

## Appendix A

This appendix lists primers used in the studies described in Chapter 3. The first section lists primers used in screening of the cDNA libraries. Section two lists primers used in the alternative polyadenylation studies. Section three lists primers used in the NXF2/TCP11-like variant studies. stSG numbers and the primer sequences are given in each section. In section one, bold-type STSs denote primary poolscreen STSs used in the transcript map. Any SSPCR nested primers designed are given in the “SSPCR STS” column. Prescreen results are given in Chapter 3. For Sections two and three, expected product sizes, pre-screen optimal annealing temperature in °C and whether the primers span introns are given. Where an STS was not pre-screened due to it spanning an intron, n/a is stated in the pre-screen column.

Section 1					
stSG number	Primer 1	Primer 2	SSPCR STS		
stSG101247	CTGTGTCACGTTGCTGCAAC	AAGCGGACTTGGCAAGCATG			
stSG101248	ACCAATCCAAGTACCATAAC	AGTGCGTACTGGATTAGTAC			
stSG101249	ATCCTTCTGCTCAAATCTCC	GAGATTTGAGCAGAAGGATC			
stSG101250	TGAAGTGGCCTGTGGCATCG	GCAACAGTAGGAAGAAGTTG			
stSG101252	GACTCTCAGAAGCTGTTACC	CCAGCTGGCACTCGGTGTAC			
<b>stSG101443</b>	ATGCATATAGAGATTATACG	ACTGACCCATTGAAACCATG			
<b>stSG101533</b>	GTGACGTGGGTGAAGGAGTT	AAACCACAGTCAGTTGATGGG			
<b>stSG118040</b>	AGACAGGTGTGAGGCACCTT	ACTGGATGAGTCCCAACAGC			
<b>stSG118961</b>	TAATGGTGAGTCCATGTAAGGC	GGAAAGGGAAAGAAAGAAGAGG			
<b>stSG118962</b>	CCACCTTCAGTGACCAGGTT	CGGCATATTGATTTGGTCCT			
<b>stSG118963</b>	GAAGCTGGGACTGAAAGTGC	TCGAGATTATTGTCTGCCAGG			
<b>stSG118964</b>	TCCGAAAGTCCCTTCTTTT	CTCACTGAAATGGTAGAGCCG			
<b>stSG118965</b>	TGGAACAGATTGTGTGTTTGC	CATATCTCACTGGCCTGAAGC			
<b>stSG118966</b>	AGCCATTAGGCAAACACCAC	TCCAGACATGTTTACATCA	119560		
<b>stSG118967</b>	CAAGTCAGCAGTAAAAATTGC	TCATTTCTCTGGTGTGGCAG			
<b>stSG118968</b>	TGAAGTCTGCACCTCCCTG	TTGTAATCGTGGTGATTTGAGG			
<b>stSG118969</b>	TGGTGAATAACAACCAGCTCC	AGTGCCTACCTTGCAGCAGT	119556		
<b>stSG118970</b>	CAGAGGGTTTAGCATGGGAA	CTATCCCATGGCCAAGATTG			

stSG118971	AGAATTAGGTCCCTGTAACCCC	TTCATGTTGGTGAATCATGTG	119557		
stSG118972	ATACCAACCCACAGAAATGAGG	ACGGGGACTGTAGGTGGAG	119558		
stSG118973	GAAAAGAAAGCCAGGATCCC	AGAAGAATGGCATGGGGAG			
stSG118974	GCACCATCTTCAAATTTGTGG	AAACAAATGGAAGAGCCAACA			
stSG118975	ATAGCATGGCAGAAAAGAGAGG	GGCACAACCTCCCCACATATT	119559		
stSG118976	CCCTGCAACTTCCTCTTCAG	GTGAAAGGAAAGATGACCTTGG			
stSG118977	ACGTGATTGCACATTTGGAA	CTGCACTCTCACTGGTCCAA	119555		
stSG118978	AGCTAGCCTTGGCATCAGAA	GTCAATGTTTTGTGTGGTCTGG			
stSG118979	CACTGTCCATCTCTCCCCAT	TTCAATGATGCAAACCTCAAATG			
stSG118980	CCTCTCCCTTGATGATCCAC	AGATGGGCATTGTGTCCCAT			
stSG119002	TGTTTGCTTGCTCTATGTTTCA	GCTGCTTTATTTTTCCACGAA	119562		
stSG119008	GAAAGAAGAAACCATCAGCCC	GCATCTTTCTCCAGAGCCTG	119565		
stSG119009	TTGCTACATTGCAGACCCTG	CCTCAGACCAGAGGCCTAAT	119566		
stSG119010	TCATGATCAGCTTCAGTGGG	ACAAAAAAAATCCCATCAGCC	119567		
stSG119011	CAGGCAAGGTCCATGATCTT	TTGGGGGAATAGGTCATTCA			
stSG119013	TGAAGTTTCCAAGCTGAGCA	CTGTTTGGAGGCAAAATGGT			
stSG119014	GCACTGTTGCTAGGTCTCT	TTTTAGTATGGGTCTGAGTATGC	119568		
stSG119015	ACTTTTGGCATTCTTCTGC	TGCAATAAACATCTTTCCATGA	119563		
stSG119016	TTGAGCTGGATCATTTTGTG	AAACAACGAATAGCAGGGTAGC	119564		
stSG119017	CCAAATGTGCGCACTCTACA	TGTTGCGGAACGAGTATCTG	119771		
stSG119018	TGCTAGGACATTTCTGAGAGCA	TGGCTCTGAATGACAGGC	119569		
stSG119022	CCTCTGTCTGTGTA AAAAGGG	TTGGAAGCAGACCTGCTTTT	119570		
stSG119023	ACCGAAGTGAATTTGAACAACA	CAGCTTCCCCTGGGTCAT	119571		
stSG119024	TGGAATGAAATGCCTCTTCC	GTA CTCAA AAGCAGCAGGATCC			
stSG119025	GTCAGAGGCCCATGTGAAAT	AGGAGAAGCAAGGAAGTGAGG	119572		
stSG119027	GTGCTGAGTCCCCGACTG	ACCTCCAACAGGGGTTTTG	119573		
stSG119075	TCAGTGGTGGTGTCACTGCT	TCAGGTCTTTGGACATGGTG			
stSG119076	GGATCAGAGCCTATGGCAGT	TGCCTTTTCATCAGCCTCTT			
stSG119098	GAAACTGCTAACAGCCCAGC	TCCTTCCTCCACGCTAAGTG			
stSG119120	ATTCCTGAAGCCCCTTCT	GTTCACTTCCCTGCATGTGG			
stSG119121	GATCACTTTACTGTAGAAGAAATGAGG	TTTCTTCTTCTTGATCTTCATTGG	119772		
stSG119555	GTGAATGTGTTTCATGTGCAC	GGTCTACTGTCCCTAGGATG			
stSG119556	TGAGCAGGAATGCAGTCTG	GTTCTGTCTGTTCAGGTA			
stSG119557	AGTGAGAAGCTACATTATCC	TAGAAATCATAAGGGAATAG			
stSG119558	TTCCTCCAGTGTATGCTGAG	CATAAGCAAATTTAACTCTG			
stSG119559	GCTCATCATTCTGAGACAAG	TGTA CTACCTAATCTAATGC			

