

Local genomic instability of the SpTransformer gene family in the purple sea urchin inferred from BAC insert deletions

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Methods

The sequence reads for each BAC insert were assembled into contigs as described in the main paper. The consensus sequences were aligned by hand in Molecular Evolutionary Genetics Analysis X (MEGAX) against the original BAC insert sequences (GenBank Accession numbers KU668451 [BAC-51], KU668452 [BAC-52]) (1). The alignments shown below were generated in BioEdit (version 5.0.9), formatted and exported as rtf files, and imported into this document.

BAC insert sequence alignments

Alignment 1. BAC-51 and BAC-51-15 identify the locations of three deletions in BAC-51-15

Page
1

Deletion 1; 96,854 bp

Deletion 2; 2,270 bp*

* likely represents an assembly artifact

Alignment 2. BAC-52 and BAC-52-2b identify the locations of one deletion in BAC-52-2b

9

Deletion 1; 108,397 bp

Alignment 1. BAC-51 and BAC-51-15

	18910	18920	18930	18940	18950	18960	18970	18980	18990	19000	
BAC-51										
BAC-51-15	TCATTCAACATACCGTAAATAGCTTCATCATGTTCTTTTCAGAAGATTTTAATTTAAAATATTTATTGTGGTTGGGGTATGTTTCTCCAACTGCAAATG										
	19010	19020	19030	19040	19050	19060	19070	19080	19090	19100	
BAC-51										
BAC-51-15	ATGTGCATTATATTTTATAAGGTTTCATTTTAAATAAGAACTGTAATAACCTAGTATTTTTGATCAAATATGTTGCTCAGAAGTCTTGAACAGCATTAAAT										

	19110	19120	19130	19140	19150	19160	19170	19180	19190	19200	
BAC-51										
BAC-51-15	ACACGACTTAACTACAGACCCGTGATTGAATTCATTTTCAGTCAGCATTGTTGCATAAATTCATTTATTTATGACTTATTTGACTTCTGCATTAAACAG										
	19210	19220	19230	19240	19250	19260	19270	19280	19290	19300	
BAC-51										
BAC-51-15	CTTGACAACCTGTTTCAGAGGCACCCCATCGGAAGTGACTTTGTGGGACTAGAGATCACCAGCAGTCGCTTTGATACTAATAGTAACCTACGTGATTGGCT										
	19310	19320	19330	19340	19350	19360	19370	19380	19390	19400	
BAC-51										
BAC-51-15	ACTCCATCTACCTGTGTGCTACCTCCCACTACAATGAGGAGAGCATCAAGGATACCTTCAATAGCGCCCTCACAGGGGCTAACATGGACACCTTTGCCGC										
	19410	19420	19430	19440	19450	19460	19470	19480	19490	19500	
BAC-51										
BAC-51-15	TTCAAATGTCATTGTGACTGATTCACTTGACTTCAGTAAGTCACTCTACCGAGTTCCAGTTTTTTTAAGGGCAGCAAACATAGACTATCTGTCTAATATT										
	19510	19520	19530	19540	19550	19560	19570	19580	19590	19600	
BAC-51										
BAC-51-15	TTATTGTAATCACTCCATGGCAGTGTTTCGCAAAGACTAAGATCGACTTTATGTTGGACTTAACTATGGCAGGCCATTTCATGCCACTGTTTGCTCTCACC										
	19610	19620	19630	19640	19650	19660	19670	19680	19690	19700	
BAC-51										
BAC-51-15	ATTTACTGGCATTGGTCTCTCAAGGGACGTACAAATCATGGTCACAAATCTACAGATTTTACATTTTGGATAATTCATTATTGAAGGAAAAATATTATC										
	19710	19720	19730	19740	19750	19760	19770	19780	19790	19800	
BAC-51										
BAC-51-15	TAAAGATCATAATGGTGAGAGCAAATAGTGGCATGAACGGCCTGCCATAGTTAAGTCCAACCTAAAGTTGGACTTTCCTCTCTCTCACATGGTGCACCTCG										
	19810	19820	19830	19840	19850	19860	19870	19880	19890	19900	
BAC-51										
BAC-51-15	CAAGCCTACTGTATAAACTTAAAGTTTATCTTACTCTATGTGAAACACTGCCATGTGCATATTATAATTTGCCTTGTTTGTGGTGTTCAAATAAACACA										
	19910	19920	19930	19940	19950	19960	19970	19980	19990	20000	
BAC-51										
BAC-51-15	ATCAGGATGACACAAGTACATGAATTATATATTTTCATGGAAACATCATCATCTCTTCTTAGCTCAAAGGTAGATAAGGATGCATTCAATAGATCCAGCCAT										
	20010	20020	20030	20040	20050	20060	20070	20080	20090	20100	
BAC-51										
BAC-51-15	ATAATGAGATCCTCCCAGCACGGTGTTGGTTCATGTATTTGACAGCTATATAATTAACCTCATGGTCTCTACTCTCTCTCTCTTTCTCTCTCTTTCTCTCT										

