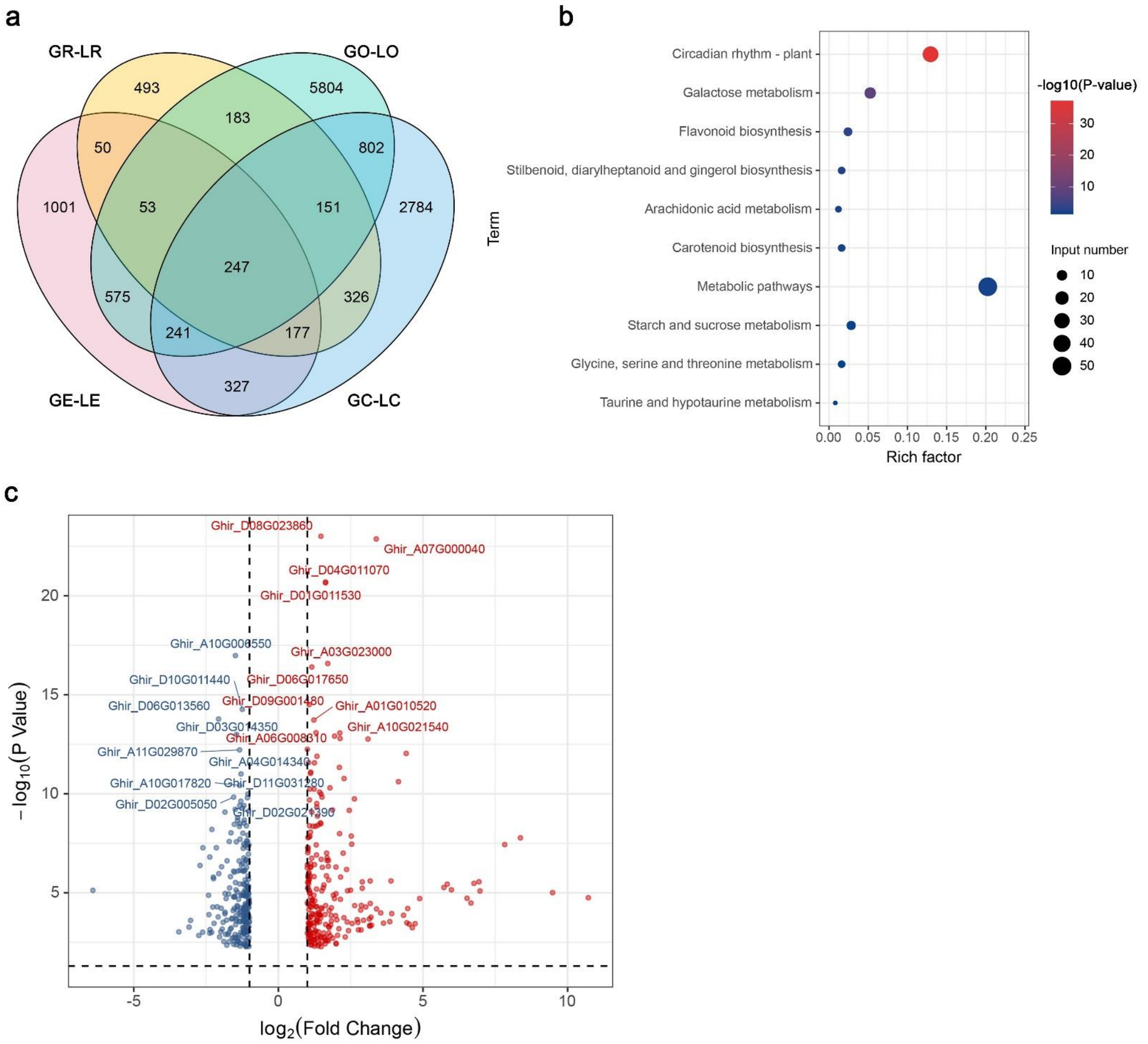


Supplemental Figure S6. Determination of relative content of anthocyanin and chlorophyll in leaves. a. Determination of chlorophyll content of E22, *Re*S$_{11}$, CK1 and OE1 in leaves. No significant difference was detected. **b.** Determination of anthocyanin content of E22, *Re*S$_{11}$, CK1 and OE1 in leaves. The anthocyanin content in *Re*S$_{11}$ and OE1 leaves was significantly higher than that in green plants. For **a** and **b**, error bars represent ±SD (3 biological replicates). The statistical significance was calculated using a *t* test (**$P < 0.01$, *$P < 0.05$).

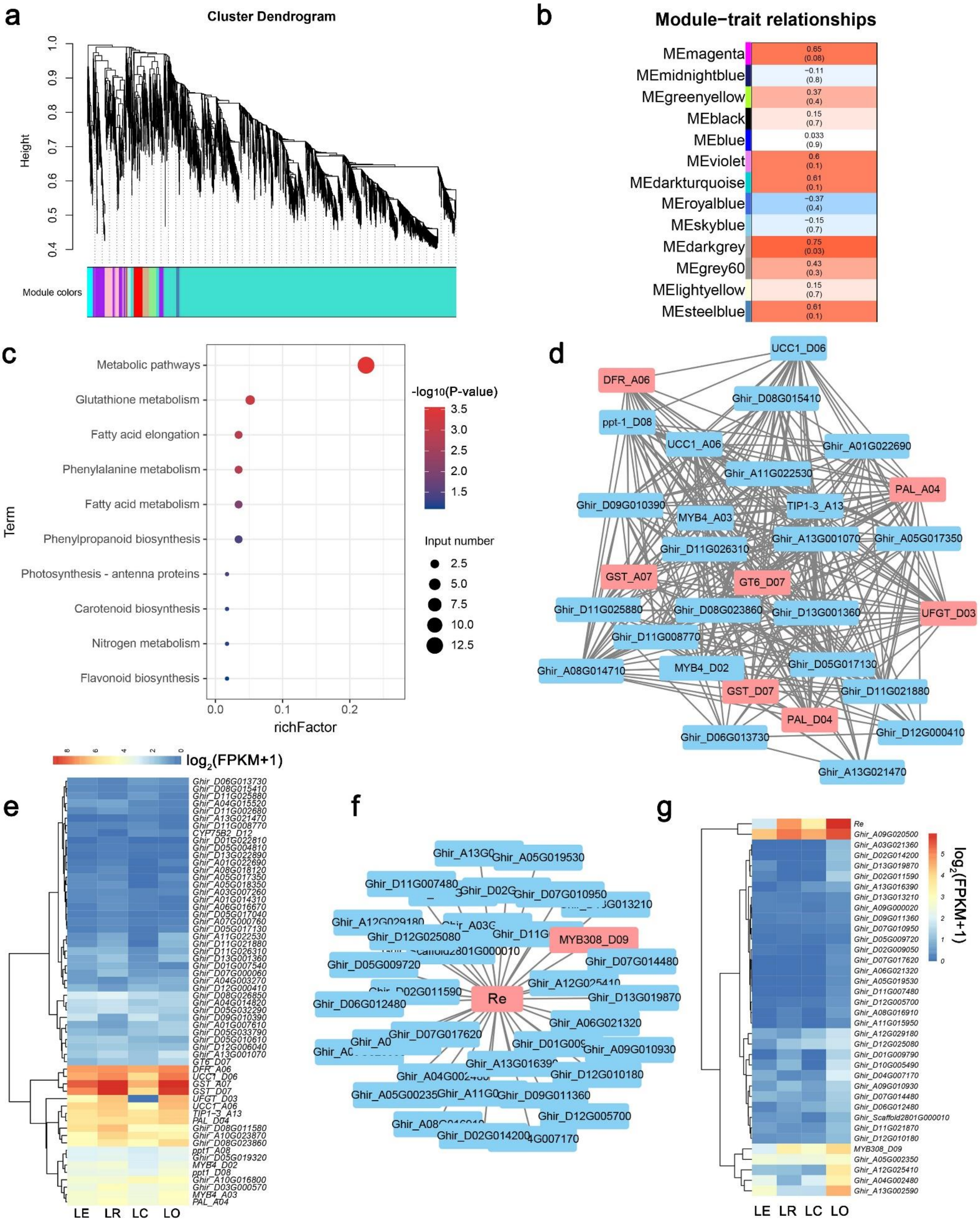


Supplemental Figure S7. Determination of relative content of PA in leaves. There was no difference in PA content of E22 and *Re*S$_{11}$ leaves. But the PA content in OE1 is significantly higher than that in CK1. Error bars represent ±SD (3 biological replicates). The statistical significance was calculated using a *t* test (**$P < 0.01$, *$P < 0.05$).

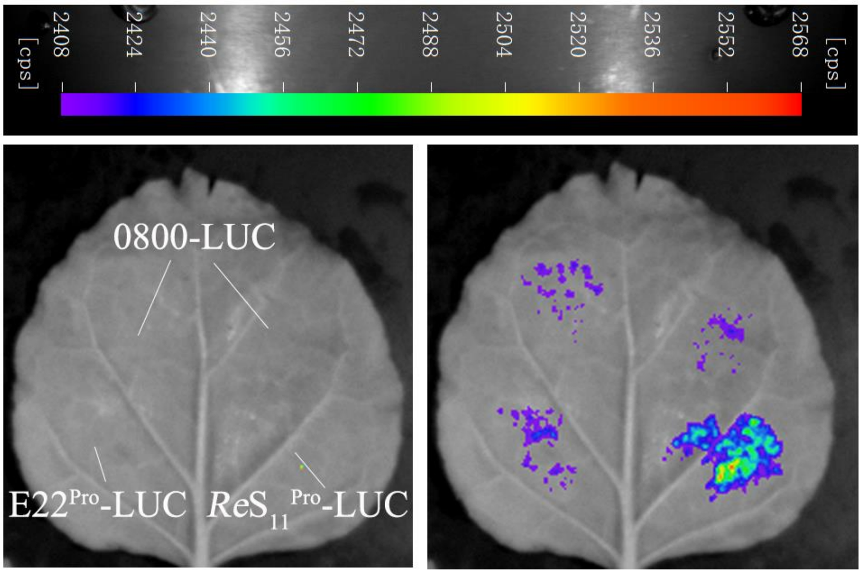
Supplemental Figure S8. The effect of natural light on leaf color. One week of bagging made *Re*S$_{11}$ leaves turn green, and there was a clear cut at the interface between bagging and non-bagging where the arrow points.



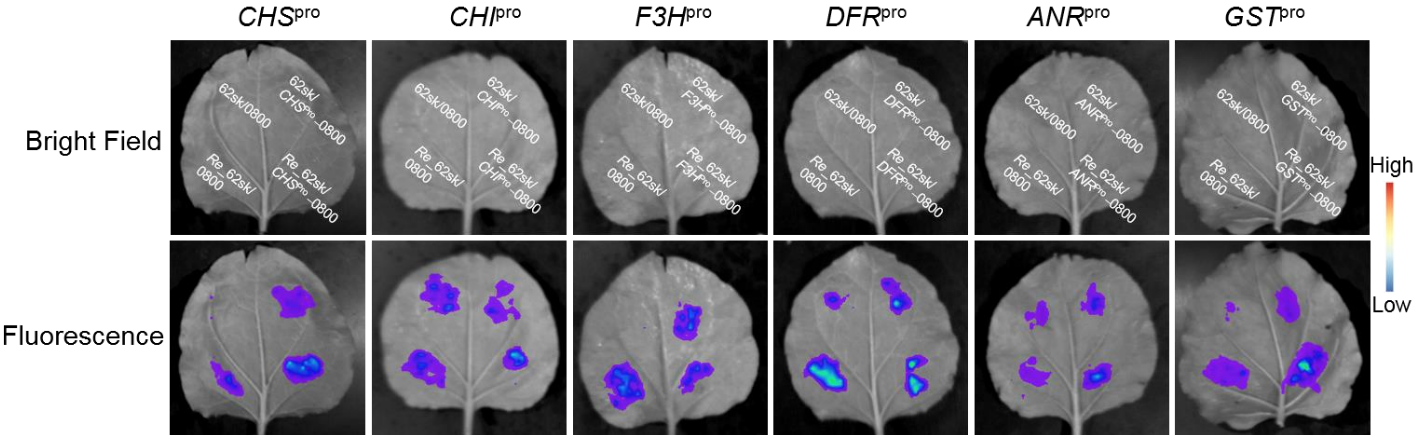
Supplemental Figure S9. DEGs under natural light and greenhouse conditions. a. Venn diagrams of DEGs of GR-LR, GO-LO, GE-LE and GC-LC. In which, "G, L" represent "greenhouse" and "natural light" conditions, respectively, and "R, E, C, O" represent *Re*S$_{11}$, E22, CK1 and OE1, respectively. **b.** KEGG enrichment analysis of the 247 overlapping genes. These genes are mainly enriched in metabolic pathway and circadian biosynthesis pathway. **c.** Changes in the expression levels of 493 GR-LR specific DEGs. Blue means down-regulation, red means up-regulation.



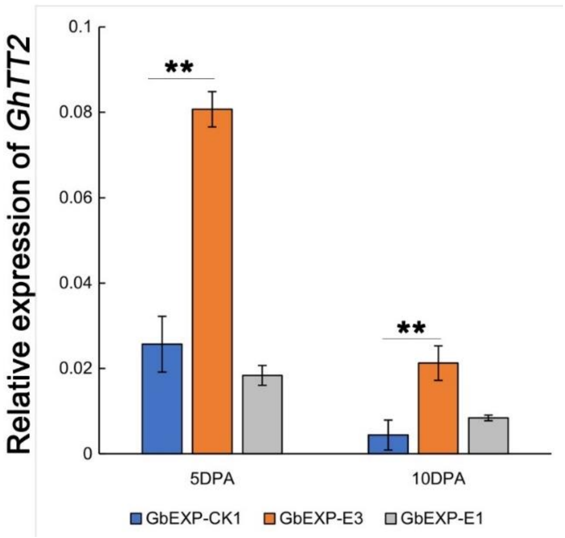
Supplemental Figure S10. WGCNA of DEGs. a. All DEGs between pairwise comparisons are clustered into 34 modules. Each color represents a module. **b.** The correlation between module and anthocyanin content. The upper value in each small rectangle represents the module-trait correlation, and the value in brackets is the corresponding P value. MEdarkgrey has the highest correlation with anthocyanin content, while *Re* belongs to MEsteelblue. **c.** KEGG enrichment analysis of genes in MEdarkgrey. **d.** Coexpression network of genes in MEdarkgrey. **e.** Heat map of gene expression in MEdarkgrey, drawn according to FPKM value by RNA-Seq. **f.** Gene network coexpressed with *Re*. **g.** Expression heatmap of genes coexpressed with *Re*, drawn according to FPKM value. "LR, LE, LC, LO" represent *Re*S$_{11}$, E22, CK1 and OE1 in "natural light" condition, respectively.



Supplemental Figure S11. LUC of *Re*S$_{11}^{pro}$ and E22^{pro}. *Re*S$_{11}^{pro}$-LUC resulted in a stronger signal in *N. benthamiana* leaves after injection.



Supplemental Figure S12. LUC of *Re* and six structural genes. The 6 structural genes are *CHS*, *CHI*, *F3H*, *DFR*, *ANR* and *GST*, and no strong fluorescent signal is detected.



Supplemental Figure S13. Relative expression of *GhTT2* in fiber-specific transgenic lines of *Re*. RT-qPCR showed that *GhTT2* had a significantly higher expression in 5DPA (days post-anthesis) and 10DPA fibers of GbEXP-E3 than that in GbEXP-CK1. However, *GhTT2* in GbEXP-E1 showed no significant expression change compared to GbEXP-CK1. Error bars represent ±SD (3 biological replicates). The statistical significance was calculated using a *t* test (**$P < 0.01$, *$P < 0.05$).

Supplemental Tables

Supplemental Table S1. Phenotypic statistics of F_2 populations in the field

Year	Total	The red plants	The intermediate type	The green plants	Chi-square value
2013	334	90	152	92	2.72
2014	954	243	484	227	0.77

Supplemental Table S2. Distribution of the 494 primers used for polymorphic analysis

Chromosome	Marker Number	Coverage (cM)	Chromosome	Marker Number	Coverage (cM)
Chr01	20	0-186.869	Chr01	17	0-164.119
Chr02	17	0-156.034	Chr02	21	0-197.102
Chr03	16	0-164.929	Chr03	11	0-94.321
Chr04	14	0-149.815	Chr04	16	0-162.228
Chr05	25	0-242.761	Chr05	15	0-146.947
Chr06	19	0-171.433	Chr06	28	0-252.267
Chr07	12	0-105.781	Chr07	13	0-117.608
Chr08	16	0-151.021	Chr08	27	0-256.028
Chr09	17	0-148.828	Chr09	18	0-169.927
Chr10	20	0-200.935	Chr10	21	0-193.185
Chr11	24	0-234.766	Chr11	21	0-198.852
Chr12	25	0-238.045	Chr12	18	0-172.192
Chr13	22	0-208.138	Chr13	21	0-211.897
At	247	2359.355	Dt	247	2336.673

Supplemental Table S3. Polymorphic rates of the primers selected from the genetic map

Origin	Primer	Nnumber of primers	Number of polymorphic primers	Number of polymorphic loci	Polymorphic rate
gSSRs	MON	106	21	23	19.81%
	Gh	9	1	1	11.11%
	BNL	24	7	10	29.17%
	CIR	7	1	1	14.29%
	DPL	12	3	4	25.00%
	JESPR	4	1	1	25.00%
	MUSB	2	0	0	0
	TMB	9	1	1	11.11%
	NBRI-gSSR	7	3	4	42.86%
	Subtotal	180	38	45	21.11%
EST-SSR	HAU	143	28	31	19.58%
	MGHES	3	0	0	0
	MUSS	5	2	2	40.00%
	NAU	109	17	18	15.60%
	STV	5	0	0	0.00%
	CCRI	11	2	2	18.18%
	NBRI-eSSR	14	2	2	14.29%
	Subtotal	290	51	55	17.59%
SNP+IDPs	Ghi	5	0	0	0
	GhIDP	7	0	0	0
	GbIDP	2	0	0	0
	Subtotal	14	0	0	0
Intron	GhPIP	2	0	0	0
subgenome	Gr-Gh	2	1	1	50.00%
fiber	gene	1	0	0	0
target	gene	3	2	2	66.67%
sequence-specific	CCRG	1	0	0	0
Pathogeness-related	CK	1	0	0	0
Total		494	92	103	18.62%