stSG119560	CTTCATGTGACCTATCACTG	AATTCTGTTCTCCAGGTTGG		
stSG119561	ATTAATGCAAATATATTTCC	TGAAATAGATTCATATTG		
stSG119562	GTAGCAGATTTTCACACATG	TCATGACGTCTCTGCAATGC		
stSG119563	TTCTGATTGGAGATTGCA	AAGTTGATGAAAGTCCTC		
stSG119564	GATGCCAAATGAATATCA	ACTTAGGTGACACAGTTC		
stSG119565	ATAGTTGAAGGACTGCGCTG	TGTTATTCTTGGAGATTGAG		
stSG119566	GAGCATTACAGTGGAAC	AGATTCTTCCTATTCACA		
stSG119567	CTGTAACAGCTATGCACATC	CGTACTGTCACGGGATAATG		
stSG119568	ATCATGTTCTGGGTCTTCT	AGACCCAGCACTCATGTTAG		
stSG119569	ATAACATTGCCTAGAAACCG	CTACATTTAACCACATCAAC		
stSG119570	CCAATCACAGTCATCATGG	CAAGGCTACCTGCTGAGCAG		
stSG119571	CATCTCAGACCCATTCTACG	GGTCATGAGAGTCTGGTGTC		
stSG119572	TATAAAGATGTACACTGTGC	GGCTGGATTCTGCAGAAGA		
stSG119573	GCTTGCCATCACACAAAG	GAGGCTGGGATGTATTC		
stSG119771	CAGGAGTTCCTATAGGCTAT	TGATACAGCTGGAACAGGAG		
stSG119772	GAGTGAGGGAGAACAACAAC	GTGCATTAGAGTTGTTGGGC		
<b>stSG46776</b>	GTCCAGGGATCAAAAATGACA	CAAAATGAAGAATTGTGTGGAA	119561	
<b>stSG84327</b>	GAAGAGGATCTCAGGACTG	AGTTGGTGCCGCTGACCAG	85560	
<b>stSG84328</b>	CTGAGGAATCACCTAAGC	CAGATCTCAGAAGTGAAC	85559	
<b>stSG84329</b>	TGAATGTACACAGCGAAC	GTGCACAGGAATCTCAGC	85558	
<b>stSG84336</b>	TCCAGGTACCATTGCTTTCC	TCCCAAACCAATACTTGTCTG	87976	
<b>stSG84337</b>	TGTGAGAGTGGCTTCCTCCT	AAACGGTTTTTCACCAATGC		
<b>stSG84338</b>	GGTTAGGGCTGAATGTTTTCC	CCCAAGGATTTTTCTTGTGTAG		
<b>stSG84339</b>	GGGGCTCCAATCCTAGAATT	GGATCCAGACTGGAATATCGG		
<b>stSG84340</b>	CATGGAGCACACTTTCTACAGC	TCGTGCACTTCCAATGTTTC	87977	
<b>stSG84341</b>	TAGAATTTGATCCCATGCTGG	CTCGTCCTCCTTGGTAGCAG		
<b>stSG85558</b>	CATTGAAGTGCGCTCTTTGC	TAATTGACCTGCGCTTCAGC		
<b>stSG85559</b>	CCTCTGAAGTCAATGTTAAC	CATACATGTGGATTAGTGG		
<b>stSG85560</b>	ACTCAACCTTCTGAGGAAG	TCCATAGAAGGACACAATG		
<b>stSG87849</b>	CTTGGATTTTCAAAGTCCTTGA	CCTCTGATGCAGCAGGATG		
<b>stSG87850</b>	CTTGTTTCGTGCTTTTAGCAGG	GGGCTCTTCCCTTGGTAAAT	88201	
<b>stSG87852</b>	TTACATAGGCAGACTGGTCCG	GGTGAAAGGGCTGAAGCTC		
<b>stSG87853</b>	TTCTGCTGTCTTTGGAACTTTG	TCTTCAACATCGCCACCC	88203	
<b>stSG87854</b>	AGCTTTTTAGGCCAAGTGGC	TTGCTAGCAGCCATGACGT		
<b>stSG87855</b>	AGCTTTTTAGGCCAAGTGGC	CAGATGTAGTTTGGCACAGCA		
<b>stSG87856</b>	TCATGAGTGGGGCAAATACA	AGACCACTCTAAGGACTGGGG		

<b>stSG87864</b>	GAATCTGCTCCCACAGTC	GTAGAATAAGGTGGTGATG		
<b>stSG87865</b>	GCGCGCACCCAATTCAGTC	CGGCAGGTGGCCAGATC		
stSG87976	AAGCCTGTTTCGACTTCTGC	GGATAAATACAGAAGCCATGCC		
stSG87977	TCAGAAGACAATGCAAATCTGG	GCTGAAATGCATCGTAACCA		
<b>stSG88115</b>	CGCTCCCGTTCGGCTCCTC	TGGCTTCGAGGAGCCGAAC		
<b>stSG88151</b>	TACTCTGAGGCAAGCACTGG	CATGGATGTCAACCAGCAAC	88152	
<b>stSG88152</b>	AGTCATCATGGAGACCTG	AAGGTGGTGATGACTGAG		
<b>stSG88153</b>	TGCACTCACGAGCTTCTGAG	ATATCTTCCCATCTGCGTTG	88154	
<b>stSG88154</b>	AGATTGCCAACCAGCAGC	TTGGCGCCTTTGCCTGCG		
<b>stSG88155</b>	TCTGTGTAACCTTCAACC	TGAGCCTGTAGTGGCATG	88156	
<b>stSG88156</b>	GAATCTGCTCCCACAGTC	AGAGGCTTAGGTGCACTG		
<b>stSG88162</b>	GCGCGCACCCAATTCAGTCG	AAGTTGGTGCCGCTGACCAG	88163	
<b>stSG88163</b>	TTCGGCTCCTCGAAGCCATG	AATGCTCCATAGAAGGACAC		
<b>stSG88169</b>	CGATTAACCTTCCAACGCAT	GAGGAGGCCAAAGCAAAAAG		
<b>stSG88170</b>	TGACTCAACCGCCATAGTTG	TATCAGCAACAGCAGCAGCT		
<b>stSG88171</b>	CCAGATTGTGAAGGTAGAAGGG	GTGTGGCTTGTGTTGACAATG		
<b>stSG88172</b>	TAAAACACTGCCCCCCT	GTAATTGTTCCCTGCCTCCTCC		
<b>stSG88173</b>	TGTGTCAAGGGCTCAGGAG	TTTCTGGCCCCTACCTCC		
<b>stSG88174</b>	CACACCCGTTAGGCATTTG	TGCGTGAATGTCTTTGCTTC		
<b>stSG88175</b>	GCAAGCAGAGGAAGCGAG	AAGAATCCATGACACTCACGG		
<b>stSG88176</b>	TTACCAACAATGCTACGAATGC	CCATCAAGGCCTTAAGGACA	93105	
stSG88201	TGATTACATGGGCCGATTC	AGCAGGTGCCAGCCCAGATC		
stSG88203	ACAGTTAGAAGATGCAGC	GAGCCCTTGGGCTGCATC		
<b>stSG88327</b>	GGAGCAGAGTCTTGGAGCC	TTCACGACATCTTGGAGCAC		
<b>stSG88328</b>	CGAGCAGTACCGCATGTG	AGCTTCGCTGTTTGCCTGT	93106	
<b>stSG88329</b>	AAGCCAAAATGTGGAGAAGC	TTTCTCCATCTTCTTCTTGAA		
<b>stSG88330</b>	ACTGAAGATGGTCACACACAGG	GAGAGCCAAAGGGAGCAAG		
<b>stSG88331</b>	TCAAAGAAGAGCAAGATGTTGG	TGGAGAGTCCATGTGGGC		
<b>stSG88332</b>	AAAATTGAGCTTGCAGGGG	GTTTCATCAGCTCCAAAGTGC		
<b>stSG88333</b>	CTCGTGTGGCCCTACACC	CACAACCCCTCTGGGTAATG		
<b>stSG88334</b>	TGTCTTCTGCTGCTGCTTGT	CCACTGGCAGTTGCCTCT		
<b>stSG88335</b>	TCTTCGGGGACAGCTTTG	CGATGCGGTCCAGTATGTC		
<b>stSG88336</b>	TTGCTTTTGGTGACCTGAGG	GATCCATGACATATTGGACCG		
<b>stSG88337</b>	CCTGAATGCCAGGATGATG	TTTTGCAGCTGTTTCTGGTG	93107	
<b>stSG88338</b>	TTGTCCGTGGTCACCTCAT	ACCGGGTGAATGTCTTCTTG		
<b>stSG88339</b>	TACCAACTATAGCACGGCCC	TCCACTGTCTTGTGCCTCAG		

