## Outline

Riboprofiling samples
Trimming reads
Removing contaminants
Genome mapping STAR
Comparing stats with references
Quantification
clustering by expression
spearman
pearson
By datatype
spearman
pearson

## Riboprofiling samples

|  | 6 h | 18 h | 120 h |
| :--- | :--- | :--- | :--- |
| Reads | $42,130,444$ | $45,982,977$ | $44,077,266$ |
| Sequence length | 50 | 50 | 50 |
| \%GC | 59 | 55 | 56 |

## Trimming



- min length: 25
- min adapter alignment length: 5
- unclipped discarded
- first base discarded


## Trimming - Cutadapt

-quality-cutoff=10 Trim low-quality bases from 3' ends of each read before adapter removal.

|  |  |  | discarded <br> id | input |
| :--- | :--- | :--- | :--- | :--- | output $\quad$| reads with |
| :--- |
| Adapter |

## Sequence length distribution after trimming - Cutadapt



(1) Sequence Length Distribution


| time | sequence length |
| :--- | :--- |
| H006 | $25-44$ |
| H018 | $25-44$ |
| H120 | $25-44$ |

## Removing contaminants - rRNA

- STAR: without split mapping; max 10 multimaps; outFilterMatchNmin 16

| id | reads <br> processed | uniquely <br> mapped | multiple <br> loci | too many <br> loci | discarded <br> too short |
| :--- | :--- | :--- | :--- | :--- | :--- |
| H006 | $34,439,444$ | $29,465,892(85.56 \%)$ | $45,281(0.13 \%)$ | $810(0.00 \%)$ | $14.31 \%$ |
| H018 | $39,441,134$ | $12,559,738(31.84 \%)$ | $193,421(0.49 \%)$ | $4,945(0.01 \%)$ | $67.65 \%$ |
| H120 | $32,501,482$ | $13,389,260(41.20 \%)$ | $119,345(0.37 \%)$ | $12,214(0.04 \%)$ | $58.39 \%$ |

## Genome mapping STAR - max 10 multimaps

- Unaligned reads from rRNA mapping
- -outFilterMatchNmin 16
- max 10 multimaps

Number of mapped reads


Proportion of mapped reads


Number of uniquely mapped reads


Proportion of uniquely mapped reads


## Genome mapping STAR - max 100 multimaps

- Unaligned reads from rRNA mapping
- -outFilterMatchNmin 16
- max 100 multimaps

Number of mapped reads


Proportion of mapped reads


Number of uniquely mapped reads


Proportion of uniquely mapped reads


## Distribution of multimaps



## Genomic regions - max 100 multimaps


uniquely mapped reads


## Genomic regions - continuous mapping - max 100 multimaps

primary alignments


## Genomic regions - split mapping - max 100 multimaps



## Genomic regions - continuous mapping

uniquely mapped reads


## Genomic regions - split mapping - max 100 multimaps

uniquely mapped reads



## Comparing stats with references

Fatima's lab

|  | RPF1 Mock | RPF1 KD | RPF2 Mock | RPF2 KD | RPF3 Mock | RPF3 KD |
| :--- | ---: | ---: | ---: | ---: | ---: | ---: |
| Total Reads | $110,347,659$ | $86,886,294$ | $70,701,122$ | $61,970,268$ | $187,463,074$ | $147,577,976$ |
| size-selected (22-36) | $105,447,994$ | $80,382,820$ | $65,538,346$ | $60,464,127$ | $159,938,111$ | $134,116,969$ |
| After rRNA,tRNA filtering | $57,452,964$ | $40,704,687$ | $8,788,516$ | $8,790,692$ | $45,542,640$ | $29,858,389$ |
| Aligned (-rRNA,tRNA) | $22,252,759$ | $15,717,018$ | $4,376,899$ | $4,232,701$ | $23,323,320$ | $12,759,154$ |
| In annotated CDSs | $16,520,263$ | $11,497,323$ | $2,451,068$ | $2,742,875$ | $17,831,699$ | $10,158,765$ |

Current stats ERC

|  | 6 h | 18 h | 120 h |
| :--- | ---: | ---: | ---: |
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| Size selected (25-44) | $34,439,444$ | $39,441,134$ | $32,501,482$ |
| After rRNA filtering | $4,928,271$ | $26,687,975$ | $18,992,877$ |
| Aligned (-rRNA, 10mm) | $2,022,381(41.04 \%)$ | $6,718,578(25.17 \%)$ | $9,117,294(48.00 \%)$ |
| Uniquely aligned (-rRNA, 10mm) | $1,095,120(54.15 \%)$ | $3,543,776(52.75 \%)$ | $4910138(53.86 \%)$ |
| Exonic mapping primary alignment | 918,722 | $3,241,787$ | $3,881,137$ |
| Exonic uniquely mapped | 697,556 | $2,486,593$ | $3,071,028$ |

## Comparing stats with references

## GBE

## Evolution of Gene Regulation during Transcription and

Translation

```
Zhe Wang }\mp@subsup{}{}{1,\dagger}\mathrm{ , Xuepeng Sun }\mp@subsup{}{}{1,2,\dagger}, Yi Zhao ', , Xiaoxian Guo', Huifeng Jiang ',4, Hongye Li', and
Zhenglong Gu'*
```

Genome Bid. Evd. 7(4):1155-1167. doi:10.1093/gbe/evv059 Advance Access publication April 14, 2015

| Mapping statistics |  |  |  |  |  |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :---: |
|  | mRNA |  |  |  | RFP |  |  |  |  |
|  | Parents rep1 | Parents rep2 | Hybrid rep1 | Hybrid rep2 | Parents rep1 | Parents rep2 | Hybrid rep1 | Hybrid rep2 |  |
| Raw re ads | $17,624,023$ | $18,867,091$ | $8,989,389$ | $11,190,803$ | $39,013,450$ | $28,194,385$ | $43,422,305$ | $28,293,665$ |  |
| rRNA re moved | $17,498,738$ | $18,780,244$ | $8,922,195$ | $11,128,519$ | $13,695,629$ | $8,022,019$ | $17,881,744$ | $10,250,293$ |  |
| Unique mapped | $8,775,097$ | $14,519,040$ | $6,138,988$ | $7,722,284$ | $5,773,238$ | $3,799,847$ | $8,588,366$ | $5,764,230$ |  |
| Assigned to Scer | $3,711,925$ | $6,234,419$ | $2,875,434$ | $3,610,498$ | $3,492,718$ | $2,367,021$ | $4,318,725$ | $2,875,927$ |  |
| Assigned to Sbay | $5,063,172$ | $8,284,621$ | $3,263,554$ | $4,111,786$ | $2,280,520$ | $1,432,826$ | $4,269,641$ | $2,888,303$ |  |
| Splicing Alignment(SA) | 6,255 | 10,645 | 13,082 | 16,222 | 6,033 | 8,432 | 11,391 | 13,122 |  |
| SA in Scer | 4,497 | 7,847 | 11,815 | 14,930 | 4,325 | 5,447 | 7,502 | 8,550 |  |
| SA in Sbay | 1,758 | 2,798 | 1,267 | 1,292 | 1,708 | 2,985 | 3,889 | 4,572 |  |

