Application of DNA Microarrays to Assess DNA Replication Timing and Chromosomal Aberrations.

Kathryn Woodfine Darwin College

This dissertation is submitted for the Degree of Doctor of Philosophy

This dissertation is the result of my own work and includes nothing which is the outcome of work done in collaboration, except where specifically indicated in the text.

This Dissertation does not exceed the word limit set by the Biology Degree Committee.

Kathryn Woodfine.

Abstract

I have developed a directly quantitative method to assess the replication timing of sequences during the S phase of the cell cycle utilizing genomic clone DNA microarrays. This is achieved by the co-hybridisation of differentially labelled S and G1 phase DNA to the arrays. The genomic resolution of the replication timing measurements is limited only by the genomic clone size and density on the arrays.

I have demonstrated the power of this approach by constructing a genome wide map of replication timing in human lymphoblastoid cells using an array with clones spaced at 1 Mb intervals. I also constructed an array using chromosome 22 tile path clones and produced a high resolution replication timing map of 22q. Tile path resolution replication timing maps have also been produced for chromosomes 1 and 6.

I have shown a positive correlation, both genome wide and at a tiling path resolution, between replication timing and a range of genome parameters including GC content, gene density and transcriptional activity.

I have further developed the replication timing assay by using an array of PCR products spanning 4.5Mb at a resolution of 10kb, and an array spanning 20Kb using overlapping 500bp PCR products. This will allow the study of correlations with sequence features at a high resolution.

Using the Chromosome 22 tile path array I have also been able to show changes in replication timing in a cell line which contains a balanced translocation between chromosomes 17 and 22. I have also used the chromosome 22 tile path array to analyse deletions in DiGeorge patients and to detect VJ recombination at the immunoglobulin light chain λ lymphoblastoid cell lines.

Acknowledgments

I would like to thank all the people, who without which the work in this thesis would not be possible.

Firstly, all the external collaborators;

Silvana Debanardi and Bryan Young from the Molecular Oncology Unit, St Bartholomew's Hospital, Katrina Prescott from the Institute of Child Health, Richard Mott from the Wellcome Centre for Human Genetics and Charles Shaw-Smith from Addenbrookes Hospital.

The Human Genetics Department at The Wellcome Trust Sanger Institute. Especially; Carol Carder, Paul Hunt, Sean Humphray, Lisa French, Carol Scott, Rob Andrew, Pawendeep Dharmi, Cordelia Langford, Oliver Dovey and David Vetrie.

The Molecular Cytogenetics group (past and present) at the Sanger Institute, paticularly;

Heike Fiegler, Philippa Carr and Eleanor Douglas for the construction of the 1 Mb resolution genomic array, Shelia Clegg for teaching me FISH and Elena Prigmore for discussion and support.

The Molecular Genetics and Proteomics group at the Sanger Institute, especially; David Beare, for his immense help with sequence analysis of chromosome 22, John Collins for advice on analysis of low copy repeats and Owen McCann for help in the assembly of the chromosome 22 clone set

I would like to thank all the people who have given me a personal input into this thesis. In particular I would like to thank;

Gary Woodfine for his support, Andy Mungall, Lisa Rickman, and Deb Burford for proof reading and their suggestions and Susan Gribble for all her help, too great to mention.

Finally I would like to thank my two supervisors, Nigel Carter and Ian Dunham for all their help, support and patience.