stSG88340	GGGAGCTGGACAGGAAGAG	GGAGACCACAGAGAAGCTGG			
stSG88341	ACCTTAGGATGACTAGGGAGCC	TGGTTGCTAATATGCAGTCCC	93108		
stSG88342	AAGCGAAAATACACAACCCG	ATGTGTCAGCTCCTGCAGG	93109		
stSG88343	CTGGGAGTTGTTCAAGGGAA	ACTTGAAGCAATGACTTGTCA	93110		
stSG88344	TCTGGTGTCTCAGGCTG	TGTCCGTTGAGTAGCGTCAG			
stSG88345	CTGGGAAAGAAGTTCGTGCT	TTCATGGTCACATGATGGCT			
stSG88346	AGCCTCTGAACATCCCCTG	CACCTTCTCTAATGTGACCTGC			
stSG88347	TCTGGGTCTGACATCAACCA	CTCAGTGGCTACCAACCCAT	93111		
stSG88348	CAAAAAGAAAAACAGACAGGGG	TCCAATGAAAACCACCCATT	93112		
stSG88349	TGGTTGCTAATATGCAGTCCC	ACCTTAGGATGACTAGGGAGCC			
stSG88350	TGCGAAAGAAGAATGAAATGG	CCAGTTCCTTGTGTATCCATCC			
stSG88351	TTCCTGAGGGAAGACCTCAA	CCATGCCTTCCACAGGTC	93113		
stSG88352	ACATAATCTTCAGCCGGGC	AGGTGATGAGGGACAACCTGG			
stSG88353	TGCAGCCCTTGTTTCACTC	AAGGAAAGCCAGAGAGTGAGG	93114		
stSG88354	TGCTAATAAAGGGGAGCCCT	TCTCACCTCCTCCCAATC			
stSG88355	CAGTGGCCCTTTTCAGATCT	TGGAAGATCTTCACCGAAGG			
stSG88356	ACTTGCAGGGGTATCGATTG	CTATTCTCATGGCGAGTCTG			
stSG88357	TGCAGTTCACGCAGTAAACC	TTGCATGTTTCAAGACAAGAAG			
stSG88358	CCCTCAAACCAGATGCAAGT	CCAGTTTGGGCCAGAATAGA	93117		
stSG88359	TCCTTATCCTGGGAGGAGGT	ACCCTGCGGTTTTGTAACCTG			
stSG88360	AAAAAGCGACTGAGAAAAGTGC	TATGGGAGGGACAAAGTTGC			
stSG88361	AGTTTCCGCGTGGTTTCTC	TCTATTTCCGTGGCTATGGC			
stSG88362	CAGTGATGGTAGCAGCTCTCC	CATCTACCTTCTGAAGATGGGG			
stSG88363	TGATTGAAACTCCTCTGGGG	CGTGATTTGCAGTGCCAG	93118		
stSG88364	AAGAAGAAAAACCCAGAGGTCC	CTTCTTGCCTCCCTCAACTG	93119		
stSG88365	CCCACAAGGGTTGAGAGTGT	ACGTGAGCCAGCTGTTCC			
stSG88366	CCACCAAAATGTAACACAATGC	TGATTTTTCATGTCACTGGTCA			
stSG88367	TCTCACCTCCTCCCAATC	TGCTAATAAAGGGGAGCCCT			
stSG88368	GGAATTCCTCCAGGTGTC	TTGGCTCAGTGACCTTGATG			
stSG88369	AGATACTCCAGTCAGCAGAGGG	CGAAGAAAGTGGTTCAACAGC			
stSG88370	AGTTAATCAAACACTGGCCCC	TCCTAAGGTTTTCTGGGCAA			
stSG88371	GAGAGGGAGGCAACGAGAG	CTCAATGGTCAGGTGCCC			
stSG88372	GTGATGCAGGAAGAGAGCG	GATCGAACCACCACAGGC			
stSG88373	TGAAGAAGGAAGCTCTCCTCC	TAACAGTGGTCCGACCATCA	93121		
stSG88374	TTGAAATCCTGATGGAGATGC	TTGTGATCTCTGCAACATGATG			
stSG88375	AGCCAGCATGAAAGGACG	CAGTCCCTGCACACATATGG			

