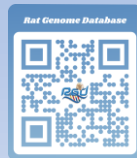


# Expansion of Rat Expression Data in the Rat Genome Database

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*20th annual Complex Trait Community | Rat Genomics Community meeting, 8-12 October 2023*



# Current Expression Data in RGD



## Summary

### Annotation

- RGD Manual Disease
- Imported Disease - ClinVar
- Imported Disease - CTD
- Imported Disease - MGI
- Imported Disease - OMIM
- Gene-Chemical Interaction
- Gene Ontology

### References

- References - curated
- PubMed References

### Genomics

- Comparative Map Data
- Variants
- miRNA Target Status
- QTLs in Region (mRatBN7.2)
- Markers in Region

### Expression

- RNA-SEQ Expression

### Sequence

- Nucleotide Sequences
- Reference Sequences
- Protein Sequences
- Reference Protein Sequences
- Protein Domains
- Protein Structures
- Transcriptome

### Additional Information

- External Database Links
- Nomenclature History
- RGD Curation Notes

## Gene: Gjb2 (gap junction protein, beta 2) Rattus norvegicus

### General Array IDs

**Symbol:** Gjb2  
**Name:** gap junction protein, beta 2  
**RGD ID:** 728891  
**Description:** Enables gap junction channel activity. Involved in several processes, including cellular response to glucagon stimulus; decidualization; and n projection, gap junction, and lateral plasma membrane. Used to study hepatocellular carcinoma and lung adenocarcinoma. Biomarker of aut urethral obstruction. Human ortholog(s) of this gene implicated in Bart-Pumphrey syndrome; Vohwinkel syndrome; autosomal dominant kera keratoderma-deafness syndrome. Orthologous to human GJB2 (gap junction protein beta 2); INTERACTS WITH 17alpha-ethynylestradiol, 1  
**Type:** protein-coding  
**RefSeq Status:** **VALIDATED**  
**Previously known as:** connexin 26; connexin e; connexin-26; Cx26; CXN-26; Cxne; gap junction beta-2 protein; gap junction channel protein connexin 26; gap jun

### RGD Orthologs



### Alliance Genes



### More Info

[more info ...](#)

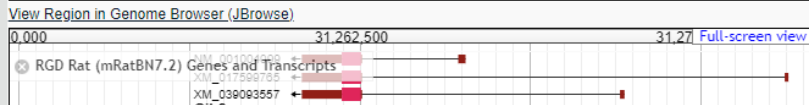
### Latest Assembly:

mRatBN7.2 - mRatBN7.2 Assembly

### Position:

Rat Assembly	Chr	Position (strand)	Source	Genome Browsers		UCSC Ensembl	
				JBrowse	NCBI		
<a href="#">mRatBN7.2</a>	15	31,260,390 - 31,278,222 (-)	NCBI	<a href="#">mRatBN7.2</a>	<a href="#">mRatBN7.2</a>		
mRatBN7.2 Ensembl	15	31,260,357 - 31,278,177 (-)	Ensembl		<a href="#">mRatBN7.2 Ensembl</a>		
UTH_Rnor_SHR_Utx	15	33,251,720 - 33,257,696 (-)	NCBI	<a href="#">Rnor_SHR</a>	<a href="#">UTH_Rnor_SHR_Utx</a>		
UTH_Rnor_SHRSP_BbbUtx_1.0	15	34,402,373 - 34,408,349 (-)	NCBI	<a href="#">Rnor_SHRSP</a>	<a href="#">UTH_Rnor_SHRSP_BbbUtx_1.0</a>		
UTH_Rnor_WKY_Bbb_1.0	15	32,660,503 - 32,666,480 (-)	NCBI	<a href="#">Rnor_WKY</a>	<a href="#">UTH_Rnor_WKY_Bbb_1.0</a>		
Rnor_6.0	15	37,377,313 - 37,394,494 (-)	NCBI	<a href="#">Rnor6.0</a>	<a href="#">Rnor_6.0</a>	<a href="#">rn6</a>	<a href="#">Rnor6.0</a>
Rnor_6.0 Ensembl	15	37,377,316 - 37,383,277 (-)	Ensembl	<a href="#">Rnor6.0</a>		<a href="#">rn6</a>	<a href="#">Rnor6.0</a>
Rnor_5.0	15	41,224,497 - 41,236,203 (-)	NCBI	<a href="#">Rnor5.0</a>	<a href="#">Rnor_5.0</a>	<a href="#">rn5</a>	<a href="#">Rnor5.0</a>
RGSC_v3.4	15	36,153,526 - 36,159,490 (-)	NCBI	<a href="#">RGSC3.4</a>	<a href="#">RGSC_v3.4</a>	<a href="#">rn4</a>	<a href="#">RGSC3.4</a>
RGSC_v3.1	15	36,169,226 - 36,175,190 (-)	NCBI				
Celera	15	30,972,813 - 30,978,777 (-)	NCBI		<a href="#">Celera</a>		
Cytogenetic Map	15	p12	NCBI				

### JBrowse:



# Current Expression Data in RGD

## RNA-SEQ Expression

High: > 1000 TPM value Medium: Between 11 and 1000 TPM  
 Low: Between 0.5 and 10 TPM Below Cutoff: < 0.5 TPM

	alimentary part of gastrointestinal system	circulatory system	endocrine system	exocrine system	hemolymphoid system	hepatobiliary system	integumental system	musculoskeletal system	nervous system	renal system	reproductive system	respiratory system	appendage
High													
Medium	2		27	21	6	21			34	23	3		
Low	1	20	22	20	13	20	3	4	38	12	27	11	3
Below cutoff		21	8				5	7	2		11		5

[View RNA-SEQ Expression Data](#)



# Current Expression Data in RGD

## RNA-SEQ Expression

High: > 1000 TPM value Medium: Between 11 and 1000 TPM  
 Low: Between 0.5 and 10 TPM Below Cutoff: < 0.5 TPM

	alimentary part of gastrointestinal system	circulatory system	endocrine system	exocrine system	hemolymphoid system	hepatobiliary system	integumental system	musculoskeletal system	nervous system	renal system	reproductive system	respiratory system
High												
Medium	2		27	21	6	21						

### Expression Data Report for gene Gjb2

[Download Expression Data](#)

