

R & OMICS

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Table of contents

About	3
1 How to use this resource	4
2 Required Data	5
3 Reading and Writing files in R	6
3.1 data.table::fread	
.	6
3.2 data.table::fwrite	
.	6
4 Exploring data in R	7
4.1 using 'str'	7
4.2 using 'skimr::skim'	8
5 Basic dplyr operations on data columns	10
5.1 'dplyr::select'	
.	11
5.2 dplyr::rename / dplyr::rename_with	15
5.3 dplyr::relocate	16
6 Basic dplyr operations on data rows	18
6.1 dplyr::filter	18
6.2 dplyr::arrange	20
6.3 dplyr::mutate / dplyr::case_when	22
7 Combining 'dplyr' functions	24
8 Working with grouped data	25
8.1 dplyr::add_count / dplyr::count	25
References	42

About

This is a Quarto book to impress Jonathan.

This web resource covers basic *R* operations on gene expression tables such as data reading/writing, exploring wrangling and plotting. It is largely based on *R tidyverse* package and can be useful for Next Generation Sequencing functional data analysis.

The resource was created and is being maintained by Jordan RAMIŁOWSKI, Associate Professor at the [Bioinformatics Laboratory](#) at Yokohama City University.

1 How to use this resource

Download the data and practice independently in RStudio using examples shown here.

2 Required Data

- Download the data directory from Dropbox (link to come)
- `setwd()`
- Install and load all required *R* packages

```
setwd('/Users/jordan/R_in_OMICS/input') # example  
library(data.table)
```

3 Reading and Writing files in *R*

3.1 data.table::fread

Simple and efficient way of reading R files:

```
library(data.table)
data = fread(file = 'connectome_1in.tsv')
data = fread(file = 'connectome_1in.tsv', nThread = 4) # can use many processors 'nThread'
```

‘fread’ vs ‘read.delim’(base) speed

```
# 'fread':
t0 = Sys.time()
data = fread(file = 'connectome_1in.tsv')
t1 = Sys.time()-t0

# 'read.delim':
t0 = Sys.time()
data = read.delim2(file = 'connectome_1in.tsv')
t2 = Sys.time()-t0
```

```
[1] "fread: Time difference of 0.18643 secs"
```

```
[1] "read.delim: Time difference of 4.577949 secs"
```

3.2 data.table::fwrite

Simple and efficient way of writing R files:

```
fwrite(data, file = 'connectome_1out.csv') # csv file (default)
fwrite(data, file = 'connectome_1out.tsv', sep = '\t') # tab-delim file (own specification)
```

4 Exploring data in R

```
library(data.table)
```

Read in and look at first 10 columns of **connectome** data set:

```
connectome_1=fread(file='connectome_1in.tsv', select = 1:10) # first 10 columns
```

```
dim(connectome_1) # number of rows / columns
```

```
[1] 17263    10
```

```
colnames(connectome_1) # names of data
```

```
[1] "ApprovedSymbol"      "Localization"      "Taxon"
[4] "F5_min"              "F5_med"            "F5_max"
[7] "Adipocyte Breast"    "Adipocyte Omental" "Adipocyte Perirenal"
[10] "Adipocyte Subcutaneous"
```

Closer look using specific *R* packages/functions:

4.1 using 'str'

```
str(connectome_1)
```

Classes 'data.table' and 'data.frame': 17263 obs. of 10 variables:

```
$ ApprovedSymbol      : chr  "A1BG" "A1CF" "A2M" "A2ML1" ...
$ Localization        : chr  "secreted" "multiple" "multiple" "secreted" ...
$ Taxon               : chr  "Eutheria" "Deuterostomia" "Euteleostomi" "Euteleostomi" ...
$ F5_min              : num  0.264 0 0 0 0 ...
```

```

$ F5_med          : num  16.94 0 1.21 0 9.72 ...
$ F5_max          : num  2378 153 1515 206 80 ...
$ Adipocyte Breast : num  36.8 0 90.3 0 24.4 ...
$ Adipocyte Omental : num  35.2 0 121.4 0 10.8 ...
$ Adipocyte Perirenal : num  49.7 0 50.6 0 17.4 ...
$ Adipocyte Subcutaneous: num  41.1 0 63.4 0 27.7 ...
- attr(*, ".internal.selfref")=<externalptr>

```

4.2 using ‘skimr::skim’

```

library(skimr)
skimr::skim(connectome_1)

```

Table 4.1: Data summary

Name	connectome_1
Number of rows	17263
Number of columns	10
Key	NULL
Column type frequency:	
character	3
numeric	7
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
ApprovedSymbol	0	1	1	10	0	17263	0
Localization	0	1	3	15	0	7	0
Taxon	0	1	0	16	614	17	0

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
F5_min	0	1	3.88	17.74	0	0.00	0.00	2.55	1451.39	
F5_med	0	1	32.14	154.02	0	0.03	5.94	22.71	6876.78	

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
F5_max	0	1	476.92	4237.26	0	23.85	75.89	211.27	309580.87	
Adipocyte	0	1	47.49	304.12	0	0.11	6.73	26.99	12064.67	
Breast										
Adipocyte	0	1	51.19	479.86	0	0.05	6.70	26.77	48575.26	
Omental										
Adipocyte	0	1	54.70	661.88	0	0.00	6.11	25.30	75911.77	
Perirenal										
Adipocyte	0	1	46.69	259.45	0	0.09	5.78	25.00	10252.56	
Subcutaneous										

5 Basic dplyr operations on data columns

```
-- Attaching packages ----- tidyverse 1.3.2 --
v ggplot2 3.3.6      v purrr   0.3.4
v tibble  3.1.8      v dplyr  1.0.9
v tidyr   1.2.0      v stringr 1.4.0
v readr   2.1.2      v forcats 0.5.1
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::between()   masks data.table::between()
x dplyr::filter()    masks stats::filter()
x dplyr::first()     masks data.table::first()
x dplyr::lag()       masks stats::lag()
x dplyr::last()      masks data.table::last()
x purrr::transpose() masks data.table::transpose()

      : 'magrittr'

      'package:purrr'      :

set_names

      'package:tidyr'      :

extract

# the entire data has 17,263 rows and 150 columns
data = fread(file = 'connectome_1in.tsv')
dim(data)

[1] 17263   150

# skim(data) #you can comment this out an run
```

5.1 'dplyr::select

```
# Simple
data %>% dplyr::select(ApprovedSymbol, F5_min, F5_med, F5_max) # selects columns by name
```

	ApprovedSymbol	F5_min	F5_med	F5_max
1:	A1BG	0.263767	16.943	2377.989
2:	A1CF	0.000000	0.000	153.024
3:	A2M	0.000000	1.212	1515.493
4:	A2ML1	0.000000	0.000	206.355
5:	A4GALT	0.000000	9.725	80.009

17259:	ZYG11A	0.000000	0.264	11.104
17260:	ZYG11B	4.388704	16.580	65.872
17261:	ZYX	20.467403	468.361	1826.202
17262:	ZZEF1	1.744677	9.323	93.429
17263:	ZZZ3	4.360941	20.657	68.401

```
data %>% dplyr::select(1:4, 50) # select columns by position
```

