Appendices

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Appendix 14: Publications arising from this work.

‘The Replication Timing of the Human Genome’ Woodfine *et al*.

Appendix 1: Reagents and buffers used.

Amino linking Buffer (10x)

500mM KCl,
25mM MgCl2,
50mM Tris/HCl pH 8.5
Made with autoclaved distilled water.

HindIII Digestion mix (for a 96 well plate)

Hind III (Boehringer 40U/ml),	55µl
Buffer B (Boehringer)	99µl
Sterilised water	286µl

Hybridisation Buffer

50% deionised formamide
2xSSC
10% dextran sulphate
0.1% SDS
10mM Tris pH 7.4
0.1% Tween 20

LB Agar

Tryptone	10g
Yeast Extract	5g
NaCl	10g
Agar	15g

Make up to 1 litre with autoclaved distilled water.

LB Broth

Tryptone	10g
Yeast Extract	5g
NaCl	10g

pH to 7.5 (using 1M NaOH)
Make up to 1 litre with autoclaved distilled water.
Autoclave at 121^{o}C for 15 minutes.

Orange G (10mls)

Orange G	0.1g
Ficoll	1.2g

Make up to 10ml with sterilised distilled water

Polyamine isolation buffer (PAB)

80mM KCl
20mM NaCl
2mM EDTA
0.5mM EGTA
15mM Tris
3mM dithiothreitol

0.25% (vol:vol) Triton X-100
pH adjusted to 7.2

Sheath Buffer

10mM Tris-HCl pH 8.0
1mM EDTA
100mM NaCl
0.5mM Sodium Azide

SSC (1x)

0.15M NaCl
0.015M Sodium Ctrate
pH 7.0

TAPS 2 Buffer (10x)

250mM TAPS pH 9.3,
166mM $(NH_4)_2SO_4$,
25m $MgCl_2$,
0.165% w/v Bovine serum albumin (Sigma),
0.7% v/v 2-mercaptoethanol
Made with autoclaved distilled water.

TBE Buffer (10x)

Tris Base	121g
Boric Acid	61.83g
EDTA	18.612g

pH 8.0
Make up to 1 litre with autoclaved distilled water.

TY Media (2x)

Bacto-tryptone	16g
Bacto-yeast Extract	10g
NaCl	5g

Make up to 1 litre with autoclaved distilled water.
Autoclave at 121^{o}C for 15 minutes.

Vista Green Stain (for 500ml – 1 gel)

1Ml Tris HCL	5ml
0.5M EDTA pH 7.4	0.5ml
Vistra Green	0.05ml

Make up to 500ml with sterilised distilled water.

Appendix 2: PCR primers for the High Resolution Array

2a: Primer sequence for PCR products in the high resolution array

STS Primer	**Forward primer**	**Reverse primer**
500bp overlapping PCR product array		
stSG494879	TGACCATGGACGGGAGAGAAAACATCCA	GAAAATGTGTGGCAGGTTCA
stSG494880	TGACCATGTGTCTCCCTTGGTGACATGA	CTCCCCACATGAGACCAGAT
stSG494881	TGACCATGAAGGCTAATGGGAAAGAGGC	TTCTGTCCCCTTTTGATTGC
stSG494882	TGACCATGCTAGGAAGAGGTTCCAGGGG	CTGAGCCTTCCTGTGTGGAT
stSG494883	TGACCATGGGAAACCATGCACCTCAGTT	GACCAGAAGGAAATGTTGGC
stSG494884	TGACCATGAAGACGGCTCTCAACCTTCA	GAAGACTCCAGCTGTGTCCC
stSG494885	TGACCATGCTCTTTGCTCGCAGTCATCA	CACAAGAGAAACACAGGCTCTC
stSG494886	No Unique Sequence	No Unique Sequence
stSG494887	TGACCATGGTCCCAACACCTCCATTTTG	CTGAACTTGGCCCATAAAACT
stSG494888	TGACCATGCGGACTCAAAAGAACAAGGC	CCTCTGAAACCGGCAGAATA
stSG494889	TGACCATGATCATTGAAGGTGCCAAGGA	TGTGCTTCAGCAAAACATCC
stSG494890	TGACCATGTACTCTTCAGTGGCCCGAAC	TATTGGCGGCCATCTACTTT
stSG494891	TGACCATGGTGCTAATTTCCACCACAGTCA	TGAAGGAAATGGAAAAGGGA
stSG494892	TGACCATGCCACTGCCTGCCAGTTAGAT	GTGCCGATCGAGACTCTTCT
stSG494893	TGACCATGGGCAAAATTCAAATCCTCCA	CTGATCTGCCTCCATCCATT
stSG494894	TGACCATGCCAGGTCACTGCCCTAAAAA	CCCAGGTCAGTTGTTTGTGA
stSG494895	TGACCATGTGAGGACTCCTGGGTTCAAG	TTCCAAACAGAGGCCTTCAT
stSG494896	TGACCATGGGTTTTCTGGACAGTTGACACA	GGAAAATGGACAAGCAGTTGA
stSG494897	TGACCATGGTGTCTTGGAGACTCCCTGG	TCCATAATTTCCGGGTTTCTA
stSG494898	TGACCATGCCTGTGGAAATCCCTCATGT	AGGACACAGGTTTGCTTTCA
stSG494899	TGACCATGGTGGCCTCTAACTCTGGCAT	CCCATACCTTTCTGAATCTGC
stSG494900	TGACCATGAATGACACCATCACCAGCAA	AGTTTCAATCACCGTGCCAT
stSG494901	TGACCATGCCCATCCTATGCCCTGTATG	GCAGCTGCAGTCAACTAACAGA
stSG494902	TGACCATGCATCTCCCAAGCTTTGCCTA	TGCACATGGTGAAATGAACA
stSG494903	TGACCATGTCCTCATGCCTCATGTCATC	TTTGGGAATACAGACAGGGG
stSG494904	TGACCATGTGGGGACAGAGGTAATCTGG	TTGCATGTGATCTGCACGTA
stSG494905	TGACCATGAAAGGTCACCCATTGCTTTT	TGGGATAAGTGAGGGTCTGC
stSG494906	TGACCATGGGAGGCTTTGGTTGTGTTTC	GTTGTTGGGGGAAGGAAAGT
stSG494907	TGACCATGAGGGTGTGACCCTGAGAGG	GCCACTGGCTGTTCAGATTA
stSG494908	TGACCATGGTGAAGGCTTGGCTGATACC	TGAAACATCTTCTGCCTCCA
stSG494909	TGACCATGGCAACTCTCCAAGTTCTGCC	GGATGGAGAAGGAAGTGCAG
stSG494910	TGACCATGTAATCTGGAAGGGCAGGAGA	CTCCCCTGAAGTGAGAGCTG
stSG494911	TGACCATGATGCCCTGACTCCAAAACTG	CCGCTGGAATTGTATCCTGT
stSG494912	TGACCATGACTCTGGAAGCCAAAAAGCA	CCAAACCGAAACAAAAAGGA
stSG494913	TGACCATGTTTTCCTTGGAACCCTTTATGA	GGTGTTTGTAAGGCAAGGAAA
stSG494914	TGACCATGCAAGTATGGCGCATCTCTCA	GGAAGTTCACGAGGGACAAA
stSG494915	TGACCATGACCCCATTCAGCTCACAAAA	ATCTGGCAGGATTTCTTGGA
stSG494916	TGACCATGAGGGGCTTGTGAAGACACAC	GGCTGGAATTCCGTCTCATA
stSG494917	No Unique Sequence	No Unique Sequence
stSG494918	TGACCATGGGAGCTCACCTTTTGGGTC	GCAGGAATAGAAGTGGGAGC
stSG494919	TGACCATGGGCCCTCCTAAGCTATTTGG	TGGGGTGTGATCACTGAGAA
stSG494920	TGACCATGGGTTCAATCTGTTGCCGTTT	GTGTTTGCATGGTTGAGCAC
stSG494921	No Unique Sequence	No Unique Sequence
stSG494922	TGACCATGGTGTACAGGGGAAGAGCGAG	GGGAAAGGAAAACTGAACCA

stSG494923	TGACCATGCTTCGTCTCTATGGTCCCCC	TAACCAACTGGAGGCAGAGG
stSG494924	TGACCATGTGTCCATTTCCTTTAGTGCG	CCGTGAACAGTAACTCCCTAGC
stSG494925	TGACCATGACAGGGTGCAGTGTAGTCCC	GGCTCCCCACAACAAGTTT
stSG494926	TGACCATGACTTCTCCCATGTGTTGTTCC	AGGCAGGGGAGCCTATCTAA
stSG494927	TGACCATGATGGGTGCTGTTCTTGTTCC	TTGGAAAACTGCAAATCAGC
stSG494928	TGACCATGTGATACCCTTCTCCTGCTCC	TGAGCACCTGGGTACAGACA
stSG494929	TGACCATGCTCACTGGGCTGGCTCTATC	TGCTTTCTTACACAAGACCCA
stSG494930	TGACCATGATCAGGTGGGAATGATGCTC	AGAGGTTGCCCAAAACACAC
stSG494931	TGACCATGAAATGAGCAAACTTGGCAGC	TCACCTGGCCAAAACAATTT
stSG494932	TGACCATGTGACTGTCTCAGAGCTGAATGA	CCAAGCCAAGATTCCTTTGA
stSG494933	TGACCATGGGTGGGTGAGACTTGAGGAA	AATTCCATGTCCCCACCATA
stSG494934	TGACCATGTGCTTCCTCCTCCTGTGACT	GTGAGCTACACCTTTGGCCT
stSG494935	TGACCATGTACCCATCAAGCCTACCTGG	TTCTCCCTTTCCTCAGTCCC
stSG494936	TGACCATGAGGCCTTTGAATAGCAAGCA	GCTGGACTATTGGCTTCTGC
stSG494937	TGACCATGTGAGAAAAACCCACTCAGGG	GGTTTCAACCCAGGAAGACA
stSG494938	TGACCATGGAGGTTAGGCTCAAGGGGAC	ACCTGTGTTGGGCTCTTGAC
stSG494939	TGACCATGTGAGTGCTTCCTGTGTCCTG	GTTTGTTAGCGTATGGGCGT
stSG494940	TGACCATGGCTTTGCTTGCTACTTGGCT	CCATCTCGTTTCCAGGACTC
stSG494941	TGACCATGTTTGTTGAGCACTGTCTGGC	TCTCTTCCACATGGACCCTC
stSG494942	TGACCATGCTCAAATCACACCACACACG	TGGTGTCAGCTGAGAAGAGC
stSG494943	TGACCATGTGGCAGCATATTCGAGTGAG	GCTCACAGCCTCTCTGCTTT
stSG494944	TGACCATGTGATCCCCAACTAGAGAAAAGG	AGCAAATGTTATTTCCCCTCC
stSG494945	TGACCATGTGTCAGCCGATCAGTCAGTC	TGGGCTCCACATATTTCCTC
stSG494946	TGACCATGGGTGAATTCTCCACCAGTCC	CTCCCTAGCTGTGCCAGAAC
stSG494947	TGACCATGTTCCTGCCTGGCTAACTGAT	GCATAGAGAAGGGACTAGAGGG
stSG494948	TGACCATGACCCGTCAAATCCTCAGATG	CGGGTACTGGGACTTTACCA
stSG494949	TGACCATGTGAGCAACGGCATAGAGATG	CCGGCCCACAATTTTAATAGA
stSG494950	TGACCATGGACACACCAGGCATCAGAGA	TGCCATGGATGGTGAGACTA
stSG494951	TGACCATGTCTGGCTTCCAGTCCTTGTT	GAGGCAAGCAGATTTTGGAG
stSG494952	TGACCATGACTTTTGGAACTTGGCATGG	CCTTTGCACTCAATGCTTCA
stSG494953	TGACCATGTACATAGGGATCTGGGCTGG	AAATCCTGTGGCTCCTTGTG
stSG494954	TGACCATGCCTGCCAGCTTCTGACTTCT	AACAGATTTCCTCCCATTGC
stSG494955	TGACCATGGGCTGACCTACTGGAGCAAA	TCAAGAGGAATTGACCTGAACA
stSG494956	TGACCATGCTAAGTTTCTCCCCGCTCCT	GCCTAAGGCCAGATTGATGA
stSG494957	TGACCATGGTCTCTGGCTCTTTGTGGCT	CCATTCTACCCAGGCATCTG
stSG494958	TGACCATGTTGACAGTAGCTGCAGGTGG	TTGGTGAGGAGGGAGATGAC
stSG494959	TGACCATGTTGGGTAGGCTGATCAGAGG	TTCTGAAGACCCTGGAATGG
stSG494960	TGACCATGAAACCCACCTTCCAAAGTCC	GTCTCCAAGAGAGGAGCGGT
stSG494961	TGACCATGGAGAGGCTAACGGACATGCT	GGCCACAGTCCTGTTCATTT
stSG494962	TGACCATGGAAACTGAGGTGTTGCGGAT	AGGGGCATCAGTTCAACATC
stSG494963	TGACCATGGCACATCTTCAGTGGGACCT	CAGGAAATACCTGAGGCCAA
stSG494964	TGACCATGGTGATTGGGGATGTGTGTGA	AGGAAAGCCATTATTTGGGG
stSG494965	TGACCATGTAGGACATGGAAGACCGGAG	GACAAAGCGGATGAAACCAT
stSG494966	TGACCATGGACGTCATCACGAAGATCTGA	CTTTCAGCATGAACCAAGCC
stSG494967	TGACCATGGTGTTTGCTTCATTGGCCTT	TTGGAACCCTCTTCCTCCTT
stSG494968	TGACCATGCAGGTCCCACATCAGGACTT	TCCAGGGAGAGGAAGACAGA
stSG494969	TGACCATGTTAAGGACCACACCCTGGAG	AGGGGACAAGTGACATCCTG
stSG494970	TGACCATGGGCCTCCTACCACACTCACT	GCAATTTCCTTAGAATGACCCA
stSG494971	TGACCATGGAGCTCCGGAGACTGACAAC	TGTGCACCTCCTTTATGGAA
stSG494972	TGACCATGCAACCTGCCACAAGACCTG	GAATTGCCTCGCCCATACT
stSG494973	TGACCATGCCCAGAAAAACCTGGGATATG	GAGTCGCCACCGTAACATTT
stSG494974	TGACCATGAATATGCACAGGGGAGAACG	AAATTGGACTAGTGGCCCAG

stSG494975	TGACCATGCAACATCAGCTTCCGTGAGA	CCCAGCAGACTAGGGAGATG
stSG494976	TGACCATGGCTGTGGAAGGAAAGACCAA	GATGGAGAAACAATGGGTGC
stSG494977	TGACCATGTCTGATGTCAAAGCAACCTGA	CACTCATCAGCCTAGATGCAA
stSG494978	No Unique Sequence	No Unique Sequence
stSG494979	TGACCATGGGCAGGAGTGGAGGTGATTA	CACAGGGCAGGTACCAAGTT
stSG494980	TGACCATGCATGCTCTGCTTTCCTTTCC	AGCAGCTCATGCTAATGCAG
stSG494981	TGACCATGGGCGCCGCATAATCTAAATA	TGGGAGATTTTCCAAGATGG
stSG494982	TGACCATGTTCAACAGAGCCGTGAACAG	GCCATTTGTGTAGCATTAGCC
stSG494983	TGACCATGAAAACAATAACGGACCGATCA	CACAAGCAATGGCCTTAACA
stSG494984	TGACCATGCAGGCACTACTGATGCTCCA	AATGCAGGAACACACATCCA
stSG494985	TGACCATGAATTTCAAACTGAGCAGGGG	ATGGCCAGCCGTTTACATAC
stSG494986	TGACCATGTTCTTAGGAAGGTTTTGAGCCT	ACAATAACCCCTGCAGTCCA
stSG494987	TGACCATGGGGCATTGAGTTTTTGGATG	GCCTCACCCAAACTGGTTAT
stSG494988	TGACCATGAATGGGCTGTACCTCATGCT	CTGCCTCCCTTGTCCATAAA
stSG494989	TGACCATGCGAGAGATACAGAGCCCAGG	TACGAAATTGGGGTTTCCAA
stSG494990	TGACCATGAGAGCACTTGCTGTAGGTCCA	GTAGGGCTCTAGACCTGGGC
stSG494991	TGACCATGACCAGGCCAACACTGGTACT	GGATGGGAGGTAAGCACTCA
stSG494992	TGACCATGGCAAAGTGAGAGAGAGATGTCC	CCATCCTTTCATTCCTTTAACC
stSG494993	TGACCATGCCCCATCTCCACCTACACAT	GGGAAAGTTTCTGGCTAATGC
stSG494994	TGACCATGCACTAAGGGAAGCACAGGGA	CTGCTTTTCAGTTTGGCCTC
stSG494995	TGACCATGTGTCCCTATCCCTCCCTCTT	GGCAGGCTCAGATCTGTAATG
stSG494996	TGACCATGGGATGACTTAGTAGGGGCCA	GGTGAGCACCACACCTCTCT
stSG494997	TGACCATGTCTTCCATGAGGGAATTTGG	CAAAATGGCATGGAGATACAAA
stSG494998	TGACCATGTGAGTGCCAAAGAATGGTGA	ATTGAGATGAATTGGCAGGC
stSG494999	TGACCATGAGAGTAAGGGTGGTGGGCTT	CCTTCAAGCTGGCTTTTGAC
stSG495000	TGACCATGAAGTGAGGAGTAGGGCTGGA	CGAATCAGGGGAAACTGAAG
stSG495001	TGACCATGGAATCCCCACGGTAGAGACA	TTAGCCATTCAGAGGGTTGG
stSG495002	TGACCATGCACCTTTCTTGCTCTGGAGG	AGAGCACTTGTTCCTGGCAT
stSG495003	TGACCATGGCAATGAAGGAATGAACCAAA	TGCCAATTACTGATCAGGCT
stSG495004	TGACCATGGCTTGCCTATGGGTGTGTCT	GATGTGGAGGAATGTGGCTT
stSG495005	TGACCATGCTCCCACAACCCTTGACCTA	AGCCTACCTTCCCCTTGAGA
stSG495006	TGACCATGGGCACTAAACTGGCTCCCTA	GCCATCCTGCAAGAGAAGTC
stSG495007	TGACCATGTTTTCCTCCCAACCACTTGT	TGCTGGCCTATCCCAAATTA
stSG495008	TGACCATGTGACTTGTGGGAAACAGCAA	TGTGGACCAATGCAAACACT
stSG495009	TGACCATGTTGGGAAGAAGGAGGGTTTT	AGAGATCTTGCTCACCCCAA
stSG495010	TGACCATGCACTGAAAGACTGGGGCTCT	ATCTGTCACCATCCTCAGCC
stSG495011	TGACCATGGGCTGAAGTCTGCAAATCCT	TATTTGTTCCCTGCCTTTGG
stSG495012	TGACCATGAATCCCTGGGAAGCTAAACG	ATGAGGTCCCCCAATTTCTC
stSG495013	TGACCATGATGCCAGCATTGATGTGTGT	TTGGTTGCAGCATCAGTAGC
stSG495014	TGACCATGTTTTCATCATTGGCTCCACA	CCGGGTAAAACAGACTCCCT
stSG495015	TGACCATGCACCTAAAAACACACCCTCCC	CCCTGGAAAGTTCCCAATTT
stSG495016	TGACCATGTTGCAGCTGCTGACTCAATC	TCTCCTCCCTCACTTCACCA
stSG495017	TGACCATGGATGAGGGTGAAGACTGGGA	TCACTTTTTCCTGCAAGGCT
stSG495018	TGACCATGTATGGCCAGTGCTTCTAGGC	GTGGGAGGGCAGTTTCTGTA
stSG495019	TGACCATGCACATGCTCCAGTGCTGAGT	AATCAGATTGGTTGGCAAGG
stSG495020	TGACCATGGAAAGGGGAGGAAACAGTCC	CTGGGGGTTTTATTGAAGACA
stSG495021	TGACCATGCAGTGATGTCAAGGCCAGTG	CCCAAACAGAGGTTCACCAT
stSG495022	TGACCATGTGGGAGATGCAGAGTTGACA	GAGGAAAGGCACAGATTGGT
stSG495023	TGACCATGGCAGTTTCTGGTGGTGACCT	TCAAGTTCAATGCCTAGGGG
stSG495024	TGACCATGGGTGTGAGATCCCAAAAGGA	CAATCTCCGGGTGCAGTTAT
stSG495025	TGACCATGGGCTGGTGGAAACAACACTT	ACAGCCTAGTGCAGCCTCAT
stSG495026	TGACCATGATCCTCCCTCTCACCCTCAT	TAAGGCAGTCCTGGAGGAGA

stSG495027	TGACCATGTTAATGGCTCCTCACCCTTG	AAGGGATGGAAGAAAGGAGG
stSG495028	TGACCATGGATGAGGTAATGCGGCTCTG	GCTTACCGATGTCGGAGTTG
stSG495029	TGACCATGGAGGTCGCAAAATGGGTAGA	ATCCTTGACAAGTGTTGGGC
stSG495030	TGACCATGGAGAGATGCCAGCAGTGACA	TGCAGGAAGTATCCCTCCAC
stSG495031	TGACCATGCCACTTGATATGTGGGGGTC	TCAGCTCCTTGCCTCAATTT
stSG495032	TGACCATGCACTTCCAGCTGCTCTCCTT	TGGGAAGCTACGTGTGATTTC
stSG495033	TGACCATGTGGTCAGCAGAGAGCTGAGA	GGATAGAAGGGCACTGACCA
stSG495034	TGACCATGTGAGTGTGAGGCACCTGAAG	AAATCATGGCTTCCCAACTG
stSG495035	TGACCATGGAGACATCCACTCCTCCCTG	TCACATGTGGGATCTTGAGG
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stSG495037	TGACCATGGCCCTGATGGATTTTTCTGA	TAAGACAGGAAAAGGGGGCT
stSG495038	TGACCATGGCTCACAGTCATCCTGCTTG	AGAGTTGGGGGTCTTCTGGT
stSG495039	TGACCATGAATAAAAGATGGCTGCACGG	ATATTGACCTCCATCGTGCC
stSG495040	TGACCATGTGGTGGAGTGGACAAAGATTC	GGTGGGGAACAAGGAAAAGT
stSG495041	TGACCATGCAAAGGAGTTAGGTCGCAGG	TCTGGCATGTTCTGGTCTTG
stSG495042	TGACCATGCCTCAAAGGCTCTGTCCTGA	CTAGCAACAAATGCGCAAAA
stSG495043	TGACCATGTTCCTCAGGCCATTCAGAGT	CAACGGGAGTCACCTCAAAT
stSG495044	TGACCATGGCTCTAAGGAGCATGGTTGG	CTGTTACCTGGGGGACTTCA
stSG495045	TGACCATGCAGAACTCACGGGTCACGTA	GTTCCAAAAGCATTGCAGGT
stSG495046	TGACCATGGACACATCCTCAGCCATCCT	ACTTGAGCCTCCAATCTTATCC
stSG495047	TGACCATGTGCCTGTGCTTTTTCCTACC	CTTGGGCAAAGTCTGAGGAG
stSG495048	TGACCATGTCCTAATCCAGACTGCCCTG	TTAGTGGTTGATGTCTGCCG
stSG495049	TGACCATGCATTTTCCAGCCACTCTGTG	TGGGCAGAAGTTACCTGAGAA
stSG495050	TGACCATGTCCAGTGATTGAACTTCCTGTG	GCCGTGTTGTGTTTACATGG
stSG495051	TGACCATGTCCCTCTGGAAAGCAGAGAA	GACCTGAGAAGGGCATGG
stSG495052	TGACCATGGTACTCCCTCTCTCCCCCTG	CCCCCACACTTTTATTTCCA
stSG495053	TGACCATGTGAGGCACACATGCCTACAT	GCTCACCAGGAGCTACAAGG
stSG495054	TGACCATGAAGGCCTCAGTGCTGTCAGT	GCCACCTTTTGTCAGCTCTC
stSG495055	TGACCATGAGAGGAGCCACAGGCTATGA	TCCCAATTTCTGATCCTTGC
stSG495056	TGACCATGTGCATGTGAAGACGTAGGGA	TAACTGGCAGAATTCCCAGC
stSG495057	TGACCATGGGGGACACAGGATGTAACCA	TGGGATGTCTCTGATCTGGTC
stSG495058	TGACCATGTGCAAGCCTCCTTTTCTCAT	CATCCTTTGGGACATGCTTT
stSG495059	TGACCATGTGGAAAGCAGAAACCCACTC	CAGGCCTTCCACTGTCTGTT
stSG495060	No Unique Sequence	No Unique Sequence
stSG495061	TGACCATGAGGTGAGAAAGCAACCATCG	CACAGAATCACAGTGGCACA
stSG495062	TGACCATGCTGAGGTTGTTCCAAGCCAT	AAAGACCAGAAGGAGCAGCA
stSG495063	No Unique Sequence	No Unique Sequence
stSG495064	TGACCATGGCTGGCTTTCTATTTCCCGT	TCCAATGTCAGACAGAGAAAGG
stSG495065	TGACCATGAGTCCACAAAGAAGGGAGCC	AGGATTTCCCTGGTGTCTCA
stSG495066	TGACCATGGGCAGGTTCAAAGGGTTTTT	TCACTCAAGTGTGAAGGGGA
stSG495067	TGACCATGTCCTAGTCCGTGGTTTCACC	GTCACTGCACTTGCCTTTCA
stSG495068	TGACCATGGGTCATCATCTGGGAGAGGT	TCATGTCAAAGCAGACCTAAGC
stSG495069	TGACCATGAATGGCAAGAGAACGACACC	GGCAATGACTCACCCACATT
stSG495070	TGACCATGGGGACCACCTGCTGAGTAAA	GGCTGGTTCCTATTTGGTGA
stSG495071	TGACCATGGAAGATTTGGAGGGGACCAT	TTTGCAGGCTGAGAGAAACA
stSG495072	TGACCATGTCTTAGCAGGTGGGAACCCT	CCCTCAAGACCCTGTGAGAA
stSG495073	TGACCATGTGCATCAGCCAGTGACTTTC	GCACTTCTTTACGAGCCAGG
stSG495074	TGACCATGCCAGAAGTTGAGGAGGGTGA	AGAAATCCTGCCCGTCTTTT
stSG495075	TGACCATGTTTTGCAATTACCTCTGCCC	CAGCCACCTTGCTTTCACTT
stSG495076	TGACCATGAGGTGCTCAGCCATCAGACT	CCAAGACTCAAACTCCAGGC
stSG495077	TGACCATGTGGCCATTTAGAAGTTCCCTT	ATCGTGACCATTGTGGGACT
stSG495078	TGACCATGTGTCTGCTTATTTGGGGCTT	TGCAGAGTCACTTGAGGTGG

stSG495079	TGACCATGAGCCAGCAGAGAGGTGAGAA	GGCTCCCAGAATGATACCAG
stSG495080	TGACCATGAATGAAGGGCTTCCAGTTCA	TTCCTGGAGCCATTTACCTG
stSG495081	TGACCATGGGGGATACTGGGGATTGTTT	AAGAAAAGAAAGAGCTGCACAA
stSG495082	TGACCATGACTGAGGGAAGGAACTGGGT	AGGAGAAAGGAGGGCAGAAC
stSG495083	TGACCATGAACACAGGGATGGGTTCTTG	GCCACCATATCATGCCTTCT
stSG495084	TGACCATGGCACTTACTCCCTGCTCTGG	GAAAGGGAAAGCAGAGGGTC
stSG495085	TGACCATGTGCTGCATGTGATTTTCAGG	TAGCACGGGAAGTTTCTTGG
stSG495086	TGACCATGGCCCTCTGTGAGGAAGAATG	CGAGCAGTGCTACAGAGACG
stSG495087	TGACCATGGTAATGACCCATGTCCCCCT	CTTTTTCCTTCCCCTTCTGG
stSG495088	TGACCATGCATCTCCATGGTTCAAGCCT	CCTCTTCATGGAGGGTGAAG
stSG495089	TGACCATGGCCTCTTCCCATCACAAATG	TGCATGTGATTTGCTTGTTTG
stSG495090	TGACCATGTCCCAGGTTGACCAATAAGG	GATGCAAAGCTGTGCTGTGT
stSG495091	TGACCATGGAGGAAGAGGCTGCCCTAGT	CCACGTCCACTTGAGGTCTT
stSG495092	TGACCATGTGTCTGAGTGCAGGATGTCTG	AGCAGCAGCTGAGTTTGAGA
stSG495093	TGACCATGCCATCACACACACAAGAGCC	GCAGCTGAGCGTTCTTTTCT
stSG495094	TGACCATGGGAGCCTGCCTATCCCTACT	CTTCTGGGGTTGAATTCATTG
stSG495095	TGACCATGCCACCCAAAATAATGCCAAT	TTGGATGGTCTTCCCATTGT
stSG495096	TGACCATGGAAACACCACCATTCACGG	TTCCAAGACTCCTGCTTTTGA
stSG495097	TGACCATGAAAAGACAATGCTCGACGCT	AGCCATAAGGCCACATCAAG
stSG495098	TGACCATGAGATCGCCTCTGTGTTTGCT	AGCTAACGTCCATGTCACCC
stSG495099	TGACCATGAAGGGTGATATTTCCCTGGC	GGAATCAAAGGAGGAAAGGC
stSG495100	TGACCATGAGTCTGCTCTGCCTGACTCC	GCCAGTGGGACATCTCATTT
stSG495101	TGACCATGAATATGTTGCACCGATGCTG	TTTGGTCCTCTTCATCCCTG
stSG495102	TGACCATGGCAAGCCGACTTTTTGACTT	CGTACAGTAGGGGCTCAACC
stSG495103	TGACCATGTGGACATGAACCTGTGCAAT	CACAGCTATTGTGGATGCGT
stSG495104	TGACCATGCCCTGGCCAATAATGGTATG	GCCAGGTCATGGAATAGGAA
stSG495105	TGACCATGGAGCATCTATGAGGCGGTGT	AGGACTGGGGGACTGAAAGT
stSG495106	TGACCATGCTGGCTTGTTTTCCATGCTT	TGACTGTGAAGGTGATGGGA
stSG495107	TGACCATGTCCACTTCCCTTCTGCTTTC	AGCTTTGGCCACAGAAAAGA
stSG495108	TGACCATGACGCTAGGGTGTGATGTGGT	TCCTGTCCTCTAACCCGATG
stSG495109	TGACCATGTGGGTGGATCATACAACAACA	AGGTCTTGGTTGTCACCTGG
stSG495110	TGACCATGTTGTCAGCGTTGGCATTAGT	CTGACCACCTTGGACCAAAT
stSG495111	TGACCATGCACCATCACTGCAGGCTAAT	TTCAGGTGTAGACAGGAAGGC
stSG495112	TGACCATGAAGAGGGCAAAGGGACTGAT	GGTCCTGTTCAGAACCTCCA
stSG495113	TGACCATGGAGCTCTTCCTATGCAAACTCC	TGCCTCAGTTTTTATTGCAGG
stSG495114	TGACCATGTGCCAGACAAATCAGCAAAG	GAACACTCTCTGGACCAGGC
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stSG495125	TGACCATGGCCAGGAGAAACTGTTCCC	GGGCAGTTTCTTGGTGTGAT
stSG495126	TGACCATGTCACACTGACGTGTTCCAGA	CTCCTCCCCAAGCTCTCTTT
stSG495127	TGACCATGTTGCTGCCTAAAGGGAAAAG	GGCCATAGTGCGTTCTGTTT
stSG495128	TGACCATGGCAAGAGTGACTGAAAACGGA	AAAAACACACAGGGAGGTAGG
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stSG495130	TGACCATGTAGCCCCAATCAATGACTCC	CTCCCAAGGGCACACATAGT