Supplemental Table S4. 470 pairs of SSR primers

Primer	Forward primer (5'-3')	Reverse primer (5'-3')
Chr01_8M-001	CGATGTTGAACACCAGCATA	GATAAGGGCAATTTCTGGGT
Chr01_8M-002	TGCACACTGACAAGATTATGC	ATTGGTGTCTTGGTTGGAAA
Chr01_8M-003	CCTTTCACCATTCAACATCC	GAAACGAGTTGGTGTATCGG
Chr01_8M-004	TCCCAAGAACAAAAACGAGT	GTTCATTTGTTTGTGCGTGA
Chr01_8M-005	AAGCCATGTGTAACCTACGTG	GTTGGACCTCGGGTAAGTTT
Chr01_8M-006	CTCAACCTAATCCAAGACAAGG	GGTAAAGTGGGGAGAGAAAGA
Chr01_8M-007	AACGTTTCGTTCATTTACGC	TCTAGGTGTATGGAGTCCCAGT
Chr01_8M-008	GCCCGATTCTGAGGTAGTTT	AGTCAACCCCATTCTTGACA
Chr01_8M-009	TAATGAAGCCTGGATCAACC	TCAGATACGGGTATGTGCCT
Chr01_8M-010	TTTCGGGAGCATAGACAAAG	CCATTTGTAAGATTGTCGGC
Chr01_8M-011	CTCTTCGTCTTCTTCTTCTCCA	TCATGCAAATCAACATCGAC
Chr01_8M-012	CCACCCAAGTCAAACACATT	ATTCTTGGTCCAGCATTGAG
Chr01_8M-013	GCCATATTGCACAGTTAGTCC	GCCCATACAGTTTCGTATGC
Chr01_8M-014	CAAATCACCCACATGGATCT	CCAAACCCACCCTAAGCTAT
Chr01_8M-015	CCATTGTTTAGGGTTTGGTG	TTGAAGATGTCTTGGTTAGTGC
Chr01_8M-016	TCTGAAATCAACCCCTGGTA	TTGGAGGGATGCTTCTCATA
Chr01_8M-017	CTTCTTCTTCTGGTGCGGTA	TGGGGATTTTACCTGACAAA
Chr01_8M-018	CGGTTGGATTTTGATGTCTC	TGTACGGTATGTCAAGACGG
Chr01_8M-019	CATCATCTTTCCATGCAACC	GCTCCCCATTGTCTCCTTAT
Chr01_8M-020	GTTCACTTGGTTTAAGGCGA	CAATTTGTCCAATAGCCACC
Chr01_8M-021	CCGTTACAGCGTAATCTCAAA	TAATTCCCCGTCAATACCCT
Chr01_8M-022	ATGGAACCCAATTAAGAGCC	GCCGAGAAAATCAACAGAGA
Chr01_8M-023	TTGGTTAGTTGGGAAGGATTC	CCTTCCAACTTAAAACAGCTACTC
Chr01_8M-024	CCTGTGATCGTAAAACCACC	CCTCCTACCCCATCAACTCT
Chr01_8M-025	TGCTTCTTCCTTGAAGCATT	GTGAGAAAAGGAGAGCCACA
Chr01_8M-026	CAGCACAACAAAATTTGGGA	TCTAGGAAAAGGAAAGCCTAGAG
Chr01_8M-027	CGAGGACTAAAACGGGAGAT	GCATGCCAACTATATCCGAC
Chr01_8M-028	TTTGCAGGGGGTTTTATGTA	ACACCTTCTAACCCCAAACC
Chr01_8M-029	TTAAATCTCACTGCCCTTCG	GGTTCTGCTCTTAGGGGTTT
Chr01_8M-030	AGGCGGCATAAGCATAAAAT	CTTTTTCTTCCCCAATTCGT
Chr01_8M-031	ACTAAGGAAATCCAATGGGC	ATCCAAAGGTTTGTAAGGGC
Chr01_8M-032	GCTGTCATGTAAGGAAAGGC	CTTCATTTTATGGGCAATGG
Chr01_8M-033	TGTATCGATGAATGGTGTGG	ATCGAGGGTGCTAATCCTTT
Chr01_8M-034	CTAAAACGCAAAACATTGCC	CGTCATGTGCTTATTGACATTG
Chr01_8M-035	TAATACATGGCAGAGCAGCA	CTTCCTGCATGTAACCCATC
Chr01_8M-036	CCATCATTTAGGAATGTGGC	GGCTTATCAGATGGAAGCAA
Chr01_8M-037	CATATGCTTGCCTTGGAACT	GCAACTATCGGAGATAGGACC
Chr01_8M-038	CGCACTTCGTATCTTTGGTT	TGCATCCCTGTATGATCCTT
Chr01_8M-039	TTTAATCAGCATATTGGCCG	ATTCAAAGGCACTAGACCCC
Chr01_8M-040	GAGTTGTCTGTCATGGCTCC	ATCATTTCCCAAACTATGCG
Chr01_8M-041	TGTAGGGCTTTCCGATACTG	AAGGCGTTCAATGTGATTTC
Chr01_8M-042	GATGTGGCTACTGTGGAACC	TCCCAGGTCTGATTTTGGTA

Chr01_8M-043	ACATTATCGGGAGGGACAGT	GACTCTCTTGGCAATTTTGAGA
Chr01_8M-044	GATGTGGCTACTGTGGAACC	TCCCAGGTCTGATTTTGGTA
Chr01_8M-045	GATAGGCGCCAATGAATAAA	CAAACATGAGGGGACAAGAC
Chr01_8M-046	GGCTACTCAAAAGCAATGGA	TCTCCCCCTCTCACTCTCTT
Chr01_8M-047	ACATTATCGGGAGGGACAGT	GACTCTCTTGGCAATTTTGAGA
Chr01_8M-048	TGGTGGCATGTTTAGAAAGG	CGTGAGCCAAATTAACAACA
Chr01_8M-049	AGGGGGAATCAAGGTTTTTA	GGGTTTTTATGGGGAATTGA
Chr01_8M-050	TTAGAGAGGGGGAAACTGAAA	GATGGAGTTGGGTGAGGTAA
Chr01_8M-051	GCTCTTTGCAAGTGGGATAA	TTCCGTCTTCTATGGTCGAA
Chr01_8M-052	GGACCAAATTGACAACTTTCAC	ATCATGAGCGTTGATTCGTT
Chr01_8M-053	GGAAACAGCCCATTAAACAA	GGATTGGCTCTCATCTCTGA
Chr01_8M-054	CAATCGGCTTCAAAAAGAGA	CAAAACAGCGTCGTTTCATA
Chr01_8M-055	TTGGTGGTTTCTTTGACGAT	GTGTGAGGAAAGGGAATGTG
Chr01_8M-056	GTTGTATGATCGCGGTTTTC	ATTCGGTCGATTATGCTTCA
Chr01_8M-057	CTGAGCAGCCTCATTCATTT	TGGGGAAGAGAAAAGGGTAG
Chr01_8M-058	TACTGGACTCAGTTCCTGCC	ATGCTTGAGATCATTGGGAA
Chr01_8M-059	TCATTAGATGGTAGCGGCTC	AGAGGAGCTGCAATTGTTGT
Chr01_8M-060	AAGTCACAAAAGCCGAGATG	AGAGGAGCTGCAATTGTTGT
Chr01_8M-061	CCCCAAATCTTGTTTCAATG	GGCATGGACATGGGTATGTA
Chr01_8M-062	TAATTTGGTAAAACAGCCCG	TCGTTCTCGTAATCGTAGGC
Chr01_8M-063	TTTATCAAGGCGAATCATGC	CAATTTGTTTCTTCTGCACG
Chr01_8M-064	AATCTTGACACACTTGACGGA	GTACATTCGCGCAAAAAGAG
Chr01_8M-065	TAAGTCGATCCCCAATCAAA	CTGAACTGTGCAACTCGGTA
Chr01_8M-066	TAAGGCCCCTCTCTTGTTTT	TTTGCACAATGAACTACCCC
Chr01_8M-067	CTCCACACCAAAAGACTGCT	CAAACATTTGTGGATTTGGG
Chr01_8M-068	TGGTGGAGGTATGTCGTTTT	ATGCCACGTAGAGAACAACC
Chr01_8M-069	GGTCCCGATTTGGTAGTGTT	CCAAGTCACTTCTTGTTGGG
Chr01_8M-070	GTTGGGGTAACAAGAAGCAA	TCCTTAAGGTGGGTTTGGAT
Chr01_8M-071	GCTTTCAAAACCCTTTTTCC	TATCCCCCATCTGCACTTTA
Chr01_8M-072	GGCAGTTTAGTGCCAAAAAG	GTTGTCATTTGGTGAGGACC
Chr01_8M-073	TGGGAAGGACCTTATGTTGA	TCAAATCCCCTTTTGTCTCA
Chr01_8M-074	ACCGACACGCTACGTTTTAG	AAATGTAGACCCATTTGCCA
Chr01_8M-075	TTCGTAAGCTTTCTTGTGGG	GAAGGCGTAATGGAAAGTGA
Chr01_8M-076	CAAAACCCAAACTCAATCCA	CCCAAAGTCAGCTCAACCTA
Chr01_8M-077	TGCTACTGTCACATGGTTGC	ATCCCCACAAATGAACAAAC
Chr01_8M-078	ACAACTTAAAGCAGATGCGG	AATACACTATGACGGCGGAA
Chr01_8M-079	CAACCGAAGAAACATCATCC	TTCCCATTTCCCATTAGACA
Chr01_8M-080	CGAGGGTGAATCTGGAAAT	CAACAAGGGCAAATACAAGG
Chr01_8M-081	CATCAACGCATATGTCCAAA	ATGTGGTTGTGAGCATTCG
Chr01_8M-082	TGTTGGACTGCTGGAAGATT	CGTTTGCCTTTGTCGTATTT
Chr01_8M-083	ATGGTTGAAGTTAGACCTGTCC	GGCTCGGGCTTATGATATTT
Chr01_8M-084	GCTTCCTCTGATTTTCGTCA	CCCAAGTCTTCCCTCATGTA
Chr01_8M-085	CACACGAAGTCATCAATCCA	TGGTGCTTTCTGGTATGGTT
Chr01_8M-086	TTCTCTCTTGTGCCTTGCTT	AGTTGCTGCTCTGCTATGCT

Chr01_8M-087	GCTTCGCCGAGTATTCTACA	CCGCCTTATTAGATCCAACC
Chr01_8M-088	CGGAAGTTCAATCTTCGTTC	ATGTATGTGTTTCGAGGCGT
Chr01_8M-089	ACCGGATTACCCGAATTAAC	ATTATCCAACCCAACCCAAT
Gr01_9-13M_001	GCCAAATTAGAACCAGCAAA	AACCTAGGCCAGTTTGGAGT
Gr01_9-13M_002	GAACTTGCCTAATCCCATGA	ATAATGGTGATGTCCATGCC
Gr01_9-13M_003	GGCCCAACTATTAAAACCCA	AGCATGAAAGAATGGGAATG
Gr01_9-13M_004	AAATTGCATGGAACTGGC	CCTGATATTGAAGGAACACGA
Gr01_9-13M_005	TAAGGATTTGGTCTGGTTGC	ACTGCTGGATCGTATGGAAG
Gr01_9-13M_006	AGAGTGTGGCGTAGAACCAG	GCTTGTCATTTCAGAGGGAA
Gr01_9-13M_007	GGGTAGAAAAATCGTGCAAA	GGCCTCTGAGAACAATGAGA
Gr01_9-13M_008	CATACAGCACCACATTTCCA	GTGTTACTGTCGCCATTTCC
Gr01_9-13M_009	TGGGTGTAGCTTACCCATGT	GAATTTTGAAGACGGCATTG
Gr01_9-13M_010	TACGCACGAGGAAGGATTAG	AGGTAGCGATCAAATGACGA
Gr01_9-13M_011	TCGAGTGTAATTTTGGGGAA	CCTTTGATGGTAATTGTGCC
Gr01_9-13M_012	GCCTCTTCTATTTCCTGCCT	AAAGAGACCAACAGGCAATG
Gr01_9-13M_013	GGTGATCCCCTTTTTGTTTT	GCAAAGAACCCTTCGATTTT
Gr01_9-13M_014	CTCTTTTTATTCCCTCCCCA	TGTGACGTTGACAAATACGG
Gr01_9-13M_015	CCTTGACAAGTGTTCGTTGA	GAGCCTAGGGACGAAATCAT
Gr01_9-13M_016	GAGAGCAGTGAGAGCGGTAG	CCTCCATTGTTGTTTCTCTCTT
Gr01_9-13M_017	TGATTTGGTGCAAAGTGGTA	CGATTTGTTTATTGCCGTTC
Gr01_9-13M_018	CTTCCACTAAGCTTCTCTCTCG	GAGCACAATATGTTCAAGTGAGG
Gr01_9-13M_019	GCCTCCCATCTTTATCCAAT	AGCAAAGCAAACTCGACAAT
Gr01_9-13M_020	GGGTTTGTATATTTGGGCCT	AGCTGCAGTGGGTTAGAATG
Gr01_9-13M_021	AAAAGTTCTTTTCGGCCACT	CGTGTAGAGGCCCAATTTAG
Gr01_9-13M_022	CATTCTTTGAAGAGGGACCA	GACAGTTTTCCGAAGGGATT
Gr01_9-13M_023	TTCCTTTTCAACTTCAACGG	GGGTGGATAAACCGATAAGG
Gr01_9-13M_024	GAATTTTGATCGCGGTAATC	TAATGCTGCCAGCTGATTTT
Gr01_9-13M_025	GCCCTTTTAACATGAGTTTCC	TTAGGGTCCCTCCAATTTTC
Gr01_9-13M_026	TTCAAGCTCGGTTGATTTTC	GTTGGGGTTCGTAAAGGATT
Gr01_9-13M_027	TGATGATGACGAATTTGCTG	AAGCACTTGTTGGGATTTGA
Gr01_9-13M_028	TGCTGGCTAGACAAATCCTT	ATCAAACATGGAGACATGGG
Gr01_9-13M_029	ACTTTGCAAGTTGATCCCTG	GCCAGAATATTCCTCAATCG
Gr01_9-13M_030	ACTTTGCAAGTTGATCCCTG	AATTTTTCCTACGTCCTCGG
Gr01_9-13M_031	TGCAAAGATTTTGGTCTGTG	CCTAAGAGTCGGGCTGAAAT
Gr01_9-13M_032	GCTTAGCTTTTGCGTTTGAA	GTTCTTCGGTGGTAGAGCAA
Gr01_9-13M_033	ACTTTCTCCACTCCACCTCC	AGCGGAACCGAGAATAAAGT
Gr01_9-13M_034	CATCTGCCATTAACATGCAC	CCACTCCTATTTCCCGTTTT
Gr01_9-13M_035	GATGGTTGCGAAATAAGCAT	TACGAGGTGTTACCGGACAT
Gr01_9-13M_036	TACAATCGGTTTTCATGGCT	ACCCGAGCCCAATAACTAAC
Gr01_9-13M_037	CAGAATCTGACAATGGGACC	ATTGTAAAGGAAGGGAGGGG
Gr01_9-13M_038	ATGGTCGGAGAGGATGTGTA	GAGCTCTCGATTGCACTGAT
Gr01_9-13M_039	CCTTTTGTATCGAGCTTCCA	ACCCCACTGCAAAACAAATA
Gr01_9-13M_040	CTCCAAAACCCAAATTTCCT	TGAGAAAGGGACTCAATCCA
Gr01_9-13M_041	GAACAATGGGCATGCTTAAC	TGATCAAGTGATGATTGGGA

Gr01_9-13M_042	CCCAAACACTAGACTCAGCC	TACATCGGACCTTCGGAATA
Gr01_9-13M_043	TGGCTGAACATTGTAGCTGA	CTCGGCCTCAGATCTTATCA
Gr01_9-13M_044	AGCCATTAAGGTTGTTAGTGGA	TTCAAGCTTCCATGGCTAAG
Gr01_9-13M_045	GTACATATGGAATTCAGCCTCTCT	CGCGTTTGAATAGGTGTTTT
Gr01_9-13M_046	GCTAAGTGCCGTGAATCTGT	TATGTCCACCTATGCCGAAT
Gr01_9-13M_047	TCCACTGGCCTAAAATGAAC	CGATTTCCGATACCATTTTG
Gr01_9-13M_048	TCATCATCCTTTTTGCAACC	GCCCGACCCGAATATATAATAA
Gr01_9-13M_049	ACCGGCCAATATAAAGGAAC	AAAGAACTGAAGGGAGCGTT
Gr01_9-13M_050	AGGTTGGTGGAAGATGATGA	GGCATCTCAAGAAAACTCCA
Gr01_9-13M_051	AGAATGGTTCTGCTAACTTCCA	CAAGTTACCTTCGACGCAAT
Gr01_9-13M_052	TGGCCAAATACATCATCTCA	ATTGCAACCCAACTGTTTGT
Gr01_9-13M_053	CTAATCAATGGAATGTGGGC	GCATGGTGCTTGTTAGCTTT
Gr01_9-13M_054	GCGTGGCTTTCGTATATTGT	CGTGTACATCATGCTGACATAA
Gr01_9-13M_055	CCATACAATCAGTGGCGAAT	TCCGCAAATGATAGAAGACC
Gr01_9-13M_056	ACAAGTGCACACAAAACCCT	TGTTGATTAGTCCCCGAAGA
Gr01_9-13M_057	CCCTCACTCACATTGGAAAG	AGGCAATGATGTTGTTGGAG
Gr01_9-13M_058	AAAAGCTTTAACCAGGGGAA	CGAAGAAACCGAATGTGACT
Gr01_9-13M_059	GATCATTTCAGCGACCATTT	GTTGAATTGCAACCTTGGTC
Gr01_9-13M_060	TCCCAAGTGGCAATAGTTGT	GTTGGGCTAGGTTTTGGATT
Gr01_9-13M_061	TTGTGGGTCCATTCAACTCT	TCCCTTCTTATCGTTCTCCTT
Gr01_9-13M_062	TGGACGAGATCTACAATGGTG	CGTTTGGTGGGAAAGAAATA
Gr01_9-13M_063	ACAACTGAGGAGGAGGCTCT	GCCTGTCAGATTGAAGCCTA
Gr01_9-13M_064	GTTTGTTTCACACTTTCTCGG	GAAAATTAGGGTCCAAAAGAGG
Gr01_9-13M_065	AAAATCTCTTCCTGGCCATT	GTCGAACCAAGCCTATTGAA
Gr01_9-13M_066	GGTTTTTGGACAAGCATGAG	GGGTTTGATTAGTGGATGCTT
Gr01_9-13M_067	TCAGGAGCTGAGTTGAGAAAA	GAAAATTACAAAGGCTCCCC
Gr01_9-13M_068	GGTGTGAAAGCATCACCTTT	GGCTTAGTTCAACCCATTTG
Gr01_9-13M_069	ATGGCAACACATTCCGTACT	AAAGGGCTAAAACCGAGAGA
Gr01_9-13M_070	GAACTCCTCAATGCATGCTC	ATGTCCTCCCATTTTCCTTC
Gr01_9-13M_071	TCCCTCTGTTTTTGCTCAAC	TGCAATATAAGGGCATGGAT
Gr01_9-13M_072	CACATGATACACTGGAAAGGG	TGGGTTTTGCTTTAGAGTGC
Gr01_9-13M_073	AGGGAAATCCAGGAAGAATG	TTGCATCCCAACATTAACCT
Gr01_9-13M_074	TATTTTTCCCCTTTCGAACC	TTCCACTGTTCGTCTTCCTC
Gr01_9-13M_075	AATTCAAAACCCCTTTGGTC	TGAATCTAGGAGAGCGTTGG
Gr01_9-13M_076	AGTTCGGTTCAGGGGAATAC	CCTTTCGTTGCATTTCATTC
Gr01_9-13M_077	TGTTTACTCCCTTTGGCTCA	AAGGTTCGGATTTGGAGTCT
Gr01_9-13M_078	AAAGCCTTAAAAAGACCCCC	GAACGAAACAACTGAGGCAT
Gr01_9-13M_079	ACAAAAGGGTTGAGTTTCCC	TTGAGGTATTAAGCCCATGC
Gr01_9-13M_080	TAACTTTTGCTCCGGTTGTC	GATTCGCCAACAAAATCAAC
Gr01_9-13M_081	TCGGGCCTATATTTTTACCC	TAGCTTAACGCCGGATTAGA
Gr01_9-13M_082	ACATCAAATATGCGGCCTAA	GTTCTGGCTAATGGGGAAAT
Gr01_9-13M_083	ACAATGCTTCTTTGGTGCTC	GGTGAAATCGGGTTCTTTTT
Gr01_9-13M_084	ATTAACCTTTTGGGCGAGTC	TGATCTCCAAAGGAGCATGT
Gr01_9-13M_085	GCTTGTCTTTGCCAATTTGT	TGTTGGAGACGAAGGGTTTA

