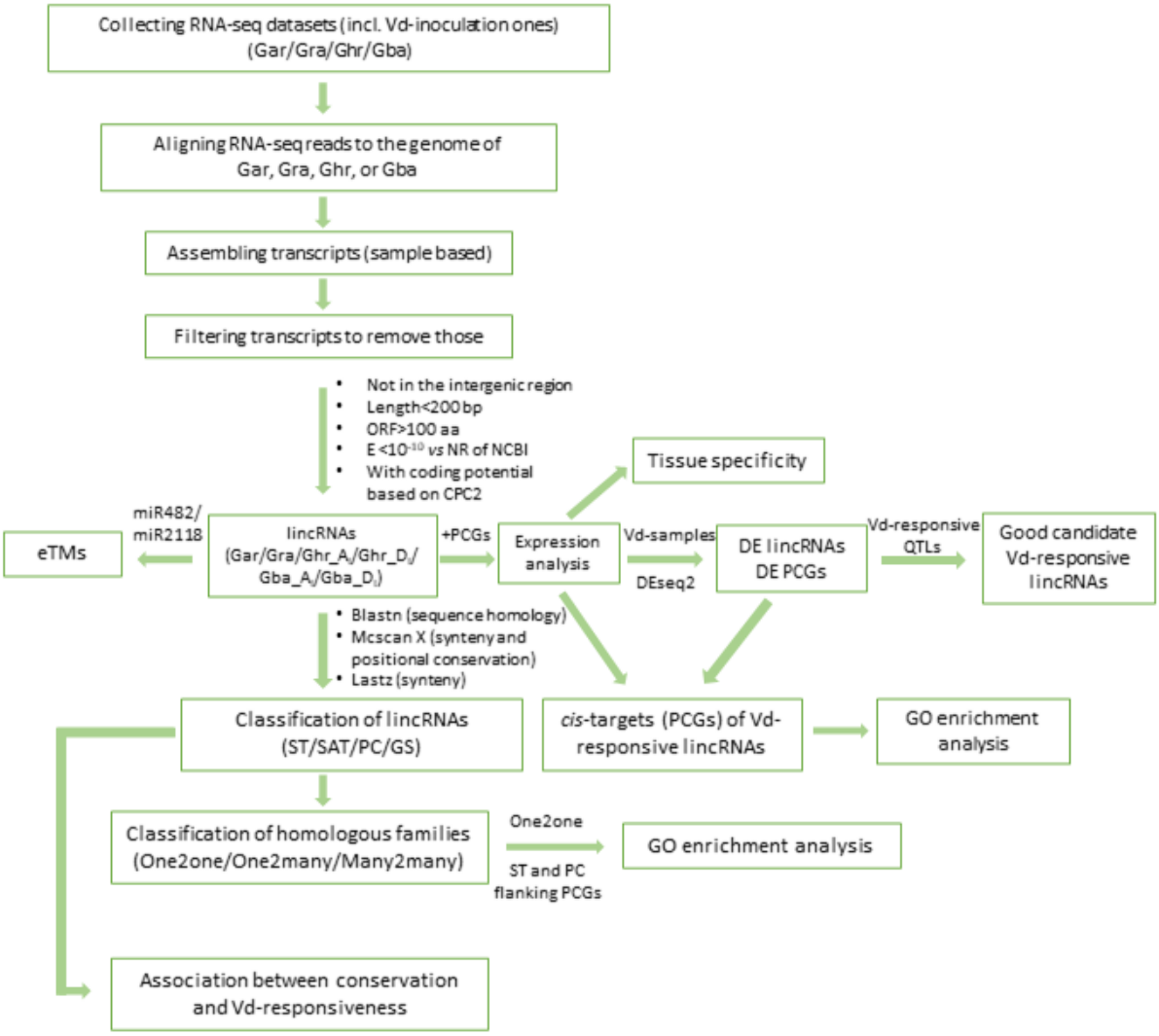
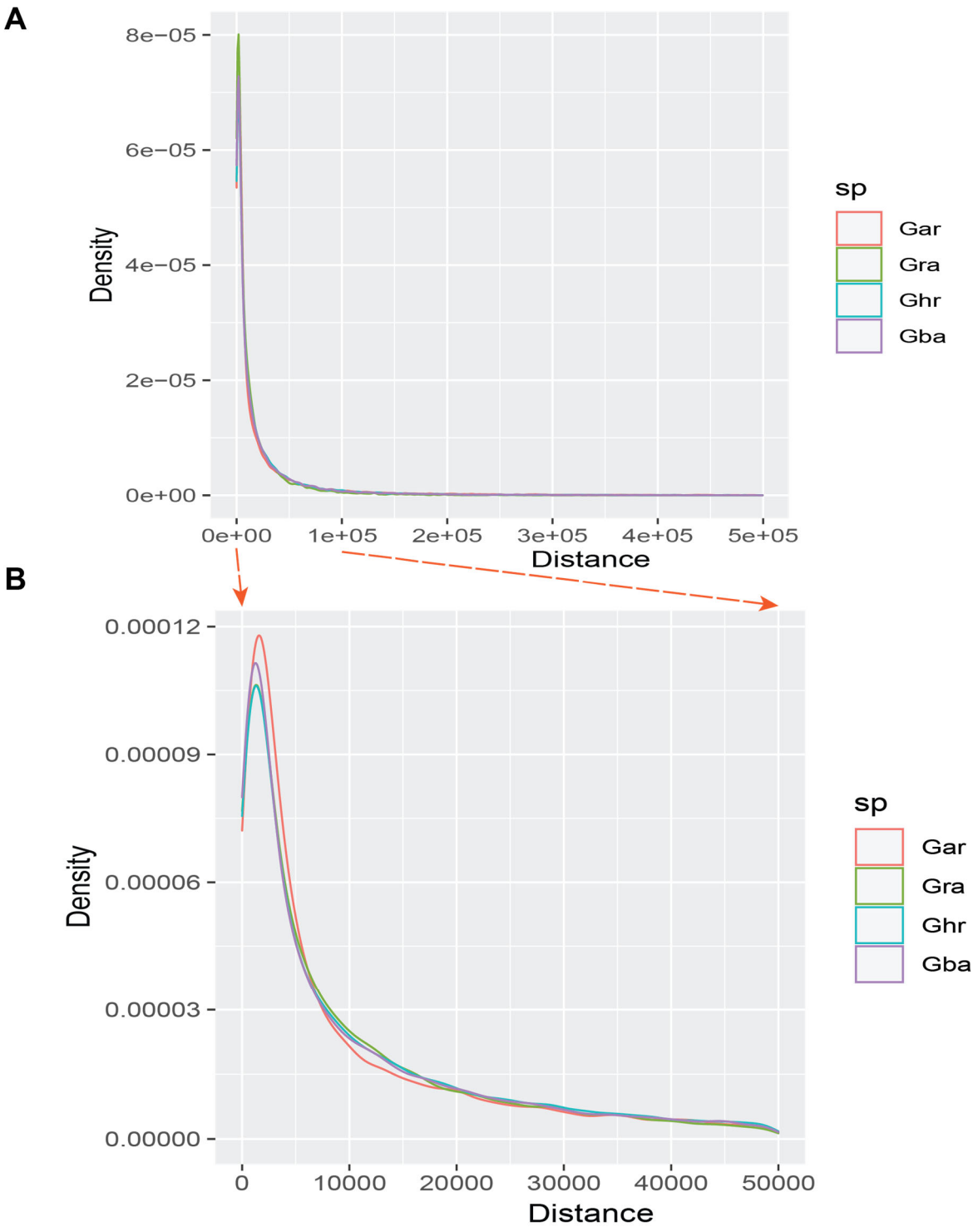
Supplemental Figure S1. The overall flowchart showing the analyses and methodology applied in the study.



