

hppRNA v1.3.3

A Snakemake-based handy parameter-free pipeline for RNA-Seq
analysis of numerous samples

Dapeng Wang

dapeng.wang@plants.ox.ac.uk

wangdp123@gmail.com

Department of Plant Sciences

University of Oxford

S Parks Rd

Oxford OX1 3RB, UK

Brief introduction

This pipeline is designed for guiding how to set up everything in your own server to perform the comprehensive RNA-Seq analysis (e.g, protein-coding genes, lncRNAs and circRNAs) for an abundance of samples you supply simultaneously through alternative 6 workflows that have integrated both well-established and recently-developed methods and tools: (1) Tophat - Cufflink - Cuffdiff; (2) Subread - featureCounts - DESeq2; (3) STAR - RSEM - EBSeq; (4) Bowtie - eXpress - edgeR; (5) kallisto - sleuth; (6) HISAT - StringTie - Ballgown. It is almost parameter-free, where parameters have been set into the optimal or sub-optimal ranges where users can alter the very important parameters such as fragment length distributions and/or sequencing orientations based on their experimental designs. It provides multiple options to cope with a variety of data types and experimental conditions as well as your specific requirements, which is formulated in a Snakemake modern pipeline management system that allows for the error handling, file surveillance and parallel processing. The first version is fitted to human or mouse species, stranded or unstranded sequencing, single-end or paired-end samples.

Outlines

1. Get ready for the computing environment of this pipeline with provided home-made scripts.
(*generate_hppRNA_installation.pl*)
2. Get all the fastq files from the sequencer in place on your server.
3. Create the snakemake file for job running with customized scripts.
(*generate_hppRNA_main_snakemake.pl* and *generate_path.pl*)

Step-by-step instructions

In order to enjoy this pipeline, please follow the instruction below step by step. The first version is only suitable for human and mouse RNA-Seq data analysis.

1. To set up the pipeline properly

Please prepare and set up the computing environment for your server in an appropriate way with the provided shell script, which will attempt to download all necessary genomes with annotations (hg19 and mm10) (Table 1) and collect and install all the compressed publicly-available software packages (Table 2) as well as home-made PERL or R scripts on your server (Table 3).

To generate the shell script for your working folder with the perl script named "generate_hppRNA_installation.pl" provided in "main_script" folder like this.

Format:

perl generate_hppRNA_installation.pl -i [the location of the software to be installed] -o [the name of the shell script for installation]

Example:

perl generate_hppRNA_installation.pl -i /data/hppRNA_software -o hppRNA_installation_script.sh

Afterwards, you can execute the shell file to install everything that is needed. It takes several hours to finish the installation depends on the computing capacity of your server and the internet connection speed.

```
./hppRNA_installation_script.sh
```

After installation, you will be able to see all the required folders encompassing the executable files as well as related files as shown in Table 4.

The unique exception in this step is that you have to download and install GATK software from <https://software.broadinstitute.org/gatk/> after registration and approval of required license, due to the fact that this software specifically require the copyright approval by the users on their own when they use it. After installation of GATK, please be noted that the path to the executable file for GATK should be properly pointed out in the sample input table file.

Table 1. The complete list of genomic files and the relevant annotation files.

(A) For human species:

Species	Version	File name	Description
Human	hg19	genes.selected.pc.gtf	The gtf file for protein-coding gene annotation for 25 major chromosomes
Human	hg19	genome.fa	Fasta-formatted genomic sequences of 25 major chromosomes
Human	hg19	genome.fa.fai	The FAIDX file for genome.fa
Human	hg19	transcript_to_gene.txt	The correspondence between transcript names and their gene names
Human	hg19	mRNA_lncRNA.gtf	The gtf file for protein-coding gene and lncRNA annotation for 25 major chromosomes
Human	hg19	mRNA_lncRNA.transcript_to_gene.txt	The correspondence between transcript names and their gene names for protein-coding genes and lncRNAs
Human	hg19	repeats.gtf	The gtf file for repetitive sequence annotation

(B) For mouse species:

Species	Version	File name	Description
Mouse	mm10	genes.selected.pc.gtf	The gtf file for protein-coding gene annotation for 22 major chromosomes
Mouse	mm10	genome.fa	Fasta-formatted genomic sequences of 22 major chromosomes
Mouse	mm10	genome.fa.fai	The FAIDX file for genome.fa
Mouse	mm10	transcript_to_gene.txt	The correspondence between transcript names and their gene names
Mouse	mm10	mRNA_lncRNA.gtf	The gtf file for protein-coding gene and lncRNA annotation for 22 major chromosomes
Mouse	mm10	mRNA_lncRNA.transcript_to_gene.txt	The correspondence between transcript names and their gene names for protein-coding genes and lncRNAs
Mouse	mm10	repeats.gtf	The gtf file for repetitive sequence annotation

Table 2. The full list of essential tools and their dependencies along with their downloadable websites.

No.	Status	Name	Original website address
1	Core	Perl	http://www.cpan.org/src/5.0/perl-5.22.2.tar.gz
2	Core	Java SE Development Kit	http://download.oracle.com/otn-pub/java/jdk/8u91-b14/jdk-8u91-linux-x64.tar.gz
3	Dependency	openssl	https://www.openssl.org/source/openssl-1.0.2h.tar.gz
4	Dependency	zlib	http://zlib.net/zlib-1.2.8.tar.gz
5	Dependency	bzip2	http://www.bzip.org/1.0.6/bzip2-1.0.6.tar.gz
6	Dependency	xz	http://tukaani.org/xz/xz-5.2.2.tar.gz
7	Dependency	pcre	ftp://ftp.csx.cam.ac.uk/pub/software/programming/pcre/pcre-8.38.tar.gz
8	Dependency	libtool	ftp://ftp.gnu.org/gnu/libtool/libtool-2.4.tar.gz
9	Dependency	curl	https://curl.haxx.se/download/curl-7.48.0.tar.gz
10	Core	Python	https://www.python.org/ftp/python/2.7.11/Python-2.7.11.tgz
11	Dependency	setuptools	https://bootstrap.pypa.io/ez_setup.py https://pypi.python.org/packages/1a/5c/57c6920bf4a1b1c11645b625e5483d778cedb3823ba21a017112730f0a12/numpy-1.11.0.tar.gz
12	Dependency	numpy	https://pypi.python.org/packages/b0/40/9c853c1dc32414263031f7f956f859ee7af145c84b8391640a1d79ce25df/cutadapt-1.9.1.tar.gz
13	Core	R	https://cloud.r-project.org/src/base/R-3/R-3.3.0.tar.gz
14	Core	FastQC	http://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.5.zip
15	Core	FASTX-Toolkit	http://hannonlab.cshl.edu/fastx_toolkit/fastx_toolkit_0.0.13_binaries_Linux_2.6_amd64.tar.bz2
16	Core	PRINSEQ-lite	http://downloads.sourceforge.net/project/prinseq/standalone/prinseq-lite-0.20.4.tar.gz
17	Core	Cutadapt	https://pypi.python.org/packages/b0/40/9c853c1dc32414263031f7f956f859ee7af145c84b8391640a1d79ce25df/cutadapt-1.9.1.tar.gz
18	Core	Bowtie2	http://downloads.sourceforge.net/project/bowtie-bio/bowtie2/2.2.9/bowtie2-2.2.9-linux-x86_64.zip
19	Core	Tophat2	https://ccb.jhu.edu/software/tophat/downloads/tophat-2.1.1.Linux_x86_64.tar.gz
20	Core	Cufflink	http://cole-trapnell-lab.github.io/cufflinks/assets/downloads/cufflinks-2.2.1.Linux_x86_64.tar.gz
21	Core	SAMtools	http://downloads.sourceforge.net/project/samtools/samtools/1.3.1/samtools-1.3.1.tar.bz2
22	Core	BlackOPs	http://downloads.sourceforge.net/project/rnaseqvariantbl/BlackOPs_v1.06.zip
23	Core	Rsubread	http://bioconductor.org/packages/3.3/bioc/src/contrib/Rsubr

			ead_1.22.0.tar.gz
24	Dependency	BiocGenerics	https://bioconductor.org/packages/3.3/bioc/src/contrib/BiocGenerics_0.18.0.tar.gz
25	Dependency	S4Vectors	https://bioconductor.org/packages/3.3/bioc/src/contrib/S4Vectors_0.10.0.tar.gz
26	Dependency	IRanges	https://bioconductor.org/packages/3.3/bioc/src/contrib/IRanges_2.6.0.tar.gz
27	Dependency	GenomeInfoDb	https://bioconductor.org/packages/3.3/bioc/src/contrib/GenomeInfoDb_1.8.0.tar.gz
28	Dependency	zlibbioc	https://bioconductor.org/packages/3.3/bioc/src/contrib/zlibbioc_1.18.0.tar.gz
29	Dependency	Xvector	https://bioconductor.org/packages/3.3/bioc/src/contrib/Xvector_0.12.0.tar.gz
30	Dependency	GenomicRanges	https://bioconductor.org/packages/3.3/bioc/src/contrib/GenomicRanges_1.24.0.tar.gz
31	Dependency	Biobase	https://bioconductor.org/packages/3.3/bioc/src/contrib/Biobase_2.32.0.tar.gz
32	Dependency	SummarizedExperiment	https://bioconductor.org/packages/3.3/bioc/src/contrib/SummarizedExperiment_1.2.0.tar.gz
33	Dependency	lambda.r	https://cran.r-project.org/src/contrib/Archive/lambda.r/lambda.r_1.1.6.tar.gz
34	Dependency	futile.options	https://cran.rstudio.com/src/contrib/futile.options_1.0.0.tar.gz
35	Dependency	futile.logger	https://cran.r-project.org/src/contrib/Archive/futile.logger/futile.logger_1.4.tar.gz
36	Dependency	snow	https://cran.r-project.org/src/contrib/Archive/snow/snow_0.3-13.tar.gz
37	Dependency	BiocParallel	https://bioconductor.org/packages/3.3/bioc/src/contrib/BiocParallel_1.6.0.tar.gz
38	Dependency	DBI	https://cran.r-project.org/src/contrib/Archive/DBI/DBI_0.3.1.tar.gz
39	Dependency	RSQLite	https://cran.r-project.org/src/contrib/Archive/RSQLite/RSQLite_0.11.4.tar.gz
40	Dependency	AnnotationDbi	https://bioconductor.org/packages/3.3/bioc/src/contrib/AnnotationDbi_1.34.0.tar.gz
41	Dependency	XML	https://cran.r-project.org/src/contrib/Archive/XML/XML_3.98-1.3.tar.gz
42	Dependency	xtable	https://cran.r-project.org/src/contrib/Archive/xtable/xtable_1.8-0.tar.gz
43	Dependency	annotate	https://bioconductor.org/packages/3.3/bioc/src/contrib/annotate_1.50.0.tar.gz
44	Dependency	genefilter	https://bioconductor.org/packages/3.3/bioc/src/contrib/genefilter_1.54.0.tar.gz
45	Dependency	locfit	https://cran.r-project.org/src/contrib/Archive/locfit/locfit_1.

			5-9.tar.gz
46	Dependency	RColorBrewer	https://cran.r-project.org/src/contrib/Archive/RColorBrewer/RColorBrewer_1.0-5.tar.gz
47	Dependency	geneplotter	https://bioconductor.org/packages/3.3/bioc/src/contrib/geneplotter_1.50.0.tar.gz
48	Dependency	digest	https://cran.r-project.org/src/contrib/Archive/digest/digest_0.6.8.tar.gz
49	Dependency	gtable	https://cran.r-project.org/src/contrib/Archive/gtable/gtable_0.1.2.tar.gz
50	Dependency	Rcpp	https://cran.r-project.org/src/contrib/Archive/Rcpp/Rcpp_0.12.3.tar.gz
51	Dependency	plyr	https://cran.r-project.org/src/contrib/Archive/plyr/plyr_1.8.2.tar.gz
52	Dependency	stringi	https://github.com/Rexamine/stringi/archive/master.zip
53	Dependency	magrittr	https://cran.r-project.org/src/contrib/Archive/magrittr/magrittr_1.0.1.tar.gz
54	Dependency	stringr	https://cran.r-project.org/src/contrib/Archive/stringr/stringr_0.6.2.tar.gz
55	Dependency	reshape2	https://cran.r-project.org/src/contrib/Archive/reshape2/reshape2_1.4.tar.gz
56	Dependency	dichromat	https://cran.r-project.org/src/contrib/Archive/dichromat/dichromat_1.2-4.tar.gz
57	Dependency	colorspace	https://cran.r-project.org/src/contrib/colorspace_1.2-6.tar.gz
58	Dependency	munsell	https://cran.r-project.org/src/contrib/Archive/munsell/munsell_0.4.2.tar.gz
59	Dependency	labeling	https://cran.r-project.org/src/contrib/Archive/labeling/labeling_0.2.tar.gz
60	Dependency	scales	https://cran.r-project.org/src/contrib/Archive/scales/scales_0.3.0.tar.gz
61	Dependency	ggplot2	https://cran.r-project.org/src/contrib/Archive/ggplot2/ggplot2_2.2.0.0.tar.gz
62	Dependency	Formula	https://cran.r-project.org/src/contrib/Archive/Formula/Formula_1.2-0.tar.gz
63	Dependency	latticeExtra	https://cran.r-project.org/src/contrib/Archive/latticeExtra/latticeExtra_0.6-26.tar.gz
64	Dependency	acepack	https://cran.r-project.org/src/contrib/Archive/acepack/acepack_1.3-3.2.tar.gz
65	Dependency	gridExtra	https://cran.r-project.org/src/contrib/Archive/gridExtra/gridExtra_2.2.0.tar.gz
66	Dependency	chron	https://cran.r-project.org/src/contrib/Archive/chron/chron_2.3-46.tar.gz
67	Dependency	data.table	https://cran.r-project.org/src/contrib/Archive/data.table/data.table_1.9.4.tar.gz
68	Dependency	Hmisc	https://cran.r-project.org/src/contrib/Archive/Hmisc/Hmisc

			_3.17-3.tar.gz
69	Dependency	RcppArmadillo	https://cran.r-project.org/src/contrib/Archive/RcppArmadillo/RcppArmadillo_0.4.500.0.tar.gz
70	Core	DESeq2	https://bioconductor.org/packages/3.3/bioc/src/contrib/DESeq2_1.12.0.tar.gz
71	Core	STAR 2.5	https://github.com/alexdobin/STAR/archive/2.5.1b.tar.gz
72	Core	RSEM	https://github.com/deweylab/RSEM/archive/v1.2.30.tar.gz
73	Dependency	blockmodeling	https://cran.rstudio.com/src/contrib/Archive/blockmodeling/blockmodeling_0.1.7.tar.gz
74	Dependency	gtools	https://cran.rstudio.com/src/contrib/Archive/gtools/gtools_3.4.2.tar.gz
75	Dependency	gdata	https://cran.rstudio.com/src/contrib/Archive/gdata/gdata_2.16.1.tar.gz
76	Dependency	bitops	https://cran.rstudio.com/src/contrib/Archive/bitops/bitops_1.0-5.tar.gz
77	Dependency	caTools	https://cran.rstudio.com/src/contrib/Archive/caTools/caTools_1.17.tar.gz
78	Dependency	gplots	https://cran.rstudio.com/src/contrib/Archive/gplots/gplots_3.0.0.tar.gz
79	Dependency	memoise	https://cran.rstudio.com/src/contrib/Archive/memoise/memoise_0.2.1.tar.gz
80	Dependency	crayon	https://cran.rstudio.com/src/contrib/Archive/crayon/crayon_1.3.0.tar.gz
81	Dependency	praise	https://cran.rstudio.com/src/contrib/praise_1.0.0.tar.gz
82	Dependency	R6	https://cran.rstudio.com/src/contrib/Archive/R6/R6_2.1.1.tar.gz
83	Dependency	testthat	https://cran.rstudio.com/src/contrib/Archive/testthat/testthat_1.0.1.tar.gz
84	Core	EBSeq	http://bioconductor.org/packages/3.3/bioc/src/contrib/EBSeq_1.12.0.tar.gz
85	Core	Bowtie	http://downloads.sourceforge.net/project/bowtie-bio/bowtie/1.1.2/bowtie-1.1.2-linux-x86_64.zip
86	Core	eXpress	http://bio.math.berkeley.edu/eXpress/downloads/express-1.5.1/express-1.5.1-linux_x86_64.tgz
87	Dependency	limma	https://bioconductor.org/packages/3.3/bioc/src/contrib/limma_3.28.2.tar.gz
88	Core	edgeR	https://bioconductor.org/packages/3.3/bioc/src/contrib/edgeR_3.14.0.tar.gz
89	Core	kallisto	https://github.com/pachterlab/kallisto/releases/download/v0.42.5/kallisto_linux-v0.42.5.tar.gz
90	Dependency	memoise	https://cran.r-project.org/src/contrib/memoise_1.0.0.tar.gz
91	Dependency	git2r	https://cran.r-project.org/src/contrib/git2r_0.15.0.tar.gz
92	Dependency	jsonlite	https://cran.r-project.org/src/contrib/jsonlite_1.0.tar.gz
93	Dependency	rstudioapi	https://cran.r-project.org/src/contrib/rstudioapi_0.6.tar.gz

94	Dependency	whisker	https://cran.r-project.org/src/contrib/whisker_0.3-2.tar.gz
95	Dependency	withr	https://cran.r-project.org/src/contrib/withr_1.0.2.tar.gz
96	Dependency	mime	https://cran.r-project.org/src/contrib/mime_0.5.tar.gz
97	Dependency	curl	https://cran.r-project.org/src/contrib/curl_1.2.tar.gz
98	Dependency	openssl	https://cran.r-project.org/src/contrib/openssl_0.9.4.tar.gz
99	Dependency	httr	https://cran.r-project.org/src/contrib/httr_1.2.1.tar.gz
100	Dependency	devtools	https://cran.r-project.org/src/contrib/Archive/devtools/devtools_1.11.0.tar.gz
101	Core	sleuth	https://rawgit.com/pachterlab/sleuth/master/inst/doc/intro.html
102	Core	HISAT	ftp://ftp.ccb.jhu.edu/pub/infphilo/hisat2/downloads/hisat2-2.0.3-beta-Linux_x86_64.zip
103	Core	StringTie	http://ccb.jhu.edu/software/stringtie/dl/stringtie-1.2.2.Linux_x86_64.tar.gz
104	Dependency	sva	https://www.bioconductor.org/packages/3.3/bioc/src/contrib/sva_3.20.0.tar.gz
105	Dependency	Biostrings	https://www.bioconductor.org/packages/3.3/bioc/src/contrib/Biostrings_2.40.0.tar.gz
106	Dependency	RCurl	https://cran.rstudio.com/src/contrib/Archive/RCurl/RCurl_1.95-4.7.tar.gz
107	Dependency	Rsamtools	https://www.bioconductor.org/packages/3.3/bioc/src/contrib/Rsamtools_1.24.0.tar.gz
108	Dependency	GenomicAlignments	https://www.bioconductor.org/packages/3.3/bioc/src/contrib/GenomicAlignments_1.8.0.tar.gz
109	Dependency	rtracklayer	https://www.bioconductor.org/packages/3.3/bioc/src/contrib/rtracklayer_1.32.0.tar.gz
110	Core	Ballgown	https://www.bioconductor.org/packages/3.3/bioc/src/contrib/ballgown_2.4.0.tar.gz
111	Dependency	iterators	https://cran.r-project.org/src/contrib/Archive/iterators/iterators_1.0.7.tar.gz
112	Dependency	foreach	https://cran.r-project.org/src/contrib/Archive/foreach/foreach_1.4.2.tar.gz
113	Dependency	doMC	https://cran.r-project.org/src/contrib/Archive/doMC/doMC_1.3.3.tar.gz
114	Dependency	caTools	https://cran.r-project.org/src/contrib/Archive/caTools/caTools_1.17.tar.gz
115	Dependency	BSgenome	https://bioconductor.org/packages/3.3/bioc/src/contrib/BSgenome_1.40.0.tar.gz
116	Dependency	hwriter	https://cran.rstudio.com/src/contrib/Archive/hwriter/hwriter_1.3.1.tar.gz
117	Dependency	ShortRead	https://bioconductor.org/packages/3.3/bioc/src/contrib/ShortRead_1.30.0.tar.gz
118	Core	ngs.plot.r	https://github.com/shenlab-sinai/ngsplot/archive/develop.zip

119	Core	wigToBigWig	http://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/wigToBigWig
120	Core	preprocessCore	http://bioconductor.org/packages/3.3/bioc/src/contrib/preprocessCore_1.34.0.tar.gz
121	Dependency	proto	https://cran.r-project.org/src/contrib/Archive/proto/proto_0.3-9.2.tar.gz
122	Dependency	assertthat	https://cran.r-project.org/src/contrib/assertthat_0.1.tar.gz
123	Dependency	lazyeval	https://cran.r-project.org/src/contrib/Archive/lazyeval/lazyeval_0.1.9.tar.gz
124	Dependency	BH	https://cran.r-project.org/src/contrib/Archive/BH/BH_1.60.0-1.tar.gz
125	Dependency	dplyr	https://cran.r-project.org/src/contrib/Archive/dplyr/dplyr_0.4.2.tar.gz
126	Dependency	tidyr	https://cran.r-project.org/src/contrib/Archive/tidyr/tidyr_0.4.0.tar.gz
127	Core	ggfortify	https://cran.r-project.org/src/contrib/Archive/ggfortify/ggfortify_0.1.0.tar.gz
128	Core	cluster	https://cran.r-project.org/src/contrib/Archive/cluster/cluster_2.0.3.tar.gz
129	Core	picard	https://github.com/broadinstitute/picard/releases/download/2.3.0/picard-tools-2.3.0.zip
130	*	GATK	https://www.broadinstitute.org/gatk/index.php
131	Core	FusionCatcher	http://sf.net/projects/fusioncatcher/files/bootstrap.py
132	Core	DCC	https://github.com/dieterich-lab/DCC/archive/v0.4.4.tar.gz
133	Dependency	aod	https://cran.r-project.org/src/contrib/aod_1.3.tar.gz
134	Core	CircTest	https://github.com/dieterich-lab/CircTest
135	Core	iSeeRNA	http://137.189.133.71/iSeeRNA/data/iSeeRNA-1.2.2.x86_64.tar.gz
136	Core	Snakemake	https://repo.continuum.io/miniconda/Miniconda3-latest-Linux-x86_64.sh

*Note: Due to the specific requirement for copyright of GATK software claimed by the authors, the script for automatically downloading and installing the tools will not include the content relating to GATK. Please manually get the GATK software from <https://software.broadinstitute.org/gatk/> after registration and approval of the license. Besides, please be advised that the path to the executable file for GATK should be properly pointed out in the sample input table file.

Table 3. The list of home-made PERL or R scripts.

No.	Programming language	Section	File	Function
1	PERL	workflow 1	classify_result_new_new.pl	To classify the annotated gene into two groups such as protein-coding genes and ncRNAs, and produce two files of which one file including all genes and the other file containing only signature genes.
2	PERL	workflow 1	classify_result_new_new_isoform.pl	To classify the annotated gene into two groups such as protein-coding genes and ncRNAs, and produce two files of which one file including all isoforms and the other file containing only signature isoforms.
3	PERL	workflow 1	clean_FPKM.pl	To make the appropriate format of FPKM matrix for PCA and heatmap analysis.
4	PERL	workflow 1	combine_cuffdiff_cufflink_isoform_new.pl	To combine the isoform-level results from cufflinks and cuffdiff for all samples.
5	PERL	workflow 1	combine_cuffdiff_cufflink_new.pl	To combine the gene-level results from cufflinks and cuffdiff for all samples.
6	PERL	workflow 1	combine_cuffdiff_results_new.pl	To combine the gene-level or isoform-level results of Cuffdiff for each sample.
7	PERL	workflow 1	combine_cufflinks_isoform_results_new.pl	To combine the isoform-level results of Cuffdiff for each sample.
8	PERL	workflow 1	combine_cufflinks_results_new.pl	To combine the gene-level results of Cufflinks for each sample.
9	PERL	workflow 1	only_FPKM.pl	To present the FPKM matrix only.
10	PERL	workflow 1	only_FPKM_isoform.pl	To present the FPKM matrix only for isoform data.
11	PERL	workflow 2	clean_RPKM_Subread_featureCounts_DESeq2.pl	To make the appropriate format of RPKM matrix for PCA and heatmap analysis.
12	PERL	workflow 2	generate_DESeq2_configure.pl	To make up the configuration file for DESeq2.
13	PERL	workflow 2	generate_DESeq2_Rscript.pl	To make up the R script file for DESeq2.
14	R	workflow 2	Subread_featureCounts_DESeq2.align.R	To align the reads against the genome.
15	R	workflow 2	Subread_featureCounts_DESeq2.buildindex.R	To construct the index files for reference genome.

16	R	workflow 2	Subread_featureCounts_DESeq2.DESeq2.R	To carry out the differential expression analysis with DESeq2.
17	R	workflow 2	Subread_featureCounts_DESeq2.featureCounts.R	To quantify the gene expression level with featureCounts.
18	PERL	workflow 3	clean_FPKM_STAR_RSEM_EBSeq.pl	To make the appropriate format of FPKM matrix for PCA and heatmap analysis.
19	PERL	workflow 3	combine_RSEM_gene_results.pl	To make up a FPKM table from results of RSEM in the level of genes.
20	PERL	workflow 3	combine_RSEM_transcript_results.pl	To make up a FPKM table from results of RSEM in the level of transcripts.
21	R	workflow 4	Bowtie_eXpress_edgeR.edgeR.R	To perform differential expression analysis with edgeR.
22	PERL	workflow 4	combine_eXpress_counts.pl	To prepare an eff_counts table for edgeR in a given comparative group.
23	PERL	workflow 4	combine_eXpress_results.pl	To make up a FPKM table from results of eXpress in the level of transcripts.
24	PERL	workflow 4	edgeR_DEG_gene.pl	To add a column showing the gene symbols to transcript DEG table.
25	PERL	workflow 5	combine_kallisto_results.pl	To produce the TPM table from kallisto results.
26	PERL	workflow 5	generate_comparison_info.pl	To create a table indicating the replicate conditions for each sample used for sleuth.
27	PERL	workflow 5	generate_sleuth_Rscript.pl	To make the R script file for sleuth.
28	PERL	workflow 5	sleuth_DEG_gene.pl	To add a column showing the gene symbols to transcript DEG table.
29	PERL	workflow 5	sleuth_transcript2gene.pl	To calculate a TPM table in the level of genes.
30	PERL	workflow 6	Ballgown_fix_FPKM_title.pl	To make the appropriate format of FPKM matrix for PCA and heatmap analysis.
31	PERL	workflow 6	generate_Ballgown_DEG_Rscript.pl	To generate the R script for Ballgown.
32	PERL	workflow 6	generate_Ballgown_matrix_Rscript.pl	To generate the R script that produces FPKM tables for genes and transcripts.
33	PERL	Post-mapping	generate_heatmap_Rscript.pl	To make up the heatmap script for plotting heatmap image.
34	PERL	Post-mapping	generate_PCA_Rscript.pl	To make up the R script for plotting PCA image.
35	PERL	lncRNA_denovo	get_transcript_to_gene_table.pl	To produce the map file including the correspondence between transcripts and genes from a gtf file.
36	PERL	lncRNA_denovo	select_cuffcompare_class_code.pl	To select the five categories of class codes that define the novel transcripts.
37	PERL	lncRNA_denovo	identify_noncoding.pl	To select the noncoding transcripts from a

		ovo		gtf file based on a file that has the classification of coding and noncoding ones.
38	PERL	lncRNA_denovo	generate_cuffmerge_assembly_list.pl	To make a file called "assembly_list.txt" with sample names.
39	PERL	lncRNA_denovo	generate_comparison_info_lncRNA.pl	To create a table indicating the replicate conditions for each sample used for sleuth, which is particularly for lncRNA analysis.
40	R	CircRNA	circTest.R	To creat the R script file for CircTest.
41	PERL	CircRNA	generate_DCC_samplesheet.pl	To generate a samplesheet file with the names of control and treatment samples as input.
42	PERL	CircRNA	generate_DCC_samplesheet_all.pl	To generate a samplesheet file with the names of a number of samples as input.

Table 4. The list of top-level folders in the specified software installation location.

Folder	Note
bedtools2	
BlackOPs_v1.06	
bowtie-1.1.2	
bowtie2-2.2.9	
bzip2-1.0.6	
cufflinks-2.2.1.Linux_x86_64	
curl-7.48.0	
cutadapt-1.9.1	
DCC-0.4.4	
express-1.5.1-linux_x86_64	
FastQC	
fastx_toolkit_0.0.13	
FusionCatcher	
GATK	
gcc-6.1.0	
hisat2-2.0.3-beta	
hppRNA_genome	genome data
iSeeRNA-1.2.2	
jdk1.8.0_91	
kallisto_linux-v0.42.5	
libtool-2.4	
my_perl	home-made
my_R	home-made
ngsplot-develop	
numpy-1.11.0	
openssl-1.0.2h	
pcre-8.38	
perl-5.22.2	
picard-tools-2.3.0	
prinseq-lite-0.20.4	
Python-2.7.11	
R-3.3.0	
R_package	R packages
RSEM-1.2.30	
samtools-1.3.1	
setuptools	
sleuth	
snakemake	
STAR-2.5.1b	

stringtie-1.2.2.Linux_x86_64

tophat-2.1.1.Linux_x86_64

wig2bigwig

xz-5.2.2

zlib-1.2.8

2. Put the fastq files with the required naming format in the correct location.

Please put the raw fastq files named in the following way, single-end or paired-end, for all samples in a folder, for example, `"/data/hppRNA_data"` for paired-end data or `"/data/hppRNA_data_single"` for single-end data.

For example, the paired-end data should end up with `".R1.fastq"` and `".R2.fastq"` in a paired fashion for each sample:

`ERR315352.R1.fastq`

`ERR315352.R2.fastq`

`ERR315391.R1.fastq`

`ERR315391.R2.fastq`

`ERR315432.R1.fastq`

`ERR315432.R2.fastq`

`ERR315455.R1.fastq`

`ERR315455.R2.fastq`

`ERR315456.R1.fastq`

`ERR315456.R2.fastq`

`ERR315477.R1.fastq`

`ERR315477.R2.fastq`

For example, the single-end data should end up with ".fastq" for each sample:

S517N701.fastq

S517N702.fastq

S517N703.fastq

S517N704.fastq

S517N705.fastq

S517N706.fastq

S502N701.fastq

S503N704.fastq

S503N705.fastq

Bear in mind that the attributes of each fastq files for each sample are supposed to be defined in the sample description table file later on so that the pipeline will be able to recognize and understand the experimental design properly.

3. To compile the snakemake file for running each module of the pipeline to fit to your data.

Please complete the sample description table as instructed.

The first step is to fill out the form with all the setting before running the pipeline as follows.

Table 5. The definition for each item in the sample description table file.

Name	Description
Project	The project name. (e.g., "hppRNA_data")
Seq	The type of sequencing. (e.g., "RNA-Seq")
Type	The sequencing strategy. (e.g., "Paired-End" or "Single-End")
Adaptor	The adaptor sequence. (e.g., "AGATCGGAAGAGC" or "No" if there is no need to remove any adaptors from the data.)
Analysis_type	The type of the analysis. (e.g., "protein-coding", "known lncRNA", "novel lncRNA" or "circRNA")
Core_workflow*	The identification of workflow to be chosen. (e.g., "1", "2", "3", "4", "5" or "6")
Fusion	If fusion gene is detected. (e.g., "No" or "Yes")
SNP	If SNP is detected. (e.g., "No" or "Yes")
Species	The species name. (e.g., "Human" or "Mouse")
Assembly_Version	The version of genome assembly. (e.g., "hg19" or "mm10")
Working_FOLDER	The folder where the raw fastq files should be placed. (e.g., "/data/hppRNA_data")
Software_FOLDER	The folder where the software installed by the provided script. (e.g., "/data/hppRNA_software")
GATK_FOLDER	The folder where the GTAK is located. (e.g., "/data/hppRNA_software/GATK")
Thread	The number of threads used in each job or rule. (e.g., "15")
Tophat: mate-inner-dist	The inner distance between the paired reads. (e.g., "50")
Tophat: mate-std-dev	The standard deviation for the inner distance distribution for paired reads. (e.g., "20")
Tophat/Cufflinks/Cuffdiff: library-type	The library type. (e.g., "fr-unstranded", "fr-firststrand" or "fr-secondstrand")
Subread: minFragLength	The minimum fragment length for valid paired-end alignments. (e.g., "50")
Subread: maxFragLength	The maximum fragment length for valid paired-end alignments. (e.g., "600")
Subread: PE_orientation	The orientation of paired reads. (e.g., "fr", "ff" or "rf")

featureCounts: strandSpecific	The strandedness of the read counting, (e.g., "0", "1" or "2")
RSEM: fragment-length-min	Minimum value of insert length for paired-end data. (e.g., "1")
RSEM: fragment-length-max	Maximum value of insert length for paired-end data. (e.g., "1000")
RSEM: fragment-length-mean	The mean value of fragment length distribution for single-end data. (e.g., "1")
RSEM: fragment-length-sd	The standard deviation of fragment length distribution for single-end data. (e.g., "0")
RSEM: forward-prob	Probability of generating a read from the forward strand of a transcript. (e.g., "0.5", "1" or "0")
Bowtie/HISAT: minins	The minimum fragment length for valid paired-end alignments. (e.g., "0")
Bowtie/HISAT: maxins	The maximum fragment length for valid paired-end alignments. (e.g., "800")
Bowtie/HISAT: PE_orientation	The orientation of paired reads. (e.g., "--fr", "--rf" or "--ff")
Bowtie/HISAT: nofw/norc	Specify which strand is not mapped. (e.g., "", "--nofw" or "--norc")
eXpress: orientation	The strand information. (e.g., "", "--fr-stranded", "--rf-stranded", "--f-stranded" or "--r-stranded")
Kallisto: l	The mean value of fragment length for single-end data. (e.g., "200")
Kallisto: s	The standard deviation of fragment length for single-end data. (e.g., "20")
DCC: strand	If the data is non-stranded, it is "-N"; otherwise, it should be " ". (e.g., "-N" or " ")

*Note: The number of core-workflow denotes: (1) Tophat - Cufflink - Cuffdiff; (2) Subread - featureCounts - DESeq2; (3) STAR - RSEM - EBSeq; (4) Bowtie - eXpress - edgeR; (5) kallisto - sleuth; (6) HISAT - StringTie - Ballgown. This parameter is only effective when Analysis_type is "protein-coding" or "known lncRNA".

The second step is to enter all necessary information for your samples one by one such as Project, Seq, Type, Species, File, Name, Length, Replicate and Platform.

The last step is to indicate which comparison groups you would like to make in the analysis.

Please also follow the instructions and examples for paired-end or single-end data we have given in the example folder. Note that you will be able to edit the table in Excel Program (e.g., *Sample_description_table_example.xlsx*) and then save it as tab-delimited text file (e.g., *workflow_1_paired.txt*), which is the input file for the main perl script called "generate_hppRNA_main_snakemake.pl".

Example 1 (Human, protein-coding, Paired-End):

	A	B	C	D	E	F	G	H	I	J	K
1	Project	hppRNA_data									
2	Seq	RNA-Seq									
3	Type	Paired-End									
4	Adaptor	AGATCGGAAGAGC									
5	Analysis_type	protein-coding									
6	Core_workflow	1									
7	Fusion	No									
8	SNP	No									
9	Species	Human									
10	Assembly_Version	hg19									
11	Working_FOLDER	/data/hppRNA_data									
12	Software_FOLDER	/data/hppRNA_software									
13	GATK_FOLDER	/data/hppRNA_software/GATK									
14	Thread	6									
15	Tophat: mate-inner-dist	50									
16	Tophat: mate-std-dev	20									
17	Tophat: library-type	fr-unstranded									
18	Cufflinks: library-type	fr-unstranded									
19	Subread: minFragLength	50									
20	Subread: maxFragLength	600									
21	Subread: PE_orientation	fr									
22	RSEM: fragment-length-min	1									
23	RSEM: fragment-length-max	1000									
24	RSEM: fragment-length-mean	-1									
25	RSEM: fragment-length-sd	0									
26	RSEM: forward-prob	0.5									
27	Bowtie/HISAT: minins	0									
28	Bowtie/HISAT: maxins	800									
29	Bowtie/HISAT: PE_orientation	--fr									
30	Bowtie/HISAT: nofw/norc										
31	eXpress: orientation										
32	Kallisto: l	200									
33	Kallisto: s	20									
34	DCC: strand	-N									
35	#Sample_title	Project	Seq	Type	Species	File	Name	Length	Replicate	Platform	
36	Sample	hppRNA_data	RNA-Seq	Paired-End	Human	ERR315477	brain_3b	101	brain	Illumina 1.9	
37	Sample	hppRNA_data	RNA-Seq	Paired-End	Human	ERR315455	brain_3c	101	brain	Illumina 1.9	
38	Sample	hppRNA_data	RNA-Seq	Paired-End	Human	ERR315432	brain_a	101	brain	Illumina 1.9	
39	Sample	hppRNA_data	RNA-Seq	Paired-End	Human	ERR315352	testis_7a	101	testis	Illumina 1.9	
40	Sample	hppRNA_data	RNA-Seq	Paired-End	Human	ERR315456	testis_7b	101	testis	Illumina 1.9	
41	Sample	hppRNA_data	RNA-Seq	Paired-End	Human	ERR315391	testis_7c	101	testis	Illumina 1.9	
42	#DEG	Control	Case								
43	DEG	testis	brain								
44											

Example 2 (Mouse, protein-coding, Single-End):

	A	E	C	D	E	F	G	H	I	J	K
1	Project	hppRNA_data									
2	Seq	RNA-Seq									
3	Type	Single-End									
4	Adaptor	AGATCGGAAGAGCC									
5	Analysis_type	protein-coding									
6	Core_workflow	1									
7	Fusion	No									
8	SNP	No									
9	Species	Mouse									
10	Assembly_Version	mm10									
11	Working_FOLDER	/data/hppRNA_data_single									
12	Software_FOLDER	/data/hppRNA_software									
13	GATK_FOLDER	/data/hppRNA_software/GATK									
14	Thread	15									
15	Tophat: mate-inner-dist	50									
16	Tophat: mate-std-dev	20									
17	Tophat/Cufflinks/Cuffdiff: library-type	fr-unstranded									
18	Subread: minFragLength	50									
19	Subread: maxFragLength	600									
20	Subread: PE_orientation	fr									
21	featureCounts: strandSpecific	0									
22	RSEM: fragment-length-min	1									
23	RSEM: fragment-length-max	1000									
24	RSEM: fragment-length-mean	-1									
25	RSEM: fragment-length-sd	0									
26	RSEM: forward-prob	0.5									
27	Bowtie/HISAT: minins	0									
28	Bowtie/HISAT: maxins	800									
29	Bowtie/HISAT: PE_orientation	--fr									
30	Bowtie/HISAT: nofw/norc										
31	eXpress: orientation										
32	Kallisto: l	200									
33	Kallisto: s	20									
34	DCC: strand	-N									
35	#Sample_title	Project	Seq	Type	Species	File	Name	Length	Replicate	Platform	
36	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S517N701	Kidney_1	76	Kidney	Illumina 1.9	
37	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S517N702	Kidney_2	76	Kidney	Illumina 1.9	
38	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S517N703	Kidney_3	76	Kidney	Illumina 1.9	
39	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S517N704	Lung_1	76	Lung	Illumina 1.9	
40	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S517N705	Lung_2	76	Lung	Illumina 1.9	
41	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S517N706	Lung_3	76	Lung	Illumina 1.9	
42	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S302N701	Spleen_1	76	Spleen	Illumina 1.9	
43	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S303N704	Spleen_2	76	Spleen	Illumina 1.9	
44	Sample	hppRNA_data_single	RNA-Seq	Single-End	Mouse	S303N705	Spleen_3	76	Spleen	Illumina 1.9	
45	#DEG	Control	Case								
46	DEG	Kidney	Lung								
47	DEG	Kidney	Spleen								
48	DEG	Lung	Spleen								
49											
50											

In addition, we exhibit the modified parameters or arguments other than default settings used in the software based on our best practice in Table 6.