Strain	Sex	Age	Tissue	Value	Unit	Assembly	Reference
F344/Nctr	female	14 days	adrenal gland	0.3	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 months	adrenal gland	0.2	TPM	Rnor_6.0	13506920
F344/Nctr	female	4 months	adrenal gland	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 years	adrenal gland	0.2	TPM	Rnor_6.0	13506920
F344/Nctr	male	14 days	adrenal gland	0.2	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 months	adrenal gland	0.4	TPM	Rnor_6.0	13506920
F344/Nctr	male	4 months	adrenal gland	0.3	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 years	adrenal gland	0.4	TPM	Rnor_6.0	13506920
F344/Nctr	female	14 days	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	4 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 years	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	14 days	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	4 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 years	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	14 days	heart	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 months	heart	0.2	TPM	Rnor_6.0	13506920
F344/Nctr	female	4 months	heart	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 years	heart	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	male	14 days	heart	0.2	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 months	heart	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	male	4 months	heart	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 years	heart	0.1	TPM	Rnor_6.0	13506920
F344/Nctr	female	14 days	kidney	29.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 months	kidney	46.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	4 months	kidney	56.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 years	kidney	53.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	14 days	kidney	31.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 months	kidney	44.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	4 months	kidney	47.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 years	kidney	56.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	14 days	lung	3.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 months	lung	5.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	4 months	lung	5.0	TPM	Rnor_6.0	13506920

all organ systems

### Expression Data Report for gene Gjb2

[Download Expression Data](#)

Strain	Sex	Age	Tissue	Value	Unit	Assembly	Reference
F344/Nctr	female	14 days	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	4 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	female	1 years	brain	6.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	14 days	brain	8.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	4 months	brain	7.0	TPM	Rnor_6.0	13506920
F344/Nctr	male	1 years	brain	7.0	TPM	Rnor_6.0	13506920
HotHsd:SD	male	11 embryonic days	brain	0.8	TPM	Rnor_6.0	14995488
HotHsd:SD	female	11 embryonic days	brain	0.8	TPM	Rnor_6.0	14995488
HotHsd:SD	female	14 days	brain	0.3	TPM	Rnor_6.0	14995488
HotHsd:SD	male	14 days	brain	0.3	TPM	Rnor_6.0	14995488
HotHsd:SD	female	1 months	brain	0.3	TPM	Rnor_6.0	14995488
HotHsd:SD	male	1 months	brain	0.3	TPM	Rnor_6.0	14995488
HotHsd:SD	male	13 embryonic days	forebrain	8.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	13 embryonic days	hindbrain	7.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	13 embryonic days	hindbrain	7.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	13 embryonic days	forebrain	8.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	14 embryonic days	brain	1.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	14 embryonic days	brain	1.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	14 embryonic days	forebrain	9.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	14 embryonic days	forebrain	9.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	15 embryonic days	brain	8.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	15 embryonic days	brain	8.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	15 embryonic days	forebrain	7.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	15 embryonic days	hindbrain	2.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	15 embryonic days	forebrain	7.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	15 embryonic days	hindbrain	2.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	16 embryonic days	forebrain	8.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	16 embryonic days	forebrain	8.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	17 embryonic days	forebrain	10.0	TPM	Rnor_6.0	14995488
HotHsd:SD	male	17 embryonic days	forebrain	10.0	TPM	Rnor_6.0	14995488
HotHsd:SD	female	18 embryonic days	hindbrain	8.0	TPM	Rnor_6.0	14995488

specific organ system



# Current Expression Data in RGD

Species	Study Source	# Studies	# Records
Human	EXPR-ATLAS	22	20,972
Rat	EXPR-ATLAS	3	313
Rat	GEO	4	448
Dog	GEO	1	75
Pig	EXPR-ATLAS	1	51
Vervet	EXPR-ATLAS	1	116