	ApprovedSymbol	Localization	Taxon	F5_min	Eosinophils
1:	A1BG	secreted	Eutheria	0.263767	2.636
2:	A1CF	multiple	Deuterostomia	0.000000	0.000
3:	A2M	multiple	Euteleostomi	0.000000	0.000
4:	A2ML1	secreted	Euteleostomi	0.000000	0.000
5:	A4GALT	multiple	Tetrapoda	0.000000	0.000

17259:	ZYG11A	nucleus	Euteleostomi	0.000000	0.000
17260:	ZYG11B	nucleus	Euteleostomi	4.388704	41.867
17261:	ZYX	multiple	Theria	20.467403	742.793
17262:	ZZEF1	other	Amniota	1.744677	93.429
17263:	ZZZ3	nucleus	Deuterostomia	4.360941	9.187

```
data %>% dplyr::select(CellCompartment=2, geneID=1, Minimum_expr=F5_min) ## dplyr::rename
```

	CellCompartment	geneID	Minimum_expr
1:	secreted	A1BG	0.263767
2:	multiple	A1CF	0.000000
3:	multiple	A2M	0.000000

```

4:      secreted  A2ML1      0.000000
5:      multiple A4GALT      0.000000
---
17259:      nucleus ZYG11A      0.000000
17260:      nucleus ZYG11B      4.388704
17261:      multiple  ZYX      20.467403
17262:      other   ZZEF1      1.744677
17263:      nucleus  ZZZ3      4.360941

```

```
head(data)[1:2,1:3] # here are the original names and order
```

```

ApprovedSymbol Localization      Taxon
1:      A1BG      secreted      Eutheria
2:      A1CF      multiple Deuterostomia

```

```
data %>% dplyr::select(contains("Macrophage")) # selects columns by pattern
```

```

Granulocyte Macrophage progenitor Macrophage Monocyte derived
1:      34.492      17.923
2:      0.000      0.000
3:      0.000      208.304
4:      0.000      0.000
5:      0.000      0.000
---
17259:      0.000      0.000
17260:      28.104      29.538
17261:      226.111      544.167
17262:      77.925      21.500
17263:      22.994      24.682

```

```
data %>% dplyr::select(starts_with("CD34+")) # selects columns by starting pattern
```

```

CD34+ Haematopoietic stem cell CD34+ progenitor
1:      23.968      34.219
2:      0.000      0.000
3:      1.317      0.280
4:      0.000      0.000
5:      2.370      0.280

```

```

---
17259:          0.527          0.000
17260:         14.750          6.768
17261:         91.394        128.700
17262:         12.379         26.067
17263:         21.861         28.870

```

```
data %>% dplyr::select(ends_with("Endothelial")) # select columns by ending pattern
```

```

      Hepatic Sinusoidal Endothelial Renal Glomerular Endothelial
1:          11.219          4.962
2:           0.000          0.000
3:         36.612         47.414
4:           0.000          0.000
5:         13.360         36.860
---
17259:          1.070          1.272
17260:         10.445          9.821
17261:        894.871        826.222
17262:          9.780         13.692
17263:         13.323         14.051

```

```
data %>% dplyr::select(where(is.character))# selects columns by data type
```

```

      ApprovedSymbol Localization      Taxon
1:           A1BG      secreted    Eutheria
2:           A1CF      multiple Deuterostomia
3:           A2M      multiple Euteleostomi
4:          A2ML1      secreted Euteleostomi
5:          A4GALT      multiple   Tetrapoda
---
17259:        ZYG11A      nucleus Euteleostomi
17260:        ZYG11B      nucleus Euteleostomi
17261:          ZYX      multiple     Theria
17262:        ZZEF1       other    Amniota
17263:        ZZZ3      nucleus Deuterostomia

```

```

# Same as above, but works by excluding columns
data %>% dplyr::select(-c(6:150)) # excludes columns by position

```

	ApprovedSymbol	Localization	Taxon	F5_min	F5_med
1:	A1BG	secreted	Eutheria	0.263767	16.943
2:	A1CF	multiple	Deuterostomia	0.000000	0.000
3:	A2M	multiple	Euteleostomi	0.000000	1.212
4:	A2ML1	secreted	Euteleostomi	0.000000	0.000
5:	A4GALT	multiple	Tetrapoda	0.000000	9.725

17259:	ZYG11A	nucleus	Euteleostomi	0.000000	0.264
17260:	ZYG11B	nucleus	Euteleostomi	4.388704	16.580
17261:	ZYX	multiple	Theria	20.467403	468.361
17262:	ZZEF1	other	Amniota	1.744677	9.323
17263:	ZZZ3	nucleus	Deuterostomia	4.360941	20.657

```
data %>% dplyr::select(!where(is.numeric))# excludes columns by type using '!'
```

	ApprovedSymbol	Localization	Taxon
1:	A1BG	secreted	Eutheria
2:	A1CF	multiple	Deuterostomia
3:	A2M	multiple	Euteleostomi
4:	A2ML1	secreted	Euteleostomi
5:	A4GALT	multiple	Tetrapoda

17259:	ZYG11A	nucleus	Euteleostomi
17260:	ZYG11B	nucleus	Euteleostomi
17261:	ZYX	multiple	Theria
17262:	ZZEF1	other	Amniota
17263:	ZZZ3	nucleus	Deuterostomia

```
# More complex
```

```
# Example:
```

```
# select and dplyr::rename column 1 and then,
```

```
# select all numeric columns starting with 'T' (character variable 'Taxon' will be excluded)
```

```
data %>% dplyr::select(geneSymbol=1, starts_with("T") & where(is.numeric))
```

	geneSymbol	Tenocyte	Trabecular	Meshwork	Tracheal	Epithelial
1:	A1BG	18.775		30.337		10.808
2:	A1CF	0.000		0.000		0.000
3:	A2M	5.266		0.000		0.223

4:	A2ML1	0.000	0.000	4.885
5:	A4GALT	61.794	6.097	11.199

17259:	ZYG11A	0.000	2.393	0.096
17260:	ZYG11B	24.898	10.372	7.905
17261:	ZYX	489.985	1313.519	616.760
17262:	ZZEF1	6.676	8.898	6.903
17263:	ZZZ3	22.721	19.108	11.410

```
#A few more 'select' arguments are: 'num_range()', 'matches()', 'any_of()', 'all_of()'
```

5.2 dplyr::rename / dplyr::rename_with

```
# renaming can also be done with 'select', but 'dplyr::rename' is easier
```

```
data=fread(file = 'connectome_1in.tsv', select = c(1,7:9))
data %>% dplyr::rename(geneSymbol = ApprovedSymbol)
```

	geneSymbol	Adipocyte	Breast	Adipocyte	Omental	Adipocyte	Perirenal
1:	A1BG		36.847		35.174		49.723
2:	A1CF		0.000		0.000		0.000
3:	A2M		90.272		121.423		50.596
4:	A2ML1		0.000		0.000		0.000
5:	A4GALT		24.386		10.811		17.447