Table 6. The usage situation for modified arguments used in the major software.

Program	Parameter
cutadapt	-m 20
fastq_quality_filter	-q 20
fastq_quality_filter	-p 50
fastq_quality_filter	-Q 33
fastx_collapser	-Q 33
kallisto quant	-b 100
ngs.plot.r	-L 3000
ngs.plot.r	-RB 0.05
ngs.plot.r	-F rnaseq
prinseq-lite	-trim_qual_left 20
prinseq-lite	-trim_qual_right 20
prinseq-lite	-min_len 20
prinseq-lite	-min_qual_mean 20
prinseq-lite	-ns_max_n 2
prinseq-lite	-out_format 3
prinseq-lite	-no_qual_header
GenomeAnalysisTK/SplitNCigarReads	-rf ReassignOneMappingQuality
GenomeAnalysisTK/SplitNCigarReads	-RMQF 255
GenomeAnalysisTK/SplitNCigarReads	-RMQT 60
GenomeAnalysisTK/SplitNCigarReads	-U ALLOW_N_CIGAR_READS
GenomeAnalysisTK/HaplotypeCaller	-dontUseSoftClippedBases
GenomeAnalysisTK/HaplotypeCaller	-stand_call_conf 20.0
GenomeAnalysisTK/HaplotypeCaller	-stand_emit_conf 20.0
GenomeAnalysisTK/VariantFiltration	-window 35
GenomeAnalysisTK/VariantFiltration	-cluster 3
GenomeAnalysisTK/VariantFiltration	-filterName FS
GenomeAnalysisTK/VariantFiltration	-filter "FS > 30.0"
GenomeAnalysisTK/VariantFiltration	-filterName QD
GenomeAnalysisTK/VariantFiltration	-filter "QD < 2.0"
CircRNA/STAR	--outSJfilterOverhangMin 15 15 15 15
CircRNA/STAR	--alignSJoverhangMin 15
CircRNA/STAR	--alignSJDBoverhangMin 15
CircRNA/STAR	--outFilterMultimapNmax 20
CircRNA/STAR	--outFilterScoreMin 1
CircRNA/STAR	--outFilterMatchNmin 1

CircRNA/STAR	--outFilterMismatchNmax 2
CircRNA/STAR	--chimSegmentMin 15
CircRNA/STAR	--chimScoreMin 15
CircRNA/STAR	--chimScoreSeparation 10
CircRNA/STAR	--chimJunctionOverhangMin 15
CircRNA/STAR (only for separate mate mapping)	--seedSearchStartLmax 30
DCC	-Nr 5 3
CircTest	filter.count = 5
CircTest	percentage = 0.1

Please utilize the main Perl script named "generate_hppRNA_main_snakemake.pl" with the sample description table as input to produce the shell file.

Format:

perl generate_hppRNA_main_snakemake.pl -i [the sample description table file] -o [the snakemake file]

Example 1 (protein-coding, paired-end, workflow 1):

perl generate_hppRNA_main_snakemake.pl -i workflow_1_protein_coding_paired.txt -o workflow_1_protein_coding_paired.snakemake

Example 2 (protein-coding, paired-end, workflow 2):

perl generate_hppRNA_main_snakemake.pl -i workflow_2_protein_coding_paired.txt -o workflow_2_protein_coding_paired.snakemake

Example 3 (protein-coding, paired-end, workflow 3):

perl generate_hppRNA_main_snakemake.pl -i workflow_3_protein_coding_paired.txt -o workflow_3_protein_coding_paired.snakemake

Example 4 (protein-coding, paired-end, workflow 4):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_4_protein_coding_paired.txt -o  
workflow_4_protein_coding_paired.snakemake
```

Example 5 (protein-coding, paired-end, workflow 5):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_5_protein_coding_paired.txt -o  
workflow_5_protein_coding_paired.snakemake
```

Example 6 (protein-coding, paired-end, workflow 6):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_6_protein_coding_paired.txt -o  
workflow_6_protein_coding_paired.snakemake
```

Example 7 (protein-coding, single-end, workflow 1):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_1_protein_coding_single.txt -o  
workflow_1_protein_coding_single.snakemake
```

Example 8 (protein-coding, single-end, workflow 2):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_2_protein_coding_single.txt -o  
workflow_2_protein_coding_single.snakemake
```

Example 9 (protein-coding, single-end, workflow 3):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_3_protein_coding_single.txt -o
```

workflow_3_protein_coding_single. snakemake

Example 10 (protein-coding, single-end, workflow 4):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_4_protein_coding_single.txt -o  
workflow_4_protein_coding_single. snakemake
```

Example 11 (protein-coding, single-end, workflow 5):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_5_protein_coding_single.txt -o  
workflow_5_protein_coding_single. snakemake
```

Example 12 (protein-coding, single-end, workflow 6):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_6_protein_coding_single.txt -o  
workflow_6_protein_coding_single. snakemake
```

Example 13 (protein-coding, paired-end, workflow 1, with DNA variation detection):

```
perl generate_hppRNA_main_snakemake.pl -i  
workflow_1_protein_coding_variation_paired.txt -o  
workflow_1_protein_coding_variation_paired. snakemake
```

Example 14 (protein-coding, single-end, workflow 1, with DNA variation detection):

```
perl generate_hppRNA_main_snakemake.pl -i  
workflow_1_protein_coding_variation_single.txt -o  
workflow_1_protein_coding_variation_single. snakemake
```

Example 15 (known lncRNA, paired-end, workflow 1):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_1_known_lncRNA_paired.txt -o workflow_1_known_lncRNA_paired.snakemake
```

Example 16 (known lncRNA, paired-end, workflow 2):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_2_known_lncRNA_paired.txt -o workflow_2_known_lncRNA_paired.snakemake
```

Example 17 (known lncRNA, paired-end, workflow 3):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_3_known_lncRNA_paired.txt -o workflow_3_known_lncRNA_paired.snakemake
```

Example 18 (known lncRNA, paired-end, workflow 4):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_4_known_lncRNA_paired.txt -o workflow_4_known_lncRNA_paired.snakemake
```

Example 19 (known lncRNA, paired-end, workflow 5):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_5_known_lncRNA_paired.txt -o workflow_5_known_lncRNA_paired.snakemake
```

Example 20 (known lncRNA, paired-end, workflow 6):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_6_known_lncRNA_paired.txt -o
```

workflow_6_known_lncRNA_paired.snakemake

Example 21 (known lncRNA, single-end, workflow 1):

perl generate_hppRNA_main_snakemake.pl -i workflow_1_known_lncRNA_single.txt -o workflow_1_known_lncRNA_single.snakemake

Example 22 (known lncRNA, single-end, workflow 2):

perl generate_hppRNA_main_snakemake.pl -i workflow_2_known_lncRNA_single.txt -o workflow_2_known_lncRNA_single.snakemake

Example 23 (known lncRNA, single-end, workflow 3):

perl generate_hppRNA_main_snakemake.pl -i workflow_3_known_lncRNA_single.txt -o workflow_3_known_lncRNA_single.snakemake

Example 24 (known lncRNA, single-end, workflow 4):

perl generate_hppRNA_main_snakemake.pl -i workflow_4_known_lncRNA_single.txt -o workflow_4_known_lncRNA_single.snakemake

Example 25 (known lncRNA, single-end, workflow 5):

perl generate_hppRNA_main_snakemake.pl -i workflow_5_known_lncRNA_single.txt -o workflow_5_known_lncRNA_single.snakemake

Example 26 (known lncRNA, single-end, workflow 6):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_6_known_lncRNA_single.txt -o  
workflow_6_known_lncRNA_single. snakemake
```

Example 27 (novel lncRNA, paired-end):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_novel_lncRNA_paired.txt -o  
workflow_novel_lncRNA_paired. snakemake
```

Example 28 (novel lncRNA, single-end):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_novel_lncRNA_single.txt -o  
workflow_novel_lncRNA_single. snakemake
```

Example 29 (circRNA, paired-end):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_circRNA_paired.txt -o  
workflow_circRNA_paired. snakemake
```

Example 30 (circRNA, single-end):

```
perl generate_hppRNA_main_snakemake.pl -i workflow_circRNA_single.txt -o  
workflow_circRNA_single. snakemake
```

To guide the program to look for the location of installed executable files, please generate the PATH file including all the necessary path headers.

Format:

perl generate_path.pl -i [the location of the software to be installed] -o [the file including the paths to executable files]

Example:

perl generate_path.pl -i /data/hppRNA_software -o path.txt

Given that your server is probably based on clusters or nodes with a job management, please combine three parts together to make up the final shell for job running. Firstly, put the content including job running information and computing resource allocation on the top as required by your server setting (Part 1). Please get in touch with the manager or administrator of your computing cluster or server for guidance if you are not sure which content you need to put here. Secondly, put the path information from the generated path file (e.g., path.txt) below (Part 2). Lastly, put the snakemake command line at the bottom (Part 3). Here is an example for your reference (*hppRNA_pipeline.sh*).

Part 1:

```
#!/bin/bash -l
```

```
# 1. Force bash as the executing shell.
```

```
#$ -S /bin/bash
```

```
# 2. Request ten minutes of wallclock time (format hours:minutes:seconds).
```

```
#$ -l h_rt=50:0:0
```

```
# 3. Request 1 gigabyte of RAM
```

```
#$ -l mem=10G
```

```
# 4. Request 15 gigabyte of TMPDIR space
```

```
#$ -l tmpfs=10G
```

```
# 5. Set the name of the job.
```

```
#$ -N hppRNA_data
```

```
# 6. Set the working directory to somewhere in your space.
```

```
#$ -wd /location_name_example/output
```

```
# 7. Run the application.
```

Part 2:

```
export PATH=/data/hppRNA_software/snakemake/Miniconda3/envs/snakemake-tutorial/bin:$PATH
```

```
export PATH=/data/hppRNA_software/perl-5.22.2/perl-5.22.2/bin:$PATH
```

```
export PATH=/data/hppRNA_software/jdk1.8.0_91/bin:$PATH
```

```
export PATH=/data/hppRNA_software/Python-2.7.11:$PATH
```

```
export PATH=/data/hppRNA_software/R-3.3.0/R-3.3.0/bin:$PATH
```

```
export PATH=/data/hppRNA_software/FastQC:$PATH
```

```
export PATH=/data/hppRNA_software/fastx_toolkit_0.0.13:$PATH
```

```
export PATH=/data/hppRNA_software/Python-2.7.11/Python-2.7.11/bin:$PATH
```

```
export PATH=/data/hppRNA_software/bowtie2-2.2.9:$PATH
```

```
export PATH=/data/hppRNA_software/tophat-2.1.1.Linux_x86_64:$PATH
```

```
export PATH=/data/hppRNA_software/cufflinks-2.2.1.Linux_x86_64:$PATH
```

```
export PATH=/data/hppRNA_software/samtools-1.3.1/samtools-1.3.1/bin:$PATH
```

```
export PATH=/data/hppRNA_software/ngsplot-develop/bin:$PATH
```

```
export NGSLOT=/data/hppRNA_software/ngsplot-develop;
```

```
export PATH=/data/hppRNA_software/hisat2-2.0.3-beta:$PATH
```



```

export PATH=/data/hppRNA_software/stringtie-1.2.2.Linux_x86_64:$PATH

export PATH=/data/hppRNA_software/kallisto_linux-v0.42.5:$PATH

export PATH=/data/hppRNA_software/STAR-2.5.1b/bin/Linux_x86_64_static:$PATH

export PATH=/data/hppRNA_software/RSEM-1.2.30:$PATH

export PATH=/data/hppRNA_software/RSEM-1.2.30/EBSeq:$PATH

export PATH=/data/hppRNA_software/express-1.5.1-linux_x86_64:$PATH

export PATH=/data/hppRNA_software/FusionCatcher/fusioncatcher/bin:$PATH

export PATH=/data/hppRNA_software/bowtie-1.1.2:$PATH

export PATH=/data/hppRNA_software/iSeeRNA-1.2.2:$PATH

```

Part 3:

```

snakemake          -p          --cores          32          --snakefile
/data/hppRNA_data/workflow_1_protein_coding_paired.snakemake

```

Note: --cores is an important argument for snakemake in order to control the maximum number of cores or CPUs that can be utilized by parallel jobs. Please set it according to your condition. -p means print all the process when running.

The final step is just to submit the job by executing the shell file.

Example:

```
qsub hppRNA_pipeline.sh
```

Example data

We have tested each module from this pipeline by means of a set of public paired-end RNA-Seq data, which includes 6 samples that have been divided into 2 groups (each group has 3 replicates). All the files in the "standard_result" folder as the example result data were calculated from this dataset.

Table 7. The basic description of the testing data.

Source Name	Accession Number	Tissue	Species	FASTQ_URI
brain_3b	ERS327019	cerebral cortex	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315477/E RR315477_1.fastq.gz
brain_3b	ERS327019	cerebral cortex	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315477/E RR315477_2.fastq.gz
brain_3c	ERS326996	cerebral cortex	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315455/E RR315455_1.fastq.gz
brain_3c	ERS326996	cerebral cortex	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315455/E RR315455_2.fastq.gz
brain_a	ERS327024	cerebral cortex	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315432/E RR315432_1.fastq.gz
brain_a	ERS327024	cerebral cortex	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315432/E RR315432_2.fastq.gz
testis_7a	ERS326963	testis	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315352/E RR315352_1.fastq.gz
testis_7a	ERS326963	testis	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315352/E RR315352_2.fastq.gz
testis_7b	ERS327017	testis	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315456/E RR315456_1.fastq.gz
testis_7b	ERS327017	testis	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315456/E RR315456_2.fastq.gz
testis_7c	ERS326984	testis	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315391/E RR315391_1.fastq.gz
testis_7c	ERS326984	testis	Homo sapiens	ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR315/ERR315391/E RR315391_2.fastq.gz

DAg (directed acyclic graph)

To facilitate the understanding of how each workflow works in this pipeline, we use the functions of Snakemake software and Graphviz to produce the directed acyclic graphs (DAgs) for our testing 6 RNA-Seq samples. Please have a look at the below small images as well as the enlarged high-resolution images (*.png) in the folder of DAg in this package.

We also show the instructions on how to generate such kinds of DAgs for the users' own datasets as follows.

Format:

```
snakemake --snakefile [the snakemake file] --dag | dot -Tsvg > [the DAg image in svg format]
```

```
convert [the DAg image in svg format] [the DAg image in png format]
```

Example 1:

```
snakemake --snakefile workflow_1_paired.snakemake.DAG --dag | dot -Tsvg > workflow_1_paired.snakemake.DAG.svg
```

```
convert workflow_1_paired.snakemake.DAG.svg workflow_1_paired.snakemake.DAG.png
```

Example 2:

```
snakemake --snakefile workflow_2_paired.snakemake.DAG --dag | dot -Tsvg > workflow_2_paired.snakemake.DAG.svg
```

convert workflow_2_paired.snakemake.DAG.svg workflow_2_paired.snakemake.DAG.png

Example 3:

*snakemake --snakefile workflow_3_paired.snakemake.DAG --dag | dot -Tsvg >
workflow_3_paired.snakemake.DAG.svg*

convert workflow_3_paired.snakemake.DAG.svg workflow_3_paired.snakemake.DAG.png

Example 4:

*snakemake --snakefile workflow_4_paired.snakemake.DAG --dag | dot -Tsvg >
workflow_4_paired.snakemake.DAG.svg*

convert workflow_4_paired.snakemake.DAG.svg workflow_4_paired.snakemake.DAG.png

Example 5:

*snakemake --snakefile workflow_5_paired.snakemake.DAG --dag | dot -Tsvg >
workflow_5_paired.snakemake.DAG.svg*

convert workflow_5_paired.snakemake.DAG.svg workflow_5_paired.snakemake.DAG.png

Example 6:

*snakemake --snakefile workflow_6_paired.snakemake.DAG --dag | dot -Tsvg >
workflow_6_paired.snakemake.DAG.svg*

convert workflow_6_paired.snakemake.DAG.svg workflow_6_paired.snakemake.DAG.png

Example 7:

```
snakemake --snakefile workflow_1_paired_variation.snakemake.DAG --dag | dot -Tsvg > workflow_1_paired_variation.snakemake.DAG.svg
```

```
convert workflow_1_paired_variation.snakemake.DAG.svg workflow_1_paired_variation.snakemake.DAG.png
```

Example 8:

```
snakemake --snakefile workflow_lncRNA_denovo_paired.snakemake.DAG --dag | dot -Tsvg > workflow_lncRNA_denovo_paired.snakemake.DAG.svg
```

```
convert workflow_lncRNA_denovo_paired.snakemake.DAG.svg workflow_lncRNA_denovo_paired.snakemake.DAG.png
```

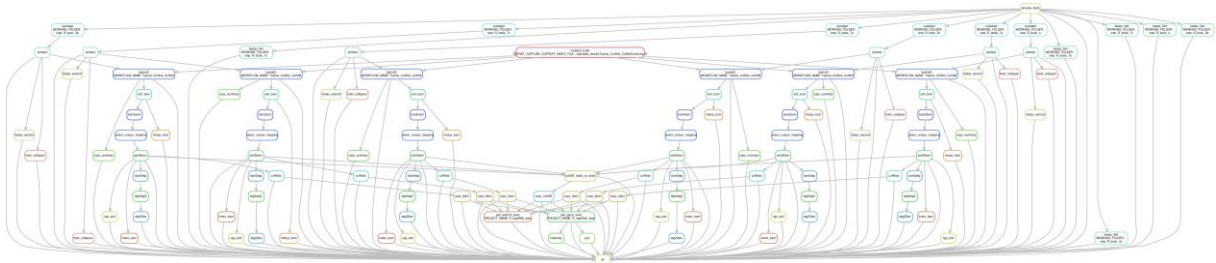
Example 9:

```
snakemake --snakefile workflow_circRNA_paired.snakemake.DAG --dag | dot -Tsvg > workflow_circRNA_paired.snakemake.DAG.svg
```

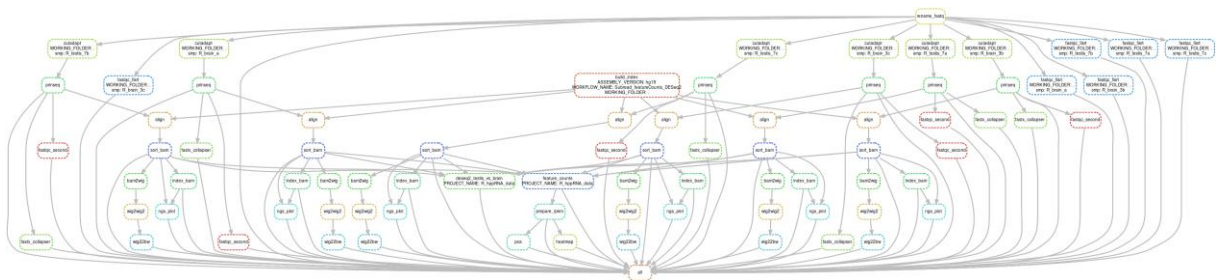
```
convert workflow_circRNA_paired.snakemake.DAG.svg workflow_circRNA_paired.snakemake.DAG.png
```

Examples for DAGs (Please check the enlarged high-resolution images in the folder of DAG)

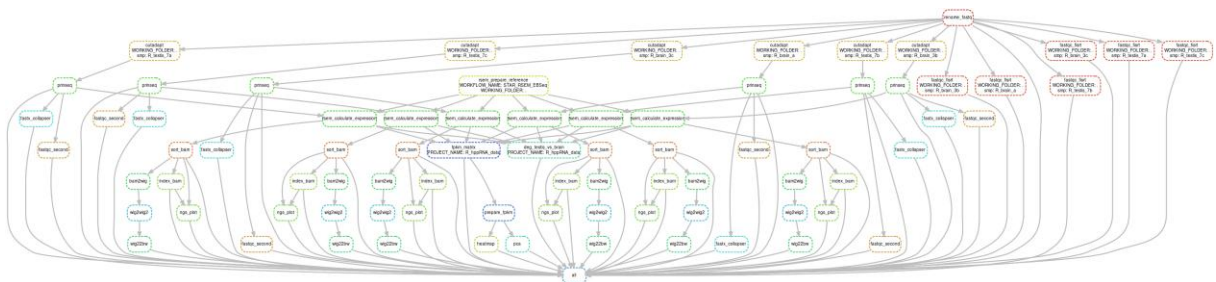
Example 1: workflow_1_paired.snakemake.DAG.png



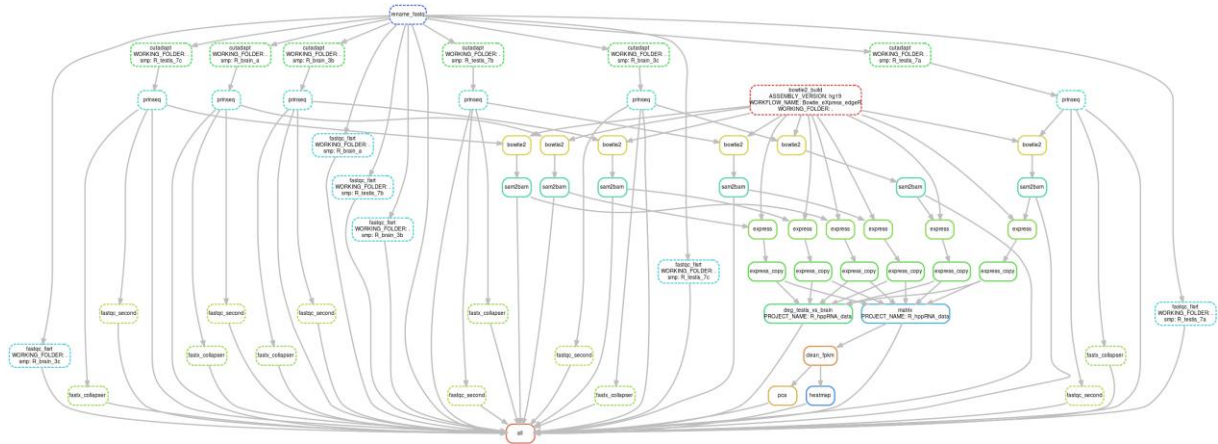
Example 2: workflow_2_paired.snakemake.DAG.png



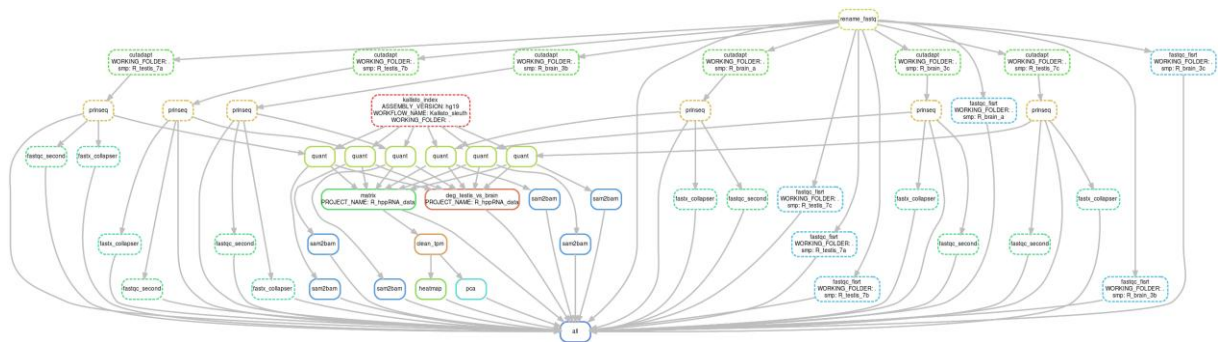
Example 3: workflow_3_paired.snakemake.DAG.png



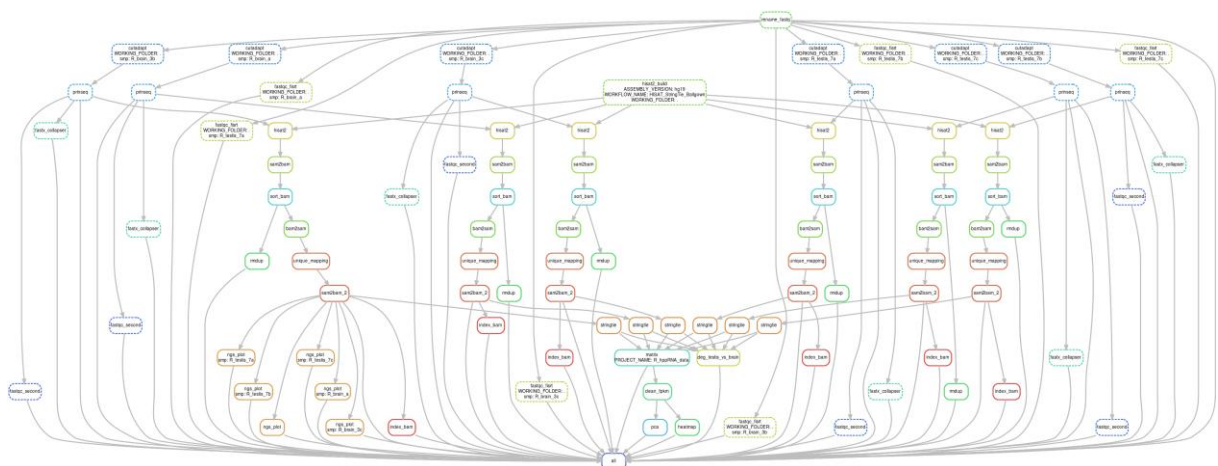
Example 4: workflow_4_paired.snakemake.DAG.png



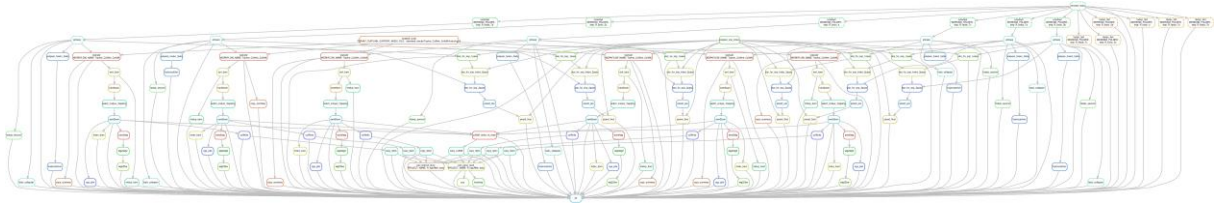
Example 5: workflow_5_paired.snakemake.DAG.png



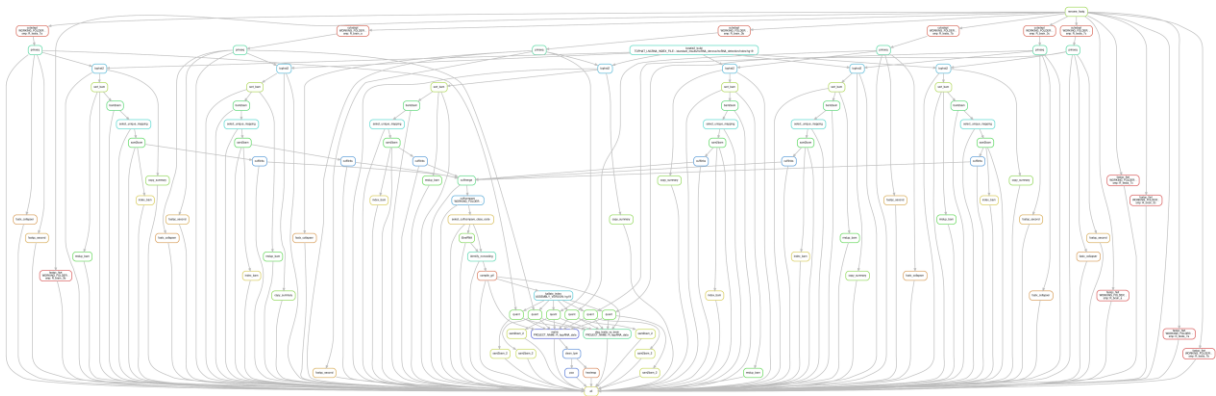
Example 6: workflow_6_paired.snakemake.DAG.png



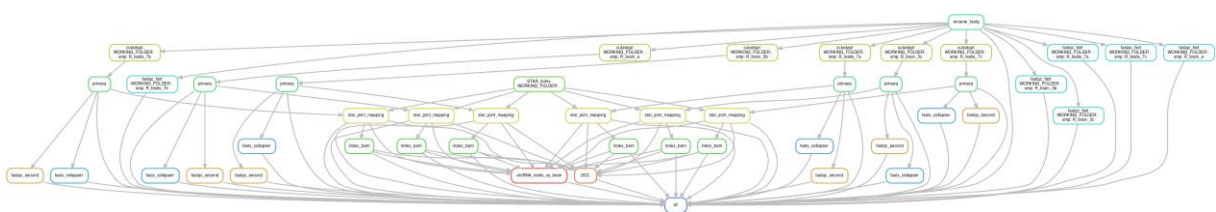
Example 7: workflow_1_paired_variation.snakemake.DAG.png



Example 8: workflow_lncRNA_denovo_paired.snakemake.DAG.png



Example 9: workflow_circRNA_paired.snakemake.DAG.png



Performance evaluation

We evaluate the performance the pipeline for each workflow by means of the testing dataset. Generally, the running time is positively correlated to the total number of bases in the raw fastq files and negatively correlated to the number of cores or CPUs, varying from workflow to workflow.

Table 8. The total sequences for each sample in the testing dataset.

<i>Sample</i>	<i>Type</i>	<i>Sequence length</i>	<i>Total Sequences</i>
<i>R_brain_3b</i>	<i>Paired-End</i>	<i>101</i>	<i>28466648</i>
<i>R_brain_3c</i>	<i>Paired-End</i>	<i>101</i>	<i>24323755</i>
<i>R_brain_a</i>	<i>Paired-End</i>	<i>101</i>	<i>17585264</i>
<i>R_testis_7a</i>	<i>Paired-End</i>	<i>101</i>	<i>35915919</i>
<i>R_testis_7b</i>	<i>Paired-End</i>	<i>101</i>	<i>32054218</i>
<i>R_testis_7c</i>	<i>Paired-End</i>	<i>101</i>	<i>39007238</i>

Table 9. The running time for various workflows for the testing dataset.

	<i>Pre-mapping+</i> <i>Workflow 1</i>	<i>Workflow</i> <i>2</i>	<i>Workflow</i> <i>3</i>	<i>Workflow</i> <i>4</i>	<i>Workflow</i> <i>5</i>	<i>Workflow</i> <i>6</i>
<i>Provided cores</i>	<i>32</i>	<i>32</i>	<i>12</i>	<i>32</i>	<i>32</i>	<i>32</i>
<i>Thread</i>	<i>6</i>	<i>6</i>	<i>6</i>	<i>6</i>	<i>6</i>	<i>6</i>
<i>Running time (h:m:s)</i>	<i>9:22:07</i>	<i>3:25:04</i>	<i>8:00:45</i>	<i>20:08:11</i>	<i>1:00:37</i>	<i>2:41:23</i>

Note: h - hour; m - minute; s - second. Thread means the number of threads used in each job or rule.

To understand the intermediate and final files of importance generated from this pipeline

* indicates the sample name you give in the sample description table

indicates the project name appearing in the sample description table

Table 10. The explanation of each essential resultant files generated by this pipeline.

Section	Folder	File	Description
Pre-mapping	Raw_FASTQ	R_*.R1.fastq	The original R1 fastq file but with the new file name defined by the correspondence between the raw file names and the user-defined names in the sample description table.
Pre-mapping	Raw_FASTQ	R_*.R2.fastq	The original R2 fastq file but with the new file name defined by the correspondence between the raw file names and the user-defined names in the sample description table.
Pre-mapping	FastQC	R_*.R1_fastqc.zip	The result generated by Fastqc for R_*.R1.fastq.
Pre-mapping	FastQC	R_*.R2_fastqc.zip	The result generated by Fastqc for R_*.R2.fastq.
Pre-mapping	Processed_FASTQ	R_*_1.fastq	The fastq file after basic processing including adaptor removal and/or base quality control for R_*.R1.fastq.
Pre-mapping	Processed_FASTQ	R_*_2.fastq	The fastq file after basic processing including adaptor removal and/or base quality control for R_*.R2.fastq.
Pre-mapping	FastQC	R_*_1_fastqc.zip	The result generated by Fastqc for R_*_1.fastq.
Pre-mapping	FastQC	R_*_2_fastqc.zip	The result generated by Fastqc for R_*_2.fastq.
Pre-mapping	Fasta	R_*_1.collapser.fasta	The fasta file including unique sequences after collapsing R_*_1.fastq.
Pre-mapping	Fasta	R_*_2.collapser.fasta	The fasta file including unique sequences after collapsing R_*_2.fastq.
workflow 1	Bigwig	R_*.wig.gz	The wig file originated from

			R_*.sorted.unique.bam.
workflow 1	Bigwig	R_*.wig.2.gz	The wig file from R_*.wig.gz without track header.
workflow 1	Bigwig	R_*.bw	The bigwig file from R_*.wig.2.gz, which is used for UCSC genome browser track display.
workflow 1	Cluster	R_#.Tophat_Cuffli nk_Cuffdiff.gene.F PKM.clean.txt	The consicely formatted file containing gene expression matrix for heatmap or PCA plot.
workflow 1	Cluster	R_#.Tophat_Cuffli nk_Cuffdiff.gene.F PKM.clean.txt.1.h eatmap.pdf	The figure shows the heatmap for clustering both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization.
workflow 1	Cluster	R_#.Tophat_Cuffli nk_Cuffdiff.gene.F PKM.clean.txt.1.m atrix.txt	The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample.
workflow 1	Cluster	R_#.Tophat_Cuffli nk_Cuffdiff.gene.F PKM.clean.txt.1.P CA.pdf	The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis.
workflow 1	Cluster	R_#.Tophat_Cuffli nk_Cuffdiff.gene.F PKM.clean.txt.1.r otation.t	The table consists of variable loadings for PCA analysis.
workflow 1	DEG	R_#.Tophat_Cuffli nk_Cuffdiff.X_vs_ Y.gene.DEG.txt	A tab-delimited text file contains the differentially-expressed-genes identified by cuffdiff.
workflow 1	DEG	R_#.Tophat_Cuffli nk_Cuffdiff.X_vs_ Y.transcript.DEG. txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by cuffdiff.
workflow 1	Gene_expression_ matrix	R_#.Tophat_Cuffli nk_Cuffdiff.gene.F PKM.txt	A tab-delimited file contains the FPKM matrix in the level of genes.
workflow 1	Gene_expression_ matrix	R_#.Tophat_Cuffli nk_Cuffdiff.transc ript.FPKM.txt	A tab-delimited file contains the FPKM matrix in the level of transcripts or isoforms.
workflow 1	NGS_plot	NGSplot. *.genebody.avgpro f.pdf	A figure shows the normalized density curve averaging all reads across gene body on the basis of build-in gene model.
workflow 1	NGS_plot	NGSplot. *.genebody.heatm	The heatmap reflects read distribution across each gene or consecutive region.

		ap.pdf	
workflow 1	NGS_plot	NGSplot. *.genebody.zip	The compressed fold includes the original matrix data for plotting average profile or heatmap.
workflow 1	Processed_BAM	R_*.sorted.bam	The sorted bam file after mapping R_*_1.fastq and R_*_2.fastq onto the given genome.
workflow 1	Processed_BAM	R_*.sorted.rmdup. bam	The bam file after removal of potential PCR duplicates with samtools rmdup from R_*.sorted.bam.
workflow 1	Processed_BAM	R_*.sorted.sam	The sam format file from R_*.sorted.bam.
workflow 1	Processed_BAM	R_*.sorted.unique. sam	The sam file containing selected unique alignments from R_*.sorted.sam.
workflow 1	Processed_BAM	R_*.sorted.unique. bam	The bam file corresponding to R_*.sorted.unique.sam.
workflow 1	Processed_BAM	R_*.sorted.unique. bam.bai	The BAI index file for R_*.sorted.unique.bam.
workflow 1	Processed_BAM	R_*_align_summa ry.txt	The file for mapping information with Tophat2.
workflow 2	Bigwig	R_*.wig.gz	The wig file originated from R_*.sorted.unique.bam.
workflow 2	Bigwig	R_*.wig.2.gz	The wig file from R_*.wig.gz without track header.
workflow 2	Bigwig	R_*.bw	The bigwig file from R_*.wig.2.gz, which is used for UCSC genome browser track display.
workflow 2	Cluster	R_#.Subread_feat ureCounts_DESeq 2.gene.RPKM.clea n.txt	The consicely formatted file containing gene expression matrix for heatmap or PCA plot.
workflow 2	Cluster	R_#.Subread_feat ureCounts_DESeq 2.gene.RPKM.clea n.txt.1.heatmap.pd f	The figure shows the heatmap for clustering both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization.
workflow 2	Cluster	R_#.Subread_feat ureCounts_DESeq 2.gene.RPKM.clea n.txt.1.matrix.txt	The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample.
workflow 2	Cluster	R_#.Subread_feat ureCounts_DESeq 2.gene.RPKM.clea n.txt.1.PCA.pdf	The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis.

workflow 2	Cluster	R_#.Subread_featureCounts_DESeq2.gene.RPKM.clean.txt.1.rotation.txt	The table consists of variable loadings for PCA analysis.
workflow 2	DEG	R_#.Subread_featureCounts_DESeq2.X_vs_Y.DESeq2.csv	A comma-seperated file contains the differentially-expressed-genes identified by DESeq2.
workflow 2	DEG	R_#.Subread_featureCounts_DESeq2.X_vs_Y.DESeq2.txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by DESeq2.
workflow 2	Gene_expression_matrix	R_#.Subread_featureCounts_DESeq2.gene.counts.csv	A comma-seperated file contains the count matrix in the level of genes.
workflow 2	Gene_expression_matrix	R_#.Subread_featureCounts_DESeq2.gene.counts.txt	A tab-delimited file contains the count matrix in the level of genes.
workflow 2	Gene_expression_matrix	R_#.Subread_featureCounts_DESeq2.gene.RPKM.csv	A comma-seperated file contains the FPKM matrix in the level of genes.
workflow 2	Gene_expression_matrix	R_#.Subread_featureCounts_DESeq2.gene.RPKM.txt	A tab-delimited file contains the FPKM matrix in the level of genes.
workflow 2	NGS_plot	NGSplot.*.genebody.avgprofile.pdf	A figure shows the normalized density curve averaging all reads across gene body on the basis of build-in gene model.
workflow 2	NGS_plot	NGSplot.*.genebody.heatmap.pdf	The heatmap reflects read distribution across each gene or consecutive region.
workflow 2	NGS_plot	NGSplot.*.genebody.zip	The compressed fold includes the original matrix data for plotting average profile or heatmap.
workflow 2	Processed_BAM	R_*.sorted.unique.bam	The sorted bam file for unique alignments.
workflow 2	Processed_BAM	R_*.sorted.unique.bam.bai	The BAI index file of R_*.sorted.unique.bam.
workflow 2	Processed_BAM	R_*.unique.bam	The BAM file for unique alignments.
workflow 3	Bigwig	R_*.wig.gz	The wig file originated from R_*.sorted.unique.bam.
workflow 3	Bigwig	R_*.wig.2.gz	The wig file from R_*.wig.gz without track header.
workflow 3	Bigwig	R_*.bw	The bigwig file from R_*.wig.2.gz, which is used for UCSC genome browser track

			display.
workflow 3	Cluster	R_#.STAR_RSEM _EBSeq.gene.FPK M.clean.txt	The concisely formatted file containing gene expression matrix for heatmap or PCA plot.
workflow 3	Cluster	R_#.STAR_RSEM _EBSeq.gene.FPK M.clean.txt.1.heat map.pdf	The figure shows the heatmap for clustering both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization.
workflow 3	Cluster	R_#.STAR_RSEM _EBSeq.gene.FPK M.clean.txt.1.matr ix.txt	The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample.
workflow 3	Cluster	R_#.STAR_RSEM _EBSeq.gene.FPK M.clean.txt.1.PCA .pdf	The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis.
workflow 3	Cluster	R_#.STAR_RSEM _EBSeq.gene.FPK M.clean.txt.1.rotat ion.txt	The table consists of variable loadings for PCA analysis.
workflow 3	DEG	R_#.STAR_RSEM _EBSeq.X_vs_Y.g ene.DEG.txt	A tab-delimited text file contains the differentially-expressed-genes identified by EBSeq.
workflow 3	DEG	R_#.STAR_RSEM _EBSeq.X_vs_Y.tr anscript.DEG.txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by EBSeq.
workflow 3	Gene_expression_ matrix	R_#.STAR_RSEM _EBSeq.gene.FPK M.txt	A tab-delimited file contains the FPKM matrix in the level of genes.
workflow 3	Gene_expression_ matrix	R_#.STAR_RSEM _EBSeq.transcript .FPKM.txt	A tab-delimited file contains the FPKM matrix in the level of transcripts or isoforms.
workflow 3	NGS_plot	NGSplot. *.genebody.avgpro f.pdf	A figure shows the normalized density curve averaging all reads across gene body on the basis of build-in gene model.
workflow 3	NGS_plot	NGSplot. *.genebody.heatm ap.pdf	The heatmap reflects read distribution across each gene or consecutive region.
workflow 3	NGS_plot	NGSplot. *.genebody.zip	The compressed fold includes the original matrix data for plotting average profile or heatmap.
workflow 3	Processed_BAM	R_*.genes.results	A tab-delimited text file contains expression quantifications in the level of genes.

workflow 3	Processed_BAM	R_*.genome.bam	The BAM file for alignments produced by RSEM in genomic coordinates.
workflow 3	Processed_BAM	R_*.genome.sorted.bam	The sorted BAM file of R_*.genome.bam.
workflow 3	Processed_BAM	R_*.genome.sorted.bam.bai	The BAI index file of R_*.genome.sorted.bam.
workflow 3	Processed_BAM	R_*.isoforms.results	A tab-delimited text file contains expression quantifications in the level of isoforms.
workflow 3	Processed_BAM	R_*.transcript.bam	The BAM file for alignments produced by RSEM in transcript coordinates.
workflow 4	Cluster	R_#.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt	The concisely formatted file containing gene expression matrix for heatmap or PCA plot.
workflow 4	Cluster	R_#.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.heatmap.pdf	The figure shows the heatmap for clustering both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization.
workflow 4	Cluster	R_#.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.matrix.txt	The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample.
workflow 4	Cluster	R_#.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.PCA.pdf	The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis.
workflow 4	Cluster	R_#.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.rotation.txt	The table consists of variable loadings for PCA analysis.
workflow 4	DEG	R_#.Bowtie_eXpress_edgeR.X_vs_Y.gene.DEG.txt	A tab-delimited text file contains the differentially-expressed-genes identified by edgeR.
workflow 4	DEG	R_#.Bowtie_eXpress_edgeR.X_vs_Y.transcript.DEG.txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by edgeR.
workflow 4	Gene_expression_matrix	R_#.Bowtie_eXpress_edgeR.gene.FPKM.txt	A tab-delimited file contains the FPKM matrix in the level of genes.
workflow 4	Gene_expression_matrix	R_#.Bowtie_eXpress_edgeR.transcript.FPKM.txt	A tab-delimited file contains the FPKM matrix in the level of transcripts or isoforms.
workflow 4	Processed_BAM	R_*.bam	The BAM file for alignments produced by Bowtie2.

workflow 4	Processed_BAM	R_*.sam	The SAM file for alignments produced by Bowtie2.
workflow 5	Cluster	R_#.Kallisto_sleuth.gene.TPM.clean.txt	The consicely formatted file containing gene expression matrix for heatmap or PCA plot.
workflow 5	Cluster	R_#.Kallisto_sleuth.gene.TPM.clean.txt.1.heatmap.pdf	The figure shows the heatmap for clustering both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization.
workflow 5	Cluster	R_#.Kallisto_sleuth.gene.TPM.clean.txt.1.matrix.txt	The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample.
workflow 5	Cluster	R_#.Kallisto_sleuth.gene.TPM.clean.txt.1.PCA.pdf	The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis.
workflow 5	Cluster	R_#.Kallisto_sleuth.gene.TPM.clean.txt.1.rotation.txt	The table consists of variable loadings for PCA analysis.
workflow 5	DEG	R_#.Kallisto_sleuth.X_vs_Y.gene.DEG.txt	A tab-delimited text file contains the differentially-expressed-genes identified by sleuth.
workflow 5	DEG	R_#.Kallisto_sleuth.X_vs_Y.transcript.DEG.txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by sleuth.
workflow 5	Gene_expression_matrix	R_#.Kallisto_sleuth.gene.TPM.txt	A tab-delimited file contains the TPM matrix in the level of genes.
workflow 5	Gene_expression_matrix	R_#.Kallisto_sleuth.transcript.TPM.txt	A tab-delimited file contains the TPM matrix in the level of transcripts or isoforms.
workflow 5	Processed_BAM	R_*.bam	The BAM file produced by kallisto.
workflow 5	Processed_BAM	R_*.sam	The SAM file produced by kallisto.
workflow 6	Bigwig	R_*.wig.gz	The wig file originated from R_*.sorted.unique.bam.
workflow 6	Bigwig	R_*.wig.2.gz	The wig file from R_*.wig.gz without track header.
workflow 6	Bigwig	R_*.bw	The bigwig file from R_*.wig.2.gz, which is used for UCSC genome browser track display.
workflow 6	Cluster	R_#.HISAT_Stripe_Ballgown.gene.FPKM.clean.txt	The consicely formatted file containing gene expression matrix for heatmap or PCA plot.
workflow 6	Cluster	R_#.HISAT_Stripe	The figure shows the heatmap for clustering

workflow 6	Cluster	gTie_Ballgown.gene.FPKM.clean.txt .1.heatmap.pdf R_#.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt .1.matrix.txt	both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization. The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample.
workflow 6	Cluster	R_#.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt .1.PCA.pdf	The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis.
workflow 6	Cluster	R_#.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt .1.rotation.txt	The table consists of variable loadings for PCA analysis.
workflow 6	DEG	R_#.HISAT_StringTie_Ballgown.X_vs_Y.gene.DEG.txt	A tab-delimited text file contains the differentially-expressed-genes identified by Ballgown.
workflow 6	DEG	R_#.HISAT_StringTie_Ballgown.X_vs_Y.transcript.DEG.txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by Ballgown.
workflow 6	Gene_expression_matrix	R_#.HISAT_StringTie_Ballgown.gene.FPKM.txt	A tab-delimited file contains the FPKM matrix in the level of genes.
workflow 6	Gene_expression_matrix	R_#.HISAT_StringTie_Ballgown.transcript.FPKM.txt	A tab-delimited file contains the FPKM matrix in the level of transcripts or isoforms.
workflow 6	NGS_plot	NGSplot. *.genebody.avgprofile.pdf	A figure shows the normalized density curve averaging all reads across gene body on the basis of build-in gene model.
workflow 6	NGS_plot	NGSplot. *.genebody.heatmap.pdf	The heatmap reflects read distribution across each gene or consecutive region.
workflow 6	NGS_plot	NGSplot. *.genebody.zip	The compressed fold includes the original matrix data for plotting average profile or heatmap.
workflow 6	Processed_BAM	R_*.1.bam	The BAM file of R_*.sam.
workflow 6	Processed_BAM	R_*.sam	The SAM file of alignments produced by hisat2.
workflow 6	Processed_BAM	R_*.sorted.bam	The sorted BAM file of R_*.1.bam.
workflow 6	Processed_BAM	R_*.sorted.rmdup.	The produced BAM file for R_*.sorted.bam

workflow 6	Processed_BAM	bam R_*.sorted.sam	after PCR duplication removal. The SAM file of R_*.sorted.bam.
workflow 6	Processed_BAM	R_*.sorted.unique. bam	The BAM file of R_*.sorted.unique.sam
workflow 6	Processed_BAM	R_*.sorted.unique. bam.bai	The BAI index file of R_*.sorted.unique.bam.
workflow 6	Processed_BAM	R_*.sorted.unique. sam	The SAM file of unique-mapping alignments from R_*.sorted.sam.
DNA variation	vcf	R_*.filter.vcf	The final VCF formatted file for sample * in terms of SNP detection.
DNA variation	Fusion_result/R_*	summary_candida te_fusions.txt	The short summary of detected fusion gene events.
DNA variation	Fusion_result/R_*	final-list_candidat e-fusion-genes.txt	The detailed information of detected fusion gene events.
lncRNA_denovo	iseeRNA	cuffcmp.combined .selected.result	The gtf file includes the filtered novel lncRNA annotation.
lncRNA_denovo	iseeRNA	cuffcmp.combined .selected.noncodin g.gtf	The file is reported from iseeRNA to include the classification of noncoding and coding transcripts.
lncRNA_denovo	iseeRNA	denovo_lncRNA.tr anscript_to_gene.t xt	The map file between transcripts and genes for novel identified lncRNAs.
lncRNA_denovo	Gene_expression_ matrix	R_#.lncRNA_deno vo.gene.TPM.txt	A tab-delimited file contains the TPM matrix in the level of genes in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.
lncRNA_denovo	Gene_expression_ matrix	R_#.lncRNA_deno vo.transcript.TPM .txt	A tab-delimited file contains the TPM matrix in the level of transcripts or isoforms in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.
lncRNA_denovo	DEG	R_#.lncRNA_deno vo.X_vs_Y.gene.D EG.txt	A tab-delimited text file contains the differentially-expressed-genes identified by sleuth in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.
lncRNA_denovo	DEG	R_#.lncRNA_deno vo.X_vs_Y.transcr ipt.DEG.txt	A tab-delimited text file contains the differentially-expressed-transcripts identified by sleuth in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.
lncRNA_denovo	Cluster	R_#.lncRNA_deno vo.gene.TPM.clea n.txt	The consicely formatted file containing gene expression matrix for heatmap or PCA plot in terms of a combined annotation set of

lncRNA_denovo	Cluster	R_#.lncRNA_denovo.gene.TPM.clean.txt.1.heatmap.pdf	<p>protein-coding genes and known and novel lncRNAs.</p> <p>The figure shows the heatmap for clustering both samples and genes after removal of extremely lowly-expressed genes and log2 transformation and quantile normalization in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.</p> <p>The matrix is made up of FPKM values for genes where FPKM is no less than 1 at least in one sample in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.</p> <p>The figure illustrates the PCA analysis by plotting PC1 against PC2 in order to observe the global tendency of all samples. The data process procedure is similar to that in heatmap analysis in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.</p> <p>The table consists of variable loadings for PCA analysis in terms of a combined annotation set of protein-coding genes and known and novel lncRNAs.</p>
lncRNA_denovo	Cluster	R_#.lncRNA_denovo.gene.TPM.clean.txt.1.matrix.txt	
lncRNA_denovo	Cluster	R_#.lncRNA_denovo.gene.TPM.clean.txt.1.PCA.pdf	
lncRNA_denovo	Cluster	R_#.lncRNA_denovo.gene.TPM.clean.txt.1.rotation.txt	
CircRNA	DCC	CircRNACount	The table contains the read counts for each identified circRNA.
CircRNA	DCC	LinearCount	The table contains the read counts for the host genes.
CircRNA	CircTest/X_vs_Y	R_#.STAR_DCC_circTest.X_vs_Y.circTest.txt	The table contains the significantly changed circRNAs across conditions in terms of their relative abundance when circRNA vs. host gene expression is taken into account.

Gene system

Due to the various resources of the different types of genes and the approach used in the identification of novel lncRNAs, there are three kinds of gene systems in the analysis. Fortunately, it is easy to tell them apart according to the below tables.

Species	Category	Protein-coding	known lncRNA	novel lncRNA
Human	Gene	-	ENSG	XLOC_
Human	Transcript	NM_/NR_	ENST	TCONS_

Species	Category	Protein-coding	known lncRNA	novel lncRNA
Mouse	Gene	-	ENSMUSG	XLOC_
Mouse	Transcript	NM_/NR_	ENSMUST	TCONS_

Troubleshooting

A couple of monitor points have been set up for quality control for the process of the analysis in the three levels of reads, alignments and samples. Briefly, when a sample is problematic in any or some of the levels, it should be cautious to consider this sample depending on your specific purpose.

Read level

FastQC is run twice before and after the fastq file processing and through comparing the two results for the same sample, it is likely to check if the adaptor sequences have been removed correctly and sufficiently and if the base quality is acceptable, and if not, a modified adaptor sequence should be considered or the sample should be eliminated when the quality is too bad. In addition, comparison of the total number of reads would help determine the general quality of the sequencing.

Alignment level

Based on the alignment, NGSplot will tell you the distribution of mapped reads across the gene model in certain organism, the shape of which reflects the quality of the alignment and RNA quality such as RIN number. Please see more on the website of this software: <https://github.com/shenlab-sinai/ngsplot>

Sample level

Heatmaps and PCA (Principle Component Analysis) plots provide an opportunity to check if any of the samples is a technical failure especially when you have replicates for each conditions. Typically, the samples from the same condition should be clustered together and the samples from different conditions should be in different clusters in heatmaps or have some

distances in PCA plots (either PC1 or PC2). If a sample falls out of the normal range or cluster, it is likely to be removed.

Appendix

The name list of all the files arranged in the directory resulted from all the functional modules of this pipeline.

standard_results:

total 384

drwxr-xr-x 9	4096 Jul 28 22:07	Bowtie_eXpress_edgeR
drwxr-xr-x 6	4096 Dec 8 15:58	CircRNA
drwxr-xr-x 2	4096 Jul 22 02:50	Fasta
drwxr-xr-x 2	8192 Jul 22 02:58	FastQC
drwxr-xr-x 4	4096 Jul 22 16:19	Fusion_gene
drwxr-xr-x 5	4096 Jul 31 01:56	HISAT_StringTie_Ballgown
drwxr-xr-x 9	4096 Jul 30 14:30	Kallisto_sleuth
drwxr-xr-x 4	4096 Dec 9 16:49	lncRNA_denovo
drwxr-xr-x 2	8192 Jul 21 19:18	Processed_FASTQ
drwxr-xr-x 2	4096 Jul 21 11:37	Raw_FASTQ
drwxr-xr-x 2	4096 Jul 31 15:05	SNP
drwxr-xr-x 9	4096 Jul 29 03:40	STAR_RSEM_EBSeq
drwxr-xr-x 9	4096 Jul 25 07:23	Subread_featureCounts_DESeq2
drwxr-xr-x 9	4096 Jul 21 11:30	Tophat_Cufflink_Cuffdiff

standard_results/Bowtie_eXpress_edgeR:

total 224

drwxr-xr-x 2	4096 Jul 28 22:07	Bigwig
drwxr-xr-x 2	4096 Jul 30 20:01	Cluster
drwxr-xr-x 3	4096 Jul 30 20:01	DEG
drwxr-xr-x 4	4096 Jul 29 19:32	Gene_expression_matrix
drwxr-xr-x 2	4096 Jul 28 22:10	Index

drwxr-xr-x 2 4096 Jul 28 22:07 NGS_plot

drwxr-xr-x 2 4096 Jul 29 17:12 Processed_BAM

standard_results/Bowtie_eXpress_edgeR/Bigwig:

total 0

standard_results/Bowtie_eXpress_edgeR/Cluster:

total 7184

-rw-r--r-- 1 1085 Jul 30 20:01 R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.heatmap.R

-rw-r--r-- 1 1428 Jul 29 19:32 R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.PCA.R

-rw-r--r-- 1 1504881 Jul 29 19:32 R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt

-rw-r--r-- 1 983304 Jul 30 20:02

R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.heatmap.pdf

-rw-r--r-- 1 1107389 Jul 29 19:32

R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.matrix.txt

-rw-r--r-- 1 4830 Jul 29 19:32 R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.PCA.pdf

-rw-r--r-- 1 2160494 Jul 29 19:32

R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.clean.txt.1.rotation.txt

standard_results/Bowtie_eXpress_edgeR/DEG:

total 14128

-rw-r--r-- 1 1333546 Jul 30 20:01 R_hppRNA_data.Bowtie_eXpress_edgeR.testis_vs_brain.eff_counts.txt

-rw-r--r-- 1 3742732 Jul 30 20:01 R_hppRNA_data.Bowtie_eXpress_edgeR.testis_vs_brain.gene.DEG.txt

-rw-r--r-- 1 3554305 Jul 30 20:01

R_hppRNA_data.Bowtie_eXpress_edgeR.testis_vs_brain.transcript.DEG.csv

-rw-r--r-- 1 3469265 Jul 30 20:01

R_hppRNA_data.Bowtie_eXpress_edgeR.testis_vs_brain.transcript.DEG.txt

drwxr-xr-x 2 4096 Jul 29 19:32 testis_vs_brain

standard_results/Bowtie_eXpress_edgeR/DEG/testis_vs_brain:

total 41584

-rw-r--r-- 1 5957259 Jul 30 20:01 R_brain_3b.results.xprs
-rw-r--r-- 1 5951998 Jul 30 20:01 R_brain_3c.results.xprs
-rw-r--r-- 1 5945776 Jul 30 20:01 R_brain_a.results.xprs
-rw-r--r-- 1 5995023 Jul 30 20:01 R_testis_7a.results.xprs
-rw-r--r-- 1 5986826 Jul 30 20:01 R_testis_7b.results.xprs
-rw-r--r-- 1 6000365 Jul 30 20:01 R_testis_7c.results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix:

total 6592

drwxr-xr-x 8 4096 Jul 29 19:00 Quantification
-rw-r--r-- 1 1504889 Jul 29 19:32 R_hppRNA_data.Bowtie_eXpress_edgeR.gene.FPKM.txt
-rw-r--r-- 1 4075243 Jul 29 19:32 R_hppRNA_data.Bowtie_eXpress_edgeR.transcript.FPKM.txt
drwxr-xr-x 2 4096 Jul 29 19:32 Summary

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification:

total 192

drwxr-xr-x 2 4096 Jul 29 19:00 R_brain_3b
drwxr-xr-x 2 4096 Jul 29 19:32 R_brain_3c
drwxr-xr-x 2 4096 Jul 29 19:27 R_brain_a
drwxr-xr-x 2 4096 Jul 29 18:15 R_testis_7a
drwxr-xr-x 2 4096 Jul 29 18:54 R_testis_7b
drwxr-xr-x 2 4096 Jul 29 18:13 R_testis_7c

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification/R_brain_3b:

total 7424

-rw-r--r-- 1 357213 Jul 29 19:00 params.xprs
-rw-r--r-- 1 5957259 Jul 29 19:00 results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification/R_brain_3c:

total 7424

-rw-r--r-- 1 357213 Jul 29 19:32 params.xprs

-rw-r--r-- 1 5951998 Jul 29 19:32 results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification/R_brain_a:

total 7424

-rw-r--r-- 1 357213 Jul 29 19:27 params.xprs

-rw-r--r-- 1 5945776 Jul 29 19:27 results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification/R_testis_7a:

total 7504

-rw-r--r-- 1 357213 Jul 29 18:15 params.xprs

-rw-r--r-- 1 5995023 Jul 29 18:15 results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification/R_testis_7b:

total 7472

-rw-r--r-- 1 357213 Jul 29 18:54 params.xprs

-rw-r--r-- 1 5986826 Jul 29 18:54 results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Quantification/R_testis_7c:

total 7504

-rw-r--r-- 1 357213 Jul 29 18:13 params.xprs

-rw-r--r-- 1 6000365 Jul 29 18:13 results.xprs

standard_results/Bowtie_eXpress_edgeR/Gene_expression_matrix/Summary:

total 41584

-rw-r--r-- 1 5957259 Jul 29 19:27 R_brain_3b.results.xprs

-rw-r--r-- 1 5951998 Jul 29 19:32 R_brain_3c.results.xprs
-rw-r--r-- 1 5945776 Jul 29 19:27 R_brain_a.results.xprs
-rw-r--r-- 1 5995023 Jul 29 19:27 R_testis_7a.results.xprs
-rw-r--r-- 1 5986826 Jul 29 19:27 R_testis_7b.results.xprs
-rw-r--r-- 1 6000365 Jul 29 19:27 R_testis_7c.results.xprs

standard_results/Bowtie_eXpress_edgeR/Index:

total 948816

-rw-r--r-- 1 53202331 Jul 28 22:09 hg19.1.bt2
-rw-r--r-- 1 281154556 Jul 28 22:09 hg19.2.bt2
-rw-r--r-- 1 382643 Jul 28 22:07 hg19.3.bt2
-rw-r--r-- 1 35144319 Jul 28 22:07 hg19.4.bt2
-rw-r--r-- 1 53202331 Jul 28 22:10 hg19.rev.1.bt2
-rw-r--r-- 1 281154556 Jul 28 22:10 hg19.rev.2.bt2
-rw-r--r-- 1 144117393 Jul 28 22:07 hg19.transcript.fa

standard_results/Bowtie_eXpress_edgeR/NGS_plot:

total 0

standard_results/Bowtie_eXpress_edgeR/Processed_BAM:

total 474972464

-rw-r--r-- 1 6935481974 Jul 29 17:12 R_brain_3b.bam
-rw-r--r-- 1 66757162178 Jul 29 12:30 R_brain_3b.sam
-rw-r--r-- 1 5674958444 Jul 29 17:20 R_brain_3c.bam
-rw-r--r-- 1 53160430320 Jul 29 15:50 R_brain_3c.sam
-rw-r--r-- 1 5041779338 Jul 29 17:26 R_brain_a.bam
-rw-r--r-- 1 33620562508 Jul 29 16:09 R_brain_a.sam
-rw-r--r-- 1 8331620721 Jul 29 16:43 R_testis_7a.bam
-rw-r--r-- 1 78854258469 Jul 29 04:35 R_testis_7a.sam

```
-rw-r--r-- 1    7376925043 Jul 29 16:57 R_testis_7b.bam
-rw-r--r-- 1    68873706840 Jul 29 09:56 R_testis_7b.sam
-rw-r--r-- 1    8534338799 Jul 29 16:27 R_testis_7c.bam
-rw-r--r-- 1    82198508692 Jul 29 04:20 R_testis_7c.sam
```

standard_results/CircRNA:

total 128

```
drwxr-xr-x 3  4096 Dec   8 15:58 CircTest
drwxr-xr-x 3  4096 Dec   8 15:58 DCC
drwxr-xr-x 2  4096 Dec   8 09:06 Index
drwxr-xr-x 8  4096 Dec   8 10:25 Mapping
```

standard_results/CircRNA/CircTest:

total 32

```
drwxr-xr-x 3  4096 Dec   8 16:12 testis_vs_brain
```

standard_results/CircRNA/CircTest/testis_vs_brain:

total 416

```
-rw-r--r-- 1    582 Dec   8 16:08 CircCoordinates
-rw-r--r-- 1    542 Dec   8 16:08 CircRNACount
-rw-r--r-- 1    544 Dec   8 16:12 CircSkipJunctions
-rw-r--r-- 1 13489 Dec   8 16:12 DCC-2016-12-08_15-58.log
-rw-r--r-- 1    619 Dec   8 16:11 LinearCount
-rw-r--r-- 1    814 Dec   8 15:58 mate1
-rw-r--r-- 1    814 Dec   8 15:58 mate2
-rw-r--r-- 1    195 Dec   8 16:12 R_hppRNA_data.STAR_DCC_circTest.testis_vs_brain.circTest.csv
-rw-r--r-- 1    162 Dec   8 16:12 R_hppRNA_data.STAR_DCC_circTest.testis_vs_brain.circTest.txt
-rw-r--r-- 1    814 Dec   8 15:58 samplesheet
```

drwxr-xr-x 2 16384 Dec 8 16:12 _tmp_DCC

standard_results/CircRNA/DCC:

total 352

-rw-r--r-- 1 599 Dec 8 15:54 CircCoordinates
-rw-r--r-- 1 542 Dec 8 15:54 CircRNACount
-rw-r--r-- 1 544 Dec 8 15:58 CircSkipJunctions
-rw-r--r-- 1 13557 Dec 8 15:58 DCC-2016-12-08_15-43.log
-rw-r--r-- 1 619 Dec 8 15:57 LinearCount
-rw-r--r-- 1 814 Dec 8 15:43 mate1
-rw-r--r-- 1 814 Dec 8 15:43 mate2
-rw-r--r-- 1 814 Dec 8 15:43 samplesheet
drwxr-xr-x 2 16384 Dec 8 15:58 _tmp_DCC

standard_results/CircRNA/Index:

total 31569408

-rw-r--r-- 1 238 Dec 8 07:00 chrLength.txt
-rw-r--r-- 1 376 Dec 8 07:00 chrNameLength.txt
-rw-r--r-- 1 138 Dec 8 07:00 chrName.txt
-rw-r--r-- 1 269 Dec 8 07:00 chrStart.txt
-rw-r--r-- 1 3099328512 Dec 8 09:03 Genome
-rw-r--r-- 1 614 Dec 8 06:59 genomeParameters.txt
-rw-r--r-- 1 23606085545 Dec 8 09:06 SA
-rw-r--r-- 1 1565873619 Dec 8 09:06 SAindex

standard_results/CircRNA/Mapping:

total 192

drwxr-xr-x 5 4096 Dec 8 09:58 R_brain_3b
drwxr-xr-x 5 4096 Dec 8 10:10 R_brain_3c

drwxr-xr-x 5 4096 Dec 8 10:25 R_brain_a
 drwxr-xr-x 5 4096 Dec 8 09:22 R_testis_7a
 drwxr-xr-x 5 4096 Dec 8 09:42 R_testis_7b
 drwxr-xr-x 5 4096 Dec 8 09:06 R_testis_7c

standard_results/CircRNA/Mapping/R_brain_3b:

total 96

drwxr-xr-x 3 4096 Dec 8 10:43 joint_mapping
 drwxr-xr-x 3 4096 Dec 8 10:08 mate1_mapping
 drwxr-xr-x 3 4096 Dec 8 10:44 mate2_mapping

standard_results/CircRNA/Mapping/R_brain_3b/joint_mapping:

total 5067712

-rw-r--r-- 1 3319569203 Dec 8 10:03 R_brain_3b.Aligned.sortedByCoord.out.bam
 -rw-r--r-- 1 3086744 Dec 8 10:43 R_brain_3b.Aligned.sortedByCoord.out.bam.bai
 -rw-r--r-- 1 73505699 Dec 8 10:02 R_brain_3b.Chimeric.out.junction
 -rw-r--r-- 1 535851538 Dec 8 10:02 R_brain_3b.Chimeric.out.sam
 -rw-r--r-- 1 1860 Dec 8 10:03 R_brain_3b.Log.final.out
 -rw-r--r-- 1 31547 Dec 8 10:03 R_brain_3b.Log.out
 -rw-r--r-- 1 600 Dec 8 10:03 R_brain_3b.Log.progress.out
 -rw-r--r-- 1 9316679 Dec 8 10:03 R_brain_3b.SJ.out.tab
 drwx----- 3 12288 Dec 8 10:03 R_brain_3b._STARtmp
 -rw-r--r-- 1 303004974 Dec 8 10:02 R_brain_3b.Unmapped.out.mate1
 -rw-r--r-- 1 292424334 Dec 8 10:02 R_brain_3b.Unmapped.out.mate2

standard_results/CircRNA/Mapping/R_brain_3b/mate1_mapping:

total 445488

-rw-r--r-- 1 31486991 Dec 8 10:08 R_brain_3b.Chimeric.out.junction
 -rw-r--r-- 1 190877432 Dec 8 10:08 R_brain_3b.Chimeric.out.sam

```

-rw-r--r-- 1      1860 Dec  8 10:08 R_brain_3b.Log.final.out
-rw-r--r-- 1     27836 Dec  8 10:08 R_brain_3b.Log.out
-rw-r--r-- 1       364 Dec  8 10:08 R_brain_3b.Log.progress.out
-rw-r--r-- 1    8327289 Dec  8 10:08 R_brain_3b.SJ.out.tab
drwx----- 2       8192 Dec  8 10:08 R_brain_3b._STARtmp
-rw-r--r-- 1 167301140 Dec  8 10:08 R_brain_3b.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_brain_3b/mate2_mapping:

total 523248

```

-rw-r--r-- 1   34892184 Dec  8 10:10 R_brain_3b.Chimeric.out.junction
-rw-r--r-- 1   34892184 Dec  8 15:58 R_brain_3b.Chimeric.out.junction.fixed
-rw-r--r-- 1  210575703 Dec  8 10:10 R_brain_3b.Chimeric.out.sam
-rw-r--r-- 1     1861 Dec  8 10:10 R_brain_3b.Log.final.out
-rw-r--r-- 1     27837 Dec  8 10:10 R_brain_3b.Log.out
-rw-r--r-- 1       364 Dec  8 10:10 R_brain_3b.Log.progress.out
-rw-r--r-- 1   8276922 Dec  8 10:10 R_brain_3b.SJ.out.tab
drwx----- 2       8192 Dec  8 10:10 R_brain_3b._STARtmp
-rw-r--r-- 1 178896931 Dec  8 10:10 R_brain_3b.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_brain_3c:

total 96

```

drwxr-xr-x 3   4096 Dec  8 10:44 joint_mapping
drwxr-xr-x 3   4096 Dec  8 10:21 mate1_mapping
drwxr-xr-x 3   4096 Dec  8 10:44 mate2_mapping

```

standard_results/CircRNA/Mapping/R_brain_3c/joint_mapping:

total 4319408

```

-rw-r--r-- 1 2819886213 Dec  8 10:16 R_brain_3c.Aligned.sortedByCoord.out.bam
-rw-r--r-- 1   2904360 Dec  8 10:44 R_brain_3c.Aligned.sortedByCoord.out.bam.bai

```

```

-rw-r--r-- 1      61361111 Dec  8 10:15 R_brain_3c.Chimeric.out.junction
-rw-r--r-- 1     443317967 Dec  8 10:15 R_brain_3c.Chimeric.out.sam
-rw-r--r-- 1          1860 Dec  8 10:16 R_brain_3c.Log.final.out
-rw-r--r-- 1         31546 Dec  8 10:16 R_brain_3c.Log.out
-rw-r--r-- 1          482 Dec  8 10:16 R_brain_3c.Log.progress.out
-rw-r--r-- 1        8775518 Dec  8 10:16 R_brain_3c.SJ.out.tab
drwx----- 3          12288 Dec  8 10:16 R_brain_3c._STARtmp
-rw-r--r-- 1     269931661 Dec  8 10:15 R_brain_3c.Unmapped.out.mate1
-rw-r--r-- 1     260588289 Dec  8 10:15 R_brain_3c.Unmapped.out.mate2

```

standard_results/CircRNA/Mapping/R_brain_3c/mate1_mapping:

total 378816

```

-rw-r--r-- 1     24956541 Dec  8 10:21 R_brain_3c.Chimeric.out.junction
-rw-r--r-- 1    151121377 Dec  8 10:21 R_brain_3c.Chimeric.out.sam
-rw-r--r-- 1         1859 Dec  8 10:21 R_brain_3c.Log.final.out
-rw-r--r-- 1        27836 Dec  8 10:21 R_brain_3c.Log.out
-rw-r--r-- 1         482 Dec  8 10:21 R_brain_3c.Log.progress.out
-rw-r--r-- 1       7841518 Dec  8 10:21 R_brain_3c.SJ.out.tab
drwx----- 2          8192 Dec  8 10:21 R_brain_3c._STARtmp
-rw-r--r-- 1    154344165 Dec  8 10:21 R_brain_3c.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_brain_3c/mate2_mapping:

total 450416

```

-rw-r--r-- 1     28589291 Dec  8 10:25 R_brain_3c.Chimeric.out.junction
-rw-r--r-- 1     28589291 Dec  8 15:58 R_brain_3c.Chimeric.out.junction.fixed
-rw-r--r-- 1    172482121 Dec  8 10:25 R_brain_3c.Chimeric.out.sam
-rw-r--r-- 1         1859 Dec  8 10:25 R_brain_3c.Log.final.out
-rw-r--r-- 1        27837 Dec  8 10:25 R_brain_3c.Log.out
-rw-r--r-- 1         482 Dec  8 10:25 R_brain_3c.Log.progress.out

```



```
-rw-r--r-- 1      7803801 Dec   8 10:25 R_brain_3c.SJ.out.tab
drwx----- 2          8192 Dec   8 10:25 R_brain_3c._STARTmp
-rw-r--r-- 1 164731681 Dec   8 10:25 R_brain_3c.Unmapped.out.mate1
```

standard_results/CircRNA/Mapping/R_brain_a:

total 96

```
drwxr-xr-x 3  4096 Dec   8 10:43 joint_mapping
drwxr-xr-x 3  4096 Dec   8 10:36 mate1_mapping
drwxr-xr-x 3  4096 Dec   8 10:44 mate2_mapping
```

standard_results/CircRNA/Mapping/R_brain_a/joint_mapping:

total 4118416

```
-rw-r--r-- 1 3111669168 Dec   8 10:30 R_brain_a.Aligned.sortedByCoord.out.bam
-rw-r--r-- 1    2777400 Dec   8 10:43 R_brain_a.Aligned.sortedByCoord.out.bam.bai
-rw-r--r-- 1    34805467 Dec   8 10:29 R_brain_a.Chimeric.out.junction
-rw-r--r-- 1  249076240 Dec   8 10:29 R_brain_a.Chimeric.out.sam
-rw-r--r-- 1     1860 Dec   8 10:30 R_brain_a.Log.final.out
-rw-r--r-- 1     31397 Dec   8 10:30 R_brain_a.Log.out
-rw-r--r-- 1      482 Dec   8 10:30 R_brain_a.Log.progress.out
-rw-r--r-- 1    7838524 Dec   8 10:30 R_brain_a.SJ.out.tab
drwx----- 3    12288 Dec   8 10:30 R_brain_a._STARTmp
-rw-r--r-- 1 145655678 Dec   8 10:29 R_brain_a.Unmapped.out.mate1
-rw-r--r-- 1 134924332 Dec   8 10:29 R_brain_a.Unmapped.out.mate2
```

standard_results/CircRNA/Mapping/R_brain_a/mate1_mapping:

total 184496

```
-rw-r--r-- 1 12971099 Dec   8 10:36 R_brain_a.Chimeric.out.junction
-rw-r--r-- 1 77763239 Dec   8 10:36 R_brain_a.Chimeric.out.sam
-rw-r--r-- 1    1857 Dec   8 10:36 R_brain_a.Log.final.out
```

```

-rw-r--r-- 1      27723 Dec  8 10:36 R_brain_a.Log.out
-rw-r--r-- 1       482 Dec  8 10:36 R_brain_a.Log.progress.out
-rw-r--r-- 1    6989223 Dec  8 10:36 R_brain_a.SJ.out.tab
drwx----- 2      8192 Dec  8 10:36 R_brain_a._STARtmp
-rw-r--r-- 1  66424316 Dec  8 10:36 R_brain_a.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_brain_a/mate2_mapping:

total 259392

```

-rw-r--r-- 1   17145277 Dec  8 10:39 R_brain_a.Chimeric.out.junction
-rw-r--r-- 1   17145277 Dec  8 15:58 R_brain_a.Chimeric.out.junction.fixed
-rw-r--r-- 1  100824913 Dec  8 10:39 R_brain_a.Chimeric.out.sam
-rw-r--r-- 1     1857 Dec  8 10:39 R_brain_a.Log.final.out
-rw-r--r-- 1     27724 Dec  8 10:39 R_brain_a.Log.out
-rw-r--r-- 1       482 Dec  8 10:39 R_brain_a.Log.progress.out
-rw-r--r-- 1   6879468 Dec  8 10:39 R_brain_a.SJ.out.tab
drwx----- 2      8192 Dec  8 10:39 R_brain_a._STARtmp
-rw-r--r-- 1   89040380 Dec  8 10:39 R_brain_a.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_testis_7a:

total 96

```

drwxr-xr-x 3   4096 Dec  8 10:41 joint_mapping
drwxr-xr-x 3   4096 Dec  8 09:37 mate1_mapping
drwxr-xr-x 3   4096 Dec  8 10:44 mate2_mapping

```

standard_results/CircRNA/Mapping/R_testis_7a/joint_mapping:

total 5995856

```

-rw-r--r-- 1  4207787443 Dec  8 09:29 R_testis_7a.Aligned.sortedByCoord.out.bam
-rw-r--r-- 1    3375536 Dec  8 10:41 R_testis_7a.Aligned.sortedByCoord.out.bam.bai
-rw-r--r-- 1   71402008 Dec  8 09:27 R_testis_7a.Chimeric.out.junction

```

```

-rw-r--r-- 1 511551446 Dec 8 09:27 R_testis_7a.Chimeric.out.sam
-rw-r--r-- 1 1865 Dec 8 09:29 R_testis_7a.Log.final.out
-rw-r--r-- 1 31698 Dec 8 09:29 R_testis_7a.Log.out
-rw-r--r-- 1 600 Dec 8 09:29 R_testis_7a.Log.progress.out
-rw-r--r-- 1 16887008 Dec 8 09:29 R_testis_7a.SJ.out.tab
drwx----- 3 12288 Dec 8 09:29 R_testis_7a._STARTmp
-rw-r--r-- 1 280455280 Dec 8 09:29 R_testis_7a.Unmapped.out.mate1
-rw-r--r-- 1 276611146 Dec 8 09:27 R_testis_7a.Unmapped.out.mate2

