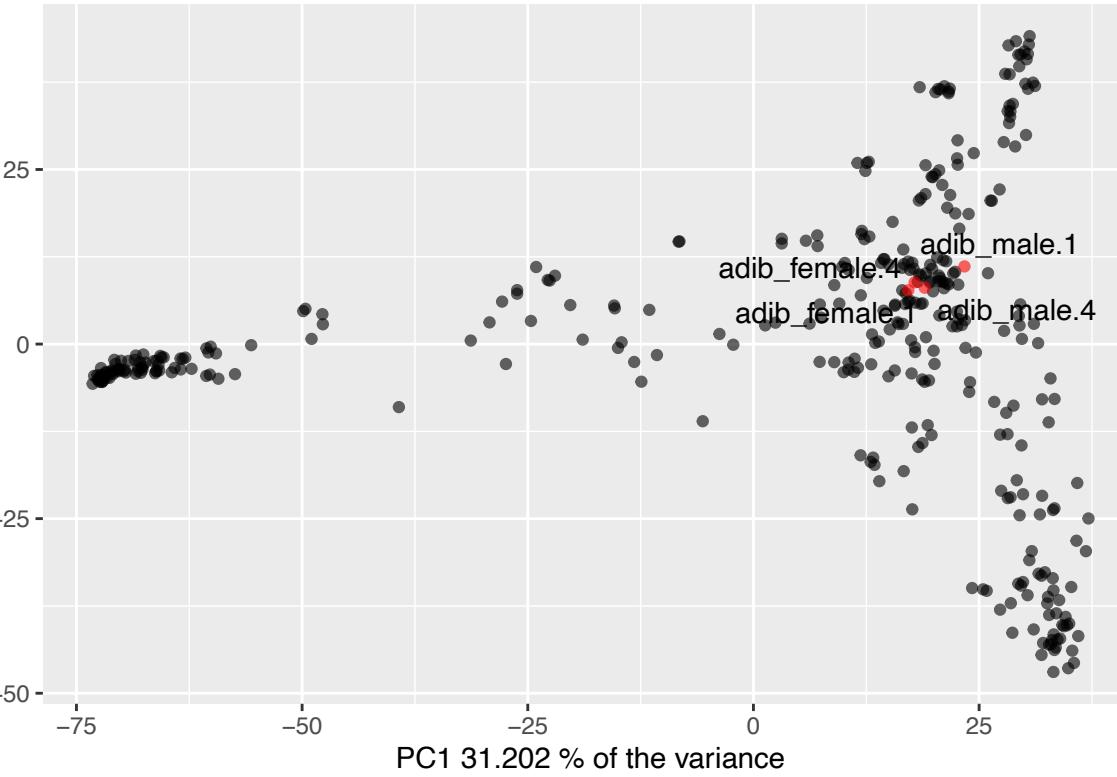
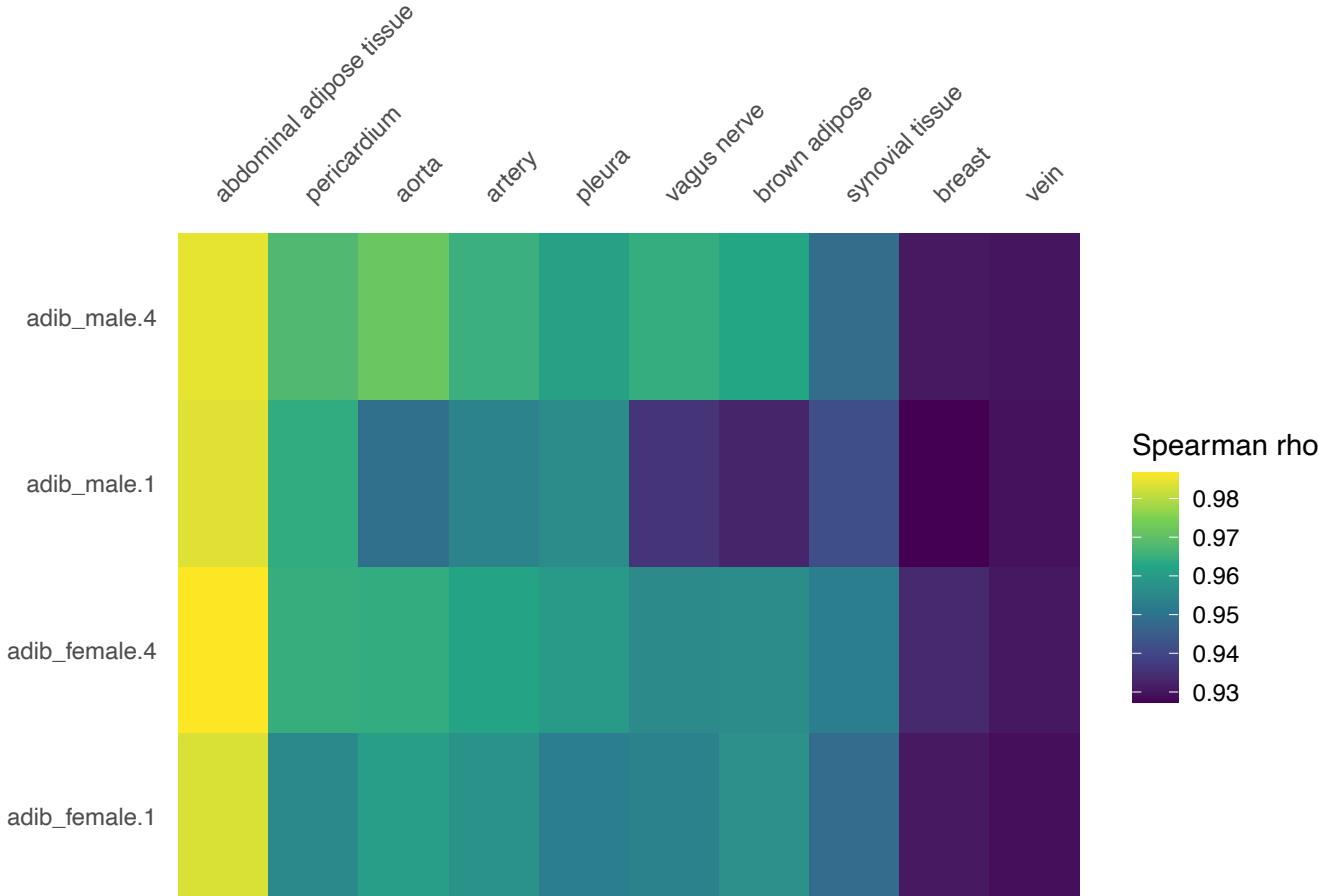


abdominal adipose tissue, PCA: TMM expression values

PC2 9.077 % of the variance



Tissue group to sample correlation



abdominal adipose tissue, UMAP: TMM expression values

UMAP2

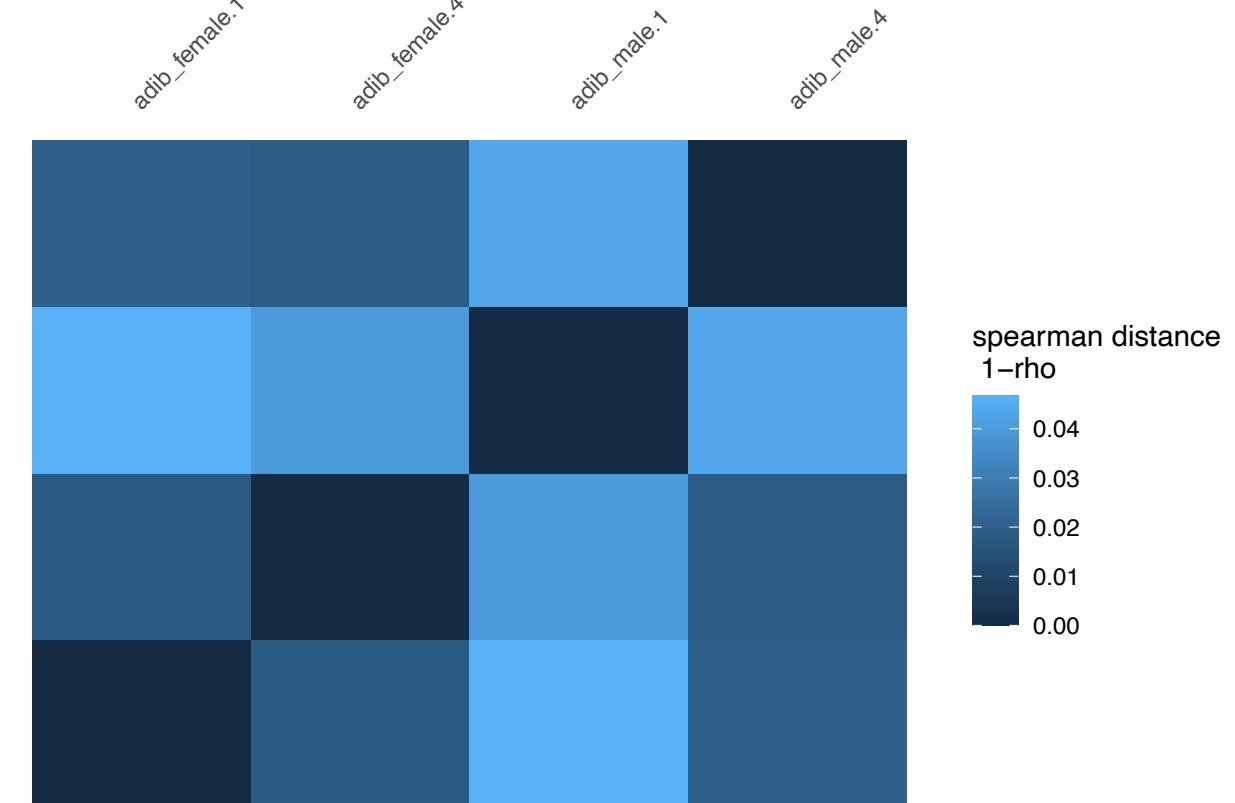
-20

-10

0

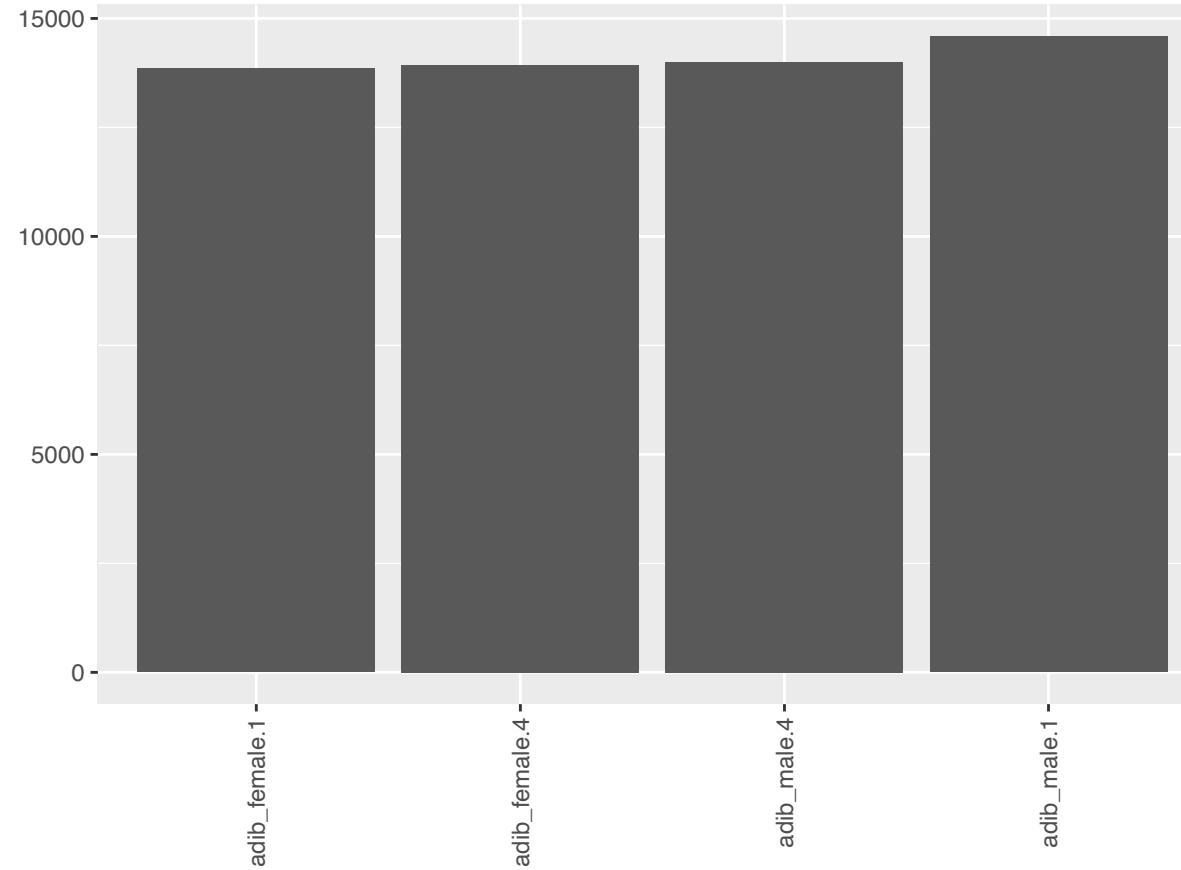
10

In tissue sample to sample Spearman Distance



abdominal adipose tissue

n(genes) >= 1 TMM



abdominal adipose tissue

log10(expression+1)

0

2

4

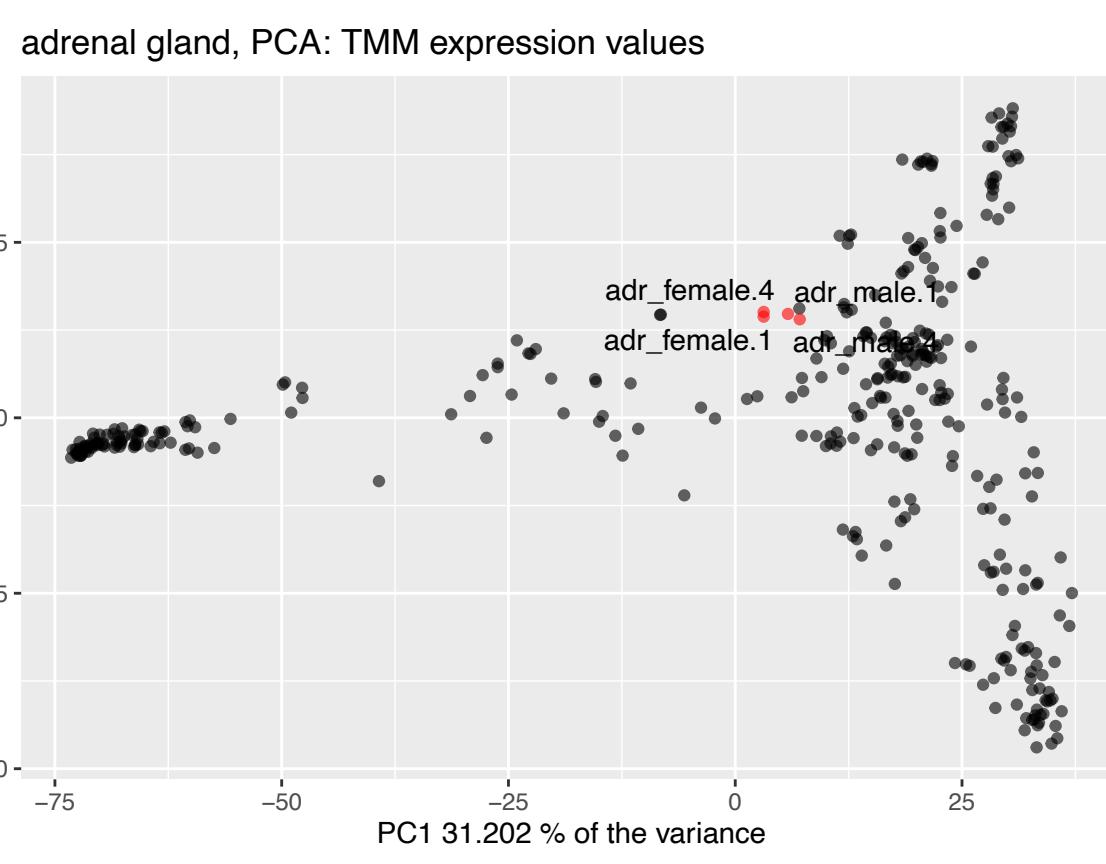
adib_female.1

adib_female.4

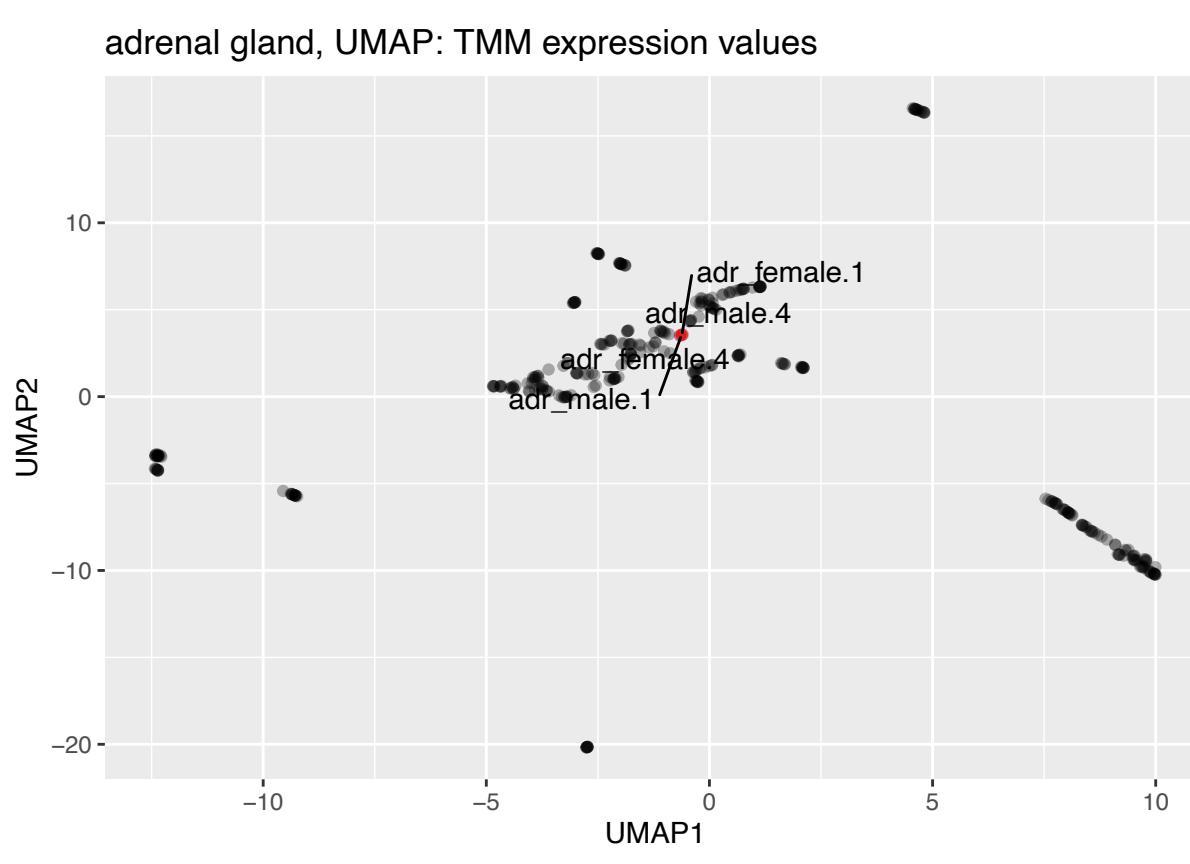
adib_male.1

adib_male.4

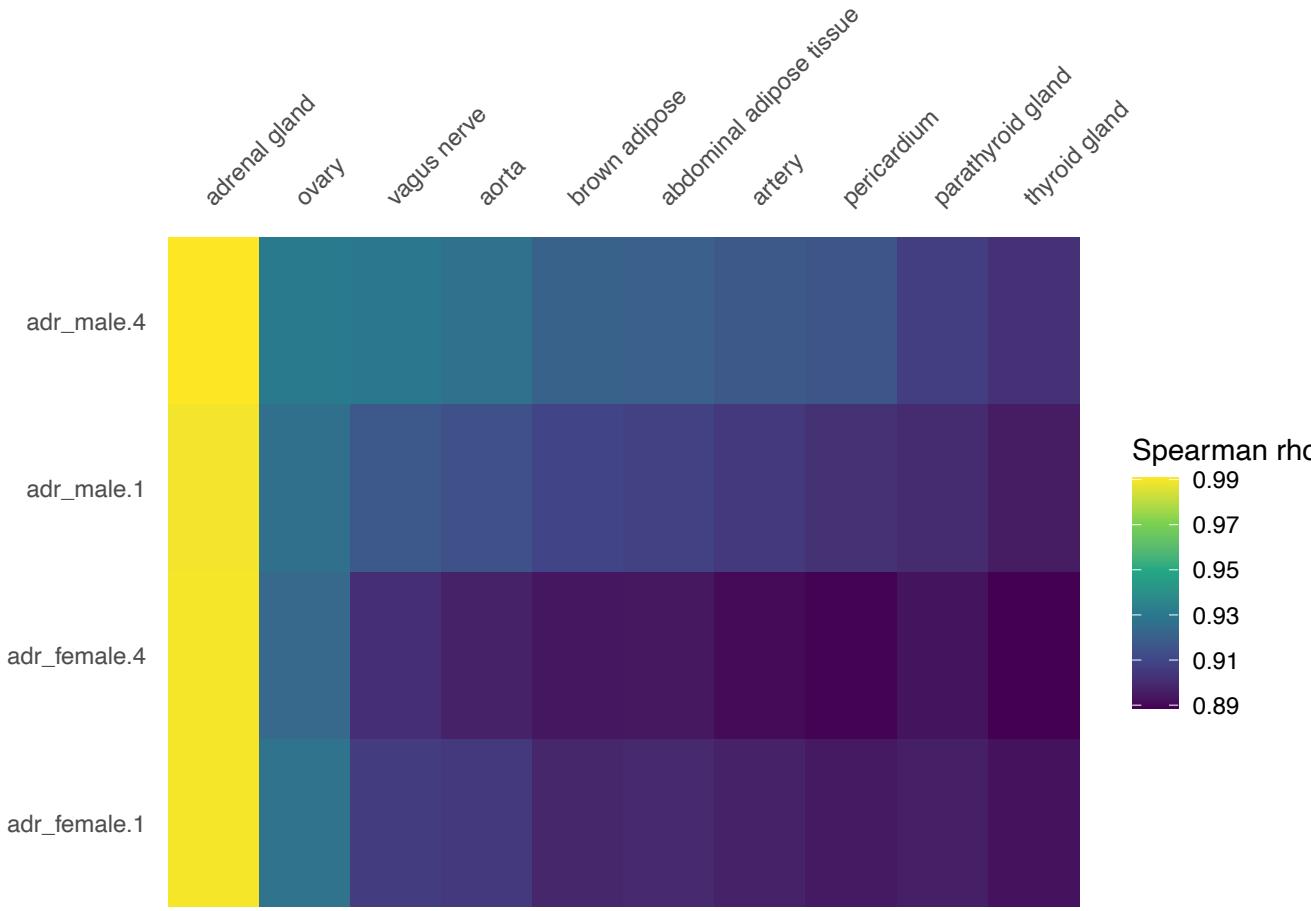
type
tmm_val
tpm_val



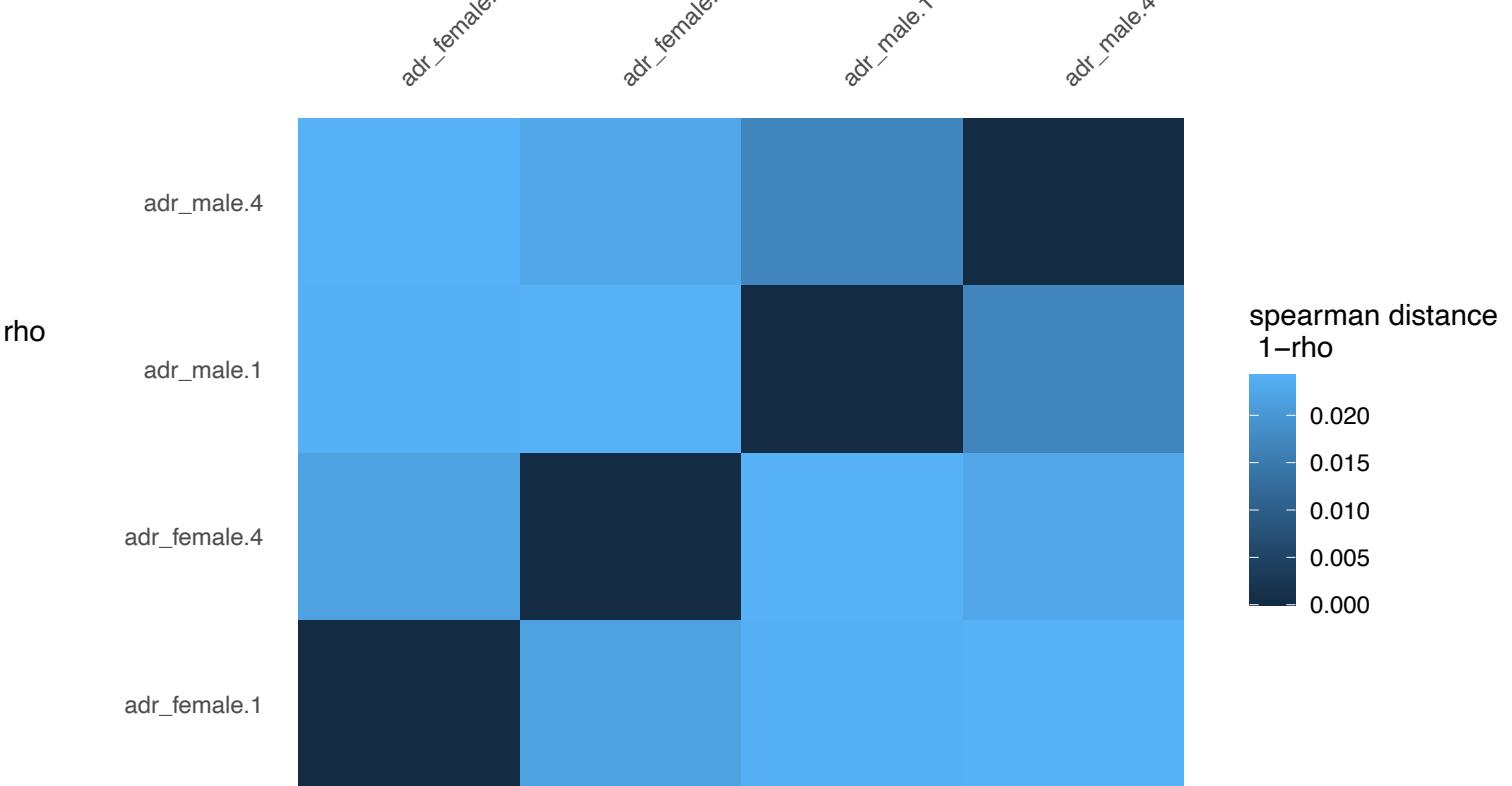
Tissue group to sample correlation



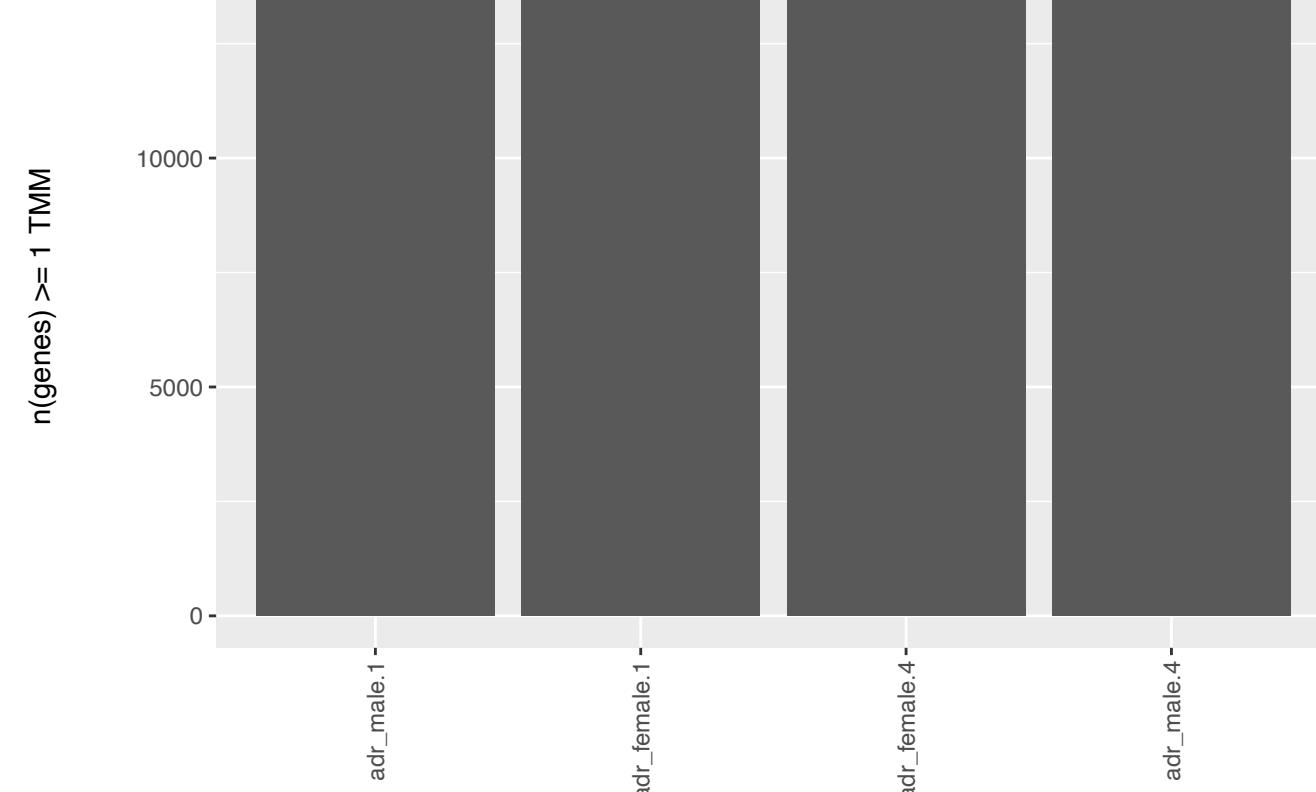
In tissue sample to sample Spearman Distance



adrenal gland

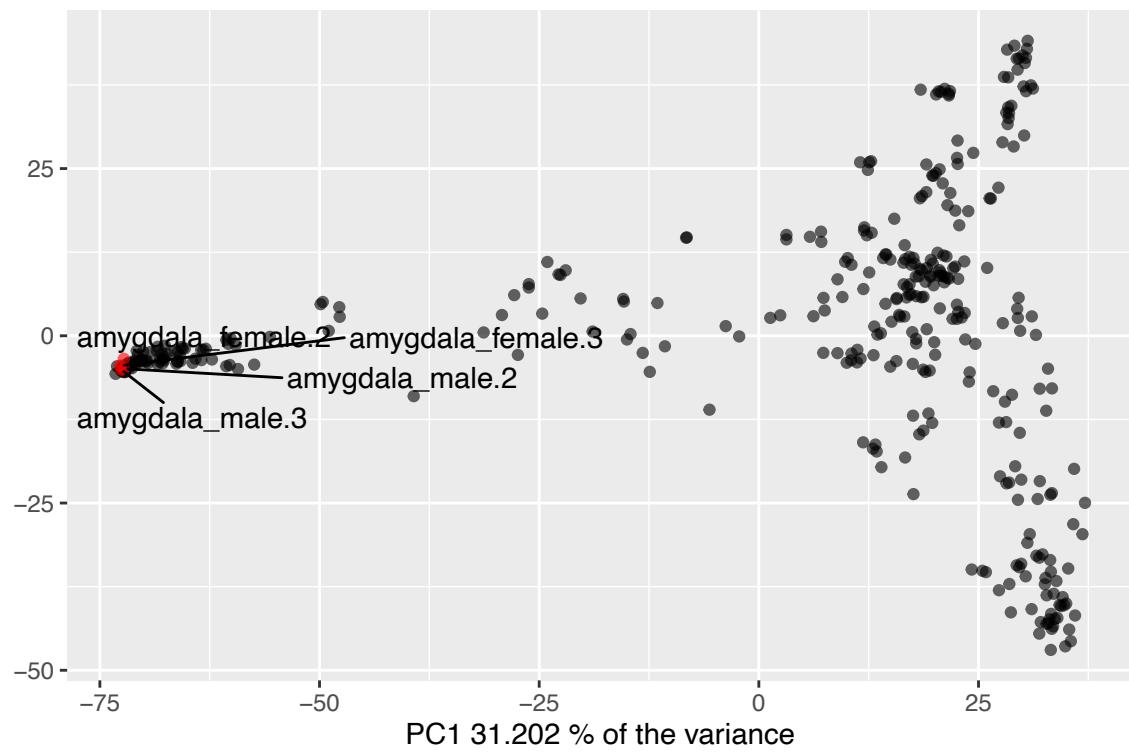


adrenal gland

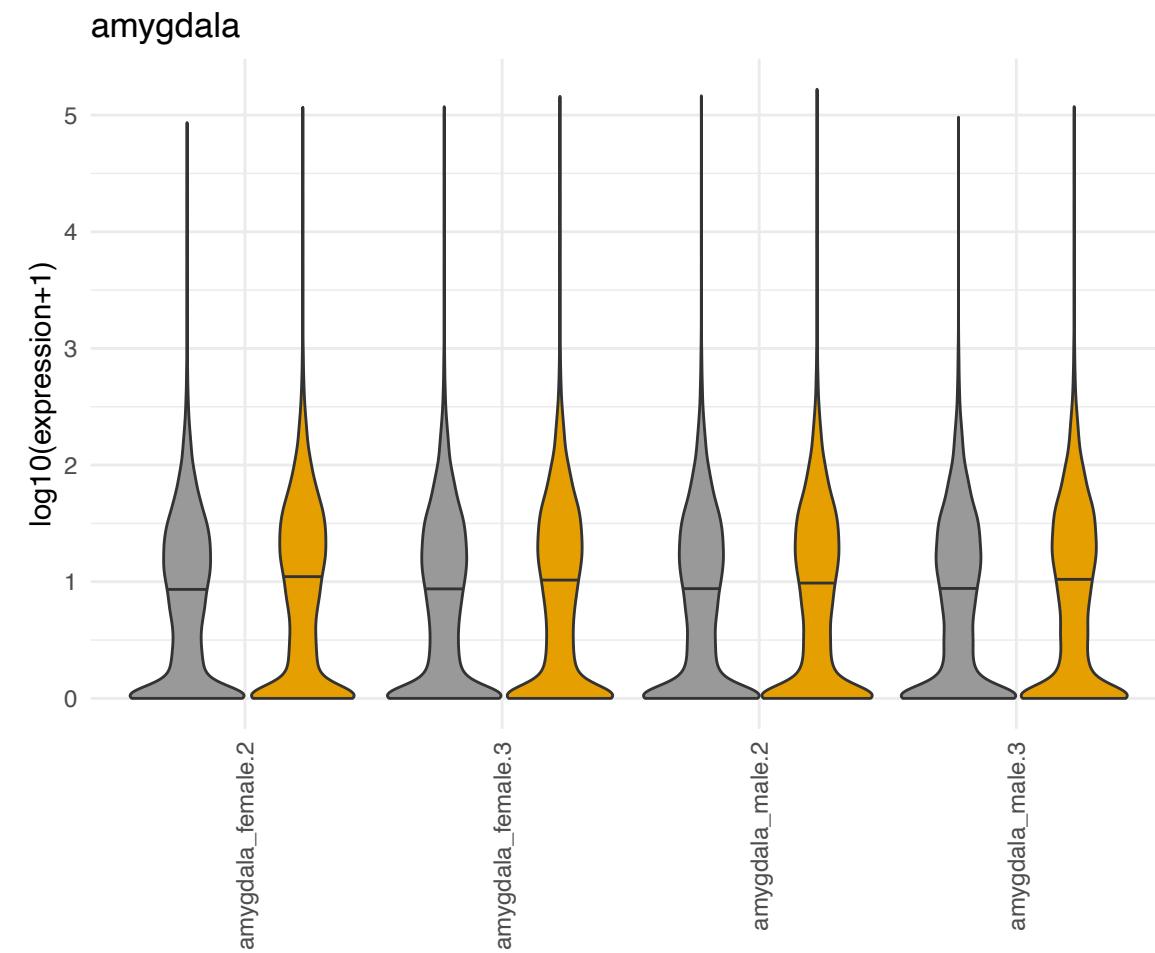
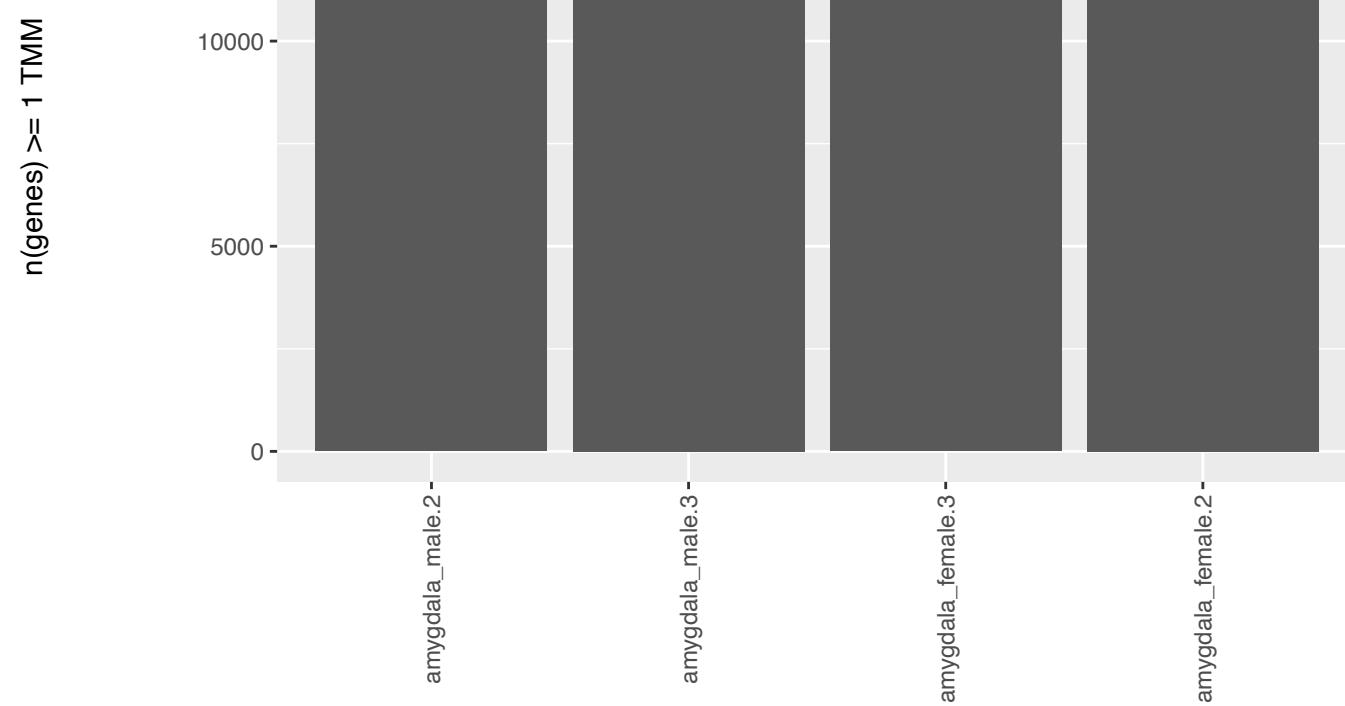
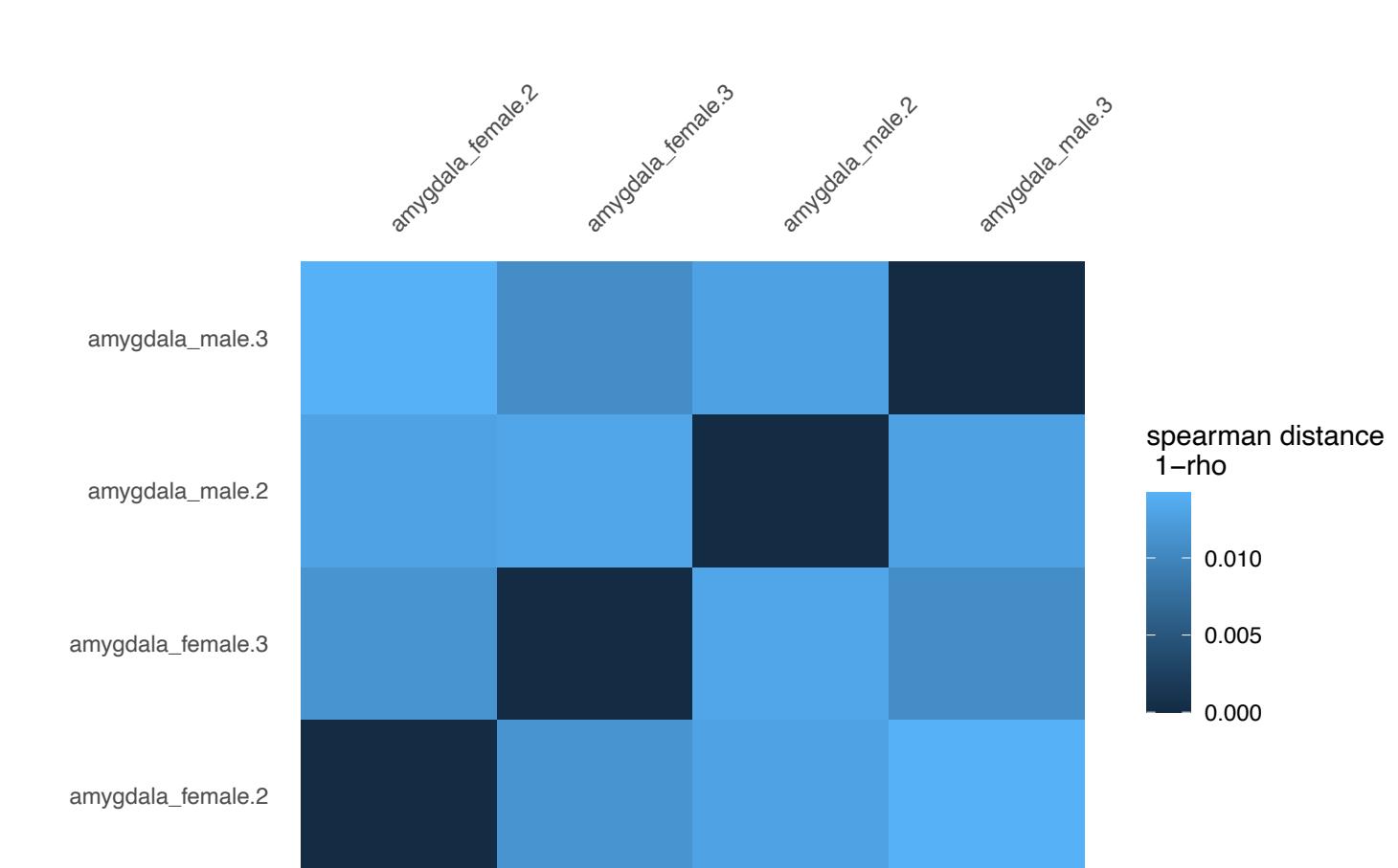
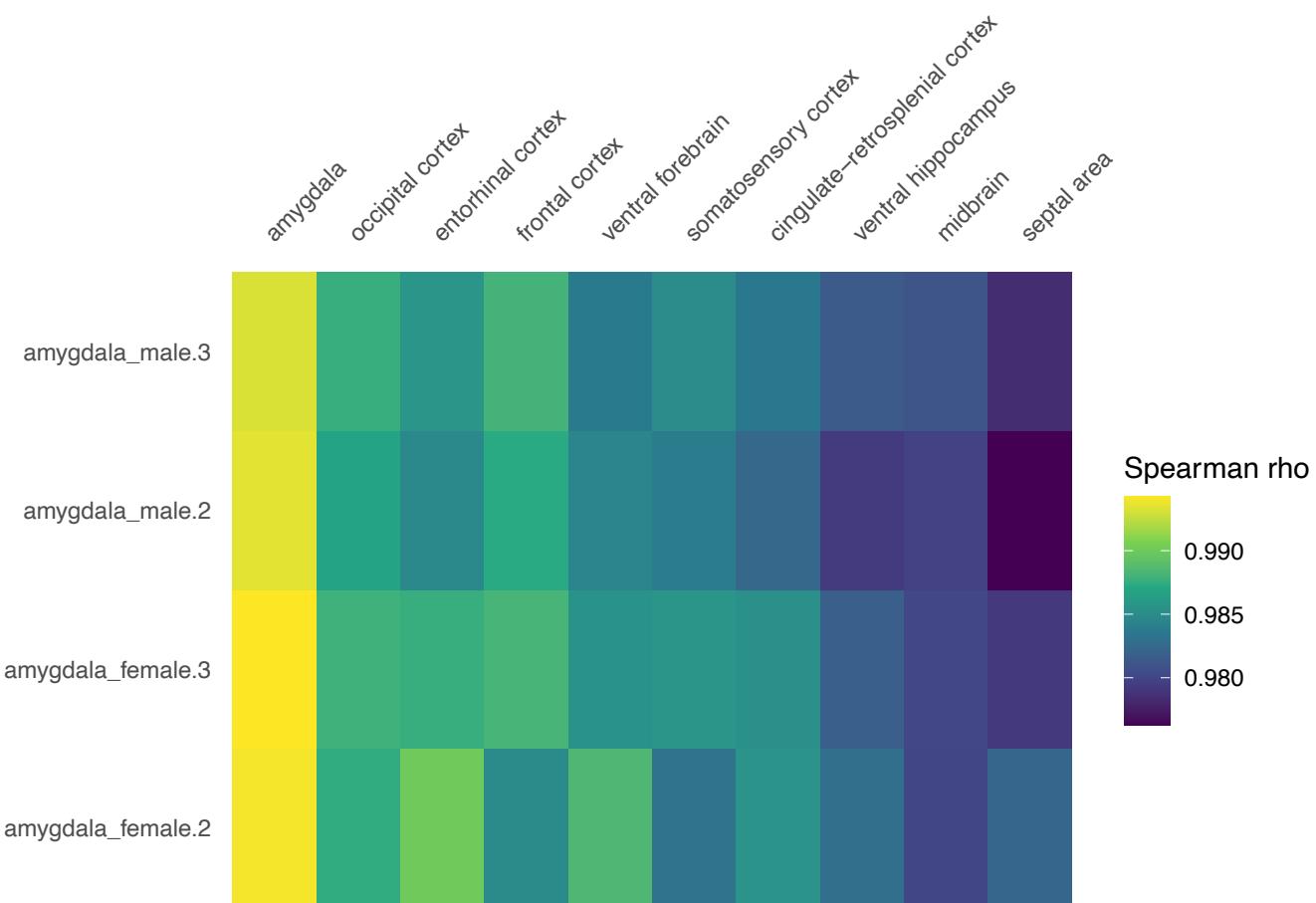
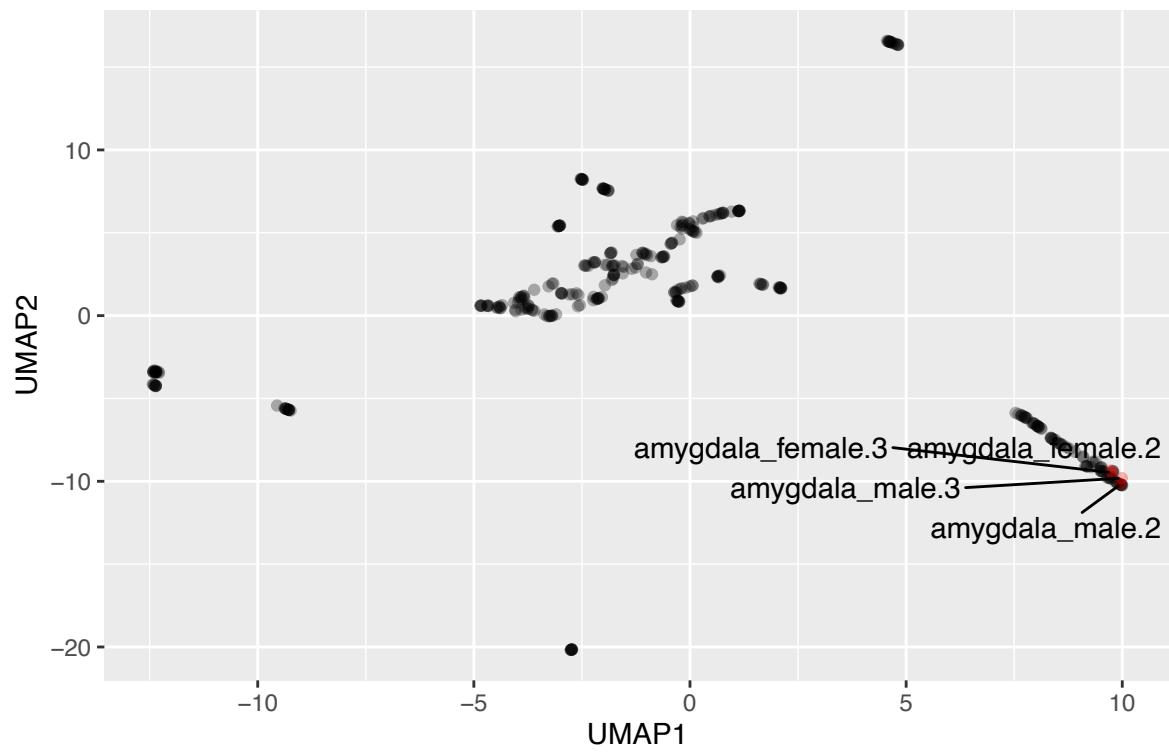


The figure consists of four side-by-side violin plots. The y-axis is labeled $\log_{10}(\text{expression}+1)$ and ranges from 0 to 4. Each plot has two violins: a grey one on the left and an orange one on the right. The x-axis labels are rotated vertically: "adr_female_1", "adr_female_4", "adr_male_1", and "adr_male_4". In each plot, the grey violin covers the lower range (0-1) and the orange violin covers the upper range (1-4). The orange violins are significantly taller than the grey ones, indicating higher expression levels.

