Genes regulating gland development in the cotton plant

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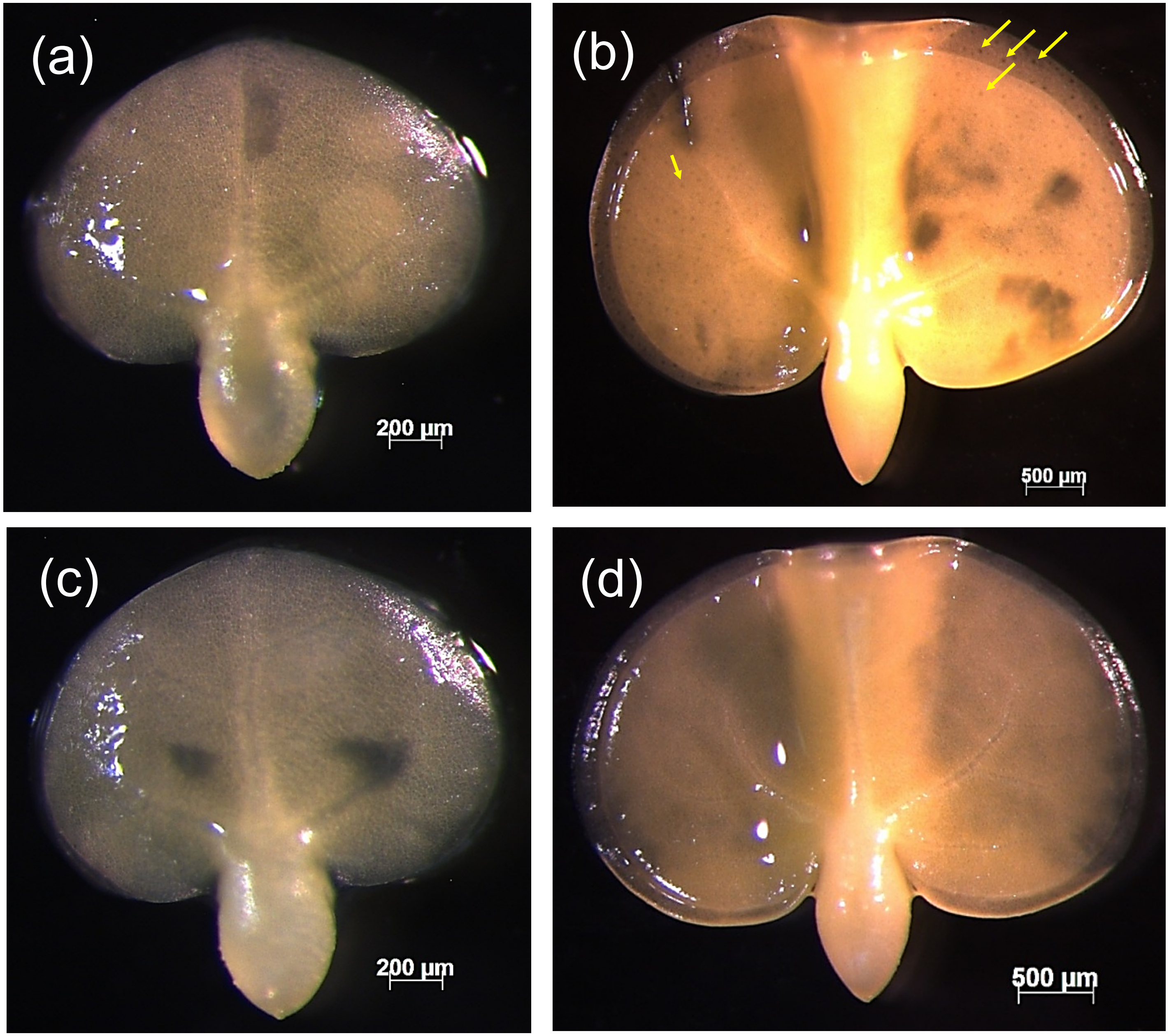


Figure S1 Microscopic images of developing embryos of Stoneville 7A glanded (GL; GVS4) and glandless (gl; GVS5), near-isogenic lines, used for comparative RNA-seq analysis. (**a**) 14-days post-anthesis (dpa) glanded embryo; (**b**) 16-dpa glanded embryo, the arrows indicate glands that are visible microscopically; (**c**) 14-dpa glandless embryo; (**d**) 16-dpa glandless embryo.

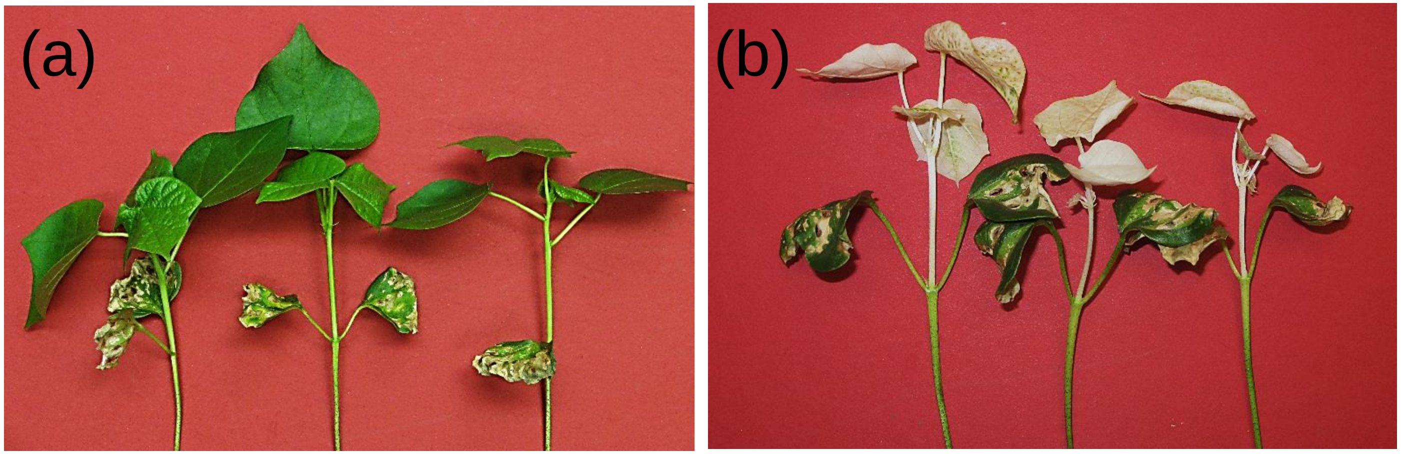


Figure S2 Virus Induced Gene Silencing (VIGS) in cotton. (**a**) empty vector (RNA1 and RNA2) infiltrated plants. (**b**) plants subjected to VIGS-mediated silencing of *GhCLA* gene. The leaves showing albino phenotype indicate the efficacy of the VIGS treatment. The photographs were taken four weeks after infiltration.

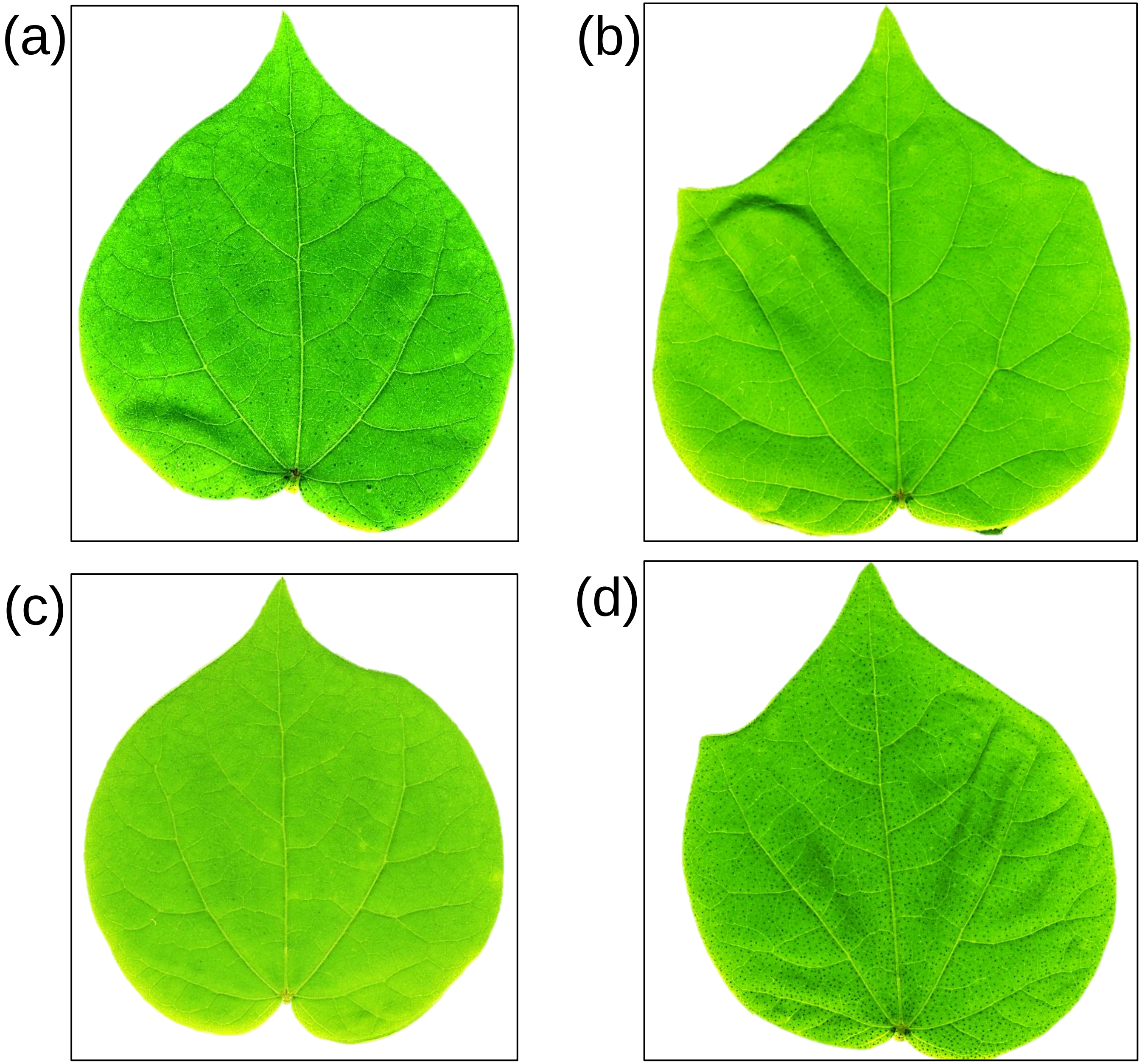
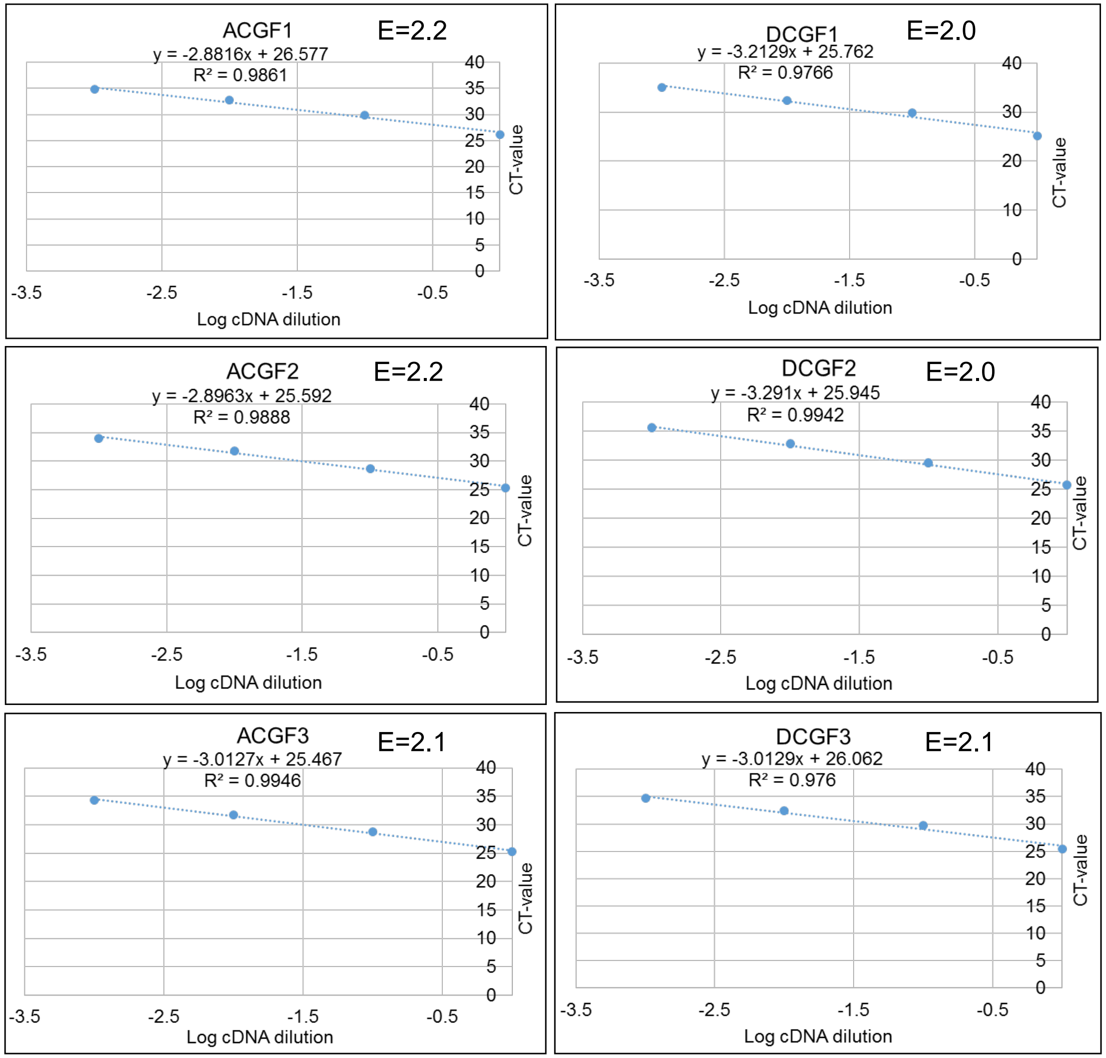


Figure S3 Leaves from plants that had undergone Virus-induced Gene Silencing against *CGF* genes showing the effects on gland formation. (**a**) silencing of *CGF1* gene, (**b**) silencing of *CGF2* gene, (**c**) silencing of *GoPGF* (synonym *CGF3*) gene, (**d**) empty vector control.



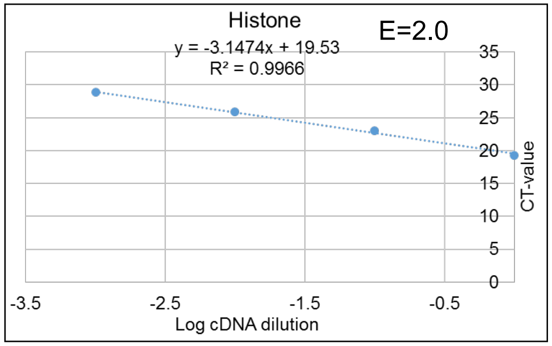
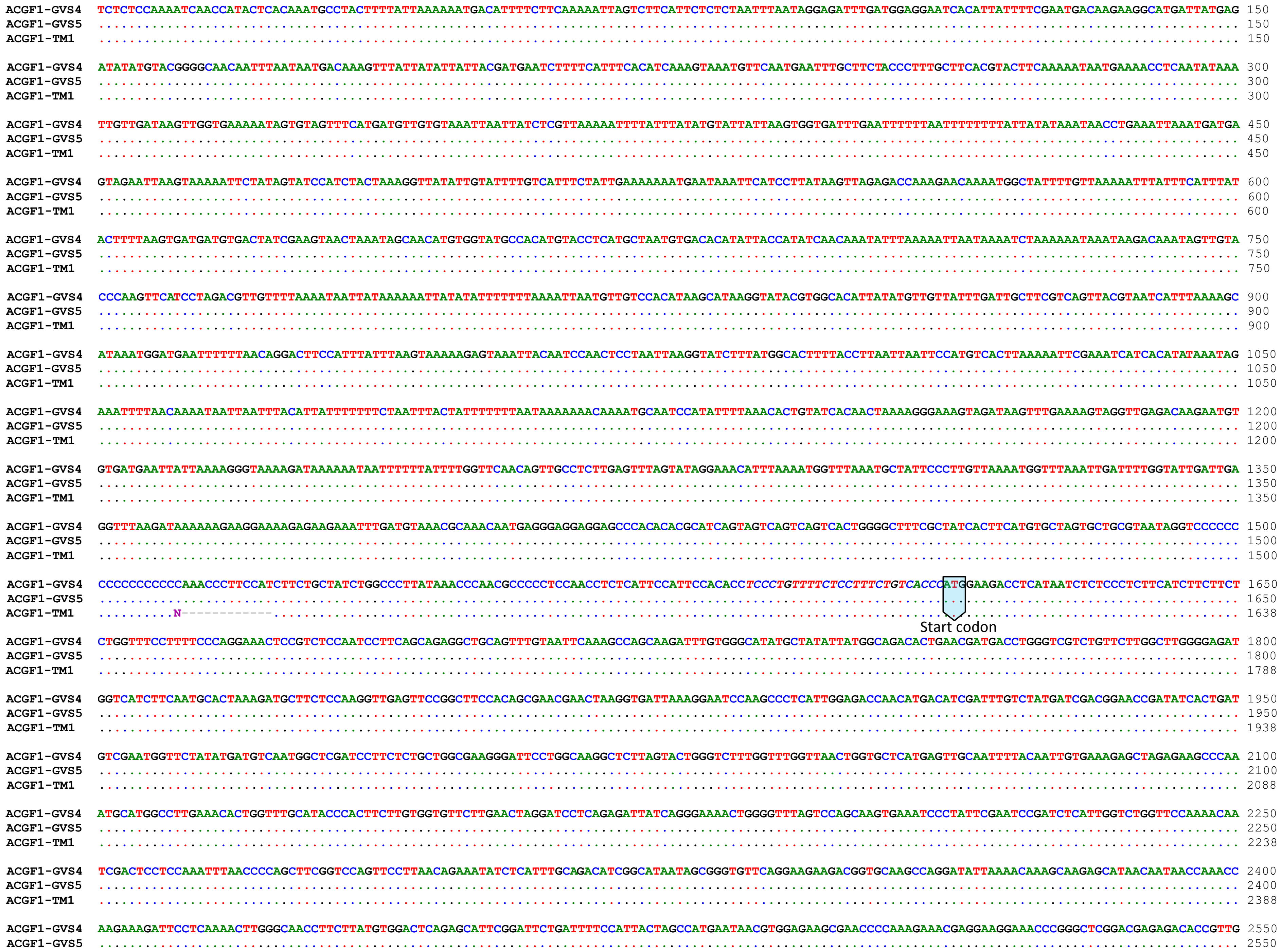


Figure S4 Real-time PCR standard curves representing PCR efficiency for each of the CGF homeologs and Histone gene.



