Additional file 2: **TinT tutorial**

http://www.compgen.uni-muenster.de/tools/tint/

1. start TinT

2. select prepared results

Alternatively you can select precomputed results (genomes) or local results (your own RepeatMasker.out file) or frequency files (previously saved projects) and load presets (configurations from previously saved projects)
3. select elements

4. change stringency for small amount of data or transposons

5. TinT matrix
element re-selection

progress of processing