amygdala, PCA: TMM expression values

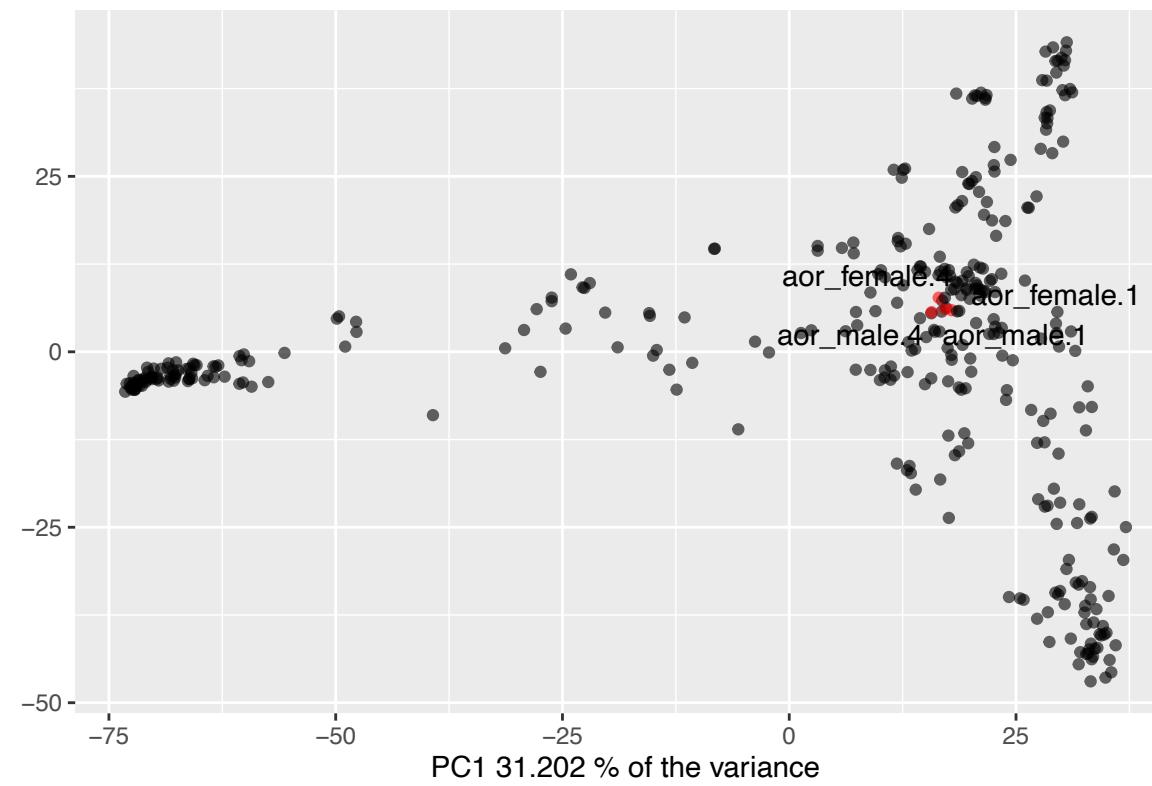


amygdala, UMAP: TMM expression values

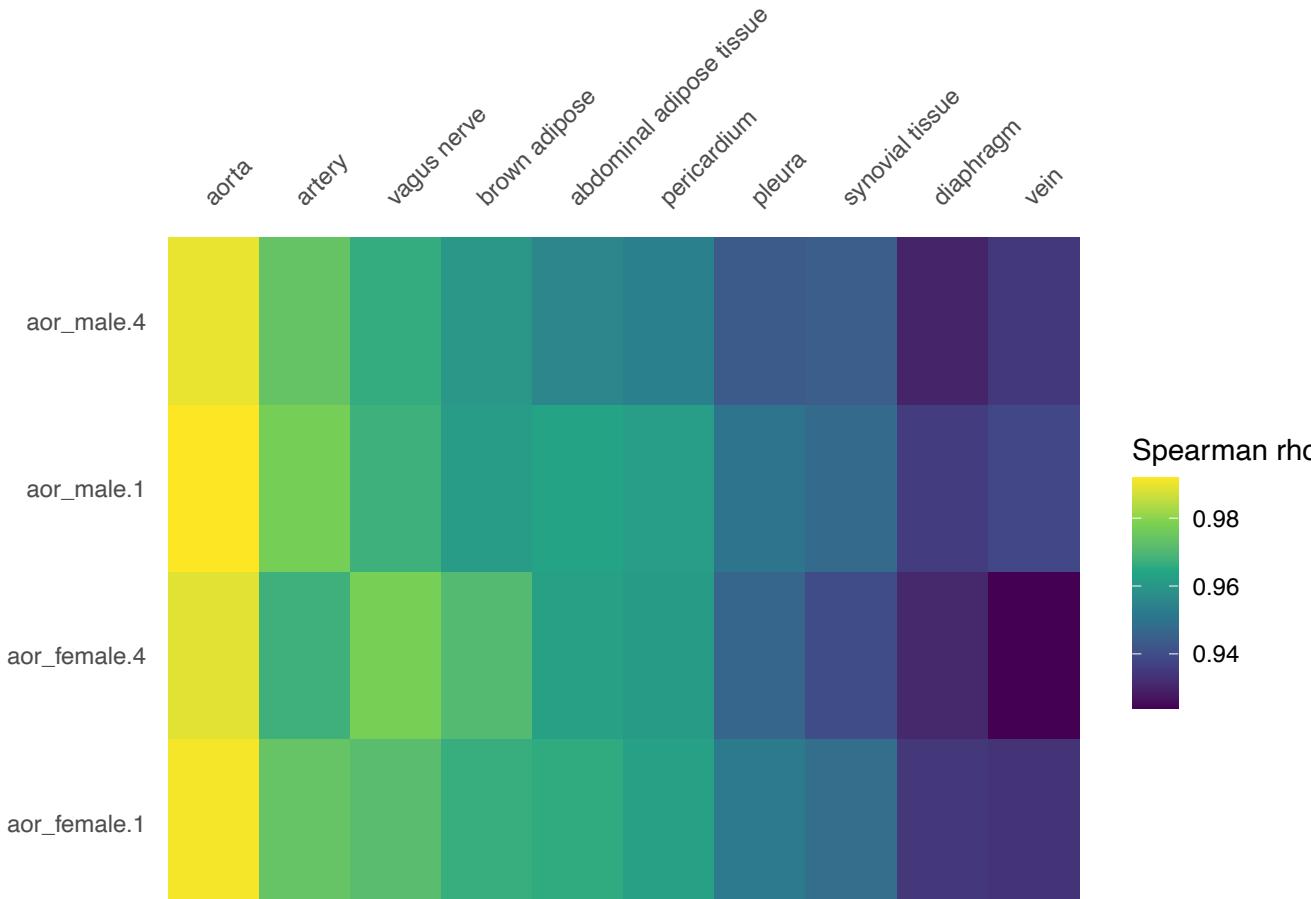


aorta, PCA: TMM expression values

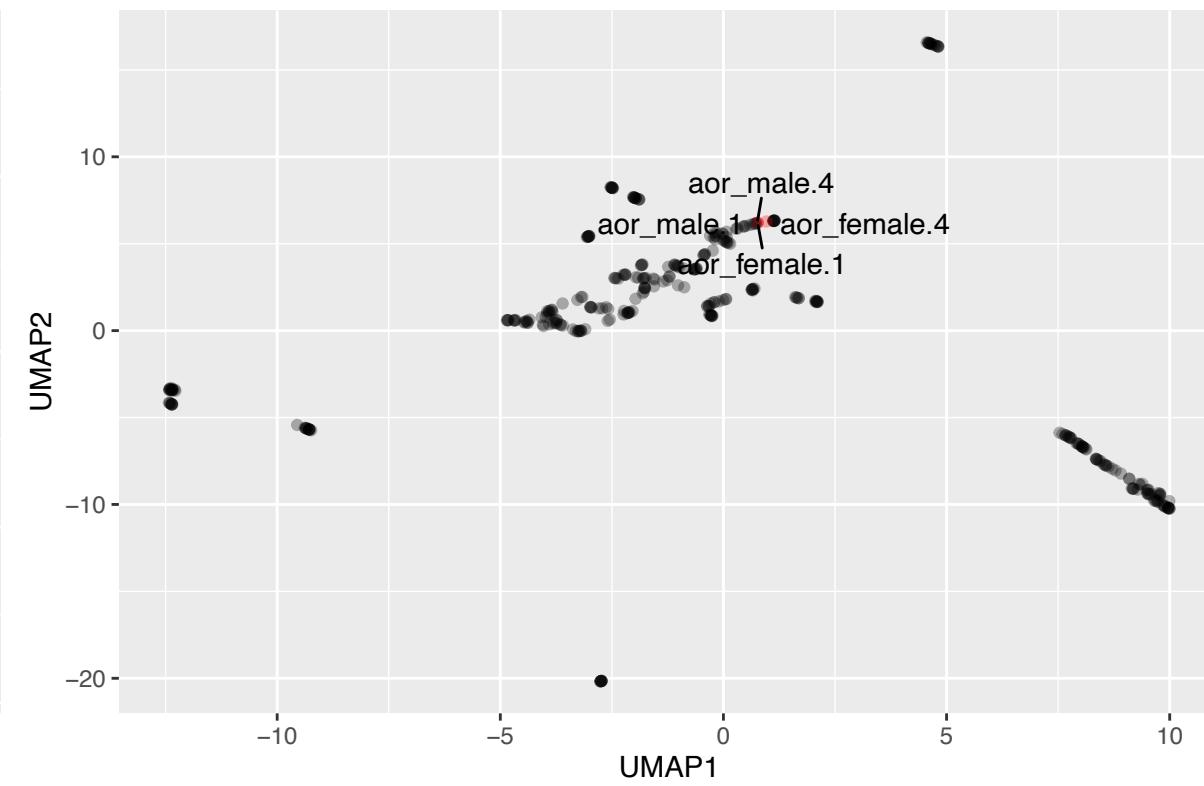
PC2 9.077 % of the variance



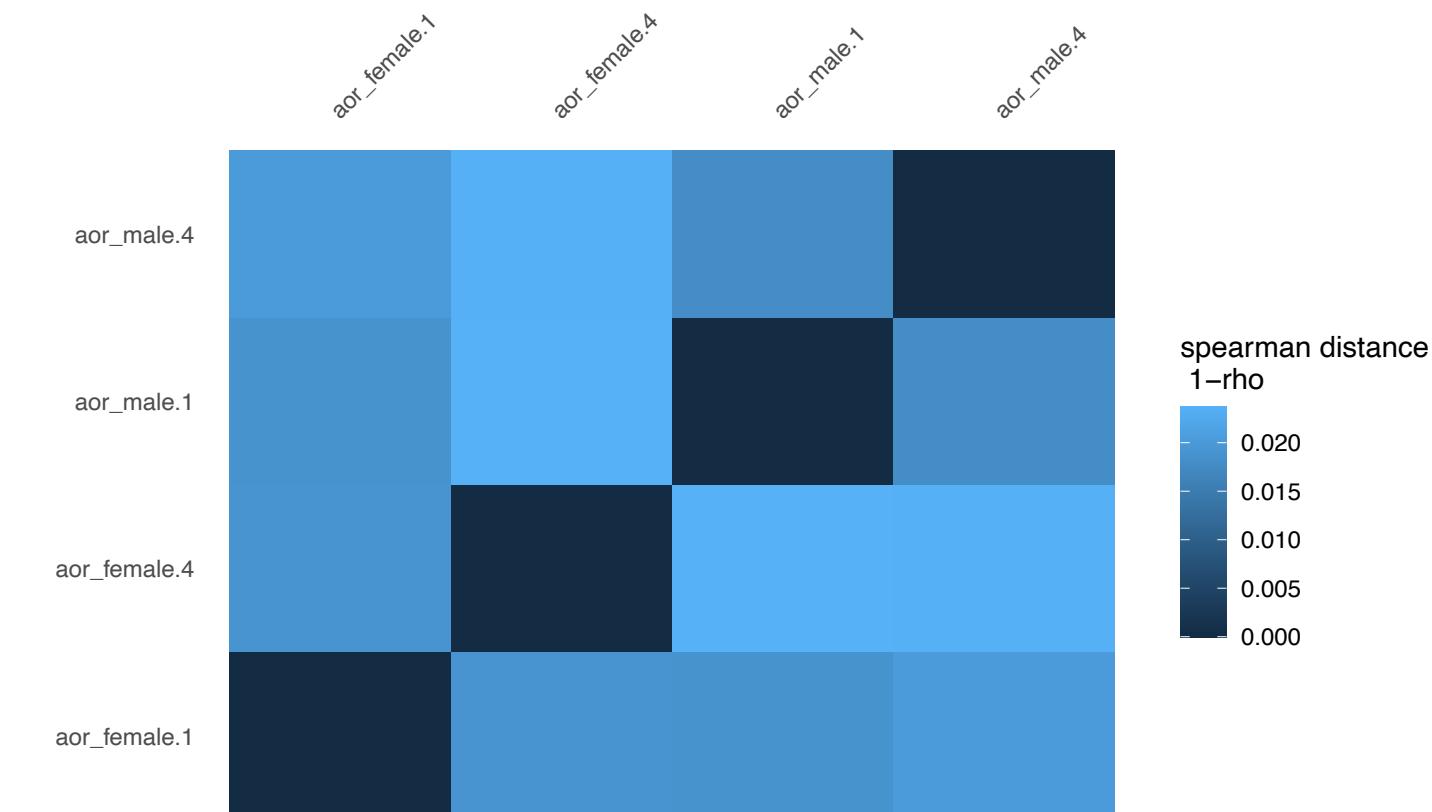
Tissue group to sample correlation



aorta, UMAP: TMM expression values

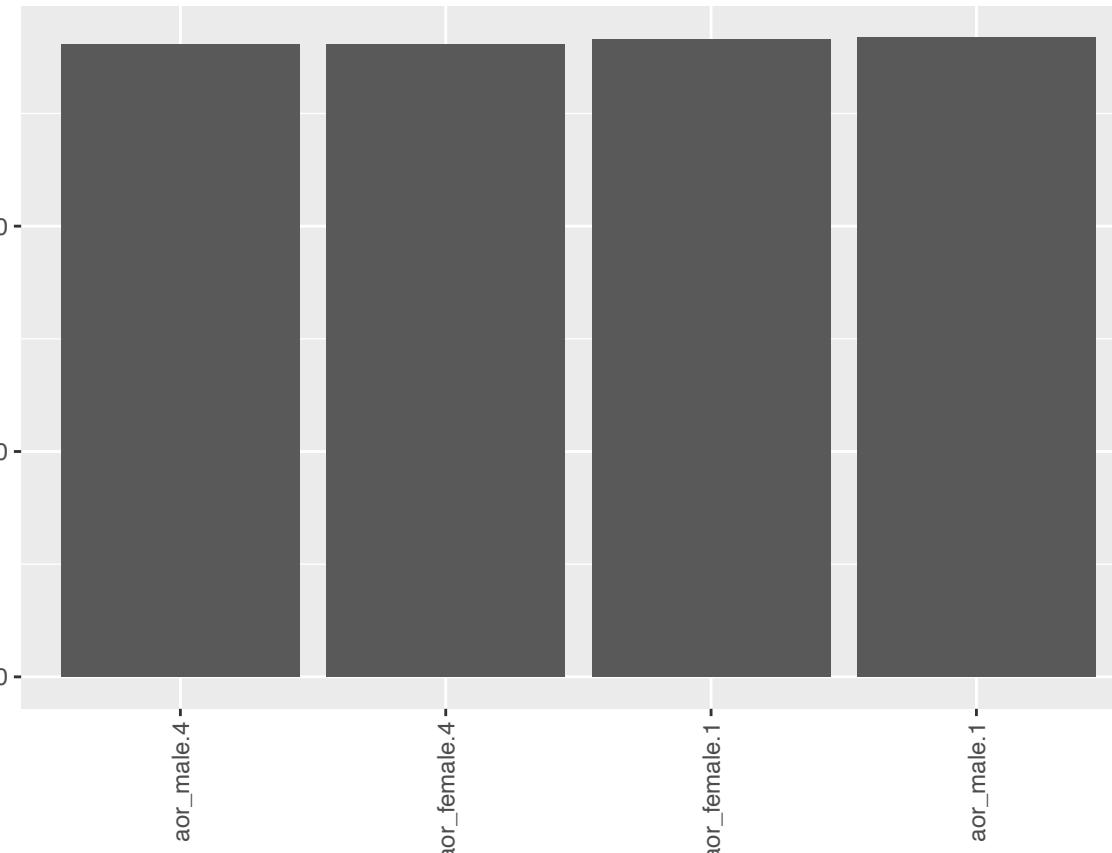


In tissue sample to sample Spearman Distance

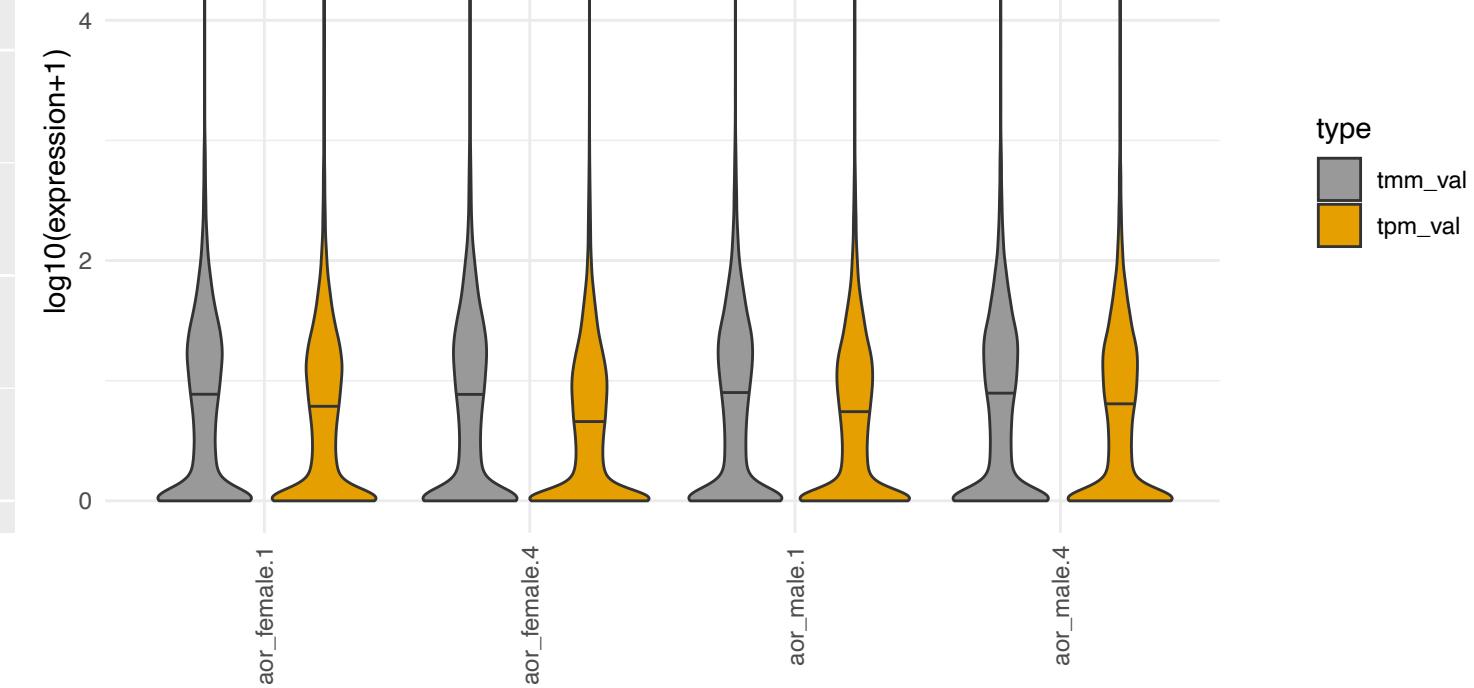


aorta

n(genes) >= 1 TMM

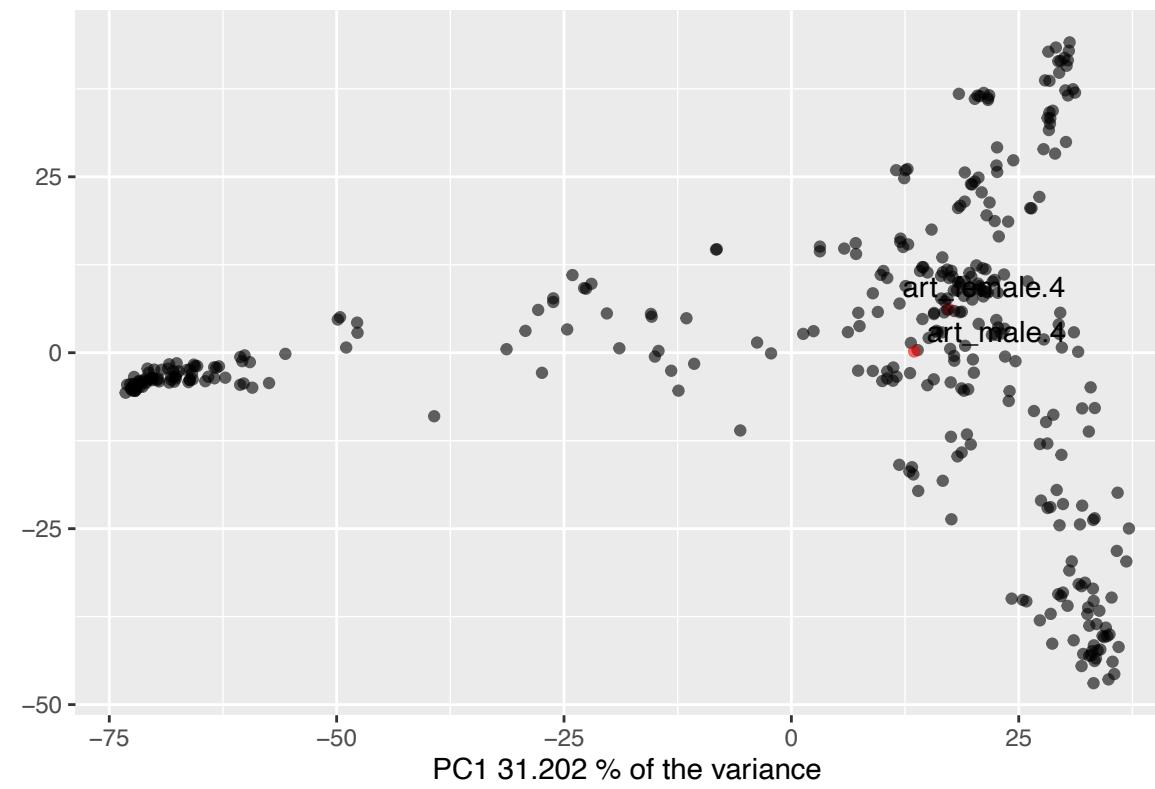


aorta

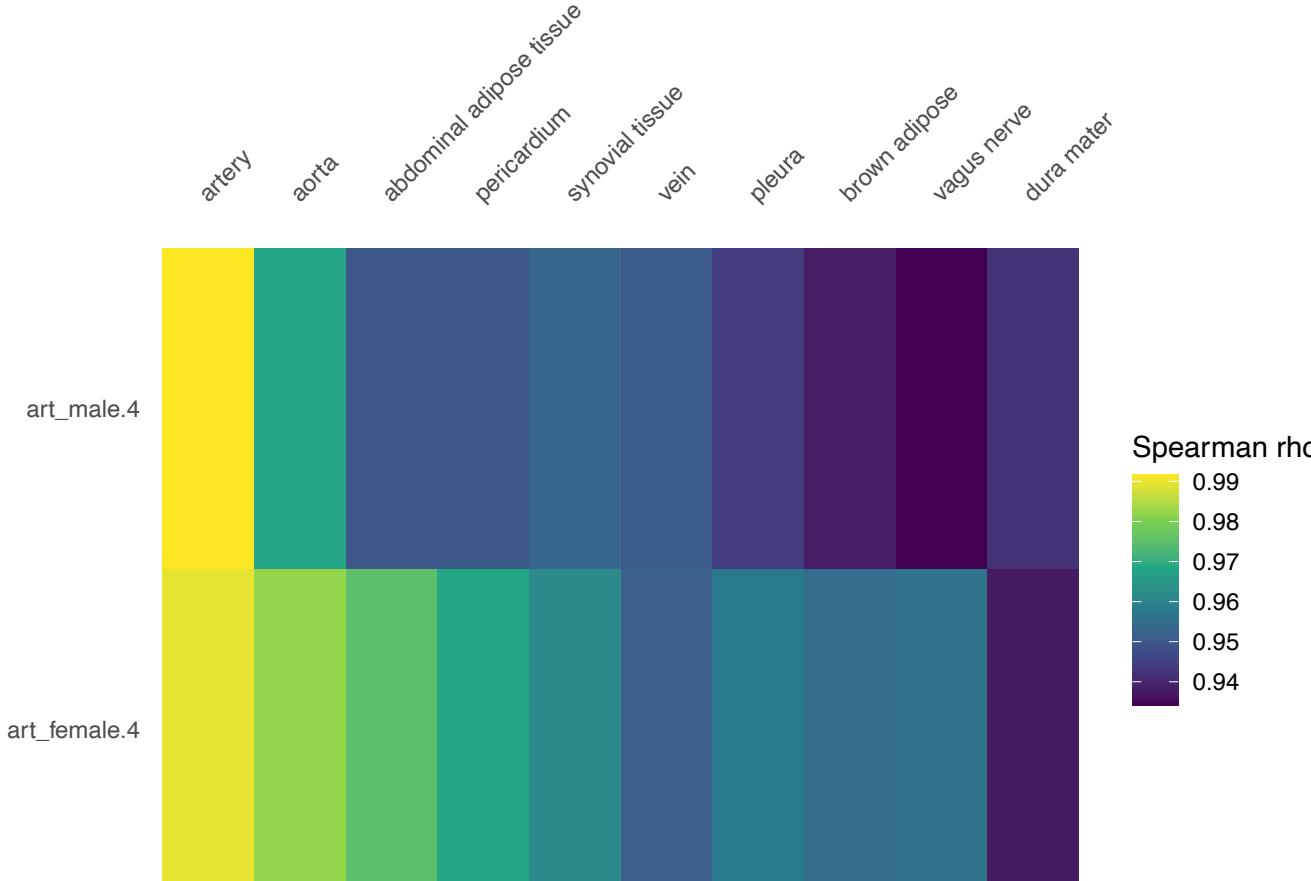


artery, PCA: TMM expression values

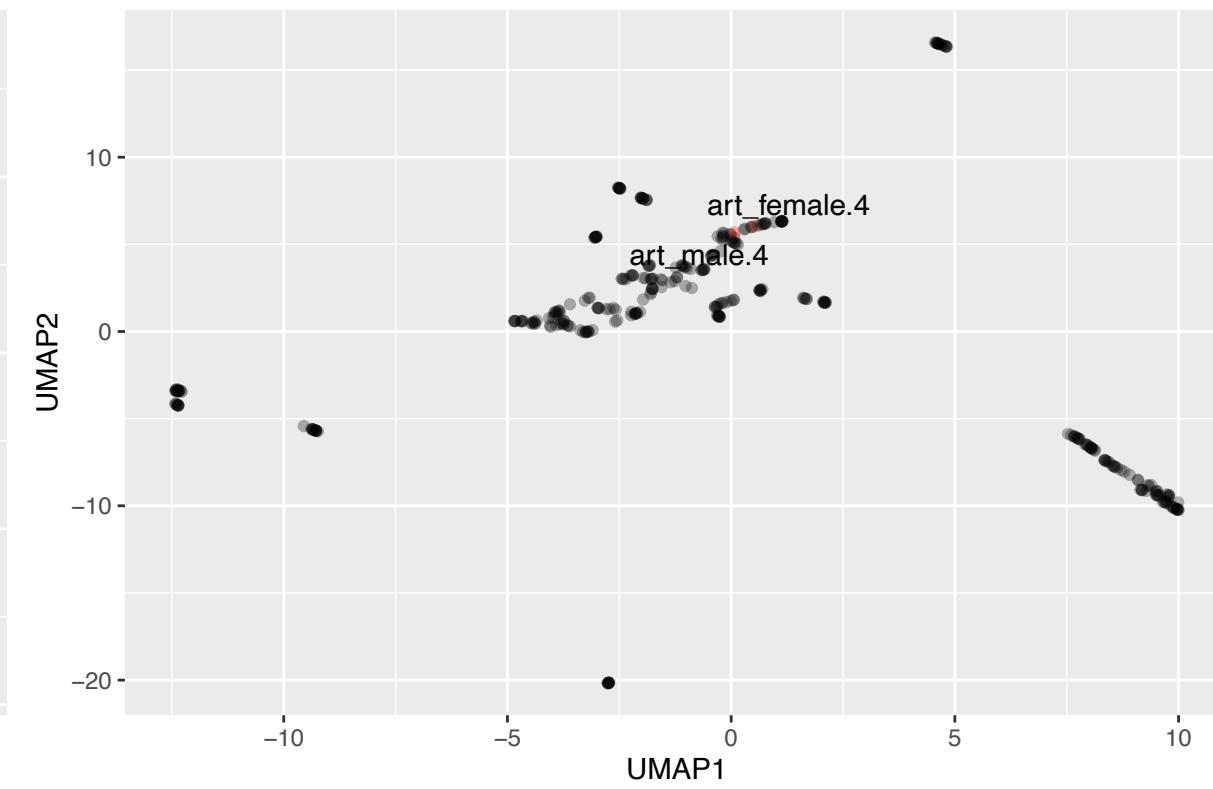
PC2 9.077 % of the variance



Tissue group to sample correlation

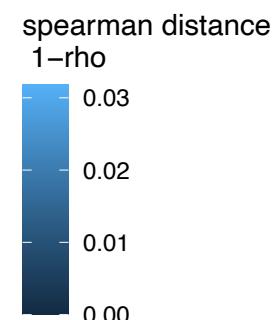


artery, UMAP: TMM expression values

art_female.4
art_male.4

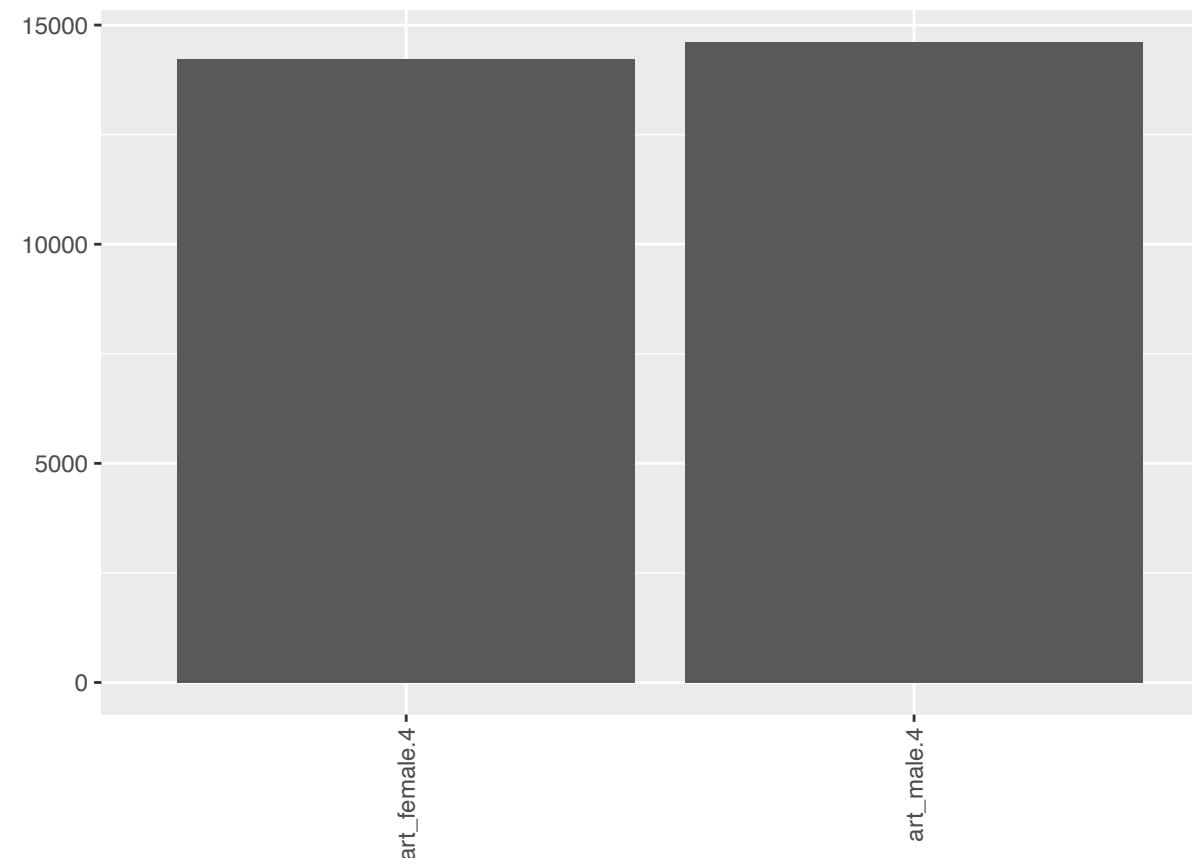
art_male.4

art_female.4



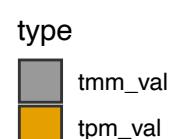
artery

n(genes) >= 1 TMM

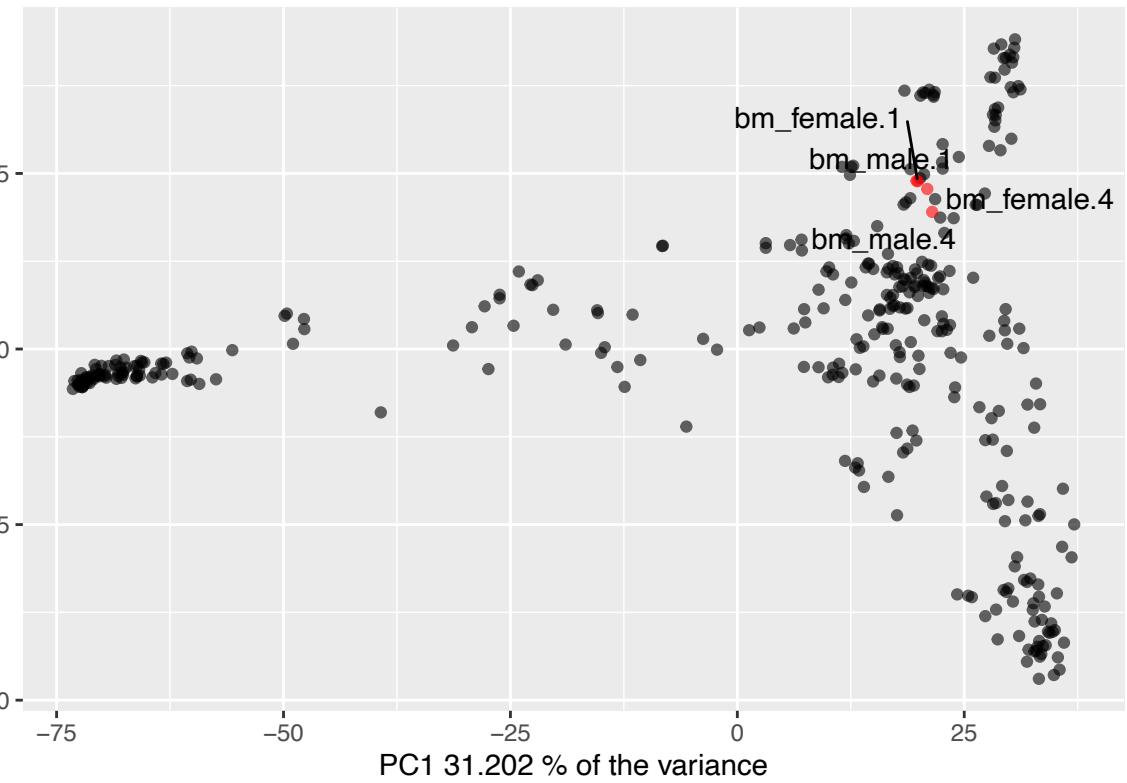


artery

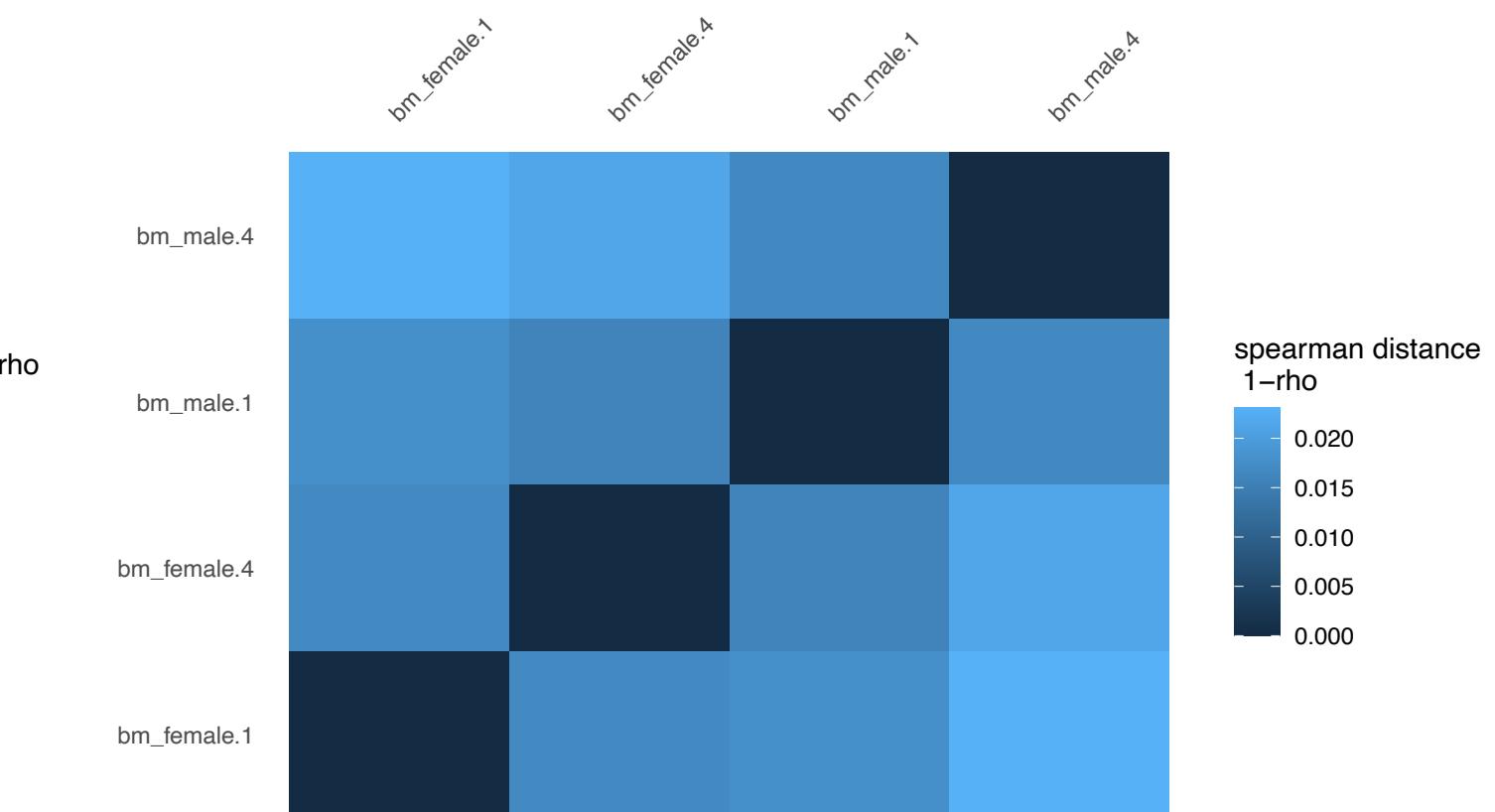
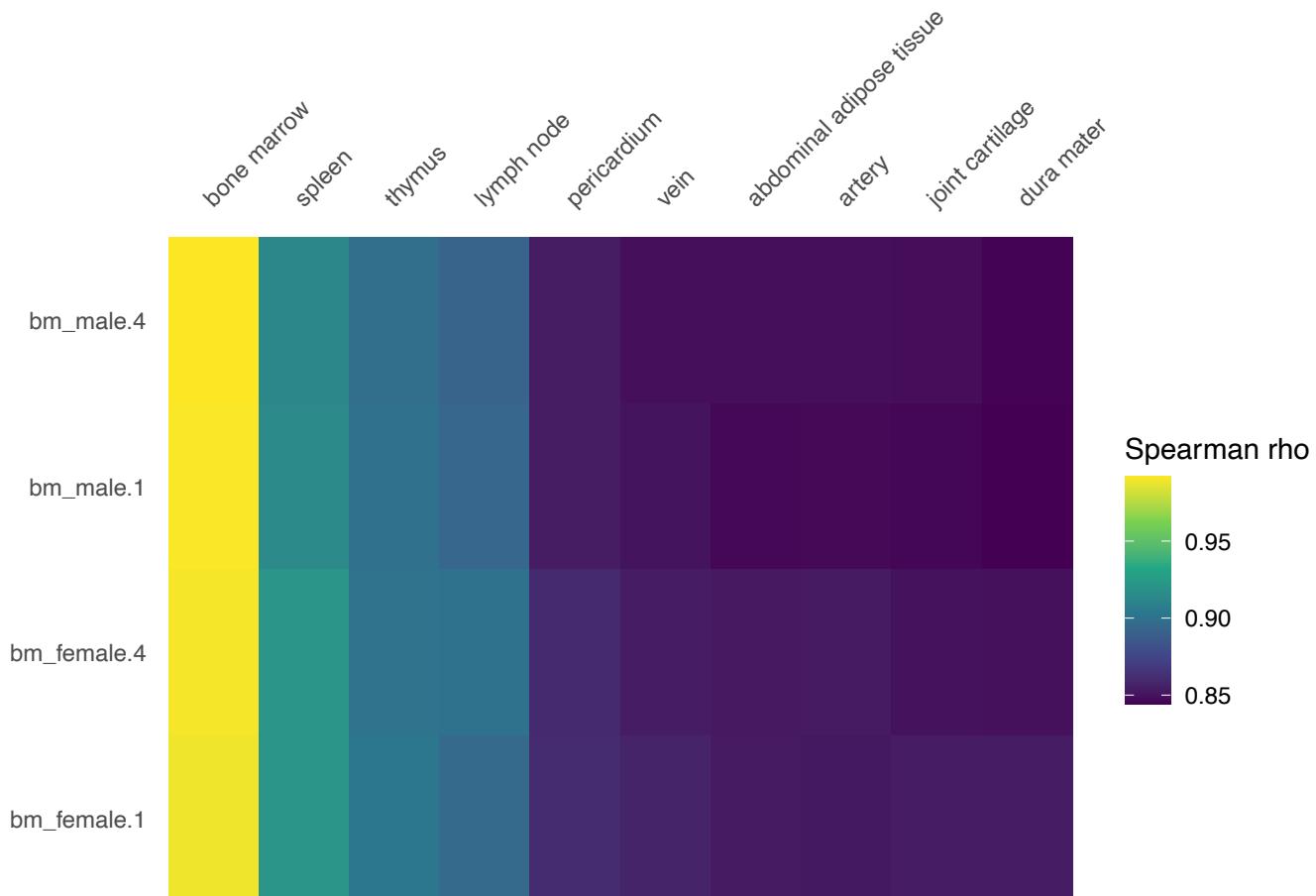
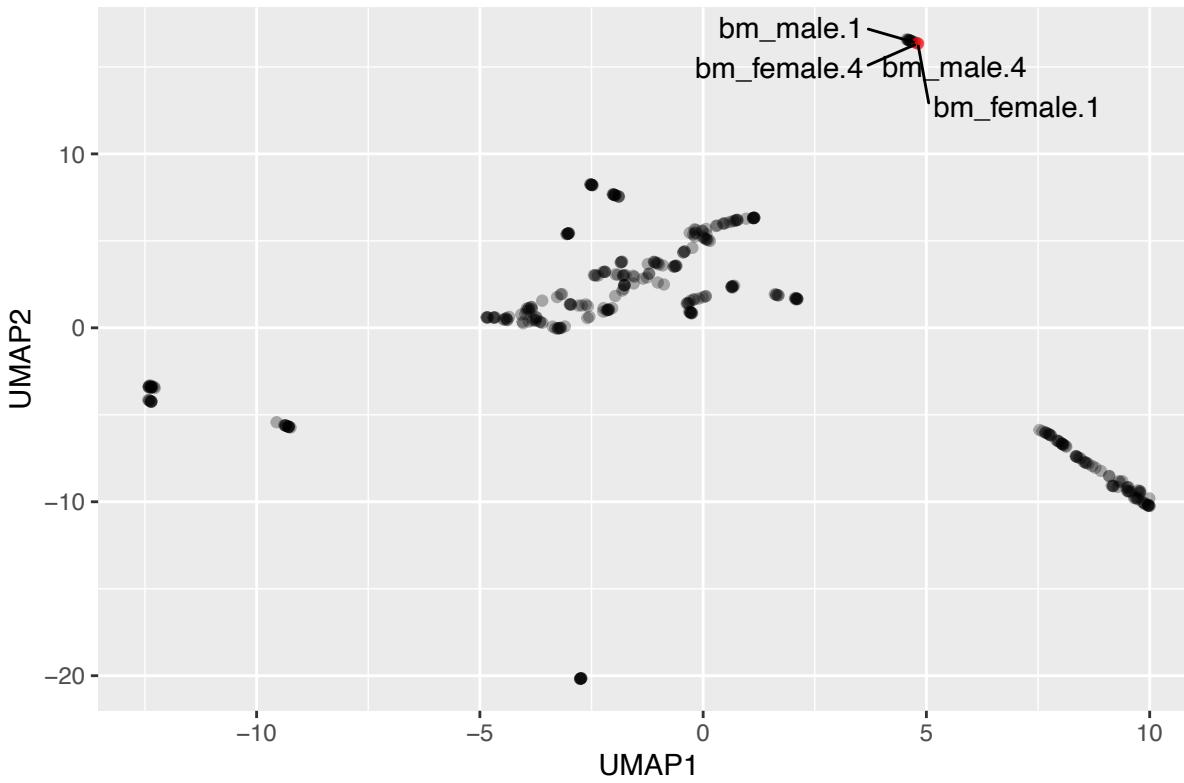
log10(expression+1)

art_female.4
art_male.4

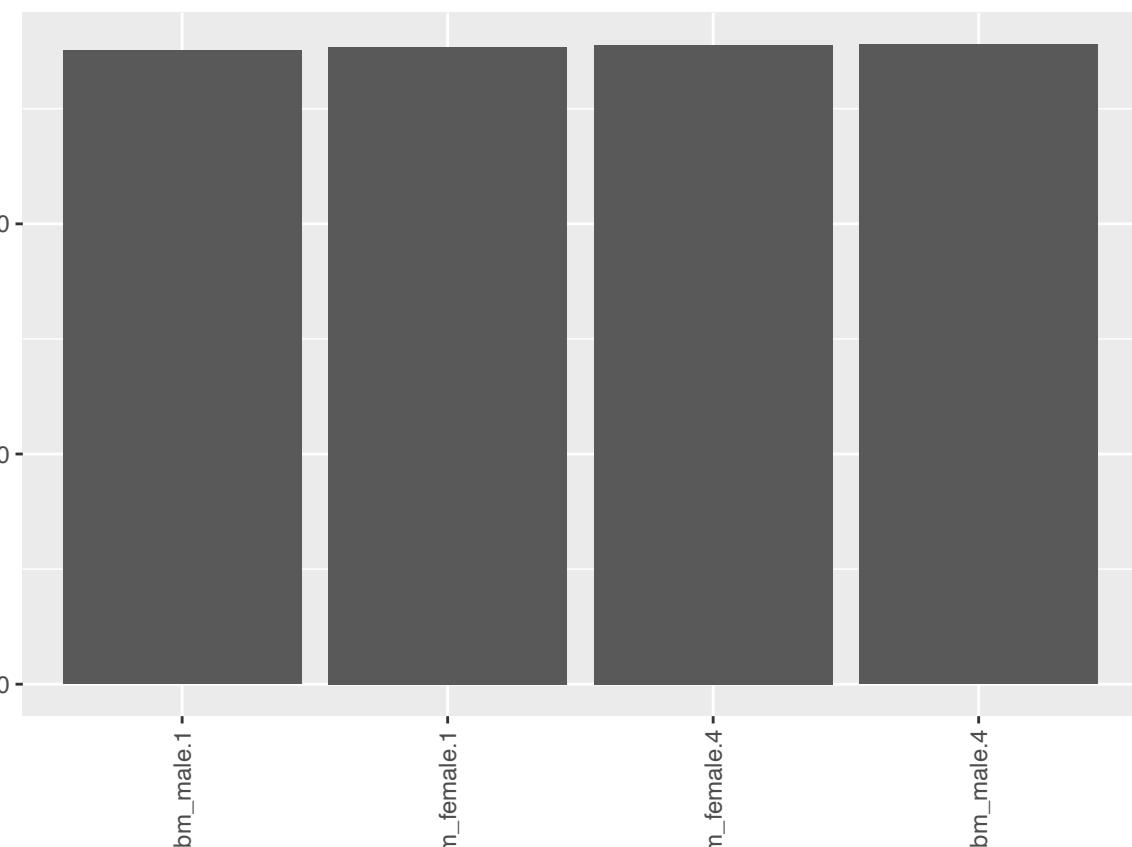
bone marrow, PCA: TMM expression values



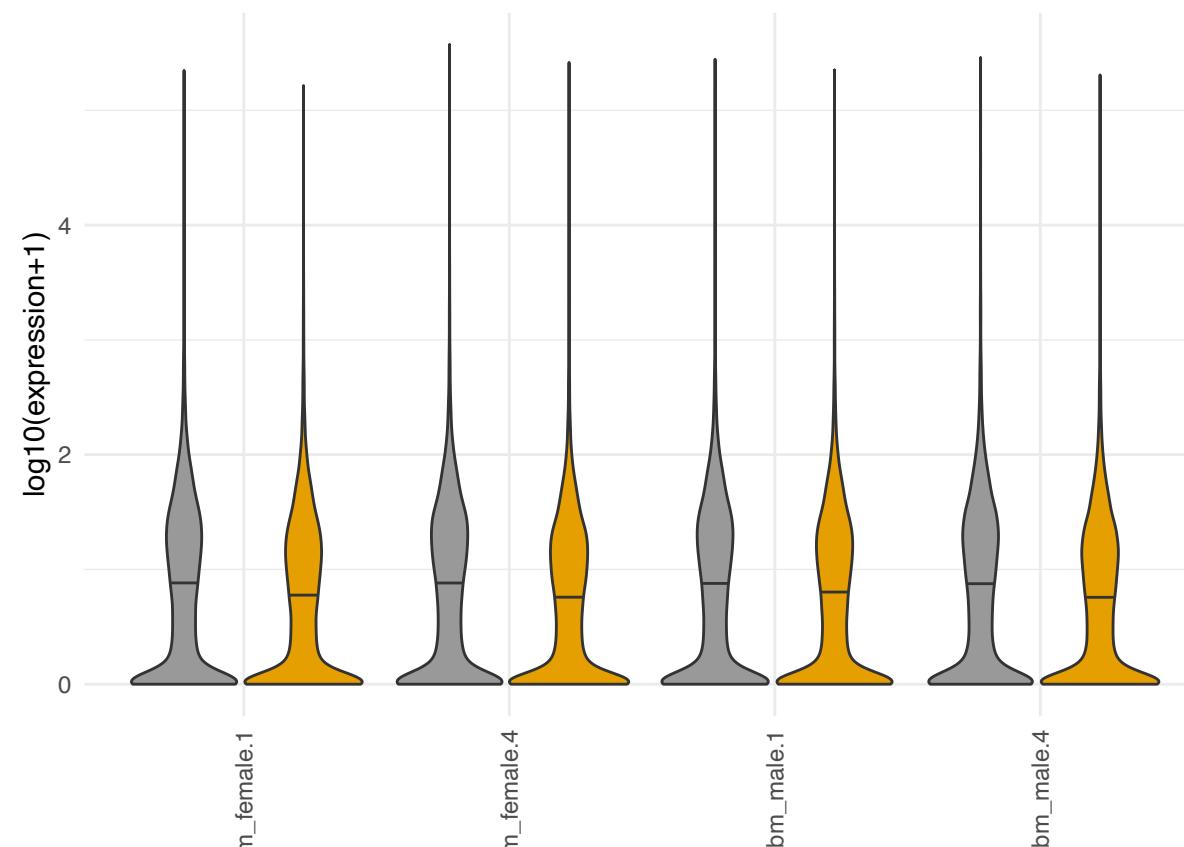
bone marrow, UMAP: TMM expression values



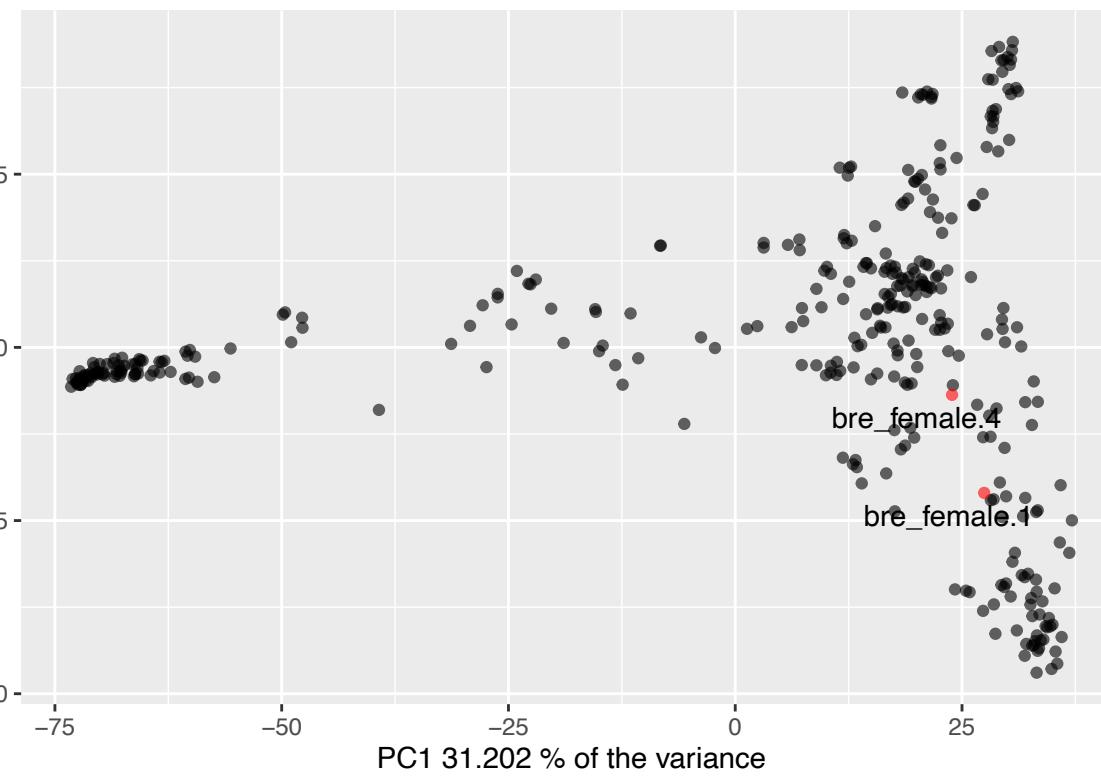
bone marrow



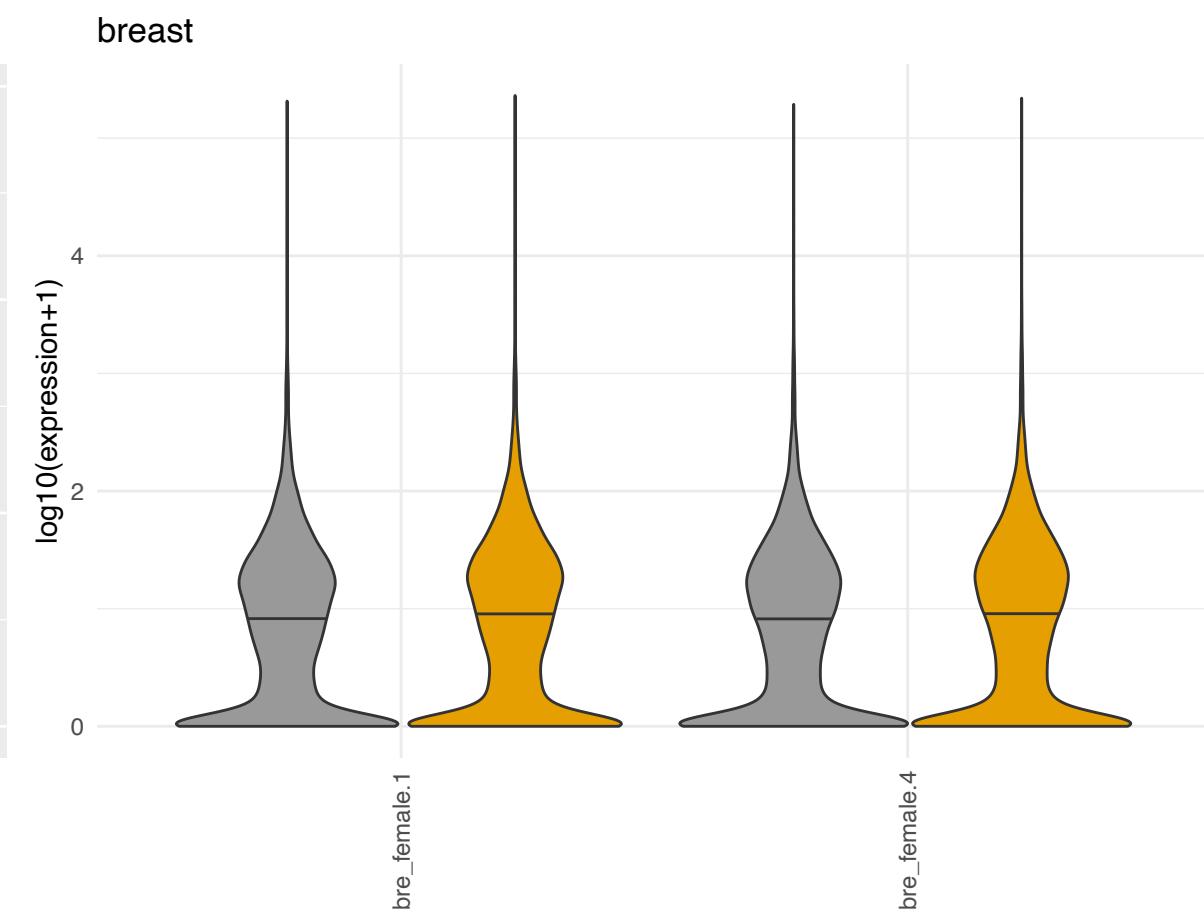
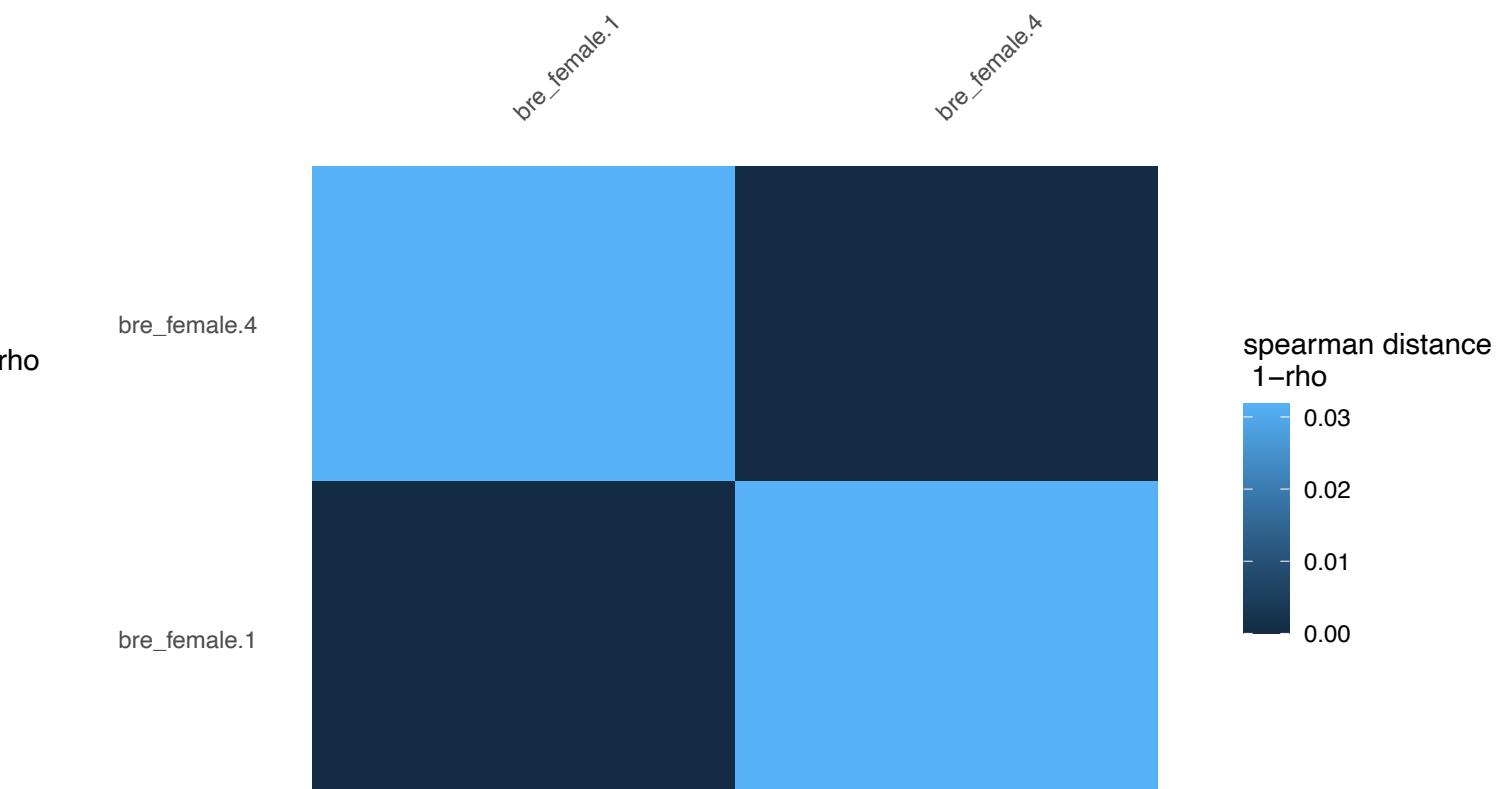
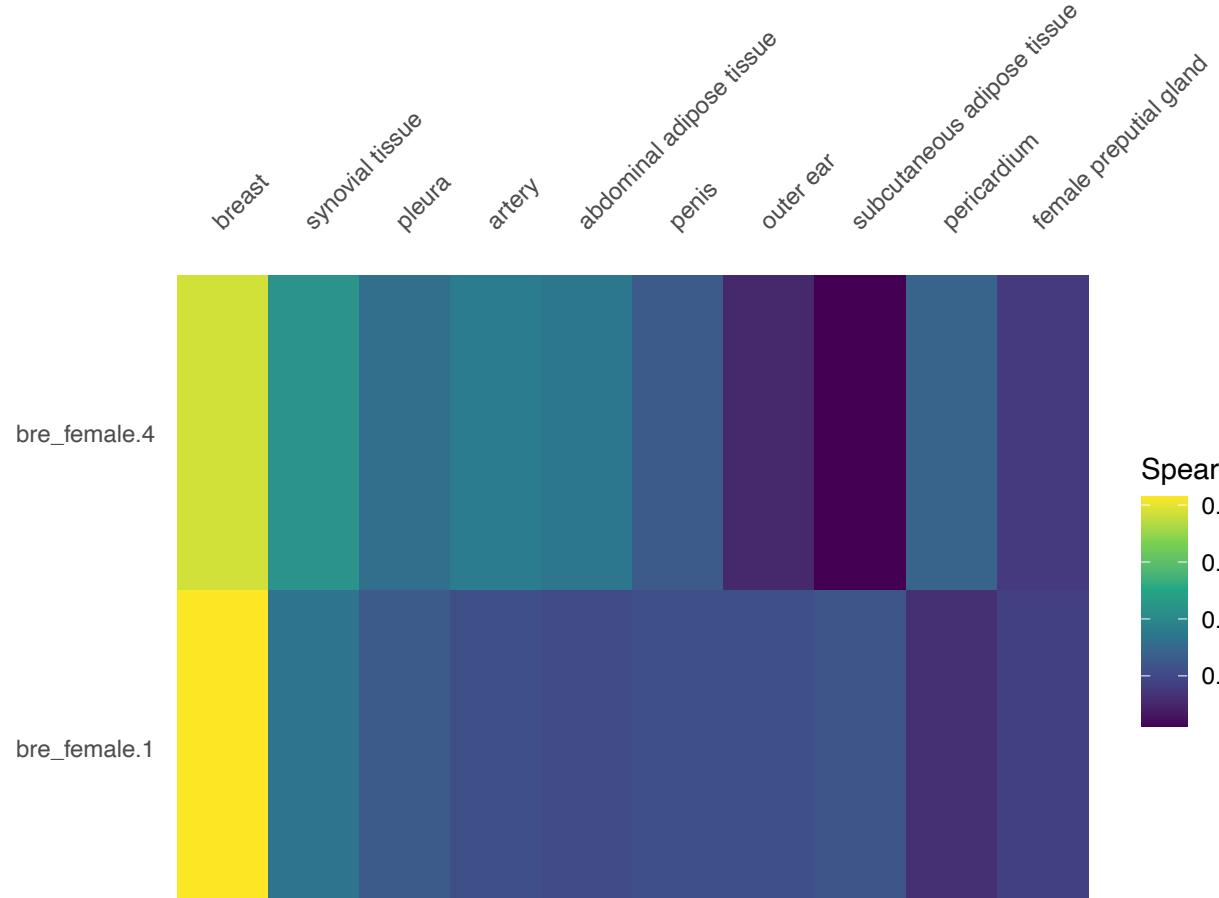
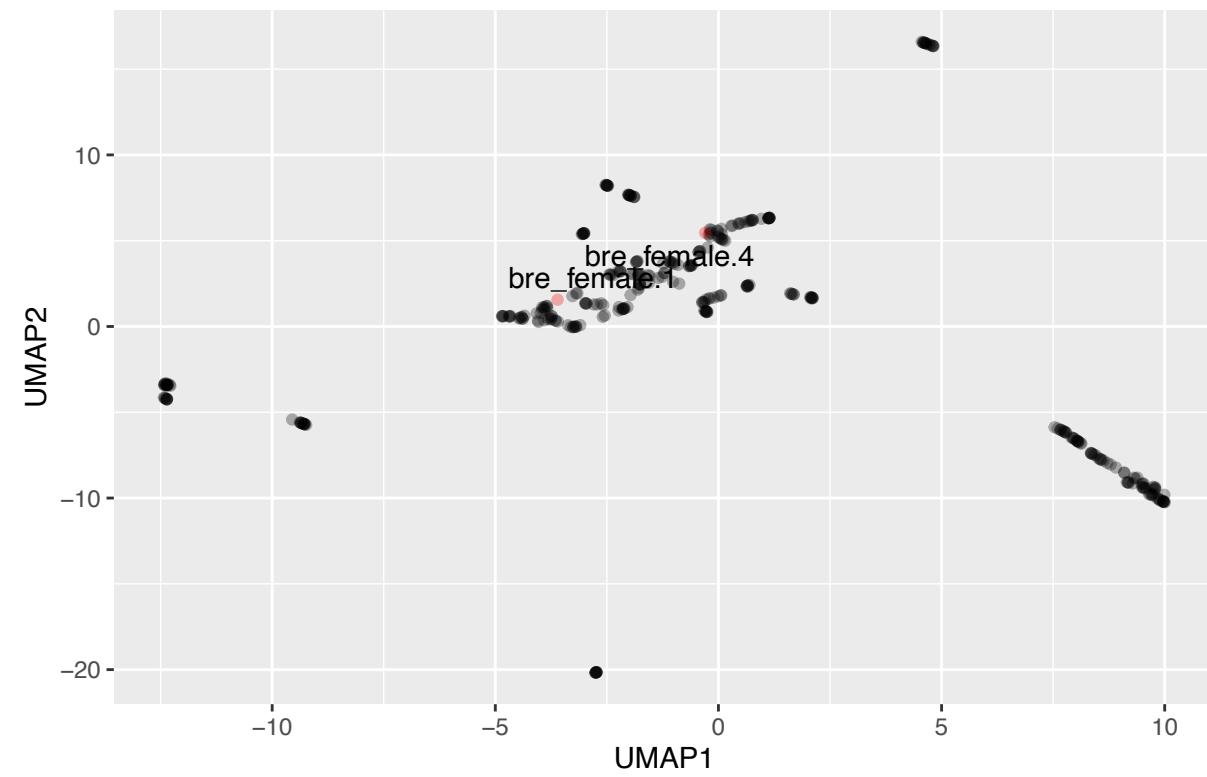
bone marrow

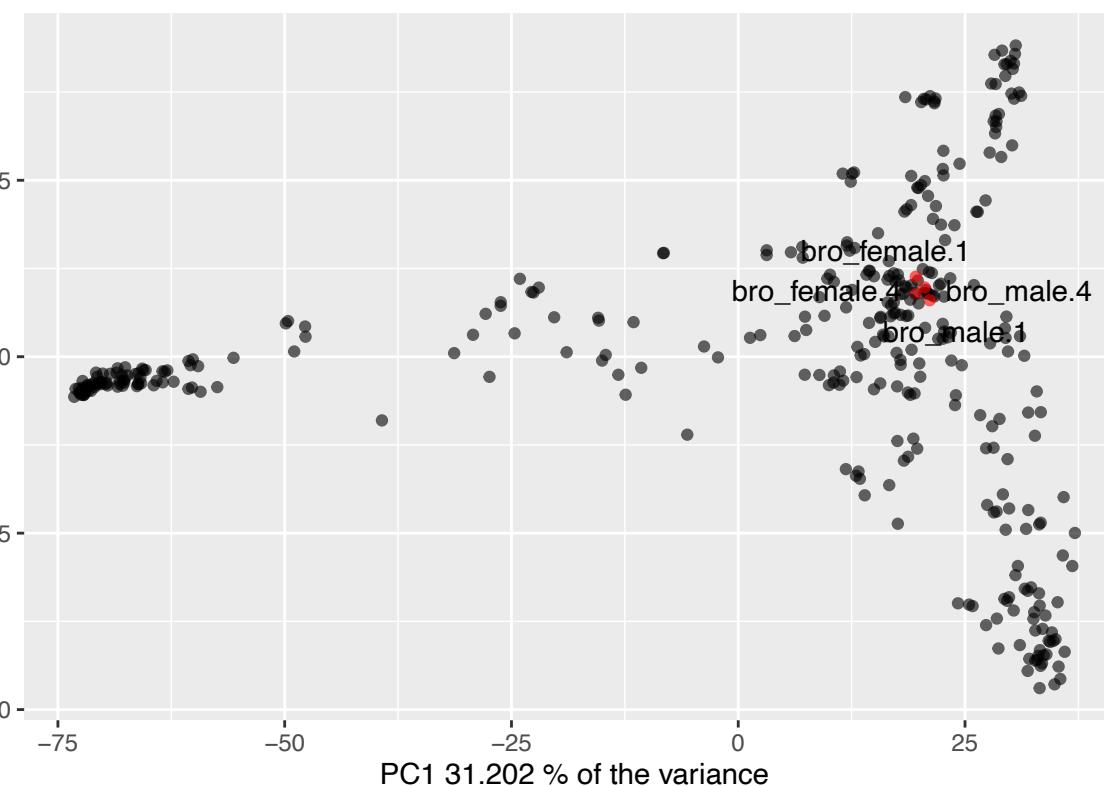


breast, PCA: TMM expression values

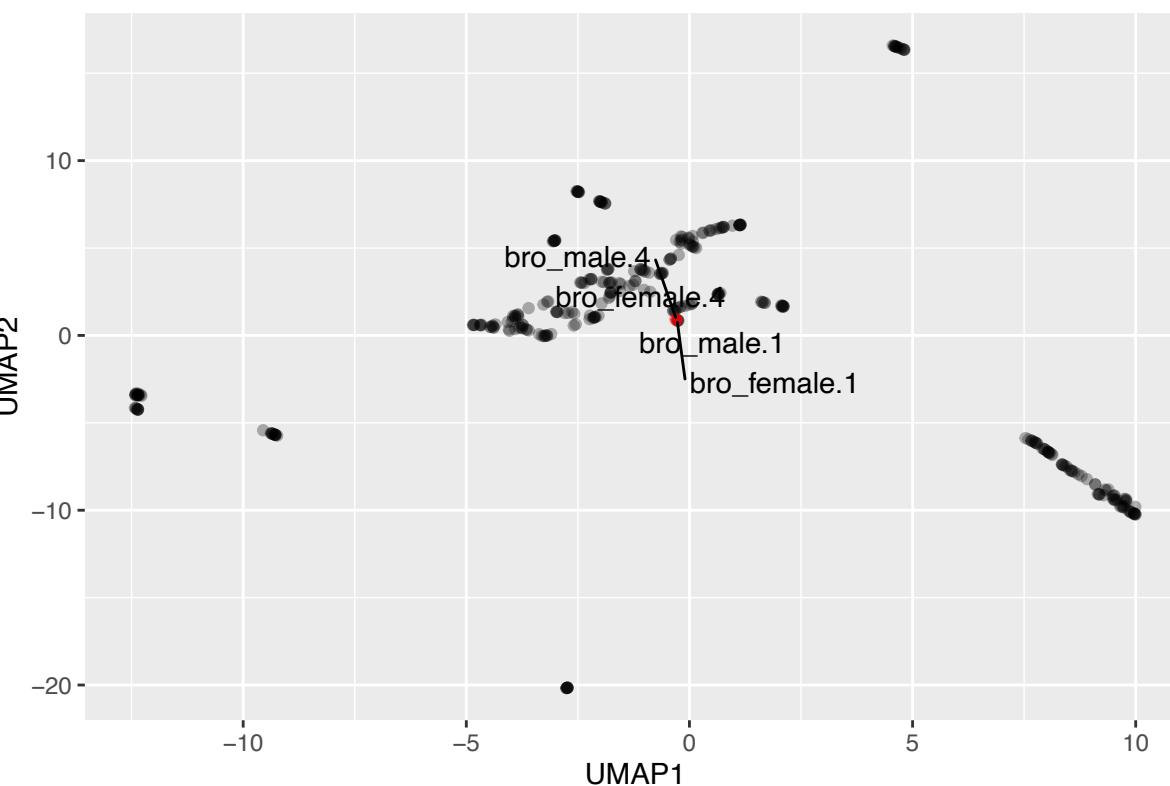


breast, UMAP: TMM expression values

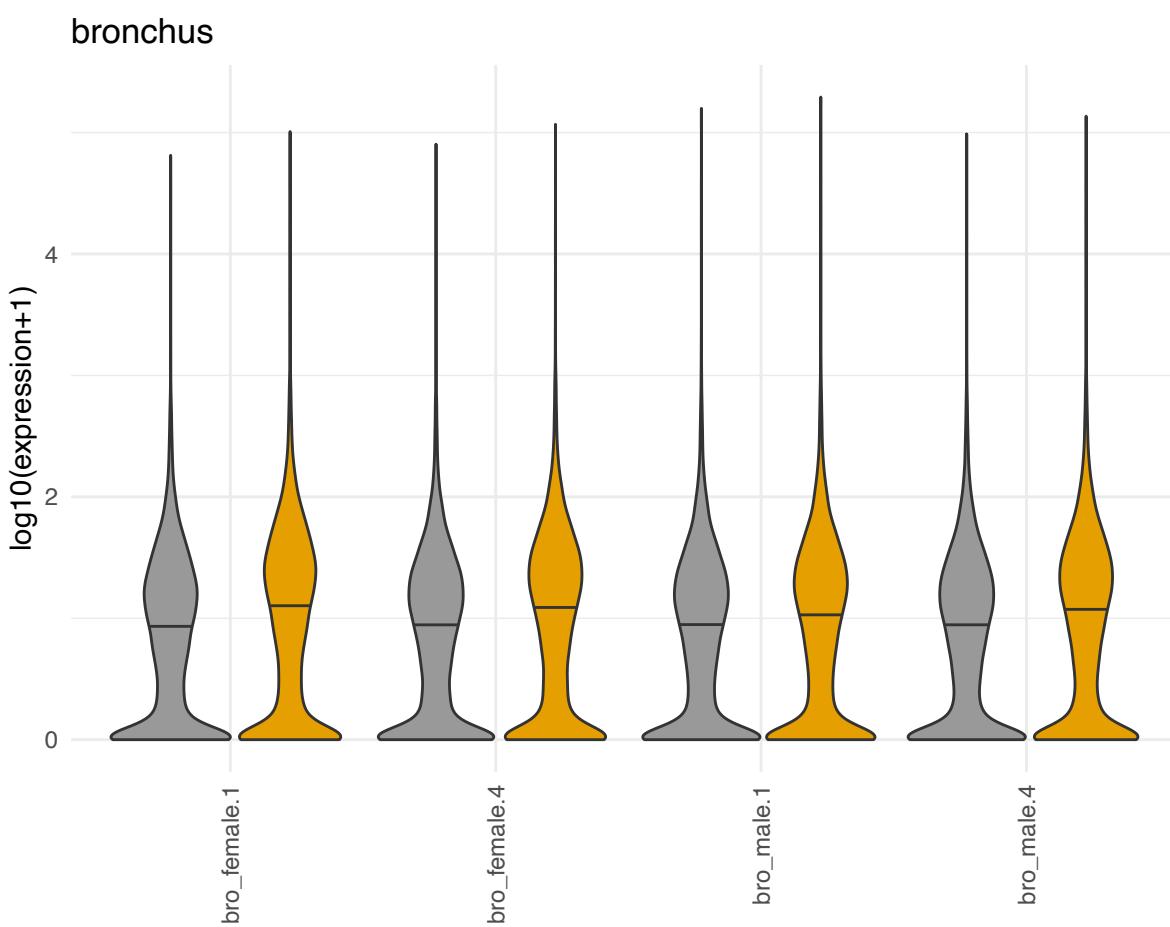
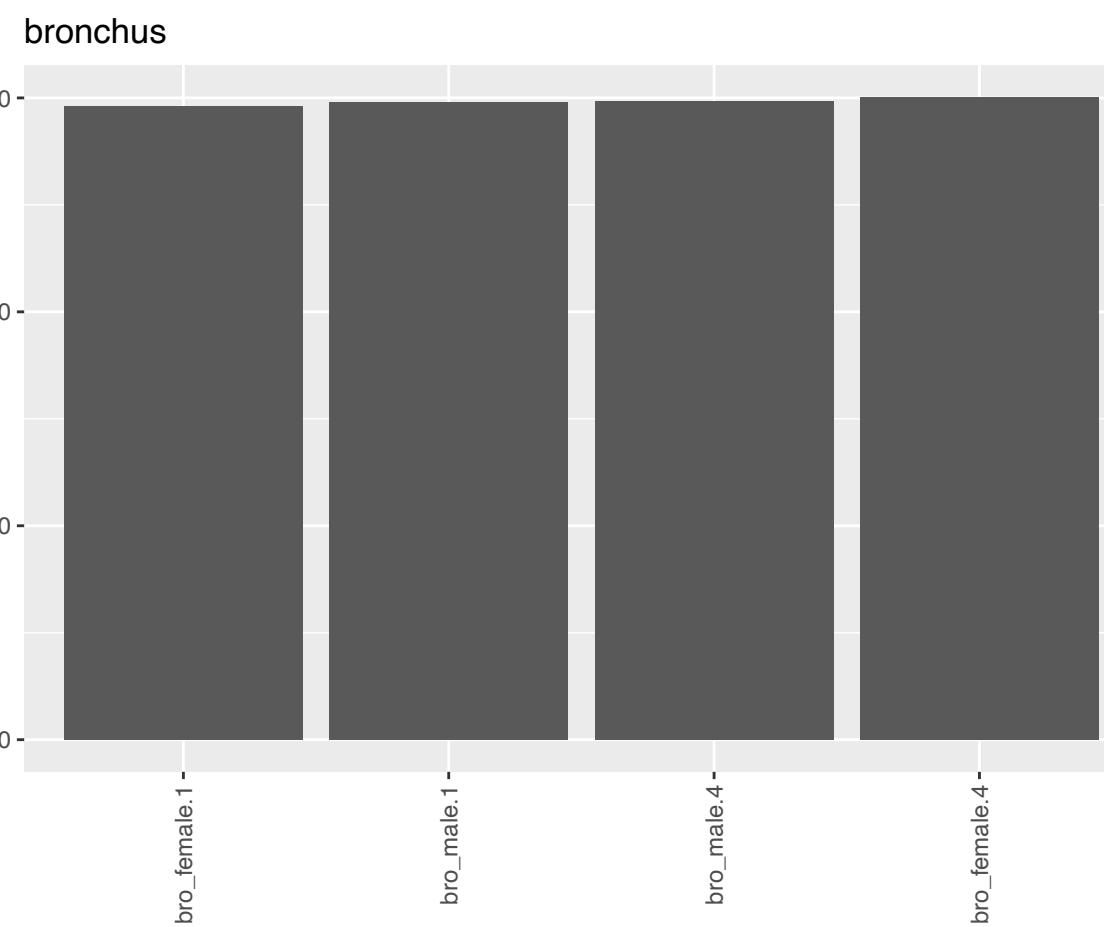
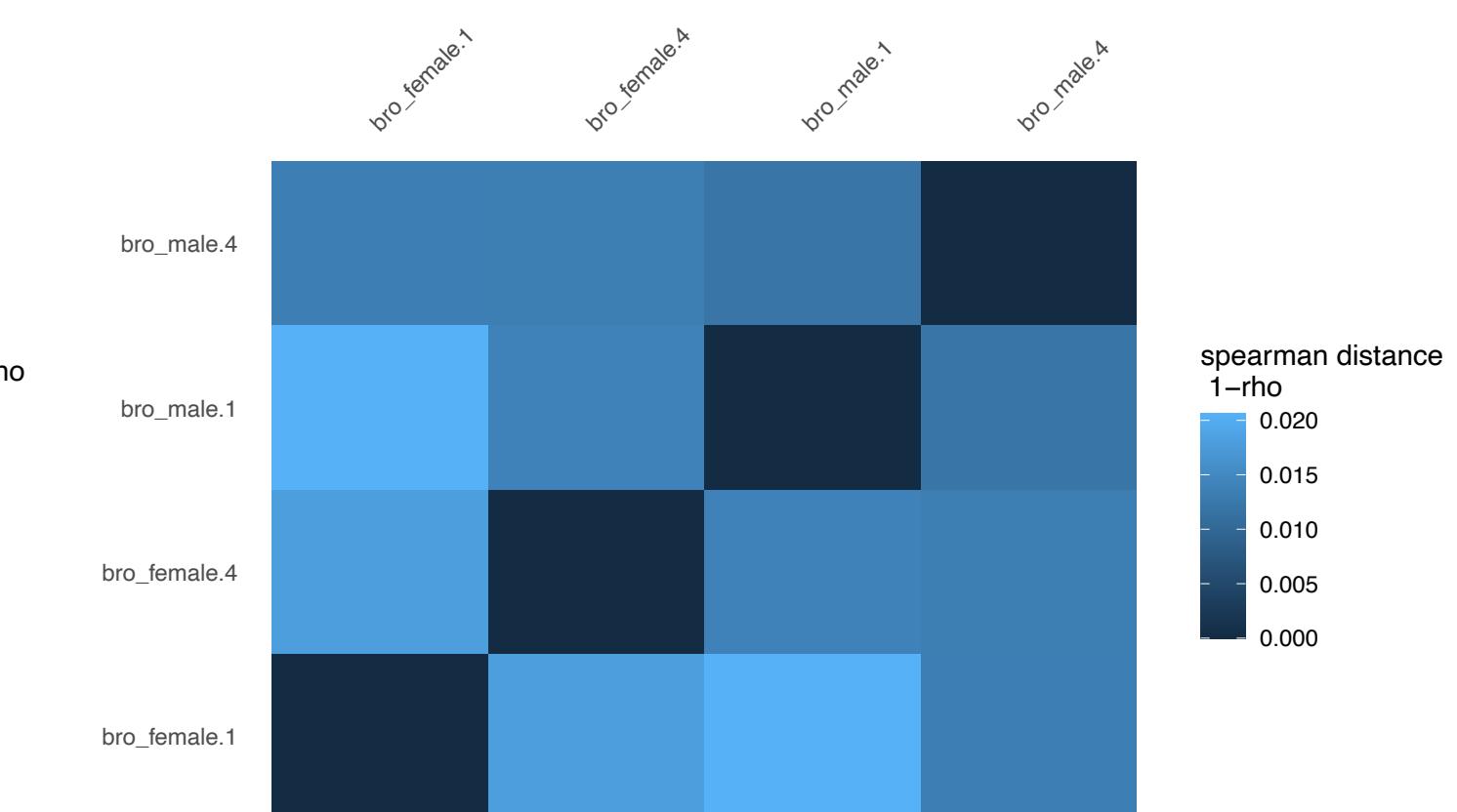
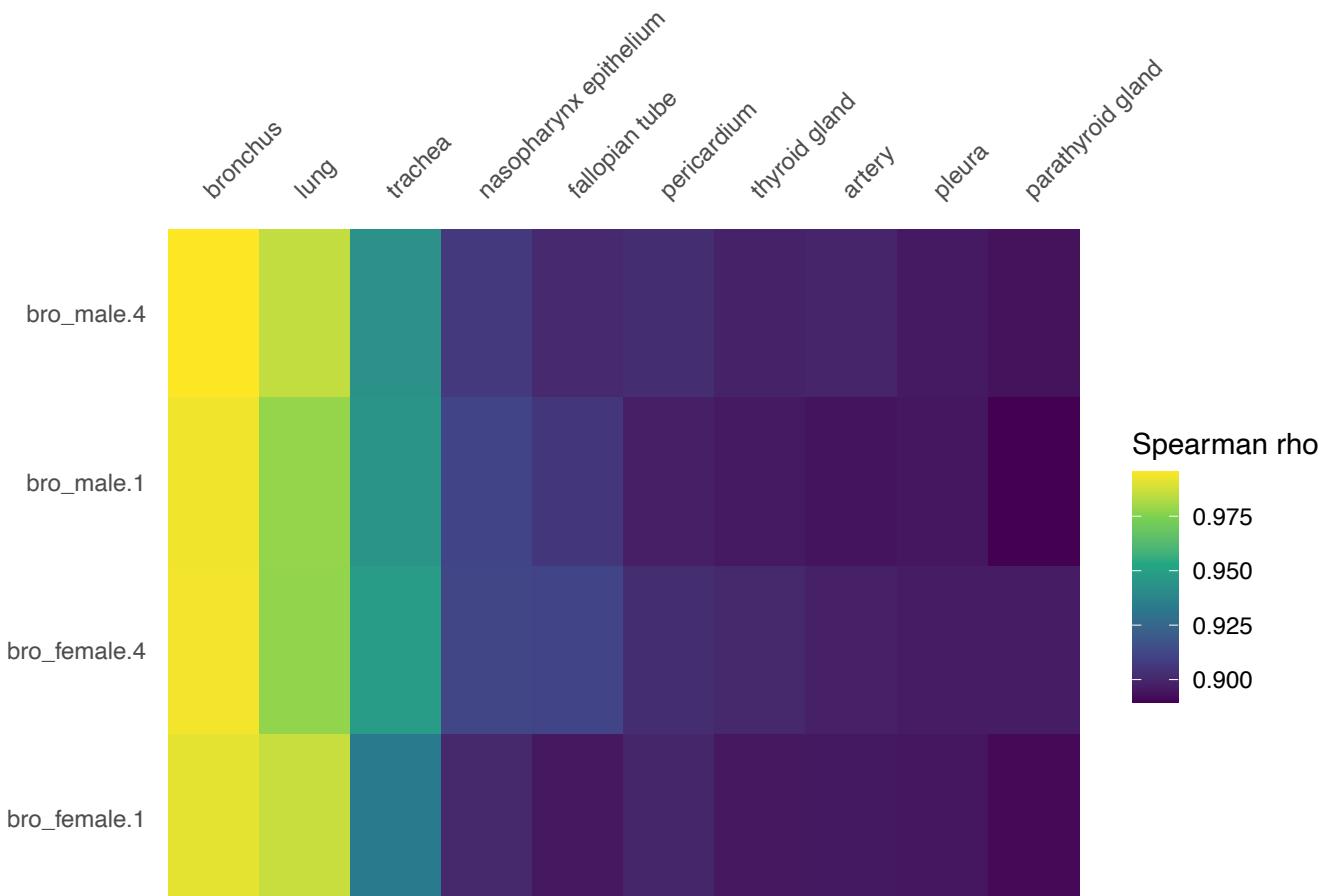