[illegible]

Deletion 1, 5' end

2010 2020 2030 2040 2050 2060 2070 2080 2090 20300
|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
 BAC-51 CTGTATGTGTCTGTTTATCTCTCTACAGATGTGGTAGAGTTTAGGGGTCAGTTTACACTGAAGAGCATTGAGAATCCTGGAACCGTTCTGTCTGAATACC
 BAC-51-15 -----

[illegible]

Sequences (96,854 bp) in BAC-51 that are deleted in BAC-51-15 are omitted

[illegible]

	116710	116720	116730	116740	116750	116760	116770	116780	116790	116800
									
BAC-51	TTCAATAGAAATCAGACAATATGTAATCAGACAATTATTTCCCTCACTTTCACTATTATATAAAATTTCTTTTGTCTATCTTCTTCTCTCTCTCCCC									
BAC-51-15	-----									

[illegible]

116910 116920 116930 116940 116950 116960 116970 116980 116990 117000

BAC-51 TGTCTTTGTCTCTTTGTCTCTCCCTCCCCCCCCCTCTCTCTCTCTCTATATATAATCAGACAATATATAATACCTATATCCCTCACTCTCACTTTTCTC

BAC-51-15 -----

[illegible]

Deletion 1, 3' end

[illegible]

	117210	117220	117230	117240	117250	117260	117270	117280	117290	117300
BAC-51									
BAC-51-15	CAATCCAGCTGCATAAGGAAAACAATTATTAGGGGCTATAATATTGAACGCTTCACAAGTATTAGTATGAGTTCAGTTATATATTTTTATTGACAAAGT									
	117310	117320	117330	117340	117350	117360	117370	117380	117390	117400
BAC-51									
BAC-51-15	CTTGACAAATTCAGTATCAATAAGAGTTTAAACAATTCGTCAACATTTTCATGCACCTTTCTACTGGCTAAGAGTCTCCTGTATCTGAATTTTAGACACAATA									
	117410	117420	117430	117440	117450	117460	117470	117480	117490	117500
BAC-51									
BAC-51-15	ATGTTTTAGTCTCTGGTAAGATATGCATTCTGTCCAAGGAAAGACATTAGTGACTATTAGTATATTTACACAAGCAATCTTTTTTATACAAATTGTACA									
	117510	117520	117530	117540	117550	117560	117570	117580	117590	117600
BAC-51									
BAC-51-15	CCTCGGCGACCACATTGACGTCTTCTTCATTGACTGCGATCTCAACCACTTCAGGTGGTGAAGATGTCGTTACGCTTTCCGTCGTTGGATGCTCCTTCTC									
	117610	117620	117630	117640	117650	117660	117670	117680	117690	117700
BAC-51									
BAC-51-15	CTCACTTTTCATTCTCACCCCAACGTCCTCGGTTACCATAGGGATGACGGTGGCCATCACGCCTGGGAGATCCTTCTTCGGTTCTGTTGCGTCTGCCGAAG									
	117710	117720	117730	117740	117750	117760	117770	117780	117790	117800
BAC-51									
BAC-51-15	GGACGGTCTCCGAAAGGCTTTCTACCGAAGGGGTTGACCAGAAGGGCCTCATCTCAAACATTGGTCTGTCTGATCTCCATCTCCGGTCTTGTGTGTAT									
	117810	117820	117830	117840	117850	117860	117870	117880	117890	117900
BAC-51									
BAC-51-15	GACGATGGGGGTGATCTCCCGTCTCATTATGACCCTGGTGACCTTCTGTGTGGTTGCGTCTGCCGAAGTGGTTGAACCGGAAGGGCCTCGTATCATTG									
	117910	117920	117930	117940	117950	117960	117970	117980	117990	118000
BAC-51									
BAC-51-15	TTTGTCTGATCTTGATCTCCCGTCTCATTATGTCTTGGTGACCCTCTGTCTGGTTATGATGACGGTGGTGGTGGCCTTGGTGGCCATGGTGGCCATGA									
	118010	118020	118030	118040	118050	118060	118070	118080	118090	118100
BAC-51									
BAC-51-15	TGGTGAGGGTGAGGACGGCCATCCTCCTCGTTGCGTTTCATTGCGCTGACCGAACGGTTGTTCTCTGGTCGGTCCTGAGGTGGACCTTGACGGTGACCAT									
	118110	118120	118130	118140	118150	118160	118170	118180	118190	118200
BAC-51									
BAC-51-15	GATGACGACGTCCATGACCATCAAACCTGACCGCGCCCTCCTAGACCATCACCAATTTGTTGGGAAGCATCAGTTTCTTCTTCTCCATCACCACGTCTTCC									