17259:	ZYG11A		0.091		0.000		0.000
17260:	ZYG11B		30.164		25.141		18.319
17261:	ZYX		473.814		442.646		389.935
17262:	ZZEF1		9.713		8.754		1.745
17263:	ZZZ3		18.076		20.905		19.191

```
data %>% dplyr::rename_with(tolower)
```

	approvesymbol	adipocyte	breast	adipocyte	omental	adipocyte	perirenal
1:	A1BG		36.847		35.174		49.723
2:	A1CF		0.000		0.000		0.000
3:	A2M		90.272		121.423		50.596
4:	A2ML1		0.000		0.000		0.000

```

      5:      A4GALT      24.386      10.811      17.447
----
17259:      ZYG11A      0.091      0.000      0.000
17260:      ZYG11B      30.164      25.141      18.319
17261:      ZYX      473.814      442.646      389.935
17262:      ZZEF1      9.713      8.754      1.745
17263:      ZZZ3      18.076      20.905      19.191

```

```
data %>% dplyr::rename_with(toupper, where(is.numeric)) # dplyr::renames to upper - here,
```

```

      ApprovedSymbol ADIPOCYTE BREAST ADIPOCYTE OMENTAL ADIPOCYTE PERIRENAL
1:      A1BG      36.847      35.174      49.723
2:      A1CF      0.000      0.000      0.000
3:      A2M      90.272      121.423      50.596
4:      A2ML1      0.000      0.000      0.000
5:      A4GALT      24.386      10.811      17.447
----
17259:      ZYG11A      0.091      0.000      0.000
17260:      ZYG11B      30.164      25.141      18.319
17261:      ZYX      473.814      442.646      389.935
17262:      ZZEF1      9.713      8.754      1.745
17263:      ZZZ3      18.076      20.905      19.191

```

5.3 dplyr::relocate

```
# moves columns to the front; this can also be done with 'select', but 'relocate' is easier
```

```
data=fread(file = 'connectome_1in.tsv', select = c(1,7:9))
data %>% relocate(starts_with('Adip'))
```

```

      Adipocyte Breast Adipocyte Omental Adipocyte Perirenal ApprovedSymbol
1:      36.847      35.174      49.723      A1BG
2:      0.000      0.000      0.000      A1CF
3:      90.272      121.423      50.596      A2M
4:      0.000      0.000      0.000      A2ML1
5:      24.386      10.811      17.447      A4GALT
----
17259:      0.091      0.000      0.000      ZYG11A
17260:      30.164      25.141      18.319      ZYG11B

```


17261:	473.814	442.646	389.935	ZYX
17262:	9.713	8.754	1.745	ZZEF1
17263:	18.076	20.905	19.191	ZZZ3

```
data %>% relocate(where(is.numeric))
```

	Adipocyte Breast	Adipocyte Omental	Adipocyte Perirenal	ApprovedSymbol
1:	36.847	35.174	49.723	A1BG
2:	0.000	0.000	0.000	A1CF
3:	90.272	121.423	50.596	A2M
4:	0.000	0.000	0.000	A2ML1
5:	24.386	10.811	17.447	A4GALT

17259:	0.091	0.000	0.000	ZYG11A
17260:	30.164	25.141	18.319	ZYG11B
17261:	473.814	442.646	389.935	ZYX
17262:	9.713	8.754	1.745	ZZEF1
17263:	18.076	20.905	19.191	ZZZ3

```
# relocate can take other arguments '.before', '.after'
?relocate #check help
```

6 Basic dplyr operations on data rows

6.1 dplyr::filter

```
# keeps rows based on desired criteria
# simple

data=fread(file = 'connectome_1in.tsv', select = c(1,5:8))
data %>% dplyr::filter(F5_max>5) #keeps rows using a numeric value
```

	ApprovedSymbol	F5_med	F5_max	Adipocyte	Breast	Adipocyte	Omental
1:	A1BG	16.943	2377.989		36.847		35.174
2:	A1CF	0.000	153.024		0.000		0.000
3:	A2M	1.212	1515.493		90.272		121.423
4:	A2ML1	0.000	206.355		0.000		0.000
5:	A4GALT	9.725	80.009		24.386		10.811

15316:	ZYG11A	0.264	11.104		0.091		0.000
15317:	ZYG11B	16.580	65.872		30.164		25.141
15318:	ZYX	468.361	1826.202		473.814		442.646
15319:	ZZEF1	9.323	93.429		9.713		8.754
15320:	ZZZ3	20.657	68.401		18.076		20.905

```
data=fread(file = 'connectome_1in.tsv', select = c(1:6))
my_genes=c('A1BG', 'CDKN3', 'ZBPB')
data %>% dplyr::filter(ApprovedSymbol %in% my_genes) #keeps rows based on custom string
```

	ApprovedSymbol	Localization	Taxon	F5_min	F5_med	F5_max
1:	A1BG	secreted	Eutheria	0.263767	16.943	2377.989
2:	CDKN3	multiple	Amniota	0.000000	14.600	226.150
3:	ZBPB	secreted	Amniota	0.000000	0.000	0.651

```
# in conjunction with 'str_detect' from stringr package; (similar to 'grep')
data %>% dplyr::filter(str_detect(ApprovedSymbol, '^HIST2')) #keeps all HIST2 genes
```

	ApprovedSymbol	Localization	Taxon	F5_min	F5_med	F5_max
1:	HIST2H2AA3	nucleus	Eukaryota	0.000000	0.431	671.790
2:	HIST2H2AA4	nucleus	Eukaryota	0.000000	0.431	671.790
3:	HIST2H2AB	nucleus	Eukaryota	9.958116	91.570	1240.587
4:	HIST2H2BE	multiple	Eukaryota	56.484107	416.034	2790.341
5:	HIST2H2BF	nucleus	Eukaryota	0.918399	21.239	457.095
6:	HIST2H3A	nucleus	Eukaryota	0.000000	0.174	797.346
7:	HIST2H3C	nucleus	Eukaryota	0.000000	0.174	797.346
8:	HIST2H3D	nucleus	Eukaryota	0.000000	0.174	797.346
9:	HIST2H4A	nucleus	Eukaryota	170.420082	1224.638	19898.334
10:	HIST2H4B	nucleus	Eukaryota	170.420082	1224.638	19898.334

```
data %>% dplyr::filter(!str_detect(ApprovedSymbol, '^HIST2')) #removes (using '!') all HIST2 genes
```

	ApprovedSymbol	Localization	Taxon	F5_min	F5_med	F5_max
1:	A1BG	secreted	Eutheria	0.263767	16.943	2377.989
2:	A1CF	multiple	Deuterostomia	0.000000	0.000	153.024
3:	A2M	multiple	Euteleostomi	0.000000	1.212	1515.493
4:	A2ML1	secreted	Euteleostomi	0.000000	0.000	206.355
5:	A4GALT	multiple	Tetrapoda	0.000000	9.725	80.009

17249:	ZYG11A	nucleus	Euteleostomi	0.000000	0.264	11.104
17250:	ZYG11B	nucleus	Euteleostomi	4.388704	16.580	65.872
17251:	ZYX	multiple	Theria	20.467403	468.361	1826.202
17252:	ZZEF1	other	Amniota	1.744677	9.323	93.429
17253:	ZZZ3	nucleus	Deuterostomia	4.360941	20.657	68.401

```
# more complex
# example:
# filter all HIST2 genes with a median expression >10TPM and localized to nucleus
```

```
data %>% dplyr::filter(str_detect(ApprovedSymbol, '^HIST2') &
  F5_med>=10 & Localization == 'nucleus')
```