## Cenik et al. 2015, Genome Res.

- To enable comparable analysis of high-throughput sequencing data sets, we used a uniform alignment and preprocessing pipeline.
- Reads were sequentially aligned using Bowtie 2 v.2.0.5 (Langmead and Salzberg 2012).
- All reads mapping to human rRNA and tRNA sequences were filtered out.
- The remaining reads were aligned to APPRIS principal transcripts (release 12) (Rodriguez et al. 2013) from the GENCODE mRNA annotation v. 15 (Harrow et al. 2012).
- For all transcript level analyses, reads that map only to coding regions were used.


## Cenik et al. 2015, Genome Res.

- The remaining reads were aligned using parameters "-L 18 -norc" to APPRIS principal transcripts (release 12) (Rodriguez et al., 2013) from the GENCODE mRNA annotation v. 15 (Harrow et al., 2012).
- This step was followed by alignment to all GENCODE transcripts and finally to the human genome (hg19).
- This strategy was preferred to avoid any differences in mappability of the exon-exon junction spanning reads due to read length differences between ribosome profiling and RNA-seq libraries.
- We only retained alignments with a mapping quality greater than two for subsequent analyses.
- Reads mapping to coding regions, 5'UTRs, and 3'UTRs were counted separately using bedtools (Quinlan and Hall, 2010) and custom scripts.
- For all transcript level analyses, reads that map only to coding regions were used.


## Comparing stats with references

Cenik et al. 2015, Genome Res.
$\rightarrow$ How many initial reads and reads mapping to coding regions you had approximately?
This varies quite a bit based on the efficiency of rRNA depletion.
Even after using the oligo-depletion a large fraction goes to rRNAs.
Just to give you an idea, I picked one of the 100 ribosome profiling libraries we sequenced:

| Reads | $16,739,559$ |
| :--- | ---: |
| After trimming | $14,866,539(88 \%)$ |
| Mapped to rRNA | $64.49 \%$ |
| Reads after rRNA removal | $5,265,866$ |
| aligned uniquely to APPRIS transcriptome | $3,355,633(63.72 \%)$ |
| aligned $>1$ times | $722,762(13.73 \%)$ |
| remaining | $1,187,471$ |
| mapped to the genome but not the transcriptome | 476,051 |

Current stats ERC

|  | 6 h | 18 h | 120 h |
| :--- | ---: | ---: | ---: |
| Reads | $42,130,444$ | $45,982,977$ | $44,077,266$ |
| Size selected (25-44) | $34,439,444$ | $39,441,134$ | $32,501,482$ |
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| Uniquely aligned (-rRNA, 10mm) | $1,095,120(54.15 \%)$ | $3,543,776(52.75 \%)$ | $4910138(53.86 \%)$ |
| Exonic mapping primary alignment | 918,722 | $3,241,787$ | $3,881,137$ |
| Exonic uniquely mapped | 697,556 | $2,486,593$ | $3,071,028$ |

## Cenik et al. 2015, Genome Res.

For our study, the primary objective is to provide and integrated analysis of RNA, protein and translation levels. Given the biology of ribosome protection, it is not possible to obtain long reads for ribosome profiling. Hence, directly mapping to the entire genome penalizes ribosome profiling reads more than it does RNA-Seq reads which are much longer. Hence, we made the simplifying assumption of concentrating on a defined transcriptome. I should note that there are very few reads that map to non-APPRIS, GENCODE transcripts.

## \{APPRIS\}

Annotating principal splice isoforms

## APPRIS Database

Access annotations for the species annotated in the database via gene name or Ensembl id.

## Access the web database

## APPRIS WebServer

Annotate splice isoforms for vertebrate genes that are not in the APPRIS Data base.
Run the web server

APPRIS Database currently houses annotations for vertebrate genomes,


Human
Assemblies: GRCh38|hg38 (Ensembl82) Assemblies: GRCh37|hg19 (Ensembl74)


Zebrafish
Assemblies: GRCZ10|danRer10 (Ensembl82) Assemblies: Zv9|danRer7 (Ensemb|77)


Rat
Assemblies: Rnor_6.0|m6 (Ensembl82)
Assemblies: Rnor_5.0|m5 (Ensemb|77)

APPRIS Database currently houses annotations for invertebrate genomes

Assemblies: BDGP6|dm6 (Ensembl82)

## APPRIS

The APPRIS WebServer [1] executes a range of computational methods to annotate splice variants for individual genes. As part of its annotation process APPRIS selects a single CDS as the principal isoform for each gene.

## Publications

[1] APPRIS WebServer and WebServices. Rodriguez JM, et al.
Nucleic Acids Res. 2015 May 18.
PUBMED:25990727 DO1:10.1093/narjgkv512

Alternative splicing generates different gene products. Recent studies have estimated that almost $100 \%$ of multi-exon human genes produce differently spliced mRNAs. It is important to designate one of the isoforms as the principal isoform in order to predict the potential changes in function, structure or localisation brought about by altemative splicing.
APPRIS annotates variants with biological data such as protein structural information, functionally important residues, conservation of functional domainsand evidence of cross-species conservation. The APPRIS Database selects a principal is oforms based on this evidence.


APFRIS Database analysis
The APPRIS Database automates a range of computational methods that are used to annotate altemative splice variants and to define principal variants. The splice isoform annotations are the results of the six modules in the APPRIS Data base; the final module selects the principal isoforms.

## 

Search gene...

## Downloads

The annotations of the following species are available.
Filter by Species: All $\hat{0}$ Assembly Version: All $\hat{0}$ Gene Dataset: All 0

| Species | Assembly version | Gene Dataset | Principal Isoforms | APPRIS scores | Functional residues | Tertiary structure | Vertebrates conservation | Whole domains | Transmembrane he |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Human | GRCh38 | gencode23/ensemb\|82 | TXT | TXT | GTFBED | GTF BED | GTFEED | GTFPED | GTF BED |
| Human | GRCh37 | gencode19/ensembl74 | TXT | TXT | GTF BED | GIF BED | GTFBED | GTFBED | GTF BED |
| Mouse | GRCm38 | gencodeM7/ensembl32 | IXI | IXI | GTE | GIF | GTE | GTF | GTF |
| Rat | Rnor_6.0 | ensembls1 | IXI | IXI | GIF | GIF | GTE | GTE | GTF |

You can download our annotations files from our server, the following README file explains the directory structure.