stSG495131	TGACCATGGCACTCTCAAGCCACTCACA	ATTATGGGAGCCCAGGAAAG
stSG495132	TGACCATGGTTTTTGAGGGAGCTTTCCA	AGGGAGACCCACACTCACAC
stSG495133	TGACCATGGGCCTTACACTTTTCCAGCA	GGCATAGTCGCTTGGTGAAT
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stSG495137	TGACCATGAGACAGGTGCAGGAAGGAGA	TGGCTTTTGAGAAGGCATTT
stSG495138	TGACCATGTCTTCCATAAAGACAATCCCCT	TTCTGCCTGTGACAAACCTG
stSG495139	TGACCATGCATGCTGGACAACAACCATC	CCTTTCTTCAGGAGTGGTGC
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stSG495145	TGACCATGAGCCCAAAGTGAGCATCAAC	CTCCCCCAATGCATAAAATAA
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stSG495161	TGACCATGTGAGGGCAGAAGCTATGACA	TATACACCAGGCAGGATGGG
stSG495162	TGACCATGGCAAAACCTAAGTGACTCCCTC	GAAGGAATGTTCCCTCTCTTTG
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stSG495166	TGACCATGACCCATAAGTTTGGCATTGG	TTGGGAAAGCCATCTGGTAA
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stSG495168	TGACCATGCCAGCTTATCAACCCGATTC	CTGGTGTTTTGCCTTCCATT
stSG495169	TGACCATGGATGATTGTCCCAGGCCTTA	CCACTGTCTAAGGGCGTTCT
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stSG495185	TGACCATGCCTGAGATTCTGGGAAGCAG	AATGCTGAAGACCCCTCTGA
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10Kb Resolution Array		
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stSG495393	TGACCATGGTCACTGAATGCCAGCTGAA	GTGCTCTCCAACTAGCCCAG
stSG495394	TGACCATGTGTGCTTGGCATAGTGGGTA	CTCAAGGACCCCAAACTTGA
stSG495395	TGACCATGATGCACACTCATTGGCACTC	ATAGGGCCTGGAAGTGTCCT
stSG495396	TGACCATGTTCTTGTTGGTTGTTTGCCC	GGCAACCACAGTAAAATGCC
stSG495397	TGACCATGTAGGCGATGCCTGAGTATCC	AAAGTGTTGCCAGTCTTGCC
stSG495398	TGACCATGGGCAAGACTGGCAACACTTT	CTTAAGCCTGAGCCCAACTG
stSG495399	TGACCATGGGGAAGTGTGTTGAATGGCT	TCACAATGGCCTCAATGGTA
stSG495400	TGACCATGTACCATTGAGGCCATTGTGA	TCGTGAAACACTGGAACTGC
stSG495401	TGACCATGAGTGTTTCACGAAAGGGGTG	GTTACCCTTTTGACAGCCCA
stSG495402	TGACCATGGATGGCCACATGCATTATAAGA	CCAAGTCAAGCACTCTTTGC
stSG495403	TGACCATGACCTGTTTCTCCCCATCTCC	GGGAAAGTTTCTGGCTAATGC
stSG495404	TGACCATGGCATTAGCCAGAAACTTTCCC	CCTGCTACTCCAACCCTTTG
stSG495405	TGACCATGCCTTATACTGCCTTTGGGGC	CCCAGATTTAAGCGGTTCTG
stSG495406	TGACCATGGCTCAAGAATTTTTGGCCTG	TGCCTCTGGCTCTATCTTCA
stSG495407	TGACCATGAACCTTGGAGGGGTCTGTTC	TCAATGATTTATGCCTCCACA
stSG495408	TGACCATGATCCAGAGCTTGGAGGAACA	TGATGTGCTGATGTGCAAAG
stSG495409	TGACCATGTTTGCACATCAGCACATCAG	GAGGGAATGGACTGCAAAAA
stSG495410	TGACCATGTCCATTCCCTCTCCACAATC	AACATGGGCTGTCTCCTGAC
stSG495411	TGACCATGACCTAGTGGGCCTGAGGTCT	GTGATGAGCCCAGGGTAAAA
stSG495412	TGACCATGGTGCCTTATGGGTTCTCCAG	CAGCAGTGATAGCTCACCCA
stSG495413	TGACCATGAGATAGAGGGAGGGGTCAGG	TTTGGCCTCCAGCAAAATAC
stSG495414	TGACCATGGGTCTTCACCTGTCTGTGGG	ATCTGTTTCGATGGATGCCT
stSG495415	TGACCATGACAGGAGGGGCCAGAGTAGT	CAGCACAGCAGAAGATCAGC
stSG495416	TGACCATGGTCCTGGAAAGGGGGATAAG	CTTTCCCATTGCATTCCATT
stSG495417	TGACCATGATGGAATGCAATGGGAAAGA	AAGGAAAATGGTGTCAAGCAA
stSG495418	TGACCATGACGTTCAAGCATCACAGTGC	ATTCCCCAGAAGCAACAAAA
stSG495419	TGACCATGTTAAAAACCCCACCAGCAAG	GCCAGAGCAAAACTAGCCAC
stSG495420	TGACCATGGTGGCTAGTTTTGCTCTGGC	GCTTTGGACACTTCCTCTGC
stSG495421	TGACCATGGCAGAGGAAGTGTCCAAAGC	ATCCACCACAAGTCCCAAAG
stSG495422	TGACCATGTCTGAAAGCATGAGGCTTGA	CAAATCCCTGGCCATCTAAA
stSG495423	TGACCATGTTAGATGGCCAGGGATTTGA	ACTCCCCTGAGAAGCTGTGA
stSG495424	TGACCATGGACGCTCTTCATGGGATCAT	TAACTTCTGCCCCAACTCCA
stSG495425	TGACCATGTGGAGTTGGGGCAGAAGTTA	GCTGCTCTGGAGAGGAGAGA
stSG495426	TGACCATGGGTCCGAGGTCTCCTCTTTC	TTCTGGGGTTTTCACCAAAG
stSG495427	TGACCATGTTGGTGAAAACCCCAGAATC	TTTTTCCCATAAATCAACCCA
stSG495428	TGACCATGTGGGTTGATTTATGGGAAAAA	CTGCTGGCTTTTGTTGTTGA
stSG495429	TGACCATGTTGTCTTTGCAGATCAGGGA	TAATCCCTCTTCCCTCCCAC
stSG495430	TGACCATGGTGGGAGGGAAGAGGGATTA	GCCTAGCAACAGCATCCTTC
stSG495431	TGACCATGGAAGGATGCTGTTGCTAGGC	CCATCGATTCCCAGATGTTT
stSG495432	TGACCATGGTGTGAGCCCAATCCAAGTAG	CCGCAAGGGCTAAACAGAAT
stSG495433	TGACCATGTTTGTCCCTATCCCTCCCTC	GGCAGGCTCAGATCTGTAATG
stSG495434	TGACCATGCTGTCGGACATAGATTACTGGC	ACAATACAGTCGCCACTCCC
stSG495435	TGACCATGGTCTGTCTGCAGCATCCCTA	AGCGTACCTGTACCCCCAG
stSG495436	TGACCATGTACCCCTCAGCTCCGGTAGT	CAGTTGTGGAAATTGTGCGT
stSG495437	TGACCATGGGTGAGTCATGGCTTCTGGT	AGGGAAACAAAGCAGCTTCA
stSG495438	TGACCATGTTGGGGACAATAATTTGGGA	TCCAGGTAACCAGCCTCAAC
stSG495439	TGACCATGGGCTGGTTACCTGGACAGAA	ATGGGTCATTTGTCACAGCA
stSG495440	TGACCATGTGCTGTGACAAATGACCCAT	ACATAGCGCAAACCCAAAAG
stSG495441	TGACCATGGGTTTGCGCTATGTTCCACT	ATTCAGACTCCAGCGCTCTC

stSG495442	TGACCATGGAGAGCGCTGGAGTCTGAAT	GGGGGACGGGATACAGTAAT
stSG495443	TGACCATGATTACTGTATCCCGTCCCCC	TCCCATATGAAGCCAAGGTC
stSG495444	TGACCATGCCACCAGCTCCAATCAGACT	CAGCCCCATATTGGTACAGG
stSG495445	TGACCATGCTGTACCAATATGGGGCTGG	TGAAAGACAGCAAGGGAACA
stSG495446	TGACCATGGCACTGCTGGTTTTCTGTGA	AACAGGTTCCAGTCTGGGTG
stSG495447	TGACCATGCTAAGCCCTTGCCAACCATA	AAAGGTGATCATTTGCACCA
stSG495448	TGACCATGTTATCTGTGTGTTTCTGCCTCA	CCTGCTACCCGTTTCTCATT
stSG495449	TGACCATGGAGGTGTGGTGCTCACCTTT	TGCAAAGCATACGTTTCGTC
stSG495450	TGACCATGTTTGCATTAAGAGTTGGGCA	AACGGGCTTGATTACTGCAC
stSG495451	TGACCATGGTGCAGTAATCAAGCCCGTT	CATTTCCCTCAATTGTGCCT
stSG495452	TGACCATGGCACAATTGAGGGAAATGCT	GGGTTCAGAAATGGGAGACA
stSG495453	TGACCATGGTCTCCCATTTCTGAACCCA	GGCAACTTGAGAGCAGGAAC
stSG495454	TGACCATGGTTCCTGCTCTCAAGTTGCC	TTTGCCATTTCCTTTCATCC
stSG495455	TGACCATGGGATGAAAGGAAATGGCAAA	CGCTCAACTTCCACTTCTCC
stSG495456	TGACCATGGAGAAGTGGAAGTTGAGCGG	AGCCATCCACAGGCATAAAG
stSG495457	TGACCATGTGCCTGTGGATGGCTTTATT	AGCCCTCCCAATCTTACCAC
stSG495458	TGACCATGCCCCCAACAAATGTCACTCT	GGGGAATGAGAACTATCCAACA
stSG495459	TGACCATGTGTTGGATAGTTCTCATTCCCC	GGCAGAAACTGTTGACACTCTG
stSG495460	TGACCATGTGTCAACAGTTTCTGCCTTCA	TGACATCACCAGAGGGTTCA
stSG495461	TGACCATGATCACTGGGCTCTTTCATGG	GCAGCTGCAATCTTTTCACA
stSG495462	TGACCATGAGGAAATGCAAGCCCATACT	CAGATCCCCTCCATATTGGTT
stSG495463	TGACCATGGGAGGGGATCTGTGTTTCAT	AGGCCTTCAAAGCAACAATG
stSG495464	TGACCATGAACTTGAAATTCCTTGGCTACG	ATTTGGCTCAAGGGCTTTTT
stSG495465	TGACCATGCCAGGTTGCTGAAGGAAAAC	ACTAGCAAACTGCAGCCGAG
stSG495466	TGACCATGCTGCAGTTTGCTAGTGCGTC	AGCTGTGCCCAACCTCTCTA
stSG495467	TGACCATGGCTAGAGAGGTTGGGCACAG	AGCAGAAAAGAGGGCAGTCA
stSG495468	TGACCATGTGACTGCCCTCTTTTCTGCT	CTAAGTGCCTGCAAAGAGCC
stSG495469	TGACCATGGGCTCTTTGCAGGCACTTAG	GCCACCATTCAACTTGACAC
stSG495470	TGACCATGCAAGTTGAATGGTGGCATGT	AGCCAATGGTCTCTTCTGTCTC
stSG495471	TGACCATGGAGACAGAAGAGACCATTGGC	CTCCACAGGAGTGGGTCATT
stSG495472	TGACCATGGGATGTTCGTTCCGTCTTGT	TGGCCTTGTAGCAGGAAATC
stSG495473	TGACCATGTACAAGGCCAAAAGCCTGAT	TTCTTGCTGCCAATTGTGAC
stSG495474	TGACCATGTCCTGAGGTCCTCTTTCTGC	CTCTGCTTTTTCTCGGTGCT
stSG495475	TGACCATGAGCACCGAGAAAAAGCAGAG	TACACCAAACTGGGCAACAA
stSG495476	TGACCATGATTCAGGACATCGTTGGGAG	CGTCCTGCATTAAACAGTGG
stSG495477	TGACCATGGAGCAGCAATGATCACCCTT	GCTGATGACTACTCCAGCACA
stSG495478	TGACCATGCAGCTGTACAGGAAGAGGCA	ACTATTCCCAAGGCCAACCT
stSG495479	TGACCATGGGTTGGCCTTGGGAATAGTT	ACCAAATGGCCTTTCAACAG
stSG495480	TGACCATGCTGTTGAAAGGCCATTTGGT	GCACATAACATTCCAAGCCA
stSG495481	TGACCATGATTGCCAATGTCTTCCTGCT	CACACATCCCCTGCATAGTG
stSG495482	TGACCATGGCAGGGGATGTGTGTATGTG	CTTGCTTGCTTCCATGACAA
stSG495483	TGACCATGTTGTCATGGAAGCAAGCAAG	CCCAGCCACATAAAACCTGT
stSG495484	TGACCATGGTGCCATATGCATGAGCAGT	GGTCACCATTCTTTGGCACT
stSG495485	TGACCATGATGGTGACCTTGCTTCTGCT	GAAGGCTGGGCATCAAGTAA
stSG495486	TGACCATGCAGCCTTCCAATTTGTCTCC	GCAGAGTTCCAAACAGCACA
stSG495487	TGACCATGCCCAAGGAGAGGTCTCATGTT	TCCGTCCCTGCTGAATTAAC
stSG495488	TGACCATGTAATTCAGCAGGGACGGAAT	GTCTCATGGCGACCCTAAAA
stSG495489	TGACCATGCTTTTTGCCCTTTCCCATTT	GCCAGGCATCCTGATTTTTA
stSG495490	TGACCATGCTGATTTGGAGCTTGGAAGG	GCAGGGTGTAACCATGAGGT
stSG495491	TGACCATGTGCCCCAGATCCTTCTAATG	GTCAGGTGATGGCAAGGAAT
stSG495492	TGACCATGTTCCAAGGGAGTGGTGAAAG	AAGCCCACCACCCTTACTCT
stSG495493	TGACCATGAGAGTAAGGGTGGTGGGCTT	CCTTCAAGCTGGCTTTTGAC

stSG495494	TGACCATGAGAGGGCAATGTGAAGAGGA	TGGAAACATTGTAGGTGCCA
stSG495495	TGACCATGTGGCACCTACAATGTTTCCA	AGGAATGCCGTTTCCTTTTT
stSG495496	TGACCATGGACCCTTTCCTTGGGAAGTC	CCTCCAGGTTCCTCAAAACA
stSG495497	TGACCATGCCTGTTTTGAGGAACCTGGA	CCCAAGACCCATTTCTTTGA
stSG495498	TGACCATGGGGCTACCCCAATCATCATA	AAAGAATTCCAAAAGCGGGT
stSG495499	TGACCATGACCCGCTTTTGGAATTCTTT	GACAGTCCCTGCGTTGAAGT
stSG495500	TGACCATGGTATACACGGAGGGTCACGG	CAAGCTCAGTCTCCTCAGCC
stSG495501	TGACCATGTCTCACGGGTATTTTCCACA	TGGCAAGAATAACCCCACTC
stSG495502	TGACCATGTGAAAACTACACCACGCAGG	TGATGCTGCAATTTAATCCAA
stSG495503	TGACCATGTGGAAGTGAGGAGTAGGGCT	CGAATCAGGGGAAACTGAAG
stSG495504	TGACCATGCTTCAGTTTCCCCTGATTCG	AATGCCCAGTGAATTAACGC
stSG495505	TGACCATGGCCTAAGCACAGACATGAAGC	TAACTAATGCAGTGCCCCGT
stSG495506	TGACCATGTCTCCTGCTTTTCCAGAAGG	TGTGCACCAAGAAACCAAAG
stSG495507	TGACCATGTTTGGTTTCTTGGTGCACAG	TGCGAGGTAAAAGTTGAGGC
stSG495508	TGACCATGGCCTCAACTTTTACCTCGCA	AGAAAGCATGCAGTGAGGGT
stSG495509	TGACCATGCTCACTGCATGCTTTCTTGC	CCCACCATGGATTACCAGAC
stSG495510	TGACCATGGTCTGGTAATCCATGGTGGG	GGGTAAGACCCTCACGATCA
stSG495511	TGACCATGCAGGATGGTGAAGAAGGGAA	GCCGAATTGAACTACCTCCA
stSG495512	TGACCATGGTCCTCCATGCAAATCACCT	CTTTGAGAACAGCCCAGCTC
stSG495513	TGACCATGGAGCTGGGCTGTTCTCAAAG	GTGGATAAGCTGTCCCGTGT
stSG495514	TGACCATGCCGTTCTCACCTGGTTTCAC	CTTGGTGGGAATTAGCCTGA
stSG495515	TGACCATGCAAGCACTGGAACAGCACAC	GGAGCCTGAGGGATCCTAGT
stSG495516	TGACCATGGGGGAAACTAGGATCCCTCA	GGGGATTCCAAAATGAACCT
stSG495517	TGACCATGGAATCCCCACGGTAGAGACA	TTAGCCATTCAGAGGGTTGG
stSG495518	TGACCATGCCAACCCTCTGAATGGCTAA	CCCACTCTGGAGAACAGCTC
stSG495519	TGACCATGTGTTCATCCTGGACTCCCTC	CCTCCATGTCTTCCCAGTGT
stSG495520	TGACCATGACACTGGGAAGACATGGAGG	ACAGGCCTAAGGGAAGGAAA
stSG495521	TGACCATGTTTCCTTCCCTTAGGCCTGT	CTTCTCTCCCTCTACCCGCT
stSG495522	TGACCATGAGCGGGTAGAGGGAGAGAAG	ACATCAAGTGGCTGGAAAGG
stSG495523	TGACCATGCCTTTCCAGCCACTTGATGT	TCTCACATGCTCCGTGCTAC
stSG495524	TGACCATGGTAGCACGGAGCATGTGAGA	CTGATCAGAGAGCCCAGAGG
stSG495525	TGACCATGCTCTCTGATCAGGGTCCTCG	CTATCCCCACAGGAGCAAAA
stSG495526	TGACCATGTTTTGCTCCTGTGGGGATAG	GCTGCACCTAATCCAGAACC
stSG495527	TGACCATGGCTGGTTCTGGATTAGGTGC	CTTAAGGCTCCTCCTCTGCC
stSG495528	TGACCATGGCTTTTTGAGTTCACAGCCC	TCTCAAGCGTCCTTCCATCT
stSG495529	TGACCATGATGGAAGGACGCTTGAGAGA	AGCAGATCAGTGACGAGGGT
stSG495530	TGACCATGTCCAGTTCCCAGAGATGGAG	GGCCTTCCTAATCTTCACCA
stSG495531	TGACCATGGGAGAATGAGGGCAGTGTGT	CTGGATTCTCCCCCAGTGTA
stSG495532	TGACCATGAGGGTGAACTGGTGAGAGGA	TTACCGAGTTTCCTGGACCTT
stSG495533	TGACCATGAAAACTGGGACAAGGTGTCG	TCTGTGTGGGTAGCTTGTGC
stSG495534	TGACCATGAGTCAGTGCCCCATAAATGC	TTCATGGCATCCCTACTGGT
stSG495535	TGACCATGCCTCTATTTCCACTGGGCAA	TTTGGGGACAAATCAAGGAG
stSG495536	TGACCATGCCAAAACCCTCAGCAAGGTA	TCATCCTCCCACACAGATCA
stSG495537	TGACCATGCACCCTATGCCAGGAACAAG	TACACACCATGCACACATGC
stSG495538	TGACCATGGCATGTGTGCATGGTGTGTA	CCTCTCTGTGTTCCTGGCTC
stSG495539	TGACCATGCAGAACAGAGGCTGACTCCC	CCCTGAGATGGTTCAAGGAA
stSG495540	TGACCATGGGTCTTTGTTAAAGCAGCCAA	TTTTGGCAATTCCGATTCTC
stSG495541	TGACCATGTTCTTTGGCACCTTGGTTTC	TGCTTTCTCCCTTTGCTCTC
stSG495542	TGACCATGAGCAAAGGGAGAAAGCACAG	GCCTCTCCTGAAGCTTTGAA
stSG495543	TGACCATGTTCAAAGCTTCAGGAGAGGC	CCTTCTAGTTTCTTGCCCCC
stSG495544	TGACCATGACGGATTCTACCCCTGGAAC	GGCTTCCTGTTTTCAGCTTG
stSG495545	TGACCATGGCCCTCAATGAGCTGTGATT	TGCAAGAGGGAAACAGATGG

stSG495546	TGACCATGAATGCCATCTGTTTCCCTCTT	AAACCCATTCAGAAGATTTGGA
stSG495547	TGACCATGTCCAGAGGTGTTTGAGAGGAA	CAGCCAATCATCAAAGAGCA
stSG495548	TGACCATGTGCTCTTTGATGATTGGCTG	TTGCATTTATTGGCCATCTG
stSG495549	TGACCATGCAGTTTGCAGATGGCCAATA	AAGGCCAGAGTAGGCTGACA
stSG495550	TGACCATGAATCTTACATGGGGGAGCAG	CATGCTGGTAAATTGCCTCC
stSG495551	TGACCATGCCTCTTACGAAAGCTGAAGGC	TACCCCTTTGGAATGAGCTG
stSG495552	TGACCATGGCAATGGGGACTTGCAAAA	CCAAAAGTCATCACATTAGGGC
stSG495553	TGACCATGTACCCAATGACCCAATGACC	GAAGACTTCTGCACCCATCC
stSG495554	TGACCATGGACGTATCCAGACAAGCCCT	GGGGCCAATCTAATCCTTCT
stSG495555	TGACCATGTTAGATTGGCCCCTCTCCTT	GATTCCAGTGGGGGATACCT
stSG495556	TGACCATGAGGTATCCCCCACTGGAATC	TTATCTTCCCACCCAACCCT
stSG495557	TGACCATGCCACCCACAAATGGGAAAG	AAAGGTCCTCTGCTGCTGAA
stSG495558	TGACCATGGCTTGCCTATGGGTGTGTCT	GATGTGGAGGAATGTGGCTT
stSG495559	TGACCATGAAGTCCTGAGGAGCCCATTT	ATGCAATGAAGGTGGGAAAG
stSG495560	TGACCATGCTTTCCCACCTTCATTGCAT	GCTTGGCTTGGTCTGTTTTC
stSG495561	TGACCATGAGGACACAGGATCAACCAGG	CAGTTGACATGACCCTCCCT
stSG495562	TGACCATGAAGTTGATGGATCAGGGTGG	AGGTCAGCTCTGCACCACTT
stSG495563	TGACCATGCGCAATCCTTAGGCAGTGAT	GTGTACAGTCCGGGAGCATT
stSG495564	TGACCATGTCCCGGACTGTACACAAACA	AAGCAGTTGTGGTCCAGGAG
stSG495565	TGACCATGGGCAATGGTTTTCTGCAAAT	CCTTCTGAAACTGGGGATCA
stSG495566	TGACCATGCTGGACTTCCACAGGGCTT	CCTAGGACACTCTCCGGTTG
stSG495567	TGACCATGCCACAAATGGAAGGTATGGC	CCTCCCTAGAAGGCAGTGTG
stSG495568	TGACCATGGCCACAATGGCTGGACTTAT	TGGGAGAGAAACATGCACAG
stSG495569	TGACCATGATGCCGCATTTAGCAACTCT	TTCCTCAGACTGCCTCCTGT
stSG495570	TGACCATGCAGGAGGCAGTCTGAGGAAG	TAGGTCAAGGGTTGTGGGAG
stSG495571	TGACCATGCTCCCACAACCCTTGACCTA	AGCCTACCTTCCCCTTGAGA
stSG495572	TGACCATGTTGGGAGAGCTTGGCTTAAA	AGTCCTGGGGCTGGTGTATT
stSG495573	TGACCATGTCCTCTGTTCCCCATCTCAC	TTACCGGCTTTCTCTGCAAT
stSG495574	TGACCATGTGCACAAATGGCTTGATTGT	CCTTCCTTCCCCTGTGAGTT
stSG495575	TGACCATGGGCCCAGTTCACTCATGTTT	TGGTGGTTTTATTTCCTGCC
stSG495576	TGACCATGCTCTCAGGGCCCTTTCCTT	TGAAACACTAGCAAGCGTGG
stSG495577	TGACCATGCCACGCTTGCTAGTGTTTCA	GTTTGAAAACCACCCGCTTA
stSG495578	TGACCATGGTCAAAAGAGCAAAGCCAGG	CTACCGTGCCCAGAGTCATT
stSG495579	TGACCATGCCTCCACTCACCAAGAGAGC	TGCTTCATTTTATTTCCGGC
stSG495580	TGACCATGCATTCTGAGCAGCTTGCTTG	CTGTGATCAAGGCAGAATGAA
stSG495581	TGACCATGCAATCAGGTGGCAAGACAAA	GTGCCAAGCTGTTTGGAGTT
stSG495582	TGACCATGTGGCACCAAATCCATCAGTA	CCTGTTGTTCCCATCACCTT
stSG495583	TGACCATGGAGCTCAAAGGTGTCCTTGC	TGTAAGCTCTGTGGACGCAC
stSG495584	TGACCATGAGTCAGGCGCTAGAGGAAGC	CACTGAATTTGGCCTTACCC
stSG495585	TGACCATGAGGCACTAAACTGGCTCCCT	GCCATCCTGCAAGAGAAGTC
stSG495586	TGACCATGCTCATGGTAATGCCTGGTCC	CAGACGGTCCTGAGCTCTTC
stSG495587	TGACCATGGCTCAGGACCGTCTGACTTC	GGAAGTGAAACCAGCCACAT
stSG495588	TGACCATGAGGAGCTTTTGGTGATTGGA	TACAAGGCAAGGAGCCAACT
stSG495589	TGACCATGTTGGCTCCTTGCCTTGTACT	AGAGTATGGGCTTTGGGCTT
stSG495590	TGACCATGAAGCCCAAAGCCCATACTCT	AATTTGCTTCCTGCCTTTGA
stSG495591	TGACCATGTGTTGCATTTGTGGAGAGGA	ACCTACCTGCCACTCCCTTT
stSG495592	TGACCATGGGAGTGGCAGGTAGGTGAGA	CAGACACCCCTGTCTGTTCC
stSG495593	TGACCATGGTCTGCAGAGGTTTCCCAAC	GAGGCTGCAGTCACAAATGA
stSG495594	TGACCATGGCCCTGAGAGCCTGAATCTA	ACCTCAGCGTTTCCATCGTA
stSG495595	TGACCATGTACGATGGAAACGCTGAGGT	CCTGACCAGCCCAATTAAGA
stSG495596	TGACCATGTTTCCTCCCAACCACTTGTC	TGCTGGCCTATCCCAAATTA
stSG495597	TGACCATGATTTGGGATAGGCCAGCAAT	CCCCAACAGGACATAAAAAGG

stSG495598	TGACCATGGCCTGAAGGGAATGGAGTTT	CTAAGCTCACCATCCCCAAA
stSG495599	TGACCATGGATGCACATGGTTTGACTGG	AGGGCTGCTGACACCTAGAA
stSG495600	TGACCATGGCTTACAACATGGCTGTGGA	CTATGGAACAAGCAGCACCC
stSG495601	TGACCATGAGTGGAAGGGCTGTTTCTCA	AAGACAGGAGTATGCCAGGAA
stSG495602	TGACCATGTTCCTGGCATACTCCTGTCTT	CTAAGGGAGGTGACGCAGAG
stSG495603	TGACCATGGTCACCTCCCTTAGGAAGCC	AGGACAGACCAGGCAAGAGA
stSG495604	TGACCATGCTGTGCATCACAAAGCCATT	TCACCATAGACACCAGGGTATG
stSG495605	TGACCATGCATACCCTGGTGTCTATGGTGA	CAGGGGCTTCAGCTGTCTAA
stSG495606	TGACCATGTTAGACAGCTGAAGCCCCTG	TGTCTCAACCTTTGGTGTGC
stSG495607	TGACCATGGGTCATGTGCAAGTCTCCAG	CCTGGTCAGAGCCTCATTTC
stSG495608	TGACCATGCCAGAGGAAATGAGGCTCTG	TCTGTTCAGCAATCACCTGC
stSG495609	TGACCATGGCAGGTGATTGCTGAACAGA	TGCTGTTTCCCACAAGTCAA
stSG495610	TGACCATGAGTTCAGGTTGCTTGGATGG	CACACTGGGGAGGTGAGATT
stSG495611	TGACCATGTGTATACACCCCTCCTCCCA	AAAATCTCCTGGACTGGCCT

*TCACCATG – Amino linking adaptor added to the 5’ end of all forward primers

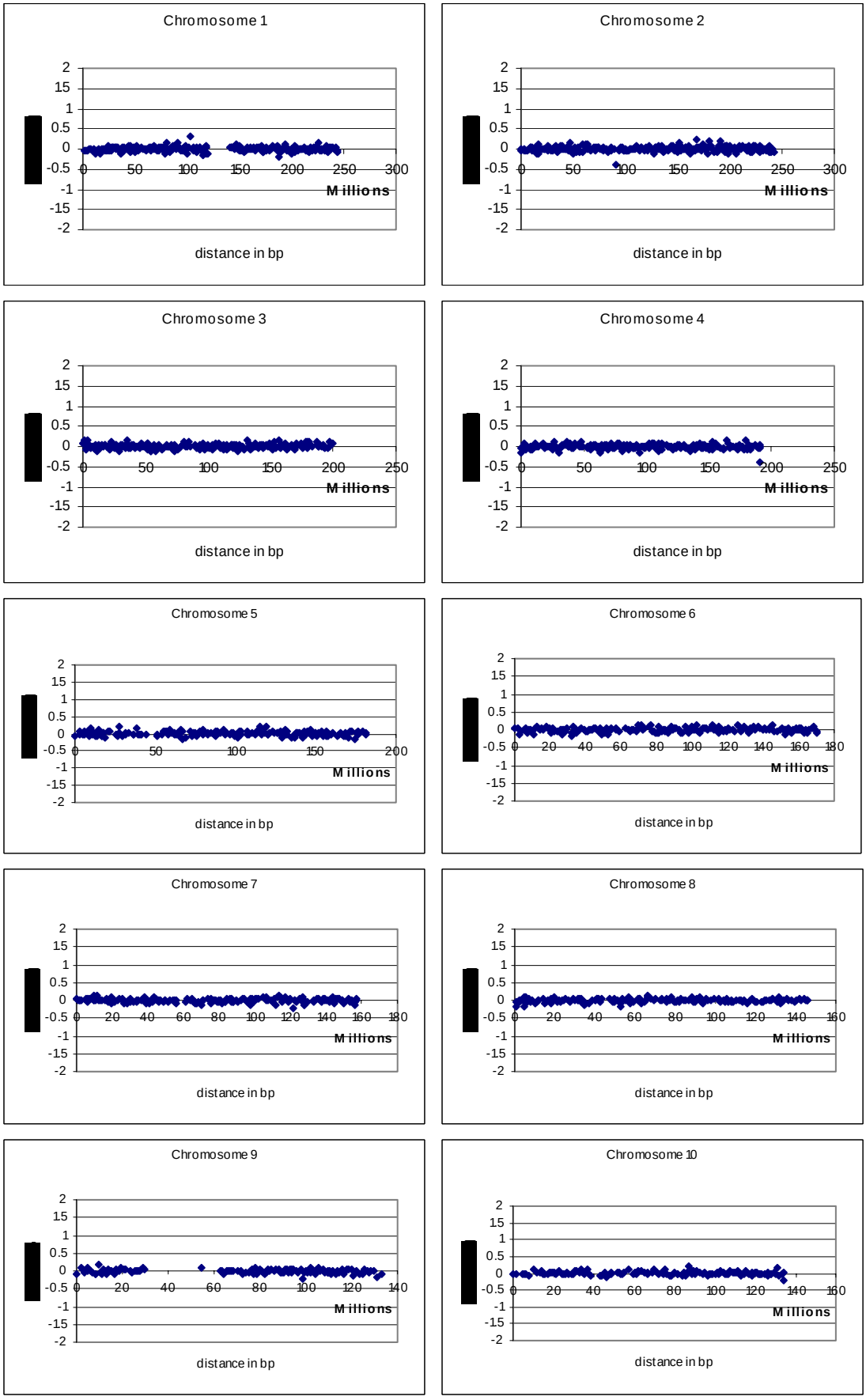
2b: The 96 well format of primers STSG 495474-495569.

