**SUPPLEMENTARY MATERIAL 4**

**System Requirement**

|  |  |
| --- | --- |
|  | Software | Version | Included | Other Setting up work|-------------|---------|-----------|--------------------- |
|  | samtools | 1.3 | No | Install and set the path |
|  | R | 3.3.0 | No | Install and set the path |
|  | java | 1.8 | No | Install and set the path |
|  | python | 2.7.3 | No | Install and set the path |
|  | perl | v5.10.1 | No | Install and set the path |
|  | STAR | 2.4.2a | YES | None |
|  | Cufflinks | 2.2.1 | YES | None |
|  | Fastqc | v0.11.3 | YES | None |
|  | Picard-Tools | 2.9.0 | YES | None |
|  | featureCoutns | 1.4.6 | YES | None |
|  | sratoolkit | 2.4.2 | YES | None |
|  | gdc-client | v1.2.1 | YES | You may need to recompile the source code(from their github) if running into GLIBC incompatibility issue for CentOS 6.8 or lower version. |
|  | CPAT | 1.2.2 | YES | You may need to recompile from source code following the instruction: http://rna-cpat.sourceforge.net/#installation |

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R session info:

R version 3.3.0 (2016-05-03)

Platform: x86\_64-pc-linux-gnu (64-bit)

Running under: CentOS release 6.8 (Final)

locale:

 [1] LC\_CTYPE=en\_US.UTF-8 LC\_NUMERIC=C

 [3] LC\_TIME=en\_US.UTF-8 LC\_COLLATE=en\_US.UTF-8

 [5] LC\_MONETARY=en\_US.UTF-8 LC\_MESSAGES=en\_US.UTF-8

 [7] LC\_PAPER=en\_US.UTF-8 LC\_NAME=C

 [9] LC\_ADDRESS=C LC\_TELEPHONE=C

[11] LC\_MEASUREMENT=en\_US.UTF-8 LC\_IDENTIFICATION=C

attached base packages:

 [1] grid tools stats4 parallel stats graphics grDevices

 [8] utils datasets methods base

other attached packages:

 [1] Gviz\_1.16.5

 [2] animation\_2.5

 [3] tidyr\_0.6.1

 [4] GGally\_1.3.0

 [5] diagram\_1.6.3

 [6] shape\_1.4.2

 [7] preprocessCore\_1.34.0

 [8] reshape2\_1.4.2

 [9] hwriter\_1.3.2

[10] ReportingTools\_2.12.2

[11] knitr\_1.15.1

[12] RColorBrewer\_1.1-2

[13] pheatmap\_1.0.8

[14] DESeq2\_1.12.4

[15] TCGAbiolinks\_2.0.13

[16] TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2

[17] GenomicFeatures\_1.24.5

[18] AnnotationDbi\_1.34.4

[19] ggthemes\_3.4.0

[20] EDASeq\_2.6.2

[21] ShortRead\_1.30.0

[22] GenomicAlignments\_1.8.4

[23] SummarizedExperiment\_1.2.3

[24] Rsamtools\_1.24.0

[25] GenomicRanges\_1.24.3

[26] GenomeInfoDb\_1.8.7

[27] Biostrings\_2.40.2

[28] XVector\_0.12.1

[29] IRanges\_2.6.1

[30] S4Vectors\_0.10.3

[31] BiocParallel\_1.6.6

[32] Biobase\_2.32.0

[33] BiocGenerics\_0.18.0

[34] cowplot\_0.7.0

[35] ggplot2\_2.2.1

[36] dplyr\_0.5.0

loaded via a namespace (and not attached):