```

standard_results/CircRNA/Mapping/R_testis_7a/mate1_mapping:

total 348368

```

-rw-r--r-- 1 25045404 Dec 8 09:37 R_testis_7a.Chimeric.out.junction
-rw-r--r-- 1 152187081 Dec 8 09:37 R_testis_7a.Chimeric.out.sam
-rw-r--r-- 1 1860 Dec 8 09:37 R_testis_7a.Log.final.out
-rw-r--r-- 1 27950 Dec 8 09:37 R_testis_7a.Log.out
-rw-r--r-- 1 718 Dec 8 09:37 R_testis_7a.Log.progress.out
-rw-r--r-- 1 14286496 Dec 8 09:37 R_testis_7a.SJ.out.tab
drwx----- 2 8192 Dec 8 09:37 R_testis_7a._STARTmp
-rw-r--r-- 1 119438296 Dec 8 09:37 R_testis_7a.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_testis_7a/mate1_mapping/R_testis_7a._STARTmp:

total 0

standard_results/CircRNA/Mapping/R_testis_7a/mate2_mapping:

total 480112

```

-rw-r--r-- 1 34140698 Dec 8 09:42 R_testis_7a.Chimeric.out.junction
-rw-r--r-- 1 34140698 Dec 8 15:58 R_testis_7a.Chimeric.out.junction.fixed
-rw-r--r-- 1 207796691 Dec 8 09:42 R_testis_7a.Chimeric.out.sam

```

```

-rw-r--r-- 1      1860 Dec  8 09:42 R_testis_7a.Log.final.out
-rw-r--r-- 1     27950 Dec  8 09:42 R_testis_7a.Log.out
-rw-r--r-- 1       600 Dec  8 09:42 R_testis_7a.Log.progress.out
-rw-r--r-- 1    14224609 Dec  8 09:42 R_testis_7a.SJ.out.tab
drwx----- 2       8192 Dec  8 09:42 R_testis_7a._STARtmp
-rw-r--r-- 1   138509033 Dec  8 09:42 R_testis_7a.Unmapped.out.mate1

```

standard_results/CircRNA/Mapping/R_testis_7b:

total 96

```

drwxr-xr-x 3   4096 Dec  8 10:42 joint_mapping
drwxr-xr-x 3   4096 Dec  8 09:55 mate1_mapping
drwxr-xr-x 3   4096 Dec  8 10:44 mate2_mapping

```

standard_results/CircRNA/Mapping/R_testis_7b/joint_mapping:

total 5301232

```

-rw-r--r-- 1   3825437803 Dec  8 09:50 R_testis_7b.Aligned.sortedByCoord.out.bam
-rw-r--r-- 1     3293096 Dec  8 10:42 R_testis_7b.Aligned.sortedByCoord.out.bam.bai
-rw-r--r-- 1     53543175 Dec  8 09:49 R_testis_7b.Chimeric.out.junction
-rw-r--r-- 1     386786073 Dec  8 09:50 R_testis_7b.Chimeric.out.sam
-rw-r--r-- 1       1865 Dec  8 09:50 R_testis_7b.Log.final.out
-rw-r--r-- 1      31697 Dec  8 09:50 R_testis_7b.Log.out
-rw-r--r-- 1       600 Dec  8 09:50 R_testis_7b.Log.progress.out
-rw-r--r-- 1    16503866 Dec  8 09:50 R_testis_7b.SJ.out.tab
drwx----- 3      12288 Dec  8 09:50 R_testis_7b._STARtmp
-rw-r--r-- 1   234278574 Dec  8 09:49 R_testis_7b.Unmapped.out.mate1
-rw-r--r-- 1   226292370 Dec  8 09:49 R_testis_7b.Unmapped.out.mate2

```

standard_results/CircRNA/Mapping/R_testis_7b/mate1_mapping:

total 313824

```
-rw-r--r-- 1 22000668 Dec 8 09:55 R_testis_7b.Chimeric.out.junction
-rw-r--r-- 1 134064902 Dec 8 09:55 R_testis_7b.Chimeric.out.sam
-rw-r--r-- 1 1860 Dec 8 09:55 R_testis_7b.Log.final.out
-rw-r--r-- 1 27949 Dec 8 09:55 R_testis_7b.Log.out
-rw-r--r-- 1 364 Dec 8 09:55 R_testis_7b.Log.progress.out
-rw-r--r-- 1 13784770 Dec 8 09:55 R_testis_7b.SJ.out.tab
drwx----- 2 8192 Dec 8 09:55 R_testis_7b._STARtmp
-rw-r--r-- 1 110187980 Dec 8 09:55 R_testis_7b.Unmapped.out.mate1
```

standard_results/CircRNA/Mapping/R_testis_7b/mate2_mapping:

total 376080

```
-rw-r--r-- 1 25190316 Dec 8 09:58 R_testis_7b.Chimeric.out.junction
-rw-r--r-- 1 25190316 Dec 8 15:58 R_testis_7b.Chimeric.out.junction.fixed
-rw-r--r-- 1 152773024 Dec 8 09:58 R_testis_7b.Chimeric.out.sam
-rw-r--r-- 1 1861 Dec 8 09:58 R_testis_7b.Log.final.out
-rw-r--r-- 1 27950 Dec 8 09:58 R_testis_7b.Log.out
-rw-r--r-- 1 364 Dec 8 09:58 R_testis_7b.Log.progress.out
-rw-r--r-- 1 13727954 Dec 8 09:58 R_testis_7b.SJ.out.tab
drwx----- 2 8192 Dec 8 09:58 R_testis_7b._STARtmp
-rw-r--r-- 1 118808452 Dec 8 09:58 R_testis_7b.Unmapped.out.mate1
```

standard_results/CircRNA/Mapping/R_testis_7c:

total 96

```
drwxr-xr-x 3 4096 Dec 8 10:40 joint_mapping
drwxr-xr-x 3 4096 Dec 8 09:17 mate1_mapping
drwxr-xr-x 3 4096 Dec 8 10:44 mate2_mapping
```

standard_results/CircRNA/Mapping/R_testis_7c/joint_mapping:

total 6163920

```
-rw-r--r-- 1 4343397564 Dec 8 09:11 R_testis_7c.Aligned.sortedByCoord.out.bam
-rw-r--r-- 1 3389584 Dec 8 10:40 R_testis_7c.Aligned.sortedByCoord.out.bam.bai
-rw-r--r-- 1 65949259 Dec 8 09:09 R_testis_7c.Chimeric.out.junction
-rw-r--r-- 1 465678239 Dec 8 09:09 R_testis_7c.Chimeric.out.sam
-rw-r--r-- 1 1865 Dec 8 09:11 R_testis_7c.Log.final.out
-rw-r--r-- 1 31702 Dec 8 09:11 R_testis_7c.Log.out
-rw-r--r-- 1 600 Dec 8 09:11 R_testis_7c.Log.progress.out
-rw-r--r-- 1 13947474 Dec 8 09:11 R_testis_7c.SJ.out.tab
drwx----- 3 12288 Dec 8 09:11 R_testis_7c._STARtmp
-rw-r--r-- 1 315462969 Dec 8 09:09 R_testis_7c.Unmapped.out.mate1
-rw-r--r-- 1 310841029 Dec 8 09:09 R_testis_7c.Unmapped.out.mate2
```

standard_results/CircRNA/Mapping/R_testis_7c/mate1_mapping:

total 395360

```
-rw-r--r-- 1 26526438 Dec 8 09:17 R_testis_7c.Chimeric.out.junction
-rw-r--r-- 1 157967246 Dec 8 09:17 R_testis_7c.Chimeric.out.sam
-rw-r--r-- 1 1860 Dec 8 09:17 R_testis_7c.Log.final.out
-rw-r--r-- 1 27949 Dec 8 09:17 R_testis_7c.Log.out
-rw-r--r-- 1 600 Dec 8 09:17 R_testis_7c.Log.progress.out
-rw-r--r-- 1 12159238 Dec 8 09:17 R_testis_7c.SJ.out.tab
drwx----- 2 8192 Dec 8 09:17 R_testis_7c._STARtmp
-rw-r--r-- 1 156460536 Dec 8 09:17 R_testis_7c.Unmapped.out.mate1
```

standard_results/CircRNA/Mapping/R_testis_7c/mate2_mapping:

total 525936

```
-rw-r--r-- 1 35443049 Dec 8 09:22 R_testis_7c.Chimeric.out.junction
-rw-r--r-- 1 35443049 Dec 8 15:58 R_testis_7c.Chimeric.out.junction.fixed
-rw-r--r-- 1 212505195 Dec 8 09:22 R_testis_7c.Chimeric.out.sam
```

```

-rw-r--r-- 1      1860 Dec  8 09:22 R_testis_7c.Log.final.out
-rw-r--r-- 1     27949 Dec  8 09:22 R_testis_7c.Log.out
-rw-r--r-- 1       600 Dec  8 09:22 R_testis_7c.Log.progress.out
-rw-r--r-- 1    12152757 Dec  8 09:22 R_testis_7c.SJ.out.tab
drwx----- 2       8192 Dec  8 09:22 R_testis_7c._STARtmp
-rw-r--r-- 1   174260981 Dec  8 09:22 R_testis_7c.Unmapped.out.mate1

```

standard_results/Fasta:

total 30292720

```

-rw-r--r-- 1   2234712604 Jul 22 02:48 R_brain_3b_1.collapser.fasta
-rw-r--r-- 1   2168036315 Jul 22 02:58 R_brain_3b_2.collapser.fasta
-rw-r--r-- 1   1880331703 Jul 22 02:46 R_brain_3c_1.collapser.fasta
-rw-r--r-- 1   1819758448 Jul 22 02:57 R_brain_3c_2.collapser.fasta
-rw-r--r-- 1   1454785722 Jul 22 02:44 R_brain_a_1.collapser.fasta
-rw-r--r-- 1   1451834774 Jul 22 02:50 R_brain_a_2.collapser.fasta
-rw-r--r-- 1   2753744835 Jul 22 02:42 R_testis_7a_1.collapser.fasta
-rw-r--r-- 1   2705809871 Jul 22 02:54 R_testis_7a_2.collapser.fasta
-rw-r--r-- 1   2496643115 Jul 22 02:50 R_testis_7b_1.collapser.fasta
-rw-r--r-- 1   2460098186 Jul 22 02:59 R_testis_7b_2.collapser.fasta
-rw-r--r-- 1   2875317487 Jul 22 02:43 R_testis_7c_1.collapser.fasta
-rw-r--r-- 1   2825550434 Jul 22 02:56 R_testis_7c_2.collapser.fasta

```

standard_results/FastQC:

total 28736

```

-rw-r--r-- 1   370641 Jul 22 02:50 R_brain_3b_1_fastqc.html
-rw-r--r-- 1   499391 Jul 22 02:50 R_brain_3b_1_fastqc.zip
-rw-r--r-- 1   367734 Jul 22 02:53 R_brain_3b_2_fastqc.html
-rw-r--r-- 1   495290 Jul 22 02:53 R_brain_3b_2_fastqc.zip
-rw-r--r-- 1   354052 Jul 22 02:43 R_brain_3b.R1_fastqc.html

```

```

-rw-r--r-- 1 480976 Jul 22 02:43 R_brain_3b.R1_fastqc.zip
-rw-r--r-- 1 368825 Jul 22 02:46 R_brain_3b.R2_fastqc.html
-rw-r--r-- 1 505243 Jul 22 02:46 R_brain_3b.R2_fastqc.zip
-rw-r--r-- 1 368558 Jul 22 02:50 R_brain_3c_1_fastqc.html
-rw-r--r-- 1 495507 Jul 22 02:50 R_brain_3c_1_fastqc.zip
-rw-r--r-- 1 356234 Jul 22 02:58 R_brain_3c_2_fastqc.html
-rw-r--r-- 1 478366 Jul 22 02:58 R_brain_3c_2_fastqc.zip
-rw-r--r-- 1 372609 Jul 22 02:50 R_brain_3c.R1_fastqc.html
-rw-r--r-- 1 509278 Jul 22 02:50 R_brain_3c.R1_fastqc.zip
-rw-r--r-- 1 360826 Jul 22 02:52 R_brain_3c.R2_fastqc.html
-rw-r--r-- 1 491025 Jul 22 02:52 R_brain_3c.R2_fastqc.zip
-rw-r--r-- 1 367309 Jul 22 02:55 R_brain_a_1_fastqc.html
-rw-r--r-- 1 480082 Jul 22 02:55 R_brain_a_1_fastqc.zip
-rw-r--r-- 1 341976 Jul 22 02:57 R_brain_a_2_fastqc.html
-rw-r--r-- 1 441972 Jul 22 02:57 R_brain_a_2_fastqc.zip
-rw-r--r-- 1 373896 Jul 22 02:54 R_brain_a.R1_fastqc.html
-rw-r--r-- 1 501482 Jul 22 02:54 R_brain_a.R1_fastqc.zip
-rw-r--r-- 1 357619 Jul 22 02:57 R_brain_a.R2_fastqc.html
-rw-r--r-- 1 474796 Jul 22 02:57 R_brain_a.R2_fastqc.zip
-rw-r--r-- 1 352102 Jul 22 02:35 R_testis_7a_1_fastqc.html
-rw-r--r-- 1 472951 Jul 22 02:35 R_testis_7a_1_fastqc.zip
-rw-r--r-- 1 333105 Jul 22 02:39 R_testis_7a_2_fastqc.html
-rw-r--r-- 1 442460 Jul 22 02:39 R_testis_7a_2_fastqc.zip
-rw-r--r-- 1 333820 Jul 22 02:35 R_testis_7a.R1_fastqc.html
-rw-r--r-- 1 451768 Jul 22 02:35 R_testis_7a.R1_fastqc.zip
-rw-r--r-- 1 340992 Jul 22 02:39 R_testis_7a.R2_fastqc.html
-rw-r--r-- 1 463234 Jul 22 02:39 R_testis_7a.R2_fastqc.zip
-rw-r--r-- 1 374909 Jul 22 02:43 R_testis_7b_1_fastqc.html
-rw-r--r-- 1 506198 Jul 22 02:43 R_testis_7b_1_fastqc.zip

```



```

-rw-r--r-- 1 382350 Jul 22 02:47 R_testis_7b_2_fastqc.html
-rw-r--r-- 1 517670 Jul 22 02:47 R_testis_7b_2_fastqc.zip
-rw-r--r-- 1 335629 Jul 22 02:43 R_testis_7b.R1_fastqc.html
-rw-r--r-- 1 453077 Jul 22 02:43 R_testis_7b.R1_fastqc.zip
-rw-r--r-- 1 353080 Jul 22 02:46 R_testis_7b.R2_fastqc.html
-rw-r--r-- 1 482098 Jul 22 02:46 R_testis_7b.R2_fastqc.zip
-rw-r--r-- 1 358361 Jul 22 02:35 R_testis_7c_1_fastqc.html
-rw-r--r-- 1 483433 Jul 22 02:35 R_testis_7c_1_fastqc.zip
-rw-r--r-- 1 342885 Jul 22 02:39 R_testis_7c_2_fastqc.html
-rw-r--r-- 1 457883 Jul 22 02:39 R_testis_7c_2_fastqc.zip
-rw-r--r-- 1 342095 Jul 22 02:35 R_testis_7c.R1_fastqc.html
-rw-r--r-- 1 462622 Jul 22 02:35 R_testis_7c.R1_fastqc.zip
-rw-r--r-- 1 353730 Jul 22 02:39 R_testis_7c.R2_fastqc.html
-rw-r--r-- 1 481632 Jul 22 02:39 R_testis_7c.R2_fastqc.zip

```

standard_results/Fusion_gene:

total 64

```

drwxr-xr-x 8 4096 Jul 22 16:25 Fusion_result
drwxr-xr-x 8 4096 Jul 22 16:14 Raw_data

```

standard_results/Fusion_gene/Fusion_result:

total 192

```

drwxr-xr-x 2 8192 Jul 22 22:12 R_brain_3b
drwxr-xr-x 2 8192 Jul 22 21:00 R_brain_3c
drwxr-xr-x 2 8192 Jul 22 19:56 R_brain_a
drwxr-xr-x 2 8192 Jul 22 23:02 R_testis_7a
drwxr-xr-x 2 8192 Jul 22 22:32 R_testis_7b
drwxr-xr-x 2 8192 Jul 22 23:23 R_testis_7c

```

standard_results/Fusion_gene/Fusion_result/R_brain_3b:

total 5536

```
-rw-r--r-- 1      19132 Jul 22 22:12 final-list_candidate-fusion-genes.caption.md.txt
-rw-r--r-- 1       3118 Jul 22 22:12 final-list_candidate-fusion-genes.GRCh37.txt
-rw-r--r-- 1       3118 Jul 22 22:12 final-list_candidate-fusion-genes.txt
-rw-r--r-- 1    420455 Jul 22 22:12 fusioncatcher.log
-rw-r--r-- 1   3949319 Jul 22 22:12 info.txt
-rw-r--r-- 1     3604 Jul 22 22:12 junk-chimeras.txt
-rw-r--r-- 1      543 Jul 22 22:12 summary_candidate_fusions.txt
-rw-r--r-- 1    15736 Jul 22 22:02 supporting-reads_gene-fusions_BLAT.zip
-rw-r--r-- 1       22 Jul 22 21:54 supporting-reads_gene-fusions_BOWTIE.zip
-rw-r--r-- 1    15736 Jul 22 22:10 supporting-reads_gene-fusions_STAR.zip
-rw-r--r-- 1     1253 Jul 22 21:35 viruses_bacteria_phages.txt
```

standard_results/Fusion_gene/Fusion_result/R_brain_3c:

total 4544

```
-rw-r--r-- 1      19132 Jul 22 21:00 final-list_candidate-fusion-genes.caption.md.txt
-rw-r--r-- 1       430 Jul 22 21:00 final-list_candidate-fusion-genes.GRCh37.txt
-rw-r--r-- 1       430 Jul 22 21:00 final-list_candidate-fusion-genes.txt
-rw-r--r-- 1    420514 Jul 22 21:00 fusioncatcher.log
-rw-r--r-- 1   3135417 Jul 22 21:00 info.txt
-rw-r--r-- 1     2520 Jul 22 21:00 junk-chimeras.txt
-rw-r--r-- 1      300 Jul 22 21:00 summary_candidate_fusions.txt
-rw-r--r-- 1       22 Jul 22 20:51 supporting-reads_gene-fusions_BLAT.zip
-rw-r--r-- 1       22 Jul 22 20:44 supporting-reads_gene-fusions_BOWTIE.zip
-rw-r--r-- 1       22 Jul 22 20:59 supporting-reads_gene-fusions_STAR.zip
-rw-r--r-- 1     1177 Jul 22 20:18 viruses_bacteria_phages.txt
```

standard_results/Fusion_gene/Fusion_result/R_brain_a:

total 1824

```
-rw-r--r-- 1 19132 Jul 22 19:56 final-list_candidate-fusion-genes.caption.md.txt
-rw-r--r-- 1 430 Jul 22 19:56 final-list_candidate-fusion-genes.GRCh37.txt
-rw-r--r-- 1 430 Jul 22 19:56 final-list_candidate-fusion-genes.txt
-rw-r--r-- 1 419173 Jul 22 19:56 fusioncatcher.log
-rw-r--r-- 1 683930 Jul 22 19:56 info.txt
-rw-r--r-- 1 1325 Jul 22 19:56 junk-chimeras.txt
-rw-r--r-- 1 247 Jul 22 19:56 summary_candidate_fusions.txt
-rw-r--r-- 1 2782 Jul 22 19:52 supporting-reads_gene-fusions_BLAT.zip
-rw-r--r-- 1 22 Jul 22 19:48 supporting-reads_gene-fusions_BOWTIE.zip
-rw-r--r-- 1 2782 Jul 22 19:56 supporting-reads_gene-fusions_STAR.zip
-rw-r--r-- 1 1067 Jul 22 19:33 viruses_bacteria_phages.txt
```

standard_results/Fusion_gene/Fusion_result/R_testis_7a:

total 6544

```
-rw-r--r-- 1 19132 Jul 22 23:02 final-list_candidate-fusion-genes.caption.md.txt
-rw-r--r-- 1 807 Jul 22 23:02 final-list_candidate-fusion-genes.GRCh37.txt
-rw-r--r-- 1 807 Jul 22 23:02 final-list_candidate-fusion-genes.txt
-rw-r--r-- 1 421617 Jul 22 23:02 fusioncatcher.log
-rw-r--r-- 1 4821106 Jul 22 23:02 info.txt
-rw-r--r-- 1 14254 Jul 22 23:02 junk-chimeras.txt
-rw-r--r-- 1 535 Jul 22 23:02 summary_candidate_fusions.txt
-rw-r--r-- 1 18728 Jul 22 22:56 supporting-reads_gene-fusions_BLAT.zip
-rw-r--r-- 1 22 Jul 22 22:51 supporting-reads_gene-fusions_BOWTIE.zip
-rw-r--r-- 1 13730 Jul 22 23:01 supporting-reads_gene-fusions_STAR.zip
-rw-r--r-- 1 1267 Jul 22 22:24 viruses_bacteria_phages.txt
```

standard_results/Fusion_gene/Fusion_result/R_testis_7b:

total 5824

```

-rw-r--r-- 1      19132 Jul 22 22:32 final-list_candidate-fusion-genes.caption.md.txt
-rw-r--r-- 1        795 Jul 22 22:32 final-list_candidate-fusion-genes.GRCh37.txt
-rw-r--r-- 1        795 Jul 22 22:32 final-list_candidate-fusion-genes.txt
-rw-r--r-- 1    421546 Jul 22 22:32 fusioncatcher.log
-rw-r--r-- 1   4211979 Jul 22 22:32 info.txt
-rw-r--r-- 1    13555 Jul 22 22:32 junk-chimeras.txt
-rw-r--r-- 1        525 Jul 22 22:32 summary_candidate_fusions.txt
-rw-r--r-- 1    10008 Jul 22 22:22 supporting-reads_gene-fusions_BLAT.zip
-rw-r--r-- 1        22 Jul 22 22:19 supporting-reads_gene-fusions_BOWTIE.zip
-rw-r--r-- 1    5028 Jul 22 22:26 supporting-reads_gene-fusions_STAR.zip
-rw-r--r-- 1    1055 Jul 22 21:57 viruses_bacteria_phages.txt

```

standard_results/Fusion_gene/Fusion_result/R_testis_7c:

total 4880

```

-rw-r--r-- 1      19132 Jul 22 23:23 final-list_candidate-fusion-genes.caption.md.txt
-rw-r--r-- 1      2900 Jul 22 23:23 final-list_candidate-fusion-genes.GRCh37.txt
-rw-r--r-- 1      2900 Jul 22 23:23 final-list_candidate-fusion-genes.txt
-rw-r--r-- 1    421638 Jul 22 23:23 fusioncatcher.log
-rw-r--r-- 1   3406039 Jul 22 23:23 info.txt
-rw-r--r-- 1    7885 Jul 22 23:23 junk-chimeras.txt
-rw-r--r-- 1        549 Jul 22 23:23 summary_candidate_fusions.txt
-rw-r--r-- 1    9518 Jul 22 23:20 supporting-reads_gene-fusions_BLAT.zip
-rw-r--r-- 1        22 Jul 22 23:17 supporting-reads_gene-fusions_BOWTIE.zip
-rw-r--r-- 1    9518 Jul 22 23:23 supporting-reads_gene-fusions_STAR.zip
-rw-r--r-- 1    899 Jul 22 22:54 viruses_bacteria_phages.txt

```

standard_results/Fusion_gene/Raw_data:

total 192

```

drwxr-xr-x 2    4096 Jul 22 16:19 R_brain_3b

```

drwxr-xr-x 2 4096 Jul 22 16:17 R_brain_3c
drwxr-xr-x 2 4096 Jul 22 16:17 R_brain_a
drwxr-xr-x 2 4096 Jul 22 16:19 R_testis_7a
drwxr-xr-x 2 4096 Jul 22 16:19 R_testis_7b
drwxr-xr-x 2 4096 Jul 22 16:20 R_testis_7c

standard_results/Fusion_gene/Raw_data/R_brain_3b:

total 15994848

-r--r--r-- 1 7192054199 Jul 22 16:19 R_brain_3b_1.fastq
-r--r--r-- 1 7131934527 Jul 22 16:22 R_brain_3b_2.fastq

standard_results/Fusion_gene/Raw_data/R_brain_3c:

total 13717120

-r--r--r-- 1 6168044007 Jul 22 16:17 R_brain_3c_1.fastq
-r--r--r-- 1 6116044175 Jul 22 16:21 R_brain_3c_2.fastq

standard_results/Fusion_gene/Raw_data/R_brain_a:

total 9131568

-r--r--r-- 1 4119497944 Jul 22 16:17 R_brain_a_1.fastq
-r--r--r-- 1 4058010312 Jul 22 16:19 R_brain_a_2.fastq

standard_results/Fusion_gene/Raw_data/R_testis_7a:

total 20067712

-r--r--r-- 1 9016611035 Jul 22 16:19 R_testis_7a_1.fastq
-r--r--r-- 1 8954611149 Jul 22 16:24 R_testis_7a_2.fastq

standard_results/Fusion_gene/Raw_data/R_testis_7b:

total 17931136

-r--r--r-- 1 8067010459 Jul 22 16:19 R_testis_7b_1.fastq

-r--r--r-- 1 7990884145 Jul 22 16:22 R_testis_7b_2.fastq

standard_results/Fusion_gene/Raw_data/R_testis_7c:

total 21168032

-r--r--r-- 1 9509030215 Jul 22 16:20 R_testis_7c_1.fastq

-r--r--r-- 1 9447615437 Jul 22 16:25 R_testis_7c_2.fastq

standard_results/HISAT_StringTie_Ballgown:

total 224

drwxr-xr-x 2 4096 Jul 9 04:39 Bigwig

drwxr-xr-x 2 4096 Jul 9 04:42 Cluster

drwxr-xr-x 3 4096 Jul 8 20:53 DEG

drwxr-xr-x 4 4096 Jul 8 20:53 Gene_expression_matrix

drwxr-xr-x 2 4096 Jul 8 01:05 Index

drwxr-xr-x 2 4096 Jul 8 21:16 NGS_plot

drwxr-xr-x 2 8192 Jul 8 20:34 Processed_BAM

standard_results/HISAT_StringTie_Ballgown/Bigwig:

total 11258448

-rw-r--r-- 1 487915873 Jul 9 04:25 R_brain_3b.bw

-rw-r--r-- 1 529576078 Jul 9 04:14 R_brain_3b.wig.2.gz

-rw-r--r-- 1 529599299 Jul 8 22:18 R_brain_3b.wig.gz

-rw-r--r-- 1 467757051 Jul 9 04:28 R_brain_3c.bw

-rw-r--r-- 1 512438117 Jul 9 04:15 R_brain_3c.wig.2.gz

-rw-r--r-- 1 512448646 Jul 8 23:18 R_brain_3c.wig.gz

-rw-r--r-- 1 431887513 Jul 9 04:31 R_brain_a.bw

-rw-r--r-- 1 479703030 Jul 9 04:16 R_brain_a.wig.2.gz

-rw-r--r-- 1 479640760 Jul 9 00:10 R_brain_a.wig.gz

```
-rw-r--r-- 1 638459905 Jul 9 04:35 R_testis_7a.bw
-rw-r--r-- 1 667429430 Jul 9 04:18 R_testis_7a.wig.2.gz
-rw-r--r-- 1 667449549 Jul 9 01:31 R_testis_7a.wig.gz
-rw-r--r-- 1 597179428 Jul 9 04:38 R_testis_7b.bw
-rw-r--r-- 1 628259929 Jul 9 04:20 R_testis_7b.wig.2.gz
-rw-r--r-- 1 628296110 Jul 9 02:47 R_testis_7b.wig.gz
-rw-r--r-- 1 582598808 Jul 9 04:42 R_testis_7c.bw
-rw-r--r-- 1 619331046 Jul 9 04:22 R_testis_7c.wig.2.gz
-rw-r--r-- 1 619325853 Jul 9 04:12 R_testis_7c.wig.gz
```

standard_results/HISAT_StringTie_Ballgown/Cluster:

total 6032

```
-rw-r--r--      1              1081      Jul      9      04:42
R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.heatmap.R
-rw-r--r-- 1      1420 Jul 9 04:42 R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.PCA.R
-rw-r--r-- 1 1213719 Jul 8 20:53 R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt
-rw-r--r--      1              808595      Jul      9      04:42
R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt.1.heatmap.pdf
-rw-r--r--      1              1034548      Jul      9      04:42
R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt.1.matrix.txt
-rw-r--r--      1              4851      Jul      9      04:42
R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt.1.PCA.pdf
-rw-r--r--      1              1730688      Jul      9      04:42
R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.clean.txt.1.rotation.txt
```

standard_results/HISAT_StringTie_Ballgown/DEG:

total 4208

```
-rw-r--r--      1              893836      Jul      8      20:53
R_hppRNA_data.HISAT_StringTie_Ballgown.testis_vs_brain.gene.DEG.txt
```

-rw-r--r-- 1 2605627 Jul 8 20:53

R_hppRNA_data.HISAT_StringTie_Ballgown.testis_vs_brain.transcript.DEG.txt

drwxr-xr-x 8 4096 Jul 8 20:52 testis_vs_brain

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain:

total 192

drwxr-xr-x 2 4096 Jul 8 20:52 R_brain_3b

drwxr-xr-x 2 4096 Jul 8 20:52 R_brain_3c

drwxr-xr-x 2 4096 Jul 8 20:52 R_brain_a

drwxr-xr-x 2 4096 Jul 8 20:52 R_testis_7a

drwxr-xr-x 2 4096 Jul 8 20:52 R_testis_7b

drwxr-xr-x 2 4096 Jul 8 20:52 R_testis_7c

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain/R_brain_3b:

total 45200

-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab

-rw-r--r-- 1 16502966 Jul 8 20:52 e_data.ctab

-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab

-rw-r--r-- 1 9055336 Jul 8 20:52 i_data.ctab

-rw-r--r-- 1 3467911 Jul 8 20:52 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain/R_brain_3c:

total 45120

-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab

-rw-r--r-- 1 16437794 Jul 8 20:52 e_data.ctab

-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab

-rw-r--r-- 1 9031405 Jul 8 20:52 i_data.ctab

-rw-r--r-- 1 3467807 Jul 8 20:52 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain/R_brain_a:

total 44912

```
-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab
-rw-r--r-- 1 16285436 Jul 8 20:52 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab
-rw-r--r-- 1 8959253 Jul 8 20:52 i_data.ctab
-rw-r--r-- 1 3466708 Jul 8 20:52 t_data.ctab
```

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain/R_testis_7a:

total 45712

```
-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab
-rw-r--r-- 1 16817397 Jul 8 20:52 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab
-rw-r--r-- 1 9178971 Jul 8 20:52 i_data.ctab
-rw-r--r-- 1 3470837 Jul 8 20:52 t_data.ctab
```

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain/R_testis_7b:

total 45648

```
-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab
-rw-r--r-- 1 16757318 Jul 8 20:52 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab
-rw-r--r-- 1 9157579 Jul 8 20:52 i_data.ctab
-rw-r--r-- 1 3470229 Jul 8 20:52 t_data.ctab
```

standard_results/HISAT_StringTie_Ballgown/DEG/testis_vs_brain/R_testis_7c:

total 45808

```
-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab
-rw-r--r-- 1 16873272 Jul 8 20:52 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab
```

-rw-r--r-- 1 9202197 Jul 8 20:52 i_data.ctab

-rw-r--r-- 1 3473492 Jul 8 20:52 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix:

total 6032

drwxr-xr-x 8 4096 Jul 8 20:48 Ballgown_input

drwxr-xr-x 2 4096 Jul 8 20:52 gff

-rw-r--r-- 1 2864 Jul 8 20:52 R_hppRNA_data.Ballgown.R

-rw-r--r-- 1 1213749 Jul 8 20:53 R_hppRNA_data.HISAT_StringTie_Ballgown.gene.FPKM.txt

-rw-r--r-- 1 3820176 Jul 8 20:53 R_hppRNA_data.HISAT_StringTie_Ballgown.transcript.FPKM.txt

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input:

total 192

drwxr-xr-x 2 4096 Jul 8 20:34 R_brain_3b

drwxr-xr-x 2 4096 Jul 8 20:37 R_brain_3c

drwxr-xr-x 2 4096 Jul 8 20:39 R_brain_a

drwxr-xr-x 2 4096 Jul 8 20:42 R_testis_7a

drwxr-xr-x 2 4096 Jul 8 20:45 R_testis_7b

drwxr-xr-x 2 4096 Jul 8 20:48 R_testis_7c

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input/R_brain_3b:

total 45200

-rw-r--r-- 1 5560283 Jul 8 20:37 e2t.ctab

-rw-r--r-- 1 16502966 Jul 8 20:37 e_data.ctab

-rw-r--r-- 1 5028539 Jul 8 20:37 i2t.ctab

-rw-r--r-- 1 9055336 Jul 8 20:37 i_data.ctab

-rw-r--r-- 1 3467911 Jul 8 20:37 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input/R_brain_3c:

total 45120

-rw-r--r-- 1 5560283 Jul 8 20:39 e2t.ctab
-rw-r--r-- 1 16437794 Jul 8 20:39 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:39 i2t.ctab
-rw-r--r-- 1 9031405 Jul 8 20:39 i_data.ctab
-rw-r--r-- 1 3467807 Jul 8 20:39 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input/R_brain_a:

total 44912

-rw-r--r-- 1 5560283 Jul 8 20:42 e2t.ctab
-rw-r--r-- 1 16285436 Jul 8 20:42 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:42 i2t.ctab
-rw-r--r-- 1 8959253 Jul 8 20:42 i_data.ctab
-rw-r--r-- 1 3466708 Jul 8 20:41 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input/R_testis_7a:

total 45712

-rw-r--r-- 1 5560283 Jul 8 20:45 e2t.ctab
-rw-r--r-- 1 16817397 Jul 8 20:45 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:45 i2t.ctab
-rw-r--r-- 1 9178971 Jul 8 20:45 i_data.ctab
-rw-r--r-- 1 3470837 Jul 8 20:45 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input/R_testis_7b:

total 45648

-rw-r--r-- 1 5560283 Jul 8 20:48 e2t.ctab
-rw-r--r-- 1 16757318 Jul 8 20:48 e_data.ctab
-rw-r--r-- 1 5028539 Jul 8 20:48 i2t.ctab
-rw-r--r-- 1 9157579 Jul 8 20:48 i_data.ctab

-rw-r--r-- 1 3470229 Jul 8 20:48 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/Ballgown_input/R_testis_7c:

total 45808

-rw-r--r-- 1 5560283 Jul 8 20:52 e2t.ctab

-rw-r--r-- 1 16873272 Jul 8 20:51 e_data.ctab

-rw-r--r-- 1 5028539 Jul 8 20:52 i2t.ctab

-rw-r--r-- 1 9202197 Jul 8 20:52 i_data.ctab

-rw-r--r-- 1 3473492 Jul 8 20:51 t_data.ctab

standard_results/HISAT_StringTie_Ballgown/Gene_expression_matrix/gff:

total 588880

-rw-r--r-- 1 78929464 Jul 8 20:37 R_brain_3b.stringtie.gff

-rw-r--r-- 1 72716570 Jul 8 20:39 R_brain_3c.stringtie.gff

-rw-r--r-- 1 64774850 Jul 8 20:41 R_brain_a.stringtie.gff

-rw-r--r-- 1 109079934 Jul 8 20:45 R_testis_7a.stringtie.gff

-rw-r--r-- 1 100560568 Jul 8 20:48 R_testis_7b.stringtie.gff

-rw-r--r-- 1 100054844 Jul 8 20:51 R_testis_7c.stringtie.gff

standard_results/HISAT_StringTie_Ballgown/Index:

total 4886256

-rw-r--r-- 1 957980047 Jul 8 01:05 hg19.1.ht2

-rw-r--r-- 1 715335932 Jul 8 01:05 hg19.2.ht2

-rw-r--r-- 1 3284 Jul 8 00:35 hg19.3.ht2

-rw-r--r-- 1 715335926 Jul 8 00:35 hg19.4.ht2

-rw-r--r-- 1 1257560445 Jul 8 01:24 hg19.5.ht2

-rw-r--r-- 1 728440442 Jul 8 01:24 hg19.6.ht2

-rw-r--r-- 1 8 Jul 8 00:35 hg19.7.ht2

-rw-r--r-- 1 8 Jul 8 00:35 hg19.8.ht2

standard_results/HISAT_StringTie_Ballgown/NGS_plot:

total 153696

-rw-r--r--	1	6711	Jul	8 20:58	NGSplot.brain_3b.genebody.avgprof.pdf
-rw-r--r--	1	1368459	Jul	8 20:58	NGSplot.brain_3b.genebody.heatmap.pdf
-rw-r--r--	1	20009589	Jul	8 20:59	NGSplot.brain_3b.genebody.zip
-rw-r--r--	1	6711	Jul	8 21:03	NGSplot.brain_3c.genebody.avgprof.pdf
-rw-r--r--	1	1309940	Jul	8 21:03	NGSplot.brain_3c.genebody.heatmap.pdf
-rw-r--r--	1	19494152	Jul	8 21:03	NGSplot.brain_3c.genebody.zip
-rw-r--r--	1	6725	Jul	8 21:07	NGSplot.brain_a.genebody.avgprof.pdf
-rw-r--r--	1	1300382	Jul	8 21:07	NGSplot.brain_a.genebody.heatmap.pdf
-rw-r--r--	1	18651200	Jul	8 21:07	NGSplot.brain_a.genebody.zip
-rw-r--r--	1	6709	Jul	8 21:10	NGSplot.testis_7a.genebody.avgprof.pdf
-rw-r--r--	1	1589403	Jul	8 21:10	NGSplot.testis_7a.genebody.heatmap.pdf
-rw-r--r--	1	23159980	Jul	8 21:10	NGSplot.testis_7a.genebody.zip
-rw-r--r--	1	6714	Jul	8 21:13	NGSplot.testis_7b.genebody.avgprof.pdf
-rw-r--r--	1	1554965	Jul	8 21:13	NGSplot.testis_7b.genebody.heatmap.pdf
-rw-r--r--	1	22662789	Jul	8 21:13	NGSplot.testis_7b.genebody.zip
-rw-r--r--	1	6714	Jul	8 21:15	NGSplot.testis_7c.genebody.avgprof.pdf
-rw-r--r--	1	1481968	Jul	8 21:15	NGSplot.testis_7c.genebody.heatmap.pdf
-rw-r--r--	1	22622680	Jul	8 21:16	NGSplot.testis_7c.genebody.zip

standard_results/HISAT_StringTie_Ballgown/Processed_BAM:

total 476734912

-rw-r--r--	1	4500623995	Jul	8 13:40	R_brain_3b.bam
-rw-r--r--	1	18744242127	Jul	8 11:47	R_brain_3b.sam
-rw-r--r--	1	2904897276	Jul	8 15:39	R_brain_3b.sorted.bam
-rw-r--r--	1	2718472780	Jul	8 17:26	R_brain_3b.sorted.rmdup.bam
-rw-r--r--	1	18744242129	Jul	8 18:26	R_brain_3b.sorted.sam

-rw-r--r--	1	2620403208	Jul	8	19:30	R_brain_3b.sorted.unique.bam
-rw-r--r--	1	2893200	Jul	8	20:31	R_brain_3b.sorted.unique.bam.bai
-rw-r--r--	1	17135059200	Jul	8	18:54	R_brain_3b.sorted.unique.sam
-rw-r--r--	1	3866263484	Jul	8	13:54	R_brain_3c.bam
-rw-r--r--	1	16032727535	Jul	8	11:47	R_brain_3c.sam
-rw-r--r--	1	2477046046	Jul	8	15:54	R_brain_3c.sorted.bam
-rw-r--r--	1	2296059127	Jul	8	17:36	R_brain_3c.sorted.rmdup.bam
-rw-r--r--	1	16032727537	Jul	8	18:29	R_brain_3c.sorted.sam
-rw-r--r--	1	2241453003	Jul	8	19:40	R_brain_3c.sorted.unique.bam
-rw-r--r--	1	2725224	Jul	8	20:31	R_brain_3c.sorted.unique.bam.bai
-rw-r--r--	1	14701677825	Jul	8	19:00	R_brain_3c.sorted.unique.sam
-rw-r--r--	1	3897872615	Jul	8	14:19	R_brain_a.bam
-rw-r--r--	1	11344348495	Jul	8	11:43	R_brain_a.sam
-rw-r--r--	1	2984525675	Jul	8	16:08	R_brain_a.sorted.bam
-rw-r--r--	1	2731738919	Jul	8	17:42	R_brain_a.sorted.rmdup.bam
-rw-r--r--	1	11344348497	Jul	8	18:32	R_brain_a.sorted.sam
-rw-r--r--	1	2970292898	Jul	8	19:47	R_brain_a.sorted.unique.bam
-rw-r--r--	1	2830248	Jul	8	20:32	R_brain_a.sorted.unique.bam.bai
-rw-r--r--	1	11283443235	Jul	8	19:02	R_brain_a.sorted.unique.sam
-rw-r--r--	1	5698146722	Jul	8	14:40	R_testis_7a.bam
-rw-r--r--	1	24446621215	Jul	8	11:49	R_testis_7a.sam
-rw-r--r--	1	3591547204	Jul	8	16:30	R_testis_7a.sorted.bam
-rw-r--r--	1	3232298335	Jul	8	17:56	R_testis_7a.sorted.rmdup.bam
-rw-r--r--	1	24446621217	Jul	8	18:37	R_testis_7a.sorted.sam
-rw-r--r--	1	3225037999	Jul	8	20:01	R_testis_7a.sorted.unique.bam
-rw-r--r--	1	3161928	Jul	8	20:33	R_testis_7a.sorted.unique.bam.bai
-rw-r--r--	1	22047399795	Jul	8	19:08	R_testis_7a.sorted.unique.sam
-rw-r--r--	1	5158857480	Jul	8	14:58	R_testis_7b.bam
-rw-r--r--	1	21843544771	Jul	8	11:51	R_testis_7b.sam

