

284s (from start codon)/cs3

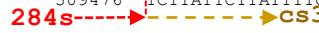
Figure S5 (1)

S352c ATGACGAGAGATAGAATGAGACAAAGCATAAAGGGGAGAGCGCTTTGCCGAGCATTAGTAGTCGTTCCGGCTGGGGGGGT 80
S352b ATGACGAGAGATAGAATGAGACAAAGCATAAAGGGGAGAGCGCTTTGCCGAGCATTAGTAGTCGTTCCGGCTGGGGGGGT 80
S352a ATGACGAGAGATAGAATGAGACAAAGCATAAAGGGGAGAGCGCTTTGCCGAGCATTAGTAGTCGTTCCGGCTGGGGGGGT 80
S356 ATGACGAGAGATAGAATGAGACAAAGCATAAAGGGGAGAGCGCTTTGCCGAGCATTAGTAGTCGTTCCGGCTGGGGGGGT 80
S367 ATGACGAGAGATAGAATGAGACAAAGCATAAAGGGGAGAGCGCTTTGCCGAGCATTAGTAGTCGTTCCGGCTGGGGGGGT 80

S352c TATCTTTAAAGTAGTGCTTAAATCACTACAGGAGCGAAAAAAGGATAAGTAGCGAAATTTTCGTCGACTATTTATTTTT 160
S352b TATCTTTAAAGTAGTGCTTAAATCACTACAGGAGCGAAAAAAGGATAAGTAGCGAAATTTTCGTCGACTATTTATTTTT 160
S352a TATCTTTAAAGTAGTGCTTAAATCACTACAGGAGCGAAAAAAGGATAAGTAGCGAAATTTTCGTCGACTATTTATTTTT 160
S356 TATCTTTAAAGTAGTGCTTAAATCACTACAGGAGCGAAAAAAGGATAAGTAGCGAAATTTTCGTCGACTATTTATTTTT 160
S367 TATCTTTAAAGTAGTGCTTAAATCACTACAGGAGCGAAAAAAGGATAAGTAGCGAAATTTTCGTCGACTATTTATTTTT 160

S352c ATATGTTATGTATTCATATTTGATCTCTTTTTGAAGATTTCCATTTTAGTTTTCTAGTCTTTTATCCGGATAGTCCTC 240
S352b ATATGTTATGTATTCATATTTGATCTCTTTTTGAAGATTTCCATTTTAGTTTTCTAGTCTTTTATCCGGATAGTCCTC 240
S352a ATATGTTATGTATTCATATTTGATCTCTTTTTGAAGATTTCCATTTTAGTTTTCTAGTCTTTTATCCGGATAGTCCTC 240
S356 ATATGTTATGTATTCATATTTGATCTCTTTTTGAAGATTTCCATTTTAGTTTTCTAGTCTTTTATCCGGATAGTCCTC 240
S367 ATATGTTATGTATTCATATTTGATCTCTTTTTGAAGATTTCCATTTTAGTTTTCTAGTCTTTTATCCGGATAGTCCTC 240

S352c CCCATAGTACAGATGTTTTCCCTTCTAACTTGTGTCCTTTCTTATCTTATCTCTCTTTTTGCCTTATTTTGACCTG 320
S352b CCCATAGTACAGATGTTTTCCCTTCTAACTTGTGTCCTTTCTTATCTTATCTCTCTTTTTGCCTTATTTTGACCTG 320
S352a CCCATAGTACAGATGTTTTCCCTTCTAACTTGTGTCCTTTCTTATCTTATCTCTCTTTTTGCCTTATTTTGACCTG 320
S356 CCCATAGTACAGATGTTTTCCCTTCTAACTTGTGTCCTTTCTTATCTTATCTCTCTTTTTGCCTTATTTTGACCTG 320
S367 CCCATAGTACAGATGTTTTCCCTTCTAACTTGTGTCCTTTCTTATCTTATCTCTCTTTTTGCCTTATTTTGACCTG 320
Sb-cs3 309476 TCTTATCTTATTTTTCGTTATTTTGACCTG 309508



