

## Descriptions of HG18 Annotation Files

Roche NimbleGen provides the following suite of human hg18 annotation files. You can import and view these files alongside your microarray data using Roche NimbleGen SignalMap software.

- **Genes.gff:** Indicates all genes for build hg18 as reported in the UCSC Genome browser (<http://genome.ucsc.edu>). Genes annotated above the baseline in each track represent features identified on the sense strand, while entries below the baseline represent features identified on the antisense strand.
- **Genes\_Exon-Intron.gff:** Indicates the exon-intron boundaries of all genes for build hg18 as reported in the UCSC Genome browser. Exons are denoted as dark blue bars, and introns are denoted as light blue bars.
- **Transcription\_Start\_Sites.gff:** Indicates all transcription initiation sites for build hg18 as reported in the UCSC Genome browser.

***Note:** Features in this file may be more easily viewed by changing the feature style from dots to bars in SignalMap software. To do this, select the track by clicking its y-axis and select **Track -> Style -> Bars**.*

- **Structural\_Variants.gff:** Displays all copy number variants as reported in the Database of Genomic Variants (<http://projects.tcag.ca/variation>).
- **Segmental\_Duplications.gff:** Displays regions of genomic duplication >1 kb in size and with >90% sequence identity after masking high-copy repeat regions (Bailey, et al. 2001; 11:1005-17) as reported in the UCSC Genome browser. The level of similarity is indicated as follows: light to dark gray bars = 90 - 98% similarity, light to dark yellow bars = 98 - 99% similarity, light to dark orange bars = >99% similarity; red = duplications of >98% that lack sufficient evidence in the Segmental Duplication database.
- **Cytogenetic\_Ideogram.gff:** Displays the cytogenetic bands, in grayscale format, for each chromosome as reported in the UCSC Genome browser.
- **miRNA.gff:** Indicates all miRNAs as reported in the miRBase database (<http://microrna.sanger.ac.uk/>). Each feature represents the entire hairpin sequence for the miRNA.

***Note:** Features in this file may be more easily viewed by changing the feature style from dots to bars in SignalMap software. To do this, select the track by clicking its y-axis and select **Track -> Style -> Bars**.*

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## Technical Support

If you have questions, contact Roche NimbleGen Technical Support:

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