Table of Contents

1: Introduction	1
1.1: Chromatin Conformation	1
1.1.1: Chromatin Condensation	1
1.1.2: The Nucleosome and Epigenetic regulation.	4
1.2: DNA Replication, the Eukaryotic Cell Cycle and Replication Origins	7
1.2.1: The Eukaryotic Cell Cycle	7
1.2.2: DNA replication during the S phase of the cell cycle	8
1.2.3: Cell cycle regulation and control checkpoints	11
1.3: Conventional ways of assessing Replication Timing	14
1.3.1: Assessment of replication timing by pulse labelling with Bromodeoxyuridine	14
1.3.2: Assessment of replication timing by fluorescence in situ hybridisation	16
1.3.3: Replication Timing by flow sorting and PCR	
1.4: Temporal control of Replication Origin Activation	20
1.4.1: DNA Replication Timing and Correlation with Sequence Features.	
1.4.2: DNA Replication Timing and Correlation with Chromatin and Epigenetic Features.	24
1.4.3: DNA Replication Timing and correlation with Nuclear Position	25
1.4.4: Asynchronous DNA Replication.	29
1.5: DNA Replication Timing and Correlation with Transcription	31
1.6: Using Genomic Arrays to investigate Copy Number Changes	37
1.6.1: Using Genomic Arrays to investigate Chromosomal Copy Number Changes	
1.6.2: Using Genomic Arrays to assess Replication Timing	
1.7 Aims of this Thesis	43
2: Materials & Methods	45
2.1 Construction of the 22 tile path array	45
2.1.1: Clone Selection and verification.	45
2.1.2: Construction of the array from the Chromosome 22 clone set	51
2.2: Construction of a High Resolution Arrays from PCR products	53
2.2.1 Primer design	53
2.2.2. PCR amplification of 500bp products	54
2.2.3 Preparation of products for spotting onto the array	54
2.2.4 Spotting of arrays.	55

2.3: Acquisition of DNA for application to the array	55
2.3.1: Extracting DNA from lymphoblastoid cell lines	55
2.3.2: Extracting DNA from sorted S phase and G phase nuclei	
2.3.3: Extraction of DNA from sorted Chromosomes	61
2.3.4: Male and Female control Pools	61
2.3.5: Obtaining DNA for Microdeletion studies	
2.4: Labelling of DNA and application to the array	63
The stages involved in the flow sorting, DNA labelling and hybridisation to the array	y is shown in
Figure 2.4	
2.4.1: Labelling of DNA	
2.4.2: Precipitation of Pre-hybridisaion and hybridisation DNA	64
2.4.3: Application of the DNA to the array	65
2.4.4: Washing the array.	66
2.5: Scanning and analysis of the array	66
2.5.1: Scanning of the slides	66
2.5.2: Analysis of the slide	67
2.6: Transcription analysis of a lymphoblastoid cell line	
2.6.1: Extraction of RNA from lymphoblastoid cell line	72
2.6.2: Synthesis of cDNA	73
2.6.3: Production and labelling of cRNA and application to the array	74
2.6.4: Washing and analysis of array.	74
2.7: FISH analysis of DiGeorge and VDJ recombination regions	75
2.7.1: Mini Prep of Bacterial clone DNA	76
2.7.2: Nick Translation	77
2.7.3: Metaphase spread preparation	77
2.7.4: Hybridisation to Metaphase spreads	
2.7.5: Detection of labelled probes	79
2.7.6: Acquisition of FISH images	79
2.8: Real-Time PCR analysis of S and G phase DNA.	80
2.8.1: Primer design	
2.8.2: Real Time PCR on S and G1 phase DNA	

3: Results 1: Pilot Replication Timing Studies Utilising a Genomic Array	
Representing 4.5Mb of Chromosome 22 Sequence	
3.1: Introduction	
3.2: Initial verification experiments on the 4.5Mb array	
3.3: S phase DNA: G1 phase DNA Hybridisation on the 4.5Mb Test Array.	
3.4: Correlation between replication timing and sequence features	
3.5: Discussion	
4: Results 2: Preparation and Verification of the Genomic Microarrays	
4.1: Introduction	
4.2: Optimisation of S phase fractions	
4.3: Preparation and initial verification of the 22q tile path array	
4.3.1: Amplification of chromosome 22 tile path clones	90
4.3.2: Male:male hybridisation onto the chromosome 22 tile path array	93
4.3.3: Male:female hybridisation onto the array.	93
4.3.4: G1 self:self phase DNA Hybridisation onto the 22q tile path array	95
4.4: Control Hybridisations on the 1Mb array	
4.4.1: Male:male hybridisation on the 1Mb array	96
4.4.2: Male:female hybridisation on the 1Mb array	97
4.5: Production of a high resolution array from PCR products.	
4.6: Detection of chromosome 22 copy number changes on clone arrays	
4.6.1: Detection of chromosome 22 copy number change on the 1 Mb tile path array.	99
4.6.2: Detection of chromosome copy number changes on the 22 tile path array	101
4.7: Discussion	
4.7.1: Control hybridisations performed on the clone arrays	103
4.7.2: Verification of the 1 Mb resolution and chromosome 22 Tile path arrays	104
4.7.3: Control hybridisations on the 500bp PCR product array	108
4.7.4: Summary	110