	118210	118220	118230	118240	118250	118260	118270	118280	118290	118300
BAC-51									
BAC-51-15	TCCTTGGCCGAAGAAAGGTCTTCCTCCAGCACCATCTGGTCTGGAGCCACCAAATCCAGGTCCGTGCAATCTCCTACCACCCATCGGACCGCCATTTTGT									
	118310	118320	118330	118340	118350	118360	118370	118380	118390	118400
BAC-51									
BAC-51-15	CTGCGTCCATCCATATGTGGGGCACCAAATCCAGGTCCATCGAACCTCCTTCCACCCATTGGTCCACCATCTTGCCTAGATCCACCCATCTGCATTCCAC									
	118410	118420	118430	118440	118450	118460	118470	118480	118490	118500
BAC-51									
BAC-51-15	CAGGCCTTCCCAAAGCGACCTTGTCTCTCTCTGCCATTCTCATTTCTCGCCGTTTCATTGAAATCTCTTCGTGCGTGAGCTGTAAGGGTTAATGA									
	118510	118520	118530	118540	118550	118560	118570	118580	118590	118600
BAC-51									
BAC-51-15	AATAATCGAATTAATTAAGTAATCACATTCTGCATTATTATATTTGGCTCTACATTGGTTTATAGCAGGTGACAAATAAGAATGGTAACTCGCCCTTCTTA									
	118610	118620	118630	118640	118650	118660	118670	118680	118690	118700
BAC-51									
BAC-51-15	TATTTTTT-TCCCTTTATGTTTAATCCTAATCCGTAAGTGCGGTTTCGATATTCAAACGCGCTAATTCTGACTGAATTAAATTTGATTACCAGATTGAACGT									
	118710	118720	118730	118740	118750	118760	118770	118780	118790	118800
BAC-51									
BAC-51-15	AAACATAATACATCCTTTGTCATTTCAGAAAACGGATTGGTGTAGGCTTAATAAATACAATTAATTATATTGTGTAACGAACAATTTAAAAATGCATAT									
	118810	118820	118830	118840	118850	118860	118870	118880	118890	118900
BAC-51									
BAC-51-15	TACAAACTATGAAATAATCATATTTACTTCTGTGAGCCCTTCGTTGGCTTTATATTTAGCACTTATCAAGTAATACCGAGTAATAATTTGATTTCTTACC									
	118910	118920	118930	118940	118950	118960	118970	118980	118990	119000
BAC-51									
BAC-51-15	CGAGATAGCAAGAGCAGCCACAATGGCAACGATCAATGTTGCTTTACCTCCATGTTTGTAAAGGTCTCTCCGATGCTACAAGCTTTCTCTAGATTTCGTTG									
	119010	119020	119030	119040	119050	119060	119070	119080	119090	119100
BAC-51									
BAC-51-15	CCTTCCAAGAGAGAAGTCTGCTTCAAACTTAACAACCTACCTGCTGGGCCACTGAATTTATAGGTTTTCTACCTAGATTGATATCTCACACTAGTACCAGA									

Matched sequences (37,500 bp) between the BACs are omitted

	156610	156620	156630	156640	156650	156660	156670	156680	156690	156700
BAC-51									
BAC-51-15	GGGCACCTTATCAGAGAAGAAAAGGAGTAGTTATAAAAAGGAG--AAGGGGCACTCTGTTTTAATGAAAAGCGCATTTATTAGAAAAGGTAAAGGGGCACT									
	GGGCACCTTATCAGAGAAGAAAAGGAGTAGTTATAAAAAG-AGAAGAAGGGGCACTCTGTTTTAATGAAAAGCGCATTTATTAGAAAAGGTAAAGGGGCACT									