	ApprovedSymbol	Localization	Taxon	F5_min	F5_med	F5_max
1:	HIST2H2AB	nucleus	Eukaryota	9.958116	91.570	1240.587

```

2:      HIST2H2BF      nucleus Eukaryota  0.918399   21.239   457.095
3:      HIST2H4A      nucleus Eukaryota 170.420082 1224.638 19898.334
4:      HIST2H4B      nucleus Eukaryota 170.420082 1224.638 19898.334

```

6.2 dplyr::arrange

```

# arranges row order
# descending - highest on top ; ascending highest at the bottom

data=fread(file = 'connectome_1in.tsv', select = 1:4)
data %>% dplyr::arrange(ApprovedSymbol) # arranges characters in descending order

```

	ApprovedSymbol	Localization	Taxon	F5_min
1:	A1BG	secreted	Eutheria	0.263767
2:	A1CF	multiple	Deuterostomia	0.000000
3:	A2M	multiple	Euteleostomi	0.000000
4:	A2ML1	secreted	Euteleostomi	0.000000
5:	A4GALT	multiple	Tetrapoda	0.000000

17259:	ZYG11A	nucleus	Euteleostomi	0.000000
17260:	ZYG11B	nucleus	Euteleostomi	4.388704
17261:	ZYX	multiple	Theria	20.467403
17262:	ZZEF1	other	Amniota	1.744677
17263:	ZZZ3	nucleus	Deuterostomia	4.360941

```

data %>% dplyr::arrange(desc(ApprovedSymbol)) # arranges characters in descending order

```

	ApprovedSymbol	Localization	Taxon	F5_min
1:	ZZZ3	nucleus	Deuterostomia	4.360941
2:	ZZEF1	other	Amniota	1.744677
3:	ZYX	multiple	Theria	20.467403
4:	ZYG11B	nucleus	Euteleostomi	4.388704
5:	ZYG11A	nucleus	Euteleostomi	0.000000

17259:	A4GALT	multiple	Tetrapoda	0.000000
17260:	A2ML1	secreted	Euteleostomi	0.000000
17261:	A2M	multiple	Euteleostomi	0.000000
17262:	A1CF	multiple	Deuterostomia	0.000000
17263:	A1BG	secreted	Eutheria	0.263767

```
data %>% dplyr::arrange(F5_min) # arranges numbers in descending order
```

	ApprovedSymbol	Localization	Taxon	F5_min
1:	A1CF	multiple	Deuterostomia	0.0000
2:	A2M	multiple	Euteleostomi	0.0000
3:	A2ML1	secreted	Euteleostomi	0.0000
4:	A4GALT	multiple	Tetrapoda	0.0000
5:	A4GNT	other	Tetrapoda	0.0000

17259:	RPS24	cytoplasm	Eukaryota	331.8715
17260:	PCBP2	multiple	Opisthokonta	344.3184
17261:	CFL1	multiple	Eukaryota	390.6739
17262:	EIF4G2	cytoplasm	Deuterostomia	402.0313
17263:	ACTB	multiple	Eukaryota	1451.3885

```
data %>% dplyr::arrange(-F5_min) # arranges numbers in ascending order
```

	ApprovedSymbol	Localization	Taxon	F5_min
1:	ACTB	multiple	Eukaryota	1451.3885
2:	EIF4G2	cytoplasm	Deuterostomia	402.0313
3:	CFL1	multiple	Eukaryota	390.6739
4:	PCBP2	multiple	Opisthokonta	344.3184
5:	RPS24	cytoplasm	Eukaryota	331.8715

17259:	ZUFSP	nucleus	Euteleostomi	0.0000
17260:	ZWINT	multiple	Eutheria	0.0000
17261:	ZXDA	nucleus	Euteleostomi	0.0000
17262:	ZXDB	nucleus	Euteleostomi	0.0000
17263:	ZYG11A	nucleus	Euteleostomi	0.0000

```
data %>% dplyr::arrange(Localization, -F5_min) # can be combined; order matters
```

	ApprovedSymbol	Localization	Taxon	F5_min
1:	EIF4G2	cytoplasm	Deuterostomia	402.0313
2:	RPS24	cytoplasm	Eukaryota	331.8715
3:	EIF1	cytoplasm	Eukaryota	301.4819
4:	FTL	cytoplasm	Theria	149.4635
5:	UBC	cytoplasm	Eukaryota	139.8899

17259:	XYLT1	secreted	Bilateria	0.0000
17260:	ZG16B	secreted	Catarrhini	0.0000
17261:	ZNF365	secreted	Tetrapoda	0.0000
17262:	ZBPB	secreted	Amniota	0.0000
17263:	ZBPB2	secreted	Amniota	0.0000

6.3 dplyr::mutate / dplyr::case_when

```
# 'mutate': adds a new variable as a column
```

```
data=fread(file = 'connectome_1in.tsv', select = c(1,2,5))
data %>% dplyr::mutate(my_new_variable = 'FANTOM_5_data') # added as last column
```

	ApprovedSymbol	Localization	F5_med	my_new_variable
1:	A1BG	secreted	16.943	FANTOM_5_data
2:	A1CF	multiple	0.000	FANTOM_5_data
3:	A2M	multiple	1.212	FANTOM_5_data
4:	A2ML1	secreted	0.000	FANTOM_5_data
5:	A4GALT	multiple	9.725	FANTOM_5_data

17259:	ZYG11A	nucleus	0.264	FANTOM_5_data
17260:	ZYG11B	nucleus	16.580	FANTOM_5_data
17261:	ZYX	multiple	468.361	FANTOM_5_data
17262:	ZZEF1	other	9.323	FANTOM_5_data
17263:	ZZZ3	nucleus	20.657	FANTOM_5_data

```
# 'case_when': now row values depend on the pattern
```

```
data %>% dplyr::mutate(expr_level = case_when(F5_med<10 ~ 'lowly-expressed gene',
                                              TRUE ~ 'highly-expressed gene'))
```

	ApprovedSymbol	Localization	F5_med	expr_level
1:	A1BG	secreted	16.943	highly-expressed gene
2:	A1CF	multiple	0.000	lowly-expressed gene
3:	A2M	multiple	1.212	lowly-expressed gene
4:	A2ML1	secreted	0.000	lowly-expressed gene
5:	A4GALT	multiple	9.725	lowly-expressed gene

17259:	ZYG11A	nucleus	0.264	lowly-expressed gene

17260:	ZYG11B	nucleus	16.580	highly-expressed gene
17261:	ZYX	multiple	468.361	highly-expressed gene
17262:	ZZEF1	other	9.323	lowly-expressed gene
17263:	ZZZ3	nucleus	20.657	highly-expressed gene

```
data=fread(file = 'connectome_lin.tsv', select = c(1,2,4))
data %>% dplyr::mutate(expr_level =
  case_when(F5_min>0 & Localization == 'secreted'~
    'highly-expressed secreted protein',
    TRUE ~ 'not so interesting')) %>%
  dplyr:: arrange(desc(Localization))
```