Supplemental Figure S2. Distribution of neighbouring protein coding genes (A) and lincRNAs (B) in the genome of *G. hirsutum*.



Supplemental Figure S3. Sequence alignment of Ghrlnc.30744 with its homologs from other five (sub)genomes and the two full-length cDNAs generated by PacBio SMART sequencing. While the length of the predicted lincRNAs is variable, the splicing event of the intron is conserved. The 2596-bp 3' end sequence of Garlnc.26799 is not shown as it is unique to *G. arboreum*.

```
PB.6980.1_gDNA      ------------------------------------------------------------     0
PB.6980.1           ------------------------------------------------------------     0
PB.23765.1          ------------------------------------------------------------     0
Ghrlnc.30744_At     CACTAGTGAAAACATTGTAAAAAATCTCCGCCGTC-CAAACAATTTCAATCACCCCCAAT     59
Garlnc.26799        ------------------------------------------------------------     0
Gbalnc.26265_At     ------------------------------------------------------------     0
Gbalnc.64928_Dt     ------------------------------------------------------------     0
Ghrlnc.74560_Dt     ------------------------------------------------------------     0
Gralnc.30550        ------------------------------------------------------------     0


PB.6980.1_gDNA      ------------------------------------------------------------     0
PB.6980.1           ------------------------------------------------------------     0
PB.23765.1          ------------------------------------------------------------     0
Ghrlnc.30744_At     CACG---------TCTCCTTTTCGTGTTGTAAAAAAGTGGAGAAAGTCATTATTATAGGA     110
Garlnc.26799        ------------------------------------------------------------     0
Gbalnc.26265_At     ------------------------------------------------------------     0
Gbalnc.64928_Dt     -------------------------------------GGAGAAAGTCATTATTATAGGAA     23
Ghrlnc.74560_Dt     ------------------------------------------------------------     0
Gralnc.30550        ------------------------------------------------------------     0


PB.6980.1_gDNA      ------------------------------------------------------------     0
PB.6980.1           ------------------------------------------------------------     0
PB.23765.1          ------------------------------------------------------------     0
Ghrlnc.30744_At     ATTGGATATGATCATACTCTGACACCCAAAAAACACATTTTTTTAATTATT---------     161
Garlnc.26799        ------------------------------------------------------------     0
Gbalnc.26265_At     ------------------------------------------------------------     0
Gbalnc.64928_Dt     TTGGATATGATCATACTCTGACACCCAAAAAACACTTTTTTTTTAATTATTATTAATAAT     83
Ghrlnc.74560_Dt     ---------------------------AAAAAACACTTTTTTTTAATTATTATTAATAAT     33
Gralnc.30550        ----------------------------------CTTTTTTTTAATTATTATTAATAAT     25


PB.6980.1_gDNA      ------------------------------------------------------------     0
PB.6980.1           ------------------------------------------------------------     0
PB.23765.1          ------------------------------------------------------------     0
Ghrlnc.30744_At     ATTAATAATTTAATAACACTCCTATTATTAGTAATTTTTAATTATATAATCATCATCGAA     221
Garlnc.26799        ---------------------------------AATTTTTAATTATATAATCATCATCGAA     28
Gbalnc.26265_At     --------------AACACTCCTATTATTAGTAATTTTTAATTATATAATCATCATCGAA     46
Gbalnc.64928_Dt     ------AATTTAATAACACTCCTATTATTAGTAATTTTTAATTATATAATCATCATCGAA     137
Ghrlnc.74560_Dt     ------AATTTAATAACACTCCTATTATTAGTAATTTTTAATTATATAATCATCATCGAA     87
Gralnc.30550        ------AATTTAATAACACTCCTATTATTAGTAATTTTTAATTATATAATCATCATCGAA     79


PB.6980.1_gDNA      ---------------------------------------------ACAGTGTTTCGGGAT--T     16
PB.6980.1           ---------------------------------------------ACAGTGTTTCGGGAT--T     16
PB.23765.1          ---------------------------------------------ACTGTATTTCGGGAT--T     16
Ghrlnc.30744_At     ACAAAGTCCAATTTATAAGCCATTTT-AGCCTCTTCTCCTTCACAGTGTTTCGGGAT---     277
Garlnc.26799        ACAAAGTCCAATTTATAAGCCATTTT-AGCCTCTTCTCCTTCACAGTGTTTCGGGAT---     84
Gbalnc.26265_At     ACAAAGTCCAATTTATAAGCCATTTT-AGCCTCTTCTCCTTCACAGTGTTTCGGGAT---     102
Gbalnc.64928_Dt     ACAAAGTCCAATTTATAAGC-ATTT-CAGCCTCTTCTCCTTCACTGTATTTCGGGAT--T     193
Ghrlnc.74560_Dt     ACAAAGTCCAATTTATAAGC-ATTT-CAGCCTCTTCTCCTTCACTGTATTTCGGGAT--T     143
Gralnc.30550        -CAAAGTCCAATTTATAAGC-ATTT-CAGCCTCTTCTCCTTCACTGTGCTTCGGGAT--T     134
                                                      ** **  ********


PB.6980.1_gDNA      --TCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     71
PB.6980.1           --TCTCGTGCTCTGTTTTTTATTTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     71
PB.23765.1          --TCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     71
Ghrlnc.30744_At     -TTCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     333
Garlnc.26799        -TTCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     140
Gbalnc.26265_At     -TTCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     158
Gbalnc.64928_Dt     --TCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     248
Ghrlnc.74560_Dt     --TCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     198
Gralnc.30550        --TCTCGTGCTCTGTTTTTTTATTCTTTGTTGAGAAAGAAG---GGATCCTTGCTTTGCT     189
                      ******************  ******************   ****************


PB.6980.1_gDNA      TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     124
PB.6980.1           TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     124
PB.23765.1          TTGATTATTTTTT------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     125
```

```
Ghrlnc.30744_At      TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     386
Garlnc.26799         TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     193
Gbalnc.26265_At      TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     211
Gbalnc.64928_Dt      TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     301
Ghrlnc.74560_Dt      TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     251
Gralnc.30550         TTGATTATTTTT-------CAATGATGATGGAGCTTTTTGTATTGGGGTGTACGGGAGTT     242
                     ************       ****************************************

PB.6980.1_gDNA       GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     181
PB.6980.1            GTGTGTGTTCCTCCACGGTGCCAATTTCTCTCTTCCATGTTCTTTTCTCAACATC--TCG     184
