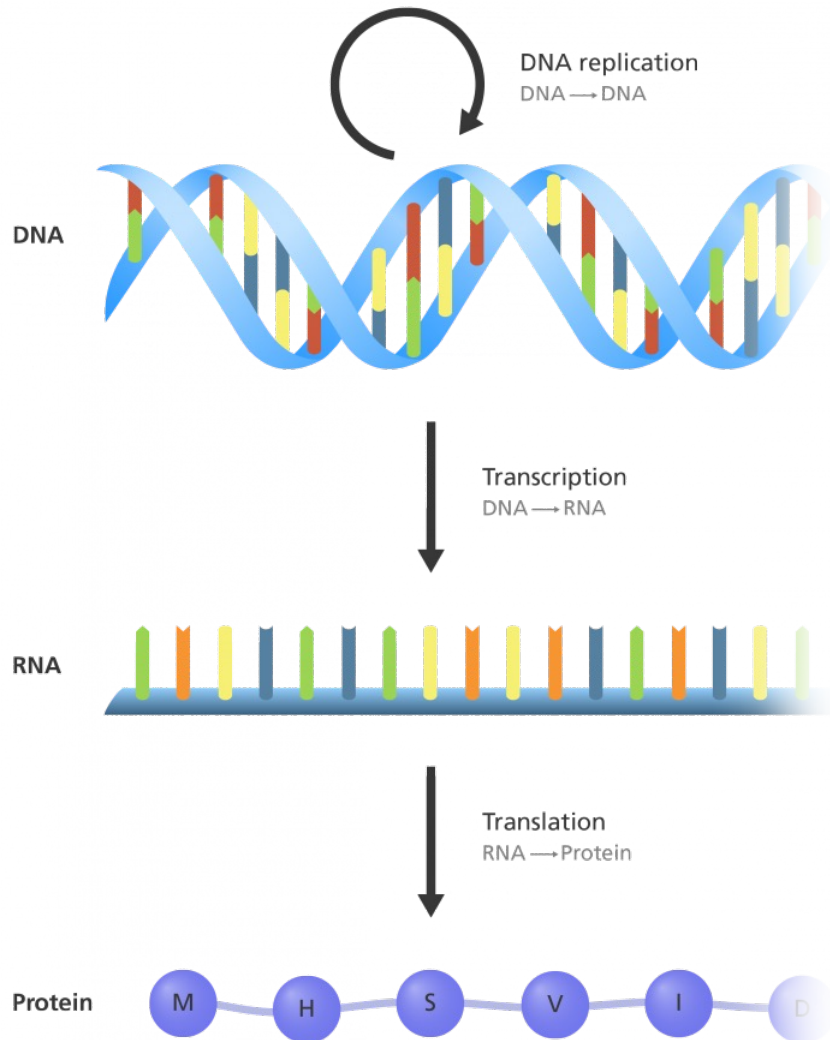


09:30-11:15 BST 10:30-12:15 CAT	13	Introduction to RNAseq analysis (45 min) Group exercise: Galaxy (both <u>RNAseq</u> & Mapping)
15 minutes		<b>Coffee Break</b>
11:30-12:30 BST 12:30-13:30 CAT	14	Transcriptomic/proteomic searches in <u>VEuPathDB</u>
1 hour		<b>Lunch Break</b>
13:30-15:15 BST 14:30-16:15 CAT	16	Orthology
15 minutes		<b>Tea Break</b>
15:30-16:45 BST 16:30-17:45 CAT		
16:45-17:30 BST 17:45-18:30 CAT	17	Catch-up

