Supplementary Figure S1

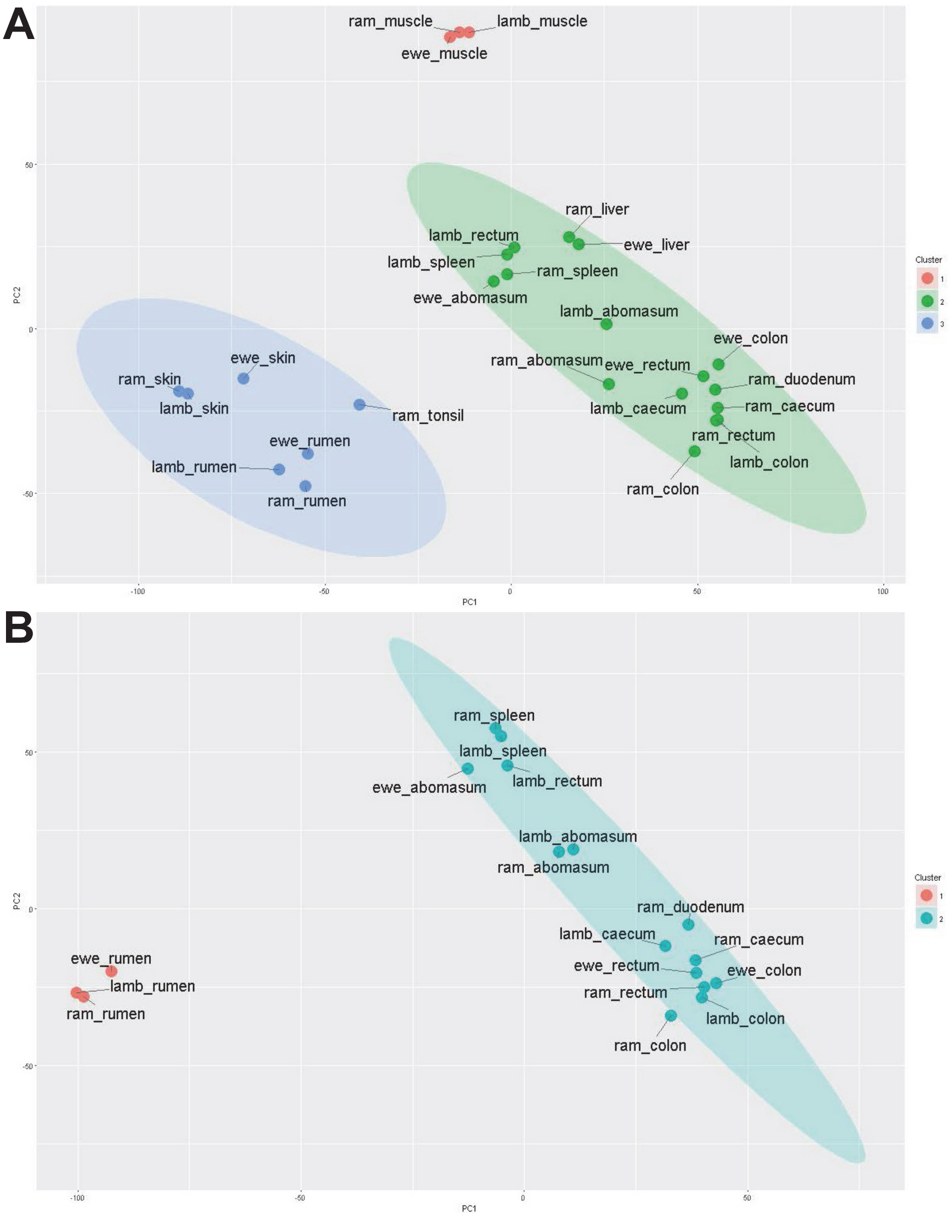
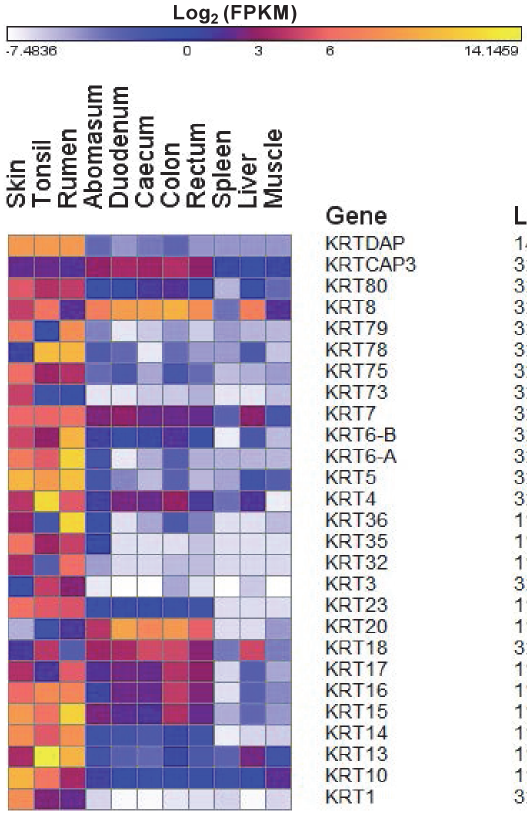


Figure S1. Raw output of PCA clustering of tissues. **A**: Three significantly separated clusters of total 26 studied tissues. **B**: Two significantly separated clusters of studied tissues without epithelial (skin and tonsil) and reference (muscle and liver) tissues. Cluster boundary significance testing is performed based on K-mean clustering and bivariate t-distribution using stat_ellipse package (https://github.com/JoFrhwld/FAAV/blob/master/r/stat-ellipse.R) and presented in ggplot2 in R.