PB.23765.1           GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATCTCTCG     182
Ghrlnc.30744_At      GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     441
Garlnc.26799         GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     248
Gbalnc.26265_At      GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     266
Gbalnc.64928_Dt      GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     356
Ghrlnc.74560_Dt      GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     306
Gralnc.30550         GTGG-TGTTCCTCCACGGTGCCAATTTCT-TCTTCCATGTTCTTT-CTCAACATC--TCG     297
                     ***  ********************** *************** *********  ***

PB.6980.1_gDNA       CTGTTCGATCTCTC--AGGTTCGTTCCATTTTTT-------TCAACAATTTCTAT-----     227
PB.6980.1            CTGTTCGATCTCTCTCAG-------------------------------------------     202
PB.23765.1           CTGTTCGATCTCTC--AG-------------------------------------------     198
Ghrlnc.30744_At      CTGTTCGATCTCTC--AG-------------------------------------------     457
Garlnc.26799         CTGTTCGATCTCTC--AG-------------------------------------------     264
Gbalnc.26265_At      CTGTTCGATCTCTC--AG-------------------------------------------     282
Gbalnc.64928_Dt      CTGTTCGATCTCTC--AG-------------------------------------------     372
Ghrlnc.74560_Dt      CTGTTCGATCTCTC--AG-------------------------------------------     322
Gralnc.30550         CTGTTCGATCTCTC--AG-------------------------------------------     313
                     **************  **

PB.6980.1_gDNA       --------AATTTTCTCACAATTA-TACCATGTCCCAAATTGCAATAAATCTGGGTAAGC     278
PB.6980.1            ---------------------------------------------------------     202
PB.23765.1           ---------------------------------------------------------     198
Ghrlnc.30744_At      ---------------------------------------------------------     457
Garlnc.26799         ---------------------------------------------------------     264
Gbalnc.26265_At      ---------------------------------------------------------     282
Gbalnc.64928_Dt      ---------------------------------------------------------     372
Ghrlnc.74560_Dt      ---------------------------------------------------------     322
Gralnc.30550         ---------------------------------------------------------     313

PB.6980.1_gDNA       TTTATTTTACAAAAAGGAA-TGATCTTTGAGTAAAAAAAAAATTCCCAACTTTCTGTTTT     337
PB.6980.1            ---------------------------------------------------------     202
PB.23765.1           ---------------------------------------------------------     198
Ghrlnc.30744_At      ---------------------------------------------------------     457
Garlnc.26799         ---------------------------------------------------------     264
Gbalnc.26265_At      ---------------------------------------------------------     282
Gbalnc.64928_Dt      ---------------------------------------------------------     372
Ghrlnc.74560_Dt      ---------------------------------------------------------     322
Gralnc.30550         ---------------------------------------------------------     313

PB.6980.1_gDNA       TTGGATGAAATTTTTTGGCTTCACAAGCATCACCTGCTAAAACTATAAATTGGGTACTGA     397
PB.6980.1            ---------------------------------------------------------     202
PB.23765.1           ---------------------------------------------------------     198
Ghrlnc.30744_At      ---------------------------------------------------------     457
Garlnc.26799         ---------------------------------------------------------     264
Gbalnc.26265_At      ---------------------------------------------------------     282
Gbalnc.64928_Dt      ---------------------------------------------------------     372
Ghrlnc.74560_Dt      ---------------------------------------------------------     322
Gralnc.30550         ---------------------------------------------------------     313

PB.6980.1_gDNA       GTAT-TTTGTAATAATTTTGTCATGT--GTTTATAAATTCTAATGTTTGGACATGTGATT     454
PB.6980.1            ---------------------------------------------------------     202
PB.23765.1           ---------------------------------------------------------     198
Ghrlnc.30744_At      ---------------------------------------------------------     457
Garlnc.26799         ---------------------------------------------------------     264
Gbalnc.26265_At      ---------------------------------------------------------     282
Gbalnc.64928_Dt      ---------------------------------------------------------     372
Ghrlnc.74560_Dt      ---------------------------------------------------------     322
Gralnc.30550         ---------------------------------------------------------     313

PB.6980.1_gDNA       TTGTTTGGTTTTTCAGTTTCTTGGGATTTGTTGGATGGTAATACCAAAAAGGGAAGAAAA     512
PB.6980.1            ----------------TTTCTTGGGATTTGTTGGATGGTAATACCAAAAAGGGAAGAAAA     246
PB.23765.1           ----------------TTTCTTGGGATTTGTTGGGTGGTAATACCAAAAAGGGGAGAAAA     242
```

```
Ghrlnc.30744_At      ----------------TTTCTTGGGATTTGTTGGATGGTAATACCAAAAAGGGAAGAAAA     501
Garlnc.26799         ----------------TTTCTTGGGATTTGTTGGATGGTAATACCAAAAAGGGAAGAAAA     308
Gbalnc.26265_At      ----------------TTTCTTGGGATTTGTTGGATGGTAATACCAAAAAGGGAAGAAAA     326
Gbalnc.64928_Dt      ----------------TTTCTTGGGATTTGTTGGGTGGTAATACCAAAAAGGGGAGAAAA     416
Ghrlnc.74560_Dt      ----------------TTTCTTGGGATTTGTTGGGTGGTAATACCAAAAAGGGGAGAAAA     366
Gralnc.30550         ----------------TTTCTTGGGATTTGTTGGGTGGTAATACCAAAAAGGGGAGAAAA     357
                                     ******************************************


PB.6980.1_gDNA       CAGAGATGATTAATATA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     568
PB.6980.1            CAGAGATGATATATATATATCTTTTTGCAAATTGAGATGTGGATCATGATGTGCTTTTGT     304
PB.23765.1           CGGAGATGATTCATTTA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     298
Ghrlnc.30744_At      CAGAGATGATTAATATA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     557
Garlnc.26799         CAGAGATGATTCATATA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     364
Gbalnc.26265_At      CAGAGATGATTAATATA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     382
Gbalnc.64928_Dt      CGGAGATGATTCATTTA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     472
Ghrlnc.74560_Dt      CGGAGATGATTCATTTA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     422
Gralnc.30550         CGGAGATGATTCATTTA--TCTTTTTGCAAATTGAGATGTGGATCATGAT--GCTTTTGT     413
                     * ********  ** **  ******************************  ********

