



Additional data file legend

Transcriptional complexity in the human genome. Recently developed high-throughput technologies have increased the capacity for surveying the transcriptional activity of the human genome, and are reporting a wealth of transcripts that had been not previously detected through 'traditional' large-scale cDNA sequencing projects. Shown here are novel transcripts discovered through a combination of directed RACE and hybridization onto the tiling arrays. Following the strategy described in Djebali *et al.* 2008 [60], 5' RACE was performed using a primer designed within an exon in the gene *KCNJ15* (potassium inwardly-rectifying channel, subfamily J, member 15, RefSeq id NM_170736), mapping to human chromosome 21. RACE products were hybridized onto genome tiling arrays, which helped reveal novel sites of transcription associated with transcripts in this locus (the so-called RACEfrags). A number of RACEfrags mapped approximately 150 kb upstream of *KCNJ15*, overlapping exons of gene *DSCR8* (Down syndrome critical region gene 8). RT-PCR reactions were carried out to verify the connectivity of one of the exons in this gene with the original exon interrogated in gene *KCNJ15*. RT-PCR products were cloned, clones were randomly selected and then sequenced. Ten new sequences were discovered, of which seven connect the two genes. Genes and transcripts are visualized here using the Genome Browser at the University of California Santa Cruz.