Table 1. Key factor analysis for simulated single exon CNV events. Results presented are for 971 identified (*true positives*) and 29 missed (*false negatives*) simulated single exon deletions with 50% of original sequencing reads removed. Data distribution plots for each factor are provided in Supp Figures S6-S13.

Factor	True positives	False negatives
Sample independent factors		
Exon size (*n* nucleotides)	**183** (12-5692; *280.9*)	**122** (11-347; *80.7*)
GC content (%)	**50.2** (28.0-76.1; *9.6*)	**54.3** (26.2-76.1; *17.4*)
Distance to neighbouring exons (*n* nucleotides)	**4186** (64-871570; *29256*)	**2621** (359-30814; *5580*)
Test sample dependent factors		
Total read depth (*n* non-duplicate reads)	**1701** (62-71020; *3408*)	**280** (0-1756; *339*)
Normalized total read depth (rpkm)	**4024** (348-16508; *1942*)	**1447** (0-5414; *1401*)
Intra-sample variability (rpkmCV, %)	**39.8** (0-102.2; *15.6*)	**52.6** (21.6-88.5; *17.3*)
Nucleotides with insufficient coverage (%)	**0.14** (0-54.1; *1.9*)	**29.8** (0-100; *40.4*)
Reference sample dependent factors		
Inter-sample variability (rpkmCV, %)	**6.1** (0.1-39.5; *4.8*)	**22.0** (0-88.6; *20.8*)

CV, coefficient of variation; *rpkm*, reads per kilobase per million. Reported statistics: mean(min-max; *sd*).