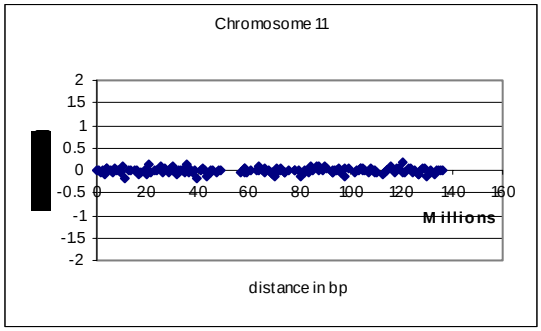
	1	2	3	4	5	6	7	8	9	10	11	12
A	stSG495474	stSG495475	stSG495476	stSG495477	stSG495478	stSG495479	stSG495480	stSG495481	stSG495482	stSG495483	stSG495484	stSG495485
B	stSG495486	stSG495487	stSG495488	stSG495489	stSG495490	stSG495491	stSG495492	stSG495493	stSG495494	stSG495495	stSG495496	stSG495497
C	stSG495498	stSG495499	stSG495500	stSG495501	stSG495502	stSG495503	stSG495504	stSG495505	stSG495506	stSG495507	stSG495508	stSG495509
D	stSG495510	stSG495511	stSG495512	stSG495513	stSG495514	stSG495515	stSG495516	stSG495517	stSG495518	stSG495519	stSG495520	stSG495521
E	stSG495522	stSG495523	stSG495524	stSG495525	stSG495526	stSG495527	stSG495528	stSG495529	stSG495530	stSG495531	stSG495532	stSG495533
F	stSG495534	stSG495535	stSG495536	stSG495537	stSG495538	stSG495539	stSG495540	stSG495541	stSG495542	stSG495543	stSG495544	stSG495545
G	stSG495546	stSG495547	stSG495548	stSG495549	stSG495550	stSG495551	stSG495552	stSG495553	stSG495554	stSG495555	stSG495556	stSG495557
H	stSG495558	stSG495559	stSG495560	stSG495561	stSG495562	stSG495563	stSG495564	stSG495565	stSG495566	stSG495567	stSG495568	stSG495569

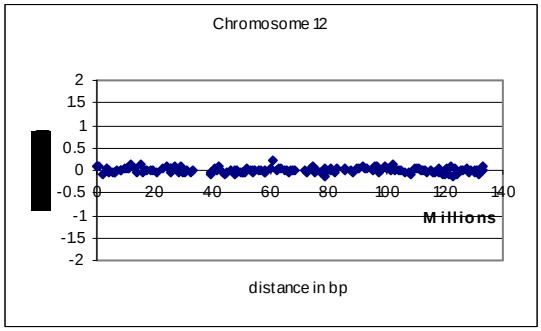
Appendix 3: Primers for quantitative PCR

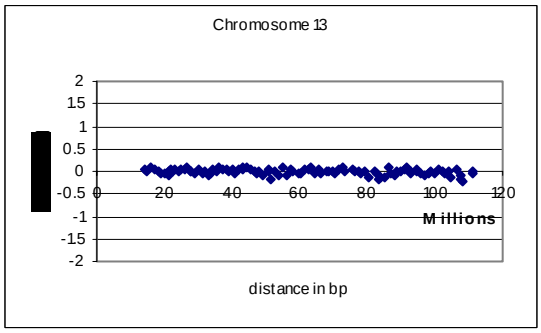
Clone	Forward Primer	Reverse Primer
cE140F8-1	TGTTCTATGAGTATGCGACTTTCCA	TTCAAACTGTGGGATGGTGAGA
cE140F8-2	TCTGCATCTTAAAGTGAGAGCTATGTTAC	TGAAGCTCTGATCTCCAGAAAGAG
cE140F8-3	GCTGATTTCCTCGTTCCCTCTATT	GTGTTAGGCAGTGGAATCATGTTC
cE140F8-4	GGATTCTGTCTTGTCTGGCCTTT	CTCCCGCGGTGCCTTT
cE140F8-5	GGCACCGCGGGAGAAG	GGCTGCATTGTTACAAATCTTTTTT
cN69F4-1	GGTTGAGGTCTGAAGCCCTTT	GGTCACTGCCCAGGCTCTT
cN69F4-2	CCTTGTCATCCCAAATACACCAT	AGACAGCTCCTGGGTCTTCCA
cN69F4-3	CAGAAACTGGCTTTGGAGAGATC	GAGACGTGGCTGAGCACAGA
cN69F4-4	GCACAAAATGTTCGAGACTGATACA	TTTACAACAAAGGCCAAATGCA
bK57G9-1	GGTGAGCCACATTTGTTATATTTGAA	GACTCACCCTTCCCCCTCTAAG
bK57G9-3	CTGTGCTGTGAATAGATCCATGTG	TGGCCGGGTGAACTCTTC
bK57G9-4	ACAATGGGTGCCAAGTTGGTA	CCCACAACCTGCTGCAGACT
bK57G9-5	TGGGCAGAGTCCCTGATTCT	AACTGGAAGGTGAACCCCAAA
bK57G9-6	GACTTCCAGGCCCTATGTCAGA	AAGTGGGAAGTTGCTGCTATGC
bK57G9-7	GATGCATGGGTGGGTGATG	TCCTGAGCCTCATTTGTTCTCA
bK57G9-8	CGGGCTTTGTCACAGCATCT	CAAAACTGGGAACAGCCTAAACA
cB13C9-1	TCAACAAGATATGTGCAAGCTTCTC	AAACTCCACCGGGCTCAAT
cB13C9-2	TTGCTGAGATTATGAATGGGTTTC	CTAGAGCTATTTTCTGTTTCCGACATACT
cB13C9-3	GCTGCACAAGCCATCCATTT	GGCCAGTGTGATTGATAAACTGAGT
cB13C9-4	GGGAGAATCCCAGCAAGTCA	CACCTCCCTGGTTGGTCATC
cB13C9-5	CTGCACCCCTCTTGTCTGTAACT	CGTCCTGAAACTTGGCATCTG

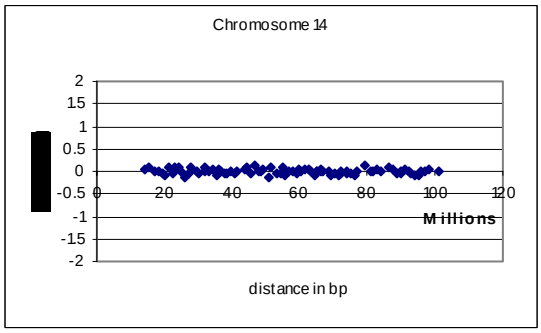
Appendix 4: Male:male hybridisation on 1Mb array

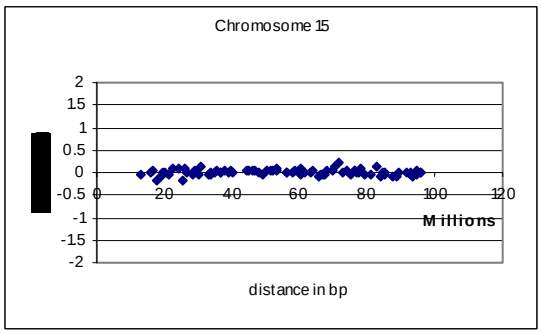


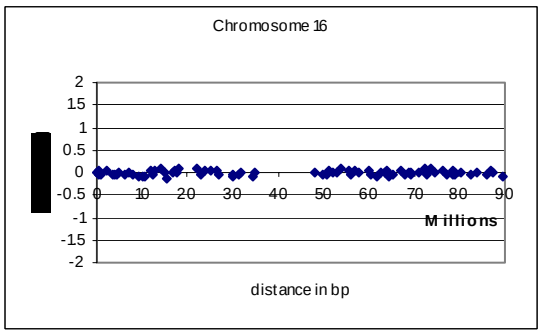

Chromosome 11
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp

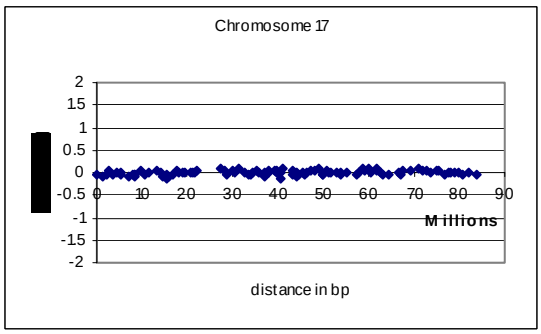

Chromosome 12
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp

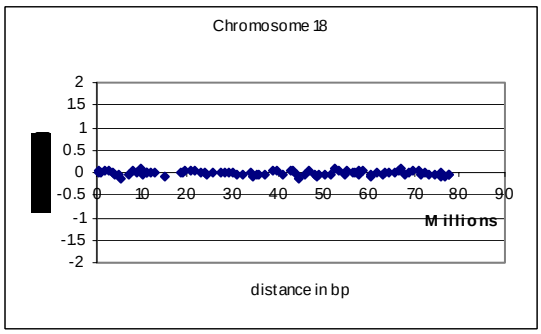

Chromosome 13
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

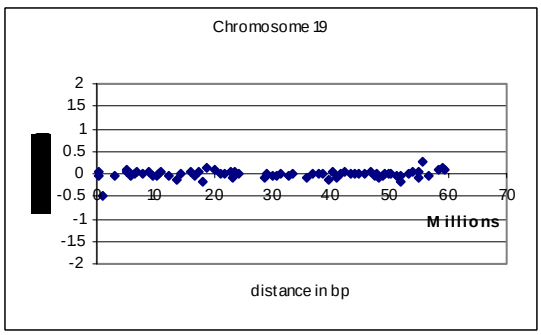

Chromosome 14
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

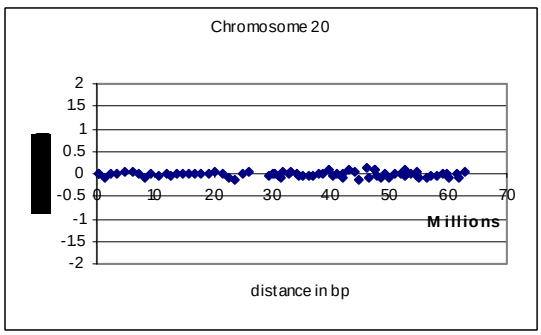

Chromosome 15
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

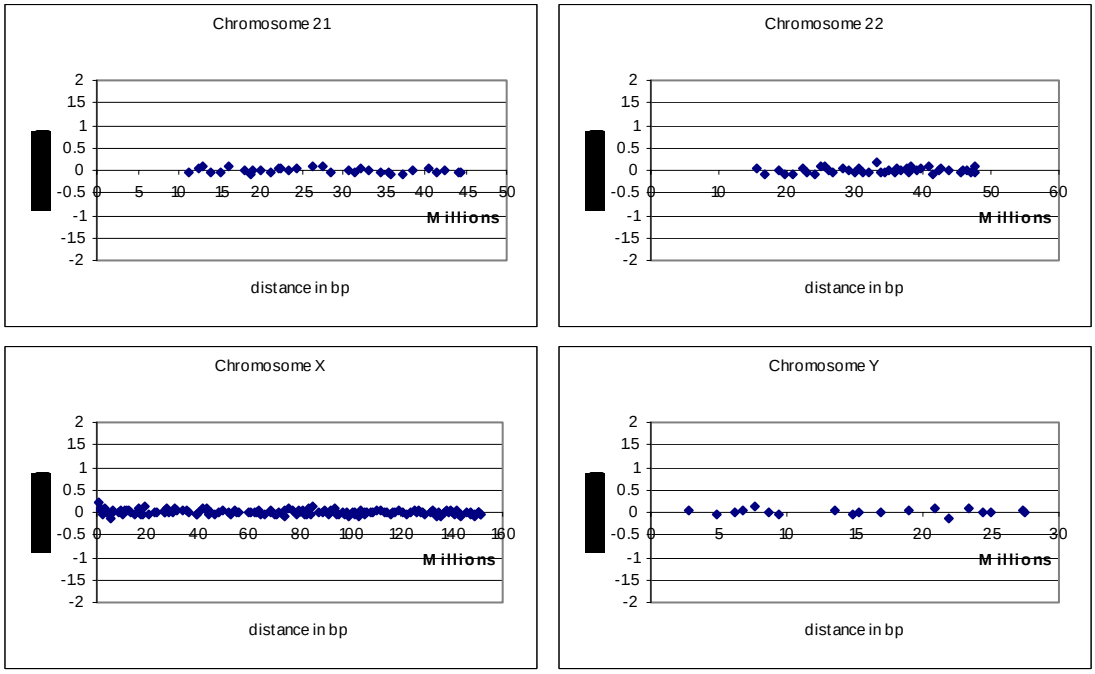

Chromosome 16
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 17
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 18
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp

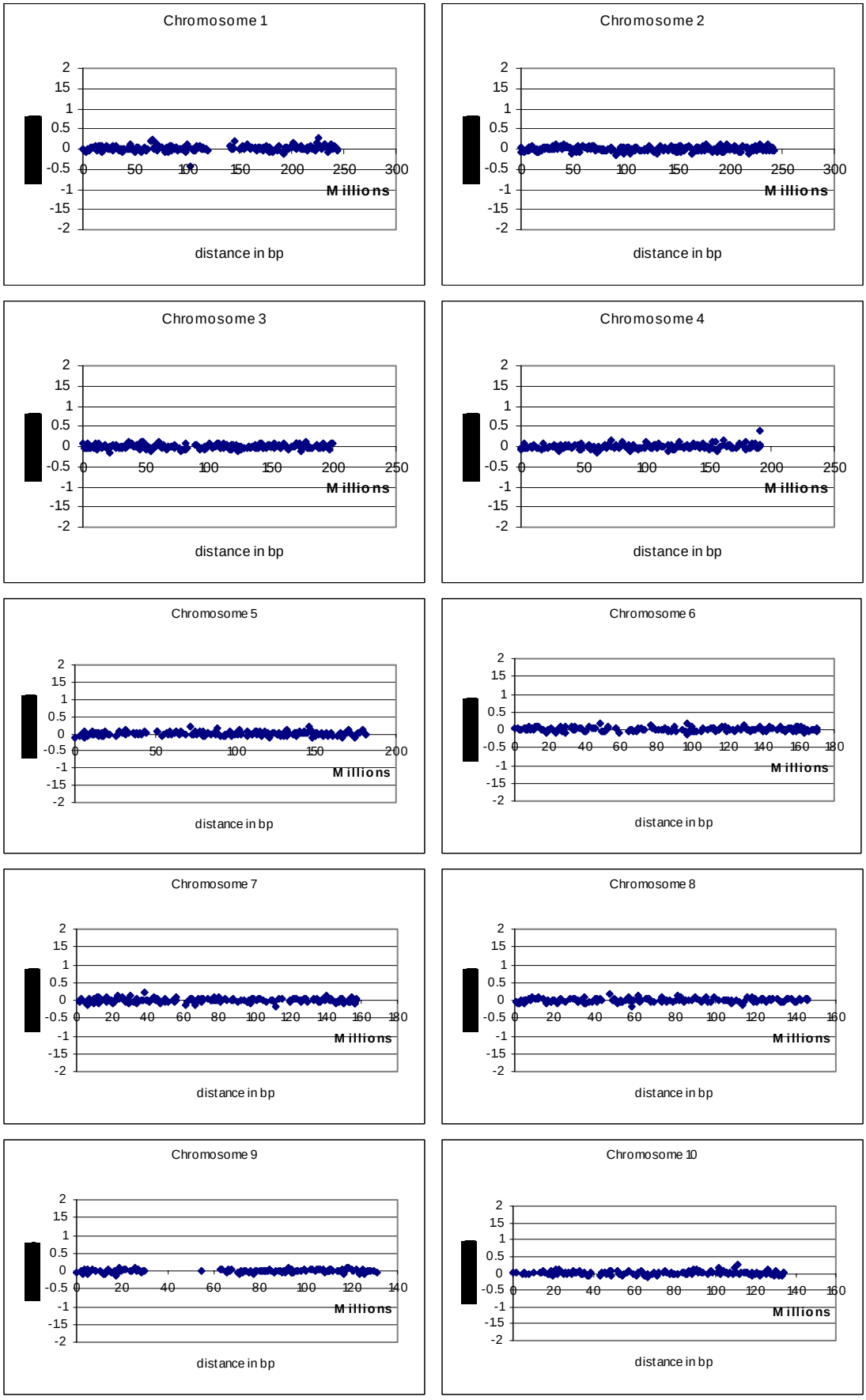

Chromosome 19
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp

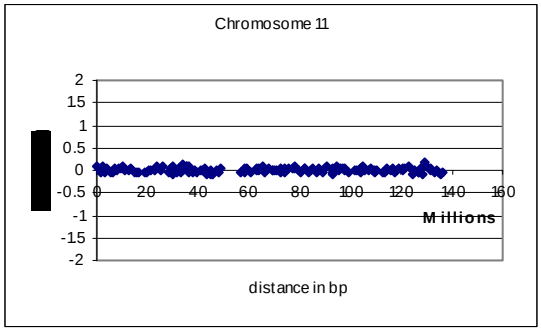

Chromosome 20
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp

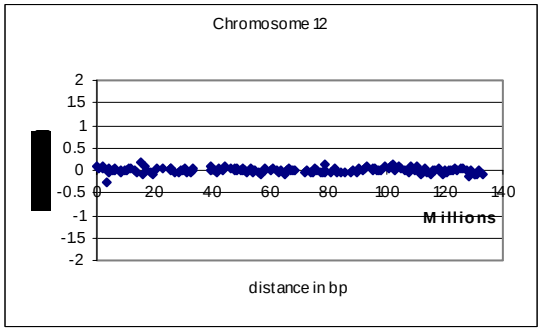


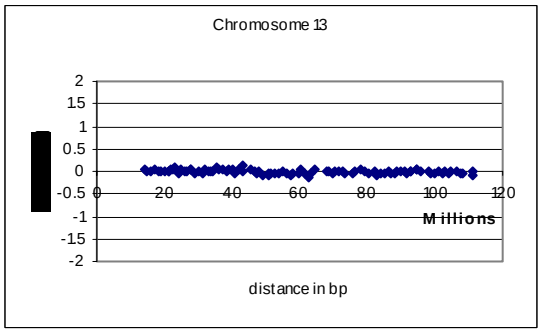
Log^2 ratios are given; therefore a 1:1 ratio will report a log^2 ratio of 0.

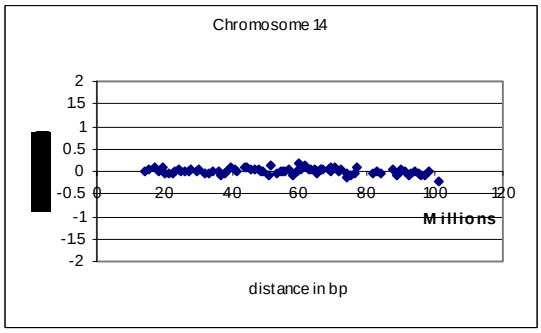
Appendix 5: Male:female hybridisation on 1Mb array

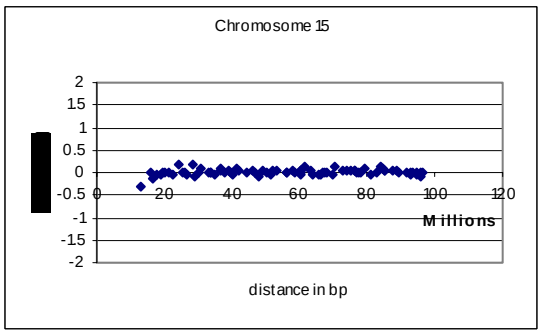


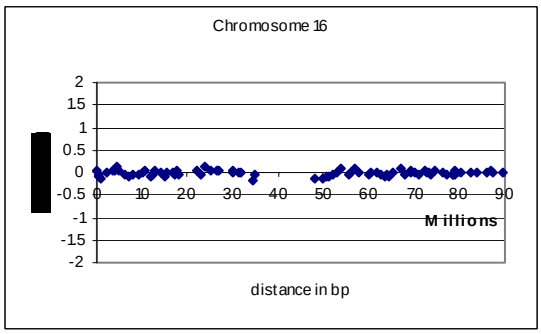

Chromosome 11
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp

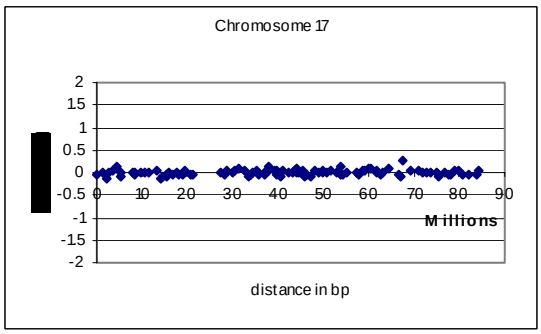

Chromosome 12
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp

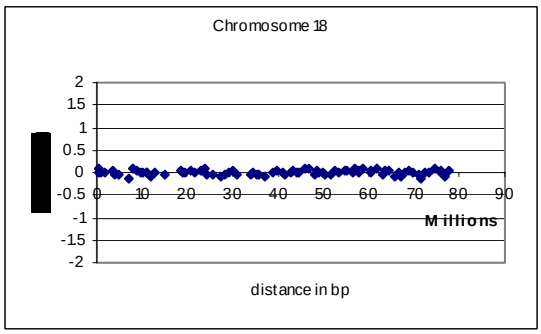

Chromosome 13
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

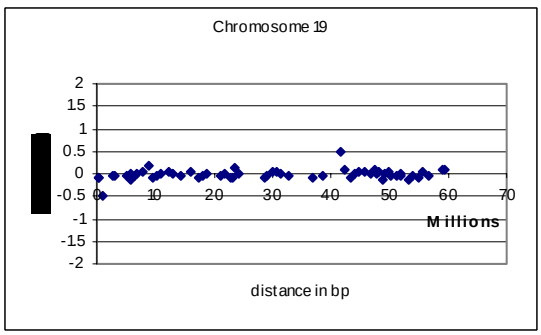

Chromosome 14
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

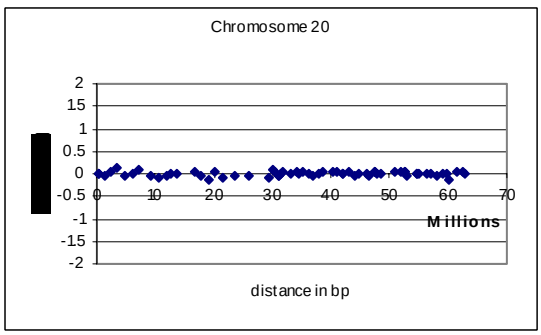

Chromosome 15
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

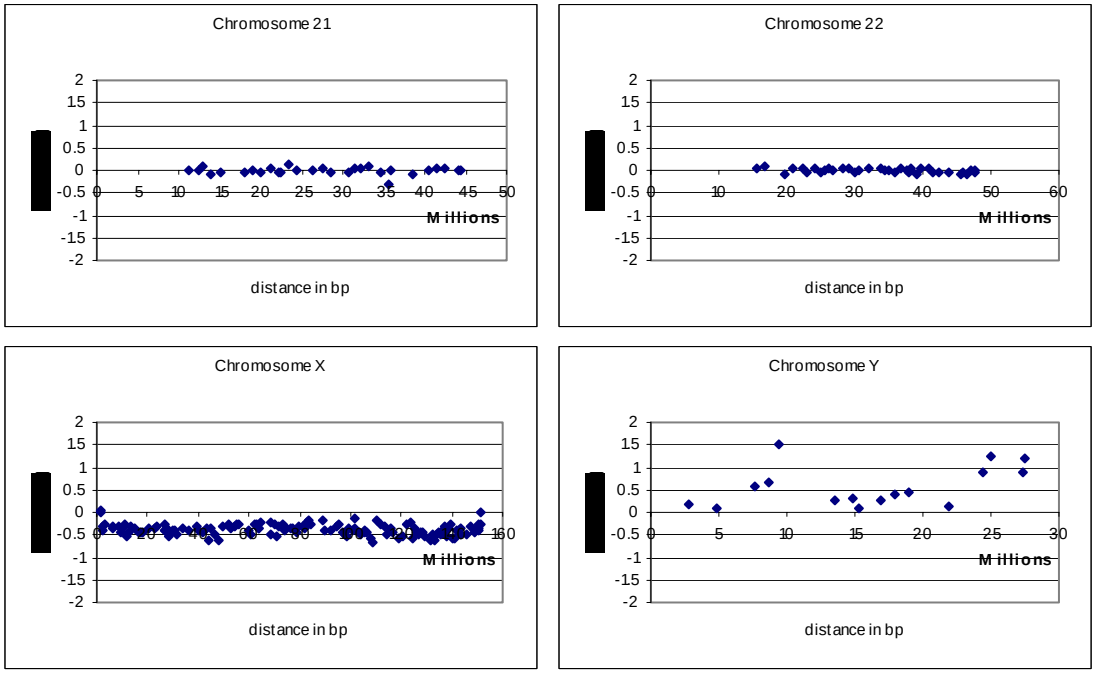

Chromosome 16
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 17
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 18
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp

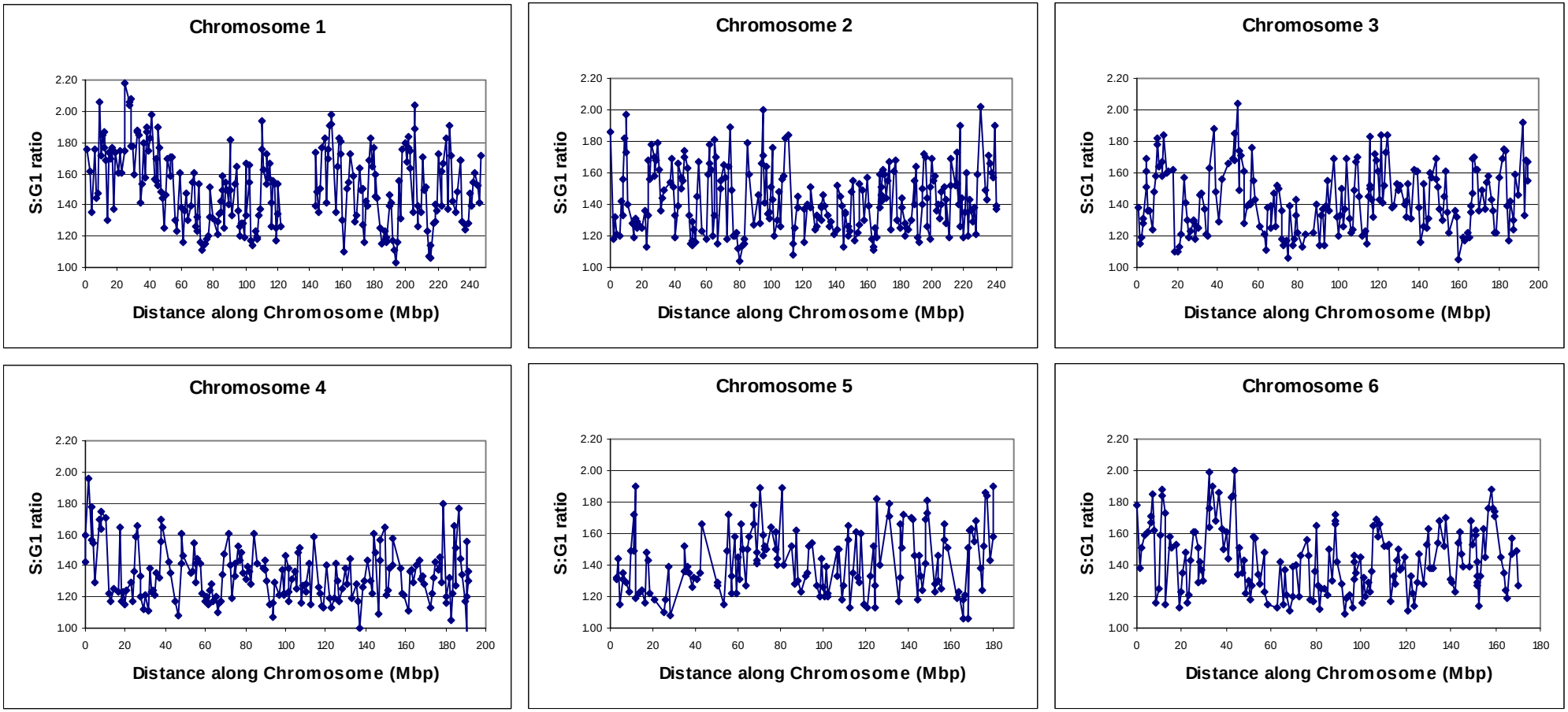

Chromosome 19
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp

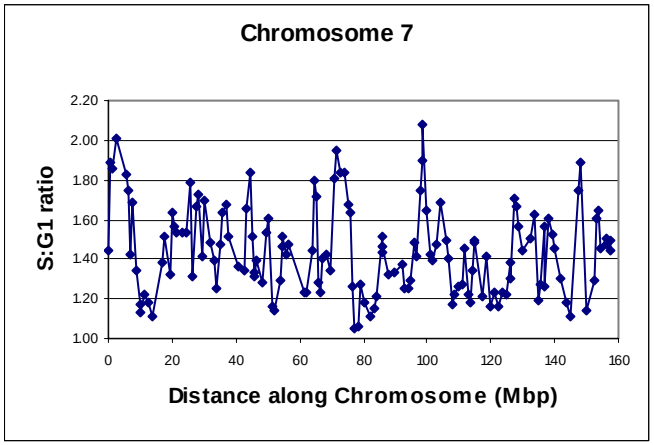

Chromosome 20
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp

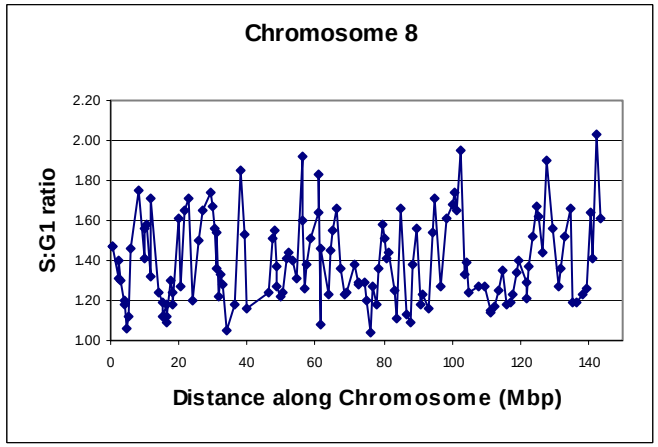


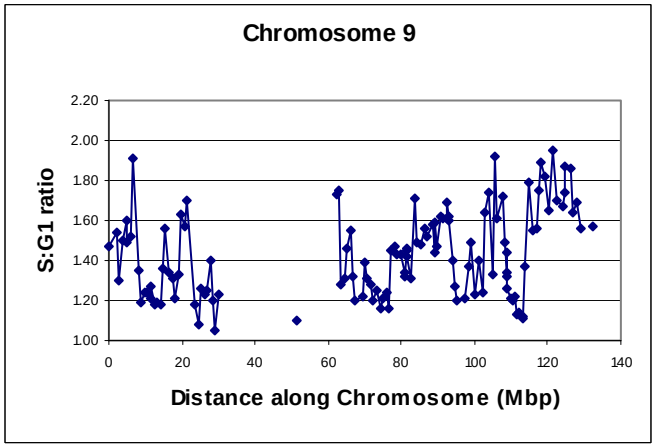
Log^2 ratios are given; therefore a 1:1 ratio will report a log^2 ratio of 0, this is seen on the autosomes. A ratio of 0.5:1 representing a single copy loss on the X clones will report a ratio of 0.5. Clones on the Y chromosome report a variety of ratios. This is because there is only Cy 3 labelled Y chromosome DNA within the hybridisation mix, so there is no Cy 5 DNA to hybridise against.

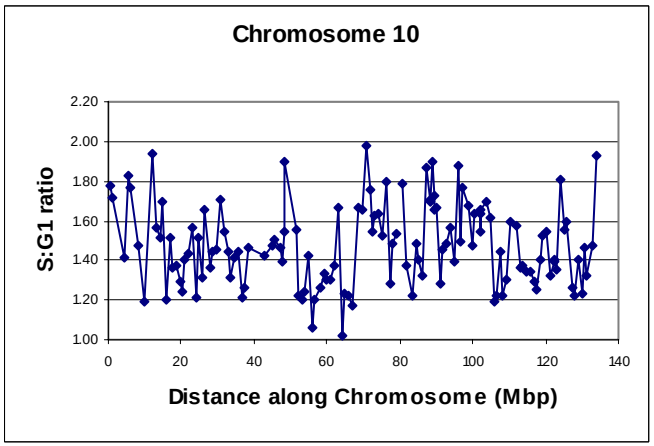
Appendix 6: Replication timing profiles for all 24 chromosomes.

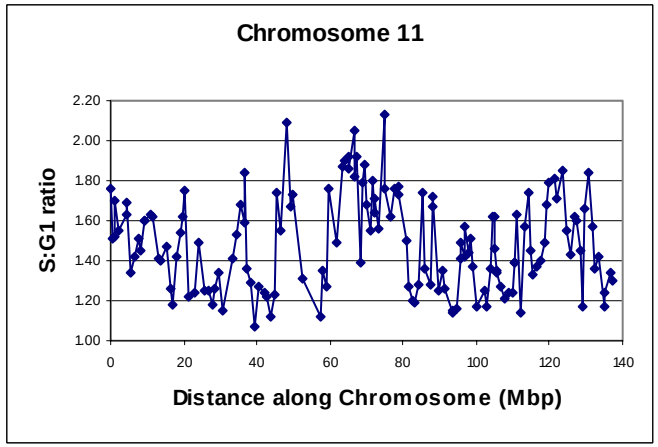


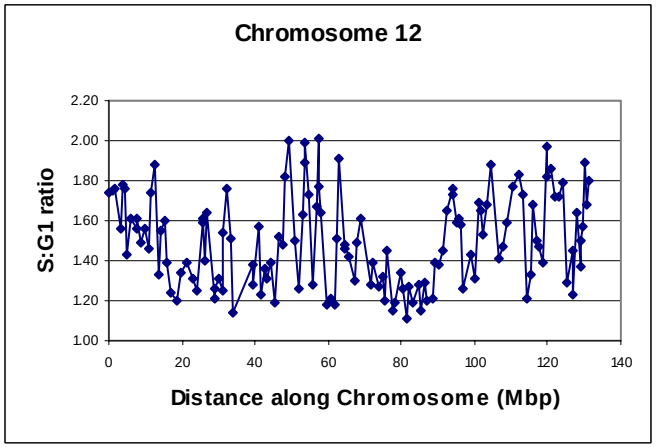

Chromosome 7
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
160
Distance along Chromosome (Mbp)

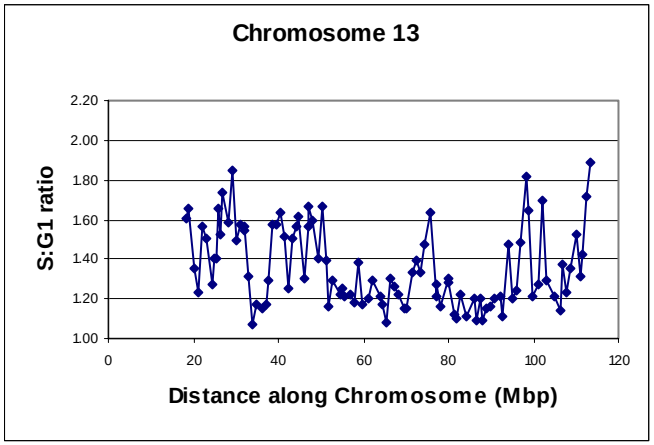

Chromosome 8
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
Distance along Chromosome (Mbp)

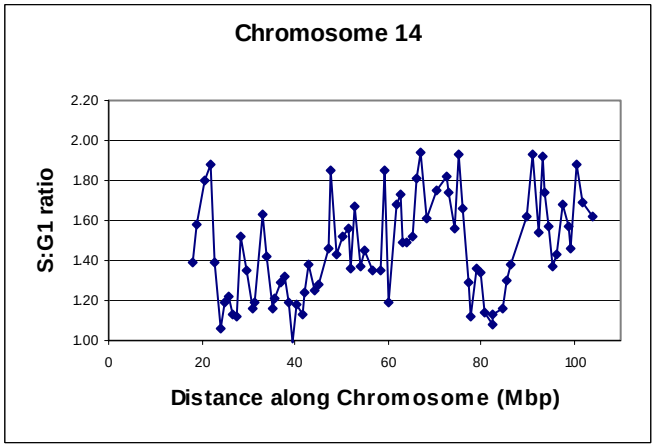

Chromosome 9
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
Distance along Chromosome (Mbp)

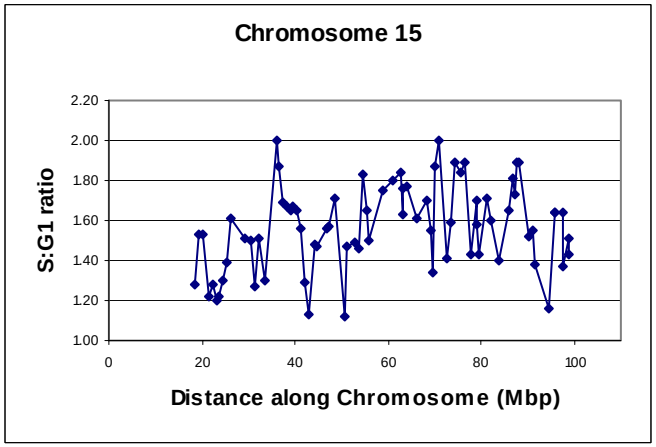

Chromosome 10
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
Distance along Chromosome (Mbp)

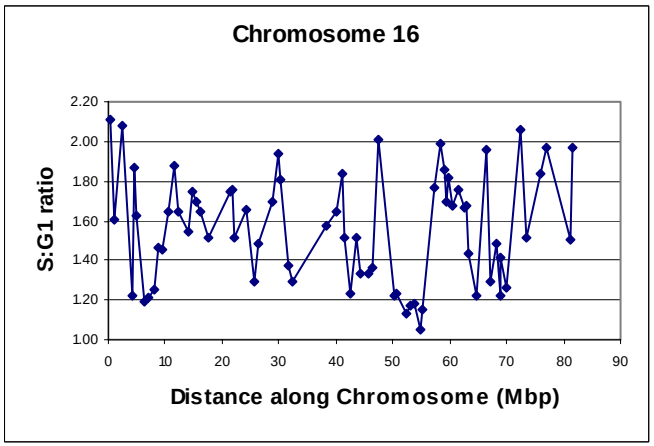

Chromosome 11
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
Distance along Chromosome (Mbp)