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ACGF1-GVS5  ...................................................................................................................................................... 150
ACGF1-TM1   ...................................................................................................................................................... 150

ACGF1-GVS4  ATATATGTACGGGGCAACAATTTAATAATGACAAAGTTTATTATATTATTACGATGAATCTTTTCATTTCACATCAAAGTAAATGTTCAATGAATTTGCTTCTACCCTTTGCTTCACGTACTTCAAAAATAATGAAAACCTCAATATAAA 300
ACGF1-GVS5  ...................................................................................................................................................... 300
ACGF1-TM1   ...................................................................................................................................................... 300

ACGF1-GVS4  TTGTTGATAAGTTGGTGAAAAATAGTGTAGTTTCATGATGTTGTGTAAATTAATTATCTCGTTAAAAATTTTATTTATATGTATTATTAAGTGGTGATTTGAATTTTTTAATTTTTTTTATTATATAAATAACCTGAAATTAAATGATGA 450
ACGF1-GVS5  ...................................................................................................................................................... 450
ACGF1-TM1   ...................................................................................................................................................... 450

ACGF1-GVS4  GTAGAATTAAGTAAAAATTCTATAGTATCCATCTACTAAAGGTTATATTGTATTTTGTCATTTCTATTGAAAAAAATGAATAAATTCATCCTTATAAGTTAGAGACCAAAGAACAAAATGGCTATTTTGTTAAAAATTTATTTCATTTAT 600
ACGF1-GVS5  ...................................................................................................................................................... 600
ACGF1-TM1   ...................................................................................................................................................... 600

ACGF1-GVS4  ACTTTTAAGTGATGATGTGACTATCGAAGTAACTAAATAGCAACATGTGGTATGCCACATGTACCTCATGCTAATGTGACACATATTACCATATCAACAAATATTTAAAAATTAATAAAATCTAAAAAATAAATAAGACAAATAGTTGTA 750
ACGF1-GVS5  ...................................................................................................................................................... 750
ACGF1-TM1   ...................................................................................................................................................... 750

ACGF1-GVS4  CCCAAGTTCATCCTAGACGTTGTTTTAAAATAATTATAAAAAATTATATATTTTTTTAAAATTAATGTTGTCCACATAAGCATAAGGTATACGTGGCACATTATATGTTGTTATTTGATTGCTTCGTCAGTTACGTAATCATTTAAAAGC 900
ACGF1-GVS5  ...................................................................................................................................................... 900
ACGF1-TM1   ...................................................................................................................................................... 900

ACGF1-GVS4  ATAAATGGATGAATTTTTTAACAGGACTTCCATTTATTTAAGTAAAAAGAGTAAATTACAATCCAACTCCTAATTAAGGTATCTTTATGGCACTTTTACCTTAATTAATTCCATGTCACTTAAAAATTCGAAATCATCACATATAAATAG 1050
ACGF1-GVS5  ...................................................................................................................................................... 1050
ACGF1-TM1   ...................................................................................................................................................... 1050

ACGF1-GVS4  AAATTTTAACAAAATAATTAATTTACATTATTTTTTTCTAATTTACTATTTTTTTAATAAAAAAACAAAATGCAATCCATATTTTAAACACTGTATCACAACTAAAAGGGAAAGTAGATAAGTTTGAAAAGTAGGTTGAGACAAGAATGT 1200
ACGF1-GVS5  ...................................................................................................................................................... 1200
ACGF1-TM1   ...................................................................................................................................................... 1200

ACGF1-GVS4  GTGATGAATTATTAAAAGGGTAAAAGATAAAAAATAATTTTTTATTTTGGTTCAACAGTTGCCTCTTGAGTTTAGTATAGGAAACATTTAAAATGGTTTAAATGCTATTCCCTTGTTAAAATGGTTTAAATTGATTTTGGTATTGATTGA 1350
ACGF1-GVS5  ...................................................................................................................................................... 1350
ACGF1-TM1   ...................................................................................................................................................... 1350

ACGF1-GVS4  GGTTTAAGATAAAAAAGAAGGAAAAGAGAAGAAATTTGATGTAAACGCAAACAATGAGGGAGGAGGAGCCCACACACGCATCAGTAGTCAGTCAGTCACTGGGGCTTTCGCTATCACTTCATGTGCTAGTGCTGCGTAATAGGTCCCCCC 1500
ACGF1-GVS5  ...................................................................................................................................................... 1500
ACGF1-TM1   ...................................................................................................................................................... 1500

ACGF1-GVS4  CCCCCCCCCCAAACCCTTCCATCTTCTGCTATCTGGCCCTTATAAACCCAACGCCCCCTCCAACCTCTCATTCCATTCCACACCTCCCTGTTTTCTCCTTTCTGTCACCCATGGAAGACCTCATAATCTCTCCCTCTTCATCTTCTTCT 1650
ACGF1-GVS5  ...................................................................................................................................................... 1650
ACGF1-TM1   .........N------------................................................................................................................................ 1638

ACGF1-GVS4  CTGGTTTCCTTTTCCCAGGAAACTCCGTCTCCAATCCTTCAGCAGAGGCTGCAGTTTGTAATTCAAAGCCAGCAAGATTTGTGGGCATATGCTATATTATGGCAGACACTGAACGATGACCTGGGTCGTCTGTTCTTGGCTTGGGGAGAT 1800
ACGF1-GVS5  ...................................................................................................................................................... 1800
ACGF1-TM1   ...................................................................................................................................................... 1788

ACGF1-GVS4  GGTCATCTTCAATGCACTAAAGATGCTTCTCCAAGGTTGAGTTCCGGCTTCCACAGCGAACGAACTAAGGTGATTAAAGGAATCCAAGCCCTCATTGGAGACCAACATGACATCGATTTGTCTATGATCGACGGAACCGATATCACTGAT 1950
ACGF1-GVS5  ...................................................................................................................................................... 1950
ACGF1-TM1   ...................................................................................................................................................... 1938

ACGF1-GVS4  GTCGAATGGTTCTATATGATGTCAATGGCTCGATCCTTCTCTGCTGGCGAAGGGATTCCTGGCAAGGCTCTTAGTACTGGGTCTTTGGTTTGGTTAACTGGTGCTCATGAGTTGCAATTTTACAATTGTGAAAGAGCTAGAGAAGCCCAA 2100
ACGF1-GVS5  ...................................................................................................................................................... 2100
ACGF1-TM1   ...................................................................................................................................................... 2088

ACGF1-GVS4  ATGCATGGCCTTGAAACACTGGTTTGCATACCCACTTCTTGTGGTGTTCTTGAACTAGGATCCTCAGAGATTATCAGGGAAAACTGGGGTTTAGTCCAGCAAGTGAAATCCCTATTCGAATCCGATCTCATTGGTCTGGTTCCAAAACAA 2250
ACGF1-GVS5  ...................................................................................................................................................... 2250
ACGF1-TM1   ...................................................................................................................................................... 2238

ACGF1-GVS4  TCGACTCCTCCAAATTTAACCCCAGCTTCGGTCCAGTTCCTTAACAGAAATATCTCATTTGCAGACATCGGCATAATAGCGGGTGTTCAGGAAGAAGACGGTGCAAGCCAGGATATTAAAACAAAGCAAGAGCATAACAATAACCAAACC 2400
ACGF1-GVS5  ...................................................................................................................................................... 2400
ACGF1-TM1   ...................................................................................................................................................... 2388

ACGF1-GVS4  AAGAAAGATTCCTCAAAACTTGGGCAACCTTCTTATGTGGACTCAGAGCATTCGGATTCTGATTTTCCATTACTAGCCATGAATAACGTGGAGAAGCGAACCCCAAAGAAACGAGGAAGGAAACCCGGGCTCGGACGAGAGACACCGTTG 2550
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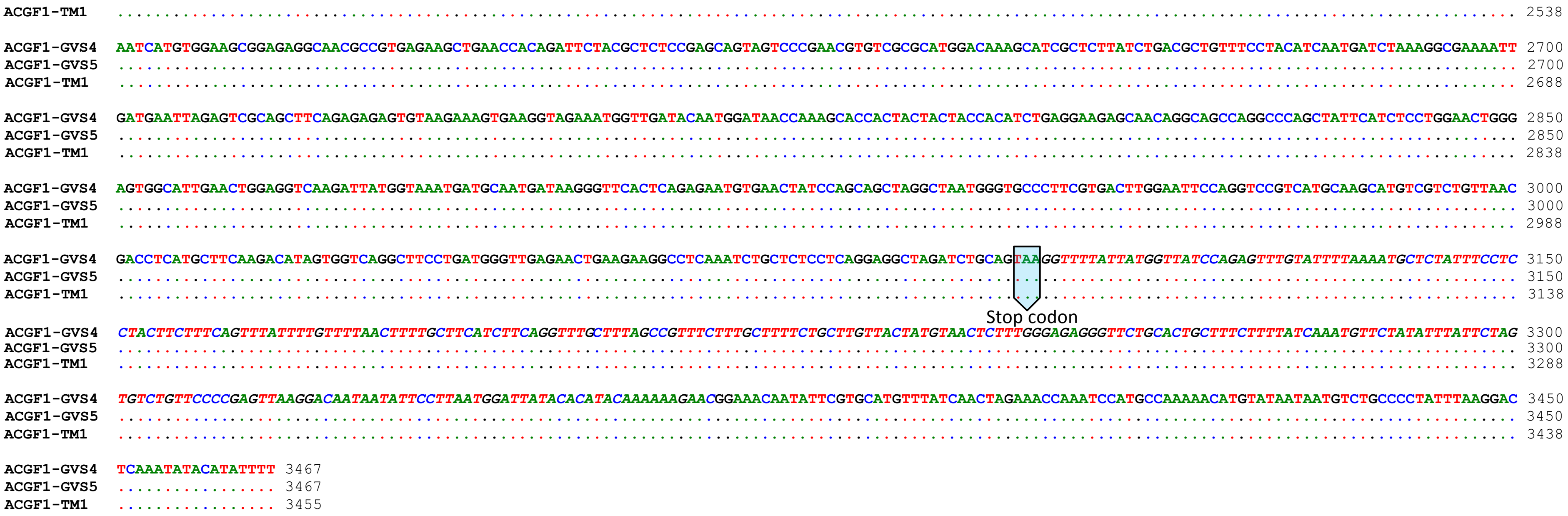

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ACGF1-GVS5  ...................................................................................................................................................... 2700
ACGF1-TM1   ...................................................................................................................................................... 2688

ACGF1-GVS4  GATGAATTAGAGTCGCAGCTTCAGAGAGAGTGTAAGAAAGTGAAGGTAGAAATGGTTGATACAATGGATAACCAAAGCACCACTACTACTACCACATCTGAGGAAGAGCAACAGGCAGCCAGGCCCAGCTATTCATCTCCTGGAACTGGG 2850
ACGF1-GVS5  ...................................................................................................................................................... 2850
ACGF1-TM1   ...................................................................................................................................................... 2838

ACGF1-GVS4  AGTGGCATTGAACTGGAGGTCAAGATTATGGTAAATGATGCAATGATAAGGGTTCACTCAGAGAATGTGAACTATCCAGCAGCTAGGCTAATGGGTGCCCTTCGTGACTTGGAATTCCAGGTCCGTCATGCAAGCATGTCGTCTGTTAAC 3000
ACGF1-GVS5  ...................................................................................................................................................... 3000
ACGF1-TM1   ...................................................................................................................................................... 2988

ACGF1-GVS4  GACCTCATGCTTCAAGACATAGTGGTCAGGCTTCCTGATGGGTTGAGAACTGAAGAAGGCCTCAAATCTGCTCTCCTCAGGAGGCTAGATCTGCAGTAAGGTTTTATTATGGTTATCCAGAGTTTGTATTTTAAAATGCTCTATTTCCTC 3150
ACGF1-GVS5  ...................................................................................................................................................... 3150
ACGF1-TM1   ...................................................................................................................................................... 3138
                                                                                                     Stop codon
ACGF1-GVS4  CTACTTCTTTCAGTTTATTTTGTTTTAACTTTTGCTTCATCTTCAGGTTTGCTTTAGCCGTTTCTTTGCTTTTCTGCTTGTTACTATGTAACTCTTTGGGAGAGGGTTCTGCACTGCTTTCTTTTATCAAATGTTCTATATTTATTCTAG 3300
ACGF1-GVS5  ...................................................................................................................................................... 3300
ACGF1-TM1   ...................................................................................................................................................... 3288

ACGF1-GVS4  TGTCTGTTCCCCGAGTTAAGGACAATAATATTCCTTAATGGATTATACACATACAAAAAAGAACGGAAACAATATTCGTGCATGTTTATCAACTAGAAACCAAATCCATGCCAAAAACATGTATAATAATGTCTGCCCCTATTTAAGGAC 3450
ACGF1-GVS5  ...................................................................................................................................................... 3450
ACGF1-TM1   ...................................................................................................................................................... 3438

ACGF1-GVS4  TCAAATATACATATTTT 3467
ACGF1-GVS5  ................. 3467
ACGF1-TM1   ................. 3455
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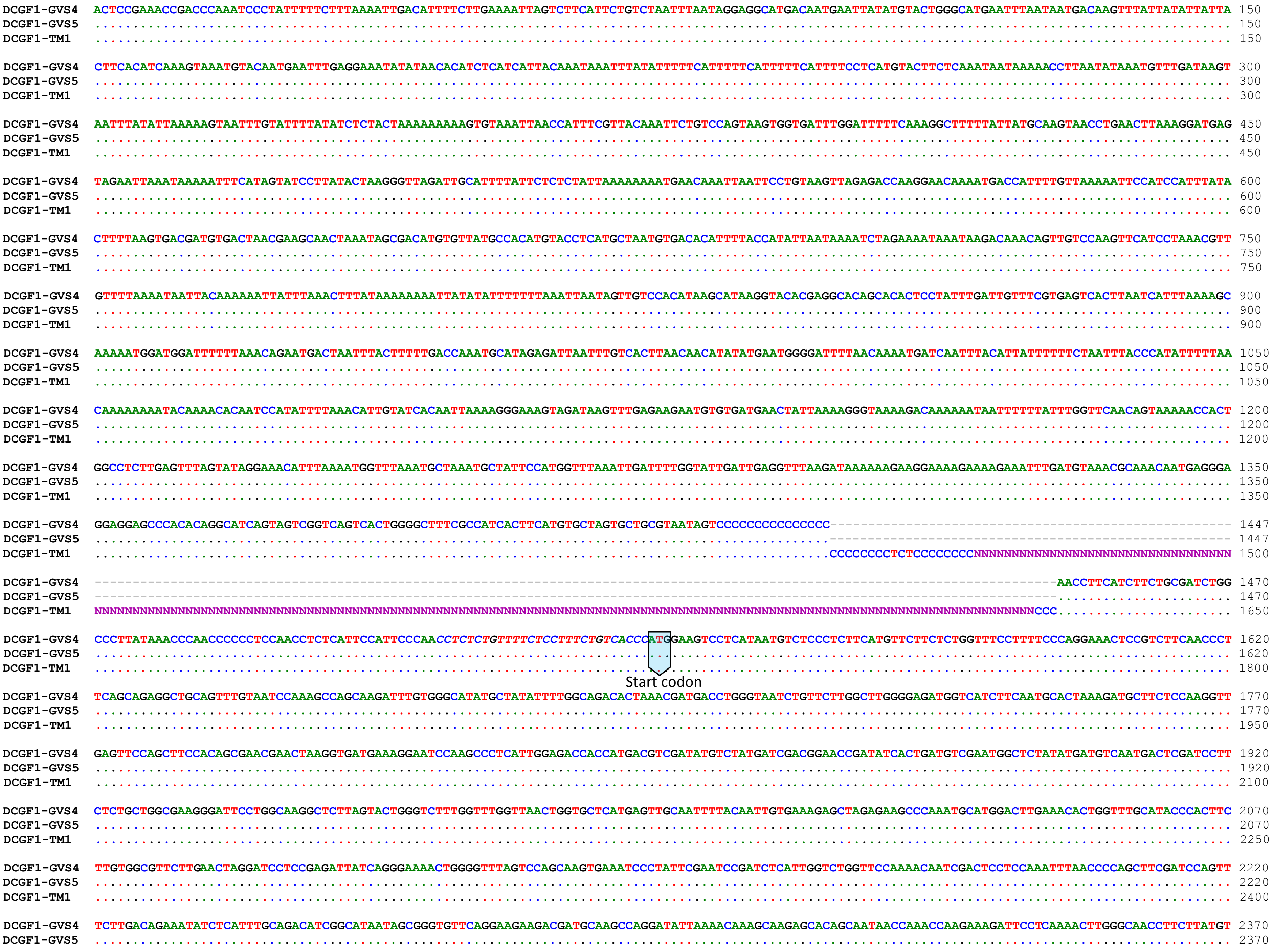
Figure S5 Alignment of A subgenome *CGF1* gene sequences from GVS4 (glanded) and GVS5 (glandless, recessive mutant) near-isogenic lines. Gene sequence of Texas Marker-1 (TM-1, a widely used genetic standard) is also provided for comparison purpose. The ~3.47 kb sequence of *A CGF1* representing the promoter region (~1.59 kb), 5'-UTR (italics), coding region, 3'-UTR (italics), and the terminator is identical between GVS4 and GVS5. Translation initiation codon and stop codon are indicated.



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DCGF1-GVS5  ...................................................................................................................................................... 150
DCGF1-TM1   ...................................................................................................................................................... 150

DCGF1-GVS4  CTTCACATCAAAGTAAATGTACAATGAATTTGAGGAAATATATAACACATCTCATCATTACAAATAAATTTATATTTTTCATTTTTCATTTTTCATTTTCCTCATGTACTTCTCAAATAATAAAAACCTTAATATAAATGTTTGATAAGT 300
DCGF1-GVS5  ...................................................................................................................................................... 300
DCGF1-TM1   ...................................................................................................................................................... 300

DCGF1-GVS4  AATTTATATTAAAAAGTAATTTGTATTTTATATCTCTACTAAAAAAAAAGTGTAAATTAACCATTTCGTTACAAATTCTGTCCAGTAAGTGGTGATTTGGATTTTTCAAAGGCTTTTTATTATGCAAGTAACCTGAACTTAAAGGATGAG 450
DCGF1-GVS5  ...................................................................................................................................................... 450
DCGF1-TM1   ...................................................................................................................................................... 450

DCGF1-GVS4  TAGAATTAAATAAAAATTTCATAGTATCCTTATACTAAGGGTTAGATTGCATTTTATTCTCTCTATTAAAAAAAATGAACAAATTAATTCCTGTAAGTTAGAGACCAAGGAACAAAATGACCATTTTGTTAAAAATTCCATCCATTTATA 600
DCGF1-GVS5  ...................................................................................................................................................... 600
DCGF1-TM1   ...................................................................................................................................................... 600

DCGF1-GVS4  CTTTTAAGTGACGATGTGACTAACGAAGCAACTAAATAGCGACATGTGTTATGCCACATGTACCTCATGCTAATGTGACACATTTTACCATATTAATAAAATCTAGAAAATAAATAAGACAAACAGTTGTCCAAGTTCATCCTAAACGTT 750
DCGF1-GVS5  ...................................................................................................................................................... 750
DCGF1-TM1   ...................................................................................................................................................... 750

DCGF1-GVS4  GTTTTAAAATAATTACAAAAAATTATTTAAACTTTATAAAAAAAATTATATATTTTTTTAAATTAATAGTTGTCCACATAAGCATAAGGTACACGAGGCACAGCACACTCCTATTTGATTGTTTCGTGAGTCACTTAATCATTTAAAAGC 900
DCGF1-GVS5  ...................................................................................................................................................... 900
DCGF1-TM1   ...................................................................................................................................................... 900

DCGF1-GVS4  AAAAATGGATGGATTTTTTAAACAGAATGACTAATTTACTTTTTGACCAAATGCATAGAGATTAATTTGTCACTTAACAACATATATGAATGGGGATTTTAACAAAATGATCAATTTACATTATTTTTTCTAATTTACCCATATTTTTAA 1050
DCGF1-GVS5  ...................................................................................................................................................... 1050
DCGF1-TM1   ...................................................................................................................................................... 1050

DCGF1-GVS4  CAAAAAAAATACAAAACACAATCCATATTTTAAACATTGTATCACAATTAAAAGGGAAAGTAGATAAGTTTGAGAAGAATGTGTGATGAACTATTAAAAGGGTAAAAGACAAAAAATAATTTTTTATTTGGTTCAACAGTAAAAACCACT 1200
DCGF1-GVS5  ...................................................................................................................................................... 1200
DCGF1-TM1   ...................................................................................................................................................... 1200

DCGF1-GVS4  GGCCTCTTGAGTTTAGTATAGGAAACATTTAAAATGGTTTAAATGCTAAATGCTATTCCATGGTTTAAATTGATTTTGGTATTGATTGAGGTTTAAGATAAAAAAGAAGGAAAAGAAAAGAAATTTGATGTAAACGCAAACAATGAGGGA 1350
DCGF1-GVS5  ...................................................................................................................................................... 1350
DCGF1-TM1   ...................................................................................................................................................... 1350

DCGF1-GVS4  GGAGGAGCCCACACAGGCATCAGTAGTCGGTCAGTCACTGGGGCTTTCGCCATCACTTCATGTGCTAGTGCTGCGTAATAGTCCCCCCCCCCCCCCC----------------------------------------------------- 1447
DCGF1-GVS5  .................................................................................................----------------------------------------------------- 1447
DCGF1-TM1   .................................................................................................CCCCCCCCTCTCCCCCCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1500

DCGF1-GVS4  -------------------------------------------------------------------------------------------------------------------------------AACCTTCATCTTCTGCGATCTGG 1470
DCGF1-GVS5  -------------------------------------------------------------------------------------------------------------------------------....................... 1470
DCGF1-TM1   NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCC....................... 1650

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DCGF1-GVS5  ...................................................................................................................................................... 1620
DCGF1-TM1   ...................................................................................................................................................... 1800