5. Results 3: Using Genomic Microarrays to assess Replication Timing in a H	Iuman
Cell line and correlation with sequence features	111
5.1: Introduction	111
5.2: Assessment of Replication Timing on the 1Mb array	112
5.2.1: Obtaining the Average Replication Timing of Individual Chromosomes	112
5.2.2: Correlating Chromosomal Replication Timing with Sequence Features of the Gene	ome. 114
5.2.3: Assessing Replication Timing at a 1 Mb resolution.	116
5.3: Assessment of Replication Timing at Tile path Resolution	118
5.3.1: The Replication Timing of Chromosome 22.	118
5.3.2: The Replication Timing of Chromosome 6.	123
5.3.3: The Replication Timing of Chromosome 1	126
5.3.4 Comparison of Replication timing between two different lymphoblastoid cell lines.	129
5.4: Assessment of Replication Timing at High Resolution Using an Array	
constructed with 500bp PCR Products	130
5.4.1: PCR Product array at 10Kb resolution	130
5.4.2: PCR product array utilising overlapping 500bp products.	133
5.5: Correlation of assessment of Replication Timing by arrays with Replicatio	n
Timing assessed by Quantitative PCR.	136
5.5.1 Correlation with published quantitative PCR data on Chromosome 11q	136
5.5.2: Verification of replication timing by arrays by analysis by Quantitative PCR	139
5.6: Replication time in flow sorted S phase fractions	140
5.7: Discussion	143
5.7.1: Correlation between Replication Timing and Sequence Features	144
5.7.2: Correlation between Replication Timing and chromosomal bands.	149
5.7.3: Rate of Replication	154
5.7.4: Comparison with other arrays assessing replication timing and limitations of the m	ethod.
	155
5.7.5: Verification of replication timing method	160
5.7.6: Assessment of replication timing using flow sorted S phase fractions	161
5.7.7: Assessment of Replication Timing using High Resolution Arrays	162
5.7.8: Summary:	165

6.1 Introduction	••••••
6.2: Correlation between Replication Timing and Transcriptional Acti	vity
6.2.1 Correlation with Expression level on the 1 Mb Chip	
6.2.2 Correlation with Expression level on the Tile path arrays.	
6.2.3: Correlation between Replication Timing and the Probability of Expression	on
6.3. Correlation between Histone Acetylation, Replication Timing and	Sequence
Features on the Chromosome 22 Tile Path Array.	••••••
6.4: Study of the Replication Timing of Chromosomal Breakpoints using	ng the Geno
Arrays	•••••
6.4.1: Assessment of the replication timing of a t(17q21.1:22q12.2) translocation	on on the
chromosome 22 array	
6.4.2 Assessment of the replication timing of constitutional breakpoints using the	he 1Mb array.
6.5.: Discussion	••••••
6.5.1: Correlation between replication timing and gene expression	
6.5.2: Assessment of Histone modifications using the tile path array	
6.5.3: The Change of Replication Timing in a Translocated Cell Line	
6.5.4: Replication Time of Constitutional Breakpoints in a Normal Cell Line	
6.5.5: Summary	
Results 5: Assessment of Chromosomal Aberrations Using Genome	ic Arrays
7.1: Introduction	
7.1.1: Microdeletion Syndromes	
7.1.2: Immunoglobulin Rearrangements	
7.1.3: Assessment of DiGeorge and IgL λ copy number change on genomic array	ays
7.2: Array analysis of DiGeorge syndrome patients	
7.2.1: Assessment of DiGeorge Patient DNA samples on the Chromosome 22q	Tile path arra
7.2.2: Assessment of patients with the DiGeorge phenotype that do not show a	deletion in 22
FISH analysis.	