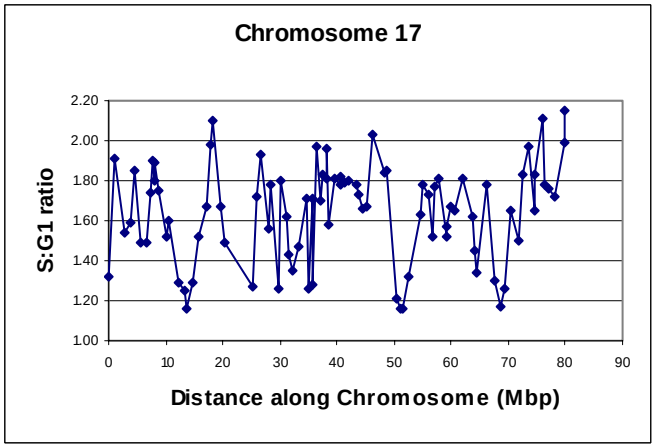

Chromosome 12
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
Distance along Chromosome (Mbp)

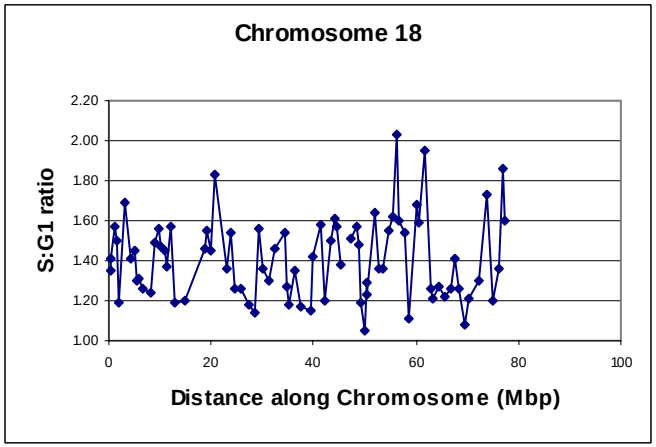

Chromosome 13
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
Distance along Chromosome (Mbp)

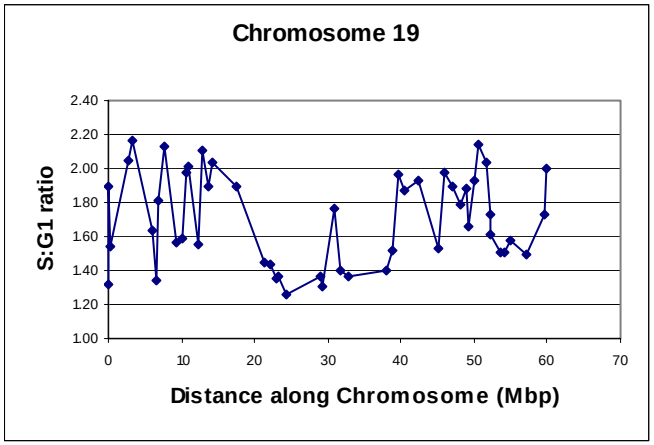

Chromosome 14
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
Distance along Chromosome (Mbp)

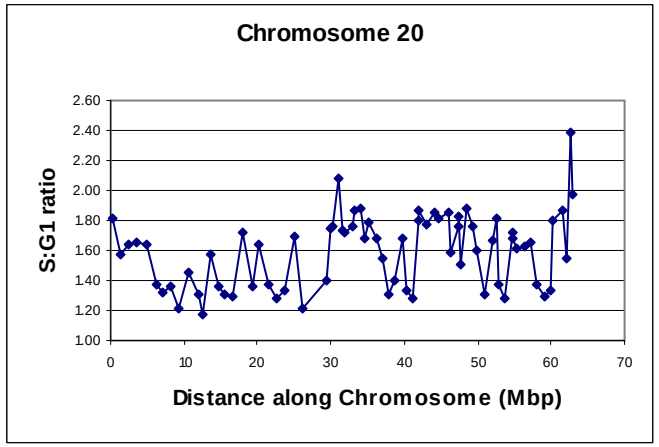

Chromosome 15
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
Distance along Chromosome (Mbp)

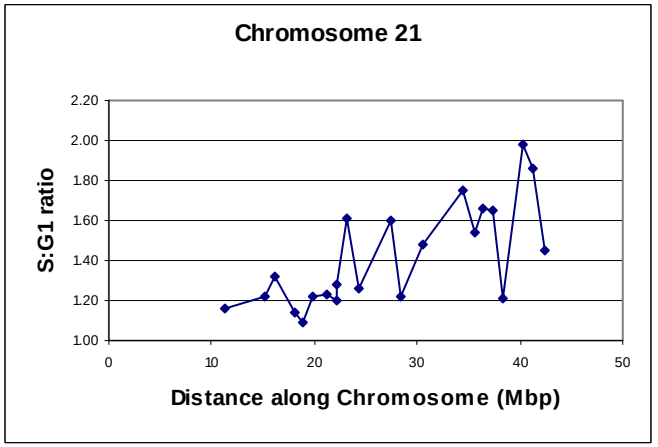

Chromosome 16
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
10
20
30
40
50
60
70
80
90
Distance along Chromosome (Mbp)

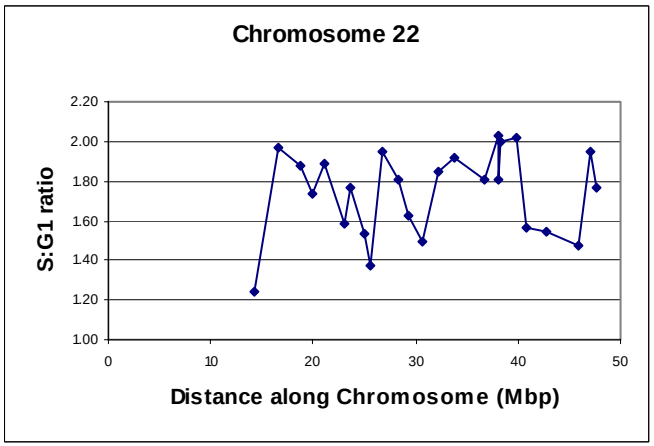

Chromosome 17
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
10
20
30
40
50
60
70
80
90
Distance along Chromosome (Mbp)

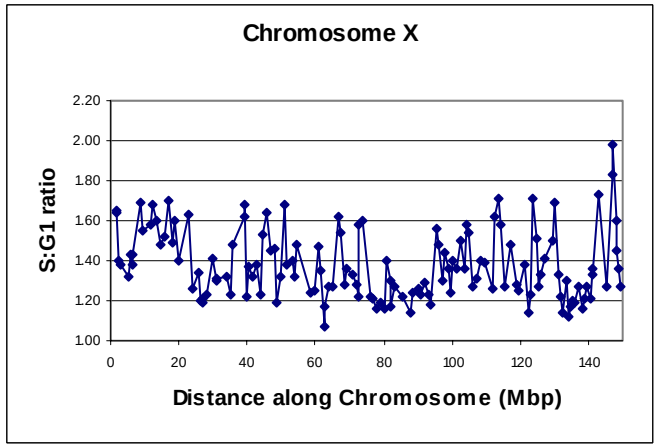

Chromosome 18
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
Distance along Chromosome (Mbp)

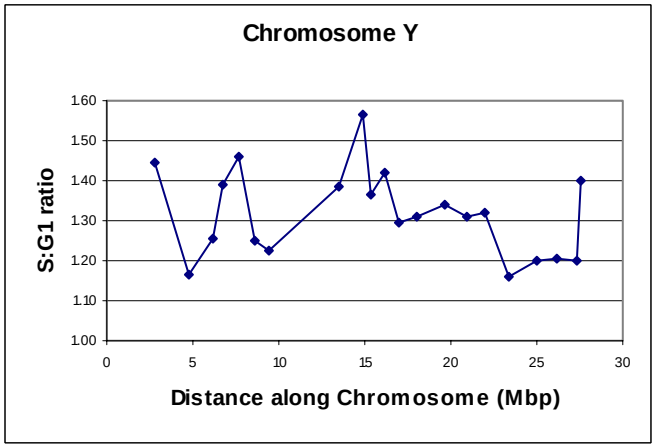

Chromosome 19
S:G1 ratio
2.40
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
10
20
30
40
50
60
70
Distance along Chromosome (Mbp)


Chromosome 20
S:G1 ratio
2.60
2.40
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
10
20
30
40
50
60
70
Distance along Chromosome (Mbp)


Chromosome 21
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
10
20
30
40
50
Distance along Chromosome (Mbp)


Chromosome 22
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
10
20
30
40
50
Distance along Chromosome (Mbp)

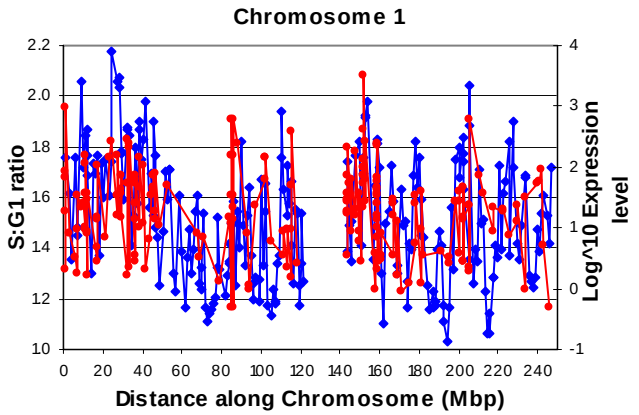

Chromosome X
S:G1 ratio
2.20
2.00
1.80
1.60
1.40
1.20
1.00
0
20
40
60
80
100
120
140
Distance along Chromosome (Mbp)

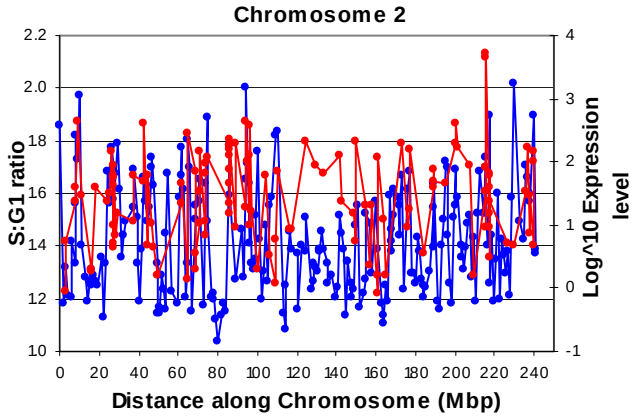

Chromosome Y
S:G1 ratio
1.60
1.50
1.40
1.30
1.20
1.10
1.00
0
5
10
15
20
25
30
Distance along Chromosome (Mbp)

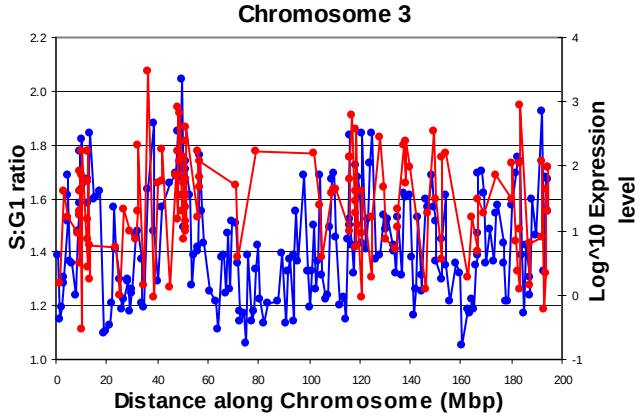
Appendix 7: Perl program to identify regions of co-ordinated replication

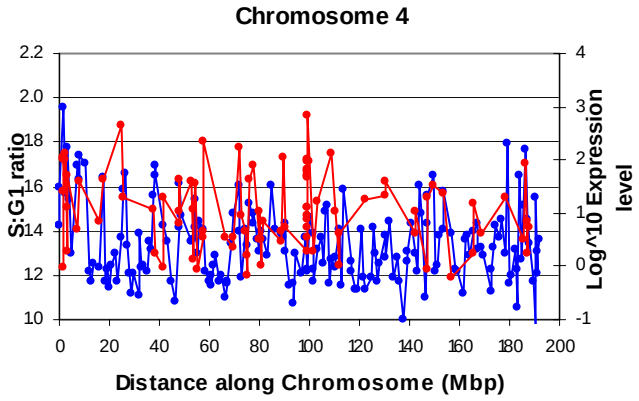
A purpose-written perl program was used to find the optimal segmentation of the replication timing (RT) data. Suppose a chromosome contains n RT signals arranged in genome order. Within each segment, starting at coordinate i and ending at coordinate j, we define the score S_{ij} equal to the sum of squared deviations of the RT values from the mean RT signal μ_{ij} for the segment. The optimal segmentation pattern (ie the number of segments and coordinates of segment boundaries) is chosen which minimises a function, W_n, based on the sum of segment scores plus a penalty score B for each segment transition. Let W_k be the score of the optimal segmentation for coordinates 1 through k. Then $W_0 = 0$ and $W_k = \min_{i<k} \{ W_{i-1}+B+S_{ik} \}$ for all $k>0$. The degree of segmentation is controlled by the value of B. The optimal segmentation is found by backtracking from the terminal value W_n. The statistical significance of W was determined by re-running the program on 1000 permuted data sets in which the order of observed RT signals was shuffled. The P-value for the test of the null hypothesis that the observed segmentation score could have arisen by chance is estimated as the proportion of times the permuted W score exceeded the observed score.

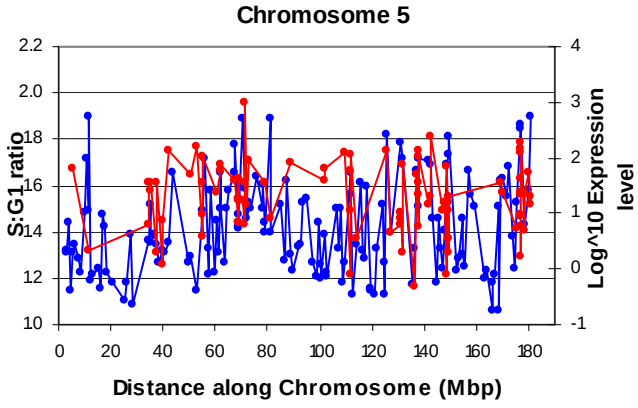
Appendix 8: Replication timing and Expression level profiles for all 24 chromosomes.

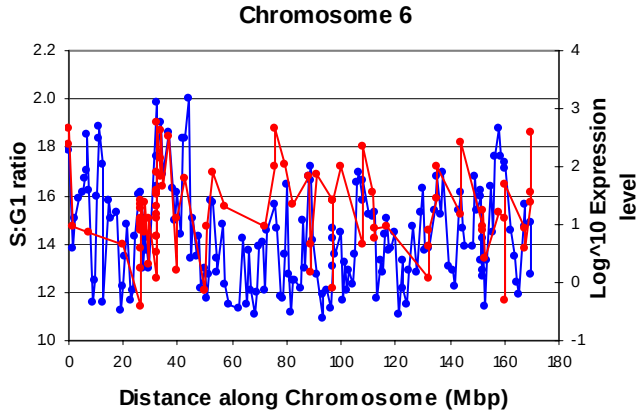


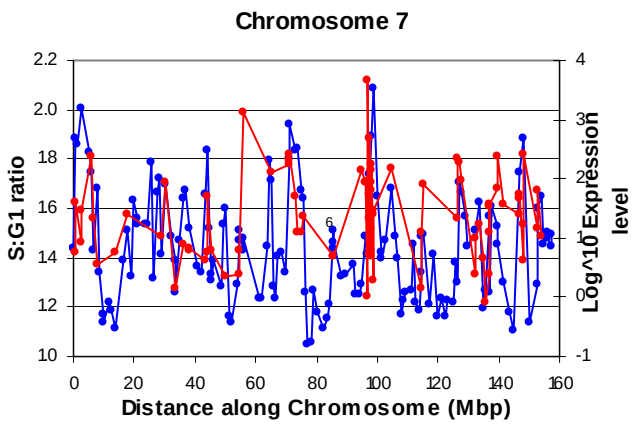


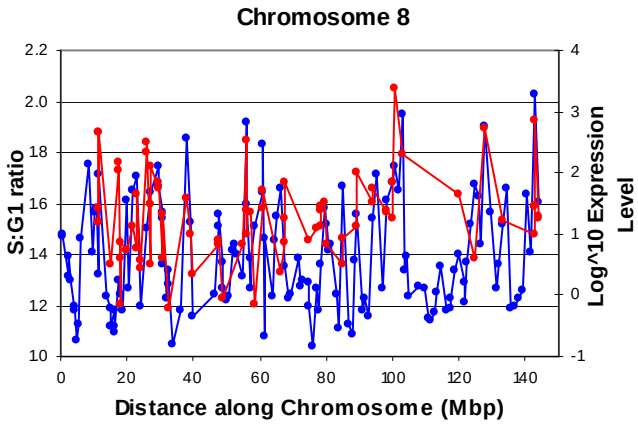


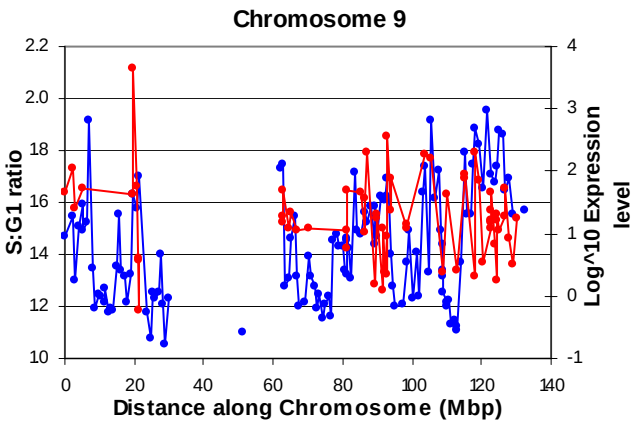


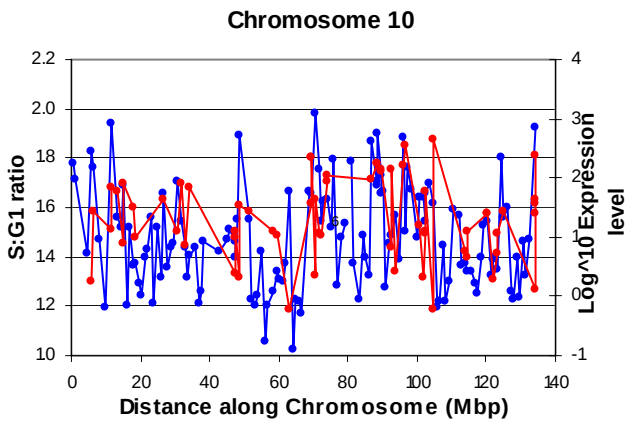


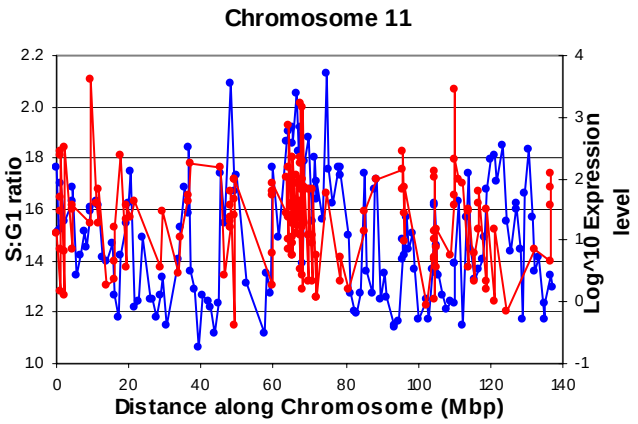


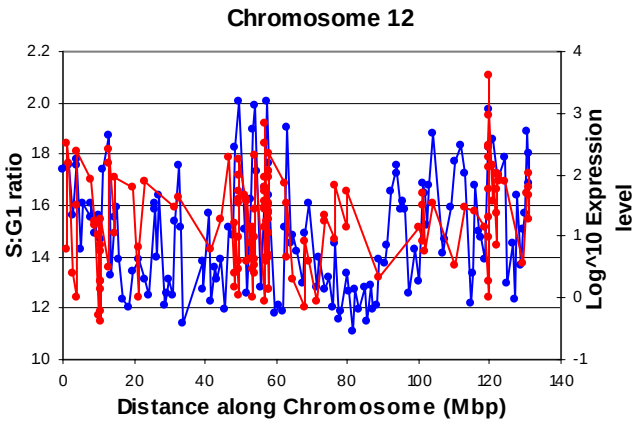

Chromosome 7
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)

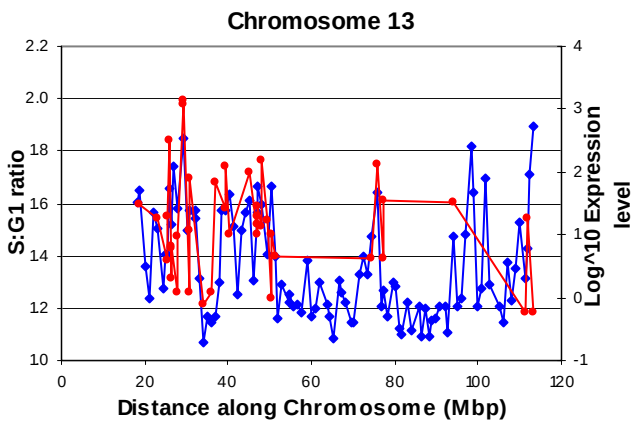

Chromosome 8
S:G1 ratio
Log^10 Expression Level
Distance along Chromosome (Mbp)

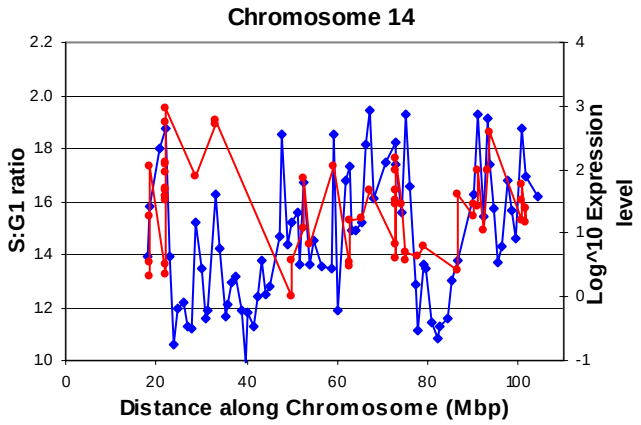

Chromosome 9
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)

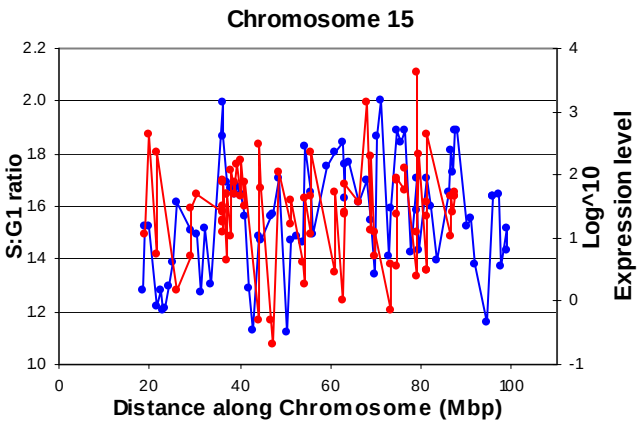

Chromosome 10
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)

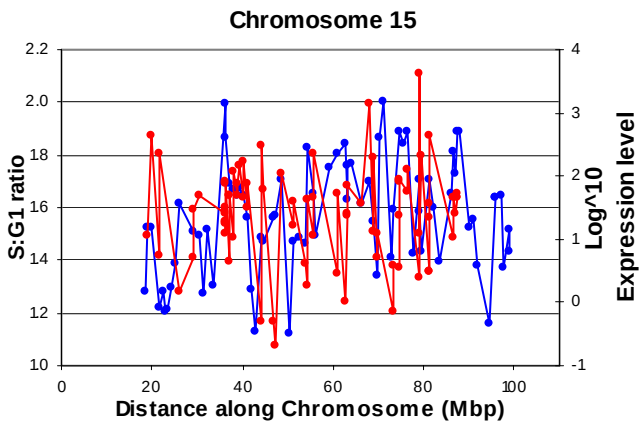

Chromosome 11
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)

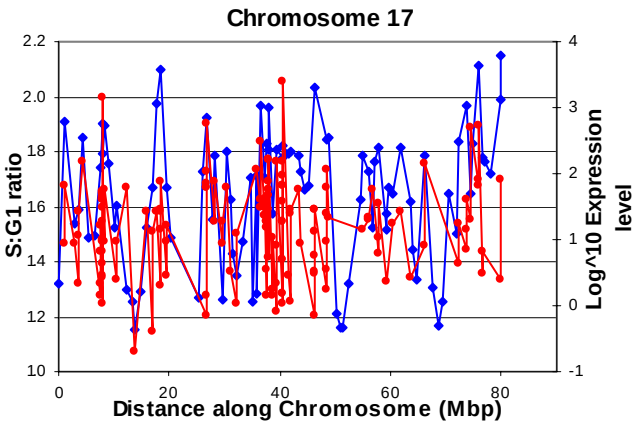

Chromosome 12
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)

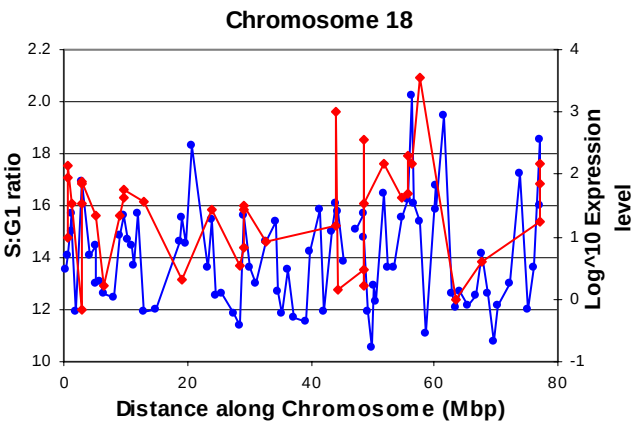

Chromosome 13
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)

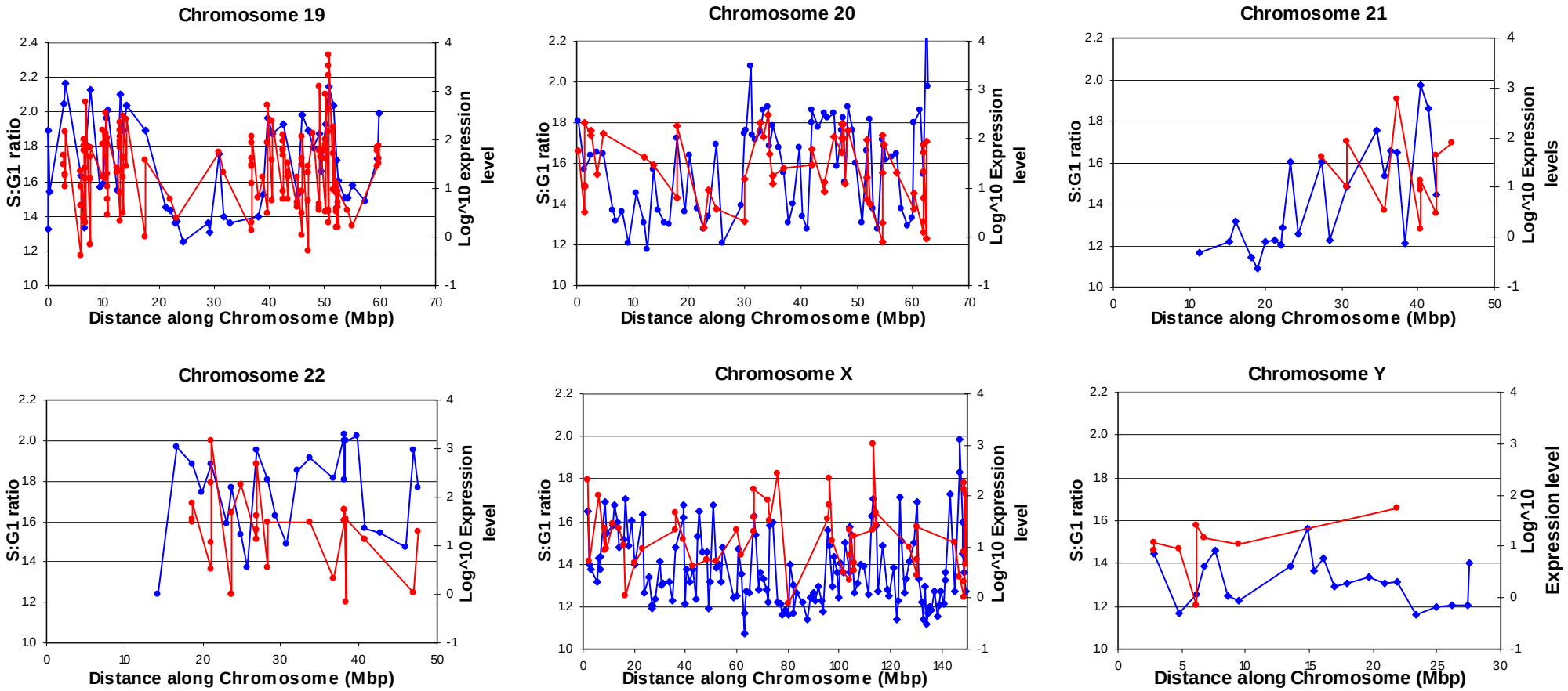

Chromosome 14
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)


Chromosome 15
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)


Chromosome 15
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)


Chromosome 17
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)


Chromosome 18
S:G1 ratio
Log^10 Expression level
Distance along Chromosome (Mbp)



Blue: Replication timing ratio. Red: Expression level of clones in the 1Mb set

Appendix 9: Chromosome 22 sequencing-clone information

9a: International Names for chromosome 22 clones

Accession No.	International Clone name	Sanger Clone name
AP000522	AP000522	cN4G1
AP000523	AP000523	c60H5
AP000524	AP000524	c70D1
AP000525	AP000525	cN14H11
AP000526	AP000526	cN64E9
AP000527	AP000527	cNN83F12
AP000528	AP000528	cN91G6
AP000529	AP000529	cN3G11
AP000530	AP000530	cN65E1
AP000531	AP000531	cN59E1
AP000532	AP000532	cN2F2
AP000533	AP000533	cN60G3
AP000534	AP000534	cN23H5
AP000535	AP000535	cN58F10
AP000536	AP000536	cN64C8
AP000537	AP000537	cN54B2
AP000538	AP000538	cN65B12
AP000539	AP000539	cN72E11
AP000540	AP000540	cN53D1
AP000541	AP000541	cN13E4
AP000542	AP000542	cN60D12
AP000543	AP000543	cN20H12
AP000544	AP000544	cN17H1
AP000545	AP000545	cN68B10
AP000546	AP000546	cN18E3
AP000547	KB-67B5	KB67B5
AP000365	KB-7G2	KB7G2
AC005301	AC005301	p15j16
AC007064	AC007064	p87o8
AC006548	AC006548	p20k14
AC006946	AC006946	p109l3
AC005300	AC005300	p143i13
AC005399	AC005399	p238m15
AC004019	AC004019	357f7
AC007666	AC007666	p273a17
AC006285	AC006285	p1087l10
AC016026	AC016026	b461k10
AC008101	XXbac-677f7	b677f7
AC008079	AC008079	bac519d21
AC008132	AC008132	pac995o6
AC008103	AC008103	pac699j1
AC007326	AC007326	p423
AC000095	AC000095	fF41C7
AC004461	AC004461	cN119F4

AC004462	AC004462	18c3
AC004471	AC004471	111f11
AC004463	AC004463	79h12
AC000081	AC000081	59c10
AC000094	AC000094	fF39E1
AC000085	AC000085	72f8
AC000092	AC000092	98c4
AC000079	AC000079	49c12
AC000068	AC000068	102g9
AC000087	AC000087	83c5
AC000088	AC000088	83e8
AC000082	AC000082	59f
AC000070	AC000070	105a
AC000086	AC000086	81h
AC000077	AC000077	31e
AC000067	AC000067	100h
AC000093	AC000093	carlaa
AC000091	AC000091	91c
AC000089	AC000089	89h
AC000076	AC000076	2h
AC000078	AC000078	33e
AC000090	AC000090	8c
AC000080	AC000080	56c
AC005663	AC005663	p888c9
AC006547	AC006547	p158l19
AC007663	AC007663	b444p24
AC007731	AC007731	b562f10
AC005500	AC005500	p52f6
AC004033	AC004033	p_M11
AC007050	AC007050	bac32
AC007308	AC007308	pac408
AC002470	AC002470	bK135H6
AC002472	AC002472	P_N5
AP000550	KB-1592A4	KB1592A4
AP000551	KB-876E2	KB876E2
AP000552	KB-1183D5	KB1183D5
AP000556	KB-1172D5	KB1172D5
AP000557	KB-1323B2	KB1323B2
AP000558	KB-1802C5	KB1802C5
AP000553	KB-1440D3	KB1440D3
AP000554	KB-666H9	KB666H9
AP000555	KB-1027C11	KB1027C11
D86995	D86995	cN109G12
D87019	D87019	cN86G7
D87012	D87012	cN61D6
D88268	D88268	cN47H9
D86993	D86993	cN23C6
D87004	D87004	cN4E7
D87022	D87022	cN88E1
D88271	D88271	cN114H4
D88269	D88269	cN33B6
D87000	D87000	cN30E12

D86996	D86996	cN23F1
D86989	D86989	cN110H3
D88270	D88270	cN123E1
D87003	D87003	cN2H8
D87018	D87018	cN80A10
D87016	D87016	cN75A1
D86999	D86999	cN22A12
D87010	D87010	cN35B9
D87009	D87009	KB288A10
D87011	D87011	cN50D10
D87013	D87013	cN63E9
D87014	D87014	cN61E11
D86991	D86991	cN29D3
D87002	D87002	cN31F3
D87006	D87006	cN52F2
D86994	D86994	cN102D1
D87007	D87007	cN48A11
D87015	D87015	cN68D6
D86998	D86998	cN24A12
D87021	D87021	cN84E4
D87024	D87024	cN92H4
D87020	D87020	cN9G6
D87023	D87023	cN9C5
D87017	D87017	cN75C12
AP000360	AP000360	cN81C12
AP000361	AP000361	cN8E4
AP000362	AP000362	cN75A12
AC000029	AC000029	bK865E9
AC000102	AC000102	bK60B5
AP000343	KB-282B12	kB282B12
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AP000347	KB-113H7	KB113H7
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AP000349	KB-1839H6	kB1839H6
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AP000357	AP000357	cN95F10
AP000358	AP000358	cN110F4
AP000359	KB-63E7	KB63E7
AL049759	RP5-930L11	dJ930L11
AL050312	RP11-9F11	bA9F11
AL022323	CTA-243E7	bK243E7
Z99916	CTA-221G9	bK221G9
AL022332	RP3-462D8	dJ462D8
AL022324	CTA-246H3	bK246H3