## Principal Isoform flags

APPRIS selects a single CDS variant for each gene as the 'PRINCIPAL' isoform based on the range of protein features. Principal isoforms are tagged with the numbers 1 to 5 , with 1 being the most reliable. The definition of the flags are as follows: - principal:1

Transcript(s) expected to code for the main functional isoform based solely on the core modules in the APPRIS database. The APPRIS core modules map protein structural and functional information and cross-species conservation to the annotated variants.

- PRINCIPAL:2

Where the APPRIS core modules are unable to choose a clear principal variant (approximately $25 \%$ of human protein coding genes), the database chooses two or more of the CDS variants as "candidates" to be the principal variant.

## Correlation between riboprofiling samples





## Correlation between riboprofiling and RNAseq samples H006-50666 genes



## Correlation between riboprofiling and RNAseq samples H018-50666 genes






## Correlation between riboprofiling and RNAseq samples H120-50666 genes








## Correlation between riboprofiling and proteomics

 samples - 6109 genes






H003.3T.9858 $0.650 .790 .790 .730 .7 \quad 0.70 .70 .870 .850 .90 .880 .880 .920 .910 .940 .940 .940 .930 .960 .950 .940 .980 .970 .940 .960 .97 \quad 1$ H000.3T. $98570.640 .770 .780 .71 \quad 0.7 \quad 0.7$ 0.7 $0.840 .840 .890 .870 .870 .910 .90 .920 .920 .940 .920 .910 .910 .930 .950 .950 .960 .94 \quad 1$

 HOO9.3T. $121080.690 .840 .840 .770 .750 .750 .740 .880 .880 .940 .920 .930 .960 .950 .980 .970 .980 .970 .960 .970 .970 .99 \quad 1 \quad 0.930 .930 .950 .97$ H006.3T. $98590.670 .820 .820 .750 .730 .730 .730 .880 .860 .920 .910 .910 .940 .930 .960 .950 .960 .950 .970 .970 .96 \quad 1 \quad 0.990 .920 .940 .950 .98$ $\quad 0$
H012.3T. $98610.690 .830 .850 .780 .760 .760 .760 .860 .880 .940 .920 .930 .950 .940 .960 .960 .970 .960 .930 .9310 .960 .970 .890 .890 .930 .94-]$ H009.2T.7308 $0.710 .860 .850 .8 \quad 0.780 .77 \quad 0.770 .860 .840 .930 .920 .920 .960 .930 .980 .960 .950 .940 .99110 .930 .970 .970 .930 .940 .910 .95 \quad 1]$ H006.2T.7307 $0.690 .830 .830 .780 .750 .750 .750 .860 .840 .910 .90 .90 .930 .910 .960 .950 .930 .92100 .990 .930 .970 .960 .920 .950 .910 .96-$

 H018.2T.7383 0.740 .880 .890 .830 .810 .810 .810 .840 .870 .970 .960 .960 .990 .980 .991100 .980 .980 .950 .960 .960 .950 .970 .920 .920 .920 .94$]$
 H036.2T.7443 $0.760 .92 \quad 0.90 .840 .840 .830 .820 .820 .860 .980 .990 .970 .99110 .960 .980 .970 .980 .910 .930 .940 .930 .950 .910 .9 \quad 0.90 .91$ H024.2T. 73840.760 .91 0.9 0.850 .830 .830 .820 .840 .860 .980 .980 .97 1 $0.990 .980 .990 .980 .980 .930 .960 .950 .940 .960 .920 .920 .910 .92-$

 H036.3T. 98640.780 .910 .930 .870 .840 .860 .850 .820 .86 H018.1RP. 118960.780 .770 .780 .720 .690 .7 0.7 0.95 1 $0.860 .840 .850 .860 .860 .870 .870 .880 .880 .840 .840 .88 \quad 0.860 .880 .810 .810 .840 .85$ H006.1RP. $118950.740 .740 .740 .680 .650 .660 .66 \quad 1 \quad 0.950 .820 .80 .810 .840 .820 .860 .840 .850 .840 .860 .860 .860 .880 .880 .820 .830 .840 .87$




H072.3T.9866 $0.880 .98100 .970 .940 .960 .950 .740 .780 .930 .930 .960 .9 \quad 0.9 \quad 0.880 .890 .880 .890 .830 .850 .850 .820 .840 .790 .790 .780 .79$ H072.2T.7445 $0.87110 .980 .960 .950 .940 .920 .740 .770 .910 .950 .940 .910 .920 .880 .880 .860 .880 .830 .860 .830 .820 .840 .8 \quad 0.810 .770 .79$ H120.1RP. $1189710.870 .88 \quad 0.9 \quad 0.9 \quad 0.9 \quad 0.9 \quad 0.740 .780 .780 .790 .810 .760 .76 \quad 0.740 .740 .730 .750 .690 .710 .690 .670 .690 .670 .680 .640 .65$


## value <br> $\begin{array}{llll}0.7 & 0.8 & 0.9 & 1.0\end{array}$

H003.3C. $95400.640 .920 .850 .840 .840 .860 .810 .770 .8 \quad 0.80 .910 .910 .910 .950 .930 .960 .980 .970 .950 .940 .960 .960 .960 .980 .950 .98 \quad 1$ H000.3C. 9539 H006.2C. 8988 H003.2C. 8987 H012.3C. 9543 H012.2C. 8990 0.6
 7
$\square$
$\square$
 H024.2C. 8992 H018.2C. 8991
 H009.3C. $95420.650 .910 .840 .840 .880 .890 .830 .8 \quad 0.820 .820 .950 .950 .940 .970 .960 .990 .99110 .970 .970 .990 .99100 .970 .970 .960 .97$ H006.3C. 9541
H009.2C. 8989 $0.660 .960 .880 .860 .850 .820 .740 .780 .790 .770 .940 .910 .870 .910 .890 .980 .970 .970 .960 .960 .950 .970 .960 .98 \quad 1 \quad 0.930 .95$ H036.3C. 99120.69 0.84 $0.80 .860 .880 .870 .80 .80 .820 .810 .960 .950 .920 .960 .941010 .990 .990 .980 .980 .980 .990 .990 .980 .980 .950 .96-1$

