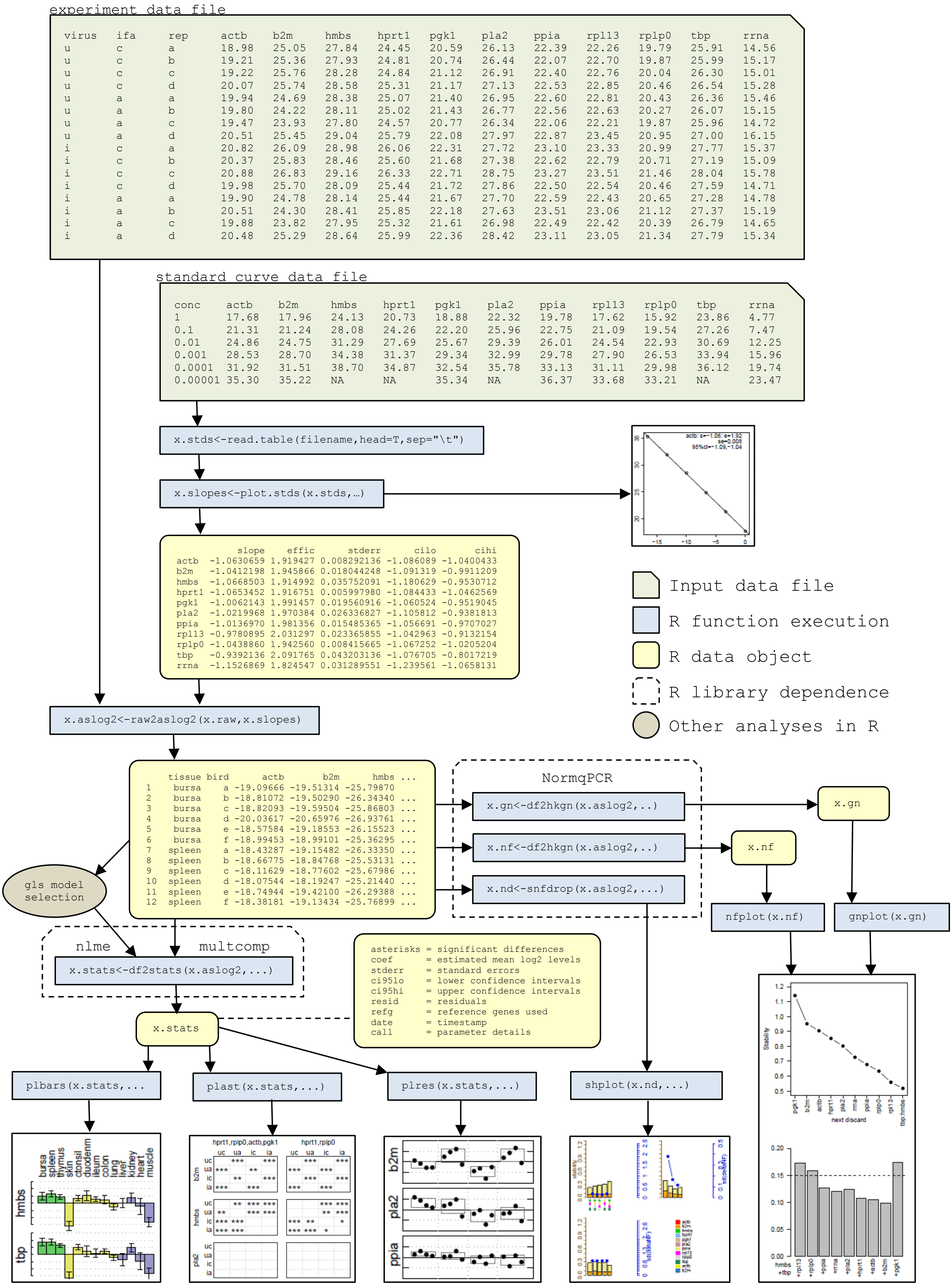

experiment data file

virus	ifa	rep	actb	b2m	hmbs	hprt1	pgk1	pla2	ppia	rpl13	rplp0	tbp	rrna
u	c	a	18.98	25.05	27.84	24.45	20.59	26.13	22.39	22.26	19.79	25.91	14.56
u	c	b	19.21	25.36	27.93	24.81	20.74	26.44	22.07	22.70	19.87	25.99	15.17
u	c	c	19.22	25.76	28.28	24.84	21.12	26.91	22.40	22.76	20.04	26.30	15.01
u	c	d	20.07	25.74	28.58	25.31	21.17	27.13	22.53	22.85	20.46	26.54	15.28
u	a	a	19.94	24.69	28.38	25.07	21.40	26.95	22.60	22.81	20.43	26.36	15.46
u	a	b	19.80	24.22	28.11	25.02	21.43	26.77	22.56	22.63	20.27	26.07	15.15
u	a	c	19.47	23.93	27.80	24.57	20.77	26.34	22.06	22.21	19.87	25.96	14.72
u	a	d	20.51	25.45	29.04	25.79	22.08	27.97	22.87	23.45	20.95	27.00	16.15
i	c	a	20.82	26.09	28.98	26.06	22.31	27.72	23.10	23.33	20.99	27.77	15.37
i	c	b	20.37	25.83	28.46	25.60	21.68	27.38	22.62	22.79	20.71	27.19	15.09
i	c	c	20.88	26.83	29.16	26.33	22.71	28.75	23.27	23.51	21.46	28.04	15.78
i	c	d	19.98	25.70	28.09	25.44	21.72	27.86	22.50	22.54	20.46	27.59	14.71
i	a	a	19.90	24.78	28.14	25.44	21.67	27.70	22.59	22.43	20.65	27.28	14.78
i	a	b	20.51	24.30	28.41	25.85	22.18	27.63	23.51	23.06	21.12	27.37	15.19
i	a	c	19.88	23.82	27.95	25.32	21.61	26.98	22.49	22.42	20.39	26.79	14.65
i	a	d	20.48	25.29	28.64	25.99	22.36	28.42	23.11	23.05	21.34	27.79	15.34

standard curve data file

conc	actb	b2m	hmbs	hprt1	pgk1	pla2	ppia	rpl13	rplp0	tbp	rrna
1	17.68	17.96	24.13	20.73	18.88	22.32	19.78	17.62	15.92	23.86	4.77
0.1	21.31	21.24	28.08	24.26	22.20	25.96	22.75	21.09	19.54	27.26	7.47
0.01	24.86	24.75	31.29	27.69	25.67	29.39	26.01	24.54	22.93	30.69	12.25
0.001	28.53	28.70	34.38	31.37	29.34	32.99	29.78	27.90	26.53	33.94	15.96
0.0001	31.92	31.51	38.70	34.87	32.54	35.78	33.13	31.11	29.98	36.12	19.74
0.00001	35.30	35.22	NA	NA	35.34	NA	36.37	33.68	33.21	NA	23.47

```
x.stds<-read.table(filename,head=T,sep="\t")
```

```
x.slopes<-plot.stds(x.stds,…)
```

```
            slope    effic      stderr      cilo       cihi
actb  -1.0630659 1.919427 0.008292136 -1.086089 -1.0400433