7.4: Discussion	
7.4.1: Segmental Duplications and the DiGeorge region	
7.4.2: Analysis of Patients showing the DiGeorge phenotype with no 22q11 deletion.	233
7.4.3: Analysis of the Immunoglobulin light chain λ recombination region	233
7.4.4. Summary	
8: Conclusions	
8.1: Construction and Validation of the Chromosome 22 arrays.	
8.2: The use of Genomic Microarrays to assess Replication Timing	
8.3: Large scale analysis of the correlation between replication timing and o	other
features of the genome	
8.4: Future Work	
8.4.1: Optimisation of the high resolution PCR product array	241
8.4.2: The assay of replication timing within other tissues and cell lines	241
8.4.3. Investigation of gene expression at regions which undergo changes in replication	on timing.
8.4.4. Investigation of other epigenetic features on the arrays	243
8.5: Conclusions	
References	
Appendices	
Appendix 1: Reagents and buffers used	
Appendix 2: PCR primers for the High Resolution Array	
2a: Primer sequence for PCR products in the high resolution array	259
2b: The 96 well format of primers STSG 495474-495569	
Appendix 3: Primers for quantitative PCR	
Appendix 4: Male:male hybridisation on 1Mb array	
Appendix 5: Male:female hybridisation on 1Mb array	
Appendix 6: Replication timing profiles for all 24 chromosomes	
Appendix 7: Perl program to identify regions of co-ordinated replication	
Appendix 8: Replication timing and Expression level profiles for all 24 chro	mosomes.

Appendix 9: Chromosome 22 sequencing-clone information 291
9a: International Names for chromosome 22 clones
9b: Clone Libraries
Appendix 10: 1Mb profiles of patients with DiGeorge phenotype and no 22q11
deletion
Appendix 11: Clones known to report an incorrect copy number change on the 1Mb
resolution array
Appendix 12: Position of Chromosomal Breakpoints on the Replication Timing
Profiles Location of breakpoints are indicated by red clones and red arrows
Appendix 13: The significance of a correlation co-efficient
Appendix 14: Publications arising from this work

List of Figures:

Fig 1.1: Levels of DNA condensation within a eukaryotic chromosome (Strachan 2001)	2
Fig 1.2: Composition of a nucleosome, the fundamental unit of chromatin adapted from	
Grewal et al, 2003. (Grewal and Moazed 2003)	4
Fig 1.3: Modification at the lysine (K) residues in the H3 and H4 tails reproduced from	
Grewal et al 2003 (Grewal and Moazed 2003)	5
Fig 1.4: The Cell cycle	7
Fig 1.5: The DNA replication fork	8
Fig 1.6: DNA replication from origins of replication	9
Fig 1.7: Formation of a Pre-RC complex to license DNA for replication reproduced from	
Nishitani et al (Nishitani and Lygerou 2002).	12
Fig 1.8: Figure from Goren and Cedar 2003. Pulse labelling of a cycling cell line with BrdU.	15
Fig 1.9: Possible DNA replication patterns displayed by the fluorescence hybridisation assay.	17
Fig 1.10: (Adapted from Azura et al, 2003) A: Cell cycle profile showing gate positions	
required to sort the nuclei into four separate S phase fractions. B. Gel photograph illustrating	
the enrichment in the S1 fraction for an early replicating locus. C. Gel photograph illustrating	
the enrichment in the S4/G2 fraction for an early replicating locus.	18
Fig 1.11: Replication timing profile of chromosome 11q using quantitative PCR. Adapted	
from Fig 3, (Watanabe, Fujiyama et al. 2002).	19
Fig 1.12: Change in Replication Timing (a) and GC content (b) across a 450Kb region of the	
MHC Class II and Class III taken from (Tenzen, Yamagata et al. 1997).	21
Fig 1.13: The correlation between GC content and replication timing profile on	
Chromosome 11q (A) and Chromosome 21q (B) (Watanabe, Fujiyama et al. 2002).	22
Fig 1.14: Different stages of replication in the interphase nucleus. Figure taken from	
(Ferreira, Paolella et al. 1997).	26
Fig 1.15: localisation of early replicating DNA (blue) and late replicating DNA (red) in	
an interphase nuclei (Schermelleh, Solovei et al. 2001).	27
Fig 1.16: Mid-late replicating chromosome domains (red) associate with lamin B (green).	
Early replicating DNA (blue) does not (Schermelleh, Solovei et al. 2001).	27
Fig 1.17: Co-localisation of DNA that is replicated in early S phase and transcriptional activity.	
For details see text (taken from (Cook 1999)).	32
Fig 1.18: Models for linking transcription and replication.	34
Fig 1.19: The initiation of replication from transcription factories.	36
Fig 1.20: From (Raghuraman, Winzeler et al. 2001) illustrating how replication timing was	
assessed in Saccharomyces cerevisiae	40
Fig 1.21: Reproduced from Schubeler et al 2002, illustrating how the replication timing of	
Drosophila melanogaster was assessed using microarray technology.	41
Fig 1.22: Replication profile of <i>Drosophilia</i> chromosome arm 2L.	42