```

-rw-r--r-- 1 3256889168 Jul 8 16:51 R_testis_7b.sorted.bam
-rw-r--r-- 1 3005418871 Jul 8 18:08 R_testis_7b.sorted.rmdup.bam
-rw-r--r-- 1 21843544773 Jul 8 18:42 R_testis_7b.sorted.sam
-rw-r--r-- 1 2933884733 Jul 8 20:15 R_testis_7b.sorted.unique.bam
-rw-r--r-- 1 3076032 Jul 8 20:34 R_testis_7b.sorted.unique.bam.bai
-rw-r--r-- 1 19731626646 Jul 8 19:12 R_testis_7b.sorted.unique.sam
-rw-r--r-- 1 5871141953 Jul 8 15:20 R_testis_7c.bam
-rw-r--r-- 1 25689640828 Jul 8 11:49 R_testis_7c.sam
-rw-r--r-- 1 3679211224 Jul 8 17:15 R_testis_7c.sorted.bam
-rw-r--r-- 1 3344268276 Jul 8 18:22 R_testis_7c.sorted.rmdup.bam
-rw-r--r-- 1 25689640830 Jul 8 18:48 R_testis_7c.sorted.sam
-rw-r--r-- 1 3313197928 Jul 8 20:30 R_testis_7c.sorted.unique.bam
-rw-r--r-- 1 3145056 Jul 8 20:34 R_testis_7c.sorted.unique.bam.bai
-rw-r--r-- 1 23294379757 Jul 8 19:17 R_testis_7c.sorted.unique.sam

```

standard_results/Kallisto_sleuth:

total 224

```

drwxr-xr-x 2 4096 Jul 30 14:30 Bigwig
drwxr-xr-x 2 4096 Jul 30 15:07 Cluster
drwxr-xr-x 3 4096 Jul 30 15:08 DEG
drwxr-xr-x 4 4096 Jul 30 15:07 Gene_expression_matrix
drwxr-xr-x 2 4096 Jul 30 14:32 Index
drwxr-xr-x 2 4096 Jul 30 14:30 NGS_plot
drwxr-xr-x 2 4096 Jul 30 15:07 Processed_BAM

```

standard_results/Kallisto_sleuth/Bigwig:

total 0

standard_results/Kallisto_sleuth/Cluster:

total 6848

```
-rw-r--r-- 1      1063 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.heatmap.R
-rw-r--r-- 1      1384 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.PCA.R
-rw-r--r-- 1 1088396 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.txt
-rw-r--r-- 1 1038067 Jul 30 15:08 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.txt.1.heatmap.pdf
-rw-r--r-- 1 1032771 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.txt.1.matrix.txt
-rw-r--r-- 1      4852 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.txt.1.PCA.pdf
-rw-r--r-- 1 2307052 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.clean.txt.1.rotation.txt
```

standard_results/Kallisto_sleuth/DEG:

total 12000

```
-rw-r--r-- 1 5345382 Jul 30 15:08 R_hppRNA_data.Kallisto_sleuth.testis_vs_brain.gene.DEG.txt
-rw-r--r-- 1      131 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.testis_vs_brain.info.txt
-rw-r--r-- 1 5071915 Jul 30 15:08 R_hppRNA_data.Kallisto_sleuth.testis_vs_brain.transcript.DEG.txt
-rw-r--r-- 1      1014 Jul 30 15:07 R_hppRNA_data.sleuth.R
drwxr-xr-x 8      4096 Jul 30 15:07 testis_vs_brain
```

standard_results/Kallisto_sleuth/DEG/testis_vs_brain:

total 192

```
drwxr-xr-x 3      4096 Jul 30 15:07 R_brain_3b
drwxr-xr-x 3      4096 Jul 30 15:07 R_brain_3c
drwxr-xr-x 3      4096 Jul 30 15:07 R_brain_a
drwxr-xr-x 3      4096 Jul 30 15:07 R_testis_7a
drwxr-xr-x 3      4096 Jul 30 15:07 R_testis_7b
drwxr-xr-x 3      4096 Jul 30 15:07 R_testis_7c
```

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_brain_3b:

total 32

```
drwxr-xr-x 2      4096 Jul 30 15:07 kallisto
```


standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_brain_3b/kallisto:

total 28208

-rw-r--r-- 1 23278572 Jul 30 15:07 abundance.h5

-rw-r--r-- 1 1583269 Jul 30 15:07 abundance.tsv

-rw-r--r-- 1 690 Jul 30 15:07 run_info.json

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_brain_3c:

total 32

drwxr-xr-x 2 4096 Jul 30 15:07 kallisto

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_brain_3c/kallisto:

total 27792

-rw-r--r-- 1 22932626 Jul 30 15:07 abundance.h5

-rw-r--r-- 1 1579743 Jul 30 15:07 abundance.tsv

-rw-r--r-- 1 690 Jul 30 15:07 run_info.json

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_brain_a:

total 32

drwxr-xr-x 2 4096 Jul 30 15:07 kallisto

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_brain_a/kallisto:

total 26496

-rw-r--r-- 1 21778612 Jul 30 15:07 abundance.h5

-rw-r--r-- 1 1526306 Jul 30 15:07 abundance.tsv

-rw-r--r-- 1 687 Jul 30 15:07 run_info.json

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_testis_7a:

total 32

drwxr-xr-x 2 4096 Jul 30 15:07 kallisto

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_testis_7a/kallisto:

total 30560

-rw-r--r-- 1 25312325 Jul 30 15:07 abundance.h5

-rw-r--r-- 1 1618982 Jul 30 15:07 abundance.tsv

-rw-r--r-- 1 693 Jul 30 15:07 run_info.json

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_testis_7b:

total 32

drwxr-xr-x 2 4096 Jul 30 15:07 kallisto

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_testis_7b/kallisto:

total 30112

-rw-r--r-- 1 24947347 Jul 30 15:07 abundance.h5

-rw-r--r-- 1 1614423 Jul 30 15:07 abundance.tsv

-rw-r--r-- 1 693 Jul 30 15:07 run_info.json

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_testis_7c:

total 32

drwxr-xr-x 2 4096 Jul 30 15:07 kallisto

standard_results/Kallisto_sleuth/DEG/testis_vs_brain/R_testis_7c/kallisto:

total 30544

-rw-r--r-- 1 25302516 Jul 30 15:07 abundance.h5

-rw-r--r-- 1 1620141 Jul 30 15:07 abundance.tsv

-rw-r--r-- 1 693 Jul 30 15:07 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix:

total 4448

drwxr-xr-x 8 4096 Jul 30 14:33 Quantification

-rw-r--r-- 1 1088404 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.gene.TPM.txt

-rw-r--r-- 1 2555977 Jul 30 15:07 R_hppRNA_data.Kallisto_sleuth.transcript.TPM.txt

drwxr-xr-x 2 4096 Jul 30 15:06 Summary

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification:

total 192

drwxr-xr-x 3 4096 Jul 30 14:33 R_brain_3b

drwxr-xr-x 3 4096 Jul 30 14:33 R_brain_3c

drwxr-xr-x 3 4096 Jul 30 14:33 R_brain_a

drwxr-xr-x 3 4096 Jul 30 14:33 R_testis_7a

drwxr-xr-x 3 4096 Jul 30 14:33 R_testis_7b

drwxr-xr-x 3 4096 Jul 30 14:33 R_testis_7c

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_brain_3b:

total 32

drwxr-xr-x 2 4096 Jul 30 14:48 kallisto

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_brain_3b/kallisto:

total 28208

-rw-r--r-- 1 23278572 Jul 30 15:02 abundance.h5

-rw-r--r-- 1 1583269 Jul 30 14:48 abundance.tsv

-rw-r--r-- 1 690 Jul 30 14:48 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_brain_3c:

total 32

drwxr-xr-x 2 4096 Jul 30 14:46 kallisto

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_brain_3c/kallisto:

total 27792

-rw-r--r-- 1 22932626 Jul 30 14:56 abundance.h5

-rw-r--r-- 1 1579743 Jul 30 14:46 abundance.tsv

-rw-r--r-- 1 690 Jul 30 14:46 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_brain_a:

total 32

drwxr-xr-x 2 4096 Jul 30 14:41 kallisto

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_brain_a/kallisto:

total 26496

-rw-r--r-- 1 21778612 Jul 30 14:48 abundance.h5

-rw-r--r-- 1 1526306 Jul 30 14:41 abundance.tsv

-rw-r--r-- 1 687 Jul 30 14:41 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_testis_7a:

total 32

drwxr-xr-x 2 4096 Jul 30 14:50 kallisto

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_testis_7a/kallisto:

total 30560

-rw-r--r-- 1 25312325 Jul 30 15:05 abundance.h5

-rw-r--r-- 1 1618982 Jul 30 14:50 abundance.tsv

-rw-r--r-- 1 693 Jul 30 14:50 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_testis_7b:

total 32

drwxr-xr-x 2 4096 Jul 30 14:49 kallisto

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_testis_7b/kallisto:

total 30112

-rw-r--r-- 1 24947347 Jul 30 15:04 abundance.h5

-rw-r--r-- 1 1614423 Jul 30 14:49 abundance.tsv

-rw-r--r-- 1 693 Jul 30 14:49 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_testis_7c:

total 32

drwxr-xr-x 2 4096 Jul 30 14:51 kallisto

standard_results/Kallisto_sleuth/Gene_expression_matrix/Quantification/R_testis_7c/kallisto:

total 30544

-rw-r--r-- 1 25302516 Jul 30 15:06 abundance.h5

-rw-r--r-- 1 1620141 Jul 30 14:51 abundance.tsv

-rw-r--r-- 1 693 Jul 30 14:51 run_info.json

standard_results/Kallisto_sleuth/Gene_expression_matrix/Summary:

total 11600

-rw-r--r-- 1 1583269 Jul 30 15:02 R_brain_3b.abundance.tsv

-rw-r--r-- 1 1579743 Jul 30 14:56 R_brain_3c.abundance.tsv

-rw-r--r-- 1 1526306 Jul 30 14:48 R_brain_a.abundance.tsv

-rw-r--r-- 1 1618982 Jul 30 15:05 R_testis_7a.abundance.tsv

-rw-r--r-- 1 1614423 Jul 30 15:04 R_testis_7b.abundance.tsv

-rw-r--r-- 1 1620141 Jul 30 15:06 R_testis_7c.abundance.tsv

standard_results/Kallisto_sleuth/Index:

total 1725872

-rw-r--r-- 1 144117393 Jul 30 14:30 hg19.transcript.fa

-rw-r--r-- 1 1401143983 Jul 30 14:33 hg19.transcript.idx

standard_results/Kallisto_sleuth/NGS_plot:

total 0

standard_results/Kallisto_sleuth/Processed_BAM:

total 230119872

-rw-r--r-- 1 4585269430 Jul 30 15:22 R_brain_3b.bam

-rw-r--r-- 1 29361970910 Jul 30 15:02 R_brain_3b.sam

-rw-r--r-- 1 3978310805 Jul 30 15:13 R_brain_3c.bam

-rw-r--r-- 1 25742464057 Jul 30 14:56 R_brain_3c.sam

-rw-r--r-- 1 3974876090 Jul 30 14:59 R_brain_a.bam

-rw-r--r-- 1 17893084791 Jul 30 14:48 R_brain_a.sam

-rw-r--r-- 1 5568145185 Jul 30 15:29 R_testis_7a.bam

-rw-r--r-- 1 34596712706 Jul 30 15:05 R_testis_7a.sam

-rw-r--r-- 1 5039154515 Jul 30 15:26 R_testis_7b.bam

-rw-r--r-- 1 31145890818 Jul 30 15:04 R_testis_7b.sam

-rw-r--r-- 1 5939094829 Jul 30 15:32 R_testis_7c.bam

-rw-r--r-- 1 38257261610 Jul 30 15:06 R_testis_7c.sam

standard_results/lncRNA_denovo:

total 64

drwxr-xr-x 6 4096 Dec 8 15:19 lncRNA_detection

drwxr-xr-x 9 4096 Dec 9 16:49 lncRNA_quantification

standard_results/lncRNA_denovo/lncRNA_detection:

total 128

drwxr-xr-x 9 4096 Dec 9 16:38 Assembly

drwxr-xr-x 2 4096 Dec 8 15:40 Index

drwxr-xr-x 3 4096 Dec 9 16:49 iseeRNA

drwxr-xr-x 8 12288 Dec 9 06:03 Processed_BAM

standard_results/lncRNA_denovo/lncRNA_detection/Assembly:

total 675584

-rw-r--r-- 1 806 Dec 9 16:33 assembly_list.txt

-rw-r--r-- 1 225042186 Dec 9 16:38 cuffcmp.combined.gtf

-rw-r--r-- 1 109874969 Dec 9 16:39 cuffcmp.combined.selected.gtf

-rw-r--r-- 1 4717231 Dec 9 16:38 cuffcmp.loci

-rw-r--r-- 1 2892066 Dec 9 16:38 cuffcmp.merged.gtf.refmap

-rw-r--r-- 1 12201016 Dec 9 16:38 cuffcmp.merged.gtf.tmap

-rw-r--r-- 1 1588 Dec 9 16:38 cuffcmp.stats

-rw-r--r-- 1 13053358 Dec 9 16:38 cuffcmp.tracking

drwxr-xr-x 2 4096 Dec 9 16:33 logs

-rw-r--r-- 1 235754814 Dec 9 16:38 merged.gtf

drwxr-xr-x 2 4096 Dec 9 05:59 R_brain_3b_clout

drwxr-xr-x 2 4096 Dec 9 06:41 R_brain_3c_clout

drwxr-xr-x 2 4096 Dec 9 05:32 R_brain_a_clout

drwxr-xr-x 2 4096 Dec 9 04:18 R_testis_7a_clout

drwxr-xr-x 2 4096 Dec 9 05:34 R_testis_7b_clout

drwxr-xr-x 2 4096 Dec 9 03:13 R_testis_7c_clout

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/logs:

total 32

-rw-r--r-- 1 4211 Dec 9 16:37 run.log

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/R_brain_3b_clout:

total 191552

```
-rw-r--r-- 1    3917496 Dec  9 06:37 genes.fpk_tracking
-rw-r--r-- 1    8610258 Dec  9 06:37 isoforms.fpk_tracking
-rw-r--r-- 1         160 Dec  9 06:37 skipped.gtf
-rw-r--r-- 1  158436411 Dec  9 06:37 transcripts.gtf
```

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/R_brain_3c_clout:
total 187760

```
-rw-r--r-- 1    3593851 Dec  9 07:09 genes.fpk_tracking
-rw-r--r-- 1    8139222 Dec  9 07:09 isoforms.fpk_tracking
-rw-r--r-- 1         160 Dec  9 07:09 skipped.gtf
-rw-r--r-- 1  155861595 Dec  9 07:09 transcripts.gtf
```

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/R_brain_a_clout:
total 181776

```
-rw-r--r-- 1    3356866 Dec  9 05:54 genes.fpk_tracking
-rw-r--r-- 1    7647896 Dec  9 05:54 isoforms.fpk_tracking
-rw-r--r-- 1         160 Dec  9 05:54 skipped.gtf
-rw-r--r-- 1  151178297 Dec  9 05:54 transcripts.gtf
```

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/R_testis_7a_clout:
total 208224

```
-rw-r--r-- 1    4813876 Dec  9 05:29 genes.fpk_tracking
-rw-r--r-- 1   10237385 Dec  9 05:29 isoforms.fpk_tracking
-rw-r--r-- 1         160 Dec  9 05:29 skipped.gtf
-rw-r--r-- 1  170800757 Dec  9 05:29 transcripts.gtf
```

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/R_testis_7b_clout:
total 201152

```
-rw-r--r-- 1    4284886 Dec  9 06:40 genes.fpk_tracking
```



```
-rw-r--r-- 1      9459381 Dec  9 06:40 isoforms.fpk_tracking
-rw-r--r-- 1          160 Dec  9 06:40 skipped.gtf
-rw-r--r-- 1  165806280 Dec  9 06:40 transcripts.gtf
```

standard_results/lncRNA_denovo/lncRNA_detection/Assembly/R_testis_7c_clout:

total 197872

```
-rw-r--r-- 1      4123294 Dec  9 04:12 genes.fpk_tracking
-rw-r--r-- 1      9123448 Dec  9 04:12 isoforms.fpk_tracking
-rw-r--r-- 1          160 Dec  9 04:12 skipped.gtf
-rw-r--r-- 1  163395220 Dec  9 04:12 transcripts.gtf
```

standard_results/lncRNA_denovo/lncRNA_detection/Index:

total 8063168

```
-rw-r--r-- 1    957980027 Dec  8 15:31 hg19.1.bt2
-rw-r--r-- 1    715335932 Dec  8 15:31 hg19.2.bt2
-rw-r--r-- 1         3284 Dec  8 15:20 hg19.3.bt2
-rw-r--r-- 1    715335926 Dec  8 15:20 hg19.4.bt2
-rwxr-xr-x 1   3157608038 Dec  8 15:20 hg19.fa
-rw-r--r-- 1    957980027 Dec  8 15:41 hg19.rev.1.bt2
-rw-r--r-- 1    715335932 Dec  8 15:41 hg19.rev.2.bt2
```

standard_results/lncRNA_denovo/lncRNA_detection/iseeRNA:

total 328864

```
-rw-r--r-- 1    2038477 Dec  9 16:49 all_cuffcmp.combined.selected.consv
drwxr-xr-x 2        12288 Dec  9 16:49 consv
-rw-r--r-- 1   195411552 Dec  9 16:47 cuffcmp.combined.selected.fa
-rw-r--r-- 1    7776046 Dec  9 16:48 cuffcmp.combined.selected.feature
-rw-r--r-- 1   42494989 Dec  9 16:46 cuffcmp.combined.selected.gtf
-rw-r--r-- 1    1041254 Dec  9 16:47 cuffcmp.combined.selected.list
```

```

-rw-r--r-- 1 20593455 Dec 9 16:49 cuffcmp.combined.selected.noncoding.gtf
-rw-r--r-- 1 3055567 Dec 9 16:47 cuffcmp.combined.selected.orf
-rw-r--r-- 1 1011737 Dec 9 16:49 cuffcmp.combined.selected.predict
-rw-r--r-- 1 1718184 Dec 9 16:49 cuffcmp.combined.selected.result
-rw-r--r-- 1 6162132 Dec 9 16:49 cuffcmp.combined.selected.scaled
-rw-r--r-- 1 10743386 Dec 9 16:49 cuffcmp.combined.selected.svm
-rw-r--r-- 1 263628 Dec 9 16:49 denovo_lncRNA.transcript_to_gene.txt
-rw-r--r-- 1 481 Dec 9 16:46 iSeeRNA.conf
-rw-r--r-- 1 3401 Dec 9 16:46 Makefile

```

standard_results/lncRNA_denovo/lncRNA_detection/iseeRNA/consv:

total 20832

```

-rw-r--r-- 1 91654 Dec 9 16:48 chr10.consv
-rw-r--r-- 1 429493 Dec 9 16:48 chr10.dat
-rw-r--r-- 1 35715 Dec 9 16:48 chr10.list
-rw-r--r-- 1 97936 Dec 9 16:48 chr11.consv
-rw-r--r-- 1 480155 Dec 9 16:48 chr11.dat
-rw-r--r-- 1 37320 Dec 9 16:48 chr11.list
-rw-r--r-- 1 102812 Dec 9 16:49 chr12.consv
-rw-r--r-- 1 571868 Dec 9 16:48 chr12.dat
-rw-r--r-- 1 39120 Dec 9 16:48 chr12.list
-rw-r--r-- 1 53348 Dec 9 16:48 chr13.consv
-rw-r--r-- 1 248008 Dec 9 16:48 chr13.dat
-rw-r--r-- 1 20970 Dec 9 16:48 chr13.list
-rw-r--r-- 1 63963 Dec 9 16:48 chr14.consv
-rw-r--r-- 1 301880 Dec 9 16:48 chr14.dat
-rw-r--r-- 1 24765 Dec 9 16:48 chr14.list
-rw-r--r-- 1 77142 Dec 9 16:48 chr15.consv
-rw-r--r-- 1 393544 Dec 9 16:48 chr15.dat

```

-rw-r--r--	1	30150	Dec	9 16:48	chr15.list
-rw-r--r--	1	78008	Dec	9 16:48	chr16.consv
-rw-r--r--	1	361268	Dec	9 16:48	chr16.dat
-rw-r--r--	1	29940	Dec	9 16:48	chr16.list
-rw-r--r--	1	96208	Dec	9 16:49	chr17.consv
-rw-r--r--	1	466072	Dec	9 16:48	chr17.dat
-rw-r--r--	1	36825	Dec	9 16:48	chr17.list
-rw-r--r--	1	41324	Dec	9 16:49	chr18.consv
-rw-r--r--	1	181852	Dec	9 16:48	chr18.dat
-rw-r--r--	1	16110	Dec	9 16:48	chr18.list
-rw-r--r--	1	107225	Dec	9 16:48	chr19.consv
-rw-r--r--	1	468060	Dec	9 16:48	chr19.dat
-rw-r--r--	1	40440	Dec	9 16:48	chr19.list
-rw-r--r--	1	194423	Dec	9 16:48	chr1.consv
-rw-r--r--	1	1048630	Dec	9 16:48	chr1.dat
-rw-r--r--	1	74070	Dec	9 16:48	chr1.list
-rw-r--r--	1	54148	Dec	9 16:48	chr20.consv
-rw-r--r--	1	216471	Dec	9 16:48	chr20.dat
-rw-r--r--	1	21015	Dec	9 16:48	chr20.list
-rw-r--r--	1	24451	Dec	9 16:49	chr21.consv
-rw-r--r--	1	104922	Dec	9 16:48	chr21.dat
-rw-r--r--	1	9555	Dec	9 16:48	chr21.list
-rw-r--r--	1	51083	Dec	9 16:48	chr22.consv
-rw-r--r--	1	211787	Dec	9 16:48	chr22.dat
-rw-r--r--	1	19890	Dec	9 16:48	chr22.list
-rw-r--r--	1	156162	Dec	9 16:49	chr2.consv
-rw-r--r--	1	892629	Dec	9 16:48	chr2.dat
-rw-r--r--	1	60210	Dec	9 16:48	chr2.list
-rw-r--r--	1	122187	Dec	9 16:49	chr3.consv

-rw-r--r--	1	661955	Dec	9 16:48	chr3.dat
-rw-r--r--	1	46785	Dec	9 16:48	chr3.list
-rw-r--r--	1	88347	Dec	9 16:48	chr4.consv
-rw-r--r--	1	447333	Dec	9 16:48	chr4.dat
-rw-r--r--	1	34005	Dec	9 16:48	chr4.list
-rw-r--r--	1	95284	Dec	9 16:49	chr5.consv
-rw-r--r--	1	456967	Dec	9 16:48	chr5.dat
-rw-r--r--	1	37080	Dec	9 16:48	chr5.list
-rw-r--r--	1	108686	Dec	9 16:49	chr6.consv
-rw-r--r--	1	526803	Dec	9 16:48	chr6.dat
-rw-r--r--	1	42270	Dec	9 16:48	chr6.list
-rw-r--r--	1	106978	Dec	9 16:49	chr7.consv
-rw-r--r--	1	539333	Dec	9 16:48	chr7.dat
-rw-r--r--	1	41505	Dec	9 16:48	chr7.list
-rw-r--r--	1	77828	Dec	9 16:48	chr8.consv
-rw-r--r--	1	368411	Dec	9 16:48	chr8.dat
-rw-r--r--	1	29985	Dec	9 16:48	chr8.list
-rw-r--r--	1	88552	Dec	9 16:49	chr9.consv
-rw-r--r--	1	468758	Dec	9 16:48	chr9.dat
-rw-r--r--	1	34200	Dec	9 16:48	chr9.list
-rw-r--r--	1	55985	Dec	9 16:48	chrX.consv
-rw-r--r--	1	321221	Dec	9 16:48	chrX.dat
-rw-r--r--	1	21090	Dec	9 16:48	chrX.list
-rw-r--r--	1	4743	Dec	9 16:48	chrY.consv
-rw-r--r--	1	25197	Dec	9 16:48	chrY.dat
-rw-r--r--	1	1860	Dec	9 16:48	chrY.list
-rw-r--r--	1	2772	Dec	9 16:48	Makefile

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM:

total 297917280

-rw-r--r--	1	565	Dec	8 22:22	R_brain_3b_align_summary.txt
-rw-r--r--	1	2618290381	Dec	8 22:37	R_brain_3b.sorted.bam
-rw-r--r--	1	2445099919	Dec	8 22:49	R_brain_3b.sorted.rmdup.bam
-rw-r--r--	1	17572624965	Dec	8 22:40	R_brain_3b.sorted.sam
-rw-r--r--	1	2467603780	Dec	8 23:01	R_brain_3b.sorted.unique.bam
-rw-r--r--	1	2764152	Dec	8 23:01	R_brain_3b.sorted.unique.bam.bai
-rw-r--r--	1	16469666297	Dec	8 22:48	R_brain_3b.sorted.unique.sam
drwxr-xr-x	3	4096	Dec	8 22:22	R_brain_3b_thout
-rw-r--r--	1	563	Dec	9 05:29	R_brain_3c_align_summary.txt
-rw-r--r--	1	2231354069	Dec	9 05:42	R_brain_3c.sorted.bam
-rw-r--r--	1	2061148928	Dec	9 05:53	R_brain_3c.sorted.rmdup.bam
-rw-r--r--	1	15003005756	Dec	9 05:45	R_brain_3c.sorted.sam
-rw-r--r--	1	2114558579	Dec	9 06:03	R_brain_3c.sorted.unique.bam
-rw-r--r--	1	2625840	Dec	9 06:03	R_brain_3c.sorted.unique.bam.bai
-rw-r--r--	1	14149506658	Dec	9 05:52	R_brain_3c.sorted.unique.sam
drwxr-xr-x	3	4096	Dec	9 05:29	R_brain_3c_thout
-rw-r--r--	1	563	Dec	8 23:51	R_brain_a_align_summary.txt
-rw-r--r--	1	2718689218	Dec	9 00:01	R_brain_a.sorted.bam
-rw-r--r--	1	2490297824	Dec	9 03:13	R_brain_a.sorted.rmdup.bam
-rw-r--r--	1	10530335240	Dec	9 03:10	R_brain_a.sorted.sam
-rw-r--r--	1	2590911442	Dec	9 03:21	R_brain_a.sorted.unique.bam
-rw-r--r--	1	2672328	Dec	9 03:21	R_brain_a.sorted.unique.bam.bai
-rw-r--r--	1	9948750913	Dec	9 03:15	R_brain_a.sorted.unique.sam
drwxr-xr-x	3	4096	Dec	8 23:51	R_brain_a_thout
-rw-r--r--	1	565	Dec	8 19:24	R_testis_7a_align_summary.txt
-rw-r--r--	1	3412667615	Dec	8 19:45	R_testis_7a.sorted.bam
-rw-r--r--	1	3066251836	Dec	8 19:59	R_testis_7a.sorted.rmdup.bam
-rw-r--r--	1	23986546636	Dec	8 19:49	R_testis_7a.sorted.sam

```

-rw-r--r-- 1 3082486500 Dec 8 20:16 R_testis_7a.sorted.unique.bam
-rw-r--r-- 1 3170816 Dec 8 20:17 R_testis_7a.sorted.unique.bam.bai
-rw-r--r-- 1 21275850927 Dec 8 20:01 R_testis_7a.sorted.unique.sam
drwxr-xr-x 3 4096 Dec 8 19:24 R_testis_7a_thout
-rw-r--r-- 1 565 Dec 8 22:20 R_testis_7b_align_summary.txt
-rw-r--r-- 1 3117027135 Dec 8 22:38 R_testis_7b.sorted.bam
-rw-r--r-- 1 2876059633 Dec 8 22:52 R_testis_7b.sorted.rmdup.bam
-rw-r--r-- 1 21583145014 Dec 8 22:42 R_testis_7b.sorted.sam
-rw-r--r-- 1 2806800092 Dec 8 23:06 R_testis_7b.sorted.unique.bam
-rw-r--r-- 1 3099176 Dec 8 23:07 R_testis_7b.sorted.unique.bam.bai
-rw-r--r-- 1 19037924900 Dec 8 22:53 R_testis_7b.sorted.unique.sam
drwxr-xr-x 3 4096 Dec 8 22:20 R_testis_7b_thout
-rw-r--r-- 1 565 Dec 8 19:03 R_testis_7c_align_summary.txt
-rw-r--r-- 1 3445850599 Dec 8 19:23 R_testis_7c.sorted.bam
-rw-r--r-- 1 3121234982 Dec 8 19:37 R_testis_7c.sorted.rmdup.bam
-rw-r--r-- 1 24707202555 Dec 8 19:27 R_testis_7c.sorted.sam
-rw-r--r-- 1 3190256420 Dec 8 19:54 R_testis_7c.sorted.unique.bam
-rw-r--r-- 1 3144208 Dec 8 19:55 R_testis_7c.sorted.unique.bam.bai
-rw-r--r-- 1 22655442614 Dec 8 19:39 R_testis_7c.sorted.unique.sam
drwxr-xr-x 3 4096 Dec 8 19:03 R_testis_7c_thout

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_brain_3b_thout:

total 3220288

```

-rw-r--r-- 1 2616751163 Dec 8 22:21 accepted_hits.bam
-rw-r--r-- 1 565 Dec 8 22:07 align_summary.txt
-rw-r--r-- 1 3212462 Dec 8 22:07 deletions.bed
-rw-r--r-- 1 4490831 Dec 8 22:07 insertions.bed
-rw-r--r-- 1 19199512 Dec 8 22:07 junctions.bed
drwxr-xr-x 2 8192 Dec 8 22:21 logs

```

```
-rw-r--r-- 1          186 Dec  8 19:41 prep_reads.info
-rw-r--r-- 1 239408344 Dec  8 22:22 unmapped.bam
```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_brain_3b_thout/logs:

total 1248

```
-rw-r--r-- 1      0 Dec  8 22:21 bam_merge_um.log
-rw-r--r-- 1 13334 Dec  8 21:50 bowtie_build.log
-rw-r--r-- 1   222 Dec  8 20:26 bowtie.left_kept_reads.log
-rw-r--r-- 1   219 Dec  8 21:15 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1   215 Dec  8 21:51 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1   215 Dec  8 21:51 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1   215 Dec  8 21:51 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1   215 Dec  8 21:51 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1   222 Dec  8 20:57 bowtie.right_kept_reads.log
-rw-r--r-- 1   219 Dec  8 21:39 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1   215 Dec  8 21:53 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1   215 Dec  8 21:54 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1   215 Dec  8 21:54 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1   215 Dec  8 21:54 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1      0 Dec  8 19:41 g2f.err
-rw-r--r-- 1   112 Dec  8 19:41 g2f.out
-rw-r--r-- 1   170 Dec  8 19:24 gtf_juncs.log
-rw-r--r-- 1   609 Dec  8 21:50 juncs_db.log
-rw-r--r-- 1   302 Dec  8 21:56 long_spanning_reads.segs.log
-rw-r--r-- 1    47 Dec  8 19:55 m2g_left_kept_reads.err
-rw-r--r-- 1   250 Dec  8 20:26 m2g_left_kept_reads.out
-rw-r--r-- 1    47 Dec  8 20:26 m2g_right_kept_reads.err
-rw-r--r-- 1   250 Dec  8 20:57 m2g_right_kept_reads.out
-rw-r--r-- 1   161 Dec  8 19:41 prep_reads.log
```

```

-rw-r--r-- 1 1013 Dec 8 22:07 reports.log
-rw-r--r-- 1 0 Dec 8 22:10 reports.merge_bam.log
-rw-r--r-- 1 40 Dec 8 22:08 reports.samtools_sort.log0
-rw-r--r-- 1 40 Dec 8 22:08 reports.samtools_sort.log1
-rw-r--r-- 1 40 Dec 8 22:08 reports.samtools_sort.log2
-rw-r--r-- 1 40 Dec 8 22:08 reports.samtools_sort.log3
-rw-r--r-- 1 40 Dec 8 22:08 reports.samtools_sort.log4
-rw-r--r-- 1 40 Dec 8 22:08 reports.samtools_sort.log5
-rw-r--r-- 1 55162 Dec 8 22:22 run.log
-rw-r--r-- 1 1540 Dec 8 21:49 segment_juncs.log
-rw-r--r-- 1 3538 Dec 8 22:22 tophat.log

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_brain_3c_thout:

total 2746192

```

-rw-r--r-- 1 2230131129 Dec 9 05:28 accepted_hits.bam
-rw-r--r-- 1 563 Dec 9 05:15 align_summary.txt
-rw-r--r-- 1 2602482 Dec 9 05:15 deletions.bed
-rw-r--r-- 1 3668977 Dec 9 05:15 insertions.bed
-rw-r--r-- 1 18384690 Dec 9 05:15 junctions.bed
drwxr-xr-x 2 8192 Dec 9 05:28 logs
-rw-r--r-- 1 186 Dec 9 03:22 prep_reads.info
-rw-r--r-- 1 203684744 Dec 9 05:29 unmapped.bam

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_brain_3c_thout/logs:

total 1248

```

-rw-r--r-- 1 0 Dec 9 05:28 bam_merge_um.log
-rw-r--r-- 1 13056 Dec 9 05:01 bowtie_build.log
-rw-r--r-- 1 222 Dec 9 03:59 bowtie.left_kept_reads.log
-rw-r--r-- 1 218 Dec 9 04:35 bowtie.left_kept_reads.m2g_um.log