Gr01_9-13M_086	GTGGGAATTAGGGGAGAAGA	AACAGCATTCGAAAACGAAG
Gr01_9-13M_087	TGCTCTTCTTTATCATGGGC	GACCCAATGCAAAGGCTTAT
Gr01_9-13M_088	CCACAACTAATCCATAGTACGAGA	GTGTAAGTTGCGGCTTCAAT
Gr01_9-13M_089	CAATGTCTTCATTTCCCGAG	CGAAAATGAAGGGAAAGGAT
Gr01_9-13M_090	CCAAACAAAGAACATACCCG	ACGGTAGTGGGCATGTTAAA
Gr01_9-13M_091	ACACGTGTCCAGATTTGGTT	GCAGAGACTAGGGATTAAATCGT
Gr01_9-13M_092	AAACCCCTAGTGATTACCCG	CCATCACCTTTCTTTTGTCG
Gr01_9-13M_093	ATTTGTTCCTTGGCCTTTTC	GAAAGGGGACGAATTTGAA
Gr01_9-13M_094	AACAAGCCATTTTCGTATGG	CGTCAGCAAAGTCAATCACA
Gr01_9-13M_095	AGTTTCGCACACTTAGTGCC	GGTTTATCGCTATCCGAGGT
Gr01_9-13M_096	TGGGGGTTCTTCTTCTCTTT	CGAATCTAGGGTCGGTTTTT
Gr01_9-13M_097	TTAATTGTAATGCCTTCGGC	CCATTCATGATTGCACATTG
Gr01_9-13M_098	AAGGTGACCTGATCACTGCT	GGCGTTAATGCTCGGTAGTA
Gr01_9-13M_099	CATGACCAGTAATGCACCAA	CTGACTCAGATAGACAGCTTTGAA
Gr01_9-13M_100	GTCAAAATTCGGTTATGGGA	AGGGGGATTCTGAGTAGTGG
Gr01_9-13M_101	GTGTCAGACCTTGGGATGAG	GCCCTTTTTAAGGTCTTTGC
Gr01_9-13M_102	TTGGCCCTCTTTTGTAATTG	GGGTGAGGACAATGGTGATA
Gr01_9-13M_103	AGCCGAAATTCTATGGGAGT	TGACCAAGGGTTTCACAGAT
Gr01_9-13M_104	TGATCTGAGGTCAAAGTCCC	TGTGTTTCAACCCTCCAGTT
Gr01_9-13M_105	CGTAGACTGAATGGTTGAAACTC	TGTTCAAGCCGACCTTTTAG
Gr01_9-13M_106	ATTCGTTGAGACTGCCTTTG	TGCAACAACTCCCAACTTTT
Gr01_9-13M_107	GTGCCTAATCGAAACCAAGA	AAAAACAAGACATGCCGAAG
Gr01_9-13M_108	GTTTTCGCATGGAGAGGATA	TAATTCCCTCATTCCCAACA
Gr01_9-13M_109	GTGGGAATTAGGGGAGAAGA	AATAGCGTGCAAAAAACGAAG
Gr01_9-13M_110	TTTCCATGAAGCTGATAGCC	ACTTGGCATTTATGGGTTGA
Gr01_9-13M_111	GGCCTCTTTTGTAAATGGGT	AAAGAGAGGCAGCTGTAGCA
Gr01_9-13M_112	GTGGGAATTAGGGGAGAAGA	TACCGAAACTAAGCGAGCAC
Gr01_9-13M_113	GCTGTGTCTTCTCGAACCAT	CCACCCGAATAGGTGTTCTA
Gr01_9-13M_114	AGGCTTGTAATTTTTGGGCT	CATTGTAGCAGGCCAATTTT
Gr01_9-13M_115	GTCTTGACTTAACCTCCCCC	TCTTCCCCGTCTCTTTTCTT
Gr01_9-13M_116	CCATCTATTCGTCGTCAACC	GGCACAGCCTCGATAGTAGA
Gr01_9-13M_117	ATAACATTCACCCCCTTGGT	CACTGTCAATCAACTCTGCG
Gr01_9-13M_118	GCTGCTTTTGAAGCTACTGC	TGTCTCTGGTTCAAGTGCAA
Gr01_9-13M_119	TTTCATTTTCAAGGTGTCCC	CTCAAAATTCGTAGGCCAAA
Gr01_9-13M_120	AGGTATAATGCATGGCACTTG	GGTGTCATTCTCTTAGAACCCA
Gr01_9-13M_121	TTCTTTCTTTGGCTCACACC	CCGCCCCGTTATAAGTAAAT
Gr01_9-13M_122	CTGCTTTGACAAGGGAGAAA	GGTTTAATTTTGCTGGGGTT
Gr01_9-13M_123	AACCCCAGCAAAATTAAACC	TGTTGTTCCTCCATTGCTTT
Gr01_9-13M_124	TAGAGGAGGTGGTGGTGGTA	ACGAGGACCAGATACATGAAA
Gr01_9-13M_125	ATGGGAGTTTTTGCGATGTA	CCTCGGTATGCATTTACAACA
Gr01_9-13M_126	CCCCTTCATTTCTCCATCTT	TTTACCATCGGATCTCTCCA
Gr01_9-13M_127	TCGACGAATGCAACTTCATA	TCACTGCTTCATCATCCAAA
Gr01_9-13M_128	ACTTCTCGCAACGTTCTGTC	GCCATTCTTGGATACTCCCT
Gr01_9-13M_129	GGCCTAGTAAACGGGCTAAA	CAAGCTTCCAAGCTCCATAA

Gr01_9-13M_130	GGTTAGGGTTAGGGTTTTTGG	CCCCGGGCATAGACATTA
Gr01_9-13M_131	TGCATGATGTTAACCCTTCA	CAATTTAATTTCGGTCCCCT
Gr01_9-13M_132	TGATCCCACAACTACTAATGTGAC	TTGCTTTGGTTACACATCCTC
Gr01_9-13M_133	GGCCGATTTTCCTTAATTCT	TAAGCTTTGGCACTGAGAGG
Gr01_9-13M_134	GAGTTGTTTTGTGCAGAGATGA	TAAGAGGCCTGAAATGACCA
Gr01_9-13M_135	AACCGAATGCTATTAACCCC	CGGTTCTAGAAGGAGGAACC
Gr01_9-13M_136	TGATTACTTCGAATAGCGCC	CCACTTGTAAAACTTCGGACA
Gr01_9-13M_137	CAAGAAACGAAGAAAACGGA	ATTTGAGCTCATCCAAATGC
Gr01_9-13M_138	GATGAATCCACGAACGAATC	TGCATGCATGTGATTTTACC
Gr01_9-13M_139	AGTCGAATTTAACGGGGAAC	GCACCGTTCAAACACTCTCT
Gr01_9-13M_140	GACATCGGAACAATTCAACC	GCCTCGCTAAAGACCAGATT
Gr01_9-13M_141	TCGAGCACACAAGTGAAAGA	ACAATGCCGCTTATCTTCAG
Gr01_9-13M_142	GGATGATGTTTCTTTGGTTGC	CTAAAATTTTGTCCAGGCCC
Gr01_9-13M_143	TCTTCAATGTCCCTCGCTAC	ACATTGCCCTTGAACTGAAA
Gr01_9-13M_144	GTTTGTCAATAATTTGCCCG	TGCCAAGGTGTCCTCATAAT
Gr01_9-13M_145	CTTCACAAAATTCCCAACCA	GTGGCACATCACACACAATAA
Gr01_9-13M_146	AATGAAGGATGCGTTTGAAG	CAAAGGCAAAAAGCTCACAT
Gr01_9-13M_147	CACACCTCTGTTTGTGTTCG	AAAATCATAACCGAGCTCCC
Gr01_9-13M_148	GAATCTCTGTGGGAGCAAAA	ATGGAAAAGTGGGGAAAAAC
Gr01_9-13M_149	GGTCTTGCTATCCTTCGTGA	TCACTACCCATTCGCTTCTC
Gr01_9-13M_150	GAGGGTTTTGGGGAGTAAAA	CGAATCGAGTTGAGTTTTCG
Gr01_9-13M_151	AAAAGTGAGAGGGACAGAAGAA	TCTTTTGATGTAGCTGAGCAAG
Gr01_9-13M_152	TTTGCAGCCAAAATAAGGAG	CCAGGAAATTTCAGTTGTGG
Gr01_9-13M_153	CAGCAGAACTCCTCTCTTGC	AACCCATCAAGGTTTTAGGG
Gr01_9-13M_154	GGTTCCCTCCTAAACAGCTC	AAAAGAGGGCAAAGTTTCGT
Gr01_9-13M_155	AAAGCCCACCATTAAAGACC	TGTTACTTGCTTGGCACTGA
Gr01_9-13M_156	CCCAAAAGTAATTGCAGCAG	CATGGTCATGAAAGCTAGGG
Gr01_9-13M_157	AGGATTTGAAGTGAATGGCA	TTGCGTTCAATAGTGCTTGA
Gr01_9-13M_158	CAGCCCAATTTGAGTGAAAC	GAGTCCATATTTGAGTGGGC
Gr01_9-13M_159	GCATGTCGATAGCTTCGTTT	TTTAAGCTGTTGCTTCCCTG
Gr01_9-13M_160	TGAATTACCCGAATTAACCG	AGGCCCACTATTCACCTAAAC
Gr01_9-13M_161	GCATGTCGATAGCTTCGTTT	TTTAAGCTGTTGCTTCCCTG
Gr01_9-13M_162	GGCATAATGGTCAAGTTTGG	GGTATTCATGTTTGACCCCA
Gr01_9-13M_163	TTATCTAACCGCTCCTGCAC	ACCGGAATCAACGTCTCTTT
Gr01_9-13M_164	CGAATCGAGTTGATTTTTCG	AAGGTTTTGAGGGTTTTTGG
Gr01_9-13M_165	CCTTTTTGGGTTTTCACCTT	CCGATGGAAGAAGAAGATCA
Gr01_9-13M_166	TGCTCAAAATCGTTGAGTGA	TAAAATATCGGCAAACCCCT
Gr01_9-13M_167	AGCAACCTCCAAACTCCTTT	GGCAAAAATATAGTCACTCCCA
Gr01_9-13M_168	GTGAGTTTAGATTGGCGGTG	TGGATTTGAACCTACGATGG
Gr01_9-13M_169	GCTTGCTCGAGAAAAAGAAG	ATTGCAGGGCATAAATCAAG
Gr01_9-13M_170	TGTAACAGGTCCAGCTCCAT	AATGGTCCCTTTTAACCGAG
Gr01_9-13M_171	CACAATGGAAAACGATCACA	TTTACTAACTTTCCGTGCCG
Gr01_9-13M_172	CAATTTTAAACCGCACCAAC	TAAGCTACAGGTGGAGTGGC
Gr01_9-13M_173	GGAGAGTGCAGGTAAGACCA	TTCTCTTACATCGGAGGCAG

Gr01_9-13M_174	TCTCGAAGCTCAACGAGAGT	TCACTTCGATCGTCTCCTTC
Gr01_9-13M_175	AATCCGACCTCTGAGCTCTT	TCCGATTAGGGTCAAAACTG
Gr01_9-13M_176	GCCATGCAACAAGAAAAATG	GGTTGGTCAGATTCAAGGAA
Gr01_9-13M_177	ACGACGTATTGGTCATCGTT	AGAAGAAAGTGCCTGGCTTT
Gr01_9-13M_178	CCTAGCCCGACTCATTTTCT	TCCTTTCTCTCTAAAAACAGCG
Gr01_9-13M_179	TGGTACGTTTTGAGGTGAGAA	GCATGCCATCTATATCCGAC
Gr01_9-13M_180	TCGAAGAAACCGATGAAAAG	TGGCGTTTTTGGTTACAAGT
Gr01_9-13M_181	AAAACCGGGATATTACAGCC	ACCACTTCCTCTTCCTCCAC
Gr01_9-13M_182	TGGTTGTAATTTGGCCTTACTC	CACCAGCCTTTTGAGCTTTA
Gr01_9-13M_183	ATGCAAGCTCACAAGTCACA	GTTAAATGCCGAAATGGATG
Gr01_9-13M_184	CTTTCCACGATCAATCAACC	GCACTTGGGTTTTCTTTTGA
Gr01_9-13M_185	AATACAATGCCTCTTTCGCA	GACTAAAACCATTAATGCCGAG
Gr01_9-13M_186	AAGAACCACCTTTGTGCTTG	AAAACCAGGCACCATTTGTA
Gr01_9-13M_187	CGTAATCTCCTTCCTCAGCA	TTCTTAGCAATGTTGACCCC
Gr01_9-13M_188	GGGTCTGAAGATGAGAAGCA	GTATTGCATTTGGAAGTGGG
Gr01_9-13M_189	CTACATCGACCACTGTTCCC	TTGTATGGGGAATTGATTGG
Gr01_9-13M_190	GGCGAACTCTGTCTAGGTGA	GGCTATAAAAAGCCATGCAA
Gr01_9-13M_191	TCTAGGTGAGCTTCCCCTTT	GGCTATAAAAAGCCATGCAA
Gr01_9-13M_192	TTTGGAGGTTTTGGCAGTAG	ATACCAGTCCCACTAAGCCC
Gr01_9-13M_193	TCATTTTGTCTAACCGCTCC	GAATCGACGTCTCTCTTTGC
Gr01_9-13M_194	CTTTAGCAGCGTTTTTGCTC	ATGTCTTCGTGGTCGTTGAT
Gr01_9-13M_195	TACATTCATGATCAACGCCA	ATCGAAGAACATGACCCAAA
Gr01_9-13M_196	TATGTCGAAGATGCTACCCC	TCAGCAGTAGGCCAAGTCTC
Gr01_9-13M_197	AACTTCATGCAACTACCCCA	CCAAAAACCTTTCTCCACCT
Gr01_9-13M_198	CCCAACATAGCGATGAAATC	AATAACAACAGCCCAACAGC
Gr01_9-13M_199	ACTTCCGAAACCCATACTCC	GAACCAAAGAGACCTCCCAT
Gr01_9-13M_200	CCCAGCCCGTTTTCTAAATA	GGCCTCAGGCACTACTTTTT
Gr01_9-13M_201	TCCAGCTCAGGTTTATTTGC	CAAAGACCAAAGGAAATGGA
Gr01_9-13M_202	AAAAGTTTTGAGGGCTTTGG	TTTACTCCTTCCCACTTCCC
Gr01_9-13M_203	AAATTTGCTAGGCCCATTGT	CCTAGGGTTTTCTGCTGCT
Gr01_9-13M_204	AATTCGTGCTGATGTTAGAGGT	GGAGCAAAGAATTGAACAGC
Gr01_9-13M_205	CCACAACAATCAGCAATCAA	ATTTTTCTCTCCCTGCTCGT
Gr01_9-13M_206	ATACAACGCGTCCAGACTTT	ATCTTATGACACAAGGGGCA
Gr01_9-13M_207	ATTGTCAAGCATGACTGGCT	TGTCTTCTCTTCCCCTGACA
Gr01_9-13M_208	GTGATTGATACCAAAGGCGA	ACTTGTTTGTATCAGGGGCA
Gr01_9-13M_209	ATTATGGGAAATCCCTGCTC	TGGTATTGGAAAGGTTGCAT
Gr01_9-13M_210	ATGGTTTTGGTCGTTGAGAA	ACCACCTTGGCCACTTAGTT
Gr01_9-13M_211	CCCCCTTGAAAAGAAAACTC	TAGTGGACTTGTGACGTGGA
Gr01_9-13M_212	CCGACATATTGATTTGGACG	CCACTTAGTTCACCGAGGAG
Gr01_9-13M_213	TTTCCTCAAGTCGAAAGTGG	GCGTAGCTTAAAATGCCAAA
Gr01_9-13M_214	AGTCCCCTCAACAGTCATCA	TAAAACGGATGAGGGTAACG
Gr01_9-13M_215	GTGTCTGGGTGCAAAGTTTC	GCCATGAGATAAGGATTGGA
Gr01_9-13M_216	TGCTGGGAGAGATATCCAAA	CATGAGCCATAGTTGAACCC
Gr01_9-13M_217	GCAAACACGAGTTTAGCGAT	TGTCCAAAGACCCTGAACAT

Gr01_9-13M_218	ACATAAGGGTCACCTGCAAA	GGGGGTGCAAATAGAGAGAT
Gr01_9-13M_219	GGAAATTCGGTCAAAGGTCT	CATCGAAACCCTCTGATACG
Gr01_9-13M_220	AAAACCAACCCAATAACCCT	ATGAGAAAATCGACCCAACC
Gr01_9-13M_221	CACGCAAAGAACAGTAGCAA	AGGAGTCTCCGATTACACCC
Gr01_9-13M_222	CATTTGACCTTCCTCCTTCC	AACTTGAGTTTCGCAAGTGG
Gr01_9-13M_223	TTTCGGTATTCCTTTTGCAG	CTTGCCTCATTGCTCTCATT
Gr01_9-13M_224	GGTGAGAGAGCCACAAAAAC	AATTTTAGGATGCACGGTGA
Gr01_9-13M_225	TCCAGGTGAAATCGTACCTC	GAGGGAAAGGGGATGTCTTA
Gr01_9-13M_226	TCAATCATTGCAACGTCAAG	ACCTCCTTTGGCATTAAACC
Gr01_9-13M_227	TGGTTTAACGGGAAGATTGA	AGCGTCACAACACGTACAAA
Gr01_9-13M_228	CGTCCCCGTATAATGAACTG	GGAGAAGAGAAGGAGATCGG
Gr01_9-13M_229	AATATTGACGTGGTGGGAGA	GCTAACGTGGCCGAATAATA
Gr01_9-13M_230	AGGATTCATTAGCTCGGCTC	GCATCGGTAACTTGAGGTTG
Gr01_9-13M_231	TCATACAAAAAGCTGCCCTC	GGGATTACGTGAGAATGGTG
Gr01_9-13M_232	TATTTTGACCCAATCCCTCA	TTGGTGCAAGTGTGCTTAAA
Gr01_9-13M_233	GAACCGCATGTAGTGAGACC	GCCTTCTCTCGTTGTGTTTG
Gr01_9-13M_234	TGTGGAAGGCTTTATCTGGA	TGGCCTCTCCTTTTTCTTTT
Gr01_9-13M_235	TTGACTGGACCTTCTTTTGC	AATAGATGTAGAGTGCGGCG
Gr01_9-13M_236	AAATTGCTAAGCTCGAACCC	GGGTAAAAATATAGGCCCGA
Gr01_9-13M_237	TCGAATTGAGTCGAGTGAGA	ATTACGATGGGTGACAGTGG
Gr01_9-13M_238	GGCTCGTTTTTGGCTTAAAT	TAGGGTGATGAATTCGGGTA
Gr01_9-13M_239	GGGAGTGAATTAGGGGAGAA	GAAAGAATGGTTTAGGGGGA
Gr01_9-13M_240	TGACACACCAGATACGGTCA	GTTTGCTTCGAAATGGAGAA
Gr01_9-13M_241	GAGCGAAGTACTGAGGTGGA	GTACCTCAGATGGATCGTGC
Gr01_9-13M_242	TCATCTGGCTGAAACCCTAC	TTTGCAGAAAATGGGTTCTC
Gr01_9-13M_243	ACAAACATGAGGGGACAAGA	GATAGGCGCCAATGAATAAA
Gr01_9-13M_244	AAACCCAAGGACAAATGATG	ATGAGACCCGATCAACTGAA
Gr01_9-13M_245	CCATAATTTTAGGTGTTGAGCG	ATTCTGGAATTCAGTGGCTG
Gr01_9-13M_246	AGGTTTTCAACCCCTTGTTC	ACAAACACGCAAAGCAGTG
Gr01_9-13M_247	TGGTACAGGTTAAGTAGATGCCT	GTAAAGTGGACTGGTGGGTG
Gr01_9-13M_248	GTTTAGGCCTTTTGGCTTTC	TGGAAAGTAAGTCAACCCCA
Gr01_9-13M_249	TTATCAACCACATCTGCCG	GCTCGAATCTTTGTGTCTGG
Gr01_9-13M_250	GGAATTTACAACTTTGGGCA	GTGACATGGCAGTTGACAGA
Gr01_9-13M_251	TCCATCCCTCCACTTTACAA	AGCAAAATAACCCTGGAACC
Gr01_9-13M_252	GTTTGCAACAAATAGGCACC	CAGCAGTTGTGGATGTTGAG
Gr01_9-13M_253	ACTGATTCGGCACTTTGTGT	TAACTTGACTCGGACTTGGC
Gr01_9-13M_254	CCGGTCTTTCTTGCTAAACA	AACCATCCTTCTCCTTGTCC
Gr01_9-13M_255	GGTTCATGAAGCATGTCTGA	CCCAGATTTGTTTGCATTCT
Gr01_9-13M_256	CAACCACCACCTCAAAACTC	TCTTCAATGGCTTTGGAGTC
Gr01_9-13M_257	TCTCATCCAACATCCGTTTT	TCAGCTTGAACAACACTCCA
Gr01_9-13M_258	AGAGCCAACCCTAGGAAGAA	TCCAGCCTTCTCTCGTTATG
Gr01_9-13M_259	CCTTATGTGGGAGGCCTTAT	AACTCAAATCCCCTTTGGTC
Gr01_9-13M_260	CGGTCTGACCCGACTATTTT	CAGCAGCAAAAGAAAGAGGA
Gr01_9-13M_261	ATGGAAAATGGATGCCTGTA	GCCATATACATGACCAAGCC