	156710	156720	156730	156740	156750	156760	156770	156780	156790	156800
BAC-51									
BAC-51-15	TGTCAAAGTAAACGAGCATCTCTCATATTTGAATAGGGGCAATTATCGGACGTGAAAGAAGCACTAGTCTTATCTGAAATGAAAAGGAGCAACTTCTTT									
	156810	156820	156830	156840	156850	156860	156870	156880	156890	156900
BAC-51									
BAC-51-15	TTACCTGAAAGGGGTCATTACCAGAGCTGAAAAGAGGCATTTATGAAAAGGAGAAGGGGATCTTTGTTTTAATGGGG-AACTAACCATCAGGAAAAGGG									
	156910	156920	156930	156940	156950	156960	156970	156980	156990	157000
BAC-51									
BAC-51-15	GCACCTCTCAAATGTTAATAAGGCAATTATCAGAGGTGAAGGGGGCACTTATTACAAGTGAAGGGCGCACGTATCGTACCTGAAAAGAGGCACCTTACTA									
	157010	157020	157030	157040	157050	157060	157070	157080	157090	157100
BAC-51									
BAC-51-15	GACATTAAGAGGCACACAGCATGAGTAGTAAACACAGCCGTGGAAAAATGTAAGCAACACAAGTTCGTATATAGTCGTACGATGAGCGATTGAAACAA									
	157110	157120	157130	157140	157150	157160	157170	157180	157190	157200
BAC-51									
BAC-51-15	CGAAGTCTGACGGATCTTTGGTCTGAAGAGCACACCTGTCTGAGCACTGGCGTACTGGTAGGGGGCTAGGGG-AGGGGGGGGGG-CGCCATCCCCCAAATAAA									
	157210	157220	157230	157240	157250	157260	157270	157280	157290	157300
BAC-51									
BAC-51-15	ATTGAACCATGACATATTTTCAATTCATATACAAGTGATGTATAAATGTTTCGTGATATCATATGATTTTCAACAAAATGCGTTTTTCTCCATTTCTGTT									
	157310	157320	157330	157340	157350	157360	157370	157380	157390	157400
BAC-51									
BAC-51-15	GCAAACTGACACATTCCCGAAGCCAGGAAGAGCATATGTTTTTTTTATAATCACTAAGGGGCTTATAGTGGCCACTAACAGTAACACTTGTATAAAAAA									
	157410	157420	157430	157440	157450	157460	157470	157480	157490	157500
BAC-51									
BAC-51-15	ACACACTCATTACAGTGTGAACACACAGTTCACACTGTGAACGGAGCCTTTTCACAGTGTGGACACTGTCACAATGTGGTAAA--CCACACAGTATTCA									
	157510	157520	157530	157540	157550	157560	157570	157580	157590	157600
BAC-51									
BAC-51-15	CATTGTAAAATTCGATTTTCACAGTGTGAATGTACCTGCTCACAGTGTGAAAATGATTTTCACAGTGTGACCAAACCTGTGATAAATAGATTTTCACAGTGTG									

Deletion 2, 5' end, this is likely an assembly artifact

	157610	157620	157630	157640	157650	157660	157670	157680	157690	157700
BAC-51									
BAC-51-15	AATACCTTACGACATACATTTACGGTGTGAACAGTAAATTTCTCAGTGTGGCCACTCTGTGAAAAATACTTCACATTGTGAAAAATAGAATTCACAGT									

	157710	157720	157730	157740	157750	157760	157770	157780	157790	157800
BAC-51									
BAC-51-15	ATGGCCGCTGGAATACTAGTGTTTTGGATCGAGGCCAATCAAGTTTCCGTGATAACAGACGAATATGTACAACTACATGTTGACGGATGAGAACATAATT									

	157810	157820	157830	157840	157850	157860	157870	157880	157890	157900
BAC-51									
BAC-51-15	GGAATGGCGGACATGGCCTGGTGAAGTTTCCCAACGGCTAGGATAGCTATCAGGCGAGGGTGTTGCCGGGCTGCTGCCGGGCTGTCATTGAATGGTGAGT									

Sequence (2,270 bp) in BAC-51 that deleted from BAC-51-15 is omitted, this is likely an assembly artifact

	159510	159520	159530	159540	159550	159560	159570	159580	159590	159600
BAC-51									
BAC-51-15	TCCTGGAGTATGCGTGCGTGACAGTGCGGGATCCTCACACCCAGGACAACATACACAGGTGGAAATGGTACAGCTCCGCAACGCCAGTTTATCACTG									

	159610	159620	159630	159640	159650	159660	159670	159680	159690	159700
BAC-51									
BAC-51-15	GAGATCACCATCATAACCAGCAGCATCGCACCAATGCTGCAACATCTCAAATGGCCATCTCTCCGAGAACGCAGGGCACGGTTTAAGATGGTGATAGTGTA									

	159710	159720	159730	159740	159750	159760	159770	159780	159790	159800
BAC-51									
BAC-51-15	CGGAACTGTCAACCTGCACTCAGAGTTTCTCAAAATGTACCTTCTATCGGTGTTAACATCTACCATGGTCATACCCAGTAATTCCAAATACAATTTACA									