Tissue group to sample correlation

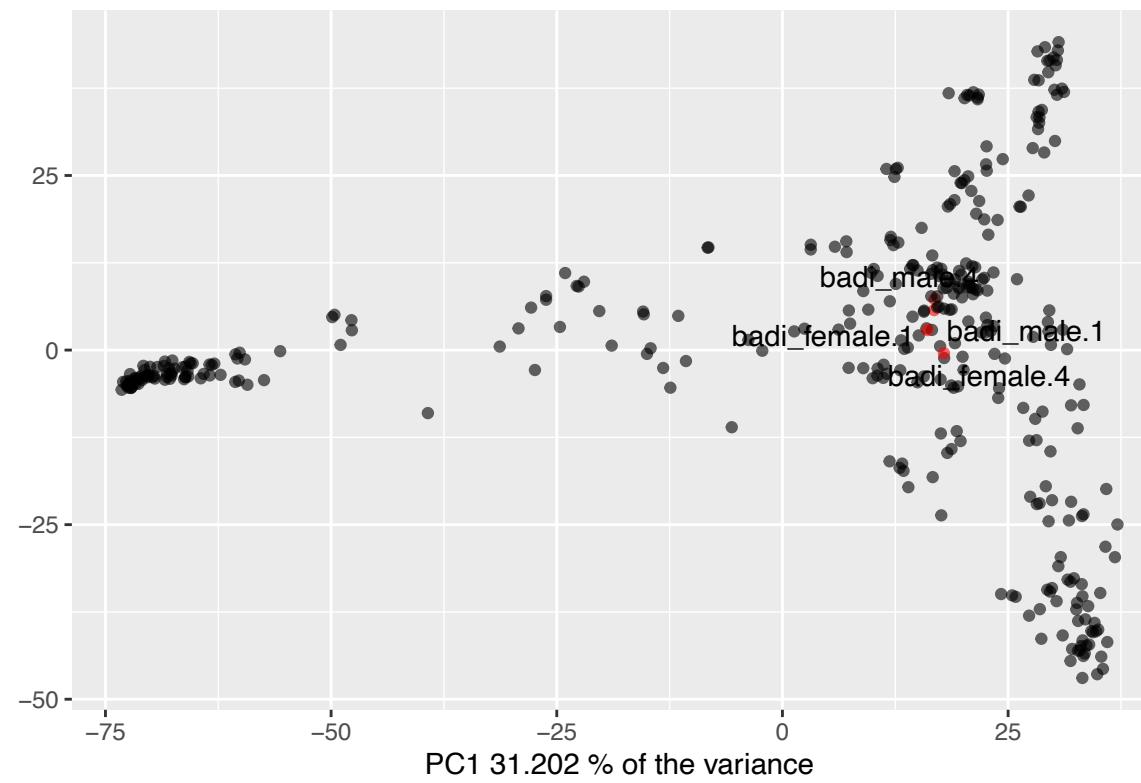


In tissue sample to sample Spearman Distance

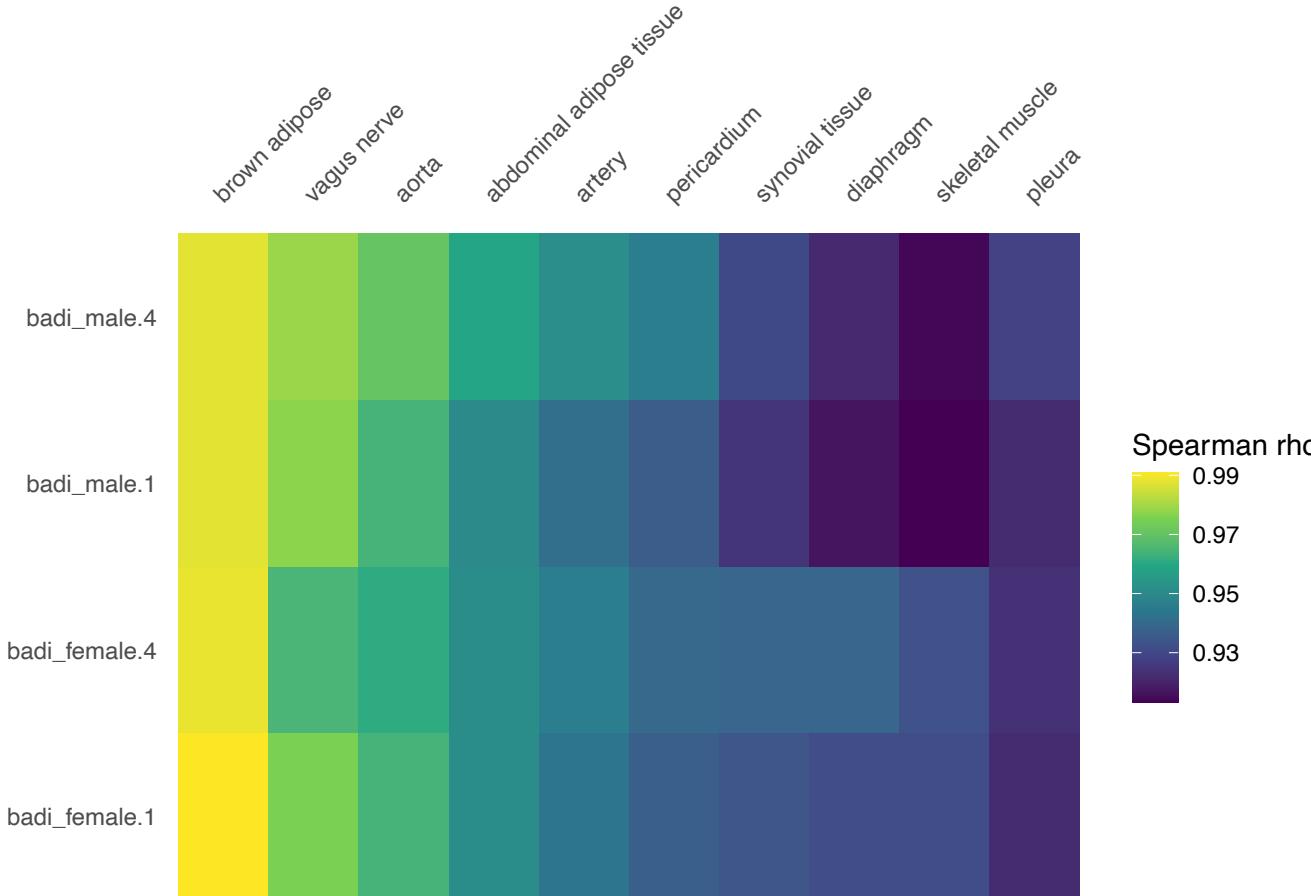


brown adipose, PCA: TMM expression values

PC2 9.077 % of the variance

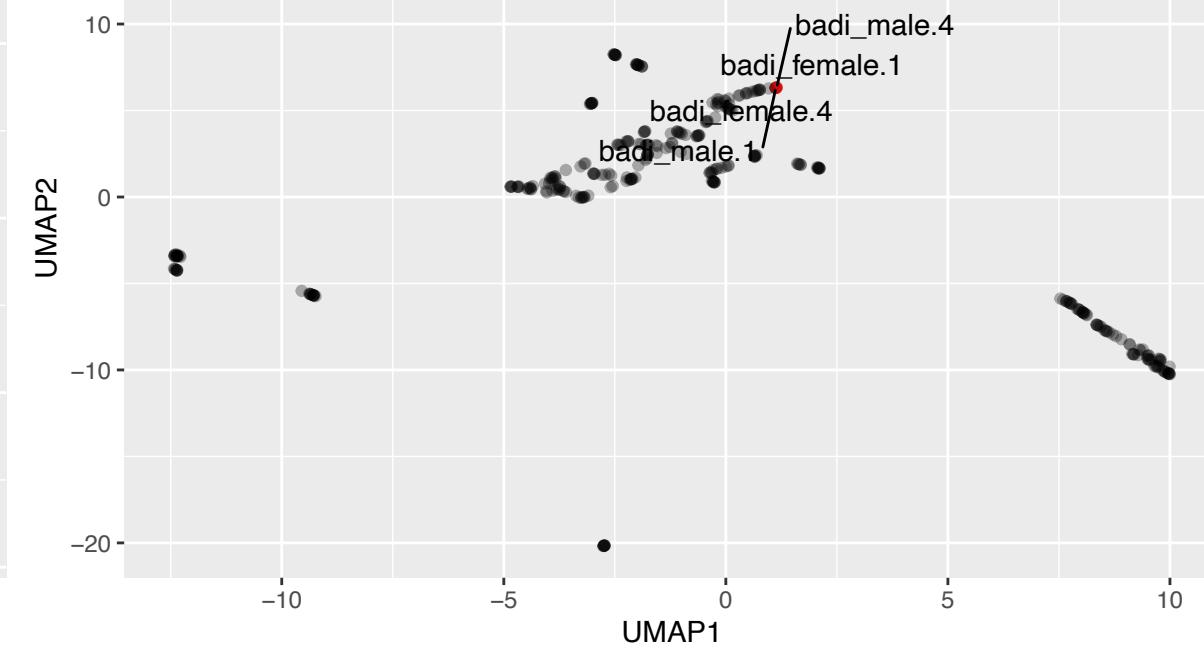


Tissue group to sample correlation

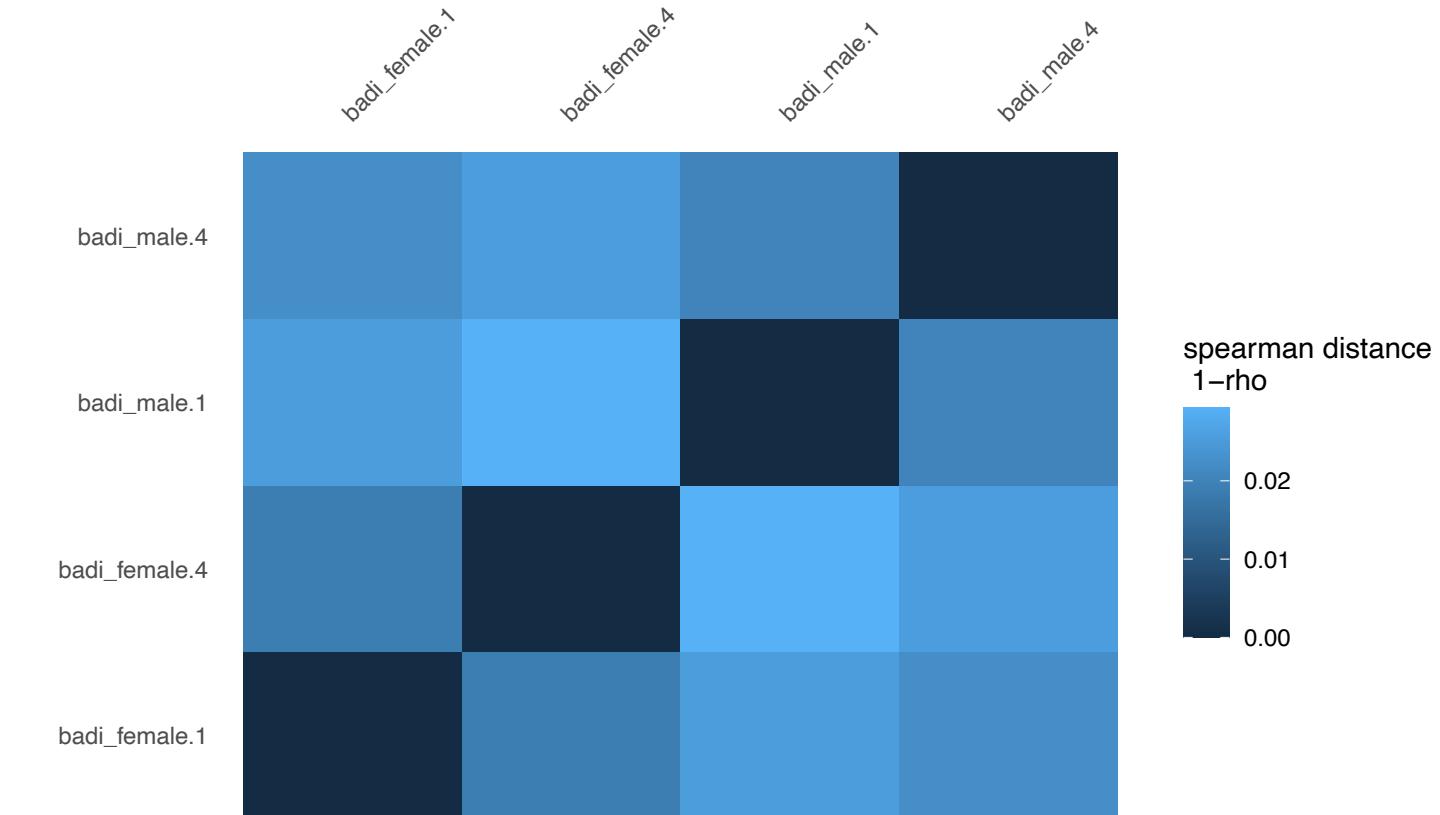


brown adipose, UMAP: TMM expression values

UMAP2

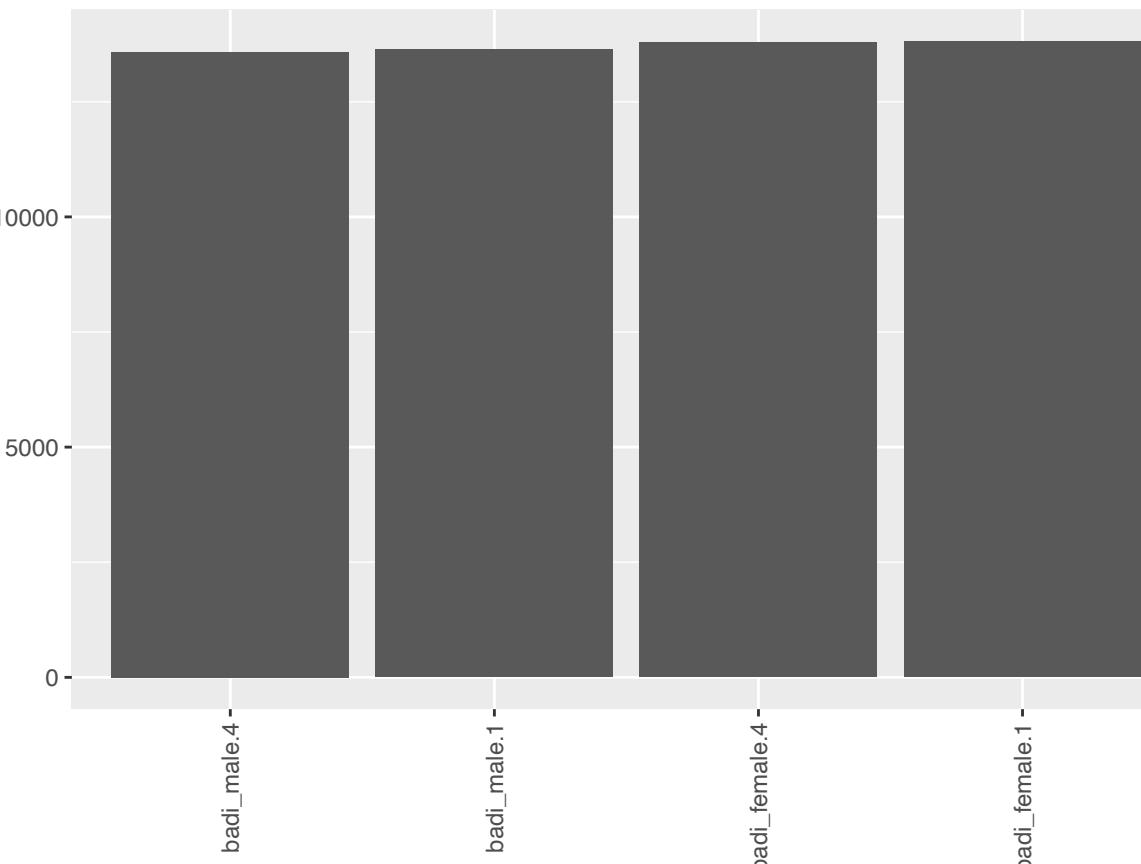


In tissue sample to sample Spearman Distance

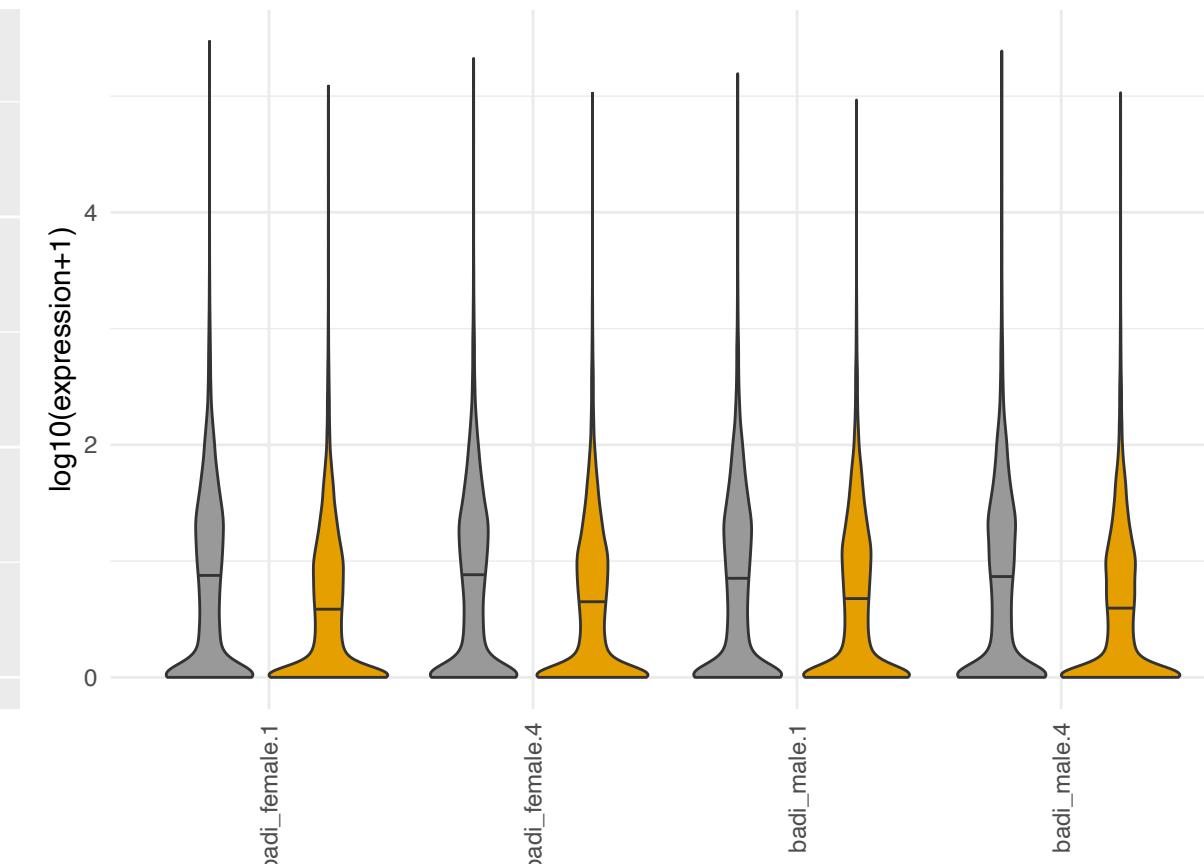


brown adipose

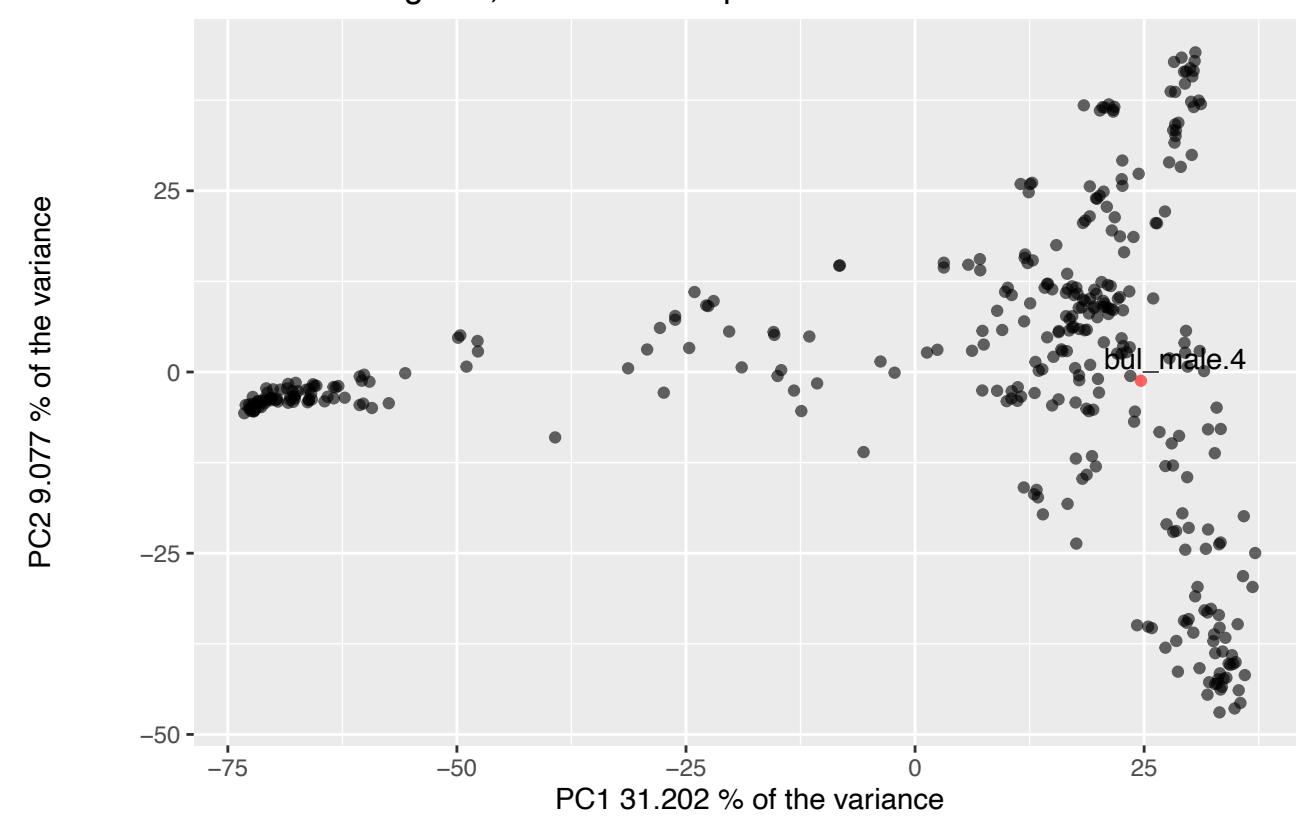
n(genes) >= 1 TMM



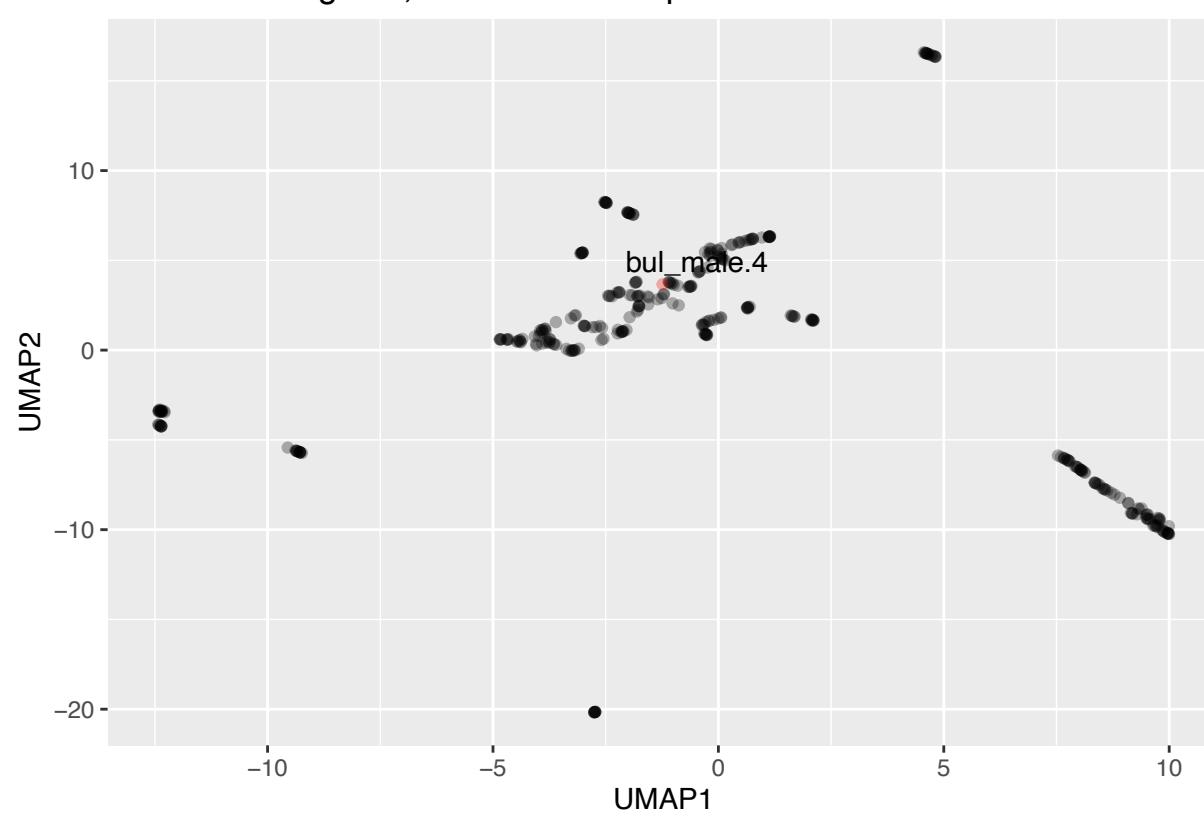
brown adipose



bulbourethral gland, PCA: TMM expression values



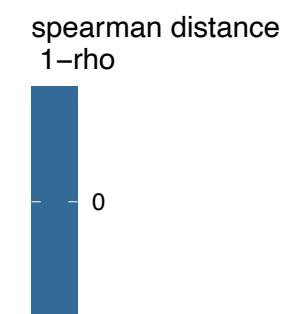
bulbourethral gland, UMAP: TMM expression values



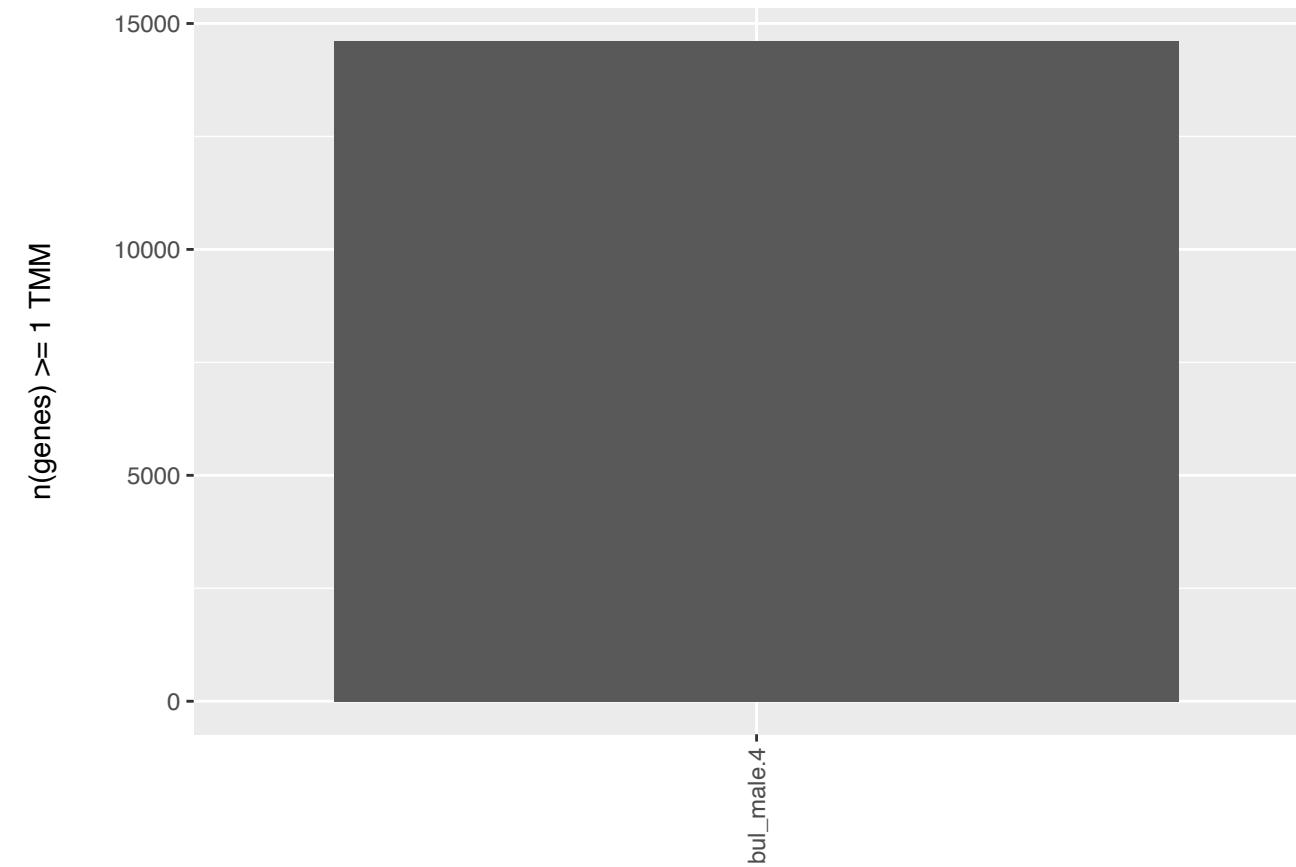
bulbourethral gland
salivary gland
thyroid gland
prostate
larynx
prostate ventral
outer ear
clitoris
trachea
breast



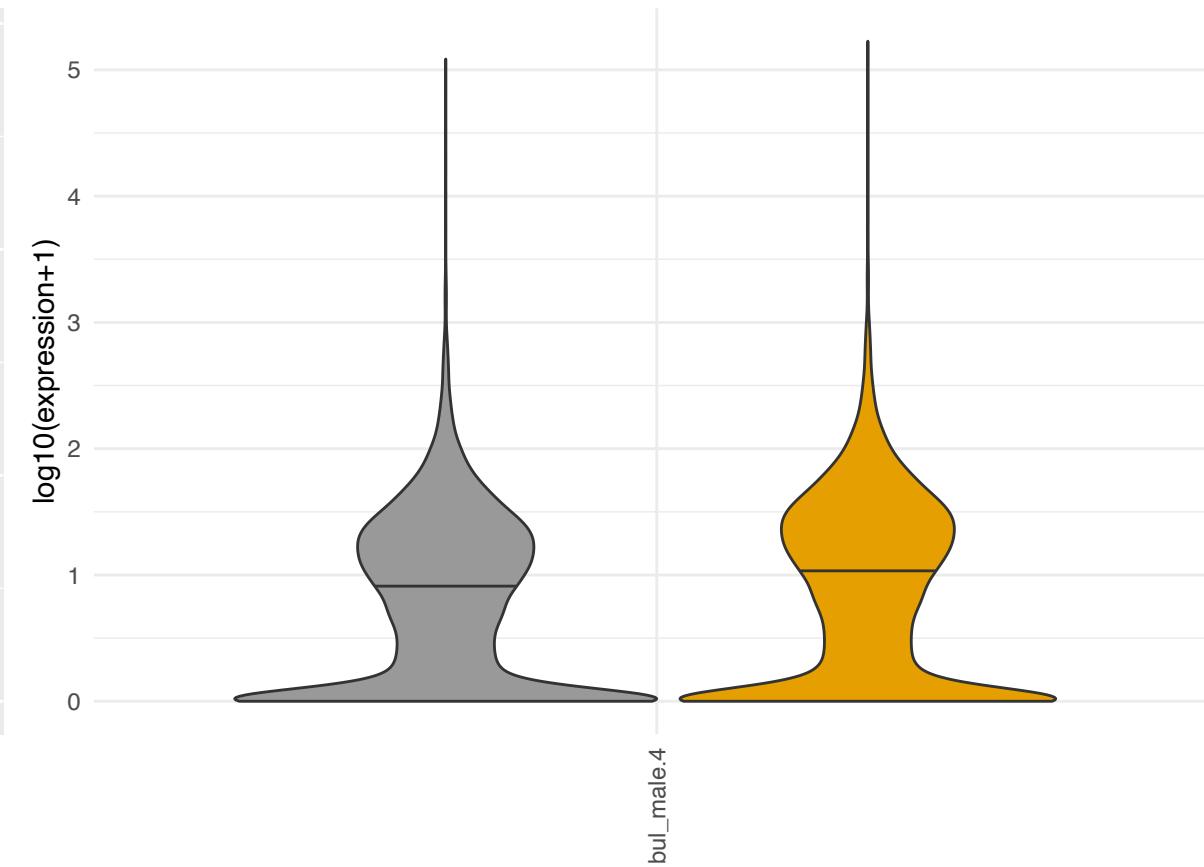
bul_male.4



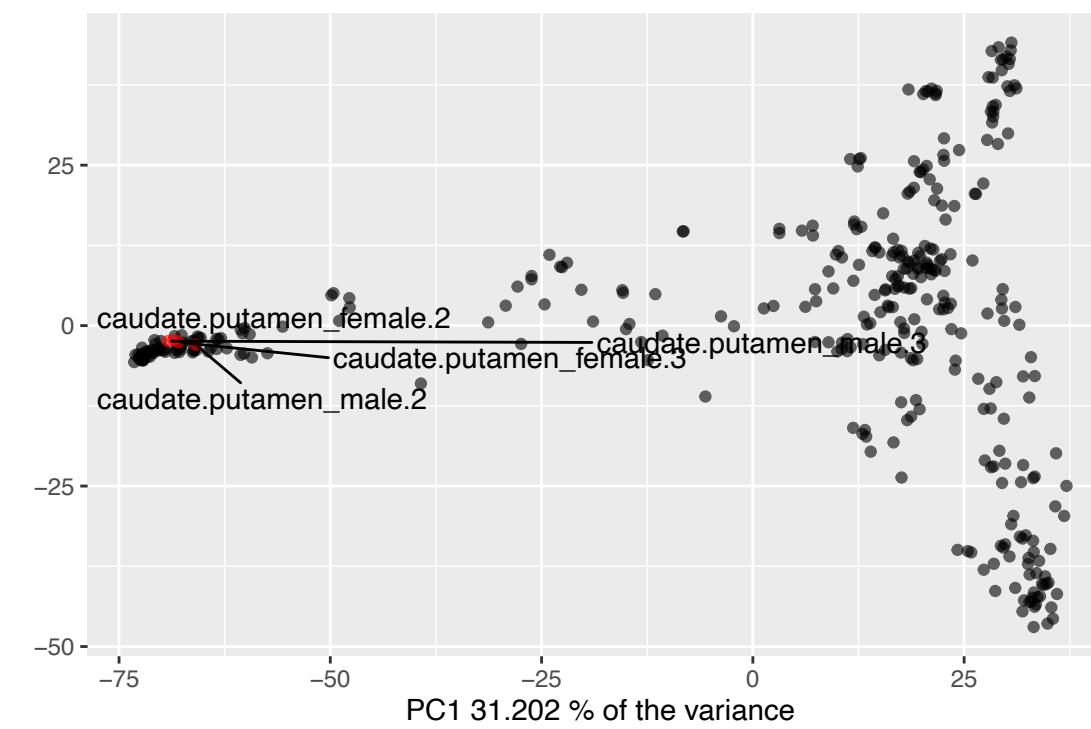
bulbourethral gland



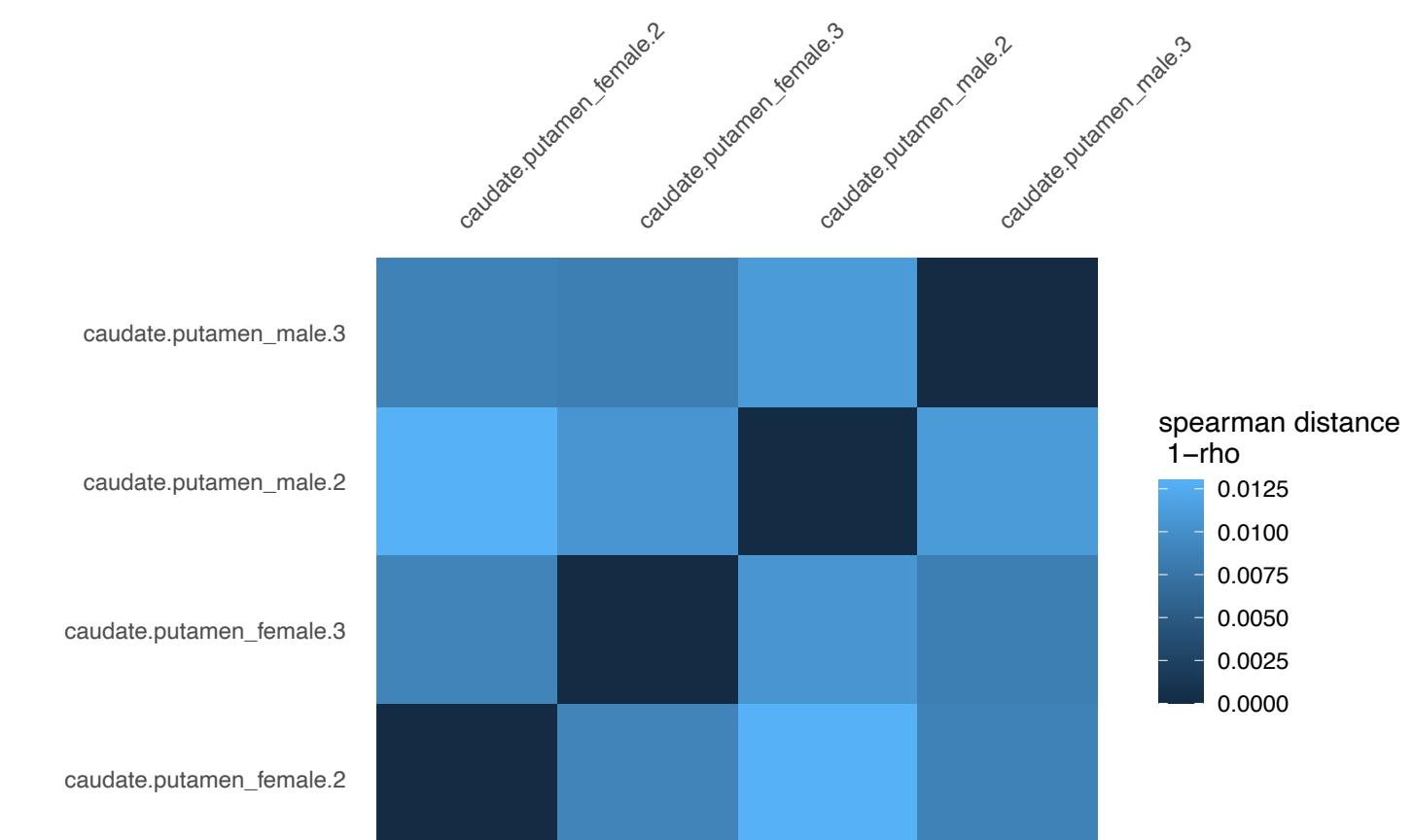
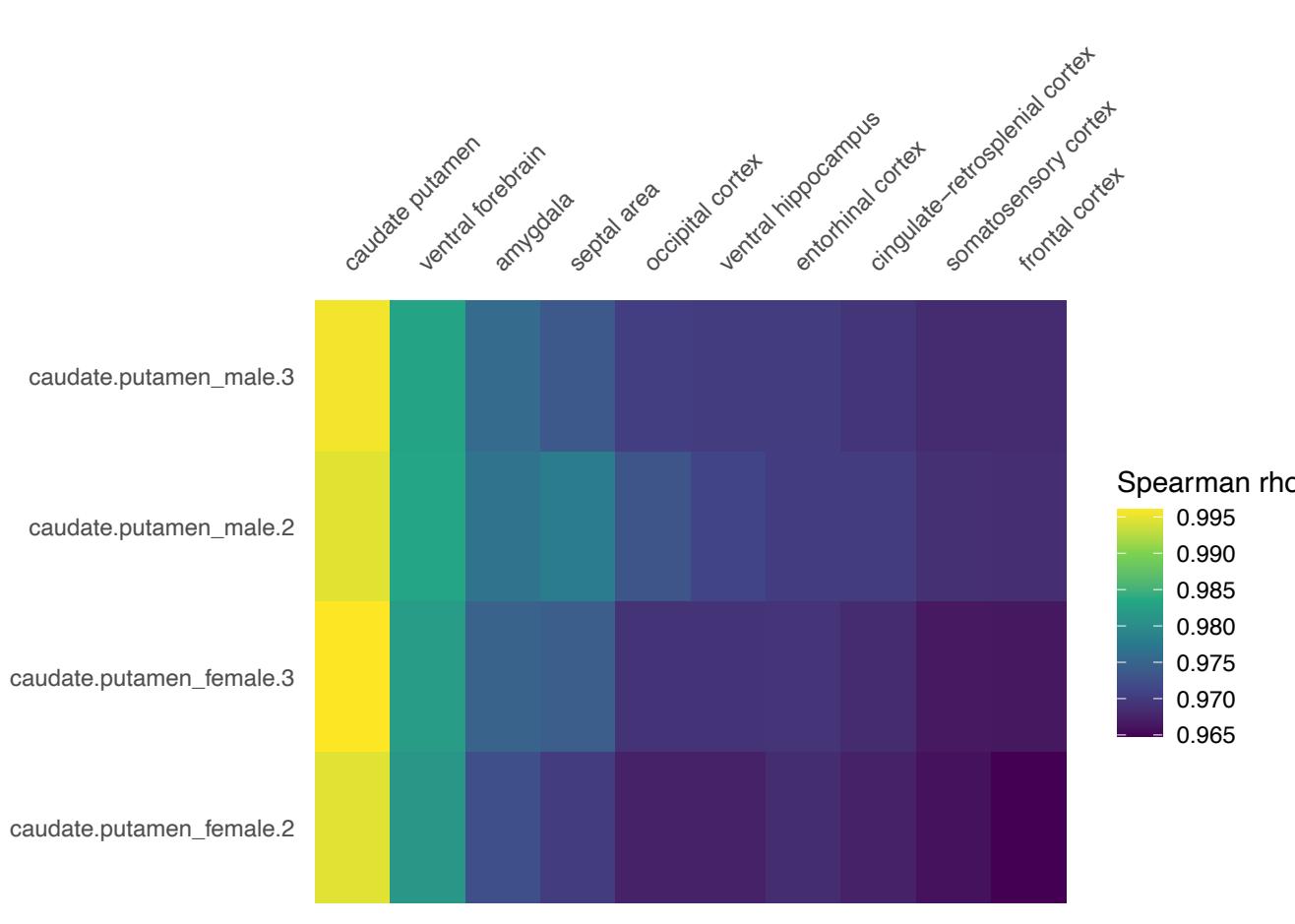
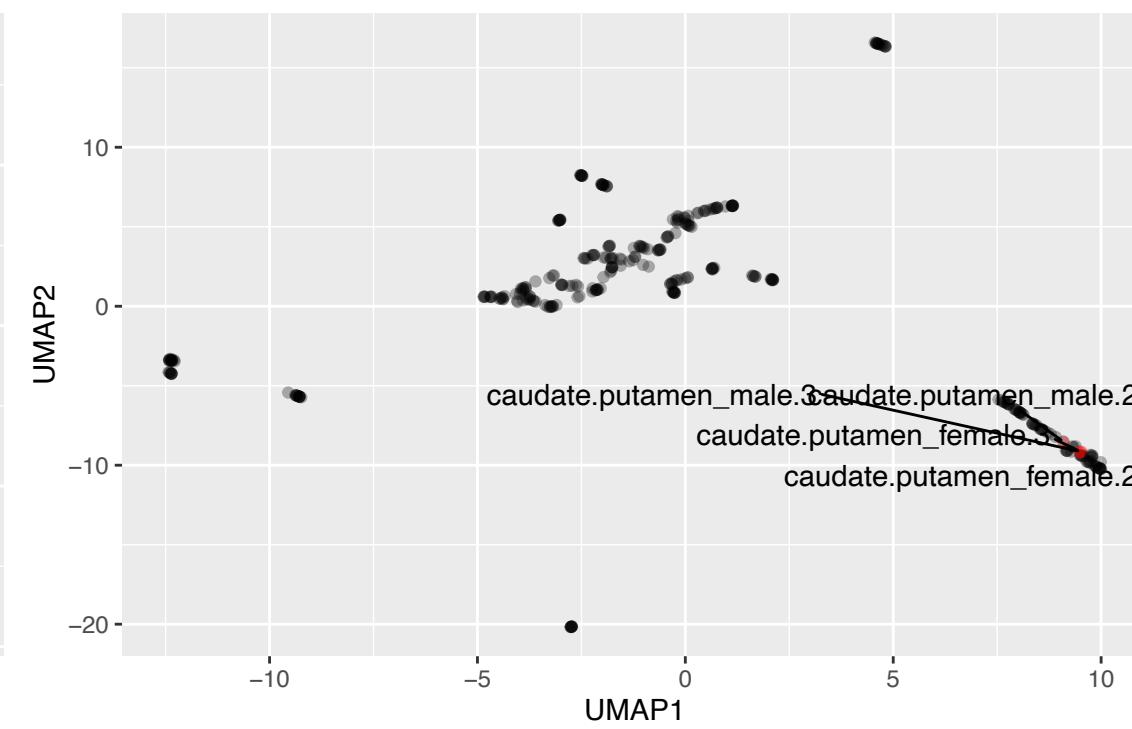
bulbourethral gland



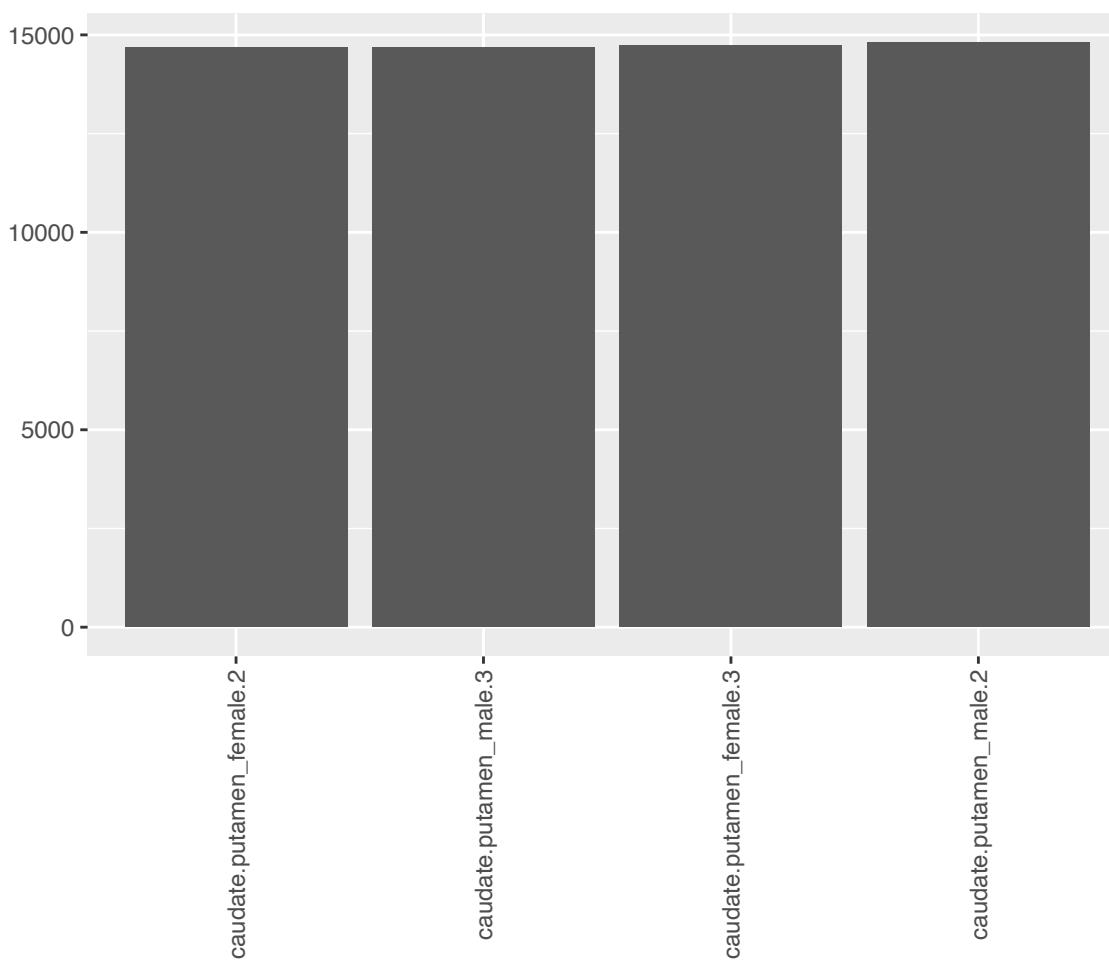
caudate putamen, PCA: TMM expression values



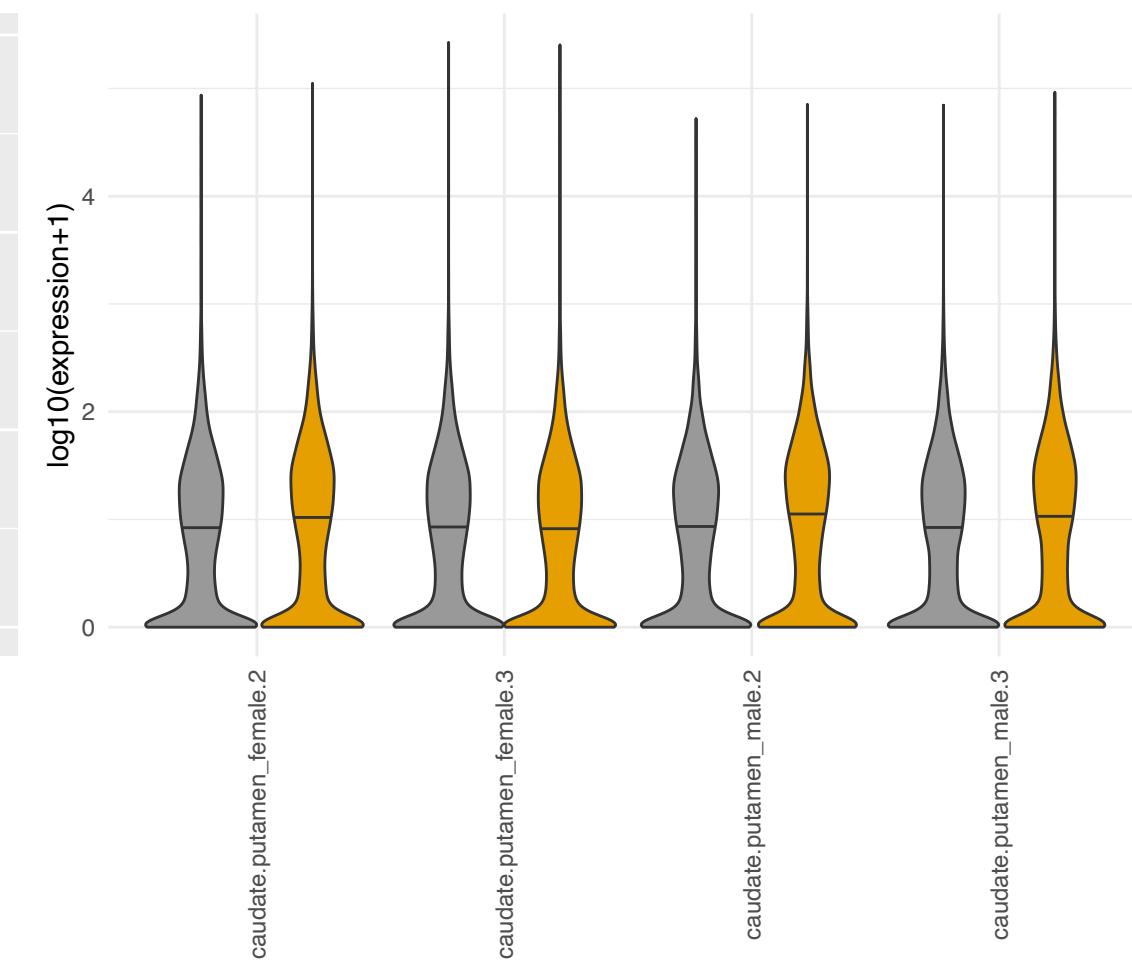
caudate putamen, UMAP: TMM expression values

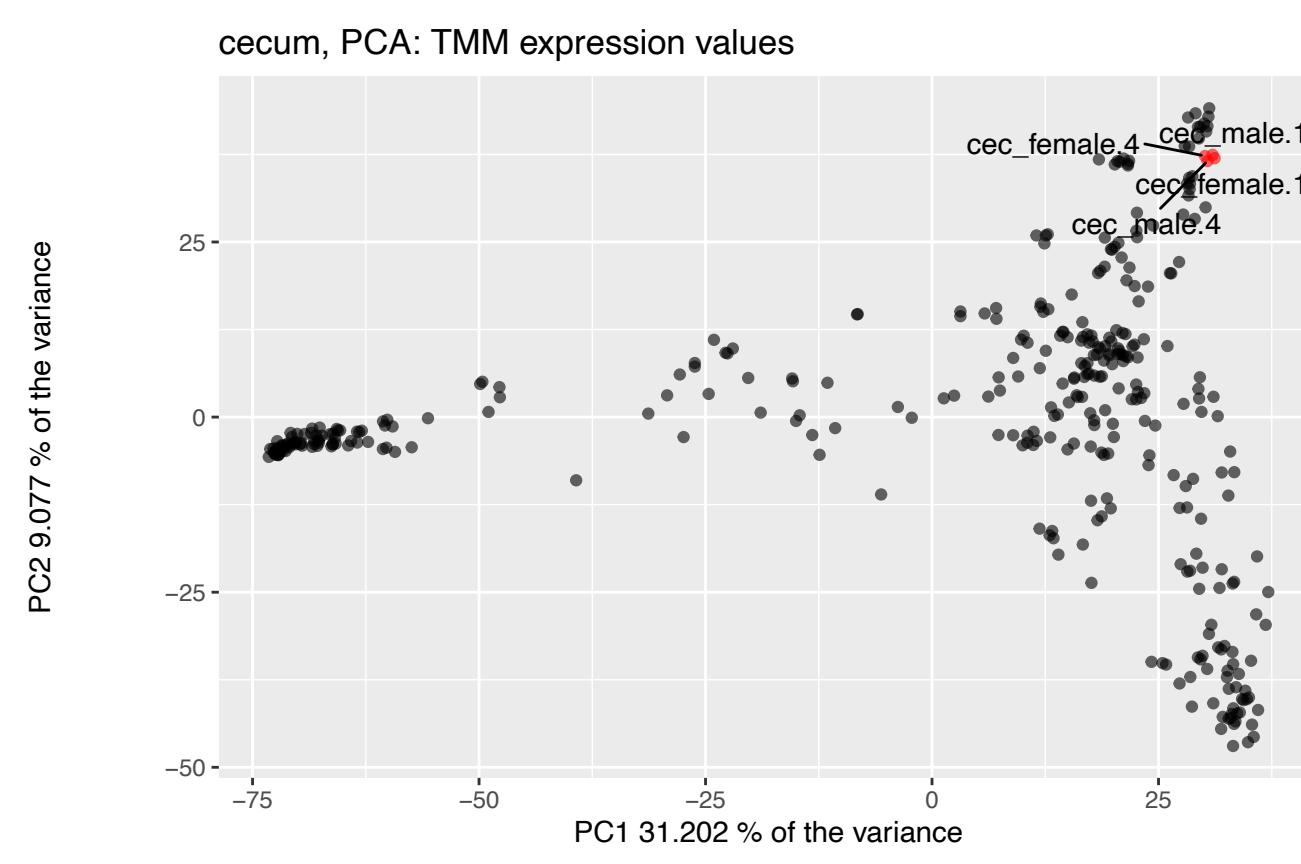


caudate putamen

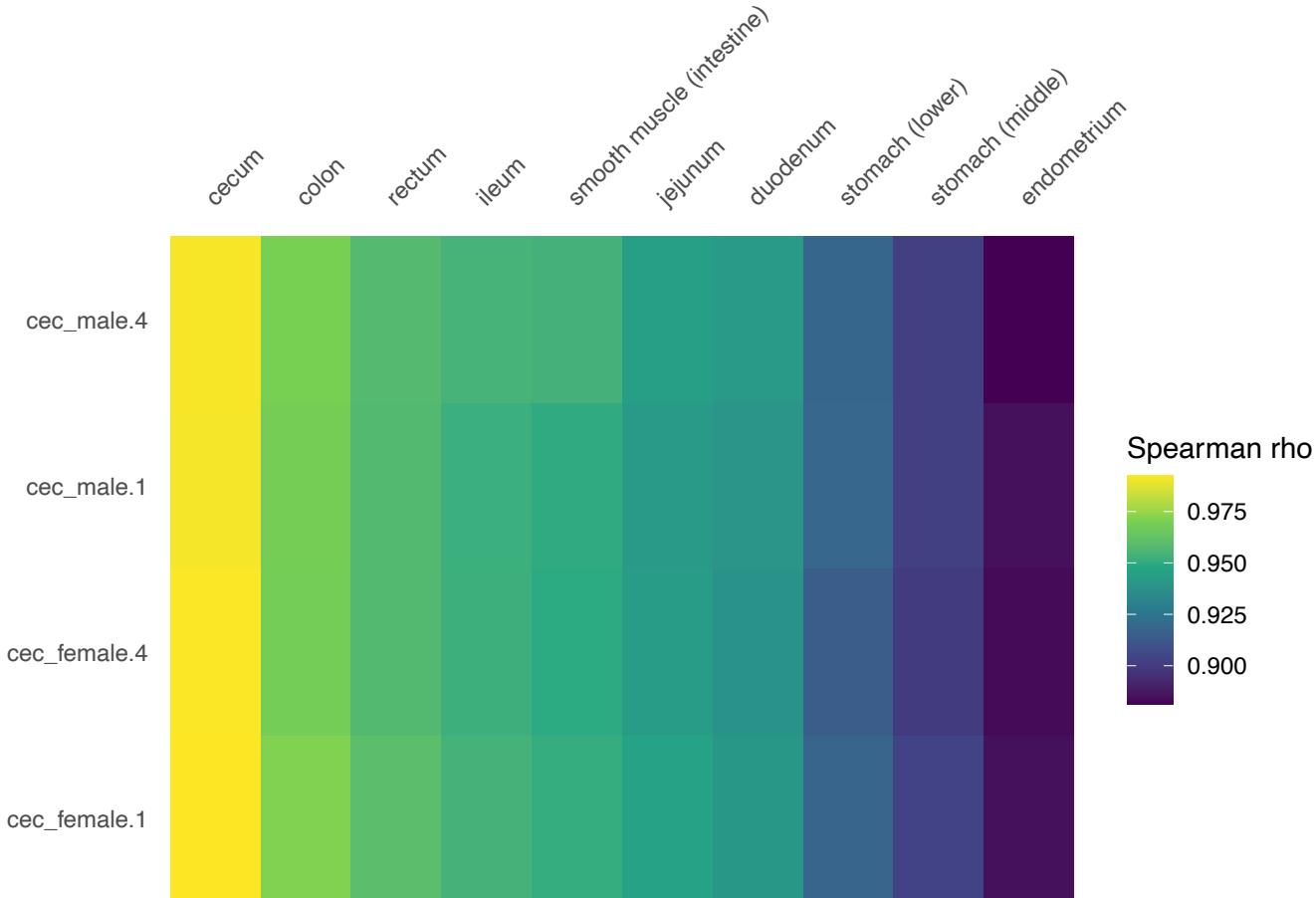


caudate putamen

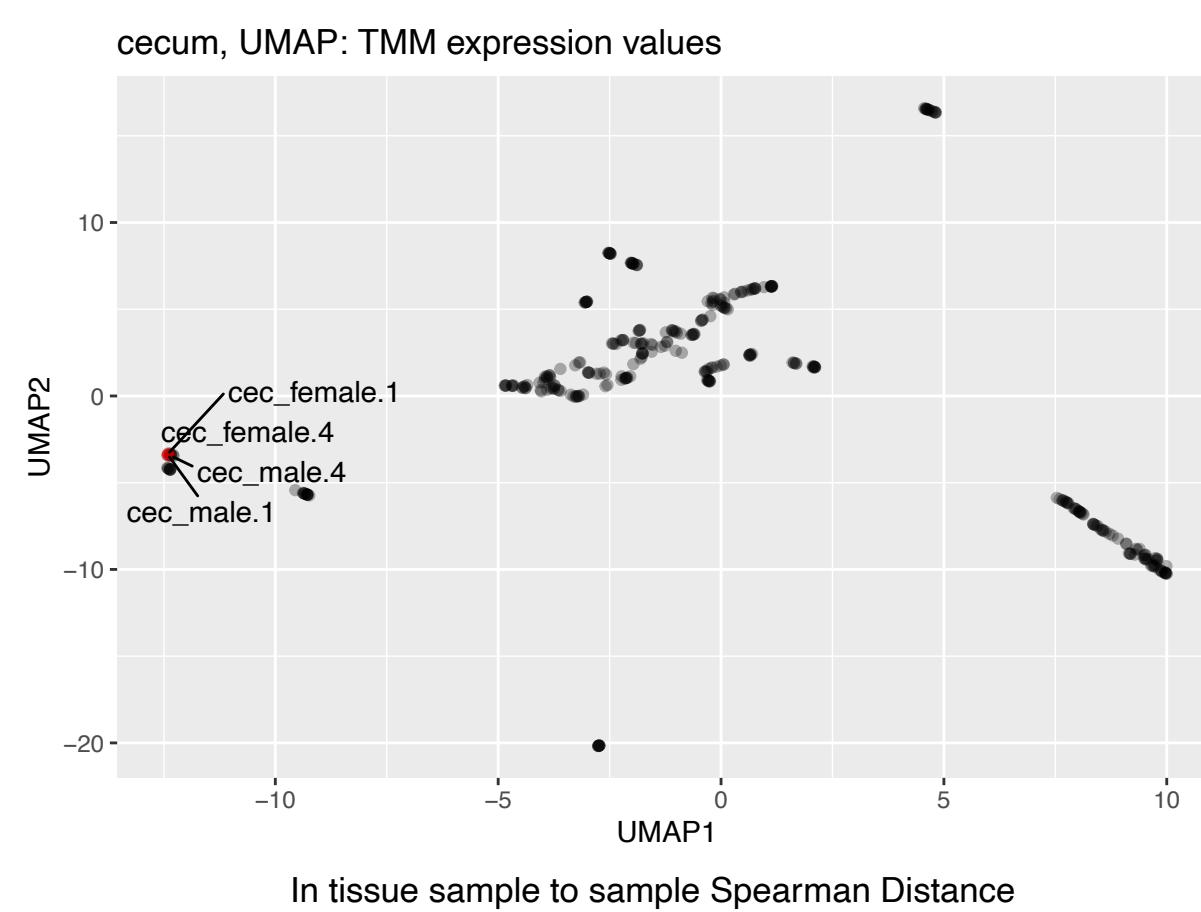




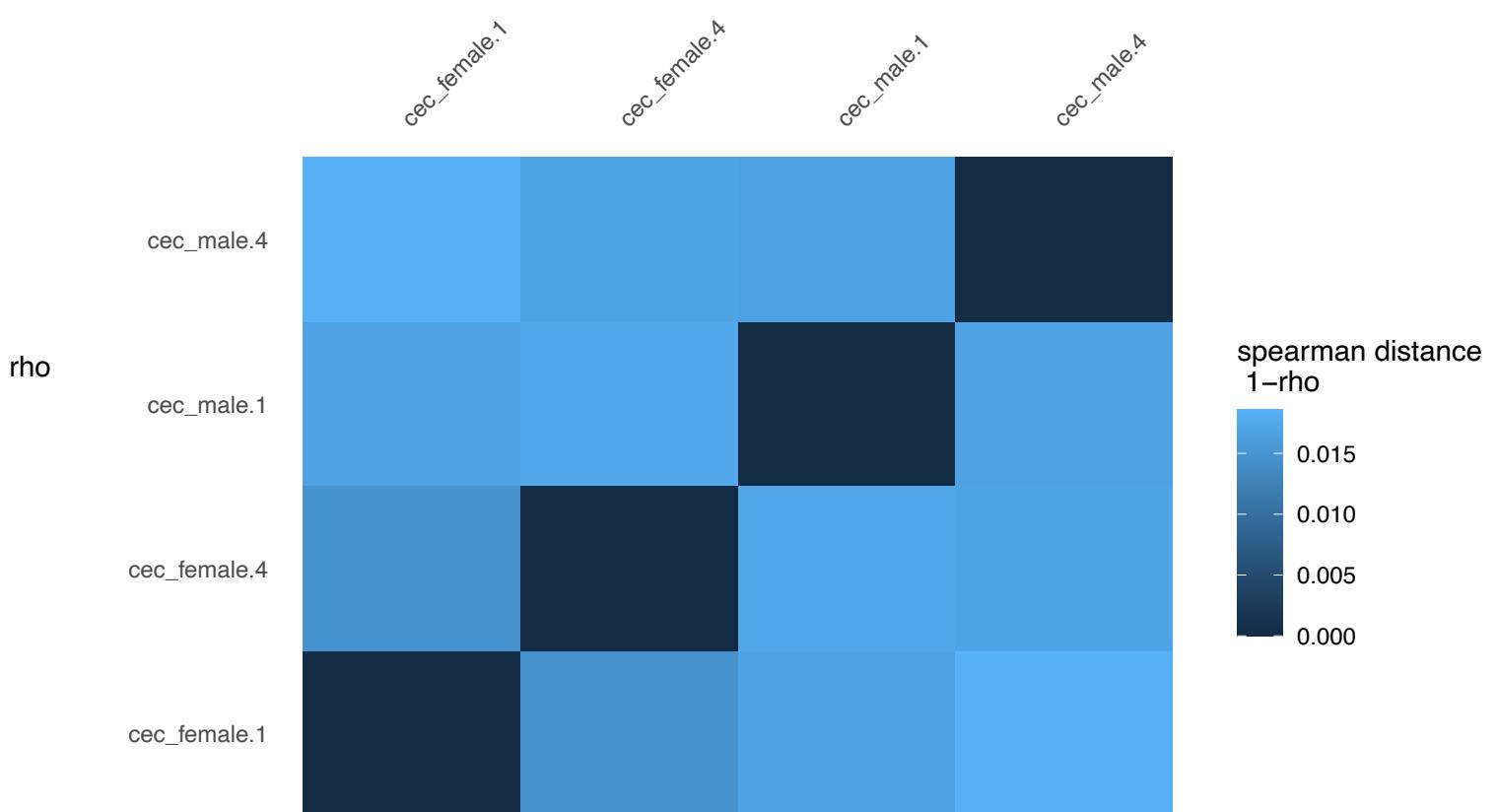
Tissue group to sample correlation



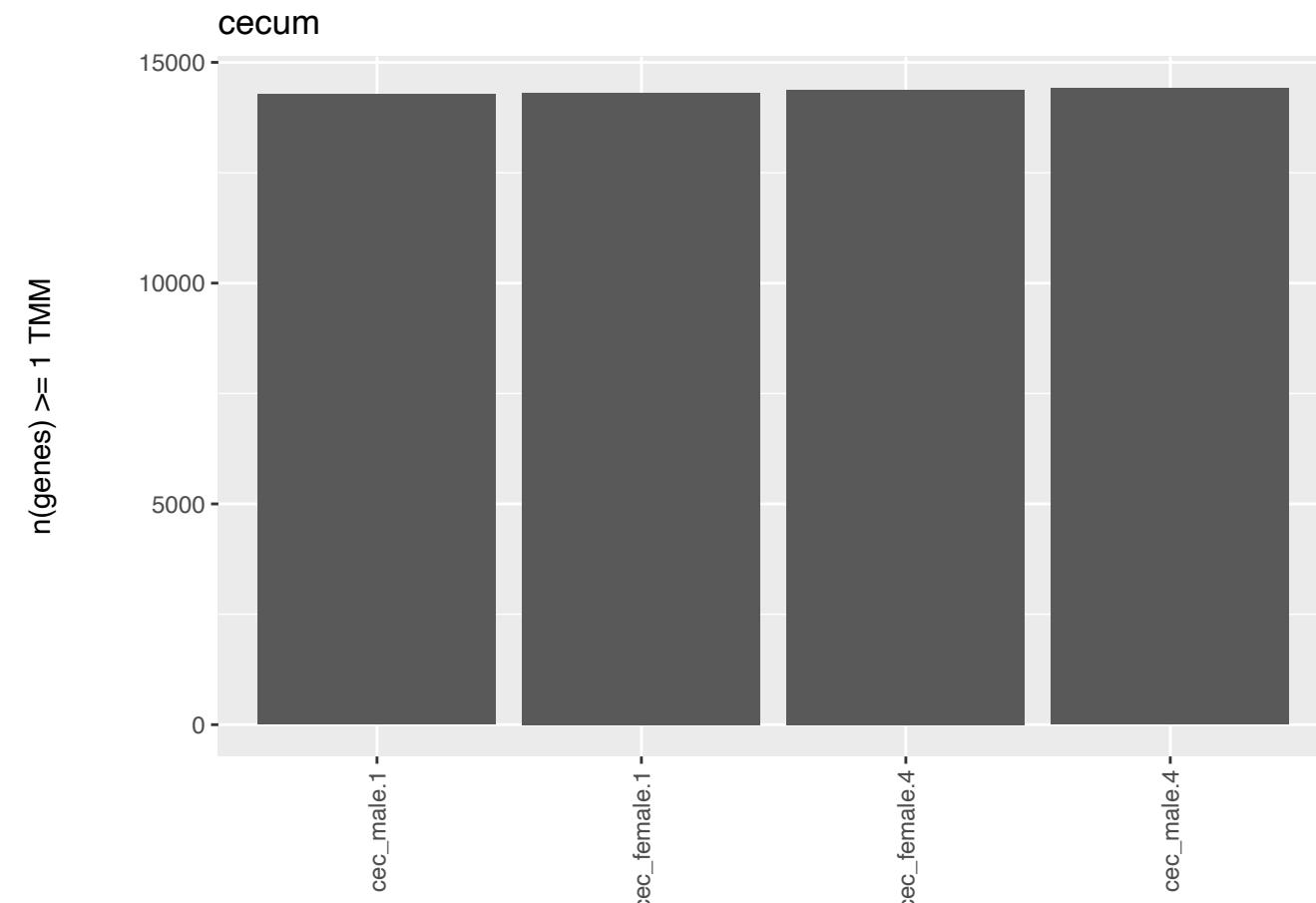
cecum



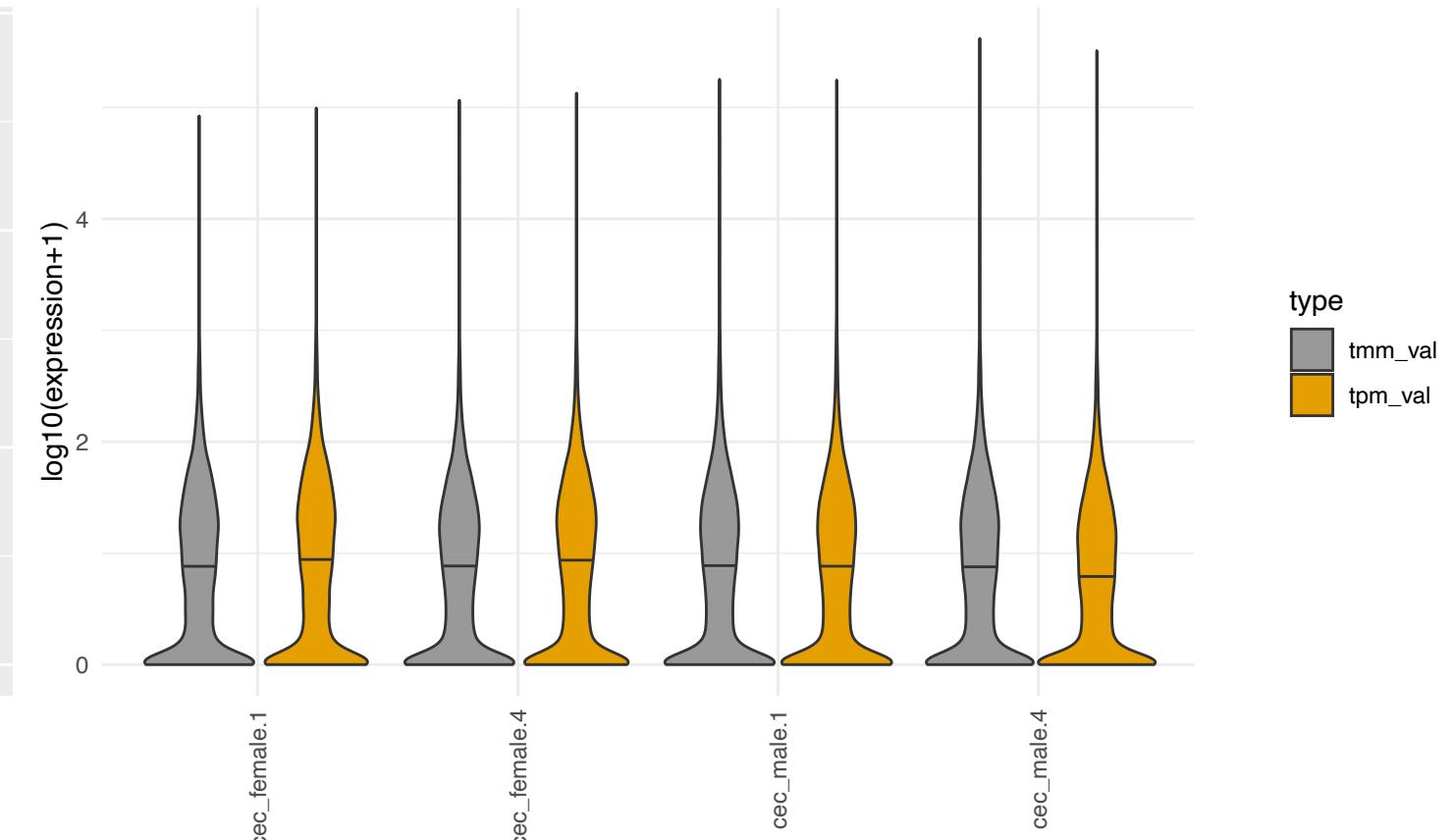
In tissue sample to sample Spearman Distance



