

# Chicken Analysis Reports

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Organism: *Gallus gallus*

Tissues: Intestine, Meat, Reproductive Tissues, Macrophage and Monocyte

Total Samples: 2 replicates for each tissue

## Differentially expressed (DE) analysis

### Method:

For each pairwise analysis, we filtered out non-expressed and low-expressed genes.

Note: `rm = rowMeans(mRNA2_meat) == 0`

The surrogate variables (batch effects) were estimated by the SVA package (Leek JT et al., 2022) and adopted in the DE analysis model. The DE analysis and normalization data were performed using (Ritchie ME et al., 2015). We considered a DE significant gene showed  $FDR < 0.05$ .

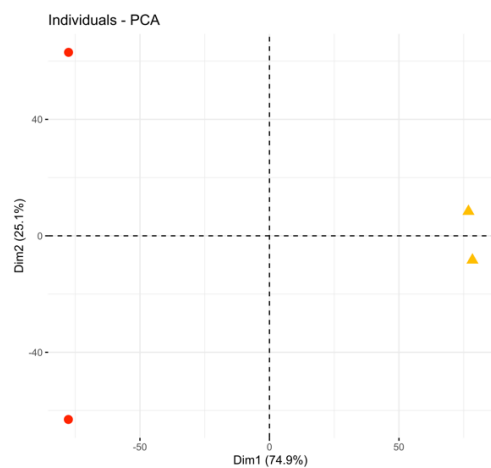
### Note:

- **Surrogate variables** are covariates constructed directly from high-dimensional data (like gene expression/RNA sequencing/methylation/brain imaging data) that can be used in subsequent analyses to adjust for unknown, unmodeled, or latent sources of noise.
- **n.sv** is the number of latent factors that need to be estimated (number of surrogate variables)