AL008721	CTA-390C10	bK390C10
AL022329	CTA-407F11	bK407F11
AL080245	RP11-89B2	bA89B2
Z98949	CTA-125H2	bK125H2
AL079300	CTA-109D1	bK109D1
AL022337	CTA-796E4	bK796E4
AL080273	RP11-259P1	bA259P1
AL023513	RP1-268D13	dJ268D13
AL078460	RP3-341O5	dJ341O5
AL035044	RP1-40G4	dJ40G4p
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Z95115	CTA-445C9	bK445C9
Z99774	CTA-373H7	bK373H7
Z95889	CTA-211A9	bK211A9
Z97353	RP1-90L6	dJ90L6
AL008638	CTA-992D9	bK992D9
AL021153	CTA-503F6	bK503F6
AL034386	RP5-1172A22	dJ1172A22
AL020994	CTA-929C8	bK929C8
AL049536	RP1-205F14	dJ205F14p
AL050402	RP11-46E17	bA46E17
AL133456	AL133456	dJ231P7p
AL390209	AL390209	bK437G10
AL121885	RP11-375H17	bA375H17
AL031591	RP3-353E16	dJ353E16
AL033538	RP3-477H23	dJ477H23
AL035453	SC22CB-42E1	cB42E1
AL050313	CTA-754D9	bK754D9
AL035397	RP6-45P1	dA45P1
AL023281	CTA-544A11	bK544A11
AL008722	CTA-732E4	bK732E4
AL080241	RP11-541J16	bA541J16
AL118497	RP11-329J7	bA329J7
AL121825	RP11-436C9	bA436C9
AL117330	RP11-444G7	bA444G7
AL023494	RP3-366L4	dJ366L4
Z93930	CTA-292E10	bK292E10
AL031596	RP4-745C22	dJ745C22
Z95113	CTA-175E3	bK175E3
AL021393	CTA-747E2	bK747E2
Z95116	CTA-57G9	bK57G9
AL031186	CTA-984G1	bK984G1
AC000026	AC000026	bK58B8
AC000041	AC000041	cE42H1
AC000035	AC000035	cN47G11
AC005529	AC005529	bK256D12
AC004882	RP1-76B20	dJ76B20
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AC004819	RP1-15I23	dJ15I23
AC003681	RP3-394A18	dJ394A18
AC003071	CTA-85E5	bK85E5
AC002378	RP3-438O4	dJ438O4

AC004264	RP1-102K2	dJ102K2
AC004997	RP1-130H16	dJ130H16
AC004832	RP4-539M6	dJ539M6
AC005006	RP1-56J10	dJ56J10
AC003072	CTA-963H5	bK963H5
AL079299	RP11-492A7	bA492A7
AL022336	RP1-78F24	dJ78F24
AC004542	RP3-430N8	dJ430N8
AC005233	RP5-1198O21	dJ1198O21
AC005005	RP3-412A9	dJ412A9
AC002073	RP3-515N1	dJ515N1
AC005003	RP3-400N23	dJ400N23
AL096702	RP11-254F5	bA254F5
AL096701	RP11-247I13	bA247I13
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AL008719	CTA-342B11	bK342B11
Z74021	SC22CB-1E7	cB1E7
Z80998	SC22CB-36G12	cB36G12
Z83849	CITF22-65B7	fF65B7
AL022321	RP1-20O8	dJ20O8
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AL008723	RP1-90G24	dJ90G24
AL021937	RP1-149A16	dJ149A16
AL035068	RP1-116G19	dJ116G19
Z71183	LL22NC03-28H9	cN28H9
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Z80902	LL22NC03-80H12	cN80H12
AL021452	CTA-285F3	bK285F3
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Z81309	LL22NC01-92H8	cE92H8
Z69714	LL22NC03-37F10	cN37F10
Z72521	LL22NC03-29F4	cN29F4
Z72520	LL22NC03-19H5	cN19H5
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Z98256	RP1-309I22	dJ309I22
AL031592	CTA-366B10	bK366B10
Z83846	CTA-415G2	bK415G2
Z82198	RP1-302D9	dJ302D9
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Z82173	SC22CB-1D7	cB1D7
AL008715	CTC-216H12	bK1216H12
AL023577	CTA-566G5	bK566G5

Z82179	LL22NC01-140F8	cE140F8
Z73421	LL22NC03-37D7	cN37D7
AL133451	LL22NC03-120B6	cN120B6
Z69943	LL22NC03-4F11	cN4F11
AL008640	SC22CB-33D11	cB33D11
Z70288	LL22NC01-78G1	cE78G1
Z97354	LL22NC03-117F11	cN117F11
Z69042	LL22NC01-95B1	cE95B1
Z68287	LL22NC03-38E12	cN38E12
Z76736	RP1-75E8	dJ75E8
Z69713	LL22NC03-20A6	cN20A6
Z68324	LL22NC03-7A10	cN7A10
AL096754	LL22NC03-2E9	cN2E9
Z49866	LL22NC03-73A10	cN73A10
Z54073	LL22NC03-13E1	cN13E1
Z77853	LL22NC03-53F3	cN53F3
Z69715	LL22NC03-74G7	cN74G7
Z73429	LL22NC03-32F9	cN32F9
Z69925	LL22NC03-116A5	cN116A5
Z68223	LL22NC01-110C7	cE110C7
Z83852	SC22CB-49C12	cB49C12
Z82182	LL22NC01-90C2	cE90C2
Z99704	LL22NC01-75B8	cE75B8
Z74581	LL22NC01-127C11	cE127C11
AL008641	LL22NC03-100B10	cN100B10
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Z68285	LL22NC03-11D4	cN11D4
AL022338	LL22NC01-82F7	cE82F7
Z82250	LL22NC03-86D4	cN86D4
AL008717	CTA-221H1	bK221H1
Z68323	LL22NC03-13G6	cN13G6
Z68288	LL22NC03-5E4	cN5E4
Z68325	LL22NC03-98E6	cN98E6
Z69712	LL22NC03-12G10	cN12G10
Z68754	LL22NC01-78H10	cE78H10
Z68758	LL22NC03-85E10	cN85E10
Z50860	LL22NC03-76A1	cN76A1
AL020992	CTA-363A12	bK363A12
Z68224	LL22NC01-129H9	cE129H9
AL049750	LL22NC01-141E2	cE141E2
Z69907	LL22NC03-22D1	cN22D1
AL031001	RP1-281O16	dJ281O16
AL021877	RP1-101G11	dJ101G11
Z82196	RP1-288L1	dJ288L1
AL024495	RP3-404L14	dJ404L14
Z82194	RP1-272J12	dJ272J12
Z83853	SC22CB-109E1	cB109E1
AL024494	RP1-215F16	dJ215F16
Z99755	CTA-714B7	bK714B7
AL031300	RP3-323A16	dJ323A16
AL008635	RP3-510H16	dJ510H16
Z82244	CTA-286B10	bK286B10

AL009049	RP5-824I19	dJ824I19
AL022334	RP4-569D19	dJ569D19
AL049747	CITF22-62D4	fF62D4
Z79996	SC22CB-33F2	cB33F2
AL049748	RP1-41P2	dJ41P2
AL079295	RP1-106I20	dJ106I20
Z82217	RP1-78B3	dJ78B3
Z95114	CTA-212A2	bK212A2
AL031426	CTA-191D12	bK191D12
Z82215	RP1-68O2	dJ68O2
AL022302	RP4-633O19	dJ633O19
AL022313	RP5-1119A7	dJ1119A7
AL031845	CTA-566H6	bK566H6
Z70289	CITF22-4G12	fF4G12
AL049749	RP1-293L6	dJ293L6
Z80897	LL22NC01-132D12	cE132D12
Z82184	CITF22-126G10	fF126G10
Z82185	CITF22-24E5	fF24E5
AL008637	CTA-833B7	bK833B7
AL133392	CITF22-45C1	fF45C1
Z82180	LL22NC01-81G9	cE81G9
Z73420	LL22NC01-146D10	cE146D10
AL022314	RP5-1170K4	dJ1170K4
Z82188	RP1-151B14	dJ151B14
Z94160	RP1-63G5	dJ63G5
AL049850	RP5-889J22	dJ889J22
Z93096	CTA-390B3	bK390B3
AL022315	RP5-1177I5	dJ1177I5
AL109980	RP4-697G8	dJ697G8
AL035496	RP3-437O22	dJ437O22
Z83844	RP1-37E16	dJ37E16
Z97630	RP3-466N1	dJ466N1
AL022311	RP5-1014D13	dJ1014D13
AL031587	RP5-1039K5	dJ1039K5
AL022322	CTA-228A9	bK228A9
AL021977	CTA-447C4	bK447C4
AL020993	RP1-5O6	dJ5O6
Z98749	RP3-449O17	dJ449O17
Z97056	RP3-434P1	dJ434P1
AL022320	RP1-199H16	dJ199H16
AL035495	RP1-319F24	dJ319F24
AL021707	RP3-508I15	dJ508I15
AL021806	RP4-779B17	dJ779B17
AL008583	RP3-327J16	dJ327J16
AL022318	CTA-150C2	bK150C2
AL031846	RP4-742C19	dJ742C19
Z81010	LL22NC03-10C3	cN10C3
AL031590	CTA-232D4	bK232D4
AL022326	RP3-333H23	dJ333H23
Z83845	RP3-407F17	dJ407F17
AL022312	RP5-1104E15	dJ1104E15
AL008716	CTA-206C7	bK206C7

AL022319	RP1-172B20	dJ172B20
AL022353	CTA-352E11	bK352E11
Z82206	RP3-370M22	dJ370M22
Z83847	RP3-496C20	dJ496C20
AL033547	RP3-340K22	dJ340K22
AL031589	RP6-11O7	dA11O7
Z93783	RP3-377F16	dJ377F16
AL022238	RP5-1042K10	dJ1042K10
AL031594	RP4-591N18	dJ591N18
Z86090	CTA-229A8	bK229A8
AL096703	RP4-735G18	dJ735G18
AL049764	RP3-362J20	dJ362J20
Z98048	RP3-408N23	dJ408N23
AL035450	RP5-1057D18	dJ1057D18
AL080242	RP11-554C12	bA554C12
AL080243	RP11-12M9	bA12M9
AL096765	RP11-422A16	bA422A16
AL035658	RP1-85F18	dJ85F18
AL035681	RP4-756G23	dJ756G23
AL035659	RP5-979N1	dJ979N1
AL008582	CTA-223H9	bK223H9
AL023553	RP3-347H13	dJ347H13
Z83840	CTA-216E10	bK216E10
AL023879	CTA-109G6	bK109G6
AL021453	RP5-821D11	dJ821D11
Z99716	CTA-250D10	bK250D10
Z82192	RP1-186O1	dJ186O1
AL021878	RP1-257I20	dJ257I20
AL031346	RP4-597B2	dJ597B2
Z83851	CTA-989H11	bK989H11
AL022316	CTA-126B4	bK126B4
AL035418	RP1-141I3	dJ141I3
Z93241	RP1-222E13	dJ222E13
Z82176	SC22CB-33B7	cB33B7
AL049757	RP1-47A17	dJ47A17
AL049758	RP3-437M21	dJ437M21
AL022476	RP3-323M22	dJ323M22
AL022237	CTB-191B2	bK1191B2
Z82214	RP3-526I14	dJ526I14
Z99756	RP1-100N22	dJ100N22
AL096761	RP4-754E20	dJ754E20
Z82172	SC22CB-13C9	cB13C9
AL118498	RP1-185D5	dJ185D5
AL031843	RP1-246D7	dJ246D7
Z82201	RP3-345P10	dJ345P10
AL023801	RP4-786D3	dJ786D3
Z97055	RP3-388M5	dJ388M5
AL023654	RP4-549K18	dJ549K18
AL035398	RP4-796I17	dJ796I17
Z82178	SC22CB-79B4	cB79B4
Z82174	SC22CB-20F6	cB20F6
AL033543	CTA-414D7	bK414D7

AL031595	RP4-671O14	dJ671O14
AL022339	LL22NC03-75B3	cN75B3
AL591914	CITF22-4H11	fF4H11
AL671760	CITF22-11D1	fF11D1
AL929500	CITF22-57B10	fF57B10
Z85994	RP1-32I10	dJ32I10
Z81308	CTA-397C4	bK397C4
AL023973	RP5-1033E15	dJ1033E15
Z75407	LL22NC03-128A12	cN128A12
AL022317	RP1-140L1	dJ140L1
AL022333	RP3-474I12	dJ474I12
Z98743	RP1-181C9	dJ181C9
Z93244	CTA-116F5	bK116F5
Z83838	RP1-127B20	dJ127B20
AL079301	RP4-753M9	dJ753M9
Z82243	CTA-217C2	bK217C2
AL008718	CTA-268H5	bK268H5
AL021391	RP1-102D24	dJ102D24
Z98047	RP1-162H14	dJ162H14
Z95331	CTA-941F9	bK941F9
Z93784	RP3-398C22	dJ398C22
Z84478	RP1-37M3	dJ37M3
AL049811	RP11-140I15	bA140I15
AL929387	RP11-398F12	bA398F12
Z94161	LL22NC03-102C10	cN102C10
AL049856	RP4-695O20	dJ695O20
AL078611	SC22cB-5E3	cB5E3
AL031034	LL22NC03-98G1	cN98G1
Z93024	LL22NC03-5H6	cN5H6
AL031844	RP3-361H15	dJ361H15
AL031588	RP5-1163J1	dJ1163J1
AL031597	RP5-996D20	dJ996D20
AL021392	RP3-439F8	dJ439F8
AL096766	RP6-59H18	dA59H18
AL118516	CTA-29F11	bK29F11
AL078642	RP5-917C11	dJ917C11
Z97351	RP1-116M15	dJ116M15
Z82187	CITF22-64F4	fF64F4
U51561	LLcos-79E2	cN79E2
AL023576	CTA-358H9	bK358H9
Z80896	RP1-67C13	dJ67C13
Z79999	CITF22-111A3	fF111A3
AL023733	SC22cB-58F5	cB58F5
Z81000	CITF22-67D6	fF67D6
AL096755	RP3-477J10	dJ477J10
U51559	LLcos-65D1	cN65D1
AL096756	RP3-477J10	dJ494G10
Z82183	LL22NC01-98F6	cE98F6
Z83836	RP1-111J24	dJ111J24
Z82186	CITF22-49D8	fF49D8
AL035069	RP3-404P13	dJ404P13
Z84496	LL22NC03-75H12	cN75H12

AL021306	CTB-109B5	bK1109B5
Z80999	LL22NC01-140G5	cE140G5
Z73416	LL22NC03-114B2	cN114B2
AL033544	LL22NC01-107C5	cE107C5
AL049568	SC22CB-23F1	cB23F1
Z80901	LL22NC03-119A7	cN119A7
AC000034	AC000034	cN119A4
Z83854	SC22CB-44H3	cB44H3
AL117329	RP11-191L9	bA191L9
AL121580	RP13-455A7	bB455A7
AL110122	CTA-280A3	bK280A3
Z73963	LL22NC03-62C4	cN62C4
AL110121	CTA-280A3	bK280A3
Z70688	LL22NC03-27C5	cN27C5
Z81002	LL22NC03-53A9	cN53A9
Z80772	CITF22-37F6	fF37F6
AL118553	CITF22-91B7	fF91B7
Z78421	LL22NC03-121E8	cN121E8
AL118554	CITF22-91B7	fF91B7
AL050314	RP1-100G10	dJ100G10
AL008720	CTA-343C1	bK343C1
Z72006	LL22NC03-69F4	cN69F4
Z82249	LL22NC03-4D6	cN4D6
AL078640	RP11-536P6	bA536P6
Z84468	CTA-299D3	bK299D3
AL096853	CITF22-96H12	fF96H12
AL096843	RP11-262A13	bA262A13
Z83837	CITF22-113D11	fF113D11
Z83855	LL22NC03-104C4	cN104C4
AL078607	RP4-619N21	dJ619N21
AL954742	CITF22-114E11	fF114E11
AL078613	RP11-354I12	bA354I12
AL078622	RP5-925J7	dJ925J7
AL078632	RP11-255N20	bA255N20
AL049773	RP5-1061O18	dJ1061O18
Z94162	LL22NC03-21F1	cN21F1
Z82202	RP1-34P24	dJ34P24
Z82189	RP1-170A21	dJ170A21
AL008636	CTA-722E9	bK722E9
AL031593	RP4-566L20	dJ566L20
Z97192	RP1-29C18	dJ29C18
AL023802	RP5-983L19	dJ983L19
Z98885	RP3-522J7	dJ522J7
AL117328	RP11-494O16	bA494O16
AL080240	RP11-232E17	bA232E17
AL022327	RP3-355C18	dJ355C18
AL034546	RP5-898I4	dJ898I4
AL022328	RP3-402G11	dJ402G11
AL954743	CITF22-49G11	fF49G11
AL671545	CITF22-53E7	fF53Et
AL096767	RP4-579N16	dJ579N16
Z94802	CTA-999D10	bK999D10

U62317	U62317	bK384D8
Z82168	RP1-104C13	dJ104C13
Z82245	CTA-799F10	bK799F10
AC000050	AC000050	cN66C4
AC000036	AC000036	cN85A3
AC002056	AC002056	cN94H12
AC002055	AC002055	cN1G3

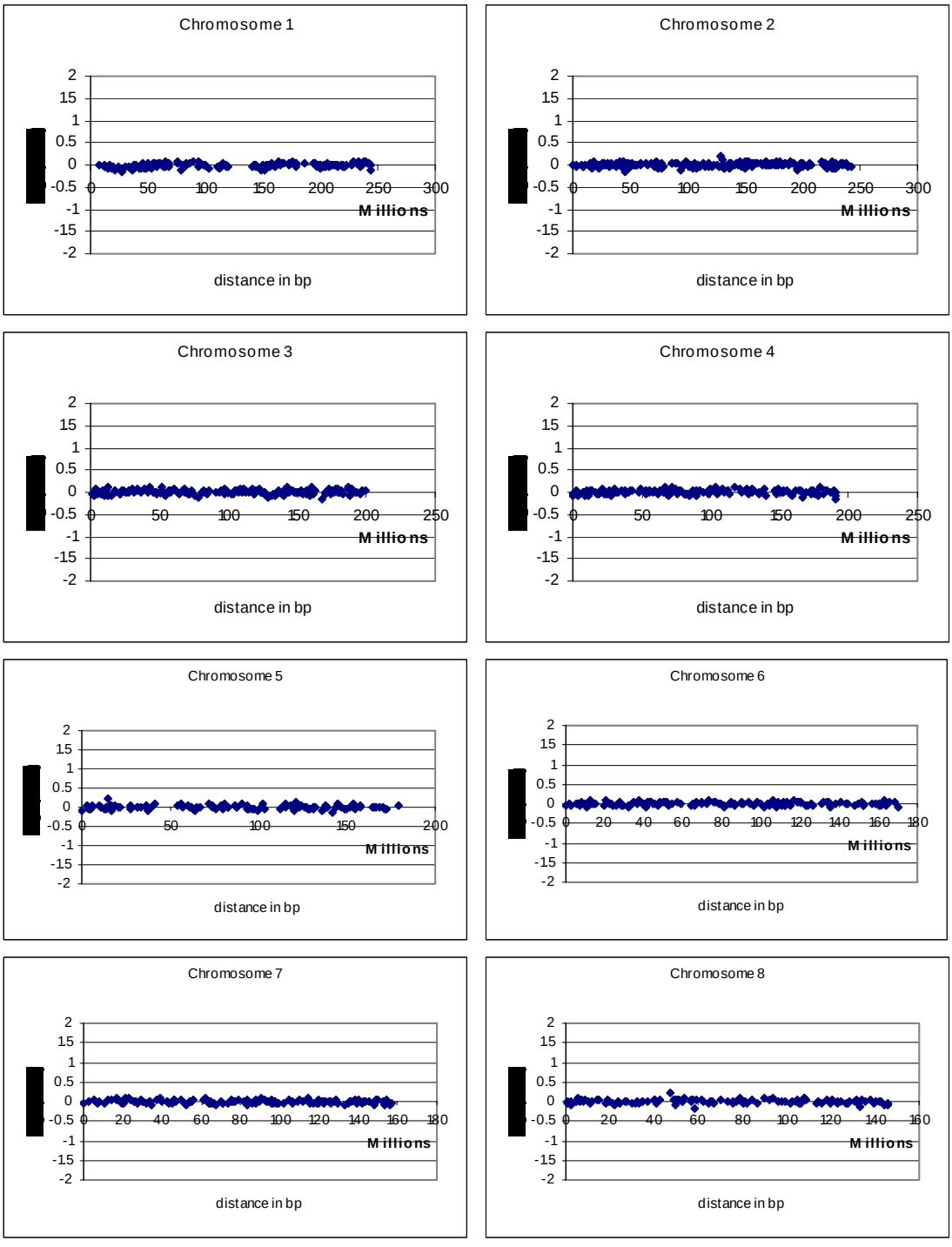
9b: Clone Libraries

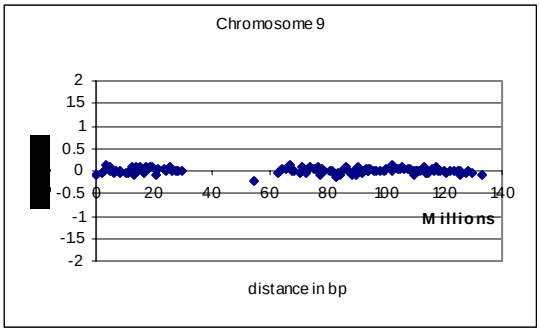
Table adapted from, http://www.sanger.ac.uk/HGP/methods/mapping/info/lib-details.shtml

Library Type	**Library**	**Library code**	**Antibiotic**
Cosmid	Sc22cB, Sanger flow sorted chromosome 22	cB	Kanamycin 30μg/ml
Cosmid	LL22NC01 “E”, Paris flow sorted chromosome 22	cE	Kanamycin 30μg/ml
Cosmid	LL22NC03 “N”, Lawerence Livermore flow sorted chromosome 22	cN	Kanamycin 30μg/ml
Fosmid	CITF22, Caltech flow sorted chromosome 22 fosmid library	fF	Chloramphenicol 25μg/ml
RPCI Human PAC	RPCI-1-5, de Jong whole genome male PAC library	dJ	Kanamycin 25μg/ml
RPCI Human PAC	RPCI-6, de Jong whole genome female PAC library	dA	Kanamycin 25μg/ml
BAC	CIT978SK (CTA, CTB and CTC) Caltech whole genome BAC library	bK	Chloramphenicol 12.5μg/ml
RPCI Human BAC	RPCI-11, Whole genome male BAC library	bA	Chloramphenicol 25μg/ml
RPCI Human BAC	RPCI-13, Whole genome female BAC library	bB	Chloramphenicol 25μg/ml

Appendix 10: 1Mb profiles of patients with DiGeorge phenotype and no 22q11 deletion.

Patient 1:




Chromosome 9
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-1
-1.5
-2
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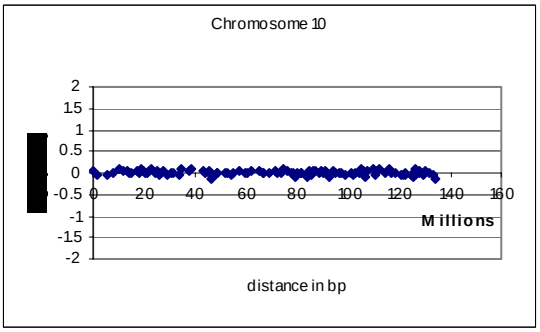
20
40
60
80
100
120
140
Millions
distance in bp


Chromosome 10
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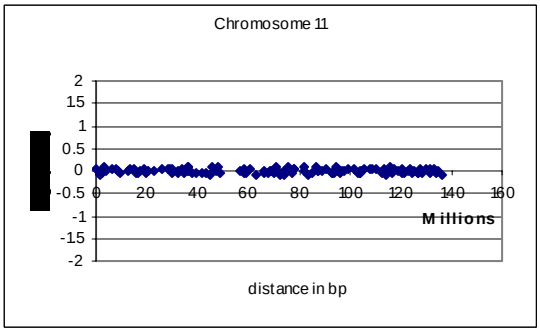
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp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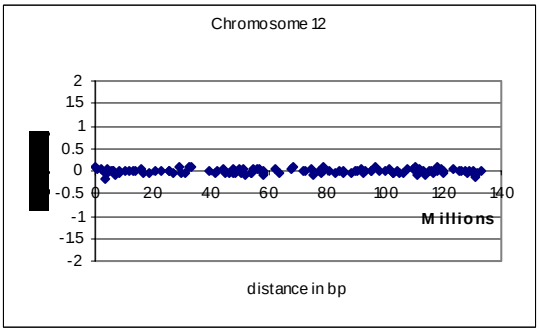
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 12
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-1
-1.5
-2
0
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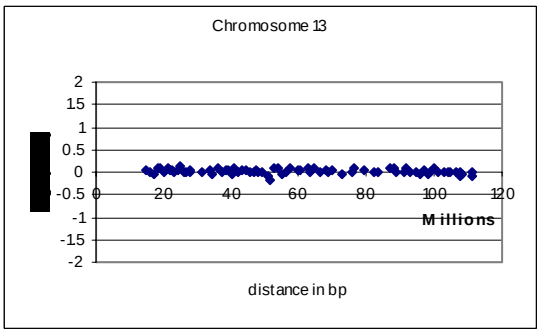
40
60
80
100
120
140
Millions
distance in bp


Chromosome 13
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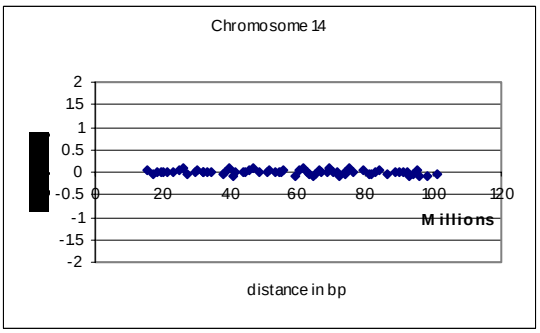
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 14
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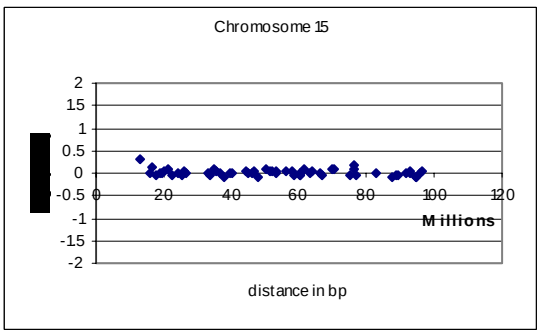
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp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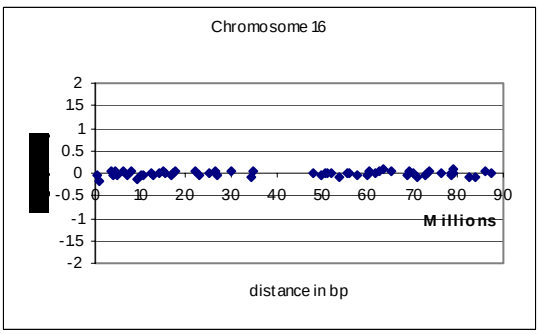
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp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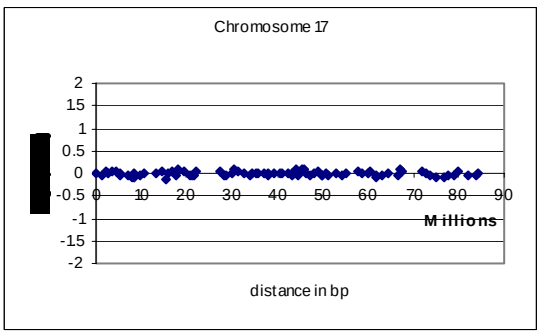
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp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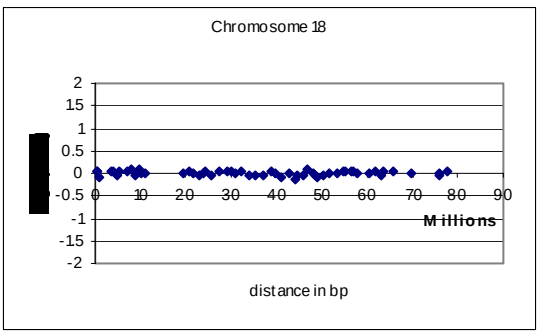
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp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0.5
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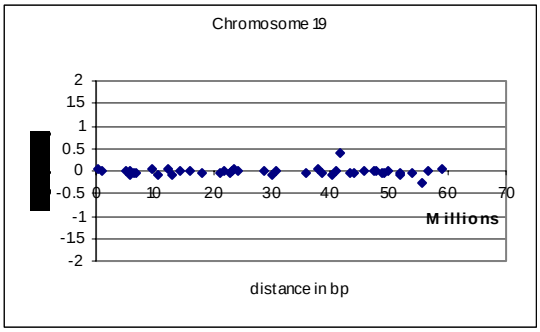
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 19
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0.5
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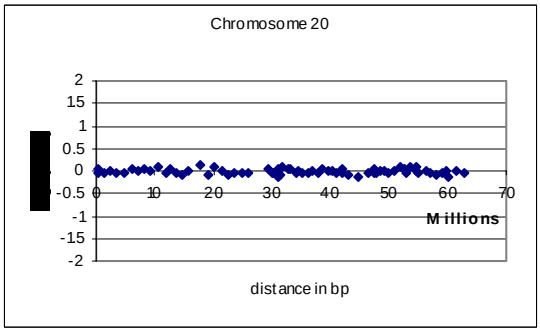
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp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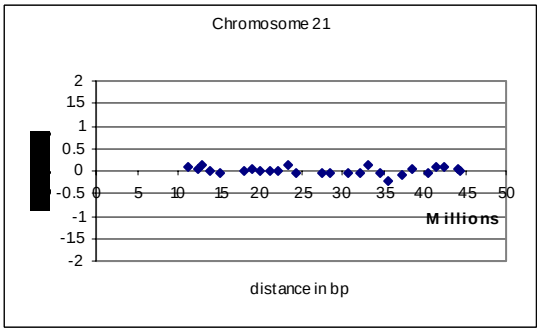
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp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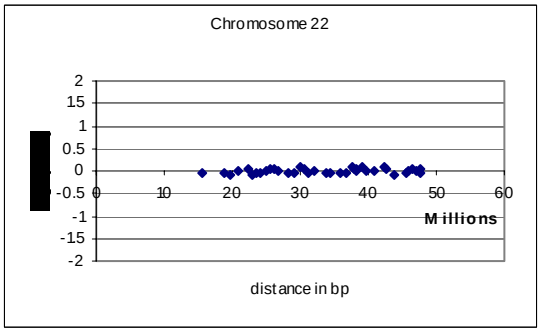
-2
0
5
10
15
20
25
30
35
40
45
50
Millions
distance in bp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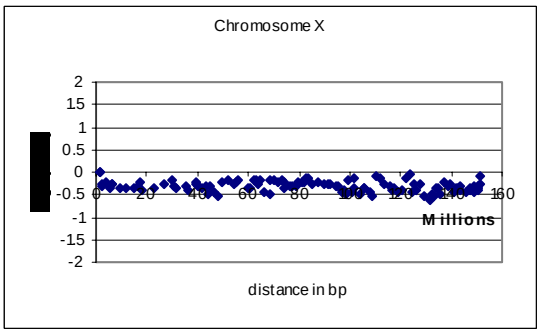
-1
-1.5
-2
0
10
20
30
40
50
60
Millions
distance in bp


Chromosome X
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-1.5
-2
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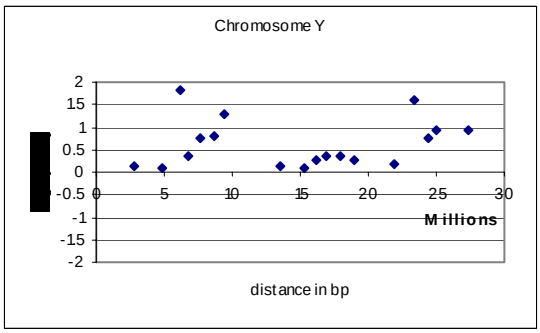
80
100
120
140
160
Millions
distance in bp


Chromosome Y
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-2
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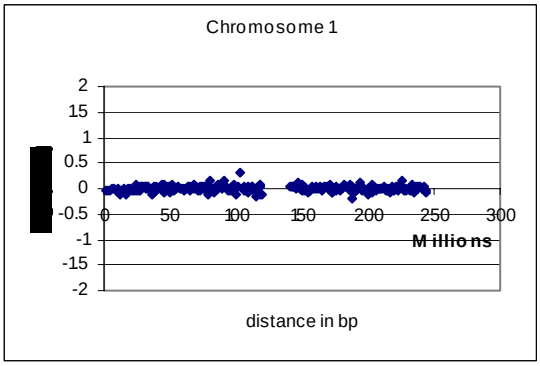
5
10
15
20
25
30
Millions
distance in bp

Patient 2:


Chromosome 1
2
1.5
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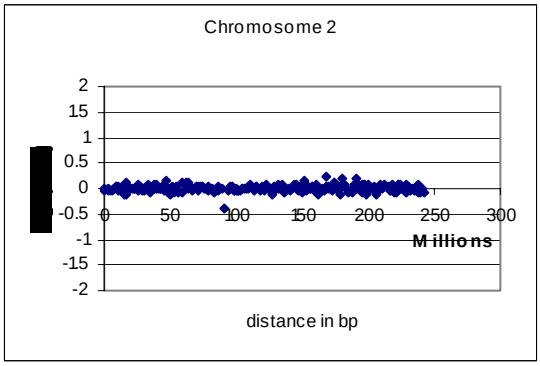
-1
-1.5
-2
0
50
100
150
200
250
300
Millions
distance in bp