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S356 TTTGATTCTTTTCCGTTTAAAGAAGAAGGAGGATTTTGCCTCCCTCCTGAAAGTATAATCTCCATTTTTTCAAGTCTTT 400
S367 TTTGATTCTTTTCCGTTTAAAGAAGAAGGAGGATTTTGCCTCCCTCCTGAAAGTATAATCTCCATTTTTTCAAGTCTTT 400
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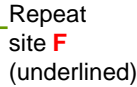
S352c TCGCTATTTTGATGGCAGTATTAGCATCGGGCCCTTCAGTTGCTTACGCTATGGGAACCC-TGGG-CCT 468
S352b TCGCTATTTTGATGGCAGTATTAGCATCGGGCCCTTCAGTTGCTTACGCTATGGGAACCC-TGGG-CCT 468
S276 -----GGCCCTTCAGTTGCTTACGCTATGGGAACCC-TGGG-CCT 240
S352a TCGCCATTTTGATGGCAGTATTAGCATCGGGCCCTTCAGTTGCTTACGCTATGGGAACCC-TGGG-CCT 468
S356 TCGCTATTTTGATGGCAGTATTAGCATCGGGCCCTTCAGTTGCTTACGCTATGGGAACCCCTGTTGGGGGTTCACT 480
S367 TCGCTATTTTGATGGCAGTATTAGCATCGGGCCCTTCAGTTGCTTACGCTATGGGAACCCCTGTTGGGGGTTCACT 480
Sb-cs3 CCGCTATTTTAAATGGCTGTATTAGCATCGGGCCCTTCAGTTGCTTACGCTATGGGAACCCCTGTTAGGGGTGAACCC 309662

S352c AGTGAAGCGGGTCTGAAGGATCCGCTGC 497
S352b AGTGAAGCGGGTCTGAAGGATCCGCTGC 497
S276 AGTGAAGCGGGTCTGAAGGATCCGCTGC 269
S352a AGTGAAGCGGGTCTGAAGGATCCGCTGC 497
S356 AGTGAAGCGGGTCTGAAGGATCCGCTGC 509
S367 AGTGAAGCGGGTCTGAAGGATCCGCTGC 509
Sb-cs3 AGT 309665

cs2/cs1

S352c ACCGCCCTCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 544
S352b ACCGCCCTCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 544
S310 ACCGCC-TCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 418
S276 ACCGCCCTCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 316
S314b ACCGCC-TCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 430
S314a ACCGCC-TCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 430
S352a ACCGCCCTCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 544
S356 ACCGCCCTCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 556
S367 ACCGCCCTCGTCCCTCTTCAAGAAAGCACGGGGGAAATGGACGCGC 589
S284b CCTCAAATTCGCCCTTATCACTTATACTT----- 340
S284a CCTCAAATTCGCCCTTATCACTTATACTT----- 340
Zmorfl179 CCTCAAATTCGCCCTTATTTACTTATACTTCCGATT 55
Gmorf271 TTATTAACGTATACAT----- 313

S352c TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 624
S352b TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 624
S310 TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 498
S276 TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 396
S314b TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 510
S314a TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 510
S352a TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 624
S356 TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTCCGGGGGGAAACCTTCGGTCAATCAACCGCTTCCAGGGGAG 636
S367 TGATGGCATCAACGACTCCTTCCGCGCCGCGGACACCCCTTCGGTCAATCAACCGCTTCCAGGGGAG 669
S284b CCGATTGGCGGAAGATTTCGGTCAGTTCGGGCGTAGTAGAAGTACCBCCTTCGGTCAATCAACCGCTTCAAGGGGAA 420
S284a CCGATTGGCGGAAGATTTCGGTCAGTTCGGGCGTAGTAGAAGTACCBCCTTCGGTCAATCAACCGCTTCAAGGGGAA 420
Zmorfl179 CCTATTTCGGTAGAGACTTCGGCCAGTTCGGGCGTAGTAGAAGTACCBCCTTCGGTCAATCAACCGCTTCAAGGGGAA 135
Gmorf271 CCGACTTGCCTCAAGACTCCGGCAAGTTCGGGCGTAGTAGTACC-----TCAGCGGTCAATCAACCGCTTCCAGGGGAA 390