PB.6980.1_gDNA       AAATATTTGATTACAACTTAGATTTTGGGCAAATATA--AAATATAATATGATAATTATG     626
PB.6980.1            AAATATTTGATTACAACTTAGATTTTGGGCAATATAAAAAATATAATAATGATAATTATG     364
PB.23765.1           AAATATTTGATTACAACTTAGATTCTGGGCAAATATC--AAATGTAATATGATAATTATG     356
Ghrlnc.30744_At      AAATATTTGATTACAACTTAGATTTTGGGCAAATATA--AAATATAATATGATAATTATG     615
Garlnc.26799         AAATATTTGATTACAACTTAGATTTTGGGCAAATATA--AAATATAATATGATAATTATG     422
Gbalnc.26265_At      AAATATTTGATTACAACTTAGATTTTGGGCAAATATA--AAATATAATATGATAATTATG     440
Gbalnc.64928_Dt      ATATATTTGATTACAACTTAGATTCTGGGCAAATATC--AAATGTAATATGATAATTATG     530
Ghrlnc.74560_Dt      AAATATTTGATTACAACTTAGATTCTGGGCAAATATC--AAATGTAATATGATAATTATG     480
Gralnc.30550         AAATATTTGATTACAACCTAGATTCTGGGCAAATATC--AAATGTAACATGATAATTATG     471
                     * ***************** ****** *******       **    *  ************

PB.6980.1_gDNA       TATTGGTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAATATAGAGCAATATCATCTT--     684
PB.6980.1            TATTGGTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAATATAGAGCAATATCATCTCTT     424
PB.23765.1           TATTGTTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAGTATAGAGCAATATCATCTT--     414
Ghrlnc.30744_At      TATTGGTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAATATAGAGCAATATCATCTT--     673
Garlnc.26799         TATTGGTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAATATAGAGCAATATCATCTT--     480
Gbalnc.26265_At      TATTGGTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAATATAGAGCAATATCATCTT--     498
Gbalnc.64928_Dt      TATTGTTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAGTATAGAGCAATATCATCTT--     588
Ghrlnc.74560_Dt      TATTGTTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAGTATAGAGCAATATCATCTT--     538
Gralnc.30550         TATTGTTAGAGCAAAAATGGAAAGGCTGTTTGCCCTCAATATAGAGCAATATCATCTT--     529
                     ***** ******************************** ******************

PB.6980.1_gDNA       TCTATACTGTATTCTATCCATTTATGTACCCCATATTTGATTAAATCTTAGATTTTGAGG     744
PB.6980.1            CTATAACTGTATTCTATCCATTTATGTACCCCATATTTGATTAAATCTTAGATTTTGAGG     484
PB.23765.1           TGTATACTGTATTTTATCCATTTATGTACCCCATCTTTGATTAAATCTTAGATTTTGAGG     474
Ghrlnc.30744_At      TCTATACTGTATTCTATCCATTTATGTACCCCATATTTGATTAAATCTTAGATTTTGAGG     733
Garlnc.26799         TCTATACTGTATTCTATCCATTTATGTACCCCATATTTGATTAAATCTTAGATTTTGAGG     540
Gbalnc.26265_At      TCTATACTGTATTCTATCCATTTATGTACCCCATATTTGATTAAATCTTAGATTTTGAGG     558
Gbalnc.64928_Dt      TGTATACTGTATTTTATCCATTTATGTACCCCATCTTTGATTAAATCTTAGATTTTGAGG     648
Ghrlnc.74560_Dt      TGTATACTGTATTTTATCCATTTATGTACCCCATCTTTGATTAAATCTTAGATTTTGAGG     598
Gralnc.30550         TGTATACTGTATTTTATCCATTTATGTACCCCATCTTTGATTAAATCTTAGATGTTGAGG     589
                          ******** ******************** ****************** ******

PB.6980.1_gDNA       GTATCAAATATAATGAAATTTATGTATCCTTAAAACCAAAAGGGAAAAGCTTTGATCCC-     803
PB.6980.1            GTATCAAATATAATGAAATTTATGTATCCTTAAAACCAAAAGGGAAAAGCTTTGATCCC-     543
PB.23765.1           GTATCAAATATAATGAAATTTATGTATCCTT-----------------------------     505
Ghrlnc.30744_At      GTATCAAATATAATGAAATTTATGTATCCTTAAAACCAAAAGGGAAAAGCTTTGATCCCA     793
Garlnc.26799         GTATCAAATATAATGAAATTTATGTATCCTTAAAACCAAAAGGGAAAAGCTTTGATCCCA     600
Gbalnc.26265_At      GTATCAAATATAATGAAATTTATGTATCCTTAAAACCAAAAGGGAAAAGCTTTGATCCCA     618
Gbalnc.64928_Dt      GTATCAAATATAATGAAATTTATGTATCCTTAAAACTAAAAGGGAAAAGCTTTGATCCCA     708
Ghrlnc.74560_Dt      GTATCAAATATAATGAAATTTATGTATCCTTAAAACTAAAAGGGAAAAGCTTTGATCCCA     658
Gralnc.30550         GTATCAAATATAATGAAATTTATGTATCCTTAAAACTAAAAGGGAAAAGCTTTGATCCCA     649
                     ********************************

PB.6980.1_gDNA       ------------------------------------------------------------     803
PB.6980.1            ------------------------------------------------------------     543
PB.23765.1           ------------------------------------------------------------     505
Ghrlnc.30744_At      CTTTGGAGCGAAATGGATGATTGTATACTTGTTACAGACA--------------------     833
Garlnc.26799         CTTTGGAGCGAAATGGATGATTGTATACTTGTTACAGACACTCCGCCGGAGACTTCATTT     660
Gbalnc.26265_At      CTTTGGAGCGAAATGGATGATTGTATACTTGTTACAGACACTCCGCCGGAGACTTCATTT     678
Gbalnc.64928_Dt      CTTTGGAGCGAAATGGATGATTGTATACTTGTTACAG----------------------     745
Ghrlnc.74560_Dt      CTTTGGAGCGAAATGGATGATTGTATACTTGTTACAGACACTCCGCCGGAGACTTCATTT     718
Gralnc.30550         CTTTGGAGCGAAATGGATGATTGTATACTTGTTACTGACACTCCGCCGGAGACTTCATTT     709


PB.6980.1_gDNA       ------------------------------------------------------------     803
```

```
PB.6980.1           ------------------------------------------------------------     543
PB.23765.1          ------------------------------------------------------------     505
Ghrlnc.30744_At     ------------------------------------------------------------     833
Garlnc.26799        GACTCCACCGGATCCATCACCTTCGCCGTCATCTCTTCTTTTGGCACAAGATTTGTTCCG     720
Gbalnc.26265_At     GACTCCAC-----------------------------------------------------     686
Gbalnc.64928_Dt     ------------------------------------------------------------     745
Ghrlnc.74560_Dt     GACTCCACTG-ATCCATCACCTTCGCCGTCATCTCTTCTTTTGGCACAAGATTTGTTCCG     777
Gralnc.30550        GACTCCACTGGATCCATCACCTTCGCCGTCATCTCTTCTTTTGGCACAAGATTTGTTCCG     769


PB.6980.1_gDNA      ------------------------------------------------------------     803
PB.6980.1           ------------------------------------------------------------     543
PB.23765.1          ------------------------------------------------------------     505
Ghrlnc.30744_At     ------------------------------------------------------------     833
Garlnc.26799        TTTAGTAATACCTAAATCCATTACCTCTAACAACTCAACAACTCCTATAAGACATGGTCA     780
Gbalnc.26265_At     ------------------------------------------------------------     686
Gbalnc.64928_Dt     ------------------------------------------------------------     745
Ghrlnc.74560_Dt     TTTAGTAGTACCTAAATCCATTACCTCTAACAACTCAACAACTCCTATAAGACATGGTCA     837
Gralnc.30550        TTTAGTAGTA---------------------------------------------------     779
```

Supplemental Figure S4. Sequence alignment of the two homologous lincRNAs predicted to be endogenous target mimics of miR2118e in *G. hirsutum* and *G. barbadense*. The two lincRNAs are identical except the 5' and 3' ends and a retained intron in Gbalnc.31516. The sequence highlighted in yellow is the binding site of miR2118e.