<b>stSG88376</b>	GCTCCTGCAGCTGAAACTG	AGCTGAAGCAAGAGCAGGAG	90808		
<b>stSG88377</b>	AGTGTTTGTGCCATTGGCA	GTCCCTTCCCCTACCACAAT			
<b>stSG88378</b>	TTTTGCAATAGGCTGGGTTT	ACCTTTTCTAGCAGCTGCCA			
<b>stSG88379</b>	AGAAGAATCCCGCCATTTG	TCTTGATTTCCATCATCTGCC			
<b>stSG88380</b>	GATGTTCAAGAAAATTCGAGGG	TAACATTGCCAGCTGTCTGTG	93122		
<b>stSG88381</b>	TTTGACTCCTGCCTTCCG	CATAATGAGAAGCTGGGGGA	93123		
<b>stSG88382</b>	AACTATGGTGGTTCTGTGAGGG	AATGGCAAAGACGAGTCCC			
<b>stSG88383</b>	TGAGACCAAGTCTGTGCCTG	AACGAGCGCCACCTACTG			
<b>stSG88384</b>	GTGTCTGTGCCCGGAAAG	AATCAGGGCCCCGAGTAG			
<b>stSG88385</b>	CAAGGTTGTTGCTGAGACGA	TCATTTTTACATGTGGAGCTGG			
<b>stSG88386</b>	TCTTCGGGGACAGCTTTG	CGATGCGGTCCAGTATGTC			
<b>stSG88387</b>	AAGAATCCATGACACTCACGG	GCAAGCAGAGGAAGCGAG			
<b>stSG88388</b>	GTGTGGTGCAAGTGACCATC	GGCTCCATCTCCTTCTTATGG	93126		
<b>stSG88389</b>	AGAAGTTGGAATCATTGTTGGG	AGTTCCGCGATGGTCTTAGA	93127		
<b>stSG88390</b>	AAAAATGTGCCGTGCCTTC	AGGGGTTTCCAGGCTGAG	93128		
<b>stSG88391</b>	CCTTCCCCGGAAAGAAATAG	ATTCCTCATTGCAGCAGCT	93129		
<b>stSG88392</b>	TATCCCAGGAGCCCTGCT	AAAGCCAGAATCTTTGTTCAGC			
stSG90808	GCTGTGGTCCCTCAGCGGTT	GGAGGAGCCGCCCCAGACGA			
stSG93106	CAGTCTAAAGCCATGGATGA	GCCTGTTTATGAAGATGCGT			
stSG93107	CACCACCAGCTCCACTCACA	TGGGCAGACGATCTCCACTT			
stSG93108	CGGTAGATCAGGAGCAGCTT	GATGGCAGAACATGCCAAG			
stSG93109	GAAACCTGTGACAATGAGA	GTGATGATCAGATTCTCAA			
stSG93110	GGATTATTCACATCTTATGA	CACTACTCATAAGATGTGAA			
stSG93111	CTCTGTTCTGTGTGTTTCT	CAAAGAGGACATATGATTCT			
stSG93112	CAAGGACTCTCAGGAGGACT	CCTTGACACATCTCCACATT			
stSG93114	CTCTCCTTCACTCTCTGGCT	GAGGGAGGGAGAGTCAGAGA			
stSG93117	GATATTGATGTGGATCTCAA	CACATGGTTGTTCCAGAGGA			
stSG93118	CCAAGATCCCACCTTATCAT	CTTCGGATTAGGCCATACT			
stSG93119	CCAAGAAGTGCTCTGAGAAG	CATTATCCTTCATTTCTGA			
stSG93121	CATCCCTAATGCCTGAAG	CTTGATCTGCCCATTTTCT			
stSG93122	GTTTACATGACTATGGCTTA	GTAGTGCATTGGAGGATCGT			
stSG93123	GTGCCAGATTATTCCTGTGT	GATGGAGCAATACAGCCAAT			
stSG93126	GACGGTTTCGTGAACGTGA	GAAAGACCACTGGATGGAA			
stSG93127	GATTGGTAGCCTGGTAGGTG	GCCTTATTCTTGCGAAGCA			
stSG93128	GTGCTGACACAGCTGGTGA	GCAGAGGTGCCCTTACTCT			
stSG93129	CATGGAGCCTAGGAGCAGAG	GACTTGCTGTAGCCATATAA			

stSG95448	AGTACGAGGGCATTGAGTTCA	TCTGGGCTTATCCTCCACAG			
stSG95449	CCCTTTGCAATATGTTGGCT	GAGCACTAGGAAGGGCACAG			
stSG95450	AAGGAAAGTCGAGAGGCTACG	CAGATAGGCAGGTAATGATCCC			
stSG95451	CAGATGTAGTTTTGGCACAGCA	TGCTTTTTTTCAGACCTCTTTCTG			
stSG95452	GATGGTGTCCCATGCTCAG	CTGGACTGGATCTGCTACTGTG			
stSG95453	CTGCAGCTGTCAAAGGTGAA	ATTCTGCCTGTCACTGTCCC	101248		
stSG95454	TACTGAGATGGGTCTTCGGG	TGCTTCAGTTTTTTCATCTGTGA	101249		
stSG95455	GAGACCGGTGGCCTGTTT	TCACCTGAGTTCTGGGCTG			
stSG95456	CAATCGGATGTCTGGGTCTT	TGCTGCTGCTAGTAGAAACTGC			
stSG95457	GGAGCTCTTACCCTGGACC	TTCTTTGAGCCTGTGGCC			
stSG95458	GACGCTTAGAAGCAGAGCGT	TAGCATGCTACCCCCTGTG			
stSG95459	CCCGACATTTGTCTTGGTCT	CCTGGGGAATCCTTCTCTTC	101252		
stSG95460	AAGGACACCACCTGGTCAAG	TCATCCATGGACAGCCCT			
stSG95461	CACACTGGAATGGCATTGAC	GAGTTGTTATCCCAGTTGGAGG			
stSG95462	CAGCCTCACAGCCCTACTTC	GCCTGATTAGGAAGGAAATGC			
stSG95463	GATCAAAGTACTCCAGCAGCG	TCGTCTCGCTTTTTCTTCCAT			
stSG95464	CATCAATGAAGTGTGTCGGG	GAACCTTAGCACATCCACTTCC	101247		
stSG95465	CAATTCCATTCTCCTCCGAA	GGAAGAAGAGCACAGCCAAC	101250		
stSG95466	AAGTTCAGATGACCCAAACAGA	CCAACCATTTGTCTGCTGC			
stSG95467	CTGAAGGAAAGCTCCACATTG	GGCATTCTACAAAGCAAAAACC			
stSG95468	GAACCTCGTGCTTTCCCC	GAAGCCTCCGAAGCCTGT			
stSG95469	AGAAGAAAGAAGGAGGAAATGG	CTTACCCACACGCTGCAGC			
stSG99719	CAGTTGTGAGCCTGAATACAGG	TCTGATAGTCACACTGTTGGCC	101254		
stSG99720	TAGGAAGTCAACCCCCATTG	TGGTACTTTGGGACATCATTG	101255		
<b>Section 2</b>					
stSG number	Primer 1	Primer 2	Product size (bp)	Pre-screen	Intron spanning?
stSG158910	CTATTCATTTTCTCCACCTTGTTT	TGTCACTTATGCAGAAGAAATAGC	225	60	no
stSG158921	TGGGTAGAAGAATAATGAGTGATCTTT	CACCTTGCTTCATTCCCAACA	130	60	no
stSG158922	CAGTTTGATGTACCTGCGTGA	TTTGCAACCCTTCACTCTGA	196	60	no
stSG158923	TAAGGCTTTGCCCTCTGAAA	TTGCTGACACACTCAAACCAG	238	60	no
stSG158924	TGTCAAGCAAAAAGAAATGCAAA	TGCATAGCCAACATCCAAGT	204	60	no
stSG158925	AGCCTGGTGTGATTGATGTG	TGAGGGGTATTCTGACAAAGAGA	199	60	no
stSG158926	TCCCCAGATCCTTCAACAAC	CCTCAGGGCTAGAATTTTCAGA	157	60	no

<b>Section 3</b>					
stSG number	Primer 1	Primer 2	Product size (bp)	Pre-screen	Intron spanning?
stSG453287	GAGATCCTAAAACACATCATCCAT	TGGCTATAGCGAGGAAGAGG	178	60	no
stSG453288	TTTCCAAGTTCGTTCTGTGAGA	CTGGCGTTTATTGAGGGAGA	150	n/a	yes
stSG453289	GGGAAGTGTAGCTCCCAGGT	AAGTGTCAGGGCTGTGGAAG	150	n/a	yes
stSG453370	GAGATCCTAAAAACCCTCATTTC	GCAGGGCCTGGGATAGAA	173	60	no
stSG453302	AGCCTAAGGCCTGGCTGAC	CAGAGCAACTGGCTCTTTGG	81	60	no

## Appendix A.1

This appendix lists the clones/accession numbers from human Xq22 and represented in the sequence contigs of Figure 3-9. The column headed 'SEQCTG' indicates which clones/accessions are contained in the numbered sequence contigs of Figure 3-9.