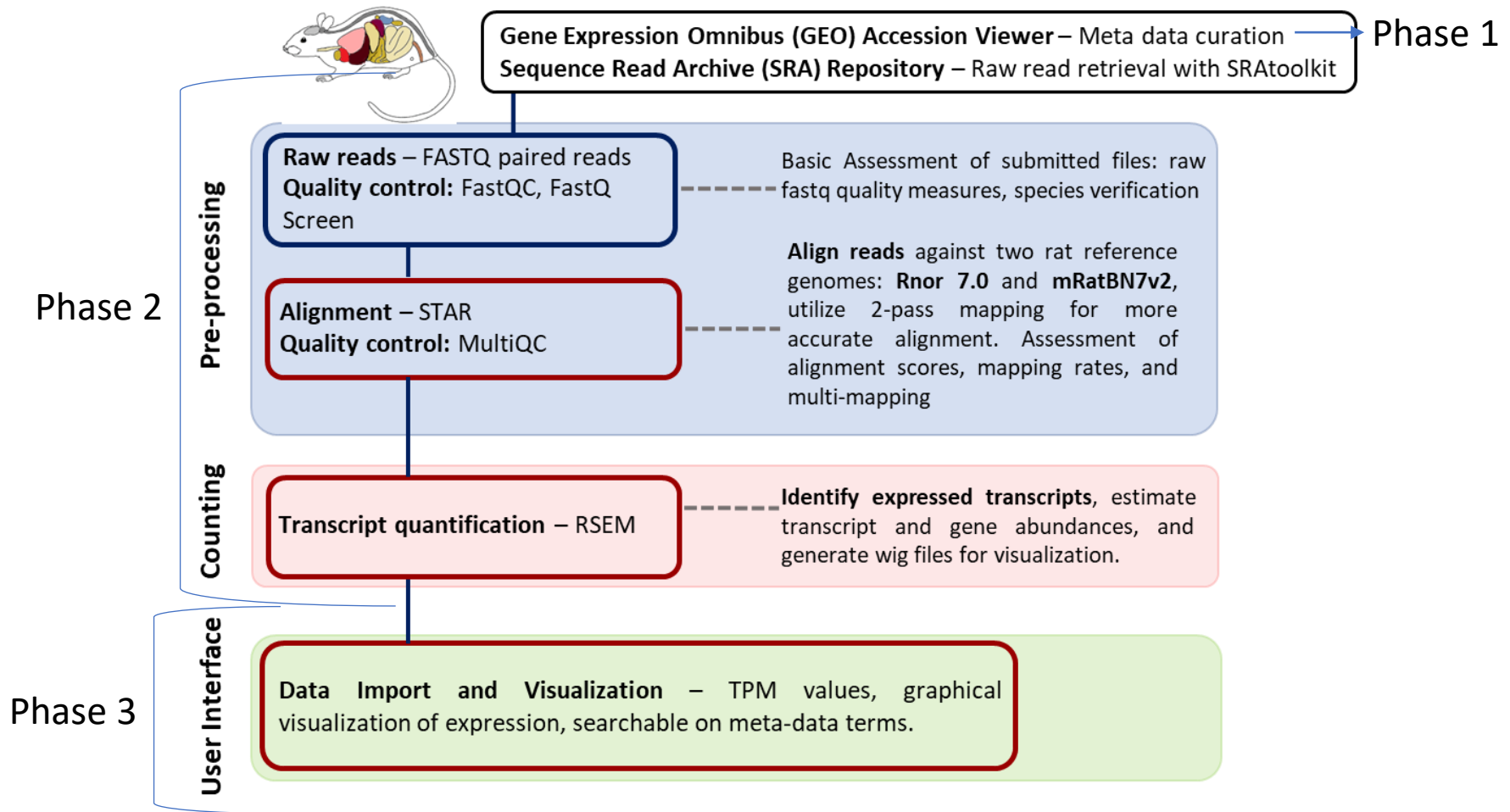
31 studies

21,975 records

Approximately 32,000 individual expression values per record



# Data Re-mapping



Dobin A, Davis C, Schlesinger F, Drenkow J, Zaleski C, Jha S, Batut P, Chaisson M, Gingeras T: **STAR: ultrafast universal RNA-seq aligner**. *Bioinformatics* 2012, Jan:29(1): 15-21

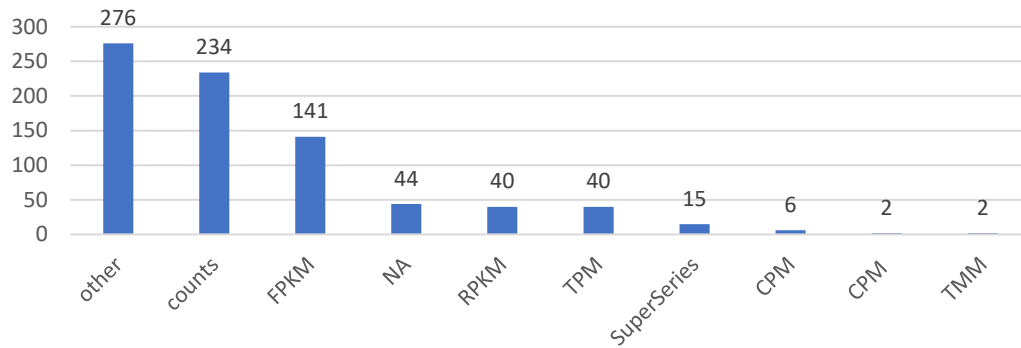
Li B, Dewey C: **RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome**. *BMC Bioinformatics* 2011 (12), 323



# GEO Rat Expression Accession Assessments

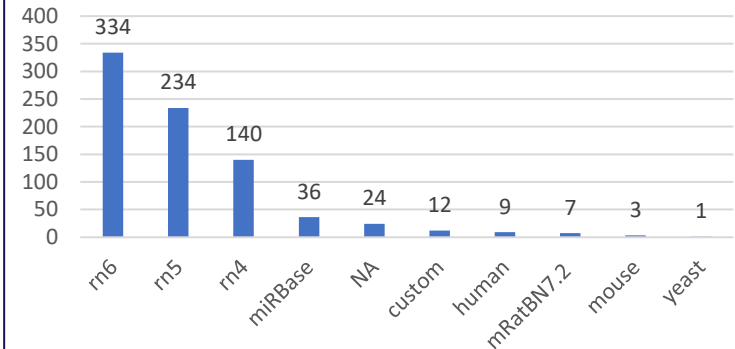
- 1,135 Rat Expression Studies imported to RGD Expression Curation Tool
- 800 studies reviewed

Data Types Reported in Submitted Data n=800

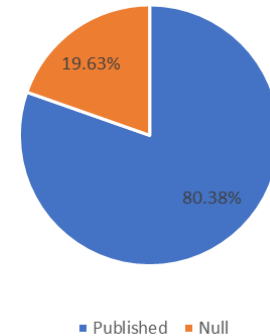


*Other*: Differential expression, methylation, UMI, etc.  
*SuperSeries*: multiple data types are often provided  
*NA*: unknown, conflicts from what is stated as submitted data type

Submitted Genome Assembly n=800



Rat Expression Data in GEO Publication



# Metadata Curation – Project Level

Geo Accession Id: GSE97047 Study Title: Wound regeneration deficit in rats correlates with low morphogenetic potential and distinct transcriptome profile of epidermis PubMed Id: 29317265 Select status: Loaded

**GEO**

PubMed Id: 29317265 **Pub Med IDs:**

Tissue: skin Tissue Id:  **Tissue Id:**

Vertebrate Trait Id:  **Vertebrate Trait Id:**

Clinical Measurement:  **Clinical Measurement:**

Strain: No strains imported! Strain Id:  **Strain Id:**

cellLine: No cell lines imported! cellLine Id:  **cellLine Id:**

cellType: No cell types imported! cellType Id:  **cellType Id:**  Culture Duration:

Age: **Age (in days) Low:**  Low:  **Age (in days) High:** 69 **Life Stage:**  embryonic  neonatal  weanling  juvenile  adult  aged

Sex:  Male  **Select Sex:**

Curator Notes:

**Experimental Conditions**

Experimental Condition 1 \*Accid: XCO:0000165 **Experimental Conditions**   
Ont Tree  
surgical manipulation

Min Value	Max Value	Unit	Min Dur	Max Dur	Application Method	*Ordinality	Notes
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/> secs	<input type="text"/> secs	<u>single full thickness excisional wound</u>	<input type="text"/>	<u>No wound dressing was applied</u>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/> secs	<input type="text"/> secs	<u>single full thickness excisional wound</u>	<input type="text"/>	<u>No wound dressing was applied</u>
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/> secs	<input type="text"/> secs	<input type="text"/>	<input type="text"/>	<input type="text"/>





# Metadata Curation – Project Level

**Geo Accession Id:** GSE97047      **Study Title:** Wound regeneration deficit in rats correlates with low morphogenetic potential and distinct transcriptome profile of epidermis      **PubMed Id:** 29317265      **Select status:** Loaded      **Update Status**