## dataType

 H048.3C.9913 $0.70 .820 .750 .790 .940 .980 .930 .860 .90 .910 .950 .98 \quad 1 \quad 0.980 .990 .920 .930 .940 .940 .940 .960 .950 .950 .890 .870 .910 .91 \quad-$
 H036.2C. 89930.750 .90 .830 .860 .940 .910 .850 .880 .90 .88 1 0.980 .950 .960 .960 .960 .940 .950 .980 .990 .970 .970 .960 .920 .940 .90 .91


 H120.3C. $99150.770 .690 .640 .680 .940 .97 \quad 1 \quad 0.930 .960 .980 .850 .90 .930 .890 .91 \quad 0.80 .810 .830 .830 .830 .86 \quad 0.830 .840 .770 .740 .810 .81$
 H072.2C. $89950.820 .790 .740 .78 \quad 1 \quad 0.970 .940 .940 .960 .950 .940 .970 .940 .910 .920 .880 .870 .88$ 0.9 0.920 .910 .90 .90 .840 .850 .830 .84 H018.1RP. $118960.780 .840 .95 \quad 1 \quad 0.780 .740 .680 .720 .730 .70 .860 .830 .790 .820 .810 .860 .840 .840 .870 .870 .860 .860 .850 .850 .860 .80 .84$ H006.1RP. $118950.740 .85 \quad 1 \quad 0.950 .74 \quad 0.70 .640 .680 .690 .660 .83 \quad 0.8 \quad 0.750 .790 .770 .860 .850 .840 .84 \quad 0.840 .830 .850 .8440 .860 .880 .810 .85$ ——


HOOO.2C.8986 0.62110 .850 .840 .790 .760 .690 .750 .750 .720 .90 .860 .820 .870 .840 .940 .920 .910 .930 .920 .910 .920 .910 .960 .960 .930 .92

H120.1RP. $1189710.620 .740 .780 .820 .760 .770 .860 .850 .820 .750 .750 .70 .680 .690 .660 .640 .650 .70 .720 .680 .680 .670 .640 .66 \quad 0.60 .6$


H036.3N. $98520.710 .830 .830 .870 .870 .860 .920 .750 .790 .80 .860 .840 .850 .840 .86 \quad 0.90 .910 .90 .970 .930 .930 .940 .950 .960 .980 .97 \quad 1$


H012.3N. $121090.670 .780 .77 \quad 0.8 \quad 0.80 .820 .860 .810 .820 .860 .910 .910 .920 .910 .920 .930 .930 .910 .920 .910 .910 .980 .98 \quad 1 \quad 0.970 .970 .96 \quad \mathrm{~L}$
H009.3N. $98480.630 .740 .730 .780 .790 .780 .840 .780 .780 .810 .860 .880 .880 .870 .890 .890 .880 .860 .920 .860 .870 .99110 .980 .950 .980 .95-$ $\square$

 H036.2N. $90050.690 .88 \quad 0.860 .840 .840 .850 .870 .680 .710 .860 .850 .870 .860 .92 \quad 0.930 .950 .970 .98 \quad 0.86 \quad 1 \quad 0.930 .88 \quad 0.860 .910 .96 \quad 0.9 \quad 0.93-$ H048.3N. $98530.750 .830 .820 .88 \quad 0.87 \quad 0.90 .940 .730 .770 .710 .780 .780 .780 .77 \quad 0.80 .820 .830 .83110 .860 .930 .90 .920 .920 .920 .92 \quad 0.97$ H024.2N. $90040.660 .840 .820 .780 .780 .820 .820 .710 .740 .910 .880 .910 .90 .950 .960 .980 .9910 .830 .980 .910 .880 .860 .910 .960 .88 \quad 0.9$ H018.2N. $90030.640 .820 .810 .780 .78 \quad 0.80 .820 .730 .750 .910 .90 .910 .910 .950 .950 .9910 .990 .830 .970 .890 .90 .880 .930 .960 .910 .91-\longrightarrow$ H012.2N. $90020.640 .80 .790 .750 .750 .790 .80 .760 .770 .930 .920 .930 .930 .960 .96 \quad 1 \quad 0.990 .980 .820 .950 .880 .910 .890 .930 .950 .90 .9$ H009.2N. $90010.630 .760 .730 .720 .710 .780 .760 .750 .750 .910 .890 .960 .930 .9910 .960 .950 .960 .8 \quad 0.930 .890 .910 .890 .920 .920 .860 .86$ H006.2N. $90000.610 .740 .72 \quad 0.7 \quad 0.70 .760 .740 .760 .740 .920 .90 .960 .94 \quad 1 \quad 0.990 .960 .950 .950 .770 .920 .870 .910 .870 .91 \quad 0.9 \quad 0.850 .84-1$ H003.3N. $98460.630 .720 .720 .690 .690 .760 .740 .820 .80 .930 .950 .97110 .940 .930 .930 .910 .90 .78 \quad 0.860 .850 .920 .880 .920 .890 .850 .85$ H003.2N. 8999
 HOOO.2N. 89980.580 .710 .710 .660 .660 .710 .690 .750 .74110 .970 .930 .930 .920 .910 .930 .910 .910 .710 .86 H018.1RP. $118960.780 .630 .640 .650 .630 .720 .70 .95110 .740 .790 .770 .8 \quad 0.740 .750 .770 .750 .740 .770 .710 .780 .790 .780 .820 .780 .780 .79$
H006.1RP. $118950.740 .59 \quad 0.6 \quad 0.6 \quad 0.590 .690 .66$

dataType Nucleus RP
replicate H072.3N. $98540.820 .930 .920 .960 .950 .96 \quad 1 \quad 0.660 .70 .690 .740 .740 .740 .740 .760 .80 .820 .820 .940 .870 .920 .830 .840 .860 .880 . .870 .92$ H072.2N. 9007 0.860.92 $0.90 .930 .89 \quad 0 \quad 0.960 .690 .720 .710 .730 .770 .760 .760 .780 .790 .80 .820 .90 .850 .950 .780 .780 .820 .830 .790 .86$ H168.3N. 9856 o.81 $0.960 .970 .99 \quad 0.890 .950 .590 .630 .66 \quad 0.70 .6770 .690 .770 .710 .750 .780 .780 .870 .840 .8440 .780 .790 .80 .840 .830 .87$ H120.3N. $98550 . .440 .970 .96 \quad 0.990 .930 .96 \quad 0.60 .650 .660 .70 .680 .690 .70 .720 .750 .780 .780 . .880 .840 .860 .770 .780 .80 .840 .820 .87$ H168.2N. $90090.820 .99+0.960 .970 .90 .920 .60 .640 .710 .730 .690 .720 .720 .730 .790 .810 .820 .820 .860 .840 .740 .730 .770 .820 .780 .83$
 H120.1RP. 1189710.830 .820 .840 .810 .860 .820 .740 .780 .580 .610 .610 .630 .610 .630 .640 .640 .660 .750 .690 .770 .630 .630 .670 .680 .650 .71