DCGF1-GVS4  TCAGCAGAGGCTGCAGTTTGTAATCCAAAGCCAGCAAGATTTGTGGGCATATGCTATATTTTGGCAGACACTAAACGATGACCTGGGTAATCTGTTCTTGGCTTGGGGAGATGGTCATCTTCAATGCACTAAAGATGCTTCTCCAAGGTT 1770
DCGF1-GVS5  ...................................................................................................................................................... 1770
DCGF1-TM1   ...................................................................................................................................................... 1950

DCGF1-GVS4  GAGTTCCAGCTTCCACAGCGAACGAACTAAGGTGATGAAAGGAATCCAAGCCCTCATTGGAGACCACCATGACGTCGATATGTCTATGATCGACGGAACCGATATCACTGATGTCGAATGGCTCTATATGATGTCAATGACTCGATCCTT 1920
DCGF1-GVS5  ...................................................................................................................................................... 1920
DCGF1-TM1   ...................................................................................................................................................... 2100

DCGF1-GVS4  CTCTGCTGGCGAAGGGATTCCTGGCAAGGCTCTTAGTACTGGGTCTTTGGTTTGGTTAACTGGTGCTCATGAGTTGCAATTTTACAATTGTGAAAGAGCTAGAGAAGCCCAAATGCATGGACTTGAAACACTGGTTTGCATACCCACTTC 2070
DCGF1-GVS5  ...................................................................................................................................................... 2070
DCGF1-TM1   ...................................................................................................................................................... 2250

DCGF1-GVS4  TTGTGGCGTTCTTGAACTAGGATCCTCCGAGATTATCAGGGAAAACTGGGGTTTAGTCCAGCAAGTGAAATCCCTATTCGAATCCGATCTCATTGGTCTGGTTCCAAAACAATCGACTCCTCCAAATTTAACCCCAGCTTCGATCCAGTT 2220
DCGF1-GVS5  ...................................................................................................................................................... 2220
DCGF1-TM1   ...................................................................................................................................................... 2400

DCGF1-GVS4  TCTTGACAGAAATATCTCATTTGCAGACATCGGCATAATAGCGGGTGTTCAGGAAGAAGACGATGCAAGCCAGGATATTAAAACAAAGCAAGAGCACAGCAATAACCAAACCAAGAAAGATTCCTCAAAACTTGGGCAACCTTCTTATGT 2370
DCGF1-GVS5  ...................................................................................................................................................... 2370
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DCGF1-TM1    ...................................................................................................................................................... 2550

DCGF1-GVS4  GGACTCAGAGCATTCAGATTCTGATTTTCCATTACTAGCCATGAATAACGTGGAGAAGCGAACCCCAAAGAAACGAGGAAGGAAACCCGGCCTCGGACGAGAGACACCGTTGAACCATGTGGAAGCGGAGAGGCAACGCCGTGAGAAGCT 2520
DCGF1-GVS5  ...................................................................................................................................................... 2520
DCGF1-TM1   ...................................................................................................................................................... 2700

DCGF1-GVS4  GAACCACAGATTCTACGCTCTCCGAGCAGTAGTCCCGAACGTGTCGCGCATGGACAAAGCATCGCTCTTATCTGACGCTGTTTCCTACATCAATGATCTAAAGGCGAAAATTGATGAATTAGAGTCGCAGCTTCAGAGAGAGCGTAAGAA 2670
DCGF1-GVS5  ...................................................................................................................................................... 2670
DCGF1-TM1   ...................................................................................................................................................... 2850

DCGF1-GVS4  AGTGAAGGTAGAAATGGTTGATACAATGGATAACCAAAGCACCACTACTACTACCACATCTGAGGAAGAGCAACAGGCAACCAGGCCCAGCTATTCATCTCCTGGAACTGGGAGTGGCATTGAACTGGAGGTCAAGATTATGGTAAATGA 2820
DCGF1-GVS5  ...................................................................................................................................................... 2820
DCGF1-TM1   ...................................................................................................................................................... 3000

DCGF1-GVS4  TGCAATGATTAGGGTTCACTCAGAGAATGTGAACTATCCAGCAGCTAGGCTAATGGGTGCCCTTCGTGACTTGGAATTCCAGGTCCATCATGCAAGCATGTCGTCTGTTAACGACCTCATGCTTCAGGACATTGTGGTCAGGCTTCCTGA 2970
DCGF1-GVS5  ...................................................................................................................................................... 2970
DCGF1-TM1   ...................................................................................................................................................... 3150

DCGF1-GVS4  TGGGTTGAGAACTGAAGAAGGCCTCAAATCTGCTCTTCTCAGGAGGCTAGATCTGCAGTAAGGTTTAATTATGGTTATCCAGAGTTTGTATTTTAAAATGCTCTATTTCCTCCTACTTATTTTTATCCCTTCCGTTTCTTTCTTCTTTCA 3120
DCGF1-GVS5  ...................................................................................................................................................... 3120
DCGF1-TM1   ...................................................................................................................................................... 3300
                                                                   Stop codon
DCGF1-GVS4  GTTTATTTTGTTTTAACTTTTGCTTCATCTTCAGGTTTGCTTTAGCCGTTTCTTTTCTTTTCTGCTTCTTACTATGTAACTCTTGGGGGAGGGGGTTCTGCGCTGCTTTCTTTTATCAAATGTTCTACATTTATTCTAGCGTCTGTTCCC 3270
DCGF1-GVS5  ...................................................................................................................................................... 3270
DCGF1-TM1   ...................................................................................................................................................... 3450

DCGF1-GVS4  CGAGTTCAGGAAAATCATATTCCTTAATGGATATACACATACAAAAAAGAACGAAAACAATATTCGTGCATGTTTATCAGCTAGAAACAAAGTCCATGCCAAAAACATATATAATCATGTCTGCCCGTTATTAAGGACTCAAATATAGAT 3420
DCGF1-GVS5  ...................................................................................................................................................... 3420
DCGF1-TM1   ...................................................................................................................................................... 3600

DCGF1-GVS4  ATTTTTGTTCTTACATATCAAATCAGATTACTATTGATGAACCTCAAAATCTAGGACTTGAAGCCAACGGAGGATGCTATGGAGACGGGACAATCGTTGCGGAATTGTGCAAAACAGAGGACCGTATACCACTATTTACCACGTATAAAG 3570
DCGF1-GVS5  ...................................................................................................................................................... 3570
DCGF1-TM1   ...................................................................................................................................................... 3750

DCGF1-GVS4  AGAAGCTTATATATATGGTAATTGCTCAGGGATCAGTCCACGAAGAAAACCTATATCTTTTCTTGAAATGAAAAAGCAAAATAAAAAATTTGTGAGAAATATTTGGAAAAAGAAAATTTATAAGTTTTGGACGTTCCTAAATTTGGCTCT 3720
DCGF1-GVS5  ...................................................................................................................................................... 3720
DCGF1-TM1   ...................................................................................................................................................... 3900