Chromosome 2
2
1.5
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-1
-1.5
-2
0
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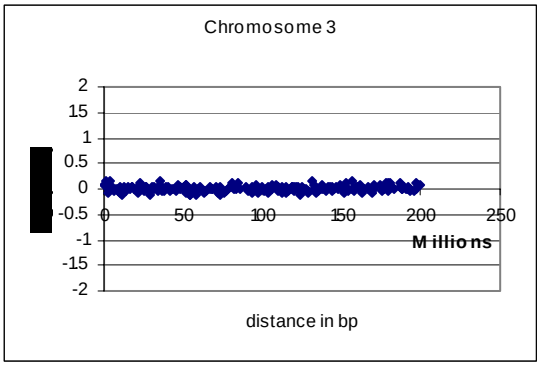
100
150
200
250
300
Millions
distance in bp


Chromosome 3
2
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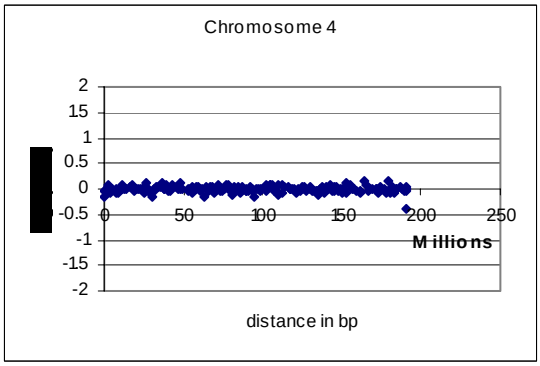
-0.5
-1
-1.5
-2
0
50
100
150
200
250
Millions
distance in bp


Chromosome 4
2
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-1
-1.5
-2
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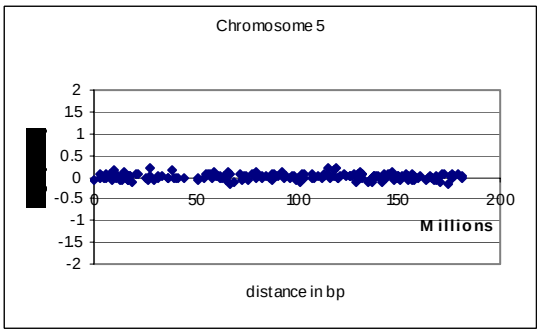
100
150
200
250
Millions
distance in bp


Chromosome 5
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-0.5
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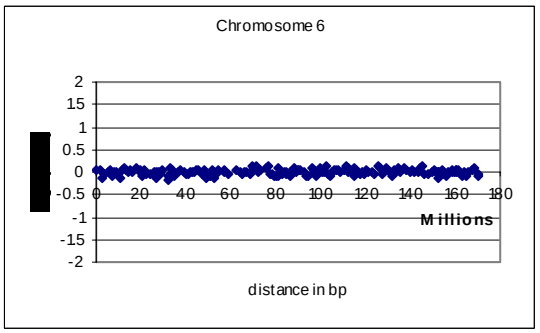
-1.5
-2
0
50
100
150
200
Millions
distance in bp


Chromosome 6
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-1.5
-2
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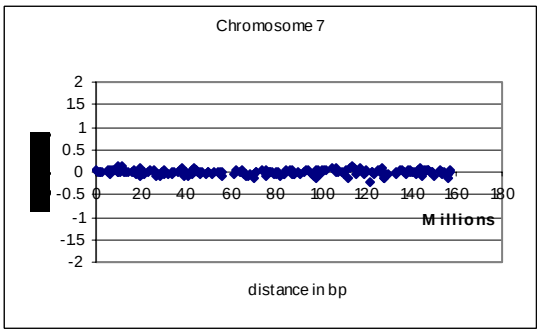
100
120
140
160
180
Millions
distance in bp


Chromosome 7
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-1.5
-2
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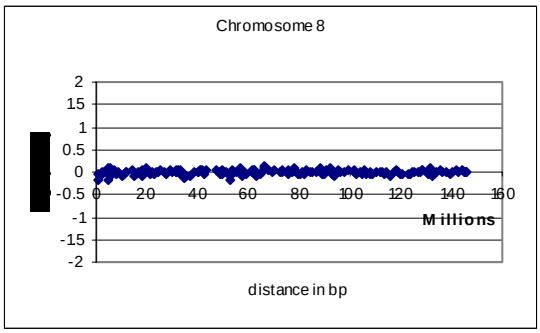
60
80
100
120
140
160
180
Millions
distance in bp


Chromosome 8
2
1.5
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0.5
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-0.5
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-1.5
-2
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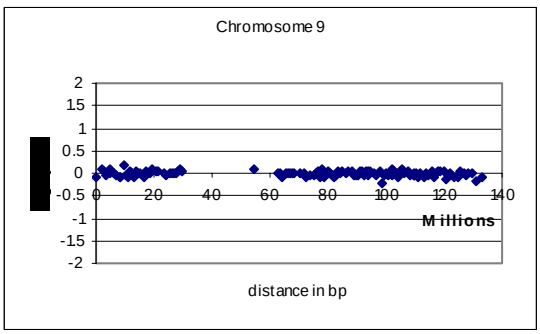
80
100
120
140
160
Millions
distance in bp


Chromosome 9
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1.5
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-1.5
-2
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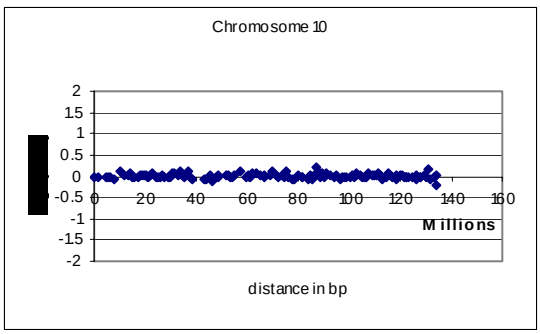
60
80
100
120
140
Millions
distance in bp


Chromosome 10
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-1
-1.5
-2
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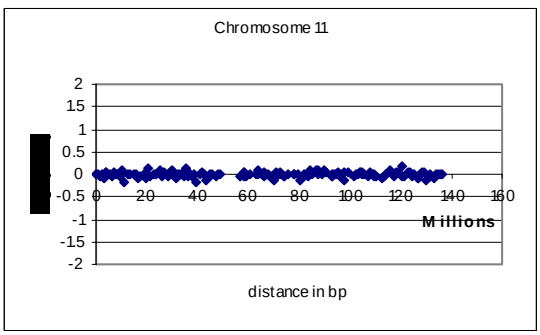
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 11
2
1.5
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0.5
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-0.5
-1
-1.5
-2
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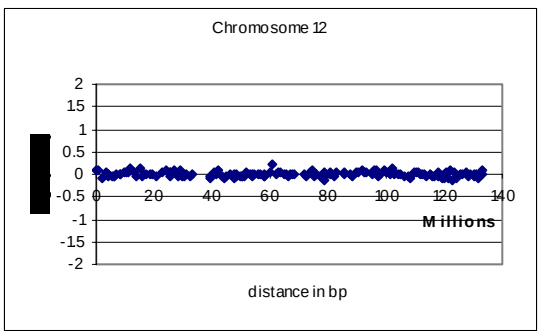
60
80
100
120
140
160
Millions
distance in bp


Chromosome 12
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1
0.5
0
-0.5
-1
-1.5
-2
0
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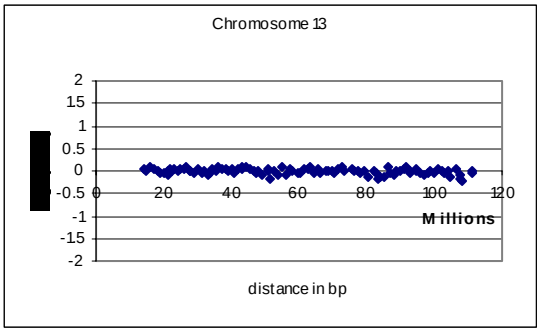
40
60
80
100
120
140
Millions
distance in bp


Chromosome 13
2
1.5
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0.5
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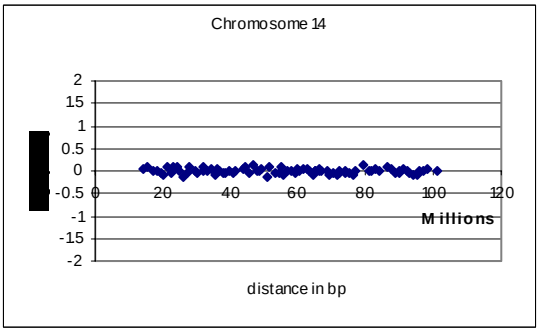
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 14
2
1.5
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-0.5
-1
-1.5
-2
0
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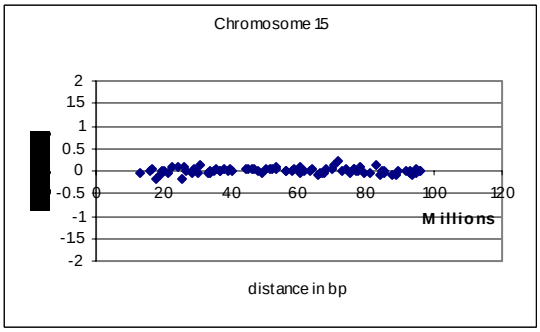
40
60
80
100
120
Millions
distance in bp


Chromosome 15
2
1.5
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0.5
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-0.5
-1
-1.5
-2
0
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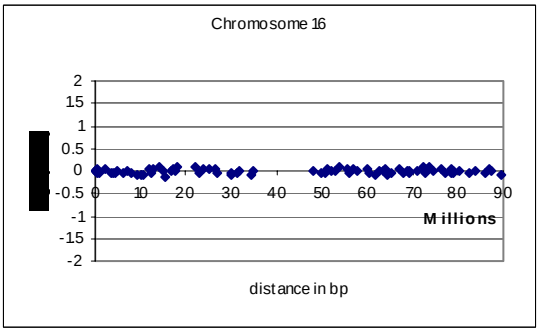
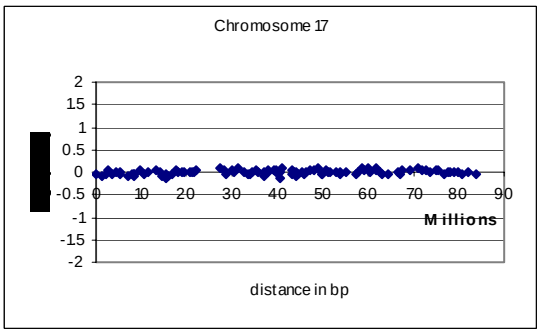
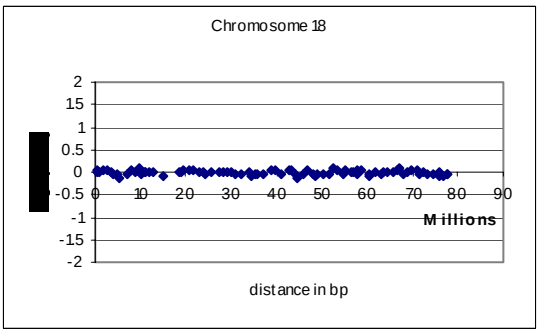
40
60
80
100
120
Millions
distance in bp


Chromosome 16
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 17
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 18
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1.5
1
0.5
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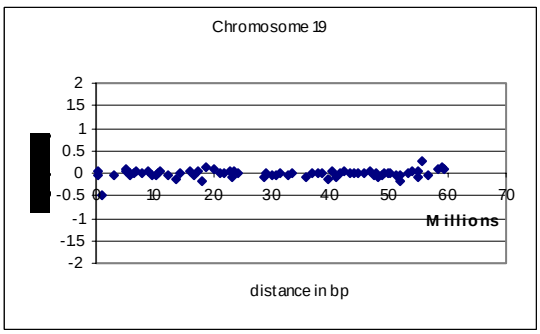
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 19
2
1.5
1
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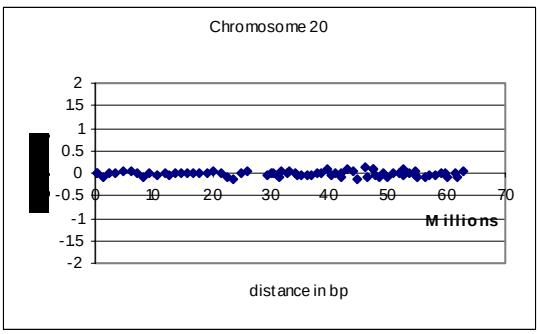
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 20
2
1.5
1
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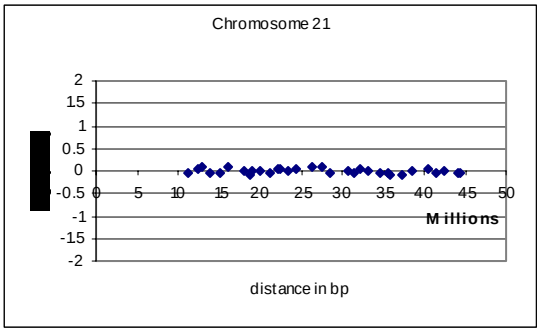
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 21
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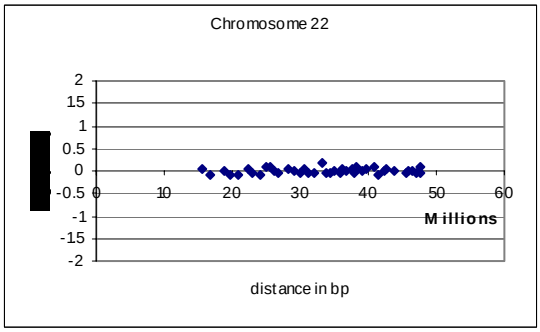
0.5
0
-0.5
-1
-1.5
-2
0 5 10 15 20 25 30 35 40 45 50
Millions
distance in bp


Chromosome 22
2
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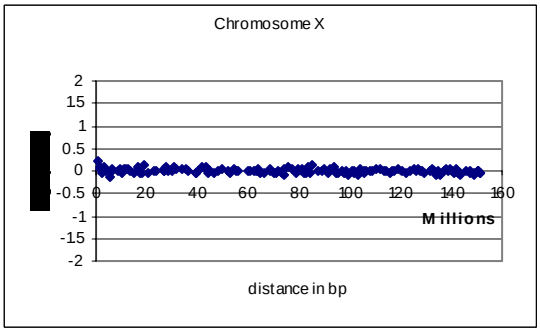
1
0.5
0
-0.5
-1
-1.5
-2
0 10 20 30 40 50 60
Millions
distance in bp


Chromosome X
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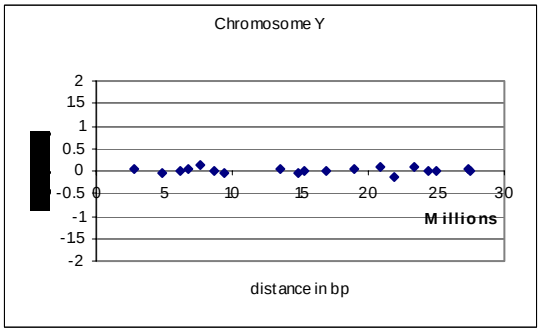
0.5
0
-0.5
-1
-1.5
-2
0 20 40 60 80 100 120 140 160
Millions
distance in bp


Chromosome Y
2
1.5
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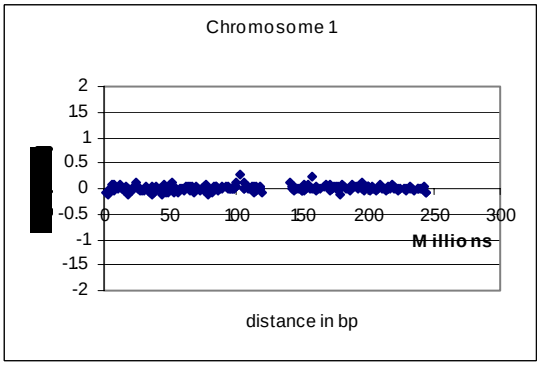
0.5
0
-0.5
-1
-1.5
-2
0 5 10 15 20 25 30
Millions
distance in bp

Patient 3:


Chromosome 1
2
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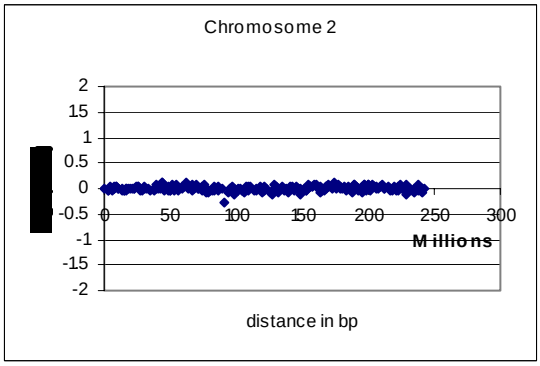
0.5
0
-0.5
-1
-1.5
-2
0 50 100 150 200 250 300
Millions
distance in bp


Chromosome 2
2
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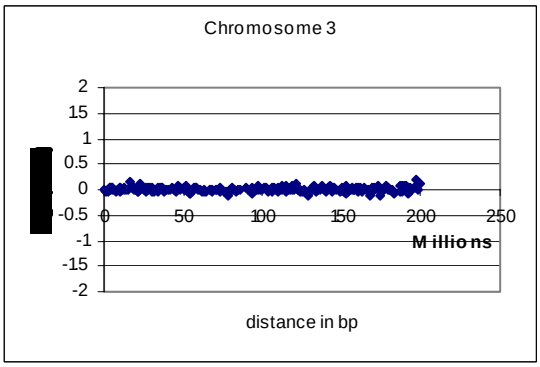
1
0.5
0
-0.5
-1
-1.5
-2
0 50 100 150 200 250 300
Millions
distance in bp


Chromosome 3
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0.5
0
-0.5
-1
-1.5
-2
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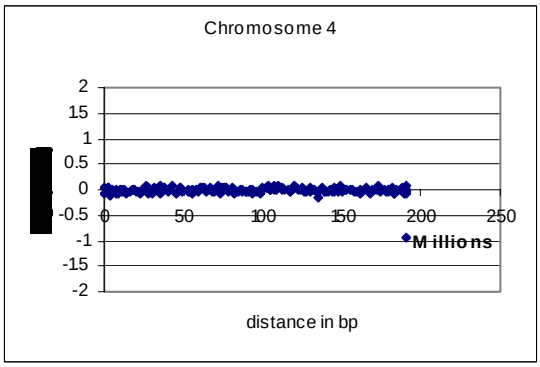
Millions
distance in bp


Chromosome 4
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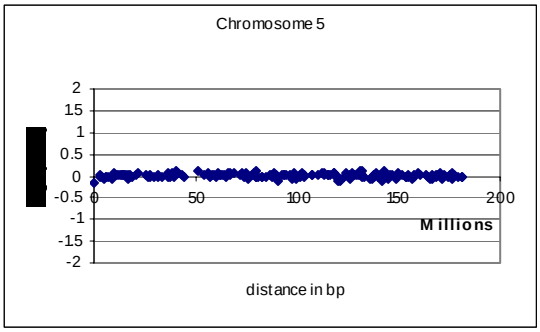
0.5
0
-0.5
-1
-1.5
-2
0 50 100 150 200 250
Millions
distance in bp


Chromosome 5
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-0.5
-1
-1.5
-2
0
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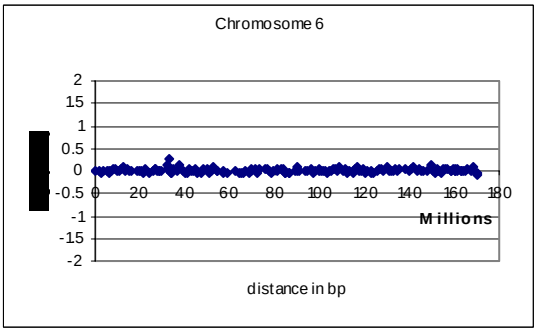
100
150
200
Millions
distance in bp


Chromosome 6
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-2
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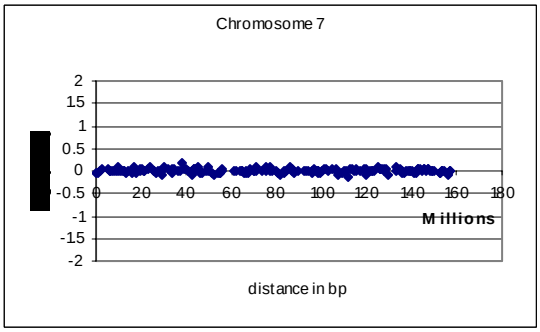
100
120
140
160
180
Millions
distance in bp


Chromosome 7
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-1.5
-2
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60
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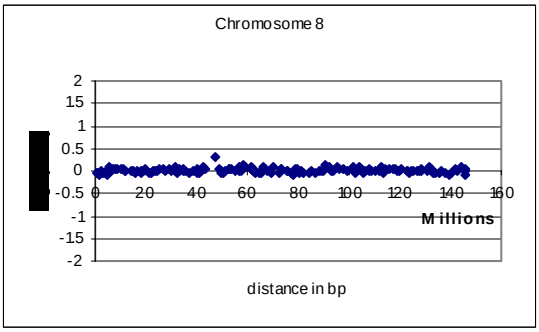
100
120
140
160
180
Millions
distance in bp


Chromosome 8
2
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-1
-1.5
-2
0
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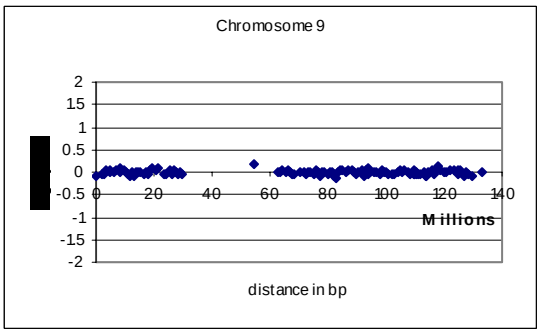
60
80
100
120
140
160
Millions
distance in bp


Chromosome 9
2
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-1
-1.5
-2
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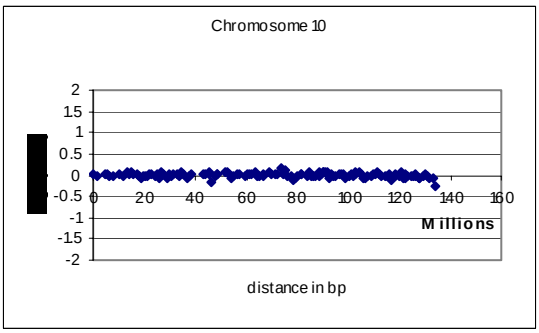
60
80
100
120
140
Millions
distance in bp


Chromosome 10
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-2
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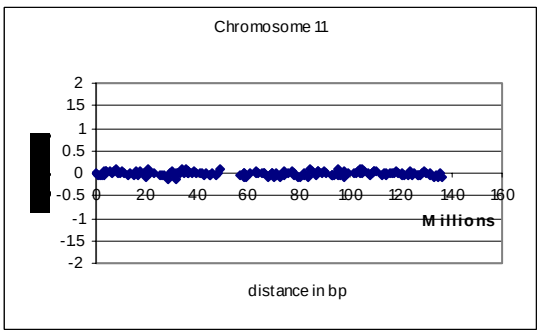
100
120
140
160
Millions
distance in bp


Chromosome 11
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-0.5
-1
-1.5
-2
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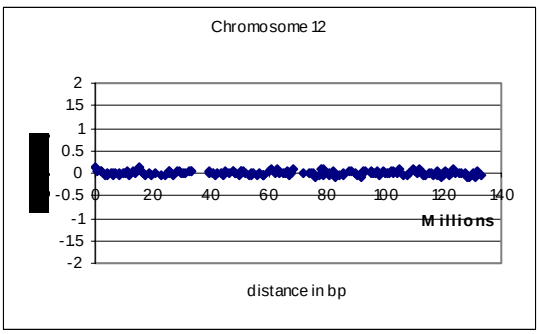
80
100
120
140
160
Millions
distance in bp


Chromosome 12
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0
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-1
-1.5
-2
0
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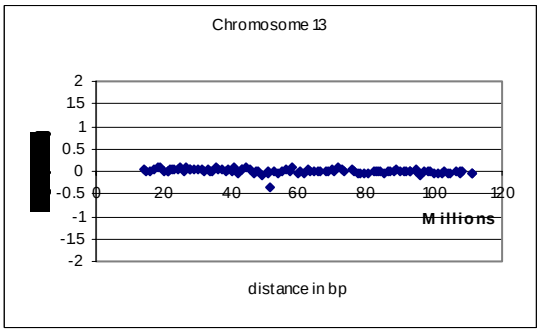
40
60
80
100
120
140
Millions
distance in bp


Chromosome 13
2
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0.5
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-0.5
-1
-1.5
-2
0
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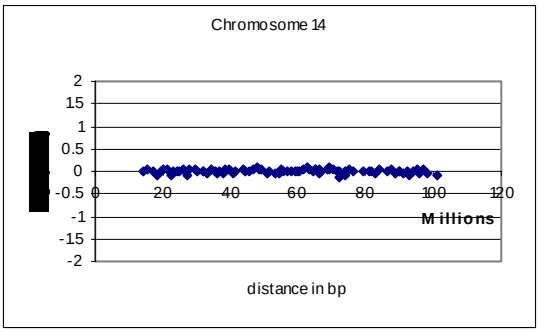
40
60
80
100
120
Millions
distance in bp


Chromosome 14
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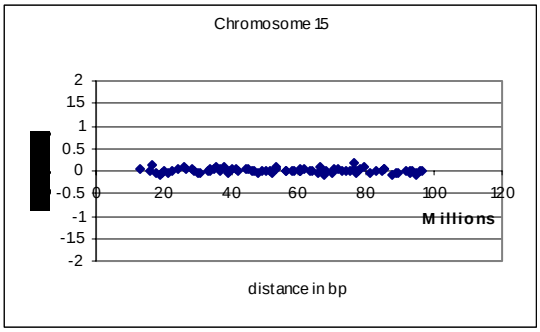
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 15
2
1.5
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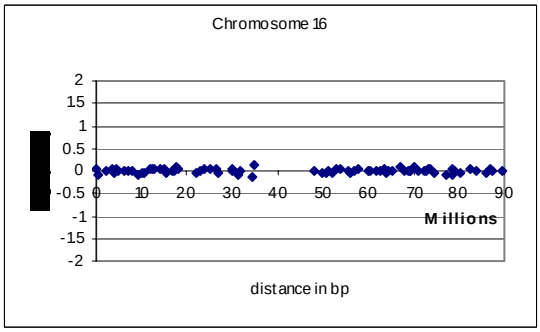
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 16
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0.5
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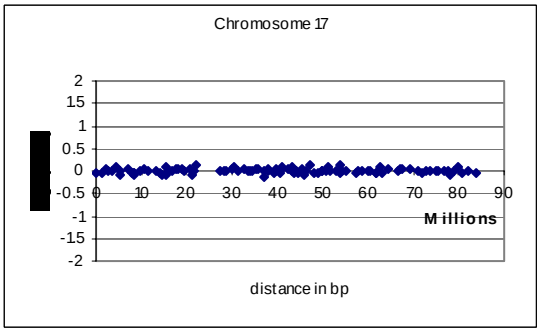
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 17
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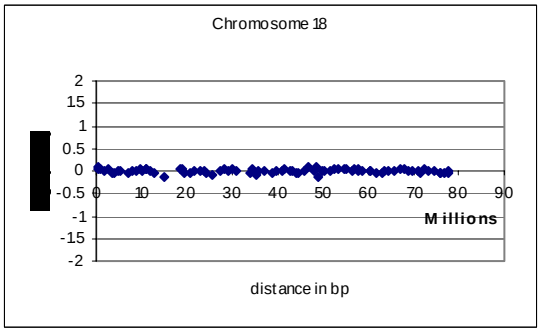
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 18
2
1.5
1
0.5
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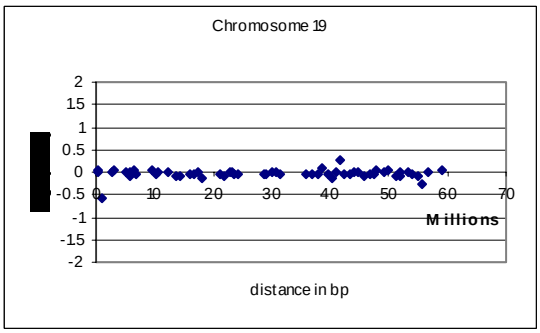
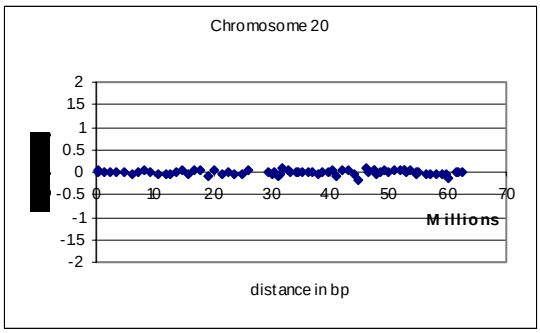
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 19
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 20
2
1.5
1
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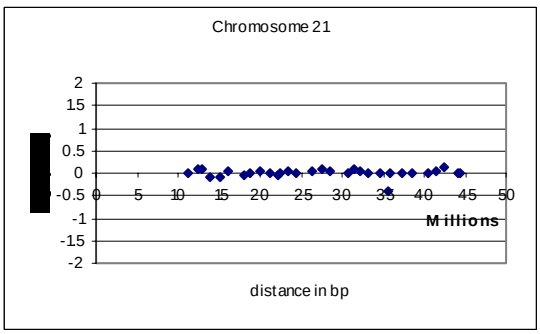
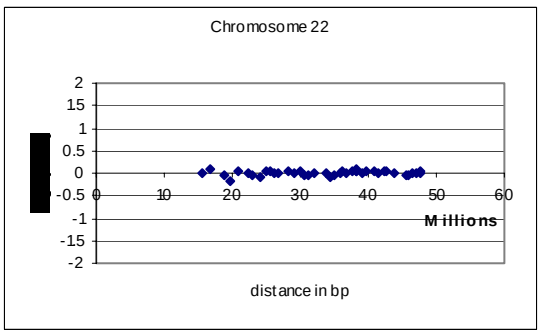
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 21
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
5
10
15
20
25
30
35
40
45
50
Millions
distance in bp


Chromosome 22
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1.5
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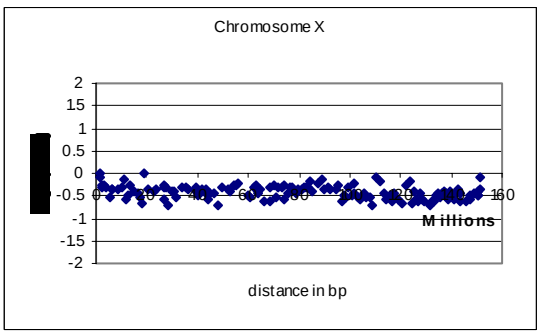
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
Millions
distance in bp


Chromosome X
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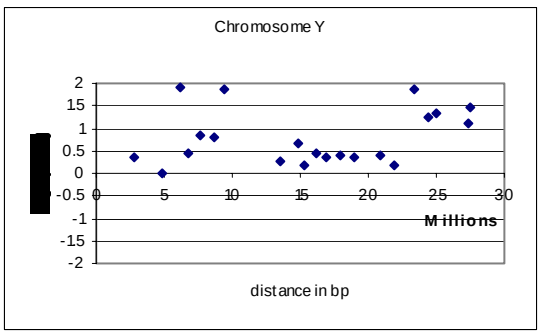
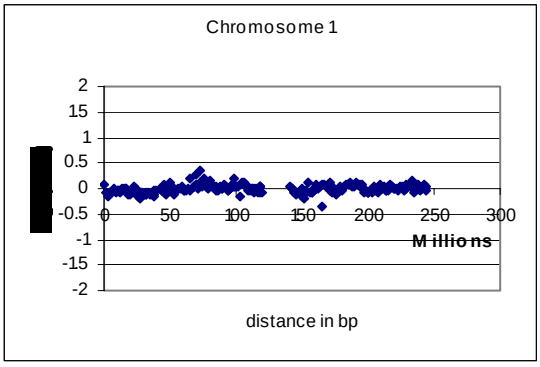
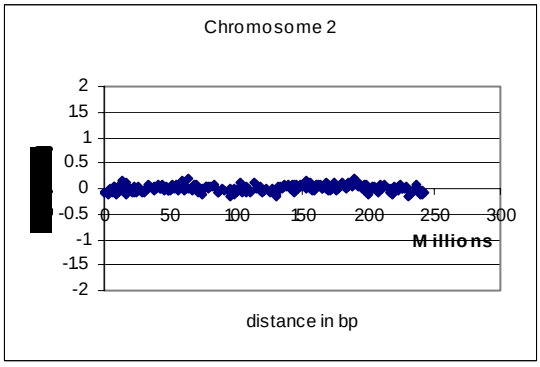
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
Millions
distance in bp


Chromosome Y
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
5
10
15
20
25
30
Millions
distance in bp

Patient 4:


Chromosome 1
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
300
Millions
distance in bp


Chromosome 2
2
1.5
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0.5
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-0.5
-1
-1.5
-2
0
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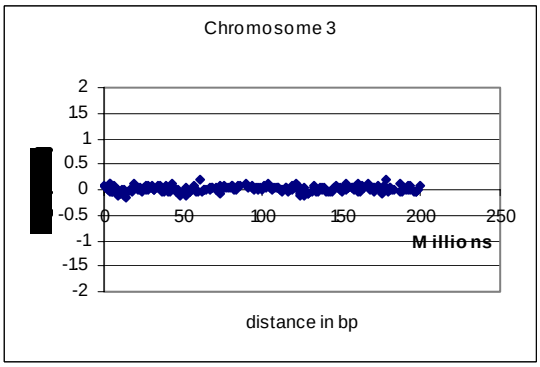
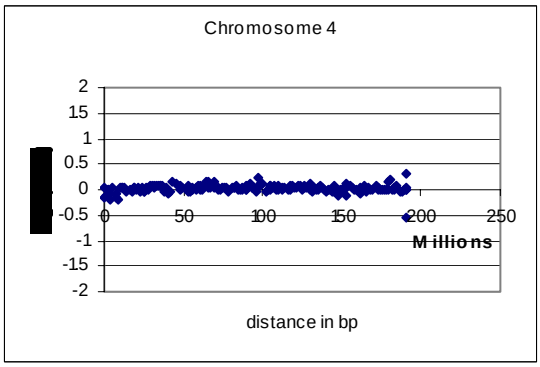
100
150
200
250
300
Millions
distance in bp


