**Supplementary File 1**. Command-line interface for the RNA-Seq Compi pipeline (<https://www.sing-group.org/compihub/explore/5d09fb2a1713f3002fde86e2>), obtained with the command compi run –p pipeline.xml --help.

usage: compi run <general-options> -- <pipeline-parameters>

 where <general-options>: [-p <pipeline>] [-pa <params>] [-n <num-tasks>] [-l <logs>] [-lt <log-only-task>] [-nl <no-log-task>] [-st <single-task>] [-f <from>] [-a <after>] [-ut <until>] [-bt <before>] [-r <runners-config>] [-o] [-q] [-w] [-h]

 --pipeline/-p

 XML pipeline file (default: pipeline.xml)

 --params/-pa

 parameters file

 --num-tasks/-n

 maximum number of tasks that can be run in parallel. This is not equivalent to the number of threads the pipeline will use, because some tasks can be parallel processes themselves (default: 6)

 --logs/-l

 Directory to save tasks' output (stdout and stderr, in separated files). By default, no output is saved. If this option is provided, all task's output will be logged by default. You can select which tasks to log with --log-only-task or --no-log-task

 --log-only-task/-lt

 Log task(s). Task id(s) whose output will be logged, other tasks' output will be ignored. This parameter is incompatible with --no-log-task. If you use this option, you must provide a log directory with --logs. This option can be specified multiple times

 --no-log-task/-nl

 Do not log task(s). Task id(s) whose output will be ignored, other tasks' output will be saved. This parameter is incompatible with --log-only-task. If you use this option, you must provide a log directory with --logs. This option can be specified multiple times

 --single-task/-st

 runs a single task without its dependencies. This option is incompatible with --from, --after, --until and --before

 --from/-f

 from task(s). Runs the pipeline from the specific task(s) without running its/their dependencies. This option is incompatible with --single-task. This option can be specified multiple times

 --after/-a

 after task(s). Runs the pipeline from the specific task(s) without running neither it/them nor its/their dependencies. This option is incompatible with --single-task. This option can be specified multiple times

 --until/-ut

 runs until a task (inclusive) including its dependencies. This option is incompatible with --single-task and --before

 --before/-bt

 runs all tasks which are dependencies of a given task. This option is incompatible with --single-task and --until

 --runners-config/-r

 XML file configuring custom runners for tasks. See the Compi documentation for more details

 --show-std-outs/-o

 Forward task stdout/stderr to the compi stdout/stderr

 --quiet/-q

 Do not output compi logs to the console

 --abort-if-warnings/-w

 Abort pipeline run if there are warnings on pipeline validation

 --help/-h

 Show help of the specified pipeline

 where <pipeline-parameters>: -ballgown\_file <ballgown\_file> -samples\_class2\_label <samples\_class2\_label> -samples\_class1\_label <samples\_class1\_label> -samples\_dir <samples\_dir> [-samtools <samtools>] -genome\_index\_dir <genome\_index\_dir> [-stringtie <stringtie>] -samples\_stringtie\_mergedannotation <samples\_stringtie\_mergedannotation> [-ballgown\_script <ballgown\_script>] -genome\_index <genome\_index> [-rscript <rscript>] -reference\_annotation <reference\_annotation> -samples\_stringtie\_mergelist <samples\_stringtie\_mergelist> -samples\_alignment\_dir <samples\_alignment\_dir> -genome\_fasta <genome\_fasta> -ballgown\_dir <ballgown\_dir> [-hisat2 <hisat2>] [-hisat2\_index <hisat2\_index>] -samples\_stringtie\_dir <samples\_stringtie\_dir>

 samtools:

 --samples\_stringtie\_mergelist/-samples\_stringtie\_mergelist

 The path to the merge list file to feed StringTie with.

 --stringtie/-stringtie

 The executable of the StringTie command. (default: /opt/stringtie-1.3.1c.Linux\_x86\_64/stringtie)

 --samtools/-samtools

 The executable of the samtools command. (default: /opt/samtools-1.3.1/samtools)

 --hisat2/-hisat2

 The executable of the HISAT2 command. (default: /opt/hisat2-2.0.5/hisat2)

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 --genome\_index/-genome\_index

 The name for the genome index.

 --reference\_annotation/-reference\_annotation

 The path to the reference GTF file for the analysis.

 --samples\_alignment\_dir/-samples\_alignment\_dir

 The directory where aligned samples reads should be placed.