SEQCTG	Accession	Clone name		SEQCTG	Accession	Clone name
seqctg1	AL109750	dJ902O5		seqctg2	Z70228	cV411C1
seqctg1	AL022148	dJ435A7		seqctg2	Z70758	cV434E11
seqctg1	AL606759	bK2319N17		seqctg2	Z69304	cV311G7
seqctg1	AL590293	bA227B10		seqctg2	Z68868	dJ3E10
seqctg1	AL137843	dJ377O6		seqctg2	Z68326	cU163D10
seqctg1	AL358953	bA552B20		seqctg2	Z80107	dJ197J16
seqctg1	AL390027	bA368G3		seqctg2	Z97355	cU230G7
seqctg1	AL590012	bA40I8		seqctg2	AL035214	dJ122O23
seqctg1	AL359641	bA402K9		seqctg2	Z70719	cV351F8
seqctg1	AL355593	bA99E24		seqctg2	AL133277	dJ158I15
seqctg1	AL590412	bA557A17		seqctg2	Z70689	cU19D8
seqctg2	Z93928	dJ127B14		seqctg2	Z70226	cV1077H7
seqctg2	AL035608	dJ479J7		seqctg2	Z68332	cV775G11
seqctg2	AL391688	bA524D16A		seqctg2	Z81367	cV618H1
seqctg2	Z73900	cU85H7		seqctg2	AL590069	bA353J17
seqctg2	AL391689	bA524D16B		seqctg2	AL035609	dJ77O19
seqctg2	Z95327	dJ347M6		seqctg2	AL035551	dJ1100E15
seqctg2	Z83819	dJ146H21		seqctg2	AL035427	dJ769N13
seqctg2	Z73417	cU131B10		seqctg2	AL590407	bA522L3
seqctg2	Z97985	dJ341D10		seqctg2	Z68871	cU157D4
seqctg2	AL133275	dJ1053B6		seqctg2	AL669904	dJ1054G24A
seqctg2	AL109952	dJ664K17		seqctg2	Z95624	cU237H1
seqctg2	AL109963	dJ1188J21		seqctg2	AL645812	dJ1054G24B
seqctg2	Z70280	cV210E9		seqctg2	Z93943	cU235H3
seqctg2	AL022155	dJ302L24		seqctg2	Z75895	cU61F10
seqctg2	Z70281	cV526F1B		seqctg2	Z73361	cU73E8
seqctg2	Z68331	cV521F8		seqctg2	AL008708	dJ198P4
seqctg2	AL109801	dJ738A13		seqctg2	Z75746	cU221F2
seqctg2	AL035422	dJ164F3		seqctg2	Z85997	cU101D3
seqctg2	Z69838	cV1164A6		seqctg2	AL035494	dJ635G19
seqctg2	Z68873	cU209G1		seqctg2	Z81014	cU65A4
seqctg2	AL133280	dJ514P16		seqctg2	Z68694	cU177E8
seqctg2	Z73913	cU61B11		seqctg2	AL133348	dJ79P11
seqctg2	AL121883	dJ545K15		seqctg2	Z92846	cU105G4
seqctg2	Z83131	cV602D8		seqctg2	AL606763	bB349O20
seqctg2	AL392164	bA269L6		seqctg3	AL079333	dJ823F3
seqctg2	AL672206	dJ232L22		seqctg3	AL117327	dJ421I20

seqctg3	Z69733	cU250H12		seqctg3	Z75747	cU96H1
seqctg3	AL035444	dJ43H13		seqctg3	AL391070	bA539A6A
seqctg3	AL021308	cU246D9		seqctg3	Z70225	cU165H7
seqctg3	Z73965	cV857G6		seqctg3	AL391071	bA539A6B
seqctg3	Z68327	cU25D11		seqctg3	Z74619	cU232G2
seqctg3	AL049610	dJ1055C14		seqctg3	AL022168	cU247E12
seqctg3	Z93848	cU35G3		seqctg3	Z70051	cU92G6
seqctg3	AL034409	dJ764D10		seqctg3	AL133272	bA229F9
seqctg3	Z73964	cV698D2		seqctg3	Z69367	cU159B9
seqctg3	AL139228	dJ540A13A		seqctg3	Z99706	cU226D1
seqctg3	Z75896	cV461C10		seqctg3	Z73967	dJ315B17
seqctg3	AL139229	dJ540A13B		seqctg3	Z68330	cU9D4
seqctg3	AL390022	bA370B6*		seqctg3	Z68908	cU227D1
seqctg3	Z70273	cU116E7		seqctg3	Z68328	cU72E5
seqctg3	Z70227	cV362H12		seqctg3	AL139813	dJ312P4
seqctg3	AL034485	dJ839M11		seqctg3	Z70274	cU84B10
seqctg3	Z73497	cU240C2		seqctg3	Z97356	cU25E4
seqctg3	Z74620	cV467E10		seqctg3	Z69734	cU71B4
seqctg3	Z82254	cU46H11		seqctg3	Z68339	cU230B10
seqctg3	AL135959	dJ233G16		seqctg3	Z83850	dJ82J11
seqctg3	AL049631	dJ513M9		seqctg3	AL512661	bA560L11
seqctg3	AL121868	bA541I12		seqctg3	Z69722	cU212C1
seqctg3	AL136977	bA230E14		seqctg3	AL135922	dJ875J13
seqctg3	AL133385	dJ81E11		seqctg3	Z68289	cU50F11
seqctg3	AL133381	dJ406H21		seqctg3	AL133271	bA155N17
seqctg3	AL050401	dJ519P24		seqctg3	AL139812	dJ19N1
seqctg3	AL121866	bA191C22		seqctg4	AL590306	bA565G2
seqctg3	AL021812	cU86H4		seqctg4	AL606515	bA575K24
seqctg3	AL008642	cU18H8		seqctg4	AL590808	bB483F6
seqctg3	Z70224	cU144A10		seqctg4	AL606833	bA647M7
seqctg3	Z80774	cU173H7		seqctg4	AL391315	bA150F24
seqctg3	AL442225	bA40K1A		seqctg4	AL591849	bA321G1
seqctg3	Z69724	cU85B5		seqctg4	AL158821	dJ75H8
seqctg3	Z95333	cU116E9		seqctg4	AL390039	bB383K5
seqctg3	AL512445	bA258F8		seqctg4	AL136112	dJ1126E12
seqctg3	Z68872	cU161B10		seqctg4	AC004081	dJ320J15
seqctg3	Z70232	cU139A4		seqctg4	AL035088	dJ3D11
seqctg3	Z75745	cU107D4		seqctg4	AL137787	dJ1070B1
seqctg3	AL133276	dJ114N20		seqctg4	AL772400	bA540N4
seqctg3	Z71182	dJ248J6		seqctg4	AL590423	bB364K23
seqctg3	Z70040	cU174H1		seqctg4	AL109946	dJ820B18
seqctg3	Z75957	cU203H4		seqctg4	AL034399	dA191P20
seqctg3	Z74477	cU42H12		seqctg4	AL953860	dJ1107B12
seqctg3	Z81144	cU129B7		seqctg4	AL031177	dJ889N15
seqctg3	Z69721	cU201H11		seqctg4	AL136080	bA448E12