Gr01_9-13M_262	TGTTTTGTTGAAAGGGAAGC	AATGAAGCTCAAGCAACCAG
Gr01_9-13M_263	CCCGATCTGGATAGTTTGAA	CTGAAATGGATCAAATTGGC
Gr01_9-13M_264	CCGGAGATTTAGACCAGGTT	CCTAGTGGACTCTCCCACCT
Gr01_9-13M_265	CAATGCATGTTGTTGTCCAC	CGTGCACTCAACAAATTCAC
Gr01_9-13M_266	GCAGTTACAGGCTAGGTGGA	AAACTTGTTCACAGGTTGGG
Gr01_9-13M_267	ACAGTGGACCTGAAAGCAAA	TGGTTGAACCGGAAATTAGA
Gr01_9-13M_268	CATGTGGCAACATCTCAGAA	TTGACCCCTCAACTTATCCA
Gr01_9-13M_269	GGACGAGTTCATACCATTGC	AGATCATTGAGCGGTTTGAG
Gr01_9-13M_270	GAAGATGATGGGTTGTTTGG	AGATCATGAAGGGCAAAATG
Gr01_9-13M_271	ATTCGAAGCAACGATCTCAA	TATCATGTTCATCTTGCCGA
Gr01_9-13M_272	TTCGTCACAGACGTCACAAC	TGTGTTTAACTTGGCTGGGT
Gr01_9-13M_273	CTGATACTTGTCCCCACCAG	ATTGTTGGTGTGCATGACTG
Gr01_9-13M_274	CCAAACCCTAATCTGTCATGC	ACGGGTAAGTTGTTGCATTT
Gr01_9-13M_275	GGTGGAATTGAGATAAGCCA	TTCCTTGATCGAGTTCATCG
Gr01_9-13M_276	AGGGTTCCTGCTCACTTTCT	GAAAGGGTTGGGTTGTTTTT
Gr01_9-13M_277	TGGGTGGATTGGGTTAAGTA	TCATTTATTTCGGGTATGGG
Gr01_9-13M_278	TTACCTCGAGACTTGCTCGT	ATTTTTCGAGCCTAGGGATG
Gr01_9-13M_279	AAAAGTACGGGGTATTTGCC	ATACACGGATTCCAACCAAA
Gr01_9-13M_280	AATAGGCTCACGTCTGAACG	AACATGTCTCGCTCAAAAGG
Gr01_9-13M_281	CGAATCGAGTCGAGTGAAAT	GGGTGACAGTGGTTACAAGG
Gr01_9-13M_282	AAGGTTTTGAGGGTTTTTGG	TACTCCTTCCCACTTTTCCC
Gr01_9-13M_283	CTTCGAAAATCCCCAAACTT	AGTATGGGCCCACTCGTATT
Gr01_9-13M_284	ATTATTTTTGGGCTGTTGGG	CACAATTGGGCTTTTCAGTC
Gr01_9-13M_285	GACACATTTCCCTATGGCTG	ACATTTGAGAGTCGAGCCAG
Gr01_9-13M_286	AATCTCCCCCAATTCACTTC	CCTTCTCTTTCTTTCTCCTTTCTC
Gr01_9-13M_287	CCCGTGTCTTCTCCTTCTTT	AGGGTGAAATGACAGACCCT
Gr01_9-13M_288	CATTTCACAGTGGGATATCGT	CAACGTGAGGAAATTTAGGG
Gr01_9-13M_289	GGTATAAGATGGTTCGGTTGG	TACTTAAAACGCATCCCAGC
Gr01_9-13M_290	GTTCGGTTGGTTAATATGCG	TACTTAAAACGCATCCCAGC
Gr01_9-13M_291	TATGAGCATGCTTTTCCAGC	TGCCTCGTCATCTTGTTGTA
Gr01_9-13M_292	AGTTTAATGACATTGGGCGT	GGAAGTTGGAGAAGCACAGA
Gr01_9-13M_293	ATCATAGACCGCCACATCAT	CGGAGAAATTCGAAAACAGA
Gr01_9-13M_294	CACAAGCAGATTTTCAGGCT	GGGATGAAGTGAACCATTTG
Gr01_9-13M_295	CAAATGGTTCACTTCATCCC	CTACATGTTCCCACCCAAAC
Gr01_9-13M_296	CTGAAATTCTCGTAATGTCGGT	ACCAAGGTAACATGCAATCC
Gr01_9-13M_297	TGGCTTTCTCCTTCCTTTCT	GCCATTGTTCTTTAATGAGGC
Gr01_9-13M_298	GGGAAACTGCAAAACGATAA	AGAATGGGGACCTTTTGTTC
Gr01_9-13M_299	GGGTGATTTGACAAAAATGC	GTAGAGGAAGCCCAAAGGAG
Gr01_9-13M_300	AAGGCCAAAATTTGTATCCC	AACAAACTGACCAAAACCCA
Gr01_9-13M_301	GGAGGCAACCCAATTTTTAT	CATTGCTCAACGGTTTTCTT
Gr01_9-13M_302	GCGTGTGTAAAATAATGACCC	ATGGAGGAATCACACTCAGG
Gr01_9-13M_303	CGTGGCATGTTAAATCATCA	AGAGATGGAGAAGGGAGGAA
Gr01_9-13M_304	AGATGGACCGTACAAGGTGA	CCCTTCCTTAAAATCCCAGA
Gr01_9-13M_305	TGCCAGCTGAATCCTCTTAT	GGCAAATAAAATCAGAGCCA

Gr01_9-13M_306	TCCAAGTAAATAGCATGAGTCG	GTTCCAAGATTATCAACGGTGT
Gr01_9-13M_307	ATGCAAGAGAACAGACTGCC	TTCCCTAATCCCAATTCCTC
Gr01_9-13M_308	GTTGGCAGGAAATGTTGAAT	CCAAGTCCCTATACATGCCA
Gr01_9-13M_309	GTTGAGGCGGCATAAGTAGA	GCTTGAAGCTCAAAAACCCT
Gr01_9-13M_310	AAGAAGAAGGCTCGGATGAT	CGTACAACAAACAACCCACA
Gr01_9-13M_311	CATATTACCGCCTTCCATTG	CTCGCCATGTTTTCAGAGAT
Gr01_9-13M_312	CCTATGCTGCTATGCCTTGT	ACTGGCACTGACTTGCTAGG
Gr01_9-13M_313	GAAGTTGGGTCAAATCATCG	TCGTAGGCGTACTCTTCCAC
Gr01_9-13M_314	TTGCTCAGTTTAGGTCCTGC	TAAACTTGGAAACCCACCAA
Gr01_9-13M_315	CCACATGTCATACTGTGTTGC	AAAAGCAATTAAGCCCCTACTC
Gr01_9-13M_316	CCGAATTAACCATATTACCCG	TCACCTAAACCCAATCCAAA
Gr01_9-13M_317	CTGGGATTGTCAGCGTAGTT	GCATGAAACCATTCATGTCA
Gr01_9-13M_318	CACAGTCGGTTCGTTAGCTT	TTAAAACCATGGAGGGATTG
Gr01_9-13M_319	CAGGCTAAGTGCTGGTGAAT	CTAATCCACATGTGCCGAAT
Gr01_9-13M_320	GGGCAAATATTGATCTTCTCAC	TGCATTGCAATCATAACCAG
Gr01_9-13M_321	CCGCCATTGAAGAACACTAT	GACATGTGAAAGATGAAGTGGA
Gr01_9-13M_322	CCAAAAATTTGTCGCAAGTC	CGCAATGCTACCGATATTCT
Gr01_9-13M_323	TTACTCCTTCCCACTTTCCC	GAGGGTTTTGGGGAGTAAAA
Gr01_9-13M_324	TGTCACTTTACGAGCTTAGGG	CCATTACTTTGTTCTTTCCCC
Gr01_9-13M_325	GATAGAGCTCACAAAGCCGA	TCGCTACTAAAATGGCTTGC
Gr01_9-13M_326	GGGAATAAACCCCTTAACAGA	GATTGATTCCCACCATTCAA
Gr01_9-13M_327	AATGGTCCAATCCAATTCCT	GCTCCCGTTTCAACTAAACA
Gr01_9-13M_328	GGCTTAATCGCGTAAAATGA	TTAGTTTCGGCCAAAAGATG
Gr01_9-13M_329	GGCCAAAATGATTACTAGACCA	AATGGGGGTAAATGGAGAAG
Gr01_9-13M_330	AGGCTGGAATCTCCCATAAG	GACAAAATCTCAGGCCCATA
Gr01_9-13M_331	GTTGATGGTGGCAGTTTTTC	AGGAAGAGTTTAGAGAGAGCTCAA
Gr01_9-13M_332	TGAACCAATCATACCTAACCG	TGTACCAACAACAGGAGAATGA
Gr01_9-13M_333	CCCACTTGGACAATAGGTTG	AAAAGACGGGAAACATCCTT
Gr01_9-13M_334	CCACCTTCCCTTTTTACACA	CCCTCTTGATAGGTAAGGGTG
Gr01_9-13M_335	CATGCCATATACCAAGCCTAA	CATTGCGTCTTATTGAAGGC
Gr01_9-13M_336	TCTGAGAAGTTGAGCAACCC	TGCCTAAGCTGGAGTAATGG
Gr01_9-13M_337	CACATTGGTTGAGGCTTTTT	ATCAGGTAGCATTTGGTTGC
Gr01_9-13M_338	GACGGTCATGATAGGGTTTCT	TGACTAAAACGCCGGTAAAG
Gr01_9-13M_339	TGTTAAGAGGACATTCGAAGC	CGTCTGTAACCCCTAAAGCA
Gr01_9-13M_340	CCCTTCGTTTTCTTTTAGGG	AAACATGTCCAACAGCATGA
Gr01_9-13M_341	CATGCAGTACAAACCGAACA	CATGCGAAAATGGCTTACTT
Gr01_9-13M_342	CGTGATCGAAGCTATCTGGT	TCACTTGTGTGAAATGGACTG
Gr01_9-13M_343	AACACCTGCAAAAACAGAGC	CCCCTTTCTTTTCTTTTTCG
Gr01_9-13M_344	ACGCATTACTCCGTTCTAGC	ATGACGATTGTTGATGCCTT
Gr01_9-13M_345	AAATGAAGCGTACCATAGCG	AGTTTTACATCCGGGTCCTC
Gr01_9-13M_346	GGATGGCAGTTTAAGGGTTT	TTTCCTCTGCTTTGACAACC
Gr01_9-13M_347	GAGACCCATGGATGACTCAG	CATGGCAGAGAGAAACAGGT
Gr01_9-13M_348	GCGTAAACACTGGGAAAGGT	CGGCTATAAAAGCCATGAAA
Gr01_9-13M_349	GACAAGACTACCACATGCCC	TTGATCGGAAGGGATAACAA

Gr01_9-13M_350	CGATCCTTTGTGAACCATGA	TCTAGATCTCTGCAAACGGC
Gr01_9-13M_351	CATGAAAAGCCTGGAAGAGA	CATTGGATCCTTCACCAAAG
Gr01_9-13M_352	TCATGTCCGAAAGGAGACAT	CAGGCCATTAAGAAAGCAAA
Gr01_9-13M_353	GCAGTAAAGGCGTCATGATT	TTCCAACATCTAGTGTGCCA
Gr01_9-13M_354	GGAGGAGAGGATGGAGGTTA	AATCAAAGCCTCTCCCACTT
Gr01_9-13M_355	ATCCCTGTCAAGGTGTCAAA	CAACATCAGTCACCAACCAA
Gr01_9-13M_356	TTAACTTGACTCGGACTCGG	AAGAGTACGGGGTATTTGCC
Gr01_9-13M_357	GGCTGATGGCAAGTAGAAGA	AAATGTCTCACCGTTTCCAA
Gr01_9-13M_358	AGCAAAGAGAGGCAGCTGTA	AAAGGATTTGGGCTATTTGG
Gr01_9-13M_359	TGTAGCAGCGTCACTCATGT	CAGCCAAGAAGCAATTAGGA
Gr01_9-13M_360	CTGAAGTCGGTCTTGCATCT	TCACATGCATTAGACACCGT
Gr01_9-13M_361	CTGAAGTCGGTCTTGCATCT	TCACATGCATTAGACACCGT
Gr01_9-13M_362	CTTGAAATCGGCCTTTTGTA	ACCCACTAAACCTAGCCCAC
Gr01_9-13M_363	TCGGTCTTTTATAGCCGAAA	CCCTAGGAGCCTATTTGCTT
Gr01_9-13M_364	AAGGCGTTTTGGAACATACA	GAACCAACATTGCAACACAA
Gr01_9-13M_365	ACTTTGGCACCTTTGGTGT	GGATGCCTTTGCTTTGTTTA
Gr01_9-13M_366	AGATGGTTGAAGTGTTGCGT	ATCCCTATCCCAATTTTCCA
Gr01_9-13M_367	TTTAGGTTCATTGCAACGGT	CCAACTGCTGACATTGTTGA
Gr01_9-13M_368	AGATTTGGAACGAGGGAAAT	TCAGCATTCTTGTTGTTTGC
Gr01_9-13M_369	CTTCCGTTAACCATTTTACACC	TCAAGAGGGTCAACTTCGAG
Gr01_9-13M_370	CGATCTTAAGACAGGGGTTG	TTGGTCATAAGTGGTACCTAAGC
Gr01_9-13M_371	GGGTAAAAATATAGGCCCGA	GAAAAATTCCTAAGCCCGAG
Gr01_9-13M_372	TTAAGTGCAACCAATCAGCA	TTGGGATGCTTGAAGTTTGT
Gr01_9-13M_373	GGTCTTGCATCTCCTTCTGA	CGTCTCTTTTCGCATTCATT
Gr01_9-13M_374	AAGTGAGGCTTTATTTAGGGCT	TCCCAACATGATTCCTTCAT
Gr01_9-13M_375	TGTAGCCAAAGACGATGACA	GCTTGAGTTGCTTCGACAAT
Gr01_9-13M_376	AATTTTAGCATAGTGTACGGGC	TGCGTTAAGGGTTTTACAGAC
Gr01_9-13M_377	GTTCCCTTTTCTACGGTGGT	AACAGAATTGAGCCGAAGTG
Gr01_9-13M_378	GAAATTCGACCAAGGGTCTT	CCCAATCAAGAAATCCACAC
Gr01_9-13M_379	TGTAGTTCCGTCTCTGCCTC	TTGTATCTGCAGCCCTCATT
Gr01_9-13M_380	AGATACTGCGCTGGCTAAGA	CATTTAGCCCACCAACTGAG
Gr01_9-13M_381	CCTAAGGAAGCAAGAGGACC	TTCTTCACCACCTCACCACT

Supplemental Table S5. 126 pairs of primers based on the 3'UTR and 5'UTR sequence of genes

