Example Plot A: Canonical Deletion, Single Sample

chr2 : 178,685,610 − 178,788,838

p(DEL) = 3.207E−05
p(DUP) = 10E−01

1,000 bp Bins

Norm. Depth t Score

- p(Dup) < Bonferroni (df=157)
- p(Del) < Bonferroni (df=157)
- Median t Score
- 1 * MAD
- 2 * MAD

Gene — *PDE11A*

SegDup

Gap

chr2 Coordinate (bp)