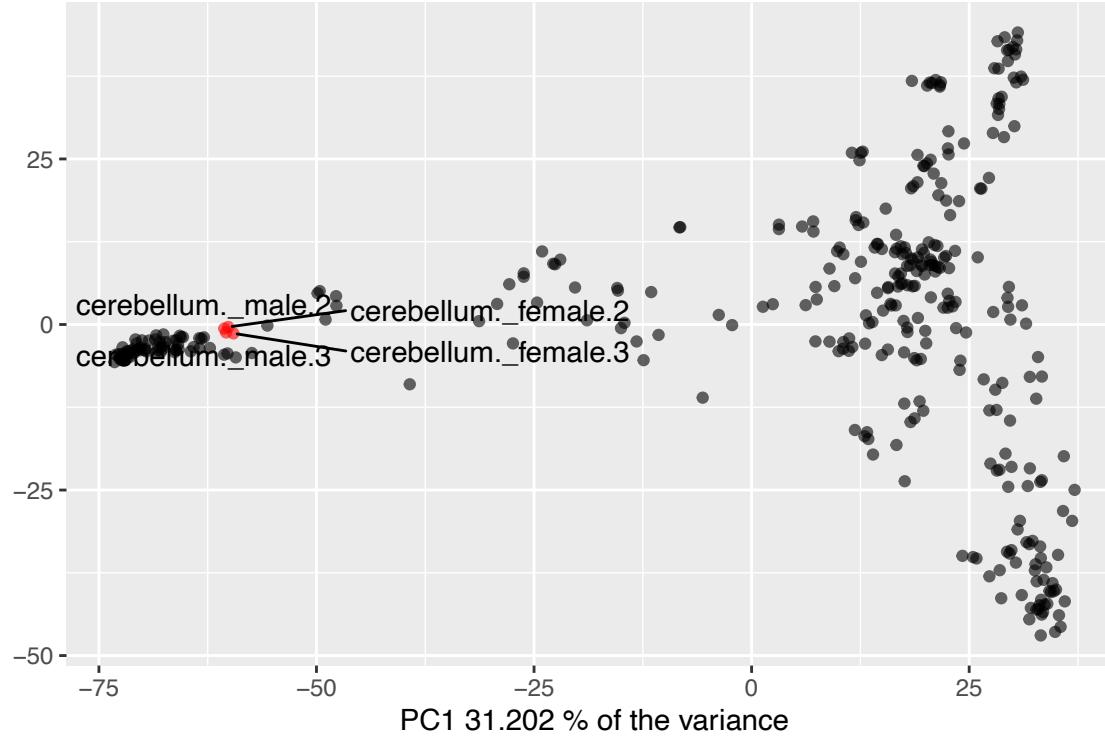
cecum



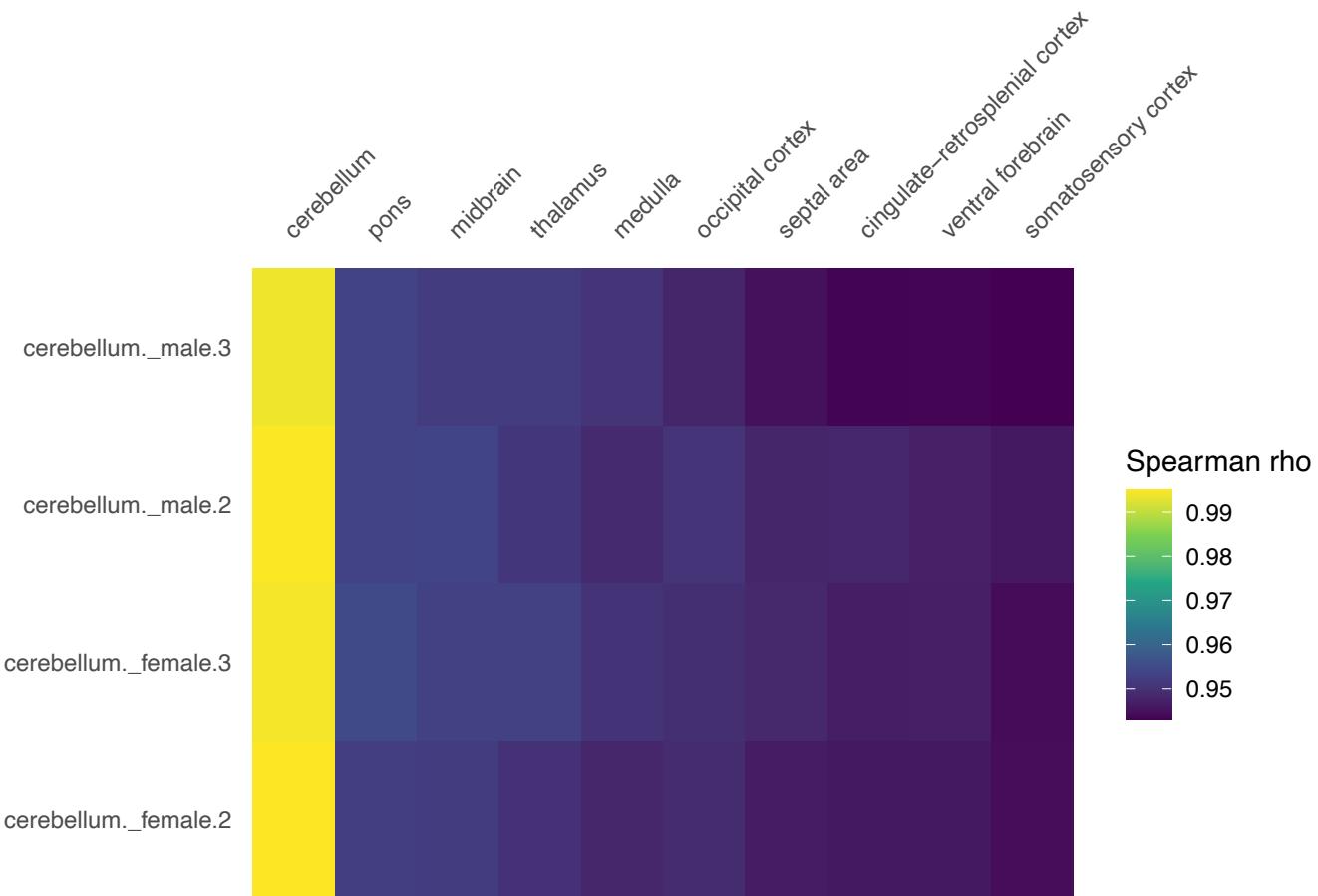
cecum



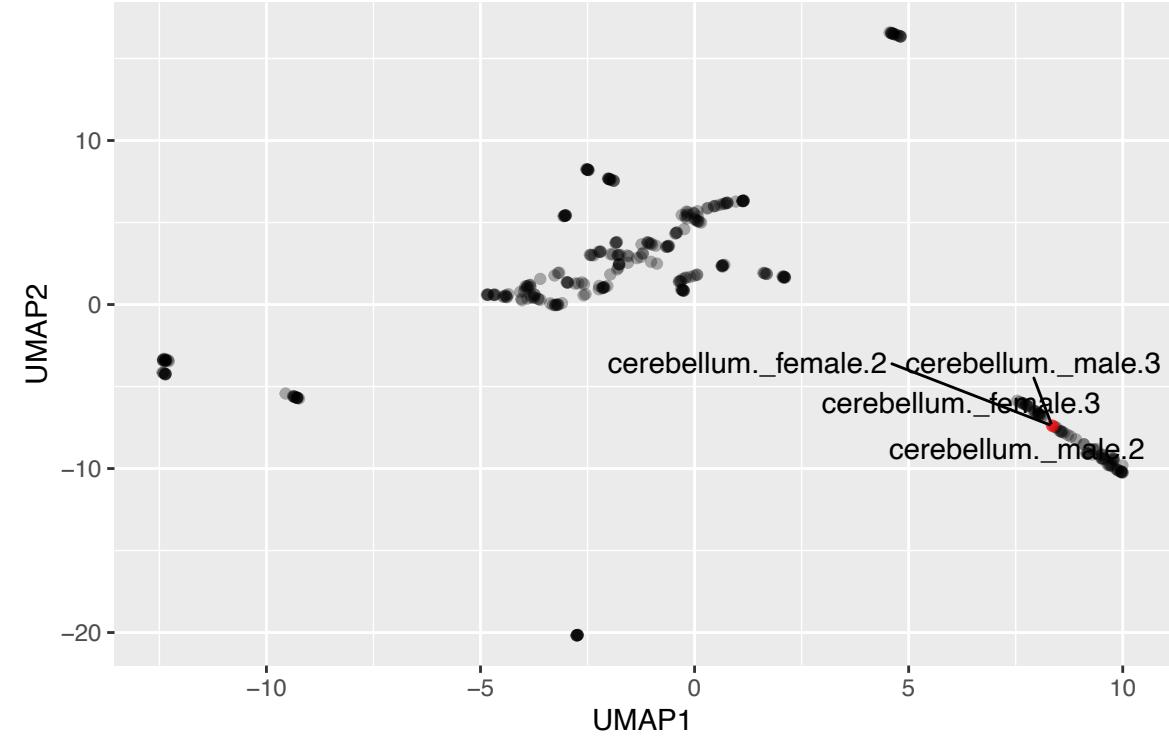
cerebellum, PCA: TMM expression values



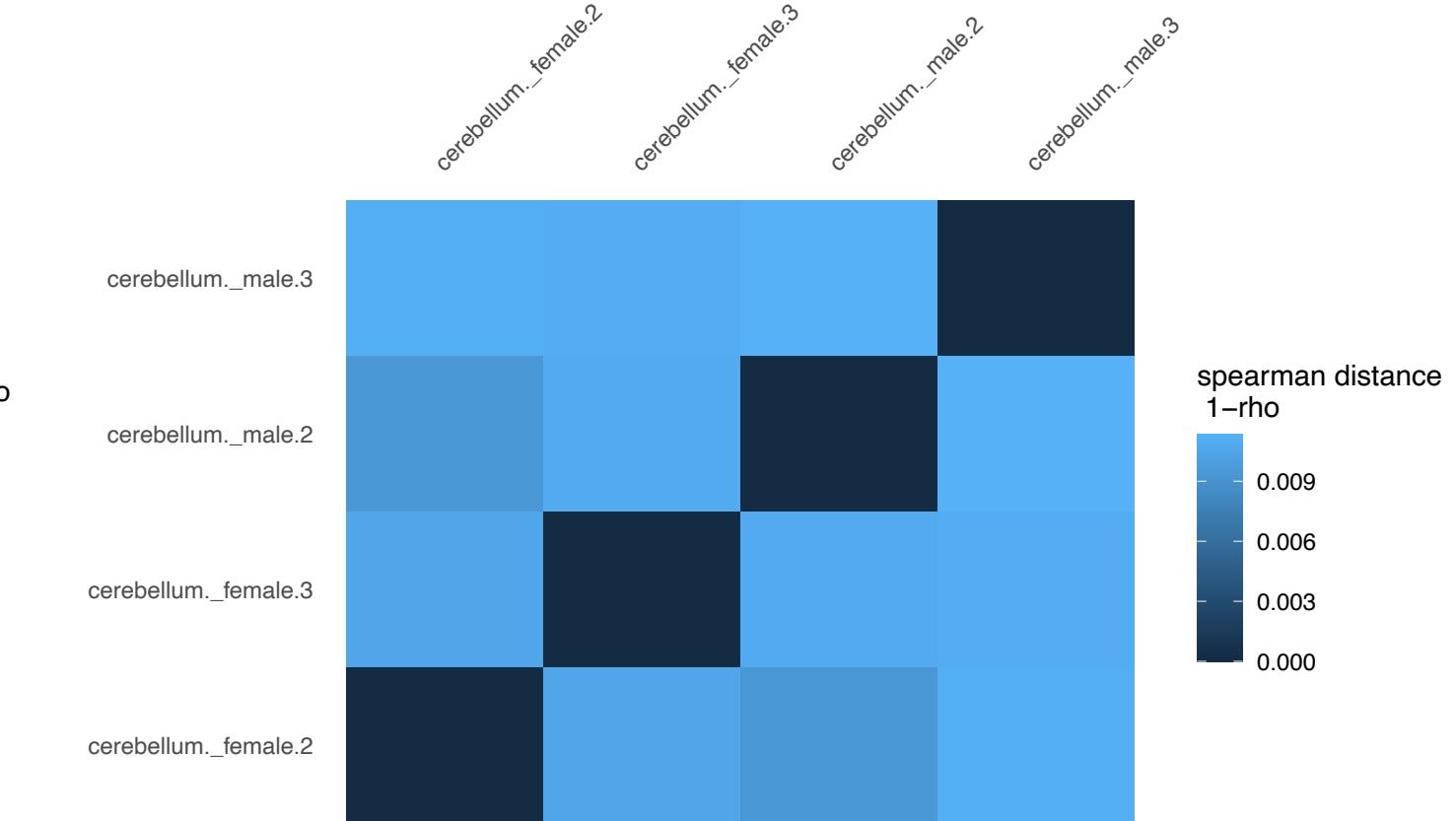
Tissue group to sample correlation



cerebellum, UMAP: TMM expression values

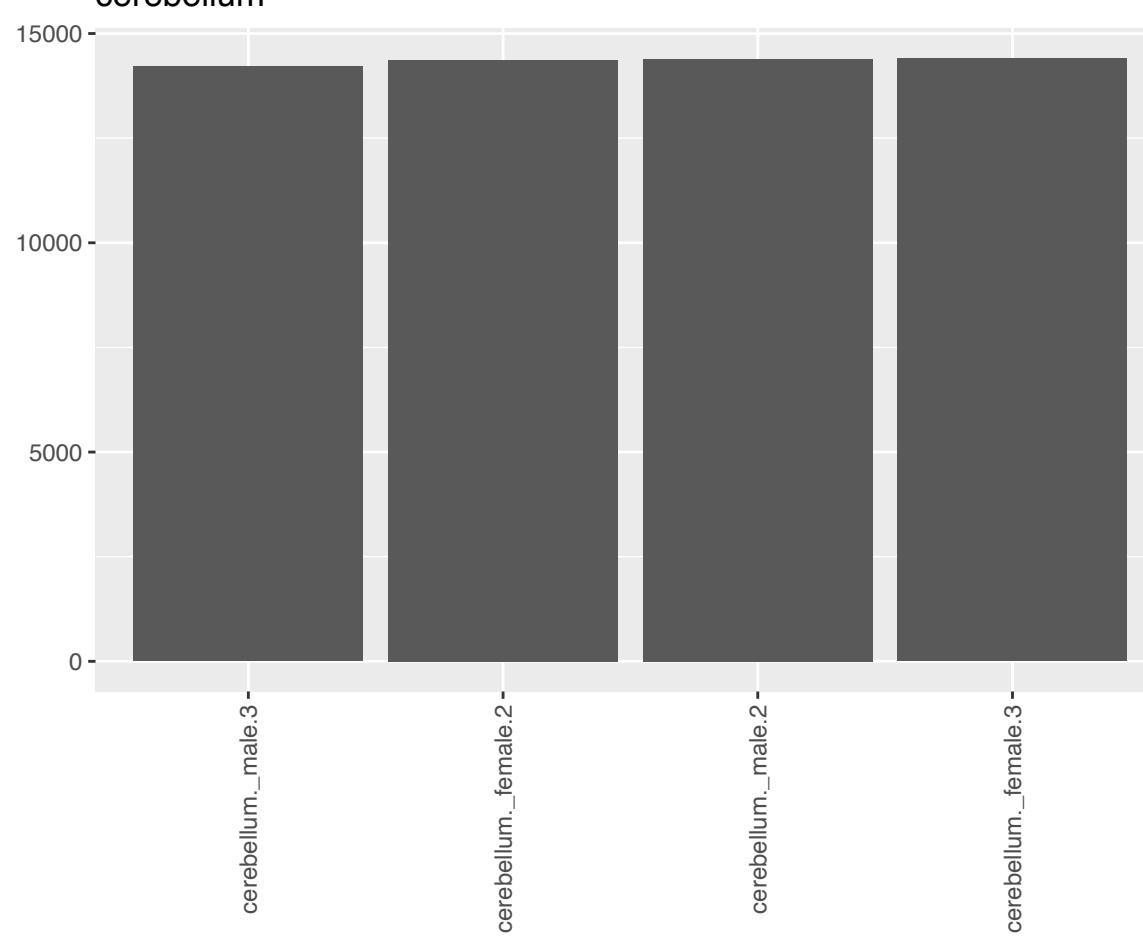


In tissue sample to sample Spearman Distance

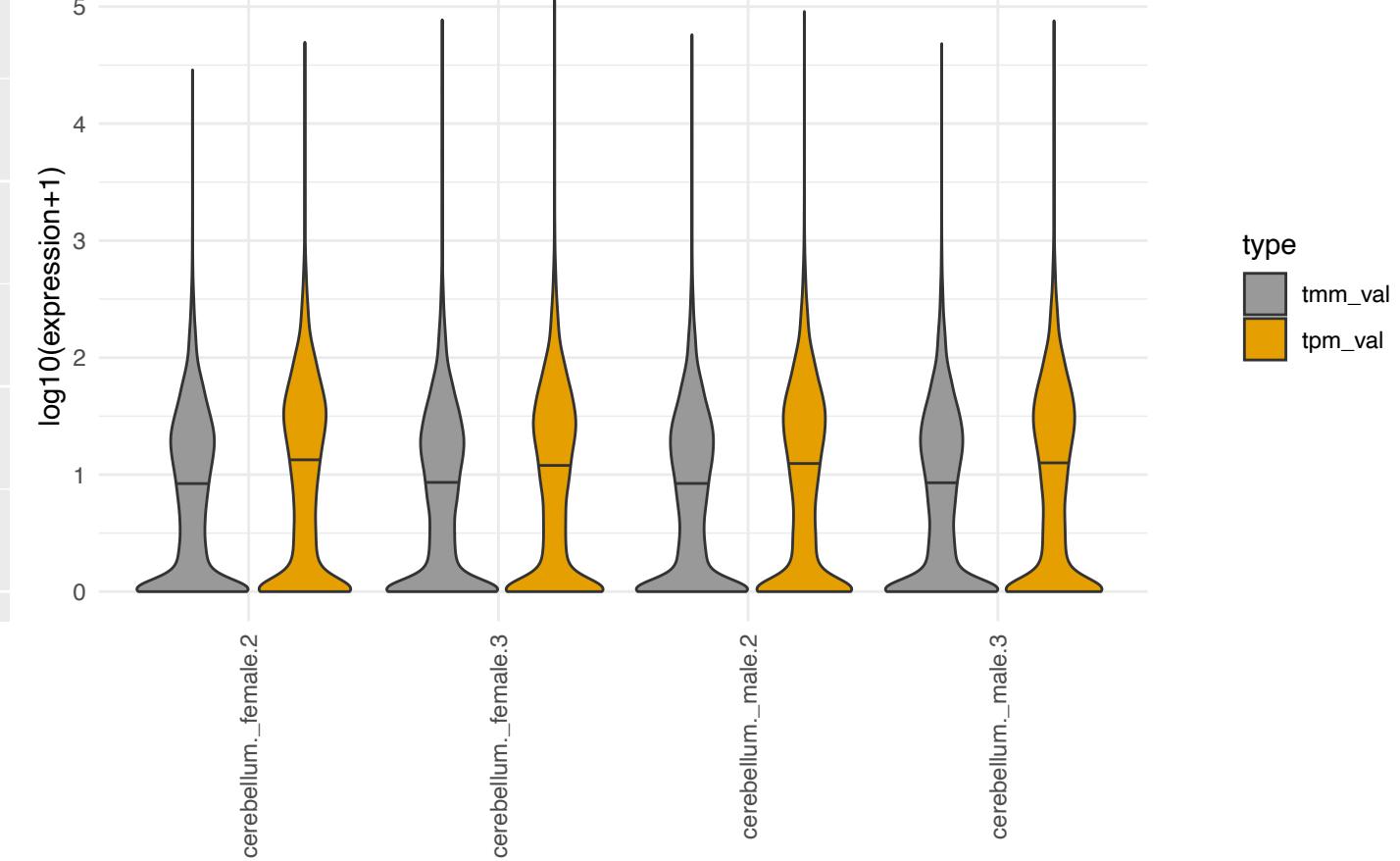


cerebellum

n(genes) >= 1 TMM

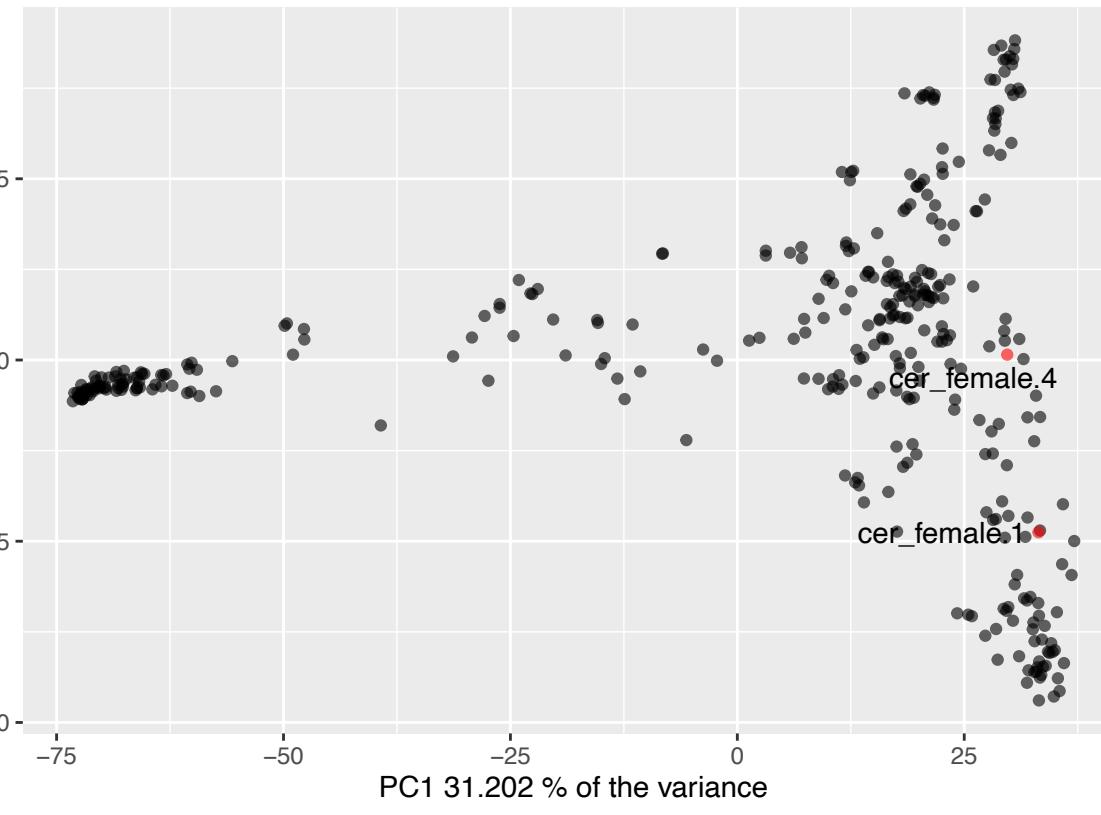


cerebellum

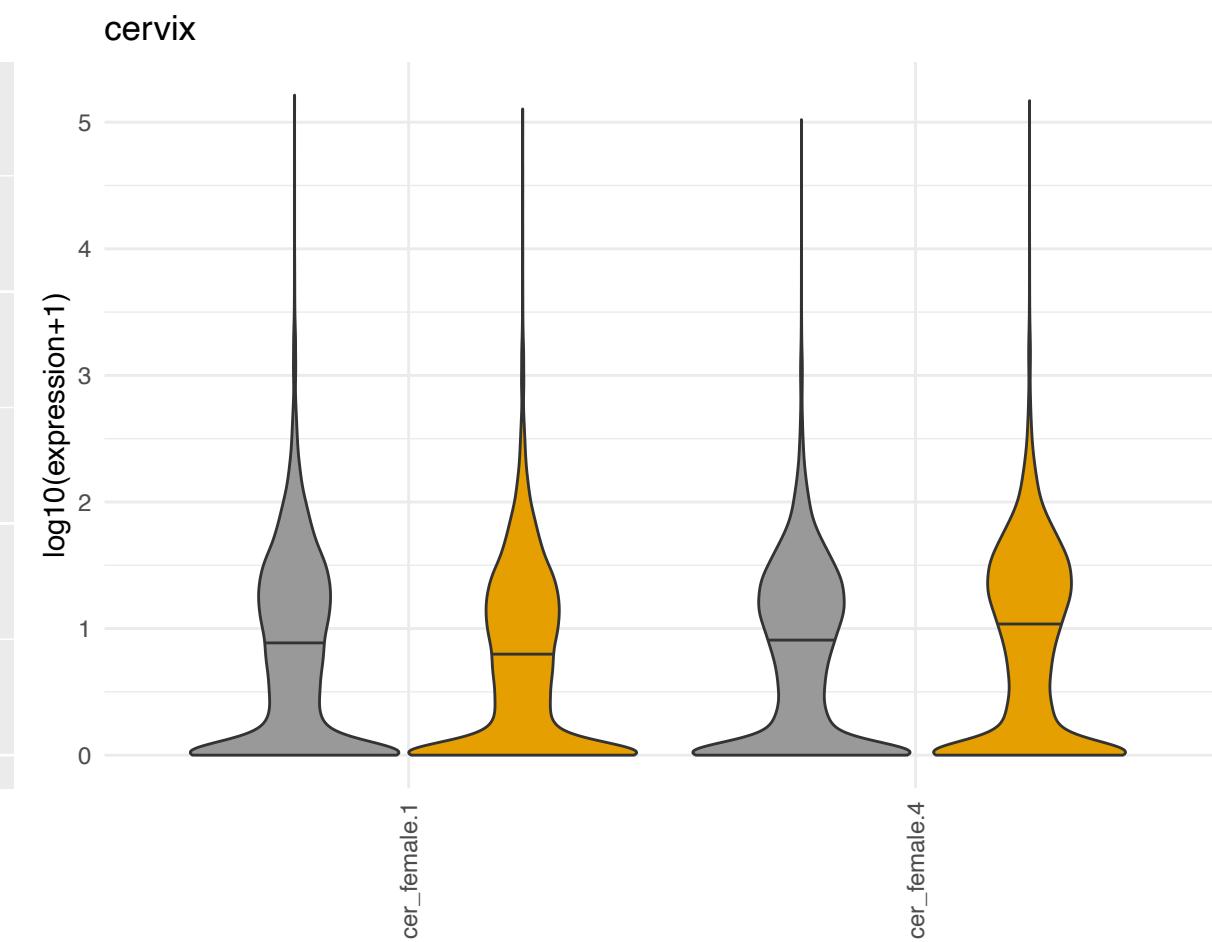
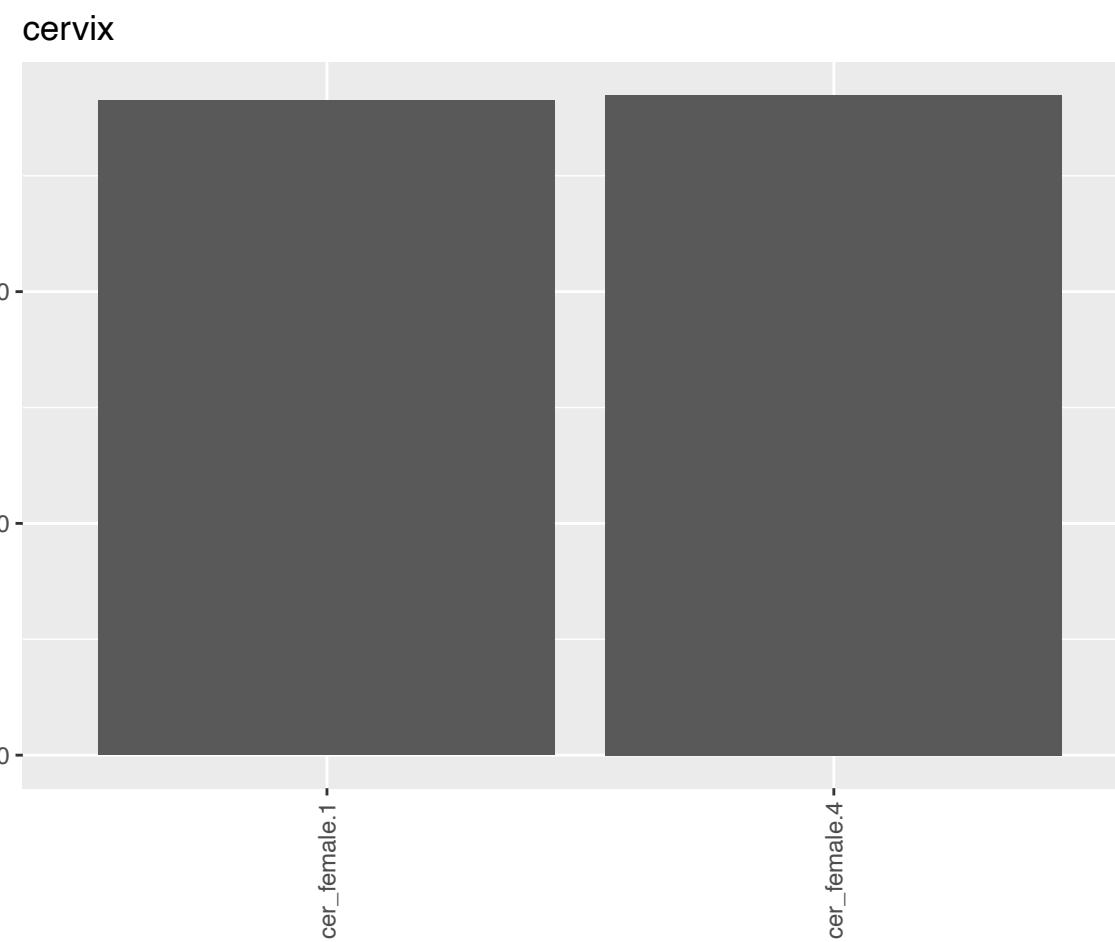
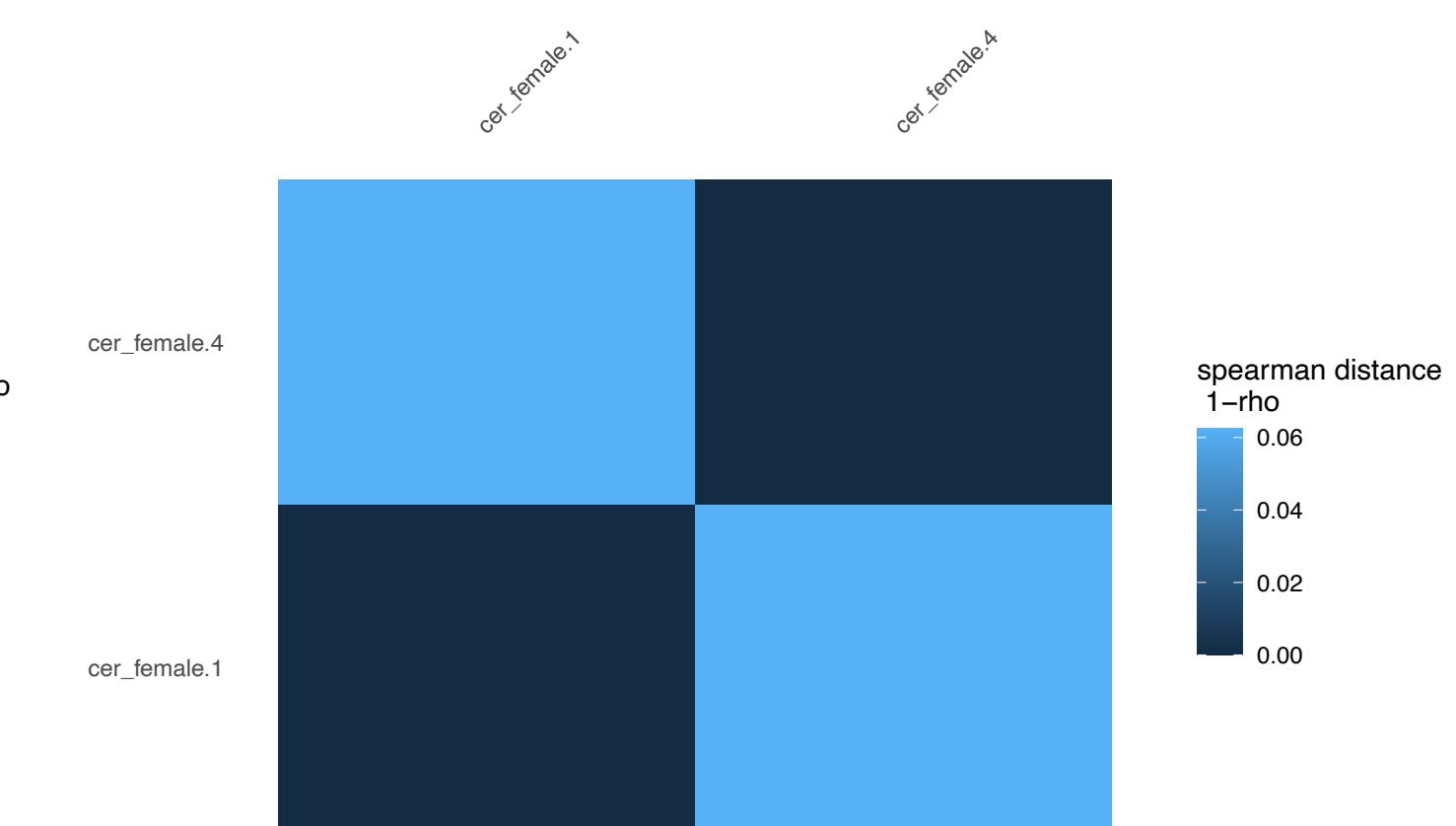
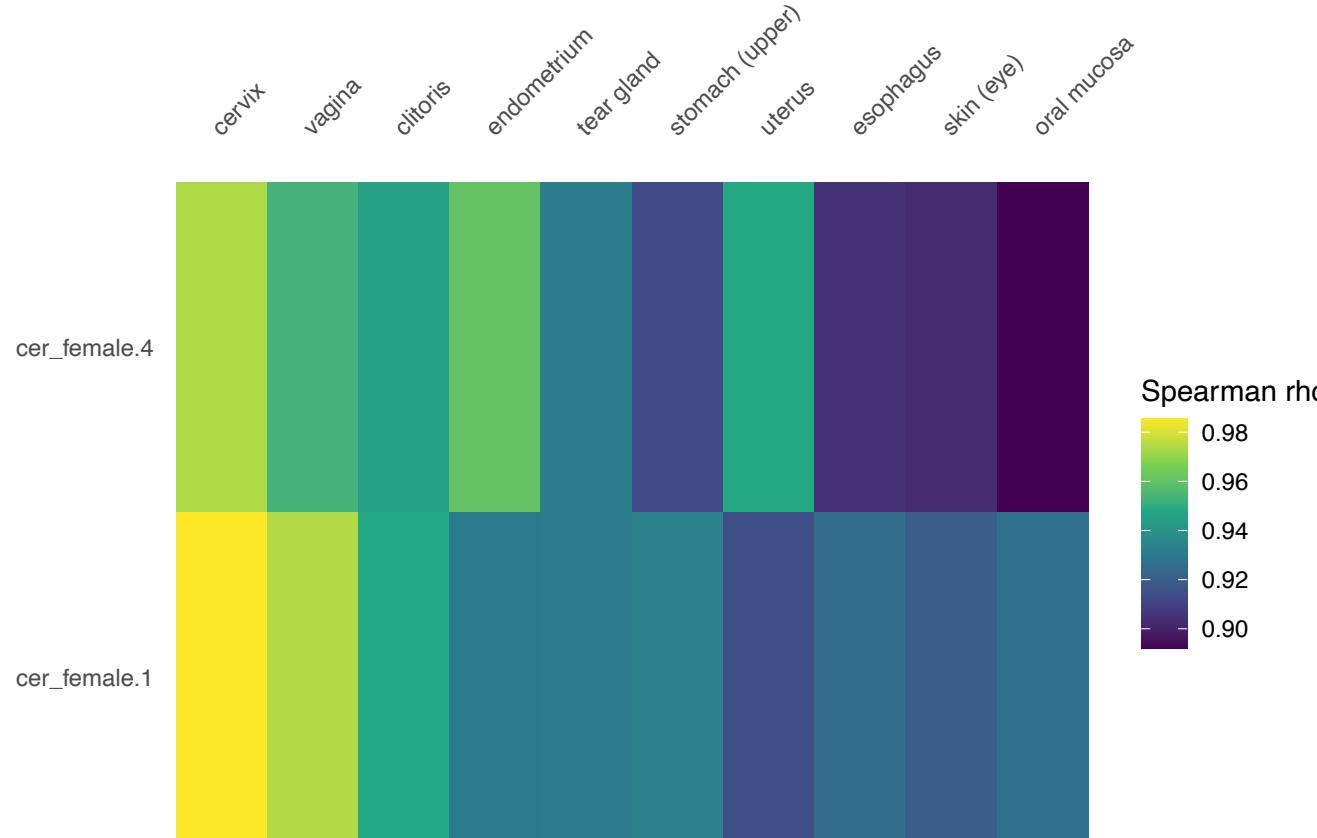
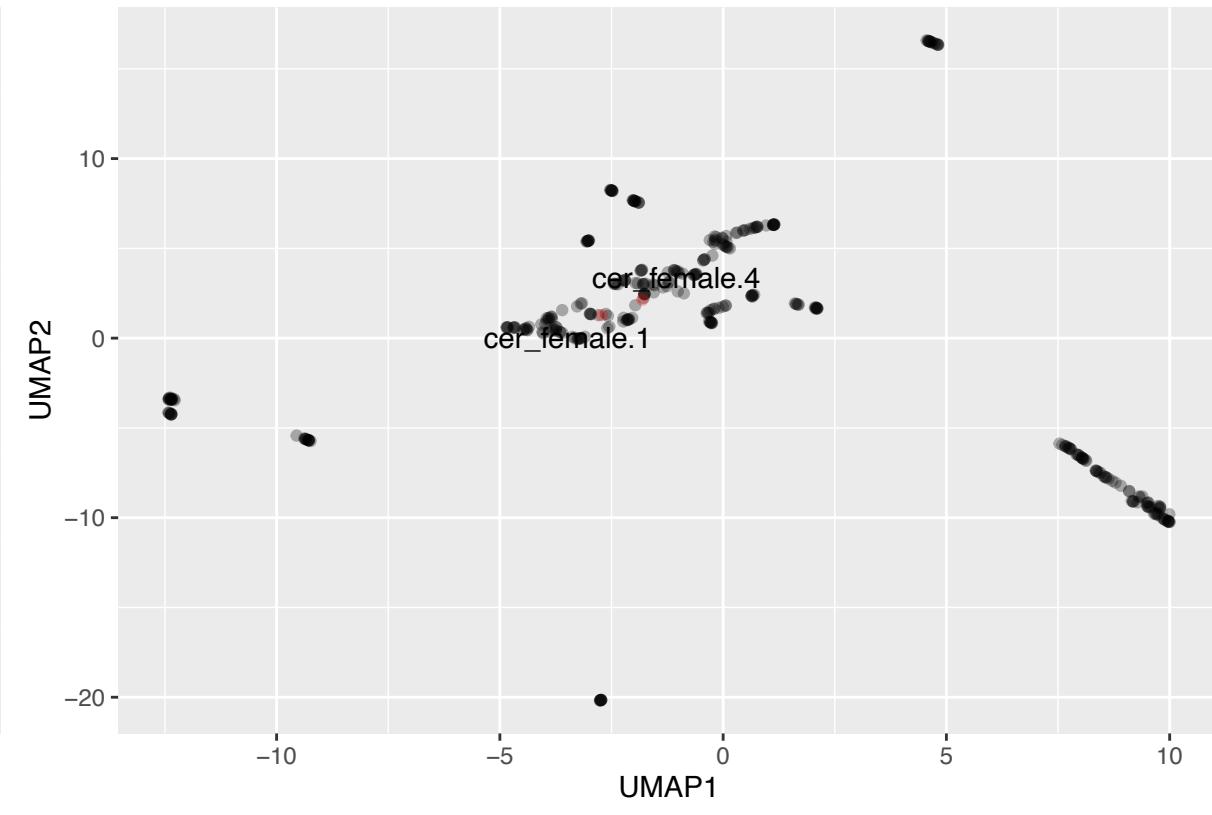


type
tmm_val
tpm_val

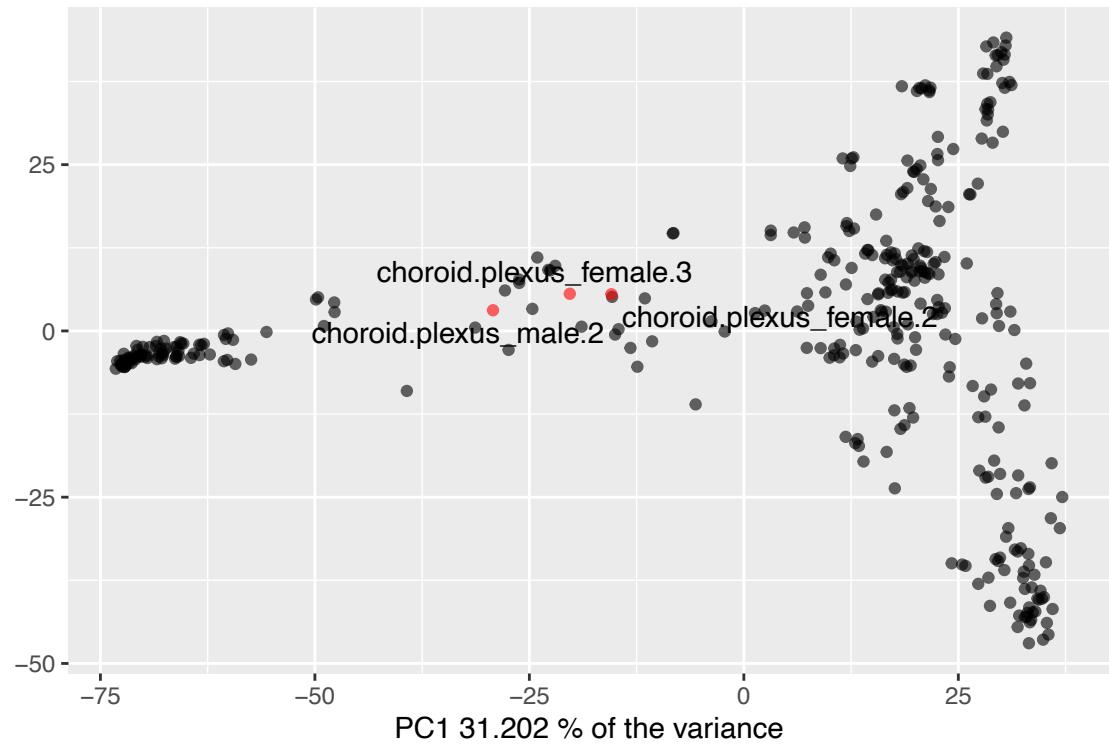
cervix, PCA: TMM expression values



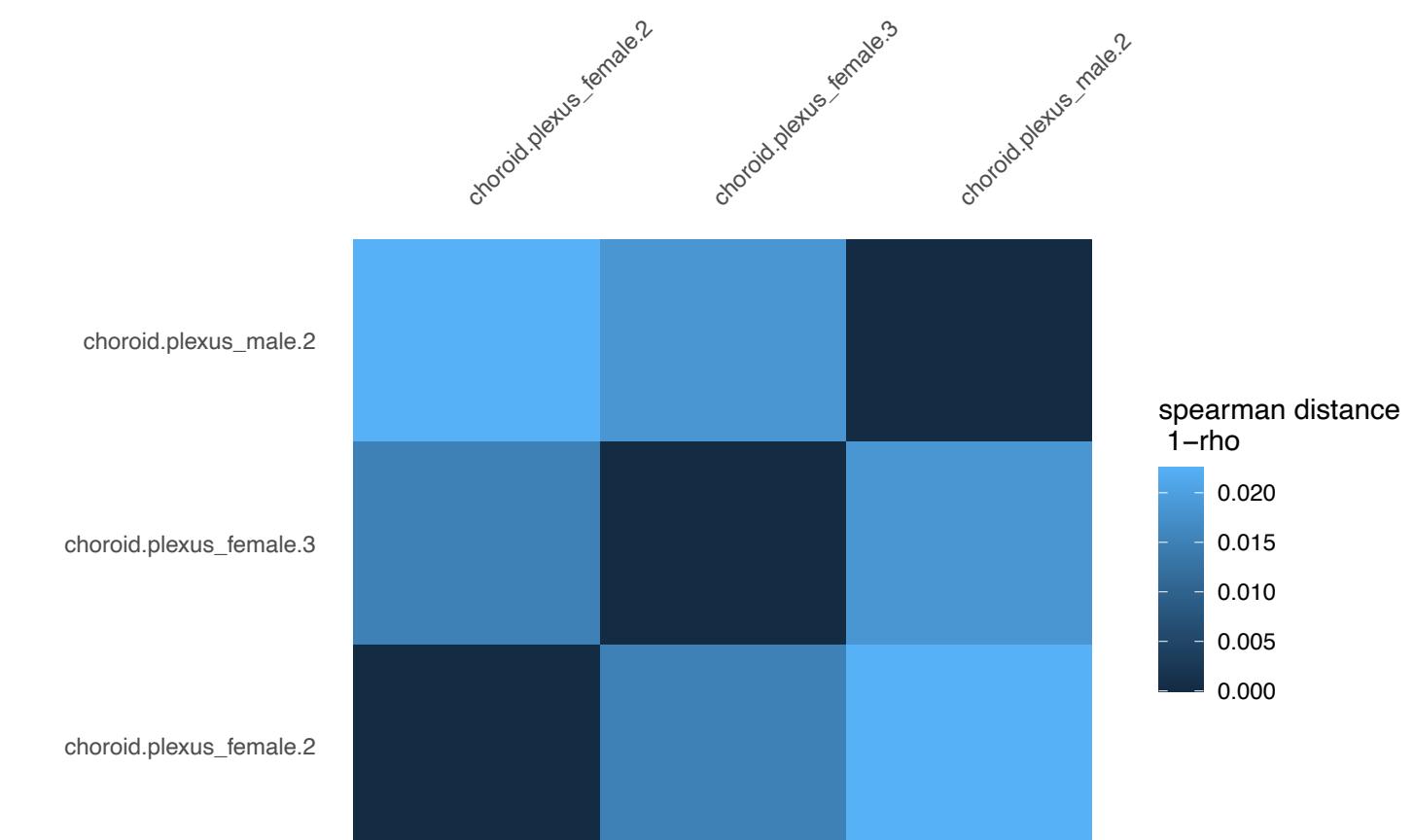
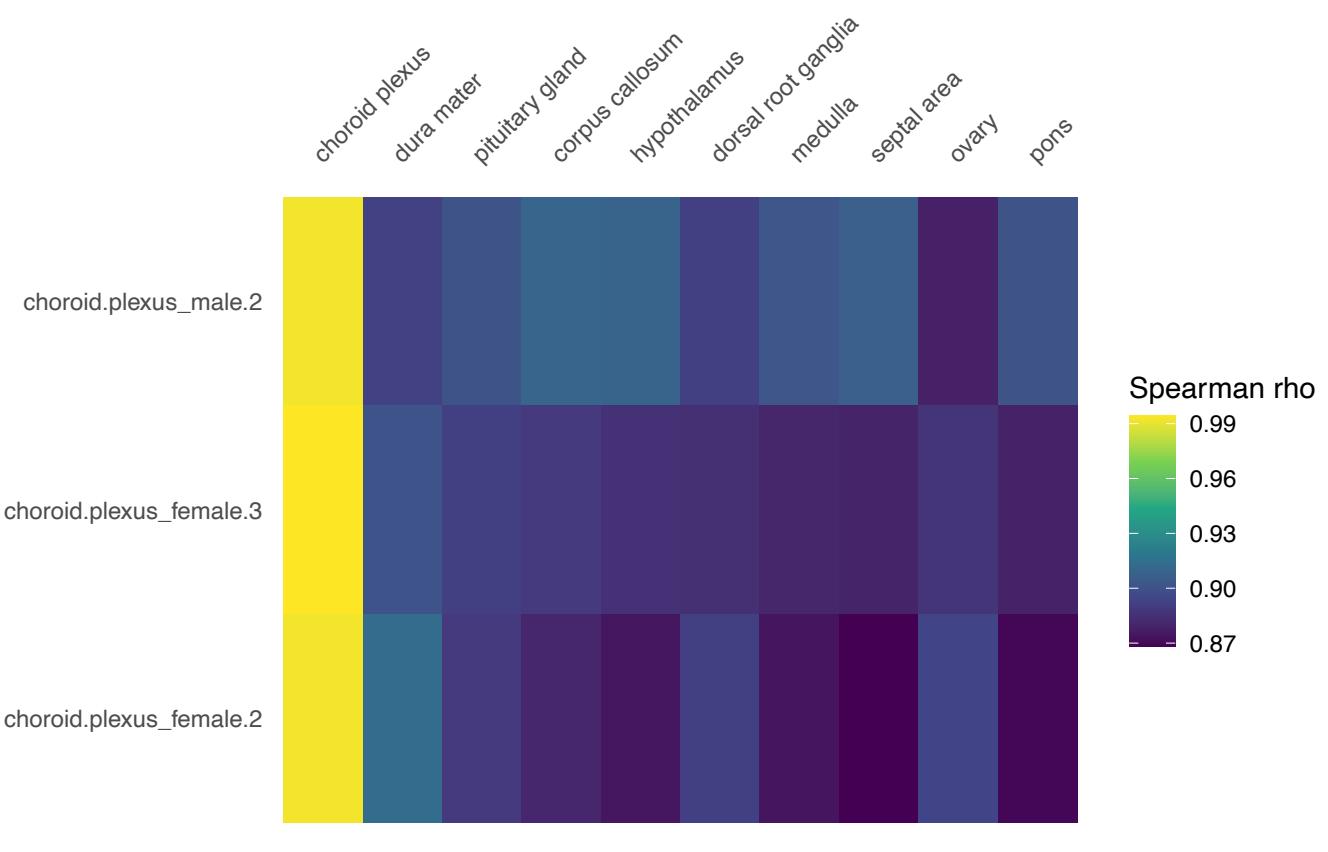
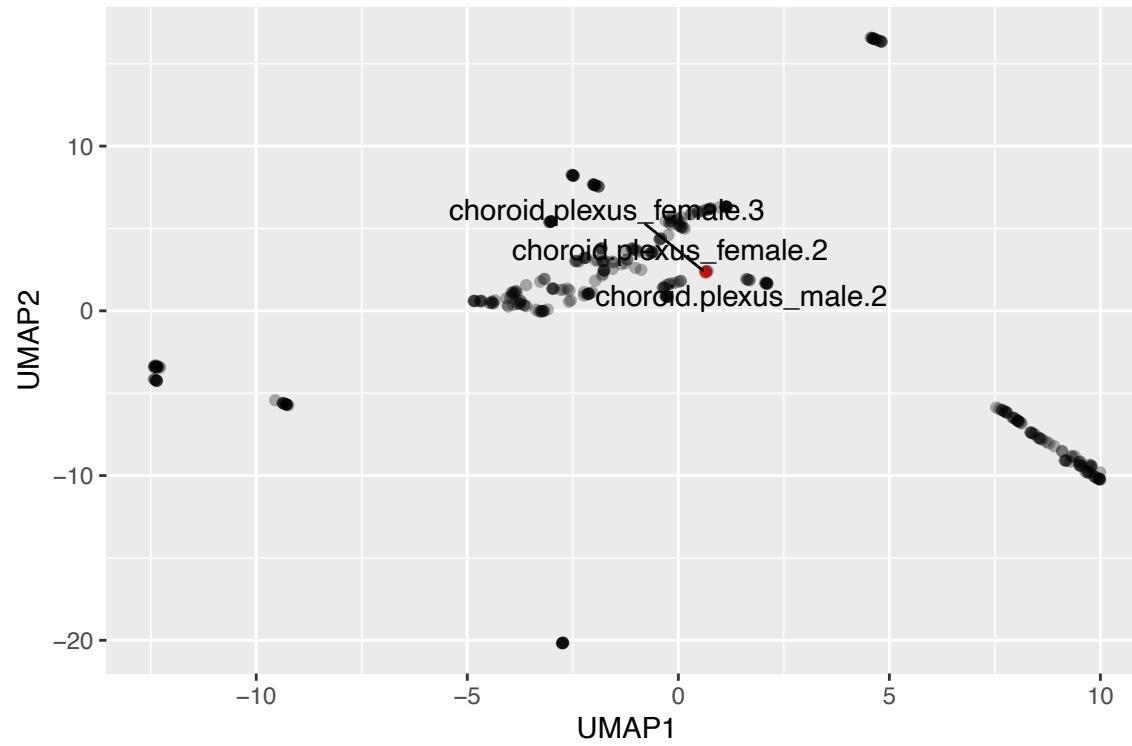
cervix, UMAP: TMM expression values



choroid plexus, PCA: TMM expression values

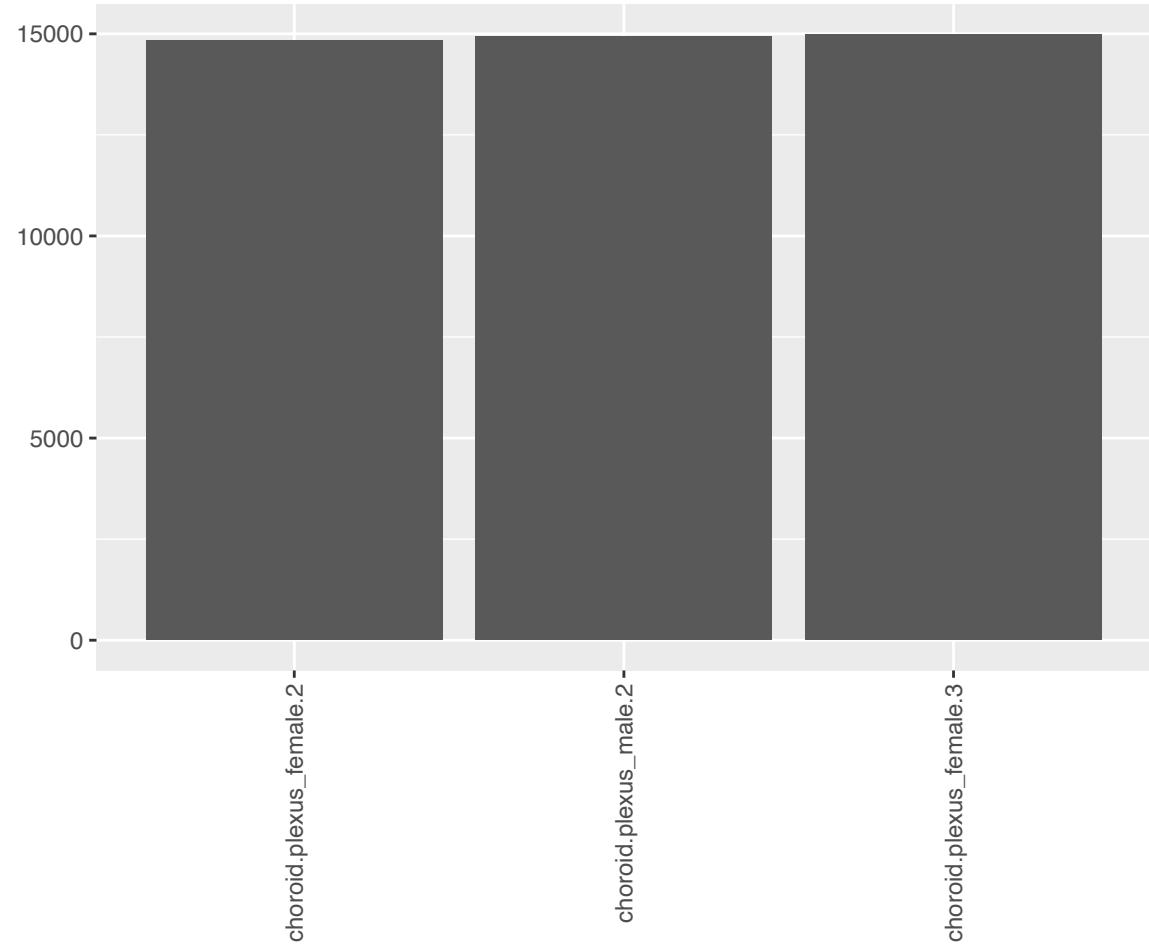


choroid plexus, UMAP: TMM expression values

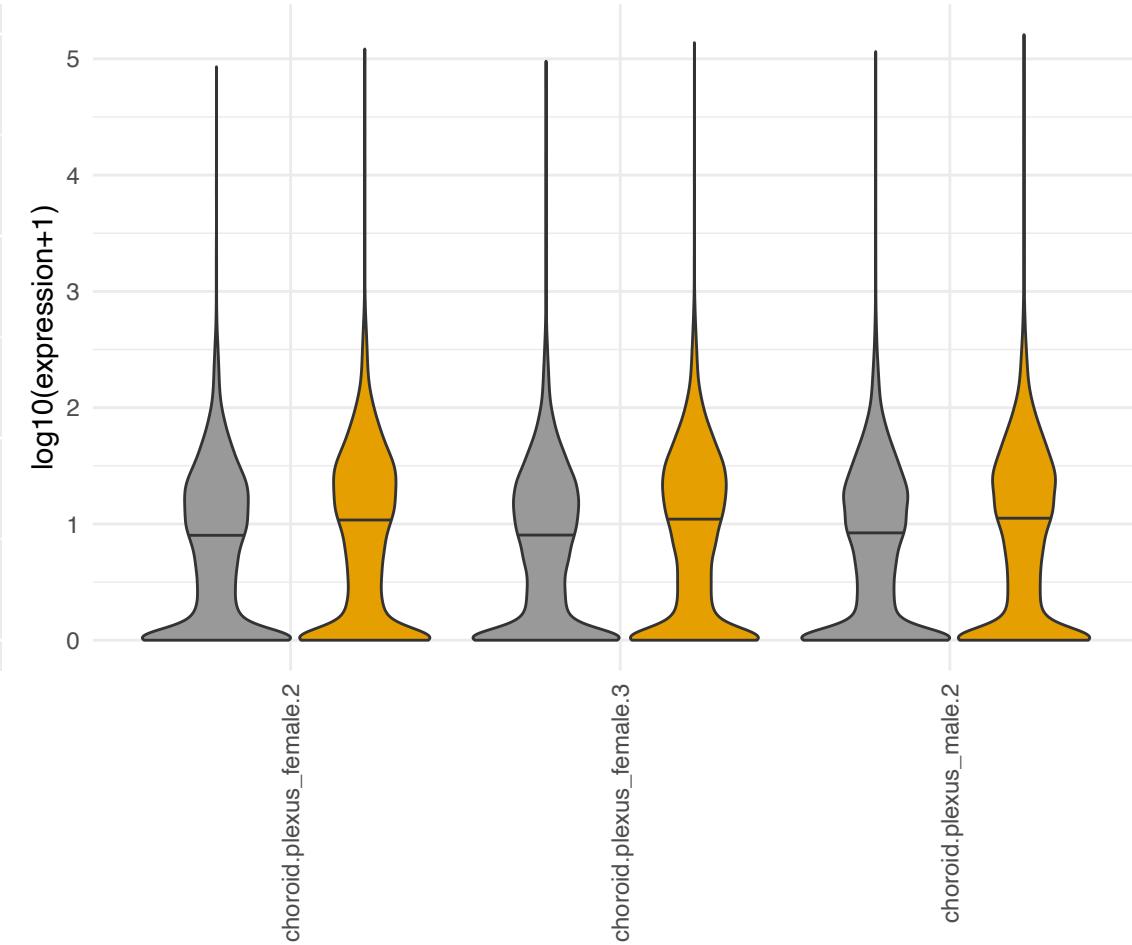


PC2 9.077 % of the variance

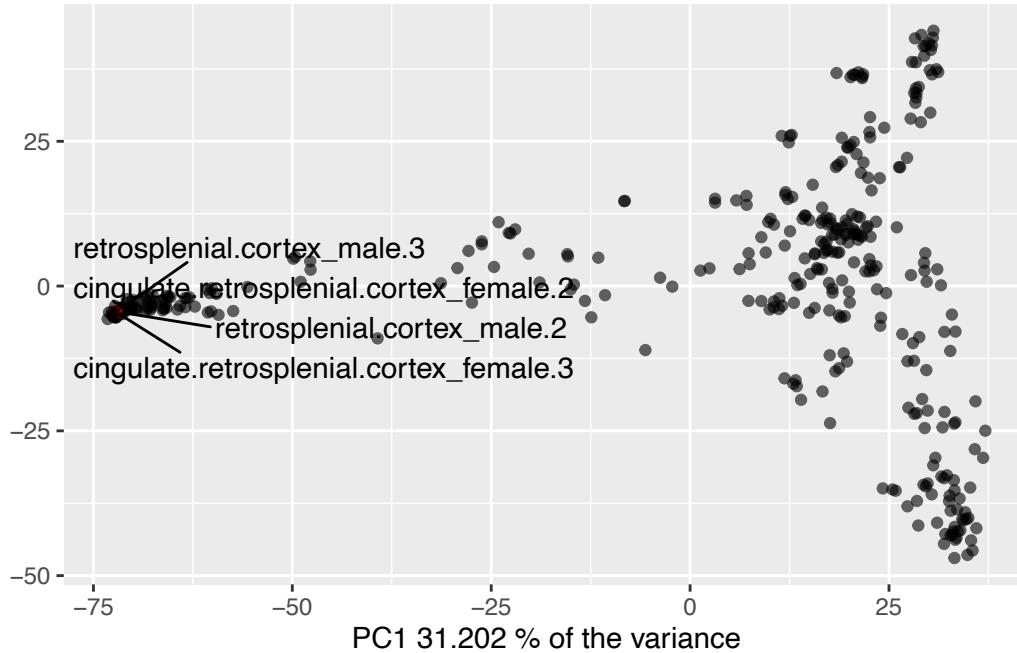
choroid plexus



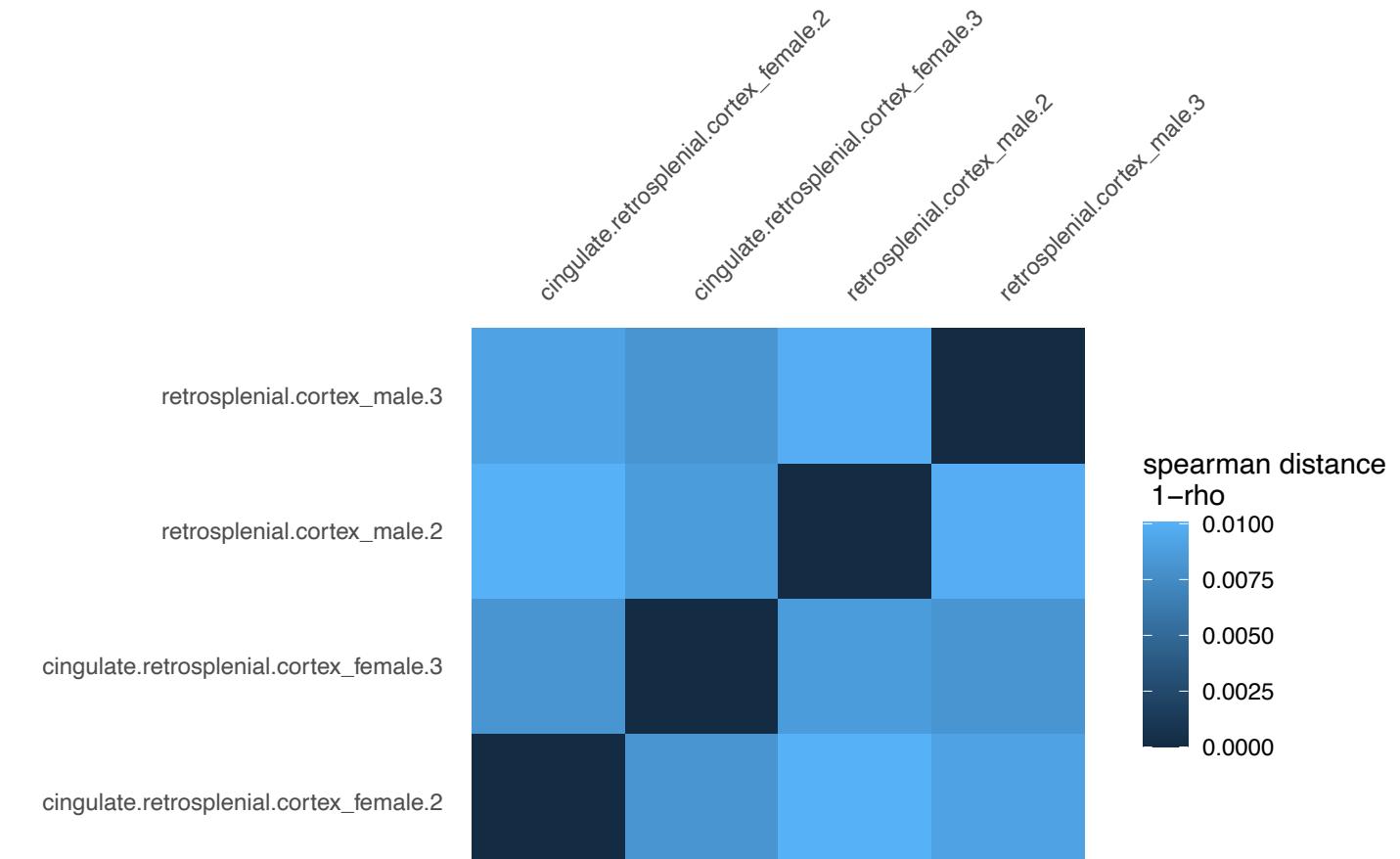
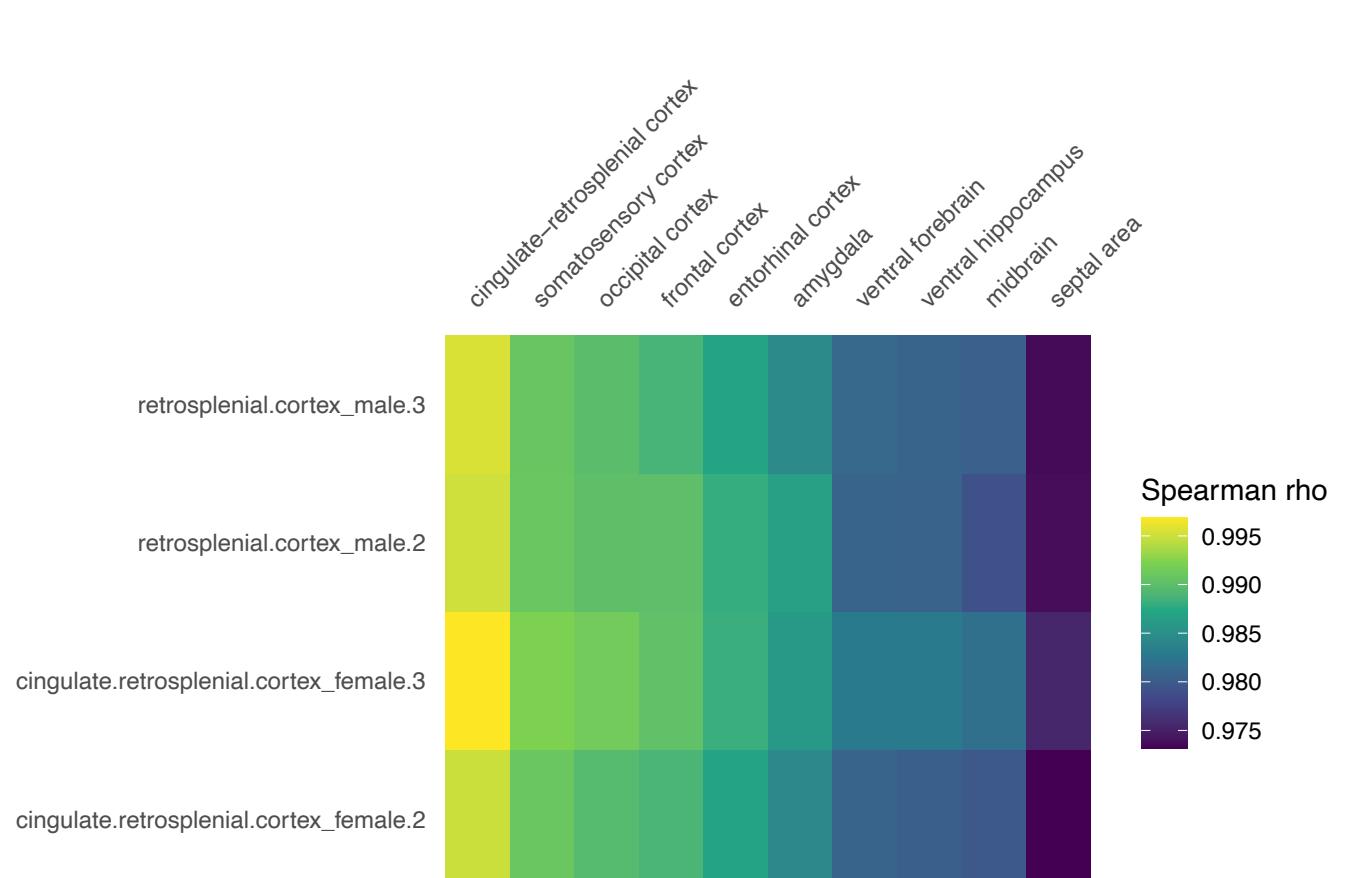
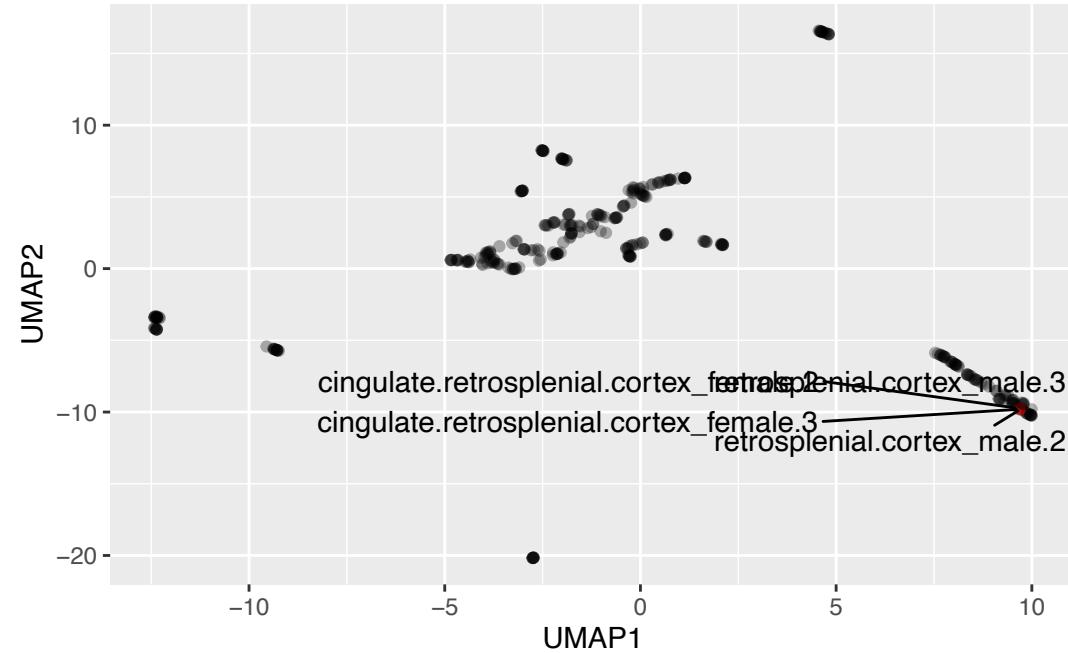
choroid plexus