seqctg4	AL109943	dJ657D12		seqctg7	AL392112	bB266I11
seqctg4	AL034369	dA149D17		seqctg7	BX088563	bA1066D24
seqctg4	AL031622	dJ740A11		seqctg7	AC000114	dJ527C21
seqctg4	AL136364	dJ734E5		seqctg7	AL034450	dJ115K14
seqctg4	AL035425	dA24A23		seqctg7	AL137124	bA485M23
seqctg4	AL928697	bK2004P2		seqctg7	AC004827	dJ44L15
seqctg4	BX322556	yR4AC12		seqctg7	AL078580	dJ874H6
segqctg5	AL732308	bA199F23		seqctg7	AC002072	dJ218B13
segqctg5	AL670405	bB148E24		seqctg7	AL023876	dA111F4
segqctg5	AL928646	bK2328D6		seqctg7	AL023877	dJ1142C11
segqctg5	AL731796	bB344M15		seqctg7	AL772262	bA444C24
segqctg5	AL390836	bB179C6		seqctg7	AL031183	dJ1168A5
segqctg5	AL034403	dJ31B8		seqctg7	AL030995	dJ1170D6
segqctg5	AL031387	dJ596C15		seqctg7	AL442070	bA468C24
segqctg5	AL118496	dJ136J15		seqctg7	AL050311	dJ964N17
segqctg5	AL138968	dA13I1		seqctg7	AL049859	dJ826A18
segqctg5	AL590647	bA130P9		seqctg7	AC002449	dJ402K21
segqctg5	AC003013	dJ205E24		seqctg7	AC003014	dJ290B4
segqctg5	AL590384	bA349A16		seqctg7	AL513476	bK2335J1
segqctg5	AL360224	bA471A8		seqctg7	AC004998	dJ164D5
segqctg5	AL359079	bB360B22		seqctg7	AC000055	dJ73F11
segqctg5	AL079334	dJ300O13		seqctg7	AL953888	dJ137P21
segqctg5	AL031319	dJ364I1				
segqctg5	AL137844	dJ557A17				
segqctg5	AC000113	dJ302C5				
segqctg5	AL360174	dJ465D4				
segqctg5	AL512882	bA441A11				
segqctg5	AL049176	dA141H5				
seqctg6	AL591489	bA814C6				
seqctg6	AL590809	bA733H21				
seqctg6	AL356578	bA14G9				
seqctg6	AL357774	bA473N15				
seqctg6	AL117326	dJ944N9				
seqctg6	AL031117	dJ914P14				
seqctg6	AL450490	bA124N4				
seqctg6	AL035067	dA170F5				
seqctg6	AL589880	bA111F16				
seqctg6	AL096764	dJ298J18				
seqctg6	AL049563	dJ68D15				
seqctg6	AC005191	dJ269O5				
seqctg6	AL031388	dJ737M10				
seqctg7	AL929583	bB530G12				
seqctg7	BX119929	dJ1150P3				
seqctg7	AL031223	dJ1041B16				
seqctg7	AL031176	dJ124K22				

## Appendix B

This appendix contains primers used in the studies presented in Chapter 4. stSG numbers, primer sequences and optimal pre-screen annealing temperatures in °C where determined are given. ND denotes pre-screen not determined. A fail denotes an instance where the pre-screen failed to give a clear result.

stSG number	Primer 1	Primer 2	Prescreen
stSG136026	TTCTGGTGTCACTTGTTC	TATACTGAGCATCTTCCC	60
stSG136027	TTCTCTGAAGATGACATG	TACGGATCTTCCCATGCA	FAIL
stSG136028	AACCAGCATGTGTTAGCC	GACCTCTCTTTGGATTCT	ND
stSG136029	GTCACCAGCTTTAAGCTGA	AGCTGAGTAGGCCATTCA	ND
stSG136030	TGGAATCTATTTCTTGGT	TGTTATTTCACTTTCCAACC	FAIL
stSG136031	ATGCTGGTGGCAATTCTAC	CGAGAACAACATTTAGAAG	60
stSG136032	ATGGACTTTCCACCTGAAC	CCCTGTTGGTCTAAGGCT	60
stSG136033	AACAAAATGAGCTTCTGAT	TGGCAAATACAATAAGCAG	60
stSG136034	GTTGATGCGTTAGTTGGT	GCTAATGTTTTCGCAAAG	60
stSG136291	TGAACAATGAAGCTGCCAC	TTTTTTTTGACACCATCTT	60
stSG136970	GCCAAGCCCTAGCCTCTC	ACAGTGGCCAGCCAAAAG	60
stSG136971	CGAACTGGAAAGCAGACTCC	ATTTGCTGCTTTTGGGTCC	60
stSG155403	TGCTGCCACTTACAACCTCG	ATCAGTGGCAAAGGCAGAG	60
stSG155404	ATCCATACTGTGACTCCCGC	AAGCTGGCAACACAAGCC	60
stSG155405	GGGTTTTGCTCATGAAGCAT	TGCGCATTGTAAATTGCATT	60
stSG155406	CGAGCAAGTACTGAGTTTGC	CATCCTGGTGTTCAAGCC	60
stSG155407	GCCAATTACGTGTCTGGGTT	GGCACTGAATAGTTTTTTG	60
stSG155408	CCTGTGGCAGGTTCTAGCTC	TGAGAGTTGGATCACAGTTT	60
stSG155409	CCCCGAAGAAGTGATAAGAG	AGGCCTGAAGCACACAGG	60
stSG155410	AATGCCTTCAGCCTTTCCTT	GCACATGGGTGAAAGTCCTT	60
stSG155411	CCCCCTAAAAGCCCCATATA	CATTTGGGGGACAAAATTTG	60
stSG155412	TCCCTGTCCAGGAACTTC	AAAAATGGAATGCTACAGAG	60
stSG155413	CACTTCCAAGTCCATGCCTT	GGAAAAGGCTTGCAGAAGAA	60
stSG155414	CCCTTGATACCCAAATCCCT	CTGTCATTTTCAGGGGCAAT	60
stSG155415	ACCCAGAAAGAGCAGAAAT	TTCCATGACAAAGAAACAGAA	ND
stSG155416	TAAGAATAAGCCCTCTTTGGG	TGCATTGGACAGAAAGAGACC	60
stSG155417	TTCTTTGGCCTTCTTCTCCA	GCCCACCTCTCAATTATGGA	60
stSG155418	AACCAAGAGAGTAAAAGGAGCC	TTCTTCAAATCCATGAGATGG	FAIL
stSG155419	ATGAAAACAAACCACTGCAGG	GCTTCTGATCAAGATTTCCCC	55
stSG155420	CCATCCAGATAGCCAAATGG	TTGCAATTAATGACAGTGATGC	60
stSG155421	TGCAAAACCTGAGTCATCCC	TTATCCAGTGAGGAATGTGGC	60
stSG155422	CGTCAGAAATTGTGGGAAGG	CTTCCTGCTATGCAGCCTCT	60
stSG155423	CATGCATAATGGACACCATAACC	GACTGCATTGCAACTGAGTCA	60
stSG155424	CAGAGAGCCACATGAATGTCA	TGGGGCAGTGACTTTACACA	ND
stSG155425	CTCCAGGAAATCCTGATGGA	TCCACTAAATAGAATGGGGGG	60
stSG155426	AAAAAAAAAAAAACAGAAGGGGC	GAGACTTGTGATGATGCTCAGC	60
stSG155427	ATGTCACGTCACTGAGCTG	GGAATTTGCCATTAGATGAGG	60
stSG155428	TGAGCTTTGTGTCAGGGATG	GGTCTCTTAGACTGGGATGCC	60