H048.2N. 9006 H036.3N. 9852 H024.3N. 9851 H018.3N. 9850 H009.3N. 9848 H012.3N. 12109 H006.3N. 9847 H048.3N. 9853 H024.2N. 9004 H018.2N. 9003 H012.2N. 9002 H009.2N. 9001 H006.2N. 9000 H003.3N. 9846 H003.2N. 8999 H000.3N. 9845 H000.2N. 8998 H072.3N. 9854 H072.2N. 9007 H168.3N. 9856 H120.3N. 9855 H168.2N. 9009 H120.2N. 9008 H 168.2 P
H 120.2 P H120.2P $00.580 .580 .590 .590 .60 .620 .640 .670 .740 .8 \quad 1$ H072.2P
 H048.2P $0.750 .760 .750 .760 .750 .770 .780 .78+0.80 .680 .670 .260 .260 .270 .25 \quad 0.330 .310 .320 .350 .330 .350 .320 .330 .340 .320 .320 .360 .350 .360 .330 .330 .340 .350 .310 .35$ H036.2P $0.750 .790 .790 .780 .820 .780 .81+0.780 .750 .680 .640 .240 .240 .250 .240 .310 .290 .330 .350 .340 .360 .330 .330 .330 .320 .320 .340 .350 .360 .340 .330 .330 .3440 .30 .34$





 H000.2P 10.830 .820 .820 .790 .780 .790 .750 .750 .70 .590 .580 .20 .210 .210 .20 .270 .250 .380 .40 .370 .390 .340 .340 .330 .310 .30 .310 .360 .350 .340 .320 .310 .310 .270 .3

time
















 H006.3T. 9859 H012.3T. 9861 H168.3T. 9868 H120.3T. 9867 H168.2T. 7447
 HO72.3T





 H036.2P $0.750 .790 .790 .780 .820 .780 .81 \quad 1 \quad 0.780 .750 .680 .640 .350 .360 .320 .290 .30 .290 .410 .420 .420 .40 .410 .390 .390 .410 .41 \quad 0.410 .4 \quad 0.4 \quad 0.410 .410 .420 .420 .420 .41$












H003.3T. $98580.80 .880 .890 .850 .860 .840 .85 \quad 0.90 .890 .970 .970 .950 .960 .960 .940 .940 .920 .930 .970 .970 .970 .990 .980 .970 .980 .98 \quad 1$ H003.2T.7306 $0.810 .890 .890 .860 .870 .860 .870 .880 .880 .970 .960 .950 .960 .950 .950 .940 .930 .920 .970 .970 .950 .970 .970 .980 .97 \quad 1$ H000.3T. $98570.780 .860 .870 .840 .840 .830 .840 .880 .880 .950 .950 .940 .940 .940 .930 .920 .910 .910 .950 .950 .960 .970 .970 .98 \quad 1 \quad 0.97$
 H009.3T. $121080.820 .910 .910 .880 .880 .870 .87 \quad 0.9 \quad 0.90 .980 .980 .970 .980 .980 .960 .960 .950 .950 .980 .980 .980 .9910 .960 .970 .970 .98$ H006.3T. $98590.810 .90 .910 .870 .870 .860 .870 .9 \quad 0.90 .980 .980 .960 .970 .970 .960 .960 .940 .940 .980 .980 .98$ 1 $0.990 .960 .970 .970 .99-7]$ H012.3T.9861 $0.830 .910 .920 .890 .890 .870 .880 .9 \quad 0.910 .980 .98 \quad 0.970 .980 .980 .970 .970 .950 .960 .970 .97 \quad 1 \quad 0.980 .980 .940 .960 .950 .97-1]$ H009.2T. $73080.820 .920 .920 .890 .890 .880 .890 .880 .880 .990 .970 .970 .980 .970 .960 .960 .950 .950 .98 \quad 1 \quad 0.970 .980 .980 .960 .950 .970 .97-]$ H006.2T.7307 $0.820 .9 \quad 0.910 .880 .880 .870 .880 .890 .890 .980 .960 .960 .970 .960 .950 .950 .940 .94 \quad 1 \quad 0.980 .970 .980 .980 .950 .950 .970 .97-$ H048.3T. $98650.880 .970 .980 .950 .950 .940 .940 .850 .880 .960 .970 .980 .970 .980 .980 .990 .9910 .940 .950 .960 .940 .950 .910 .910 .920 .93-$ H048.2T. $74440.880 .980 .970 .950 .950 .940 .940 .850 .880 .960 .970 .980 .970 .970 .990 .98 \quad 1 \quad 0.990 .940 .950 .950 .940 .950 .920 .910 .930 .92]$ H036.3T. $98640.870 .960 .960 .930 .940 .920 .930 .86 \quad 0.90 .980 .980 .980 .980 .990 .99110 .980 .990 .950 .960 .970 .960 .960 .920 .920 .940 .94$ H036.2T. $74430.870 .960 .960 .930 .930 .920 .920 .870 .90 .980 .980 .990 .980 .98 \quad 1 \quad 0.990 .990 .98 \quad 0.950 .960 .970 .960 .960 .930 .930 .950 .94$ H024.3T. $98630.850 .940 .950 .910 .920 .90 .910 .880 .910 .980 .990 .990 .98 \quad 1 \quad 0.98 \quad 0.990 .970 .98 \quad 0.960 .970 .980 .970 .980 .940 .940 .950 .96$ H018.2T. $73830.840 .940 .940 .910 .920 .90 .910 .870 .890 .990 .990 .99 \quad 1 \quad 0.980 .980 .980 .970 .970 .970 .980 .980 .970 .980 .950 .940 .960 .96-$ H024.2T. $73840.850 .950 .950 .930 .930 .920 .920 .870 .890 .990 .98 \quad 1 \quad 0.990 .990 .990 .980 .980 .980 .960 .970 .970 .960 .970 .940 .940 .950 .95-$ H018.3T. $98620.840 .930 .940 .90 .910 .890 .90 .890 .910 .98 \quad 1 \quad 0.980 .990 .990 .980 .980 .970 .970 .960 .970 .980 .980 .980 .950 .950 .960 .97-$ H012.2T.7309 $0.840 .930 .940 .910 .91 \quad 0.9 \quad 0.90 .890 .9 \quad 1 \quad 0.980 .990 .990 .980 .980 .980 .960 .960 .980 .990 .980 .980 .980 .960 .950 .970 .97$ 0
 H006.1RP. 118950.810 .810 .820 .790 .780 .770 .78110 .930 .890 .890 .870 .870 .880 .870 .860 .850 .850 .890 .880 .90 .90 .90 .870 .880 .880 .9 H168.3T. $98680.90 .960 .970 .980 .990 .98 \quad 1 \quad 0.780 .81 \quad 0.9 \quad 0.90 .920 .910 .910 .920 .930 .940 .940 .880 .890 .88 \quad 0.870 .870 .860 .840 .870 .85$
 H120.3T. $98670.910 .970 .980 .98 \quad 1 \quad 0.980 .990 .780 .820 .910 .910 .930 .920 .920 .930 .940 .950 .950 .88 \quad 0.890 .890 .870 .880 .860 .840 .870 .86$
 H072.3T. 98660.90 .98100 .980 .980 .970 .970 .820 .850 .940 .940 .950 .940 .950 .960 .960 .970 .980 .910 .920 .920 .910 .910 .870 .870 .890 .89 H072.2T.7445 0.9110 .980 .980 .970 .970 .960 .810 .850 .930 .930 .950 .940 .940 .960 .960 .980 .970 .90 .920 .910 .90 .910 .870 .860 .890 .88 H120.1RP. 11897 + $0.90 .90 .910 .910 .910 .90 .810 .860 .840 .840 .850 .840 .850 .870 .870 .880 .88 \quad 0.820 .820 .830 .810 .820 .790 .780 .81 \quad 0.8$
time