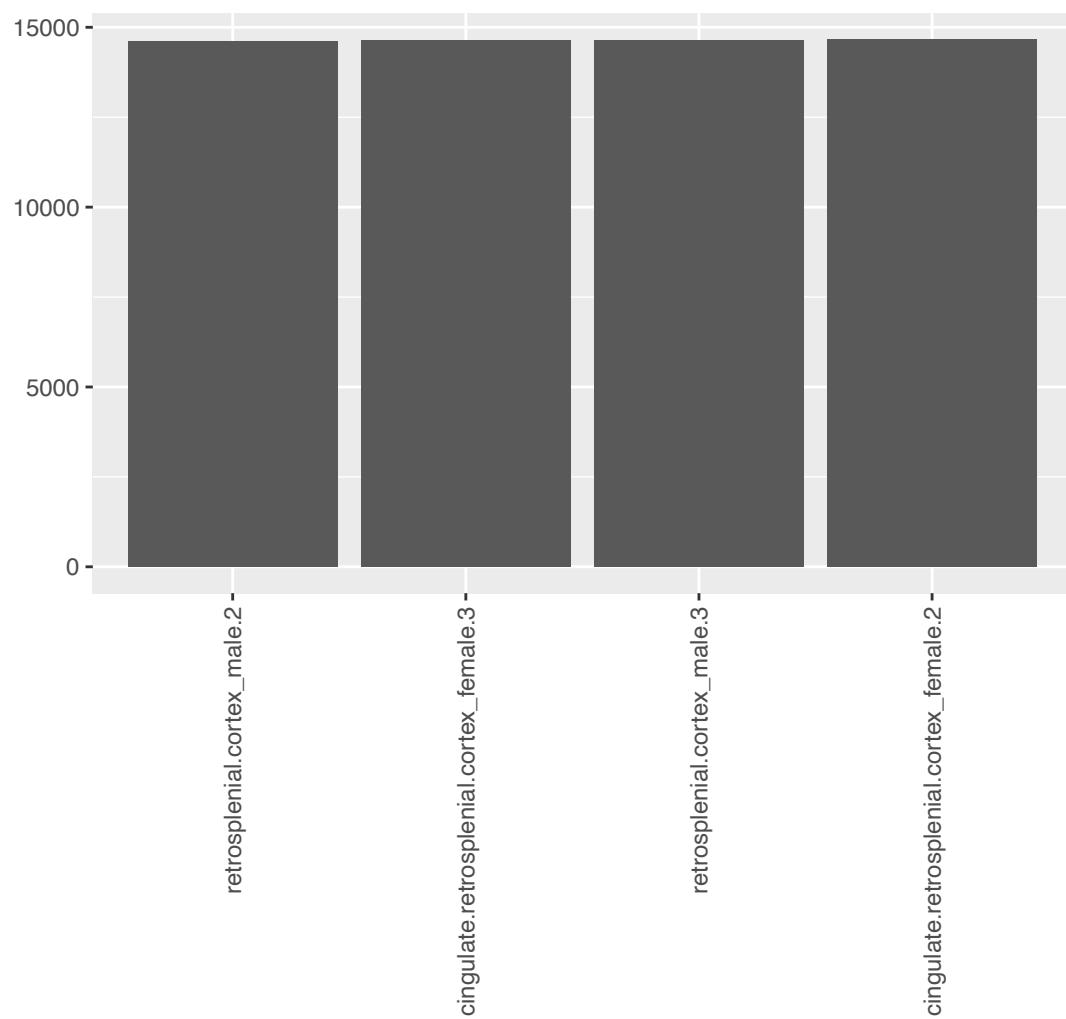
cingulate–retrosplenial cortex, PCA: TMM expression values



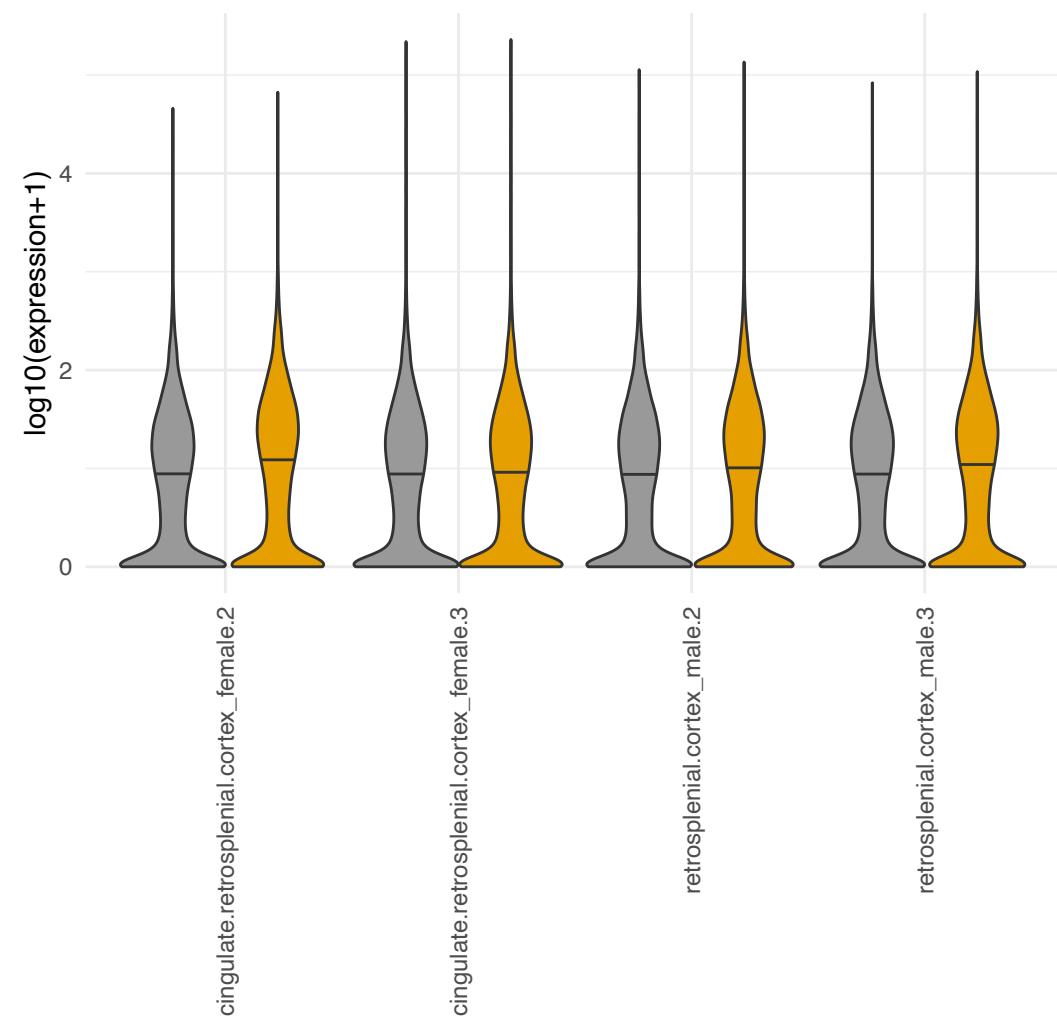
cingulate–retrosplenial cortex, UMAP: TMM expression values



cingulate–retrosplenial cortex

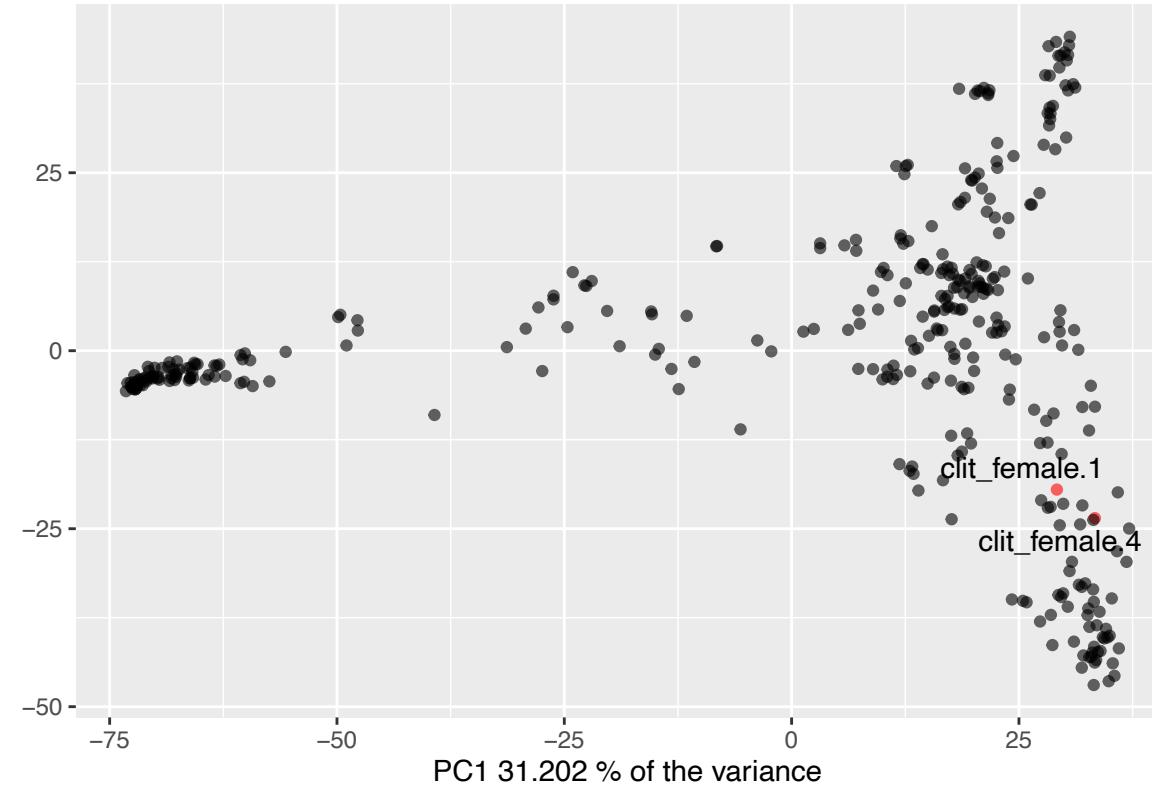


cingulate–retrosplenial cortex

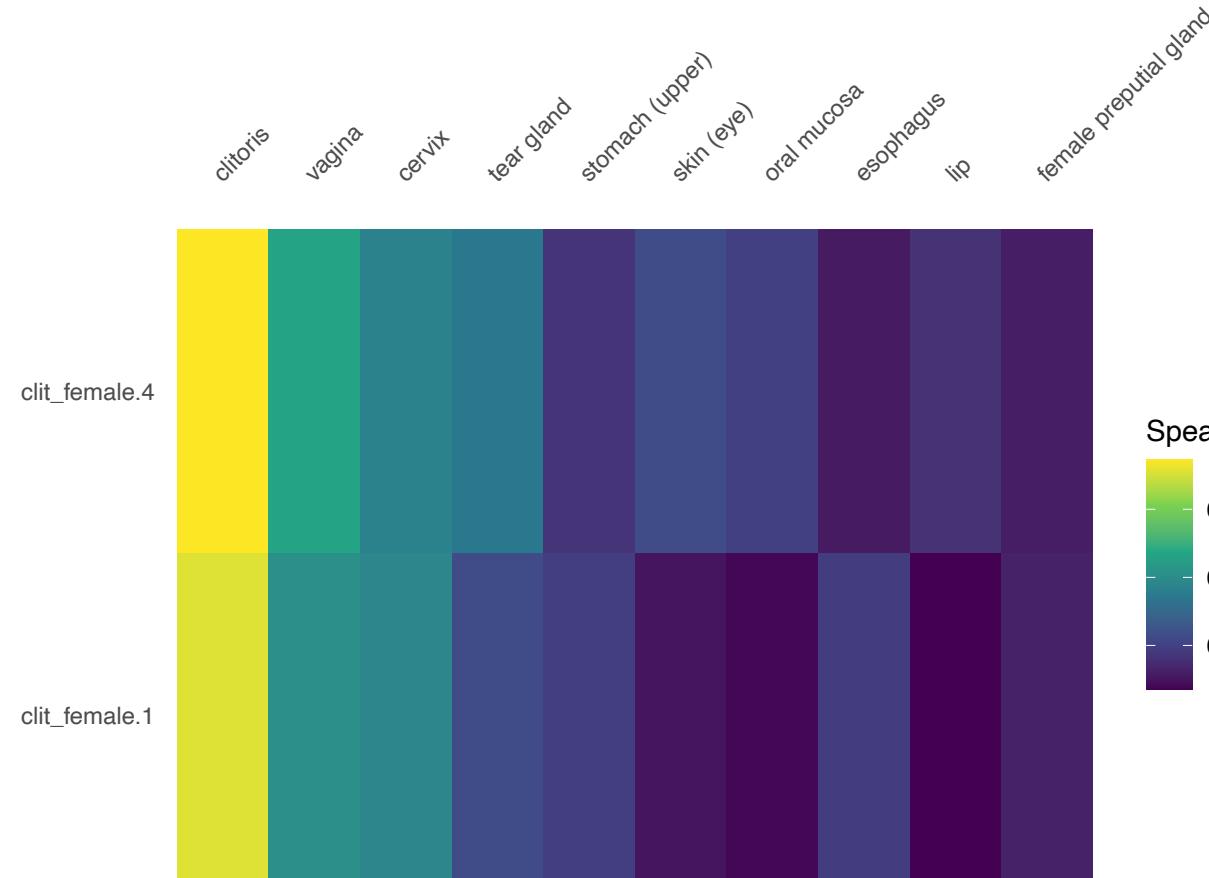


clitoris, PCA: TMM expression values

PC2 9.077 % of the variance



Tissue group to sample correlation

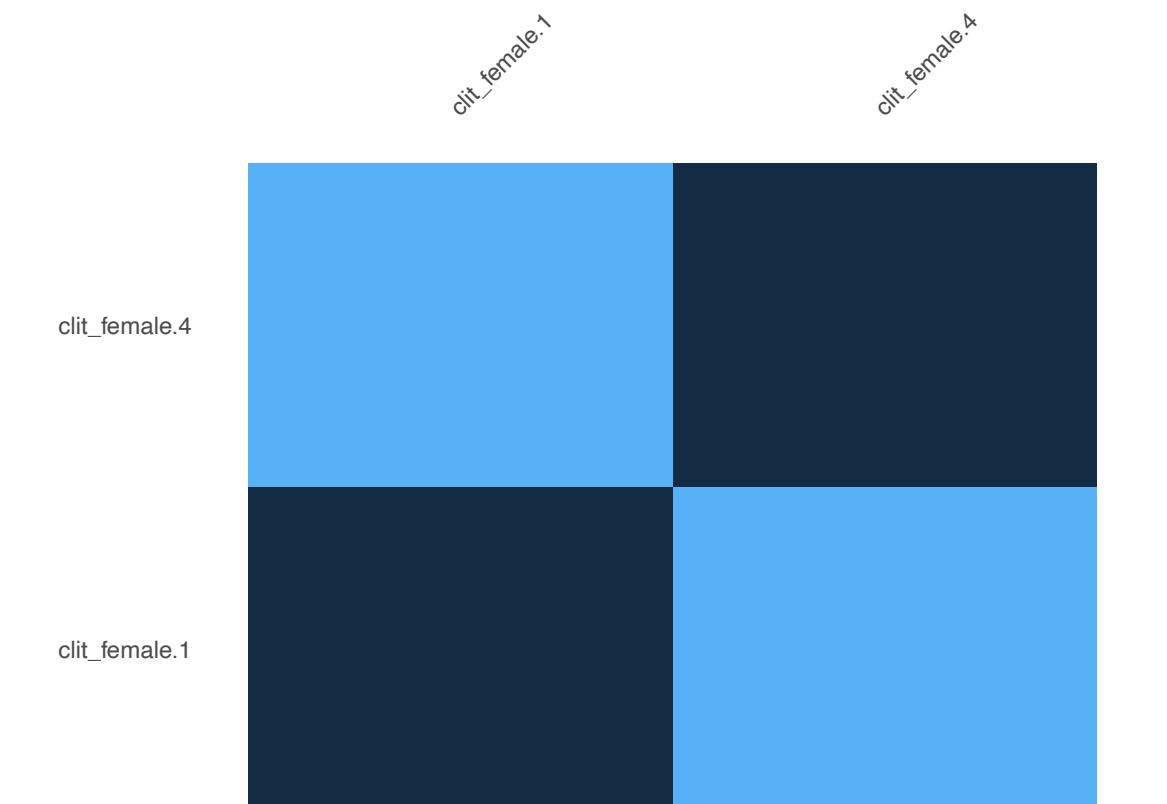


clitoris, UMAP: TMM expression values

UMAP2

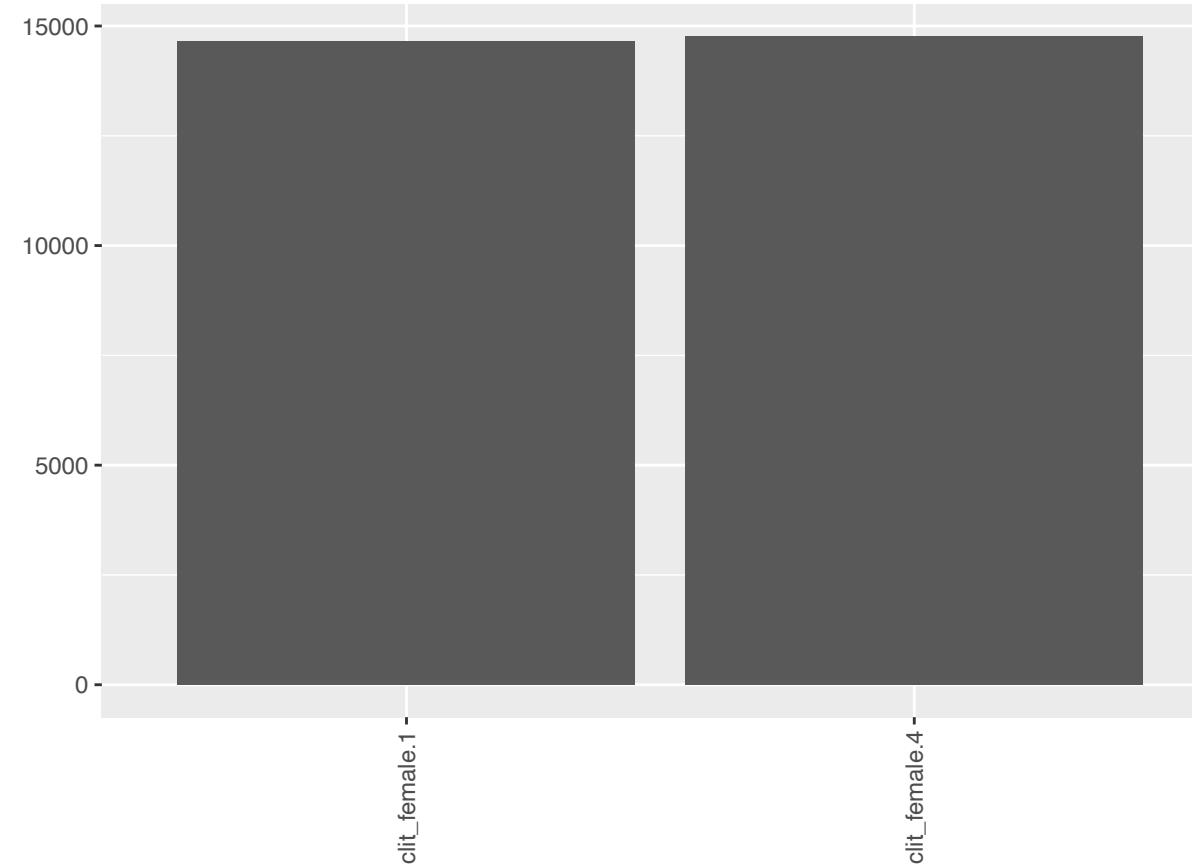
UMAP1

In tissue sample to sample Spearman Distance



clitoris

n(genes) >= 1 TMM



clitoris

log10(expression+1)

UMAP1

clit_female.1

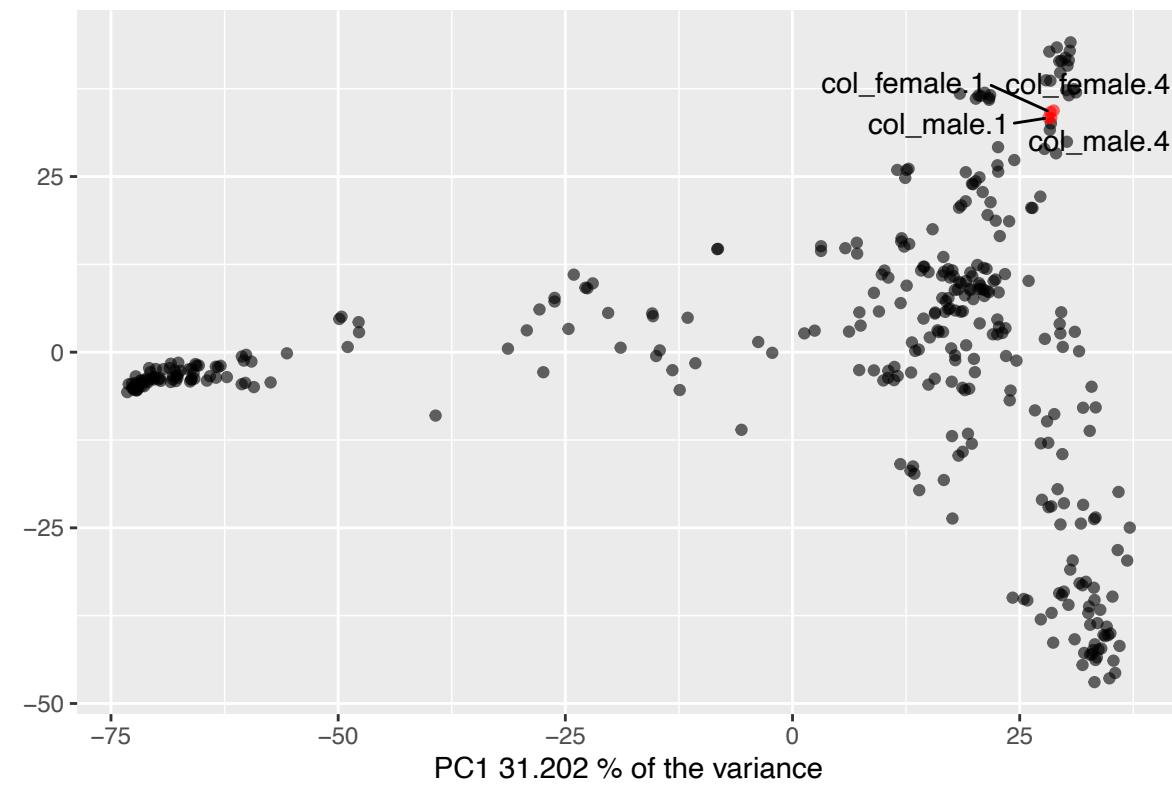
clit_female.4

type
tmm_val
tpm_val

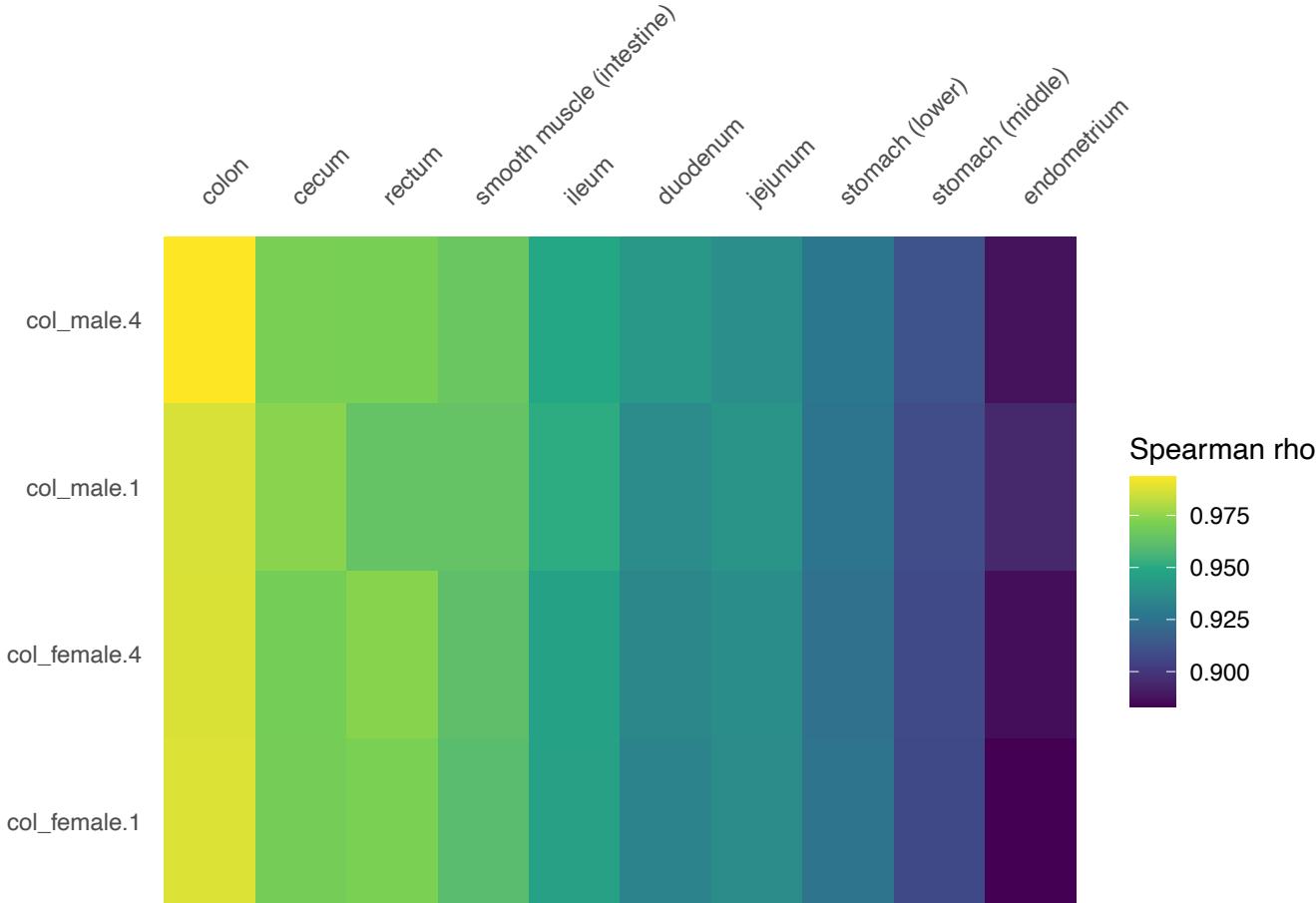
clit_female.4

colon, PCA: TMM expression values

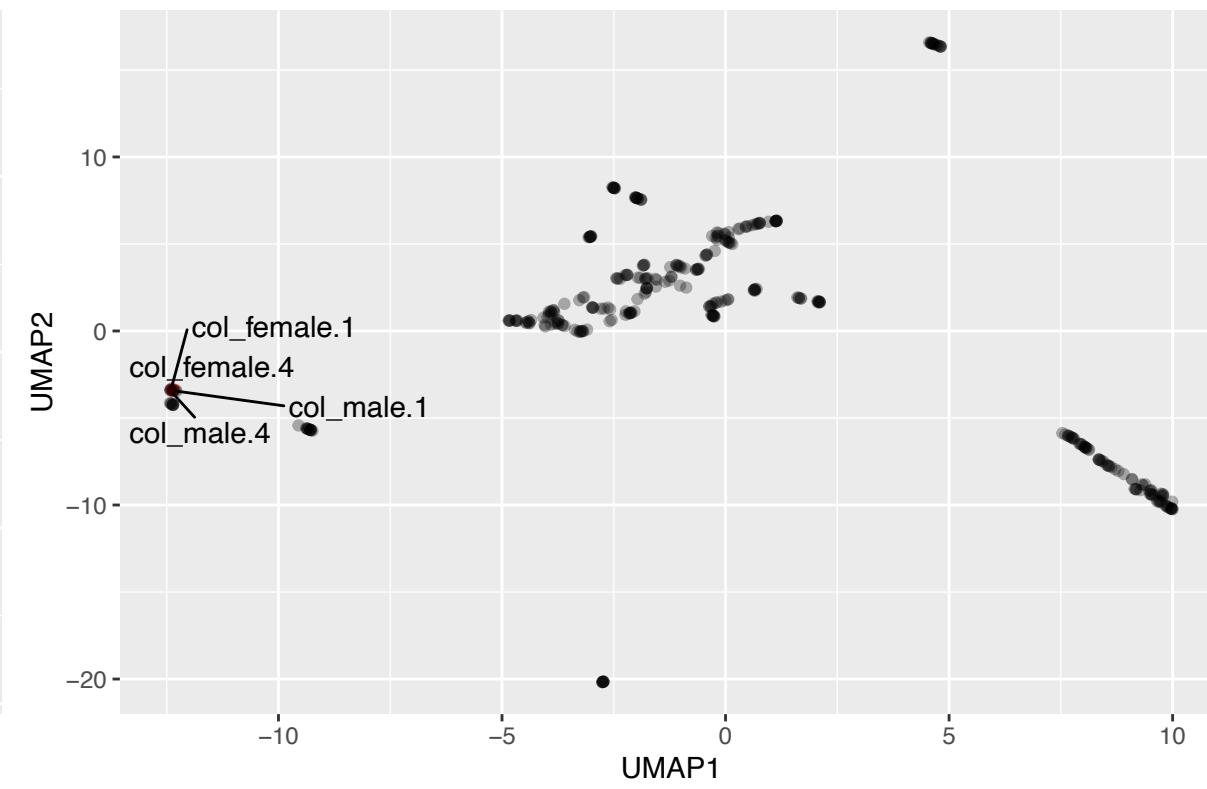
PC2 9.077 % of the variance



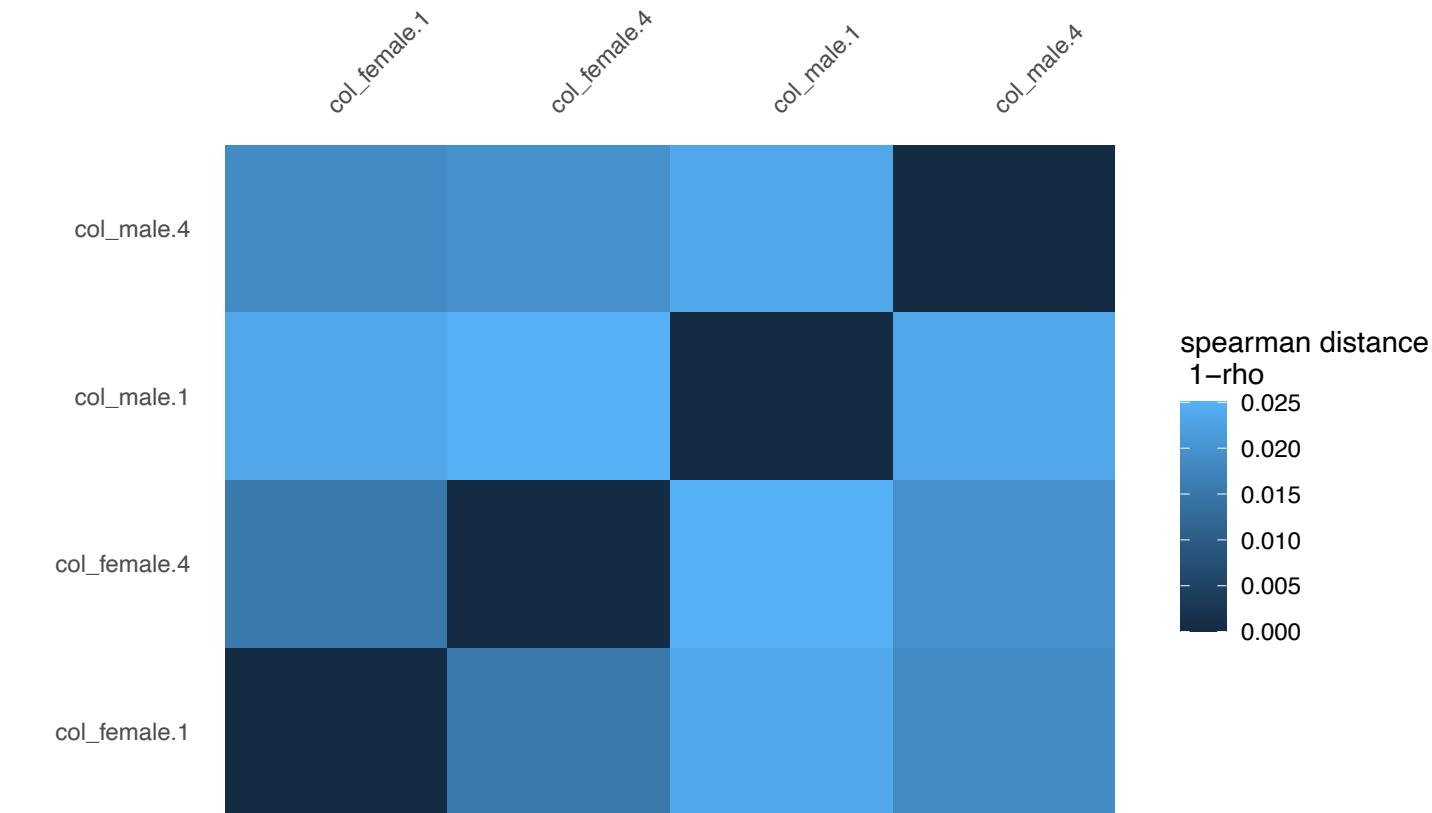
Tissue group to sample correlation



colon, UMAP: TMM expression values

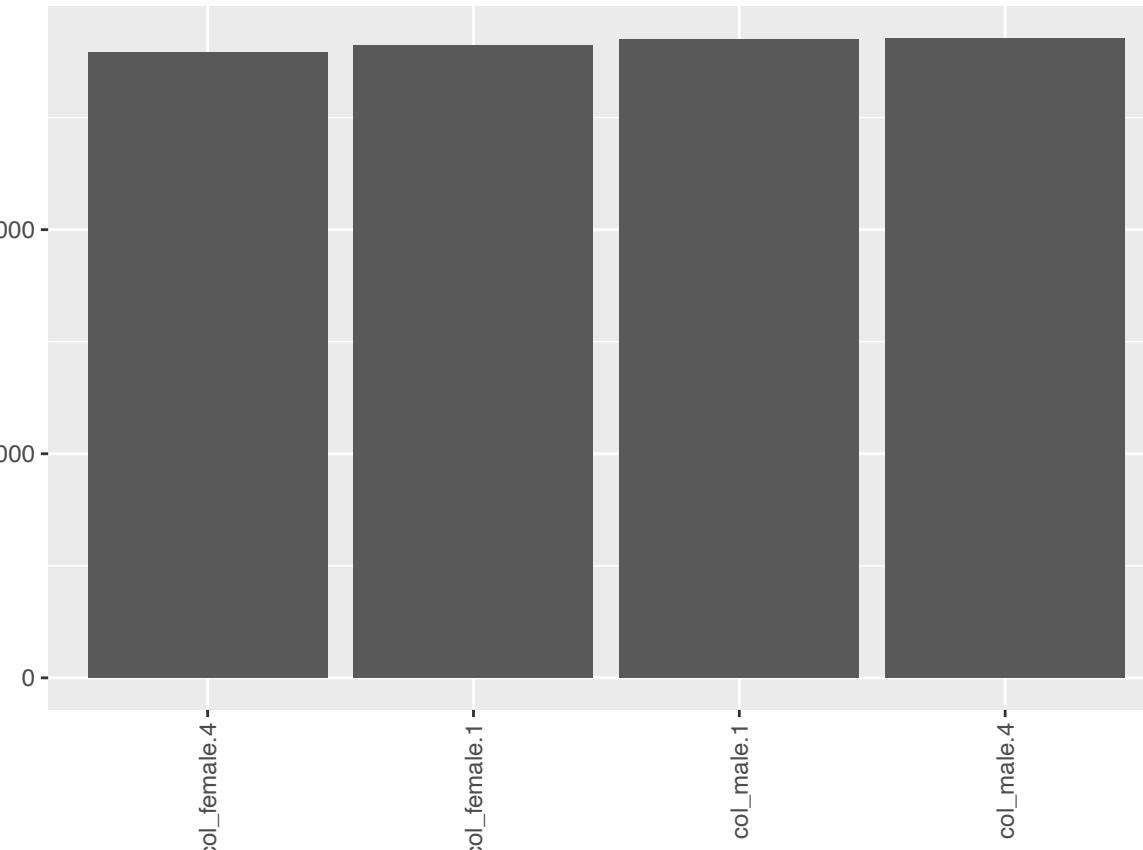


In tissue sample to sample Spearman Distance

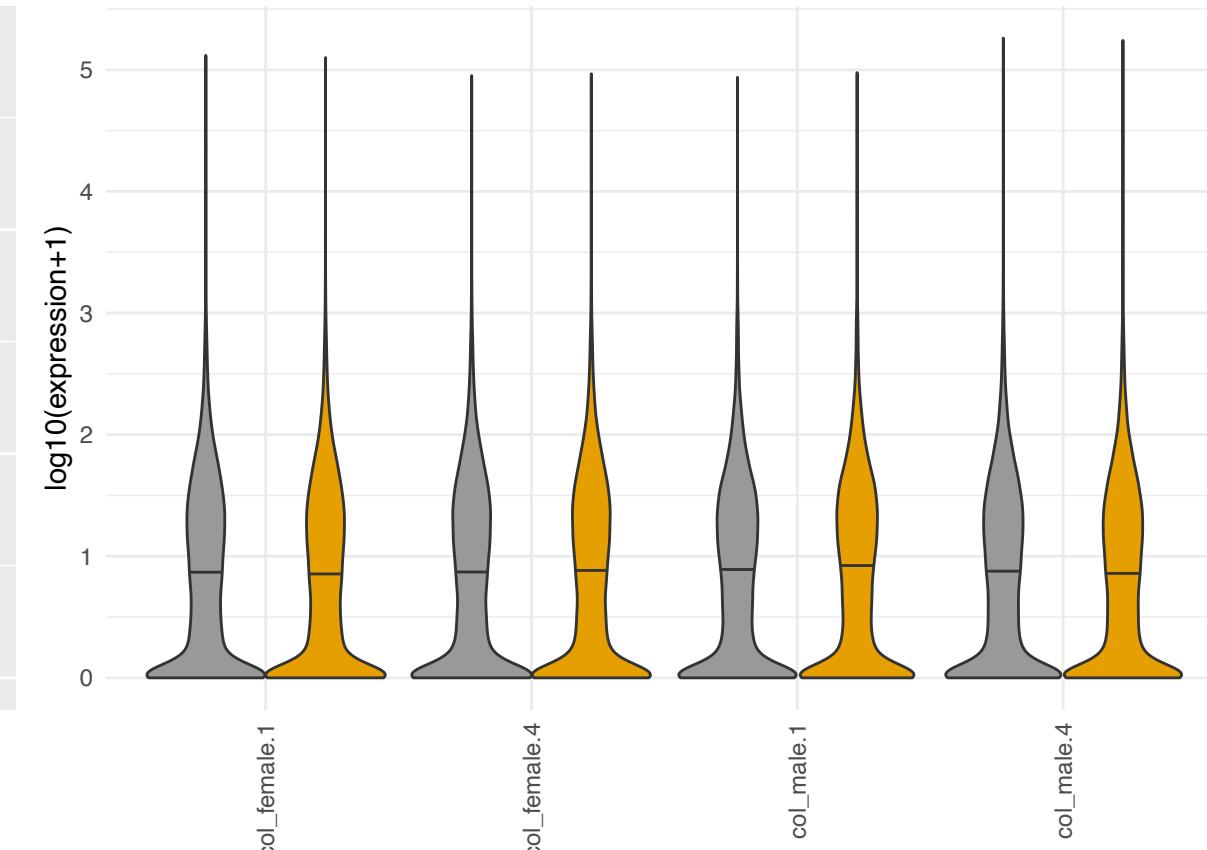


colon

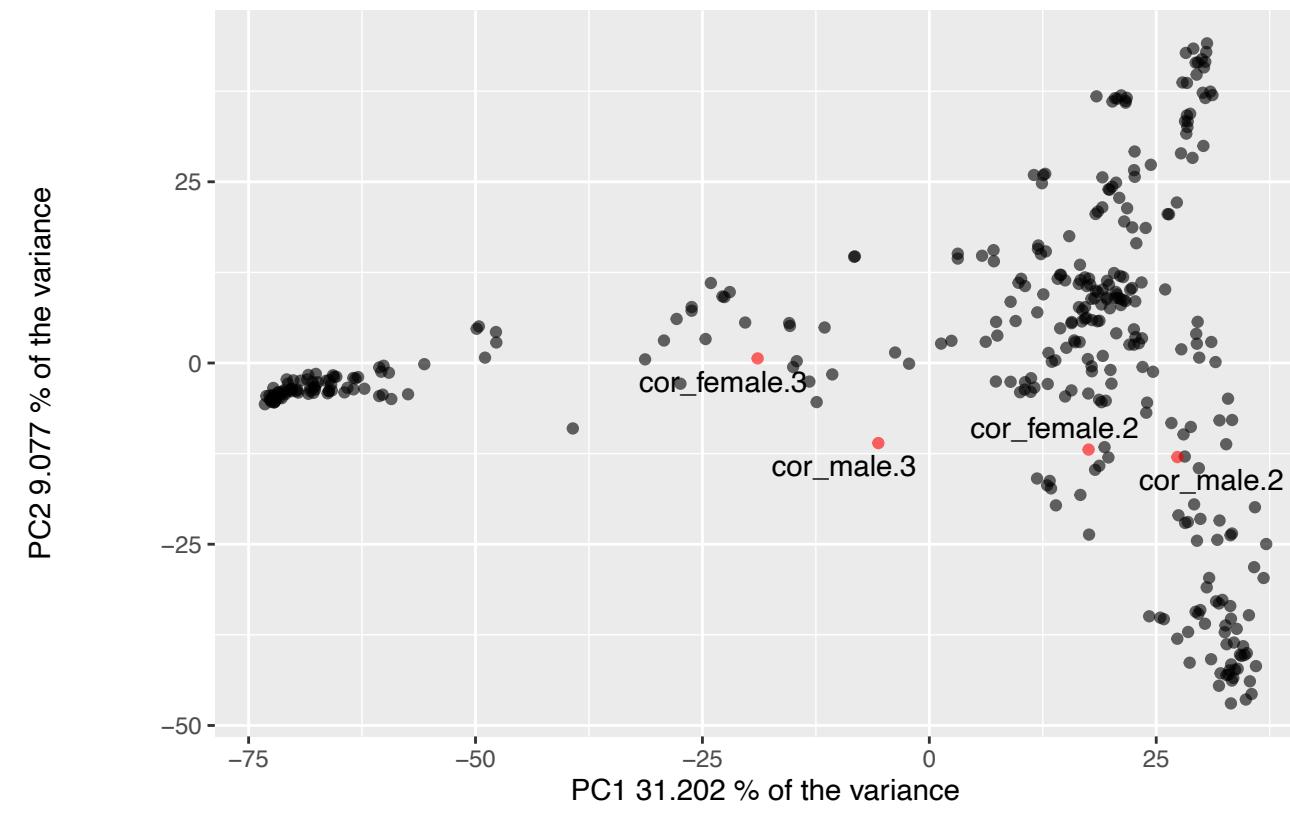
n(genes) >= 1 TMM



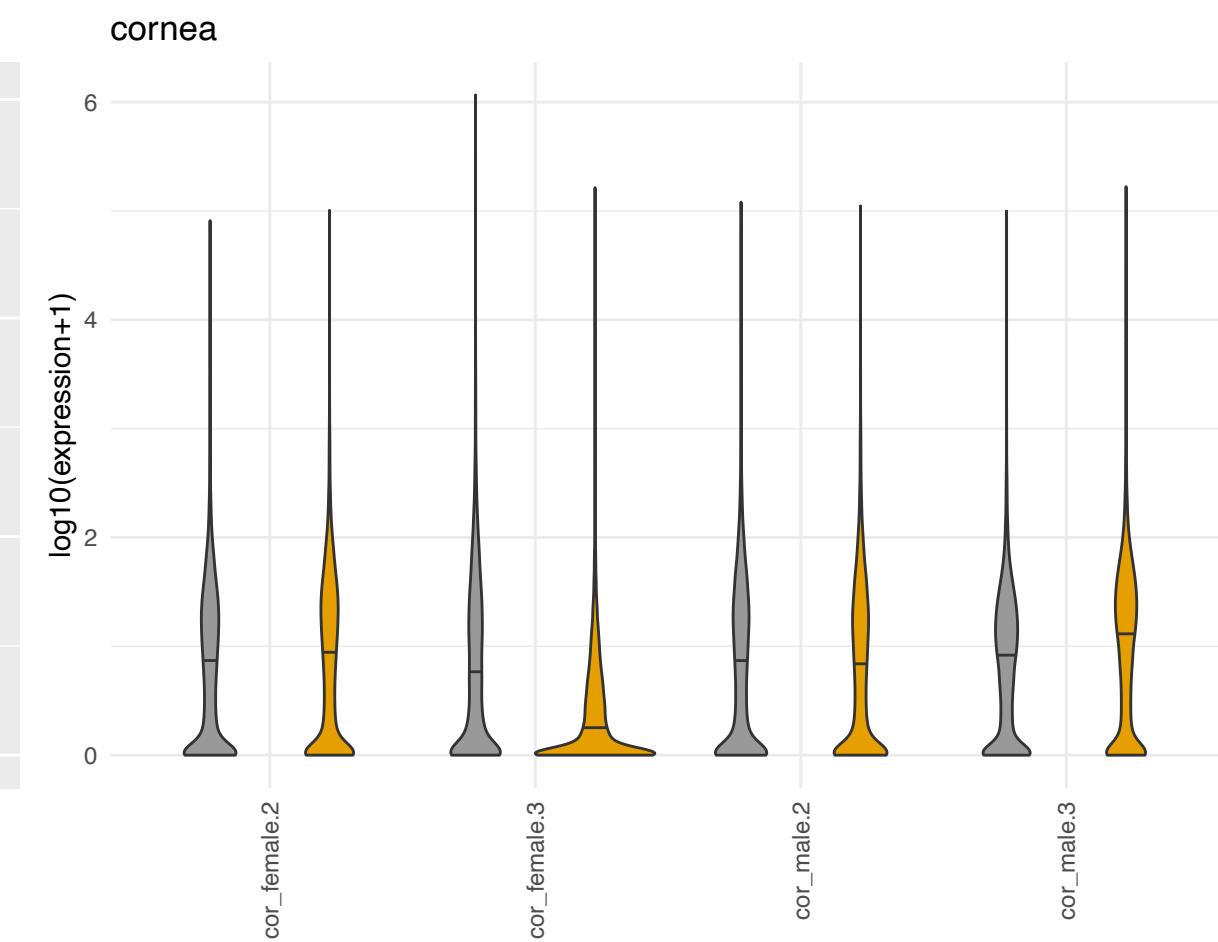
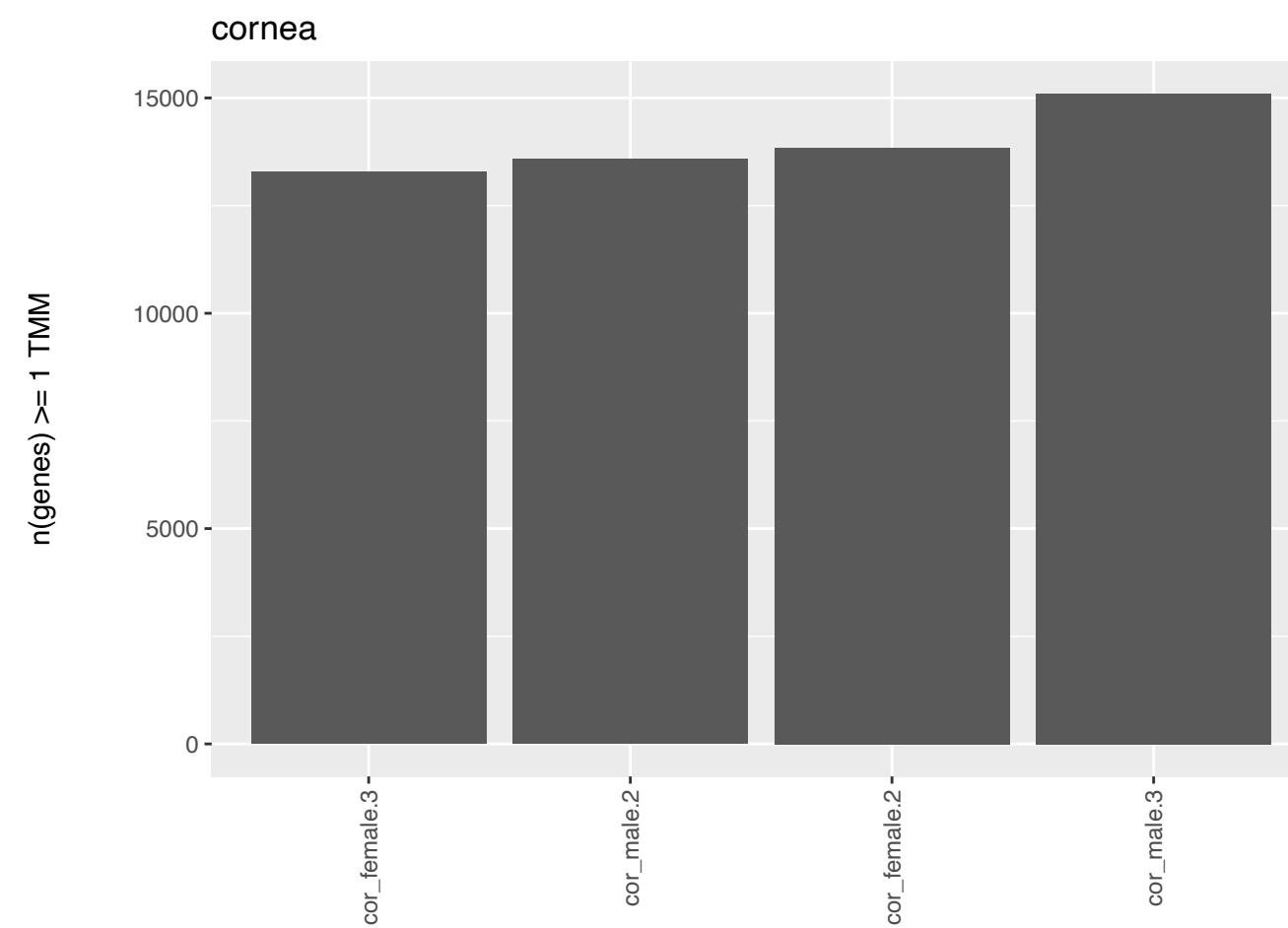
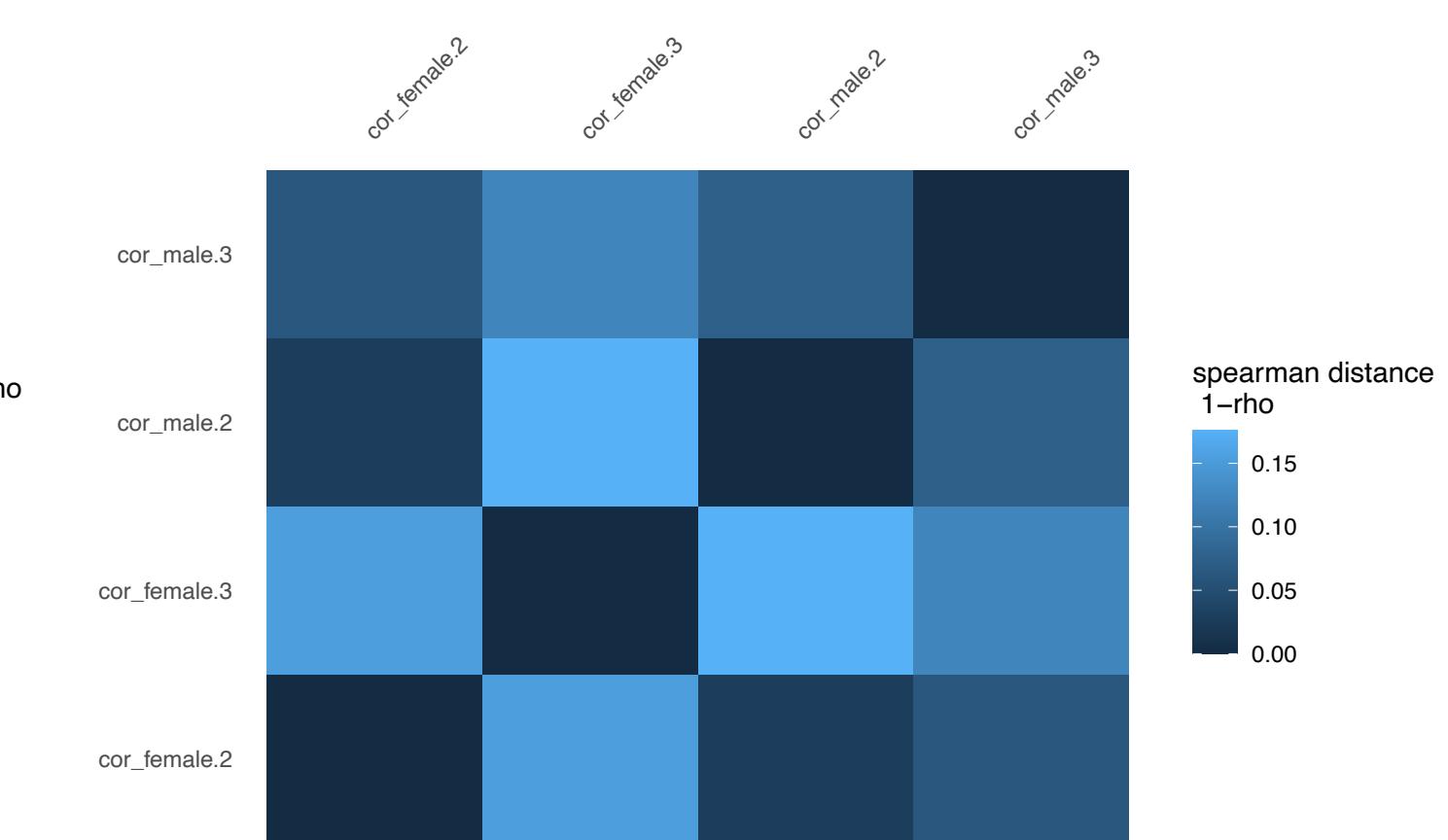
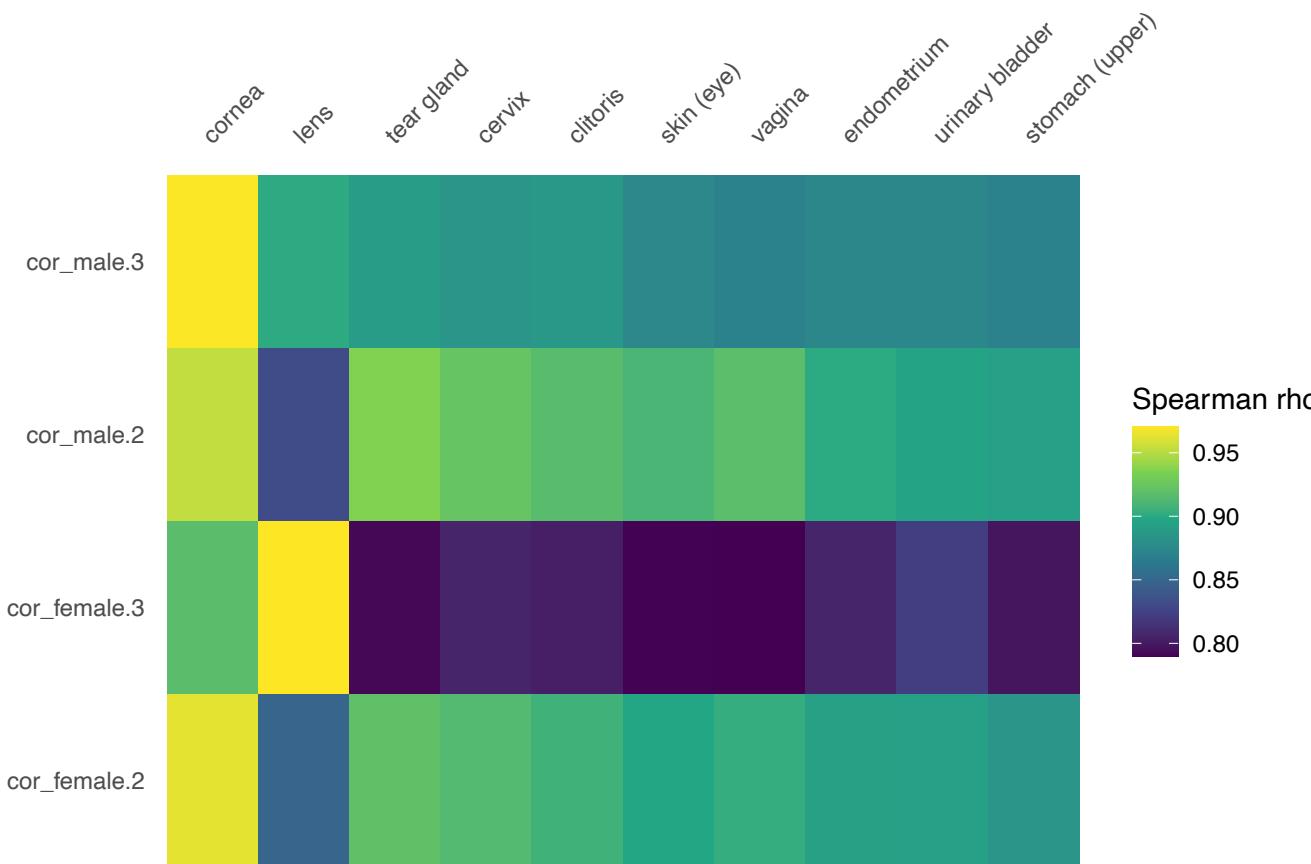
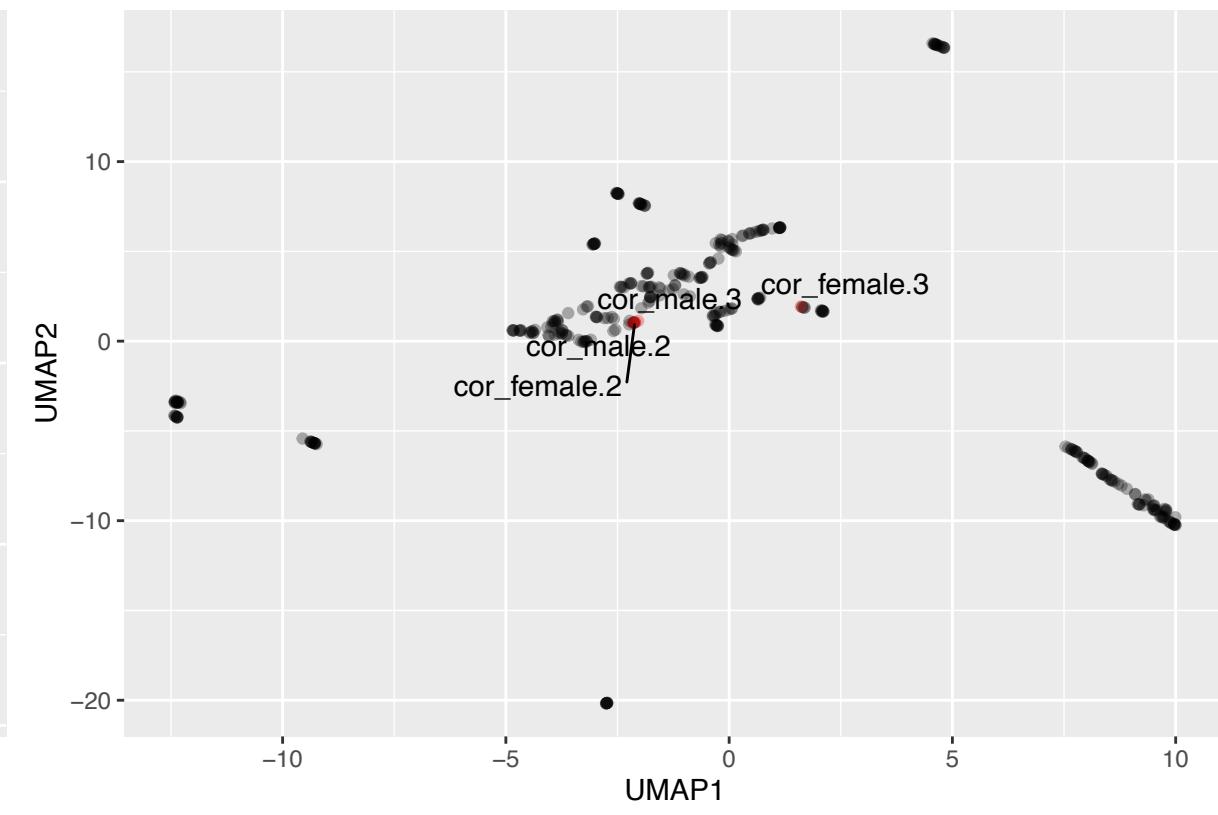
colon