Note 3

S352c CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 704  
 S352b CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 704  
 S310 CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 578  
 S276 CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 476  
 S314b CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 590  
 S314a CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 590  
 S352a CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 704  
 S356 CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 716  
 S367 CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 749  
 S284b CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 500  
 S284a CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 500  
 Zmorf179 CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTACGCGCCCTACCCGTATCCAGT 215  
 Gmorf271 CAAGCTATGCCTCCCGCTCTTCCCGTTATGCAGGAAGCTGCTAATCGGTCCTCCGCCCTAC---CCCT----ATCAA 46

Note 3

S352c TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 784  
 S352b TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 784  
 S310 TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 658  
 S276 TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 556  
 S314b TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 670  
 S314a TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 670  
 S352a TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 784  
 S356 TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 796  
 S367 TGACGAGATAATAGGAGGGGATAGCGTGCAATCCATTCAAAGAAGACTTTGGGGACTAATTGGAATCCTTCGCCCCATG 829  
 S284b AATGAAATAATAGGAGGGGATAGCGTAGAATCCATTCAAAGGAGGCTGTGGGGACTAATTGGAATCCTTCAGCCCCATG 580  
 S284a AATGAAATAATAGGAGGGGATAGCGTAGAATCCATTCAAAGGAGGCTGTGGGGACTAATTGGAATCCTTCAGCCCCATG 580  
 Zmorf179 AATGAAATAATAGGAGGGGATAGCGTAGAATCCATTCAAAGGAGGCTGTGGGGACTAATTGGAATCCTTCAGCCCCATG 295  
 Gmorf271 AATGAGATATAGGAGGGGATAGCGTAGAATCCATTCAAAGGAGGCTGTGGGGACTAATTGGAATCCTTCAGCCCCATG 541

Note 3

S352c ACATGCAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGGGCCTGCAT 864  
 S352b ACATGCAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGGGCCTGCAT 864  
 S310 ACATGCAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGCAATCATAAGAAGATGGCGGGCCTGCAT 738  
 S276 ACATGCAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGGGCCTGCAT 636  
 S314b ACATGCAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGCAATCATAAGAAGATGGCGACCCCTGCAT 750  
 S314a ACATGCAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGACCCCTGCAT 750  
 S352a ACATAAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGGGCCTGCAT 864  
 S356 ACATAAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGGGCCTGCAT 876  
 S367 AATAAAAATGTCGGGATTC AAGCGGAGGATCTATTTGAACTGAAAGTGGAATCATAAGAAGATGGCGGGCCTGCAT 909  
 S284b ACATAAGAATGGCCGGATTC AAGCGGAGGATCTATTTGAGGTGAAGGTGACATAATCCGGAAGATGGCGGGCCTGCAT 660  
 S284a ACATAAGAATGGCCGGATTC AAGCTGAAGCTTTTGGAGTGAAGGTGACATAATCCGGAAGATGGCGGGCCTGCAT 660  
 Zmorf179 ACATAAGAATGGCCGGATTC AAGCGGAGGATCTATTTGAGGTGAAGGTGACATAATCCGGAAGATGGCGGGCCTGCAT 375  
 Gmorf271 AGATTC AAGATGGCCGGATTC AAGCGGAGGATCTATTTGAGGTGAAGGTGACATAATCCGGAAGATGGCGGGCCTGCAT 621