```
Ghrlnc.36832      ATTCATTATTAGGTTTTTGAAGTTCTTAAGTTTCAACGACCACCAGAAAATTTACAACAC        60
Gbalnc.31516      -----------GGTTTTTGAAGTTCTTAAGTTTCAACGACCACCAGAAAATTTACAACAC        49
                           **************************************************

Ghrlnc.36832      GTTTGGTTGGCATGAATAGCCAAACTATTCCTGGATGATTCGGTGATAAGCAGCTATTCA        120
Gbalnc.31516      GTTTGGTTGGCATGAATAGCCAAACTATTCCTGGATGATTCGGTGATAAGCAGCTATTCA        109
                  ************************************************************

Ghrlnc.36832      TTAGTTTGGTTCACTGAATCCTCCATTCGACAGAATTTCATTCATCTCCCATTCCGCCTC        180
Gbalnc.31516      TTAGTTTGGTTCACTGAATCCTCCATTCGACAGAATTTCATTCATCTCCCATTCCGCCTC        169
                  ************************************************************

Ghrlnc.36832      TTCCCGTAATAGCCATTCCCCACCTGATTTAAAGAATAGCAATACAGAGCCTCCACCGAA        240
Gbalnc.31516      TTCCCGTAATAGCCATTCCCCACCTGATTTAAAGAATAGCAATACAGAGCCTCCACCGAA        229
                  ************************************************************

Ghrlnc.36832      TAAGAAAAAAAAACATAACCTCCCATTCTTGCCCTTTACCACTCTCCCTCAGCAAACACCT        300
Gbalnc.31516      TAAGAAAAAAAAACATAACCTCCCATTCTTGCCCTTTACCACTCTCCCTCAGCAAACACCT        289
                  ************************************************************

Ghrlnc.36832      CAAGCCACCACACCCCAACCCTGTCTCCTAGTTCTCGTTTAGTTATTCTCATCCCACGAC        360
Gbalnc.31516      CAAGCCACCACACCCCAACCCTGTCTCCTAGTTCTCGTTTAGTTATTCTCATCCCACGAC        349
                  ************************************************************

Ghrlnc.36832      CATCATCGACAGAGATCTCGACATTATAAAAAGCATCCCCAAAGTTGAGACGAGTAAG--        420
Gbalnc.31516      CATCATCGACAGAGATCTCGACATTATAAAAAGCATCCCCAAAGTTGAGACGAGTAAGGT        409
                  ************************************************************

Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      TATTATTTCCCTCAATCTCACCTCCATTGTGAGAATTTCATCTCTTTACTTCTCTGCTTG        469

Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      TATTTCACTAGAAAGGGGTTGTGAAAAAAATGAGTTTTCGAAAAAAAATTGGTCAACTGG        529

Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      TTGATCCGATTATTTTAGGGCAATTTAGGGTTAGAAAGCTAAGCTTGGTTTATTCGAATT        589

Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      GTTGGGCATTTCTGTTTATTGTAAGGGATTTCAGGTTGCTTGTCTCAATAGTAAGAGATT        649

Ghrlnc.36832      ----------GTTGGAATTTGTTGTTTGTGGTAAATGGGTTGAAGGGGTTTTGGATTTTG        468
Gbalnc.31516      TCAATTTCAGGTTGGAATTTGTTGTTTGTGGTAAATGGGTTGAAGGGGTTTTGGATTTTG        709
                            **************************************************

Ghrlnc.36832      AGCTTTGAATCAGTTATAGAGTTTTTGAGCAAGAAAAAGAAAAAGAAAATAGAGGCGGGG        528
Gbalnc.31516      AGCTTTGAATCAGTTATAGAGTTTTTGAGCAAGAAAAAGAAAAAGAAAATAGAGGCGGGG        769
                  ************************************************************

Ghrlnc.36832      GAGATGAGGAAATCGTTTTACTGGCTCACATGCTCAAACTTATGATACTTTGAAGGGCAA        588
Gbalnc.31516      GAGATGAGGAAATCGTTTTACTGGCTCACATGCTCAAACTTATGATACTTTGAAGGGCAA        829
                  ************************************************************

Ghrlnc.36832      CAGTGGTGGTCAATCATGTATGCTCAGCCTATCAGAAGATAATATCCTGGACACTGTGGG        648
Gbalnc.31516      CAGTGGTGGTCAATCATGTATGCTCAGCCTATCAGAAGATAATATCCTGGACACTGTGGG        889
                  ************************************************************

Ghrlnc.36832      AGTCATTTGTGTTGACACTGAAAGAAATATAGCATAGGAGCCTCCAGTGGTGGTATTGTA        708
Gbalnc.31516      AGTCATTTGTGTTGACACTGAAAGAAATATAGCATAGGAGCCTCCAGTGGTGGTATTGTA        949
                  ************************************************************

Ghrlnc.36832      CTGAAGGTCTCTGGTCGTGTGGGATTAGCAGCAATGTATGGTGCAGGCTGTTGGGCCTCC        768
Gbalnc.31516      CTGAAGGTCTCTGGTCGTGTGGGATTAGCAGCAATGTATGGTGCAGGCTGTTGGGCCTCC        1009
                  ************************************************************

Ghrlnc.36832      TCAAAAGGACCCTTTGGGGCTCGTTTCATAGTTGGTTGTTGTGTTAGCGGTGCTGGAGAA        828
Gbalnc.31516      TCAAAAGGACCCTTTGGGGCTCGTTTCATAGTTGGTTGTTGTGTTAGCGGTGCTGGAGAA        1069
```

```
                ************************************************************

Ghrlnc.36832    CACCTAATGAAAGGATTTTCAGCTCGGGAGTGCTGTGTCTCATCGTCACTGTAGGATTCT        888
Gbalnc.31516    CACCTAATGAAAGGATTTTCAGCTCGGGAGTGCTGTGTCTCATCGTCACTGTAGGATTCT        1129
                ************************************************************


Ghrlnc.36832    TTTGGATTTATATGACTAACAGGAATTTGTTCCCTTTACATGAAGAAAGTTTTAGTTATC        948
Gbalnc.31516    TTTGGATTTATATGACTAACAGGAATTTGTTCCCTTTACATGAAGAAAGTTTTAGTTATC        1189
                ************************************************************

Ghrlnc.36832    CTAAATGGACCTTGTCGAGTTAGGTTGTCTCTGCTTGTATCTCTTTTTATTAATACAAAA        1008
Gbalnc.31516    CTAAATGGACCTTGTCGAGTTAGGTTGTCTCTGCTTGTATCTCTTTTTATTAATACAAAA        1249
                ************************************************************

Ghrlnc.36832    GTAGTATAATAGGATACGATCTTTTGAAACATTAATTGTCTACTTGATTCTGAGCATGGG        1068
Gbalnc.31516    GTAGTATAATAGGATACGATCTTTTGAAACATTAATTGTCTACTTGATTCTGAGCATGGG        1309
                ************************************************************

Ghrlnc.36832    TGTTGAAATCGGTAAGGGTCTATGTTTGGTGAGAACTAGAAGTGATAAATCATATAATAG        1128
Gbalnc.31516    TGTTGAAATCGGTAAGGGTCTATGTTTGGTGAGAACTAGAAGTGATAAATCATATAATAG        1369
                ************************************************************

Ghrlnc.36832    AAGTTGAATTTGTTCGATCTTAAATTATTTGCTTAAATTCGAAGATTTATCATCTTTGAT        1188
Gbalnc.31516    AAGTTGAATTTGTTCGATCTTAAATTATTTGCTTAAATTCGAAGATTTATCATCTTTGAT        1429
                ************************************************************

Ghrlnc.36832    CCCATTTAGAAT        1200
Gbalnc.31516    CC----------        1431
                **
```

Supplemental Figure S5. Sequence alignment of the two homologous endogenous target mimicries of miR2118e and their homologous PacBio full-length cDNAs. The sequence shown in red is the miR2118e binding site.