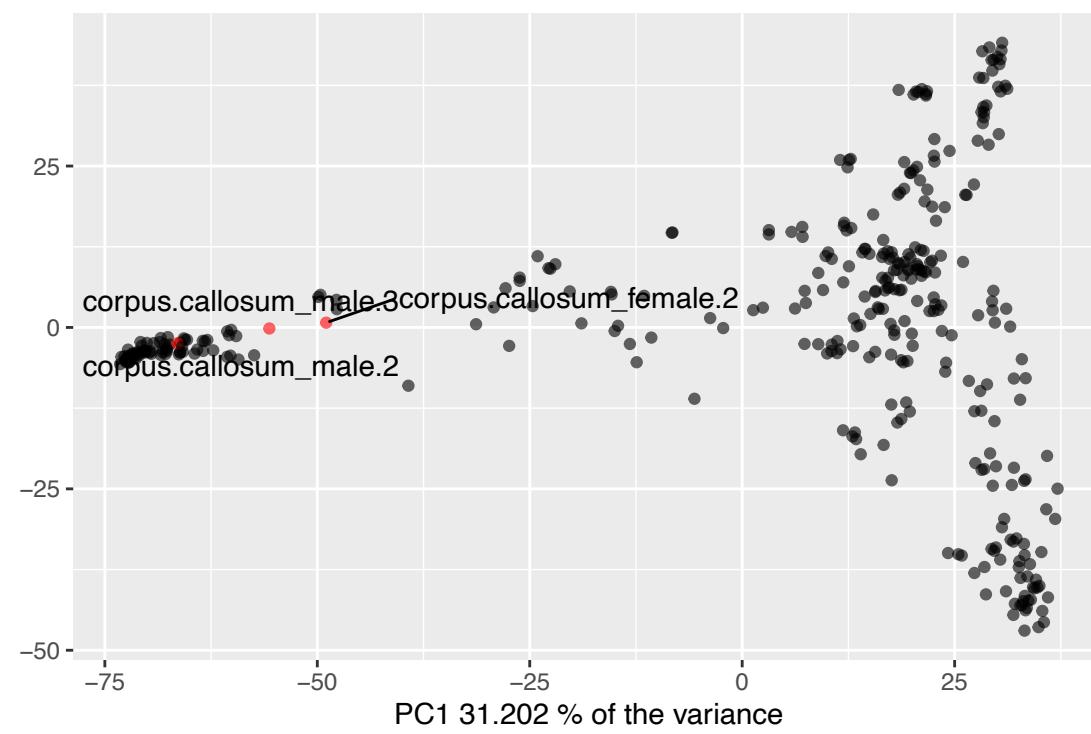
cornea, PCA: TMM expression values



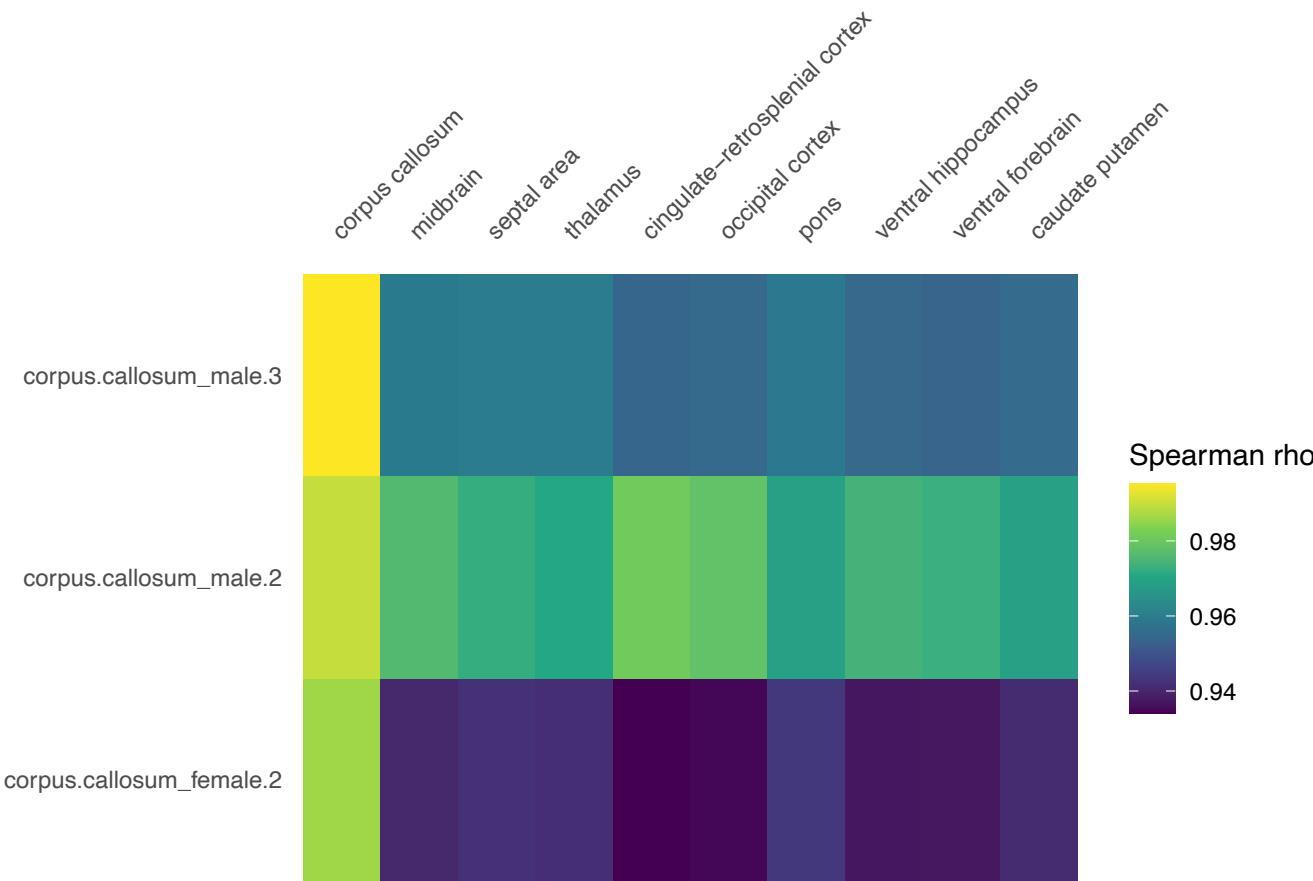
cornea, UMAP: TMM expression values



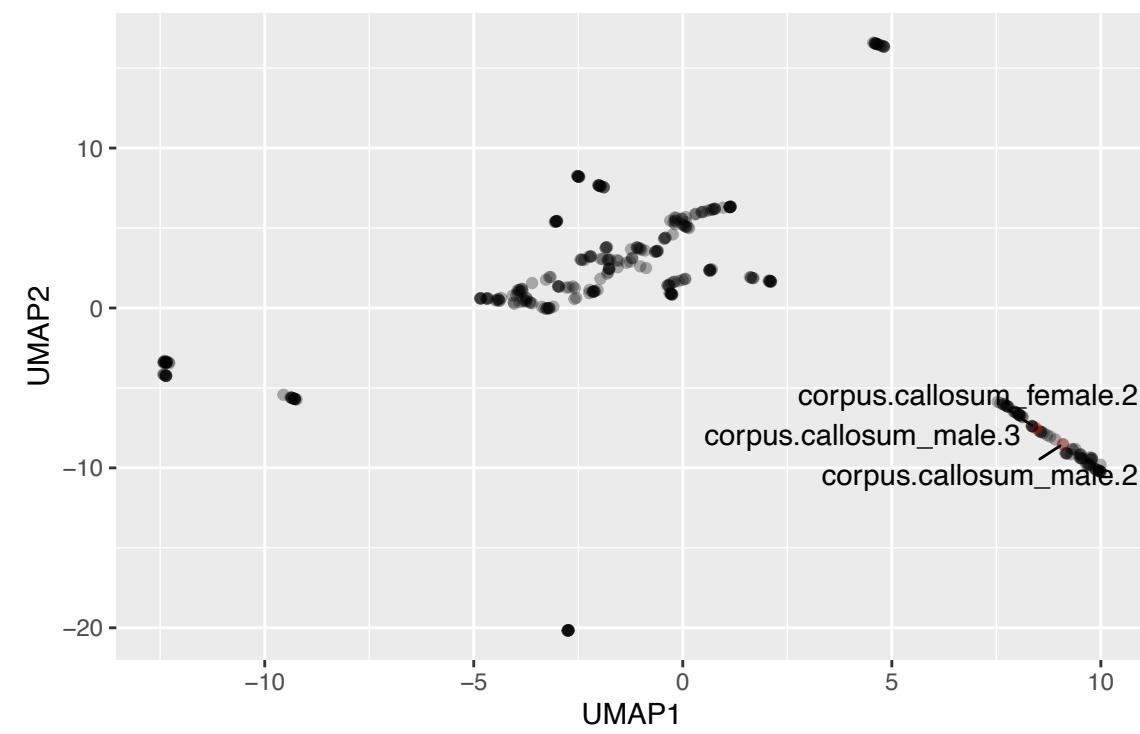
corpus callosum, PCA: TMM expression values



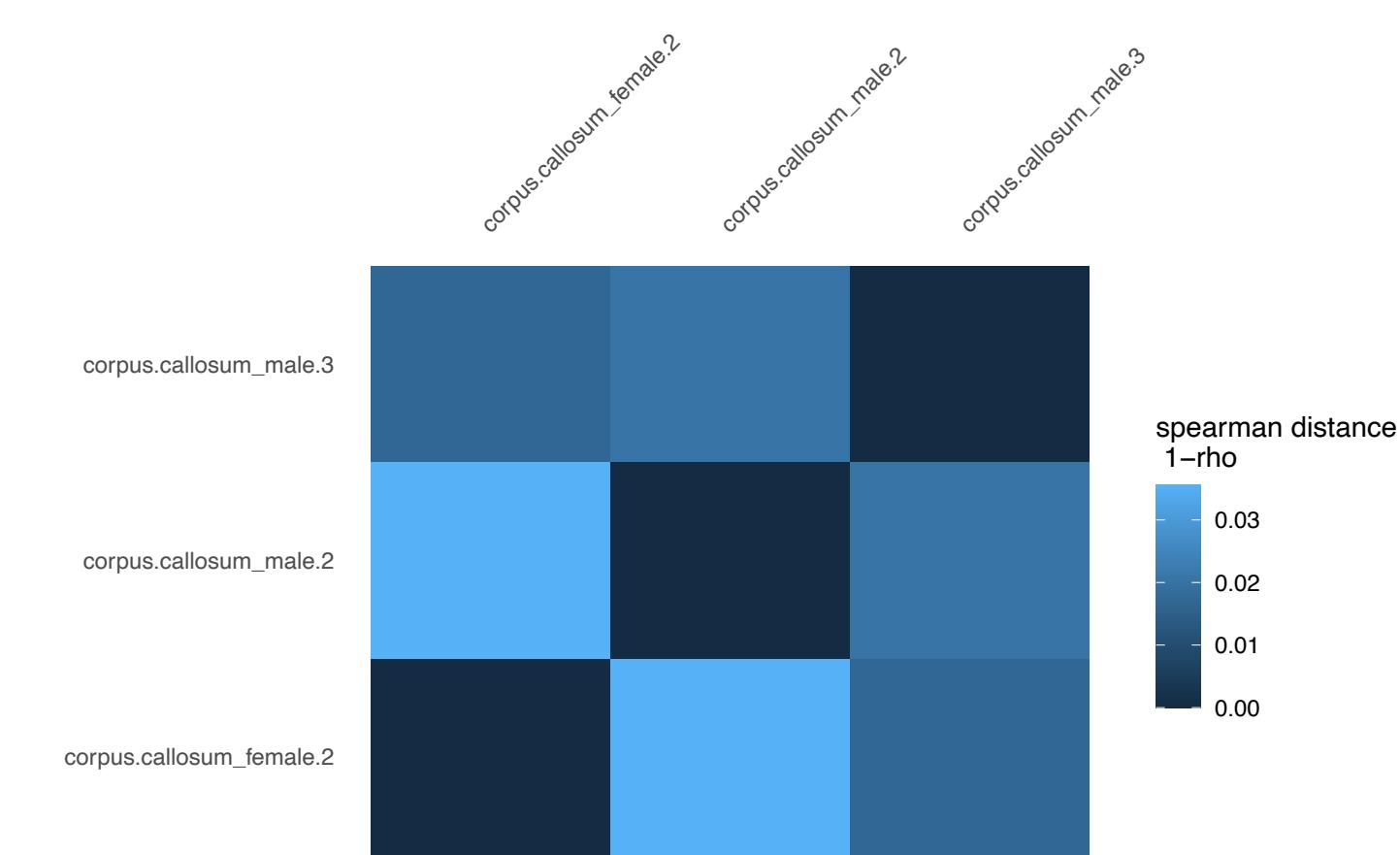
Tissue group to sample correlation



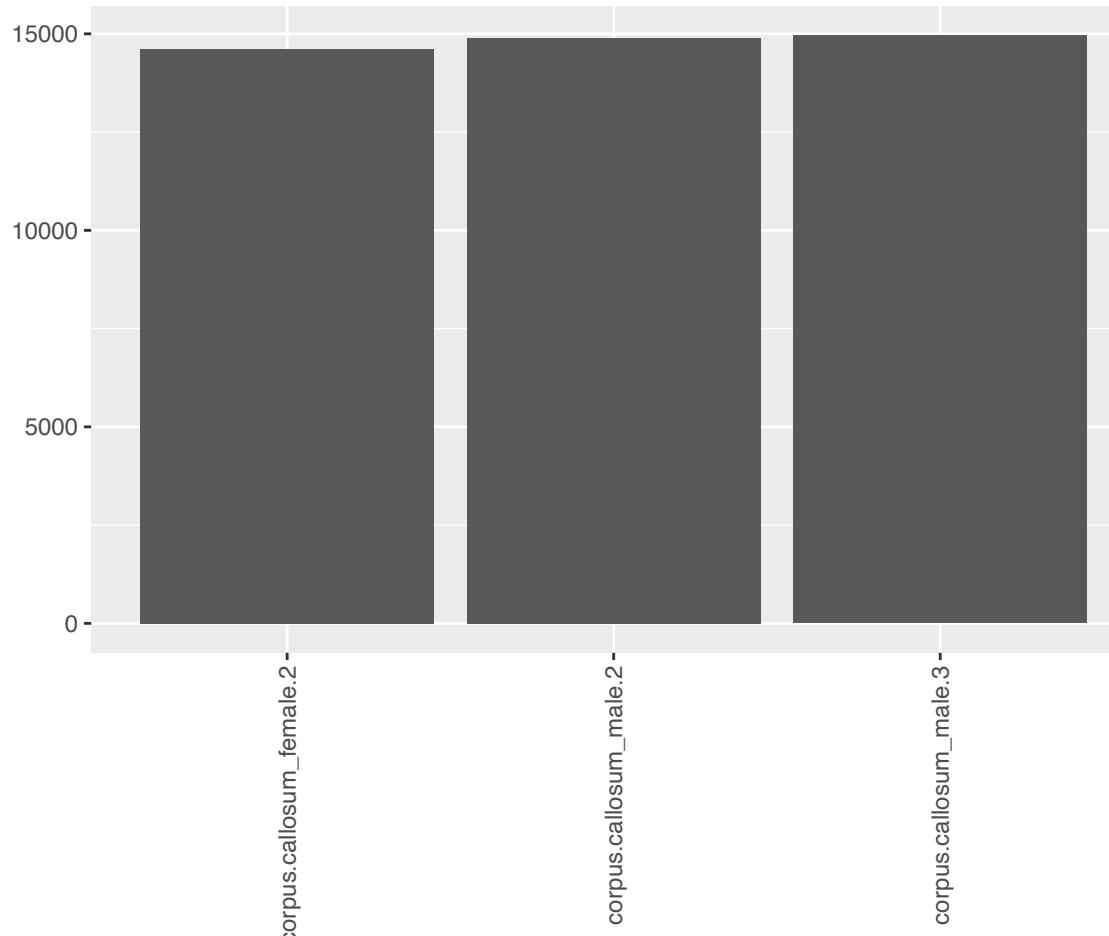
corpus callosum, UMAP: TMM expression values



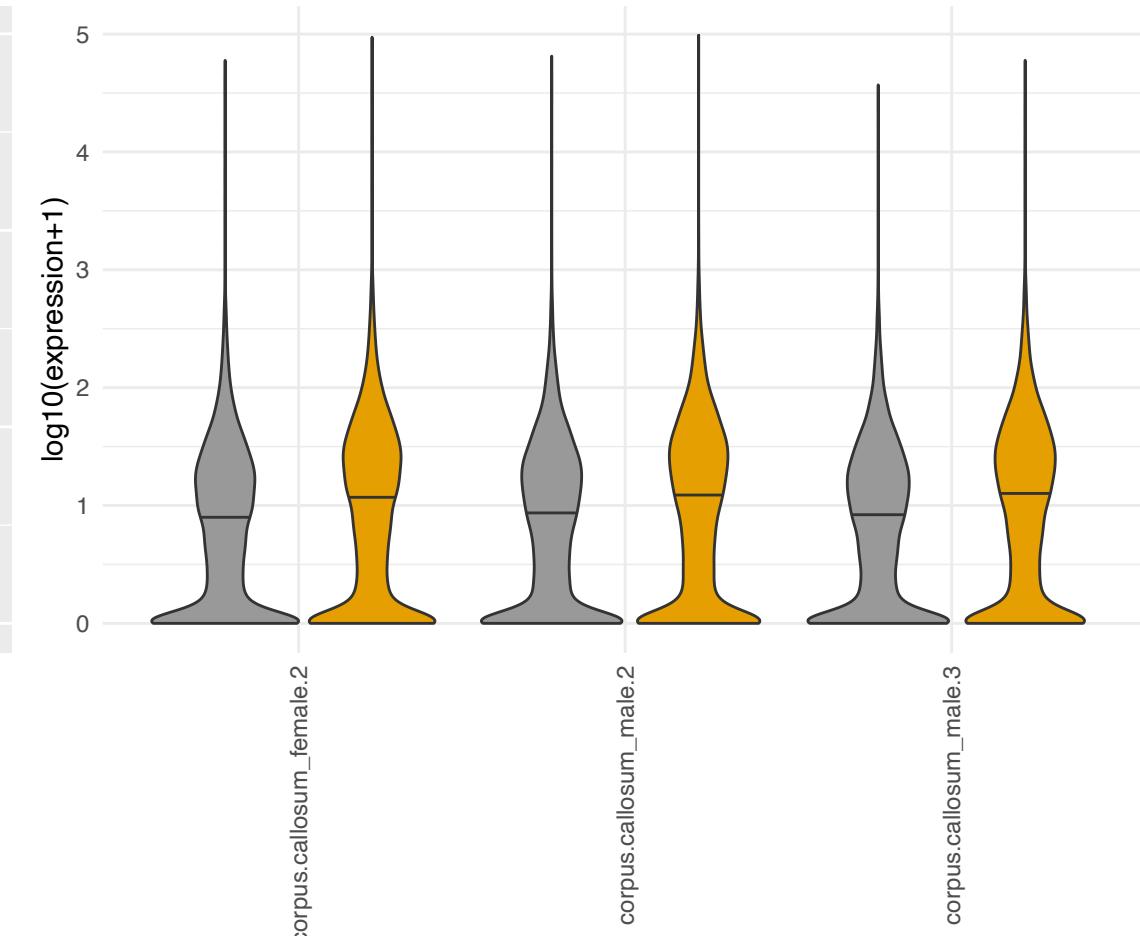
In tissue sample to sample Spearman Distance



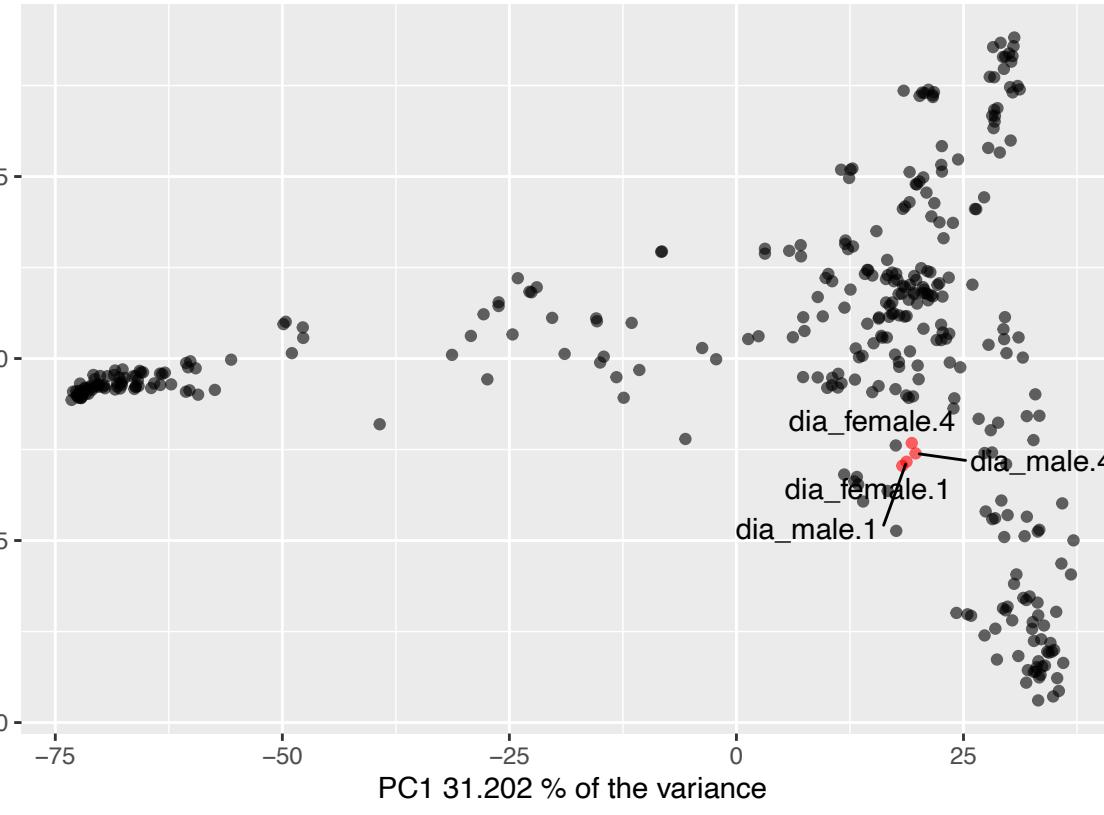
corpus callosum



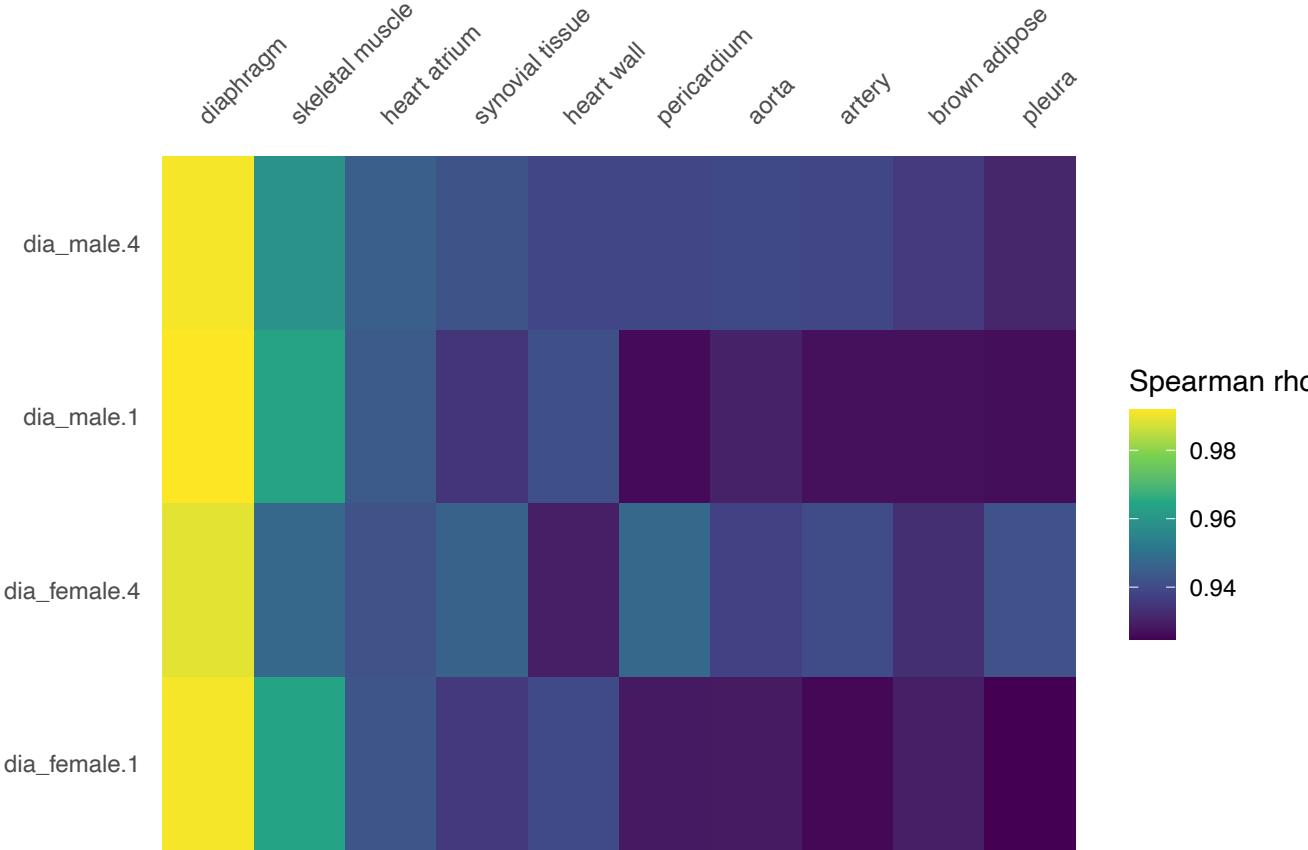
corpus callosum



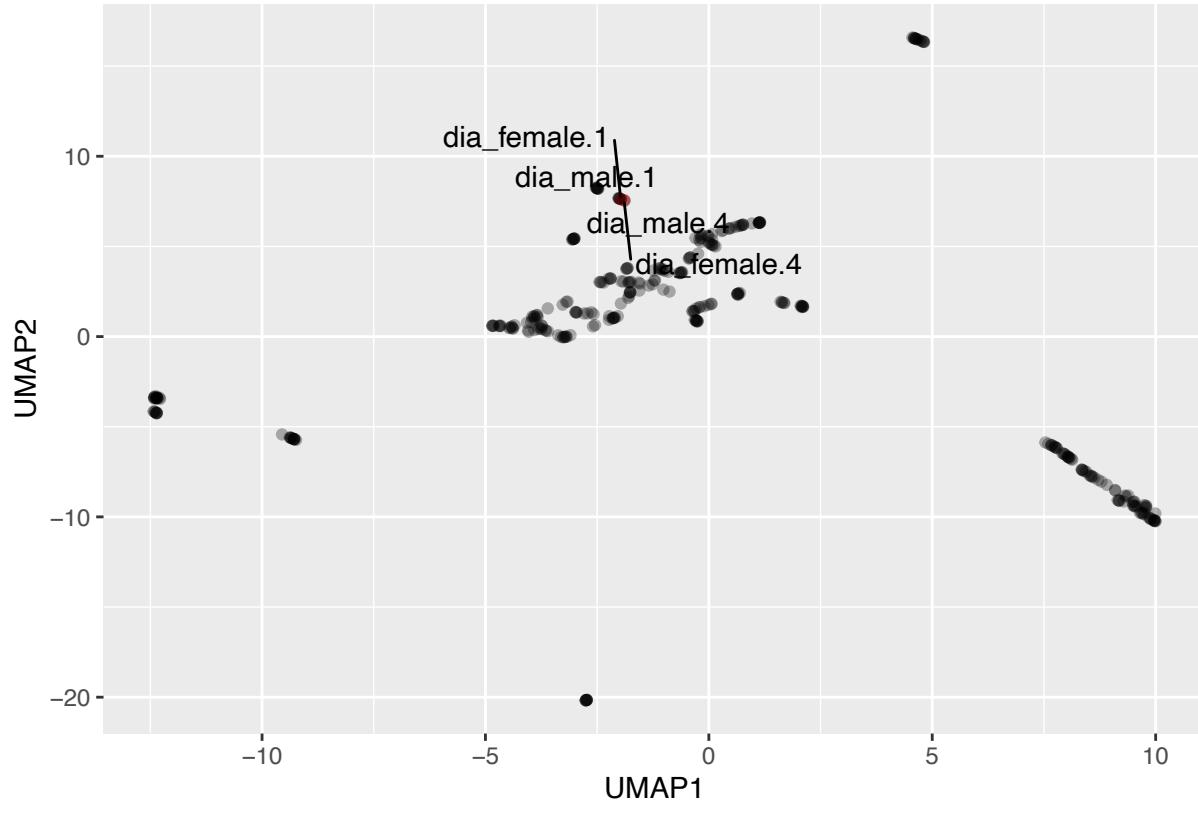
diaphragm, PCA: TMM expression values



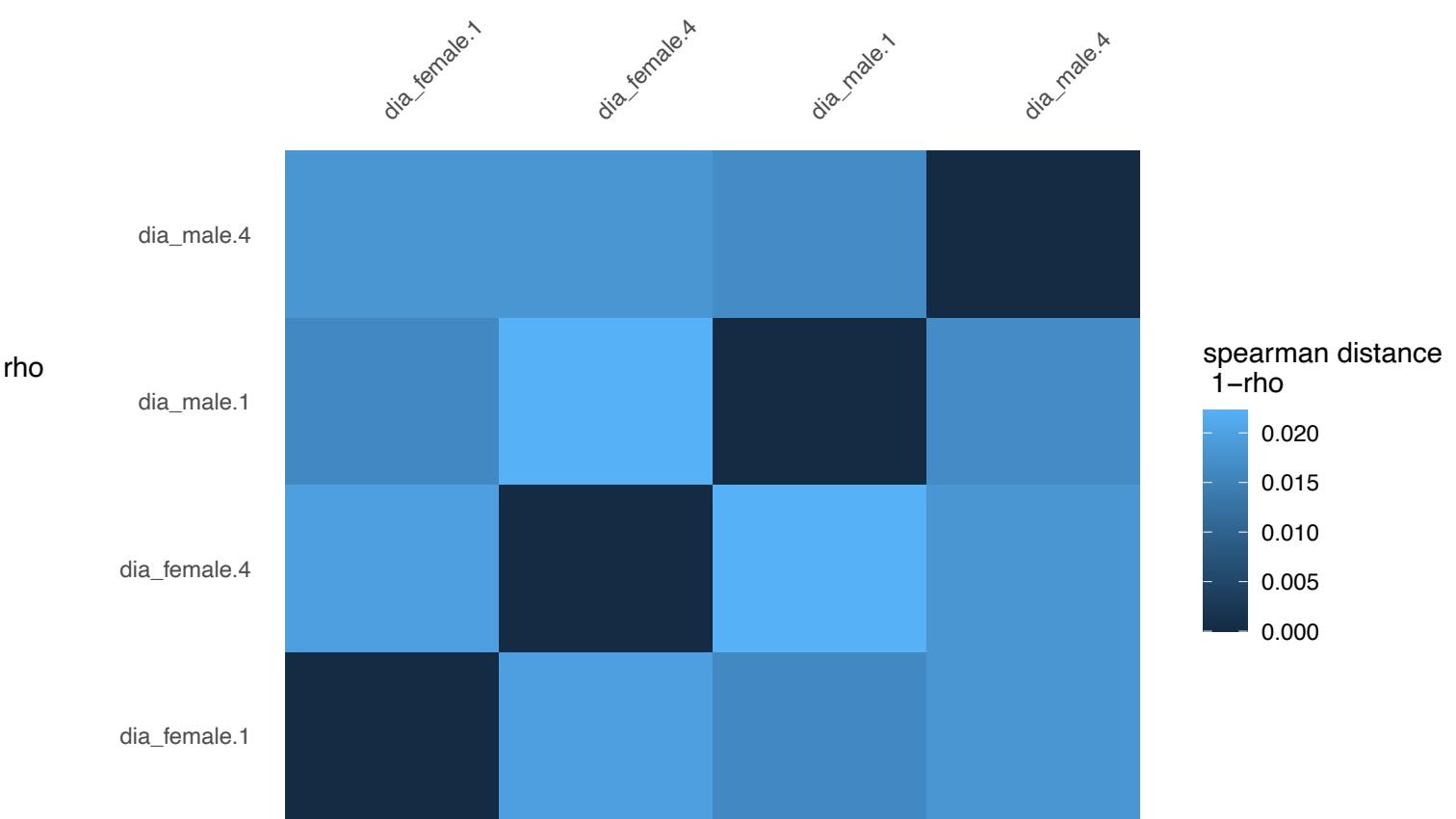
Tissue group to sample correlation



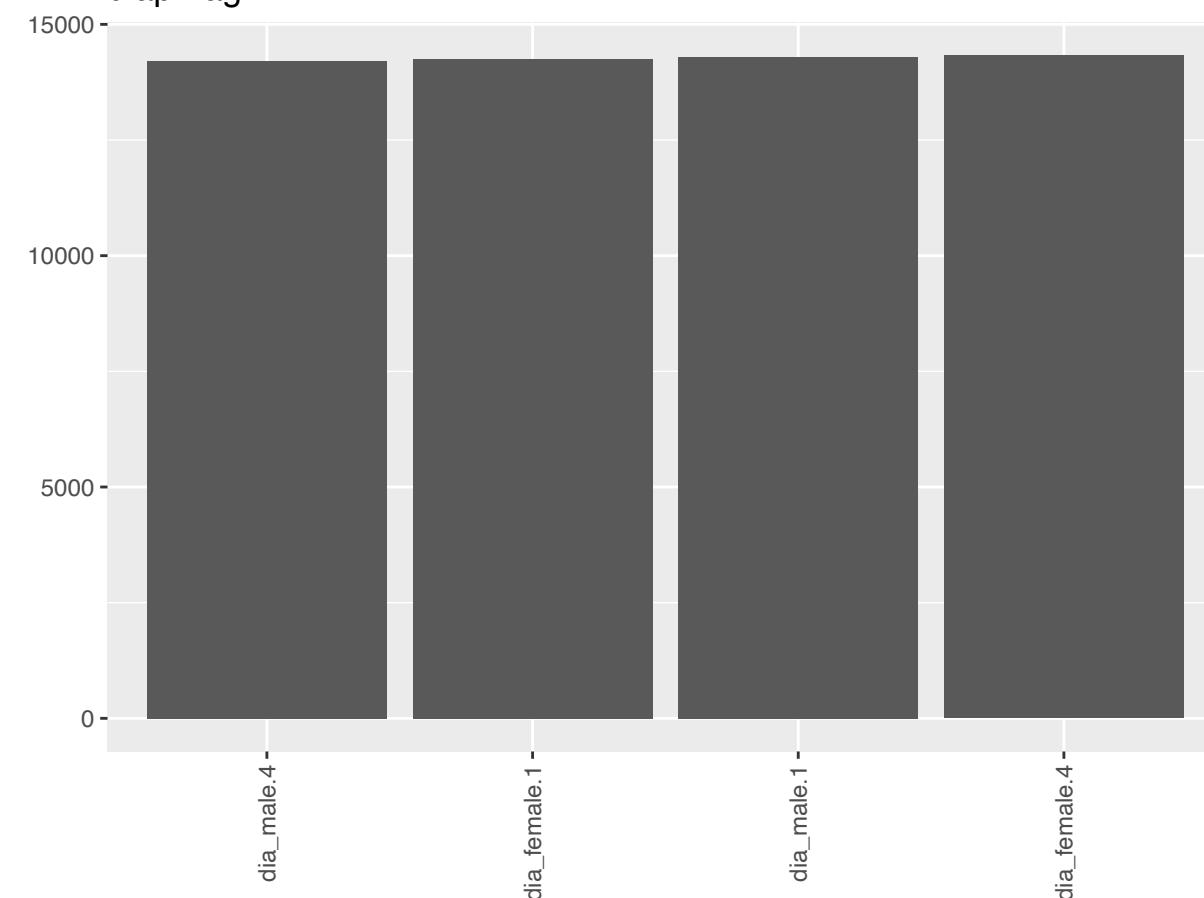
diaphragm, UMAP: TMM expression values



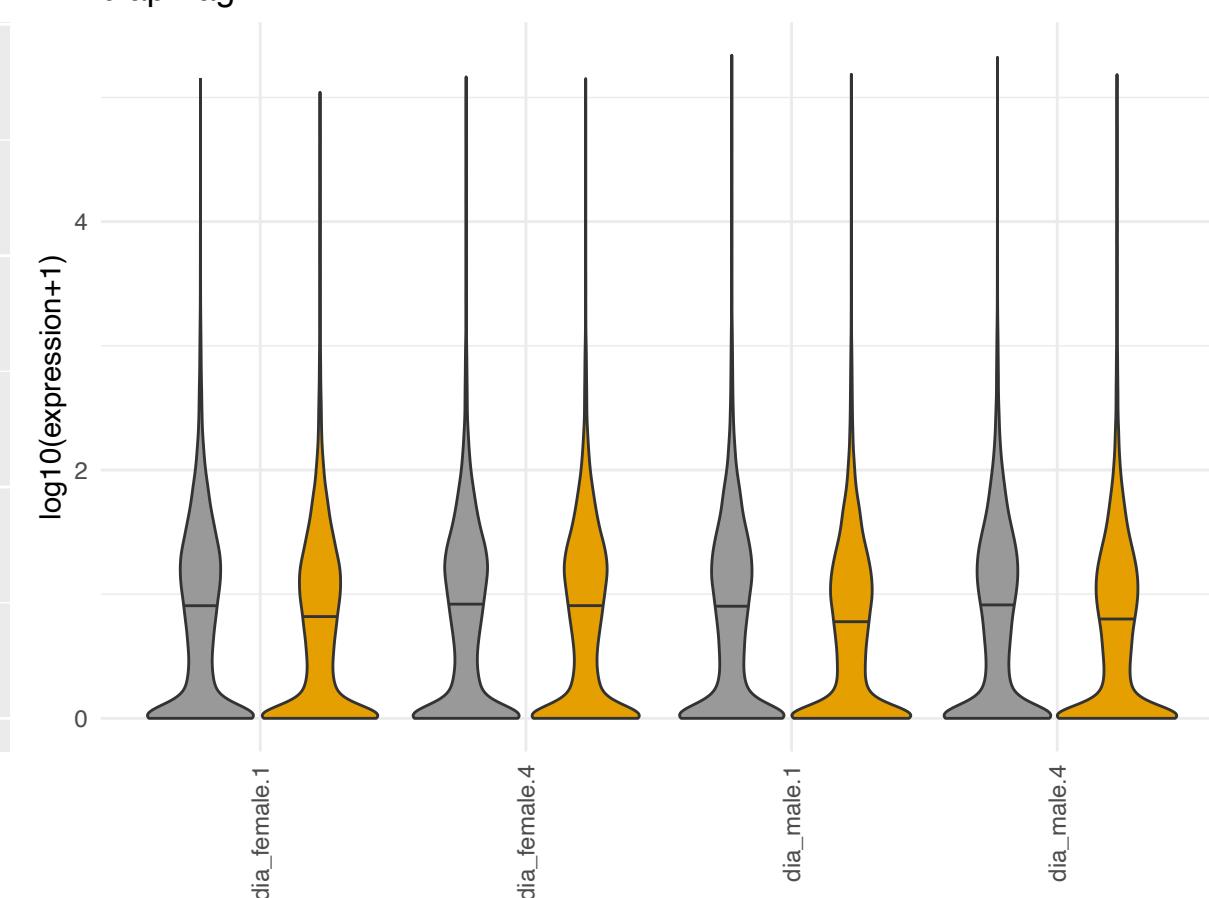
In tissue sample to sample Spearman Distance



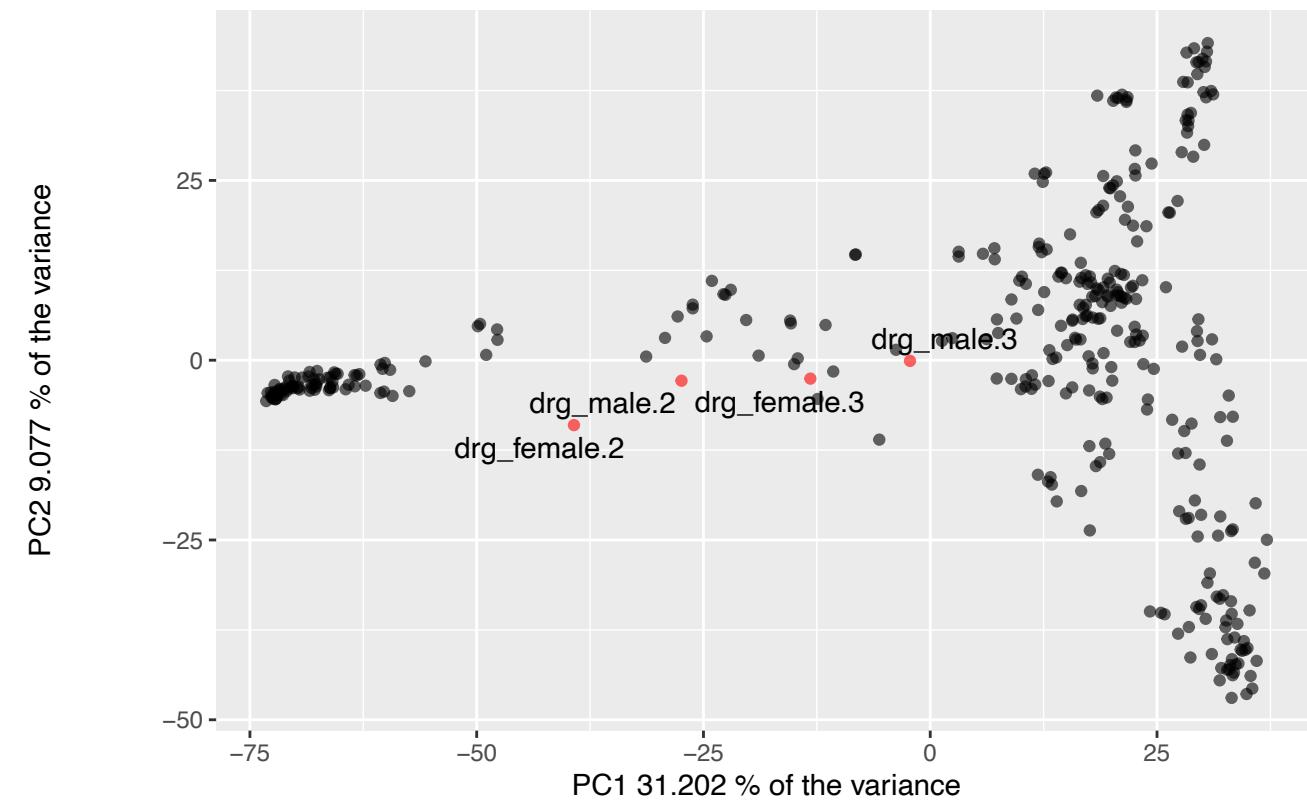
diaphragm



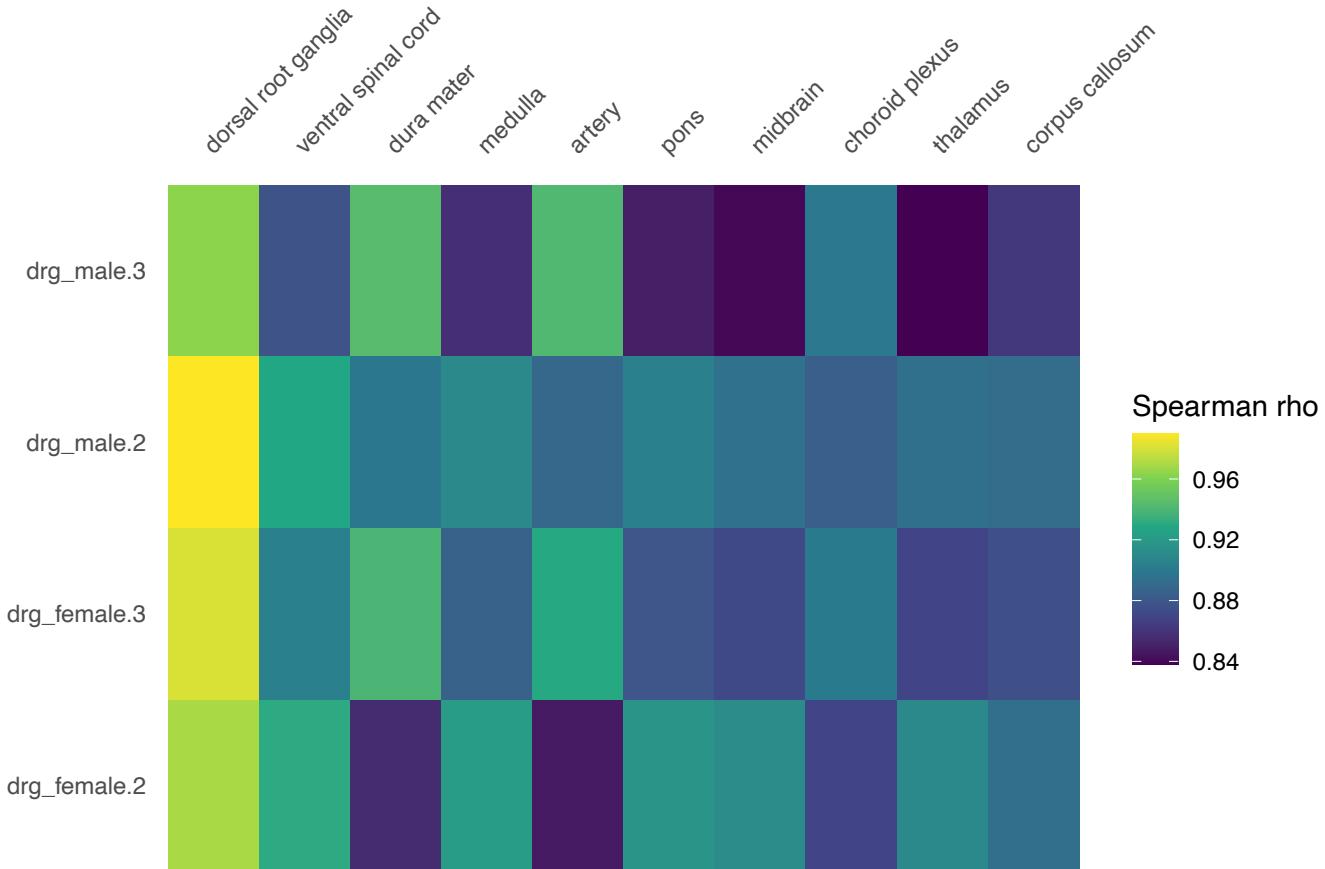
diaphragm



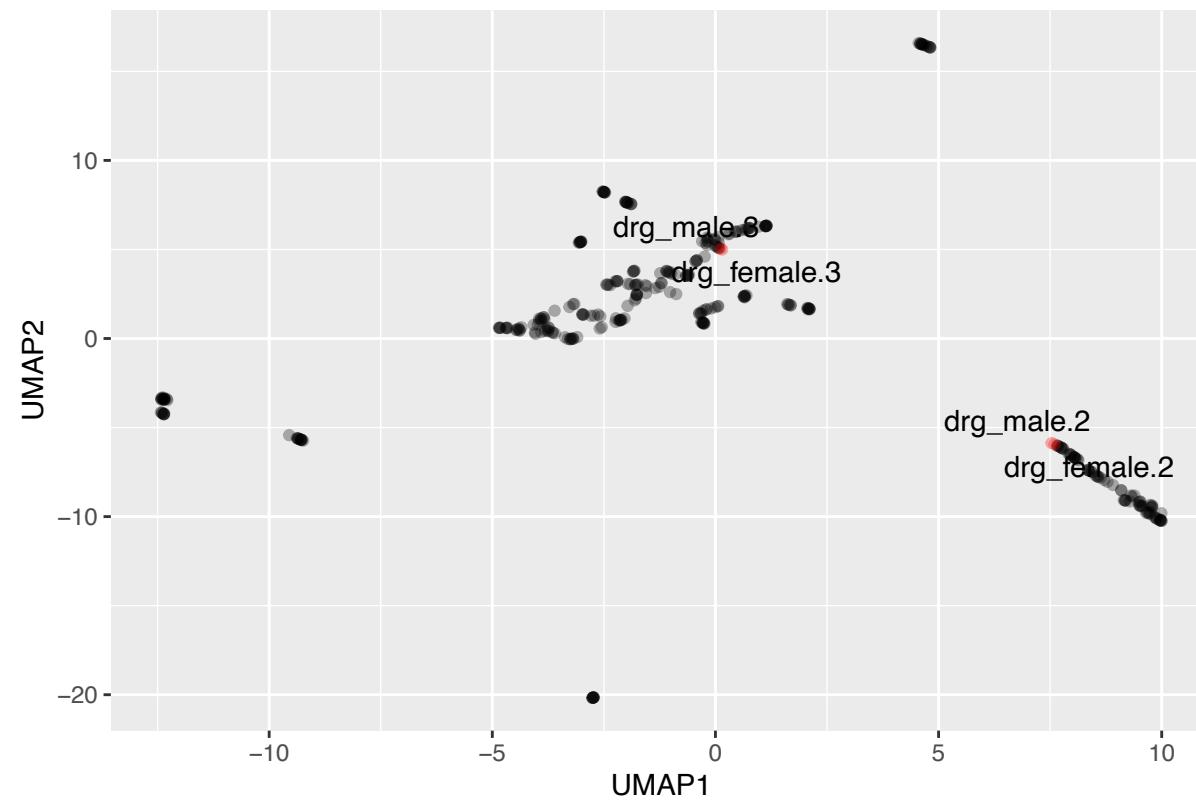
dorsal root ganglia, PCA: TMM expression values



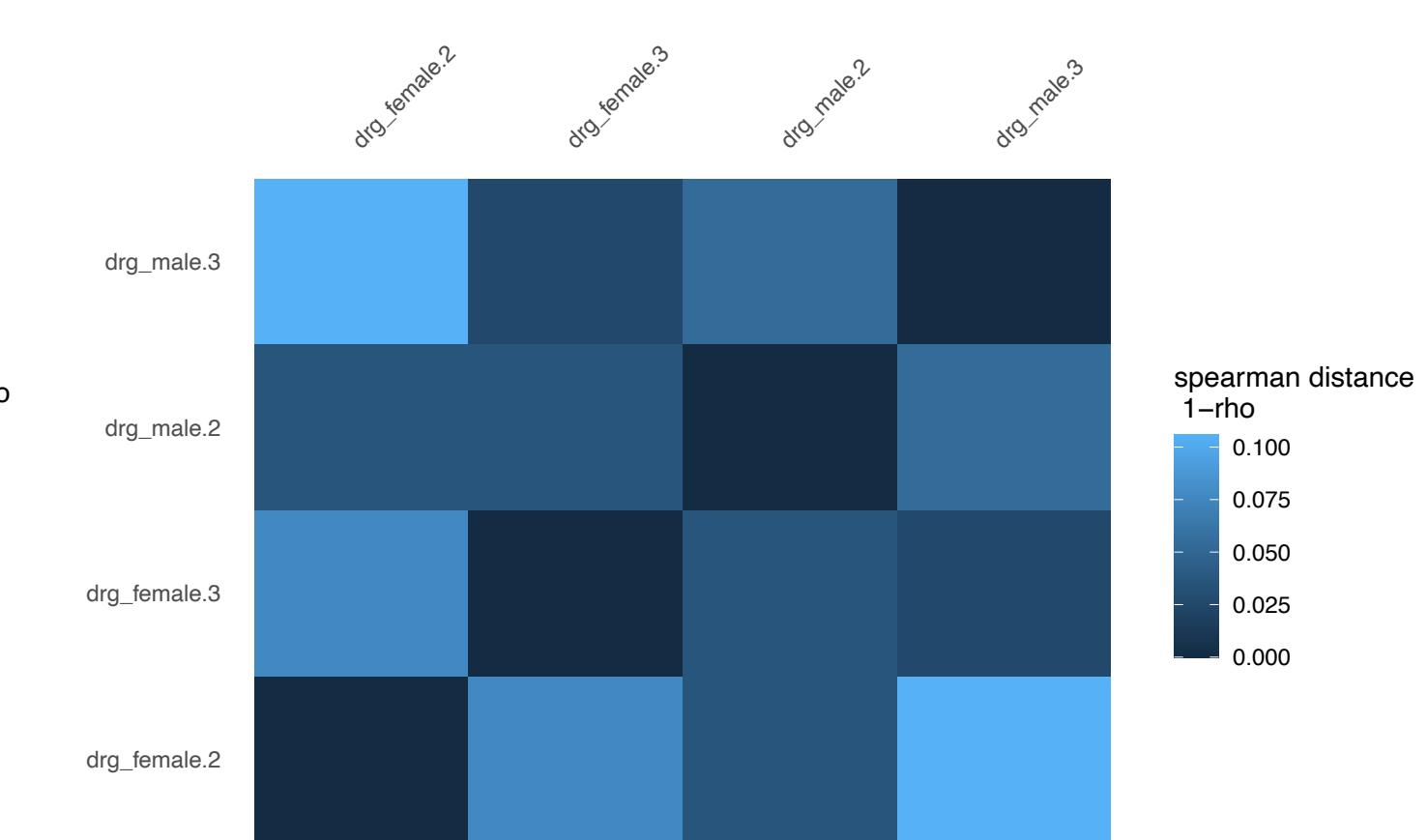
Tissue group to sample correlation



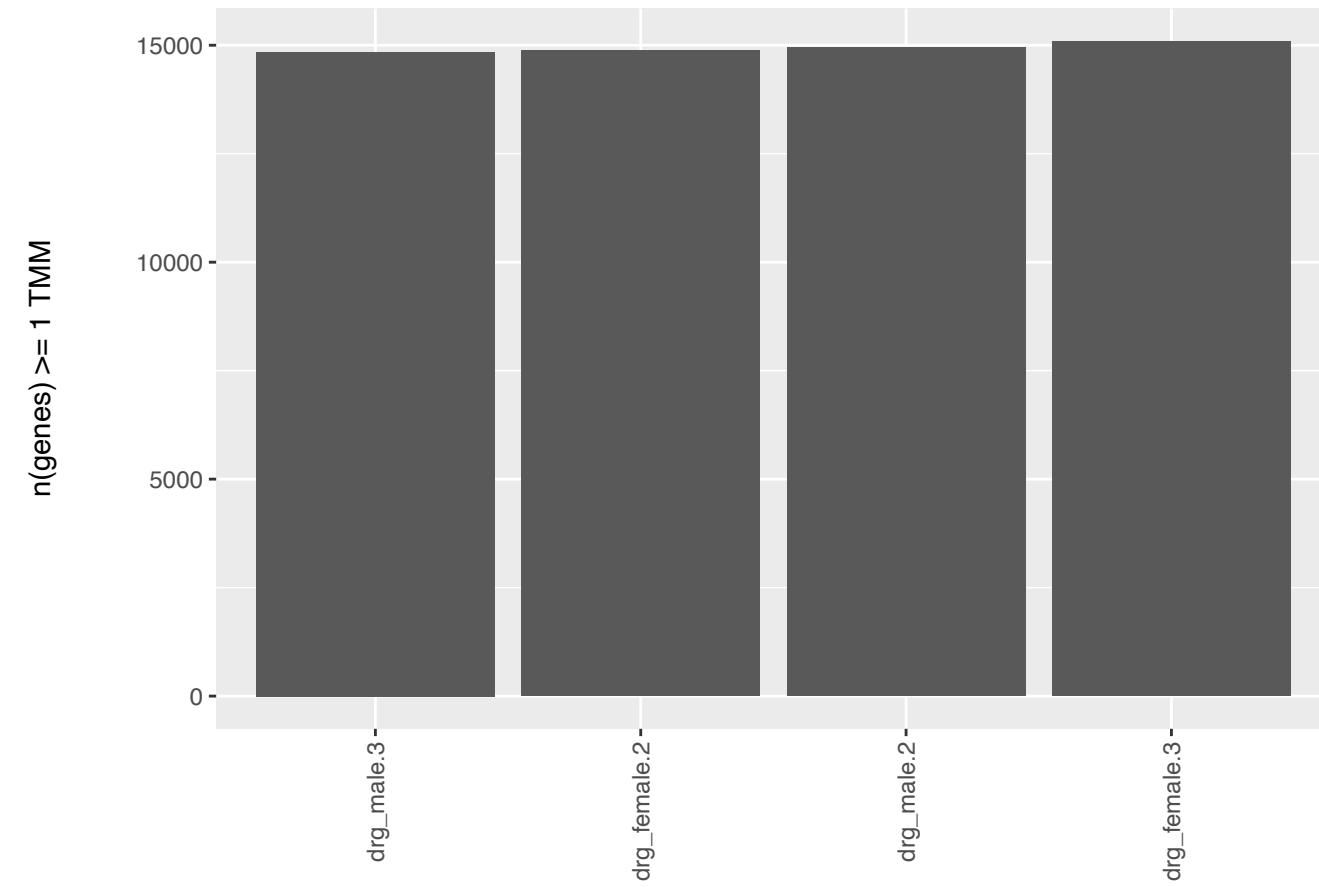
dorsal root ganglia, UMAP: TMM expression values



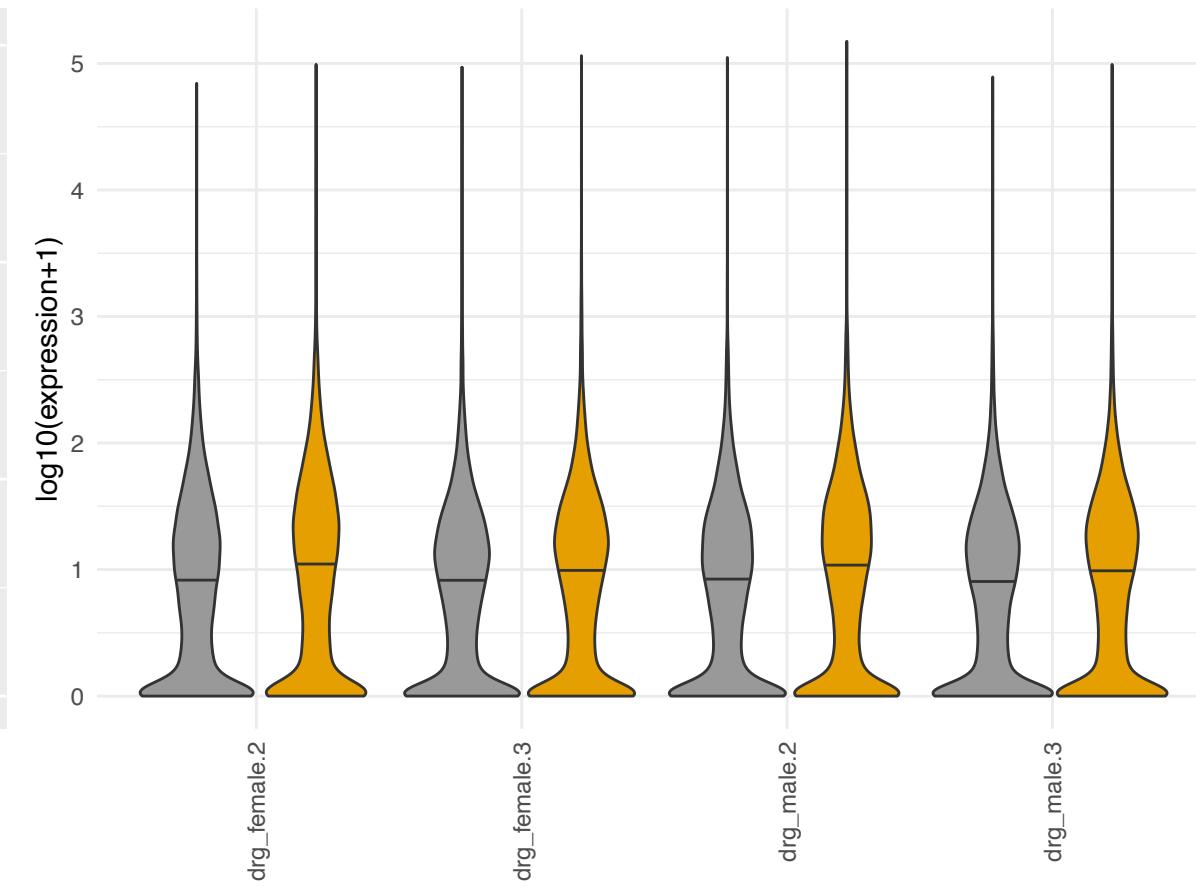
In tissue sample to sample Spearman Distance



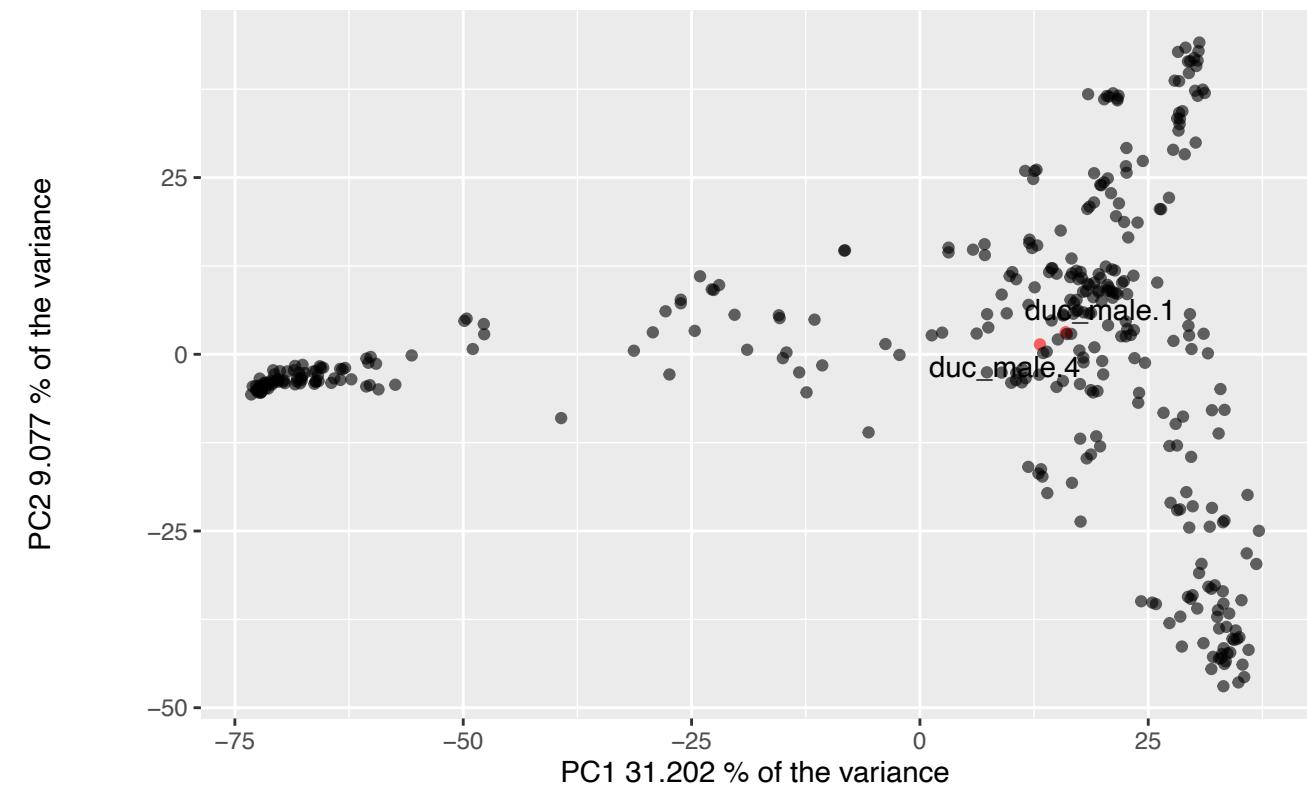
dorsal root ganglia



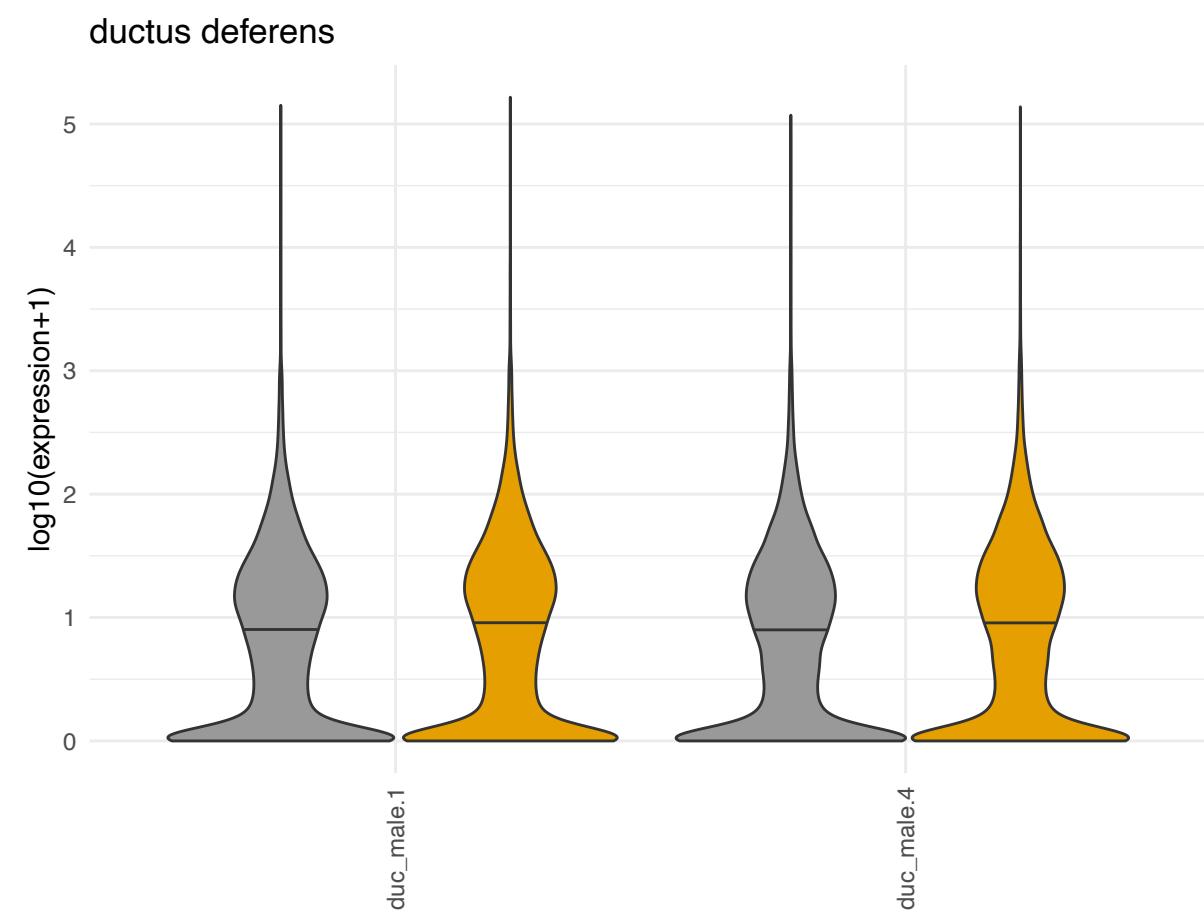
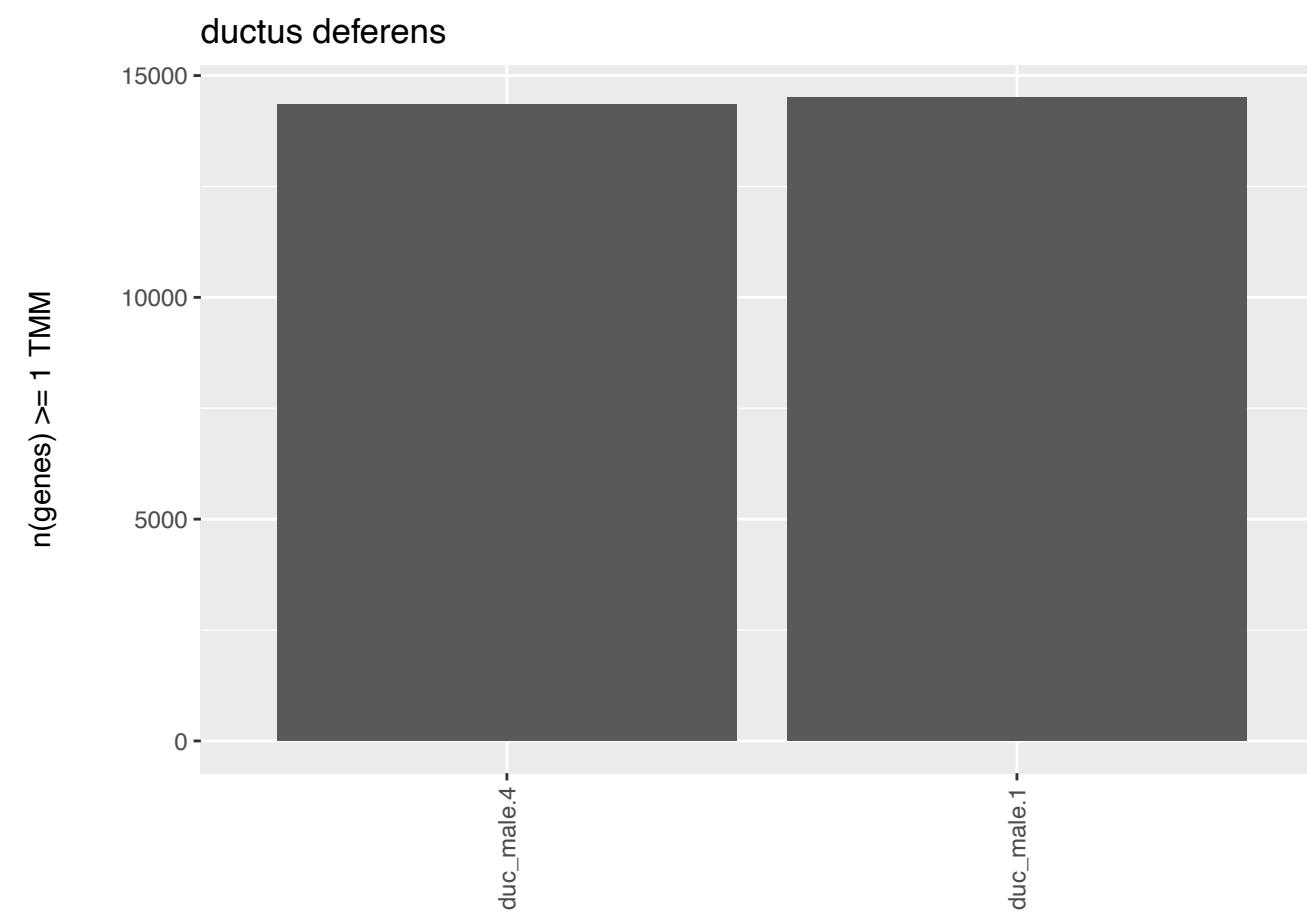
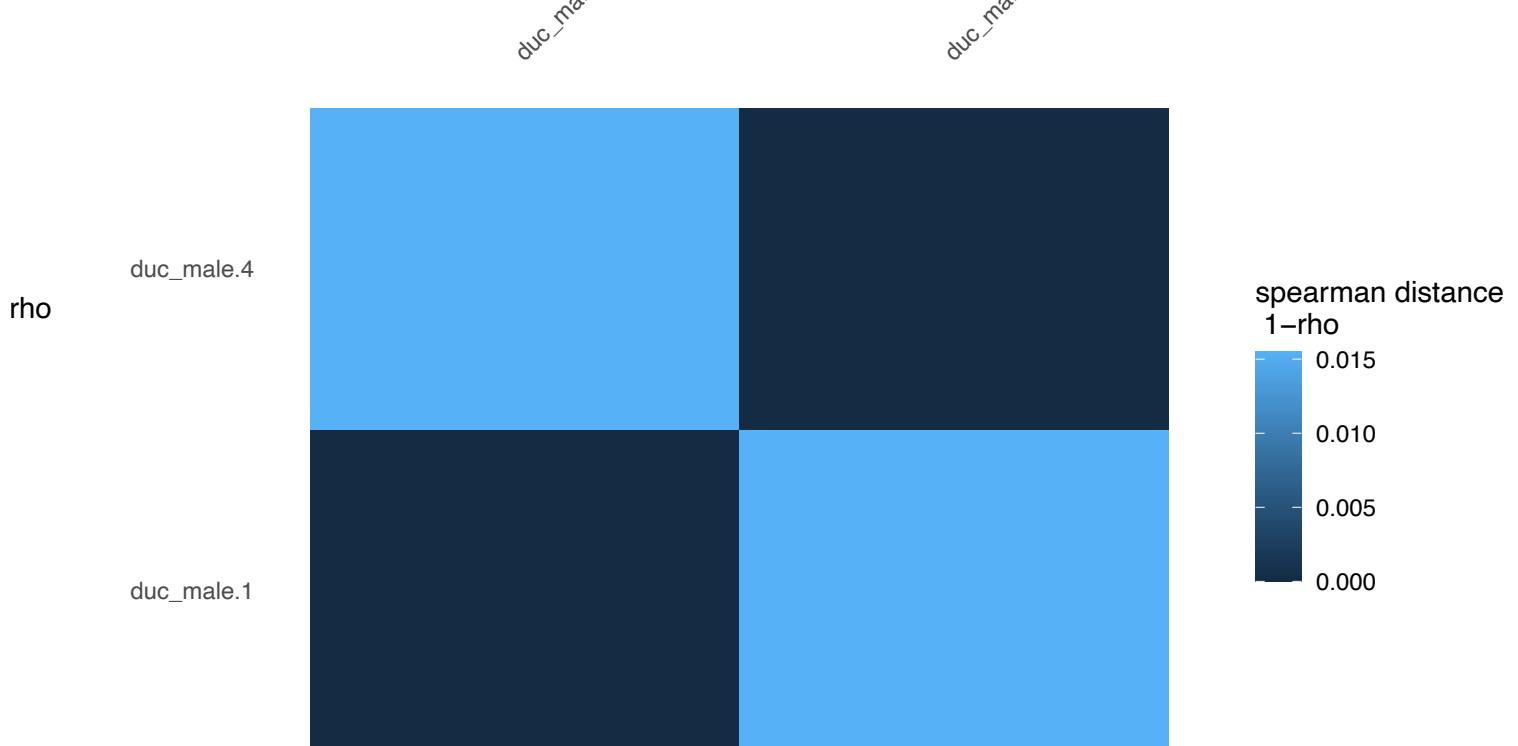
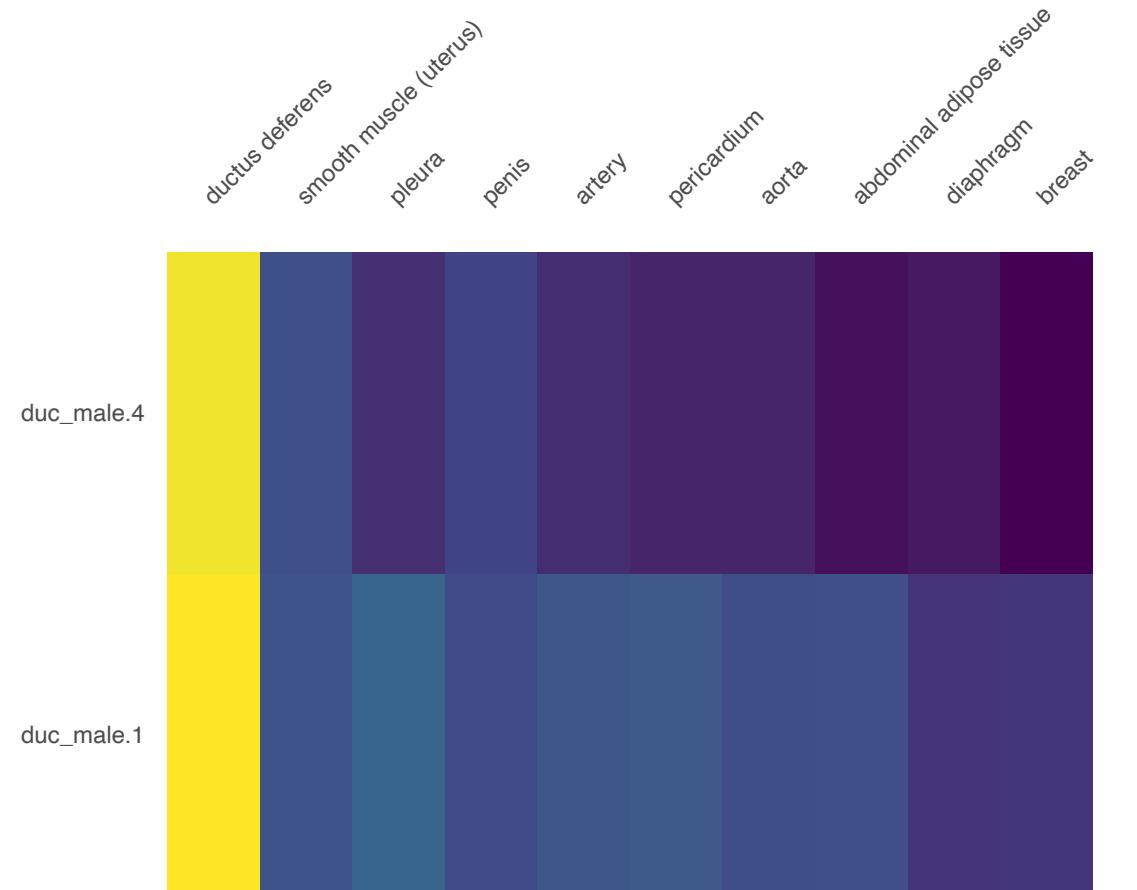
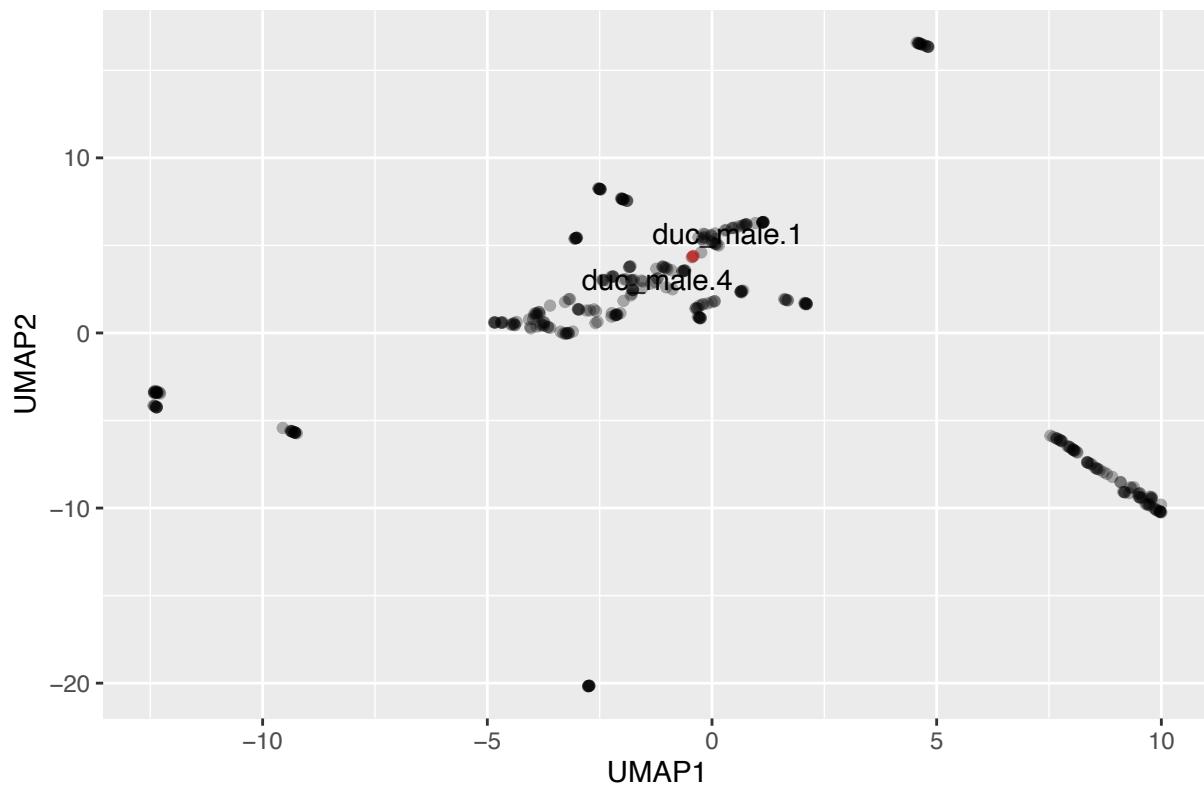
dorsal root ganglia