S352c CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 944  
 S352b CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 944  
 S310 CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 818  
 S276 CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 716  
 S314b CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAA 830  
 S314a CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 830  
 S352a CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 944  
 S356 CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 956  
 S367 CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCGAGGAAGACTTGGCTAG 989  
 S284b CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGCTGAGGAAGACTTGGCTAG 660  
 S284a CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGTGAAGGAAGACTTGGCTAG 660  
 Zmorf179 CCAAGTGGCGATTGGATGGGATGGGGCGCGGGGCCTTGGACAACCCCGTACGGCCACTGGTGAAGACACTTGGCTAG 455  
 Gmorf271 CCAAGCGGGGATTGGATGGGACGGGGGCCTAGAGCTCTGGAATACTTCGTACCGCCACTGGAGAGGAGTCCTTAAGTAA 701

S352c GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 1024  
 S352b GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 1024  
 S310 GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 898  
 S276 GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 796  
 S314b GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 910  
 S314a GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 910  
 S352a GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 1024  
 S356 GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 1036  
 S367 GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 1069  
 S284b GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 740  
 S284a GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATGAGCAATCAGCTACCTTCTGGCGCTTGGTCAAAGAGTCCGCT 740  
 Zmorf179 GTTGCAACCAATGCTCGACGACCTACAGAGCCGGAATTTCCATCTGCAACCTCTG-----TCGAAAGAGTCCGCT 527

S352c TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 1081  
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 S310 TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 955  
 S276 TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 853  
 S314b TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 967  
 S314a TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 967  
 S352a TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 1081  
 S356 TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 1093  
 S367 TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTGAGAGAAGGGTGAA 1126  
 S284b TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTCAAAACGAGGGGTAAAGCCAAAGTGTCTTAAACAA 820  
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 Zmorf179 TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTCAAAACGAGGGGTAAAGCCAAAGTGTCTTAAACAA 607  
 Gmorf271 TACGGGCGGATGAGGATCAAAACTCAGCCTCCTAG-ACATGGCTCAAAACGAGGGGTAAAGCCAAAGTGTCTTAAACAA 832