```
PB.25815.1        ------------------------------------------------------------        0
PB.13303.1        ------------------------------------------------------------        0
PB.8185.1         ------------------------------------------------------------        0
Ghrlnc.36832      ATTCATTATTAGGTTTTTGAAGTTCTTAAGTTTCAACGACCACCAGAAAATTTACAACAC        60
Gbalnc.31516      -----------GGTTTTTGAAGTTCTTAAGTTTCAACGACCACCAGAAAATTTACAACAC        49


PB.25815.1        ------------------------------------------------------------        0
PB.13303.1        --------------------------ATTCCGGATGATTAGGTGATAAGTAGCTATTCA        33
PB.8185.1         -------------------------------------------GGTGATAAGCAGCTATTCA        19
Ghrlnc.36832      GTTTGGTTGGCATGAATAGCCAAACTATTCCTGGATGATTCGGTGATAAGCAGCTATTCA        120
Gbalnc.31516      GTTTGGTTGGCATGAATAGCCAAACTATTCCTGGATGATTCGGTGATAAGCAGCTATTCA        109


PB.25815.1        -----------------ATCTTCCATTCGACAGAATTTCATTCATCTTCC-ATTCCGCCT        42
PB.13303.1        TTAGTTTGGTTCACCGAATCCTCCATTCGACAGGATTTCATTCATCTCCC-ATTCCGTCT        92
PB.8185.1         TTAGTTTAATTCACCGAATCTCCA-TTCGACAGAATTTTATTCATCTCCCATTCCGCCCT        78
Ghrlnc.36832      TTAGTTTGGTTCACTGAATCCTCCATTCGACAGAATTTCATTCATCTCCC-ATTCCGCCT        179
Gbalnc.31516      TTAGTTTGGTTCACTGAATCCTCCATTCGACAGAATTTCATTCATCTCCC-ATTCCGCCT        168
                                  ***  *  ******** **** ******** **  * *   **


PB.25815.1        CCTCCTGTAATAGCCATTCCCTACCTGATCTAAAGAATAGCAATACAGAGCCTCCACCGA        102
PB.13303.1        TCTCCCATAATAGCCATTCCCCACCTGATCTAAAGAATAGCAATACTGAGCCTCCATCGG        152
PB.8185.1         CTACCCATAATAGCCATTCCCCACCTGATCTAAAGAATAGCAATACAGAGCCTCTACCGA        138
Ghrlnc.36832      CTTCCCGTAATAGCCATTCCCCACCTGATTTAAAGAATAGCAATACAGAGCCTCCACCGA        239
Gbalnc.31516      CTTCCCGTAATAGCCATTCCCCACCTGATTTAAAGAATAGCAATACAGAGCCTCCACCGA        228
                     **  ************** ******* ********************* ******* * **


PB.25815.1        ATAAGAAAAAAAAAACATAACCTCCCATTCTTGCGCCTTTACCACTCTTCCTCAGCAAACA        162
PB.13303.1        ATAAGAAAAAAAAACATAA-CCT-CCCATTCTTGCCCTTTACCACTCTTCCTCAGCAAACA        210
PB.8185.1         ATAAGAAAA-AAACATAA-CCT-CCCATTCTTGCCCTTTACCATTCTCCCTCAGCAAAC-        194
Ghrlnc.36832      ATAAGAAAAAAAAACATAA-CCT-CCCATTCTTGCCCTTTACCACTCTCCCTCAGCAAACA        297
Gbalnc.31516      ATAAGAAAAAAAAACATAA-CCT-CCCATTCTTGCCCTTTACCACTCTCCCTCAGCAAACA        286
                  ********* ***    * *** **  *  *   ********* *** ***********


PB.25815.1        CCTCAAGCCACCACACCCCAACCCTATCTCCTAGTTCTCGTTTAGTTATTCTCATCCCAC        222
PB.13303.1        CCTCAAGCCACCACACACCAGCCGTG-----------------------------------        236
PB.8185.1         ACTCAAGCCACCACACCTCAACCTTGTCTCATAGTTCTCGTTTAGTTATTGTTATCCCAG        254
Ghrlnc.36832      CCTCAAGCCACCACACCCCAACCCTGTCTCCTAGTTCTCGTTTAGTTATTCTCATCCCAC        357
Gbalnc.31516      CCTCAAGCCACCACACCCCAACCCTGTCTCCTAGTTCTCGTTTAGTTATTCTCATCCCAC        346
                   ***************  ** ** *


PB.25815.1        AACCATCTTCGACAAAGATCTCGACATTGTAAAAAGCG----------------------        260
PB.13303.1        ------------------------------------------------------------        236
PB.8185.1         GACCATTATAGACAAAGATCTCGACATTGTAAAAAGCTTCCCCAAAGTTGAGACGAGCTC        314
Ghrlnc.36832      GACCATCATCGACAGAGATCTCGACATTATAAAAAGCATCCCCAAAGTTGAGACGAGTAA        417
Gbalnc.31516      GACCATCATCGACAGAGATCTCGACATTATAAAAAGCATCCCCAAAGTTGAGACGAGTAA        406


PB.25815.1        ------------------------------------------------------------        260
PB.13303.1        ------------------------------------------------------------        236
PB.8185.1         GACCTTTGCTTACTGAAGCAATTGAACATCA---AGACTTTGATATGTTGGTGGATCCGA        371
Ghrlnc.36832      G-----------------------------------------------------------        420
Gbalnc.31516      GGTTATTATTTCCCTCAATCTCACCTCCATTGTGAGAATTTCATCTCTTTACTTCTCTGC        466


PB.25815.1        ------------------------------------------------------------        260
PB.13303.1        ------------------------------------------------------------        236
PB.8185.1         GGCTGGAAAAGAACTACGTGGATCACGAAAT------GTTTCGA--------------AT        411
Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      TTGTATTTCACTAGAAAGGGGTTGTGAAAAAAATGAGTTTTCGAAAAAAAATTGGTCAAC        526


PB.25815.1        ------------------------------------------------------------        260
PB.13303.1        ------------------------------------------------------------        236
PB.8185.1         TTGATG------TTAATAATGGTAAACAAAGGGCTACAAGATTTAGTTATGTTGCTTACG        465
Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      TGGTTGATCCGATTATTTTAGGGCAATTTAGGGTTAGAAAGCTAAGCTTGGTTTATTCGA        586
```

```
PB.25815.1        ------------------------------------------------------------        260
PB.13303.1        ------------------------------------------------------------        236
PB.8185.1         T--------TCTCATTATGTATGCCAAAATATTGCAGACTGGATGGCAATCTGTAATGAG        517
Ghrlnc.36832      ------------------------------------------------------------        420
Gbalnc.31516      ATTGTTGGGCATTTCTGTTTATTGTAAGGGATTTCAGGTTGCTTGTCTCAAT----AGTA        642


PB.25815.1        ------------------------------------------------------------        260
PB.13303.1        ------------------------------------------------------------TCT        239
PB.8185.1         AATGAGTGCAAACTTACAGGACCTATTTCTATATGAGGCATTTTTGTATTATAATCATCT        577
Ghrlnc.36832      -------------------GTTGGAATTTGTTGTTTGTGGTAAATGGGTTGAAGGGGTTT        459
Gbalnc.31516      AGAGATT--TCAATTTCAGGTTGGAATTTGTTGTTTGTGGTAAATGGGTTGAAGGGGTTT        700


PB.25815.1        ------------------------------------------------------------        260