Chromosome 3
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
Millions
distance in bp


Chromosome 4
2
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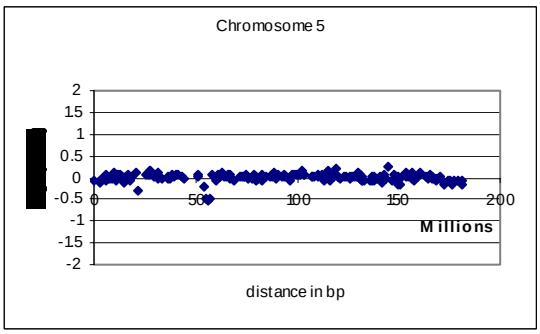
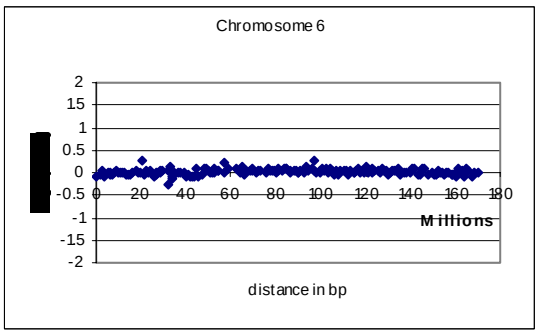
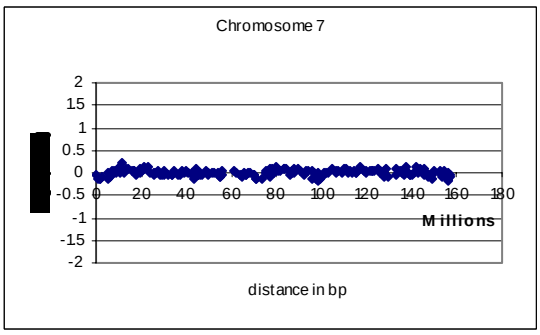
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
Millions
distance in bp


Chromosome 5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
Millions
distance in bp


Chromosome 6
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
180
Millions
distance in bp


Chromosome 7
2
1.5
1
0.5
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-0.5
-1
-1.5
-2
0
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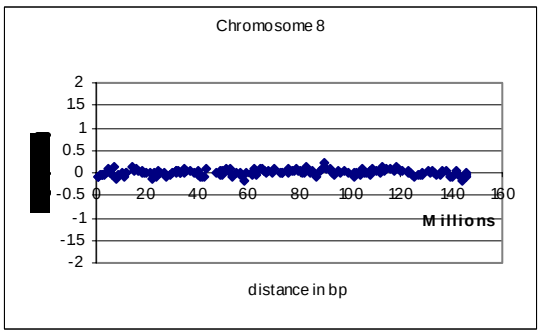
60
80
100
120
140
160
180
Millions
distance in bp


Chromosome 8
2
1.5
1
0.5
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-0.5
-1
-1.5
-2
0
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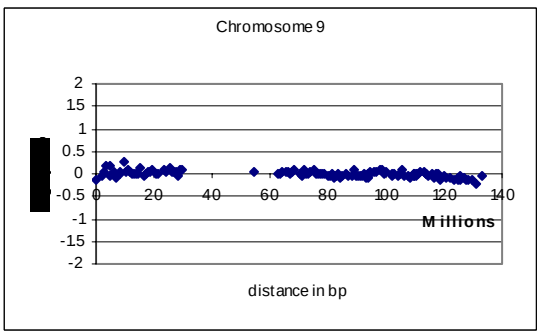
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 9
2
1.5
1
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0
-0.5
-1
-1.5
-2
0
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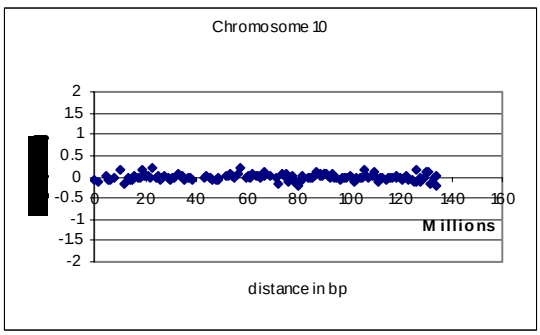
40
60
80
100
120
140
Millions
distance in bp


Chromosome 10
2
1.5
1
0.5
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-0.5
-1
-1.5
-2
0
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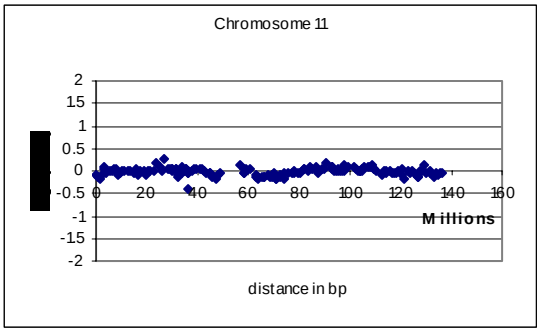
60
80
100
120
140
160
Millions
distance in bp


Chromosome 11
2
1.5
1
0.5
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-0.5
-1
-1.5
-2
0
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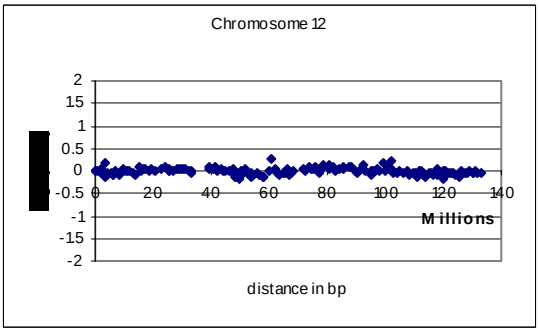
60
80
100
120
140
160
Millions
distance in bp


Chromosome 12
2
1.5
1
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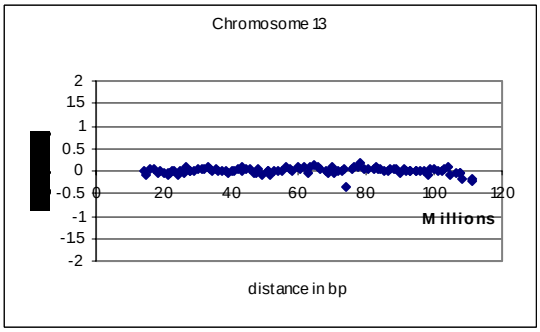
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp


Chromosome 13
2
1.5
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0.5
0
-0.5
-1
-1.5
-2
0
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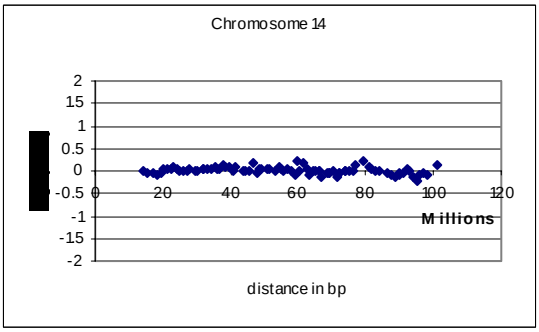
40
60
80
100
120
Millions
distance in bp


Chromosome 14
2
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0.5
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-0.5
-1
-1.5
-2
0
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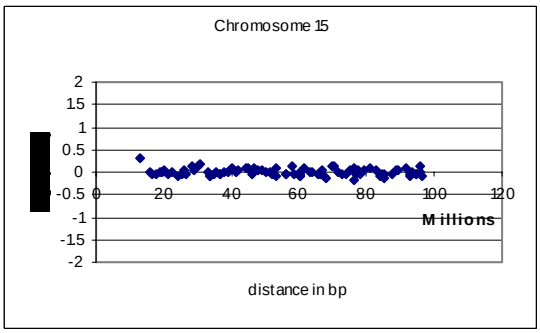
40
60
80
100
120
Millions
distance in bp


Chromosome 15
2
1.5
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0.5
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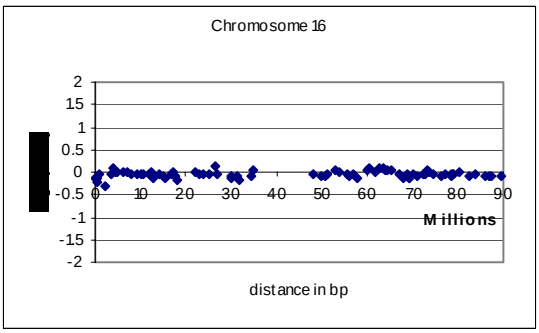
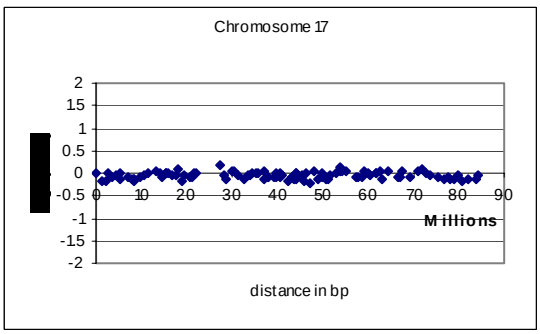
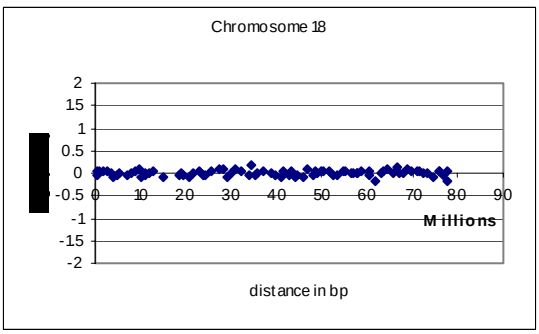
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 16
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 17
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 18
2
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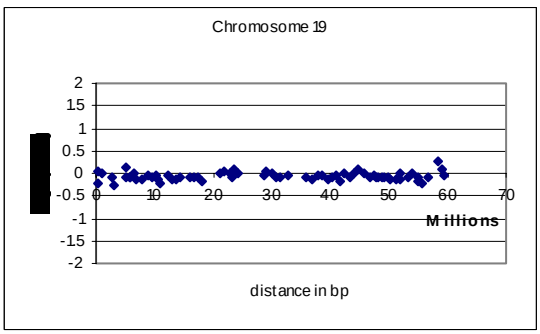
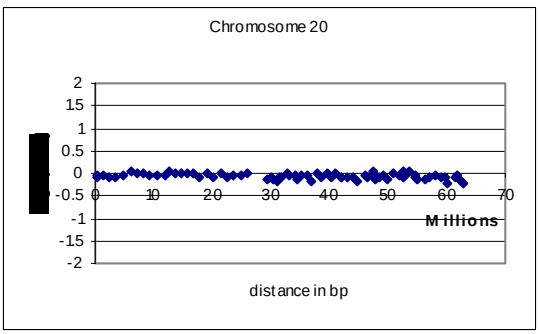
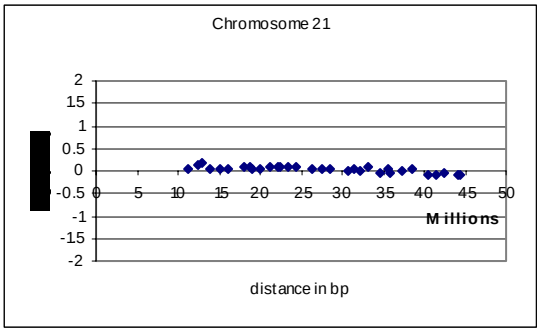
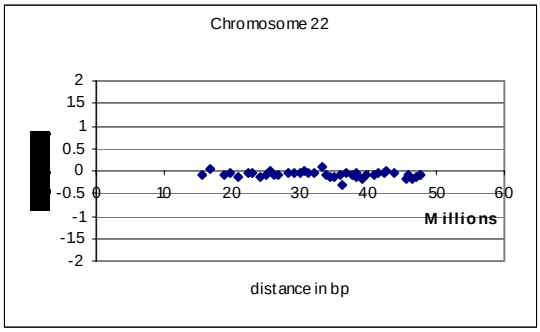
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 19
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 20
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 21
2
15
1
0.5
0
-0.5
-1
-15
-2
0 5 10 15 20 25 30 35 40 45 50
Millions
distance in bp


Chromosome 22
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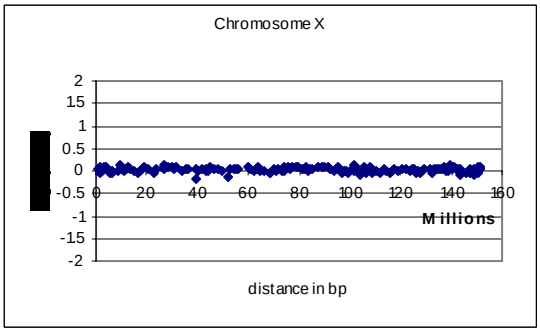
15
1
0.5
0
-0.5
-1
-15
-2
0 10 20 30 40 50 60
Millions
distance in bp


Chromosome X
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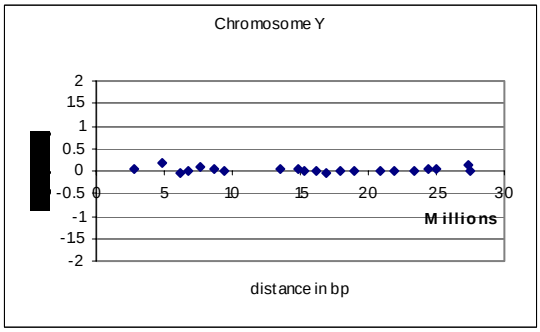
1
0.5
0
-0.5
-1
-15
-2
0 20 40 60 80 100 120 140 160
Millions
distance in bp


Chromosome Y
2
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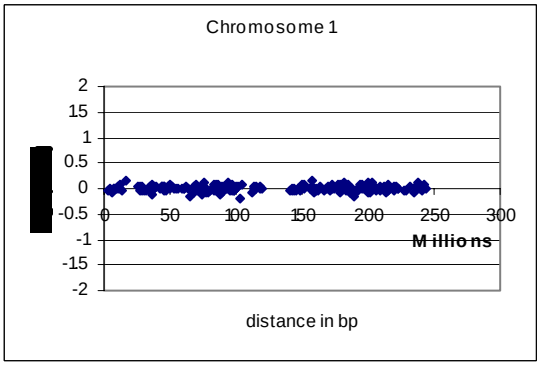
0.5
0
-0.5
-1
-15
-2
0 5 10 15 20 25 30
Millions
distance in bp

Patient 5:


Chromosome 1
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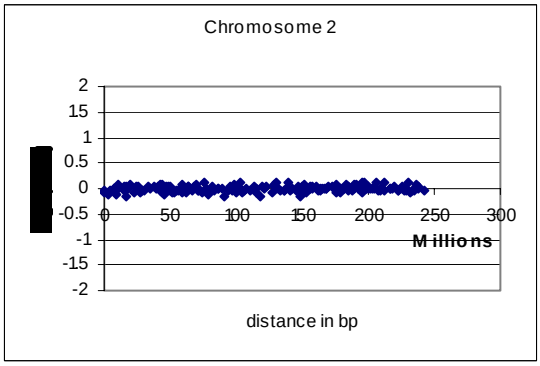
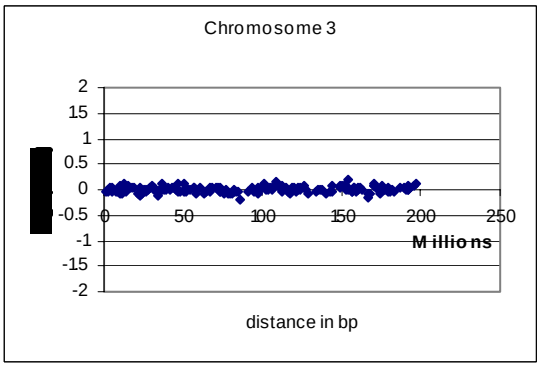
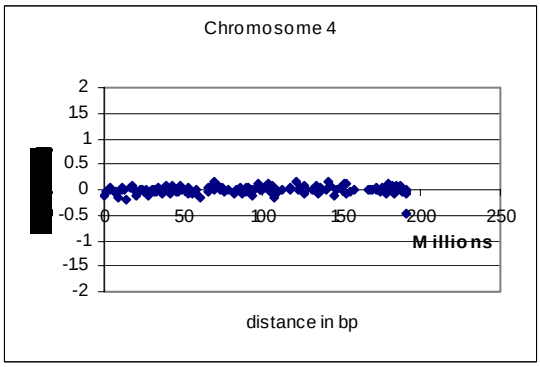
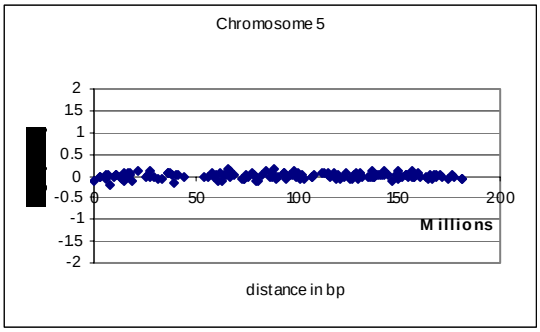
1
0.5
0
-0.5
-1
-15
-2
0 50 100 150 200 250 300
Millions
distance in bp


Chromosome 2
2
15
1
0.5
0
-0.5
-1
-15
-2
0 50 100 150 200 250 300
Millions
distance in bp


Chromosome 3
2
15
1
0.5
0
-0.5
-1
-15
-2
0 50 100 150 200 250
Millions
distance in bp


Chromosome 4
2
15
1
0.5
0
-0.5
-1
-15
-2
0 50 100 150 200 250
Millions
distance in bp


Chromosome 5
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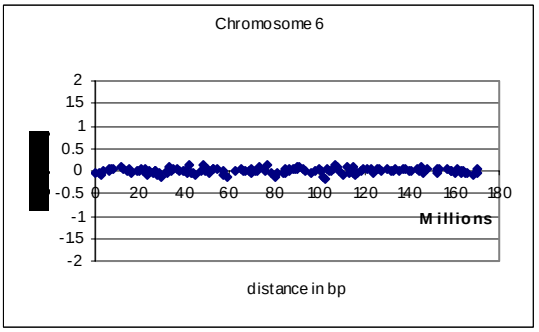
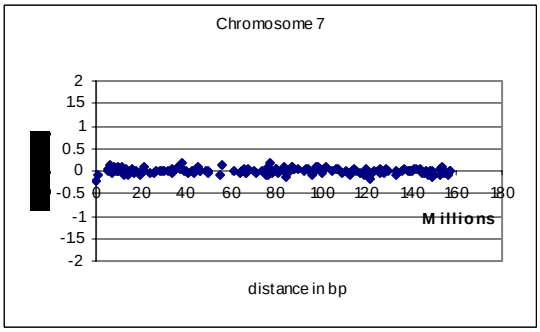
0
-0.5
-1
-1.5
-2
0
50
100
150
200
Millions
distance in bp


Chromosome 6
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
180
Millions
distance in bp


Chromosome 7
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
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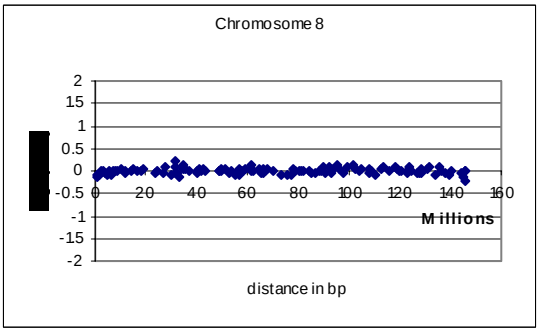
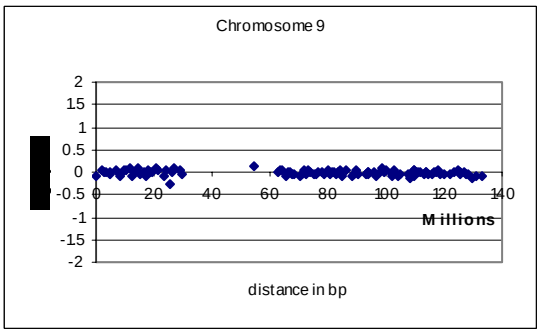
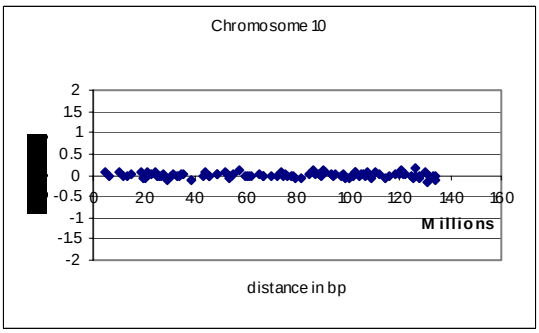
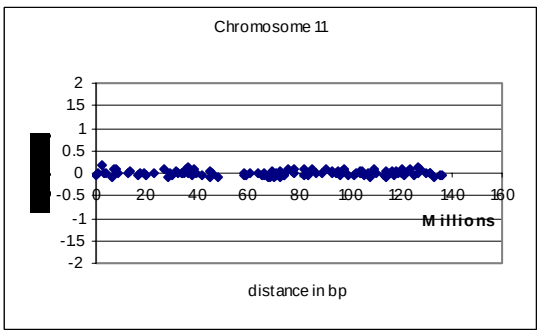
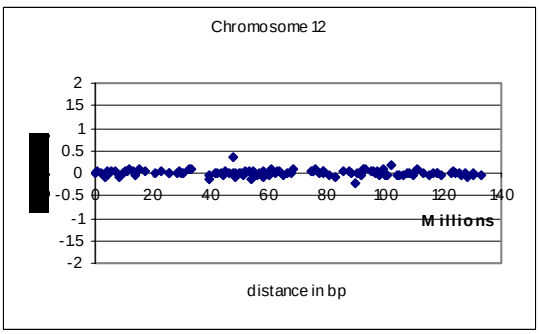
60
80
100
120
140
160
180
Millions
distance in bp

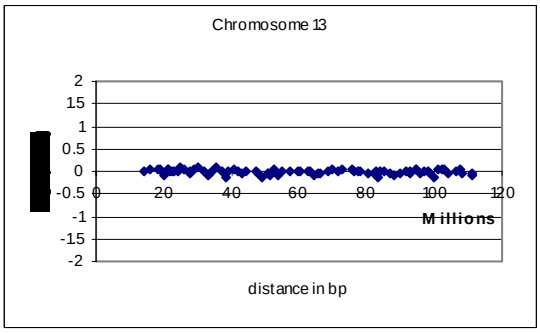

Chromosome 8
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 9
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp


Chromosome 10
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 11
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 12
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp


Chromosome 13
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1.5
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0.5
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-0.5
-1
-1.5
-2
0
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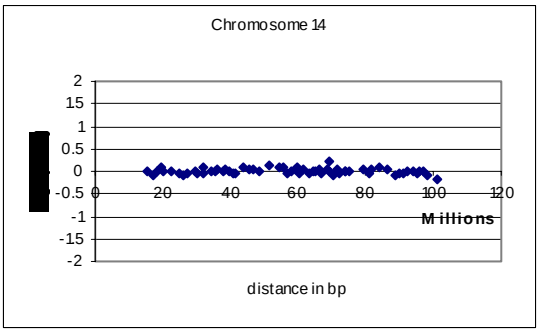
40
60
80
100
120
Millions
distance in bp


Chromosome 14
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1.5
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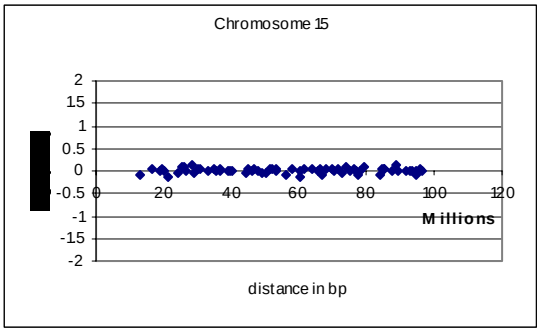
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 15
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1.5
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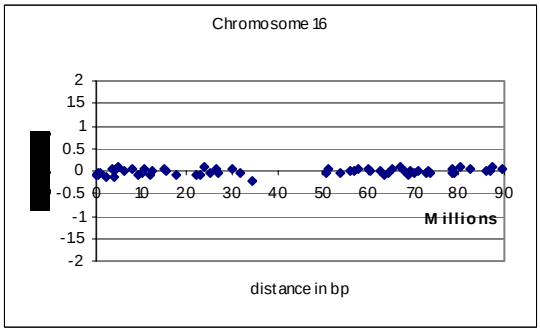
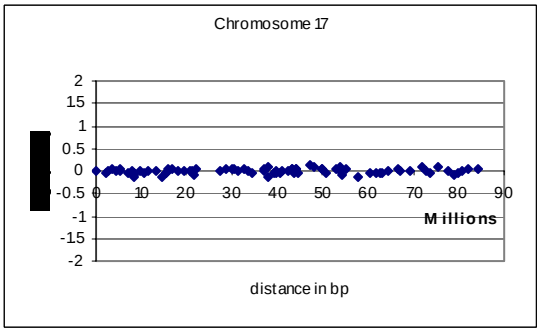
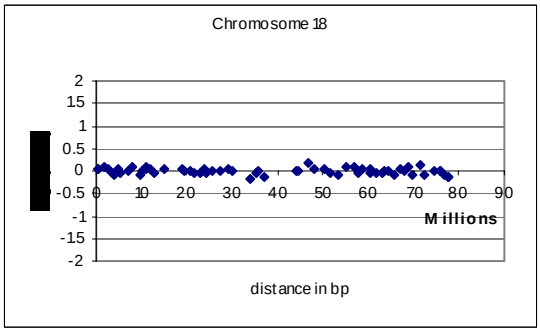
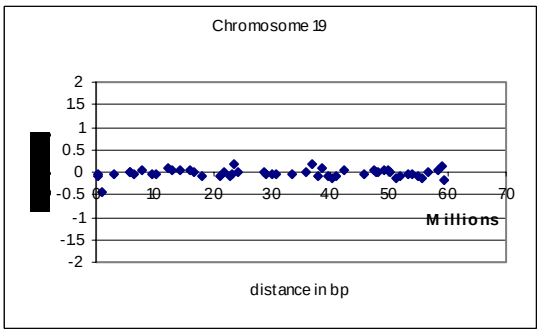
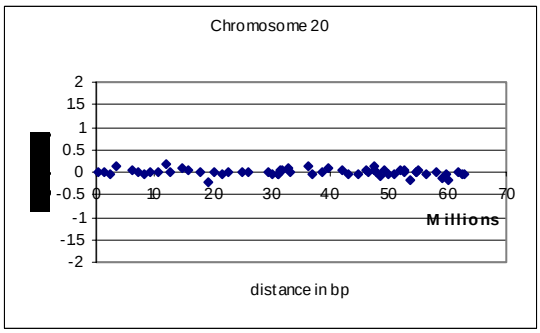
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp

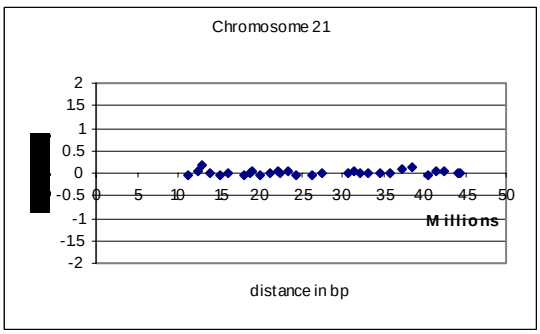

Chromosome 16
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp

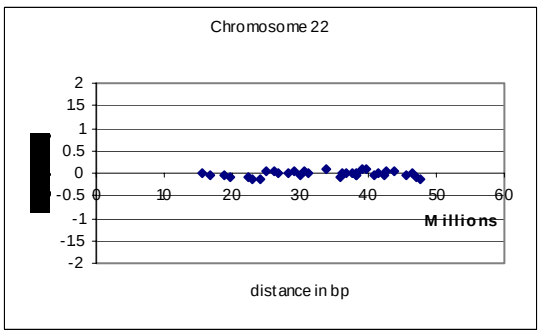

Chromosome 17
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp

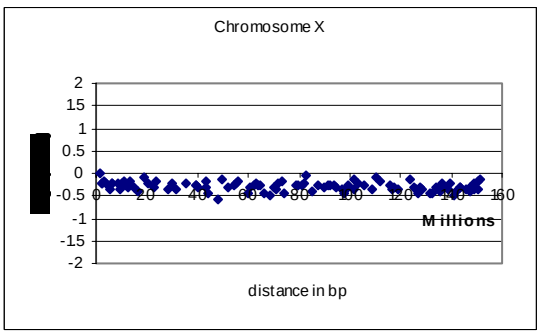

Chromosome 18
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp

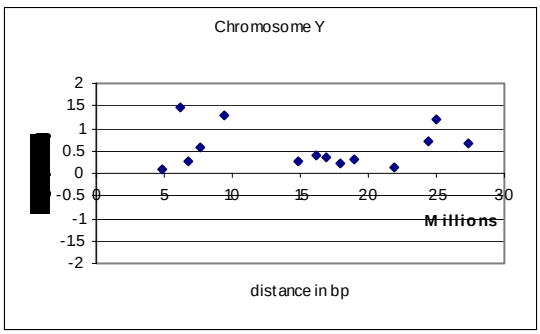

Chromosome 19
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 20
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp

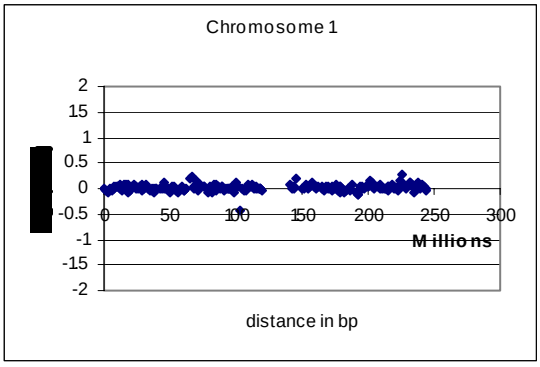

Chromosome 21
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
5
10
15
20
25
30
35
40
45
50
Millions
distance in bp

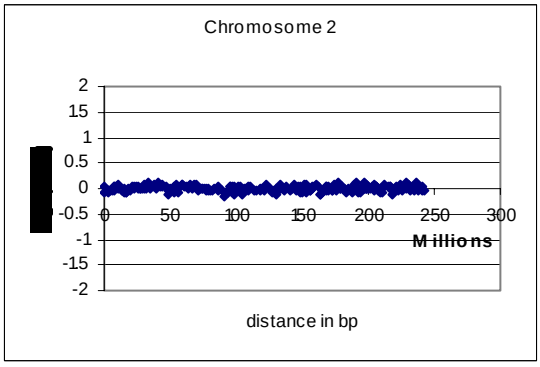

Chromosome 22
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
Millions
distance in bp

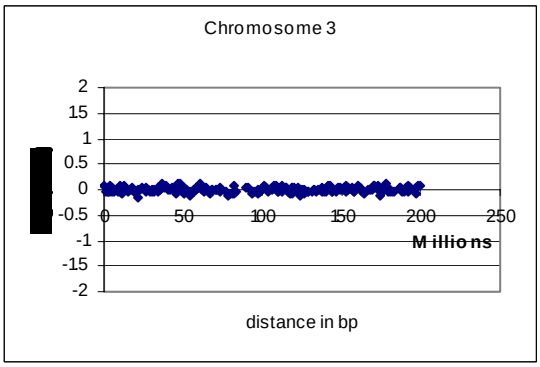

Chromosome X
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp

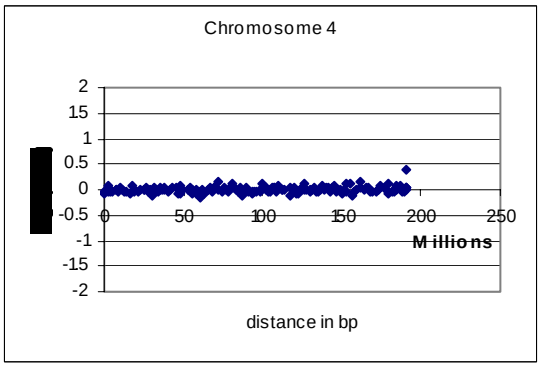

Chromosome Y
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
5
10
15
20
25
30
Millions
distance in bp

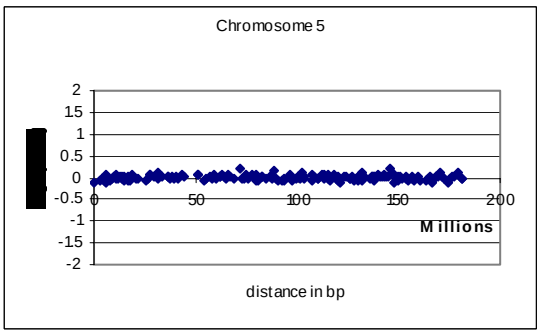
Patient 6:

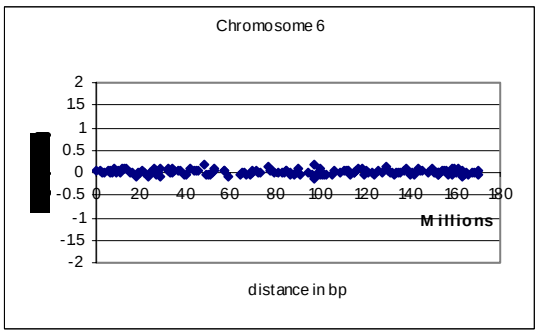

Chromosome 1
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
300
Millions
distance in bp

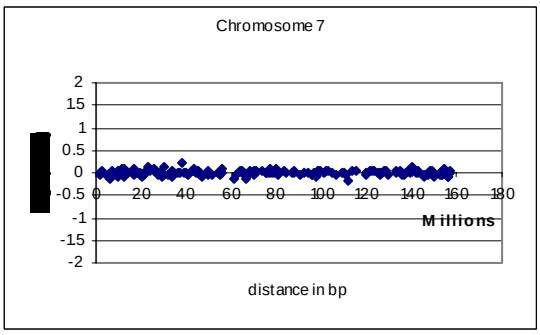

Chromosome 2
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
300
Millions
distance in bp