DCGF1-GVS4  TAAAAATTTAATGATGACAAATCTCTACAAATTTTTTATATTACAAAAC 3769
DCGF1-GVS5  ................................................. 3769
DCGF1-TM1   ................................................. 3949
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Figure S6 Alignment of D subgenome *CGF1* gene sequences from GVS4 (glanded) and GVS5 (glandless, recessive mutant) near-isogenic lines. Sequence of Texas Marker-1 (TM-1, a widely used genetic standard) is also provided for comparison purpose. The ~3.77 kb sequence of *D CGF1* representing the promoter region (~1.5 kb), 5'-UTR (italics), coding region, 3'-UTR (italics), and the terminator is identical between GVS4 and GVS5. Translation initiation codon and stop codon are indicated.

```
ACGF2-GVS4  CAATATTACCTTGGCTAGTAATGAACTTAATTAGGGCTTCAATCTTCTCTTCAGGCATAAAAGAATGTTTAGGAATTGGTGGATTGTTCAACAAAGTGTTGACTTCAGCAATCACTTGTAGTAACATCCATAGCCTTCAATGAGGTTTCT 150
ACGF2-GVS5  ...................................................................................................................................................... 150
ACGF2-TM1   ...................................................................................................................................................... 150
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  CCCTCTACCTCAGTAGTAACTATAAAAAATATCATTTGCCTTTTCAATAACAGTCACTTTGATGACAATTTTTTTTAGGCAAAGATTAGAGCATCTTTGTAACAAGCTCTAAGTTTGAGTATTCTTCACCAAAGGCAAAAACCTAATTTT 300
ACGF2-GVS5  ...................................................................................................................................................... 300
ACGF2-TM1   ...................................................................................................................................................... 300
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  AAATGTCATAAAGCTTTGCATAGAATTTAGATAAGGTCTTATTGTCATACATTGTTAAAGTTTCAAATCTCGTAGTCAGCATTTGAAGTTTGGATTACTTCACAATTGGTCCTTTATAAGTAGTTTCAAGAATAGTCTAAGCTTCTCTAG 450
ACGF2-GVS5  ...................................................................................................................................................... 450
ACGF2-TM1   ...................................................................................................................................................... 450
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  CAAATGATCATTTAGATATTGACCTAAAATCTTGAGGATTAACTCTAGAGAAAATTACCTTAAAGTCTTAGAGTTTGCATTAGCCAATTTCTCTTCATCATTAGTCTAAGTTAGTTTAGGTTTGAGATTTCTCACACCATATACACTAGT 600
ACGF2-GVS5  ...................................................................................................................................................... 600
ACGF2-TM1   ...................................................................................................................................................... 600
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  TATTAGTAGCTCCTAACCAGTCAAAATTGAGTGCCAAGATTTTTCATCCATGAACTTGATAAAGCATCATCCTTACCTTCTACTAGGCATAGTTTGTACCATCCAACATGGGGGAACTTGGGGCTATTAGTCCTTCCATCTTAATTGCAA 750
ACGF2-GVS5  ...................................................................................................................................................... 750
ACGF2-TM1   ...................................................................................................................................................... 750
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  ATCAAAAATAGGATCACAACTTAGTACATTAAGTGTCTAGCTCTGATACCAAATATGGATTCTTTGAAATTTGCCTTGCAATTTTTCATCCAATTGTAACTAGATGAAGTGACTAATAGTTATGAAACGAGAGATGGAAAAAAAGAGTTT 900
ACGF2-GVS5  ...................................................................................................................................................... 900
ACGF2-TM1   ...................................................................................................................................................... 900
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  GGTTTCGCAGTTCAAAAACTTTCTACATTTGTAGAGCTTTACCCAAAGAGTAATCTACTATAAATCAATATGTATAAGACGTTATTTAAGTTCAACTCACTCACTAAGTTGCAACCCTACTCCTATACTTCAATCTAGATCACTTTCCAA 1050
ACGF2-GVS5  ...................................................................................................................................................... 1050
ACGF2-TM1   ...................................................................................................................................................... 1050
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  CTAAGTATAGCTTAGCTACAAATTGATGTACAAAACAATTTACGTACACAAGTATGCATTGGAAATAAGTTCCTCAATGAACAAGTTAAGTGCTCTCTCTAATGCTCTTAACCTTCAAACAAGTTGCCTCTTAAATAAGTGTAATTAACG 1200
ACGF2-GVS5  ...................................................................................................................................................... 1200
ACGF2-TM1   ...................................................................................................................................................... 1200
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  TGTTAAAATACAATCAATGTAAATATCTAATTCTTCAAAAGGAGCCCTAGAAAATGTCTTCAATAAAGAATATACTTGTAGAGATCTTCTCGATATTAAATTTATTGTAGATCTAATCTCTCAAATAAGAGAACTTCTAATCACATCGAG 1350
ACGF2-GVS5  ...................................................................................................................................................... 1350
ACGF2-TM1   ...................................................................................................................................................... 1350
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  AGTATTCACAAAGTTCATGCTAGACTTGATTCTTACACGATCTGTCTTAATAGATTGCAAAAAACCTTCAAGGATATACATTTAAAAGTTCCAACAATTTTAATTAAAATATGGTAATCACATAAGATATCTTACAATATTTTGCTAGAT 1500
ACGF2-GVS5  ...................................................................................................................................................... 1500
ACGF2-TM1   ...................................................................................................................................................... 1500
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  GTGGTGTTGCCTCACACCCTTAAGAGACCCTAACAATATATGCATAACATATCTTAAAGTATATATTTGACATTGGATTTCCCAAAATTTTCTAAGGTGTCCTATCATGAAATGTTTGGTGCTAGGTGTTTGAAACATGAAAGAAATCAA 1650
ACGF2-GVS5  ...................................................................................................................................................... 1650
ACGF2-TM1   ...................................................................................................................................................... 1650
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  GACTCTTTCGAAGCTGATTGGGGCTTCTTTGTGCATAATAAGTCAATAATTTGATTTTGACCCGAGCAACCGGCAAGTGGGACGACTCCCCCCCAAACATTATTTAAGAAGGTTCCATAATGTTCAAAACTAGCAGCTAGCTTCTCTCTG 1800
ACGF2-GVS5  ...................................................................................................................................................... 1800
ACGF2-TM1   ...................................................................................................................................................... 1800
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

ACGF2-GVS4  TAAGTTTGATTGACGATTTCATGCCACTGTACACACCAAAATTGAATGATTAACACTAATCTTTGATTTCTTTCCCGAGCTTGATCCACACTTAGCCAGCTTCGTCAAAGATGATGAACGTCGACGACGTCCAAGGTGTTAACGATAACA 1950
ACGF2-GVS5  ...................................................................................................................................................... 1950
ACGF2-TM1   ...................................................................................................................................................... 1950
CDS         --------------------------------------------------------------------------------------------------------------........................................ 40
                                                                                                                                      Start codon

ACGF2-GVS4  AGGCCGATCACGAAGATATTCAACTTCCTGGGTTCCGGTTTCATCCTACTGATGAAGAGCTCGTAGGGTTTTATCTTAAACGCAAAGTTGAAAAGAAACCCCTAAGATTCGAGCTTATCAAACAGATTGATATTTACAAATTTGATCCCT 2100
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ACGF2-GVS5  ...................................................................................................................................................... 2100
ACGF2-TM1   ...................................................................................................................................................... 2100
CDS         ...................................................................................................................................................... 190

ACGF2-GVS4  GGGATCTCCCGAgtatgttctcagctcctcctcgttcatttttattatatatgtttgcagatagtgagattccaatattaaatttacggtttgattgaataaagcaggcgtagatcataaaataaaaattaaaaaaatggaaggataatc 2250
ACGF2-GVS5  ...................................................................................................................................................... 2250
ACGF2-TM1   ...................................................................................................................................................... 2250
CDS         ............------------------------------------------------------------------------------------------------------------------------------------------ 202

ACGF2-GVS4  aaaacccaatttcattaaaattttcctattttgtgatgtgaatgaaaatataaacctttattttctttaagttgatgatgtgtgttggtgatgaatgaaatagcagAAGCTAGCATGGTGGGGGGAGGAGGAGAGAGTGAATCGTACTTC 2400
ACGF2-GVS5  ...................................................................................................................................................... 2400
ACGF2-TM1   ...................................................................................................................................................... 2400
CDS         ----------------------------------------------------------------------------------------------------------.......................................... 246

ACGF2-GVS4  TTCTGCAAACGAGGAAGGAAATACAGGAACAGCGTGAGACCAAACAGGGTAACAGGGTCTGGTTTTTGGAAAGCAACCGGCATTGACAAGCCTGTTTATGCTCAAACAGGTGATCATCAAGGCCTTGCCTGCATTGGGTTAAAGAAAACC 2550
ACGF2-GVS5  ...................................................................................................................................................... 2550
ACGF2-TM1   ...................................................................................................................................................... 2550
CDS         ...................................................................................................................................................... 396

ACGF2-GVS4  TTAGTGTATTACCGTGGAGCCGCCGGAAAAGGGACCAAAACCGATTGGATGATGCACGAGTTTCGTCTTCCTTATCCCCATGAGAGTACCACTGTCGTCGCCTTTTCCAATCCCAAATTTGCTGCACAAGAAGCTGtaagtataaaatac 2700
ACGF2-GVS5  ...................................................................................................................................................... 2700
ACGF2-TM1   ...................................................................................................................................................... 2700
CDS         ........................................................................................................................................-------------- 532

ACGF2-GVS4  tgctcaagttgggttaatcaatgttattttatttaagggttaatttcatcagaagtccctgattaacttcaaaatgttctgattgagtcatgataatatcaatattgtatcaatcagttcattttattagcctagcagttaatttaggca 2850
ACGF2-GVS5  ...................................................................................................................................................... 2850
ACGF2-TM1   ...................................................................................................................................................... 2850
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 532

ACGF2-GVS4  ttaaataccaattcagatataatatagaatatatttaaagcacatggatgatcaaactgtaaacacatgtgtacctcttgcttcgacaaattagatattttaaggaaaacaaataatgtcaataaaattaaagaggactatttgtttta 3000
ACGF2-GVS5  ...................................................................................................................................................... 3000
ACGF2-TM1   ...................................................................................................................................................... 3000
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 532

ACGF2-GVS4  aggcatcatattcaaattgtatgtatagtaggcacacacgtatttaccgttcattatatccaaaatgcctgagtacgaaatgcctagagtgataggatgttgatactttgaggatttgattgtaacattttgaagtttttggattgattt 3150
ACGF2-GVS5  ...................................................................................................................................................... 3150
ACGF2-TM1   ...................................................................................................................................................... 3150
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 532

ACGF2-GVS4  agaatttaagcaatagtttaaccctttatgtaaataacttctgatacgataataataattgtctggaattacaggAAGTATGGACCATATGTCGAATCTTCAAGCGAAATTCATCACTCAAAAAACACAAACAAGATTGGAGACAAGTCA 3300
ACGF2-GVS5  ...................................................................................................................................................... 3300
ACGF2-TM1   ...................................................................................................................................................... 3300
CDS         ---------------------------------------------------------------------------........................................................................... 607

ACGF2-GVS4  CAGCAAAACGAGCTTCACTGACAACAGCGCCAACCTCTCAAACATGTAGTGTGGAGTCCAAATCCAACGTTCAAGGGAAGTACATTACCTTCGGTTCTCCATTTATAGTAGATTATCATCATCATAACGACGAGGAGAAGCCATCAATGC 3450
ACGF2-GVS5  ...................................................................................................................................................... 3450
ACGF2-TM1   ...................................................................................................................................................... 3450
CDS         ...................................................................................................................................................... 757

ACGF2-GVS4  TTGTGAATCATCATAATATAAGTGGAAAGAACCAAAGCCAATGGCATGTTACAGATAGAATGAGTAGTGCTGCAATGGCTCAAATACCTTCATCAATGGCGGCATCATCTTCTAGCTTTTCAAACGATGATTTCTTCACTGAGGCCAATT 3600
ACGF2-GVS5  ...................................................................................................................................................... 3600
ACGF2-TM1   ...................................................................................................................................................... 3600
CDS         ...................................................................................................................................................... 907

ACGF2-GVS4  GGGATGAGCTGAAATCAGTTGTGGAGTTTGCTCTTGAACCCTTTCCTATGTAAATATATATAATATGCTTTATAGGGTTGCACTTTTTTTTTTAATTTTGATGATGAGGGAATATTATTAATTAATAATTAGTTGCTAATTTTATATTTA 3750
ACGF2-GVS5  ...................................................................................................................................................... 3750
ACGF2-TM1   ...................................................................................................................................................... 3750
CDS         .....................................................------------------------------------------------------------------------------------------------- 960
                                                         Stop codon

ACGF2-GVS4  ATAATGGAATATTTTATAGAGACTGACATGGATGTACTCCAGTTTTTTTTTCTTTTTTTCTTTTTGTAAGTATCTTTCTTTATTTTTATTTTTTGAAACTTCGTTTTATTTTATTTCTTTTACCTTAATTCAATATTATTATGAATTTGA 3900
ACGF2-GVS5  ...................................................................................................................................................... 3900
ACGF2-TM1   ...................................................................................................................................................... 3900
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 960

ACGF2-GVS4  GAATCTTGGATTTATATTTCATATGCTATATTAATTAATTGGTATTTAATATGATTATATACTAGACAAAAATATATGAATATTAAGTTCACAAGTATTTATAAAAATTCTCAAATTTTAATTTTAAGATTATTTTGTATTTAAATATTT 4050
ACGF2-GVS5  ...................................................................................................................................................... 4050
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ACGF2-TM1    ...................................................................................................................................................... 4050
CDS          ------------------------------------------------------------------------------------------------------------------------------------------------------ 960

ACGF2-GVS4   TTTTAGAAATTTATGATTTTTAATTTTTTTATAGAAATTTATGATTCTTTTTATTGGAATTATAACAAAAATTTATTAATAATTTACTCAAAATGAAGTCATTATATATGGTTTTTTTTCTAATGGTGTATACTAAAATTTATTAATTAT 4200
ACGF2-GVS5   ...................................................................................................................................................... 4200
ACGF2-TM1    ...................................................................................................................................................... 4200
CDS          ------------------------------------------------------------------------------------------------------------------------------------------------------ 960

ACGF2-GVS4   GATTCTATTTTGCATTGATGGATGTAATTTCATCAAAATAATAATTATATATTTTTCTACAAAG 4264
ACGF2-GVS5   ................................................................ 4264
ACGF2-TM1    ................................................................ 4264
CDS          ---------------------------------------------------------------- 960
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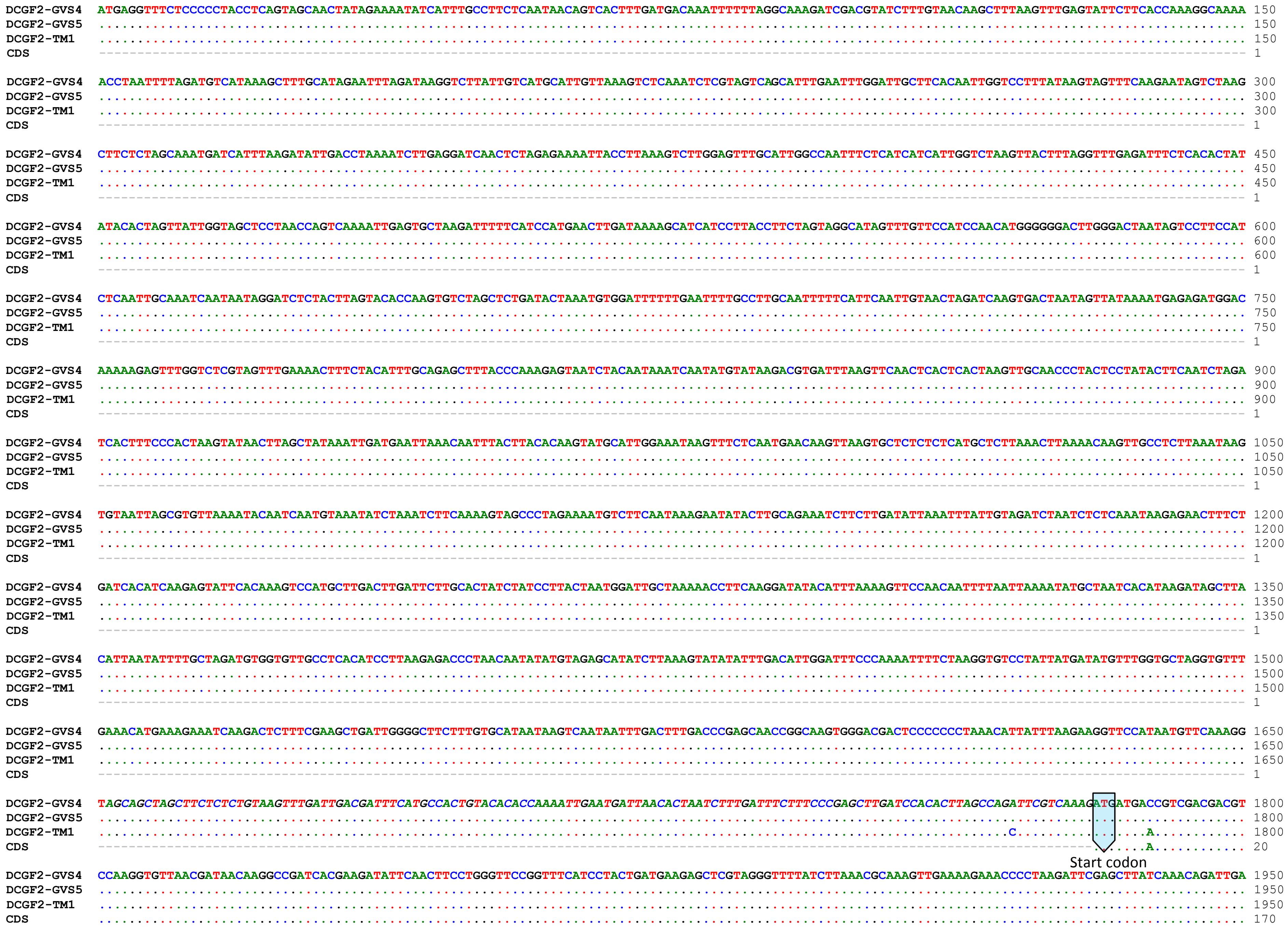
Figure S7 Alignment of A subgenome *CGF2* gene sequences from GVS4 (glanded) and GVS5 (glandless, recessive mutant) near-isogenic lines. Sequence of Texas Marker-1 (TM-1, a widely used genetic standard) is also provided for comparison purpose. The ~4.26 kb sequence of *A CGF2* representing the promoter region (~1.8 kb), 5’-UTR (italics), coding region (including two introns, shown in small case), 3’-UTR (italics), and the terminator is identical between GVS4 and GVS5. Translation initiation codon and stop codon are indicated.



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DCGF2-GVS4  ATGAGGTTTCTCCCCCTACCTCAGTAGCAACTATAGAAAATATCATTTGCCTTCTCAATAACAGTCACTTTGATGACAAATTTTTTAGGCAAAGATCGACGTATCTTTGTAACAAGCTTTAAGTTTGAGTATTCTTCACCAAAGGCAAAA 150
DCGF2-GVS5  ...................................................................................................................................................... 150
DCGF2-TM1   ...................................................................................................................................................... 150
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  ACCTAATTTTAGATGTCATAAAGCTTTGCATAGAATTTAGATAAGGTCTTATTGTCATGCATTGTTAAAGTCTCAAATCTCGTAGTCAGCATTTGAATTTGGATTGCTTCACAATTGGTCCTTTATAAGTAGTTTCAAGAATAGTCTAAG 300
DCGF2-GVS5  ...................................................................................................................................................... 300
DCGF2-TM1   ...................................................................................................................................................... 300
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  CTTCTCTAGCAAATGATCATTTAAGATATTGACCTAAAATCTTGAGGATCAACTCTAGAGAAAATTACCTTAAAGTCTTGGAGTTTGCATTGGCCAATTTCTCATCATCATTGGTCTAAGTTACTTTAGGTTTGAGATTTCTCACACTAT 450
DCGF2-GVS5  ...................................................................................................................................................... 450
DCGF2-TM1   ...................................................................................................................................................... 450
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  ATACACTAGTTATTGGTAGCTCCTAACCAGTCAAAATTGAGTGCTAAGATTTTTCATCCATGAACTTGATAAAAGCATCATCCTTACCTTCTAGTAGGCATAGTTTGTTCCATCCAACATGGGGGGACTTGGGACTAATAGTCCTTCCAT 600
DCGF2-GVS5  ...................................................................................................................................................... 600
DCGF2-TM1   ...................................................................................................................................................... 600
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  CTCAATTGCAAATCAATAATAGGATCTCTACTTAGTACACCAAGTGTCTAGCTCTGATACTAAATGTGGATTTTTTGAATTTTGCCTTGCAATTTTTCATTCAATTGTAACTAGATCAAGTGACTAATAGTTATAAAATGAGAGATGGAC 750
DCGF2-GVS5  ...................................................................................................................................................... 750
DCGF2-TM1   ...................................................................................................................................................... 750
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  AAAAAGAGTTTGGTCTCGTAGTTTGAAAACTTTCTACATTTGCAGAGCTTTACCCAAAGAGTAATCTACAATAAATCAATATGTATAAGACGTGATTTAAGTTCAACTCACTCACTAAGTTGCAACCCTACTCCTATACTTCAATCTAGA 900
DCGF2-GVS5  ...................................................................................................................................................... 900