	159810	159820	159830	159840	159850	159860	159870	159880	159890	159900
BAC-51									
BAC-51-15	ATGACTCTCGTATACCAGAAGTCATTCTTCCCGATTCCATCATGCTTTGGAACTTGCTACCTGCTGGATTGTCAACTGTACTTTTCGCTAAAGCTTTTA									
	-----CATCATGCTTTGGAACTTGCTACCTGCTGGATTGTCAACTGTACTTTTCGCTAAAGCTTTTA									

Deletion 2, 3' end, this is likely an assembly artifact

	159910	159920	159930	159940	159950	159960	159970	159980	159990	160000
BAC-51									
BAC-51-15	AGCAAGAGGTACAAAATTTCCATCTCCGTTAGAAGGGGAAGAAGGATTTTAACTGCTCATAGAATATTATAGAAAGTTTAAATTCGCACTGTATATTC									
	AGCAAGAGGTACAAAATTTCCATCTCCGTTAGAAGGGGAAGAAGGATTTTAACTGCTCATAGAATATTATAGAAAGTTTAAATTCGCACTGTATATTC									

	160010	160020	160030	160040	160050	160060	160070	160080	160090	160100
BAC-51									
BAC-51-15	GCGACACCAGACCTGACGTACGTGATACACCATACGGTGGACTGGAGTGATATCTCAAGATCTGGGGGATGATAATTCCGGGCTTTAACAAATTGTGTGAT									
	GCGACACCAGACCTGACGTACGTGATACACCATACGGTGGACTGGAGTGATATCTCAAGATCTGGGGGATGATAATTCCGGGCTTTAACAAATTGTGTGAT									

	160110	160120	160130	160140	160150	160160	160170	160180	160190	160200
BAC-51									
BAC-51-15	AGTGGAGGTATTATTTTTGACTGCACAGTCGGAAGTTCCATCTAGTTATAATATCCTAACATCAGTATATTATCGCTAGAACAAAAAATCATAAGTTACT									
	AGTGGAGGTATTATTTTTGACTGCACAGTCGGAAGTTCCATCTAGTTATAATATCCTAACATCAGTATATTATCGCTAGAACAAAAAATCATAAGTTACT									

	160210	160220	160230	160240	160250	160260	160270	160280	160290	160300
BAC-51									
BAC-51-15	TATGTAGTTTAGGAAGTACATATATTTTTGTATGCCATTCTGCTTTTTTCTGTGCCACCGTATATAGAGTGTATGGTTATTTATTTGTAAAAAGATGAGC									
	160310	160320	160330	160340	160350	160360	160370	160380	160390	160400
BAC-51									
BAC-51-15	AAAATCTGTTTTTTTCTCATCTTCAGGTATTTATTAGTATTAGTTGTAGAAATTTATGTAGCCATAACAGTAAAACGTGTCTGCCTAAAATAGATTGT									
	160410	160420	160430	160440	160450	160460	160470	160480	160490	160500
BAC-51									
BAC-51-15	TTTCAACTTTTTTTTCAAGATGTATTGACAGAGATATTTTGAACCTTTTTATCATTTTTAATAGGTTTATGAAGAACCTGTATGTGCCAAAGATTTTCTGAT									
	160510	160520	160530	160540	160550	160560	160570	160580	160590	160600
BAC-51									
BAC-51-15	ACATTGCAATTGCCAAAGTTACATGTCATGTGTGGATATTTCTATACTTGGAAATGTGACTAGCCATACTAATGTATCTTCATAAATTTAATATACCTAC									
	160610	160620	160630	160640	160650	160660	160670	160680	160690	160700
BAC-51									
BAC-51-15	AGAAATGTTTAAAGAGATATTGCCAGAGATGCTCTAAACCTATTTT-ATTACTGACGTAACATGCTAATGTGCTTTTATTATGTTTTACGAGTGTGAGTAC									
	160710	160720	160730	160740	160750	160760	160770	160780	160790	160800
BAC-51									
BAC-51-15	GAGTTCAGGGAAATATTGATGATATGTGCAATTTTTGCCGTCACCTGTAATTTATTCCTCGATGTTATACAGTGGAAACCTCTATAACTCTATTTCACAAGT									
	160810	160820	160830	160840	160850	160860	160870	160880	160890	160900
BAC-51									
BAC-51-15	CCACGTTTTTCTGTAATTCATTGTTTTAAACCCTTGTACAATAAGATATCTGATATAAAGAGGTCAATTTAGTGGACACCAATGTGCTCATTATAATGAG									
	160910	160920	160930	160940	160950	160960	160970	160980	160990	161000
BAC-51									
BAC-51-15	GTTTCACTGTAGATAGCAAGTTCTGTTTTTCAAGATATCTCTACTATCTAATTTAAACTGTTTGGATTCAATTTGTCTTTGTTTTCACTCTGGTTCACATC									
	161010	161020	161030	161040	161050	161060	161070	161080	161090	161100
BAC-51									
BAC-51-15	ATGTTGGCATTACAGAGTAAAATTTGTTTATCTGTAAGTATAGTATTACTGCAATCTTTGTATACCTAAGAGGTATATGTTTCATAAGTCCTTTTAGCGA									
	161110	161120	161130	161140	161150	161160	161170	161180	161190	161200
BAC-51									
BAC-51-15	AAAGTACATCAATATAAGCTTTTGAATACATTTTAAGTTACCTCATAAAGGCTATAACATGTATATGTTTAAGATTACTGTATTATTTTCAGATGTTTC									