	ApprovedSymbol	Localization	F5_min	expr_level
1:	A1BG	secreted	0.263767	highly-expressed secreted protein
2:	A2ML1	secreted	0.000000	not so interesting
3:	AADACL2	secreted	0.000000	not so interesting
4:	ABHD12	secreted	5.284597	highly-expressed secreted protein
5:	ABHD12B	secreted	0.000000	not so interesting

17259:	ZNF503	cytoplasm	0.000000	not so interesting
17260:	ZNF706	cytoplasm	6.065311	not so interesting
17261:	ZNFX1	cytoplasm	6.826872	not so interesting
17262:	ZNRF4	cytoplasm	0.000000	not so interesting
17263:	ZSWIM8	cytoplasm	1.970653	not so interesting

7 Combining ‘dplyr’ functions

Example:

1. find all highly expressed in CD14+ Monocytes (>10TPM) putative ligands (secreted genes)
2. order the genes from most highly expressed down, annotate them and save to a file
3. ApprovedSymbol (dplyr::rename to geneSymbol), Localization and the cell of interest
4. after excluding all ‘orf’ genes (ex: C1orf162, etc)

```
data=fread(file = 'connectome_1in.tsv')
data %>% dplyr::filter(Localization=='secreted' & `CD14+ Monocytes` > 10) %>%
  dplyr::arrange(-`CD14+ Monocytes`) %>%
  dplyr::select(ApprovedSymbol, Localization, `CD14+ Monocytes`) %>%
  dplyr::rename(geneSymbol=ApprovedSymbol) %>%
  dplyr::mutate(Class='Monocyte Ligand') %>%
  dplyr::filter(!str_detect(geneSymbol, 'orf'))
```

	geneSymbol	Localization	CD14+ Monocytes	Class
1:	LYZ	secreted	13533.670	Monocyte Ligand
2:	IL8	secreted	12834.926	Monocyte Ligand
3:	B2M	secreted	7159.262	Monocyte Ligand
4:	CCL3	secreted	3027.740	Monocyte Ligand
5:	CXCL2	secreted	2427.316	Monocyte Ligand

169:	PF4	secreted	10.554	Monocyte Ligand
170:	NID1	secreted	10.457	Monocyte Ligand
171:	TCTN3	secreted	10.359	Monocyte Ligand
172:	FOLR3	secreted	10.122	Monocyte Ligand
173:	THBS3	secreted	10.065	Monocyte Ligand

8 Working with grouped data

```
-- Attaching packages ----- tidyverse 1.3.2 --
v ggplot2 3.3.6      v purrr   0.3.4
v tibble  3.1.8      v dplyr   1.0.9
v tidyr   1.2.0      v stringr 1.4.0
v readr   2.1.2      v forcats 0.5.1
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::between()   masks data.table::between()
x dplyr::filter()    masks stats::filter()
x dplyr::first()     masks data.table::first()
x dplyr::lag()       masks stats::lag()
x dplyr::last()      masks data.table::last()
x purrr::transpose() masks data.table::transpose()

      : 'magrittr'

      'package:purrr'      :

set_names

      'package:tidyr'      :

extract
```

8.1 dplyr::add_count / dplyr::count

```
data = fread(file = 'connectome_1in.tsv')
data %>% dplyr::add_count(ApprovedSymbol) %>% dplyr::arrange(-n)
```

	ApprovedSymbol	Localization	Taxon	F5_min	F5_med	F5_max
1:	A1BG	secreted	Eutheria	0.263767	16.943	2377.989

2:	A1CF	multiple	Deuterostomia	0.000000	0.000	153.024
3:	A2M	multiple	Euteleostomi	0.000000	1.212	1515.493
4:	A2ML1	secreted	Euteleostomi	0.000000	0.000	206.355
5:	A4GALT	multiple	Tetrapoda	0.000000	9.725	80.009

17259:	ZYG11A	nucleus	Euteleostomi	0.000000	0.264	11.104
17260:	ZYG11B	nucleus	Euteleostomi	4.388704	16.580	65.872
17261:	ZYX	multiple	Theria	20.467403	468.361	1826.202
17262:	ZZEF1	other	Amniota	1.744677	9.323	93.429
17263:	ZZZ3	nucleus	Deuterostomia	4.360941	20.657	68.401
Adipocyte Breast Adipocyte Omental Adipocyte Perirenal						
1:	36.847		35.174		49.723	
2:	0.000		0.000		0.000	
3:	90.272		121.423		50.596	
4:	0.000		0.000		0.000	
5:	24.386		10.811		17.447	

17259:	0.091		0.000		0.000	
17260:	30.164		25.141		18.319	
17261:	473.814		442.646		389.935	
17262:	9.713		8.754		1.745	
17263:	18.076		20.905		19.191	
Adipocyte Subcutaneous Alveolar Epithelial Amniotic Epithelial						
1:	41.076		4.143		0.264	
2:	0.000		0.000		0.000	
3:	63.397		0.000		0.000	
4:	0.000		0.000		21.168	
5:	27.730		11.608		19.070	

17259:	0.000		0.123		1.733	
17260:	18.911		4.978		15.027	
17261:	663.910		1012.799		495.516	
17262:	9.769		6.561		12.725	
17263:	11.938		10.109		6.001	
Amniotic Membrane Annulus Pulposus Astrocyte Cerebellum						
1:	4.915		31.099		16.943	
2:	0.000		0.000		0.000	
3:	0.819		0.000		1.364	
4:	206.355		0.000		0.000	
5:	30.631		42.725		6.146	

17259:	0.396		0.000		1.195	
17260:	21.576		17.402		7.212	

17261:	81.118	638.182	597.896
17262:	12.789	8.083	9.124
17263:	25.542	26.437	10.307
	Astrocyte Cerebral Cortex	Basophils	Bronchial Epithelial
1:	7.498	17.908	9.793
2:	0.000	0.103	0.000
3:	8.824	0.128	0.000
4:	0.000	0.619	3.187
5:	0.655	0.334	16.745

17259:	1.115	0.128	0.100
17260:	27.474	14.586	6.326
17261:	251.642	440.993	641.173
17262:	8.411	33.169	9.038
17263:	27.943	17.550	13.487
	CD133+ Haematopoietic stem cell		
1:	50.206		
2:	0.000		
3:	0.000		
4:	0.000		
5:	0.000		

17259:	0.000		
17260:	8.514		
17261:	116.266		
17262:	11.450		
17263:	31.122		
	CD14+ Monocyte derived Endothelial progenitor	CD14+ Monocytes	
1:	21.596	16.290	
2:	0.000	0.000	
3:	144.359	0.185	
4:	0.000	0.000	
5:	0.075	0.217	

17259:	0.000	0.000	
17260:	43.930	17.754	
17261:	270.955	476.539	
17262:	59.266	49.950	
17263:	68.401	23.115	
	CD14+CD16+ Monocytes	CD14+CD16- Monocytes	CD14-CD16+ Monocytes
1:	16.181	23.447	10.928
2:	0.000	0.000	0.000
3:	0.141	0.050	0.127