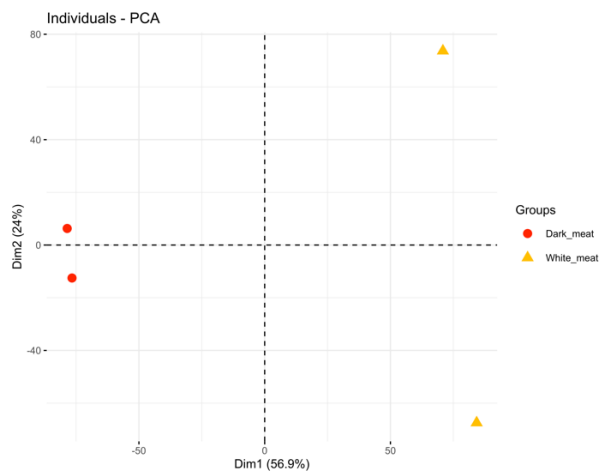
## DE analysis: meat tissues

Note: total n.sv=2

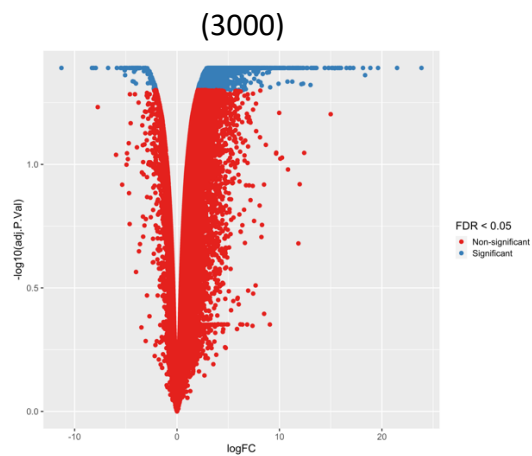
### Using sva with n.sv=1



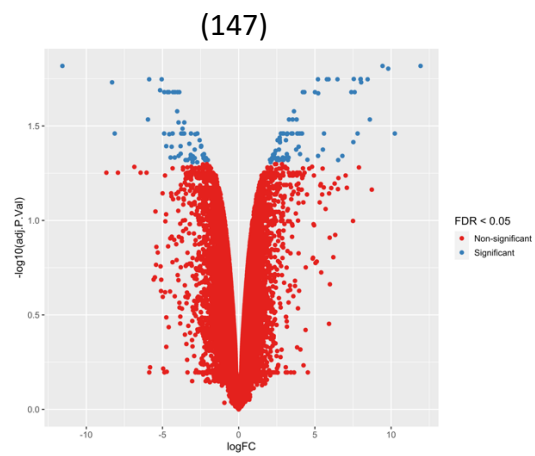
### Not using sva



### Using sva with n.sv=1



### Not using sva

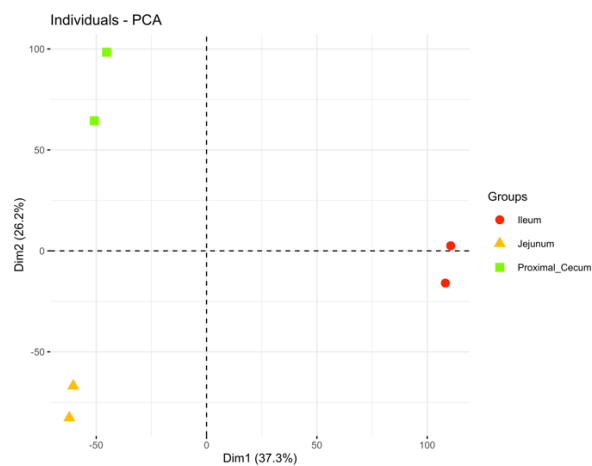


Note: the values in brackets are the number of significant DE

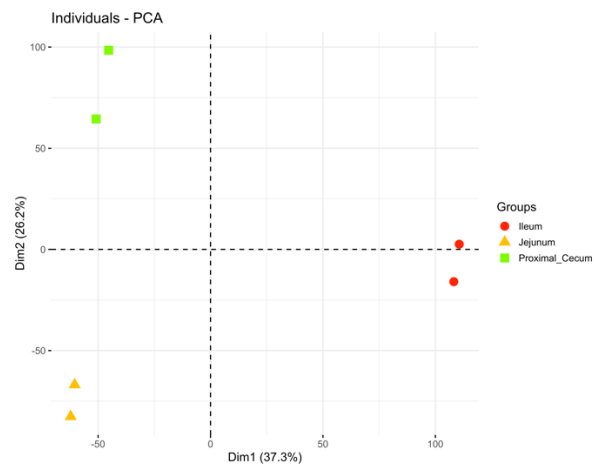
## DE analysis: intestine tissues

Note: total n.sv=3, but only n.sv=1 can work in svaseq() function

### Using sva with n.sv=1



### Not using sva



Note: The two PCA are the same.