```


-rw-r--r--	1	213 Dec	9 05:01	bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r--	1	214 Dec	9 05:02	bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r--	1	213 Dec	9 05:02	bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r--	1	212 Dec	9 05:02	bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r--	1	222 Dec	9 04:23	bowtie.right_kept_reads.log
-rw-r--r--	1	218 Dec	9 04:52	bowtie.right_kept_reads.m2g_um.log
-rw-r--r--	1	213 Dec	9 05:04	bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r--	1	214 Dec	9 05:04	bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r--	1	214 Dec	9 05:05	bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r--	1	212 Dec	9 05:05	bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r--	1	0 Dec	9 03:22	g2f.err
-rw-r--r--	1	112 Dec	9 03:22	g2f.out
-rw-r--r--	1	170 Dec	9 03:07	gtf_juncs.log
-rw-r--r--	1	609 Dec	9 05:01	juncs_db.log
-rw-r--r--	1	302 Dec	9 05:06	long_spanning_reads.segs.log
-rw-r--r--	1	47 Dec	9 03:36	m2g_left_kept_reads.err
-rw-r--r--	1	250 Dec	9 03:59	m2g_left_kept_reads.out
-rw-r--r--	1	47 Dec	9 04:00	m2g_right_kept_reads.err
-rw-r--r--	1	250 Dec	9 04:23	m2g_right_kept_reads.out
-rw-r--r--	1	161 Dec	9 03:22	prep_reads.log
-rw-r--r--	1	1013 Dec	9 05:15	reports.log
-rw-r--r--	1	0 Dec	9 05:18	reports.merge_bam.log
-rw-r--r--	1	40 Dec	9 05:16	reports.samtools_sort.log0
-rw-r--r--	1	40 Dec	9 05:16	reports.samtools_sort.log1
-rw-r--r--	1	40 Dec	9 05:16	reports.samtools_sort.log2
-rw-r--r--	1	40 Dec	9 05:16	reports.samtools_sort.log3
-rw-r--r--	1	40 Dec	9 05:16	reports.samtools_sort.log4
-rw-r--r--	1	40 Dec	9 05:16	reports.samtools_sort.log5
-rw-r--r--	1	55162 Dec	9 05:29	run.log

```
-rw-r--r-- 1    1538 Dec   9 04:59 segment_juncs.log
-rw-r--r-- 1    3538 Dec   9 05:29 tophat.log
```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_brain_a_thout:

total 3308176

```
-rw-r--r-- 1 2718972161 Dec   8 23:51 accepted_hits.bam
-rw-r--r-- 1          563 Dec   8 23:42 align_summary.txt
-rw-r--r-- 1    1314058 Dec   8 23:42 deletions.bed
-rw-r--r-- 1    1989593 Dec   8 23:42 insertions.bed
-rw-r--r-- 1    16748306 Dec   8 23:42 junctions.bed
drwxr-xr-x 2          8192 Dec   8 23:51 logs
-rw-r--r-- 1          186 Dec   8 22:31 prep_reads.info
-rw-r--r-- 1 222742070 Dec   8 23:51 unmapped.bam
```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_brain_a_thout/logs:

total 1248

```
-rw-r--r-- 1          0 Dec   8 23:51 bam_merge_um.log
-rw-r--r-- 1    12426 Dec   8 23:31 bowtie_build.log
-rw-r--r-- 1     221 Dec   8 22:57 bowtie.left_kept_reads.log
-rw-r--r-- 1     217 Dec   8 23:16 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1     210 Dec   8 23:31 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1     210 Dec   8 23:32 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1     210 Dec   8 23:32 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1     211 Dec   8 23:32 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1     221 Dec   8 23:10 bowtie.right_kept_reads.log
-rw-r--r-- 1     218 Dec   8 23:24 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1     212 Dec   8 23:34 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1     210 Dec   8 23:34 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1     210 Dec   8 23:34 bowtie.right_kept_reads.m2g_um_seg3.log
```

```

-rw-r--r-- 1    211 Dec  8 23:34 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1      0 Dec  8 22:31 g2f.err
-rw-r--r-- 1   112 Dec  8 22:31 g2f.out
-rw-r--r-- 1   170 Dec  8 22:22 gtf_juncs.log
-rw-r--r-- 1   609 Dec  8 23:31 juncs_db.log
-rw-r--r-- 1   302 Dec  8 23:35 long_spanning_reads.segs.log
-rw-r--r-- 1    47 Dec  8 22:44 m2g_left_kept_reads.err
-rw-r--r-- 1   249 Dec  8 22:57 m2g_left_kept_reads.out
-rw-r--r-- 1    47 Dec  8 22:57 m2g_right_kept_reads.err
-rw-r--r-- 1   249 Dec  8 23:10 m2g_right_kept_reads.out
-rw-r--r-- 1   161 Dec  8 22:31 prep_reads.log
-rw-r--r-- 1  1012 Dec  8 23:42 reports.log
-rw-r--r-- 1      0 Dec  8 23:45 reports.merge_bam.log
-rw-r--r-- 1    40 Dec  8 23:43 reports.samtools_sort.log0
-rw-r--r-- 1    40 Dec  8 23:43 reports.samtools_sort.log1
-rw-r--r-- 1    40 Dec  8 23:43 reports.samtools_sort.log2
-rw-r--r-- 1    40 Dec  8 23:43 reports.samtools_sort.log3
-rw-r--r-- 1    40 Dec  8 23:43 reports.samtools_sort.log4
-rw-r--r-- 1    40 Dec  8 23:43 reports.samtools_sort.log5
-rw-r--r-- 1  54922 Dec  8 23:51 run.log
-rw-r--r-- 1   1536 Dec  8 23:30 segment_juncs.log
-rw-r--r-- 1   3536 Dec  8 23:51 tophat.log

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_testis_7a_thout:

total 4086976

```

-rw-r--r-- 1 3411332745 Dec  8 19:23 accepted_hits.bam
-rw-r--r-- 1      565 Dec  8 19:04 align_summary.txt
-rw-r--r-- 1  4908948 Dec  8 19:04 deletions.bed
-rw-r--r-- 1  5073730 Dec  8 19:04 insertions.bed

```

```

-rw-r--r-- 1      32584436 Dec  8 19:04 junctions.bed
drwxr-xr-x 2          8192 Dec  8 19:23 logs
-rw-r--r-- 1          186 Dec  8 16:00 prep_reads.info
-rw-r--r-- 1    205351398 Dec  8 19:24 unmapped.bam

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_testis_7a_thout/logs:

total 1248

```

-rw-r--r-- 1      0 Dec  8 19:23 bam_merge_um.log
-rw-r--r-- 1  12721 Dec  8 18:44 bowtie_build.log
-rw-r--r-- 1   224 Dec  8 16:49 bowtie.left_kept_reads.log
-rw-r--r-- 1   221 Dec  8 17:53 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1   216 Dec  8 18:44 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1   217 Dec  8 18:45 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1   217 Dec  8 18:45 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1   217 Dec  8 18:46 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1   224 Dec  8 17:26 bowtie.right_kept_reads.log
-rw-r--r-- 1   221 Dec  8 18:25 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1   215 Dec  8 18:48 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1   217 Dec  8 18:49 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1   217 Dec  8 18:49 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1   217 Dec  8 18:50 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1      0 Dec  8 16:00 g2f.err
-rw-r--r-- 1   112 Dec  8 16:00 g2f.out
-rw-r--r-- 1   170 Dec  8 15:42 gtf_juncs.log
-rw-r--r-- 1   609 Dec  8 18:43 juncs_db.log
-rw-r--r-- 1   302 Dec  8 18:51 long_spanning_reads.segs.log
-rw-r--r-- 1    47 Dec  8 16:12 m2g_left_kept_reads.err
-rw-r--r-- 1   251 Dec  8 16:49 m2g_left_kept_reads.out
-rw-r--r-- 1    47 Dec  8 16:50 m2g_right_kept_reads.err

```

```

-rw-r--r-- 1    251 Dec  8 17:27 m2g_right_kept_reads.out
-rw-r--r-- 1    161 Dec  8 16:00 prep_reads.log
-rw-r--r-- 1   1014 Dec  8 19:04 reports.log
-rw-r--r-- 1      0 Dec  8 19:09 reports.merge_bam.log
-rw-r--r-- 1    40 Dec  8 19:06 reports.samtools_sort.log0
-rw-r--r-- 1    40 Dec  8 19:06 reports.samtools_sort.log1
-rw-r--r-- 1    40 Dec  8 19:06 reports.samtools_sort.log2
-rw-r--r-- 1    40 Dec  8 19:06 reports.samtools_sort.log3
-rw-r--r-- 1    40 Dec  8 19:06 reports.samtools_sort.log4
-rw-r--r-- 1    40 Dec  8 19:06 reports.samtools_sort.log5
-rw-r--r-- 1  55402 Dec  8 19:24 run.log
-rw-r--r-- 1   1540 Dec  8 18:42 segment_juncs.log
-rw-r--r-- 1   3540 Dec  8 19:24 tophat.log

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_testis_7b_thout:

total 3719312

```

-rw-r--r-- 1 3116214465 Dec  8 22:20 accepted_hits.bam
-rw-r--r-- 1      565 Dec  8 22:03 align_summary.txt
-rw-r--r-- 1   4414591 Dec  8 22:03 deletions.bed
-rw-r--r-- 1   4298550 Dec  8 22:03 insertions.bed
-rw-r--r-- 1  31686563 Dec  8 22:03 junctions.bed
drwxr-xr-x 2      8192 Dec  8 22:20 logs
-rw-r--r-- 1      186 Dec  8 19:21 prep_reads.info
-rw-r--r-- 1  173317307 Dec  8 22:20 unmapped.bam

```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_testis_7b_thout/logs:

total 1248

```

-rw-r--r-- 1      0 Dec  8 22:20 bam_merge_um.log
-rw-r--r-- 1  12721 Dec  8 21:43 bowtie_build.log

```

-rw-r--r--	1	222 Dec	8 20:06 bowtie.left_kept_reads.log
-rw-r--r--	1	219 Dec	8 21:02 bowtie.left_kept_reads.m2g_um.log
-rw-r--r--	1	216 Dec	8 21:44 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r--	1	217 Dec	8 21:44 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r--	1	217 Dec	8 21:45 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r--	1	217 Dec	8 21:45 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r--	1	222 Dec	8 20:39 bowtie.right_kept_reads.log
-rw-r--r--	1	219 Dec	8 21:29 bowtie.right_kept_reads.m2g_um.log
-rw-r--r--	1	215 Dec	8 21:47 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r--	1	217 Dec	8 21:48 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r--	1	217 Dec	8 21:48 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r--	1	217 Dec	8 21:49 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r--	1	0 Dec	8 19:21 g2f.err
-rw-r--r--	1	112 Dec	8 19:21 g2f.out
-rw-r--r--	1	170 Dec	8 19:03 gtf_juncs.log
-rw-r--r--	1	609 Dec	8 21:42 juncs_db.log
-rw-r--r--	1	302 Dec	8 21:50 long_spanning_reads.segs.log
-rw-r--r--	1	47 Dec	8 19:34 m2g_left_kept_reads.err
-rw-r--r--	1	251 Dec	8 20:07 m2g_left_kept_reads.out
-rw-r--r--	1	47 Dec	8 20:07 m2g_right_kept_reads.err
-rw-r--r--	1	251 Dec	8 20:39 m2g_right_kept_reads.out
-rw-r--r--	1	161 Dec	8 19:21 prep_reads.log
-rw-r--r--	1	1014 Dec	8 22:03 reports.log
-rw-r--r--	1	0 Dec	8 22:07 reports.merge_bam.log
-rw-r--r--	1	40 Dec	8 22:04 reports.samtools_sort.log0
-rw-r--r--	1	40 Dec	8 22:04 reports.samtools_sort.log1
-rw-r--r--	1	40 Dec	8 22:04 reports.samtools_sort.log2
-rw-r--r--	1	40 Dec	8 22:04 reports.samtools_sort.log3
-rw-r--r--	1	40 Dec	8 22:04 reports.samtools_sort.log4

```
-rw-r--r-- 1      40 Dec  8 22:04 reports.samtools_sort.log5
-rw-r--r-- 1 55402 Dec  8 22:20 run.log
-rw-r--r-- 1   1540 Dec  8 21:41 segment_juncs.log
-rw-r--r-- 1   3540 Dec  8 22:20 tophat.log
```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_testis_7c_thout:
total 4134400

```
-rw-r--r-- 1 3441130951 Dec  8 19:02 accepted_hits.bam
-rw-r--r-- 1      565 Dec  8 18:42 align_summary.txt
-rw-r--r-- 1 4532288 Dec  8 18:42 deletions.bed
-rw-r--r-- 1 4341191 Dec  8 18:42 insertions.bed
-rw-r--r-- 1 27455127 Dec  8 18:42 junctions.bed
drwxr-xr-x 2      8192 Dec  8 19:02 logs
-rw-r--r-- 1      186 Dec  8 16:01 prep_reads.info
-rw-r--r-- 1 224295988 Dec  8 19:03 unmapped.bam
```

standard_results/lncRNA_denovo/lncRNA_detection/Processed_BAM/R_testis_7c_thout/logs:
total 1248

```
-rw-r--r-- 1      0 Dec  8 19:02 bam_merge_um.log
-rw-r--r-- 1 12709 Dec  8 18:22 bowtie_build.log
-rw-r--r-- 1   223 Dec  8 16:48 bowtie.left_kept_reads.log
-rw-r--r-- 1   219 Dec  8 17:43 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1   215 Dec  8 18:22 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1   215 Dec  8 18:23 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1   215 Dec  8 18:23 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1   215 Dec  8 18:24 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1   223 Dec  8 17:24 bowtie.right_kept_reads.log
-rw-r--r-- 1   219 Dec  8 18:07 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1   215 Dec  8 18:26 bowtie.right_kept_reads.m2g_um_seg1.log
```

```

-rw-r--r-- 1    215 Dec  8 18:26 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1    215 Dec  8 18:27 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1    215 Dec  8 18:27 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1      0 Dec  8 16:01 g2f.err
-rw-r--r-- 1   112 Dec  8 16:01 g2f.out
-rw-r--r-- 1   170 Dec  8 15:42 gtf_juncs.log
-rw-r--r-- 1   609 Dec  8 18:21 juncs_db.log
-rw-r--r-- 1   302 Dec  8 18:28 long_spanning_reads.segs.log
-rw-r--r-- 1    47 Dec  8 16:14 m2g_left_kept_reads.err
-rw-r--r-- 1   251 Dec  8 16:49 m2g_left_kept_reads.out
-rw-r--r-- 1    47 Dec  8 16:49 m2g_right_kept_reads.err
-rw-r--r-- 1   251 Dec  8 17:24 m2g_right_kept_reads.out
-rw-r--r-- 1   161 Dec  8 16:01 prep_reads.log
-rw-r--r-- 1  1014 Dec  8 18:42 reports.log
-rw-r--r-- 1      0 Dec  8 18:47 reports.merge_bam.log
-rw-r--r-- 1    40 Dec  8 18:44 reports.samtools_sort.log0
-rw-r--r-- 1    40 Dec  8 18:44 reports.samtools_sort.log1
-rw-r--r-- 1    40 Dec  8 18:44 reports.samtools_sort.log2
-rw-r--r-- 1    40 Dec  8 18:44 reports.samtools_sort.log3
-rw-r--r-- 1    40 Dec  8 18:44 reports.samtools_sort.log4
-rw-r--r-- 1    40 Dec  8 18:44 reports.samtools_sort.log5
-rw-r--r-- 1  55402 Dec  8 19:03 run.log
-rw-r--r-- 1   1540 Dec  8 18:20 segment_juncs.log
-rw-r--r-- 1   3540 Dec  8 19:03 tophat.log

```

standard_results/lncRNA_denovo/lncRNA_quantification:

total 224

drwxr-xr-x 2 4096 Dec 9 16:49 Bigwig

drwxr-xr-x 2 4096 Dec 9 17:39 Cluster


```

drwxr-xr-x 3 4096 Dec  9 23:40 DEG
drwxr-xr-x 4 4096 Dec  9 17:39 Gene_expression_matrix
drwxr-xr-x 2 4096 Dec  9 16:52 Index
drwxr-xr-x 2 4096 Dec  9 16:49 NGS_plot
drwxr-xr-x 2 4096 Dec  9 17:39 Processed_BAM

```

standard_results/lncRNA_denovo/lncRNA_quantification/Bigwig:

total 0

standard_results/lncRNA_denovo/lncRNA_quantification/Cluster:

total 12464

```

-rw-r--r-- 1      1079 Dec  9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.heatmap.R
-rw-r--r-- 1      1412 Dec  9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.PCA.R
-rw-r--r-- 1 2251039 Dec  9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.txt
-rw-r--r-- 1 1738592 Dec  9 17:42 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.txt.1.heatmap.pdf
-rw-r--r-- 1 2011648 Dec  9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.txt.1.matrix.txt
-rw-r--r-- 1      4768 Dec  9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.txt.1.PCA.pdf
-rw-r--r-- 1 4580777 Dec  9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.clean.txt.1.rotation.txt

```

standard_results/lncRNA_denovo/lncRNA_quantification/DEG:

total 20352

```

-rw-r--r-- 1 9221735 Dec  9 23:40 R_hppRNA_data.lncRNA_denovo.testis_vs_brain.gene.DEG.txt
-rw-r--r-- 1      131 Dec  9 23:37 R_hppRNA_data.lncRNA_denovo.testis_vs_brain.info.txt
-rw-r--r-- 1     1020 Dec  9 23:37 R_hppRNA_data.lncRNA_denovo.testis_vs_brain.sleuth.R
-rw-r--r-- 1 8400573 Dec  9 23:40 R_hppRNA_data.lncRNA_denovo.testis_vs_brain.transcript.DEG.txt
drwxr-xr-x 8      4096 Dec  9 23:37 testis_vs_brain

```

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain:

total 192

drwxr-xr-x 3 4096 Dec 9 23:37 R_brain_3b
drwxr-xr-x 3 4096 Dec 9 23:37 R_brain_3c
drwxr-xr-x 3 4096 Dec 9 23:37 R_brain_a
drwxr-xr-x 3 4096 Dec 9 23:37 R_testis_7a
drwxr-xr-x 3 4096 Dec 9 23:37 R_testis_7b
drwxr-xr-x 3 4096 Dec 9 23:37 R_testis_7c

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_brain_3b:

total 32

drwxr-xr-x 2 4096 Dec 9 23:37 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_brain_3b/kallisto:

total 44512

-rw-r--r-- 1 36570887 Dec 9 23:37 abundance.h5

-rw-r--r-- 1 2881948 Dec 9 23:37 abundance.tsv

-rw-r--r-- 1 690 Dec 9 23:37 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_brain_3c:

total 32

drwxr-xr-x 2 4096 Dec 9 23:37 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_brain_3c/kallisto:

total 43344

-rw-r--r-- 1 35487620 Dec 9 23:37 abundance.h5

-rw-r--r-- 1 2910828 Dec 9 23:37 abundance.tsv

-rw-r--r-- 1 690 Dec 9 23:37 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_brain_a:

total 32

drwxr-xr-x 2 4096 Dec 9 23:37 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_brain_a/kallisto:

total 40240

-rw-r--r-- 1 32743217 Dec 9 23:37 abundance.h5

-rw-r--r-- 1 2874611 Dec 9 23:37 abundance.tsv

-rw-r--r-- 1 687 Dec 9 23:37 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_testis_7a:

total 32

drwxr-xr-x 2 4096 Dec 9 23:37 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_testis_7a/kallisto:

total 51952

-rw-r--r-- 1 43126396 Dec 9 23:37 abundance.h5

-rw-r--r-- 1 3041158 Dec 9 23:37 abundance.tsv

-rw-r--r-- 1 693 Dec 9 23:37 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_testis_7b:

total 32

drwxr-xr-x 2 4096 Dec 9 23:37 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_testis_7b/kallisto:

total 50864

-rw-r--r-- 1 42144984 Dec 9 23:37 abundance.h5

-rw-r--r-- 1 3027498 Dec 9 23:37 abundance.tsv

-rw-r--r-- 1 693 Dec 9 23:37 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_testis_7c:

total 32

drwxr-xr-x 2 4096 Dec 9 23:37 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/DEG/testis_vs_brain/R_testis_7c/kallisto:

total 51024

-rw-r--r-- 1 42252104 Dec 9 23:37 abundance.h5

-rw-r--r-- 1 3030231 Dec 9 23:37 abundance.tsv

-rw-r--r-- 1 693 Dec 9 23:37 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix:

total 8336

drwxr-xr-x 8 4096 Dec 9 16:52 Quantification

-rw-r--r-- 1 2251047 Dec 9 17:39 R_hppRNA_data.lncRNA_denovo.gene.TPM.txt

-rw-r--r-- 1 4927209 Dec 9 17:39 R_hppRNA_data.lncRNA_denovo.transcript.TPM.txt

drwxr-xr-x 2 4096 Dec 9 17:39 Summary

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification:

total 192

drwxr-xr-x 3 4096 Dec 9 16:52 R_brain_3b

drwxr-xr-x 3 4096 Dec 9 16:52 R_brain_3c

drwxr-xr-x 3 4096 Dec 9 16:52 R_brain_a

drwxr-xr-x 3 4096 Dec 9 16:52 R_testis_7a

drwxr-xr-x 3 4096 Dec 9 16:52 R_testis_7b

drwxr-xr-x 3 4096 Dec 9 16:52 R_testis_7c

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_brain_3b:

total 32

drwxr-xr-x 2 4096 Dec 9 17:09 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_brain_3b/

kallisto:

total 44512

-rw-r--r-- 1 36570887 Dec 9 17:32 abundance.h5

-rw-r--r-- 1 2881948 Dec 9 17:09 abundance.tsv

-rw-r--r-- 1 690 Dec 9 17:09 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_brain_3c:

total 32

drwxr-xr-x 2 4096 Dec 9 17:06 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_brain_3c/

kallisto:

total 43344

-rw-r--r-- 1 35487620 Dec 9 17:27 abundance.h5

-rw-r--r-- 1 2910828 Dec 9 17:06 abundance.tsv

-rw-r--r-- 1 690 Dec 9 17:06 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_brain_a:

total 32

drwxr-xr-x 2 4096 Dec 9 17:02 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_brain_a/k

allisto:

total 40240

-rw-r--r-- 1 32743217 Dec 9 17:16 abundance.h5

-rw-r--r-- 1 2874611 Dec 9 17:02 abundance.tsv

-rw-r--r-- 1 687 Dec 9 17:02 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_testis_7a:

total 32

drwxr-xr-x 2 4096 Dec 9 17:11 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_testis_7a/

kallisto:

total 51952

-rw-r--r-- 1 43126396 Dec 9 17:39 abundance.h5

-rw-r--r-- 1 3041158 Dec 9 17:11 abundance.tsv

-rw-r--r-- 1 693 Dec 9 17:11 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_testis_7b:

total 32

drwxr-xr-x 2 4096 Dec 9 17:09 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_testis_7b/

kallisto:

total 50864

-rw-r--r-- 1 42144984 Dec 9 17:33 abundance.h5

-rw-r--r-- 1 3027498 Dec 9 17:09 abundance.tsv

-rw-r--r-- 1 693 Dec 9 17:09 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_testis_7c:

total 32

drwxr-xr-x 2 4096 Dec 9 17:11 kallisto

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Quantification/R_testis_7c/

kallisto:

total 51024

-rw-r--r-- 1 42252104 Dec 9 17:38 abundance.h5
-rw-r--r-- 1 3030231 Dec 9 17:11 abundance.tsv
-rw-r--r-- 1 693 Dec 9 17:11 run_info.json

standard_results/lncRNA_denovo/lncRNA_quantification/Gene_expression_matrix/Summary:

total 20784

-rw-r--r-- 1 2881948 Dec 9 17:32 R_brain_3b.abundance.tsv
-rw-r--r-- 1 2910828 Dec 9 17:27 R_brain_3c.abundance.tsv
-rw-r--r-- 1 2874611 Dec 9 17:16 R_brain_a.abundance.tsv
-rw-r--r-- 1 3041158 Dec 9 17:39 R_testis_7a.abundance.tsv
-rw-r--r-- 1 3027498 Dec 9 17:33 R_testis_7b.abundance.tsv
-rw-r--r-- 1 3030231 Dec 9 17:38 R_testis_7c.abundance.tsv

standard_results/lncRNA_denovo/lncRNA_quantification/Index:

total 2558480

-rw-r--r-- 1 182341234 Dec 9 16:49 all_lncRNA_mRNA.gtf
-rw-r--r-- 1 1883300 Dec 9 16:49 all_lncRNA_mRNA.transcript_to_gene.txt
-rw-r--r-- 1 205012115 Dec 9 16:49 hg19.transcript.fa
-rw-r--r-- 1 1901358664 Dec 9 16:52 hg19.transcript.idx

standard_results/lncRNA_denovo/lncRNA_quantification/NGS_plot:

total 0

standard_results/lncRNA_denovo/lncRNA_quantification/Processed_BAM:

total 262286832

-rw-r--r-- 1 4840364363 Dec 9 17:53 R_brain_3b.bam
-rw-r--r-- 1 33986955735 Dec 9 17:32 R_brain_3b.sam
-rw-r--r-- 1 4193496387 Dec 9 17:46 R_brain_3c.bam
-rw-r--r-- 1 29671920518 Dec 9 17:27 R_brain_3c.sam

```

-rw-r--r-- 1 4149603900 Dec 9 17:28 R_brain_a.bam
-rw-r--r-- 1 20692553477 Dec 9 17:16 R_brain_a.sam
-rw-r--r-- 1 5865308603 Dec 9 18:04 R_testis_7a.bam
-rw-r--r-- 1 39981769917 Dec 9 17:39 R_testis_7a.sam
-rw-r--r-- 1 5302796183 Dec 9 17:56 R_testis_7b.bam
-rw-r--r-- 1 35927164835 Dec 9 17:33 R_testis_7b.sam
-rw-r--r-- 1 6253391173 Dec 9 18:04 R_testis_7c.bam
-rw-r--r-- 1 44024102823 Dec 9 17:38 R_testis_7c.sam

```

standard_results/Processed_FASTQ:

total 200613264

```

-r--r--r-- 1 7192054199 Jul 21 18:28 R_brain_3b_1.fastq
-rw-r--r-- 1 125098552 Jul 21 18:28 R_brain_3b_1_singletons.fastq
-r--r--r-- 1 7131934527 Jul 21 18:28 R_brain_3b_2.fastq
-rw-r--r-- 1 11978485 Jul 21 18:28 R_brain_3b_2_singletons.fastq
-rw-r--r-- 1 7424055839 Jul 21 17:53 R_brain_3b.adapt.R1.fastq
-rw-r--r-- 1 7424443325 Jul 21 17:53 R_brain_3b.adapt.R2.fastq
-r--r--r-- 1 6168044007 Jul 21 19:11 R_brain_3c_1.fastq
-rw-r--r-- 1 110879555 Jul 21 19:11 R_brain_3c_1_singletons.fastq
-r--r--r-- 1 6116044175 Jul 21 19:11 R_brain_3c_2.fastq
-rw-r--r-- 1 14510804 Jul 21 19:11 R_brain_3c_2_singletons.fastq
-rw-r--r-- 1 6378340473 Jul 21 18:39 R_brain_3c.adapt.R1.fastq
-rw-r--r-- 1 6378704315 Jul 21 18:39 R_brain_3c.adapt.R2.fastq
-r--r--r-- 1 4119497944 Jul 21 19:41 R_brain_a_1.fastq
-rw-r--r-- 1 71598313 Jul 21 19:41 R_brain_a_1_singletons.fastq
-r--r--r-- 1 4058010312 Jul 21 19:41 R_brain_a_2.fastq
-rw-r--r-- 1 3444518 Jul 21 19:41 R_brain_a_2_singletons.fastq
-rw-r--r-- 1 4415172551 Jul 21 19:18 R_brain_a.adapt.R1.fastq
-rw-r--r-- 1 4415161733 Jul 21 19:18 R_brain_a.adapt.R2.fastq

```



```

-r--r--r-- 1 9016611035 Jul 21 16:49 R_testis_7a_1.fastq
-rw-r--r-- 1 137200541 Jul 21 16:49 R_testis_7a_1_singletons.fastq
-r--r--r-- 1 8954611149 Jul 21 16:49 R_testis_7a_2.fastq
-rw-r--r-- 1 9949570 Jul 21 16:49 R_testis_7a_2_singletons.fastq
-rw-r--r-- 1 9270242710 Jul 21 16:05 R_testis_7a.adapt.R1.fastq
-rw-r--r-- 1 9270808522 Jul 21 16:05 R_testis_7a.adapt.R2.fastq
-r--r--r-- 1 8067010459 Jul 21 17:41 R_testis_7b_1.fastq
-rw-r--r-- 1 136675830 Jul 21 17:41 R_testis_7b_1_singletons.fastq
-r--r--r-- 1 7990884145 Jul 21 17:41 R_testis_7b_2.fastq
-rw-r--r-- 1 3721798 Jul 21 17:41 R_testis_7b_2_singletons.fastq
-rw-r--r-- 1 8290555536 Jul 21 17:02 R_testis_7b.adapt.R1.fastq
-rw-r--r-- 1 8290845864 Jul 21 17:02 R_testis_7b.adapt.R2.fastq
-r--r--r-- 1 9509030215 Jul 21 15:50 R_testis_7c_1.fastq
-rw-r--r-- 1 148593385 Jul 21 15:50 R_testis_7c_1_singletons.fastq
-r--r--r-- 1 9447615437 Jul 21 15:50 R_testis_7c_2.fastq
-rw-r--r-- 1 7995762 Jul 21 15:50 R_testis_7c_2_singletons.fastq
-rw-r--r-- 1 9770708492 Jul 21 15:03 R_testis_7c.adapt.R1.fastq
-rw-r--r-- 1 9771229174 Jul 21 15:03 R_testis_7c.adapt.R2.fastq

```

standard_results/Raw_FASTQ:

total 105285184

```

-rw-r--r-- 1 7689156452 Jul 21 11:31 R_brain_3b.R1.fastq
-rw-r--r-- 1 7689156452 Jul 21 11:32 R_brain_3b.R2.fastq
-rw-r--r-- 1 6568492582 Jul 21 11:32 R_brain_3c.R1.fastq
-rw-r--r-- 1 6568492582 Jul 21 11:33 R_brain_3c.R2.fastq
-rw-r--r-- 1 4516969123 Jul 21 11:33 R_brain_a.R1.fastq
-rw-r--r-- 1 4516969123 Jul 21 11:33 R_brain_a.R2.fastq
-rw-r--r-- 1 9524311147 Jul 21 11:34 R_testis_7a.R1.fastq
-rw-r--r-- 1 9524311147 Jul 21 11:35 R_testis_7a.R2.fastq

```

```
-rw-r--r-- 1      8499034613 Jul 21 11:35 R_testis_7b.R1.fastq
-rw-r--r-- 1      8499034613 Jul 21 11:36 R_testis_7b.R2.fastq
-rw-r--r-- 1     10345040836 Jul 21 11:37 R_testis_7c.R1.fastq
-rw-r--r-- 1     10345040836 Jul 21 11:38 R_testis_7c.R2.fastq
```

standard_results/SNP:

total 224

```
drwxr-xr-x 2    8192 Jul  8 12:27 Index
drwxr-xr-x 7    4096 Jul  8 12:27 R_brain_3b
drwxr-xr-x 7    4096 Jul  8 13:06 R_brain_3c
drwxr-xr-x 7    4096 Jul  8 13:47 R_brain_a
drwxr-xr-x 7    4096 Jul  8 14:31 R_testis_7a
drwxr-xr-x 7    4096 Jul  8 15:22 R_testis_7b
drwxr-xr-x 7    4096 Jul  8 16:12 R_testis_7c
```

standard_results/SNP/Index:

total 35095520

```
-rw-r--r-- 1          238 Jul  8 11:57 chrLength.txt
-rw-r--r-- 1          376 Jul  8 11:57 chrNameLength.txt
-rw-r--r-- 1          138 Jul  8 11:57 chrName.txt
-rw-r--r-- 1          269 Jul  8 11:57 chrStart.txt
-rw-r--r-- 1    3099328512 Jul  8 12:24 Genome
-rw-r--r-- 1          628 Jul  8 11:56 genomeParameters.txt
-rw-r--r-- 1          3899 Jul  8 11:56 hg19.genome.dict
-rwxr-xr-x 1    3157608038 Jul  8 11:56 hg19.genome.fa
-rw-r--r-- 1          783 Jul  8 11:56 hg19.genome.fa.fai
-rw-r--r-- 1    23606085545 Jul  8 12:27 SA
-rw-r--r-- 1    1565873619 Jul  8 12:27 SAindex
```

standard_results/SNP/R_brain_3b:

total 160

drwxr-xr-x 2 4096 Jul 8 12:31 1pass
drwxr-xr-x 2 4096 Jul 8 13:06 2pass
drwxr-xr-x 2 4096 Jul 8 19:41 BAM
drwxr-xr-x 2 8192 Jul 8 13:00 Index_2pass
drwxr-xr-x 2 4096 Jul 8 22:27 vcf

standard_results/SNP/R_brain_3b/1pass:

total 17677568

-rw-r--r-- 1 15820839890 Jul 8 12:31 R_brain_3b.Aligned.out.sam
-rw-r--r-- 1 1856 Jul 8 12:31 R_brain_3b.Log.final.out
-rw-r--r-- 1 17287 Jul 8 12:31 R_brain_3b.Log.out
-rw-r--r-- 1 600 Jul 8 12:31 R_brain_3b.Log.progress.out
-rw-r--r-- 1 9718216 Jul 8 12:31 R_brain_3b.SJ.out.tab

standard_results/SNP/R_brain_3b/2pass:

total 17680528

-rw-r--r-- 1 15823470499 Jul 8 13:06 R_brain_3b.Aligned.out.sam
-rw-r--r-- 1 1865 Jul 8 13:06 R_brain_3b.Log.final.out
-rw-r--r-- 1 17597 Jul 8 13:06 R_brain_3b.Log.out
-rw-r--r-- 1 836 Jul 8 13:06 R_brain_3b.Log.progress.out
-rw-r--r-- 1 9720591 Jul 8 13:06 R_brain_3b.SJ.out.tab

standard_results/SNP/R_brain_3b/BAM:

total 9745232

-rw-r--r-- 1 5448672 Jul 8 17:26 R_brain_3b.deduplicated.bai
-rw-r--r-- 1 2807990105 Jul 8 17:26 R_brain_3b.deduplicated.bam
-rw-r--r-- 1 2910 Jul 8 17:26 R_brain_3b.output.metrics

```
-rw-r--r-- 1 2756856157 Jul 8 17:13 R_brain_3b.rg_added_sorted.bam
-rw-r--r-- 1 4651408 Jul 8 20:17 R_brain_3b.split.bai
-rw-r--r-- 1 3151692313 Jul 8 20:17 R_brain_3b.split.bam
```

standard_results/SNP/R_brain_3b/Index_2pass:

total 31989136

```
-rw-r--r-- 1 238 Jul 8 12:32 chrLength.txt
-rw-r--r-- 1 376 Jul 8 12:32 chrNameLength.txt
-rw-r--r-- 1 138 Jul 8 12:32 chrName.txt
-rw-r--r-- 1 269 Jul 8 12:32 chrStart.txt
-rw-r--r-- 1 3138602404 Jul 8 12:58 Genome
-rw-r--r-- 1 899 Jul 8 12:31 genomeParameters.txt
-rw-r--r-- 1 23927948793 Jul 8 13:00 SA
-rw-r--r-- 1 1565873619 Jul 8 13:00 SAindex
-rw-r--r-- 1 7622059 Jul 8 12:55 sjdbInfo.txt
-rw-r--r-- 1 6722725 Jul 8 12:55 sjdbList.out.tab
```

standard_results/SNP/R_brain_3b/vcf:

total 101584

```
-rw-r--r-- 1 40849601 Jul 8 22:25 R_brain_3b.call.vcf
-rw-r--r-- 1 3872596 Jul 8 22:25 R_brain_3b.call.vcf.idx
-rw-r--r-- 1 41668861 Jul 8 22:27 R_brain_3b.filter.vcf
-rw-r--r-- 1 3872598 Jul 8 22:27 R_brain_3b.filter.vcf.idx
```

standard_results/SNP/R_brain_3c:

total 160

```
drwxr-xr-x 2 4096 Jul 8 13:12 1pass
drwxr-xr-x 2 4096 Jul 8 13:47 2pass
drwxr-xr-x 2 4096 Jul 8 22:27 BAM
```

drwxr-xr-x 2 8192 Jul 8 13:43 Index_2pass

drwxr-xr-x 2 4096 Jul 9 00:49 vcf

standard_results/SNP/R_brain_3c/1pass:

total 15075136

-rw-r--r-- 1 13490985679 Jul 8 13:11 R_brain_3c.Aligned.out.sam

-rw-r--r-- 1 1855 Jul 8 13:12 R_brain_3c.Log.final.out

-rw-r--r-- 1 17287 Jul 8 13:12 R_brain_3c.Log.out

-rw-r--r-- 1 600 Jul 8 13:12 R_brain_3c.Log.progress.out

-rw-r--r-- 1 9118420 Jul 8 13:12 R_brain_3c.SJ.out.tab

standard_results/SNP/R_brain_3c/2pass:

total 15098352

-rw-r--r-- 1 13511748738 Jul 8 13:47 R_brain_3c.Aligned.out.sam

-rw-r--r-- 1 1864 Jul 8 13:47 R_brain_3c.Log.final.out

-rw-r--r-- 1 17597 Jul 8 13:47 R_brain_3c.Log.out

-rw-r--r-- 1 718 Jul 8 13:47 R_brain_3c.Log.progress.out

-rw-r--r-- 1 9120444 Jul 8 13:47 R_brain_3c.SJ.out.tab

standard_results/SNP/R_brain_3c/BAM:

total 8310368

-rw-r--r-- 1 5195856 Jul 8 17:47 R_brain_3c.dedupped.bai

-rw-r--r-- 1 2390359105 Jul 8 17:47 R_brain_3c.dedupped.bam

-rw-r--r-- 1 2911 Jul 8 17:47 R_brain_3c.output.metrics

-rw-r--r-- 1 2345241900 Jul 8 17:36 R_brain_3c.rg_added_sorted.bam

-rw-r--r-- 1 4480408 Jul 8 22:58 R_brain_3c.split.bai

-rw-r--r-- 1 2696278469 Jul 8 22:58 R_brain_3c.split.bam

standard_results/SNP/R_brain_3c/Index_2pass:

total 31963296

-rw-r--r--	1	238 Jul	8 13:12	chrLength.txt
-rw-r--r--	1	376 Jul	8 13:12	chrNameLength.txt
-rw-r--r--	1	138 Jul	8 13:12	chrName.txt
-rw-r--r--	1	269 Jul	8 13:12	chrStart.txt
-rw-r--r--	1	3136177948 Jul	8 13:39	Genome
-rw-r--r--	1	899 Jul	8 13:12	genomeParameters.txt
-rw-r--r--	1	23908080095 Jul	8 13:43	SA
-rw-r--r--	1	1565873619 Jul	8 13:43	SAindex
-rw-r--r--	1	7150086 Jul	8 13:37	sjdbInfo.txt
-rw-r--r--	1	6308434 Jul	8 13:37	sjdbList.out.tab

standard_results/SNP/R_brain_3c/vcf:

total 77664

-rw-r--r--	1	31588164 Jul	9 00:48	R_brain_3c.call.vcf
-rw-r--r--	1	2459517 Jul	9 00:48	R_brain_3c.call.vcf.idx
-rw-r--r--	1	32225882 Jul	9 00:49	R_brain_3c.filter.vcf
-rw-r--r--	1	2503031 Jul	9 00:49	R_brain_3c.filter.vcf.idx

standard_results/SNP/R_brain_a:

total 160

drwxr-xr-x	2	4096 Jul	8 13:52	1pass
drwxr-xr-x	2	4096 Jul	8 14:31	2pass
drwxr-xr-x	2	4096 Jul	9 00:49	BAM
drwxr-xr-x	2	8192 Jul	8 14:27	Index_2pass
drwxr-xr-x	2	4096 Jul	9 02:20	vcf

standard_results/SNP/R_brain_a/1pass:

total 10714288

```
-rw-r--r-- 1 9586565814 Jul 8 13:52 R_brain_a.Aligned.out.sam
-rw-r--r-- 1 1855 Jul 8 13:52 R_brain_a.Log.final.out
-rw-r--r-- 1 17265 Jul 8 13:52 R_brain_a.Log.out
-rw-r--r-- 1 482 Jul 8 13:52 R_brain_a.Log.progress.out
-rw-r--r-- 1 8141098 Jul 8 13:52 R_brain_a.SJ.out.tab
```

standard_results/SNP/R_brain_a/2pass:

total 10777184

```
-rw-r--r-- 1 9642768510 Jul 8 14:31 R_brain_a.Aligned.out.sam
-rw-r--r-- 1 1861 Jul 8 14:31 R_brain_a.Log.final.out
-rw-r--r-- 1 17568 Jul 8 14:31 R_brain_a.Log.out
-rw-r--r-- 1 600 Jul 8 14:31 R_brain_a.Log.progress.out
-rw-r--r-- 1 8155314 Jul 8 14:31 R_brain_a.SJ.out.tab
```

standard_results/SNP/R_brain_a/BAM:

total 9817328