DCGF2-TM1   ...................................................................................................................................................... 900
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  TCACTTTCCCACTAAGTATAACTTAGCTATAAATTGATGAATTAAACAATTTACTTACACAAGTATGCATTGGAAATAAGTTTCTCAATGAACAAGTTAAGTGCTCTCTCTCATGCTCTTAAACTTAAAACAAGTTGCCTCTTAAATAAG 1050
DCGF2-GVS5  ...................................................................................................................................................... 1050
DCGF2-TM1   ...................................................................................................................................................... 1050
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  TGTAATTAGCGTGTTAAAATACAATCAATGTAAATATCTAAATCTTCAAAAGTAGCCCTAGAAAATGTCTTCAATAAAGAATATACTTGCAGAAATCTTCTTGATATTAAATTTATTGTAGATCTAATCTCTCAAATAAGAGAACTTTCT 1200
DCGF2-GVS5  ...................................................................................................................................................... 1200
DCGF2-TM1   ...................................................................................................................................................... 1200
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  GATCACATCAAGAGTATTCACAAAGTCCATGCTTGACTTGATTCTTGCACTATCTATCCTTACTAATGGATTGCTAAAAACCTTCAAGGATATACATTTAAAAGTTCCAACAATTTTAATTAAAATATGCTAATCACATAAGATAGCTTA 1350
DCGF2-GVS5  ...................................................................................................................................................... 1350
DCGF2-TM1   ...................................................................................................................................................... 1350
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  CATTAATATTTTGCTAGATGTGGTGTTGCCTCACATCCTTAAGAGACCCTAACAATATATGTAGAGCATATCTTAAAGTATATATTTGACATTGGATTTCCCAAAATTTTCTAAGGTGTCCTATTATGATATGTTTGGTGCTAGGTGTTT 1500
DCGF2-GVS5  ...................................................................................................................................................... 1500
DCGF2-TM1   ...................................................................................................................................................... 1500
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  GAAACATGAAAGAAATCAAGACTCTTTCGAAGCTGATTGGGGCTTCTTTGTGCATAATAAGTCAATAATTTGACTTTGACCCGAGCAACCGGCAAGTGGGACGACTCCCCCCCTAAACATTATTTAAGAAGGTTCCATAATGTTCAAAGG 1650
DCGF2-GVS5  ...................................................................................................................................................... 1650
DCGF2-TM1   ...................................................................................................................................................... 1650
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 1

DCGF2-GVS4  TAGCAGCTAGCTTCTCTCTGTAAGTTTGATTGACGATTTCATGCCACTGTACACACCAAAATTGAATGATTAACACTAATCTTTGATTTCTTTCCCGAGCTTGATCCACACTTAGCCAGATTCGTCAAAGATGATGACCGTCGACGACGT 1800
DCGF2-GVS5  ...................................................................................................................................................... 1800
DCGF2-TM1   .......................................................................................................................C.................A............ 1800
CDS         ----------------------------------------------------------------------------------------------------------------------------------.......A............ 20
                                                                                                                                            Start codon
DCGF2-GVS4  CCAAGGTGTTAACGATAACAAGGCCGATCACGAAGATATTCAACTTCCTGGGTTCCGGTTTCATCCTACTGATGAAGAGCTCGTAGGGTTTTATCTTAAACGCAAAGTTGAAAAGAAACCCCTAAGATTCGAGCTTATCAAACAGATTGA 1950
DCGF2-GVS5  ...................................................................................................................................................... 1950
DCGF2-TM1   ...................................................................................................................................................... 1950
CDS         ...................................................................................................................................................... 170
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DCGF2-GVS4  TATTTACAAATTTGATCCCTGGGATCTCCCAAgtatgttctcagctcctcttctttcatttttattatatatgtttgcagatagtgagattccaatattaaatttacggtttgattgaataaagcaggcctagatcataaaatagaaatt 2100
DCGF2-GVS5  ...................................................................................................................................................... 2100
DCGF2-TM1   ...................................................................................................................................................... 2100
CDS         ................................---------------------------------------------------------------------------------------------------------------------- 202

DCGF2-GVS4  ttaaaaatggaaaggataaccaaaacccaatttcattaaagttttccaattttgtggtgtgaatgaaaatataaagctttattttctttaagttgatgatgtgtgttggtgatgaatgaaatagcagAAGCTAGCATGGTGGGGGGAGGA 2250
DCGF2-GVS5  ...................................................................................................................................................... 2250
DCGF2-TM1   ...................................................................................................................................................... 2250
CDS         -------------------------------------------------------------------------------------------------------------------------------....................... 225

DCGF2-GVS4  GGAGAGAGTGAATCGTACTTCTTCTGCAAACGAGGAAGGAAATACAGGAACAGCGTGAGACCAAACAGGGTAACAGGGTCTGGTTTTTGGAAAGCAACCGGCATTGACAAGCCTGTTTATGCTCAAACAGGTGATCATCAAGGCCTTGCC 2400
DCGF2-GVS5  ...................................................................................................................................................... 2400
DCGF2-TM1   ...................................................................................................................................................... 2400
CDS         ...................................................................................................................................................... 375

DCGF2-GVS4  TGCATTGGGTTAAAGAAAACCTTAGTGTATTACCGTGGAGCCGCCGGAAAAGGGACCAAAACCGATTGGATGATGCACGAGTTTCGTCTTCCTTATCCCCATGAGAGCACCACTGTCGTCGCCTTTTCCAATCCCAAATTTGCTGCACAA 2550
DCGF2-GVS5  ...................................................................................................................................................... 2550
DCGF2-TM1   ...................................................................................................................................................... 2550
CDS         ...................................................................................................................................................... 525

DCGF2-GVS4  GAAGCTGtaagtataaaatattgctcaagttgggttaatcaatgttattttgtttaagggttaatttcattagaagtccctgattaacttcaaaatgttctgattgagtcatgataatatcaatatcgtatcaatcagtttattttatta 2700
DCGF2-GVS5  ...................................................................................................................................................... 2700
DCGF2-TM1   ...................................................................................................................................................... 2700
CDS         .......----------------------------------------------------------------------------------------------------------------------------------------------- 532

DCGF2-GVS4  gcctagcagttaatttaggtgttaaataccaattcagatataatatcgagtatatttaaagcacatggatgatcaaactgtaaacacatgtgtacctcttgcttcgtcaacttagatatgatattttaaggaaaacaaataatgtcaata 2850
DCGF2-GVS5  ...................................................................................................................................................... 2850
DCGF2-TM1   ...................................................................................................................................................... 2850
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 532

DCGF2-GVS4  aaatgtaagaggactatttgtttttaaggcatcagattcaaattgtatgtatagtaggcacacacgtatttaccgttcattatatccaaaatgtccgagtacgaaatgcctagagtgataggatgttgatactttgaggatttgattgta 3000
DCGF2-GVS5  ...................................................................................................................................................... 3000
DCGF2-TM1   ...................................................................................................................................................... 3000
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 532

DCGF2-GVS4  acattttgaagtttttggatcgatttagaatttaagcaataatttaacccttcatgtaaataacttgtgatacgatagtaataattatcgggaattacaggAAGTATGGACCATATGTCGAATCTTCAAGCGAAATTCATCACTCAAAAA 3150
DCGF2-GVS5  ...................................................................................................................................................... 3150
DCGF2-TM1   ...................................................................................................................................................... 3150
CDS         -----------------------------------------------------------------------------------------------------................................................. 581

DCGF2-GVS4  ACACAAACAAGATTGGAGACAAATCACAGCAAAACGAGCTTCACTGACAACAGCACCAACCTCCCAAACATGTAGTGTGGAATCCAAATCCAACGTTCAAGGGAAGTACATTACCTTCGGTTCTCCATTTATAGTAGATTATCATCAATA 3300
DCGF2-GVS5  ...................................................................................................................................................... 3300
DCGF2-TM1   ...................................................................................................................................................... 3300
CDS         ...................................................................................................................................................... 731

DCGF2-GVS4  TCATAACGACGAGGAGAAGCCATCAACGCTTGTGAATCATCATAATATCAGTGGAAAGAACCAAAGCCAATGGCATGTTACAGATAGAATGAGTAGTGCTGCAACGGCTCAAATACCTTCATCAATGGCGGCATCATCTTCTAGCTTTTC 3450
DCGF2-GVS5  ...................................................................................................................................................... 3450
DCGF2-TM1   ...................................................................................................................................................... 3450
CDS         ...................................................................................................................................................... 881

DCGF2-GVS4  AAATGATGATTTCTTCACTGAGGCCAATTGGGATGAGCTGAAATCAGTTGTGGAGTTTGCTCTTGAACCCTTTCCTATGTAAATATATATAATATGCTTTATAGGGTTGCACTTTTTTTTTTTAATTTTGATGATGAGGGAATATTATTA 3600
DCGF2-GVS5  ...................................................................................................................................................... 3600
DCGF2-TM1   ...................................................................................................................................................... 3600
CDS         ..................................................................................-------------------------------------------------------------------- 963
                                                                                     Stop codon

DCGF2-GVS4  ATTAATAATTAGTTGCTAATTTTATATTTAATAATGGAATATTTTATAGAGACTGACATGGATGTACTCCAGTTTTTTTTTCTTTTTTTGTAAGTATCTTTCTTTATTTTTATTTTTTGAAACTTCGTTTTATTTTATTTCTTTTACCTT 3750
DCGF2-GVS5  ...................................................................................................................................................... 3750
DCGF2-TM1   ...................................................................................................................................................... 3750
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 963

DCGF2-GVS4  AATTCAATATTATTATGAATTTGAGAATCTTGGATTAATATTTCATATGCTATATTAATTAATTGGTATTTAATATGATTATATACTAGAGACAAATATATGAATATAAAGTTCACAAGTATTTATAAAAATTCTCAAATTTTAATTTTA 3900
DCGF2-GVS5  ...................................................................................................................................................... 3900
DCGF2-TM1   ...................................................................................................................................................... 3900
CDS         ------------------------------------------------------------------------------------------------------------------------------------------------------ 963
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DCGF2-GVS4  AGATTCTTTTGTATTTCAATATTTTTTTTAGAATTTTATGATTTTTAGTTTTTTTTTATAGAAATTTATGATTCTTTTTATTGAAATTATAATGATACGTAACATACGAAAACCATTTTGTTACG 4023
DCGF2-GVS5  ............................................................................................................................. 4023
DCGF2-TM1   ............................................................................................................................. 4023
CDS         ----------------------------------------------------------------------------------------------------------------------------- 963
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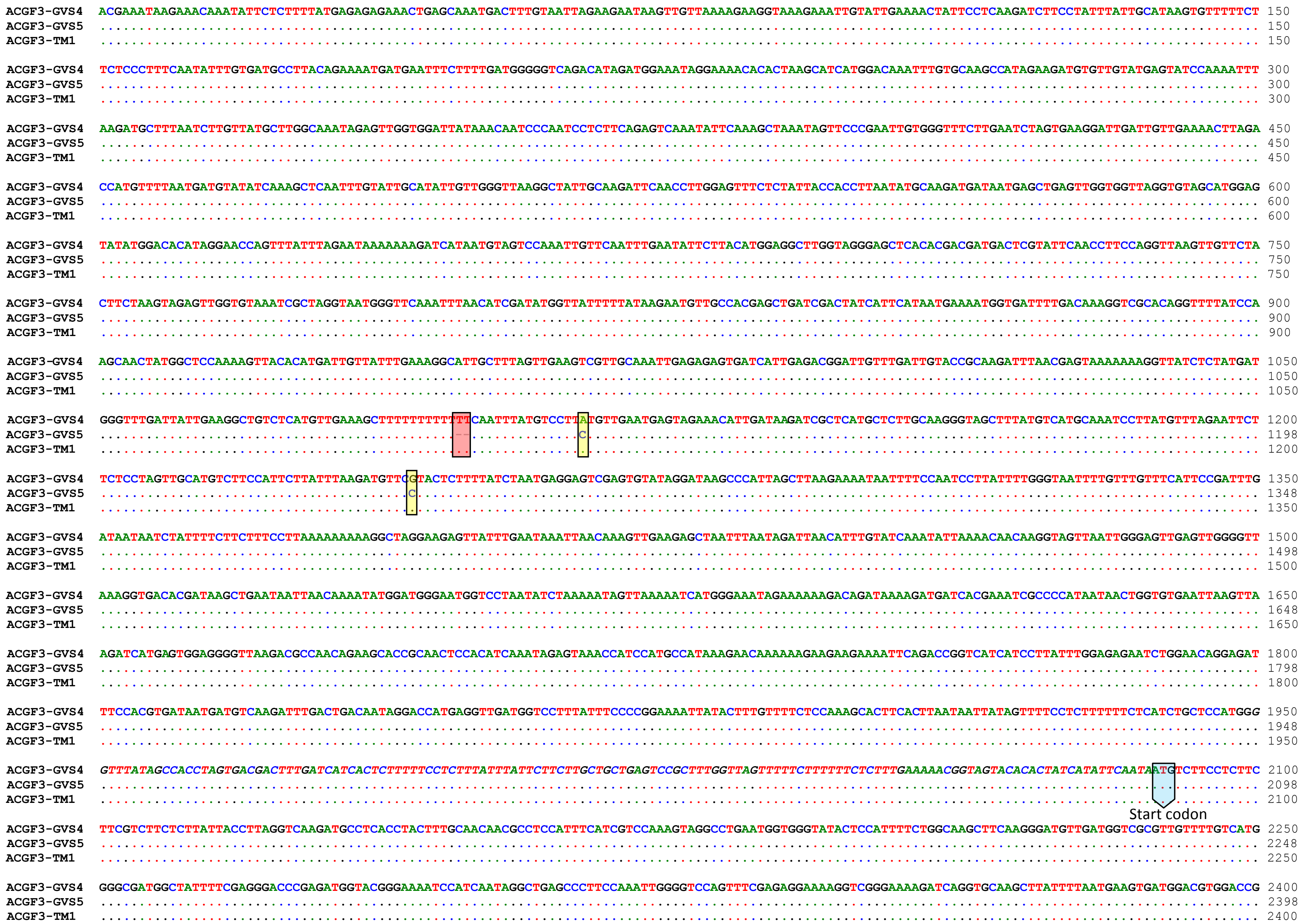
Figure S8 Alignment of D subgenome *CGF2* gene sequences from GVS4 (glanded) and GVS5 (glandless, recessive mutant) near-isogenic lines. Sequence of Texas Marker-1 (TM-1, a widely used genetic standard) is also provided for comparison purpose. The ~4.02 kb sequence of *D CGF2* representing the promoter region (~1.65 kb), 5’-UTR (italics), coding region (including two introns, shown in small case), 3’-UTR (italics), and the terminator is identical between GVS4 and GVS5. Translation initiation codon and stop codon are indicated.


ACGF3-GVS4
ACGF3-GVS5
ACGF3-TM1
150
300
450
600
750
900
1050
1200
1198
1350
1348
1500
1498
1650
1648
1800
1798
1950
1948
2100
2098
2250
2248
2400
2398
Start codon

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ACGF3-GVS4  TATGGTAGATGGCGATGTGACTGATTATGAGTGGTACTATACCGTATC------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  ................................................TGTTGCGGAAAGGATCGATTCGAGAACTCCGATATGACTACAAGTAAATTGACCGGAACGAAAAATAAAGTGAACACAAGGATTTACGTGGTTCGGCTTTAA 2548
ACGF3-TM1   ................................................------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TGCCTACGTCCACGGGCAGAGGCGAAAAGAAATTTCACTATAACAAGATGAAGATTACAAGTGTTTTACACTCAAGACACAACCCGAGAACCTCACAACTCTCAACCCCTATAGAAAACCCGAAAGCTAAAATCCTAGCTTTCAAAGAAC 2698
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  AAGCTTTGCTCTCTCTTGGTTTGGGATGATGAATATGGCTAATGAACCTCTCTATTTATAAGAGAGTTCAAGGACATAATTGTCCAAAACTTTGGCAAAGATTTGTGGTTGAAAATGGACACCAACAACCATCCACTAATCCACTACCAC 2848
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CAACAACCCACTACCAACAACAACAATCCACTACCAATTTTAAGCCATTTCTTAACAAATCTCCACCTTGGCTTGAAATTTACCAAGCTGAACATCATAGTGAATTCCTCGAACTGGATCACCTCTTCCAAACGCCTCTCTGGCGCTAAT 2998
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CAATCCCGAATACCTATCAAGTCCAAGCAATGCTTGAACTTATATGCAGGGATCACCTTAGTTAACATATCTGCAGGATTCTTCTCGGTAGCAACCTTGCTGATAACAATGTCACCTTGCGTAACATGTTCCCGAACAAAATGATATCTG 3148
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  ACATCAATGTGTTTGGTCCGTTCATGAAACATCTGATTTTTAGTCAGATGTATGGCACTCTGGCTATCGCAAAATACAACAGTGAAATCCTGTTGTAAACCCAAACTGCTTACTAGACCTTTCATCCACAATGCTTCTTTCACTGCTTCT 3298
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GCTAACGCCATATATTCCGCCTCAGTCGTAGATAAGGCTACGGTAGACTGTAACACAGCTTTCCAACTAATGGCTCCTCCAGAATAAGTGAAAACATAACCCGTCAGAGATCTTCTTTTGTCCAGATCTCCAGCATAATCAGAGTCCACA 3448
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TAGCCCGTGACACTGCTAGTGCAGTCACTCTGATCATATACCAAGCATAAATCTGCAGAACCTCTCAAGTACCTGAGAATCCATTTCACGGCCTGCCAGTGTTCCTTGCCAGGACAACTCATGTATCTGCTGACCACACTAACTGCATGT 3598
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GAAATGTCTGGACGAGTGCAAACCATTGCATACATCACGCTTCCAACTGCACTCGAGTATGGAATGTGAGACATTTGCTGCTTTTCTTCATCAGATTGTGGTGACAACTCTGCAGAGAGTTTGAAATGTGGTGCCAACGGAGTACTCACA 3748
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GTTTTCGCTTTATCCATGCCGAAGCGTTGAAGAACCTTTTCAATGTAGTTCTTCTGCGACACACGAAGCTTGCCCGCCTTGCGATCTCTGTGAATATCCATGCCCAAAATTTTCTTGGCAGCACCCAGATCCTTCATCTCGAACTCACCA 3898
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CTCAACTGCGACTTTAACTTGTTGATTTCCGACATGTTTTTGGAAGCAATTAACATGTCATCAACATACAGCAACAAATAAATGTGCGAACCATCTGAGAGCTTCCGATGATAGACACAAGCATCATAGTCACATCTTGTGTAACCATGC 4048
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TGAATCATGAAGCTATCAAACCGCTTGTACCACTGCCTTGGGGATTGTTTCAATCCATATAAAGACTTCTTTAATAGACAGACATGGTCTTCTTTACCAGGAACTGTAAAACCCTCTGGTTGACGCATGTAGATTGTTTCCTCGAGCTCA 4198
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CCATGCAAGAACGCCGTTTTTACGTCAAGCTGCTCAAGTTCTAGATCAGACTTGGCCACCATGGCAAGTAATACACGAATGGAAGAATGCTTTACGACTGGGGAGAAAACTTCATTGTAGTCAATCCCCTCTTTCTGAGTGAAGCCTTTA 4348
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GCAACCAATCGTGCCTTGAATCTAGTTGCTTCAACCCCTAGGATGCCTTCCTTTTTCTTGAAGACCCATTTGCAACCAACTATCTTCTGGTTACTTGGCGGCTTAACCAACTCCCAAGTATGGTTCTTGTGAAGAGATTCTATCTCCTCA 4498
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CTCATAGCAATTGCCCACTGTGCCGATTCATCACACGTGACAGCCTCATTATAACTGGAAGGTTCTATACCAATGGACTCCGCCACACTGAGCGCGAAAGACACCAGATTAGCGTAACGCGGATTTGGTTTGATTTGTCTCTTCGTTCTT 4648
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CCAGTGGCAATGCTATATGGTTTTTCTTGAGGTGACTCATCTTCATCGGAATCTTGCACCTCAACTTGATCATCCTGGACTGAAGTACCTTCCGTAGGAATTGGAGCGTCCACCTGACACTCCACCTGCTTCTCAACACCGTGATCTCCC 4798
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
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ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  ATTCTATCTGACTCCTCCTTTTCCCGGGAATTTGTGGTGGATCGAAGCATGGATGACTCATCAAAAGTCACATCTCTGCTGATGATGAACTTGGACGAAACCGGATCAGGACACCACAACCTGTATCCTTTCACCCCTTGGCCGTATCCA 4948
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  AGAAATATGCATTTCTTCGCCCTCGGTTTGAGTTTTCCCTCATTTACATGAGCATACGCAGGGCAGCCAAACACTCTTAAACCAGAGTAATCAGCAGGAGAACCAGACCATACTTCCTCAGGAGTCTTCAGCTCAATAGCTGTTGATGGA 5098
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GATCTGTTAACCAAATAACAAGCAGTATTAACAGCTTCAGCCCAAAATTCTTCACCGAGCCCAGCATTTGATCGCATGCAACGAGCTCGCTCCAAGAGAGTTCTATTCATGCGTTCTGCAACTCCATTTTGTTGTGGTGTTCGACGAACA 5248
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GTGCGGTGTCTCACTATTCCTTCATTTTTGCAGAACTCATTGAATTCACCTGAGCAAAACTCCAAGCCATTATCCGTCCGGAATCGCTTGATCTTCTTTCCTGTTTGATTTTCGATCAAAGCTTTAAATTGCTTGAAGTTGATGAGAACC 5398
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TCATACTTGCTCTTCAGAAAATACACCCAAACCTTTCTCGAGTAATCATCGATAAAGGTAAGCAGATATCTGTAACCACCTTTAGAAATTGTCGGAGAAGGCCCCCAAAGGTCAGAATGGAAGTAATCCACTGTGCCTTTTGTCTTGTGA 5548
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  ATCCCAGTGCTGAACTTTACCCGAGTCTGCTTACCGAAGACGCAGTGCTCACAGAAATTCAACTTTCCTGTACACTGCCCAGACAATAATCCTCGTTTGCTTAGCACCGATAAGCCTCTCTCGCTCATATGCCCGAGCCGCATATGCCAT 5698
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  AACTTCGTGGTGTCAGAATCTAGATCATCTGATGATGACACTCCCGCAACACCTGTAACCGAGGAACCATCGAGGAAGTAAAGGCCCCGCTCCAAATTACCACGTATCACAGTCAAAGCACCCGAGAATACCTTGAGAACTCCACCTTCA 5848
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  GCAGAGTACCGAAAGCCTTTCTTGTCCAACGTACTCAAAGAGATCAAATTTTTCTTCATTTCTGGAATGTGCCGAACATCAGTTAGAGTTCTAACAATACCGTCAAACATCTTTATACGAACTGTGCCAATCCCCATGACTTGACATGCG 5998
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TGGTCATTTCCCATTAGTACTGAACCAGAATGCTTCTCGTATGTTGAGAATGCATCTTTCGAAGTACTTATATGAAATGTAGCTCCCGTATCAAGAATCCATCTCCCACCAGCGTAAGAGTCGGATACTGCAAGAACGATCTCGGCATCA 6148
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CTTGAAGAATCTGCATCAGCTACATTCGCACGATCATTTTGTTGCTCCTGTGATTCTGATTTCTCCTTCCTTTTCGGACAATCTACCTTCATGTGCCCGTACTTCTTACAGTAGTAGCACTGTATTCTCTTCTTGGACTGCGATCTAGGA 6298
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TGGCTTTTACTTGAACTTCCACCCTTTGCCTTGGATCTTCCTCGAGCAACCAAGCCTTCGCCTTCATTGTTTTCGACCACCTTACCAGTGATTTTCTTCCTCAACTCACTGGAACTTAAGGCATTTTTCACCTCCTCTAGAGTCAGGTCA 6448
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TCACGACCGTACATCATTGTATCAACAAAATTCTCATACGAGGGAGGCAAAGAACACAAAACAATTATTGCTTGGTCCTCATCATCGATTTTGTTATCGATATTATTCAAATCCATGATAATGGAATTGAATTTATCCAGGTGCTGGGAA 6598
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  ACAGGTGTACCTTCCTCCATCTTCAGGGCATAGAGTCTTTGCTTGAGGTAGAGCCGGTTCGTCAATGACTTCGTCATGTACTTGCTCTCTAACCGGAGCCACAAACCGGACGCGGTTTTCTCATCCGCTACTTCTCGTAGCACTTCATCT 6748
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CCTAGACATAGCAGAATAGCACTATGTGCTCTTTCTAGCATGTCATCCTTTTGCTCTTCCGAAAGCGTGCTTGGTAATTTATCTTTACCAGACAATGCTTTTAGCAATCCTTGTTGAACCAGCACTGCCCGCATCTTGATGCGCCATAAA 6898
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  CTGAAACTATTTTTCCCGGTAAATTTCTCGACATCATACTTAGTCGATGAAACACTTGTAGCCATAATTTGGAACCTTTGAATGAATGATAATATTTTCTTCCTGATGTGAAAGATCAGACAAAGCTGCAGTCACAGGGCAATTCAGAAA 7048
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  ATATTATCACTCCTTCAACTACGCTCTGATACCAATTTGTTGCGGAAAGGATCGATTCGAGAACTCCGATATGACTACAAGTAAATTGACCGGAACGAAAAATAAAGTGAACACAAGGATTTACGTGGTTCGGCTTTAATGCCTACGTCC 7198
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
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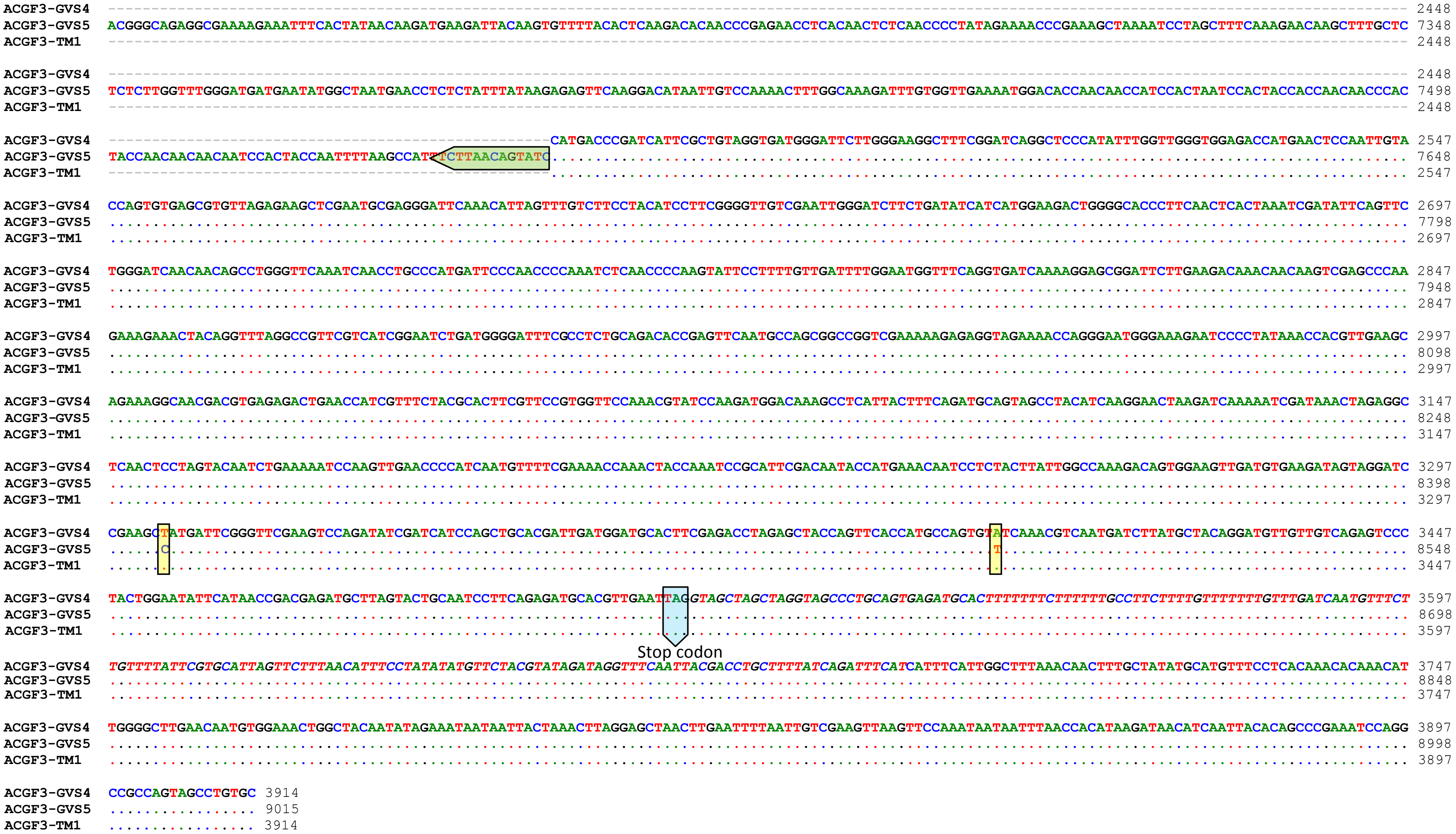

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ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448
ACGF3-GVS5  TCTCTTGGTTTGGGATGATGAATATGGCTAATGAACCTCTCTATTTATAAGAGAGTTCAAGGACATAATTGTCCAAAACTTTGGCAAAGATTTGTGGTTGAAAATGGACACCAACAACCATCCACTAATCCACTACCACCAACAACCCAC 7498
ACGF3-TM1   ------------------------------------------------------------------------------------------------------------------------------------------------------ 2448

ACGF3-GVS4  ---------------------------------------------------CATGACCCGATCATTCGCTGTAGGTGATGGGATTCTTGGGAAGGCTTTCGGATCAGGCTCCCATATTTGGTTGGGTGGAGACCATGAACTCCAATTGTA 2547