PB.13303.1        C------CTAGTTTTCGTTTAGTTATTCTCATC-CCACGACCATCATCGACAGAGATCTC        292
PB.8185.1         -------TCTTCTGGTGGTTAGTTAAAATTTTATGATATATAAAAAATTTATGTTATACT        630
Ghrlnc.36832      TGGATTTTGAGCTTTGAATCAGTTATAGAGTTTTTGAGCAAGAAAAAGAAAAAGAAAATA        519
Gbalnc.31516      TGGATTTTGAGCTTTGAATCAGTTATAGAGTTTTTGAGCAAGAAAAAGAAAAAGAAAATA        760


PB.25815.1        ----------------------TCCCTAAAGTTGAACGAGCTCACATGCTCAAACTTGTG        298
PB.13303.1        GACATTATAAAGCTTCCCTAAAGTTGAGAC----GAG---CTCACATTCTCAAACTTGTG        345
PB.8185.1         AATTTTTTCAATATGAGTGCAATTTTATGTTGTGTGTTTAAGGACTTGTAAGAGATTATT        690
Ghrlnc.36832      GAGGCGGGGGAGATGAGGAAATCGTTTTAC----TGG---CTCACATGCTCAAACTTATG        572
Gbalnc.31516      GAGGCGGGGGAGATGAGGAAATCGTTTTAC----TGG---CTCACATGCTCAAACTTATG        813
                                                          ** *     *  ** *


PB.25815.1        ATACTTTGGAGGACAACAGTGGTGGTCAATCATGCGTGGTCAATCATTTGATGCCCAGCC        358
PB.13303.1        ATACTTTGGAGGACAACAGTGGTGGTCAATCA----------------TGTATGCTCAGCC        390
PB.8185.1         CTCCTTGTTTTGATATC--------ACAGACT---------------ACAATGGTATGGC        727
Ghrlnc.36832      ATACTTTGAAGGGCAACAGTGGTGGTCAATCA----------------TGTATGCTCAGCC        617
Gbalnc.31516      ATACTTTGAAGGGCAACAGTGGTGGTCAATCA----------------TGTATGCTCAGCC        858
                   * ***     *  * *         **  *                  ***    * *


PB.25815.1        CATCACAAGACAATATCATGGACACTGTGGGAGTCATTTGGGTTGACACTGAAGGAAATA        418
PB.13303.1        CATCAGAAGACAATATCATGGACACTGTGGGAGTCATTTGTTTTTAACACTGAAGGAAAT        450
PB.8185.1         TTTGGGGAATCAATTTATGGGTCTTTTCTTAGTTCATTCCTC---------TTTGAGGCT        778
Ghrlnc.36832      TATCAGAAGATAATATCCTGGACACTGTGGGAGTCATTTGTGTTGACACTGAAAGAA-AT        676
Gbalnc.31516      TATCAGAAGATAATATCCTGGACACTGTGGGAGTCATTTGTGTTGACACTGAAAGAA-AT        917
                    *    *   *** *   ** *  *       *****                 *


PB.25815.1        TAGCATCAGGAGCCTCCAGGCAGCGGTATTGCACTGAAGGTCTCTGTTCGTATGGGATTA        478
PB.13303.1        ATAGCATC-----------AAGAGCCTCCAGCGGTGAAGGTCTCCAGTCGTGTGAGATTA        499
PB.8185.1         ATAATTTA--TGAGACACTTTTTCCCACAATTGTGACAGGTCTCTGGTCATGTGGGATTA        836
Ghrlnc.36832      ATAGCATA-GGAGCCTCCAGTGGTGGTATTGTACTGAAGGTCTCTGGTCGTGTGGGATTA        735
Gbalnc.31516      ATAGCATA-GGAGCCTCCAGTGGTGGTATTGTACTGAAGGTCTCTGGTCGTGTGGGATTA        976
                                              *******   ** * ** *****


PB.25815.1        GCAGCAATGTATGGTGCAGGCTGTTGGGGCCTCCTCAAAAGGACCCTTTGGGGCTTCTTT        538
PB.13303.1        GCAACAATGTACGGTGCAGGCTGTTGGG-CCTCCTCAAAAGGACCTTTTGGGGCTCCTTT        558
PB.8185.1         GCAGCAATGTATGGTGCAGGCTGTTGGG-CATCCTCAAAAGGACCTTTTGGGGCTCCTTT        895
Ghrlnc.36832      GCAGCAATGTATGGTGCAGGCTGTTGGG-CCTCCTCAAAAGGACCCTTTGGGGCTCGTTT        794
Gbalnc.31516      GCAGCAATGTATGGTGCAGGCTGTTGGG-CCTCCTCAAAAGGACCCTTTGGGGCTCGTTT       1035
                  *** ******* ***************** * ************** *********  ***


PB.25815.1        CATAGTTGGTTGTTGTGTTAGCGGTGCTGGGAGAATACCTAATGAAAAGATTTGCAGCTC        598
PB.13303.1        CATAGTTGCTTGTTGTATTAGCAGTGCTGGAGAAA-CACTAATGAAAGGATTTGCAGCTC        617
PB.8185.1         CACAGTTGGTTGTTGTGTTAGCGATGCTGGAGAAC-ACCTAATGAAAAGATTTGCAGCTC        954
Ghrlnc.36832      CATAGTTGGTTGTTGTGTTAGCGGTGCTGGAGAAC-ACCTAATGAAAGGATTTTCAGCTC        853
Gbalnc.31516      CATAGTTGGTTGTTGTGTTAGCGGTGCTGGAGAAC-ACCTAATGAAAGGATTTTCAGCTC       1094
                  ** ***** ******* *****  ******   *    ********** ***** ******


PB.25815.1        GGGAGTGCGTGTGTCTCATCGTCACTATAAGATTCTTTTGGATTTATATGCCTAATAGGA        658
PB.13303.1        GGGA-GTGCTGTGTCTCATCGTCACTGTAAGATTCTTTTGGATTTATATGCCTAACAGGA        676
PB.8185.1         GGGA-GTGCTGTGTCTCATCGTACT-GTAAGATTCTTTTGGATTTATATGCCTAACATGA       1012
Ghrlnc.36832      GGGA-GTGCTGTGTCTCATCGTCACTGTAGGATTCTTTTGGATTTATATGACTAACAGGA        912
Gbalnc.31516      GGGA-GTGCTGTGTCTCATCGTCACTGTAGGATTCTTTTGGATTTATATGACTAACAGGA       1153
                  ****     *************     ** ********************* **** * **


PB.25815.1        ATTTGCTCCCTTTACATGAAGAAAGTTTTAGTTATCCTAAATGGACCTTGTTGAGTTAGG        718
PB.13303.1        ATTTGTTCCCTTTACATGAAGAAAGTTTCAGTTATCCTAAATGGACCTTGTTGAGTTAGG        736
PB.8185.1         ATTTGATCCTT--TACATGAGAAAGTTTCAGTTATCCTAAATGGACCTTGTTGAGTTAGG       1070
Ghrlnc.36832      ATTTGTTCCCTTTACATGAAGAAAGTTTTAGTTATCCTAAATGGACCTTGTCGAGTTAGG        972
Gbalnc.31516      ATTTGTTCCCTTTACATGAAGAAAGTTTTAGTTATCCTAAATGGACCTTGTCGAGTTAGG       1213
                  ***** *** *        ********* ********************** ********
```

```
PB.25815.1        TTGTCTCTGCTTGTATCGCTTTCTATTAATACAAAAGTAGTATAATAGGATGGCGATCTT        778
PB.13303.1        TTGTCTCTGCTTTTATCTCTTTCTATTAATACAAAAGTAGTATAGTAGGATAC-GATCTT        795
PB.8185.1         TTGTCTCTGCTTGTATCTCTTTCTATTAATACAAAAGTAGTATAATAGGATAC-GATCTT       1129
Ghrlnc.36832      TTGTCTCTGCTTGTATCTCTTTTTATTAATACAAAAGTAGTATAATAGGATAC-GATCTT       1031
Gbalnc.31516      TTGTCTCTGCTTGTATCTCTTTTTATTAATACAAAAGTAGTATAATAGGATAC-GATCTT       1272
                  ************ **** **** ********************** ******   ******

PB.25815.1        TTGAAACATTAATTATCTACTTGATTCCGAGCATGGGTGTGTTGAAATCGGTAACGGTCT        838
PB.13303.1        TTAAAACATTAATTGTCTACTTGATTCCGAGCATGGGTG--TTGAAATCGGTAACGGTCT        853
PB.8185.1         TTAAAACATTAATTGTCTACTTGATTCAGAGCATGGGTG--TTGAAATTGGTAACGGTCT       1187
Ghrlnc.36832      TTGAAACATTAATTGTCTACTTGATTCTGAGCATGGGTG--TTGAAATCGGTAAGGGTCT       1089
Gbalnc.31516      TTGAAACATTAATTGTCTACTTGATTCTGAGCATGGGTG--TTGAAATCGGTAAGGGTCT       1330
                  ** *********** ************ ***********  ******* ***** *****

