

# 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
<b>Output report file</b>	Path to the report output file. Result for CEAS analysis.		<b>image-file</b>	<i>string</i>
<b>Output annotations file</b>	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).		<b>anns-file</b>	<i>string</i>
<b>Gene annotations table</b>	Path to gene annotation table (e.g. a refGene table in sqlite3 db format (--gt).	hg19	<b>anns-table</b>	<i>string</i>
<b>Span size</b>	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	<b>span</b>	<i>numeric</i>
<b>Wiggle profiling resolution</b>	Wiggle profiling resolution. WARNING: Value smaller than the wig interval (resolution) may cause aliasing error. (--pf-res).	50	<b>profiling-resolution</b>	<i>numeric</i>
<b>Promoter /downstream interval</b>	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	<b>promoter-sizes</b>	<i>numeric</i>
<b>BiPromoter ranges</b>	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	<b>promoter-bisizes</b>	<i>string</i>
<b>Relative distance</b>	Relative distance to TSS/TTS in WIGGLE file profiling (--rel-dist).	3000	<b>relative-distance</b>	<i>string</i>
<b>Gene group files</b>	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).		<b>group-files</b>	<i>string</i>
<b>Gene group names</b>	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).		<b>group-names</b>	<i>string</i>

## 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
<b>Enrichment signal</b>	<b>enrichment-signal</b>	<i>ann-table-list</i>
<b>Peak regions</b>	<b>peak-regions</b>	<i>string</i>