ACGF3-GVS5  TACCAACAACAACAATCCACTACCAATTTTAAGCCATTTCTTAACAGTATC................................................................................................... 7648
ACGF3-TM1   ---------------------------------------------------................................................................................................... 2547

ACGF3-GVS4  CCAGTGTGAGCGTGTTAGAGAAGCTCGAATGCGAGGGATTCAAACATTAGTTTGTCTTCCTACATCCTTCGGGGTTGTCGAATTGGGATCTTCTGATATCATCATGGAAGACTGGGGCACCCTTCAACTCACTAAATCGATATTCAGTTC 2697
ACGF3-GVS5  ...................................................................................................................................................... 7798
ACGF3-TM1   ...................................................................................................................................................... 2697

ACGF3-GVS4  TGGGATCAACAACAGCCTGGGTTCAAATCAACCTGCCCATGATTCCCAACCCCAAATCTCAACCCCAAGTATTCCTTTTGTTGATTTTGGAATGGTTTCAGGTGATCAAAAGGAGCGGATTCTTGAAGACAAACAACAAGTCGAGCCCAA 2847
ACGF3-GVS5  ...................................................................................................................................................... 7948
ACGF3-TM1   ...................................................................................................................................................... 2847

ACGF3-GVS4  GAAAGAAACTACAGGTTTAGGCCGTTCGTCATCGGAATCTGATGGGGATTTCGCCTCTGCAGACACCGAGTTCAATGCCAGCGGCCGGTCGAAAAAGAGAGGTAGAAAACCAGGGAATGGGAAAGAATCCCCTATAAACCACGTTGAAGC 2997
ACGF3-GVS5  ...................................................................................................................................................... 8098
ACGF3-TM1   ...................................................................................................................................................... 2997

ACGF3-GVS4  AGAAAGGCAACGACGTGAGAGACTGAACCATCGTTTCTACGCACTTCGTTCCGTGGTTCCAAACGTATCCAAGATGGACAAAGCCTCATTACTTTCAGATGCAGTAGCCTACATCAAGGAACTAAGATCAAAAATCGATAAACTAGAGGC 3147
ACGF3-GVS5  ...................................................................................................................................................... 8248
ACGF3-TM1   ...................................................................................................................................................... 3147

ACGF3-GVS4  TCAACTCCTAGTACAATCTGAAAAATCCAAGTTGAACCCCATCAATGTTTTCGAAAACCAAACTACCAAATCCGCATTCGACAATACCATGAAACAATCCTCTACTTATTGGCCAAAGACAGTGGAAGTTGATGTGAAGATAGTAGGATC 3297
ACGF3-GVS5  ...................................................................................................................................................... 8398
ACGF3-TM1   ...................................................................................................................................................... 3297

ACGF3-GVS4  CGAAGCTATGATTCGGGTTCGAAGTCCAGATATCGATCATCCAGCTGCACGATTGATGGATGCACTTCGAGACCTAGAGCTACCAGTTCACCATGCCAGTGTATCAAACGTCAATGATCTTATGCTACAGGATGTTGTTGTCAGAGTCCC 3447
ACGF3-GVS5  ......C..............................................................................................T................................................ 8548
ACGF3-TM1   ...................................................................................................................................................... 3447

ACGF3-GVS4  TACTGGAATATTCATAACCGACGAGATGCTTAGTACTGCAATCCTTCAGAGATGCACGTTGAATTAGGTAGCTAGCTAGGTAGCCCTGCAGTGAGATGCACTTTTTTTCTTTTTTGCCTTCTTTTGTTTTTTTGTTTGATCAATGTTTCT 3597
ACGF3-GVS5  ...................................................................................................................................................... 8698
ACGF3-TM1   ...................................................................................................................................................... 3597

ACGF3-GVS4  TGTTTTATTCGTGCATTAGTTCTTTAACATTTCCTATATATGTTCTACGTATAGATAGGTTTCAATTACGACCTGCTTTTATCAGATTTCATCATTTCATTGGCTTTAAACAACTTTGCTATATGCATGTTTCCTCACAAACACAAACAT 3747
ACGF3-GVS5  ...................................................................................................................................................... 8848
ACGF3-TM1   ...................................................................................................................................................... 3747

ACGF3-GVS4  TGGGGCTTGAACAATGTGGAAACTGGCTACAATATAGAAATAATAATTACTAAACTTAGGAGCTAACTTGAATTTTAATTGTCGAAGTTAAGTTCCAAATAATAATTTAACCACATAAGATAACATCAATTACACAGCCCGAAATCCAGG 3897
ACGF3-GVS5  ...................................................................................................................................................... 8998
ACGF3-TM1   ...................................................................................................................................................... 3897

ACGF3-GVS4  CCGCCAGTAGCCTGTGC 3914
ACGF3-GVS5  ................. 9015
ACGF3-TM1   ................. 3914
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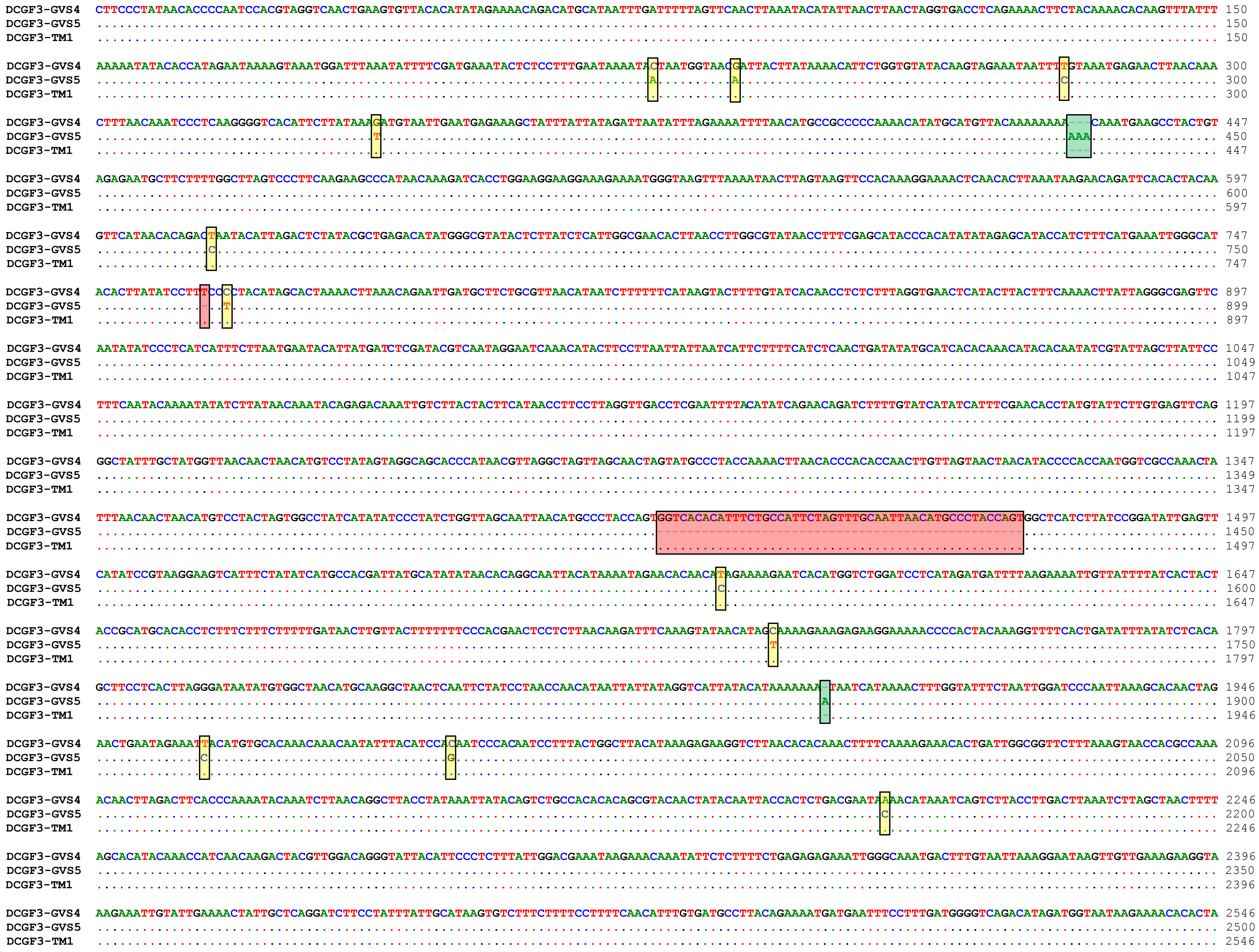
Figure S9 Alignment of A subgenome *GoPGF* (synonym *CGF3*) gene sequences from GVS4 (glanded) and GVS5 (glandless, recessive mutant) near-isogenic lines. Sequence of Texas Marker-1 (TM-1, a widely used genetic standard) is also provided for comparison purpose. The ~1.95 kb sequence upstream of the start codon, representing the promoter region of*A CGF3* in the glandless GVS5, has 2 SNPs (yellow box) and one deletion (2 bp long; red box) compared to the glanded GVS4. In addition, this homeolog in the GVS5 has two SNPs and a ~5.1 kb transposon insertion (indicated with two opposing green arrows) in the coding sequence. 5'-UTR and 3'-UTR are shown in italics. Translation initiation codon and stop codon are indicated.



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DCGF3-GVS5  ...................................................................................................................................................... 150
DCGF3-TM1   ...................................................................................................................................................... 150

DCGF3-GVS4  AAAAATATACACCATAGAATAAAAGTAAATGGATTTAAATATTTTCGATGAAATACTCTCCTTTGAATAAAATACTAATGGTAACGATTACTTATAAAACATTCTGGTGTATACAAGTAGAAATAATTTTGTAAATGAGAACTTAACAAA 300
DCGF3-GVS5  ..........................................................................A..........A...........................................C.................... 300
DCGF3-TM1   ...................................................................................................................................................... 300

DCGF3-GVS4  CTTTAACAAATCCCTCAAGGGGTCACATTCTTATAAAGATGTAATTGAATGAGAAAGCTATTTATTATAGATTAATATTTAGAAAATTTTAACATGCCGCCCCCAAAACATATGCATGTTACAAAAAAAA---CAAATGAAGCCTACTGT 447
DCGF3-GVS5  .....................................T............................................................................................AAA................. 450
DCGF3-TM1   ..................................................................................................................................---................. 447

DCGF3-GVS4  AGAGAATGCTTCTTTTGGCTTAGTCCCTTCAAGAAGCCCATAACAAAGATCACCTGGAAGGAAGGAAAGAAAATGGGTAAGTTTAAAATAACTTAGTAAGTTCCACAAAGGAAAACTCAACACTTAAATAAGAACAGATTCACACTACAA 597
DCGF3-GVS5  ...................................................................................................................................................... 600
DCGF3-TM1   ...................................................................................................................................................... 597

DCGF3-GVS4  GTTCATAACACAGACTAATACATTAGACTCTATACGCTGAGACATATGGGCGTATACTCTTATCTCATTGGCGAACACTTAACCTTGGCGTATAACCTTTCGAGCATACCCACATATATAGAGCATACCATCTTTCATGAAATTGGGCAT 747
DCGF3-GVS5  ...............C...................................................................................................................................... 750
DCGF3-TM1   ...................................................................................................................................................... 747

DCGF3-GVS4  ACACTTATATCCTTTCCCCTACATAGCACTAAAACTTAAACAGAATTGATGCTTCTGCGTTAACATAATCTTTTTTCATAAGTACTTTTGTATCACAACCTCTCTTTAGGTGAACTCATACTTACTTTCAAAACTTATTAGGGCGAGTTC 897
DCGF3-GVS5  ..............-..T.................................................................................................................................... 899
DCGF3-TM1   ...................................................................................................................................................... 897

DCGF3-GVS4  AATATATCCCTCATCATTTCTTAATGAATACATTATGATCTCGATACGTCAATAGGAATCAAACATACTTCCTTAATTATTAATCATTCTTTTCATCTCAACTGATATATGCATCACACAAACATACACAATATCGTATTAGCTTATTCC 1047
DCGF3-GVS5  ...................................................................................................................................................... 1049
DCGF3-TM1   ...................................................................................................................................................... 1047

DCGF3-GVS4  TTTCAATACAAAATATATCTTATAACAAATACAGAGACAAATTGTCTTACTACTTCATAACCTTCCTTAGGTTGACCTCGAATTTTACATATCAGAACAGATCTTTTGTATCATATCATTTCGAACACCTATGTATTCTTGTGAGTTCAG 1197
DCGF3-GVS5  ...................................................................................................................................................... 1199
DCGF3-TM1   ...................................................................................................................................................... 1197

DCGF3-GVS4  GGCTATTTGCTATGGTTAACAACTAACATGTCCTATAGTAGGCAGCACCCATAACGTTAGGCTAGTTAGCAACTAGTATGCCCTACCAAAACTTAACACCCACACCAACTTGTTAGTAACTAACATACCCCACCAATGGTCGCCAAACTA 1347
DCGF3-GVS5  ...................................................................................................................................................... 1349
DCGF3-TM1   ...................................................................................................................................................... 1347

DCGF3-GVS4  TTTAACAACTAACATGTCCTACTAGTGGCCTATCATATATCCCTATCTGGTTAGCAATTAACATGCCCTACCAGTGGTCACACATTTCTGCCATTCTAGTTTGCAATTAACATGCCCTACCAGTGGCTCATCTTATCCGGATATTGAGTT 1497
DCGF3-GVS5  ...........................................................................-------------------------------------------------.......................... 1450
DCGF3-TM1   ...................................................................................................................................................... 1497

DCGF3-GVS4  CATATCCGTAAGGAAGTCATTTCTATATCATGCCACGATTATGCATATATAACACAGGCAATTACATAAAATAGAACACAACATAGAAAAGAATCACATGGTCTGGATCCTCATAGATGATTTTAAGAAAATTGTTATTTTATCACTACT 1647
DCGF3-GVS5  ...................................................................................C.................................................................. 1600
DCGF3-TM1   ...................................................................................................................................................... 1647

DCGF3-GVS4  ACCGCATGCACACCTCTTTCTTTCTTTTTGATAACTTGTTACTTTTTTTCCCACGAACTCCTCTTAACAAGATTTCAAAGTATAACATAGCAAAAGAAAGAGAAGGAAAAACCCCACTACAAAGGTTTTCACTGATATTTATATCTCACA 1797
DCGF3-GVS5  ..........................................................................................T........................................................... 1750
DCGF3-TM1   ...................................................................................................................................................... 1797

DCGF3-GVS4  GCTTCCTCACTTAGGGATAATATGTGGCTAACATGCAAGGCTAACTCAATTCTATCCTAACCAACATAATTATTATAGGTCATTATACATAAAAAAA-TAATCATAAAACTTTGGTATTTCTAATTGGATCCCAATTAAAGCACAACTAG 1946
DCGF3-GVS5  .................................................................................................A.................................................... 1900
DCGF3-TM1   .................................................................................................-.................................................... 1946

DCGF3-GVS4  AACTGAATAGAAATTACATGTGCACAAACAAACAATATTTACATCCACAATCCCACAATCCTTTACTGGCTTACATAAAGAGAAGGTCTTAACACACAAACTTTTCAAAAGAAACACTGATTGGCGGTTCTTTAAAGTAACCACGCCAAA 2096
DCGF3-GVS5  ..............C................................G...................................................................................................... 2050
DCGF3-TM1   ...................................................................................................................................................... 2096

DCGF3-GVS4  ACAACTTAGACTTCACCCAAAATACAAATCTTAACAGGCTTACCTATAAATTATACAGTCTGCCACACACAGCGTACAACTATACAATTACCACTCTGACGAATAAAACATAAATCAGTCTTACCTTGACTTAAATCTTAGCTAACTTTT 2246
DCGF3-GVS5  .........................................................................................................C............................................ 2200
DCGF3-TM1   ...................................................................................................................................................... 2246

DCGF3-GVS4  AGCACATACAAACCATCAACAAGACTACGTTGGACAGGGTATTACATTCCCTCTTTATTGGACGAAATAAGAAACAAATATTCTCTTTTCTGAGAGAGAAATTGGGCAAATGACTTTGTAATTAAAGGAATAAGTTGTTGAAAGAAGGTA 2396
DCGF3-GVS5  ...................................................................................................................................................... 2350
DCGF3-TM1   ...................................................................................................................................................... 2396

DCGF3-GVS4  AAGAAATTGTATTGAAAACTATTGCTCAGGATCTTCCTATTTATTGCATAAGTGTCTTTCTTTTCCTTTTCAACATTTGTGATGCCTTACAGAAAATGATGAATTTCCTTTGATGGGGTCAGACATAGATGGTAATAAGAAAACACACTA 2546
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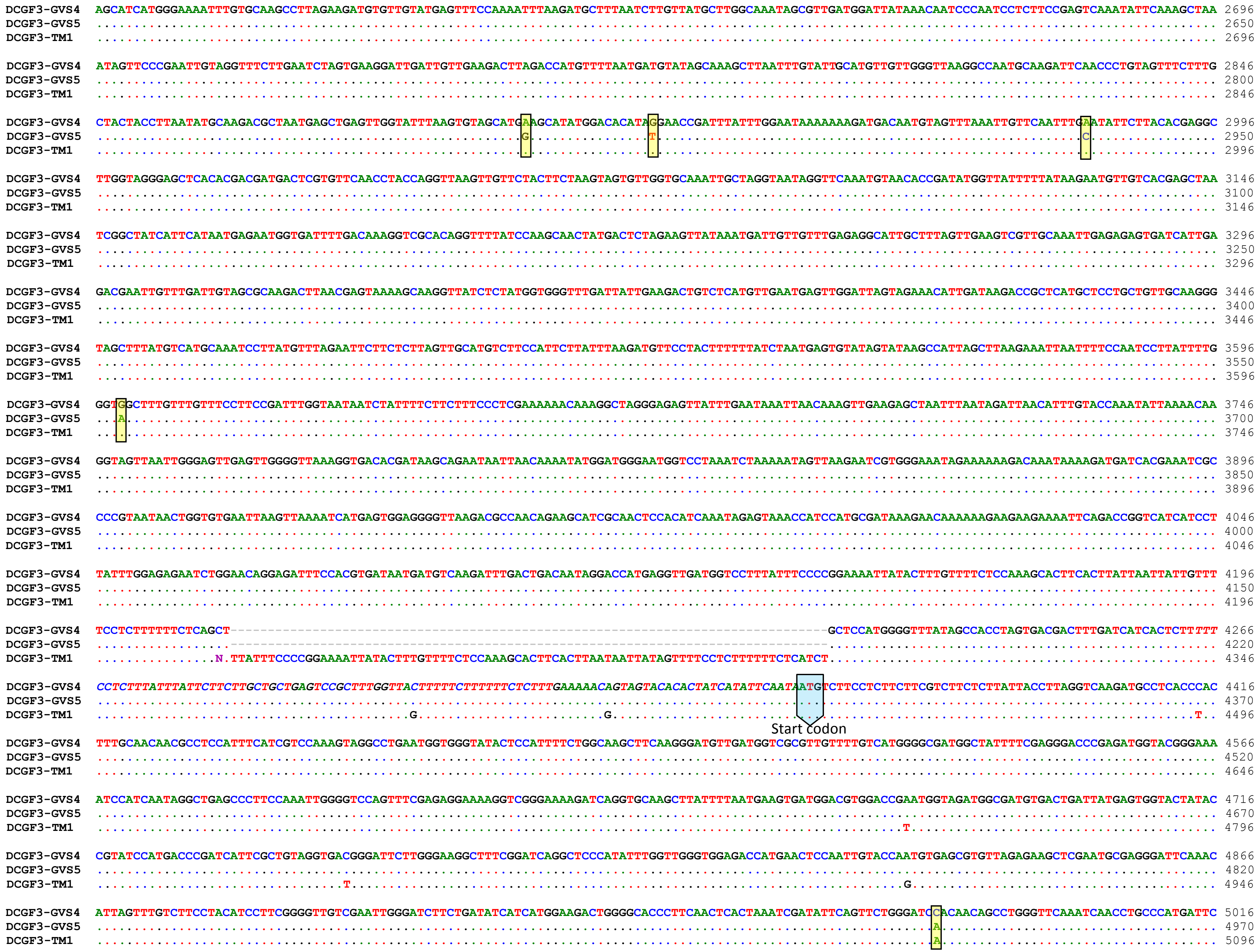

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DCGF3-GVS5  ...................................................................................................................................................... 2650
DCGF3-TM1   ...................................................................................................................................................... 2696

DCGF3-GVS4  ATAGTTCCCGAATTGTAGGTTTCTTGAATCTAGTGAAGGATTGATTGTTGAAGACTTAGACCATGTTTTAATGATGTATAGCAAAGCTTAATTTGTATTGCATGTTGTTGGGTTAAGGCCAATGCAAGATTCAACCCTGTAGTTTCTTTG 2846
DCGF3-GVS5  ...................................................................................................................................................... 2800
DCGF3-TM1   ...................................................................................................................................................... 2846

DCGF3-GVS4  CTACTACCTTAATATGCAAGACGCTAATGAGCTGAGTTGGTATTTAAGTGTAGCATGAAGCATATGGACACATAGGAACCGATTTATTTGGAATAAAAAAAGATGACAATGTAGTTTAAATTGTTCAATTTGAATATTCTTACACGAGGC 2996
DCGF3-GVS5  .........................................................G................T.........................................................C................. 2950
DCGF3-TM1   ...................................................................................................................................................... 2996

DCGF3-GVS4  TTGGTAGGGAGCTCACACGACGATGACTCGTGTTCAACCTACCAGGTTAAGTTGTTCTACTTCTAAGTAGTGTTGGTGCAAATTGCTAGGTAATAGGTTCAAATGTAACACCGATATGGTTATTTTTATAAGAATGTTGTCACGAGCTAA 3146
DCGF3-GVS5  ...................................................................................................................................................... 3100
DCGF3-TM1   ...................................................................................................................................................... 3146

DCGF3-GVS4  TCGGCTATCATTCATAATGAGAATGGTGATTTTGACAAAGGTCGCACAGGTTTTATCCAAGCAACTATGACTCTAGAAGTTATAAATGATTGTTGTTTGAGAGGCATTGCTTTAGTTGAAGTCGTTGCAAATTGAGAGAGTGATCATTGA 3296
DCGF3-GVS5  ...................................................................................................................................................... 3250
DCGF3-TM1   ...................................................................................................................................................... 3296

DCGF3-GVS4  GACGAATTGTTTGATTGTAGCGCAAGACTTAACGAGTAAAAGCAAGGTTATCTCTATGGTGGGTTTGATTATTGAAGACTGTCTCATGTTGAATGAGTTGGATTAGTAGAAACATTGATAAGACCGCTCATGCTCCTGCTGTTGCAAGGG 3446
DCGF3-GVS5  ...................................................................................................................................................... 3400
DCGF3-TM1   ...................................................................................................................................................... 3446

DCGF3-GVS4  TAGCTTTATGTCATGCAAATCCTTATGTTTAGAATTCTTCTCTTAGTTGCATGTCTTCCATTCTTATTTAAGATGTTCCTACTTTTTTATCTAATGAGTGTATAGTATAAGCCATTAGCTTAAGAAATTAATTTTCCAATCCTTATTTTG 3596
DCGF3-GVS5  ...................................................................................................................................................... 3550
DCGF3-TM1   ...................................................................................................................................................... 3596

DCGF3-GVS4  GGTGGCTTTGTTTGTTTCCTTCCGATTTGGTAATAATCTATTTTCTTCTTTCCCTCGAAAAAACAAAGGCTAGGGAGAGTTATTTGAATAAATTAACAAAGTTGAAGAGCTAATTTAATAGATTAACATTTGTACCAAATATTAAAACAA 3746
DCGF3-GVS5  ...A.................................................................................................................................................. 3700
DCGF3-TM1   ...................................................................................................................................................... 3746

DCGF3-GVS4  GGTAGTTAATTGGGAGTTGAGTTGGGGTTAAAGGTGACACGATAAGCAGAATAATTAACAAAATATGGATGGGAATGGTCCTAAATCTAAAAATAGTTAAGAATCGTGGGAAATAGAAAAAAGACAAATAAAAGATGATCACGAAATCGC 3896
DCGF3-GVS5  ...................................................................................................................................................... 3850
DCGF3-TM1   ...................................................................................................................................................... 3896

DCGF3-GVS4  CCCGTAATAACTGGTGTGAATTAAGTTAAAATCATGAGTGGAGGGGTTAAGACGCCAACAGAAGCATCGCAACTCCACATCAAATAGAGTAAACCATCCATGCGATAAAGAACAAAAAAGAAGAAGAAAATTCAGACCGGTCATCATCCT 4046
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DCGF3-GVS5  ...................................................................................................................................................... 4150
DCGF3-TM1   ...................................................................................................................................................... 4196

DCGF3-GVS4  TCCTCTTTTTTCTCAGCT--------------------------------------------------------------------------------GCTCCATGGGGTTTATAGCCACCTAGTGACGACTTTGATCATCACTCTTTTT 4266
DCGF3-GVS5  ..................--------------------------------------------------------------------------------.................................................... 4220
DCGF3-TM1   ................N.TTATTTCCCCGGAAAATTATACTTTGTTTTCTCCAAAGCACTTCACTTAATAATTATAGTTTTCCTCTTTTTTCTCATCT.................................................... 4346

DCGF3-GVS4  CCTCTTTATTTATTCTTCTTGCTGCTGAGTCCGCTTTGGTTACTTTTTCTTTTTTCTCTTTGAAAAACAGTAGTACACACTATCATATTCAATAATGTCTTCCTCTTCTTCGTCTTCTCTTATTACCTTAGGTCAAGATGCCTCACCCAC 4416
DCGF3-GVS5  ...................................................................................................................................................... 4370
DCGF3-TM1   ..........................................G.........................G..............................................................................T.. 4496

DCGF3-GVS4  TTTGCAACAACGCCTCCATTTCATCGTCCAAAGTAGGCCTGAATGGTGGGTATACTCCATTTTCTGGCAAGCTTCAAGGGATGTTGATGGTCGCGTTGTTTTGTCATGGGGCGATGGCTATTTTCGAGGGACCCGAGATGGTACGGGAAA 4566
DCGF3-GVS5  ...................................................................................................................................................... 4520
DCGF3-TM1   ...................................................................................................................................................... 4646

DCGF3-GVS4  ATCCATCAATAGGCTGAGCCCTTCCAAATTGGGGTCCAGTTTCGAGAGGAAAAGGTCGGGAAAAGATCAGGTGCAAGCTTATTTTAATGAAGTGATGGACGTGGACCGAATGGTAGATGGCGATGTGACTGATTATGAGTGGTACTATAC 4716
DCGF3-GVS5  ...................................................................................................................................................... 4670
DCGF3-TM1   ............................................................................................................T......................................... 4796

DCGF3-GVS4  CGTATCCATGACCCGATCATTCGCTGTAGGTGACGGGATTCTTGGGAAGGCTTTCGGATCAGGCTCCCATATTTGGTTGGGTGGAGACCATGAACTCCAATTGTACCAATGTGAGCGTGTTAGAGAAGCTCGAATGCGAGGGATTCAAAC 4866
DCGF3-GVS5  ...................................................................................................................................................... 4820
DCGF3-TM1   .................................T..........................................................................G......................................... 4946

DCGF3-GVS4  ATTAGTTTGTCTTCCTACATCCTTCGGGGTTGTCGAATTGGGATCTTCTGATATCATCATGGAAGACTGGGGCACCCTTCAACTCACTAAATCGATATTCAGTTCTGGGATCCACAACAGCCTGGGTTCAAATCAACCTGCCCATGATTC 5016
DCGF3-GVS5  ................................................................................................................A..................................... 4970
DCGF3-TM1   ................................................................................................................A..................................... 5096
```

