

STA1

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chr2_53943-54143      TGGTTTGGACACATAAAAGTATGGAAAAGTCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGATAGGCTATGTGCGAGCTGTGACAGG
chr2_54144-54343      TGGTTTGGACACATAAAAGTATGGAAAAGGCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGATAGGCTATCTCGAGCTGTGACAAAG
chr2_54344-54524      TGGTTTCTACACATAAAAGTATGAAAAAGTCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGATAGGCTCTCTCGAGCTGT-----
chr7_47381-47580      TGGTTTGGACTCATCAAAGTATGGAAAAGTCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCACCTGTGATAGGCTCTCTCGAGCTATGATAGG
chr7_47581-47782      TGGTTTGGACACATAAAAGTATGGAAAAGTCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCACCTGTGATAGGCTCTCTCGAGCTATGATAGG
chr7_47783-47963      TGGTTTGGACACATAAAAGTATGAAAAAGTCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGATAGGCTCTCTCGAGCTGT-----
chr9_8128-8306        TGGTTTGGACACATAAAAGTATGGAAAAGTCTAGAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGAT--GGCTCTCTCGAGCTGT-----
chr9_8307-8487        TGGTTTGAACACATAAAAGTATGGAAAAGTCTAGAATTTTACAATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGATAGGCTCTCTCGAGCTGT-----
chr9_8488-8667        -GGTTTGGACACATAAAAGTATGGAAAAGTCTAAAATTTTACCATGGTTTGGAGTCTAGACTTTTTTCAGCTGTGATAGGCTCTCTCGAGCTAT-----
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chr2_53943-54143      GTCCCTCGAGGTGTGATAGGCTCCCTCTAGCTATGAACCTATTGGTCCCTCAAACCTTCACAAA-A-AAATATTACCATACCTTGAACACATGGAATTTTACTA
chr2_54144-54343      GTCCCTCGAGGTGTGATGGGGTCCCTCTAGCTATGAACCTATTGGTCCCTCAAGCTTCACAAA-A-AAATATTACCATACCTTGA-ACATATGGAATTTTAAATA
chr2_54344-54524      -----GATAGGGTCCCTCTAGCTATGACCTATTGGACCTCAAGCTTCACAAA-AAAAATATTACCATACCTTGA-ACACATGGAATTTTACTA
chr7_47381-47580      GTCTCTCGAGGTGTGATAGGCTCCCTCTAGCTATGAATATTGGTCCCTCAAGCTTCACAAA-A-AAATATTACCATACCTTGA-ACACATGGAATTTTACTA
chr7_47581-47782      GTCTCTCGAGGTGTGATAGGCTCCCTCTAGCTATGAACCTATTGGTCCCTCAAGCTTCACAAA-AAAAATATTACCATACCTTGA-ACACATGGAATTTTACTA
chr7_47783-47963      -----GATAGGGTCCCTCTAGCTATGACCTATTGGTCCCTCAAGCTTCACAAA-AAAAATATTACCATACCTTGA-ACACATGGAATTTTACTA
chr9_8128-8306        -----GATAGGGTCCCTCTAGCTATGACCTATTGGTCCCTCAAGCTTCACAAA-A-AAATATTACCATACCTTGA-ACACATGGAATTTTACTA
chr9_8307-8487        -----GATAGGGTCTCTCTAGCTATGACCTATTGGTCCCTCAAGCTTCACAAA-AAAAATATTACCATACCTTGC-ACACATGGAATTTTACTA
chr9_8488-8667        -----GATAGGGTCCCTCTAGCTATGACCTATTGGTCCCTCAAGCTTCACAAA-AGAAATATTACCATACCTTGA-ACACATGGAATTTTACTA
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STA2

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chr4_35658-35834      TGGTATTGACACATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGACGTGTCACAGACAAGGCCCTATAGGTGAGATAA
chr4_35835-36011      TGGTATAAACACATGAAATATGGTAAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGACAAGGCCCTATGGGTGTGACAA
chr4_36012-36188      TGGTATGGAACATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCATAGACAAGGCCCTATAGGTGTGACAA
chr7_65495504-65495680 TGGTATGGACACATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGGCAAGGCCCTATAGGTGTGACAA
chr7_65495681-65495857 TGGTATGGACACATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGGCAAGGCCCTACAGGTGTGACAA
chr7_65495858-65496034 TGGTATGGACACATAAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGGCAAGGCCCTATAGGTGTGACAA
chr9_59414161-59414337 TGGTATGGACATATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGACGAGGCCCTATAGTTGTGACAA
chr9_59414338-59414514 TGGTATAGACACATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGACGAGGCCCTATAGGTGTGACAA
chr9_59414515-59414691 TGGTATAGACACATGAAATATGGTTAAGTCTAGATTTTTTACCATGGTTTGGAGTCTAGAAATTTTCGAGGGGTTCACAGACGAGGCCCTATAGGTGTGACAA
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chr4_35658-35834      GTTGTGACAAGGGTCTGATAGCTGTGACAGGCTGTGACAAGGGTCTTATACCTATGACACACATGACAAGAATTCT
chr4_35835-36011      GCTGTGACAAGGGTCCGATAGCTGTGACAGGCTGTGACAAGGGTCTTATACCTATGACAGGCTATGACAAGGATTCT
chr4_36012-36188      GCTGTGACAAGGGTCCGATAGCTGTGACAGGCTGTGACAAGGGTCTTATACCTATGACAGGTTGTGACAAGGATTCT
chr7_65495504-65495680 GGTGTGACAAGGGTCCGATAGCTGTGACAGGCTGTGACAAGGGTCTTATACCTATGACAGGATGTGACAAGGATTCT
chr7_65495681-65495857 GCTGTGACAAGGGTCCGATAGCTGTGACAGGCTGTGACAAGGGTCTTATACCTATGACAGGCTGTGACAAGGTTCT
chr7_65495858-65496034 GATATGACAAGGGTCCGATAGCTGTGACAGGCTGTGACAAGGGTCTTATACCTATGACAGGCTGTGACAAGGATTCT
chr9_59414161-59414337 GCTGTGACAAGGGTCCGATAGCCGTGACAGGCTGTGACAAGGGTCTTATACCTATGACGGTCTGTGACAAGGATTCT
chr9_59414338-59414514 GCTGTGACAAGGGTCTAATAGCTGTGATAGGCTGTGACAAGGGTCTTACACCTATGACAGGCTGTGACAAGGATTCT
chr9_59414515-59414691 GCTGTGACAAGGGTCTAATAGCTGTGATAGGCTGTGACAAGGGTCTTACCTATGACAGGCTATGACAAGGATTCT
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Supplemental Figure S4: Multiple sequence alignment of nine STA1 and nine STA2 sequences corresponding to 3 monomers from each of 3 arrays on different chromosome arms. Nucleotide sequences, including the consensus sequence for STA1 and STA2, is contained in Supplemental File S2.