Fig 2.1: Flow diagram illustrating the construction of the tile-path array	46
Fig 2.2: Flow sorter profiles and gate positions of sorted cell lines.	60
Fig 2.3: Purified S and G1 phase DNA.	61
Fig 2.4: Flow diagram illustrating how DNA was applied to the constructed array.	63
Fig 2.5: Labelled S and G1 phase DNA	64
Fig 2.6: The 22q Tile path array.	67
Fig 3.1: G1 self:self Hybridisation performed on a 4.5Mb array.	83
Fig 3.2: Replication Timing profiles for a 4.5 Mb region of Chromosome 22q.	84
Fig 3.3: Correlation between replication timing and GC content over a 4.5 Mb region.	85
Fig 3.4: Correlation between replication timing and Intragenic DNA over a 4.5 Mb region	86
Fig 4.1: The change in the proportion of the cells in S phase at times after subculture for a	
lymphoblastoid cell line.	89
Fig 4.2: Lymphoblastoid nuclei flow sort profile after harvest 26 hours from subculture.	90
Fig 4.3: DOP-PCR amplification of a selection of chromosome 22 tile path clones, as indicated	
in the key.	91
Fig 4.4: Amino-linking PCR amplification of a selection of Chromosome 22 tile path clones as	
indicated in the key.	92
Fig 4.5: Male self:self hybridisation on the chromosome 22q array	93
Fig 4.6: Male:female hybridisation on the constructed 22q array.	94
Fig 4.7: G1:G1 Hybridisation on the 22q array.	96
Fig 4.8: PCR products obtained from the amplification of primers STSG 495474 –	
STSG 495569 in a 96 well format	97
Fig 4.9: A G1:G1 hybridisation on the high resolution PCR product array.	98
Fig 4.10: A male:female hybridisation on the high resolution PCR product array.	99
Fig 4.11: A genomic DNA + Chr 22 : genomic DNA hybridisation on the 1 Mb array.	100
Fig 4.12: Response of the chromosome 22 clones to a chromosome 22 add-in experiment.	100
Fig 4.13: Hybridisation ratios reported by chromosome 11 clones after a genomic	
DNA + 22: genomic DNA hybridisation.	101
Fig 4.14: Ratios reported when different amounts of chromosome 22 are added into the	
hybridisation mix.	102
Fig 4.15: Correlation between GC content of PCR product and the ratio reported by a self:self	
hybridisation.	110
Fig 5.1: The average replication times of all 24 chromosomes	113
Fig 5.2: Correlation between replication timing and sequence features of the genome.	115
Fig 5.3: Replication timing profiles of; A: chromosomes 6 and B: chromosome 12	116
Fig 5.4: Correlation between replication timing and sequence features of the genome.	117

