Figure 6.7: Correlation between replication and probability of expression at a tile path resolution. The red line shows the line of logistic regression and the equation is indicated in Table 5.3. A: Chromosome 1, B: Chromosome 6, C: Chromosome 22.

Table 6.2: features of the logistic regression performed, correlating replication timing ratio with probability of gene transcription. The equation for the regression line is $y = e^{a+bx}/(1+e^{a+bx})$.

Array	Intercept (a)	Regression co-efficient (b)	Correlation co-efficient
1Mb Genome wide	-2.13	1.31	0.62
1	-5.29	3.35	0.83
6	-8.28	5.56	0.93
22	-10.13	5.71	0.89

This analysis shows that there is a strong correlation between replication timing and the probability of expression. This correlation with the probability of expression is stronger than the correlation with level of expression. The correlation also improves when an individual chromosome is studied, opposed to the entire genome.

6.3. Correlation between Histone Acetylation, Replication Timing and Sequence Features on the Chromosome 22 Tile Path Array.

To correlate replication timing with histone acetylation, separate chromatin immunoprecipitations were performed using an antibody binding to acetylated Histone H3 and a second antibody binding to acetylated Histone H4. The immunoprecipitated DNA was labelled in one colour and the same DNA that was used as the input to the immunoprecipitation was labelled in a second colour. The DNA was co-hybridised to the chromosome 22 tile path array. The ratio of chromatin immunoprecipitated DNA: input DNA was then plotted against chromosome position (Figure 6.8).
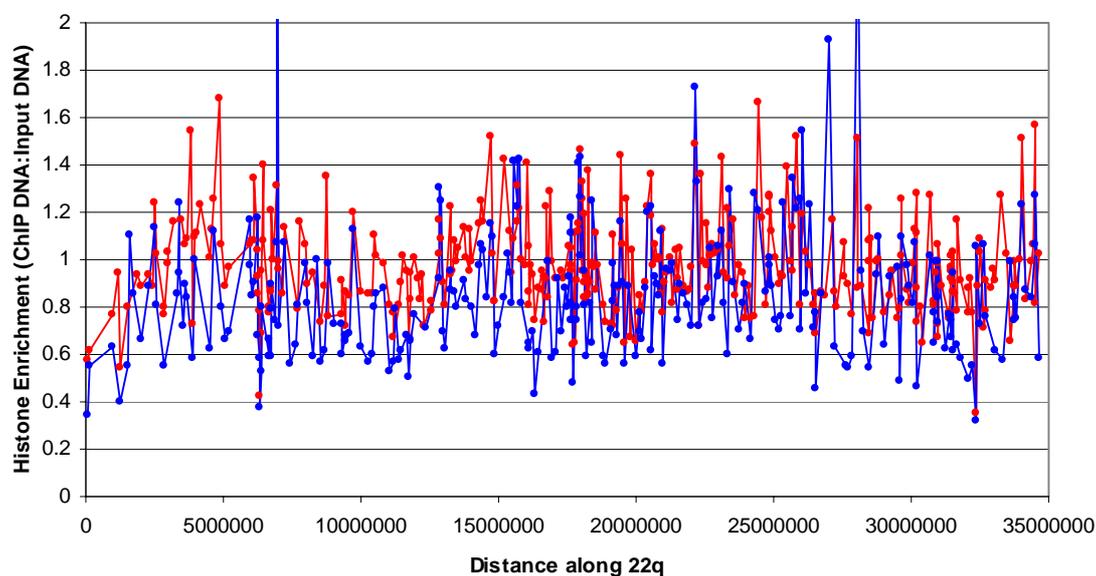

Figure 6.8: The ratio of Chromatin immunoprecipitated DNA:Input DNA plotted against position on chromosome 22. Red: H3 enrichment, Blue: H4 enrichment.

The relationship between histone H3 and histone H4 enrichment with acetylation was then plotted on Figure 6.9.