**Search:** skin epidermis      **View Samples**

**GEO**      **RGD**

**PubMed Id:** 29317265      **Pub Med IDs:**

**Tissue:** skin      **Tissue Id:** UBERON:0001003 skin epidermis **Ont Tree**

**Vertebrate Trait Id:** VT:0011025 skin ribonucleic acid amount **Ont Tree**

**Clinical Measurement:** CMO:0003932 epidermis ribonucleic acid level **Ont Tree**

**Strain:** No strains imported      **Strain Id:** RS:000681 SD **Ont Tree**

**cellLine:** No cell lines imported      **cellLine Id:**

**cellType:** No cell types imported      **cellType Id:** **Ont Tree**      **Culture Duration:**

**Age:**      **Age (in days) Low:** 55      **Age (in days) High:** 69      **Life Stage:**

embryonic     neonatal     weanling  
 juvenile     adult     aged

**Sex:** Select Sex: Male **Public Notes:**      **Curator Notes:**

**Experimental Conditions**      **Add Condition**

**Experimental Condition 1**      \*Accid      XCO:0000165 **Ont Tree**      surgical manipulation

Min Value	Max Value	Unit	Min Dur	Max Dur	Application Method	*Ordinality	Notes
			secs		single full thickness excisional wound	1	No wound dressing was applied

**Experimental Condition 2**      \*Accid      XCO:0000099 **Ont Tree**      control condition

Min Value	Max Value	Units	Min Dur	Max Dur	Application Method	*Ordinality	Notes
			secs			1	

**skin epidermis (UBERON:0001003)**  
 Annotations: Rat\_(0) Mouse\_(0) Human\_(0) Chinchilla\_(0) Bonobo\_(0) Dog\_(0) Squirrel\_(0) Pig\_(0) Naked Mole-rat\_(0) Green Monkey\_(0)

Parent Terms	Term With Siblings	Child Terms
<ul style="list-style-type: none"> <li>external integument</li> <li>outer epithelium</li> <li>skin of body</li> </ul>	<ul style="list-style-type: none"> <li>epidermal scale</li> <li>head external integument structure</li> <li>hyposcrotium</li> <li>limb external integument structure</li> <li>pad</li> <li>skin crest</li> <li>skin papilloma</li> <li>skin flap</li> <li>skin stand</li> <li>tail external integument structure</li> <li>Yemen's gland</li> <li>zone of skin</li> </ul>	<ul style="list-style-type: none"> <li>actinotrichium</li> <li>couplep gland</li> <li>dural limb integumentary appendage</li> <li>epidermal egg tooth</li> <li>epidermal intermediate stratum</li> <li>epidermal ridge of skin</li> <li>epidermal scale</li> <li>epidermal superficial stratum</li> <li>epidermis gland</li> <li>epidermis of feather</li> <li>follicle</li> </ul>

**NCBI**      **Gene Expression Omnibus**

**Accession Display**

**Scope:** List    **Format:** HTML    **Amount:** Full    **Geo Accession:** GSE97047

**Series GSE97047**      **Query Database for**

**Status:** Public on Jan 03, 2018

**Title:** Wound regeneration deficit in rats correlates with low morphogenetic and distinct transcriptome profile of epidermis

**Organisms:** Mus musculus; Rattus norvegicus

**Experiment type:** Expression profiling by high throughput sequencing

**Summary:** the report whole tissue transcriptomes from rat and mouse wounds rat inter-follicular epidermis

**Overall design:** Total RNA was isolated from adult rat and mouse whole tissue included rat and mouse wound dermis and wound epidermis collect after each detachment, the time point that coincides with a regeneration in mice, and vacuum suction isolated rat inter-follicular

**Laboratory:** Irvine PIH, Institute for Regenerative Medicine

**Citation(s):** Gweryn-Gratier CP, Adrienot A, Hurst R, Dang CT et al. Wound Regeneration Deficit in Rats Correlates with Low Morphogenetic and Distinct Transcriptome Profile of Epidermis. J Invest Dermatol 2018

**NH grant(s):**

Grant ID	Grant title	Affiliation
AR67273	Induction of rat regeneration in skin wounds by hair follicle signaling	The Regents of the University of California

**Submission date:** Mar 27, 2017  
**Last update date:** Mar 15, 2018

**Contact name:** Makim V Pilkus  
**Email(s):** mpil@uci.edu  
**Phone:** 949-924-1260

**Organization name:** University of California, Irvine  
**Department:** Developmental and Cell Biology  
**Street address:** 845 Health Sciences Road  
**City:** Irvine  
**State/province:** California  
**ZIP/Postal code:** 92697  
**Country:** USA

**Platforms (2):** GPL19057 Illumina NextSeq 500 (Mus musculus); GPL20084 Illumina NextSeq 500 (Rattus norvegicus)

**Samples (18) of 18:**

GSM2550441	Mouse_dermis_rep1
GSM2550442	Mouse_dermis_rep2
GSM2550443	Mouse_dermis_rep3
GSM2550444	Mouse_epidermis_rep1
GSM2550445	Mouse_epidermis_rep2
GSM2550446	Mouse_epidermis_rep3
GSM2550447	Rat_dermis_rep1
GSM2550448	Rat_dermis_rep2
GSM2550449	Rat_dermis_rep3
GSM2550450	Rat_epidermis_rep1
GSM2550451	Rat_epidermis_rep2
GSM2550452	Rat_epidermis_rep3
GSM2550453	Rat_epidermis_rep4
GSM2550454	Rat_IFE_rep1
GSM2550455	Rat_IFE_rep2
GSM2550456	Rat_IFE_rep3
GSM2550457	Rat_IFE_rep4
GSM2550458	Rat_IFE_rep5

**Relations:**

Bioproject	PRJNA380783
ISA	SRP125507

**Download family**

Format	
SOFT	SOFT
FASTQ	FASTQ
FASTQ	FASTQ
Series Matrix	Matrix
Series Matrix	Matrix

**Supplementary file**

File Type	Size	Download
GSE97047_Mouse_TPM.txt.gz	465.3 KB	(R) (H) TXT
GSE97047_Rat_TPM.txt.gz	384.0 KB	(R) (H) TXT

**SRX Run Selector**

Raw data are available in SRA  
 Download data from SRA using the SRA Toolkit



# Sample Level Curation

The screenshot shows the GEO database interface with a search bar at the top. Below the search bar, there are several columns for filtering and viewing samples. The columns include: GEO Sample ID, Sample Organization, Strain (Source), Strain ID (Curated), Cell Type (Source), Cell Type ID (Curated), Culture Duration (Curated), Cell Line (Source), Cell Line ID (Curated), Tissue (Source), Tissue ID (Curated), Vertebrate Trait ID (Curated), Chemical Measurement ID (Curated), Sex (Curated), Age (Source), Age in days (Low (Curated)), Age in days (High (Curated)), Life Stage (Curated), Public Notes, Curator Notes, Status/Action, and two columns for Acid 1 and Acid 2. The interface also includes a navigation menu with options like HOME, SEARCH, and SITE MAP, and a login status indicator.