stSG155429	GCTGCGGTGTTTATACCTATG	CACATAAACGAAATCATGCTCA	60
stSG155430	ATGACATGGAGAAAGCAGGG	GGCACTAAGCAATTGGTGGT	60
stSG155431	TTGTCCCTGAAACAAAAGCA	TTTGTTATGTACAATGTTGGCC	60
stSG155432	TGTATCCATTTCCCTCATTGC	CAAGTACCCACCTGATGCT	60
stSG155433	GATGGATCATTTCATGGATGG	ACAACAGCCAAATACAGCCC	60
stSG155434	ACCTTTCCTGGAACCCTCAT	CTGGAAAATAAGTTTCATGGCA	60
stSG155435	ATCATTCTCTAGGCCTGCCA	CCCAGCAAACATTCCATTG	60
stSG155436	TCTCCAGGCTGCTAGGATGT	GAAAAAACCCAAGCAGAAAGG	60
stSG155437	AGGGCAGCGATCTGTTTG	GGATTATCCCAGGGACACCT	60
stSG155438	CTGCTCATAACCCAAATCTTCC	ATTTCCACGGAGTGAGATGC	60
stSG155439	CCATTGTTCCACACAGCAAG	TTTACCCAAAGGGAGTGTGC	60
stSG155440	TCTAGCACGGCAACAGTCAC	ACTAACAGAAAGGGCCTTTGG	60
stSG155441	TTTCCTCTGAATGGACAGTGG	GGGGGGGAGGTGAGATATAA	60
stSG155442	TAGGCAGCGTTGATAAGTTCTG	CAACATGCCTATCCACAAAGG	60
stSG155443	TGGTTACGTGTTTTCTTTGC	GTGGCAATATGCTACAGACTGC	60
stSG155444	AGTCGAAAGGGCTGTGAGAA	GGGTTACAGCTTGCTCTTCG	60
stSG155445	TCCTTTTTGTTGTTGTTGTTGC	AACACCTATCCACCCAAAACC	60
stSG155446	CCAGCCAGTTTTTAGTGGCA	AGGAGTCAATGGGATTTATCCT	ND
stSG155447	TTATGTACTGCGTGGAAGCG	GGGAATCTTCTGTTGACACCA	60
stSG156835	TGGGATTTATCCTAGGGCTTA	CATTGAAAATAACACTTCCATGACA	ND
stSG156883	CCATCCAGATAGCCAAATGG	TTGCAATTAATGACAGTGATGC	ND
stSG156884	TGTCAAACCTGAGTCATCCC	TTATCCAGTGAGGAATGTGGC	ND

## Appendix C

This appendix contains information for primers used in the studies presented in Chapter 5. stSG numbers, the locus the STS was designed to, the primer sequences, expected product sizes, optimal pre-screening annealing temperatures in °C and indication if the primers span introns are given. N/A denotes instances where a pre-screen was not performed as the primers span an intron.

stSG number	Locus	Primer 1	Primer 2	Product size (bp)	Pre-screen	Intron spanning?
stSG158852	dJ77O19.CX.1	AAACTTACCATTGGTGCATATG	CAATGGAAGCACCCATCA	137	60	no
stSG158853	cV362H12.CX.1	AAACTTCCCATTGGTATGTAAG	AACTATTGAGGCACCCATTG	139	60	no
stSG158855	dJ198P4.CX.1	CCCTAAAGTTATTACGGAAACAGA	CCACGTAACAAGTGACAGGT	96	60	no
stSG158856	dJ79P11.1	CCCTGAAGTTAATAGGGAGACC	CCCACAAGAAATAGGTAACATCA	95	60	no
stSG158857	dJ635G19.2	AGGCACTATATGCGCTTCC	CATTAACCTCAGCGAAAACCTT	94	60	no
stSG158858	cV351F8.CX.2	ATGTGAACCTTTTGGCATTCT	ATGAAAGTTGATGAAAGTCCTCT	103	60	no
stSG158860	NGFRAP1	GAACCCTATGTTATTTCCATGTGTC	ACTACTGCTGACAGAACTTACACTG	99	60	no
stSG158862	dJ769N13.1	GTCCTGGTTCTGGGATGGA	CCACAGTTGCTTCCATTGT	246	60	no
stSG158864	dJ769N13.CX.2	CCATTTTCAGGGAAGTTAAAGAG	CTTACTTAAAACGAACTGGTTTGC	291	60	no
stSG158865	dJ1100E15.CX.3	TAAGACAAAACCCCTGGCAGA	AATGCTGGTCTCTTCCCTTC	199	60	no
stSG158866	dJ769N13.CX.1	GGTCCAAGCTCAGGACAAATAG	TTTCTGGGCCCTGAGTTTCA	161	60	no
stSG158869	cU250H12.CX.1	GCTCCAGGAAAACTCTGGTTA	CCCGTGAGAACTGAAAACCTA	82	55	no
stSG158870	cU237H1.1	GCTCCAGGAAAACTCTGAATG	CCCATGAGAACTGAAAACGT	87	55	no
stSG158871	cU237H1.1	ACAAGATGTTCTACAAGATATGAAGC	TCTTACTGACCCATTGAAACCA	100	55	no
stSG158905	cU116E7.CX.3	CCATTTCCCTTTCATCTTTTC	CTGGAGCCTCTGCTTGTGTT	112	n/a	yes
stSG158906	cU46H11.CX.1	CATTTCCCTTTCATCCGTGA	TTTCTGGAGCCTCTGCTC	119	n/a	yes
stSG158907	cU209G1.CX.1	TCTGGAAGTAATGCACATTGTAAG	CCACACAAAGGACCAAAGATTAC	226	60	no
stSG158908	cU61B11.CX.1	TATTGAGATATTTGCAGTTGGTACG	AACCAATTCATTGTCAGTTTAGGT	285	60	no
stSG158909	dJ545K15.1	GTGGACAAAGAACATCAAATTAC	GCGTGTAGAAGAAAGAGCAAA	174	60	no
stSG158910	dJ545K15.2	CTATTCATTTTCTCCACCTTGTTT	TGCTACTTATGCAGAAGAAATAGC	225	60	no
stSG158911	cV602D8.CX.1	CCCTCTATAATTCTTACGTGGAATC	GAAATTTCTTCAAGTCTTTTGACG	269	60	no
stSG158900	dJ122O23.CX.1	GGCTAGGGTGGAGGATAAAAG	CTGAAACATAGAGCAAGCAAACAC	289	60	no
stSG158901	cV351F8.CX.1	CTGCTGTGCACATCCCTATG	TGAGTATGCAGACCCAGCAC	115	60	no