4:	0.000	0.000	0.000
5:	0.000	0.037	0.000

17259:	0.000	0.000	0.000
17260:	15.776	20.266	16.119
17261:	359.648	580.106	329.579
17262:	19.920	23.946	30.071
17263:	15.776	17.156	13.928
CD19+ B cells CD34+ Haematopoietic stem cell CD34+ progenitor			
1:	24.777	23.968	34.219
2:	0.000	0.000	0.000
3:	0.000	1.317	0.280
4:	0.000	0.000	0.000
5:	0.217	2.370	0.280

17259:	1.290	0.527	0.000
17260:	17.912	14.750	6.768
17261:	26.779	91.394	128.700
17262:	27.082	12.379	26.067
17263:	35.293	21.861	28.870
CD4+ T cells CD4+CD25+CD45RA+ naive regulatory T cells			
1:	15.572		13.057
2:	0.000		0.000
3:	0.000		0.000
4:	0.000		0.000
5:	0.000		0.000

17259:	0.262		0.118
17260:	25.652		16.660
17261:	156.419		76.060
17262:	45.869		23.929
17263:	51.262		38.660
CD4+CD25+CD45RA- memory regulatory T cells			
1:		15.473	
2:		0.000	
3:		0.000	
4:		0.000	
5:		0.341	

17259:		0.062	
17260:		15.991	
17261:		154.997	
17262:		20.953	

17263:	31.162			
	CD4+CD25-CD45RA+ naive conventional T cells			
1:	16.530			
2:	0.000			
3:	0.000			
4:	0.000			
5:	0.000			

17259:	0.101			
17260:	20.752			
17261:	111.837			
17262:	26.076			
17263:	40.911			
	CD4+CD25-CD45RA- memory conventional T cells	CD8+ T cells		
1:	17.132	25.467		
2:	0.000	0.000		
3:	0.000	0.000		
4:	0.000	0.000		
5:	0.028	0.000		

17259:	0.152	0.149		
17260:	15.595	17.183		
17261:	115.866	130.069		
17262:	24.326	29.854		
17263:	34.308	42.319		
	Cardiac Myocyte	Chondroblast	Chondrocyte	Chorionic Membrane
1:	8.595	9.231	17.668	7.071
2:	0.000	0.000	0.000	0.000
3:	17.161	4.198	28.522	30.713
4:	0.000	0.000	0.000	18.666
5:	12.142	31.842	19.033	27.820

17259:	0.309	0.241	0.000	0.153
17260:	22.829	18.431	23.253	18.167
17261:	432.366	341.704	127.448	287.212
17262:	10.602	9.115	9.840	11.830
17263:	24.197	20.446	22.374	21.327
	Ciliary Epithelial	Corneal Epithelial		
1:	5.169	10.818		
2:	0.000	0.000		
3:	1.474	0.000		
4:	0.029	16.614		
5:	3.882	62.267		

```

---
17259:          1.246          1.103
17260:          22.091          5.705
17261:         425.145         416.233
17262:          9.560          6.434
17263:         26.001          4.983
      Dendritic Monocyte Immature derived Dendritic Plasmacytoid ES cells
      1:          19.102          93.768      10.198
      2:          0.000          0.000      0.000
      3:         622.499          0.966      0.044
      4:          0.000          0.000      0.125
      5:          3.082          1.999      5.704
---
17259:          0.044          0.000      11.104
17260:         30.346          4.601      18.448
17261:        345.054        103.197     177.084
17262:         22.906         23.909       4.880
17263:         17.190         50.876     34.292
      Endothelial Aortic Endothelial Artery Endothelial Lymphatic
      1:         14.159         12.190         2.268
      2:          0.000          0.000          0.000
      3:          0.849          7.317        112.864
      4:          0.000          0.000          0.000
      5:         16.708         22.830         17.733
---
17259:          0.514          0.737          0.291
17260:         16.580         10.450         25.263
17261:        760.351        951.401        430.343
17262:         14.401         10.641         16.899
17263:         12.937         11.703         37.392
      Endothelial Microvascular Endothelial Thoracic
      1:          15.821          16.751
      2:          0.000          0.000
      3:         22.919          4.527
      4:          0.000          0.000
      5:         48.154          23.226
---
17259:          0.760          0.000
17260:         14.217         12.139
17261:        678.548        810.633
17262:         12.125         12.915
17263:         12.092         14.897
      Endothelial Umbilical Vein Endothelial Vein Eosinophils

```

1:	1.460	8.301	2.636
2:	0.000	0.000	0.000
3:	6.203	0.938	0.000
4:	0.000	0.000	0.000
5:	6.894	3.753	0.000

17259:	1.584	1.011	0.000
17260:	21.824	17.400	41.867
17261:	351.405	857.603	742.793
17262:	12.374	13.511	93.429
17263:	31.748	12.787	9.187
Esophageal Epithelial Fibroblast Aortic Adventitial Fibroblast Cardiac			
1:	8.286	9.701	24.256
2:	0.000	0.000	0.000
3:	0.436	5.699	10.457
4:	17.008	0.000	0.000
5:	18.752	19.151	15.473

17259:	0.872	0.988	0.465
17260:	7.414	20.302	21.306
17261:	593.088	515.496	597.537
17262:	3.489	8.258	10.805
17263:	4.361	20.657	22.829
Fibroblast Choroid Plexus Fibroblast Conjunctival Fibroblast Dermal			
1:	35.255	20.855	22.007
2:	0.000	0.000	0.000
3:	7.497	0.234	1.313
4:	0.000	0.000	0.095
5:	44.240	7.264	6.952

17259:	0.378	1.875	0.965
17260:	14.575	9.139	14.446
17261:	452.713	698.512	493.593
17262:	11.345	6.561	8.834
17263:	19.612	19.917	29.152
Fibroblast Gingival Fibroblast Lymphatic Fibroblast Periodontal Ligament			
1:	26.186	34.565	20.547
2:	0.000	0.000	0.000
3:	0.465	0.000	1.168
4:	0.000	0.000	0.000
5:	21.772	28.743	13.828

17259:	0.414	0.000	0.613

17260:	26.905	5.509	25.036
17261:	458.303	1757.244	560.575
17262:	10.650	4.431	9.916
17263:	36.798	8.407	29.337

Fibroblast Pulmonary Artery Fibroblast Skin Normal Gingival Epithelial

1:	15.881	32.488	5.443
2:	0.000	0.000	0.000
3:	0.340	23.182	0.064
4:	0.000	0.000	26.966
5:	12.364	11.766	11.276

17259:	0.227	0.235	1.261
17260:	14.860	16.632	17.275
17261:	468.361	479.812	359.155
17262:	5.785	8.612	7.890
17263:	12.931	29.297	17.675

Granulocyte Macrophage progenitor Hair Follicle Dermal Papilla

1:	34.492	35.204
2:	0.000	0.000
3:	0.000	9.592
4:	0.000	0.000
5:	0.000	6.254

17259:	0.000	0.460
17260:	28.104	13.679
17261:	226.111	941.256
17262:	77.925	13.769
17263:	22.994	26.221