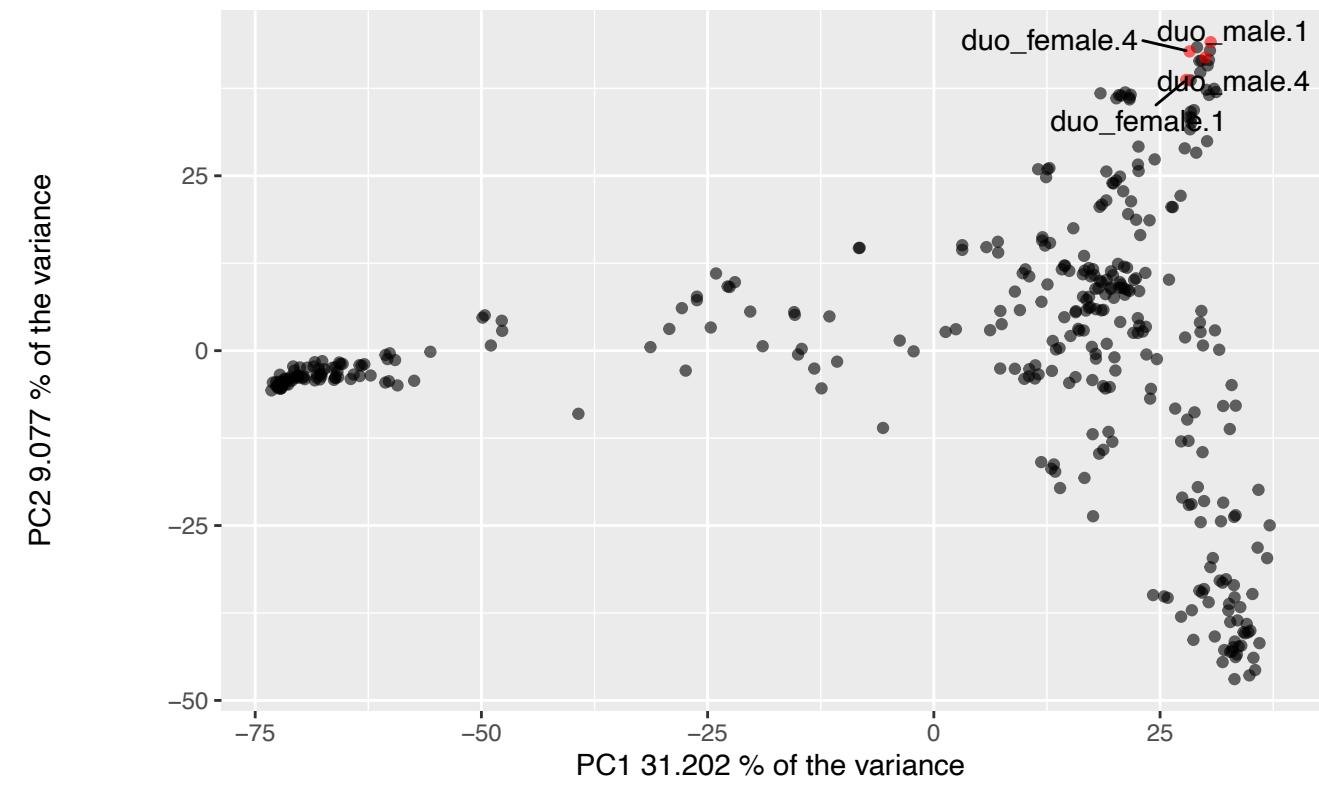
ductus deferens, PCA: TMM expression values



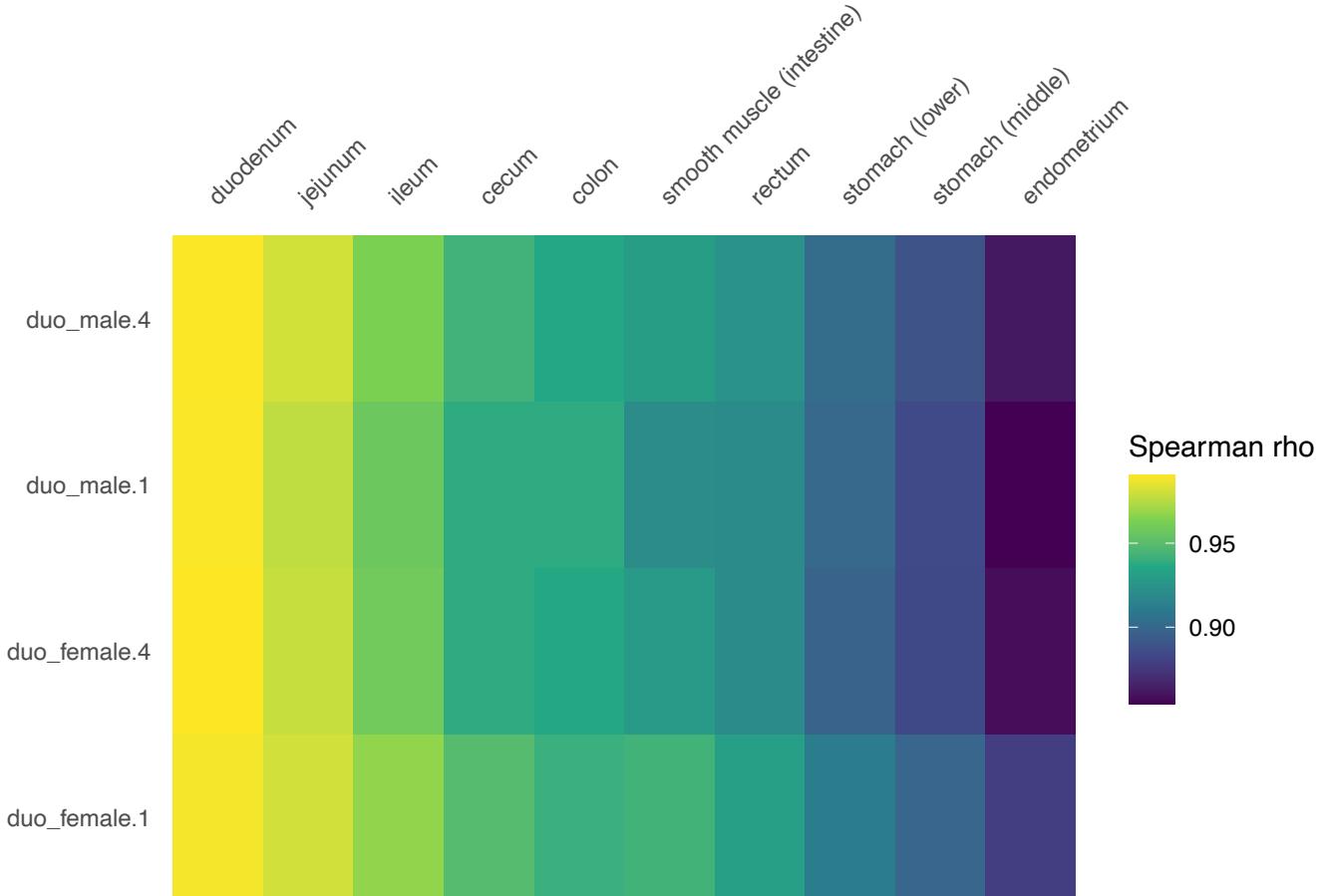
ductus deferens, UMAP: TMM expression values



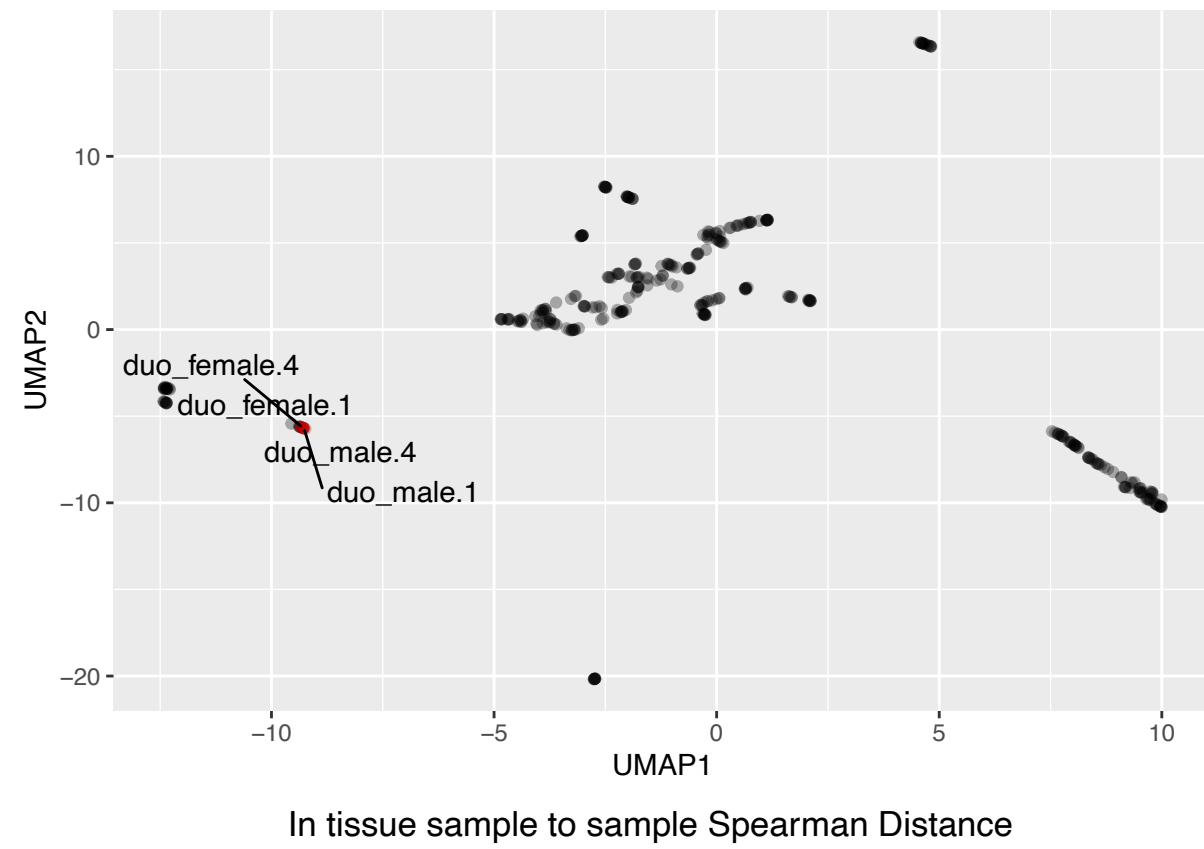
duodenum, PCA: TMM expression values



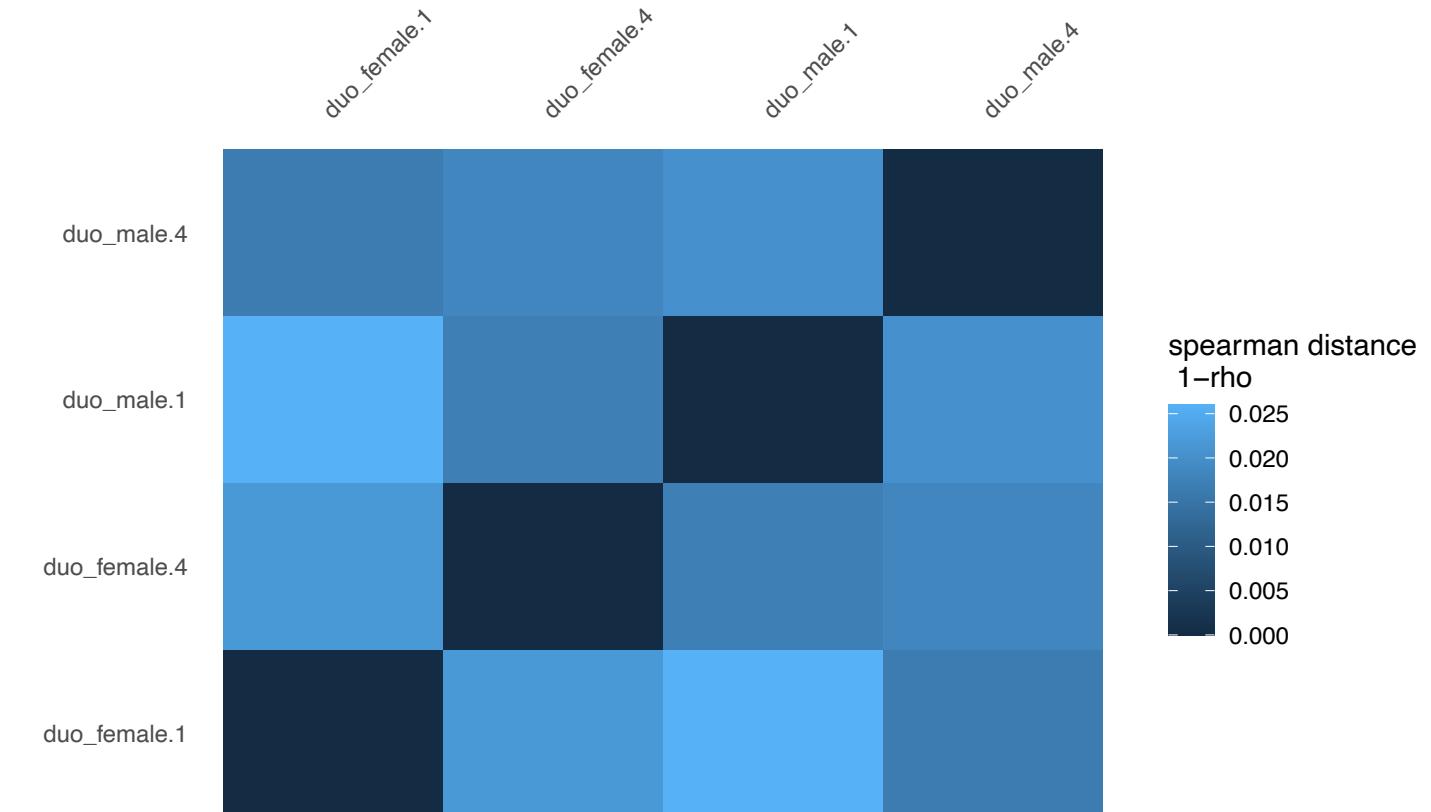
Tissue group to sample correlation



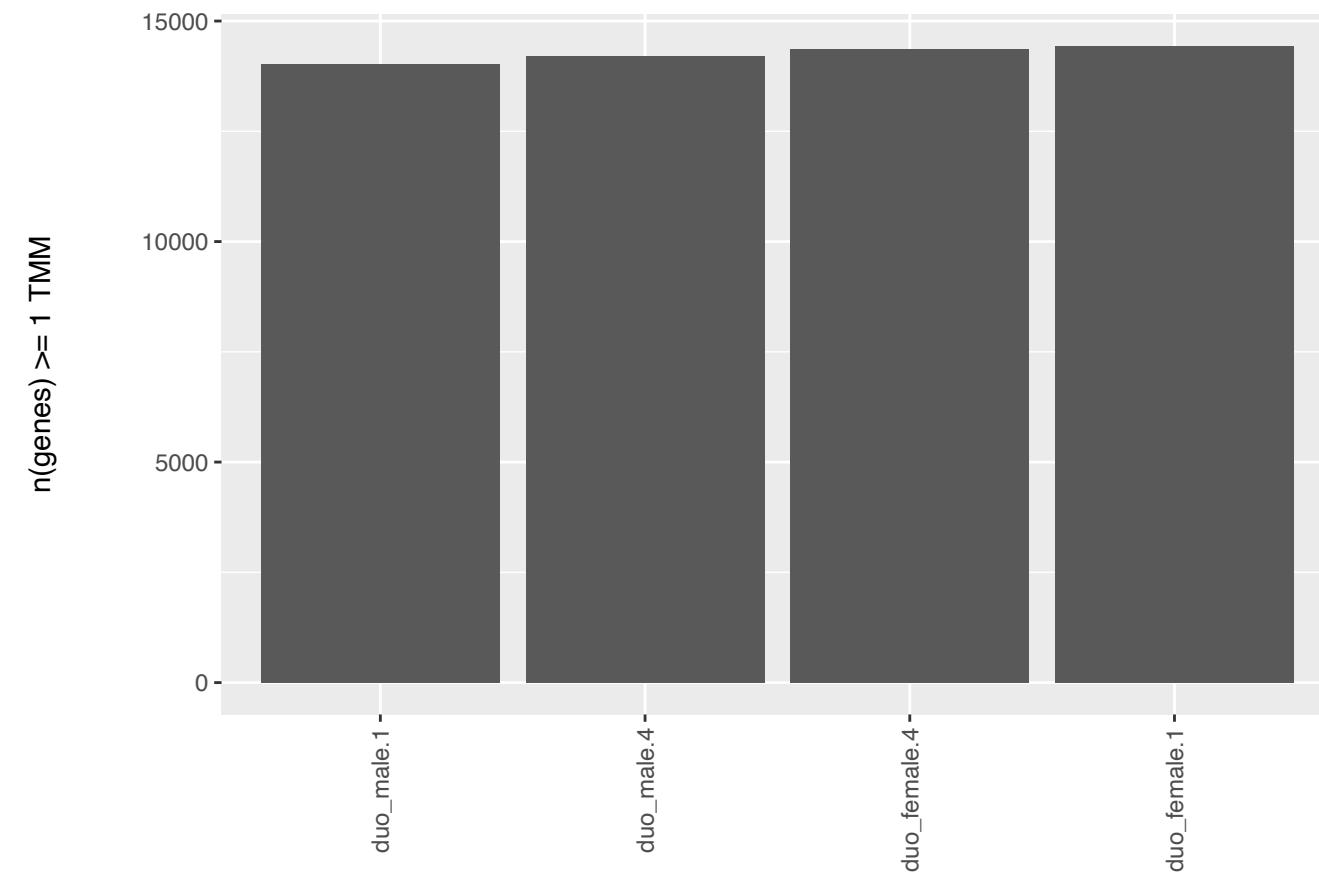
duodenum, UMAP: TMM expression values



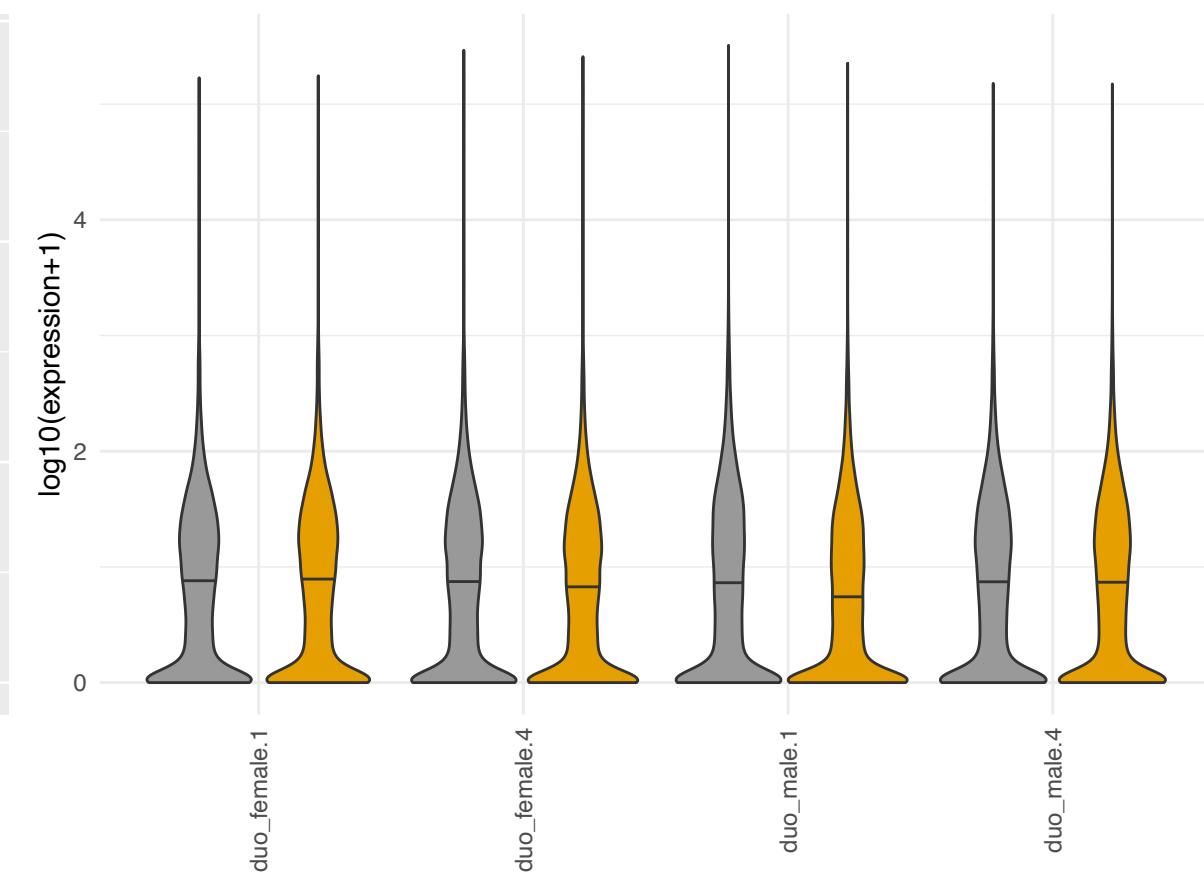
In tissue sample to sample Spearman Distance



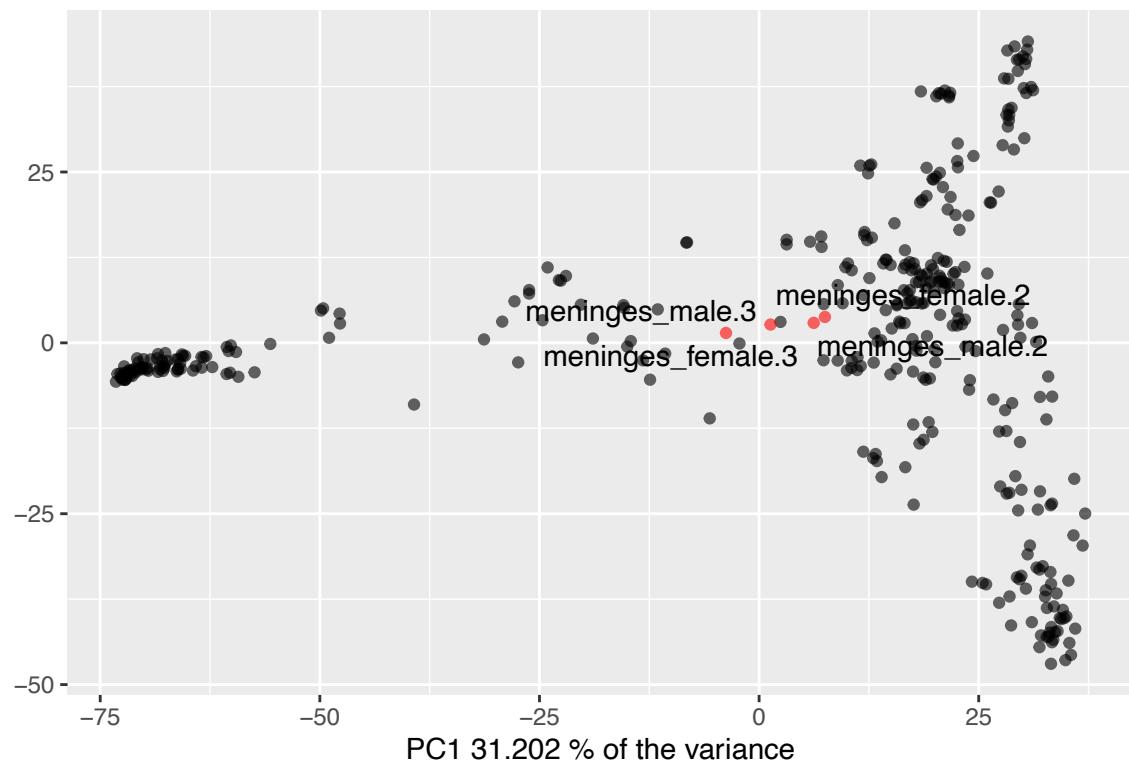
duodenum



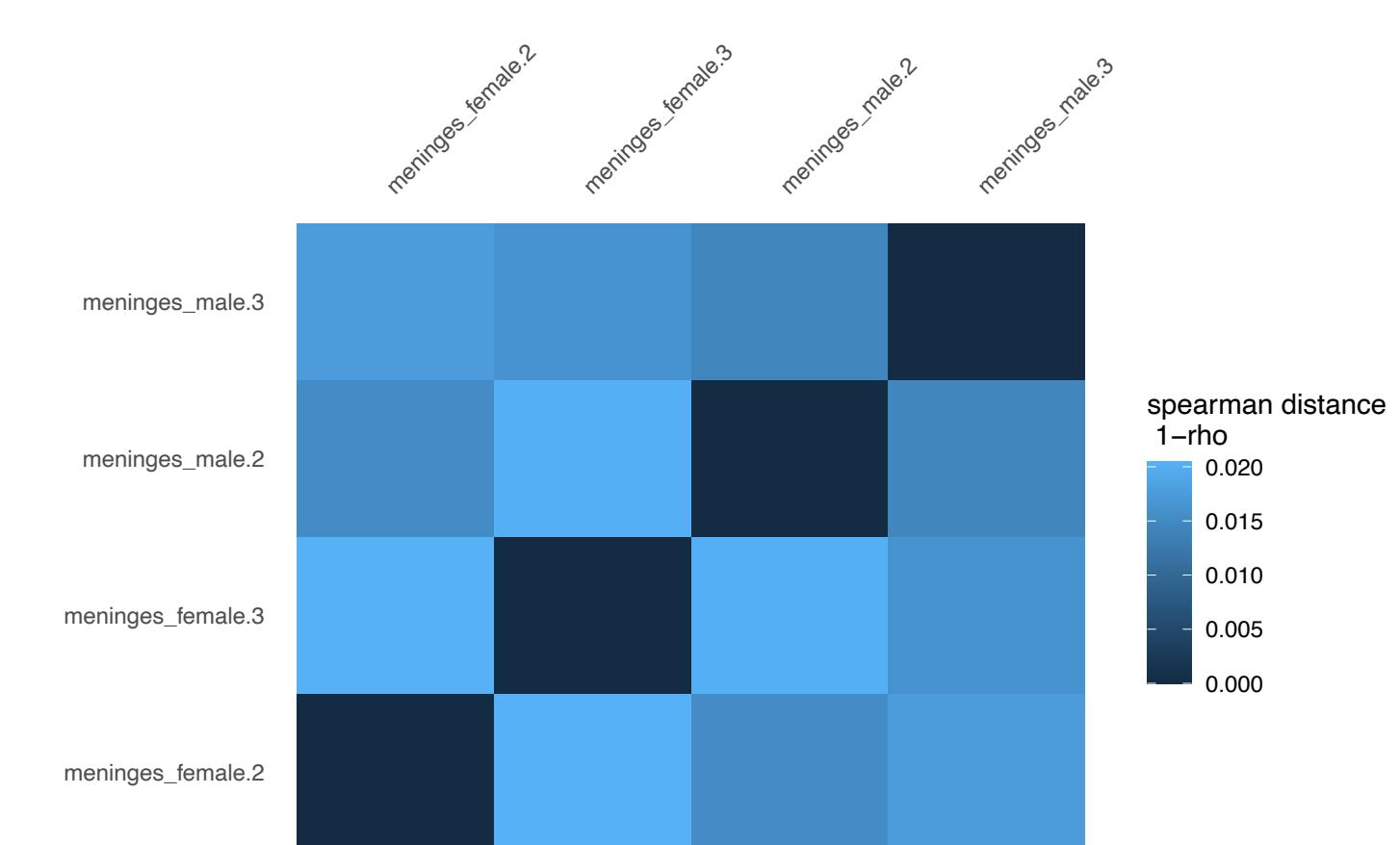
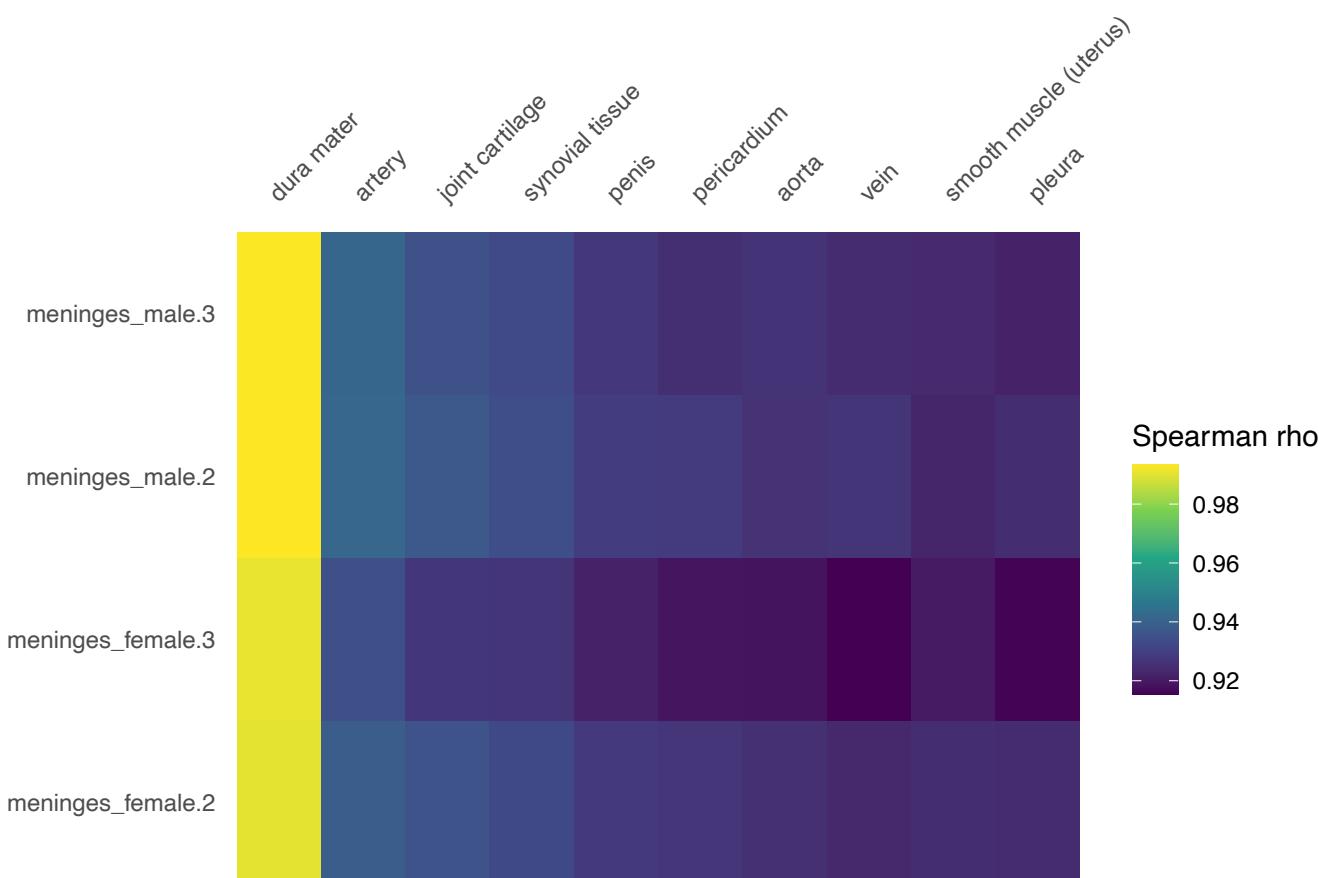
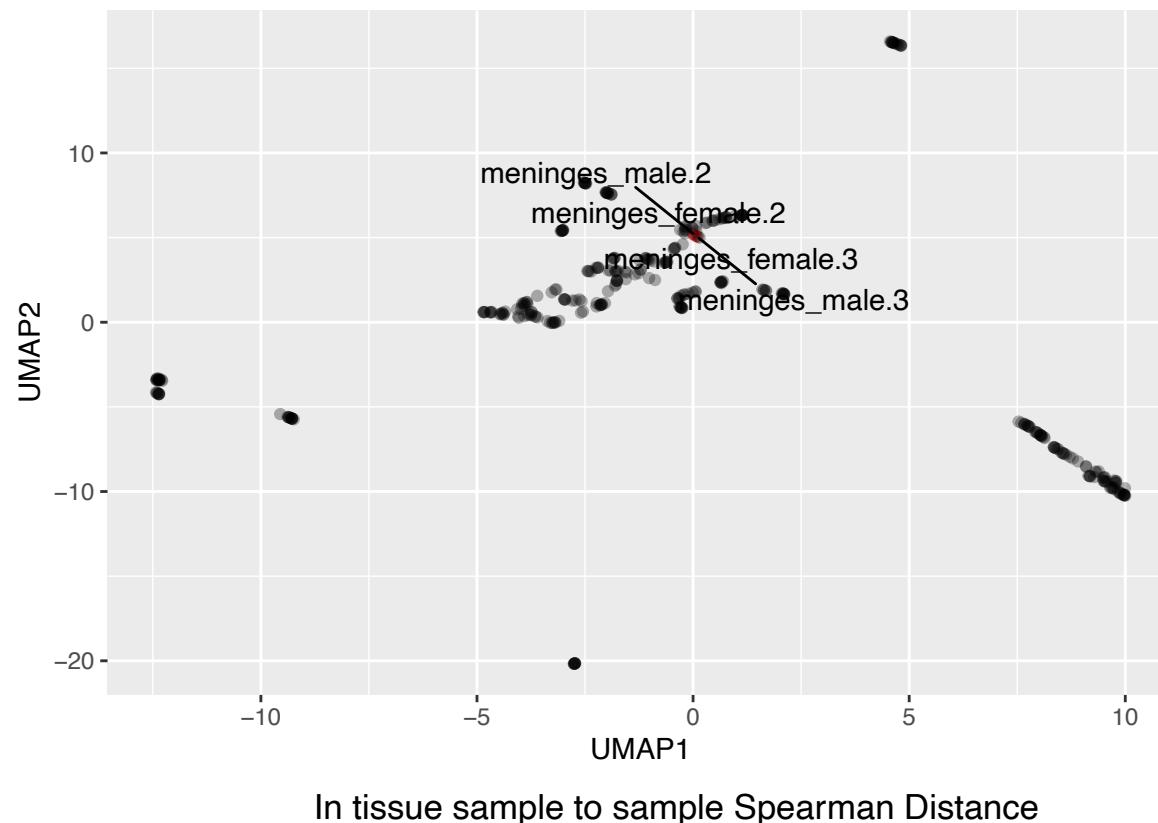
duodenum



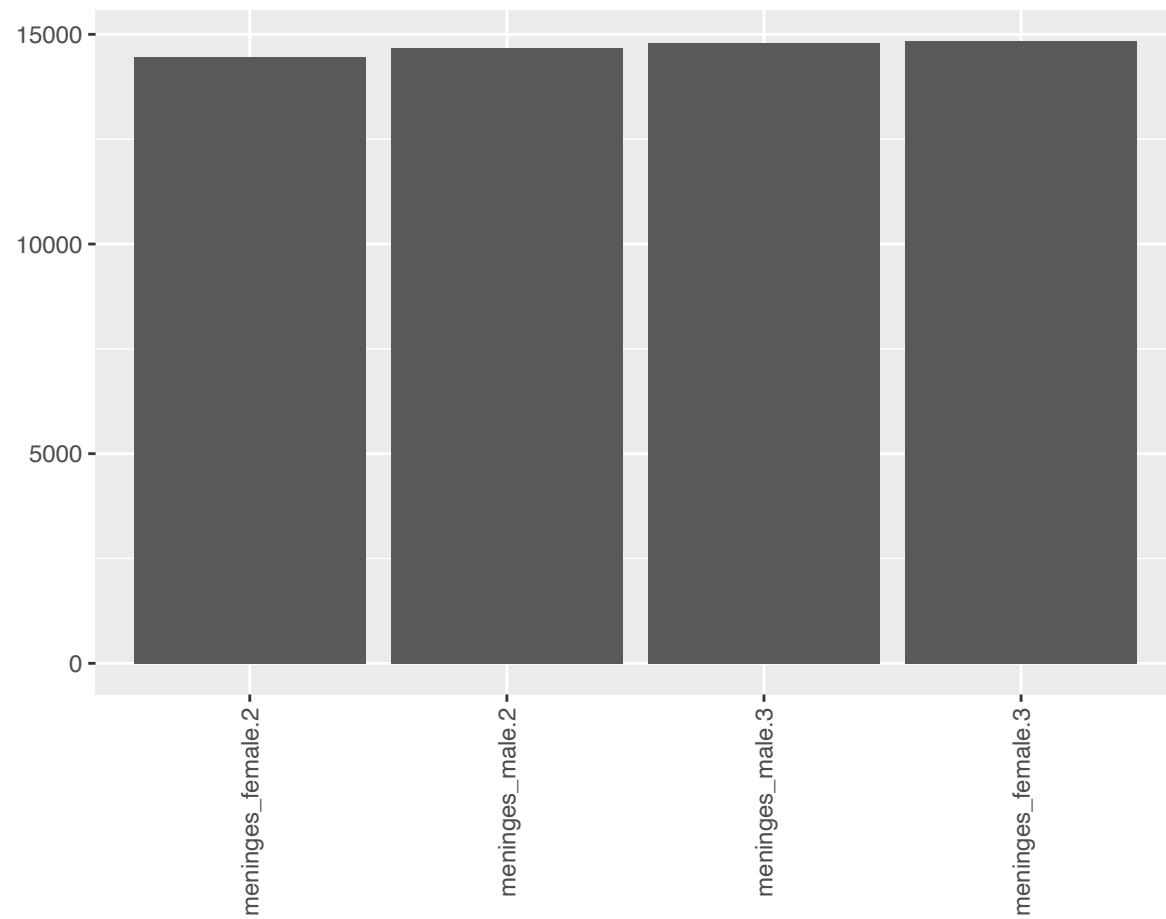
dura mater, PCA: TMM expression values



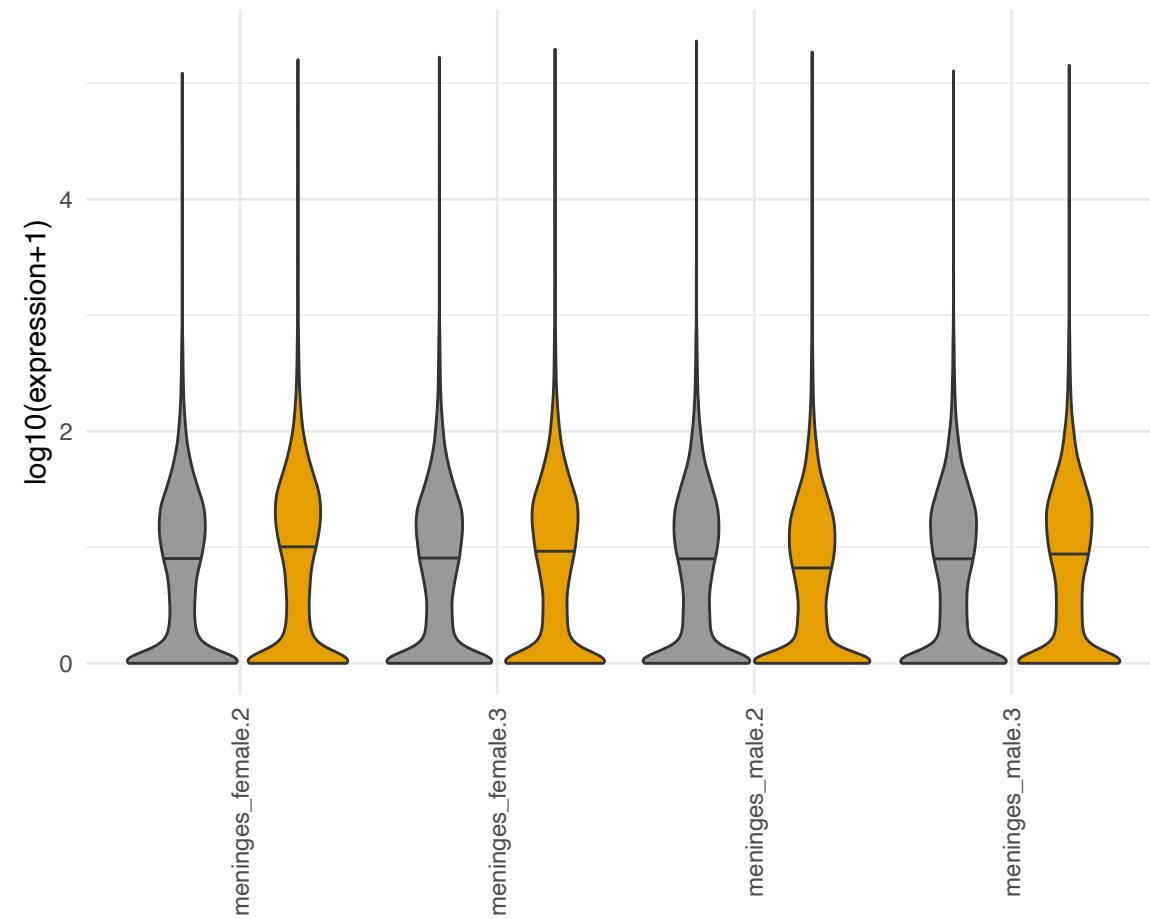
dura mater, UMAP: TMM expression values



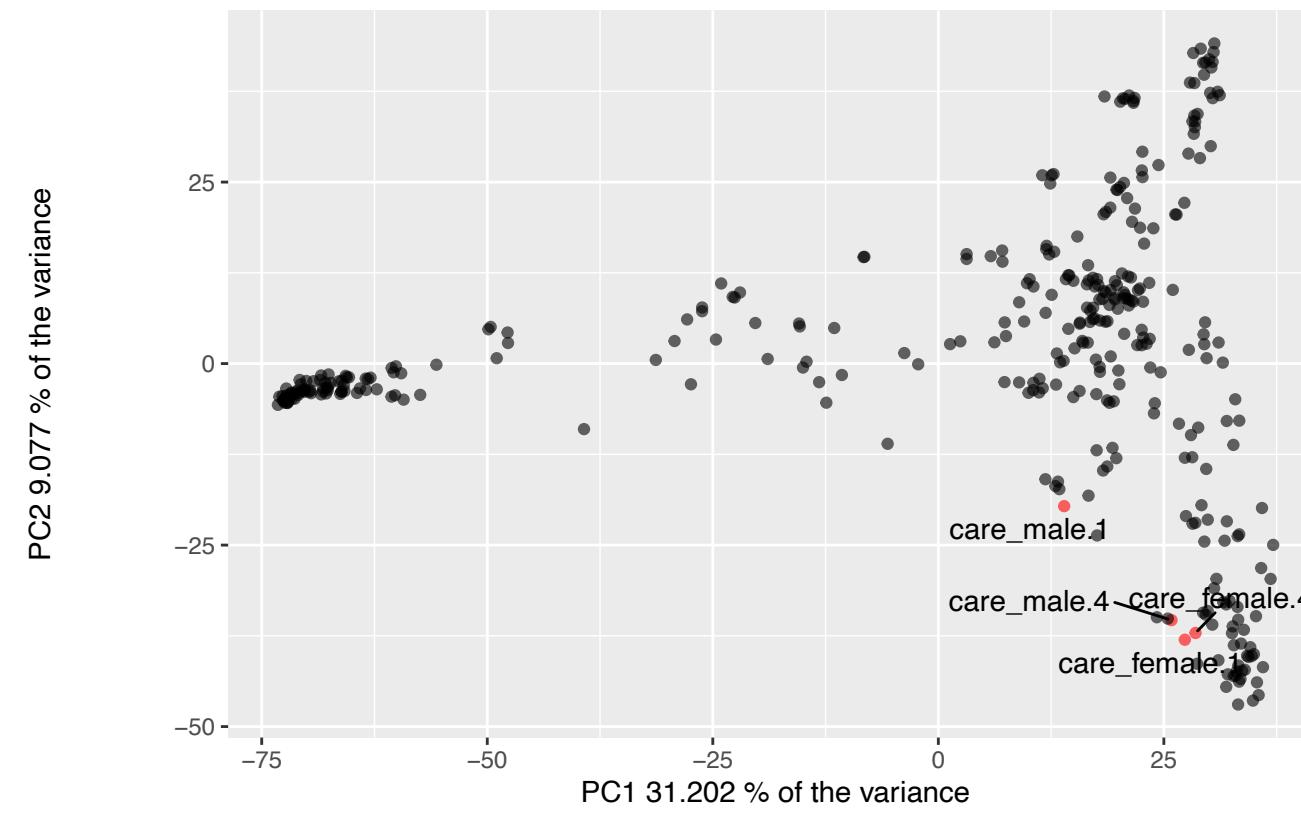
dura mater



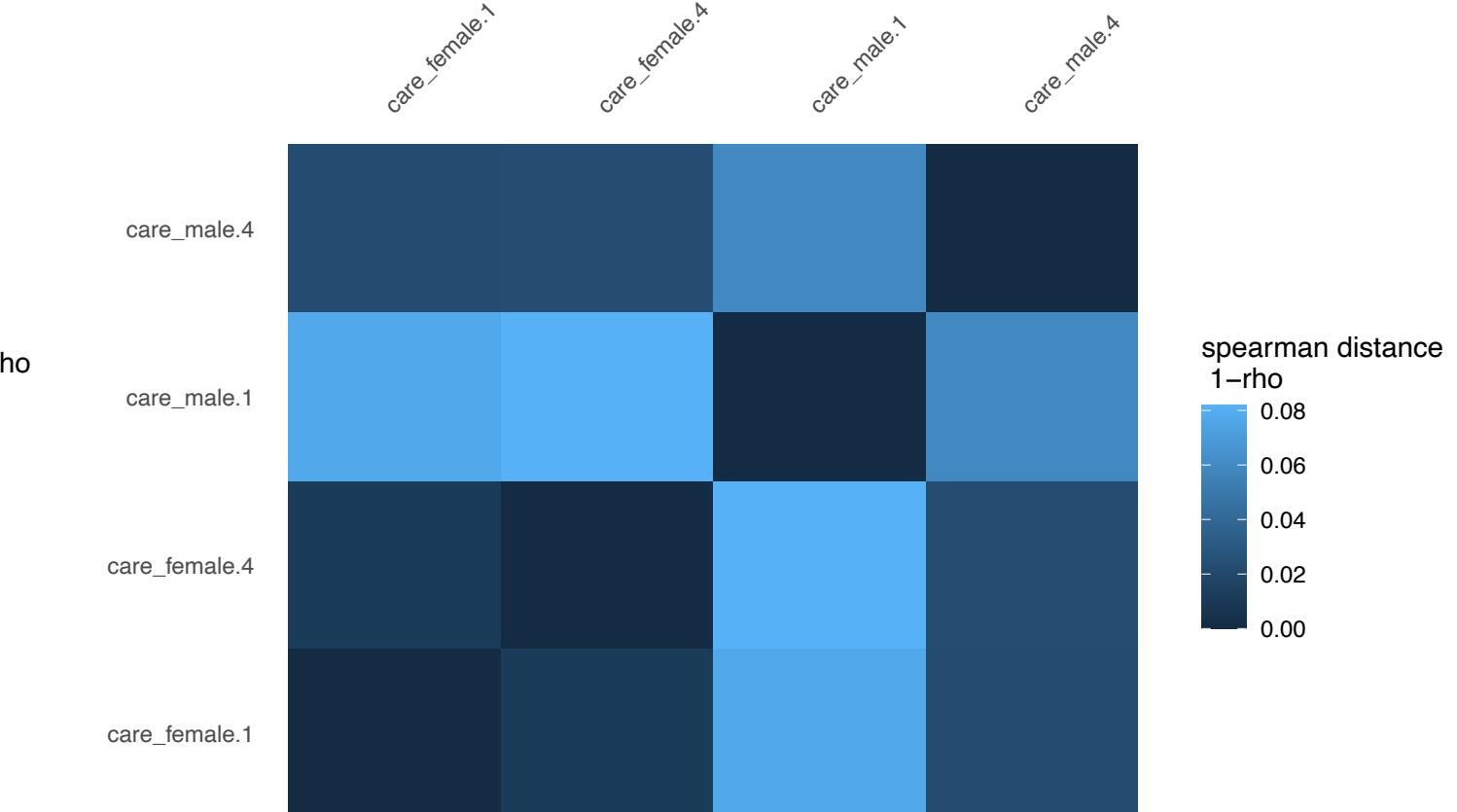
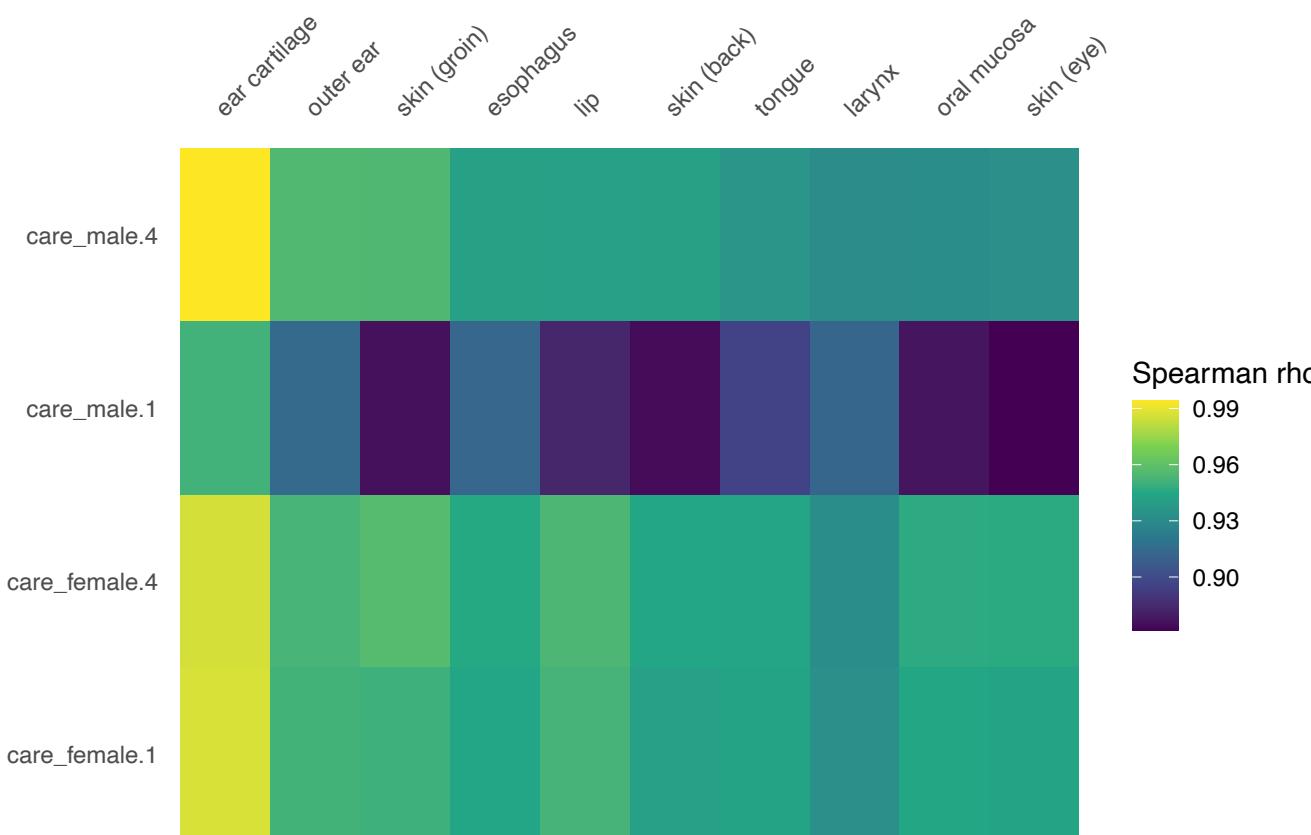
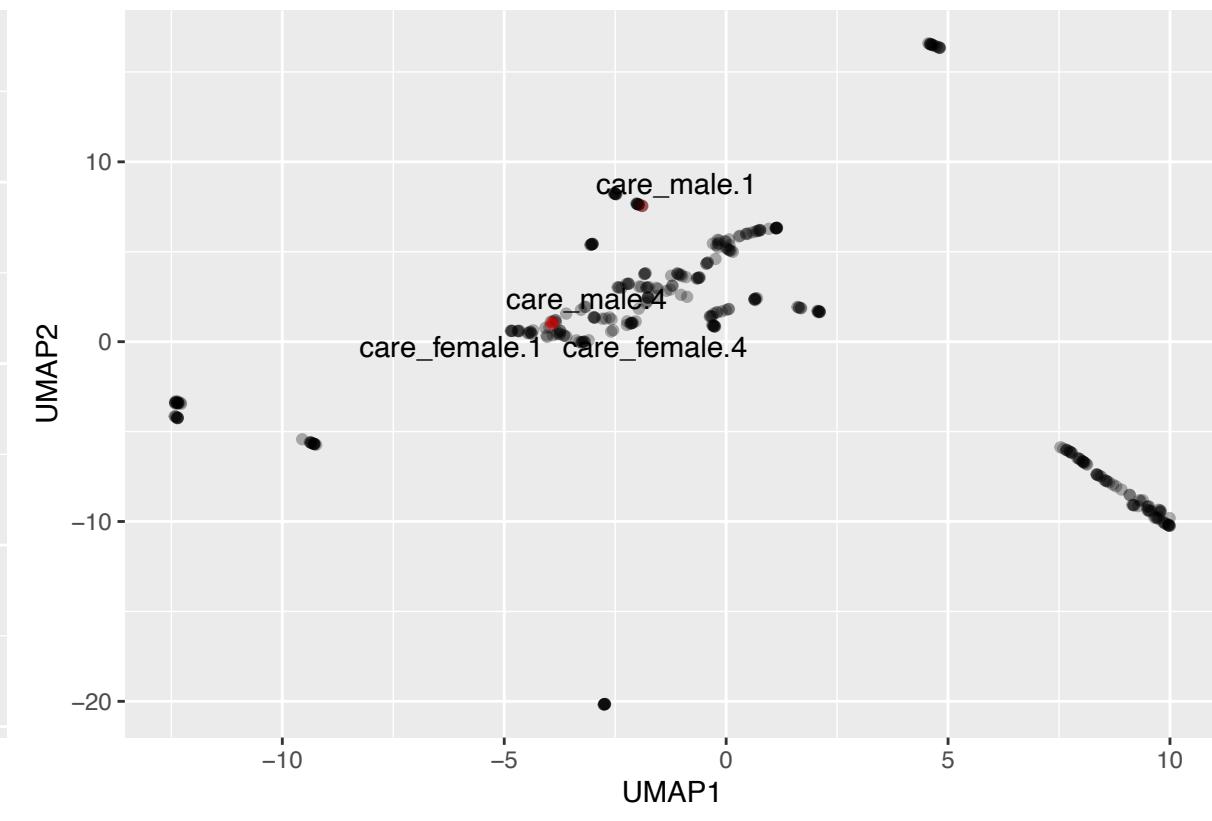
dura mater



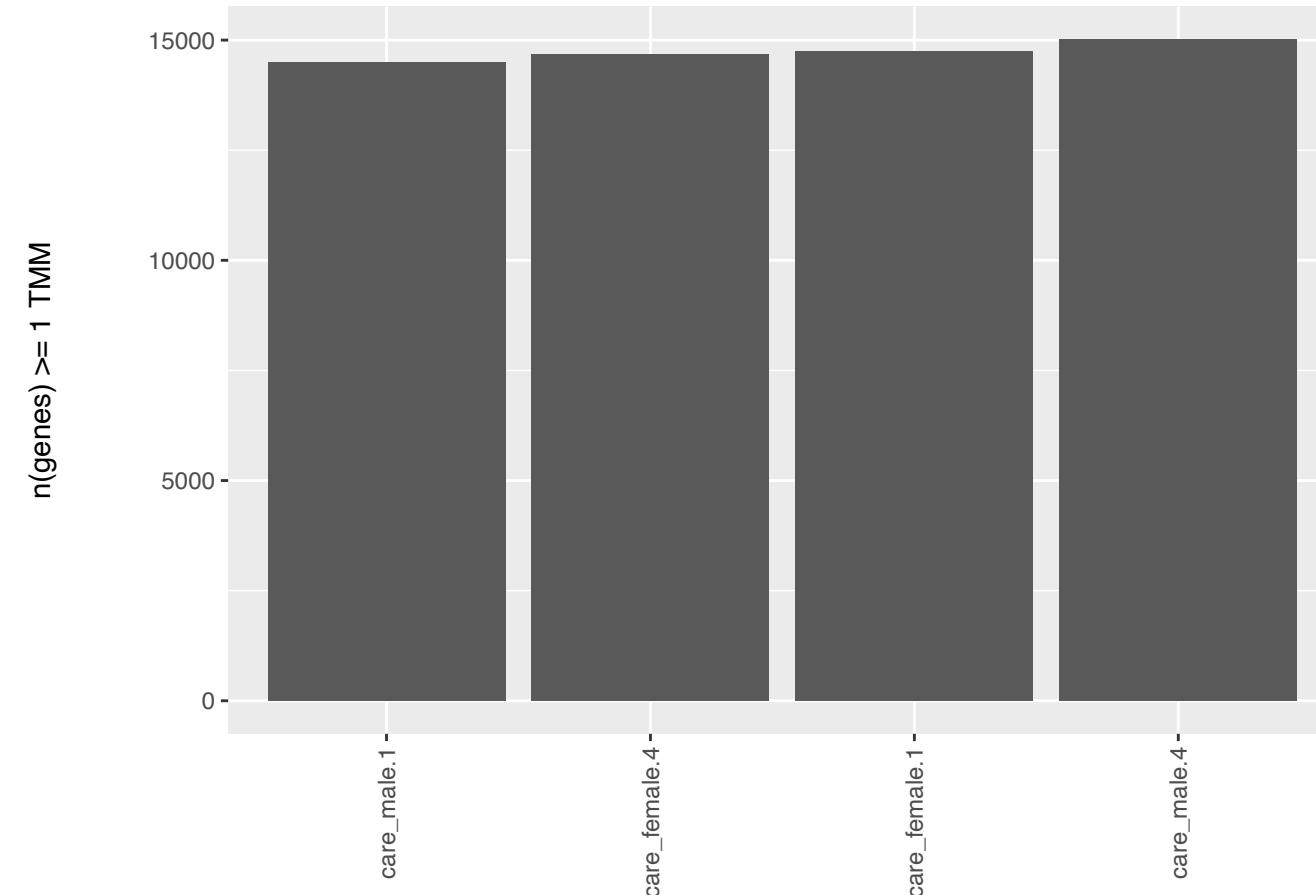
ear cartilage, PCA: TMM expression values