Supplementary Figure S2



Gene	Location
KRTDAP	14:45254953-45258246
KRTCAP3	3:34364032-34365125
KRT80	3:134021407-134042991
KRT8	3:133375727-133383019
KRT79	3:133433601-133443905
KRT78	3:133420696-133428181
KRT75	3:133772163-133781755
KRT73	3:133608720-133618332
KRT7	3:133962047-133975095
KRT6-B	3:133739439-133744414
KRT6-A	3:133722475-133727191
KRT5	3:133704094-133709834
KRT4	3:133453262-133459729
KRT36	11:41180429-41184184
KRT35	11:41168178-41172256
KRT32	11:41156442-41163908
KRT3	3:133471252-133477730
KRT23	11:40690641-40707235
KRT20	11:40637777-40646750
KRT18	3:133329883-133333811
KRT17	11:41324173-41338864
KRT16	11:41315077-41317232
KRT15	11:41206815-41224898
KRT14	11:41277222-41284786
KRT13	11:41198168-41202367
KRT10	11:40583329-40587120
KRT1	3:133566405-133604565

Figure S2. Expression profile of gastrointestine related keratin genes. Keratin genes are selected based on their average count per million values in gastrointestinal tissues > 3.

Supplementary Figure S3

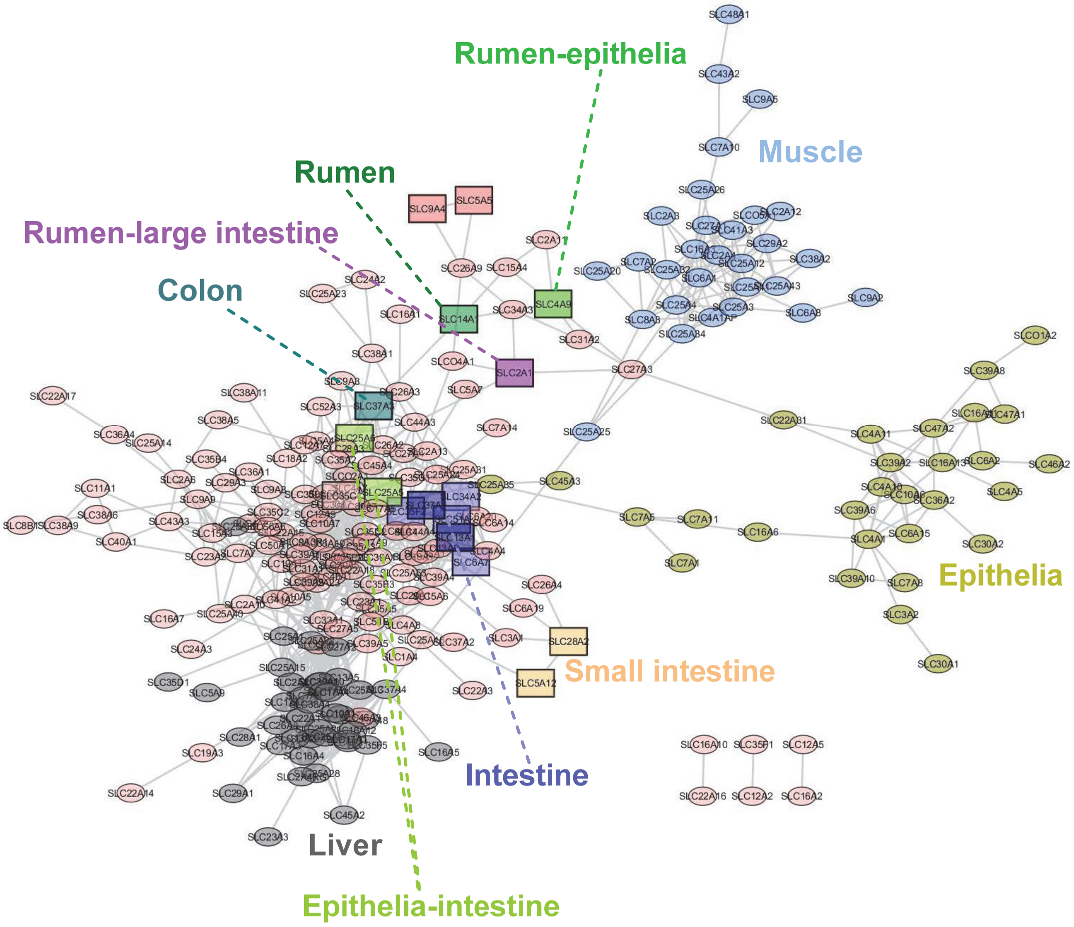


Figure S3. Clustering of transporter genes. Genes in boxes are assigned with sheep clusters as shown in table S1.