Hair Follicle Outer Root Sheath Hepatic Sinusoidal Endothelial

1:	50.829	11.219
2:	0.000	0.000
3:	69.227	36.612
4:	0.000	0.000
5:	26.718	13.360

17259:	0.000	1.070
17260:	18.619	10.445
17261:	492.240	894.871
17262:	10.575	9.780
17263:	21.046	13.323

Hepatic Stellate Hepatocyte Immature Langerhans

1:	26.137	2377.989	46.017
2:	0.000	153.024	0.000

3:	1.235	1515.493	9.836	
4:	0.000	0.000	10.474	
5:	8.997	0.000	0.000	

17259:	0.000	4.341	0.000	
17260:	12.112	33.607	5.106	
17261:	1114.881	94.638	161.451	
17262:	8.467	16.168	20.296	
17263:	7.909	42.797	27.800	
Intestinal Epithelial (polarized) Iris Pigment Epithelial				
1:		0.984	7.206	
2:		53.254	0.000	
3:		9.593	0.172	
4:		0.000	0.000	
5:		6.026	4.975	

17259:		1.599	0.515	
17260:		16.111	15.098	
17261:		118.807	471.983	
17262:		7.379	5.319	
17263:		15.988	19.730	
Keratinocyte Epidermal Keratinocyte Oral Keratocytes Lens Epithelial				
1:	4.995	1.852	31.620	12.195
2:	0.000	0.000	0.000	0.000
3:	0.034	0.000	0.000	0.663
4:	20.528	13.148	0.000	0.000
5:	2.383	11.574	9.466	6.038

17259:	0.488	1.204	1.497	0.676
17260:	9.766	21.388	6.804	19.175
17261:	473.740	258.600	535.837	469.660
17262:	9.513	5.185	10.281	8.082
17263:	16.939	29.165	12.492	20.688
Macrophage Monocyte derived Mallassez derived Mammary Epithelial				
1:	17.923	9.523	4.266	
2:	0.000	0.000	0.000	
3:	208.304	0.000	2.494	
4:	0.000	5.063	1.235	
5:	0.000	14.173	1.850	

17259:	0.000	0.794	0.765	
17260:	29.538	11.063	11.799	
17261:	544.167	391.202	360.113	

17262:		21.500		6.146		7.575
17263:		24.682		19.728		27.103
	Mast cells	Mast cells stimulated	Mature Adipocyte	Melanocyte	Meningeal	
1:	21.826	11.824	1.629	24.663	6.175	
2:	0.000	0.000	0.000	0.000	0.000	
3:	1.178	0.000	85.879	423.667	2.797	
4:	0.496	0.000	0.000	0.209	0.000	
5:	0.883	0.000	5.599	0.575	7.811	

17259:	0.119	0.000	0.300	0.554	1.516	
17260:	23.254	8.868	38.571	15.233	14.621	
17261:	130.957	205.441	75.078	176.569	725.339	
17262:	24.955	4.434	17.865	11.846	8.827	
17263:	26.307	38.920	14.656	16.781	16.446	
	Mesenchymal precursor	Adipose Mesenchymal precursor	Bone Marrow			
1:		19.417	15.766			
2:		0.000	0.000			
3:		3.791	4.242			
4:		0.000	0.000			
5:		10.586	23.057			

17259:		0.412	0.063			
17260:		10.694	15.663			
17261:		404.482	398.606			
17262:		6.075	7.430			
17263:		26.862	22.748			
	Mesenchymal precursor	Cardiac Mesenchymal stem cell	Adipose			
1:		16.772	123.496			
2:		0.000	0.000			
3:		2.287	42.790			
4:		0.000	0.000			
5:		22.477	80.009			

17259:		0.687	0.109			
17260:		12.000	14.489			
17261:		281.751	1794.597			
17262:		6.228	8.004			
17263:		23.183	16.787			
	Mesenchymal stem cell	Amniotic Membrane				
1:		21.221				
2:		0.000				
3:		64.543				
4:		0.000				

5:	6.722	

17259:	0.653	
17260:	21.727	
17261:	805.240	
17262:	6.710	
17263:	25.101	
	Mesenchymal stem cell Bone Marrow	Mesenchymal stem cell Hepatic
1:	10.101	25.629
2:	0.000	0.000
3:	1.121	5.059
4:	0.000	0.000
5:	4.531	4.491

17259:	1.463	1.818
17260:	12.460	28.307
17261:	739.854	348.455
17262:	8.035	8.266
17263:	10.272	27.484
	Mesenchymal stem cell Umbilical	Mesenchymal stem cell Wharton's Jelly
1:	50.172	28.828
2:	0.000	0.000
3:	0.000	0.129
4:	0.000	0.000
5:	13.804	4.395

17259:	0.264	0.259
17260:	10.866	18.486
17261:	485.315	305.986
17262:	7.237	7.756
17263:	10.922	19.520
	Mesothelial Migratory Langerhans	
1:	34.815	22.289
2:	0.000	0.000
3:	91.831	100.280
4:	0.000	0.065
5:	9.413	2.969

17259:	0.067	0.000
17260:	17.012	8.426
17261:	471.516	641.794
17262:	8.412	16.995
17263:	13.762	26.937

	Multipot.	Cord Blood	Unrestrict.	Somatic stem cell	Myoblast	Myotube	
1:				15.398	24.219	24.929	
2:				0.000	0.000	0.000	
3:				0.000	1.243	29.737	
4:				0.000	0.000	0.000	
5:				4.718	12.731	8.903	

17259:				0.694	0.176	0.267	
17260:				22.414	22.962	24.039	
17261:				541.254	368.368	462.343	
17262:				7.854	9.323	8.992	
17263:				26.099	24.100	22.347	
	NK cells	Nasal	Epithelial	Neural stem cell	Neurons	Neutrophils	
1:	10.954		10.309	6.114	6.177	0.802	
2:	0.000		0.000	0.000	0.000	0.000	
3:	0.066		0.311	96.416	22.745	0.000	
4:	0.000		21.389	0.254	0.000	0.000	
5:	0.171		9.087	0.127	0.223	0.000	

17259:	0.229		0.140	0.905	0.000	0.000	
17260:	16.003		14.102	45.513	32.986	65.872	
17261:	150.932		224.852	348.359	176.113	1826.202	
17262:	43.102		12.315	13.429	12.432	78.486	
17263:	39.510		23.803	32.353	28.234	11.961	
	Nucleus Pulposus	Olfactory	Epithelial	Osteoblast	Osteocyte		
1:	28.643		28.786	2.784	27.879		
2:	0.000		0.000	0.000	0.000		
3:	1.212		2.805	0.849	16.605		
4:	0.000		0.000	0.000	0.000		
5:	34.574		3.817	1.863	27.933		

17259:	0.000		0.717	0.184	0.000		
17260:	21.465		29.622	22.979	15.396		
17261:	807.148		589.053	598.789	447.318		
17262:	7.636		11.644	10.015	12.868		
17263:	28.063		26.305	22.024	18.103		
	Pancreatic	Stromal	Pericytes	Placental	Epithelial	Preadipocyte	Breast
1:	25.804		81.360		2.573		26.514
2:	0.000		0.000		0.000		0.000
3:	6.343		1.740		0.101		17.948
4:	0.000		0.000		18.928		0.000
5:	9.818		13.108		8.783		23.957