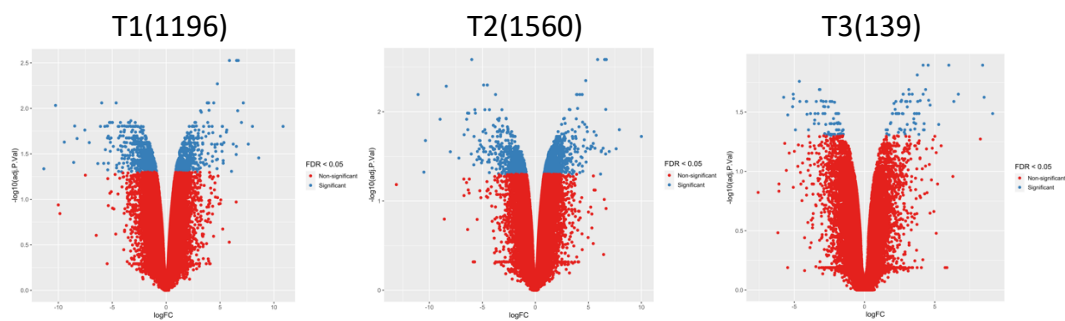
```
> contrast.matrix_intestine
```

	T1	T2	T3
Ileum	1	1	0
Jejunum	-1	0	1
Proximal_Cecum	0	-1	-1

### Using sva with n.sv=1



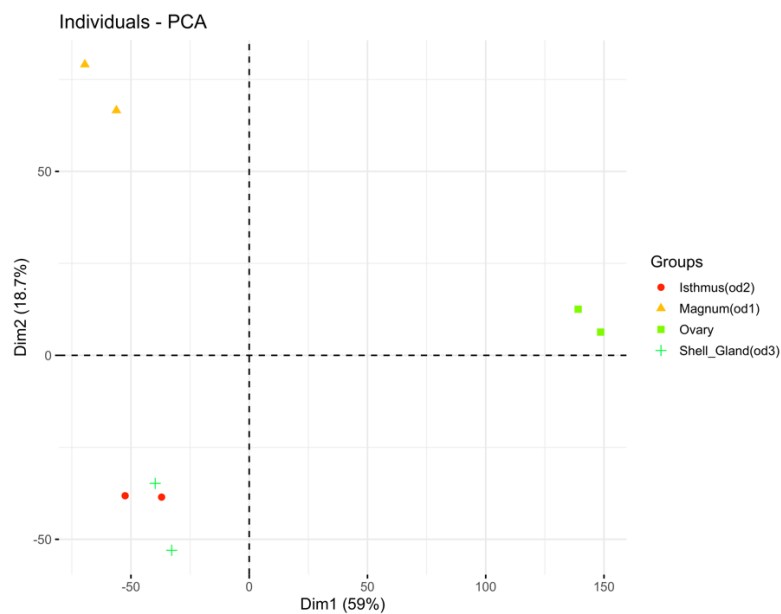
### Not using sva



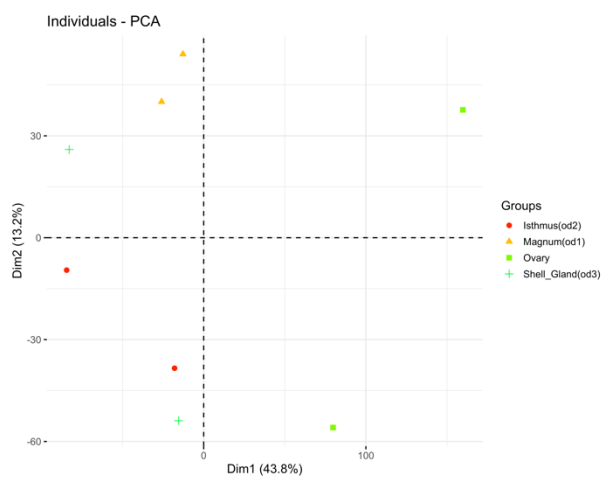
## DE analysis: reproductive tissues

Note: total n.sv=4, there are no significance DE among all tissue comparisons when n.sv=2 or 3