S352c	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>ATACTA</b> ATA	1098
S352b	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>ATACTA</b> ATA	1098
S310	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>ATACTA</b> ATA	1029
S276	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>ATACTA</b> ATA	927
S314b	AGACATGGCTGAGAGAAGGGGGAA	991
S314a	AGACATGGCTGAGAGAAGGGTGAA <b>ATGAAA</b> AAAAAAG-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>ATACTA</b> ATA	1047
S352a	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>TAGCAA</b> ATA	1098
S356	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>TAGCAA</b> ATA	1167
S367	AGACATGGCTGAGAGAAGGGTGAA-----AAAAAAT-AATTGGAACTATTGAGCGCTGTAGGTATCCATCT <b>TAGCAA</b> ATA	1200
Ta-cs4	62763 AAACAATGAATTGGAACTATTGAGTGGTGTAGGTATCCATCT <b>TAGCAA</b> ATA	62699
As-cs4	413869 AAACAATGAATTGGAACTATTGAGTGGTGTAGGTATCCATCT <b>TAGCAA</b> ATA	413919
Sc-cs4	739 TCT <b>CAGGAA</b> ATA	750
Zm-cs4	4566 TGTAGGTATCTCTCT <b>TTGCAA</b> ATA	4589
	<b>Note 5</b>	<b>Note 4</b>
S352c	GAT <b>ATA</b> ACCGAGGCC	1113
S352b	GAT <b>ATA</b> ACCGAGGCC <b>CCCA</b> ACCTACTAGTTGTTGGT <b>G</b> ----GGGAAAGAAGAGTGGGAAT <b>GTGGG</b> CTTCTTTCA <b>---</b> TTT	1172
S310	GAT <b>ATA</b> ACCGAGGCC <b>CCCA</b> ACCTACTAGTTGTTGGT <b>G</b> ----GGGAAAGAAGAGTGGGAAT <b>GTGGG</b> CTTCTTTCA <b>---</b> TTT	1103
S276	GAT <b>ATA</b> ACCGAGGCC <b>CCCA</b> ACCTACTAGTTGTTGGT <b>G</b> ----GGGAAAGAAGAGTGGGAAT <b>GTGGG</b> CTTCTTTCA <b>---</b> TTT	1001
S314a	GAT <b>ATA</b> ACCGAGGCC <b>CA</b> CAACCTACTAGTTGTTGGT <b>TTGGT</b> GGGAAAGAAGAGTGGGTAT <b>AGGGC</b> TTCTTTCA <b>CTTT</b> TTT	1128
S352a	GAGATACCGAGGCC <b>CA</b> CAACCTACTACTTGTGGT <b>TTGGT</b> GGGAAAGAAGAGTGGGTAT <b>AGGGC</b> TTCTTTCA <b>CTTT</b> TTT	1179
S356	GAGATACCGAGGCC <b>CA</b> CAACCTACTACTTGTGGT <b>TTGGT</b> GGGAAAGAAGAGTGGGTAT <b>AGGGC</b> TTCTTTCA <b>CTTT</b> TTT	1248
S367	GAGATACCGAGGCC <b>CA</b> CAACCTACTACTTGTGGT <b>TTGGT</b> GGGAAAGAAGAGTGGGTAT <b>AGGGC</b> TTCTTTCA <b>CTTT</b> TTT	1281
Ta-cs4	GAGATACCGAGGCC <b>CA</b> CAACCTACTACTTGTGGT <b>TTGGT</b> GGGAAAGAAGAGTGGGTAT <b>AGGGC</b> TTCTTTCA <b>CTTT</b> TTT	62632
As-cs4	GAGATACCGAGGCC <b>CA</b> CAACCTACTACTTGTGGT <b>TTGGT</b> GGGAAAGAAGAGTGGGTAT <b>AGGGC</b> TTCTTTCA <b>CTTT</b> TTT	414000
Sc-cs4	GAGATACCGAGGCC <b>CA</b> CAACCTACTACTTGTGGT <b>TTGGT</b> GGGAAAGAAGAG <b>CGGG</b> AAC <b>AGGGC</b> TTCTTTCA <b>CTG</b> TTT	831
Zm-cs4	GAGAT <b>G</b> CCGAGGCC <b>---</b> CTACTTAC <b>---</b> CTTCTGGT <b>TTTG</b> GGGAAAGAAGAGTGGGT <b>TAG</b> CGGGCTTCTTTCA <b>CTGT</b> TTT	4666
	<b>Note 4</b>	<b>Note 4</b>
S352b	GATTTT <b>T</b> GGTTGGTGA	1188
S310	GATTTT <b>T</b> GGTTGGTGA	1119
S276	GATTTT <b>T</b> GGTTGGTGA	1017
S314a	GT <b>TTT</b> TGTGGTGA	1144
S352a	GT <b>TTT</b> TGT <b>AG</b> GTGA	1195
S356	GT <b>TTT</b> TGTGGTGA	1264
S367	GT <b>TTT</b> TGTGGTGA	1294
	<b>Note 4</b>	

**Figure S5.** Comparison among the conserved sequences of the recombinant structures and those from other plant species as references. *Sb*, sorghum bicolor; *Zm*, Zea mays; *Gm*, Glycine max; *Ta*, Triticum aestivum; *As*, Aegilops speltoides, *Sc*, Secale cereale. The start and stop codons are shown in green. The nucleotide variations are shown in red. The repeat site E is for recombination between S367 and S276 to produce S352b, and the site F is for recombination between S314a and S276 to produce S310 (see Fig. 4). Note 1: these base mutations and the two 6-bp deletions (in red) occurred to produce S352a and the mutated sequence inherited into S276, then S352b, and S352c (see Fig. 4). Note 2: the 33-bp segment in S367 was deleted between the two CCGCC repeats to produce S356. Note 3: the three SNPs indicate that S367 is the most primitive sequence among the recombinant structures after generation of S284b. Note 4: these nucleotide variations (in blue) indicate the primitive forms (conserved in other species) and the diverged forms (in red) of the cs4 sequences. Note 5: S314a contains both the ancestral and diverged types of the nucleotides in the sites, thus may be an intermediate form.