

Gene Expression and Methylation from Lung Genomic Research Consortium (LGRC)

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The data is also available at <https://www.lung-genomics.org/research/>. We provide them here in a processed form to accompany the methods in the package `COPDSexualDimorphism`.

1 Clinical Data

Clinical phenotypes of 254 LGRC samples are given as a `data.frame` named `meta`. It has six fields: `tissueid`, `newid`, `GENDER`, `age`, `cigever`, `pkys`, and `diagn`. `tissueid` identifies the samples and `newid` identifies the subjects. Some subjects might have more than one sample from left/right/upper/lower lung or blood. These are designated by the last two letters of the tissue ID. The information for these samples have been adjudicated as described in Sathirapongsasuti et al (in review).

```
> library(COPDSexualDimorphism.data)
> `%%` <- function(x,y) paste(x,y,sep="")
> data(lgrc.meta)
> head(meta)
```

	tissueid	newid	GENDER	age	cigever	pkys	diagn
LT196199RU	LT196199RU	202158	1-Male	82	2-Ever (>100)	60	2-COPD/Emphysema
LT073345RU	LT073345RU	84736	1-Male	74	3-Never	0	3-Control
LT156041LU	LT156041LU	299693	2-Female	70	2-Ever (>100)	77	2-COPD/Emphysema
LT095342LU	LT095342LU	198904	1-Male	60	2-Ever (>100)	19	2-COPD/Emphysema
LT155982RU	LT155982RU	79946	2-Female	48	2-Ever (>100)	28	2-COPD/Emphysema
LT083759RL	LT083759RL	221323	1-Male	73	2-Ever (>100)	120	2-COPD/Emphysema

2 Gene Expression

Gene expression profile for 229 LGRC samples are available in two parts. One is `expr`, a `matrix` of 14497 Ensembl genes (rows) by 229 samples (columns), and the other is `expr.meta`, a `data.frame` of 229 samples (rows) by the subjects' clinical metadata. The subjects are arranged in the same order in the two objects.

```
> data(lgrc.expr)
> data(lgrc.expr.meta)
> dim(expr)
```

```
[1] 14497 229
```

```
> head(expr.meta)
```

	tissueid	sample_name	newid	GENDER	age	cigever	pkys
1	LT001098RU	LT001098RU_COPD	161745	2-Female	46	2-Ever (>100)	35
2	LT001796RU	LT001796RU_CTRL	212671	1-Male	48	2-Ever (>100)	19

```

3 LT005419RU LT005419RU_COPD 291396 1-Male 70 2-Ever (>100) 43
4 LT007392RU LT007392RU_COPD 169067 1-Male 46 2-Ever (>100) 45
5 LT009615LU LT009615LU_CTRL 49801 2-Female 49 2-Ever (>100) 45
6 LT010491LL LT010491LL_COPD 180409 1-Male 78 2-Ever (>100) 51
      diagmaj gender
1 2-COPD/Emphysema 2-Female
2      3-Control 1-Male
3 2-COPD/Emphysema 1-Male
4 2-COPD/Emphysema 1-Male
5      3-Control 2-Female
6 2-COPD/Emphysema 1-Male

```

Corresponding to the Ensembl genes in the expression profile is the data frame `genes`. This is a result of a query to BiomaRt database, stored here for convenience.

```

> data(lgrc.genes)
> head(lgrc.genes)

```

	ensembl_gene_id	hgnc_symbol
ENSG000000000003	ENSG000000000003	TSPAN6
ENSG000000000005	ENSG000000000005	TNMD
ENSG000000000419	ENSG000000000419	DPM1
ENSG000000000457	ENSG000000000457	SCYL3
ENSG000000000460	ENSG000000000460	C1orf112
ENSG000000000938	ENSG000000000938	FGR

ENSG000000000003	tetraspanin 6 [Source:HGNC Symbol]
ENSG000000000005	tenomodulin [Source:HGNC Symbol]
ENSG000000000419	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit [Source:HGNC Symbol]
ENSG000000000457	SCY1-like 3 (S. cerevisiae) [Source:HGNC Symbol]
ENSG000000000460	chromosome 1 open reading frame 112 [Source:HGNC Symbol]
ENSG000000000938	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog [Source:HGNC Symbol]

	chromosome_name	band	strand	start_position	end_position
ENSG000000000003	X	q22.1	-1	99883667	99894988
ENSG000000000005	X	q22.1	1	99839799	99854882
ENSG000000000419	20	q13.13	-1	49551404	49575092
ENSG000000000457	1	q24.2	-1	169821804	169863408
ENSG000000000460	1	q24.2	1	169631245	169823221
ENSG000000000938	1	p36.11	-1	27938575	27961788

	ensembl_gene_id.1	entrezgene
ENSG000000000003	ENSG000000000003	7105
ENSG000000000005	ENSG000000000005	64102
ENSG000000000419	ENSG000000000419	8813
ENSG000000000457	ENSG000000000457	57147
ENSG000000000460	ENSG000000000460	55732
ENSG000000000938	ENSG000000000938	2268

3 Methylation

Methylation data for 245 LGRC subjects is provided as a data frame `methp` which contains percent methylation for 12094 variably methylated regions (VMRs). Each row provides average median absolute deviation (MAD), length, and the number of probes for a VMR.

```

> data(lgrc.methp)
> methp[1:5, c("name", "ave.mad", "length", "num.probes")]

```

	name	ave.mad	length	num.probes
1	vmr_chr1_932668_932806	0.03778364	139	5
2	vmr_chr1_939506_939647	0.04619729	142	5
3	vmr_chr1_966705_966843	0.05257659	139	5
4	vmr_chr1_989551_989797	0.04155331	247	5
5	vmr_chr1_1006424_1006565	0.04367978	142	5

4 Session Information

```
> sessionInfo()
```

```
R version 3.1.0 RC (2014-04-02 r65358)
```

```
Platform: x86_64-apple-darwin10.8.0 (64-bit)
```

```
locale:
```

```
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
other attached packages:
```

```
[1] COPDSexualDimorphism.data_1.0.0
```

```
loaded via a namespace (and not attached):
```

```
[1] tools_3.1.0
```