# Types of data in VEuPathDB

BIOLOGICAL PROCESS

ASSAY TECHNIQUE



RNA Sequencing  
Microarray

Ribosome profiling

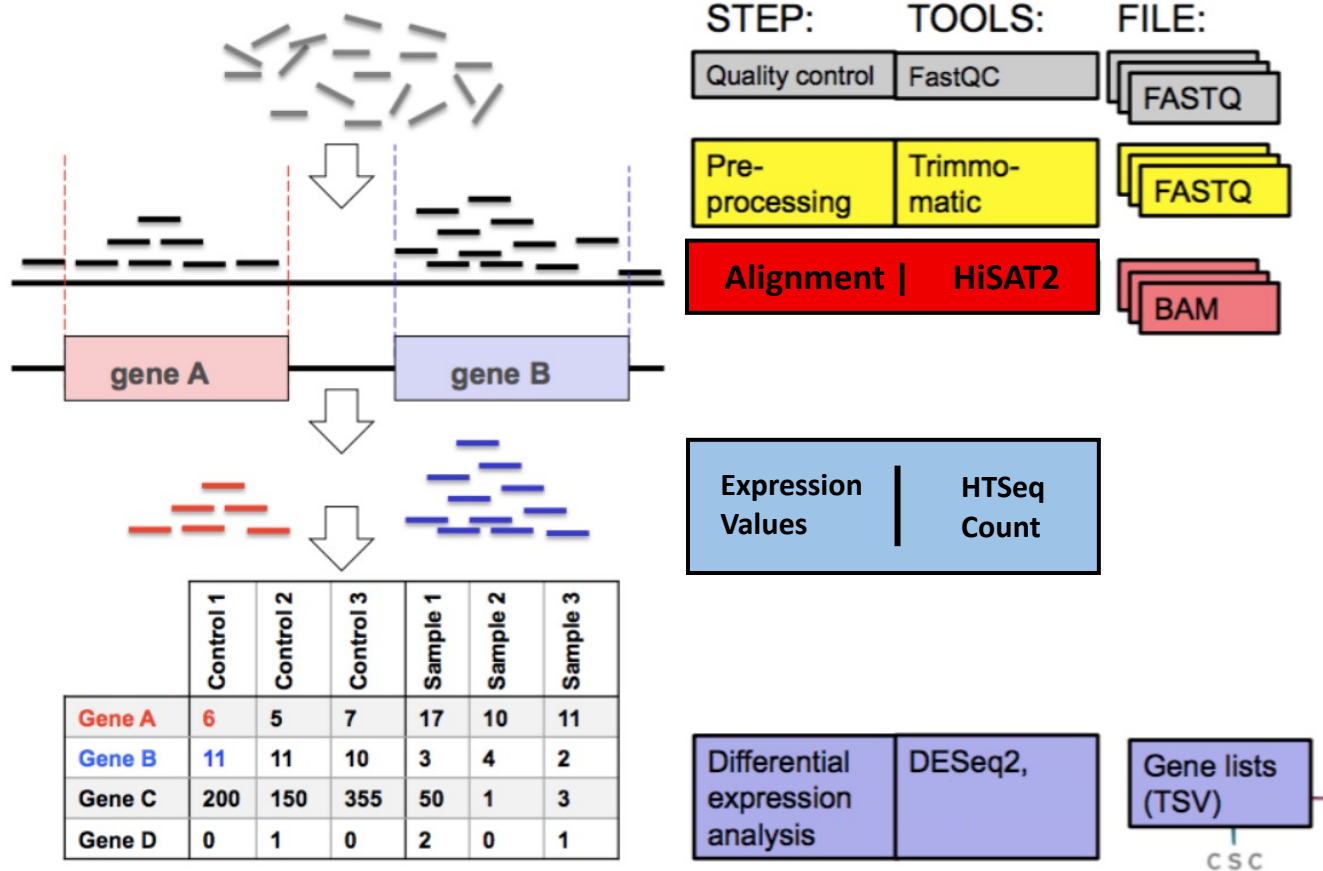
Proteomics  
peptides  
quantitative  
post trans modifications