**Sample GSM2550549**  
 Status: Public on Jan 03, 2018  
 Title: Rat\_dermis\_rep3  
 Sample type: SRA  
 Source name: Rat wound dermis  
 Organism: [Rattus norvegicus](#)  
 Characteristics: tissue: skin; tissue compartment: dermis; skin status: Skin wound; Stage: Scab detachment day 1  
 Extracted molecule: total RNA  
 Extraction protocol: Whole tissue was homogenized using Precellys with beta-mercapto ethanol to preserve RNA integrity using RNeasy micro kit as per manufacturer DNase treatment. Total RNA was eluted in optimal RIN scores were considered for library preparation. SMART-seq2 was performed on total RNA as desc 10 ng and 100 ng total RNA was used for RT. Result for 12 and 10 cycles, respectively and tagmentated 20 ng cDNA using the Nextera DNA Sample Fragments were amplified for 8 continuous cycles single-end (86bp and 43bp) on a NextSeq (Illumina).

**Sample GSM2550550**  
 Status: Public on Jan 03, 2018  
 Title: Rat\_epidermis\_rep1  
 Sample type: SRA  
 Source name: Rat wound epidermis  
 Organism: [Rattus norvegicus](#)  
 Characteristics: tissue: skin; tissue compartment: epidermis; skin status: Skin wound; Stage: Scab detachment day 1  
 Extracted molecule: total RNA  
 Extraction protocol: Whole tissue was homogenized using Precellys with beta-mercapto ethanol to preserve RNA integrity using RNeasy micro kit as per manufacturer's suggestion DNase treatment. Total RNA was eluted in optimal RIN scores were considered for library preparation. SMART-seq2 was performed on total RNA as desc 10 ng and 100 ng total RNA was used for RT. Result for 12 and 10 cycles, respectively and tagmentated 20 ng cDNA using the Nextera DNA Sample Fragments were amplified for 8 continuous cycles single-end (86bp and 43bp) on a NextSeq 500 II

**Sample GSM2550555**  
 Status: Public on Jan 03, 2018  
 Title: Rat\_IFE\_rep2  
 Sample type: SRA  
 Source name: Rat inter-follicular epidermis  
 Organism: [Rattus norvegicus](#)  
 Characteristics: tissue: skin; tissue compartment: epidermis; skin status: Normal skin; Stage: Adult

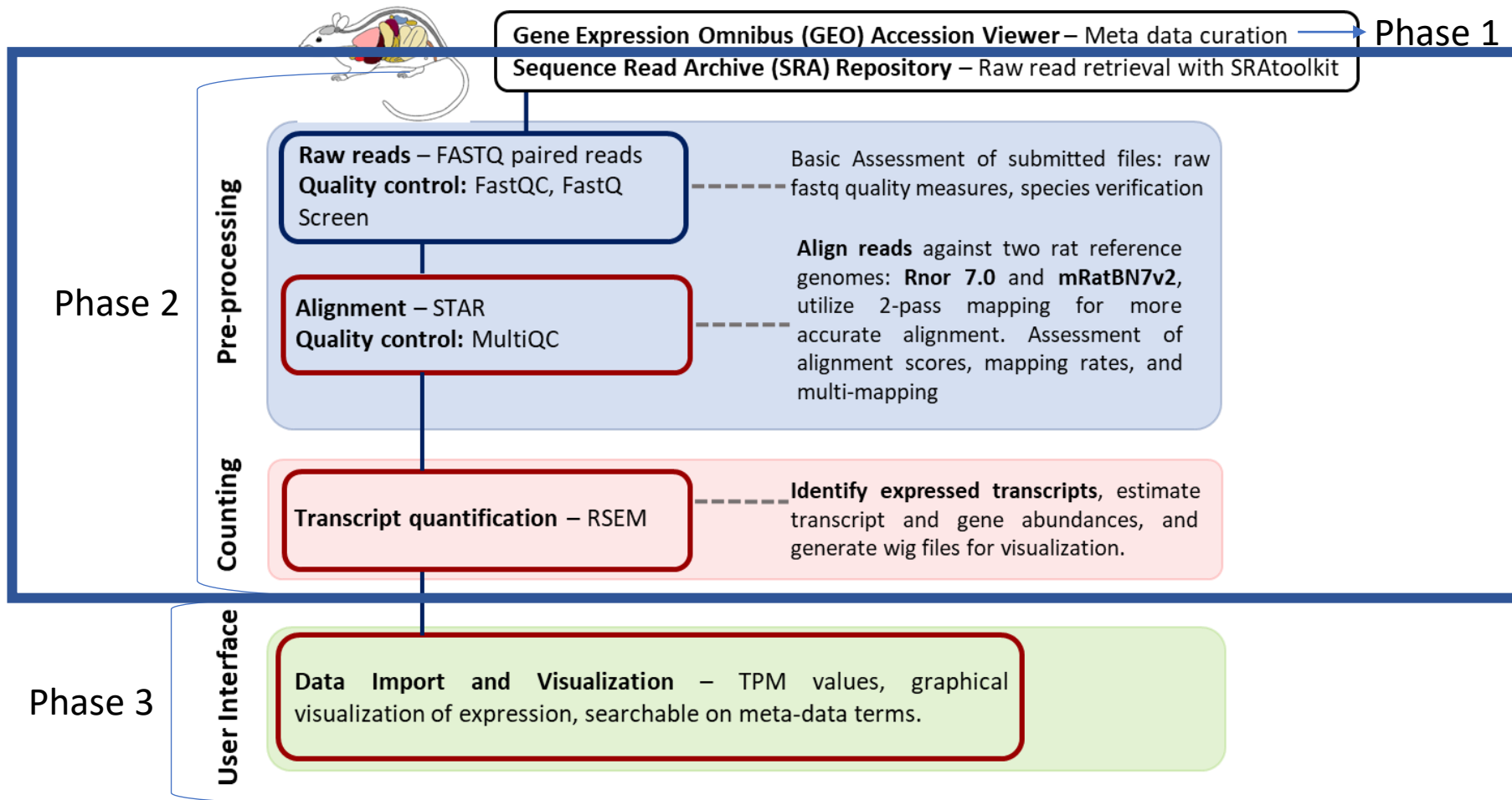
Load Samples



# Summary of Curation Status

- Metadata for 101 studies have been loaded to the database via the new Expression Curation Tool.
- 529 categorized for future curation.
- 24 categorized not for curation (due to lack of information or species).
- We have notified GEO of 15 publications that are associated with GEO Accession IDs but not displayed on the interface.
- We have connected to 21 authors for data clarifications on aspects such as strain, data type, sample to experimental condition relationship.