Primer	Forward primer (5'-3')	Reverse primer (5'-3')
G077500.1-3'	TCGATTACACCCCTAAACCA	GGTTGCTCATGGTTGACATT
G077500.2-5'	AGAATTGGGGGAAAGGAAC	TCGTTGACAAGGTGTTTTACTC
G077600.1-5'	AGAGAAGTGGGAAAGGAGGA	ATCTCATAAGCAGCGAGTGG
G077600.3-3'	GGTTAATCGACCATCATCCA	GGAATTGCATTGGCTGTAAC
G077800.4-3'	GCCTTCATGTTGAAGAGGAC	AACCACCGACTAACTGACCA
G077900.1-5'	CAGACTTTGCTTTTGATGTGTG	AATCAAAGAAAGGGGGAAGA
G078000.1-3'	CTTGAATTCCAGCTTTCAGC	TCTTACCCTCCAGAAAATCAAC
G078000.5-5'	GCAAAGACACATCCCTTTCA	AAAAGCATCACTTGGATGGA
G078100.1-5'	TGCAGAAACGTAAATGCAGA	TTTCAAATTTCTGGCTCTCG
G078100.5-3'	AACCTGCGTTTGACACTCAT	ATTCCATGCGCACATAACTT
G078200.1-3'	GAAGCATTTCATTGCACCA	CGCCACAAAAGGACATAGAT
G078200.1-5'	TTCCTAGGGTTAGGGTTCGT	TGAGACCAAACTAGCTGAAGG
G078300.1-5'	ATCAAAGCATGCATGAGAGA	CAACAAAATGCCATGACAAG
G078400.1-3'	TGCAAAATATCAGGGCTACG	GAAAAACGATCAGACGGAGA
G078400.1-5'	GATGCCCGTTCTCTCTCTCT	AGATGGAAAGGGATCGTAGC
G078500.2-5'	GCTGCAGATTGAAACAAAAC	GCCATGTTAGCTCTGCAACT
G078600.1-3'	GAAAAACAATATGCGGTTGC	GCCTTCAGGGCCTTAGAATA
G078600.1-5'	CCGGGATGTAGAGATGAAGT	TGGGTTTCTACTCTCCCGTA
G078700.1-3'	CCATTTTCGGCAATTACAAG	GATCAACCCTCCTCTTCCTG
G078700.1-5'	ATGCCATATCTTCAAACACG	GCTTATCCAATCTCCACTAACC
G078800.1-5'	TTGGGGTTATGCATTGACTT	AGTGAGTCCGGTGAGTGAAG
G078800.2-3'	CATTCGATGCTACACAGCAC	CGACATAACAGACACCACCA
G078900.1-3'	GAGCTATGGGCGTCAGTAGA	GCCAAACTTAATGGCAGATG
G078900.1-5'	CACGTCTTCCCCTATTGTTG	AATGAGAGGTCCTCGTTTCC
G079000.1-3'	TTTCGTTCTTCCTTTTCTGG	GGGGTATGGATCAAGCTTTT
G079000.1-5'	ATGCAAACGTAGCCTCAACT	AAAAACACCCCCAATGAGTC
G079100.1-5'	CGGCCCTTAGTCAAGAAGAT	GAATGCGAAGAGAAATTCCA
G079300.1-5'	AAATTCCCCACCAAGAAAAC	CGCCTTTGCTTGCTAATCTA
G079300.2-3'	TGTTTGCCTGGCTTAGTAGC	CACCAAGACAGATGATGTGC
G079700.3-3'	TGGTTCTGGTTTAGGGATTG	TGCCAACACTCATGATCCTA
G079700.3-5'	CGATGAATCAAAAACTCTAGGC	CAGCGAAACCCTAGTTAAAGC
G079800.1-5'	AGAACGGACGGCTTAAATCT	TGCTTTGGGTTCTGCTCTTA
G079800.3-3'	GGAGAGAATGGGCTGTTGTA	ACATGCAGAGAAACATGCAA
G079900.1-3'	CGTAGTGGGTTTTGGTTTTG	CAGCAATGAACCAACATTCA
G079900.1-5'	ATTGGACCACCCTCTCTTTC	GATCGACGACTTTTTCGTTG
G080000.1-5'	TGCCTAGTTCTCTTTTCTTCTCTC	CTGCTTCCCGCTACTACAAG
G080000.2-3'	AAGTCAGCTGCAAGAAAAGG	ATGGCTTCCAGGTCATTGTA
G080100.1-3'	CGTGAACACTGAGAGAGCTG	TCCCTCCTTTTTGGAAGAAC
G080100.3-5'	ATCCAGGAGATGAAGCAGTG	CCATGGAGCAATCTTCTTGTA
G080200.1-3'	TGCAAATACTTTGTGCATGG	GGACAACGATGGACTTTGAG
G080200.1-5'	ATTGACTCGGTAAGCCCAAG	GAATTTTCTGCTGGGAAATG

G080300.5-3'	ATGCCTTCATGTCTTTTCCA	GTTGCAACCTCTGAATGCTC
G080900.1-5'	TTTGTCTTTTGCTTCCGAAC	AGTGGGTGCTGAGAAGAGAA
G081000.1-3'	AATTCATGGAACCTGCTTTG	CCAGGATAGCAGTCACCAAC
G081000.1-5'	TGAGAATAATAGCAGGCAGCA	CATGTCAGGGGAAGATTTTG
G081100.5-3'	GCATTGGGTAAGTCACCATC	TGCTCGTCTACTCATGTCCA
G081100.8-5'	CTCCATTGCTGCTCTCTCTC	TTCACCAAAGCAAGGGAATA
G081200.6-3'	TTGCCTTCTTCGTCACTAGG	TACAACACATGTCGGACTGC
G081200.7-5'	GGGGAAGAGGGTACCATAGA	CCCCCTTGTTATTTGTCTTG
G081600.1-3'	AATGCGACTGCTTAATTTGG	CTACCAAATTGGGACGAAAA
G081600.1-5'	TGATGGTGACATAAGCGAAA	TAGGGCCAGTCTTGAAAATG
G081700.1-5'	TTGCTGAGAAGAAAGGGTTG	TTGCTGTAAATGATGGGTCA
G081800.1-3'	AGAACCATTTGCCATCTCCT	ATTTCCAGGGGATTAATGGA
G081800.3-5'	GAAATGGGTATCCTCGGAAG	GGAGAACATAAGGGGTCCAT
G081900.1-3'	GCGACCTTCCATTTTCATTA	AACATGATGTCCCCTTACCA
G081900.1-5'	TTTTTATCCCGCTACAAGGT	CTGGGCTTTCAGCAGTTAAA
G082000.1-3'	TCCACCATTCCCGTCTATTA	ATTCGGTCGATTATGCTTCA
G082000.1-5'	GGACAGTTGAAATGAAACGAC	TGTATGACCTGAAGCAAGCA
G082100.1-5'	ACCACGCCTTTTTGTGTTT	GGGTTTGAATTGAGGAAGAAG
G082200.1-3'	TGTGATTGCTGCTTAATGCT	GCTTGAGATCATTGGGAAAC
G082200.1-5'	TTCCCCTTAACTTCCAATCC	GGCGGAAATAAAGGAAAGTT
G082300.4-3'	GAATTGTGGAGCAAGTGGAC	TAAGAGGGCAGCAAGTTTTG
G082300.5-5'	CAATTTCAGGAAAGGAGCAA	ACCTGGGTGTTGAATGGTTA
G082400.1-3'	CAACATTGAACATCGACAGC	TTCGCATCACTTTCTTGACA
G082400.1-5'	TTTGGGTCGATGAACATAGG	TGTCGCCAAAAATGGTTACT
G082500.4-5'	GGTGTTTGATTTGCAGGTTC	TACCCGAGATATCGAAGCAG
G082500.5-3'	GATCATGTGGTTTCCGTCAT	AATGGATGCTGCAAGGAATA
G082600.1-3'	TTAGGACCACGTAGCACCTT	TTTTTGGCCTACTTGTTCTAGG
G082600.1-5'	TGTTTTGCCTTTAACGAAGG	GTTTGGTTTTTGGATTGTCG
G082700.2-3'	CAAAAGCAAAGGCCTAATCA	TGAGGGTGGTGCTAGAAATC
G082700.2-5'	CTTTCGCTCTCTGAAACTGC	CGGCCACTAACACCTCTAAC
G082800.1-3'	CCCAACATAACCATCCCTCT	AGGCTACCCAACACCTCATT
G082800.2-5'	CTTTTGCAGTACGTCGGTTT	CTTTTCTTTACCGCGCTCTT
G082900.1-3'	CTCGGGGTAAACAGAACCTT	GTTGATGCACAATGGGTACA
G083100.1-5'	CAATTTCGTTGGTTCGGTTA	TTTGAATGAGATCGGAAACC
G083100.2-3'	ATGGTCTTCCCTGTTCACAA	GCAAAGTTTTTGTTGGCATC
G083200.1-5'	GTTGTACGGTTGCTTTCAGG	GCAGATCTCGGTATTTCACG
G083300.1-3'	CATGGTTGACATGGTCTTCA	AGGGTAGAATTGGCGACTTT
G083300.1-5'	CCAATTGCCATTTCAGTCTT	CACAACCCTAACGCTTTTTG
G083400.2-3'	AACCTGAAGCTCATTTGCTG	TCAACACTGATCTGCAATGG
G083700.3-3'	GCACTGCAGGTACCAAGTTC	GTTGATGAGTGTGCCTGTGA
G083700.6-5'	CACAAATTTCACCACAACGA	GGTCACTGTGATGTCAACCA
G083800.1-3'	TGCAATGTGGCAAATACTGT	TCAACCCTACTACGCAAATCA
G083800.1-5'	GCAAACCAAAGATCCAGAAA	TTTGTCTCGCTTCGCTTAGT
G083900.2-5'	CTTGGGGTGAGGGAATAAAT	CGTGTCGGTGCAAATACTAA

G084000.1-3'	TGCATCGTCTCTTAGTTATGGA	TCCGTATTCTTCACTCACCTC
G084000.1-5'	CGGCTATGTGCTCTGCTTAT	AACAACCAACCGATCTTCAG
G084100.1-5'	CTTTCATACCACGCCAAAAC	TTTTGTCTCCTCCCACAAGA
G084200.1-3'	TGGAGAGTCTAACCCTCAACA	AAATTGCCATCGTGTTGTCT
G084200.1-5'	TGGCAACTTTCCTTTTCTTG	ATACTCGGCGAAGCGTATAA
G084400.1-3'	TTGCTCACAAATCACAATGC	TTGCAAGTTGCGAGCTTT
G084600.1-3'	GCTAGGTCTTTGGGATTGGT	TTTTGTTCCAGCAAAAGGAG
G084700.1-5'	GGATTTTGAGGAGGCTAGGT	TGCAGCAAAAACCATCAGT
G084900.1-5'	TGCTGTTGCTGTTGTTTTGT	TTCAAAGACACGTGGTTGTC
G085000.2-3'	TGGAAGGAGCAAACAGTTCT	TGGAAATGTGGTGCTGTATG
G085300.3-3'	AGAGGGGCATATCCAATAGC	TGAAAGAGTTCGTGGCTACC
G085500.1-3'	CTCCAATTACCAACGACCAC	AGGTGGGATTCTTGCACATA
G085600.2-5'	GAGAGGAACTGCAGCCATTA	TTGAATCTTTCCAGCGAGTT
G085600.3-3'	TCCAAATCCAAAAACACCAC	TGTGGAAAAACAGGTGAAAG
G085900.1-3'	TCGTGTGTTCCAGCTTCATA	GGTTTGAAAAACCAACATGG
G086100.1-3'	GCTTAAGCTTTTAGGGTTACCA	ACACTGTCGTCAAAAATCCA
G086300.1-3'	AAATACACAACCGTCGCTTT	TTGCAGCAAGAATCAGTTCA
G086400.1-3'	AATCAAGCCGAGGTATAGGG	AGGTTTTGTTGTGCAGGTGT
G086400.1-5'	CATTGCCTTAAACACATTGG	CCAGCTCAGTCCTTTTCTCA
G086600.1-3'	GCATTTCAGCCCCAATACTA	CCAACCATTTGGAAGAAGTG
G087000.1-5'	GAAGGATGGGTTAGCAACAA	CAAATGAAGAACAGCCGAAG
G087000.3-3'	CAACAGCATCATCGTATGGA	AGAAGCCGTAGACACCACTG
G087100.1-3'	TAACTTAGAGGCGCAAATGG	CCTACATATGGATGGCGAGA
G087400.1-5'	GCCTGCTAGCTAGGTGTGTT	GGAATGGTAGCTGCAATCAA
G087600.3-3'	TTTCCCATTCCCCTGAGTAT	TGTAGTGCAAGAATGGCTCA
G087800.1-3'	GACCGTACAACAAGCTGCTAA	TGCCTCCTATAAGTGTCGAA
G087800.1-5'	AGGCGAAAGAGATGTCTCAA	TAACGAAATTACCGGGTCTG
G088000.1-5'	GCAAAGTGTGTAATGGAGGGTA	CCACATTTCCCTTTGTCCTA
G088100.1-3'	AAAAGTGCGAGTGACTGGAG	TGAAAACCCTTCAAAACACC
G088100.1-5'	ACCATCCTGGTTATCCCATT	GGCTGAAAATGAGGAATTTG
G088300.1-3'	AGATGGTCGAGGTGATCAGA	GGGCAACATGTACAGTTCTTTT
G088300.1-5'	TTCCGAGACCAGTTATCCAA	AATGGGAGCTGAAGAGTGTG
G088500.3-3'	GGGTATTTGTTGTTGCCAAG	AGGGAGCAAGCAGAACTTTT
G088600.2-3'	AGACCAGGACTTCGGTCAA	AACTTTGCATGGTGCTTGTT
G088600.2-5'	TGCTTTTGCTATTTGCACCT	TTGGCAAAGTGATGAAAGAG
G088700.2-5'	CAACTTCGCCATCAAAAGAC	TCAAAGGGTGTTTCATTGGT
G088700.5-3'	TTTCCGAGTGTCCACATAGA	CTAATTGCAGGCAAGTGATG
G088800.1-3'	CCTCGTGCATAACTGACTCC	TGGCTCTATCACTGTTGTCG
G089100.1-5'	TAGCTAACCGTCCGAAGTTG	AATCTTGTGACAGCCTCACC
G089200.1-3'	CGGAGTTCCGATTTTTCAGT	CTCTTGACCAAGGGTTACCA
G089300.4-3'	TCTTCACCCCGTTGATAAAA	GCATGCAAATGAGATCAAAG

Supplemental Table S6. 80 pairs of SSR primers on D07

Primer	Forward primer (5'-3')	Reverse primer (5'-3')
Gh_D07_8-9M_01	AGTATATTATCGGGCCTCCG	GATTTTTCCATCTATTGCCG
Gh_D07_8-9M_02	GAGAACCTTGGTCTCAGCAG	CGCTAGCGCTATCAAGTTGT
Gh_D07_8-9M_03	TCCTTGGCTTAAGAACATGC	AGGTGAAGTTGGGTTGAGTAAA
Gh_D07_8-9M_04	GCCCGACTTTGAGGTAGTTT	AGTCAACCCCATTCTTGACA
Gh_D07_8-9M_05	TTTCGGGAGCATAGACAAAG	CCATTTGTAAGACTGTCGGC
Gh_D07_8-9M_06	AAAGAGGAAAGGGAAACTGTG	GCATTTACGTTTCTGCAGGT
Gh_D07_8-9M_07	CCTTGTTGTTCTTGAGCGTT	ATTAAGGGGATCCAGCAAAC
Gh_D07_8-9M_08	GGTCATATTGCACAGTTAGTCCT	GCCCATACAGTTTCGTATGC
Gh_D07_8-9M_09	TTTGAAATCAACCCCTGGTA	AGCCTAGTGGCATCATCATC
Gh_D07_8-9M_10	GGGTTACGAAGCATTACCAG	GTTTTTAATTGCAGGGGGTT
Gh_D07_8-9M_11	GCGGATACACAGATTCCAAC	AAAAGTACGGGGTATTTGCC
Gh_D07_8-9M_12	TGTACACCATCAACACCATACA	TGGTGAAAAGATGGTACAAGTG
Gh_D07_8-9M_13	GTCACAAAAGGCCATGGTT	TGCTCCAATTACTTTCCAACTC
Gh_D07_8-9M_14	CAAAGTGGAGATTACGGTGG	CATGTGACACCTTGGGATTT
Gh_D07_8-9M_15	GGGCTTGAGCAAAATTCTAGT	CATTGGACAACCACAGGAGT
Gh_D07_8-9M_16	GTTAACAAGCCACGTTGGAC	GCCGAGAAAATCAACAGAGA
Gh_D07_8-9M_17	CCCTTTTCTTCAAGTTGGGT	TCTCCAAACAACTCACCCTC
Gh_D07_8-9M_18	AAGGGAAGACAAGGTTGAGG	CCTTCCAACTTAAAACAGCTACTC
Gh_D07_8-9M_19	GTAACATTGGGTCACCCTGA	TCATGGGGAAATGAGGTAGA
Gh_D07_8-9M_20	AAGTTTGCTCATGAAGTGCC	TTCATGTTACTGGCCCTTGT
Gh_D07_8-9M_21	AAAAACCACGGGTAGAGGAG	GAATTAAGTGACCCGAATCCT
Gh_D07_8-9M_22	TCGACTCACTTTGAATTGTCC	GTGAGAAAAGGAGAGCCACA
Gh_D07_8-9M_23	CAGCACAACAAAATTTGGGA	AAATCTAGGAAAGGGAAAGCC
Gh_D07_8-9M_24	AAATTTGCAGGGGGTTTTAC	TGTAACACCCTCTAACCCCA
Gh_D07_8-9M_25	TGTGTGTGTGTATGAGGAGTGA	AATTGGATCTCTGGATCCCT
Gh_D07_8-9M_26	ACTAAGGAAATCCAATGGGC	TGACAAATCTAAGGGCTTGC
Gh_D07_8-9M_27	TTTCCCAACACACCAGTTTT	GACACATTTCCAAACGCAAT
Gh_D07_8-9M_28	GAGTTGTCTGTCATGGCTCC	CATTTCCCAAACTATGCACC
Gh_D07_8-9M_29	GGAGAAAGTGGGATTTTGATG	TTCAACATCCATGACACAGC
Gh_D07_8-9M_30	CCGATATCTAAACAATCCGGT	CCTAATGCTCCTTCTCCCTC
Gh_D07_8-9M_31	TTCACCATCATACACCCCTC	CCTAATGCTCCTTCTCCCTC
Gh_D07_8-9M_32	CAAGGTCAACTCCTCCACAC	ACAATGGAGCAGGAAAATGA
Gh_D07_8-9M_33	GGGTTACATTTTTCATTGGTGC	CAAACATGAGGGGACAAGAC
Gh_D07_8-9M_34	TCTTGTCCCCTCATGTTTGT	TCATCTGGCTGAAACCCTAC
Gh_D07_8-9M_35	CAAAGCAGGAAGGGTCCTAT	TCTACTCCACGAAGTCGCTC
Gh_D07_8-9M_36	AGTGAAGATTGGTGGCATGT	CGTGAGCCAAATTAACAACA
Gh_D07_8-9M_37	AATTGGGCTTCACCTAATCC	TTGCTCATGTGTGCATGG
Gh_D07_8-9M_38	TGGCAATCCACCTCTACTTC	AATGTTAGCATGGAAGCCTG
Gh_D07_8-9M_39	GGACCAAATTCACAACTTTCAC	ATCATGAGCGTTGATTCGTT
Gh_D07_8-9M_40	TTTAGGCTCTGCCATTGTTC	AATTATCATGCAGGAACCCA
Gh_D07_8-9M_41	AGAGCAGCCTCATTCATTTG	TGGGGAAGAGAAAAGGGTAG
Gh_D07_8-9M_42	CTGGACTCAGTTTCTGCCAT	ATGCTTGAGATCATTGGGAA

