

# Create CEAS Report Element

It provides summary statistics on ChIP enrichment in important genomic regions such as individual chromosomes, promoters, gene bodies or exons, and infers the genes most likely to be regulated by the binding factor under study.

Element type: ceas-report

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output report file	Path to the report output file. Result for CEAS analysis.		image-file	string
Output annotations file	Name of tab-delimited output text file, containing a row of annotations for every RefSeq gene. (file is not generated if no peak location data is supplied).		anns-file	string
Gene annotations table	Path to gene annotation table (e.g. a refGene table in sqlite3 db format (--gt).	hg19	anns-table	string
Span size	Span from TSS and TTS in the gene-centered annotation (base pairs). ChIP regions within this range from TSS and TTS are considered when calculating the coverage rates in promoter and downstream (--span).	3000	span	numeric
Wiggle profiling resolution	Wiggle profiling resolution. WARNING: Value smaller than the wig interval (resolution) may cause aliasing error. (--pf-res).	50	profiling-resolution	numeric
Promoter /downstream interval	Promoter/downstream intervals for ChIP region annotation are three values or a single value can be given. If a single value is given, it will be segmented into three equal fractions (e.g. 3000 is equivalent to 1000,2000,3000) (--rel-dist).	3000	promoter-sizes	numeric
BiPromoter ranges	Bidirectional-promoter sizes for ChIP region annotation. It's two values or a single value can be given. If a single value is given, it will be segmented into two equal fractions (e.g. 5000 is equivalent to 2500,5000) (--bisizes).	5000	promoter-bisizes	string
Relative distance	Relative distance to TSS/TTS in WIGGLE file profiling (--rel-dist).	3000	relative-distance	string
Gene group files	Gene groups of particular interest in wig profiling. Each gene group file must have gene names in the 1st column. The file names are separated by commas (--gn-groups).		group-files	string
Gene group names	Set this parameter empty for using default values. The names of the gene groups from "Gene group files" parameter. These names appear in the legends of the wig profiling plots. Values range: comma-separated list of strings. Default value: 'Group 1, Group 2,...Group n' (--gn-group-names).		group-names	string

## Input/Output Ports

The element has 1 *input port*:

Name in GUI: CEAS data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Enrichment signal	enrichment-signal	ann-table-list
Peak regions	peak-regions	string