# Data Re-mapping

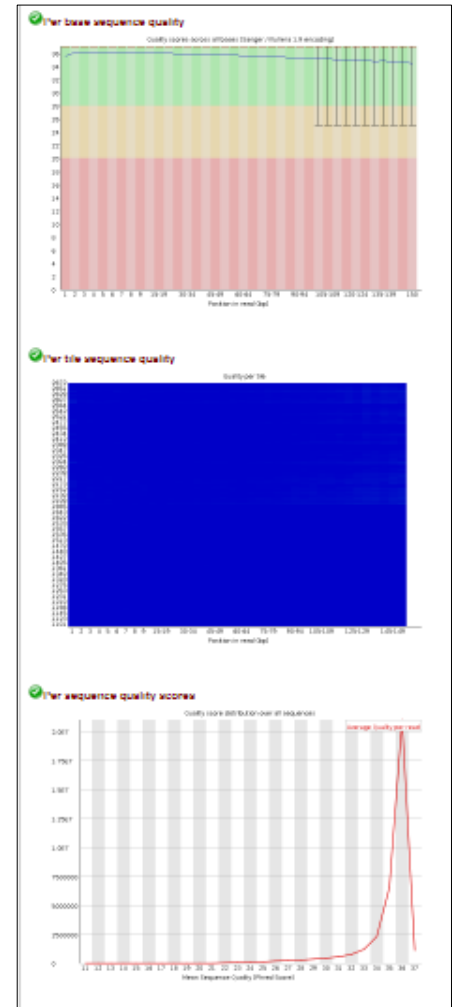
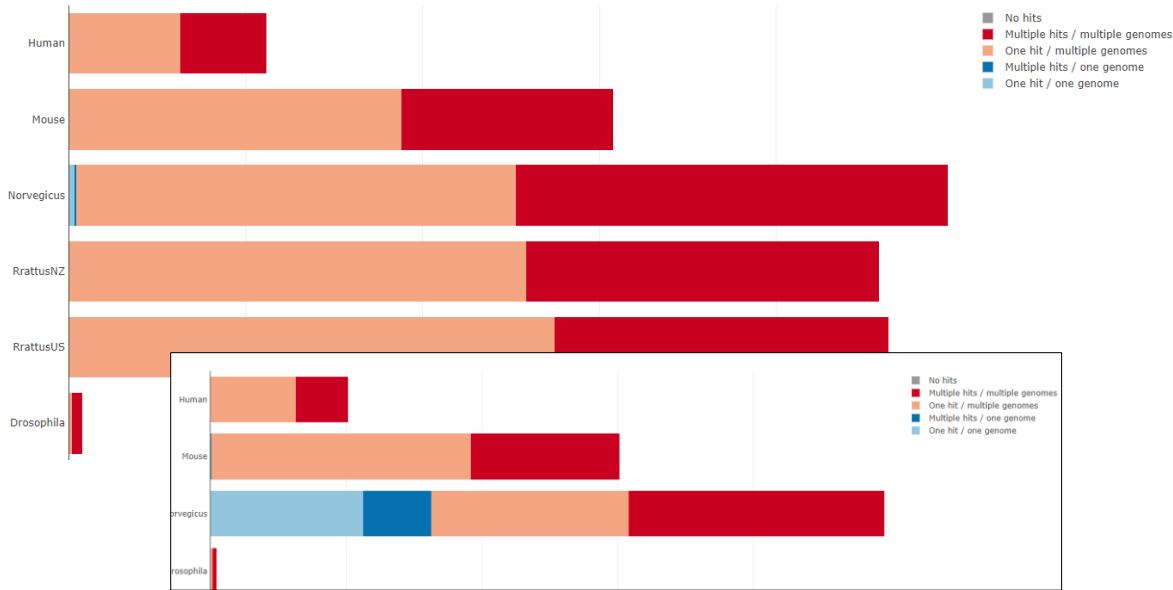


Dobin A, Davis C, Schlesinger F, Drenkow J, Zaleski C, Jha S, Batut P, Chaisson M, Gingeras T: **STAR: ultrafast universal RNA-seq aligner**. *Bioinformatics* 2012, Jan:29(1): 15-21

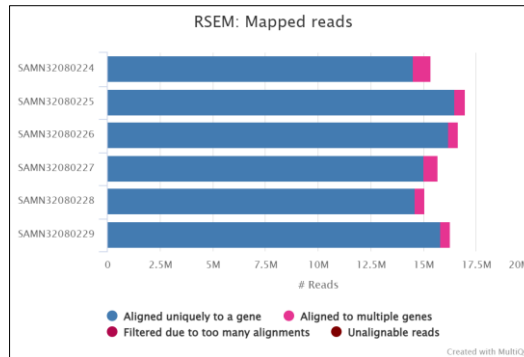
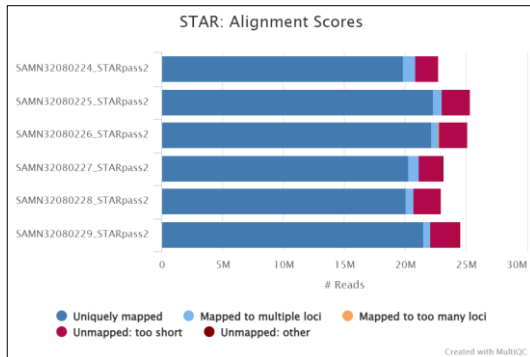
Li B, Dewey C: **RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome**. *BMC Bioinformatics* 2011 (12), 323



# Data Remapping QC



Wingett SW and Andrews S. **FastQ Screen: A tool for multi-genome mapping and quality control [version 2; referees: 4 approved].** *F1000Research* 2018, 7:1338



Andrews S. **FastQC: a quality control tool for high throughput sequence data.** 2010.

