

This document briefly describes the data file types available from the Auble Lab web site pertaining to:

K. Poorey, R.O. Sprouse, M.N. Wells, R. Viswanathan, S. Bekiranov, and D.T. Auble. RNA Synthesis Precision Is Regulated by Preinitiation Complex Turnover. *Genome Res.* 20:1679-1688, 2010.

If you have a question about these files or formats please send your query to David Auble: auble@virginia.edu

All of these files are compatible with IGB (Integrated genome Browser) available at the Affymetrix website.

File types:

<file> .sgr: graph files representing absolute RNA signal or CHIP occupancy levels computed by the TAS program.

They are in the format: Chromosome Genomic Coordinate Signal Value

For the absolute total RNA for WT (*MOT1*), WT (*SET2*), *mot1-42*, and *set2Δ* strains, the data was smoothed over a 100 bp window. For the differential RNA ($\log_2(\text{mutant}/\text{WT})$) the data was smoothed over a 500 bp window.

For the TBP and TFIIB whole genome CHIP-Chip studies, the data was smoothed over a 500 bp window.

This format is also used to display the TBP and TFIIB ChIP-chip peak locations.

<file> .bed: These are bar files that describe the length change defects and annotations in this study.

They are in the format: Chromosome Start Stop

The .bed files follow the UCSC format

(<http://genome.ucsc.edu/FAQ/FAQformat.html#format1>).

<genelist> .txt: These files contain the lists of genes with specific transcript length changes.

Expression_profile_all.xls : These are excel files that contain the differential expression profiles for *mot1-42*/WT and *set2Δ*/WT.