Fig 5.5: Replication timing profile of chromosome 22.	119
Fig 5.6: Correlation between replication timing and other genome features on the 22TP array.	120
Fig 5.7: Replication timing profile of chromosome 22 with other genome features.	122
Fig 5.8: The Replication Timing profile of chromosome 6.	124
Fig 5.9: Correlation between replication timing and other genome features on the chromosome	
6 tile path array.	125
Fig 5.10: The replication timing profile of chromosome 1. The ratios reported are the average	
of two arrays.	127
Fig 5.11: Correlation between replication timing and other genome features on the chromosome	
1 tile-path array.	128
Fig 5.12: Replication time profiles of two different lymphoblastoid cell lines.	129
Fig 5.13: Replication timing profile of the region 15.4-20Kb along 22q at a 10Kb resolution.	131
Fig 5.14: Replication Timing Profile of a region of 22q represented on the array by overlapping	
500bp PCR products.	134
Fig 5.15: Comparison of the replication timing profile obtained on the 22 TP array, 10Kb	
resolution PCR product array and a 500bp resolution array.	135
Fig 5.16: Comparison of Replication Timing on 11q.	137
Fig 5.17: Correlation between quantitative PCR data and array data of loci within 100Kb	
of each other.	138
Fig 5.18: Replication timing data of the MHC region collected from the chromosome 6 tile	
path array.	139
Fig 5.19: Comparison of S:G1 as determined by the replication timing arrays and by	
quantitative PCR	140
Fig 5.20: Ratio obtained for each S phase fraction when hybridised against G1.	141
Fig 5.21: Ratio obtained for each S phase fraction when hybridised against G1 for clones	
across a transition region.	142
Fig 5.22: Ratio obtained on loci representing chromosome X for each S phase fraction when	
hybridised against G1.	143
Fig 5.23: Replication timing of chromosomes 13 and 14. Gene deserts are marked.	145
Fig 5.24: Comparison between replication timing ratio and high resolution giemsa banding of	
chromosomes.	150
Fig 5.25: Statistical analysis to identify regions of the genome with similar replication timing.	153
Fig 5.26: The rate of replication during the S phase of the cell cycle.	155
Fig 5.27: A: Comparison between drosophilia flow sort profile from (Schubeler, Scalzo	
et al. 2002) and the human lymphoblastoid flow sort profile obtained from sorting HRC575.	
B: Purity of the flow sort showing the G1 and S phase fractions.	157
Fig 5.28: Comparison of the flow sort profiles of a lymphoblastoid cell line and a fibroblastoid	
cell line.	159
Fig 5.30: Correction against ratios reported for a self:self hybridisation on the high resolution	
array.	163

Fig 6.1: RNA prepared from a lymphoblastoid cell line.	168
Fig 6.2: The correlation between replication timing ratio and log ₁₀ expression level of clones	
on the 1Mb array.	169
Fig 6.3: Replication timing and expression level profiles on Chromosome 2.	170
Fig 6.4: Replication timing ratio plotted against expression level.	171
Fig 6.5: Replication timing ratio and Expression level (Log ¹⁰ -red) plotted against chromosome	
position.	173
Fig 6.6: Correlation between replication timing and probability of expression for windows of	
50 clones.	174
Fig 6.7: Correlation between replication and probability of transcription at a tile-path resolution.	174
Fig 6.8: The ratio of Chromatin immunoprecipitated DNA : Input DNA plotted against position	
on chromosome 22.	177
Fig 6.9: Relationship between H3 enriched DNA and H4 enriched DNA. Linear regression was	
performed.	178
Fig 6.10: The ratio of immunoprecipitated DNA: Input DNA plotted with replication timing ratio,	
against position on chromosome 22.	178
Fig 6.11: Correlation between replication timing and histone acetylation.	180
Fig 6.12: Replication timing profile of the 22 clones on the translocated cell line	182
Fig 6.13: A: Comparison of the replication timing profile from a normal lymphoblastoid cell line	
and a lymphoblastoid cell line with a translocation between chromosomes 17 and 22.	183
Figure 6.14: The correlation between the replication timing of the first and second breakpoint	186
on a congenital translocation.	
Fig 6.15: Ensembl view of a region of chromosome 2 (75-86Mb) to illustrate the position of the	
1Mb clones in relation to genes in this region.	187
Fig 6.16: Ensembl pages illustrating those regions that are late replicating and under represented	
on the Affymetrix array are gene poor.	188
Fig 7.1: Mechanisms for segmental duplications	199
Fig 7.2: Segmental duplications on the sequenced q arm of chromosome 22.	200
Fig 7.3: Patterns of deletion in DiGeorge patients.	201
Fig 7.4: Mechanisms for deletion in DiGeorge patients (Maynard, Haskell et al. 2002).	202
Fig 7.5: Detection of the DiGeorge deletion on patient metaphases. The commercially available	
probe set from Vysis.	202
Fig 7.6: Basic four chain structure of an immunoglobulin protein.	204
Fig 7.7: Recombination of the lambda chain of the immunoglobulin light chain.	205
Fig 7.8: Hybridisation of DNA from a DiGeorge patient onto the 22q tile-path array.	208
Fig 7.9: DNA from the same DiGeorge patient hybridised to two different arrays using two	
different control samples.	209
Fig 7.10: Patient: Control ratio profiles for five separate DiGeorge Patient DNA samples.	210

