Blahnik: Supplementary Figure S5

A

Input files for Sole-search: Eland_extended.txt or eland_results.txt

Output files from Sole-search

- Run statistics and parameters (Summary_Job.txt)
- Sgr files for visualization of the raw data (rawbinning.sgr)
- Summary: # of peaks, average and median peak height, highest and lowest peak, average peak width (signifpeaks.txt)
- Sgr file of all tags corresponding to called peaks (redbin.sgr)
- Gff file of all peaks, ranked by tag height (signifpeaks.gff)
- Gff file of all peaks, ranked by significance over background (effectsize.gff)
- Sgr files for visualization of the amplified and deleted regions (smear.sgr)
- Gff file of the amplified regions of the genome (duplications.gff)
- Gff file of the deleted regions of the genome (deletions.gff)

B

Input files for Gff-Overlap Tool

Peaks files from Sole-search (signifpeaks.gff)

Output files from Gff-Overlap Tool

Summary file
Gff file of the overlapping peaks
Gff file of the non-overlapping peaks
Gff file of the union of both peaks files

C

Input files for Location-Analysis Tool

Peaks files from Sole-search (signifpeaks.gff)

Output files from Location-Analysis Tool

chrom_count: Hits per chromosome
loc_analysis: Location analysis
gene_count: number of binding sites per target gene
dist_analysis: location of sites with respect to TSS of nearest gene
pos_info: sites identified as upstream, downstream or within a gene
Intron information: intragenic sites divided into exons and introns