```
-rw-r--r-- 1 4883800 Jul 8 18:05 R_brain_a.deduplicated.bai
-rw-r--r-- 1 2867808937 Jul 8 18:05 R_brain_a.deduplicated.bam
-rw-r--r-- 1 2910 Jul 8 18:05 R_brain_a.output.metrics
-rw-r--r-- 1 2837554669 Jul 8 17:56 R_brain_a.rg_added_sorted.bam
-rw-r--r-- 1 4261192 Jul 9 01:15 R_brain_a.split.bai
-rw-r--r-- 1 3076454275 Jul 9 01:15 R_brain_a.split.bam
```

standard_results/SNP/R_brain_a/Index_2pass:

total 31921824

```
-rw-r--r-- 1 238 Jul 8 13:53 chrLength.txt
-rw-r--r-- 1 376 Jul 8 13:53 chrNameLength.txt
-rw-r--r-- 1 138 Jul 8 13:53 chrName.txt
-rw-r--r-- 1 269 Jul 8 13:53 chrStart.txt
```

```

-rw-r--r-- 1 3132301778 Jul 8 14:22 Genome
-rw-r--r-- 1 894 Jul 8 13:52 genomeParameters.txt
-rw-r--r-- 1 23876313470 Jul 8 14:27 SA
-rw-r--r-- 1 1565873619 Jul 8 14:28 SAindex
-rw-r--r-- 1 6389225 Jul 8 14:19 sjdbInfo.txt
-rw-r--r-- 1 5640595 Jul 8 14:19 sjdbList.out.tab

```

standard_results/SNP/R_brain_a/vcf:

total 46576

```

-rw-r--r-- 1 17976308 Jul 9 02:19 R_brain_a.call.vcf
-rw-r--r-- 1 2261283 Jul 9 02:19 R_brain_a.call.vcf.idx
-rw-r--r-- 1 18324882 Jul 9 02:20 R_brain_a.filter.vcf
-rw-r--r-- 1 2396805 Jul 9 02:20 R_brain_a.filter.vcf.idx

```

standard_results/SNP/R_testis_7a:

total 160

```

drwxr-xr-x 2 4096 Jul 8 14:43 1pass
drwxr-xr-x 2 4096 Jul 8 15:22 2pass
drwxr-xr-x 2 4096 Jul 9 02:20 BAM
drwxr-xr-x 2 8192 Jul 8 15:13 Index_2pass
drwxr-xr-x 2 4096 Jul 9 05:23 vcf

```

standard_results/SNP/R_testis_7a/1pass:

total 23206560

```

-rw-r--r-- 1 20764470662 Jul 8 14:43 R_testis_7a.Aligned.out.sam
-rw-r--r-- 1 1860 Jul 8 14:43 R_testis_7a.Log.final.out
-rw-r--r-- 1 17309 Jul 8 14:43 R_testis_7a.Log.out
-rw-r--r-- 1 836 Jul 8 14:43 R_testis_7a.Log.progress.out
-rw-r--r-- 1 17705446 Jul 8 14:43 R_testis_7a.SJ.out.tab

```


standard_results/SNP/R_testis_7a/2pass:

total 23256176

-rw-r--r-- 1 20808904370 Jul 8 15:22 R_testis_7a.Aligned.out.sam

-rw-r--r-- 1 1868 Jul 8 15:22 R_testis_7a.Log.final.out

-rw-r--r-- 1 17626 Jul 8 15:22 R_testis_7a.Log.out

-rw-r--r-- 1 1190 Jul 8 15:22 R_testis_7a.Log.progress.out

-rw-r--r-- 1 17716406 Jul 8 15:22 R_testis_7a.SJ.out.tab

standard_results/SNP/R_testis_7a/BAM:

total 12435152

-rw-r--r-- 1 7035680 Jul 8 18:38 R_testis_7a.dedupped.bai

-rw-r--r-- 1 3558426478 Jul 8 18:38 R_testis_7a.dedupped.bam

-rw-r--r-- 1 2933 Jul 8 18:38 R_testis_7a.output.metrics

-rw-r--r-- 1 3478889919 Jul 8 18:21 R_testis_7a.rg_added_sorted.bam

-rw-r--r-- 1 5776984 Jul 9 03:13 R_testis_7a.split.bai

-rw-r--r-- 1 4085242467 Jul 9 03:13 R_testis_7a.split.bam

standard_results/SNP/R_testis_7a/Index_2pass:

total 32335952

-rw-r--r-- 1 238 Jul 8 14:44 chrLength.txt

-rw-r--r-- 1 376 Jul 8 14:44 chrNameLength.txt

-rw-r--r-- 1 138 Jul 8 14:44 chrName.txt

-rw-r--r-- 1 269 Jul 8 14:44 chrStart.txt

-rw-r--r-- 1 3171088242 Jul 8 15:10 Genome

-rw-r--r-- 1 904 Jul 8 14:43 genomeParameters.txt

-rw-r--r-- 1 24194181936 Jul 8 15:13 SA

-rw-r--r-- 1 1565873619 Jul 8 15:13 SAindex

-rw-r--r-- 1 13924886 Jul 8 15:07 sjdbInfo.txt

-rw-r--r-- 1 12287376 Jul 8 15:07 sjdbList.out.tab

standard_results/SNP/R_testis_7a/vcf:

total 135088

-rw-r--r-- 1 54446201 Jul 9 05:22 R_testis_7a.call.vcf

-rw-r--r-- 1 4945974 Jul 9 05:22 R_testis_7a.call.vcf.idx

-rw-r--r-- 1 55488967 Jul 9 05:23 R_testis_7a.filter.vcf

-rw-r--r-- 1 5432344 Jul 9 05:24 R_testis_7a.filter.vcf.idx

standard_results/SNP/R_testis_7b:

total 160

drwxr-xr-x 2 4096 Jul 8 15:31 1pass

drwxr-xr-x 2 4096 Jul 8 16:12 2pass

drwxr-xr-x 2 4096 Jul 9 05:24 BAM

drwxr-xr-x 2 8192 Jul 8 16:04 Index_2pass

drwxr-xr-x 2 4096 Jul 9 08:13 vcf

standard_results/SNP/R_testis_7b/1pass:

total 20785744

-rw-r--r-- 1 18596823597 Jul 8 15:31 R_testis_7b.Aligned.out.sam

-rw-r--r-- 1 1860 Jul 8 15:31 R_testis_7b.Log.final.out

-rw-r--r-- 1 17309 Jul 8 15:31 R_testis_7b.Log.out

-rw-r--r-- 1 718 Jul 8 15:31 R_testis_7b.Log.progress.out

-rw-r--r-- 1 17321285 Jul 8 15:31 R_testis_7b.SJ.out.tab

standard_results/SNP/R_testis_7b/2pass:

total 20816528

-rw-r--r-- 1 18624417744 Jul 8 16:12 R_testis_7b.Aligned.out.sam

-rw-r--r-- 1 1868 Jul 8 16:12 R_testis_7b.Log.final.out

```
-rw-r--r-- 1          17626 Jul  8 16:12 R_testis_7b.Log.out
-rw-r--r-- 1          954 Jul  8 16:12 R_testis_7b.Log.progress.out
-rw-r--r-- 1       17326105 Jul  8 16:12 R_testis_7b.SJ.out.tab
```

standard_results/SNP/R_testis_7b/BAM:

total 11323152

```
-rw-r--r-- 1       6768920 Jul  8 19:08 R_testis_7b.dedupped.bai
-rw-r--r-- 1   3235069883 Jul  8 19:08 R_testis_7b.dedupped.bam
-rw-r--r-- 1        2925 Jul  8 19:08 R_testis_7b.output.metrics
-rw-r--r-- 1   3168049472 Jul  8 18:53 R_testis_7b.rg_added_sorted.bam
-rw-r--r-- 1       5634544 Jul  9 06:16 R_testis_7b.split.bai
-rw-r--r-- 1   3724149419 Jul  9 06:16 R_testis_7b.split.bam
```

standard_results/SNP/R_testis_7b/Index_2pass:

total 32319584

```
-rw-r--r-- 1        238 Jul  8 15:32 chrLength.txt
-rw-r--r-- 1        376 Jul  8 15:32 chrNameLength.txt
-rw-r--r-- 1        138 Jul  8 15:32 chrName.txt
-rw-r--r-- 1        269 Jul  8 15:32 chrStart.txt
-rw-r--r-- 1   3169558159 Jul  8 16:01 Genome
-rw-r--r-- 1        904 Jul  8 15:31 genomeParameters.txt
-rw-r--r-- 1   24181641548 Jul  8 16:04 SA
-rw-r--r-- 1   1565873619 Jul  8 16:05 SAindex
-rw-r--r-- 1   13633821 Jul  8 15:58 sjdbInfo.txt
-rw-r--r-- 1   12021604 Jul  8 15:58 sjdbList.out.tab
```

standard_results/SNP/R_testis_7b/vcf:

total 118736

```
-rw-r--r-- 1   46806749 Jul  9 08:11 R_testis_7b.call.vcf
```

-rw-r--r-- 1 5543397 Jul 9 08:11 R_testis_7b.call.vcf.idx
-rw-r--r-- 1 47697180 Jul 9 08:13 R_testis_7b.filter.vcf
-rw-r--r-- 1 5543399 Jul 9 08:13 R_testis_7b.filter.vcf.idx

standard_results/SNP/R_testis_7c:

total 160

drwxr-xr-x 2 4096 Jul 8 16:21 1pass
drwxr-xr-x 2 4096 Jul 8 17:00 2pass
drwxr-xr-x 2 4096 Jul 9 08:13 BAM
drwxr-xr-x 2 8192 Jul 8 16:52 Index_2pass
drwxr-xr-x 2 4096 Jul 9 11:34 vcf

standard_results/SNP/R_testis_7c/1pass:

total 24484048

-rw-r--r-- 1 21911624041 Jul 8 16:21 R_testis_7c.Aligned.out.sam
-rw-r--r-- 1 1860 Jul 8 16:21 R_testis_7c.Log.final.out
-rw-r--r-- 1 17309 Jul 8 16:21 R_testis_7c.Log.out
-rw-r--r-- 1 836 Jul 8 16:21 R_testis_7c.Log.progress.out
-rw-r--r-- 1 14589009 Jul 8 16:21 R_testis_7c.SJ.out.tab

standard_results/SNP/R_testis_7c/2pass:

total 24436160

-rw-r--r-- 1 21868722814 Jul 8 17:00 R_testis_7c.Aligned.out.sam
-rw-r--r-- 1 1868 Jul 8 17:00 R_testis_7c.Log.final.out
-rw-r--r-- 1 17626 Jul 8 17:00 R_testis_7c.Log.out
-rw-r--r-- 1 1072 Jul 8 17:00 R_testis_7c.Log.progress.out
-rw-r--r-- 1 14593923 Jul 8 17:00 R_testis_7c.SJ.out.tab

standard_results/SNP/R_testis_7c/BAM:

total 12828000

```
-rw-r--r-- 1      6562216 Jul  8 19:41 R_testis_7c.dedupped.bai
-rw-r--r-- 1 3664683899 Jul  8 19:41 R_testis_7c.dedupped.bam
-rw-r--r-- 1      2932 Jul  8 19:41 R_testis_7c.output.metrics
-rw-r--r-- 1 3582481108 Jul  8 19:24 R_testis_7c.rg_added_sorted.bam
-rw-r--r-- 1      5404648 Jul  9 09:08 R_testis_7c.split.bai
-rw-r--r-- 1 4228174866 Jul  9 09:08 R_testis_7c.split.bam
```

standard_results/SNP/R_testis_7c/Index_2pass:

total 32199936

```
-rw-r--r-- 1      238 Jul  8 16:22 chrLength.txt
-rw-r--r-- 1      376 Jul  8 16:22 chrNameLength.txt
-rw-r--r-- 1      138 Jul  8 16:22 chrName.txt
-rw-r--r-- 1      269 Jul  8 16:22 chrStart.txt
-rw-r--r-- 1 3158347164 Jul  8 16:48 Genome
-rw-r--r-- 1      904 Jul  8 16:21 genomeParameters.txt
-rw-r--r-- 1 24089764581 Jul  8 16:52 SA
-rw-r--r-- 1 1565873619 Jul  8 16:53 SAindex
-rw-r--r-- 1 11456592 Jul  8 16:45 sjdbInfo.txt
-rw-r--r-- 1 10105575 Jul  8 16:45 sjdbList.out.tab
```

standard_results/SNP/R_testis_7c/vcf:

total 116864

```
-rw-r--r-- 1 46876426 Jul  9 11:33 R_testis_7c.call.vcf
-rw-r--r-- 1 4615030 Jul  9 11:33 R_testis_7c.call.vcf.idx
-rw-r--r-- 1 47824562 Jul  9 11:34 R_testis_7c.filter.vcf
-rw-r--r-- 1 4615032 Jul  9 11:34 R_testis_7c.filter.vcf.idx
```

standard_results/STAR_RSEM_EBSeq:

total 224

drwxr-xr-x 2	4096	Jul 31 00:02	Bigwig
drwxr-xr-x 2	4096	Jul 31 00:00	Cluster
drwxr-xr-x 2	4096	Jul 30 14:34	DEG
drwxr-xr-x 4	4096	Jul 29 09:32	Gene_expression_matrix
drwxr-xr-x 2	4096	Jul 30 14:29	Index
drwxr-xr-x 2	4096	Jul 31 00:04	NGS_plot
drwxr-xr-x 8	12288	Jul 30 14:24	Processed_BAM

standard_results/STAR_RSEM_EBSeq/Bigwig:

total 7677760

-rw-r--r-- 1	351305409	Jul 31 00:03	R_brain_3b.bw
-rw-r--r-- 1	404391709	Jul 30 14:25	R_brain_3b.wig.2.gz
-rw-r--r-- 1	404392045	Jul 29 09:41	R_brain_3b.wig.gz
-rw-r--r-- 1	348953056	Jul 31 00:04	R_brain_3c.bw
-rw-r--r-- 1	401926224	Jul 31 00:01	R_brain_3c.wig.2.gz
-rw-r--r-- 1	401932044	Jul 30 15:02	R_brain_3c.wig.gz
-rw-r--r-- 1	326954051	Jul 31 00:04	R_brain_a.bw
-rw-r--r-- 1	376526873	Jul 31 00:01	R_brain_a.wig.2.gz
-rw-r--r-- 1	376509866	Jul 30 14:57	R_brain_a.wig.gz
-rw-r--r-- 1	352781471	Jul 29 08:18	R_testis_7a.bw
-rw-r--r-- 1	400922410	Jul 29 08:15	R_testis_7a.wig.2.gz
-rw-r--r-- 1	400927848	Jul 29 08:14	R_testis_7a.wig.gz
-rw-r--r-- 1	344493647	Jul 29 09:30	R_testis_7b.bw
-rw-r--r-- 1	391151189	Jul 29 09:28	R_testis_7b.wig.2.gz
-rw-r--r-- 1	391095717	Jul 29 09:27	R_testis_7b.wig.gz
-rw-r--r-- 1	365623368	Jul 29 08:47	R_testis_7c.bw
-rw-r--r-- 1	416482269	Jul 29 08:44	R_testis_7c.wig.2.gz
-rw-r--r-- 1	416490992	Jul 29 08:43	R_testis_7c.wig.gz

standard_results/STAR_RSEM_EBSeq/Cluster:

total 5728

```
-rw-r--r-- 1      1065 Jul 31 00:00 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.heatmap.R
-rw-r--r-- 1      1384 Jul 31 00:00 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.PCA.R
-rw-r--r-- 1    752946 Jul 31 00:00 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.txt
-rw-r--r-- 1          1          975299          Jul          31          00:01
R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.txt.1.heatmap.pdf
-rw-r--r-- 1    632612 Jul 31 00:00 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.txt.1.matrix.txt
-rw-r--r-- 1      4828 Jul 31 00:00 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.txt.1.PCA.pdf
-rw-r--r-- 1          1          2132317          Jul          31          00:00
R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.txt.1.rotation.txt
```

standard_results/STAR_RSEM_EBSeq/DEG:

total 18144

```
-rw-r--r-- 1    2057104 Jul 30 14:25 R_hppRNA_data.STAR_RSEM_EBSeq.testis_vs_brain.gene.DEG.txt
-rw-r--r-- 1          1          1965383          Jul          30          14:25
R_hppRNA_data.STAR_RSEM_EBSeq.testis_vs_brain.gene.DEG.txt.normalized_data_matrix
-rw-r--r-- 1    944574 Jul 30 14:24 R_hppRNA_data.STAR_RSEM_EBSeq.testis_vs_brain.GeneMat.txt
-rw-r--r-- 1    2149134 Jul 30 14:29 R_hppRNA_data.STAR_RSEM_EBSeq.testis_vs_brain.IsoMat.txt
-rw-r--r-- 1    4433865 Jul 30 14:34 R_hppRNA_data.STAR_RSEM_EBSeq.testis_vs_brain.transcript.DEG.txt
-rw-r--r-- 1          1          3899581          Jul          30          14:34
R_hppRNA_data.STAR_RSEM_EBSeq.testis_vs_brain.transcript.DEG.txt.normalized_data_matrix
```

standard_results/STAR_RSEM_EBSeq/Gene_expression_matrix:

total 3536

```
-rw-r--r-- 1    752954 Jul 29 09:32 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.txt
-rw-r--r-- 1    2085693 Jul 29 09:32 R_hppRNA_data.STAR_RSEM_EBSeq.transcript.FPKM.txt
drwxr-xr-x 2      4096 Jul 29 09:32 Summary_gene
```

drwxr-xr-x 2 4096 Jul 29 09:32 Summary_transcript

standard_results/STAR_RSEM_EBSeq/Gene_expression_matrix/Summary_gene:

total 9264

-rw-r--r-- 1 1255915 Jul 29 08:46 R_brain_3b.genes.results
-rw-r--r-- 1 1254577 Jul 29 09:30 R_brain_3c.genes.results
-rw-r--r-- 1 1251744 Jul 29 09:32 R_brain_a.genes.results
-rw-r--r-- 1 1263383 Jul 29 07:11 R_testis_7a.genes.results
-rw-r--r-- 1 1262062 Jul 29 08:28 R_testis_7b.genes.results
-rw-r--r-- 1 1264014 Jul 29 07:33 R_testis_7c.genes.results

standard_results/STAR_RSEM_EBSeq/Gene_expression_matrix/Summary_transcript:

total 15920

-rw-r--r-- 1 2258514 Jul 29 08:46 R_brain_3b.isoforms.results
-rw-r--r-- 1 2256181 Jul 29 09:30 R_brain_3c.isoforms.results
-rw-r--r-- 1 2250881 Jul 29 09:32 R_brain_a.isoforms.results
-rw-r--r-- 1 2273189 Jul 29 07:11 R_testis_7a.isoforms.results
-rw-r--r-- 1 2270910 Jul 29 08:28 R_testis_7b.isoforms.results
-rw-r--r-- 1 2273847 Jul 29 07:33 R_testis_7c.isoforms.results

standard_results/STAR_RSEM_EBSeq/Index:

total 32706800

-rw-r--r-- 1 238 Jul 29 03:42 chrLength.txt
-rw-r--r-- 1 376 Jul 29 03:42 chrNameLength.txt
-rw-r--r-- 1 138 Jul 29 03:42 chrName.txt
-rw-r--r-- 1 269 Jul 29 03:42 chrStart.txt
-rw-r--r-- 1 15663347 Jul 29 05:40 exonGeTrInfo.tab
-rw-r--r-- 1 7088712 Jul 29 05:40 exonInfo.tab
-rw-r--r-- 1 125244 Jul 29 05:40 geneInfo.tab


```

-rw-r--r-- 1 3141143748 Jul 29 05:46 Genome
-rw-r--r-- 1 967 Jul 29 03:41 genomeParameters.txt
-rw-r--r-- 1 365 Jul 29 03:41 hg19.chrlist
-rw-r--r-- 1 110586 Jul 29 03:41 hg19.grp
-rw-r--r-- 1 141147827 Jul 29 03:41 hg19.idx.fa
-rw-r--r-- 1 20886 Jul 29 05:50 hg19Log.out
-rw-r--r-- 1 141147827 Jul 29 03:41 hg19.n2g.idx.fa
-rw-r--r-- 1 85030 Jul 30 14:29 hg19.ngvec
-rw-r--r-- 1 150352226 Jul 29 03:41 hg19.seq
-rw-r--r-- 1 14184875 Jul 29 03:41 hg19.ti
-rw-r--r-- 1 141147827 Jul 29 03:41 hg19.transcripts.fa
-rw-r--r-- 1 780282 Jul 30 14:29 hg19.ump
-rw-r--r-- 1 23949344928 Jul 29 05:49 SA
-rw-r--r-- 1 1565873619 Jul 29 05:50 SAindex
-rw-r--r-- 1 6093930 Jul 29 05:40 sjdbInfo.txt
-rw-r--r-- 1 5386351 Jul 29 05:40 sjdbList.fromGTF.out.tab
-rw-r--r-- 1 5386325 Jul 29 05:40 sjdbList.out.tab
-rw-r--r-- 1 2322293 Jul 29 05:40 transcriptInfo.tab

```

standard_results/STAR_RSEM_EBSeq/NGS_plot:

total 116464

```

-rw-r--r-- 1 6690 Jul 29 09:02 NGSplot.R_brain_3b.genebody.avgprof.pdf
-rw-r--r-- 1 1133730 Jul 29 09:02 NGSplot.R_brain_3b.genebody.heatmap.pdf
-rw-r--r-- 1 15074578 Jul 29 09:02 NGSplot.R_brain_3b.genebody.zip
-rw-r--r-- 1 6708 Jul 31 00:04 NGSplot.R_brain_3c.genebody.avgprof.pdf
-rw-r--r-- 1 1104683 Jul 31 00:04 NGSplot.R_brain_3c.genebody.heatmap.pdf
-rw-r--r-- 1 14952616 Jul 31 00:04 NGSplot.R_brain_3c.genebody.zip
-rw-r--r-- 1 6682 Jul 31 00:03 NGSplot.R_brain_a.genebody.avgprof.pdf
-rw-r--r-- 1 1060688 Jul 31 00:03 NGSplot.R_brain_a.genebody.heatmap.pdf

```

```

-rw-r--r-- 1 14570367 Jul 31 00:03 NGSplot.R_brain_a.genebody.zip
-rw-r--r-- 1 6717 Jul 29 07:28 NGSplot.R_testis_7a.genebody.avgprof.pdf
-rw-r--r-- 1 1271006 Jul 29 07:28 NGSplot.R_testis_7a.genebody.heatmap.pdf
-rw-r--r-- 1 16758880 Jul 29 07:28 NGSplot.R_testis_7a.genebody.zip
-rw-r--r-- 1 6742 Jul 29 08:44 NGSplot.R_testis_7b.genebody.avgprof.pdf
-rw-r--r-- 1 1280817 Jul 29 08:44 NGSplot.R_testis_7b.genebody.heatmap.pdf
-rw-r--r-- 1 16550222 Jul 29 08:44 NGSplot.R_testis_7b.genebody.zip
-rw-r--r-- 1 6712 Jul 29 07:54 NGSplot.R_testis_7c.genebody.avgprof.pdf
-rw-r--r-- 1 1262676 Jul 29 07:55 NGSplot.R_testis_7c.genebody.heatmap.pdf
-rw-r--r-- 1 16899165 Jul 29 07:55 NGSplot.R_testis_7c.genebody.zip

```

standard_results/STAR_RSEM_EBSeq/Processed_BAM:

total 61686624

```

-rw-r--r-- 1 1255915 Jul 29 08:34 R_brain_3b.genes.results
-rw-r--r-- 1 2972980349 Jul 29 08:46 R_brain_3b.genome.bam
-rw-r--r-- 1 1787391421 Jul 29 09:00 R_brain_3b.genome.sorted.bam
-rw-r--r-- 1 2020144 Jul 29 09:00 R_brain_3b.genome.sorted.bam.bai
-rw-r--r-- 1 2258514 Jul 29 08:34 R_brain_3b.isoforms.results
drwxr-xr-x 2 4096 Jul 29 08:29 R_brain_3b.stat
-rw-r--r-- 1 3777677169 Jul 29 08:34 R_brain_3b.transcript.bam
-rw-r--r-- 1 1254577 Jul 29 09:18 R_brain_3c.genes.results
-rw-r--r-- 1 2692198657 Jul 29 09:30 R_brain_3c.genome.bam
-rw-r--r-- 1 1617507390 Jul 29 09:40 R_brain_3c.genome.sorted.bam
-rw-r--r-- 1 1990064 Jul 30 14:24 R_brain_3c.genome.sorted.bam.bai
-rw-r--r-- 1 2256181 Jul 29 09:18 R_brain_3c.isoforms.results
drwxr-xr-x 2 4096 Jul 29 09:14 R_brain_3c.stat
-rw-r--r-- 1 3420760592 Jul 29 09:18 R_brain_3c.transcript.bam
-rw-r--r-- 1 1251744 Jul 29 09:25 R_brain_a.genes.results
-rw-r--r-- 1 2734716046 Jul 29 09:32 R_brain_a.genome.bam

```

```

-rw-r--r-- 1 2029395573 Jul 29 09:39 R_brain_a.genome.sorted.bam
-rw-r--r-- 1 2052656 Jul 30 14:24 R_brain_a.genome.sorted.bam.bai
-rw-r--r-- 1 2250881 Jul 29 09:25 R_brain_a.isoforms.results
drwxr-xr-x 2 4096 Jul 29 09:22 R_brain_a.stat
-rw-r--r-- 1 3336615078 Jul 29 09:25 R_brain_a.transcript.bam
-rw-r--r-- 1 1263383 Jul 29 06:56 R_testis_7a.genes.results
-rw-r--r-- 1 3556306092 Jul 29 07:11 R_testis_7a.genome.bam
-rw-r--r-- 1 2052875357 Jul 29 07:25 R_testis_7a.genome.sorted.bam
-rw-r--r-- 1 2114056 Jul 29 07:26 R_testis_7a.genome.sorted.bam.bai
-rw-r--r-- 1 2273189 Jul 29 06:56 R_testis_7a.isoforms.results
drwxr-xr-x 2 4096 Jul 29 06:51 R_testis_7a.stat
-rw-r--r-- 1 4342389177 Jul 29 06:56 R_testis_7a.transcript.bam
-rw-r--r-- 1 1262062 Jul 29 08:13 R_testis_7b.genes.results
-rw-r--r-- 1 3293637961 Jul 29 08:28 R_testis_7b.genome.bam
-rw-r--r-- 1 1909347914 Jul 29 08:41 R_testis_7b.genome.sorted.bam
-rw-r--r-- 1 2090480 Jul 29 08:42 R_testis_7b.genome.sorted.bam.bai
-rw-r--r-- 1 2270910 Jul 29 08:13 R_testis_7b.isoforms.results
drwxr-xr-x 2 4096 Jul 29 08:08 R_testis_7b.stat
-rw-r--r-- 1 4006176612 Jul 29 08:13 R_testis_7b.transcript.bam
-rw-r--r-- 1 1264014 Jul 29 07:16 R_testis_7c.genes.results
-rw-r--r-- 1 4137990392 Jul 29 07:33 R_testis_7c.genome.bam
-rw-r--r-- 1 2412057368 Jul 29 07:52 R_testis_7c.genome.sorted.bam
-rw-r--r-- 1 2156912 Jul 29 07:52 R_testis_7c.genome.sorted.bam.bai
-rw-r--r-- 1 2273847 Jul 29 07:16 R_testis_7c.isoforms.results
drwxr-xr-x 2 4096 Jul 29 07:10 R_testis_7c.stat
-rw-r--r-- 1 5124795368 Jul 29 07:16 R_testis_7c.transcript.bam

```

standard_results/STAR_RSEM_EBSeq/Processed_BAM/R_brain_3b.stat:

total 2128

-rw-r--r-- 1 418 Jul 29 07:59 R_brain_3b.cnt

-rw-r--r-- 1 130542 Jul 29 08:29 R_brain_3b.model

-rw-r--r-- 1 1511009 Jul 29 08:29 R_brain_3b.theta

standard_results/STAR_RSEM_EBSeq/Processed_BAM/R_brain_3c.stat:

total 2128

-rw-r--r-- 1 484 Jul 29 08:45 R_brain_3c.cnt

-rw-r--r-- 1 130520 Jul 29 09:14 R_brain_3c.model

-rw-r--r-- 1 1514853 Jul 29 09:14 R_brain_3c.theta

standard_results/STAR_RSEM_EBSeq/Processed_BAM/R_brain_a.stat:

total 2128

-rw-r--r-- 1 464 Jul 29 09:01 R_brain_a.cnt

-rw-r--r-- 1 154563 Jul 29 09:22 R_brain_a.model

-rw-r--r-- 1 1486077 Jul 29 09:22 R_brain_a.theta

standard_results/STAR_RSEM_EBSeq/Processed_BAM/R_testis_7a.stat:

total 2240

-rw-r--r-- 1 569 Jul 29 06:17 R_testis_7a.cnt

-rw-r--r-- 1 130459 Jul 29 06:51 R_testis_7a.model

-rw-r--r-- 1 1632062 Jul 29 06:51 R_testis_7a.theta

standard_results/STAR_RSEM_EBSeq/Processed_BAM/R_testis_7b.stat:

total 2224

-rw-r--r-- 1 578 Jul 29 07:34 R_testis_7b.cnt

-rw-r--r-- 1 130443 Jul 29 08:08 R_testis_7b.model

-rw-r--r-- 1 1613668 Jul 29 08:08 R_testis_7b.theta

standard_results/STAR_RSEM_EBSeq/Processed_BAM/R_testis_7c.stat:

total 2240

-rw-r--r-- 1 622 Jul 29 06:22 R_testis_7c.cnt
-rw-r--r-- 1 130457 Jul 29 07:10 R_testis_7c.model
-rw-r--r-- 1 1622345 Jul 29 07:10 R_testis_7c.theta

standard_results/Subread_featureCounts_DESeq2:

total 224

drwxr-xr-x 2 4096 Jul 26 03:34 Bigwig
drwxr-xr-x 2 4096 Jul 30 14:24 Cluster
drwxr-xr-x 2 4096 Jul 25 07:23 DEG
drwxr-xr-x 2 4096 Jul 25 07:23 Gene_expression_matrix
drwxr-xr-x 2 4096 Jul 25 04:43 Index
drwxr-xr-x 2 4096 Jul 25 07:24 NGS_plot
drwxr-xr-x 2 12288 Jul 25 07:23 Processed_BAM

standard_results/Subread_featureCounts_DESeq2/Bigwig:

total 1430528

-rw-r--r-- 1 78963471 Jul 25 06:55 R_brain_3b.bw
-rw-r--r-- 1 61968199 Jul 25 06:54 R_brain_3b.wig.2.gz
-rw-r--r-- 1 61968416 Jul 25 06:54 R_brain_3b.wig.gz
-rw-r--r-- 1 65642261 Jul 25 06:36 R_brain_3c.bw
-rw-r--r-- 1 50381642 Jul 25 06:36 R_brain_3c.wig.2.gz
-rw-r--r-- 1 50381819 Jul 25 06:36 R_brain_3c.wig.gz
-rw-r--r-- 1 49356614 Jul 25 06:03 R_brain_a.bw
-rw-r--r-- 1 36954726 Jul 25 06:03 R_brain_a.wig.2.gz
-rw-r--r-- 1 36955018 Jul 25 06:03 R_brain_a.wig.gz
-rw-r--r-- 1 114931470 Jul 26 03:35 R_testis_7a.bw
-rw-r--r-- 1 87797193 Jul 26 03:34 R_testis_7a.wig.2.gz
-rw-r--r-- 1 87797319 Jul 25 07:28 R_testis_7a.wig.gz

```
-rw-r--r-- 1 98892299 Jul 25 07:09 R_testis_7b.bw
-rw-r--r-- 1 75522980 Jul 25 07:09 R_testis_7b.wig.2.gz
-rw-r--r-- 1 75523114 Jul 25 07:08 R_testis_7b.wig.gz
-rw-r--r-- 1 96776272 Jul 26 03:34 R_testis_7c.bw
-rw-r--r-- 1 73746679 Jul 26 03:34 R_testis_7c.wig.2.gz
-rw-r--r-- 1 73746697 Jul 25 07:31 R_testis_7c.wig.gz
```

standard_results/Subread_featureCounts_DESeq2/Cluster:

total 8320

```
-rw-r--r-- 1 3594 Jul 30 16:03 R_hppRNA_data.STAR_RSEM_EBSeq.gene.FPKM.clean.txt.1.PCA.pdf
-rw-r--r-- 1 1117 Jul 26 03:34
R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.heatmap.R
-rw-r--r-- 1 1492 Jul 26 03:34
R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.PCA.R
-rw-r--r-- 1 1960300 Jul 26 03:34 R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.txt
-rw-r--r-- 1 963074 Jul 26 03:34
R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.txt.1.heatmap.pdf
-rw-r--r-- 1 1742254 Jul 26 03:34
R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.txt.1.matrix.txt
-rw-r--r-- 1 4833 Jul 26 03:34
R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.txt.1.PCA.pdf
-rw-r--r-- 1 2112894 Jul 26 03:34
R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.clean.txt.1.rotation.txt
```

standard_results/Subread_featureCounts_DESeq2/DEG:

total 11584

```
-rw-r--r-- 1 226 Jul 25 07:19 R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.col.csv
-rw-r--r-- 1 2209485 Jul 25 07:23
R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.DESeq2.csv
```

-rw-r--r--	1	2170974	Jul	25	07:23	
R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.DESeq2.txt						
-rw-r--r--	1	601822	Jul	25	07:23	
R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.gene.counts.csv						
-rw-r--r--	1	563311	Jul	25	07:23	
R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.gene.counts.txt						
-rw-r--r--	1	1998919	Jul	25	07:23	
R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.gene.RPKM.csv						
-rw-r--r--	1	1960408	Jul	25	07:23	
R_hppRNA_data.Subread_featureCounts_DESeq2.testis_vs_brain.gene.RPKM.txt						

standard_results/Subread_featureCounts_DESeq2/Gene_expression_matrix:

total 6384

-rw-r--r--	1	601822	Jul	25	07:23	R_hppRNA_data.Subread_featureCounts_DESeq2.gene.counts.csv
-rw-r--r--	1	563311	Jul	25	07:23	R_hppRNA_data.Subread_featureCounts_DESeq2.gene.counts.txt
-rw-r--r--	1	1998919	Jul	25	07:23	R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.csv
-rw-r--r--	1	1960408	Jul	25	07:23	R_hppRNA_data.Subread_featureCounts_DESeq2.gene.RPKM.txt

standard_results/Subread_featureCounts_DESeq2/Index:

total 6557504

-rw-r--r--	1	773938533	Jul	25	04:43	hg19.00.b.array
-rw-r--r--	1	5098240981	Jul	25	04:43	hg19.00.b.tab
-rw-r--r--	1	1245	Jul	25	04:35	hg19.files
-rw-r--r--	1	0	Jul	25	04:16	hg19.log
-rw-r--r--	1	404	Jul	25	04:43	hg19.reads

standard_results/Subread_featureCounts_DESeq2/NGS_plot:

total 153008

-rw-r--r--	1	6735	Jul	25	06:48	NGSplot.R_brain_3b.genebody.avgprof.pdf
------------	---	------	-----	----	-------	---

```

-rw-r--r-- 1      1342248 Jul 25 06:48 NGSplot.R_brain_3b.genebody.heatmap.pdf
-rw-r--r-- 1      19994125 Jul 25 06:48 NGSplot.R_brain_3b.genebody.zip
-rw-r--r-- 1          6705 Jul 25 06:31 NGSplot.R_brain_3c.genebody.avgprof.pdf
-rw-r--r-- 1      1282513 Jul 25 06:31 NGSplot.R_brain_3c.genebody.heatmap.pdf
-rw-r--r-- 1      19468525 Jul 25 06:31 NGSplot.R_brain_3c.genebody.zip
-rw-r--r-- 1          6719 Jul 25 06:00 NGSplot.R_brain_a.genebody.avgprof.pdf
-rw-r--r-- 1      1276272 Jul 25 06:00 NGSplot.R_brain_a.genebody.heatmap.pdf
-rw-r--r-- 1      18488661 Jul 25 06:00 NGSplot.R_brain_a.genebody.zip
-rw-r--r-- 1          6722 Jul 25 07:17 NGSplot.R_testis_7a.genebody.avgprof.pdf
-rw-r--r-- 1      1494756 Jul 25 07:17 NGSplot.R_testis_7a.genebody.heatmap.pdf
-rw-r--r-- 1      23088438 Jul 25 07:18 NGSplot.R_testis_7a.genebody.zip
-rw-r--r-- 1          6735 Jul 25 07:00 NGSplot.R_testis_7b.genebody.avgprof.pdf
-rw-r--r-- 1      1515146 Jul 25 07:00 NGSplot.R_testis_7b.genebody.heatmap.pdf
-rw-r--r-- 1      22589527 Jul 25 07:00 NGSplot.R_testis_7b.genebody.zip
-rw-r--r-- 1          6728 Jul 25 07:23 NGSplot.R_testis_7c.genebody.avgprof.pdf
-rw-r--r-- 1      1440570 Jul 25 07:23 NGSplot.R_testis_7c.genebody.heatmap.pdf
-rw-r--r-- 1      22525927 Jul 25 07:24 NGSplot.R_testis_7c.genebody.zip

```

standard_results/Subread_featureCounts_DESeq2/Processed_BAM:

total 49817056

```

-rw-r--r-- 1      2659820842 Jul 25 06:45 R_brain_3b.sorted.unique.bam
-rw-r--r-- 1          3297632 Jul 25 06:45 R_brain_3b.sorted.unique.bam.bai
-rw-r--r-- 1      4239709835 Jul 25 06:27 R_brain_3b.unique.bam
-rw-r--r-- 1          10306775 Jul 25 06:27 R_brain_3b.unique.bam.indel
-rw-r--r-- 1      2271281236 Jul 25 06:28 R_brain_3c.sorted.unique.bam
-rw-r--r-- 1          3248184 Jul 25 06:29 R_brain_3c.sorted.unique.bam.bai
-rw-r--r-- 1      3647934354 Jul 25 06:13 R_brain_3c.unique.bam
-rw-r--r-- 1          8454794 Jul 25 06:13 R_brain_3c.unique.bam.indel
-rw-r--r-- 1      2770516737 Jul 25 05:57 R_brain_a.sorted.unique.bam

```



```

-rw-r--r-- 1      3382616 Jul 25 05:57 R_brain_a.sorted.unique.bam.bai
-rw-r--r-- 1    3666553944 Jul 25 05:46 R_brain_a.unique.bam
-rw-r--r-- 1      4405981 Jul 25 05:46 R_brain_a.unique.bam.indel
-rw-r--r-- 1    3266929872 Jul 25 07:14 R_testis_7a.sorted.unique.bam
-rw-r--r-- 1      3776960 Jul 25 07:15 R_testis_7a.sorted.unique.bam.bai
-rw-r--r-- 1    5329167028 Jul 25 06:53 R_testis_7a.unique.bam
-rw-r--r-- 1     12948906 Jul 25 06:53 R_testis_7a.unique.bam.indel
-rw-r--r-- 1    2960478496 Jul 25 06:57 R_testis_7b.sorted.unique.bam
-rw-r--r-- 1      3750840 Jul 25 06:58 R_testis_7b.sorted.unique.bam.bai
-rw-r--r-- 1    4820552746 Jul 25 06:38 R_testis_7b.unique.bam
-rw-r--r-- 1     11265641 Jul 25 06:38 R_testis_7b.unique.bam.indel
-rw-r--r-- 1    3376186815 Jul 25 07:19 R_testis_7c.sorted.unique.bam
-rw-r--r-- 1      3785368 Jul 25 07:20 R_testis_7c.sorted.unique.bam.bai
-rw-r--r-- 1    5520662320 Jul 25 06:56 R_testis_7c.unique.bam
-rw-r--r-- 1     11422862 Jul 25 06:56 R_testis_7c.unique.bam.indel

```

standard_results/Tophat_Cufflink_Cuffdiff:

total 256