Fig 7.11: Patient: Control ratios obtained when five different patients are plotted on the same axis	. 212
Fig 7.12: FISH analysis of the region that the array indicated is not deleted on patient 5.	213

Fig 7.13: Probes hybridised to chromosomes prepared from a normal (46 XY) lymphoblastoid cell line.

cell line.	215
Fig 7.14: DiGeorge region probes hybridised to chromosomes isolated from patient 1.	217
Fig 7.15: DiGeorge Region Probes hybridised to chromosomes isolated from patient 4	218
Fig 7.16: Patient: Control ratios obtained when six different patients are plotted against	
position on chromosome 22.	220
Fig 7.17: Deletion detected in chromosome 5 of patient 4 on the 1Mb array.	222
Fig 7.18: DNA from five lymphoblastoid cell lines with a normal karyotype were hybridised	
against DNA from a pool of 20 individuals.	223
Fig 7.19: Fluorescence <i>in situ</i> hybridisation of clones from the immunoglobulin light chain λ	
locus (red) and a control probe (bK57G9 - green) to metaphases from the cell lines.	226
Fig 7.20: Segmental duplications on chromosome 22. Blue: Intrachromosomal deletions. Red:	
Interchromosomal deletions. DiGeorge region is indicated in green. Figure from	
(Bailey, Yavor et al. 2002).	229
Fig 7.21: Correlation between DiGeorge ratios reported and the slope obtained from the	
chromosome 22 add-in experiments, for the clones in the DiGeorge region.	230

List of Tables:

Table 1.1: A summary of chromatin and associated epigenetic features.	6
Table 2.1: Cell lines cultured for DNA extraction (names in brackets denote internal names)	55
Table 2.2: Concentration of DNA extracted from cell lines	57
Table 2.3: Cell lines cultured for S and G1 flow sorting (names in brackets denote internal names)	57
Table 2.4: Table to indicate where gates are positioned on cell profiles (Fig 2.2).	59
Table 2.5: Scaling factors for Microarray experiments	70
Table 2.6: Chromosome 22 add in experiments performed	71
Table 2.7: Scaling factor applied for the S phase fraction experiments	71
Table 2.8: Clones picked from the VDJ recombination region;	75
Table 2.9: Clones picked from the DiGeorge Region;	75
Table 4.1: Clones showing unexpected ratios in a male:female hybridisation	95
Table 4.2: Clone not mapped to chromosome 22 that responded to extra chromosome	
22 in the hybridisation mix	105
Table 4.3: Clones not responding with the correct copy number change when chromosome	
add-in experiments were performed on the tiling path arrays.	107
Table 5.1: The average replication times of all 24 chromosomes (Early-late)	114
Table 5.2: Linear regression performed between replication timing and genome statistics.	115
Table 5.3: Linear regression performed between replication timing and genome statistics at	
a 1 Mb resolution.	118
Table 5.4: Linear regression performed between replication timing and genome statistics	
at a 78Kb resolution on the 22 tile path array.	121
Table 5.5: Linear regression performed between replication timing and genome statistics	
at a 94Kb resolution on the chromosome 6 tile path array.	126
Table 5.6: Linear regression performed between replication timing and genome statistics	
at a 94Kb resolution on the chromosome 1 tile path array.	129
Table 5.7: Clones used for the analysis displayed in figure 5.21	141
Table 5.8: Regression coefficients for correlations between replication timing and sequence	
features of the genome.	144
Table 6.1: Regression features of Replication timing versus expression levels at tile path	
resolution.	172
Table 6.2: features of the logistic regression performed, correlating replication timing	
ratio with probability of gene transcription.	176
Table 6.3: Linear regression statistics performed when replication timing was plotted	
against Histone acetylation enrichment levels.	180