stSG158902	cU177E8.CX.1	TCGAGGTGAGGGAAGAGAGA	CTTCTTCGGAAGGTTGAGGA	203	n/a	yes
stSG158903	cU177E8.CX.3	AAGGCAACTGCCCTACAGC	TTCTAGGTTTCTTTTCATTCTCTGG	178	n/a	yes
stSG158904	cV857G6.CX.1	GGCTAAGGTGCAGGATGAGAA	TCCTACTGAGAACACTGCATTGC	284	60	no
stSG158913	cV857G6.CX.2	GAGATGTGTCAAGGGCTCAA	CCAGCAATATTCTCATCAGAGAAA	219	60	no
stSG158914	TCEAL1	CTCGCTTAAAGTTGAGGTTTCC	CAACCACTGTTATGCCTTTGAA	225	60	no
stSG158930	pp21 homolog	CCGTGGAAGGAGTCAAACCT	GGATTTTCATCTTGTATCTGTCTACC	193	n/a	yes
stSG453302	NXF2	AGCCTAAGGCCTGGCTGAC	CAGAGCAACTGGCTCTTTGG	81	60	no
stSG453303	NXF5	CACCAGCCTAAGACCACTCTAAG	CACAGAACAACCTGGCTCTTCAG	112	60	no
stSG453304	NXF4	TACCAGCCTAAGGCCGTG	CACAGAACAACCTGGTTCTTCAA	112	60	no
stSG453305	NXF3	GGGCTGACTCTCATCCTTCC	CCATACTTTATTGTGAAAAGGAACA	98	not tested	no
stSG453306	NXF1	CTCGCCTGCCTTCTGGAA	TAAGGAGGTCCTGGGGTTAAGT	135	60	no
stSG482247	cV857G6.CX.2	TGGAGGTAGGGGCCAGAGG	ACCAGGGAAAGCAGGGCCA	108	tested	no
stSG482248	cV857G6.CX.2	GCTTCCGCGAGCCGGAGA	TCCTCCTTTTTAGGCCTCGC	93	n/a	yes
stSG482249	TMSB4X	TGCAAAGAGGTTGGATCAAG	CTTCCTTCACCAACATGCAA	152	not tested	

## Appendix D

This appendix contains information for primers used in the studies presented in Chapter 6. stSG numbers, the gene the STS was designed to, the primer sequences, expected product size and optimal pre-screen annealing temperature in °C are given.

stSG number	Gene	Primer 1	Primer 2	Product size (bp)	Prescreen
stSG427961	ALEX1	AGATGGCTGGGCTAAGACTG	GATGCGAGCCCTTCATTTT	307	60
stSG187942	ALEX2	AAAATCAGGGCCGGCTTC	GATGCTGGCACTTGGGTACT	280	60
stSG407290	BMX	CCCACCTGCTGGTCAAGTA	TGCTTCCCAGAGGGTACATC	104	60
stSG407309	BTK	CCGGTACAACAGTGATCTGG	TTCCATTCTGTTCTCCAAA	125	60
stSG427959	cU46H11.CX.1	TCAGCATTCTCAAGGAATTCAA	GCATGTTCTGCCATCCAATA	282	60
stSG427962	cU209G1.CX.1	TGTGCAGTTGGCTGGACTAA	TCAGTGATGTTGGTGCATTG	212	60
stSG187911	CYBB	TCACCCTTTCAAACCATCG	CCACGCATCTTAAAACCTCT	235	60
stSG427960	dJ545K15.1	GCGGCAGGACTGATGATT	GAATGGCCGCTGTTTTATTG	285	60
stSG407294	DMD	TCCAGCATTACTGCCAAAGTT	GCTCCCCTCTTTCCTCACTC	102	60
stSG407311	DRP2	CTTTAACCACAGCCCTGGAA	CATTGAGGAGCCAATTGAGG	180	60
stSG407317	GLRA4	TCGTTTCTATTTCCGTGGCTA	CTGGTGGATATCTTCTGACCA	259	60
stSG187917	GLRA2	CCTGCATTGAGGTCAAGTTTC	CCTGAACCTCTGGGTGGTCAT	184	60
stSG187903	GPM6B	ATGCTGCATCAAGTGTCTGG	CTCAGCAAGGCATGGTCAC	171	60
stSG187941	GRPR	CCAGACCTTCATTAGCTGTGC	CCTTCCACGGGAAGATTGTA	174	60
stSG187907	IL1RAPL1	TTGAAGATGTGGCAAGATGTG	CATTTTGGTCCATGCCATTT	253	60
stSG407310	IL1RAPL2	TATTCTCAGACGGGGATGGA	TTTTGGATCCCTTCCACTTG	188	60
stSG407318	KIAA0316-like	TGGCATCAGCCATGTTATTG	CCATGATGCTGGTCTCCAC	128	60
stSG407292	KIAA0316	TGACACAGGCAATCCCTTTT	TACTGAGCGAACGACCACTG	149	60
stSG187894	MID1	GAGGTCTAGACGGGCTCAAG	ATGTGAGAGTCCGGAATTGG	307	60
stSG407305	MID2	GCATCACCTGTGAGGTCTCC	AATCGATCATTCAGGGATGC	247	60
stSG187946	NADE	TGGCAAATATTCACCAGGAA	ATTTCTGCAGGCTGGTG	104	60
stSG407312	NOX1	TTGAAGTGGATGGTCCCTTT	TTTGAGGTTGTGGTCTGCAC	152	60
stSG187944	NXF2	GTCTTTGAACTTGTGCAACAACA	ATTTTTGGAGAGATTGAGGGTCT	100	60
stSG407308	PLP	CCATGCCTTCCAGTATGTCA	CCTAGCCATTTTCCCAAACA	246	60

stSG187936	POLA	CGGAGTGGATTTGGTGAAG	TTTTCCATTGGGATTACAACC	155	60
stSG407306	PRPS1	GTGACCTCCATTGCAGACAG	AGTGTGAGCCATGTCATCCA	144	60
stSG187896	PRPS2	CAGGTTGAATGTGGAATTTGC	AGTGTGAGCCATGTCATCCA	127	60
stSG187898	RAB9A	TACCATGCAGATTTGGGACA	TGGCATCTTTTGCACCTTGTT	308	60
stSG407307	RAB9B	GGAGGTAGATGGACGCTTTG	GGGTAATCCCCATTCTCCAT	300	60
stSG187938	RAI2	TTCTGTGGCAAGATCAAAGG	TTTTTGATTGGGAGCATGTG	209	60
stSG187923	SAT	GCAGCATGCACTTCTTGGA	TCACTCCTCTGTTGCCATTTT	149	60
stSG407313	SRPUL	AACGTCAACGTCAACTCAGC	TGCATTTTATAATATCGGTTGGAA	107	60
stSG187914	SRPX	ACGTCAATGTGGGTGTCAGA	ATTCCTAGCTGGAGCCGGTA	121	60
stSG407315	SYTL4	TAAAAAGGAAAGGGGCAAG	CACCTCCAGGTACCATTGCT	169	60
stSG187916	TM4SF2	ATCACTGGGGTGATCCTGCT	GTTTCAGCATCCATGGGCTA	187	60
stSG407314	TM4SF6	ACTGGCGTTATCCTTCTTGC	TAGCATCCATGCAGAAGCTC	180	60
stSG427958	TMSNB	GATAAGCCAGACTTGTCGGAAG	TTTCCTTTGAGGGAAGAGTATTTT	94	60
stSG407316	XKL	ATCCTCTTTGAGCCCTGGAT	TCTCTGTCTGCCAACCTCAA	176	60
stSG187919	XK	CTTCCTGTGGAGGAGCTTTG	ATGGGACTTGCTGATGAGGT	304	60
stSG187921	SYTL5	ACCTGCTCCCTGATGATAGC	CAAACGAACCTCCTCCAGAA	194	60