 --samples\_dir/-samples\_dir

 The directory containing the samples reads.

 genome-index:

 --genome\_fasta/-genome\_fasta

 The reference genome.

 --hisat2\_index/-hisat2\_index

 The executable of the HISAT2 index command. (default: /opt/hisat2-2.0.5/hisat2-build)

 --genome\_index/-genome\_index

 The name for the genome index.

 initialization:

 --ballgown\_file/-ballgown\_file

 The path to the Ballgown CSV file with the input data.

 --ballgown\_dir/-ballgown\_dir

 The directory where Ballgown files should be placed.

 --samples\_stringtie\_mergelist/-samples\_stringtie\_mergelist

 The path to the merge list file to feed StringTie with.

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 --genome\_index\_dir/-genome\_index\_dir

 The directory where genome indexes should be created.

 --samples\_alignment\_dir/-samples\_alignment\_dir

 The directory where aligned samples reads should be placed.

 stringtie:

 --samples\_stringtie\_mergelist/-samples\_stringtie\_mergelist

 The path to the merge list file to feed StringTie with.

 --stringtie/-stringtie

 The executable of the StringTie command. (default: /opt/stringtie-1.3.1c.Linux\_x86\_64/stringtie)

 --samtools/-samtools

 The executable of the samtools command. (default: /opt/samtools-1.3.1/samtools)

 --hisat2/-hisat2

 The executable of the HISAT2 command. (default: /opt/hisat2-2.0.5/hisat2)

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 --genome\_index/-genome\_index

 The name for the genome index.

 --reference\_annotation/-reference\_annotation

 The path to the reference GTF file for the analysis.

 --samples\_alignment\_dir/-samples\_alignment\_dir

 The directory where aligned samples reads should be placed.

 --samples\_dir/-samples\_dir

 The directory containing the samples reads.

 ballgown-class-1:

 --ballgown\_file/-ballgown\_file

 The path to the Ballgown CSV file with the input data.

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 --samples\_class1\_label/-samples\_class1\_label

 The label for the first class.

 stringtie-merge:

 --samples\_stringtie\_mergelist/-samples\_stringtie\_mergelist

 The path to the merge list file to feed StringTie with.

 --stringtie/-stringtie

 The executable of the StringTie command. (default: /opt/stringtie-1.3.1c.Linux\_x86\_64/stringtie)

 --reference\_annotation/-reference\_annotation

 The path to the reference GTF file for the analysis.

 --samples\_stringtie\_mergedannotation/-samples\_stringtie\_mergedannotation

 The path to the merged annotation file created by StringTie.

 ballgown-class-2:

 --ballgown\_file/-ballgown\_file

 The path to the Ballgown CSV file with the input data.

 --samples\_class2\_label/-samples\_class2\_label

 The label for the second class.

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 ballgown-analysis:

 --ballgown\_dir/-ballgown\_dir

 The directory where Ballgown files should be placed.

 --rscript/-rscript

 The executable of the RScript command. (default: Rscript)

 --ballgown\_script/-ballgown\_script

 The path to the Ballgown DE script. (default: /opt/ballgown-differential-expression.R)

 alignment:

 --samples\_stringtie\_mergelist/-samples\_stringtie\_mergelist

 The path to the merge list file to feed StringTie with.

 --stringtie/-stringtie

 The executable of the StringTie command. (default: /opt/stringtie-1.3.1c.Linux\_x86\_64/stringtie)

 --samtools/-samtools

 The executable of the samtools command. (default: /opt/samtools-1.3.1/samtools)

 --hisat2/-hisat2

 The executable of the HISAT2 command. (default: /opt/hisat2-2.0.5/hisat2)

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 --genome\_index/-genome\_index

 The name for the genome index.

 --reference\_annotation/-reference\_annotation

 The path to the reference GTF file for the analysis.

 --samples\_alignment\_dir/-samples\_alignment\_dir

 The directory where aligned samples reads should be placed.

 --samples\_dir/-samples\_dir

 The directory containing the samples reads.

 stringtie-analysis:

 --stringtie/-stringtie

 The executable of the StringTie command. (default: /opt/stringtie-1.3.1c.Linux\_x86\_64/stringtie)

 --samples\_stringtie\_dir/-samples\_stringtie\_dir

 The directory where StringTie files should be placed.

 --samples\_alignment\_dir/-samples\_alignment\_dir

 The directory where aligned samples reads should be placed.

 --samples\_stringtie\_mergedannotation/-samples\_stringtie\_mergedannotation

 The path to the merged annotation file created by StringTie.