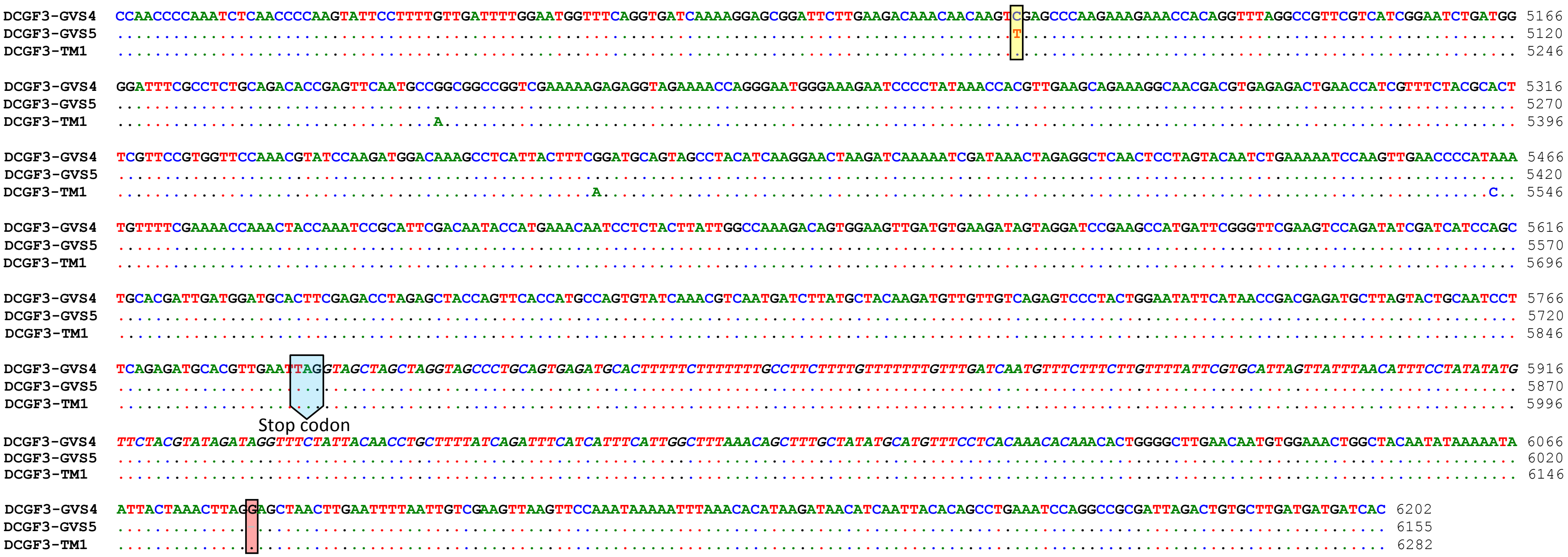

Figure S10 Alignment of D subgenome *GoPGF* (synonym *CGF3*) gene sequences from GVS4 (glanded) and GVS5 (glandless, recessive mutant) near-isogenic lines. Sequence of Texas Marker-1 (TM-1, a widely used genetic standard) is also provided for comparison purpose. The ~4.2 kb sequence upstream of the start codon, representing the promoter region of*D CGF3* in the glandless GVS5, has 15 SNPs (yellow box), two deletions (1 and 49 bp long; red box), and two insertions (1 and 3 bp; green box) compared to the glanded GVS4. In addition, the GVS5 has two SNPs in the coding sequence and one base pair deletion in the terminator. 5'-UTR and 3'-UTR are shown in italics. Translation initiation codon and stop codon are indicated.

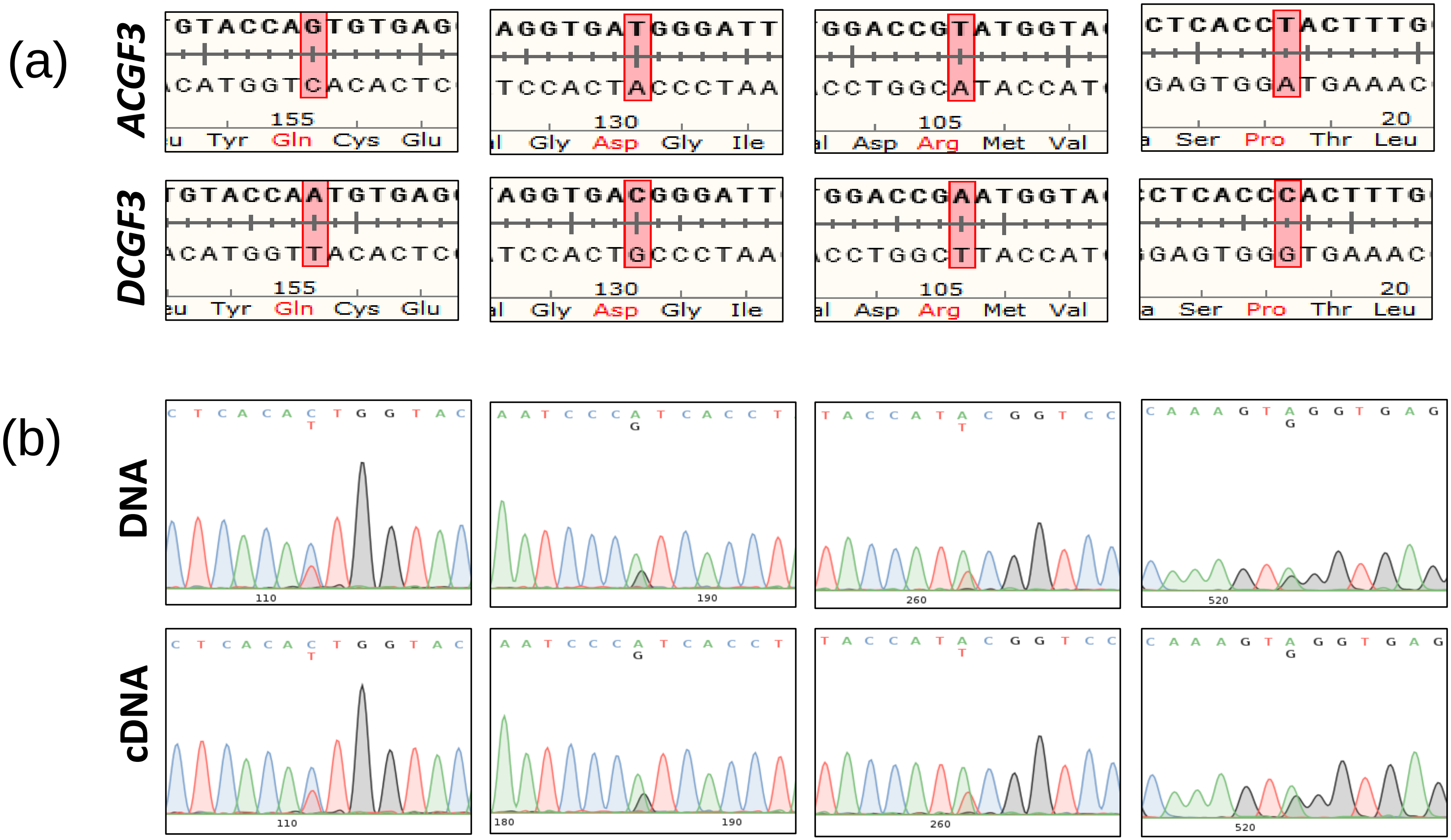

Figure S11 Sequencing results showing four different SNPs that differentiate A and D subgenome *GoPGF* (synonym *CGF3*) genes. (**a**) Segments of *GoPGF* (synonym *CGF3*) gene sequence showing four SNPs between A and D homeologs; (**b**) chromatograms showing the expected SNPs between the two homeologs of the *GoPGF* (synonym *CGF3*) gene in genomic DNA and cDNA samples.

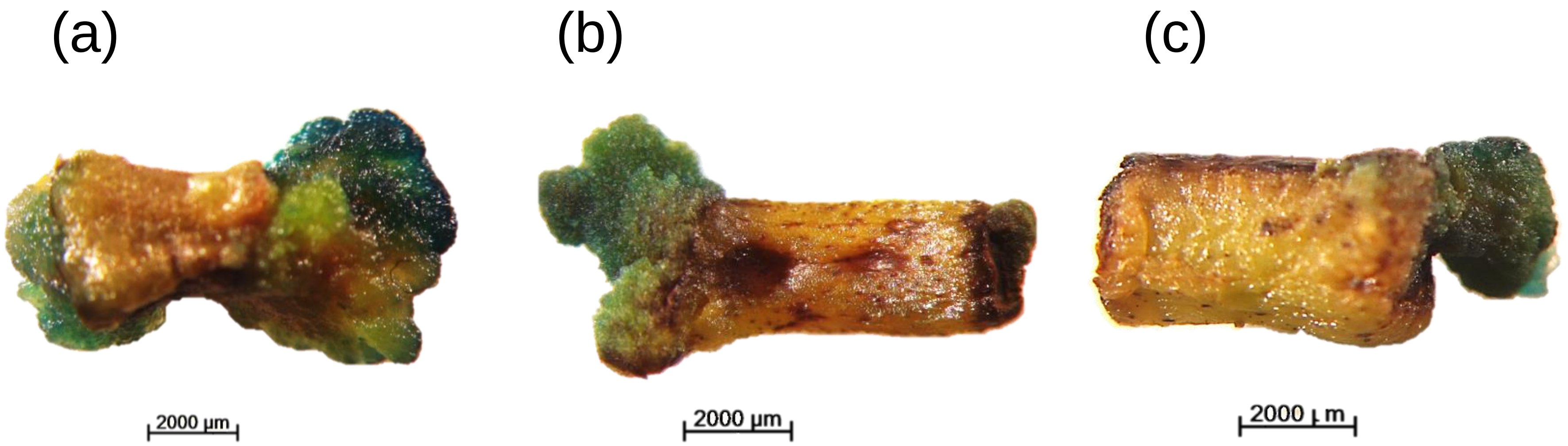

Figure S12 Promoter (2.05 kb) activity evaluation of the D subgenome *GoPGF* (synonym *CGF3*) gene from glanded and glandless cotton using *gusA* as the reporter gene. (**a**) CaMV 35S promoter (used as a positive control); (**b**) 2 kb promoter from glanded cotton; (**c**) 2 kb promoter from glandless cotton.

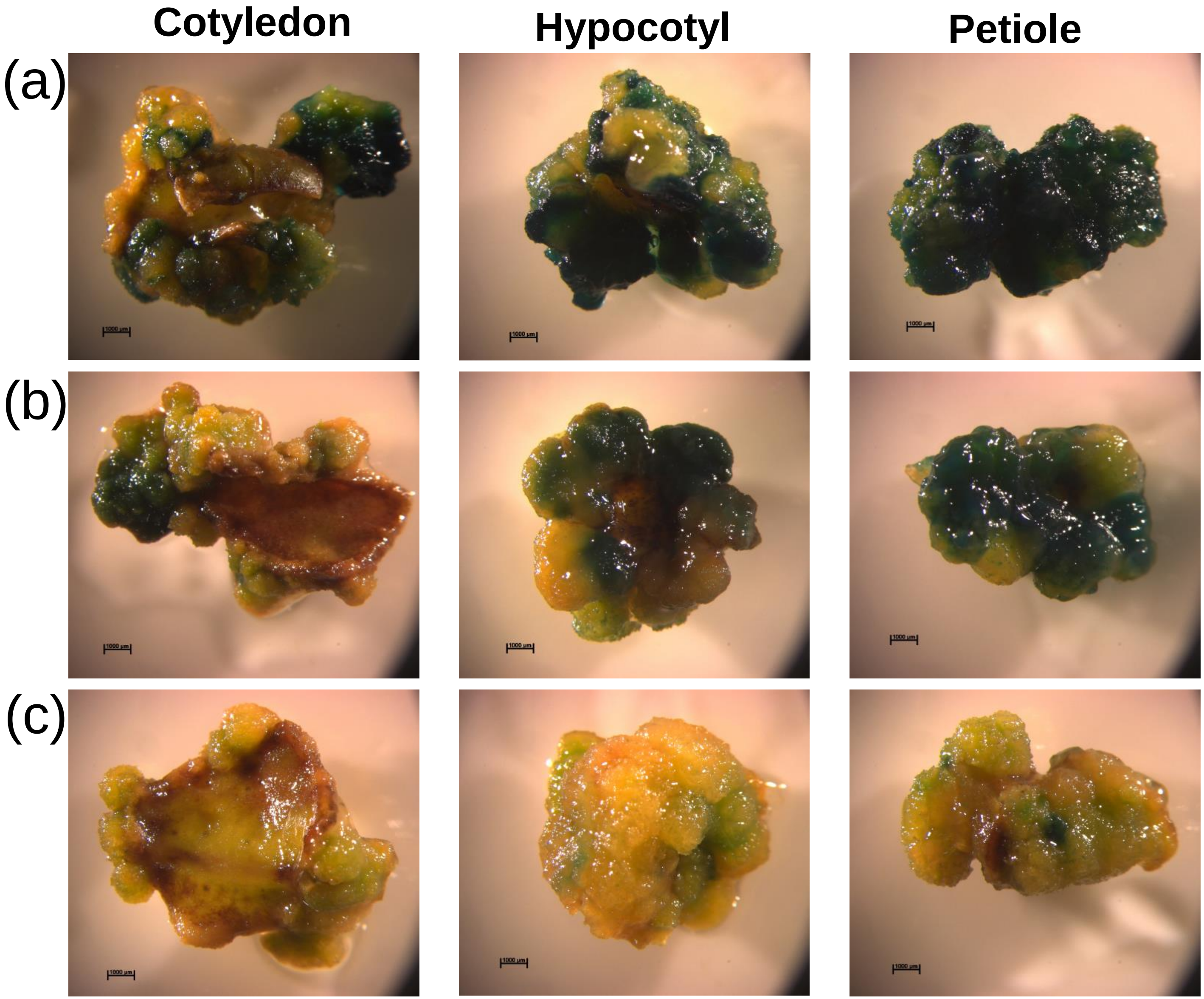

Figure S13 Promoter (~4.2 kb) activity evaluation of the D subgenome *GoPGF* (synonym *CGF3*) gene from glanded and glandless cotton using *gusA* as the reporter gene. (**a**) CaMV 35S promoter (used as a positive control); (**b**) ~4.2 kb promoter from glanded cotton; (**c**) ~4.2 kb promoter from glandless cotton.

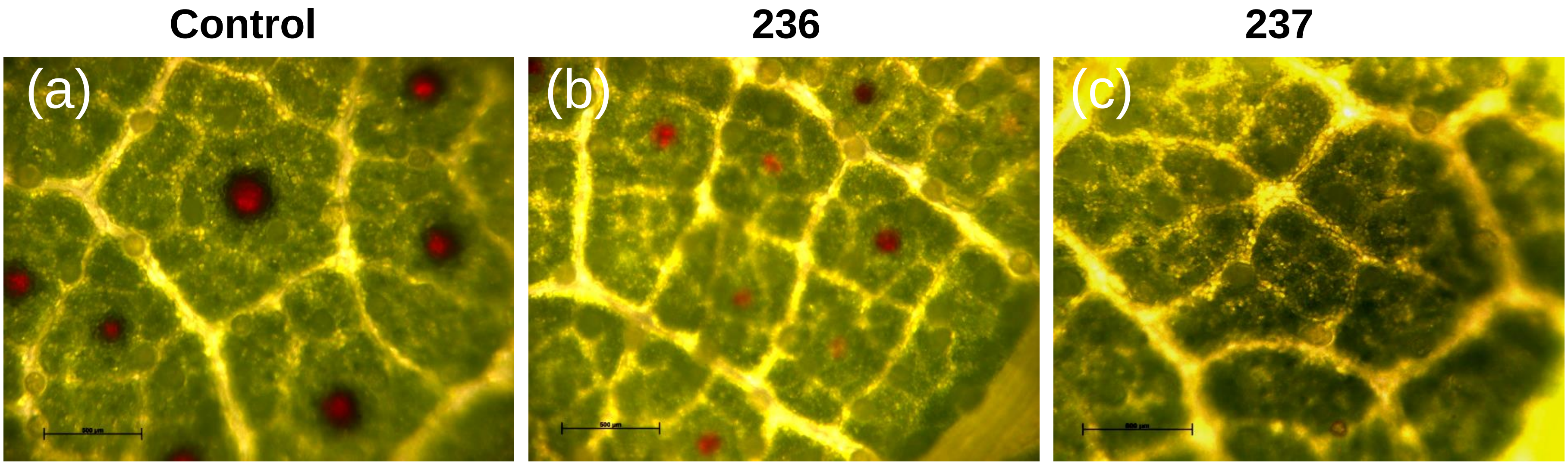

Figure S14 Effect of CRISPR/Cas9-mediated knockout of *CGF2* and *GoPGF* (synonym *CGF3*) genes on gland formation in T0 plants in comparison to glanding pattern seen in a wild-type, control cotton plant. Microscopic images of leaves undergoing expansion: (**a**) control plant showing well developed glands, (**b**) line 236-10 showing smaller and malformed glands, (**c**) line 237-3 showing complete absence of glands.