Gh_D07_8-9M_43	AAGTCACAAAAGCCGAGATG	GAGGAGCTGCAATTGTTATGA
Gh_D07_8-9M_44	GAAATCACAACATTCCAGGG	TCTTAGAGGTGCTAATGGGC
Gh_D07_8-9M_45	TGTCTCCTCTCTGCCAGAAT	AACTTGCAGCAAACAAAAGC
Gh_D07_8-9M_46	CTCCACACCAAAAGACTGCT	CACTAACATTTGTGGATTTGGG
Gh_D07_8-9M_47	TGGTGGAGGTATGTCGTTTT	ACATGCCACGTAGACAACAA
Gh_D07_8-9M_48	GCATCAATTTCACCTGTCAAC	TCATAAGCAATCATCCTCTTCC
Gh_D07_8-9M_49	GTCTATTTCGGGTCTGGGTT	GTAGGCCTATTTTGGCCAGG
Gh_D07_8-9M_50	TTCGTAAGCTTTCTTGTGGG	CAGGGAGCGTAGATGAGAAA
Gh_D07_8-9M_51	ACAACTTAAAGCAGATGCGG	GCGTTTACCTGCGGTTAGTA
Gh_D07_8-9M_52	CTGATTTGGAAGAAAAACGG	AAGATGAATGGACCTAGCCC
Gh_D07_8-9M_53	CGAGGGTGAATCTGGAAAT	ATGCTGTTGTGGTGGAGATT
Gh_D07_8-9M_54	TATGTTCACATCAACGCACA	ATGTGGTTGTGAGCATTCG
Gh_D07_8-9M_55	CACACGAAGTCATCAATCCA	CACTTCGGTGCTCTCTGATT
Gh_D07_8-9M_56	CGGAAATTCAATCTTCGTTC	CCAAATCTGGCATGAAATGT
Gh_D07_8-9M_57	CAGGAAAGTGAAATACCCGA	GTTTTCTTGCTGAGCCAAAG
Gh_D07_8-9M_58	AGAATTACCCGAATTACCCG	ATTATCCAACCCAACCCAAT
Gh_D07_8-9M_59	GTTTTAGGGGAAAAGTGGGA	CCAAACTCCCAAACCTTTTT
Gh_D07_8-9M_60	CCAAAAGACCTTTCGCATAC	AAAACCACCTTTGGTCACAA
Gh_D07_8-9M_61	CATACAGCACCACATTTCCA	CTCGAGGCAGCTAGTCGTAG
Gh_D07_8-9M_62	CCTACTCCTGTCTTCCCACA	GCGGTATAACCCAAAATTCC
Gh_D07_8-9M_63	TGAGTTTGGGAGTCGGTTAC	AGGTAGCGATCAAATGACGA
Gh_D07_8-9M_64	TCGAGTGTAATTTTGGGGAA	CCTTTGATGGTAATTGTGCC
Gh_D07_8-9M_65	CTTGGCACTTGTTTAAGCGT	CGAGCTCCTGAAAATGATGT
Gh_D07_8-9M_66	TGAAGAACCAGCTCAAGGAG	TAAATGAAAAGATGAGGCGG
Gh_D07_8-9M_67	AATACCAAAGAGTCGTGGCA	TCCTAAACGTACTCCTTGCCT
Gh_D07_8-9M_68	CCTTGACAAGTGTTCGTTGA	GCCTAGGGACAAAATCATCA
Gh_D07_8-9M_69	AAAACACCACCACCGATTTA	GGATGATGTGGAAAAACAGG
Gh_D07_8-9M_70	GTAGCGGAAGTGGTAGTGGA	CCTCCATTGTTGTTTCTCTCTT
Gh_D07_8-9M_71	TTGGACCTAGATTTGCCTGA	TGGATGATTTGAAGAAGGGA
Gh_D07_8-9M_72	TACCCATTAGGGCAAAAGTG	GCCCTCTGAATATGCTTCAA
Gh_D07_8-9M_73	TCGCAAGTTACTCGACTTCA	CGTGTTCAAATGGTAGAGGG
Gh_D07_8-9M_74	AGCCATTAAGGTTGTTAGTGGA	TCCCGGAAACATAGAAATCA
Gh_D07_8-9M_75	ACCGGCCAATATAAAGGAAC	AAGAGCGAAACATTCACTGG
Gh_D07_8-9M_76	ATTGTAGGTTGGCACCAAAA	GAGCATCAACATTAAGACCCA
Gh_D07_8-9M_77	ACAAGTGCACACAAAACCCT	TAGATCAAGAACCGGACCAA
Gh_D07_8-9M_78	TGTGCATAGTATAGGGTCAAGACT	TCTAAGGGCTTTTCGTTGGT
Gh_D07_8-9M_79	ACTCACGTTGGAAAGATGGA	AGGCAATGATGTTGTTGGAG
Gh_D07_8-9M_80	AAACCGACGGTCAAGATACA	TTTGGCCTACGAGAACTGAC

Supplemental Table S7. The markers involved in gene mapping

Primer	Forward primer (5'-3')	Reverse primer (5'-3')
Chr01_8M-004	TCCCAAGAACAAAAACGAGT	GTTCATTTGTTTGTGCGTGA
Gr01_9-13M_056	ACAAGTGCACACAAAACCCT	TGTTGATTAGTCCCCGAAGA
Gr01_9-13M_061	TTGTGGGTCCATTCAACTCT	TCCCTTCTTATCGTTCTCCTT
Gr01_9-13M_064	GTTTGTTTCACACTTTCTCGG	GAAAATTAGGGTCCAAAAGAGG
Gr01_9-13M_079	ACAAAAGGGTTGAGTTTCCC	TTGAGGTATTAAGCCCATGC
Gr01_9-13M_110	TTTCCATGAAGCTGATAGCC	ACTTGGCATTTATGGGTTGA
Gr01_9-13M_245	CCATAATTTTAGGTGTTGAGCG	ATTCTGGAATTCAGTGGCTG
Gr01_9-13M_263	CCCGATCTGGATAGTTTGAA	CTGAAATGGATCAAATTGGC
Gh_D07_8-9M_77	ACAAGTGCACACAAAACCCT	TAGATCAAGAACCGGACCAA
G089200.1-3’	CGGAGTTCCGATTTTTCAGT	CTCTTGACCAAGGGTTACCA
MON_DC40065	TGAAGCAAATGCTCTTCC	AGCCGGTGATCTTAGTGC

Supplemental Table S8. RT-PCR primers for candidate genes

Primer	Forward primer (5'-3')	Reverse primer (5'-3')
Gh_D07G0690	GAAGATGGAGCAGGTGAAAGC	TCTGGGTTGCACCAAGATTTT
Gh_D07G0691	CATTTCGCATCATGGACAGG	AACTGACCAGCAAGTACCGTGA
Gh_D07G0692	TGTGGCATGACCGACCTATCT	AGCCGCACTCCTAAACTACCTC
Gh_D07G0693	GGTCCTTGAACTTTCGGATACTG	AATGCATACATTCTTGCGATATTTA
Gh_D07G0694	GGCAAAACAAAAGTCTGAATGG	GCATATTTCTGGGATTGTCGTAAC
Gh_D07G0695	GTAGCGACGGAGGAGTTAGTGTA	ATTTGTTATCTTTGTAAGTTCGGTTT
Gh_D07G0696	ATCGCAGGTGGAGCAAGAG	CGAAAGATTGAACCTTGGACAA
Gh_D07G0697	TTCTTCTGGGACCTTGGCTAG	TGAAGTCCTCGCCATTCTCTAC
Gh_D07G0698	TCTCTTCCTCCTCTATTGCACCTT	ACTGCTGGCTGTCTCTGTCGT
Gh_D07G0699	TTGGGAACATCAGTTATGCCTAC	TAAAAACATGGTAATGCTGCGG
Gh_D07G0700	ATCAAGAATGCTCGCAAATACC	TATTGGACAACGAGTGTTAGGCT
Gh_D07G0701	GGCTCCCAACTGATGAGAACTT	AAACAACATTTATACCCTACCCCAA
Gh_D07G0702	ATGCCCCTTTGAGCAAGTTAC	ACTGACGCCCATAGCTCGTG
Gh_D07G0703	CCGCTTTGACATTGGCTTTA	GCATAGTTGAGGCTACGTTTGC
Gh_D07G0704	CCTCTTCCTGATGGACGCTT	AACCGCTCTGGATCTTGTGG
Gh_D07G0705	TTGTTGTTTGCCTGGCTTAGTA	TTACACAGCTCACTACCAGTCACC
Gh_D07G0706	AAGAAGTTTCAAAGGCAGGCTAA	TAAGAGTGAGTCAACGCTTTTCC
Gh_D07G0707	CCAGCAATACTTCTCAGATTCTTACG	CCACCAGGCACTACGATACAACTA
Gh_D07G0709	AACCGATGGCATACGCAAA	TCCCTAAACCAGAACCAGGCT
Gh_D07G0710	CACAATAGGGAGAGAATGGGC	AATCCGTCTGTCACCTTCTAACC
Gh_D07G0711	GGGGAACAAGGGAGGCTAAG	GCTGCTGCCTTTTTTTCTAACA
Gh_D07G0712	TGTTTCTGCCATTTGCTTAGTG	GATGCTTACGGGCTGACGAT
Gh_D07G0713	TTAGTGGTCGTGCTTTCTGGA	GCCATTGGTTGAATTGCATACT
Gh_D07G0714	TCTTCTGTTTTCCCTCGTTTTAGC	CCTCAGGCTTTTGTGGGCA
Gh_D07G0715	TTGCCCTCACAAATCACCCTAT	TTTTATTCTCATCGCTACAACATCC
Gh_D07G0716	GGAGCAAGATGAAGCAAAAGGC	AGCACAGGAAATGGGAATGAGC
Gh_D07G0717	TTATTGATGTCTGAGACGCATAGAC	AATCTTCTCCCTGTTACCTCCG

Gh_D07G0718	TCTGGATGGTATTCCTGTTGGG	GGTTCCGTGTTCCTTTGCTG
Gh_D07G0719	AGAAAGGGGAAATGAAAGGCT	CGCTGGACAAACAGGCAAA
Gh_D07G0720	TCATTTGAAGGATTTGTGGAGTCT	TGGATGTGACGAACCGTAGTGTA
Gh_D07G0721	TCTCCTTTCTATGTTTGCCCACT	TTGCCACCTGTTGTCTCATCC
Gh_D07G0722	TGGGGTTTCAAAAGGAGTAGTAGC	TGTGTTTAGGGTTATTGGGCGA
Gh_D07G0723	CTTGCTCTGAATCCGACGACTT	GCTACCGTGCTTCTGAAAACTG
Gh_D07G0724	TGGATGCTTGGAACCCTACG	TACTGTTGCTCCCCCTACCC
Gh_D07G0725	GCACCAAAAAAAGAAAGCATCC	AATAGCATCATTCAAAACAAAATCAT
Gh_D07G0726	TTTTCAAACGGTATTGTCAGCC	CAGCCAGGTATAGTCTGTATTTGTATG
Gh_D07G0727	GGAGTTCGTGATTCAAGCCTATG	GGCTGATTTTCTTCCTGATGTGTAT
Gh_D07G0728	CAAGGTGGATTCGGAACTGTAT	ACTTCTAACTGTTCAGGTTTATCTGG
Gh_D07G0729	ATTTTGATTGTTGTGCTGGGTG	TCTATTTTCTGCTCCTTTCCAGTG
Gh_D07G0730	ATGTGACGAGCCAAATCGAG	CCAAGTAAAACATGATGTCCCC
Gh_D07G0731	CAGCACCCCTGAATAATGGAC	GTGGACTCTTGCACTCGGATC
Gh_D07G0732	GAGAAACAAACCACAACTCAAGGA	GAGGAGGGTAAAAAAAGGGAAA
Gh_D07G0733	CTTTGGTTTGCTCCTCCTGACT	GCAATCACAGAAGAAAATGGCAG
Gh_D07G0734	TGGCATCCATTTGGAGGAA	ATGAGAAGACCAGGGCAGACA
Gh_D07G0735	GGCGAAGATCGGGAGGACT	AGACTCAATTCAAGGGTTGTAGGA
Gh_D07G0736	CTCTTGCCAAGGATGCTTCG	AAATGACACCAAACGCTGCC
Gh_D07G0737	TATGTGGCACAAACCATGACG	TCTAATAACCAAGCAATCTCCCG
Gh_D07G0738	GCAATGATAATAGCAGGTCTGAGA	GTTCCGTCCCAAATAAAGGC
Gh_D07G0739	GCACAATCTCGGGCAGTTC	CATTGACTCCCCCTGACCA
Gh_D07G0740	GCCACCAGGAACTGCACAAA	ACCCCGAGACAGGCTAACTAAAA
Gh_D07G0741	TGTGAGTAGGAAGTTGGATGGTC	AAATCGGGACCCAACACAA
Gh_D07G0742	AAGGCATAGCGATTACAGCGT	TGGGATGACTTGATGGGGAC
Gh_D07G0743	TCTTCGTGTCAGTTCTCATCAGCA	GCCTCGAATTGCTTTCCTTCA
Gh_D07G0744	GTCACGACTTCAAAGGTAGCTGC	GGGTATTTTTTTGGGGGGC
Gh_D07G0745	TTTCCTCCTTCGTCAACCG	CACTAAGACCGTATCACCCTGC
Gh_D07G0746	TGGGCTATCTATGTCTGGTGTCG	AAGTCCATCCTCATTCCTTCTATCAT
Gh_D07G0747	AGCCTATAGATCGATGCTTCACTC	TCTTCGGCACACAGAAAAACC
Gh_D07G0748	TGCTTCTGCTAGAAATGAGCCT	TTGGATGCCCTTTCTCGACT
Gh_D07G0749	TGCTGGGCTCGTAGTGGCT	GGTTCGCAATCTGAATCTCTCC
Gh_D07G0750	GAAAAAGTGGCGGATTTGAAC	TGGCAATGGTCAGCGTAGG
Gh_D07G0751	CGAAACCCTAAACGGACAAGC	CGAGAAACTGATAGCCAATGCC
Gh_D07G0752	TAGTTGAGGAGCCTATTCGTGC	CCTCCAACACATTTTTTCACCAT
Gh_D07G0753	CGCTAAAAAGGGCTTCGTATT	ACCTCATGTGGATGTTCAGGG
Gh_D07G0754	AATACAATCAAGGACCGAGAAACAC	CAGAGCCACTTGGGAGACAGAC
Gh_D07G0755	AAGGAGAGAATAGAGGTGGTGAAG	GAAAAAAGGCAAAGGAAAAGAGT
Gh_D07G0756	TGATTGGCTTCAAAGTGCAGA	GGCAACCAGACCAAATCCTT
Gh_D07G0757	AACGCCTAACGAAATCTAAACCTG	CTCTCTCACACAAACACACGCAC
Gh_D07G0759	ATGGGTGTGGATACTCCGTGT	CAAAAGAACCTGTTGCCGC
Gh_D07G0760	TGCGACTCGTAAGATTAGAGATGA	AGTTGTGGGAAGACAGGAGTAGG
Gh_D07G0761	GTGATAATGACAGCGTTCGGG	AATACTCCAATGGCGGCTCC
Gh_D07G0762	AAGTTTCGGTATTGCTATGGTGGT	TGTCATTTCCTACTACGATAAGCCTG

Gh_D07G0763	ATACTGGCATTGTTGTGGCTCT	TTATCGGAGTGGTCTGGTTGTC
Gh_D07G0764	GGATGATGTGGAAAAACAGGTG	AATGAGGTCTTTCCTTACAGGCA
Gh_D07G0765	TGCTCCCTTCAACTTTCCACA	GCAGATCGAAGTAGATACAGACCG
Gh_D07G0766	TGCGTTTCTCTTGGCTACCG	TCTTTGCTTTCTTGCTCCCTTC
Gh_D07G0767	TTTTGGAATGGTTTACGTGGTC	GCTGGAACACACGAACCTGG
Gh_D07G0768	ATGGACTGCGATGGATGTGA	CAGAACTCCGCTCTCTTGCC
Gh_D07G0769	AGAACCAAACGCAAACCAATG	TTCCGAACAAATCCCGCC
Gh_D07G0770	ATGAGGAACCGTGGAATGTGT	TTTTGGTTACCCAATTATCTTGGA
Gh_D07G0771	GAAGGGAAATGGCATCAAGTG	TCCAATTATTCCTCATTCTTACAGTT
Gh_D07G0772	CACTGAACGCTCCCAGACCT	TTACTCGGCCAACGAATCG
Gh_D07G0773	CTCAGAATGGAACAAGGGGGA	GCTAACATAGTGGGGGTGCTAATAC
Gh_D07G0774	CGGAACCGAAAATCGTAGTG	AGGGCGAAAAAGAGAGTAGAGAA
Gh_D07G0775	AAATCTCCATCCCATTCAAGTG	AAACCTCTCTCCCCATTACCC
Gh_D07G0776	CTCAGCGAGTGATGGGGCTA	GAATGTGGGGAATGAATAAGTGTG
Gh_D07G0777	ATGGCAAACTGTGTCGTATTCA	TCATCATCAACCTTCACTCGC

Supplemental Table S9. The genes that are relevant to biosynthesis and transport of pigment metabolic pathways

Upland cotton gene	Arabidopsis gene	The description of function	Metabolic pathways
RE1	*AT2G20340*	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	Tyrosine metabolism Isoquinoline alkaloid biosynthesis
RE2	*AT3G02580*	sterol 1	Steroid biosynthesis
RE3	*AT5G17220*	glutathione S-transferase phi 12	Glutathione metabolism
RE4	*AT5G17230*	PHYTOENE SYNTHASE	Carotenoid biosynthesis
RE5	*AT3G02360*	6-phosphogluconate dehydrogenase family protein	Pentose phosphate pathway Glutathione metabolism Carbon metabolism
RE6	*AT1G66370*	MYB113	Regulation of anthocyanin biosynthesis
RE7	*AT1G66370*	MYB113	Regulation of anthocyanin biosynthesis

Supplemental Table S10. DEGs between pairwise comparisons

Table S10 can be found at figshare Dataset. https://doi.org/10.6084/m9.figshare.15350091.v1

Supplemental Table S11. Co-expression analysis of genes in MEdarkgrey module

FromNode	ToNode	Weight	FromNode	ToNode	Weight
Ghir_A07G008080	*Ghir_D07G008160*	0.21	*Ghir_D02G015000*	*Ghir_D07G020010*	0.04
Ghir_A07G008080	*Ghir_D06G017430*	0.22	*Ghir_D02G015000*	*Ghir_A13G001070*	0.05
Ghir_A07G008080	*Ghir_A06G000790*	0.10	*Ghir_D02G015000*	*Ghir_D11G021880*	0.03
Ghir_A07G008080	*Ghir_A06G016540*	0.21	*Ghir_D02G015000*	*Ghir_D13G001360*	0.12
Ghir_A07G008080	*Ghir_D03G005110*	0.08	*Ghir_D02G015000*	*Ghir_D11G026310*	0.09
Ghir_A07G008080	*Ghir_A13G024190*	0.02	*Ghir_D02G015000*	*Ghir_A11G022530*	0.04
Ghir_A07G008080	*Ghir_D08G023860*	0.09	*Ghir_D02G015000*	*Ghir_D11G008770*	0.07
Ghir_A07G008080	*Ghir_A03G013820*	0.05	*Ghir_D02G015000*	*Ghir_D12G000410*	0.04
Ghir_A07G008080	*Ghir_A04G008120*	0.02	*Ghir_D02G015000*	*Ghir_D06G013730*	0.06
Ghir_A07G008080	*Ghir_D02G015000*	0.04	*Ghir_D02G015000*	*Ghir_A05G017350*	0.07
Ghir_A07G008080	*Ghir_D03G000570*	0.02	*Ghir_D02G015000*	*Ghir_A05G018350*	0.03
Ghir_A07G008080	*Ghir_D08G015520*	0.08	*Ghir_D02G015000*	*Ghir_D11G025880*	0.05
Ghir_A07G008080	*Ghir_D09G010390*	0.05	*Ghir_D02G015000*	*Ghir_D05G017130*	0.17
Ghir_A07G008080	*Ghir_A08G014710*	0.03	*Ghir_D02G015000*	*Ghir_D12G015390*	0.04
Ghir_A07G008080	*Ghir_D05G019320*	0.02	*Ghir_D02G015000*	*Ghir_A13G021470*	0.12
Ghir_A07G008080	*Ghir_A13G001070*	0.08	*Ghir_D02G015000*	*Ghir_D08G015410*	0.05
Ghir_A07G008080	*Ghir_D11G021880*	0.07	*Ghir_D02G015000*	*Ghir_A01G022690*	0.02
Ghir_A07G008080	*Ghir_D13G001360*	0.03	*Ghir_D03G000570*	*Ghir_D05G032290*	0.03
Ghir_A07G008080	*Ghir_A11G022530*	0.07	*Ghir_D03G000570*	*Ghir_D12G015390*	0.02
Ghir_A07G008080	*Ghir_D11G025880*	0.02	*Ghir_D03G000570*	*Ghir_D11G002680*	0.02
Ghir_A07G008080	*Ghir_D05G017130*	0.03	*Ghir_D03G000570*	*Ghir_A07G000760*	0.05
Ghir_A07G008080	*Ghir_A07G000760*	0.02	*Ghir_D03G000570*	*Ghir_D13G022890*	0.03
Ghir_D07G008160	*Ghir_D06G017430*	0.21	*Ghir_D08G015520*	*Ghir_A08G014710*	0.18
Ghir_D07G008160	*Ghir_A06G000790*	0.05	*Ghir_D08G015520*	*Ghir_D07G020010*	0.17
Ghir_D07G008160	*Ghir_A06G016540*	0.21	*Ghir_D08G015520*	*Ghir_A13G001070*	0.23
Ghir_D07G008160	*Ghir_D03G005110*	0.16	*Ghir_D08G015520*	*Ghir_D11G021880*	0.05
Ghir_D07G008160	*Ghir_A13G024190*	0.03	*Ghir_D08G015520*	*Ghir_D13G001360*	0.06
Ghir_D07G008160	*Ghir_D08G023860*	0.07	*Ghir_D08G015520*	*Ghir_A11G022530*	0.13
Ghir_D07G008160	*Ghir_A03G013820*	0.03	*Ghir_D08G015520*	*Ghir_D11G008770*	0.15
Ghir_D07G008160	*Ghir_A04G008120*	0.06	*Ghir_D08G015520*	*Ghir_A05G017350*	0.04
Ghir_D07G008160	*Ghir_D02G015000*	0.04	*Ghir_D08G015520*	*Ghir_D05G017130*	0.06
Ghir_D07G008160	*Ghir_D03G000570*	0.03	*Ghir_D08G015520*	*Ghir_A01G022690*	0.03
Ghir_D07G008160	*Ghir_D08G015520*	0.06	*Ghir_D09G010390*	*Ghir_A08G014710*	0.04
Ghir_D07G008160	*Ghir_D09G010390*	0.14	*Ghir_D09G010390*	*Ghir_A13G001070*	0.05
Ghir_D07G008160	*Ghir_A08G014710*	0.05	*Ghir_D09G010390*	*Ghir_D11G021880*	0.12
Ghir_D07G008160	*Ghir_A13G001070*	0.11	*Ghir_D09G010390*	*Ghir_D13G001360*	0.10
Ghir_D07G008160	*Ghir_D11G021880*	0.14	*Ghir_D09G010390*	*Ghir_A11G022530*	0.08
Ghir_D07G008160	*Ghir_D13G001360*	0.10	*Ghir_D09G010390*	*Ghir_D12G000410*	0.07
Ghir_D07G008160	*Ghir_A11G022530*	0.13	*Ghir_D09G010390*	*Ghir_D06G013730*	0.04
Ghir_D07G008160	*Ghir_D11G025880*	0.05	*Ghir_D09G010390*	*Ghir_D11G025880*	0.11
Ghir_D07G008160	*Ghir_D05G017130*	0.07	*Ghir_D09G010390*	*Ghir_D05G017130*	0.09