	161210	161220	161230	161240	161250	161260	161270	161280	161290	161300
BAC-51									
BAC-51-15	GGGGGTATATTCTATTTAAGTTGAGTTTATAAGTGAGACATTGATTATAAACCTTTTCTCCTTCGTATTTATACGTACTAAGCTCTACATGACTACATT									
	161310	161320	161330	161340	161350	161360	161370	161380	161390	161400
BAC-51									
BAC-51-15	TTCATAGTTTGAAATATTTACACAGAATTCAAAAATAAACTTGTATCACAGTGTGGTGGGCGTTTCACAGTGTGGTAATCTCATACAATATAATGTGT									
	161410	161420	161430	161440	161450	161460	161470	161480	161490	161500
BAC-51									
BAC-51-15	CACAATGTAACGTAGTGGGCGTTTCACAGTGTGTTTGGTGTTCACAGTGTGGTGGGCGTTTCACAGTGTGGTAATCTCATACAATATAATGTGT									
	161510	161520	161530	161540	161550	161560	161570	161580	161590	161600
BAC-51									
BAC-51-15	TCACATTGTGGTTGCTTCGTTTACAGTGTGGTTCACAGTGTGGATATCTACACTGAAACGACGCGACCACAATGTGAAAATACCCCAATGTAACATTGT									
	161610	161620	161630	161640	161650	161660	161670	161680	161690	161700
BAC-51									
BAC-51-15	GGGCGTTTCACAGTGTGTTTCTGTTTCAAAGTGTGCTGGGCATTTCACTGTGTGAGTGTTTACAATGTTAAATTGGGGCGTTTCACATTGTGGTCGCTT									
	161710	161720	161730	161740	161750	161760	161770	161780	161790	161800
BAC-51									
BAC-51-15	CGTTTCACAGTTGGGTTACACAGTATGAAACGACGCGACCACAATGTGAAAACGCCCAATTTAACATTGTGGGCGTTACACAGTGTGGTGGGCATTTTAC									
	161810	161820	161830	161840	161850	161860	161870	161880	161890	161900
BAC-51									
BAC-51-15	TGTGTGAGTGTTTACAATGTTAAATTGGGGCGTTTTCACAGTGTGATTACACTGTGTTTACACTGTGAATGAGTGTTGTGGTCTGGTCTGGTCGCGAC									

Alignment 2. BAC-52 and BAC-52-2b

	9910	9920	9930	9940	9950	9960	9970	9980	9990	10000
BAC52									
BAC52-2b	CATACTGAAT ACTAAAAATT GTAAAAATAA -GATGTAGCT GAACCTCATAC GAAGGTAATG TGCAATAATA AAGCCCCGAA TATTTTCCTG ACGCAGATGA									
	10010	10020	10030	10040	10050	10060	10070	10080	10090	10100
BAC52									
BAC52-2b	ATTGATCATT GTTATTGAAT CAATGAGGAA GACGAAATGA AGGAAAAAGG AATACAATGT ATATAGAGAT AGAGAGAGAG AGAGAGAGAG --ATAGAGAG									