Available from:

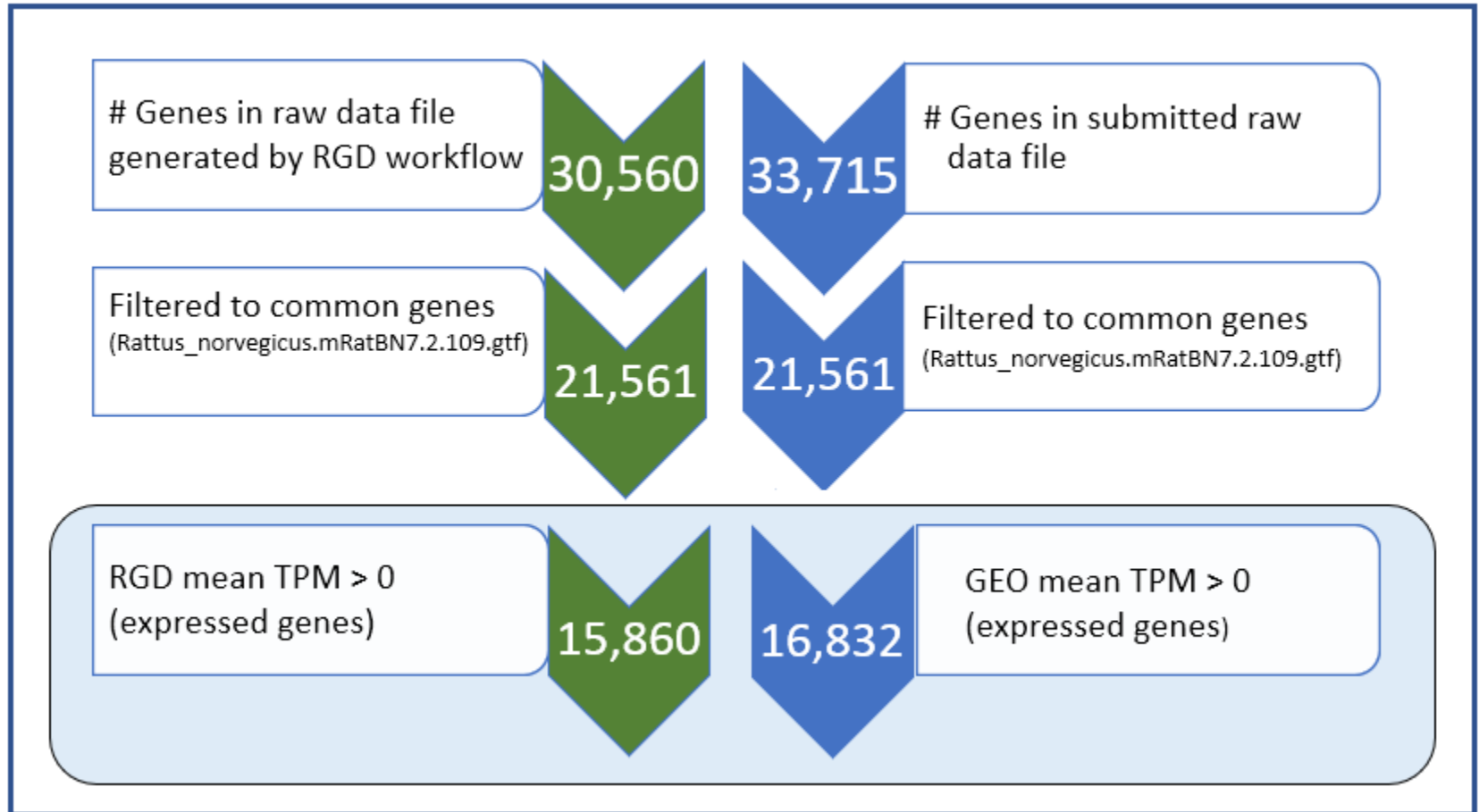
<https://www.bioinformatics.babraham.ac.uk/projects/fastqc>

Ewels P, Magnusson M, Lundin S, Källér M: **MultiQC: Summarize analysis results for multiple tools and samples in a single report.** *Bioinformatics* (2016)

Contact us: <https://rgd.mcw.edu/rgdweb/contact/contactus.html>



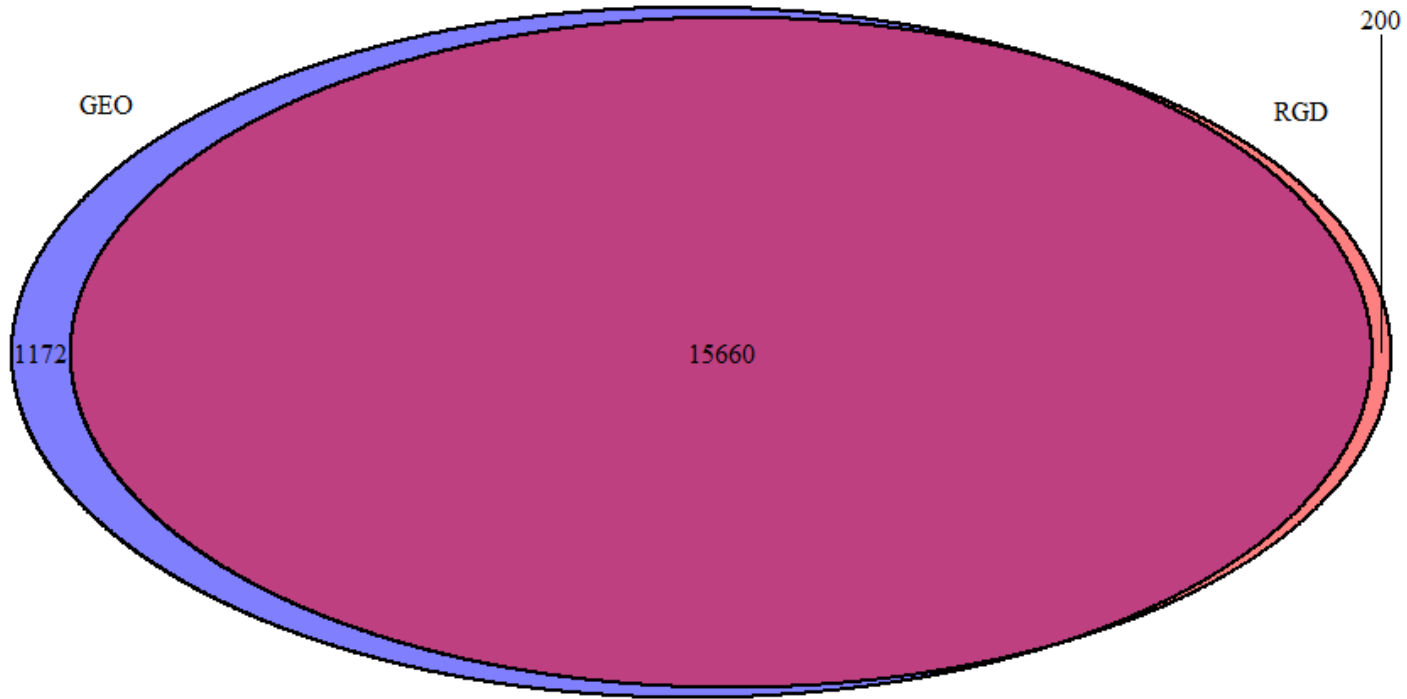
# Data Re-mapping Evaluation



Li X: GSE220261 Available from: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE220261>