# Prioritize data

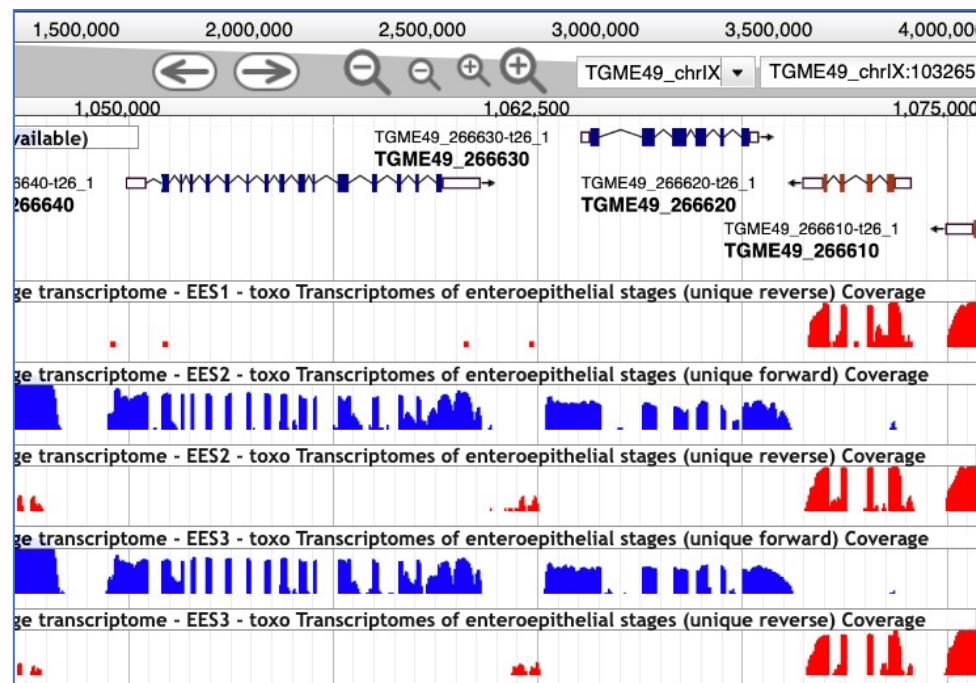
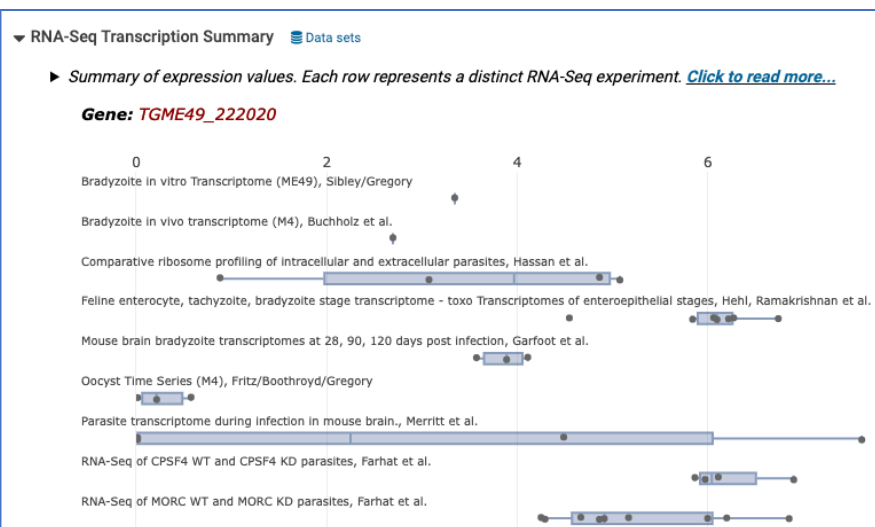
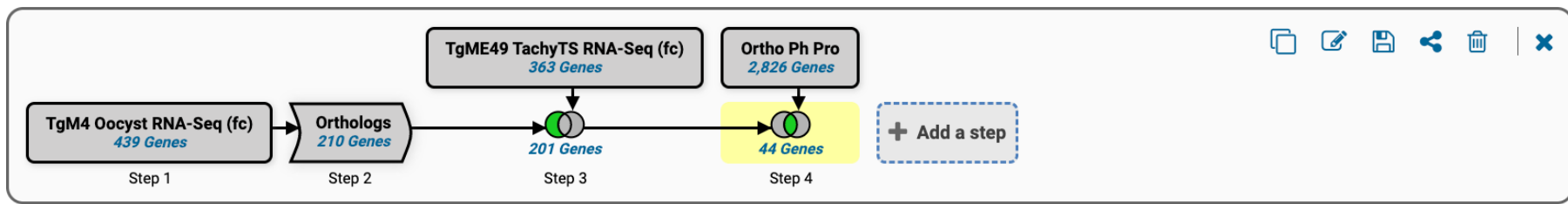
- Suggestions from researchers
- Publication
- Repository
  - SRA – <https://www.ncbi.nlm.nih.gov/sra>
  - ENA – <https://www.ebi.ac.uk/ena>
  - DDBJ – <https://www.ddbj.nig.ac.jp/dra/index-e.html>
  - ArrayExpress
  - ProteomeXchange
  - PRIDE