|  | H000 |
| :---: | :---: |
|  | H003 |
|  | H006 |
|  | H009 |
|  | H012 |
|  | H018 |
|  | H024 |
| J | H036 |
|  | H048 |
|  | H072 |
|  | H120 |
| L | H168 |

replicate
rep1
rep2
rep3


## value <br> 0.800 .850 .900 .951 .00



## time H000 H003 H006 H009 H012 H018 H024 H036 H048 H072 H120 H168

## dataType

 H048.3C. 9913 0.84 $0.820 .860 .970 .980 .950 .9220 .940 .940 . .880 .910 .92 \quad 1 \quad 0.970 .980 .980 .990 .960 .960 .970 .960 .960 .940 .940 .950 .920 .92$
 H000.2C. 8986 0.78 0.89 0.880 .860 .84 0.8 $0.840 .8440 .83 \quad 1 \quad 0.960 .950 .880 .920 .90 .920 .90 .940 .9440 .940 .950 .940 .950 .960 .940 .970 .97$


 H072.3C.9914 0.85 0.79 0.83 0.98 $+0.980 .940 .960 .960 .840 .880 .890 .980 .950 .970 .950 .970 .930 .940 .940 .920 .930 .910 .910 .920 . .880 .88$



H120.1RP. 11897 1 $0.810 .860 .890 .850 .860 .890 .890 .880 .780 .760 .790 .840 .860 .870 .820 .830 .840 .850 .820 .820 .810 .80 .810 .8 \quad 0.80 .81$


H048.3N. 98530.870 .960 .970 .940 .930 .920 .910 .830 .860 .850 .860 .890 .90 .890 .880 .940 .930 .940 .950 .960 .920 .920 .930 .950 .980 .971





H168
dataType
Nucleus
RP
replicate
rep1
rep2
rep3

 $\mathrm{H} 0 \mathrm{O} .2 \mathrm{P} 0.270 .280 .270 .280 .220 .230 .210 .240 .250 .240 .260 .250 .250 .240 .160 .160 .160 .160 .220 .20 .20 .210 .180 .180 .810 .61 \quad 1 \quad 0.720 .690 .60 .650 .870 .640 .530 .410 .4$ H048.2P 0.230 .250 .220 .240 .230 .220 .210 .230 .230 .220 .240 .230 .240 .240 .190 .180 .190 .190 .230 .210 .220 .230 .210 .210 .66100 .610 .620 .590 .590 .640 .610 .590 .670 .520 .52
 H072.3N. $98540.860 .850 .830 .830 .940 .910 .920 .90 .870 .880 .890 .90 .920 .920 .980 .970 .970 .950 .960 .940 .970 .970 .98 \quad 1$
 H048.3N. $98530.890 .880 .850 .860 .960 .920 .930 .920 .890 .90 .930 .940 .940 .950 .940 .930 .920 .910 .980 .950 .97 \quad 1 \quad 0.960 .970$ H048.2N. $90060.920 .9 \quad 0.880 .88 \quad 0.980 .960 .960 .940 .930 .940 .920 .980 .950 .940 .940 .930 .940 .920 .970 .97 \quad 1 \quad 0.970 .980 .970$ H036.2N. $90050.930 .910 .910 .890 .980 .980 .990 .970 .950 .950 .930 .940 .960 .960 .920 .920 .940 .920 .97 \quad 1 \quad 0.970 .950 .940 .94$ H036.3N. $98520.920 .920 .9 \quad 0.90 .980 .960 .960 .960 .980 .940 .960 .960 .970 .980 .930 .920 .920 .91 \quad 1 \quad 0.970 .970 .980 .940 .960$ H168.2N. $90090.840 .830 .820 .820 .9 \quad 0.89 \quad 0.9 \quad 0.880 .850 .860 .850 .850 .870 .880 .980 .980 .98$ 1 0.910 .920 .920 .910 .950 .950