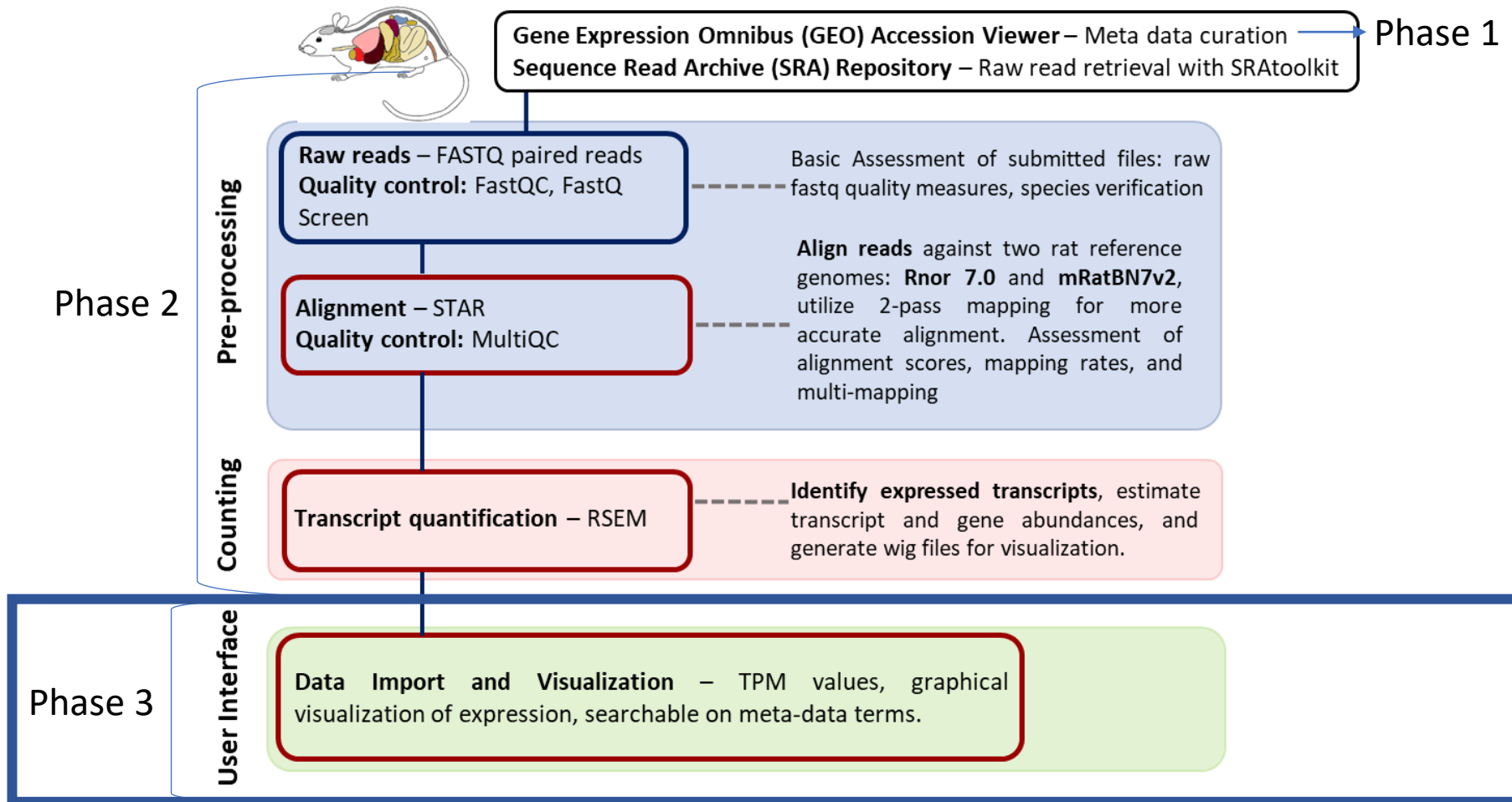
# Data Re-mapping Evaluation



Li X: GSE220261 Available from: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE220261>



# Data Re-mapping



Dobin A, Davis C, Schlesinger F, Drenkow J, Zaleski C, Jha S, Batut P, Chaisson M, Gingeras T: **STAR: ultrafast universal RNA-seq aligner**. *Bioinformatics* 2012, Jan:29(1): 15-21

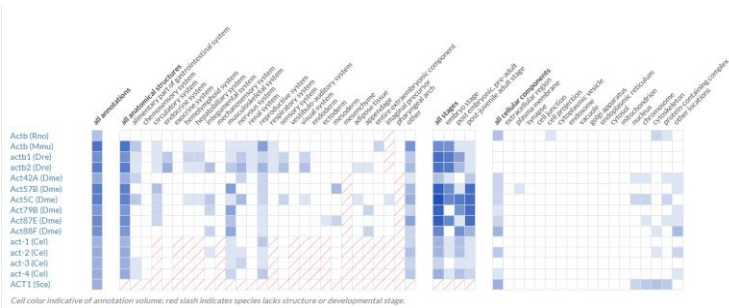
Li B, Dewey C: **RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome**. *BMC Bioinformatics* 2011 (12), 323





# JBrowse2

JBrowse 2 developed by The JBrowse Consortium (<https://jbrowse.org/>; <https://github.com/GMOD/jbrowse-components>)



<https://www.alliancegenome.org/gene/RGD:628837/#expression>



# Acknowledgments

## Rat Genome Database

Principal Investigator  
Anne Kwitek, PhD

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Jennifer Smith, MSc

Research Scientists and Curators  
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Tom Hayman, PhD  
Mary Kaldunski, BSc  
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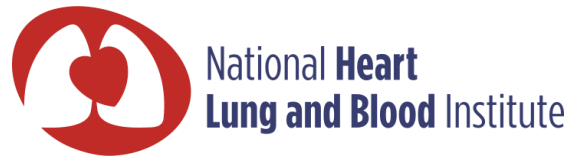
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## We gratefully acknowledge our funders:

*RGD is funded by the National Heart, Lung, and Blood Institute (NHLBI; R01HL064541), and the National Human Genome Research Institute (NHGRI) as part of the Alliance of Genome Resources (U24HG010859).*

And to the researchers who contribute data and faithfully use our website and data!



# Thank you



Special CTC-RG meeting attendee  
deadline extension is October 13<sup>th</sup>,  
2023

Please send your high-resolution  
images to  
[RGD.Community@mcw.edu](mailto:RGD.Community@mcw.edu)