```

drwxr-xr-x  2    4096 Jul 26 03:35 Bigwig
drwxr-xr-x  2    4096 Jul 26 04:26 Cluster
drwxr-xr-x  2    4096 Jul 26 04:26 DEG
drwxr-xr-x  2    4096 Jul 26 04:26 Gene_expression_matrix
drwxr-xr-x  2    4096 Jul 22 02:59 Index
drwxr-xr-x  2    4096 Jul 26 04:04 NGS_plot
drwxr-xr-x 19   24576 Jul 26 03:42 Processed_BAM

```

standard_results/Tophat_Cufflink_Cuffdiff/Bigwig:

total 8351216

```

-rw-r--r-- 1    397698187 Jul 26 03:34 R_brain_3b.bw

```

```

-rw-r--r-- 1 433314504 Jul 26 03:31 R_brain_3b.wig.2.gz
-rw-r--r-- 1 433307530 Jul 25 05:49 R_brain_3b.wig.gz
-rw-r--r-- 1 387941583 Jul 26 03:35 R_brain_3c.bw
-rw-r--r-- 1 427182291 Jul 26 03:31 R_brain_3c.wig.2.gz
-rw-r--r-- 1 427208844 Jul 25 05:40 R_brain_3c.wig.gz
-rw-r--r-- 1 364480917 Jul 26 03:37 R_brain_a.bw
-rw-r--r-- 1 406790386 Jul 26 03:32 R_brain_a.wig.2.gz
-rw-r--r-- 1 406815587 Jul 25 05:25 R_brain_a.wig.gz
-rw-r--r-- 1 413263294 Jul 26 03:35 R_testis_7a.bw
-rw-r--r-- 1 431721038 Jul 26 03:31 R_testis_7a.wig.2.gz
-rw-r--r-- 1 431668241 Jul 25 06:00 R_testis_7a.wig.gz
-rw-r--r-- 1 388073404 Jul 26 03:37 R_testis_7b.bw
-rw-r--r-- 1 409980263 Jul 26 03:33 R_testis_7b.wig.2.gz
-rw-r--r-- 1 409981491 Jul 25 05:50 R_testis_7b.wig.gz
-rw-r--r-- 1 416918874 Jul 26 03:34 R_testis_7c.bw
-rw-r--r-- 1 444933042 Jul 26 03:31 R_testis_7c.wig.2.gz
-rw-r--r-- 1 444961224 Jul 25 06:10 R_testis_7c.wig.gz

```

standard_results/Tophat_Cufflink_Cuffdiff/Cluster:

total 6192

```

-rw-r--r-- 1 1101 Jul 26 04:26 R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.heatmap.R
-rw-r--r-- 1 1460 Jul 26 04:26 R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.PCA.R
-rw-r--r-- 1 1010132 Jul 26 04:26 R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.txt
-rw-r--r-- 1 950076 Jul 26 04:27
R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.txt.1.heatmap.pdf
-rw-r--r-- 1 868344 Jul 26 04:26
R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.txt.1.matrix.txt
-rw-r--r-- 1 4832 Jul 26 04:26
R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.txt.1.PCA.pdf

```

-rw-r--r-- 1 2084059 Jul 26 04:26

R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.clean.txt.1.rotation.txt

standard_results/Tophat_Cufflink_Cuffdiff/DEG:

total 7984

-rw-r--r-- 1 2131709 Jul 26 04:26 R_hppRNA_data.Tophat_Cufflink_Cuffdiff.testis_vs_brain.gene.DEG.txt

-rw-r--r-- 1 4736290 Jul 26 04:26

R_hppRNA_data.Tophat_Cufflink_Cuffdiff.testis_vs_brain.transcript.DEG.txt

standard_results/Tophat_Cufflink_Cuffdiff/Gene_expression_matrix:

total 56960

-rw-r--r-- 1 548624 Jul 26 04:26 R_hppRNA_data.cuffdiff.combine

-rw-r--r-- 1 2164710 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink.combine

-rw-r--r-- 1 2452866 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink.combine.class

-rw-r--r-- 1 2452866 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink.combine.class.pc

-rw-r--r-- 1 1086869 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink.combine.signature

-rw-r--r-- 1 7935052 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink_isoform.combine

-rw-r--r-- 1 8566228 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink_isoform.combine.class

-rw-r--r-- 1 8566228 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink_isoform.combine.class.pc

-rw-r--r-- 1 1266830 Jul 26 04:26 R_hppRNA_data.cuffdiff_cufflink_isoform.combine.signature

-rw-r--r-- 1 1306270 Jul 26 04:26 R_hppRNA_data.cuffdiff_isoform.combine

-rw-r--r-- 1 1654508 Jul 26 04:26 R_hppRNA_data.cufflink.combine

-rw-r--r-- 1 6712940 Jul 26 04:26 R_hppRNA_data.cufflink_isoform.combine

-rw-r--r-- 1 1010257 Jul 26 04:26 R_hppRNA_data.Tophat_Cufflink_Cuffdiff.gene.FPKM.txt

-rw-r--r-- 1 2920839 Jul 26 04:26 R_hppRNA_data.Tophat_Cufflink_Cuffdiff.transcript.FPKM.txt

standard_results/Tophat_Cufflink_Cuffdiff/Index:

total 4537120

-rw-r--r-- 1 957980027 Jul 22 02:47 hg19.1.bt2

```
-rw-r--r-- 1 715335932 Jul 22 02:47 hg19.2.bt2
-rw-r--r-- 1 3284 Jul 22 02:32 hg19.3.bt2
-rw-r--r-- 1 715335926 Jul 22 02:32 hg19.4.bt2
-rw-r--r-- 1 957980027 Jul 22 03:00 hg19.rev.1.bt2
-rw-r--r-- 1 715335932 Jul 22 03:00 hg19.rev.2.bt2
```

standard_results/Tophat_Cufflink_Cuffdiff/NGS_plot:

total 152624

```
-rw-r--r-- 1 6703 Jul 26 04:02 NGSplot.R_brain_3b.genebody.avgprof.pdf
-rw-r--r-- 1 1354747 Jul 26 04:02 NGSplot.R_brain_3b.genebody.heatmap.pdf
-rw-r--r-- 1 19918432 Jul 26 04:02 NGSplot.R_brain_3b.genebody.zip
-rw-r--r-- 1 6724 Jul 26 04:04 NGSplot.R_brain_3c.genebody.avgprof.pdf
-rw-r--r-- 1 1299987 Jul 26 04:04 NGSplot.R_brain_3c.genebody.heatmap.pdf
-rw-r--r-- 1 19407700 Jul 26 04:04 NGSplot.R_brain_3c.genebody.zip
-rw-r--r-- 1 6723 Jul 25 04:48 NGSplot.R_brain_a.genebody.avgprof.pdf
-rw-r--r-- 1 1282778 Jul 25 04:48 NGSplot.R_brain_a.genebody.heatmap.pdf
-rw-r--r-- 1 18417237 Jul 25 04:48 NGSplot.R_brain_a.genebody.zip
-rw-r--r-- 1 6716 Jul 26 03:57 NGSplot.R_testis_7a.genebody.avgprof.pdf
-rw-r--r-- 1 1572140 Jul 26 03:57 NGSplot.R_testis_7a.genebody.heatmap.pdf
-rw-r--r-- 1 22999135 Jul 26 03:57 NGSplot.R_testis_7a.genebody.zip
-rw-r--r-- 1 6714 Jul 26 03:59 NGSplot.R_testis_7b.genebody.avgprof.pdf
-rw-r--r-- 1 1534323 Jul 26 03:59 NGSplot.R_testis_7b.genebody.heatmap.pdf
-rw-r--r-- 1 22512541 Jul 26 03:59 NGSplot.R_testis_7b.genebody.zip
-rw-r--r-- 1 6721 Jul 26 03:54 NGSplot.R_testis_7c.genebody.avgprof.pdf
-rw-r--r-- 1 1460454 Jul 26 03:54 NGSplot.R_testis_7c.genebody.heatmap.pdf
-rw-r--r-- 1 22463173 Jul 26 03:54 NGSplot.R_testis_7c.genebody.zip
```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM:

total 277612528

drwxr-xr-x 2	4096 Jul 26 04:26 cuffdiff
drwxr-xr-x 2	4096 Jul 26 04:26 cuffdiff_isoform
drwxr-xr-x 2	4096 Jul 26 03:51 cufflink
drwxr-xr-x 2	4096 Jul 26 03:51 cufflink_isoform
-rw-r--r-- 1	565 Jul 25 04:16 R_brain_3b_align_summary.txt
drwxr-xr-x 2	4096 Jul 25 05:01 R_brain_3b_clout
-rw-r--r-- 1	2608253600 Jul 25 04:31 R_brain_3b.sorted.bam
-rw-r--r-- 1	17525299242 Jul 25 04:35 R_brain_3b.sorted.sam
-rw-r--r-- 1	2448263628 Jul 25 04:56 R_brain_3b.sorted.unique.bam
-rw-r--r-- 1	2827488 Jul 25 04:56 R_brain_3b.sorted.unique.bam.bai
-rw-r--r-- 1	16368669259 Jul 25 04:44 R_brain_3b.sorted.unique.sam
drwxr-xr-x 3	4096 Jul 22 21:48 R_brain_3b_thout
-rw-r--r-- 1	563 Jul 25 04:16 R_brain_3c_align_summary.txt
drwxr-xr-x 2	4096 Jul 25 04:53 R_brain_3c_clout
-rw-r--r-- 1	2227415455 Jul 25 04:29 R_brain_3c.sorted.bam
-rw-r--r-- 1	15001712465 Jul 25 04:32 R_brain_3c.sorted.sam
-rw-r--r-- 1	2098721751 Jul 25 04:50 R_brain_3c.sorted.unique.bam
-rw-r--r-- 1	2702744 Jul 25 04:50 R_brain_3c.sorted.unique.bam.bai
-rw-r--r-- 1	14065945296 Jul 25 04:40 R_brain_3c.sorted.unique.sam
drwxr-xr-x 3	4096 Jul 23 23:42 R_brain_3c_thout
-rw-r--r-- 1	563 Jul 25 04:16 R_brain_a_align_summary.txt
drwxr-xr-x 2	4096 Jul 25 04:41 R_brain_a_clout
-rw-r--r-- 1	2709482958 Jul 25 04:25 R_brain_a.sorted.bam
-rw-r--r-- 1	10497168564 Jul 25 04:27 R_brain_a.sorted.sam
-rw-r--r-- 1	2575528056 Jul 25 04:38 R_brain_a.sorted.unique.bam
-rw-r--r-- 1	2739264 Jul 25 04:39 R_brain_a.sorted.unique.bam.bai
-rw-r--r-- 1	9898211782 Jul 25 04:32 R_brain_a.sorted.unique.sam
drwxr-xr-x 3	4096 Jul 22 22:24 R_brain_a_thout
-rw-r--r-- 1	565 Jul 25 04:16 R_testis_7a_align_summary.txt

```

drwxr-xr-x 2          4096 Jul 26 03:45 R_testis_7a_clout
-rw-r--r-- 1    3369102499 Jul 25 04:36 R_testis_7a.sorted.bam
-rw-r--r-- 1    23751151361 Jul 25 04:41 R_testis_7a.sorted.sam
-rw-r--r-- 1    3018292012 Jul 25 05:08 R_testis_7a.sorted.unique.bam
-rw-r--r-- 1      3467592 Jul 25 05:09 R_testis_7a.sorted.unique.bam.bai
-rw-r--r-- 1    20922796563 Jul 25 04:53 R_testis_7a.sorted.unique.sam
drwxr-xr-x 3          4096 Jul 22 22:37 R_testis_7a_thout
-rw-r--r-- 1          565 Jul 25 04:16 R_testis_7b_align_summary.txt
drwxr-xr-x 2          4096 Jul 25 05:11 R_testis_7b_clout
-rw-r--r-- 1    3078787283 Jul 25 04:34 R_testis_7b.sorted.bam
-rw-r--r-- 1    21400472294 Jul 25 04:38 R_testis_7b.sorted.sam
-rw-r--r-- 1    2749264366 Jul 25 05:03 R_testis_7b.sorted.unique.bam
-rw-r--r-- 1      3396376 Jul 25 05:03 R_testis_7b.sorted.unique.bam.bai
-rw-r--r-- 1    18731048186 Jul 25 04:49 R_testis_7b.sorted.unique.sam
drwxr-xr-x 3          4096 Jul 22 22:26 R_testis_7b_thout
-rw-r--r-- 1          565 Jul 25 04:16 R_testis_7c_align_summary.txt
drwxr-xr-x 2          4096 Jul 26 03:35 R_testis_7c_clout
-rw-r--r-- 1    3416847560 Jul 25 04:37 R_testis_7c.sorted.bam
-rw-r--r-- 1    24531744865 Jul 25 04:42 R_testis_7c.sorted.sam
-rw-r--r-- 1    3151290954 Jul 25 05:10 R_testis_7c.sorted.unique.bam
-rw-r--r-- 1      3403720 Jul 25 05:11 R_testis_7c.sorted.unique.bam.bai
-rw-r--r-- 1    22446752496 Jul 25 04:54 R_testis_7c.sorted.unique.sam
drwxr-xr-x 3          4096 Jul 22 21:49 R_testis_7c_thout
drwxr-xr-x 2          4096 Jul 26 03:30 testis_vs_brain_diff_out

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/cuffdiff:

total 2528

```

-rw-r--r-- 1    2131709 Jul 26 04:26 testis_vs_brain.gene_exp.diff

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/cuffdiff_isoform:

total 5456

-rw-r--r-- 1 4736290 Jul 26 04:26 testis_vs_brain.isoform_exp.diff

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/cufflink:

total 12288

-rw-r--r-- 1 1698110 Jul 25 05:07 R_brain_3b.genes.fpkms_tracking

-rw-r--r-- 1 1697960 Jul 25 04:58 R_brain_3c.genes.fpkms_tracking

-rw-r--r-- 1 1696346 Jul 25 04:44 R_brain_a.genes.fpkms_tracking

-rw-r--r-- 1 1727507 Jul 26 03:51 R_testis_7a.genes.fpkms_tracking

-rw-r--r-- 1 1725792 Jul 25 05:17 R_testis_7b.genes.fpkms_tracking

-rw-r--r-- 1 1725460 Jul 26 03:42 R_testis_7c.genes.fpkms_tracking

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/cufflink_isoform:

total 29328

-rw-r--r-- 1 4193174 Jul 25 05:07 R_brain_3b.isoforms.fpkms_tracking

-rw-r--r-- 1 4195983 Jul 25 04:58 R_brain_3c.isoforms.fpkms_tracking

-rw-r--r-- 1 4192234 Jul 25 04:44 R_brain_a.isoforms.fpkms_tracking

-rw-r--r-- 1 4251532 Jul 26 03:51 R_testis_7a.isoforms.fpkms_tracking

-rw-r--r-- 1 4247399 Jul 25 05:17 R_testis_7b.isoforms.fpkms_tracking

-rw-r--r-- 1 4247346 Jul 26 03:42 R_testis_7c.isoforms.fpkms_tracking

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_3b_clout:

total 119520

-rw-r--r-- 1 1698110 Jul 25 05:07 genes.fpkms_tracking

-rw-r--r-- 1 4193174 Jul 25 05:07 isoforms.fpkms_tracking

-rw-r--r-- 1 0 Jul 25 05:01 skipped.gtf

-rw-r--r-- 1 100625285 Jul 25 05:07 transcripts.gtf

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_3b_thout:

total 3223696

```
-rw-r--r-- 1 2606713453 Jul 22 21:47 accepted_hits.bam
-rw-r--r-- 1 565 Jul 22 21:26 align_summary.txt
-rw-r--r-- 1 3204279 Jul 22 21:27 deletions.bed
-rw-r--r-- 1 4482835 Jul 22 21:27 insertions.bed
-rw-r--r-- 1 13533272 Jul 22 21:27 junctions.bed
drwxr-xr-x 2 8192 Jul 22 21:47 logs
-rw-r--r-- 1 186 Jul 22 16:25 prep_reads.info
-rw-r--r-- 1 258022120 Jul 22 21:48 unmapped.bam
```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_3b_thout/logs:

total 1248

```
-rw-r--r-- 1 0 Jul 22 21:47 bam_merge_um.log
-rw-r--r-- 1 12800 Jul 22 20:19 bowtie_build.log
-rw-r--r-- 1 0 Jul 22 16:06 bowtie_inspect_recons.log
-rw-r--r-- 1 222 Jul 22 17:32 bowtie.left_kept_reads.log
-rw-r--r-- 1 219 Jul 22 19:14 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 20:19 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 20:19 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 20:20 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 20:20 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1 222 Jul 22 18:31 bowtie.right_kept_reads.log
-rw-r--r-- 1 219 Jul 22 20:04 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 20:33 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 20:34 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 20:34 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 20:34 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1 0 Jul 22 16:25 g2f.err
```



```

-rw-r--r-- 1      118 Jul 22 16:25 g2f.out
-rw-r--r-- 1      176 Jul 22 16:09 gtf_juncs.log
-rw-r--r-- 1      609 Jul 22 20:18 juncs_db.log
-rw-r--r-- 1      302 Jul 22 20:36 long_spanning_reads.segs.log
-rw-r--r-- 1       47 Jul 22 16:38 m2g_left_kept_reads.err
-rw-r--r-- 1      260 Jul 22 17:32 m2g_left_kept_reads.out
-rw-r--r-- 1       47 Jul 22 17:33 m2g_right_kept_reads.err
-rw-r--r-- 1      260 Jul 22 18:31 m2g_right_kept_reads.out
-rw-r--r-- 1      161 Jul 22 16:25 prep_reads.log
-rw-r--r-- 1     1011 Jul 22 21:27 reports.log
-rw-r--r-- 1        0 Jul 22 21:32 reports.merge_bam.log
-rw-r--r-- 1      40 Jul 22 21:29 reports.samtools_sort.log0
-rw-r--r-- 1      40 Jul 22 21:28 reports.samtools_sort.log1
-rw-r--r-- 1      40 Jul 22 21:28 reports.samtools_sort.log2
-rw-r--r-- 1      40 Jul 22 21:28 reports.samtools_sort.log3
-rw-r--r-- 1      40 Jul 22 21:28 reports.samtools_sort.log4
-rw-r--r-- 1      40 Jul 22 21:28 reports.samtools_sort.log5
-rw-r--r-- 1    50036 Jul 22 21:48 run.log
-rw-r--r-- 1     4069 Jul 22 21:48 tophat.log

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_3c_clout:

total 119504

```

-rw-r--r-- 1    1697960 Jul 25 04:58 genes.fpk_tracking
-rw-r--r-- 1    4195983 Jul 25 04:58 isoforms.fpk_tracking
-rw-r--r-- 1          0 Jul 25 04:53 skipped.gtf
-rw-r--r-- 1   100604679 Jul 25 04:58 transcripts.gtf

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_3c_thout:

total 2752224

```

-rw-r--r-- 1 2226106614 Jul 22 20:23 accepted_hits.bam
-rw-r--r-- 1 563 Jul 22 20:00 align_summary.txt
-rw-r--r-- 1 2598912 Jul 22 20:01 deletions.bed
-rw-r--r-- 1 3659498 Jul 22 20:01 insertions.bed
-rw-r--r-- 1 13542146 Jul 22 20:01 junctions.bed
drwxr-xr-x 2 8192 Jul 22 20:23 logs
-rw-r--r-- 1 186 Jul 22 16:23 prep_reads.info
-rw-r--r-- 1 217962284 Jul 22 20:24 unmapped.bam

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_3c_thout/logs:

total 1248

```

-rw-r--r-- 1 0 Jul 22 20:23 bam_merge_um.log
-rw-r--r-- 1 12800 Jul 22 19:17 bowtie_build.log
-rw-r--r-- 1 0 Jul 22 16:06 bowtie_inspect_recons.log
-rw-r--r-- 1 222 Jul 22 17:13 bowtie.left_kept_reads.log
-rw-r--r-- 1 218 Jul 22 18:24 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 19:18 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 19:18 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 19:18 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 19:18 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1 222 Jul 22 17:57 bowtie.right_kept_reads.log
-rw-r--r-- 1 218 Jul 22 19:02 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 19:22 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 19:22 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 19:22 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 19:23 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1 0 Jul 22 16:23 g2f.err
-rw-r--r-- 1 118 Jul 22 16:23 g2f.out
-rw-r--r-- 1 176 Jul 22 16:09 gtf_juncs.log

```

```

-rw-r--r-- 1      609 Jul 22 19:17 juncs_db.log
-rw-r--r-- 1     302 Jul 22 19:25 long_spanning_reads.segs.log
-rw-r--r-- 1      47 Jul 22 16:35 m2g_left_kept_reads.err
-rw-r--r-- 1     260 Jul 22 17:13 m2g_left_kept_reads.out
-rw-r--r-- 1      47 Jul 22 17:14 m2g_right_kept_reads.err
-rw-r--r-- 1     260 Jul 22 17:57 m2g_right_kept_reads.out
-rw-r--r-- 1     161 Jul 22 16:23 prep_reads.log
-rw-r--r-- 1    1011 Jul 22 20:01 reports.log
-rw-r--r-- 1       0 Jul 22 20:07 reports.merge_bam.log
-rw-r--r-- 1     40 Jul 22 20:03 reports.samtools_sort.log0
-rw-r--r-- 1     40 Jul 22 20:02 reports.samtools_sort.log1
-rw-r--r-- 1     40 Jul 22 20:02 reports.samtools_sort.log2
-rw-r--r-- 1     40 Jul 22 20:01 reports.samtools_sort.log3
-rw-r--r-- 1     40 Jul 22 20:01 reports.samtools_sort.log4
-rw-r--r-- 1     40 Jul 22 20:03 reports.samtools_sort.log5
-rw-r--r-- 1   50036 Jul 22 20:24 run.log
-rw-r--r-- 1    4069 Jul 22 20:24 tophat.log

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_a_clout:

total 119440

```

-rw-r--r-- 1   1696346 Jul 25 04:44 genes.fpkms_tracking
-rw-r--r-- 1   4192234 Jul 25 04:44 isoforms.fpkms_tracking
-rw-r--r-- 1         0 Jul 25 04:41 skipped.gtf
-rw-r--r-- 1  100540060 Jul 25 04:44 transcripts.gtf

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_a_thout:

total 3309776

```

-rw-r--r-- 1 2709801214 Jul 22 22:23 accepted_hits.bam
-rw-r--r-- 1       563 Jul 22 22:12 align_summary.txt

```

```

-rw-r--r-- 1      1310140 Jul 22 22:12 deletions.bed
-rw-r--r-- 1      1988059 Jul 22 22:12 insertions.bed
-rw-r--r-- 1     13059483 Jul 22 22:12 junctions.bed
drwxr-xr-x 2          8192 Jul 22 22:23 logs
-rw-r--r-- 1          186 Jul 22 20:41 prep_reads.info
-rw-r--r-- 1    237051642 Jul 22 22:24 unmapped.bam

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_brain_a_thout/logs:

total 1248

```

-rw-r--r-- 1          0 Jul 22 22:23 bam_merge_um.log
-rw-r--r-- 1    12794 Jul 22 21:51 bowtie_build.log
-rw-r--r-- 1          0 Jul 22 20:24 bowtie_inspect_recons.log
-rw-r--r-- 1     221 Jul 22 21:07 bowtie.left_kept_reads.log
-rw-r--r-- 1     217 Jul 22 21:35 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1     208 Jul 22 21:51 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1     208 Jul 22 21:51 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1     208 Jul 22 21:52 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1     208 Jul 22 21:52 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1     221 Jul 22 21:22 bowtie.right_kept_reads.log
-rw-r--r-- 1     218 Jul 22 21:45 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1     211 Jul 22 21:54 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1     208 Jul 22 21:54 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1     208 Jul 22 21:55 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1     208 Jul 22 21:55 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1          0 Jul 22 20:41 g2f.err
-rw-r--r-- 1     118 Jul 22 20:41 g2f.out
-rw-r--r-- 1     176 Jul 22 20:29 gtf_juncs.log
-rw-r--r-- 1     609 Jul 22 21:51 juncs_db.log
-rw-r--r-- 1     302 Jul 22 21:56 long_spanning_reads.segs.log

```

```

-rw-r--r-- 1      47 Jul 22 20:54 m2g_left_kept_reads.err
-rw-r--r-- 1    259 Jul 22 21:08 m2g_left_kept_reads.out
-rw-r--r-- 1      47 Jul 22 21:09 m2g_right_kept_reads.err
-rw-r--r-- 1    259 Jul 22 21:23 m2g_right_kept_reads.out
-rw-r--r-- 1     161 Jul 22 20:41 prep_reads.log
-rw-r--r-- 1   1010 Jul 22 22:12 reports.log
-rw-r--r-- 1        0 Jul 22 22:16 reports.merge_bam.log
-rw-r--r-- 1     40 Jul 22 22:13 reports.samtools_sort.log0
-rw-r--r-- 1     40 Jul 22 22:13 reports.samtools_sort.log1
-rw-r--r-- 1     40 Jul 22 22:13 reports.samtools_sort.log2
-rw-r--r-- 1     40 Jul 22 22:13 reports.samtools_sort.log3
-rw-r--r-- 1     40 Jul 22 22:13 reports.samtools_sort.log4
-rw-r--r-- 1     40 Jul 22 22:14 reports.samtools_sort.log5
-rw-r--r-- 1  49825 Jul 22 22:24 run.log
-rw-r--r-- 1   4066 Jul 22 22:24 tophat.log

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7a_clout:

total 119776

```

-rw-r--r-- 1 1727507 Jul 26 03:51 genes.fpkms_tracking
-rw-r--r-- 1 4251532 Jul 26 03:51 isoforms.fpkms_tracking
-rw-r--r-- 1        0 Jul 26 03:45 skipped.gtf
-rw-r--r-- 1 100790839 Jul 26 03:51 transcripts.gtf

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7a_thout:

total 4093008

```

-rw-r--r-- 1 3367673358 Jul 22 22:35 accepted_hits.bam
-rw-r--r-- 1        565 Jul 22 22:08 align_summary.txt
-rw-r--r-- 1 4883043 Jul 22 22:08 deletions.bed
-rw-r--r-- 1 5047352 Jul 22 22:08 insertions.bed

```

```
-rw-r--r-- 1      15221140 Jul 22 22:09 junctions.bed
drwxr-xr-x 2          8192 Jul 22 22:35 logs
-rw-r--r-- 1          186 Jul 22 16:29 prep_reads.info
-rw-r--r-- 1    271691309 Jul 22 22:37 unmapped.bam
```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7a_thout/logs:

total 1248

```
-rw-r--r-- 1          0 Jul 22 22:35 bam_merge_um.log
-rw-r--r-- 1    12806 Jul 22 21:02 bowtie_build.log
-rw-r--r-- 1          0 Jul 22 16:06 bowtie_inspect_recons.log
-rw-r--r-- 1     224 Jul 22 17:55 bowtie.left_kept_reads.log
-rw-r--r-- 1     221 Jul 22 19:59 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1     212 Jul 22 21:02 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1     212 Jul 22 21:03 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1     212 Jul 22 21:03 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1     212 Jul 22 21:03 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1     224 Jul 22 19:07 bowtie.right_kept_reads.log
-rw-r--r-- 1     221 Jul 22 20:46 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1     212 Jul 22 21:27 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1     212 Jul 22 21:27 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1     212 Jul 22 21:27 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1     212 Jul 22 21:28 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1          0 Jul 22 16:29 g2f.err
-rw-r--r-- 1     118 Jul 22 16:29 g2f.out
-rw-r--r-- 1     176 Jul 22 16:09 gtf_juncs.log
-rw-r--r-- 1     609 Jul 22 21:01 juncs_db.log
-rw-r--r-- 1     302 Jul 22 21:31 long_spanning_reads.segs.log
-rw-r--r-- 1      47 Jul 22 16:43 m2g_left_kept_reads.err
-rw-r--r-- 1     261 Jul 22 17:55 m2g_left_kept_reads.out
```

```

-rw-r--r-- 1      47 Jul 22 17:56 m2g_right_kept_reads.err
-rw-r--r-- 1    261 Jul 22 19:08 m2g_right_kept_reads.out
-rw-r--r-- 1    161 Jul 22 16:29 prep_reads.log
-rw-r--r-- 1   1012 Jul 22 22:09 reports.log
-rw-r--r-- 1        0 Jul 22 22:15 reports.merge_bam.log
-rw-r--r-- 1    40 Jul 22 22:11 reports.samtools_sort.log0
-rw-r--r-- 1    40 Jul 22 22:11 reports.samtools_sort.log1
-rw-r--r-- 1    40 Jul 22 22:10 reports.samtools_sort.log2
-rw-r--r-- 1    40 Jul 22 22:11 reports.samtools_sort.log3
-rw-r--r-- 1    40 Jul 22 22:11 reports.samtools_sort.log4
-rw-r--r-- 1    40 Jul 22 22:10 reports.samtools_sort.log5
-rw-r--r-- 1  50247 Jul 22 22:37 run.log
-rw-r--r-- 1   4072 Jul 22 22:37 tophat.log

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7b_clout:

total 119760

```

-rw-r--r-- 1  1725792 Jul 25 05:17 genes.fpkms_tracking
-rw-r--r-- 1  4247399 Jul 25 05:17 isoforms.fpkms_tracking
-rw-r--r-- 1        0 Jul 25 05:11 skipped.gtf
-rw-r--r-- 1 100782858 Jul 25 05:17 transcripts.gtf

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7b_thout:

total 3722480

```

-rw-r--r-- 1 3077913656 Jul 22 22:25 accepted_hits.bam
-rw-r--r-- 1      565 Jul 22 21:52 align_summary.txt
-rw-r--r-- 1 4398996 Jul 22 21:52 deletions.bed
-rw-r--r-- 1 4272912 Jul 22 21:52 insertions.bed
-rw-r--r-- 1 15070029 Jul 22 21:52 junctions.bed
drwxr-xr-x 2      8192 Jul 22 22:25 logs

```

```
-rw-r--r-- 1          186 Jul 22 16:27 prep_reads.info
-rw-r--r-- 1 231059509 Jul 22 22:26 unmapped.bam
```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7b_thout/logs:

total 1248

```
-rw-r--r-- 1          0 Jul 22 22:25 bam_merge_um.log
-rw-r--r-- 1 12806 Jul 22 20:31 bowtie_build.log
-rw-r--r-- 1          0 Jul 22 16:06 bowtie_inspect_recons.log
-rw-r--r-- 1 222 Jul 22 17:40 bowtie.left_kept_reads.log
-rw-r--r-- 1 219 Jul 22 19:30 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 20:31 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1 222 Jul 22 18:40 bowtie.right_kept_reads.log
-rw-r--r-- 1 219 Jul 22 20:18 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 20:35 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 20:35 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 20:35 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 20:36 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1          0 Jul 22 16:27 g2f.err
-rw-r--r-- 1 118 Jul 22 16:27 g2f.out
-rw-r--r-- 1 176 Jul 22 16:09 gtf_juncs.log
-rw-r--r-- 1 609 Jul 22 20:31 juncs_db.log
-rw-r--r-- 1 302 Jul 22 20:37 long_spanning_reads.segs.log
-rw-r--r-- 1 47 Jul 22 16:40 m2g_left_kept_reads.err
-rw-r--r-- 1 261 Jul 22 17:41 m2g_left_kept_reads.out
-rw-r--r-- 1 47 Jul 22 17:42 m2g_right_kept_reads.err
-rw-r--r-- 1 261 Jul 22 18:40 m2g_right_kept_reads.out
```



```

-rw-r--r-- 1      161 Jul 22 16:27 prep_reads.log
-rw-r--r-- 1    1012 Jul 22 21:52 reports.log
-rw-r--r-- 1         0 Jul 22 22:03 reports.merge_bam.log
-rw-r--r-- 1     40 Jul 22 21:53 reports.samtools_sort.log0
-rw-r--r-- 1     40 Jul 22 21:53 reports.samtools_sort.log1
-rw-r--r-- 1     40 Jul 22 21:53 reports.samtools_sort.log2
-rw-r--r-- 1     40 Jul 22 21:53 reports.samtools_sort.log3
-rw-r--r-- 1     40 Jul 22 21:53 reports.samtools_sort.log4
-rw-r--r-- 1     41 Jul 22 21:56 reports.samtools_sort.log5
-rw-r--r-- 1   50247 Jul 22 22:26 run.log
-rw-r--r-- 1    4072 Jul 22 22:26 tophat.log

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7c_clout:

total 119792

```

-rw-r--r-- 1 1725460 Jul 26 03:42 genes.fpk_tracking
-rw-r--r-- 1 4247346 Jul 26 03:42 isoforms.fpk_tracking
-rw-r--r-- 1         0 Jul 26 03:35 skipped.gtf
-rw-r--r-- 1 100807983 Jul 26 03:42 transcripts.gtf

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7c_thout:

total 4134816

```

-rw-r--r-- 1 3412213260 Jul 22 21:48 accepted_hits.bam
-rw-r--r-- 1      565 Jul 22 21:21 align_summary.txt
-rw-r--r-- 1 4523739 Jul 22 21:21 deletions.bed
-rw-r--r-- 1 4316865 Jul 22 21:21 insertions.bed
-rw-r--r-- 1 15149739 Jul 22 21:21 junctions.bed
drwxr-xr-x 2      8192 Jul 22 21:48 logs
-rw-r--r-- 1      186 Jul 22 16:31 prep_reads.info
-rw-r--r-- 1 265802878 Jul 22 21:49 unmapped.bam

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/R_testis_7c_thout/logs:

total 1248

```
-rw-r--r-- 1      0 Jul 22 21:48 bam_merge_um.log
-rw-r--r-- 1 12806 Jul 22 20:31 bowtie_build.log
-rw-r--r-- 1      0 Jul 22 16:06 bowtie_inspect_recons.log
-rw-r--r-- 1 223 Jul 22 17:50 bowtie.left_kept_reads.log
-rw-r--r-- 1 219 Jul 22 19:33 bowtie.left_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 20:32 bowtie.left_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1 223 Jul 22 18:55 bowtie.right_kept_reads.log
-rw-r--r-- 1 219 Jul 22 20:18 bowtie.right_kept_reads.m2g_um.log
-rw-r--r-- 1 212 Jul 22 20:35 bowtie.right_kept_reads.m2g_um_seg1.log
-rw-r--r-- 1 212 Jul 22 20:35 bowtie.right_kept_reads.m2g_um_seg2.log
-rw-r--r-- 1 212 Jul 22 20:36 bowtie.right_kept_reads.m2g_um_seg3.log
-rw-r--r-- 1 212 Jul 22 20:36 bowtie.right_kept_reads.m2g_um_seg4.log
-rw-r--r-- 1      0 Jul 22 16:31 g2f.err
-rw-r--r-- 1 118 Jul 22 16:31 g2f.out
-rw-r--r-- 1 176 Jul 22 16:09 gtf_juncs.log
-rw-r--r-- 1 609 Jul 22 20:31 juncs_db.log
-rw-r--r-- 1 302 Jul 22 20:37 long_spanning_reads.segs.log
-rw-r--r-- 1 47 Jul 22 16:45 m2g_left_kept_reads.err
-rw-r--r-- 1 261 Jul 22 17:50 m2g_left_kept_reads.out
-rw-r--r-- 1 47 Jul 22 17:51 m2g_right_kept_reads.err
-rw-r--r-- 1 261 Jul 22 18:55 m2g_right_kept_reads.out
-rw-r--r-- 1 161 Jul 22 16:31 prep_reads.log
-rw-r--r-- 1 1012 Jul 22 21:21 reports.log
```

```

-rw-r--r-- 1      0 Jul 22 21:29 reports.merge_bam.log
-rw-r--r-- 1    40 Jul 22 21:25 reports.samtools_sort.log0
-rw-r--r-- 1    40 Jul 22 21:24 reports.samtools_sort.log1
-rw-r--r-- 1    40 Jul 22 21:24 reports.samtools_sort.log2
-rw-r--r-- 1    40 Jul 22 21:23 reports.samtools_sort.log3
-rw-r--r-- 1    40 Jul 22 21:24 reports.samtools_sort.log4
-rw-r--r-- 1    40 Jul 22 21:23 reports.samtools_sort.log5
-rw-r--r-- 1 50247 Jul 22 21:49 run.log
-rw-r--r-- 1   4072 Jul 22 21:49 tophat.log

```

standard_results/Tophat_Cufflink_Cuffdiff/Processed_BAM/testis_vs_brain_diff_out:

total 90288

```

-rw-r--r-- 1      53 Jul 26 04:26 bias_params.info
-rw-r--r-- 1 2027956 Jul 26 04:26 cds.count_tracking
-rw-r--r-- 1 1591283 Jul 26 04:26 cds.diff
-rw-r--r-- 1 3734190 Jul 26 04:26 cds_exp.diff
-rw-r--r-- 1 3662370 Jul 26 04:26 cds.fpkm_tracking
-rw-r--r-- 1 9822617 Jul 26 04:26 cds.read_group_tracking
-rw-r--r-- 1 2131709 Jul 26 04:26 gene_exp.diff
-rw-r--r-- 1 1164844 Jul 26 04:26 genes.count_tracking
-rw-r--r-- 1 2156804 Jul 26 04:26 genes.fpkm_tracking
-rw-r--r-- 1 5342150 Jul 26 04:26 genes.read_group_tracking
-rw-r--r-- 1 4736290 Jul 26 04:26 isoform_exp.diff
-rw-r--r-- 1 2651531 Jul 26 04:26 isoforms.count_tracking
-rw-r--r-- 1 4770739 Jul 26 04:26 isoforms.fpkm_tracking
-rw-r--r-- 1 13176469 Jul 26 04:26 isoforms.read_group_tracking
-rw-r--r-- 1 1549136 Jul 26 04:26 promoters.diff
-rw-r--r-- 1    1174 Jul 26 04:26 read_groups.info
-rw-r--r-- 1    1168 Jul 26 04:26 run.info

```

-rw-r--r--	1	2115308	Jul 26 04:26	splicing.diff
-rw-r--r--	1	2815677	Jul 26 04:26	tss_group_exp.diff
-rw-r--r--	1	1562886	Jul 26 04:26	tss_groups.count_tracking
-rw-r--r--	1	2752788	Jul 26 04:26	tss_groups.fpk_tracking
-rw-r--r--	1	7449293	Jul 26 04:26	tss_groups.read_group_tracking
-rw-r--r--	1	2456800	Jul 26 03:47	var_model.info