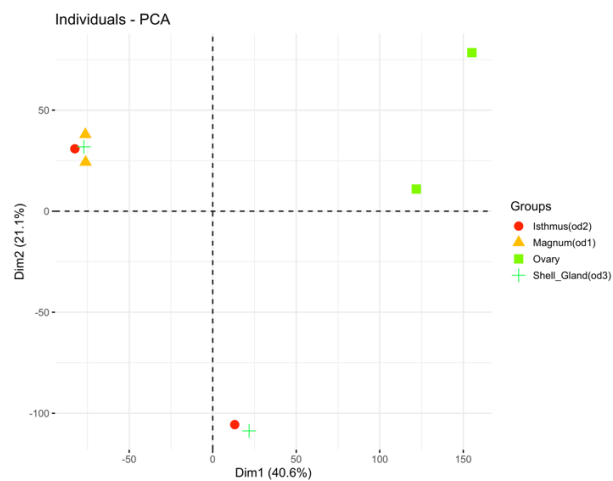
### using sva with n.sv=3



### Using sva with n.sv=1



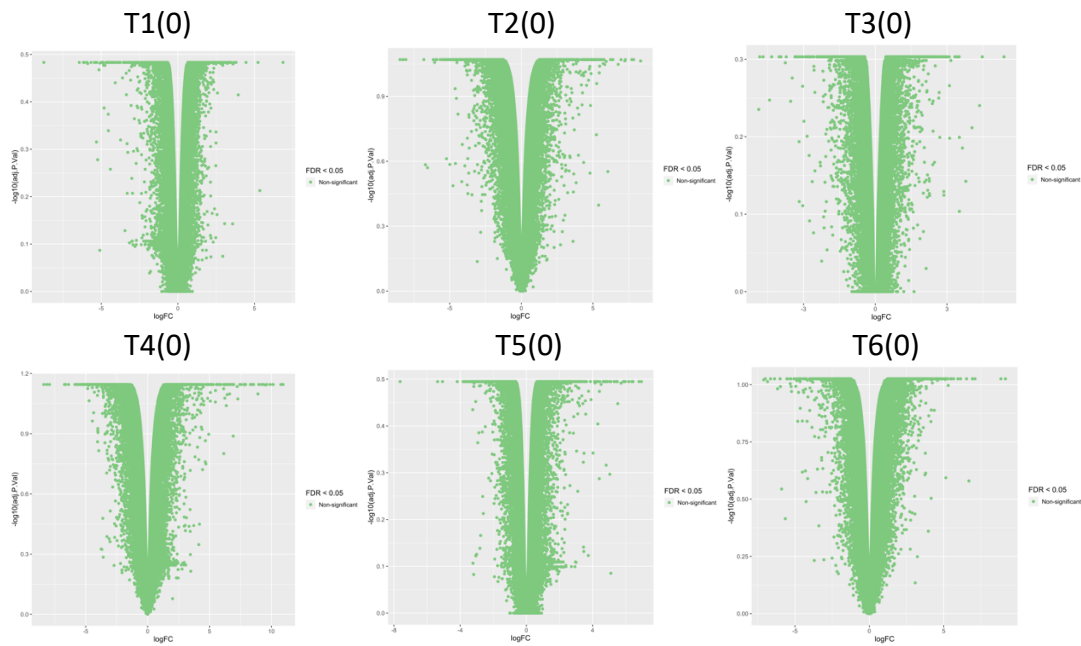
### not using sva



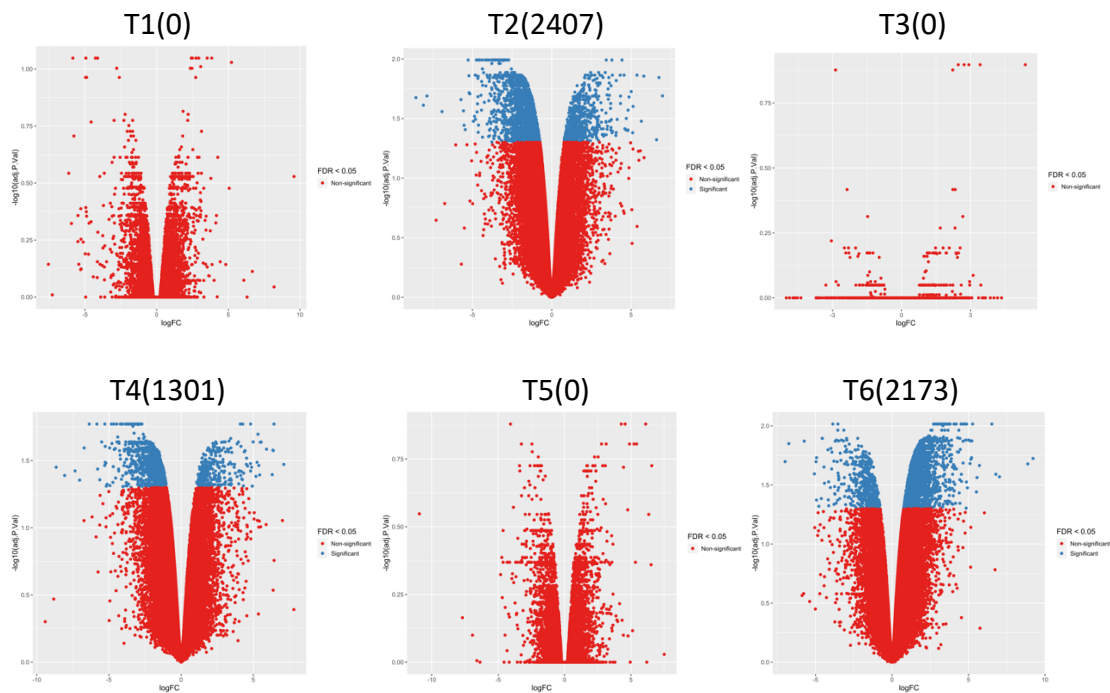
> contrast.matrix

	T1	T2	T3	T4	T5	T6
Isthmus(od2)	1	1	1	0	0	0
Magnum(od1)	-1	0	0	1	1	0
Ovary	0	-1	0	-1	0	1
Shell_Gland(od3)	0	0	-1	0	-1	-1