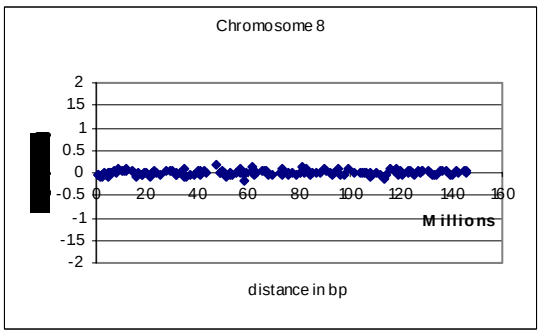

Chromosome 3
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
Millions
distance in bp

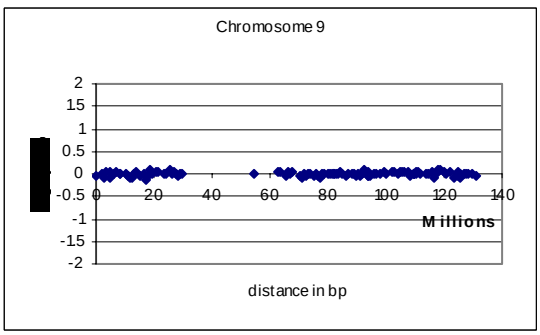

Chromosome 4
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
250
Millions
distance in bp

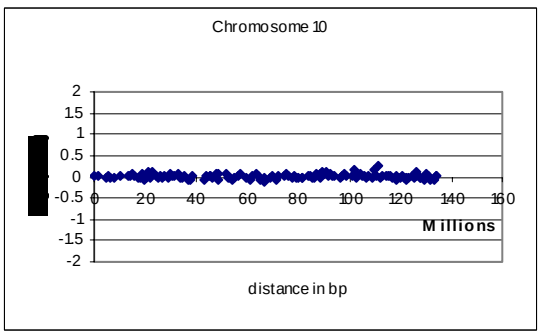

Chromosome 5
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
50
100
150
200
Millions
distance in bp

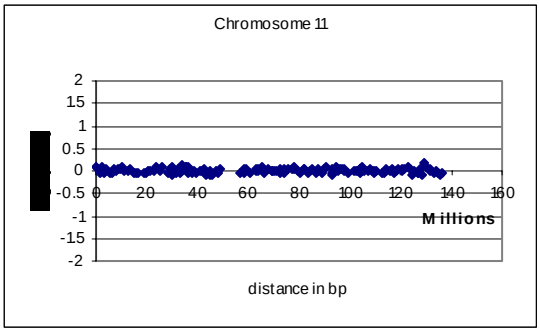

Chromosome 6
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
180
Millions
distance in bp

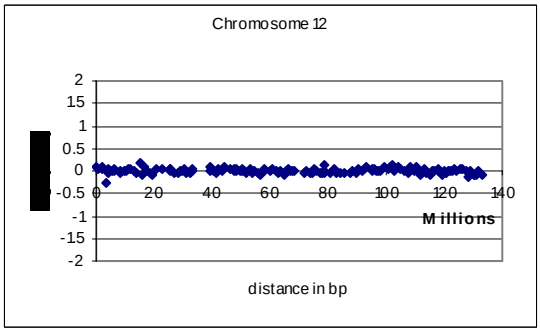

Chromosome 7
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
180
Millions
distance in bp

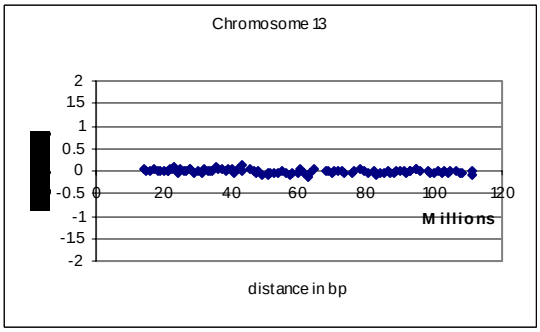

Chromosome 8
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp

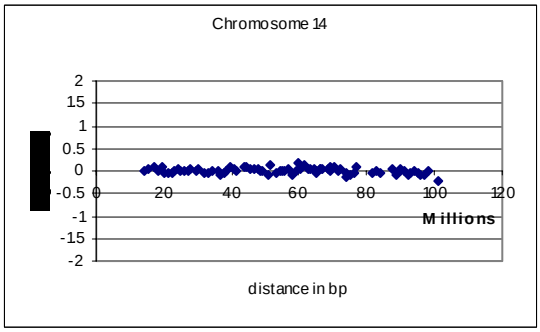

Chromosome 9
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp


Chromosome 10
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 11
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome 12
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
Millions
distance in bp


Chromosome 13
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 14
2
1.5
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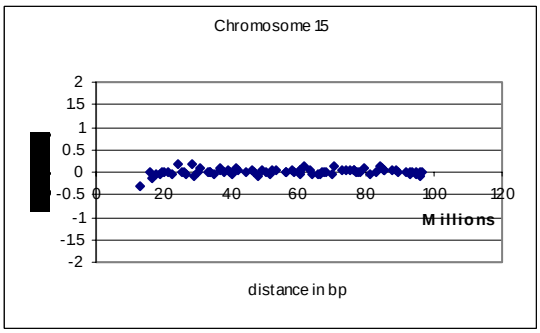
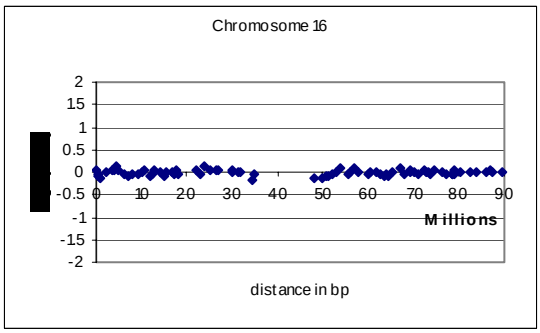
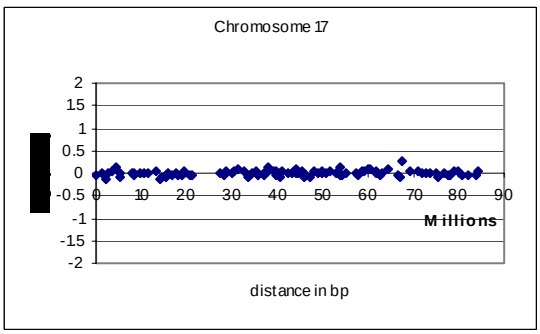
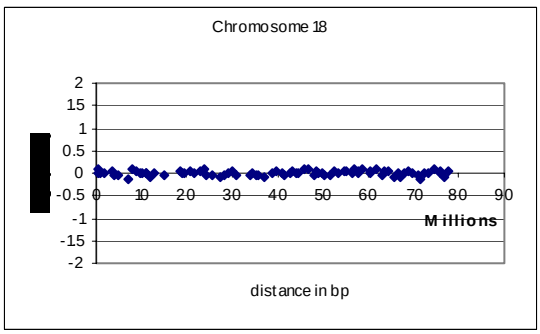
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 15
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
Millions
distance in bp


Chromosome 16
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 17
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 18
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0.5
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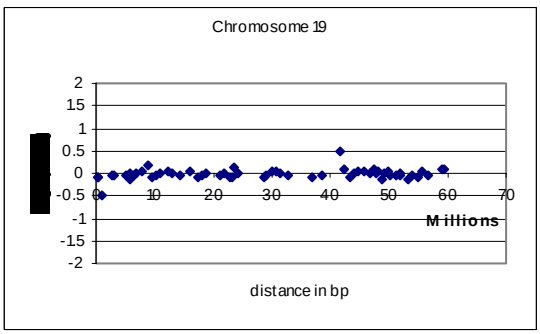
-1.5
-2
0
10
20
30
40
50
60
70
80
90
Millions
distance in bp


Chromosome 19
2
1.5
1
0.5
0
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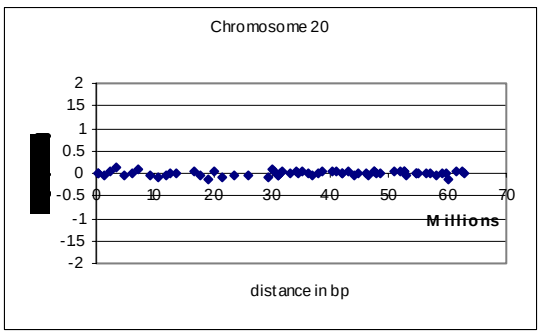
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 20
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1.5
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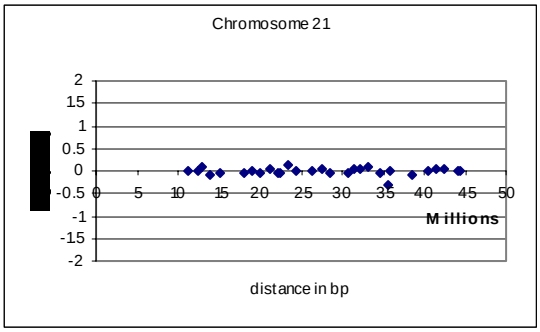
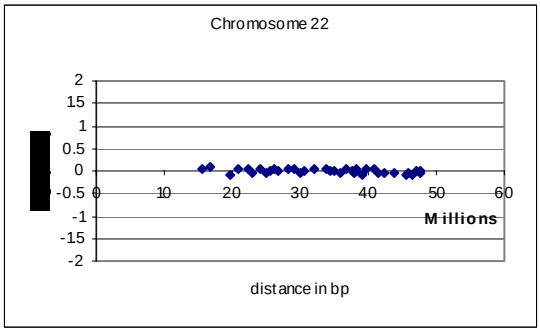
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
70
Millions
distance in bp


Chromosome 21
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
5
10
15
20
25
30
35
40
45
50
Millions
distance in bp


Chromosome 22
2
1.5
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0.5
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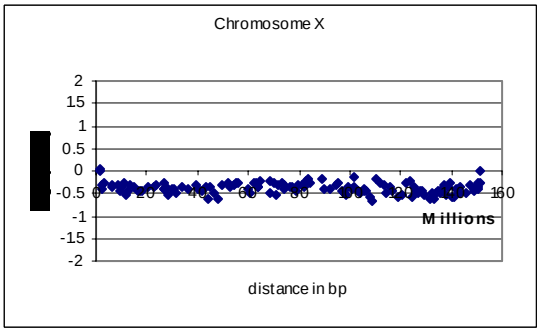
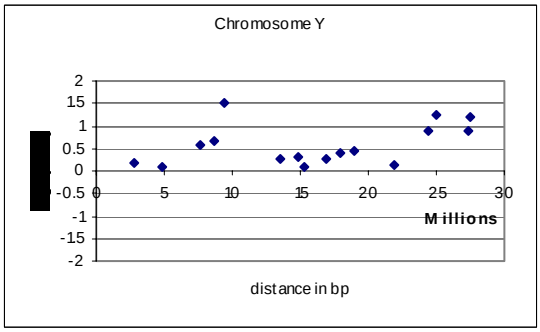
-0.5
-1
-1.5
-2
0
10
20
30
40
50
60
Millions
distance in bp


Chromosome X
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
20
40
60
80
100
120
140
160
Millions
distance in bp


Chromosome Y
2
1.5
1
0.5
0
-0.5
-1
-1.5
-2
0
5
10
15
20
25
30
Millions
distance in bp

Appendix 11: Clones known to report an incorrect copy number change on the 1Mb resolution array

Autosomes reporting an unexpected linear ratio

Clone	Chr	Position (bp)
bA326G21	1	143533568
bA5K23	1	159201779.5
dJ1108M17	1	104815713
dJ97P20	1	167462445
bA32C20	2	128082133
bA400O18	2	184873490
963K6	4	191632378
bA94E2	5	18186914.5
dJ159G19	6	80412976
dJ93N13	6	32596730.5
bA17M8	8	136548513.5
bA350F16	8	46413667
bB445N5	10	38414815
bA13E1	10	48233085
221K18	12	131110572
bA25J23	13	78143302
bA279F15	13	55656472
820M16	14	104124908
bA2F9	15	18507931
bA161M6	16	1085464
dJ843B9	17	43741286
bA220N20	17	44390565.5
bA416K7	17	45289524.5
bA294I20	19	86263
bA50L23	22	19845427.5

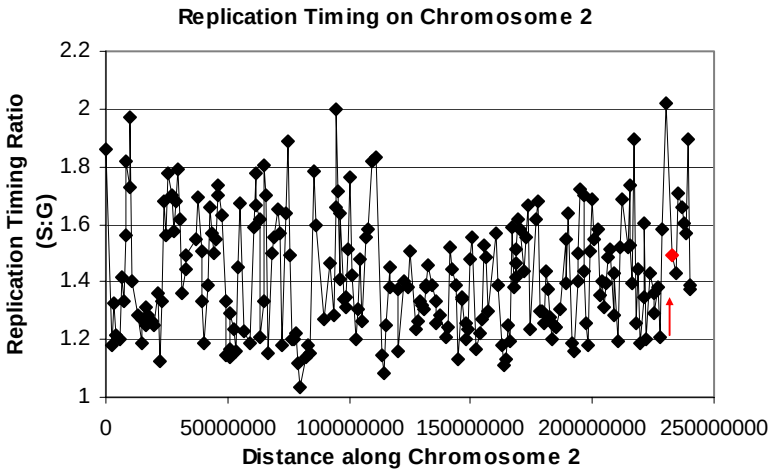
X Clones reporting an unexpected linear ratio

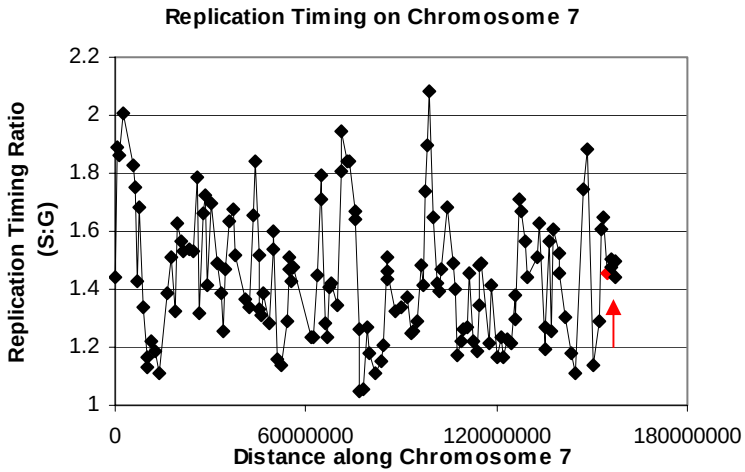
Clone	Chr	Position (bp)
98C4	X	490000
bA155F12	X	1834539.5
bA457M7	X	2000055.5
bA418N20	X	2326367.5
bA483M24	X	5959670
bA323F16	X	6434519
bA431J24	X	15946832
bA2J15	X	16774468
bA268G12	X	25943688.5
bA163L4	X	39575156.5
bA56H2	X	49574586.5

bB188A5	X	53052560
bA445O16	X	53863026
dJ966K21	X	54681885
dJ323B6	X	60874153.5
bB130F17	X	61742036.5
dJ583H20	X	66927306.5
bB260P4	X	68630583
bA236O12	X	70675479
dJ411B6	X	71885166.5
dJ875J14	X	72373814
dJ93L7	X	80445116.5
dJ225D2	X	80937973.5
bB166C10	X	85629051
bA122L9	X	86374786.5
bA156J23	X	87618715.5
dJ421I20	X	98011402
dJ312P4	X	100360142.5
dJ290B4	X	108330281
dJ93I3	X	109797538
bA434C1	X	111084399
dJ428A13	X	121210464
bA218L14	X	148668646
225F6	X	149149818

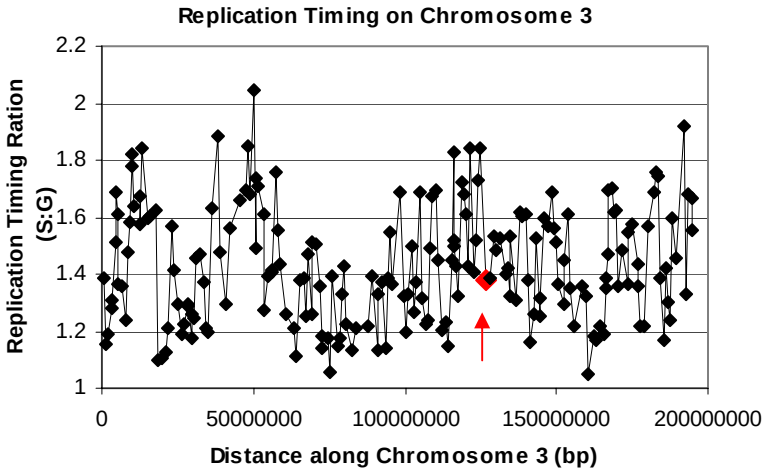
Appendix 12: Position of Chromosomal Breakpoints on the Replication Timing Profiles Location of breakpoints are indicated by red clones and red arrows.

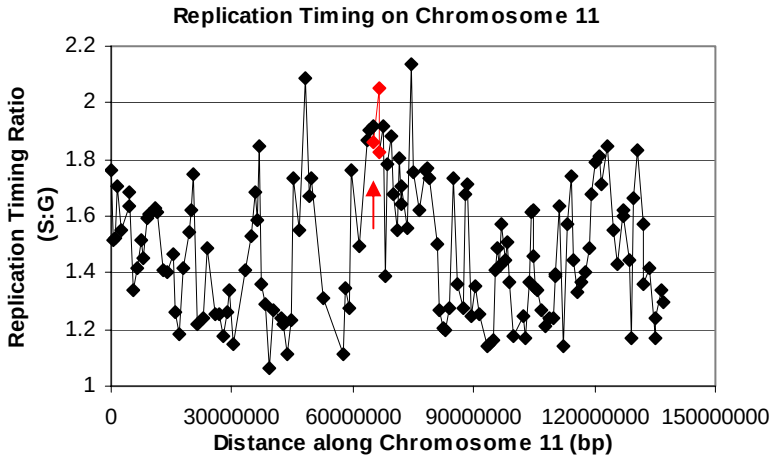
t(2:7)a



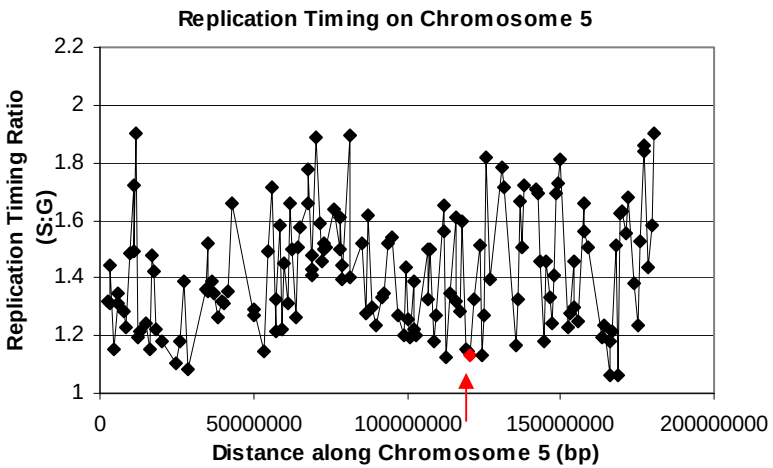


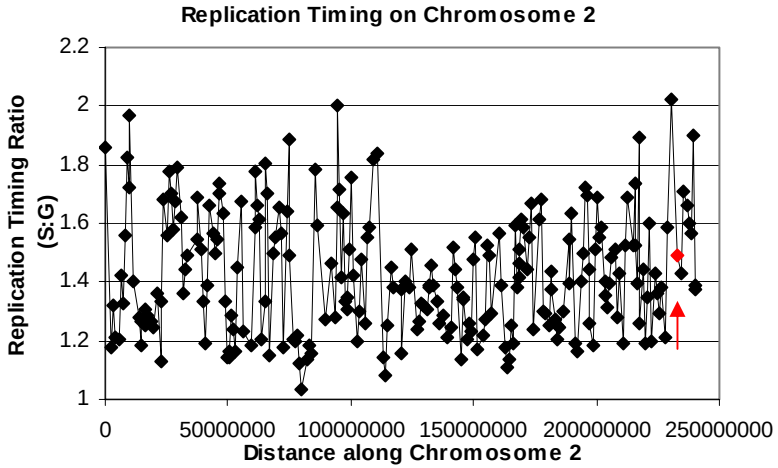
(3:11)



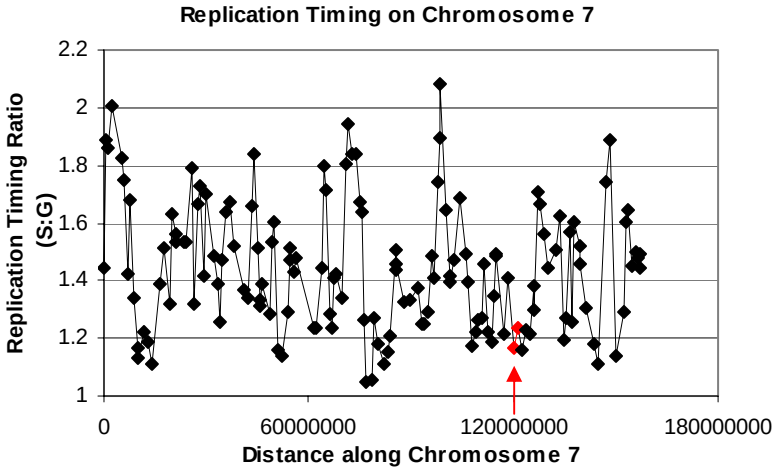


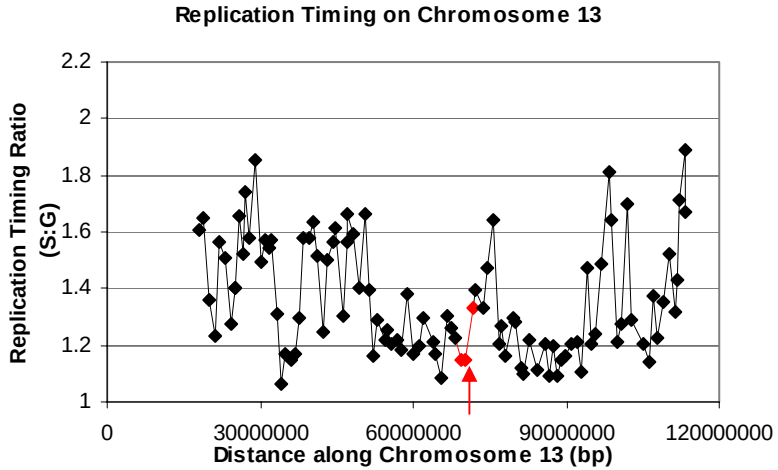
t(2:5)


Replication Timing on Chromosome 5
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
50000000
100000000
150000000
200000000
Distance along Chromosome 5 (bp)

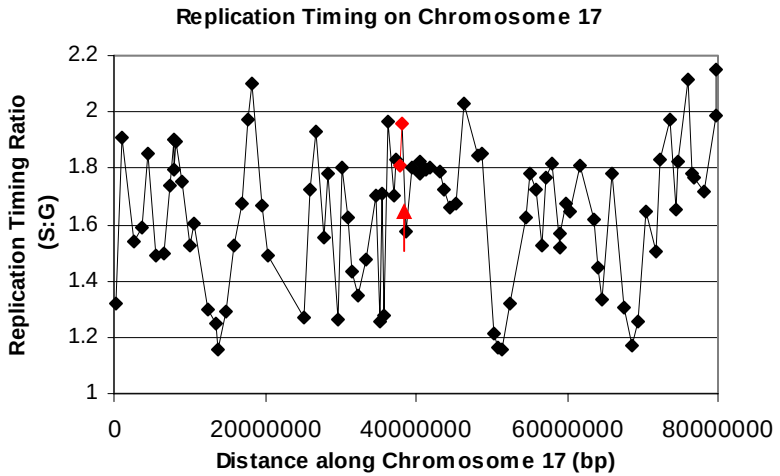

Replication Timing on Chromosome 2
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
50000000
100000000
150000000
200000000
250000000
Distance along Chromosome 2

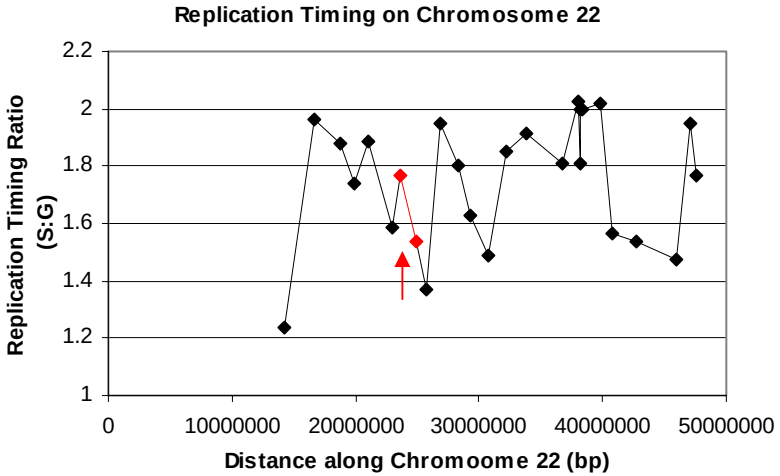
t(7:13)


Replication Timing on Chromosome 7
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
60000000
120000000
180000000
Distance along Chromosome 7

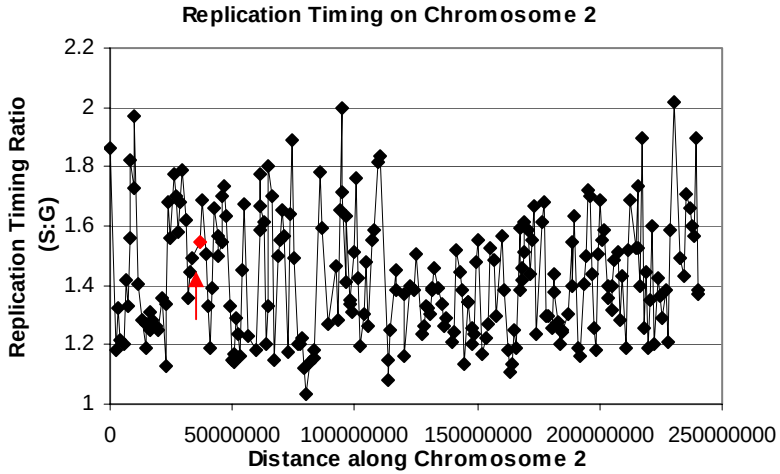

Replication Timing on Chromosome 13
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
30000000
60000000
90000000
120000000
Distance along Chromosome 13 (bp)

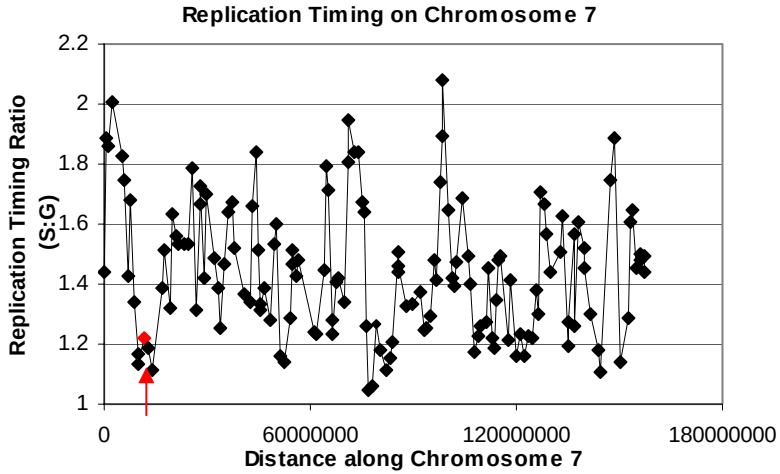
t(17:22)


Replication Timing on Chromosome 17
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
20000000
40000000
60000000
80000000
Distance along Chromosome 17 (bp)

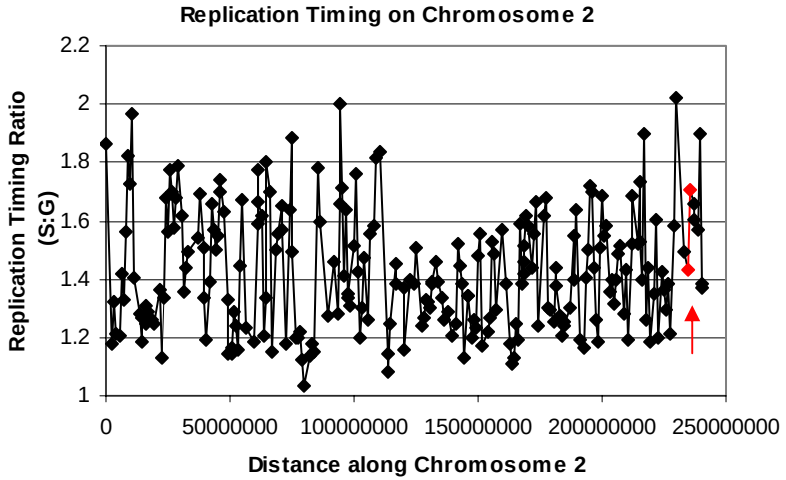

Replication Timing on Chromosome 22
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
10000000
20000000
30000000
40000000
50000000
Distance along Chromoome 22 (bp)

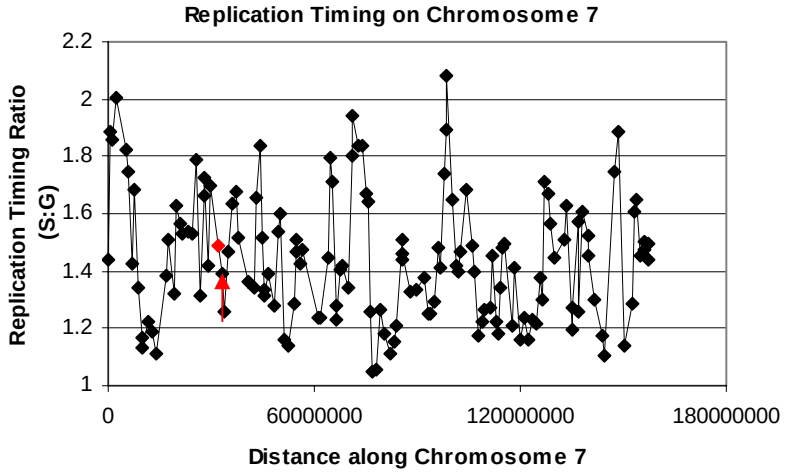
t(2:7)b


Replication Timing on Chromosome 2
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
50000000
100000000
150000000
200000000
250000000
Distance along Chromosome 2

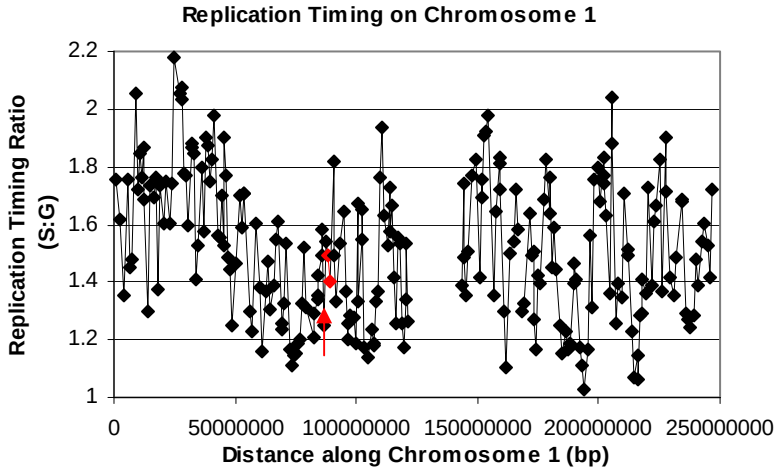

Replication Timing on Chromosome 7
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
60000000
120000000
180000000
Distance along Chromosome 7

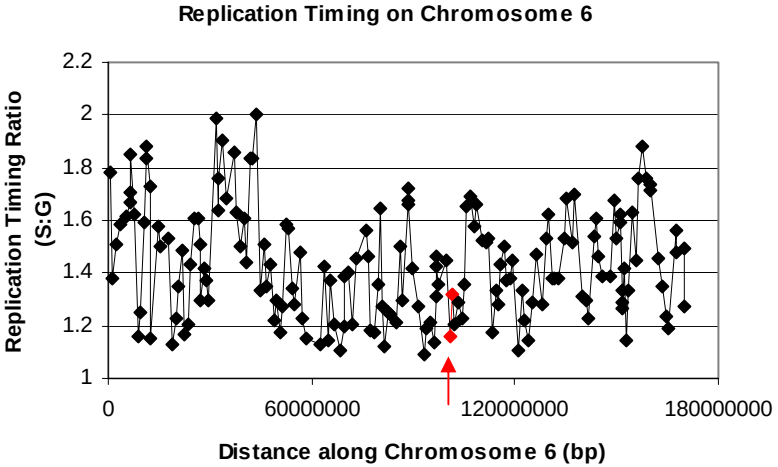
t(2:7)c


Replication Timing on Chromosome 2
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
50000000
100000000
150000000
200000000
250000000
Distance along Chromosome 2


Replication Timing on Chromosome 7
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
60000000
120000000
180000000
Distance along Chromosome 7

t(1:6)


Replication Timing on Chromosome 1
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
50000000
100000000
150000000
200000000
250000000
Distance along Chromosome 1 (bp)


Replication Timing on Chromosome 6
Replication Timing Ratio (S:G)
2.2
2
1.8
1.6
1.4
1.2
1
0
60000000
120000000
180000000
Distance along Chromosome 6 (bp)

Appendix 13: The significance of a correlation co-efficient.

Value of Coefficient (r)	**Meaning**
0.00-0.19	A very weak correlation
0.20-0.39	A weak correlation
0.40-0.69	A modest correlation
0.70-0.89	A strong correlation
0.90-1.00	A very strong correlation

Table from ‘Practical Statistics for Field Biologists’ (Fowler 1998).

Appendix 14: Publications arising from this work.

‘The Replication timing of the human genome.’ Woodfine et al. Human Molecular Genetics