 H120.3N. $98550.840 .830 .810 .810 .910 .890 .90 .880 .850 .860 .870 .870 .890 .9 \quad 1 \quad 0.990 .980 .980 .930 .920 .940 .940 .960 .980$ H018.3N. $98500.930 .930 .910 .910 .980 .960 .960 .960 .940 .950 .970 .980 .98 \quad 1 \quad 0.90 .90 .890 .880 .980 .960 .940 .950 .90 .920$ H012.3N. $121090.960 .950 .940 .940 .980 .970 .960 .970 .960 .970 .980 .99 \quad 1 \quad 0.980 .890 .88 \quad 0.88 \quad 0.870 .970 .960 .950 .940 .910 .92$ H009.3N. $98480.960 .940 .920 .980 .970 .960 .940 .960 .950 .960 .98 \quad 1 \quad 0.990 .98 \quad 0.870 .870 .860 .85 \quad 0.960 .940 .930 .940 .89 \quad 0.9$ H006.3N. $98470.970 .960 .940 .940 .960 .950 .940 .960 .960 .96 \quad 1 \quad 0.980 .980 .970 .870 .860 .860 .850 .960 .930 .920 .960 .880 .890$ H009.2N. $90010.980 .980 .950 .930 .980 .970 .970 .980 .99 \quad 1 \quad 0.960 .960 .970 .950 .860 .850 .870 .860 .940 .950 .940 .90 .890 .88$ H006.2N. $90000.980 .960 .960 .940 .980 .970 .970 .98 \quad 1 \quad 0.990 .960 .950 .960 .9440 .850 .840 .860 .850 .930 .950 .930 .890 .880 .870$ H012.2N. $90020.960 .950 .950 .940 .980 .990 .98 \quad 1 \quad 0.980 .980 .960 .960 .970 .960 .880 .870 .890 .880 .960 .970 .940 .920 .9 \quad 0.9$ H024.2N. $90040.950 .930 .930 .910 .980 .99 \quad 1 \quad 0.980 .970 .970 .9440 .940 .960 .960 .90 .890 .910 .90 .960 .990 .960 .980 .920 .920$ H018.2N. $90030.950 .940 .940 .920 .98 \quad 1 \quad 0.990 .990 .970 .970 .960 .950 .970 .960 .890 .880 .90 .990 .960 .980 .950 .920 .910 .91$ H024.3N. $98510.940 .930 .930 .92 \quad 1 \quad 0.980 .980 .98 \quad 0.960 .960 .960 .970 .980 .980 .910 .90 .910 .90 .980 .980 .960 .960 .920 .94$ $0.190 .210 .180 .150 .15 \quad 0.2 \quad 0.22 \quad 0.16 \quad 0.170 .24 \quad 0.220 .22$ 0.20 .210 .180 .160 .160 .210 .220 .160 .170 .250 .220 .22 0.220 .230 .210 .190 .190 .240 .250 .20 .210 .250 .210 .21 $\begin{array}{llllll}0.21 & 0.22 & 0.2 & 0.18 & 0.18 & 0.23 \\ 0.24 & 0.19 & 0.2 & 0.23 & 0.19 & 0.19\end{array}$ $0.20 .210 .20 .180 .180 .230 .230 .190 .20 .210 .160 .15-7$
 0.170 .190 .160 .130 .130 .180 .190 .140 .150 .220 .210 .21 170.190 .160 .130 .130 .180 .190 .140 .150 .230 .210 .21 $0.170 .180 .180 .130 .130 .180 .190 .14 \quad 0.150 .220 .220 .22$ .180 .190 .160 .14 0.14 0.18 .0 .190 .140 .150 .230 .220 .22 0.240 .240 .240 .220 .220 .260 .270 .230 .240 .220 .180 .17 240.240 .250 .230 .240 .280 .280 .240 .250 .220 .170 .16 0.240 .230 .250 .230 .240 .280 .280 .240 .250 .220 .160 .15
 H000.2N. $89980.960 .95+0.980 .930 .940 .930 .950 .980 .950 .940 .920 .940 .910 .810 .810 .830 .820 .90 .940 .880 .850 .840 .830 .220 .220 .270 .250 .250 .280 .270 .250 .260 .180 .130 .12$
 H003.2N. $8999+0.970 .960 .950 .9440 .950 .950 .960 .980 .980 .970 .950 .960 .930 .840 .930 .840 .840 .920 .930 .920 .890 .880 .860 .240 .230 .270 .250 .260 .290 .280 .260 .260 .020 .140 .13$

time
H000
H003 H006 H009 H012 H012
H018
 —] H072.2P $0.220 .230 .260 .260 .260 .280 .280 .260 .260 .260 .280 .250 .250 .250 .270 .280 .270 .260 .280 .280 .260 .250 .260 .250 .60 .670 .530 .540 .520 .510 .570 .540 .52 \quad 10.570 .58 \quad-$

 H024.2P 0.310 .320 .31 0.31 0.310 .31 0.3 0.3 0.32 0.320 .320 .320 .33 0.33 $0.280 .290 .290 .290 .280 .25 \quad 0.220 .220 .230 .22$ H018.2P 0.320 .320 .31 0.31 0.3 0.3 0.30 .290 .320 .320 .320 .330 .330 .330 .260 .280 .280 .280 .250 .240 .210 .210 .210 .21 H006.2P 0.290 .290 .270 .270 .260 .260 .250 .250 .280 .280 .280 .290 .30 .30 .220 .240 .230 .230 .20 .190 .170 .160 .170 .16 H003.2P 0.290 .30 .270 .270 .280 .260 .250 .250280 .280 .280 .290 .3 0.3 $0.220 .240 .240 .240 .2 \quad 0.2 \quad 0.17 .0 .160 .170 .17$ HOOO.2P 0.310 .310 .280 .280 .280 .280 .270 .260 .3 0.3 0.3 0.3 0.32 0.320 .240 .260 .250 .250 .220 .22 0.19 0.190 .190 .19
H048.2P 0.280 .270 .280 .280 .280 .280 .280 .270 .280 .280 .280 .280 .280 .280 .280 .280 .270 .270 .260 .250 .230 .220 .230 .220
H036.2P $0.270 .270 .280 .280 .280 .28 \quad 0.270 .270 .280 .28 \quad D \quad .280 .280 .280 .290 .260 .270 .260 .280 .240 .230210 .20 .210 .2$ H168.3C. 9916 0.83 $0.850 .890 .9 \quad 0.9 \quad 0.9 \quad 0.910 .910 .880 .880 .880 .860 .860 .860 .940 .940 .960 .930 .960 .960 .980 .980 .99$ H120.2C. $89960.840 .85 \quad 0.9 \quad 0.9 \quad 0.920 .910 .920 .920 .88 \quad 0.890 .890 .880 .870 .860 .940 .960 .940 .930 .970 .960 .970 .99 \quad 1 \quad 0.99$ H168.2C. $89970.840 .840 .890 .890 .9 \quad 0.90 .910 .90 .870 .880 .880 .870 .860 .850 .920 .930 .980 .910 .960 .940 .96 \quad 1 \quad 0.990 .98$ H120.3C. 9915 0.8 $0.850 .890 .890 .890 .9 \quad 0.9 \quad 0.920 .870 .870 .880 .840 .850 .860 .950 .940 .920 .940 .960 .98 \quad 1 \quad 0.950 .970 .98$ H072.3C. $99140.840 .880 .920 .930 .930 .940 .940 .950 .910 .910 .920 .880 .880 .890 .980 .970 .950 .970 .98 \quad 1 \quad 0.980 .940 .960 .96$ H072.2C. $89950.860 .870 .930 .930 .940 .940 .950 .940 .910 .920 .920 .90 .90 .890 .970 .980 .960 .95 \quad 1 \quad 0.980 .960 .980 .970 .960$