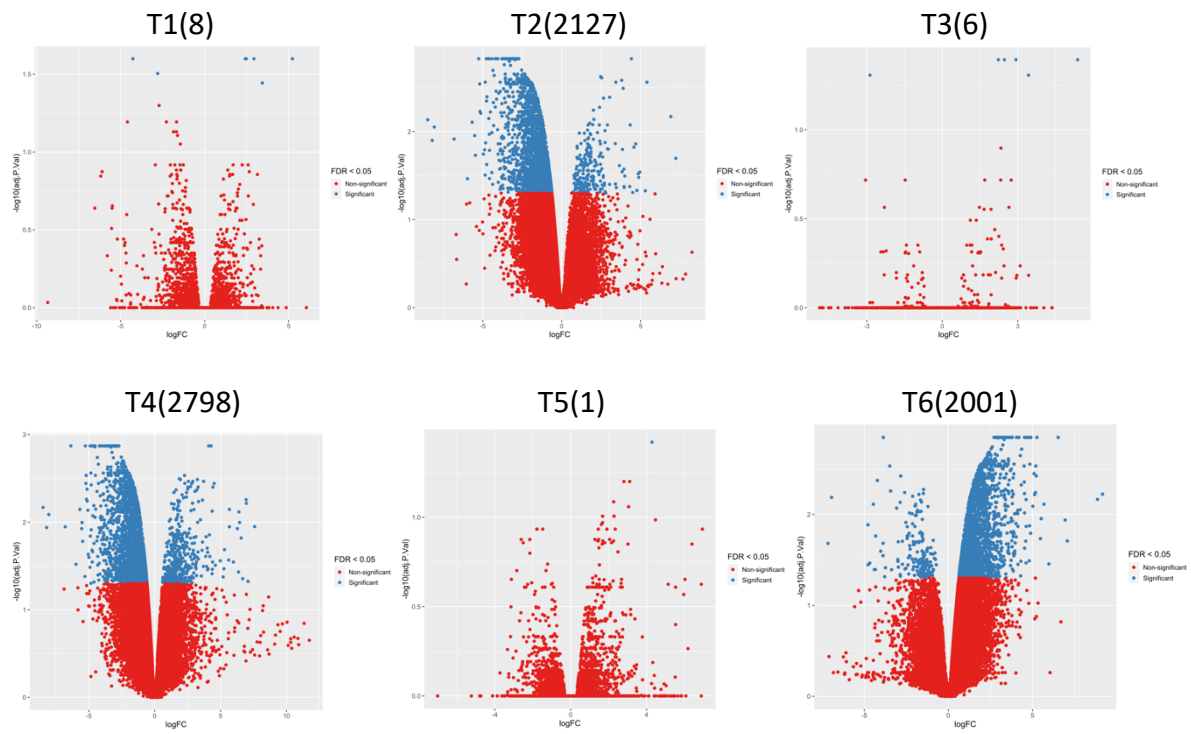
### Using sva with n.sv=3



### Using sva with n.sv=1



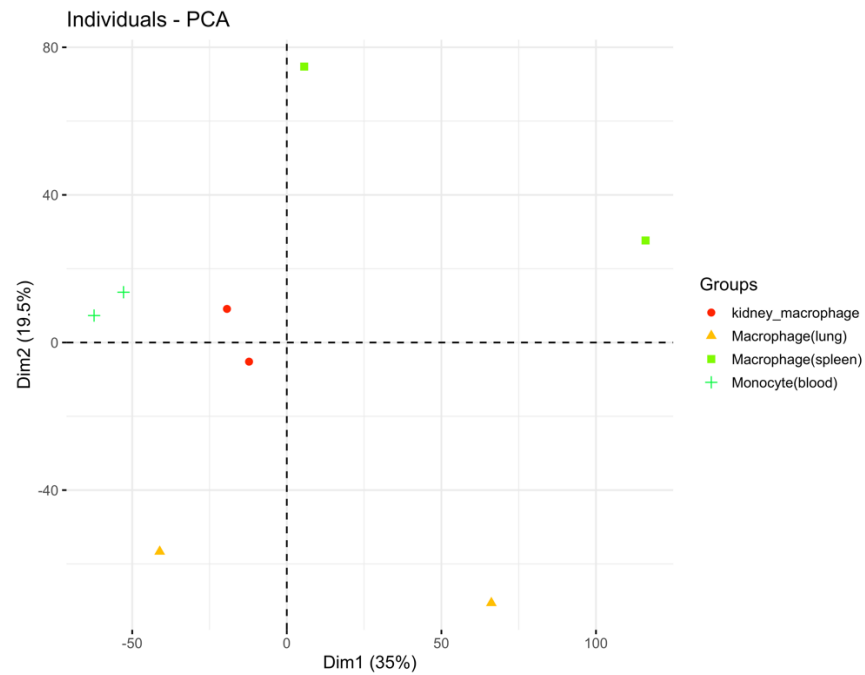
## Not using sva



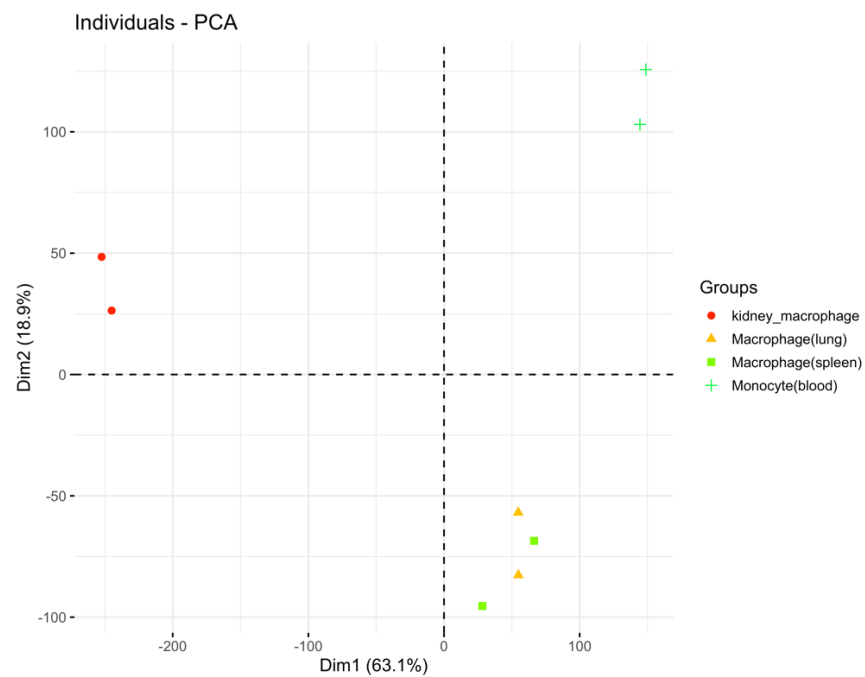
## DE analysis: macrophage tissues and monocyte

Note: total n.sv=4, there are no significance DE among all tissue comparisons when n.sv=2 or 3

### Using sva with n.sv=2



### Using sva with n.sv=1



```
> contrast.matrix
```

	T1	T2	T3	T4	T5	T6
macrophage_kidney	1	1	1	0	0	0
Macrophage_lung	-1	0	0	1	1	0
Macrophage_spleen	0	-1	0	-1	0	1
Monocyte	0	0	-1	0	-1	-1

Using sva with n.sv=1