17259:	0.695	0.098	0.202	0.140
17260:	27.281	4.923	13.618	23.652
17261:	504.272	790.225	427.509	494.841
17262:	9.210	8.964	8.024	6.965
17263:	29.106	9.846	11.451	24.937

	Preadipocyte Omental	Preadipocyte Perirenal	Preadipocyte Subcutaneous
1:	31.362	57.883	31.618
2:	0.000	0.000	0.000
3:	20.348	7.421	3.173
4:	0.000	0.000	0.000
5:	8.280	17.810	6.012

17259:	0.428	0.000	0.397
17260:	28.414	14.842	20.294
17261:	485.452	552.115	647.132
17262:	7.652	4.453	6.832
17263:	21.306	11.873	16.432

	Preadipocyte Visceral Prostate	Epithelial Prostate	Stromal
1:	17.867	3.093	16.122
2:	0.000	7.816	0.000
3:	0.622	0.138	13.502
4:	0.000	15.235	0.000
5:	17.783	13.987	10.854

17259:	0.570	0.242	1.390
17260:	20.144	16.644	19.337
17261:	504.228	313.816	457.992
17262:	8.435	7.171	8.223
17263:	25.769	19.604	20.297

	Renal Cortical Epithelial	Renal Epithelial	Renal Glomerular Endothelial
1:	3.642	8.393	4.962
2:	0.000	0.000	0.000
3:	0.000	0.000	47.414
4:	0.039	0.000	0.000
5:	12.396	31.502	36.860

17259:	1.133	2.336	1.272
17260:	11.790	12.459	9.821
17261:	339.622	581.510	826.222
17262:	8.704	4.548	13.692
17263:	16.972	16.062	14.051

	Renal Mesangial	Renal Proximal Tubular	Epithelial Reticulocyte
1:	19.607	4.602	1.113

2:	0.000		0.000	0.000
3:	0.251		0.000	0.131
4:	0.000		0.000	0.000
5:	36.755		26.727	41.660

17259:	0.522		2.278	0.000
17260:	7.441		10.504	9.483
17261:	925.429		314.538	20.467
17262:	7.887		6.491	14.248
17263:	8.118		11.819	15.576
	Retinal Pigment	Epithelial	Salivary Acinar	Sebocyte Sertoli
1:		4.445	8.125	9.870 3.214
2:		0.000	0.000	0.000 0.000
3:		0.194	2.552	0.000 35.350
4:		0.000	35.931	24.871 0.000
5:		4.433	21.075	5.033 27.316

17259:		1.083	0.069	1.912 0.000
17260:		16.906	12.555	9.280 25.709
17261:		369.460	268.938	1059.838 393.676
17262:		8.508	18.132	11.290 19.282
17263:		22.610	33.129	8.857 17.675
	Skeletal Muscle	Skeletal Muscle	Satellite	Small Airway Epithelial
1:	12.024		14.713	3.268
2:	0.000		0.000	0.000
3:	5.353		4.979	0.132
4:	0.000		0.000	4.941
5:	9.673		13.759	14.181

17259:	0.487		0.227	0.055
17260:	15.615		24.160	12.988
17261:	444.258		468.990	406.527
17262:	8.857		9.533	6.950
17263:	28.755		34.142	27.946
	Smooth Muscle Aortic	Smooth Muscle	Brachiocephalic	
1:	40.748		45.693	
2:	0.000		0.000	
3:	0.174		0.093	
4:	0.000		0.000	
5:	16.562		17.797	

17259:	1.135		0.000	
17260:	11.313		14.311	

17261:	744.286	547.700
17262:	10.759	8.519
17263:	9.526	17.754
	Smooth Muscle Brain Vascular	Smooth Muscle Bronchial
1:	25.877	33.998
2:	0.000	0.000
3:	3.687	22.458
4:	0.000	0.000
5:	4.468	13.933

17259:	0.890	0.726
17260:	24.562	11.288
17261:	414.742	1125.933
17262:	10.198	8.764
17263:	27.923	18.051
	Smooth Muscle Carotid	Smooth Muscle Colonic
1:	39.639	15.752
2:	0.000	0.000
3:	0.159	10.153
4:	0.000	0.000
5:	19.114	7.930

17259:	0.000	0.331
17260:	12.293	21.923
17261:	970.678	358.749
17262:	9.186	9.284
17263:	13.333	28.665
	Smooth Muscle Coronary Artery	Smooth Muscle Esophageal
1:	100.375	21.456
2:	0.000	0.000
3:	0.669	0.975
4:	0.000	0.000
5:	19.340	15.604

17259:	0.202	2.926
17260:	8.915	4.389
17261:	732.392	1411.700
17262:	14.216	6.339
17263:	8.280	8.777
	Smooth Muscle Internal Thoracic Artery	Smooth Muscle Prostate
1:		43.965
2:		21.860
3:		0.000
4:		0.000
5:		0.122
6:		6.740

4:	0.000	0.000		
5:	31.124	9.725		

17259:	0.244	1.311		
17260:	8.531	17.391		
17261:	534.323	374.423		
17262:	10.441	9.558		
17263:	13.609	24.070		
	Smooth Muscle Pulmonary Artery	Smooth Muscle Subclavian Artery		
1:	48.593	18.313		
2:	0.000	0.000		
3:	2.260	0.146		
4:	0.000	0.000		
5:	30.512	25.372		

17259:	0.000	0.146		
17260:	16.951	11.053		
17261:	679.179	688.957		
17262:	6.780	10.125		
17263:	6.780	11.370		
	Smooth Muscle Tracheal	Smooth Muscle Umbilical Artery		
1:	26.873	34.897		
2:	0.000	0.000		
3:	37.598	2.324		
4:	0.000	0.000		
5:	24.153	8.914		

17259:	0.328	0.237		
17260:	20.024	10.054		
17261:	740.403	977.311		
17262:	6.578	9.201		
17263:	15.163	9.848		
	Smooth Muscle Umbilical Vein	Smooth Muscle Uterine	Synoviocyte	Tenocyte
1:	13.021	18.802	9.504	18.775
2:	0.000	0.000	0.000	0.000
3:	0.143	3.193	2.208	5.266
4:	0.000	0.000	0.000	0.000
5:	1.855	2.129	65.447	61.794

17259:	0.430	1.064	0.481	0.000
17260:	17.677	18.448	21.608	24.898
17261:	510.591	433.518	467.281	489.985
17262:	5.382	9.933	7.342	6.676

17263:		23.406	24.833	25.040	22.721
	Trabecular Meshwork	Tracheal Epithelial	Urothelial	n	
1:	30.337	10.808	2.750	1	
2:	0.000	0.000	0.000	1	
3:	0.000	0.223	0.000	1	
4:	0.000	4.885	10.780	1	
5:	6.097	11.199	26.715	1	

17259:	2.393	0.096	0.000	1	
17260:	10.372	7.905	11.614	1	
17261:	1313.519	616.760	540.465	1	
17262:	8.898	6.903	6.794	1	
17263:	19.108	11.410	10.543	1	

References