 H006.3C. $95410.950 .970 .980 .990 .980 .980 .970 .97 \quad 1 \quad 0.990 .990 .980 .980 .980 .940 .960 .950 .960 .910 .910 .870 .870 .880 .880$ H024.3C. 99110.920 .950 .980 .980 .980 .990 .98 1 0.970 .970 .980 .950 .950 .950 .980 .970 .980 .990 .940 .950 .920 .90 .920 .910 .27 H024.2C. $89920.940 .940 .990 .980 .990 .99 \quad 1 \quad 0.980 .970 .980 .980 .970 .960 .950 .980 .980 .990 .98 \quad 0.950 .94 \quad 0.90 .910 .920 .910 .27$ H018.3C. $95440.940 .960 .990 .990 .99 \quad 1 \quad 0.990 .990 .980 .980 .990 .970 .970 .960 .970 .970 .990 .980 .940 .940 .90 .90 .910 .90$ H018.2C. $89910.940 .950 .990 .98 \quad 1 \quad 0.990 .990 .980 .980 .980 .980 .970 .970 .960 .960 .970 .980 .970 .940 .930 .890 .90 .920 .9$

 H000.3C. $95390.96 \quad 1 \quad 0.960 .960 .950 .960 .940 .950 .970 .960 .960 .960 .970 .980 .91 \quad 0.910 .920 .930 .870 .88 \quad 0.850 .840 .850 .85$ H000.2C. $8986 \quad 1 \quad 0.960 .950 .940 .940 .940 .940 .920 .960 .960 .940 .970 .970 .950 .880 .90 .920 .90 .860 .840 .80 .840 .840 .83$

H024
H036
H048
H072
H120
H168

## dataType

 Cytoplasmicreplicate


 H048.2P $0.230 .230220 .210 .270 .20 .250 .260 .250 .250 .260 .250 .250 .250 .250 .270 .260 .260 .270 .280 .240 .250 .250 .280 .66 \quad 1 \quad 0.590 .610 .620 .590 .640 .610 .590 .670 .520 .52$
 H003.3T. $98580.880 .890 .850 .840 .860 .850 .970 .970 .950 .960 .960 .920 .960 .940 .940 .970 .990 .980 .970 .970 .970 .980 .98 \quad 1$
 H000.3T. $98570.860 .870 .840 .830 .840 .8440 .950 .950 .940 .940 .940 .910 .910 .930 .920 .960 .970 .970 .950 .950 .98 \quad 1 \quad 0.970 .980 .260 .250 .310 .30 .280 .28 \quad 0.30 .280 .290 .220 .16015$







 H048.3T. $98650.970 .980 .950 .940 .950 .940 .960 .970 .980 .970 .980 .99 \quad 1 \quad 0.980 .990 .960 .940 .950 .940 .950 .910 .910 .920 .980 .240 .250 .260 .230 .210210 .260 .220 .230 .260 .210 .21$, H048.2T. $74440.980 .970 .950 .940 .950 .940 .960 .970 .980 .970 .97 \quad 1 \quad 0.990 .990 .980 .950 .940 .950 .940 .950 .920 .910 .930 .920 .240 .250 .26 \quad 0.240 .220 .220 .270 .220 .230 .280 .210 .21$, H024.3T. $98630.940 .950 .910 .90 .920 .910 .980 .990 .990 .98 \quad 1 \quad 0.970 .980 .980 .990 .980 .970 .98 \quad 0.960 .970 .940 .940 .950 .960 .250 .260 .290 .260 .240 .240 .290 .250 .250 .250 .190 .18$



 H168.3T. $98680.960 .970 .980 .980 .99 \quad 1 \quad 0.9 \quad 0.90 .920 .910 .910 .940 .940 .920 .980 .880 .870 .870 .880 .890 .860 .840 .870 .850 .190 .20 .20 .180 .150 .150 .210 .160 .160 .240 .230 .23$


 H072.3T. $98660.98 \quad 1 \quad 0.980 .970 .980 .970 .940 .940 .950 .940 .950 .970 .980 .960 .960 .920 .910 .910 .910 .920 .870 .870 .890 .890 .220 .230 .23 \quad 0.20 .180 .180 .240 .190 .20 .280 .240 .23$ (W


 H018.3T.S862 Н018.2Т.7383 н ния
 H018.3N. 9850
H036.2T.7443
H036.2T.7443
H024.2T.7384
H036 3T. H 036.3 T .9864
H 036.3 N .0852 H036.3N. 9852
H036.3C. 9912 H036.3C. 9912
H024.3C. 9911 H024.3C. 9911
H036.2C.8993
H012.3C. 9543 H012.2C.85990 H018.3C. 9544 H024.2C.8992
H018.2C.8991 H024.2N. 9004 H012.2N. 9002
H036. 2 N .9005
$\qquad$ zewe owe wh co

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$$
\begin{aligned}
& \mathrm{H}, 72.2 \mathrm{~N} .9007 \\
& \mathrm{H} 072.3 \mathrm{~T} .9866
\end{aligned}
$$

$$
\begin{array}{r}
\mathrm{H} 072.3 \mathrm{~T} .9866 \\
\mathrm{H} 072.2 \mathrm{~T} .7445
\end{array}
$$

H048.3C. 9913
H048.2.8994
H009 2 T 7308
H009.2T.7308

## H006.2T.7307 H009.3T.12108

## H009.3T. 12108 H006. 3 T .9859

H006.3T.9858
H009.3N. 9848
H006.3N. 9847
H009.2C. 8989
H006.2C.8988
H009.3C.9542
H006.3C.9541
H003.2C.8987

| H003.2C.8987 |
| :--- |
| H003.3C.9540 |
|  |

$H 000.3 \mathrm{C} .9539$
H 000 .2С. 8986
H000. H 000.3 C .89856
H
H000.2T.7305
H003.3N. 9846
$H 003$
$H$
H003.2N. 8999
H003.3T. 9858
H003.3T.9858
$H 003.2 \mathrm{~T} .7306$
H009.2N. 9001
H006. 2 N .900
H006.2N. 9000
H000. N .9845
H000.2N. 8998
H072.3C 9914
$H 0722 \mathrm{C}$
H072.2C.8995
H168.2C.8997
H120.2C.8996
H120.2C.8996
H168.3C. 9916
H120.3C. 9915
H 168.3 N .9856
H120.3N. 9855
$H 168$
H




H168.3T.9868
H168.2T.7447
 К









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 7


dataType Zaytolasmic | Nutoplas |
| :--- |
| Totalaus |






## Extras

## Genomic regions - max 10 multimaps


uniquely mapped reads


## Genomic regions - continuous mapping - max 10 multimaps

primary alignments


## Genomic regions - split mapping - max 10 multimaps



## Genomic regions - continuous mapping

uniquely mapped reads


## Genomic regions - split mapping - max 10 multimaps

uniquely mapped reads



