

**RNA-seq data
(DuF2 dataset)**

Sscrofa10.2
Gene
annotation

Raw
reads

Data
QC

Reads after
QC

Alignment
(TopHat/BWA)

Aligned reads

Readcount
(BEDTools)

Normalized expression
data

Normalization
(Limma voom)

Gene expression
(read counts)

**Microarray data
(Duroc, Landrace datasets)**

Normalized
microarray
Expression data

GEOQuery

Normalized and mapped
Microarray data

BLAST

Microarray
Probe id → Fasta

NCBI
Sscrofa10.2
cDNA
Entrez id → Fasta

NCBI GEO
GSE11073

Correlation coefficients
Rank order statistics
Joint CDF computation

LA HA co-expression
clusters

Infomap
Consensus clustering
Statistical significance
of clusters

Result 2.
LA – HA clusters GO KEGG
enrichment

GO KEGG Enrichment

GO enriched clusters

Functional similarity assessment

Result 4.
LA – HA functional similarity graph

Result 1.
Statistically significant
LA HA co-expression
clusters

Physical similarity assessment

Result 3.
LA – HA physical similarity graph