Table 6.4: Linear regression statistics performed when genome features were plotted	
against histone enrichment levels	181
Table 6.5: Replication timings of chromosomal breakpoints on a normal cell line.	185
Table 7.1: The region of 22q which exhibited a gain when the cell line HRC 575 DNA was used,	
and yet showed normal ratios when hybridised against a pool DNA control.	210
Table 7.2: Patient: Control ratios of clones in the DiGeorge region of chromosome 22.	211
Table 7.3: Clones chosen for FISH analysis, and results on the patient metaphases.	214
Table 7.4: The phenotype characteristics of patients showing some characteristics of DiGeorge	
syndrome, but with no 22q11 deletion when analysed by FISH.	220
Table 7.5: Clones showing amplification or deletion on the DiGeorge phenotype patients when	
analysed on the 1 MB array.	221
Table 7.6: The chromosome 5 clones deleted in patient 4	222
Table 7.7: Clones from the immunoglobulin light chain λ locus hybridised to metaphases from	
two different lymphoblastoid cell lines.	225
Table 7.8: Results from FISH experiments performed with clones from the VJ recombination	
region hybridised to metaphases from two different lymphoblastoid cell lines.	227
Table 7.9: Results from FISH experiments performed on metaphase chromosomes from	
patient 4.	233

List of Abbreviations:

approx.	Approximately
ATP	Adenosine Triphosphate
BAC	Bacterial artificial chromosome
bp	base pair
BrdU	Bromodeoxyuridine
cdk	cyclin dependant kinase
cDNA	Complementary DNA
CpG	Cytosine and Guanosine dinucleotide
Су	Cyanine dye
D. melanogaster	Drosophila melanogaster
dATP	2'-Deoxyadenosine 5'-triphosphate
dCTP	2'-Deoxycytosine 5'-triphosphate
dGTP	2'-Deoxyguanosine 5'-triphosphate
DMSO	Dimethyl sulphoxide
DNase	Deoxyribonuclease
dNTP	2'-Deoxynucleoside 5'-triphosphate
DOP	Degenerate Oligonucleotide Primer
dsDNA	Double stranded DNA
dTTP	2'-Deoxythymidine 5'-triphosphate
E. Coli	Escherichia coli
EDTA	Ethylenedinediaminetetraacetic acid
EST	Expressed sequence tag
Fig.	Figure
FISH	Florescence in-situ hybridisation
G	Giemsa
G1	Growth 1 phase of the cell cycle
G2	Growth 2 phase of the cell cycle
GC	Guanosine + Cytosine
Н	Histone
HCl	Hydrochloric acid
HPLC	High
IgH	Immunoglobulin heavy chain
IgL	Immunoglobulin light chain
J	Joining region (IgL)
Κ	Lysine
Kb	kilobase
LB Agar	Luria-Bertani agar
log	logarithmic
Μ	molar
Μ	Mitosis phase of the cell cycle
Mb	Megabase
MCM	Mini chromosome maintainance

μg	microgram
mg	miligram
μl	microlitre
μΜ	micromolar
mM	milimolar
mRNA	Messenger RNA
NaAc	Sodium Acetate
NaCl	Sodium Chloride
nm	namometer
ORC	Origin Recognition Complex
Ori	Origin of Replication
PAC	P1-derived artificial chromosome
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
PI	Propidium iodide
Pre-RC	Pre-Replication Complex
r.p.m	revolutions per minute
RNA	ribonucleic acid
RNase	Ribonuclease
S	Synthesis phase of the cell cycle
SDS	Sodium dodecyl sulphate
SSC	Sodium chloride/citrate solution
STS	Sequence tagged site
TDP	Timing Decision Point
TE	Tris (hydroxymethyl) aminomethane-
	Ethylenedinediaminetetraacetic acid
V	Variable region (IgL)