Figure S15 Mutations observed in two *CGF2* knockout lines, (**a**) 236-8 and (**b**) 236-10. The two target sites are highlighted yellow and PAM sequences red. Nucleotide insertions are shown in lower case and highlighted grey.

Figure S16 Mutations observed in two *GoPGF* (synonym *CGF3*) knockout lines, (**a**) 237-3 and (**b**) 237-4. The two target sites are highlighted yellow and PAM sequences red. Nucleotide insertions are shown in lower case and highlighted grey.

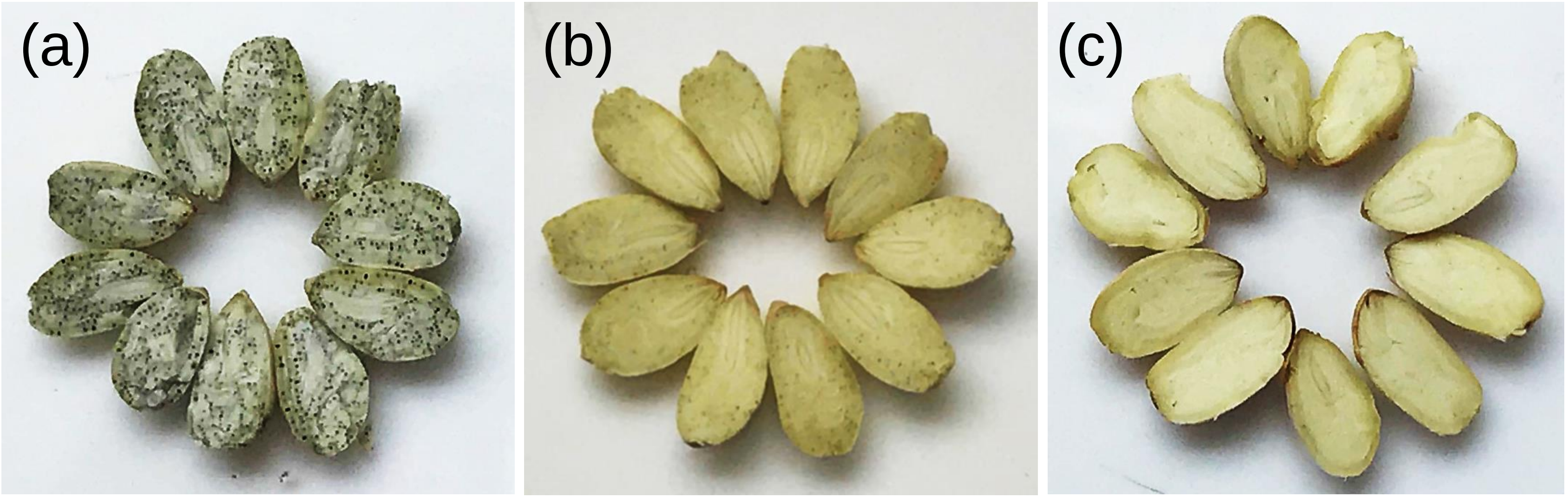

Figure S17 Effect of CRISPR/Cas9-mediated knockout of *CGF2* and *GoPGF* (synonym *CGF3*) genes on gland formation observed in cottonseed kernels. (**a**) Seeds of control plant showing well developed glands;(**b**) T1 seeds of line 236-10 showing smaller and malformed glands; (**c**) T1 seeds of line 237-3 showing complete absence of glands.

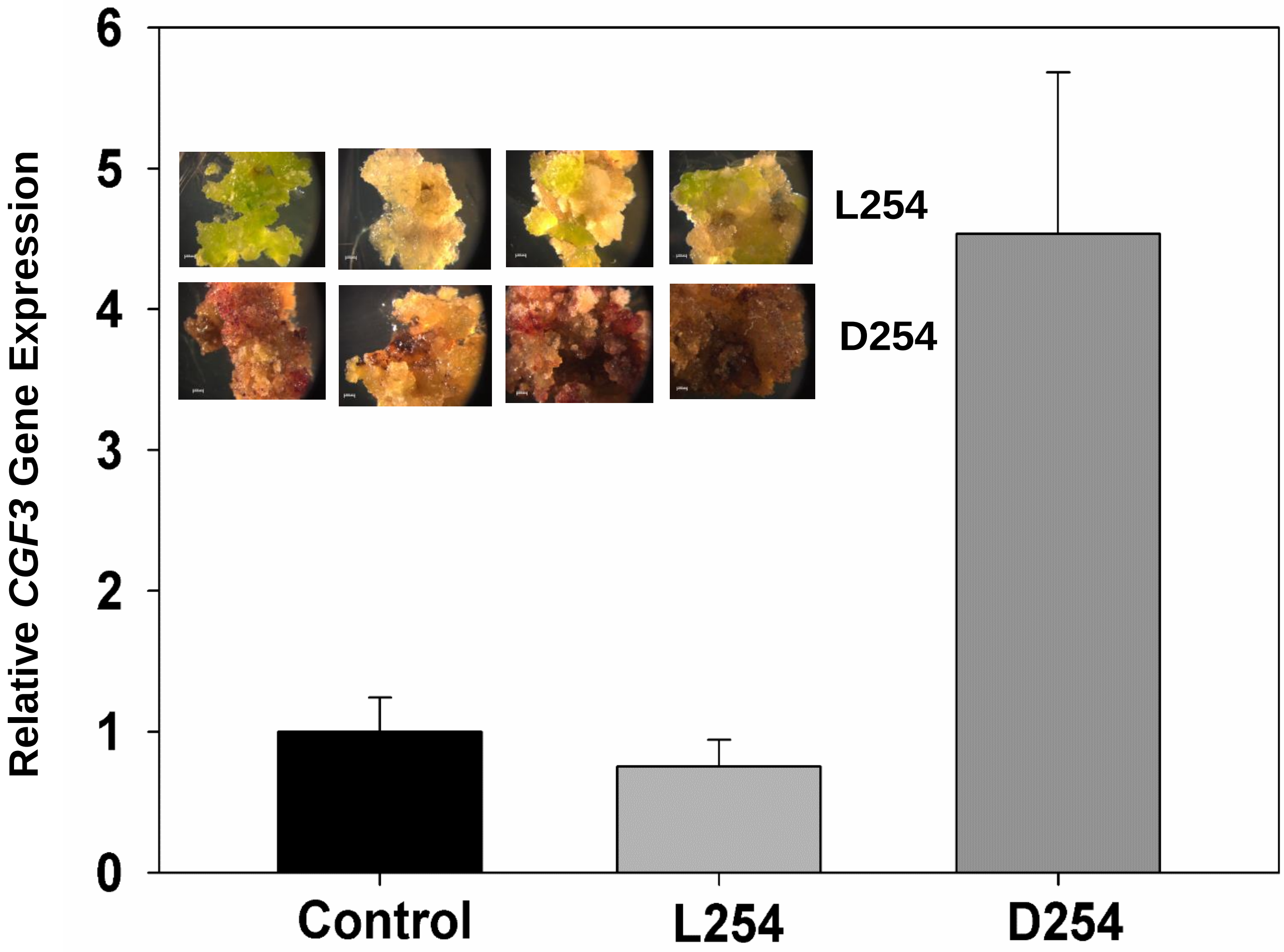

Figure S18 qRT-PCR analysis of *GoPGF* (synonym *CGF3*) transcripts in cotton callus cultures obtained following transformation with *ACGF3* overexpression construct. L254: light-colored callus lines; D254 dark-colored callus lines; Control: non transgenic callus.

Table S1 RNA-seq reads for glanded (GL; GVS4) and glandless (gl; GVS5) embryos at 14-, 16- and 32-days post-anthesis and their mapping to the reference genome.

Tissue	Quality filtered paired reads	Uniquely mapped reads	Reads mapped >1 time	Total mapped reads	Reads not mapped	% of reads not mapped	% of reads mapped one time	% of reads mapped >1 time	% total mapped
14GL	57,526,347	41,539,721	13,219,522	54,759,243	2,767,104	4.81	72.21	22.98	95.19
14gl	55,574,944	39,411,172	13,043,137	52,454,309	3,120,635	5.62	70.92	23.47	94.38
16GL	45,027,488	31,957,244	10,240,975	42,198,219	2,829,269	6.28	70.97	22.74	93.72
16gl	58,872,534	41,914,607	13,567,579	55,482,186	3,390,348	5.76	71.2	23.05	94.24
32GL	78,953,741	57,667,091	18,523,395	76,190,486	2,763,255	3.5	73.04	23.46	96.5
32gl	81,721,688	60,837,058	17,351,295	78,188,353	3,533,335	4.32	74.44	21.23	95.68
	377,676,742	**273,326,893**	**85,945,903**	**359,272,796**	**18,403,946**	**5.05**	**72.13**	**22.82**	**94.95**

Table S2 Genes that expressed at higher levels in the glanded embryos (STV GL; GVS4; $Gl_2Gl_2Gl_3Gl_3$) in comparison to those in the glandless (STV gl; GVS5; $gl_2gl_2gl_3gl_3$) embryos at 14-days post-anthesis stage of development based on RNA-seq analysis. Genes encoding putative transcription factors were tested for their role in gland formation using virus-induced gene silencing (VIGS). Note that because of a high degree of homology between the two homeologs, the same VIGS construct will silence both the copies in A and D subgenomes.

Gene	***G. hirsutum* Chromosome Number**	**Shrunken log fold change**	**FDR**	**Putative Function**	**Size bp**	**VIGS**	**Laboratory Designation**
Gh_A11G0909	11 (A11)	3.459546	0.000000	Basic helix-loop-helix (bHLH) DNA-binding family protein	1488	Yes	*CGF1*
Gh_D11G1055	24 (D11)	6.412898	0.000000	Basic helix-loop-helix (bHLH) DNA-binding family protein	1488		*CGF1*
Gh_A01G0267	01 (A01)	4.992123	0.000001	NAC domain containing protein 42	960	Yes	*CGF2*
Gh_D01G0278	14 (D01)	4.656837	0.000013	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	963		*CGF2*
Gh_A12G2172	12 (A12)	6.231119	0.000000	Basic helix-loop-helix (bHLH) DNA-binding family protein	1428	Yes	*CGF3*
Gh_D12G2351	25 (D12)	4.284841	0.001531	Basic helix-loop-helix (bHLH) DNA-binding family protein	1428		*CGF3*
Gh_A10G0388		4.903984	0.000002	Jasmonate-zim-domain protein 8	363	Yes	
Gh_D10G0403		3.747897	0.003033	Jasmonate-zim-domain protein 8	363		
Gh_A12G1233		5.43426	0.000000	B-box type zinc finger family protein	393	Yes	
Gh_D12G1358		2.11097	0.000000	B-box type zinc finger family protein	393		
Gh_A01G0135		2.064435	0.000139	Zinc finger C-x8-C-x5-C-x3-H type family protein	1020	No	
Gh_A04G0546		4.370138	0.001173	HEAT repeat ;WD domain, G-beta repeat protein protein	192	No	
Gh_A05G0334		2.677935	0.000088	NAD(P)-binding Rossmann-fold superfamily protein	987	No	
Gh_A05G2973		2.888822	0.000000	Lysine histidine transporter 1	1077	No	
Gh_A06G0017		2.788916	0.000000	Thioredoxin superfamily protein	555	No	
Gh_A06G0018		2.25659	0.008180	Expansin 11	768	No	

Gh_A06G0213		2.775923	0.012662	Uncharacterized protein	957	No	
Gh_A06G1947		4.176235	0.000392	NAC domain containing protein 42	930	Yes	
Gh_A08G2056		2.912436	0.000230	NAC domain containing protein 42	867	Yes	
Gh_A10G0667		5.494345	0.000000	Pectin lyase-like superfamily protein	2202	No	
Gh_A12G1784		1.995549	0.000013	Integrase-type DNA-binding superfamily protein	711	No	
Gh_A12G2056		2.388568	0.000000	Uncharacterized protein	1251	No	
Gh_A13G0385		2.137374	0.023065	S-methyl-5-thioribose kinase	660	No	
Gh_D04G0529		3.720997	0.028702	Phosphoenolpyruvate (pep)/phosphate translocator 2	1251	No	
Gh_D05G0292		2.546437	0.031860	myb-like transcription factor family protein	768	Yes	
Gh_D05G0439		2.126081	0.007311	NAD(P)-binding Rossmann-fold superfamily protein	894	No	
Gh_D06G1859		2.756698	0.000000	P-loop containing nucleoside triphosphate hydrolases superfamily protein	987	No	
Gh_D07G2328		4.295568	0.000100	WRKY family transcription factor family protein	501	Yes	
Gh_D08G2336		3.448213	0.031860	Uncharacterized protein	345	No	
Gh_D11G0631		3.446236	0.007958	Uncharacterized protein	417	No	
Gh_D11G0996		4.052173	0.008242	Cytokinin response factor 6	894	No	
Gh_D12G1160		5.449322	0.000000	Basic helix-loop-helix (bHLH) DNA-binding family protein	1464	Yes	
Gh_Sca007330G01		4.131307	0.000000	Plant invertase/pectin methylesterase inhibitor superfamily protein	630	No	

Table S3 Primers used to amplify segments of the coding sequence of the target gene for cloning into TRV2 binary vector to conduct VIGS experiments.

Primers	Sequences (5' to 3')	size
GhA01G0267 EcoRI-F	CGgaattcCTGGGATCTCCCGAAAGCTAGC	634
GhA01G0267 SacI-R	ACGCgagctcCTCATTCTATCTGTAACATGCCATTGGC	
GhA10G0388 EcoRI-F	CGgaattcATGAGACGAAACTGCAACTTGGAG	357
GhA10G0388 SacI-R	ACGCgagctcGTAAGGAGAGGTAGCTTGGATTCG	
GhA12G2172 EcoRI-F	CGgaattcATGTCTTCCTCTTCTTCGTCTTCTC	600
GhA12G2172 SacI-R	ACGCgagctcCGATTTAGTGAGTTGAAGGGTGC	
GhA12G1233 XbaI-F	GCtctagaATGTGCAAAGGTTTACAACAAGGAAG	366
GhA12G1233 XmaI-R	TCCCcccgggGGTTGTTGAAGACTCGGTTTCCGTG	
GhD07G2328 XbaI-F	GCtctagaTCAAATGTTCTTCCCTATCTCGG	491
GhD07G2328 XmaI-R	TCCCcccgggTCAGAAGGGAGTGTAAATCTGCA	
GhD11G1055 XbaI-F	GCtctagaATGGAAGTCCTCATAATGTCTCCCTC	628
GhD11G1055 XmaI-R	TCCCcccgggCCAGACCAATGAGATCGGATTC	
GhA06G1947 XbaI-F	GCtctagaATGGAAGATGTGGAGATGGAGA	505
GhA06G1947 XmaI-R	TCCCcccgggCTTCAAAGTTGTCTTTGGCATG	
GhD05G0292 XbaI-F	GCtctagaATGGGCAGGAAATGCTCACATTG	614
GhD05G0292 XmaI-R	TCCCcccgggAATCAATGCATCCGTACTGCAAC	
GhD12G1160 XbaI-F	GCtctagaATGGAAGAACTAATCATCTCTCCATC	587
GhD12G1160 XmaI-R	TCCCcccgggGATCCAAGTTCAAGAACACCACG	
GhA08G2056 XbaI-F	GCtctagaATGAGCATGGTCCATGGCACCA	630
GhA08G2056 XmaI-R	TCCCcccgggTATCTTAACGATGGCTGCATGAACC	

Table S4 Primers used to amplify and isolate *CGF* genes from A and D subgenomes of glanded (GVS4) and glandless (GVS5) cotton plants.

Primer	Sequence 5' to 3'	Purpose
A11GhCGF-prom-3F	CTCTCCAAAATCAACCATACTCACAAATGCCTAC	To amplify CGF1 from A genome
A11GhCGF-term-R	CTCCATGGCATCCTCAAGTCACAG	
D11GhCGF-prom-F	ATCTTCTCACTCCGAAACCGACC	To amplify CGF1 from D genome
D11GhCGF-term-R	TGGAAGAAACAAGATCGGATGTGGC	
A01CGF2-P-F	GGCTGTCAGATGTAGTAAAATCAGTATTGGT	To amplify CGF2 from A genome
A01CGF2-T-R	CAAATATATATGGGTCTGATATGCATGTCTCC	
D01CGF2-P-F	CAAAGTGTTGATTTCAGCAATAACTTGTAGC	To amplify CGF2 from D genome
D01CGF2-T-R	CGTAACAAAATGGTTTTCGTATGTTACGTATC	
A12CGF-prom-F	CATCCCATACAAACTATTAACAAGATTACGTCGGATG	To amplify CGF3 from A genome
A12CGF-term-R	GTGATCATCATCAAGCACAGGCTACTG	
D12CGF-Prom-F	CAAACCATCAACAAGACTACGTTGGACA	To amplify CGF3 from D genome
D12CGF-term-R	CTAATTTAAGTGATCATCATCAAGCACAGTCTAATC	

Table S5 Guide sequences used to target *CGF2* and *GoPGF* (synonym *CGF3*) genes.

Target name	Sequence 5' to 3'
CGF2-guide-1	GCTCAAACAGGTGATCATCA
CGF2-guide-2	GATTGGAAAAGGCGACGACAG
CGF3-guide-1	AATTGGGGTCCAGTTTCGAG
CGF3-guide-2	AGTGATGGACGTGGACCGTA
CGF3-guide-3	GCTTCTCTAACACGCTCACAC

Table S6 Primers used for amplicon sequencing of regenerated plants targeted with LCT236, LCT237 and LCT238 constructs. These primers contained barcodes to distinguish amplicons from different plants.

Primers	**Sequences (5'-3')**
A_CGF2.Ampseq-F	gtactcAAGTTGATGATGTGTGTTGGTGATG
B_CGF2.Ampseq-F	tctagcAAGTTGATGATGTGTGTTGGTGATG
C_CGF2.Ampseq-F	gagtcaAAGTTGATGATGTGTGTTGGTGATG
D_CGF2.Ampseq-F	gctagtAAGTTGATGATGTGTGTTGGTGATG
E_CGF2.Ampseq-F	atgctaAAGTTGATGATGTGTGTTGGTGATG
F_CGF2.Ampseq-F	ctgcgaAAGTTGATGATGTGTGTTGGTGATG
G_CGF2.Ampseq-R	cgactgATAACATTGATTAACCCAACTTGAGC
H_CGF2.Ampseq-R	tgatagATAACATTGATTAACCCAACTTGAGC
I_CGF2.Ampseq-R	gtcacgATAACATTGATTAACCCAACTTGAGC
J_CGF2.Ampseq-R	atgatgATAACATTGATTAACCCAACTTGAGC
K_CGF2.Ampseq-R	cagtcaATAACATTGATTAACCCAACTTGAGC
L_CGF2.Ampseq-R	acgtcaATAACATTGATTAACCCAACTTGAGC
A_CGF3.Ampseq-F	gtactcCTTCAAGGGATGTTGATGGTCG
B_CGF3.Ampseq-F	tctagcCTTCAAGGGATGTTGATGGTCG
C_CGF3.Ampseq-F	gagtcaCTTCAAGGGATGTTGATGGTCG
D_CGF3.Ampseq-F	gctagtCTTCAAGGGATGTTGATGGTCG
E_CGF3.Ampseq-F	atgctaCTTCAAGGGATGTTGATGGTCG
F_CGF3.Ampseq-F	ctgcgaCTTCAAGGGATGTTGATGGTCG
G_CGF3.Ampseq-R	cgactgATCGATTTAGTGAGTTGAAGGGTGC
H_CGF3.Ampseq-R	tgatagATCGATTTAGTGAGTTGAAGGGTGC
I_CGF3.Ampseq-R	gtcacgATCGATTTAGTGAGTTGAAGGGTGC
J_CGF3.Ampseq-R	atgatgATCGATTTAGTGAGTTGAAGGGTGC
K_CGF3.Ampseq-R	cagtcaATCGATTTAGTGAGTTGAAGGGTGC
L_CGF3.Ampseq-R	acgtcaATCGATTTAGTGAGTTGAAGGGTGC