Ghir_D07G008160	*Ghir_A01G022690*	0.05	*Ghir_D09G010390*	*Ghir_D08G015410*	0.05
Ghir_D07G008160	*Ghir_A07G000760*	0.02	*Ghir_D09G010390*	*Ghir_A01G022690*	0.03
Ghir_D06G017430	*Ghir_A06G000790*	0.09	*Ghir_A08G014710*	*Ghir_D07G020010*	0.18
Ghir_D06G017430	*Ghir_A06G016540*	0.31	*Ghir_A08G014710*	*Ghir_A13G001070*	0.19
Ghir_D06G017430	*Ghir_D03G005110*	0.22	*Ghir_A08G014710*	*Ghir_D11G021880*	0.07
Ghir_D06G017430	*Ghir_A13G024190*	0.05	*Ghir_A08G014710*	*Ghir_D13G001360*	0.13
Ghir_D06G017430	*Ghir_D04G012180*	0.05	*Ghir_A08G014710*	*Ghir_A11G022530*	0.13
Ghir_D06G017430	*Ghir_D08G023860*	0.13	*Ghir_A08G014710*	*Ghir_D11G008770*	0.18
Ghir_D06G017430	*Ghir_A03G013820*	0.08	*Ghir_A08G014710*	*Ghir_D12G000410*	0.02
Ghir_D06G017430	*Ghir_A04G008120*	0.08	*Ghir_A08G014710*	*Ghir_A05G017350*	0.09
Ghir_D06G017430	*Ghir_D02G015000*	0.05	*Ghir_A08G014710*	*Ghir_D11G025880*	0.03
Ghir_D06G017430	*Ghir_D08G015520*	0.14	*Ghir_A08G014710*	*Ghir_D05G017130*	0.16
Ghir_D06G017430	*Ghir_D09G010390*	0.10	*Ghir_A08G014710*	*Ghir_D08G015410*	0.02
Ghir_D06G017430	*Ghir_A08G014710*	0.10	*Ghir_A08G014710*	*Ghir_A01G022690*	0.07
Ghir_D06G017430	*Ghir_D07G020010*	0.05	*Ghir_D08G026850*	*Ghir_A01G007610*	0.07
Ghir_D06G017430	*Ghir_A13G001070*	0.21	*Ghir_D08G026850*	*Ghir_D05G033790*	0.09
Ghir_D06G017430	*Ghir_D11G021880*	0.19	*Ghir_D08G026850*	*Ghir_D05G032290*	0.07
Ghir_D06G017430	*Ghir_D13G001360*	0.12	*Ghir_D08G026850*	*Ghir_A04G003270*	0.06
Ghir_D06G017430	*Ghir_A11G022530*	0.22	*Ghir_D08G026850*	*Ghir_D05G010610*	0.21
Ghir_D06G017430	*Ghir_D11G008770*	0.04	*Ghir_D08G026850*	*Ghir_D01G007540*	0.03
Ghir_D06G017430	*Ghir_A05G017350*	0.03	*Ghir_D08G026850*	*Ghir_A04G015520*	0.10
Ghir_D06G017430	*Ghir_D11G025880*	0.05	*Ghir_D08G026850*	*Ghir_A01G014310*	0.02
Ghir_D06G017430	*Ghir_D05G017130*	0.08	*Ghir_D08G026850*	*Ghir_D12G015390*	0.02
Ghir_D06G017430	*Ghir_D08G015410*	0.02	*Ghir_D05G019320*	*Ghir_A04G014820*	0.03
Ghir_D06G017430	*Ghir_A01G022690*	0.07	*Ghir_D05G019320*	*Ghir_D12G006040*	0.05
Ghir_A06G000790	*Ghir_A06G016540*	0.07	*Ghir_D05G019320*	*Ghir_A07G000760*	0.05
Ghir_A06G000790	*Ghir_D03G005110*	0.04	*Ghir_D05G019320*	*Ghir_A03G007260*	0.13
Ghir_A06G000790	*Ghir_A13G024190*	0.04	*Ghir_D07G020010*	*Ghir_A13G001070*	0.15
Ghir_A06G000790	*Ghir_D04G012180*	0.08	*Ghir_D07G020010*	*Ghir_D11G021880*	0.02
Ghir_A06G000790	*Ghir_D08G023860*	0.09	*Ghir_D07G020010*	*Ghir_D13G001360*	0.06
Ghir_A06G000790	*Ghir_A03G013820*	0.15	*Ghir_D07G020010*	*Ghir_A11G022530*	0.07
Ghir_A06G000790	*Ghir_A04G008120*	0.04	*Ghir_D07G020010*	*Ghir_D11G008770*	0.16
Ghir_A06G000790	*Ghir_D02G015000*	0.04	*Ghir_D07G020010*	*Ghir_A05G017350*	0.05
Ghir_A06G000790	*Ghir_D08G015520*	0.17	*Ghir_D07G020010*	*Ghir_D05G017130*	0.08
Ghir_A06G000790	*Ghir_A08G014710*	0.07	*Ghir_D07G020010*	*Ghir_A01G022690*	0.02
Ghir_A06G000790	*Ghir_D05G019320*	0.04	*Ghir_A04G014820*	*Ghir_D12G006040*	0.03
Ghir_A06G000790	*Ghir_D07G020010*	0.06	*Ghir_A04G014820*	*Ghir_A05G018350*	0.07
Ghir_A06G000790	*Ghir_A13G001070*	0.10	*Ghir_A04G014820*	*Ghir_A04G015520*	0.03
Ghir_A06G000790	*Ghir_D13G001360*	0.02	*Ghir_A04G014820*	*Ghir_D12G015390*	0.03
Ghir_A06G000790	*Ghir_A11G022530*	0.04	*Ghir_A04G014820*	*Ghir_A08G018120*	0.11
Ghir_A06G000790	*Ghir_D11G008770*	0.07	*Ghir_A04G014820*	*Ghir_A07G000760*	0.03
Ghir_A06G000790	*Ghir_D05G017130*	0.03	*Ghir_A04G014820*	*Ghir_A03G007260*	0.06
Ghir_A06G016540	*Ghir_D03G005110*	0.17	*Ghir_A04G014820*	*Ghir_D05G004810*	0.23
Ghir_A06G016540	*Ghir_A13G024190*	0.03	*Ghir_A01G007610*	*Ghir_D05G033790*	0.15

Ghir_A06G016540	*Ghir_D04G012180*	0.03	*Ghir_A01G007610*	*Ghir_D05G032290*	0.03
Ghir_A06G016540	*Ghir_D08G023860*	0.08	*Ghir_A01G007610*	*Ghir_A04G003270*	0.02
Ghir_A06G016540	*Ghir_A03G013820*	0.06	*Ghir_A01G007610*	*Ghir_D05G010610*	0.06
Ghir_A06G016540	*Ghir_A04G008120*	0.05	*Ghir_A01G007610*	*Ghir_A04G015520*	0.03
Ghir_A06G016540	*Ghir_D02G015000*	0.05	*Ghir_A13G001070*	*Ghir_D11G021880*	0.14
Ghir_A06G016540	*Ghir_D08G015520*	0.11	*Ghir_A13G001070*	*Ghir_D13G001360*	0.13
Ghir_A06G016540	*Ghir_D09G010390*	0.06	*Ghir_A13G001070*	*Ghir_A11G022530*	0.23
Ghir_A06G016540	*Ghir_A08G014710*	0.06	*Ghir_A13G001070*	*Ghir_D11G008770*	0.12
Ghir_A06G016540	*Ghir_D07G020010*	0.02	*Ghir_A13G001070*	*Ghir_A05G017350*	0.06
Ghir_A06G016540	*Ghir_A13G001070*	0.14	*Ghir_A13G001070*	*Ghir_D11G025880*	0.03
Ghir_A06G016540	*Ghir_D11G021880*	0.14	*Ghir_A13G001070*	*Ghir_D05G017130*	0.09
Ghir_A06G016540	*Ghir_D13G001360*	0.08	*Ghir_A13G001070*	*Ghir_A01G022690*	0.09
Ghir_A06G016540	*Ghir_D11G026310*	0.02	*Ghir_D05G033790*	*Ghir_D05G032290*	0.06
Ghir_A06G016540	*Ghir_A11G022530*	0.16	*Ghir_D05G033790*	*Ghir_D12G006040*	0.02
Ghir_A06G016540	*Ghir_D11G008770*	0.02	*Ghir_D05G033790*	*Ghir_A04G003270*	0.03
Ghir_A06G016540	*Ghir_A05G017350*	0.03	*Ghir_D05G033790*	*Ghir_D05G010610*	0.08
Ghir_A06G016540	*Ghir_D11G025880*	0.04	*Ghir_D05G033790*	*Ghir_A04G015520*	0.05
Ghir_A06G016540	*Ghir_D05G017130*	0.06	*Ghir_D05G033790*	*Ghir_A01G014310*	0.04
Ghir_A06G016540	*Ghir_D08G015410*	0.02	*Ghir_D11G021880*	*Ghir_D13G001360*	0.14
Ghir_A06G016540	*Ghir_A01G022690*	0.04	*Ghir_D11G021880*	*Ghir_A11G022530*	0.20
Ghir_D03G005110	*Ghir_A13G024190*	0.09	*Ghir_D11G021880*	*Ghir_D12G000410*	0.03
Ghir_D03G005110	*Ghir_D04G012180*	0.06	*Ghir_D11G021880*	*Ghir_A05G017350*	0.02
Ghir_D03G005110	*Ghir_D08G023860*	0.09	*Ghir_D11G021880*	*Ghir_D11G025880*	0.07
Ghir_D03G005110	*Ghir_A03G013820*	0.07	*Ghir_D11G021880*	*Ghir_D05G017130*	0.08
Ghir_D03G005110	*Ghir_A04G008120*	0.16	*Ghir_D11G021880*	*Ghir_D08G015410*	0.07
Ghir_D03G005110	*Ghir_D02G015000*	0.07	*Ghir_D11G021880*	*Ghir_A01G022690*	0.06
Ghir_D03G005110	*Ghir_D08G015520*	0.11	*Ghir_D13G001360*	*Ghir_D11G026310*	0.02
Ghir_D03G005110	*Ghir_D09G010390*	0.11	*Ghir_D13G001360*	*Ghir_A11G022530*	0.17
Ghir_D03G005110	*Ghir_A08G014710*	0.14	*Ghir_D13G001360*	*Ghir_D11G008770*	0.06
Ghir_D03G005110	*Ghir_D07G020010*	0.07	*Ghir_D13G001360*	*Ghir_D12G000410*	0.04
Ghir_D03G005110	*Ghir_A13G001070*	0.20	*Ghir_D13G001360*	*Ghir_D06G013730*	0.02
Ghir_D03G005110	*Ghir_D11G021880*	0.21	*Ghir_D13G001360*	*Ghir_A05G017350*	0.09
Ghir_D03G005110	*Ghir_D13G001360*	0.22	*Ghir_D13G001360*	*Ghir_D11G025880*	0.05
Ghir_D03G005110	*Ghir_A11G022530*	0.26	*Ghir_D13G001360*	*Ghir_D05G017130*	0.21
Ghir_D03G005110	*Ghir_D11G008770*	0.06	*Ghir_D13G001360*	*Ghir_A13G021470*	0.02
Ghir_D03G005110	*Ghir_A05G017350*	0.06	*Ghir_D13G001360*	*Ghir_D08G015410*	0.05
Ghir_D03G005110	*Ghir_D11G025880*	0.05	*Ghir_D13G001360*	*Ghir_A01G022690*	0.17
Ghir_D03G005110	*Ghir_D05G017130*	0.14	*Ghir_D05G032290*	*Ghir_A04G003270*	0.07
Ghir_D03G005110	*Ghir_D08G015410*	0.03	*Ghir_D05G032290*	*Ghir_D05G010610*	0.09
Ghir_D03G005110	*Ghir_A01G022690*	0.18	*Ghir_D05G032290*	*Ghir_A04G015520*	0.02
Ghir_A13G024190	*Ghir_D04G012180*	0.18	*Ghir_D05G032290*	*Ghir_A01G014310*	0.05
Ghir_A13G024190	*Ghir_D08G023860*	0.04	*Ghir_D05G032290*	*Ghir_D12G015390*	0.02
Ghir_A13G024190	*Ghir_A03G013820*	0.11	*Ghir_D05G032290*	*Ghir_D11G002680*	0.04
Ghir_A13G024190	*Ghir_A04G008120*	0.17	*Ghir_D05G032290*	*Ghir_A07G000760*	0.02

Ghir_A13G024190	*Ghir_D02G015000*	0.05	*Ghir_D05G032290*	*Ghir_D13G022890*	0.02
Ghir_A13G024190	*Ghir_D08G015520*	0.09	*Ghir_D12G006040*	*Ghir_A04G003270*	0.04
Ghir_A13G024190	*Ghir_D09G010390*	0.02	*Ghir_D12G006040*	*Ghir_A01G014310*	0.11
Ghir_A13G024190	*Ghir_A08G014710*	0.18	*Ghir_D12G006040*	*Ghir_A07G000760*	0.03
Ghir_A13G024190	*Ghir_D07G020010*	0.18	*Ghir_D12G006040*	*Ghir_A03G007260*	0.08
Ghir_A13G024190	*Ghir_A13G001070*	0.12	*Ghir_D12G006040*	*Ghir_D05G004810*	0.02
Ghir_A13G024190	*Ghir_D11G021880*	0.03	*Ghir_D11G026310*	*Ghir_D12G000410*	0.04
Ghir_A13G024190	*Ghir_D13G001360*	0.10	*Ghir_D11G026310*	*Ghir_D06G013730*	0.08
Ghir_A13G024190	*Ghir_A11G022530*	0.06	*Ghir_D11G026310*	*Ghir_A05G017350*	0.03
Ghir_A13G024190	*Ghir_D11G008770*	0.17	*Ghir_D11G026310*	*Ghir_A05G018350*	0.03
Ghir_A13G024190	*Ghir_A05G017350*	0.04	*Ghir_D11G026310*	*Ghir_D11G025880*	0.05
Ghir_A13G024190	*Ghir_D05G017130*	0.11	*Ghir_D11G026310*	*Ghir_D05G017130*	0.04
Ghir_A13G024190	*Ghir_A01G022690*	0.04	*Ghir_D11G026310*	*Ghir_D12G015390*	0.03
Ghir_D04G012180	*Ghir_D08G023860*	0.08	*Ghir_D11G026310*	*Ghir_A13G021470*	0.11
Ghir_D04G012180	*Ghir_A03G013820*	0.21	*Ghir_D11G026310*	*Ghir_D08G015410*	0.08
Ghir_D04G012180	*Ghir_A04G008120*	0.13	*Ghir_A04G003270*	*Ghir_D05G010610*	0.10
Ghir_D04G012180	*Ghir_D02G015000*	0.04	*Ghir_A04G003270*	*Ghir_A04G015520*	0.03
Ghir_D04G012180	*Ghir_D08G015520*	0.19	*Ghir_A04G003270*	*Ghir_A01G014310*	0.07
Ghir_D04G012180	*Ghir_A08G014710*	0.18	*Ghir_A04G003270*	*Ghir_D11G002680*	0.03
Ghir_D04G012180	*Ghir_D07G020010*	0.22	*Ghir_A04G003270*	*Ghir_A07G000760*	0.03
Ghir_D04G012180	*Ghir_A13G001070*	0.16	*Ghir_A04G003270*	*Ghir_A06G016670*	0.03
Ghir_D04G012180	*Ghir_D13G001360*	0.05	*Ghir_A04G003270*	*Ghir_A03G007260*	0.05
Ghir_D04G012180	*Ghir_A11G022530*	0.07	*Ghir_A11G022530*	*Ghir_D11G008770*	0.05
Ghir_D04G012180	*Ghir_D11G008770*	0.18	*Ghir_A11G022530*	*Ghir_A05G017350*	0.04
Ghir_D04G012180	*Ghir_A05G017350*	0.05	*Ghir_A11G022530*	*Ghir_D11G025880*	0.04
Ghir_D04G012180	*Ghir_D05G017130*	0.08	*Ghir_A11G022530*	*Ghir_D05G017130*	0.09
Ghir_D08G011580	*Ghir_A10G016800*	0.02	*Ghir_A11G022530*	*Ghir_D08G015410*	0.02
Ghir_D08G011580	*Ghir_D08G026850*	0.04	*Ghir_A11G022530*	*Ghir_A01G022690*	0.13
Ghir_D08G011580	*Ghir_A04G014820*	0.09	*Ghir_D05G010610*	*Ghir_A04G015520*	0.10
Ghir_D08G011580	*Ghir_D05G032290*	0.02	*Ghir_D05G010610*	*Ghir_A01G014310*	0.04
Ghir_D08G011580	*Ghir_D12G006040*	0.02	*Ghir_D05G010610*	*Ghir_D12G015390*	0.03
Ghir_D08G011580	*Ghir_A04G003270*	0.06	*Ghir_D05G010610*	*Ghir_A08G018120*	0.03
Ghir_D08G011580	*Ghir_D05G010610*	0.07	*Ghir_D05G010610*	*Ghir_A07G000760*	0.03
Ghir_D08G011580	*Ghir_A05G018350*	0.02	*Ghir_D05G010610*	*Ghir_A06G016670*	0.02
Ghir_D08G011580	*Ghir_D07G000060*	0.05	*Ghir_D11G008770*	*Ghir_A05G017350*	0.09
Ghir_D08G011580	*Ghir_A04G015520*	0.06	*Ghir_D11G008770*	*Ghir_D05G017130*	0.10
Ghir_D08G011580	*Ghir_A01G014310*	0.04	*Ghir_D11G008770*	*Ghir_A13G021470*	0.03
Ghir_D08G011580	*Ghir_D12G015390*	0.03	*Ghir_D11G008770*	*Ghir_A01G022690*	0.03
Ghir_D08G011580	*Ghir_A08G018120*	0.18	*Ghir_D01G007540*	*Ghir_A05G018350*	0.02
Ghir_D08G011580	*Ghir_A07G000760*	0.08	*Ghir_D01G007540*	*Ghir_A04G015520*	0.08
Ghir_D08G011580	*Ghir_A06G016670*	0.06	*Ghir_D01G007540*	*Ghir_A08G018120*	0.03
Ghir_D08G011580	*Ghir_A03G007260*	0.06	*Ghir_D01G007540*	*Ghir_D01G022810*	0.06
Ghir_D08G011580	*Ghir_D13G022890*	0.05	*Ghir_D12G000410*	*Ghir_D06G013730*	0.19
Ghir_D08G011580	*Ghir_D05G004810*	0.12	*Ghir_D12G000410*	*Ghir_D11G025880*	0.22