	10110	10120	10130	10140	10150	10160	10170	10180	10190	10200
BAC52
BAC52-2b	GGATATATAT	ATATATATAT	ATATATATAG	AGAGAGAGAG	AGAGAGAGAG	AGA--GAATG	AGATAGAGAG	AAATAAAAGA	GAGAGAGAGA	GAA-GAAAGA
	10210	10220	10230	10240	10250	10260	10270	10280	10290	10300
BAC52
BAC52-2b	GAGAGG-AGA	GGTGAGATAG	ATAGAAAGGG	TAGAGAGAGA	TGAAGAGACA	AAAGAAATAG	AGATATGTAG	AGATAGAGAG	AGCGAGAGGG	AGAGACAAAG
	10310	10320	10330	10340	10350	10360	10370	10380	10390	10400
BAC52
BAC52-2b	AGACAGAGAG	ACAAAGAGAA	TATGAGAGTG	AGATGGAGAG	AGATATGAGT	GTGAGAGAAA	GAGG-AGAGA	GAGAGAGAGA	GAGAGAGAGA	GAGAAGATAG
	10410	10420	10430	10440	10450	10460	10470	10480	10490	10500
BAC52
BAC52-2b	ATAAGATTAT	TTATATATAC	AATGCGTATA	AAAAAAAGTG	TGCCCAACTT	TAGTAACCTC	TACTTAAAAA	TTTATAACAT	ATAAACTGAT	ATCCTGTCTA
	10510	10520	10530	10540	10550	10560	10570	10580	10590	10600
BAC52
BAC52-2b	ATGATTTTAT	ATTTCATAATT	GTACTGCCAT	GGATGATTGA	GCAGCAGGCT	TTTTATAAAG	TTTTTTTCAA	ATCCTTTTTG	AACCAAGTTT	GGGCCGAAGC
	10610	10620	10630	10640	10650	10660	10670	10680	10690	10700
BAC52
BAC52-2b	AATGGATGCG	GGTCAAAAGT	CATTATGTGT	GGGTTATCTC	ATTCCATAAA	CAATTGTTCT	CTTATGAATA	CTAACTATTA	GGCTGTTGAA	GATAAAAGGT
	10710	10720	10730	10740	10750	10760	10770	10780	10790	10800
BAC52
BAC52-2b	GTGAATATCA	ACTCAAGCTA	TAAAGGAAAT	TTTATCACAA	ACAAAATGTA	TGATATTCTC	TTTGTTATGA	TGAATAAAAT	CTTAAATTCA	TTCGTATCCC
	10810	10820	10830	10840	10850	10860	10870	10880	10890	10900
BAC52
BAC52-2b	TTGTTTAAGG	AAACCTTTCT	CAGTGATAAA	AAACCGATCG	GGACGTTATC	TTCTTTATTA	AAGTCTCATC	GTAATAATAA	TATGAAAAAT	TTATATAGCG
	10910	10920	10930	10940	10950	10960	10970	10980	10990	11000
BAC52
BAC52-2b	CTTGTGACAA	AAGTTTCAAA	GCACTCGTGT	GTTTCGTTCT	GCATTTGGAT	GTAGTAACCT	TTGAGTTTTT	ATTCGCTATT	CAATATAAAC	ACCATAATGT
	11010	11020	11030	11040	11050	11060	11070	11080	11090	11100
BAC52
BAC52-2b	GCTCATTACG	CGTGTGAAAT	TGTGTAGAGG	ACAAGTGAGC	AGAGAGAAAT	TAGATATAAT	GAAACAAGAA	GTTAGTTGGC	TGTTCAAAAT	AACTAAAAGT

	11110	11120	11130	11140	11150	11160	11170	11180	11190	11200
BAC52
BAC52-2b	TTTCCCCGGG	GTCGTAACAA	GGTTCTGCGA	AACAGGGGCG	GATCTAGCCG	GCGGCGAGGG	TGGGGGGGGG	GGGG----CA	ATTTAAGAAA	ATAGTTAGCG

	11210	11220	11230	11240	11250	11260	11270	11280	11290	11300
BAC52
BAC52-2b	CCGAATTAGC	CGGCGAAAAA	GCAATAGGGG	GGG--TTAAT	GAGCAATAAA	TTGTTATTTC	TTTTTTGCTC	AACGGGGGGG	GGGGTAGTGC	ATGCGCGGAT

Deletion 1, 5' end

	11310	11320	11330	11340	11350	11360	11370	11380	11390	11400
BAC52
BAC52-2b	CCAGGGGAGG	CCCCCGCCCC	CCCAAAAAAG	TTTTTAATTT	TTTGTTTTTT	TAAATGGAGA	CAGATAAAAA	TTAGTGCTC	ACTACCACCC	CCCCCCCCCC

	11410	11420	11430	11440	11450	11460	11470	11480	11490	11500
BAC52
BAC52-2b	CCCCCTACTG	AGCAAAATTT	ATCGGCCGGC	ACGATTTTCG	AATTTACACCA	CGCTAAATTA	AAAATTGATT	TCAAATTTGG	GTCTCCCCTA	AGGAATCTGT