 [1] R.utils\_2.5.0 RSQLite\_1.1-2

 [3] htmlwidgets\_0.8 trimcluster\_0.1-2

 [5] DESeq\_1.24.0 munsell\_0.4.3

 [7] codetools\_0.2-15 colorspace\_1.3-2

 [9] BiocInstaller\_1.22.3 Category\_2.38.0

 [11] OrganismDbi\_1.14.1 supraHex\_1.10.0

 [13] robustbase\_0.92-7 downloader\_0.4

 [15] TH.data\_1.0-8 biovizBase\_1.20.0

 [17] diptest\_0.75-7 R6\_2.2.0

 [19] doParallel\_1.0.10 locfit\_1.5-9.1

 [21] flexmix\_2.3-13 bitops\_1.0-6

 [23] reshape\_0.8.6 assertthat\_0.2.0

 [25] scales\_0.4.1 multcomp\_1.4-6

 [27] nnet\_7.3-12 gtable\_0.2.0

 [29] affy\_1.50.0 ggbio\_1.20.2

 [31] sandwich\_2.3-4 ensembldb\_1.4.7

 [33] genefilter\_1.54.2 GlobalOptions\_0.0.11

 [35] splines\_3.3.0 rtracklayer\_1.32.2

 [37] lazyeval\_0.2.0 acepack\_1.4.1

 [39] dichromat\_2.0-0 hexbin\_1.27.1

 [41] checkmate\_1.8.2 backports\_1.0.5

 [43] httpuv\_1.3.3 Hmisc\_4.0-2

 [45] RBGL\_1.48.1 affyio\_1.42.0

 [47] gplots\_3.0.1 Rcpp\_0.12.10

 [49] plyr\_1.8.4 base64enc\_0.1-3

 [51] zlibbioc\_1.18.0 RCurl\_1.95-4.8

 [53] rpart\_4.1-10 GetoptLong\_0.1.6

 [55] viridis\_0.3.4 zoo\_1.8-0

 [57] ggrepel\_0.6.5 cluster\_2.0.5

 [59] magrittr\_1.5 data.table\_1.10.4

 [61] dnet\_1.0.10 circlize\_0.3.10

 [63] mvtnorm\_1.0-6 whisker\_0.3-2

 [65] matrixStats\_0.52.2 aroma.light\_3.2.0

 [67] hms\_0.3 mime\_0.5

 [69] xtable\_1.8-2 XML\_3.98-1.5

 [71] mclust\_5.2.3 gridExtra\_2.2.1

 [73] biomaRt\_2.28.0 tibble\_1.3.0

 [75] KernSmooth\_2.23-15 R.oo\_1.21.0

 [77] htmltools\_0.3.5 GOstats\_2.38.1

 [79] Formula\_1.2-1 geneplotter\_1.50.0

 [81] DBI\_0.6 matlab\_1.0.2

 [83] ComplexHeatmap\_1.10.2 MASS\_7.3-45

 [85] fpc\_2.1-10 Matrix\_1.2-8

 [87] readr\_1.1.0 parmigene\_1.0.2

 [89] R.methodsS3\_1.7.1 gdata\_2.17.0

 [91] igraph\_1.0.1 coin\_1.1-3

 [93] foreign\_0.8-67 xml2\_1.1.1

 [95] foreach\_1.4.3 annotate\_1.50.1

 [97] AnnotationForge\_1.14.2 rvest\_0.3.2

 [99] stringr\_1.2.0 VariantAnnotation\_1.18.7

[101] digest\_0.6.12 ConsensusClusterPlus\_1.36.0

[103] graph\_1.50.0 htmlTable\_1.9

[105] dendextend\_1.5.2 edgeR\_3.14.0

[107] GSEABase\_1.34.1 kernlab\_0.9-25

[109] shiny\_1.0.1 gtools\_3.5.0

[111] modeltools\_0.2-21 rjson\_0.2.15

[113] nlme\_3.1-131 jsonlite\_1.4

[115] PFAM.db\_3.3.0 limma\_3.28.21

[117] BSgenome\_1.40.1 lattice\_0.20-34

[119] httr\_1.2.1 DEoptimR\_1.0-8

[121] survival\_2.40-1 GO.db\_3.3.0

[123] interactiveDisplayBase\_1.10.3 prabclus\_2.2-6

[125] iterators\_1.0.8 Rgraphviz\_2.16.0

[127] class\_7.3-14 stringi\_1.1.5

[129] AnnotationHub\_2.4.2 latticeExtra\_0.6-28

[131] caTools\_1.17.1 memoise\_1.0.0

[133] ape\_4.1

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You are using pip version 7.1.0, however version 9.0.1 is available.

