Target Expression profiling for APOE

- Template WIP - Not finished yet!! -

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# Introduction

Cross-tissue mRNA expression of APOE was assessed in available tissues of the following species: **Homo sapiens, Canis familiaris, Macaca fascicularis and Mus Musculus**.

# Results

APOE is statistically enriched in the following tissues: **digestive system, endocrine system**. By specie, the tissues where the gene is enriched are:

| Species | Enrichment |
| --- | --- |
| Canis familiaris | digestive system |
| Homo Sapiens | digestive system, endocrine system |
| Macaca fascicularis | digestive system |
| Mus musculus | digestive system |

From the point of view of the tissues, the different species that are statistically enriched are:

| Tissues | Species |
| --- | --- |
| adrenal gland | Homo Sapiens |
| liver | Homo Sapiens, Macaca fascicularis, Canis familiaris, Mus musculus |

###### (\*\*\* ZScore > 3 | \*\* 3 > ZScore > 2 | \* 2 > ZScore > 1)

Expression values per tissue in individual species and data sets can be found in Section 4. A summary heatmap can be found in **Figure 4-10**. The list of tissues per species and datasets expressing APOE are shown in **Table 5-2**.

# Tables

## Summary table

## Databases row data

### GTEx