# RNA sequence analysis

- Standard workflows - compare across data sets
- determine expression levels
- TPM values



# VEuPathDB



# Proteomic analysis

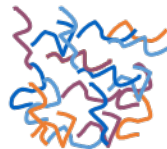
Protein of  
your sample

Protein  
mixture



*Chemical  
treatment*  
**→**  
*Digestion*

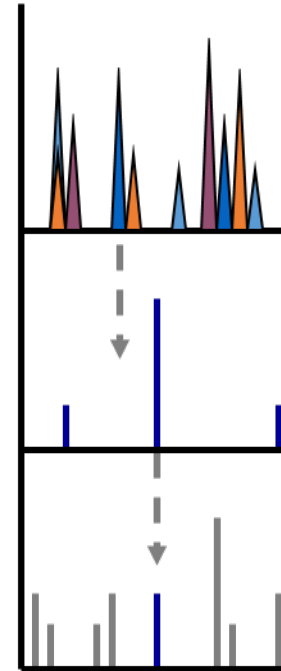
Peptide  
mixture



HPLC



MS

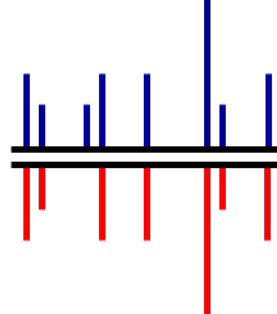


MS/MS

Database  
searching

*Correlation  
analysis*

Experimental

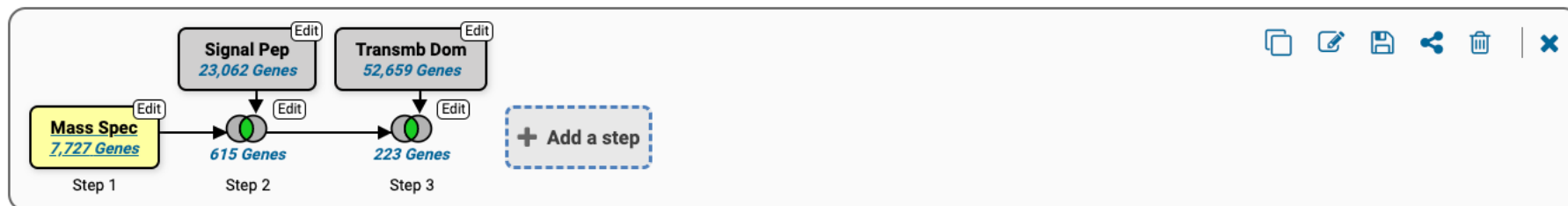


Theoretical

Identification of proteins

*Computational translation of MS/MS spectra to amino  
acid sequences using genomic or protein databases*