You should consider upgrading via the 'pip install --upgrade pip' command.

argh==0.26.1

argparse==1.2.1

Babel==0.9.4

backports.ssl-match-hostname==3.4.0.2

bayesian-optimization==0.1.0

biom-format==1.1.2

biopython==1.66

boto==2.45.0

bx-python==0.7.1

cas==0.15

chardet==2.2.1

cogent==1.5.3

configobj==4.6.0

Counter==1.0.0

coverage==4.0a6

CPAC==0.3.0

CPAT==1.2.2

CrossMap==0.2.2

csvkit==0.9.0

cutadapt==1.7.1

Cython==0.22

dbf==0.94.3

docutils==0.6

elementtree===1.2.7-20070827-preview

empy==3.1

eta===0.9.8f

ethtool==0.6

firstboot==1.110

foolscap==0.4.2

fpconst==0.7.3

freeipa==2.0.0a0

h5py==1.3.1

HTSeq===0.5.4p3

iniparse==0.3.1

iotop==0.3.2

ipapython==3.0.0

ipdb==0.7

ipython==0.13.2

iwlib==1.0

jdcal==1.0

Jinja2==2.2.1

kerberos==1.1

libgenders==1.2

lockfile==0.9.1

lxml==2.2.3

M2Crypto==0.20.2

MACS==1.4.3

Magic-file-extensions==0.1

matplotlib==1.3.1

memory-profiler==0.31

mercurial==1.4

mglob==0.4

MySQL-python==1.2.3rc1

nest==1.3.0

netaddr==0.7.5

networkx==1.8.1

nibabel==1.3.0

nipype==0.9.2

nose==1.3.1

Numeric==24.2

numexpr==2.4

numpy==1.10.1

openpyxl==2.1.1

ordereddict==1.2

pandas==0.17.1

paramiko==1.7.5

patsy==0.3.0

pexpect==2.3

PIL==1.1.6

Pmw==1.3.2

protobuf==2.4.1

psutil==2.2.1

psycopg2==2.6

pyasn1==0.0.12a0

pycassa==1.9.0

pycrypto==2.0.1

pycurl==7.19.0

Pygments==1.1.1

pygpgme==0.1

pymc==2.3.4

pymol==1.8.0.0

pymongo==2.6.3

pyOpenSSL==0.13.1

pyparsing==2.0.1

pysam==0.8.2.1

python-dateutil==2.4.2

python-default-encoding==0.1

python-dmidecode==3.10.13

python-ldap==2.3.10

python-nss==0.16.0

pytz==2015.7

PyVCF==0.6.7

PyXML==0.8.4

PyYAML==3.10

pyzmq==14.3.1

reportlab==2.3

requests==2.6.0

riak==2.0.2

riak-pb==1.4.4.0

rsa==3.4.1

s3cmd==1.6.1

scdate==1.9.60

scikit-learn==0.16b1

scipy==0.15.1

simplegeneric==0.8

simplejson==3.6.4

six==1.10.0

snp-pipeline==0.3.4

SOAPpy==0.11.6

Sphinx==0.6.6

SQLAlchemy==0.9.7

SSSDConfig==1.13.3

statsmodels==0.6.1

swalign==0.3.3

tables==3.1.1

Theano==0.6.0

thrift==0.9.1

tornado==3.2

traits==4.4.0

Twisted-Core==8.2.0

Twisted-Web==8.2.0

urlgrabber==3.9.1

urllib3==1.10.2

wxPython==2.8.12.0

wxPython-common==2.8.12.0

xlrd==0.9.3

yum-metadata-parser==1.1.2

zope.interface==3.5.2

ZSI==2.0