b2m   -1.0412198 1.945866 0.018044248 -1.091319 -0.9911209
hmbs  -1.0668503 1.914992 0.035752091 -1.180629 -0.9530712
hprt1 -1.0653452 1.916751 0.005997980 -1.084433 -1.0462569
pgk1  -1.0062143 1.991457 0.019560916 -1.060524 -0.9519045
pla2  -1.0219968 1.970384 0.026336827 -1.105812 -0.9381813
ppia  -1.0136970 1.981356 0.015485365 -1.056691 -0.9707027
rpl13 -0.9780895 2.031297 0.023365855 -1.042963 -0.9132154
rplp0 -1.0438860 1.942560 0.008415665 -1.067252 -1.0205204
tbp   -0.9392136 2.091765 0.043203136 -1.076705 -0.8017219
rrna  -1.1526869 1.824547 0.031289551 -1.239561 -1.0658131
```

Input data file

R function execution

R data object

R library dependence

Other analyses in R

```
x.aslog2<-raw2aslog2(x.raw,x.slopes)
```

```
   tissue bird      actb       b2m      hmbs ...
1   bursa    a -19.09666 -19.51314 -25.79870
2   bursa    b -18.81072 -19.50290 -26.34340 ...
3   bursa    c -18.82093 -19.59504 -25.86803 ...
4   bursa    d -20.03617 -20.65976 -26.93761 ...
5   bursa    e -18.57584 -19.18553 -26.15523 ...
6   bursa    f -18.99453 -18.99101 -25.36295 ...
7  spleen    a -18.43287 -19.15482 -26.33350 ...
8  spleen    b -18.66775 -18.84768 -25.53131 ...
9  spleen    c -18.11629 -18.77602 -25.67986 ...
10 spleen    d -18.07544 -18.19247 -25.21440 ...
11 spleen    e -18.74944 -19.42100 -26.29388 ...
12 spleen    f -18.38181 -19.13434 -25.76899 ...
```

NormqPCR

```
x.gn<-df2hkgn(x.aslog2,..)
x.nf<-df2hkgn(x.aslog2,..)
x.nd<-snfdrop(x.aslog2,...)
```

x.gn

x.nf

```
nfplot(x.nf)
gnplot(x.gn)
```

gls model selection

nlme

multcomp

```
x.stats<-df2stats(x.aslog2,...)
```

x.stats

```
asterisks = significant differences
coef      = estimated mean log2 levels
stderr    = standard errors
ci95lo    = lower confidence intervals
ci95hi    = upper confidence intervals
resid     = residuals
refg      = reference genes used
date      = timestamp
call      = parameter details
```

```
plbars(x.stats,...
plast(x.stats,...)
plres(x.stats,...)
shplot(x.nd,...)
```