	11510	11520	11530	11540	11550	11560	11570	11580	11590	11600
BAC52
BAC52-2b	GACCCGCGCC	AGTAGTAAGC	ACTATTTTTA	TTTACTGAAC	CCCCCCCCTT	GAGCAAAAAC	AAAAAGAAGG	TAAGATTGTG	GATACTATCT	TTGTTTAAAT

	119410	119420	119430	119440	119450	119460	119470	119480	119490	119500
BAC52
BAC52-2b	TGCCTGAAAA	AAAAATCACA	GTAGAAATAT	CCCCTGAAAA	GGATTGATCA	TCGTTTTCGA	AATATTACCG	GAGGTAGCTG	GAAATTTGTT	GATAAATATT

	119510	119520	119530	119540	119550	119560	119570	119580	119590	119600
BAC52
BAC52-2b	CCATGCCACA	TGTGTAGTTT	AATATTAGCC	TACCCAATTT	CGTTTATGTG	TGCACTAAAA	AGTCATTTGT	CAGCATTTTC	AGACATTCTG	ATTAAATTTT

	119610	119620	119630	119640	119650	119660	119670	119680	119690	119700
BAC52
BAC52-2b	TTGTAATTTT	GATGAATTCA	AACCTTACAC	TTCTGTACTA	AACAGGCGCG	TACGCAGGAT	TTTTTCAAGT	GGGGGGGGGG	GGGGGTTTAA	CATTTTTTAA

Deletion 1, 3' end

	119710	119720	119730	119740	119750	119760	119770	119780	119790	119800
BAC52
BAC52-2b	TCGGGCCGAA	AATTTTCGCAT	CGACTCAGCC	AGCCGCTGAA	TAAGCGGGGG	GGGGGGGGGG	GG--AAGAGG	ACACTTTTTC	TTTTCTTTT	TTGGTCTCGA

	119810	119820	119830	119840	119850	119860	119870	119880	119890	119900
BAC52
BAC52-2b	AATTTGAAAA	TTTGACATTT	TGCTCTGTTG	GGGGGGGGGG	GG-TAAGGTC	GCCTTTTTTTA	GGTCAGCCAT	GGGAATAGTT	TTTTT-ATTA	TTATTTTTTTT
	119910	119920	119930	119940	119950	119960	119970	119980	119990	120000
BAC52
BAC52-2b	TTT-ATTATT	CAAAAAACA	AAAAACA AAA	CAAAACAAAG	GGGGGGGGGG	TTGTTTTTTTT	AGGGGGGTTT	ATACACATAA	AAATACCAA	GGGGGGGGG-
	120010	120020	120030	120040	120050	120060	120070	120080	120090	120100
BAC52
BAC52-2b	TTAACCCCTA	AACACCCCC	CCCCCCC--T	GCGTACGCGC	CTGGTACTAC	ATACATATTA	AACCTTTCTA	TGTAAATTTT	AGCCCATTTC	TTTCAAAACG
	120110	120120	120130	120140	120150	120160	120170	120180	120190	120200
BAC52
BAC52-2b	TAATCACATG	ACCAGTACTA	GATTTATTTT	GAAACATCCG	TCTTGATGTT	TATAATGATA	GATGACGTTA	TACGACCCTG	TCTTATGGGG	TACCTTGTC
	120210	120220	120230	120240	120250	120260	120270	120280	120290	120300
BAC52
BAC52-2b	TTCGTGCCAT	TTTGGGGGGA	GGGTGGAGAC	CCGCAGACTT	CCCCCTCTAG	AACCACTACT	GAATACCACT	GAACGCAACT	GAAGAATATG	TTATCGTCAT
	120310	120320	120330	120340	120350	120360	120370	120380	120390	120400
BAC52
BAC52-2b	AGAGGTCGGT	TATACATTTT	TTTCCATGCA	GGTTTTCATT	CACTGTGAGG	TGCTCATTTG	TAATGATAAT	GACCCATCGT	CTCGGTGTTC	CCAGGGATGT
	120410	120420	120430	120440	120450	120460	120470	120480	120490	120500
BAC52
BAC52-2b	AAGTCTAGAT	TCAGACGTGG	TAGCCGTCAC	ACCCGTGGAG	CAAGCTCCAC	TCCTCATCTA	ATCTCTAATG	GACCTCTTTC	AACTGCCAC	ACTATGCATG
	120510	120520	120530	120540	120550	120560	120570	120580	120590	120600
BAC52
BAC52-2b	CCGCAGAAGC	ACACAACCT	GGTAATTACC	TTTTTAAAGA	ACACAACACT	TAACCTTTAAA	GGTGTCGTGT	TTGTCTAGTG	AAAACGTCGT	TGGACTGTGG

Reference

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