Figure 10.9. Side-by-side whole genome plots comparing expression levels in ALL1/AF4 and E2A/PBX1.

+ axes = FALSE, xlab = "", ylab = ""
> axis(2, at = (1:10), labels = levels(sidec), las = 1)

The result is shown in Figure 10.9. Genes are represented by short vertical lines which go up if the gene is on the sense strand and down if it is on the anti-sense strand. Although not all differences are obvious, some inspection reveals that there appear to be some real differences on Chromosomes 20 and 22. We will explore Chromosome 22 further using a related, but more detailed, chromosomal plotting mechanism, provided by the function plotChr.

plotChr produces one plot per chromosome. Each sample has two smooth lines. The one in the top half of the plot represents genes on the sense strand and the line in the bottom half of the plot represents expression for genes encoded on the anti-sense strand. Low expression values are near the center line, and high expression values are toward the edge of the plot.

> par(mfrow = c(1, 1))
> msobj <- Makesense(ALLs, "hgu95av2")
Chromosome 22

Figure 10.10. Plot of the expression data of individual ALL1/AF4 and E2A/PBX1 samples. Each sample is plotted as a continuous line, the $x$-values are determined by the location of the gene on the chromosome and the $y$ values are expression values. To remove some of the noise, the lines have been smoothed.

```r
> plotChr("22", msobj, col = ifelse(ALLs$mol.biol ==
+ "ALL1/AF4", "#EF8A62", "#67A9CF"), log = FALSE)
```

We can see in the plot of Chromosome 22 in Figure 10.10 that there are a few loci of interest, two on the anti-sense strand and one of the sense strand. Next we could try to extract the relevant genes and try to understand whether these differences in expression might be related to the outcome.

### 10.6.1 Cumulative Expression

The function `alongChrom` plots gene expression with the genes ordered by their chromosomal location. It can sometimes be useful to look at cumulative expression, that is, the running sum of expression values along the chromosome. The motivation for this is that on the level of individual loci, the technical and biological variability between samples can be large enough to obscure systematic differences due to copy number changes, while the cumulative values are more precise.

J.-P. Bourquin compared gene expression profiles between children with Down’s syndrome (trisomy 21) and a transient myeloid disorder and