# VEuPathDB



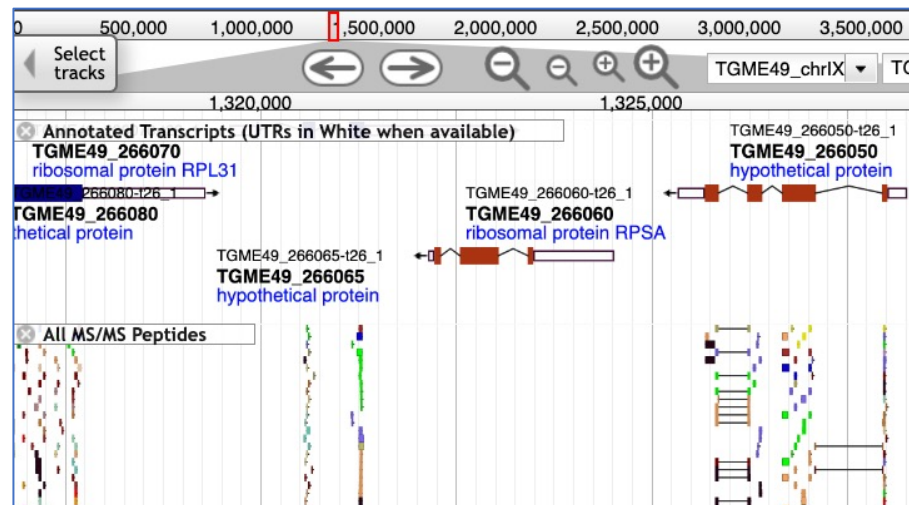
## 18 Proteomics

► Mass Spec.-based Expression Evidence [Data sets](#)

► Mass Spec.-based expression evidence in Protein Browser [Data sets](#)

▼ Post Translational Modifications [Download](#) [Data sets](#)

Experiment	Sample	Modification Type
Tachyzoite Intra- and Extracellular Lysine-Acetylomes (RH)	extracellular acetylome	acetylation site



# Exercise

## 6a\_Transcriptomics.pdf

- ▼ Genes
  - ▶ Annotation, curation and identifiers
  - ▶ Function prediction
  - ▶ Gene models
  - ▶ Genomic Location
  - ▶ Immunology
  - ▶ Orthology and synteny
  - ▶ Pathways and interactions
  - ▶ Phenotype
  - ▶ Protein features and properties
  - ▶ Protein targeting and localization
  - ▶ Proteomics
  - ▶ Sequence analysis
  - ▶ Structure analysis
  - ▶ Taxonomy
  - ▶ Text
- ▼ Transcriptomics
  - Q [Microarray Evidence](#)
  - Q [RNA-Seq Evidence](#)
  - Q [RT PCR Evidence](#)
  - Q [Single Cell RNA-Seq Evidence](#)
- ▶ Organisms
- ▶ Popset Isolate Sequences

## 6b\_Proteomics.pdf

- ▼ Genes
  - ▶ Annotation, curation and identifiers
  - ▶ Epigenomics
  - ▶ Function prediction
  - ▶ Gene models
  - ▶ Genetic variation
  - ▶ Genomic Location
  - ▶ Immunology
  - ▶ Orthology and synteny
  - ▶ Pathways and interactions
  - ▶ Phenotype
  - ▶ Protein features and properties
  - ▶ Protein targeting and localization
- ▼ Proteomics
  - Q [Mass Spec. Evidence](#)
  - Q [Post-Translational Modification](#)
  - Q [Quantitative Mass Spec. Evidence](#)
- ▶ Sequence analysis
- ▶ Structure analysis
- ▶ Taxonomy
- ▶ Text
- ▶ Transcriptomics
- ▶ Organisms