Ghir_A10G023870	*Ghir_D12G006040*	0.03	*Ghir_D12G000410*	*Ghir_D05G017130*	0.06
Ghir_A10G023870	*Ghir_D07G000060*	0.08	*Ghir_D12G000410*	*Ghir_D08G015410*	0.08
Ghir_A10G023870	*Ghir_A01G014310*	0.04	*Ghir_D06G013730*	*Ghir_D11G025880*	0.17
Ghir_A10G023870	*Ghir_D11G002680*	0.06	*Ghir_D06G013730*	*Ghir_D05G017130*	0.05
Ghir_A10G023870	*Ghir_A07G000760*	0.02	*Ghir_D06G013730*	*Ghir_A13G021470*	0.04
Ghir_A10G023870	*Ghir_A06G016670*	0.04	*Ghir_D06G013730*	*Ghir_D08G015410*	0.09
Ghir_A10G023870	*Ghir_D13G022890*	0.09	*Ghir_D06G013730*	*Ghir_D05G017040*	0.02
Ghir_D08G023860	*Ghir_A03G013820*	0.10	*Ghir_A05G017350*	*Ghir_A05G018350*	0.03
Ghir_D08G023860	*Ghir_A04G008120*	0.04	*Ghir_A05G017350*	*Ghir_D05G017130*	0.08
Ghir_D08G023860	*Ghir_D08G015520*	0.17	*Ghir_A05G017350*	*Ghir_A13G021470*	0.06
Ghir_D08G023860	*Ghir_A08G014710*	0.07	*Ghir_A05G017350*	*Ghir_A01G022690*	0.07
Ghir_D08G023860	*Ghir_D07G020010*	0.07	*Ghir_A05G018350*	*Ghir_D05G017130*	0.02
Ghir_D08G023860	*Ghir_A13G001070*	0.18	*Ghir_A05G018350*	*Ghir_A04G015520*	0.04
Ghir_D08G023860	*Ghir_D11G021880*	0.04	*Ghir_A05G018350*	*Ghir_D12G015390*	0.04
Ghir_D08G023860	*Ghir_D13G001360*	0.03	*Ghir_A05G018350*	*Ghir_A13G021470*	0.02
Ghir_D08G023860	*Ghir_A11G022530*	0.12	*Ghir_A05G018350*	*Ghir_A08G018120*	0.04
Ghir_D08G023860	*Ghir_D11G008770*	0.04	*Ghir_A05G018350*	*Ghir_D01G022810*	0.03
Ghir_D08G023860	*Ghir_D05G017130*	0.02	*Ghir_A05G018350*	*Ghir_D05G004810*	0.05
Ghir_A10G016800	*Ghir_D02G015000*	0.02	*Ghir_D11G025880*	*Ghir_D05G017130*	0.07
Ghir_A10G016800	*Ghir_D08G026850*	0.05	*Ghir_D11G025880*	*Ghir_D08G015410*	0.09
Ghir_A10G016800	*Ghir_A01G007610*	0.02	*Ghir_D07G000060*	*Ghir_A01G014310*	0.03
Ghir_A10G016800	*Ghir_D05G033790*	0.03	*Ghir_D07G000060*	*Ghir_D11G002680*	0.03
Ghir_A10G016800	*Ghir_D05G032290*	0.05	*Ghir_D07G000060*	*Ghir_A08G018120*	0.04
Ghir_A10G016800	*Ghir_A04G003270*	0.05	*Ghir_D07G000060*	*Ghir_A07G000760*	0.05
Ghir_A10G016800	*Ghir_D05G010610*	0.08	*Ghir_D07G000060*	*Ghir_A06G016670*	0.03
Ghir_A10G016800	*Ghir_D12G015390*	0.06	*Ghir_D07G000060*	*Ghir_D01G022810*	0.03
Ghir_A10G016800	*Ghir_A13G021470*	0.03	*Ghir_D07G000060*	*Ghir_D13G022890*	0.12
Ghir_A10G016800	*Ghir_A07G000760*	0.02	*Ghir_D07G000060*	*Ghir_D05G004810*	0.03
Ghir_A03G013820	*Ghir_A04G008120*	0.15	*Ghir_D05G017130*	*Ghir_A13G021470*	0.05
Ghir_A03G013820	*Ghir_D02G015000*	0.07	*Ghir_D05G017130*	*Ghir_D08G015410*	0.04
Ghir_A03G013820	*Ghir_D08G015520*	0.22	*Ghir_D05G017130*	*Ghir_A01G022690*	0.09
Ghir_A03G013820	*Ghir_A08G014710*	0.20	*Ghir_A04G015520*	*Ghir_A01G014310*	0.02
Ghir_A03G013820	*Ghir_D07G020010*	0.20	*Ghir_A04G015520*	*Ghir_D12G015390*	0.02
Ghir_A03G013820	*Ghir_A13G001070*	0.16	*Ghir_A04G015520*	*Ghir_A08G018120*	0.07
Ghir_A03G013820	*Ghir_D11G021880*	0.03	*Ghir_A04G015520*	*Ghir_D05G004810*	0.04
Ghir_A03G013820	*Ghir_D13G001360*	0.07	*Ghir_A01G014310*	*Ghir_D11G002680*	0.04
Ghir_A03G013820	*Ghir_A11G022530*	0.07	*Ghir_A01G014310*	*Ghir_A08G018120*	0.03
Ghir_A03G013820	*Ghir_D11G008770*	0.21	*Ghir_A01G014310*	*Ghir_A07G000760*	0.03
Ghir_A03G013820	*Ghir_A05G017350*	0.06	*Ghir_A01G014310*	*Ghir_A06G016670*	0.02
Ghir_A03G013820	*Ghir_D05G017130*	0.08	*Ghir_A01G014310*	*Ghir_A03G007260*	0.04
Ghir_A03G013820	*Ghir_A13G021470*	0.03	*Ghir_A01G014310*	*Ghir_D13G022890*	0.04
Ghir_A03G013820	*Ghir_A01G022690*	0.02	*Ghir_D12G015390*	*Ghir_A08G018120*	0.03
Ghir_A04G008120	*Ghir_D02G015000*	0.14	*Ghir_D12G015390*	*Ghir_A07G000760*	0.07
Ghir_A04G008120	*Ghir_D08G015520*	0.11	*Ghir_D12G015390*	*Ghir_D01G022810*	0.08

Ghir_A04G008120	*Ghir_D09G010390*	0.07	*Ghir_D12G015390*	*Ghir_D05G004810*	0.04
Ghir_A04G008120	*Ghir_A08G014710*	0.20	*Ghir_A13G021470*	*Ghir_D08G015410*	0.03
Ghir_A04G008120	*Ghir_D07G020010*	0.13	*Ghir_D11G002680*	*Ghir_A07G000760*	0.03
Ghir_A04G008120	*Ghir_A13G001070*	0.15	*Ghir_D11G002680*	*Ghir_A06G016670*	0.04
Ghir_A04G008120	*Ghir_D11G021880*	0.08	*Ghir_D11G002680*	*Ghir_D13G022890*	0.10
Ghir_A04G008120	*Ghir_D13G001360*	0.18	*Ghir_A08G018120*	*Ghir_A07G000760*	0.05
Ghir_A04G008120	*Ghir_D11G026310*	0.02	*Ghir_A08G018120*	*Ghir_A06G016670*	0.03
Ghir_A04G008120	*Ghir_A11G022530*	0.12	*Ghir_A08G018120*	*Ghir_A03G007260*	0.03
Ghir_A04G008120	*Ghir_D11G008770*	0.14	*Ghir_A08G018120*	*Ghir_D01G022810*	0.03
Ghir_A04G008120	*Ghir_D12G000410*	0.04	*Ghir_A08G018120*	*Ghir_D13G022890*	0.03
Ghir_A04G008120	*Ghir_D06G013730*	0.03	*Ghir_A08G018120*	*Ghir_D05G004810*	0.15
Ghir_A04G008120	*Ghir_A05G017350*	0.10	*Ghir_A07G000760*	*Ghir_A06G016670*	0.02
Ghir_A04G008120	*Ghir_D11G025880*	0.05	*Ghir_A07G000760*	*Ghir_A03G007260*	0.06
Ghir_A04G008120	*Ghir_D05G017130*	0.23	*Ghir_A07G000760*	*Ghir_D01G022810*	0.03
Ghir_A04G008120	*Ghir_A13G021470*	0.03	*Ghir_A07G000760*	*Ghir_D13G022890*	0.06
Ghir_A04G008120	*Ghir_D08G015410*	0.03	*Ghir_A07G000760*	*Ghir_D05G004810*	0.05
Ghir_A04G008120	*Ghir_A01G022690*	0.09	*Ghir_A06G016670*	*Ghir_D13G022890*	0.14
Ghir_D02G015000	*Ghir_D08G015520*	0.05	*Ghir_A03G007260*	*Ghir_D05G004810*	0.04
Ghir_D02G015000	*Ghir_D09G010390*	0.04	*Ghir_D01G022810*	*Ghir_D05G017040*	0.02
Ghir_D02G015000	*Ghir_A08G014710*	0.09	*Ghir_D01G022810*	*Ghir_D05G004810*	0.02

Supplemental Table S12. Genes co-expressed with *Re*

FromNode	ToNode	Weight	FromNode	ToNode	Weight
Re	*Ghir_A09G020500*	0.22	*Re*	*Ghir_Scaffold2801G000010*	0.17
Re	*Ghir_D09G017850*	0.19	*Re*	*Ghir_D13G019870*	0.10
Re	*Ghir_A04G002480*	0.16	*Re*	*Ghir_D02G011590*	0.15
Re	*Ghir_A13G002590*	0.15	*Re*	*Ghir_A13G016390*	0.08
Re	*Ghir_A12G029180*	0.08	*Re*	*Ghir_D02G009050*	0.12
Re	*Ghir_D12G025080*	0.11	*Re*	*Ghir_A09G000020*	0.10
Re	*Ghir_D01G009790*	0.12	*Re*	*Ghir_D13G013210*	0.12
Re	*Ghir_D04G007170*	0.11	*Re*	*Ghir_D09G011360*	0.13
Re	*Ghir_D10G005490*	0.14	*Re*	*Ghir_A11G015950*	0.19
Re	*Ghir_A05G002350*	0.14	*Re*	*Ghir_D12G005700*	0.24
Re	*Ghir_A09G010930*	0.19	*Re*	*Ghir_D07G017620*	0.15
Re	*Ghir_A12G025410*	0.21	*Re*	*Ghir_A03G021360*	0.19
Re	*Ghir_D11G021870*	0.08	*Re*	*Ghir_A05G019530*	0.03
Re	*Ghir_A08G016910*	0.08	*Re*	*Ghir_D07G010950*	0.12
Re	*Ghir_D07G014480*	0.09	*Re*	*Ghir_D05G009720*	0.10
Re	*Ghir_D12G010180*	0.04	*Re*	*Ghir_D02G014200*	0.22
Re	*Ghir_D06G012480*	0.11	*Re*	*Ghir_D11G007480*	0.06
			Re	*Ghir_A06G021320*	0.14

Supplemental Table S13. Primers for vector construction and functional verification

Forward primer (5'-3')	Reverse primer (5'-3')	Target
AATATGGTGAAGGGAAATGGC	GGTTATGGAGGCGAATAATGAG	RT primer for *Re*
GATGAGATGATGTGGTGGGAA	CAAACAAACATATATATTTCTGGCT	RT primer for *RE8*
GTATTGGCTAACTGCGGTGAC	ATCAAAAACAACAAACAACCATATT	RT primer for *RE3*
TAGCATTGCCCCATTCCC	CTTGTCCCATCCTGACCTG	genome sequencing of gene RE3
AGCAGGTCAGGATGGGACA	GTGATCAATAATTAGCGAGCTTCAT	
ACCGAATGAACAACCCTACA	TAGACTGTAGGGTTGTTCATTCG	genome sequencing of gene *RE*8
AAAGATCCCCAAGGAAACAAAT	GTTTCCTTGGGGATCTTTTTC	
CACTCTTTACCCACTACTTATGTTA	GGGTGAAACGTGAATGGACC	
TTATTAAGGCTTTTCTATCTCCCC	GAATGAACAACCCTACAGTCTAATG	
AACCAGGCACTATTGACGAA	CTAACTCTTAAAGATGAGCCTTCCAT	promoter region sequencing of gene *RE8*
TTGATATCGAATTCCTGAAGATGGAGCGGCGTAAG	TAGAACTAGTGGATCATAAAAGCTGTTATAGTTAGCTTGC	primer for LUC
GGGGACAAGTTTGTACAAAAAAGCAGGCTGCATGGAAGGCTCATCTTTAAGAGTTA	GGGGACCACTTTGTACAAGAAAGCTGGGTGCTATGGGTTGAACACATTCCACAG	Construction of 35S/Gb-EXP2 overexpression vector by BP reaction
ACCTTCGTGAAGTTGGGCTTAC	CGTGCCTTGTGGCTCGTA	RT primer for *CHS*
TGATGCAGAAGCAAAAGCCAT	AGCTCAGTACCAGAAGGTGGGA	RT primer for *CHI*
CAGTCACCGACGGCGAGAT	CGAAGTCCATAGGCGTGGC	RT primer for *DFR*
GGGCCTAGCTTGCAAGCTTCTT	AAGCAAGAGTGTGATGGTGCCTG	RT primer for *F3H*
GAGGCCTAGCGAGCAAAATAC	GTGAGCTTCGACACCGAGAG	RT primer for *ANR*

TCTTCTCCGCATCCCAACTA	TCCATTGCCTTCCTCAGATT	RT primer for *UFGT*
CCGCAGCTGTGTCTATCAACAC	AGCAAATTTCCAAGCTGCCTT	RT primer for *ANS*
CGCTCTAGAACTAGTGGATCCCTGCTTAGCAATGAACCACTGTAGT	CTTGATATCGAATTCCTGCAGATTAATTGGCTGCAACACAATAAGT	primers for *PIF4*_62sk
CGCTCTAGAACTAGTGGATCCATGGAAGGCTCATCTTTAAGAGTTA	CTTGATATCGAATTCCTGCAGCTATGGGTTGAACACATTCCACAG	primers for *Re*_62sk
CTTGATATCGAATTCCTGCAGTGTGCAATTTGCCAATATTCGTA	CGCTCTAGAACTAGTGGATCCCTTTCTACTCTAGGTAGCACTGAGG	primers for *ANS*Pro_0800
CTTGATATCGAATTCCTGCAGGCGGTGGGATGCGTTTATT	CGCTCTAGAACTAGTGGATCCGGTAGTTGTGATTTGTGGAGGAAAA	primers for *CHI*Pro_0800
CTTGATATCGAATTCCTGCAGCAGGTCGCAAACTGTCAAAC	CGCTCTAGAACTAGTGGATCCTAGGACGCTCATCTTCATCAC	primers for *F3H*Pro_0800
CTTGATATCGAATTCCTGCAGTGGAGGATTGTCGGCGCA	CGCTCTAGAACTAGTGGATCCCCAGCAATGACGCAACGAAT	primers for *ANR*Pro_0800
CTTGATATCGAATTCCTGCAGTTAGGCATTCCAATCACCAA	CGCTCTAGAACTAGTGGATCCAGATCCCATCGTTGTCTAGAAGATC	primers for *DFR*Pro_0800
CTTGATATCGAATTCCTGCAGACCACATGGGCGGCACAGT	CGCTCTAGAACTAGTGGATCCTCTTTTTCGGATGATTACAAACAGC	primers for *CHS*Pro_0800
CTTGATATCGAATTCCTGCAGGCACTACGAGCCAACCTCTCTC	CGCTCTAGAACTAGTGGATCCACCGTACACTTTCACTACCATTCTT	primers for *GST*Pro_0800
CTTGATATCGAATTCCTGCAGAACTGGTCTAAATCTTCTATTGGAG	CGCTCTAGAACTAGTGGATCCCGGGAAAGGTTGAGTTTGGAT	primers for *UFGT*Pro_0800
CAGATTACGCTCATATGTTTAAATCTGAAAGTTAATGGCG	TGCTTGGGTGGAATTCATTATGGTATTATTTGATTTATCGC	*TT8*_AD

Supplemental Table S14. Vectors used in this study

Purpose	Vector	Construct method	Restriction sites1 and Adapter sequence	Restriction sites2 and Adapter sequence
Overexpression vector	pk2GW7	BP-LR	-	-
Fiber-specific expression vector	PGbEXPA2	BP-LR	-	-
Subcellular localization	pMDC83	BP-LR	-	-
LUC assay	pGreen II 0800-62sk	infusion	PstI: CGCTCTAGAACTAGTGGATCC	BamHI: CTTGATATCGAATTCCTGCAG
	pGreen II 0800-LUC	infusion	PstI:CTTGATATCGAATTCCTGCAG	BamHI: CGCTCTAGAACTAGTGGATCC
Yeast two-hybrid assay	pGBKT7	infusion	BamHI: ATGGAGGCCGAATTC	EcoR1: GCAGGTCGACGGATCC
	pGADT7	infusion	NdeI: CAGATTACGCTCATATG	EcoR1: TGCTTGGGTGGAATTC
LCI assay	JW771	infusion	BamHI: CTCGGTACCCGGGATCC	SalI: TACGAGATCTGGTCGAC
	JW772	infusion	BamHI: GGCGGTACCCGGGATCCA	SalI: AAGCTCTGCAGGTCGAC
BiFC assay	pXY104	infusion	BamHI: CAGGTACCCGGGGATCC	SalI: GCGCTGCCCGCGTCGAC
	pXY106	infusion	BamHI: AGGACGCCGGCGGATCC	SalI:AAGCTCTGCAGGTCGAC