PB.25815.1        ATGCTTGGTGAGAACTTAGAAGTGATAAATCATATAATAGAAGTTGAATTTGTTCAATCT        898
PB.13303.1        ATGTTTGGTGAGAACTAGAAGTGATAAATCATATATATAGAAGTTGAATTTGTTCGATCT        913
PB.8185.1         ATGCTTGGTGAGACTA-GAAGTGATAAATCATAT-AATAGAAGTTGAATTTGTTCGATCT       1245
Ghrlnc.36832      ATGTTTGGTGAGAACTAGAAGTGATAAATCATATAA-TAGAAGTTGAATTTGTTCGATCT       1148
Gbalnc.31516      ATGTTTGGTGAGAACTAGAAGTGATAAATCATATAA-TAGAAGTTGAATTTGTTCGATCT       1389
                  *** *********      *      **         ****************** ****

PB.25815.1        TAAATTATTTGCTTAAATTTGAAGCTATAGAAATTGCAGCTGCGTACTCATCCTTGTCTT        958
PB.13303.1        TAAATTATTTGCTTAAATTCGAAGATTTATCATCTTTGATCCCATTTAGAATATTTAAGG        973
PB.8185.1         TAAATTATTTGCTTAAATTCGAAGATTTATCATCTTTGATCCCATTTAGAATATTTAAGG       1305
Ghrlnc.36832      TAAATTATTTGCTTAAATTCGAAGATTTATCATCTTTGATCCCATTTAGAAT--------       1200
Gbalnc.31516      TAAATTATTTGCTTAAATTCGAAGATTTATCATCTTTGATCC------------------       1431
                  ****************** **** * **  *  *

PB.25815.1        TTGGGATAGGATATTT---------------------------------TGGAAGTGGC        984
PB.13303.1        TAAGCTAAAAAGAGAAATGAATGACACAAGTAAATAATTTTG-GCTCCTTTGAAACATAC       1032
PB.8185.1         TAAGCTAAAAGAGAAATG-AAGGACACAAGTAAATAATTTTGGCTACCTTTGAAAAATAC       1364
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431

PB.25815.1        ATAGGAA---------------------------GGCCTAAG------------------       999
PB.13303.1        ATTAGATTCATTGCAAT-----------------------------TTGCATGAAAGT       1061
PB.8185.1         ATTAGATTCATTGCAATTTGCAATACTTGGGGTACTAATAAGGTCATTTTCATGCTTAGT       1424
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431

PB.25815.1        -----GTATGATGCTTGCAATTAAAACATGCATGTTTTTGGAGTAGATGGTATATTCATT       1054
PB.13303.1        TTACAGGCAGGTCCTGCCTCTGCTTGCATGAAAGTTCTTTGCTCCGTTGCTCAAGATAGT       1121
PB.8185.1         TTATAGGCAGGTCCTGCCTCTGCTTGCATGAAAGTTCTTCGCTCTATTGCTCAAGATAGT       1484
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431

PB.25815.1        GATGTAGCAAA---TTATAAGTGTG---TGGTTAAGAT----------------------       1086
PB.13303.1        AATCAAGCTGATACTGATAAAAGTGATGGGATTTTAATCGTGCAAGCGGGTGCTCCTATC       1181
PB.8185.1         AATCAAGCTGATACTGATAAAAGTGCTGGGATTTTAATCGTGCAAGCGGATGCTCCTATT       1544
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431

PB.25815.1        ------------------------------------------ACTGCATTAATTATGTATG       1105
PB.13303.1        AGGGCGAGTTCTCAATTAAACAACAATATATCTTTAAAAAAAATACATTTATCGGATTAG       1241
PB.8185.1         AGGGCGAGATCTCAATTAAACCACAATACATCTTTCG-----------------------       1581
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431

PB.25815.1        GTTATGAAGT---------CCCAATTATTTCCAGCAATGCTTTGACAGCCATTAGAGATG       1156
PB.13303.1        TTTTTATATGTGAGTTTATTGGTTTAGGTTCCAGGAAATCCTCCAAAACTGAAAGCTATA       1301
PB.8185.1         ------------------------------------------------------------       1581
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431

PB.25815.1        AAAATATTT---ATGTA-----CTC------------TCTATCTGTTGTTTATGCTTTTT       1196
PB.13303.1        TAGAAATTGCAGCTGCGTACTCATCCTTGTCTTTTGGGATAGGATATTTTGGAAGTGGCA       1361
PB.8185.1         ------------------------------------------------------------       1581
Ghrlnc.36832      ------------------------------------------------------------       1200
Gbalnc.31516      ------------------------------------------------------------       1431
```

```
PB.25815.1        TTTTCTTGATTCAGGTTTCTATTCTTAGGAGAAGTAAACAACAGAATAGAAGTGGAATCG        1256
PB.13303.1        TGGAACGGCCTAAGGTTTCTATTCTTAGAAAAAGTAAACAGCAGAATAGAAGTGGAATCG        1421
PB.8185.1         ------------------------------------------------------------        1581
Ghrlnc.36832      ------------------------------------------------------------        1200
Gbalnc.31516      ------------------------------------------------------------        1431

PB.25815.1        ATCATTTTGAAGCTCGAGTTGATGTTTCTACATGACTGGTTTTTGTTAACATGTTTTTTT        1316
PB.13303.1        ATCATTTTGAAGCTCAAGTTGATGTTTCTACATGACTGATTTTTGTTTAACCTATTTT--        1479
PB.8185.1         ------------------------------------------------------------        1581
Ghrlnc.36832      ------------------------------------------------------------        1200
Gbalnc.31516      ------------------------------------------------------------        1431

PB.25815.1        TTTAAGGATAAATTATCATATCAAATCAAATTCTCTCCAATTTACTTGGTTTCTTTGGGA        1376
PB.13303.1        TTCAAGGATAAATTACCATATCAA-ATCAAAACTCTCCAATTTACTTAGTTTCTTTGGGA        1538
PB.8185.1         ------------------------------------------------------------        1581
Ghrlnc.36832      ------------------------------------------------------------        1200
Gbalnc.31516      ------------------------------------------------------------        1431

PB.25815.1        GTGTATGTAGTACTATAAAGAGAAAGTAACTTGTCCCCCTTCGAGATTGCCATTTATTGT        1436
PB.13303.1        GTGTATGTAGTACTATAAAAGAAAGTA-ACCTGTCCCCCTTTGAGATTGTCATTTA-ATG        1596
PB.8185.1         ------------------------------------------------------------        1581
Ghrlnc.36832      ------------------------------------------------------------        1200
Gbalnc.31516      ------------------------------------------------------------        1431

PB.25815.1        GTTAATATCGATGAATAAAAGTTAAAGTGATCAAATCGATATGATCTTAACTCTCATC          1494
PB.13303.1        GTTAATATCGATGAATAAAAGTTAAAGTGATCAAATCGATATGATCTTAACCTT----          1650
PB.8185.1         ------------------------------------------------------------        1581
Ghrlnc.36832      ------------------------------------------------------------        1200
Gbalnc.31516      ------------------------------------------------------------        1431
```