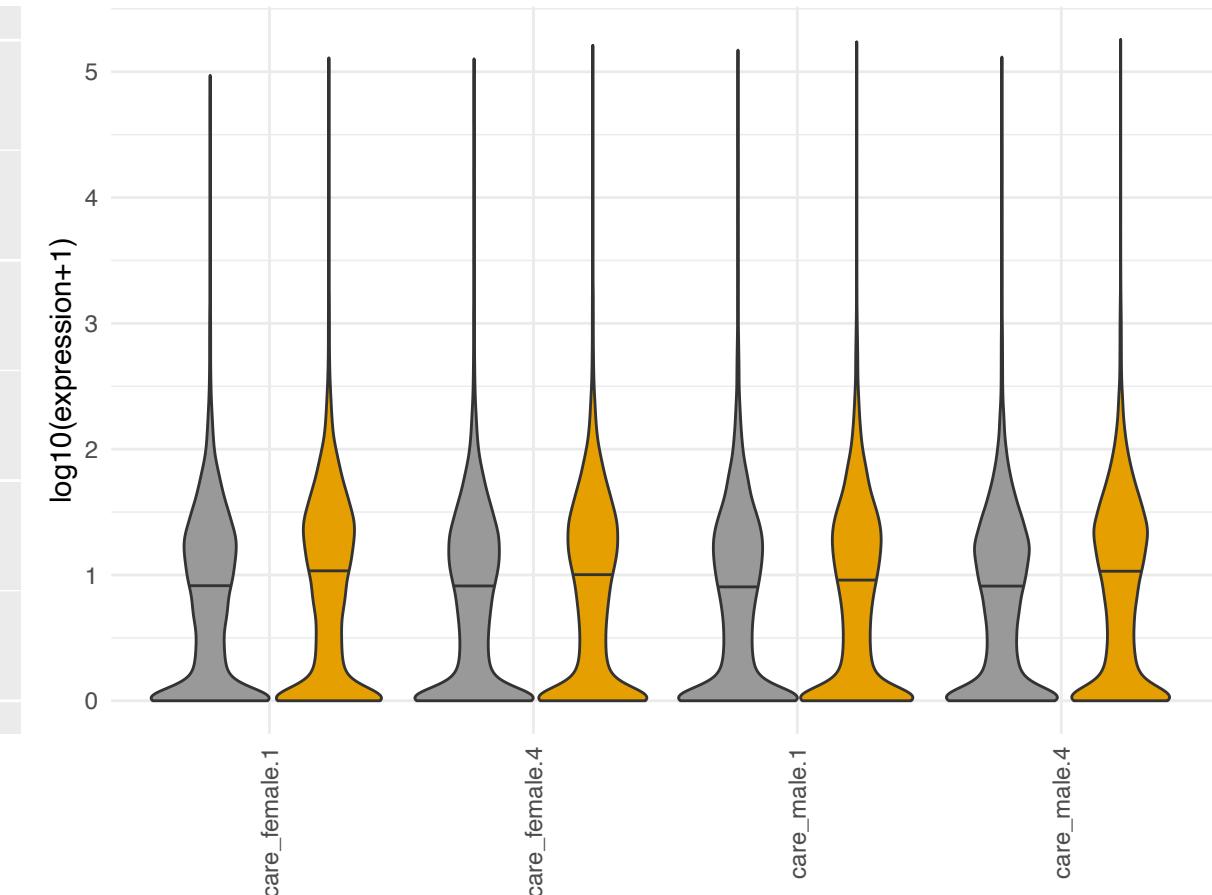
ear cartilage, UMAP: TMM expression values



ear cartilage

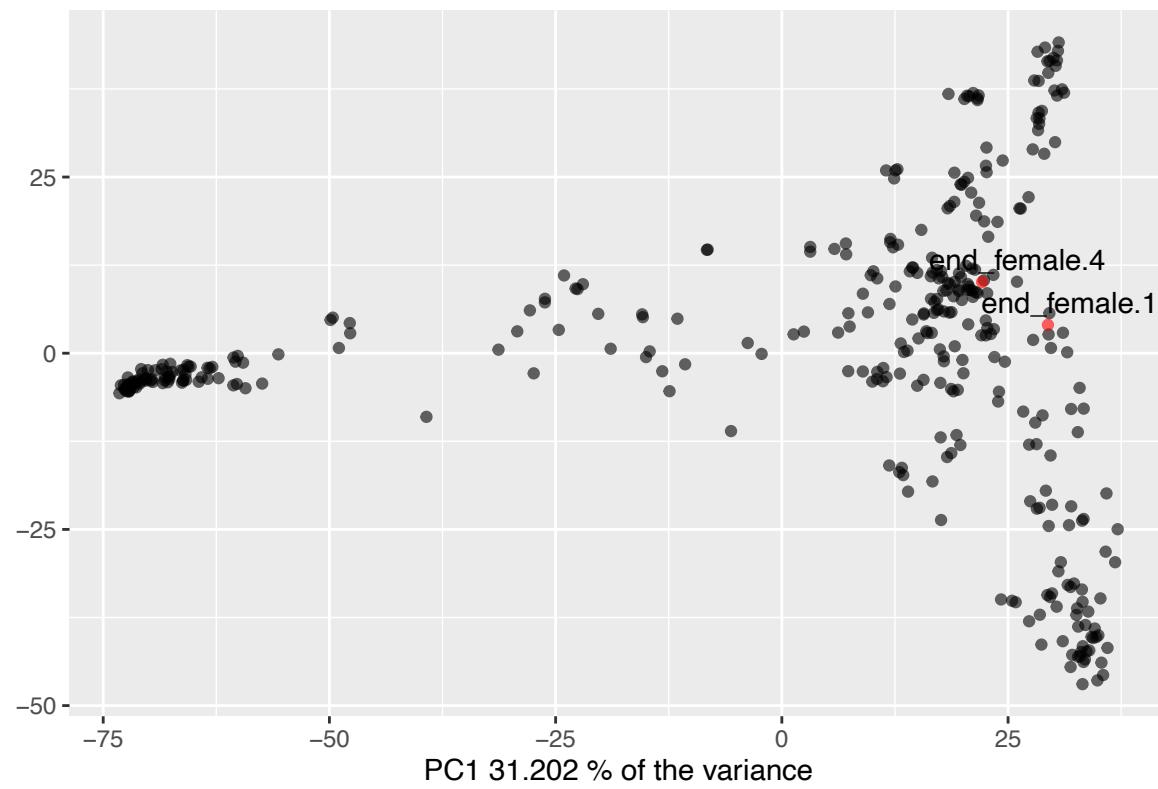


ear cartilage

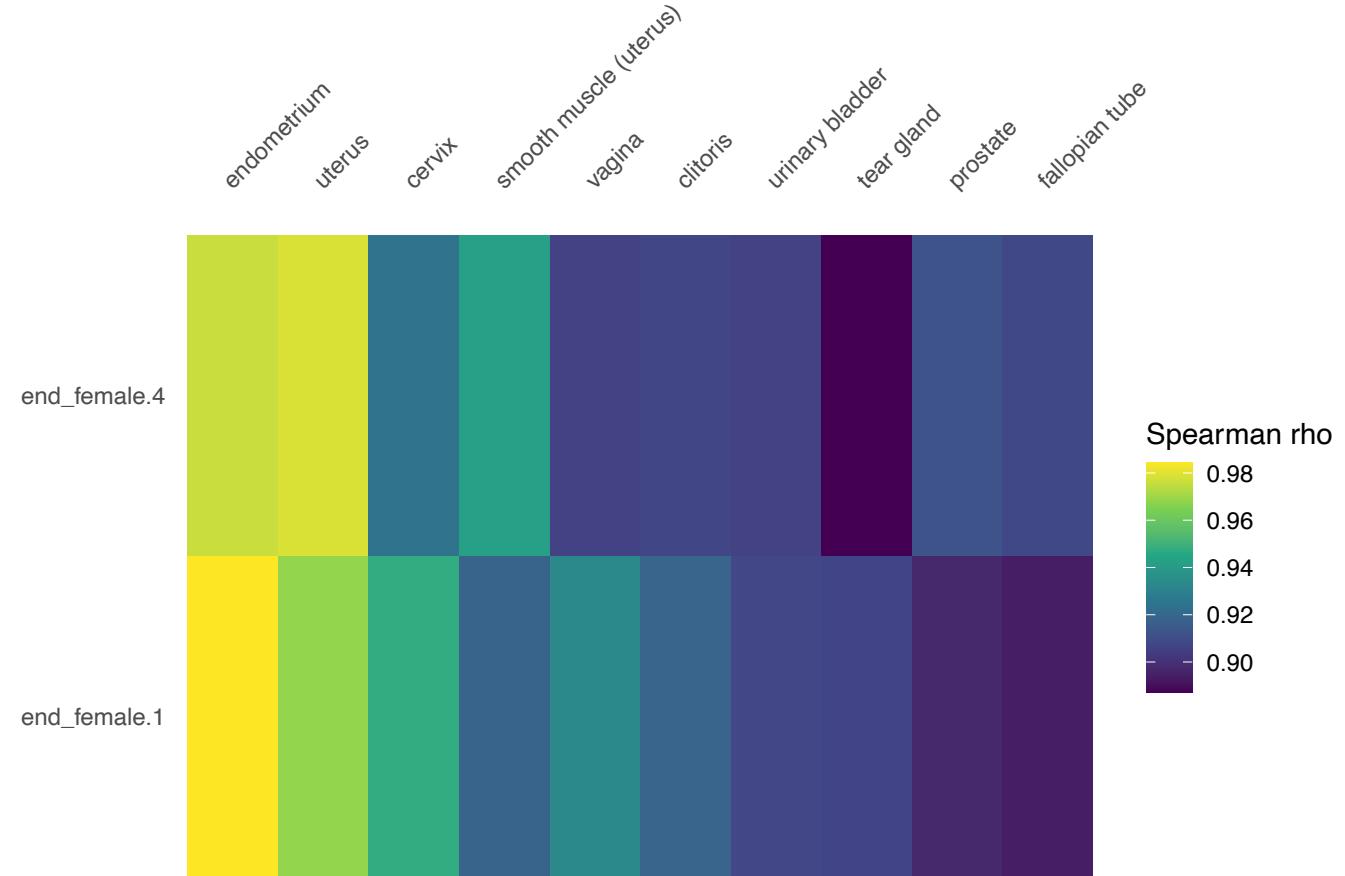


endometrium, PCA: TMM expression values

PC2 9.077 % of the variance



Tissue group to sample correlation

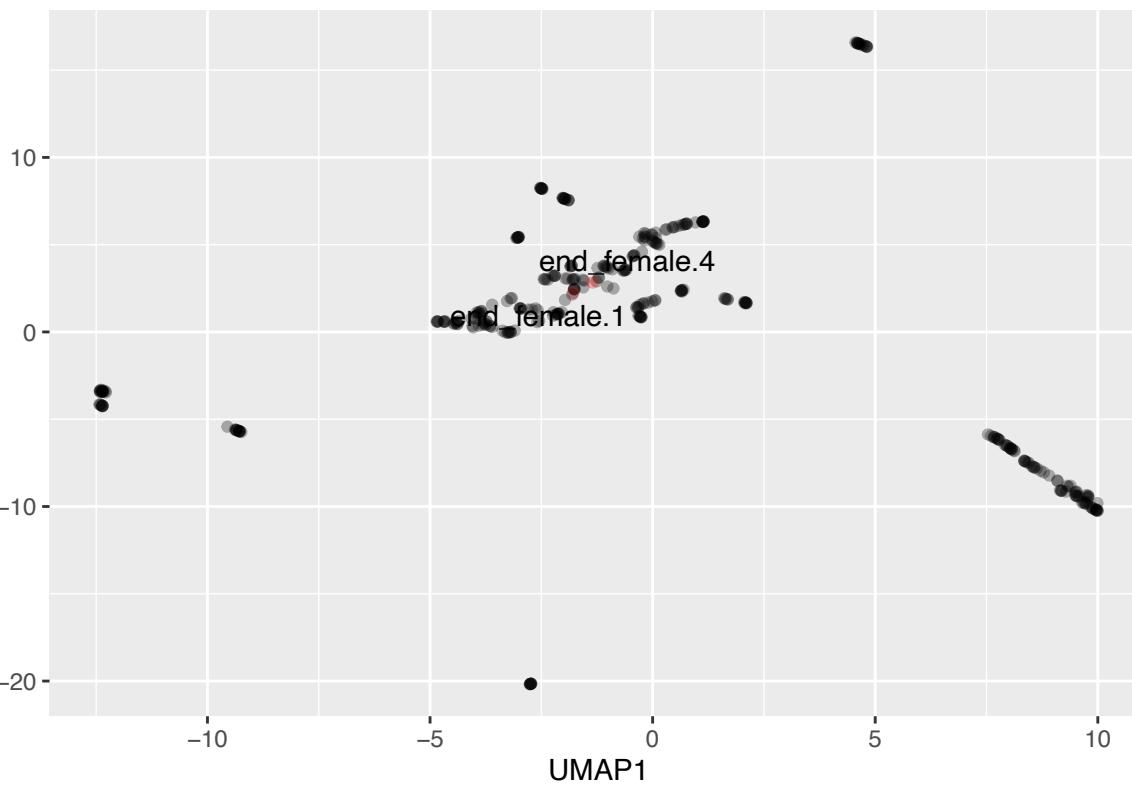


endometrium, UMAP: TMM expression values

UMAP2

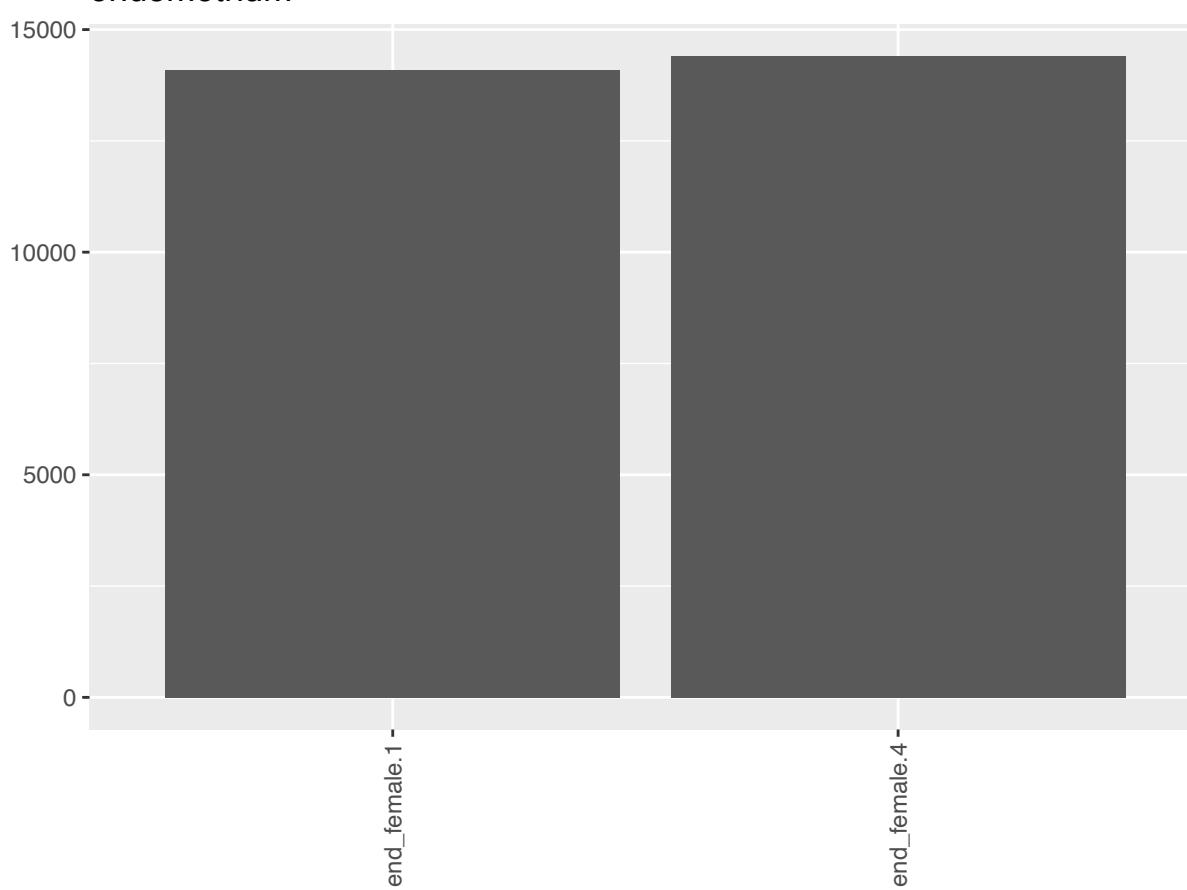
UMAP1

In tissue sample to sample Spearman Distance



endometrium

n(genes) >= 1 TMM

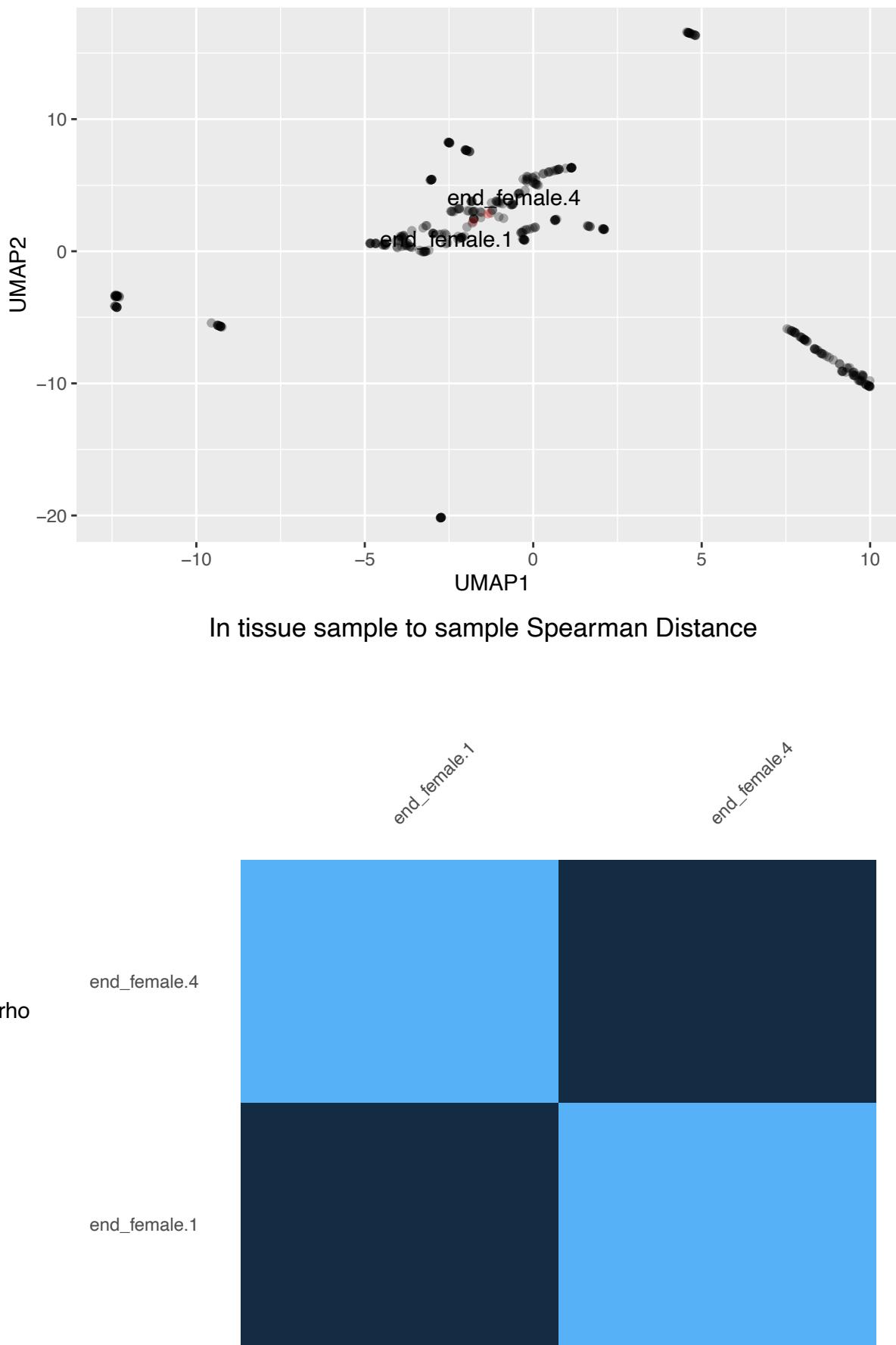


endometrium

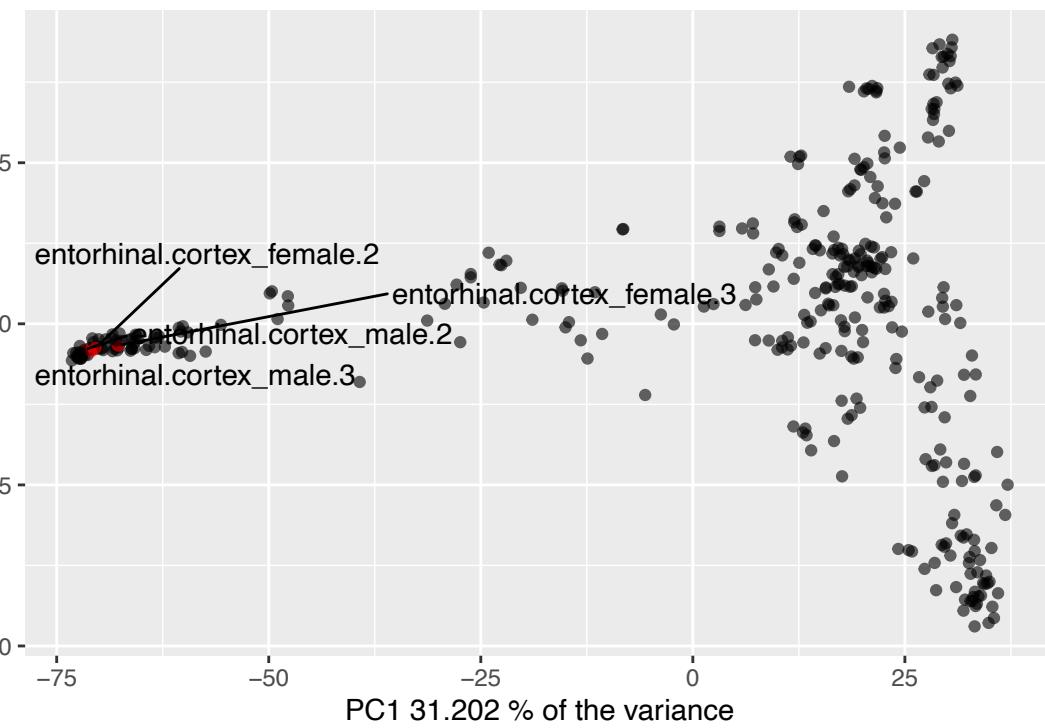
log10(expression+1)

end_female.1
end_female.4

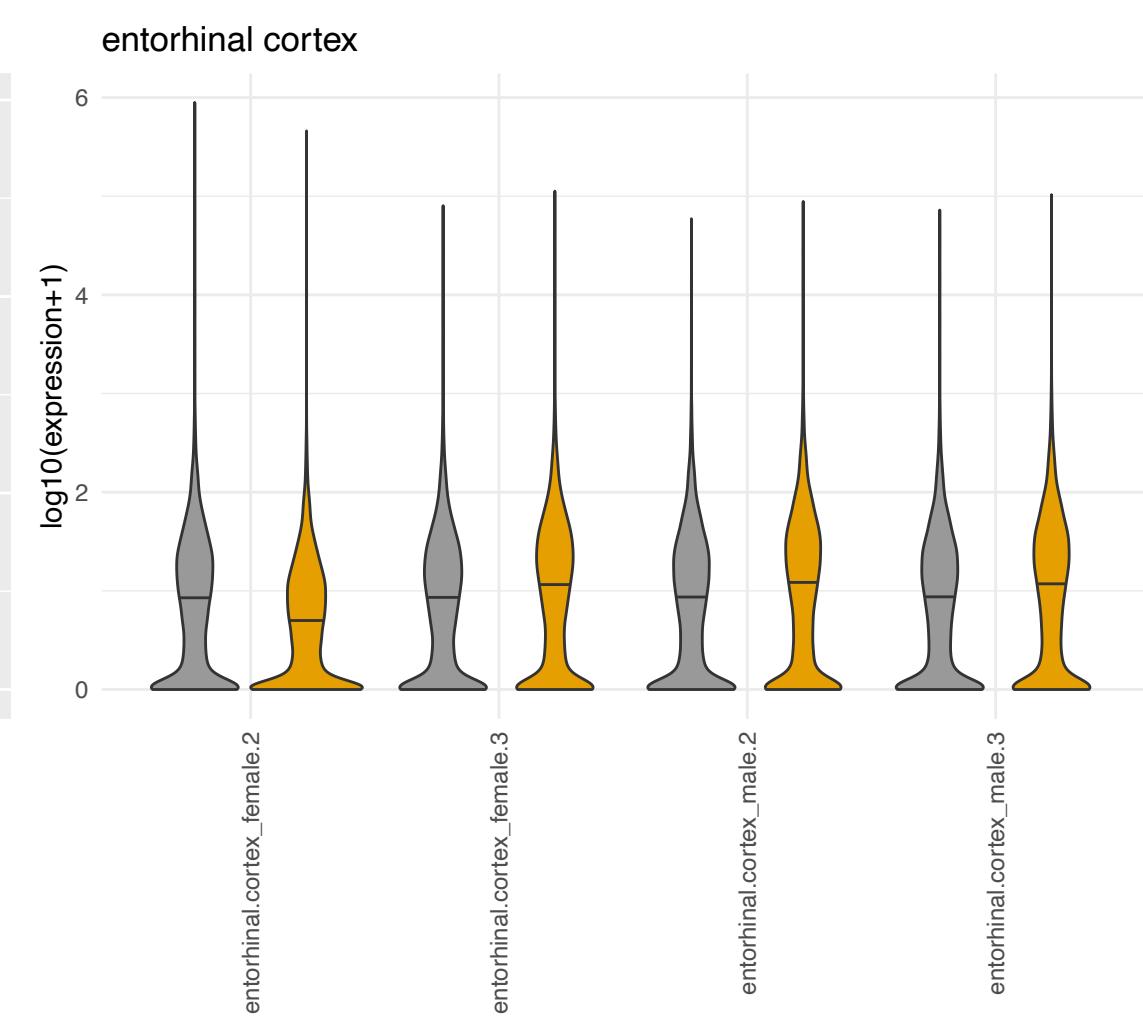
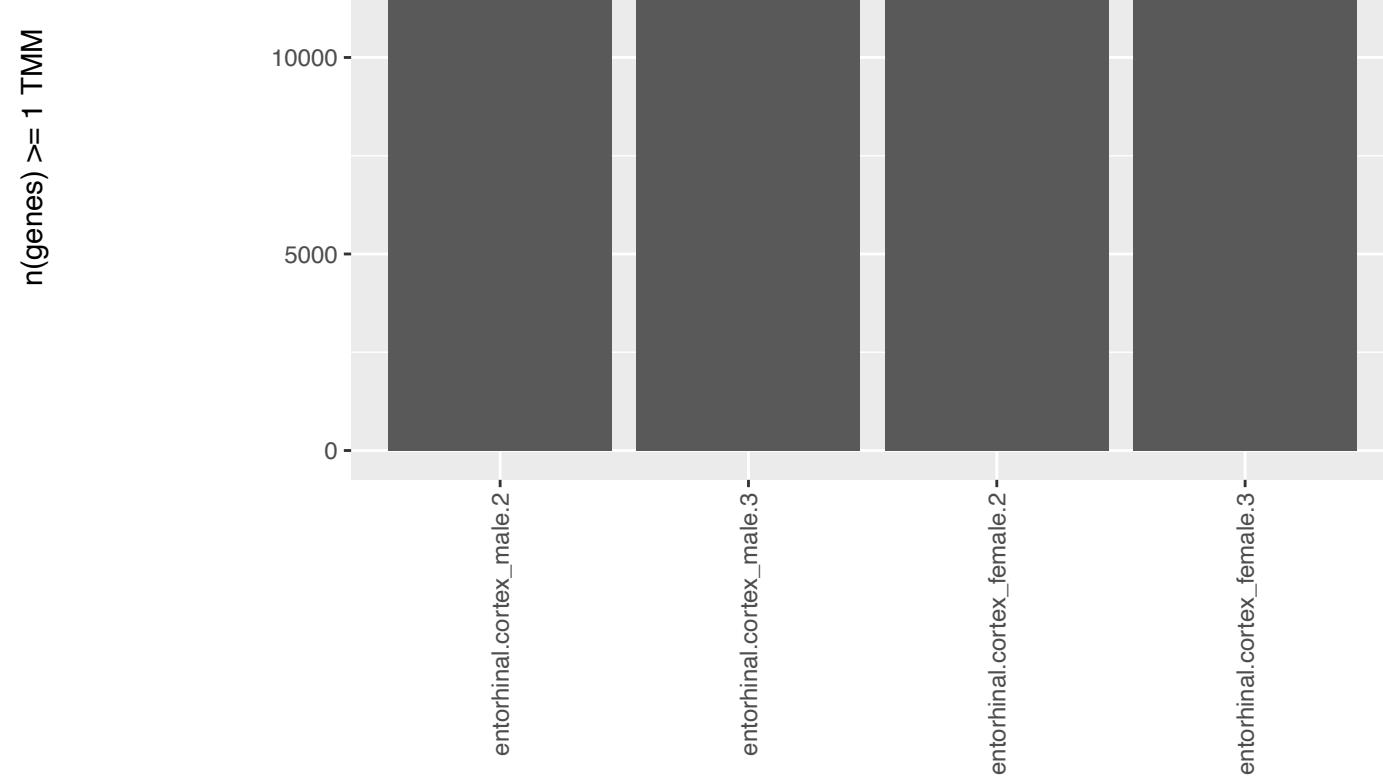
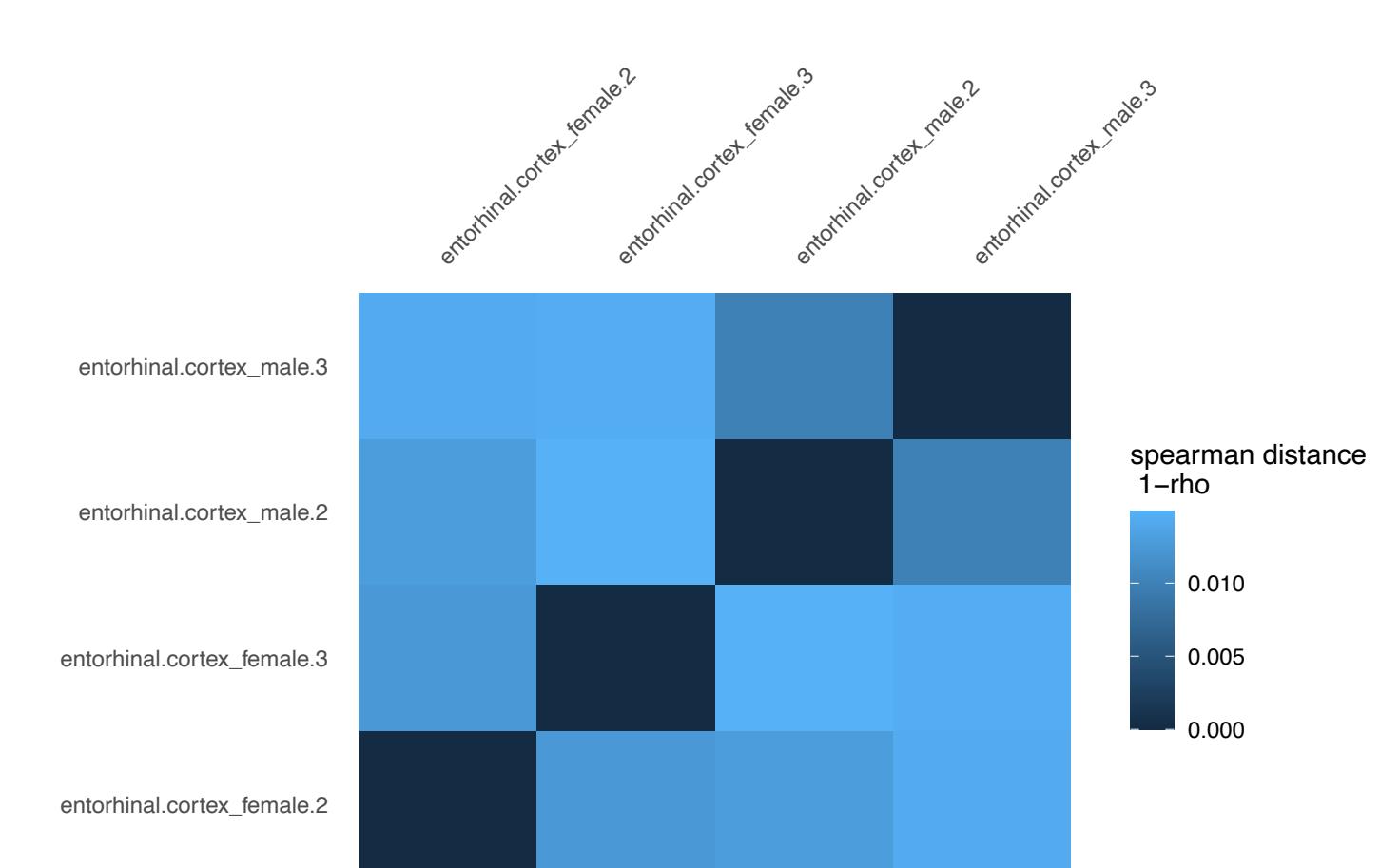
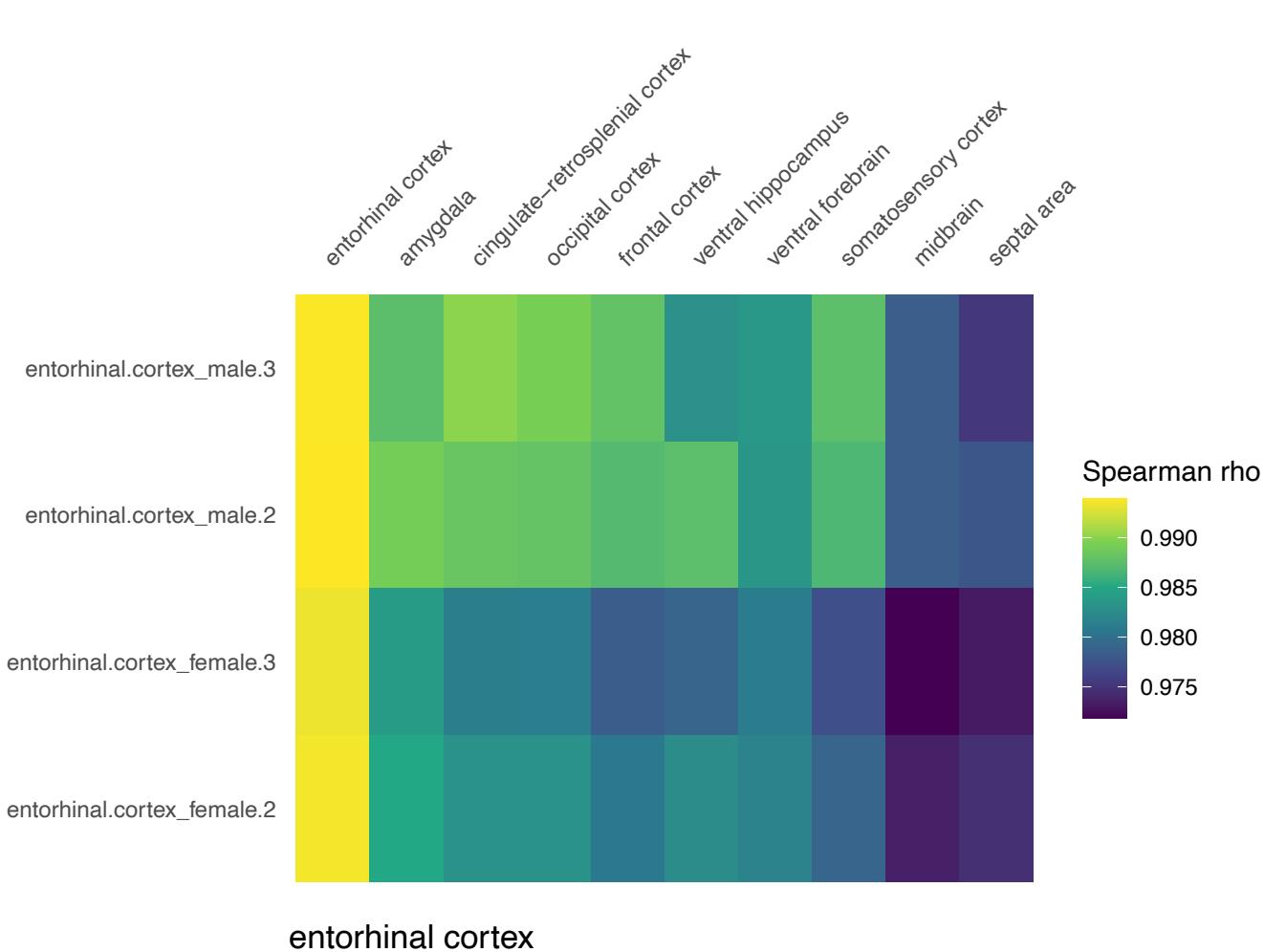
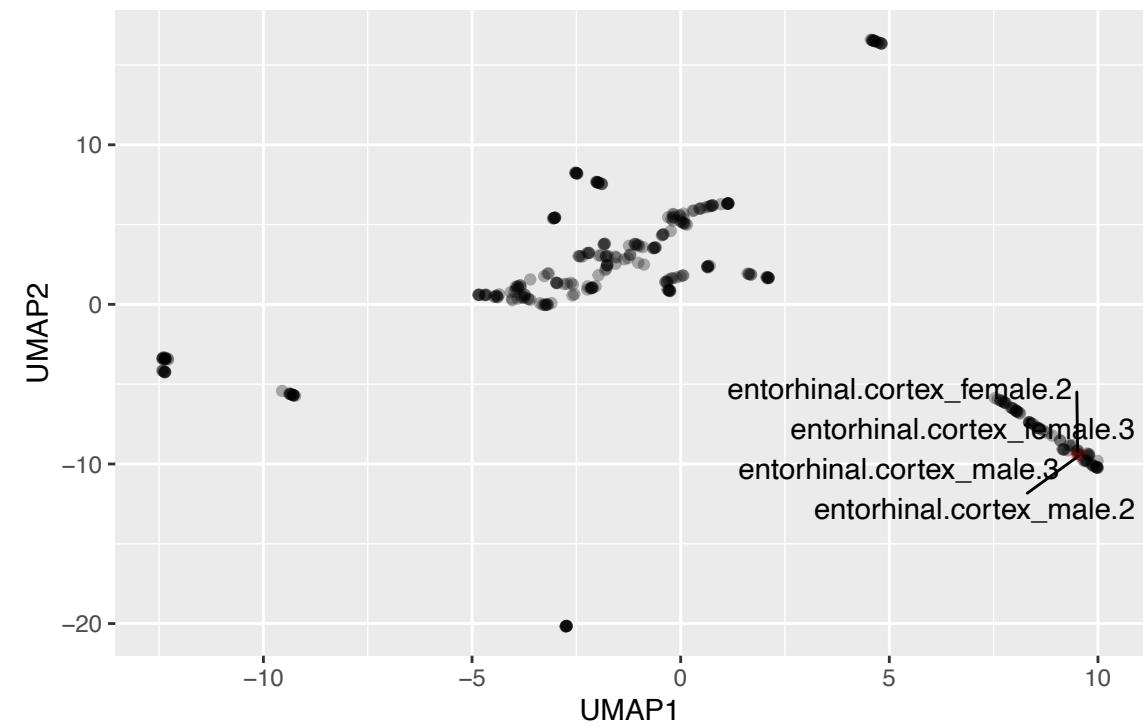
type
tmm_val
tpm_val



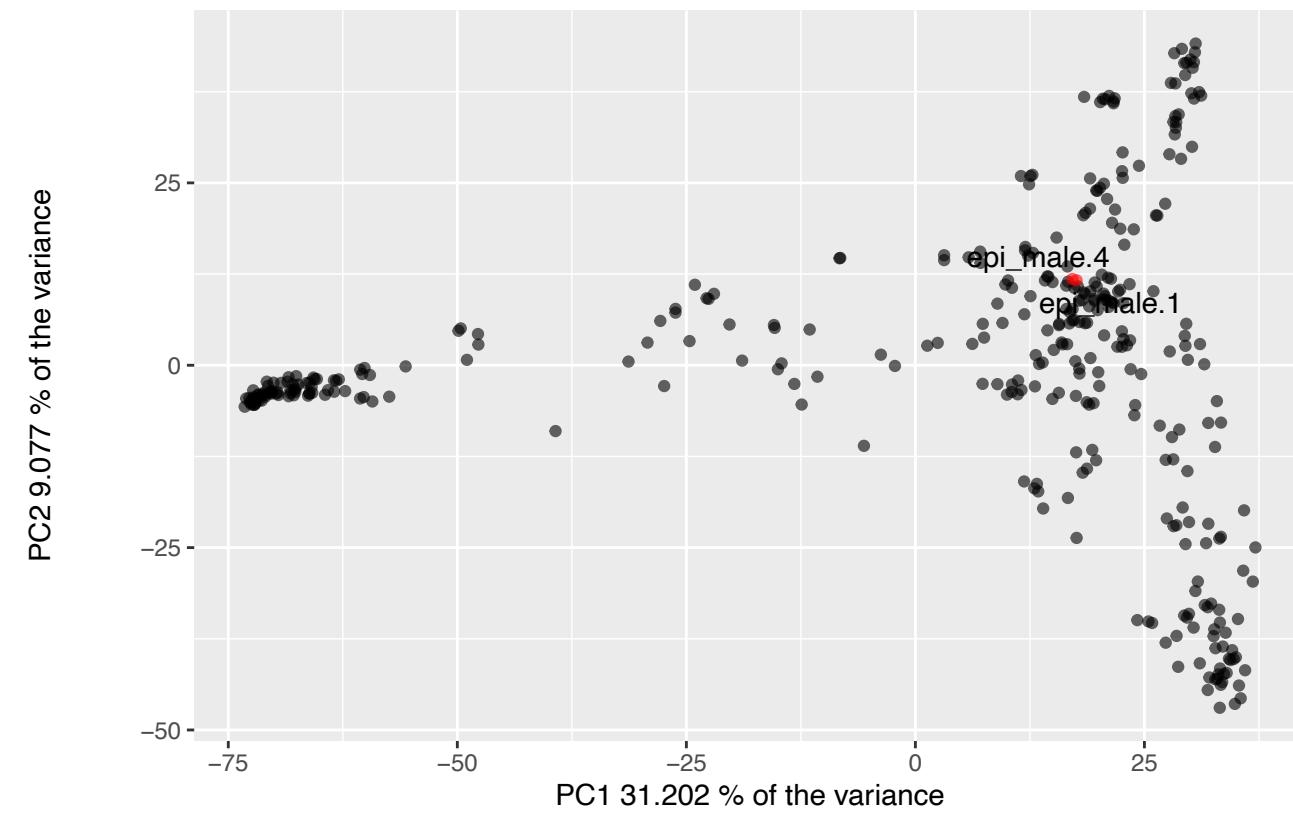
entorhinal cortex, PCA: TMM expression values



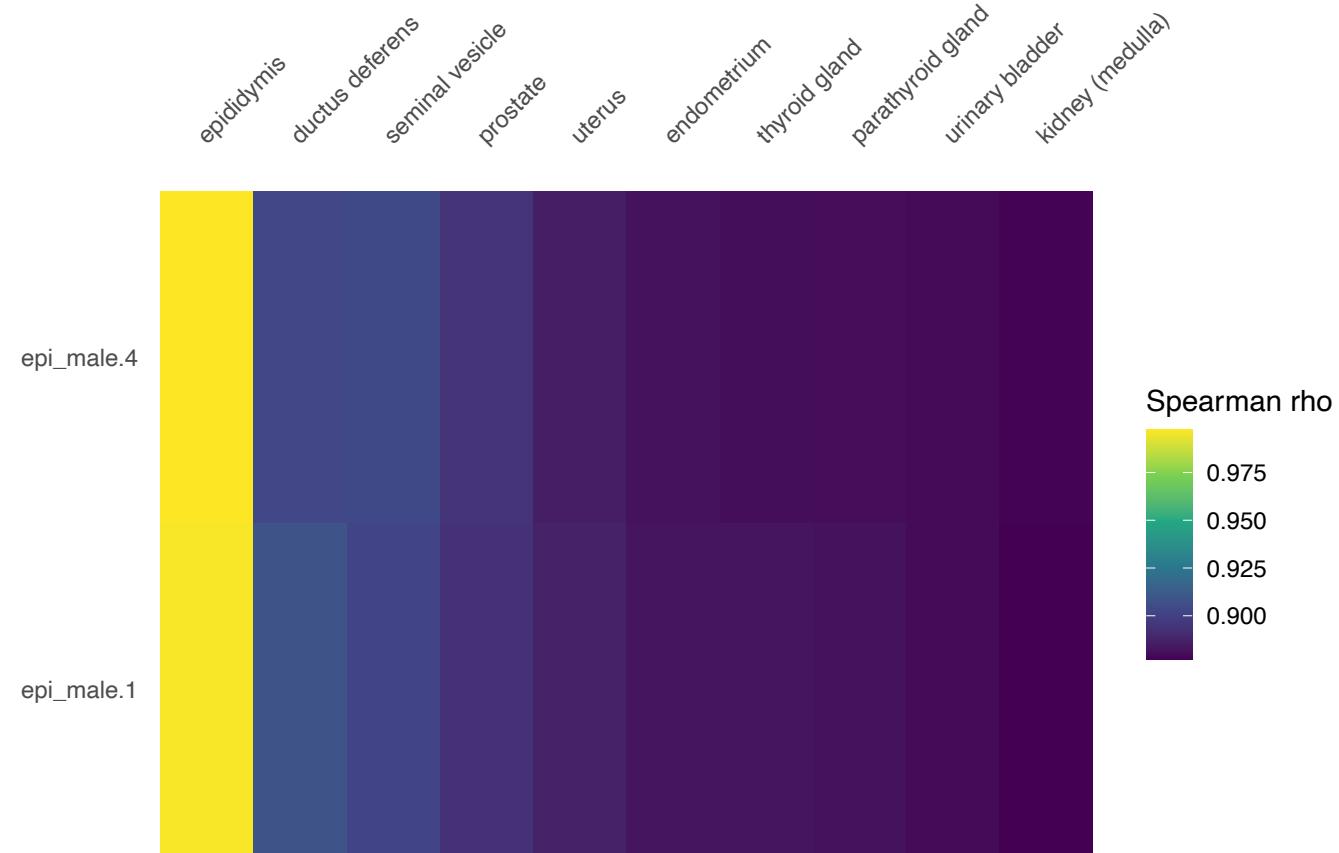
entorhinal cortex, UMAP: TMM expression values



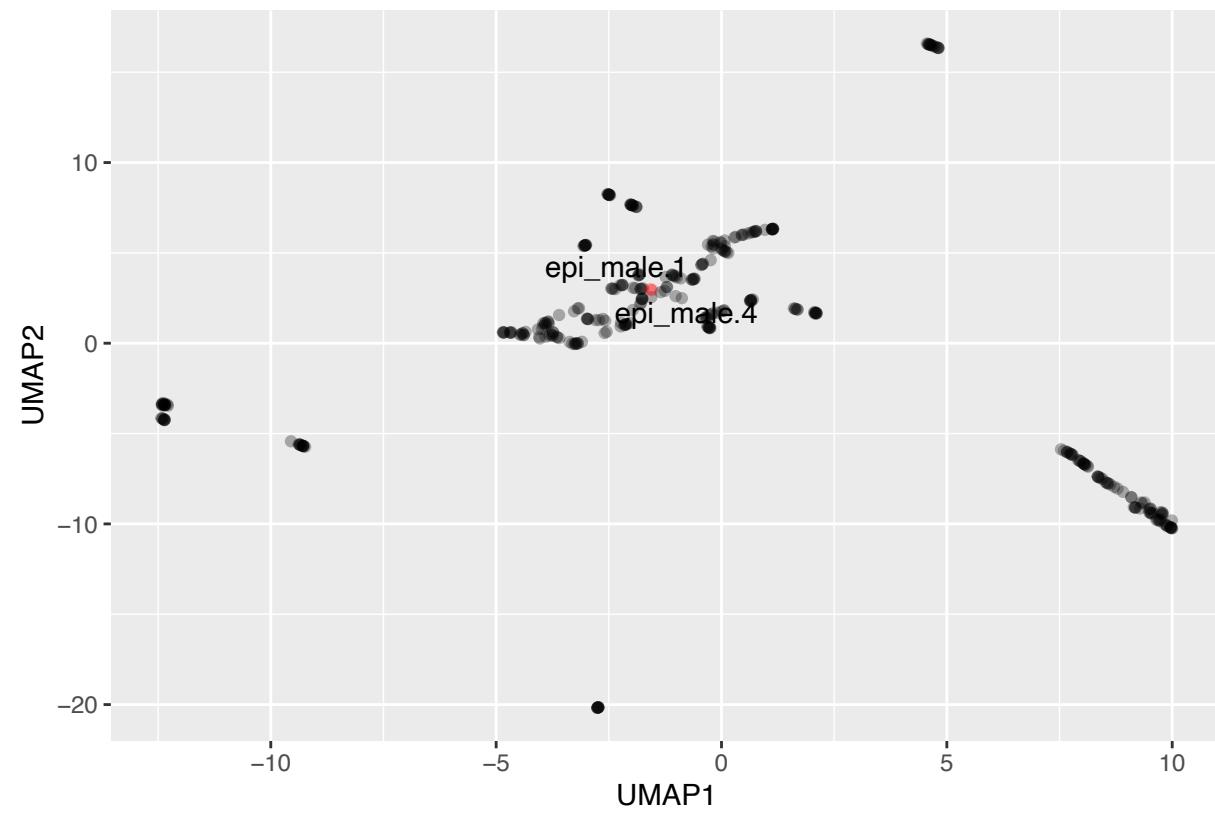
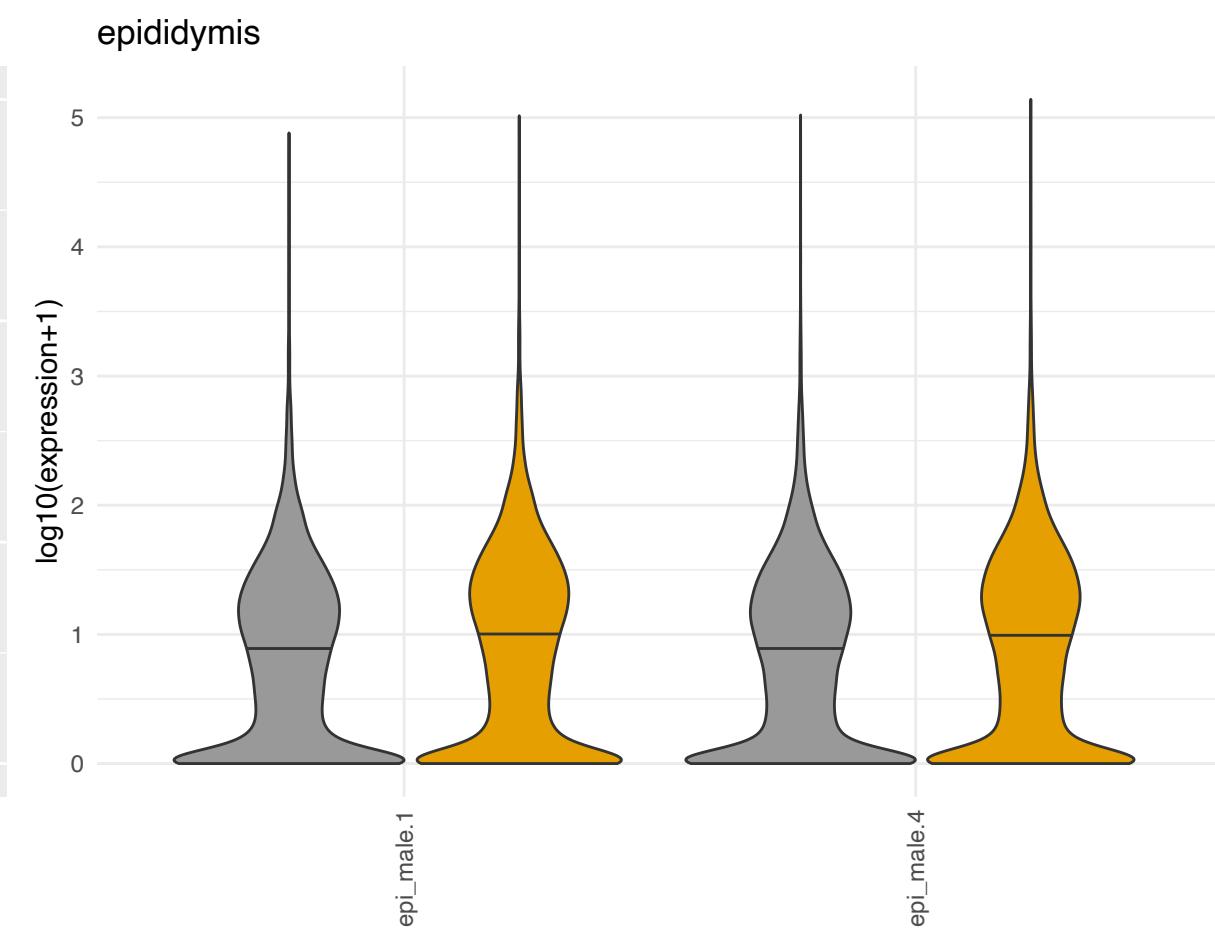
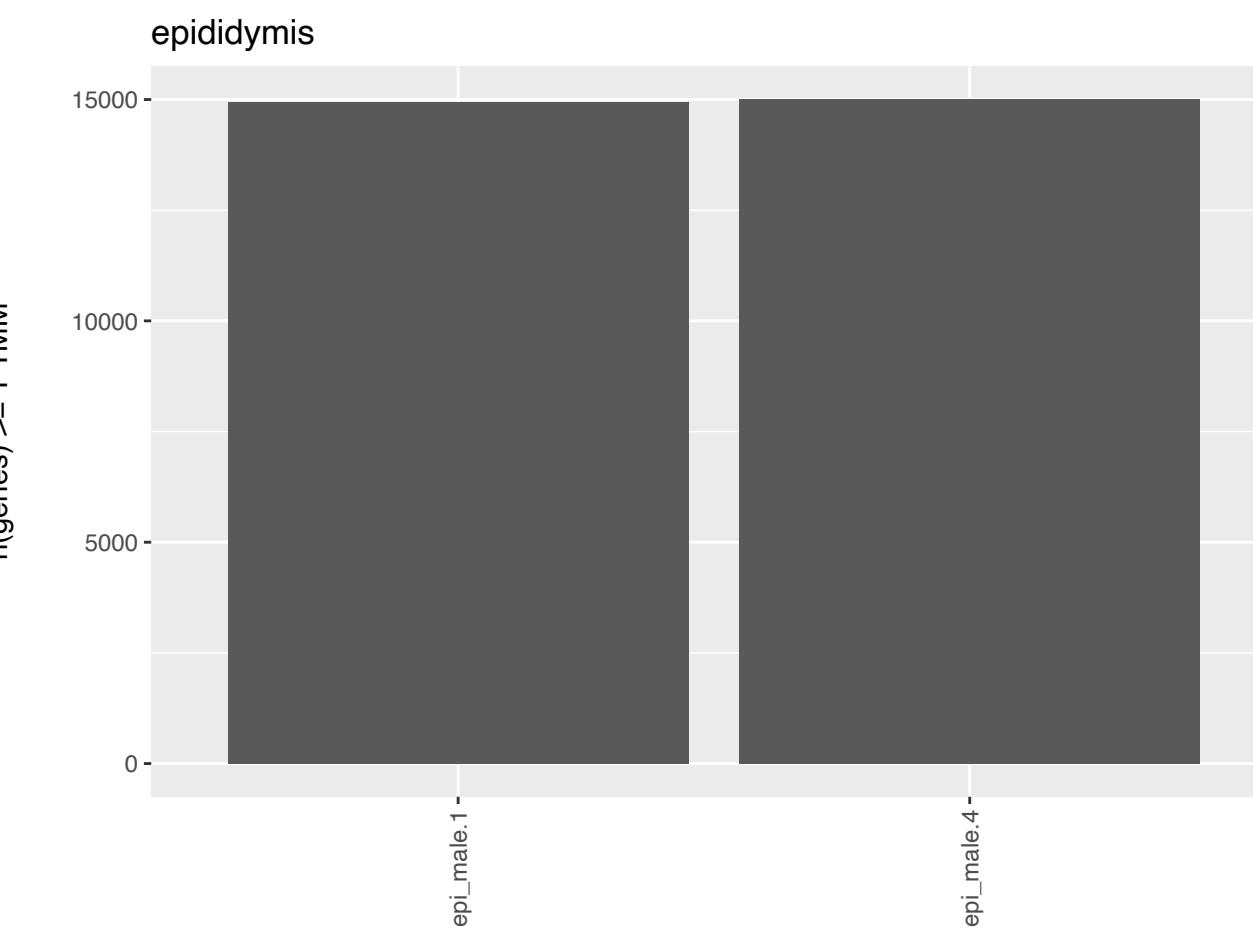
epididymis, PCA: TMM expression values



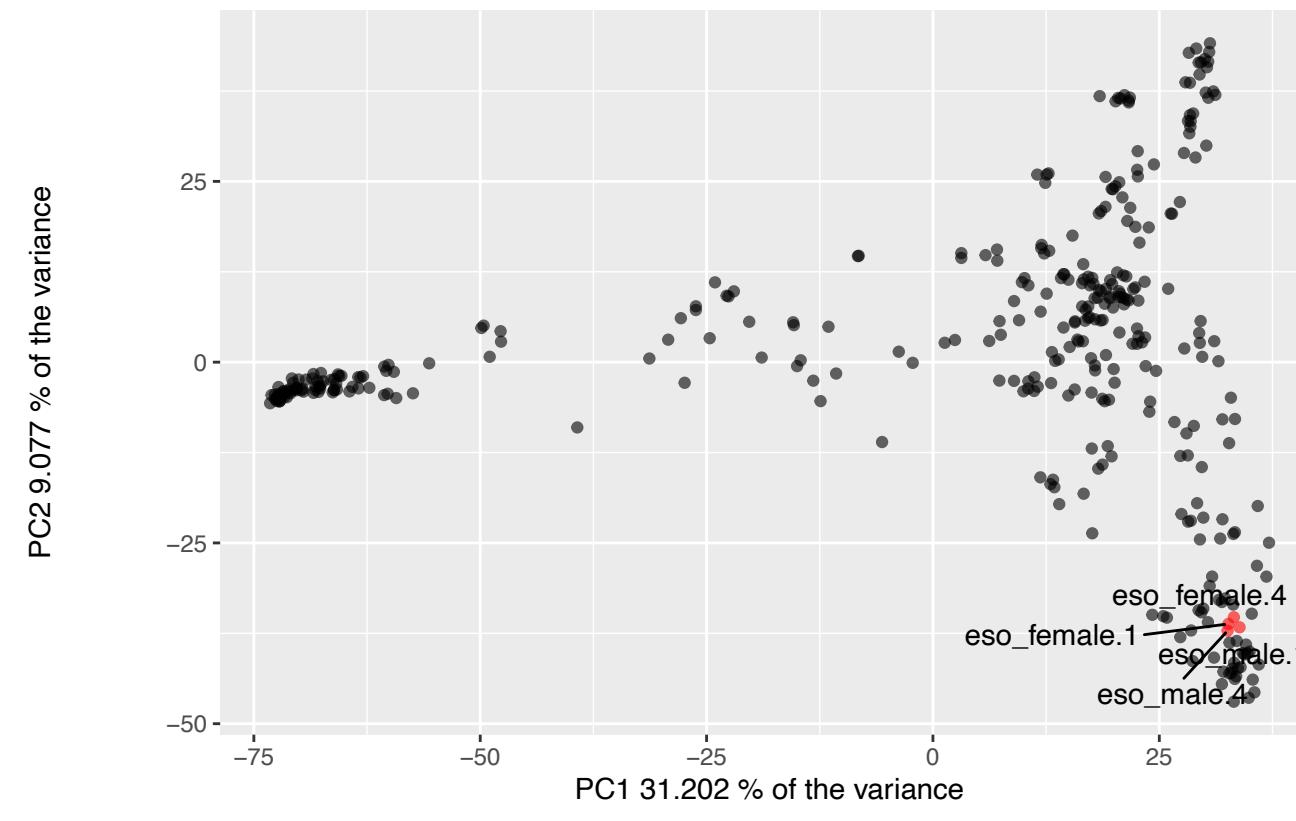
Tissue group to sample correlation



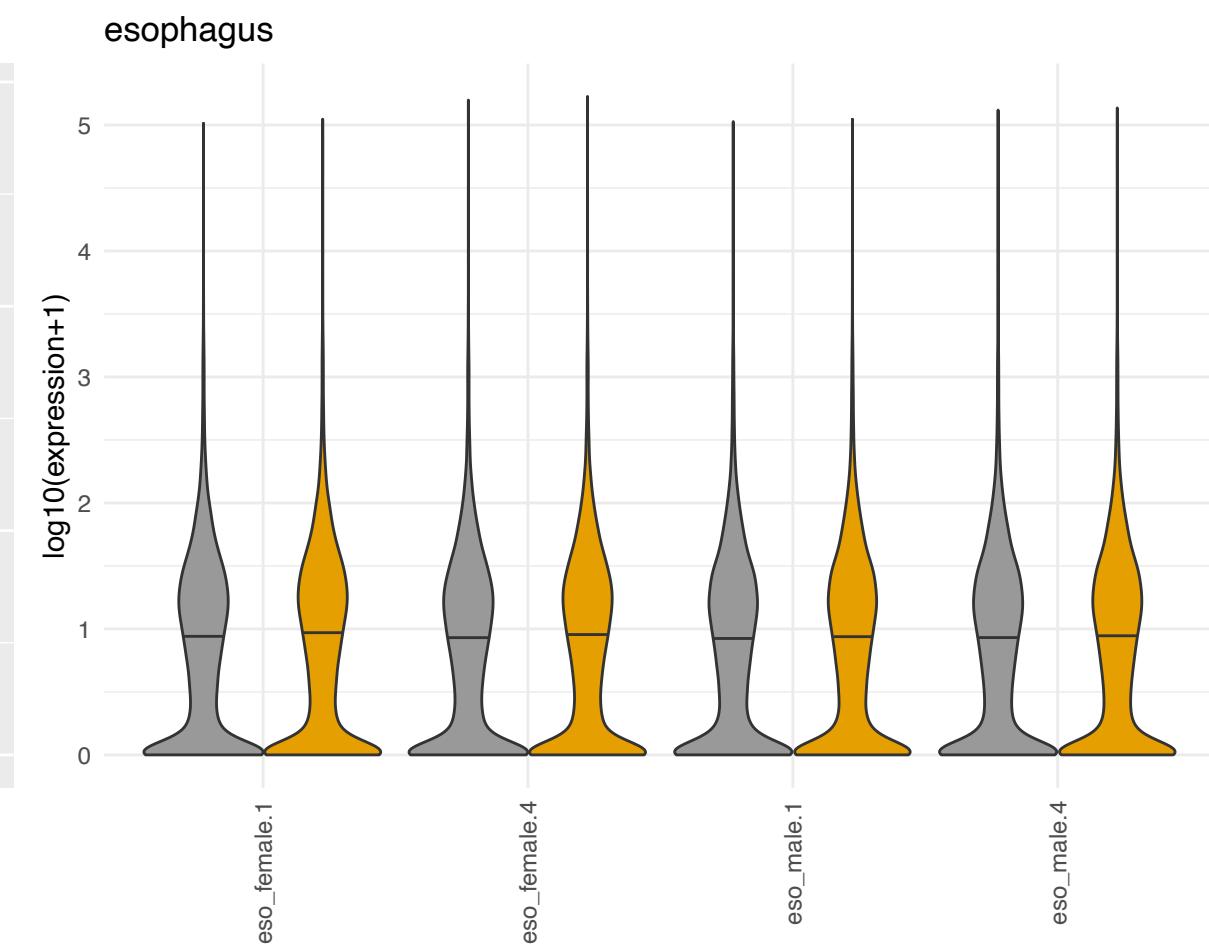
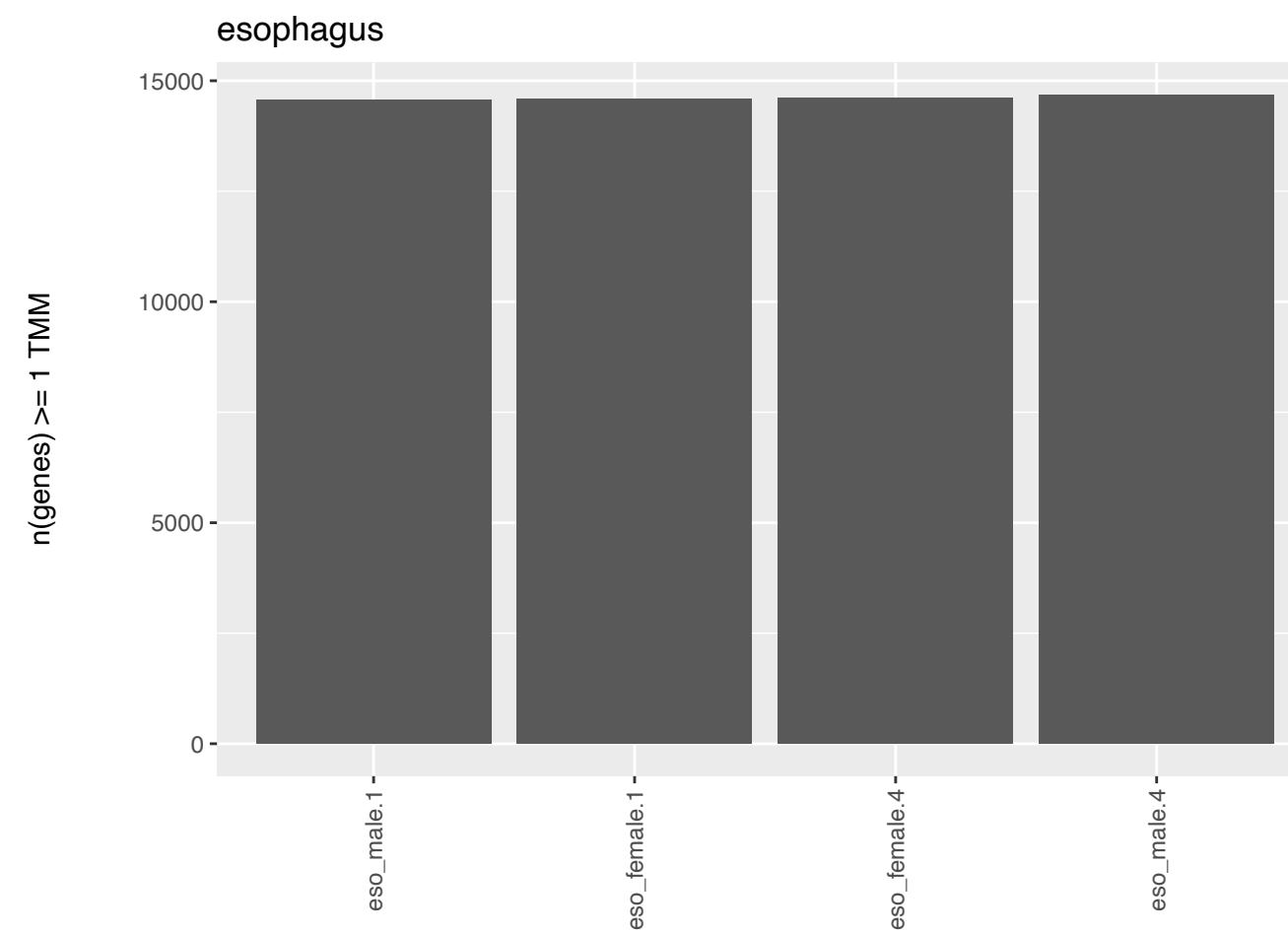
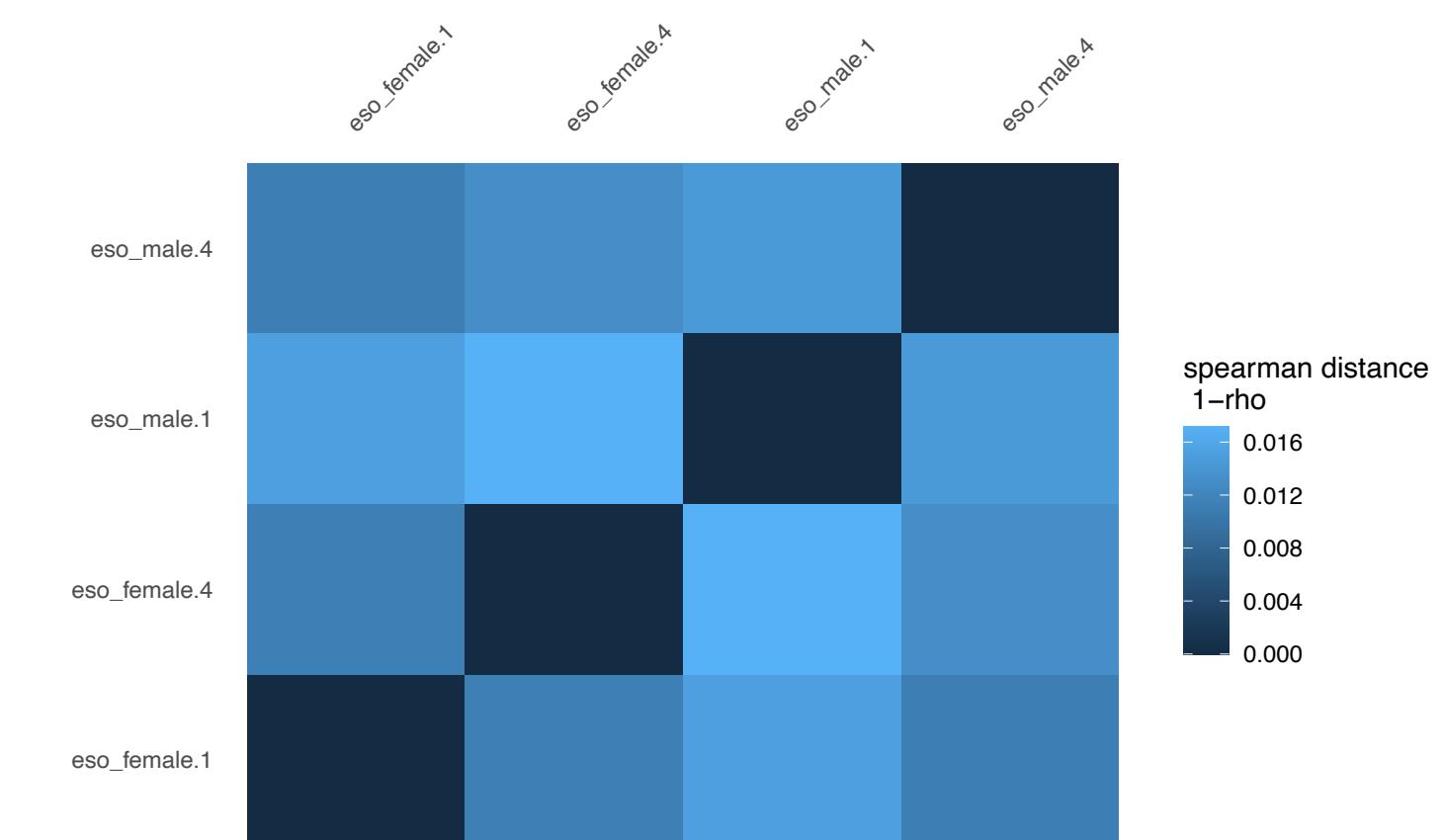
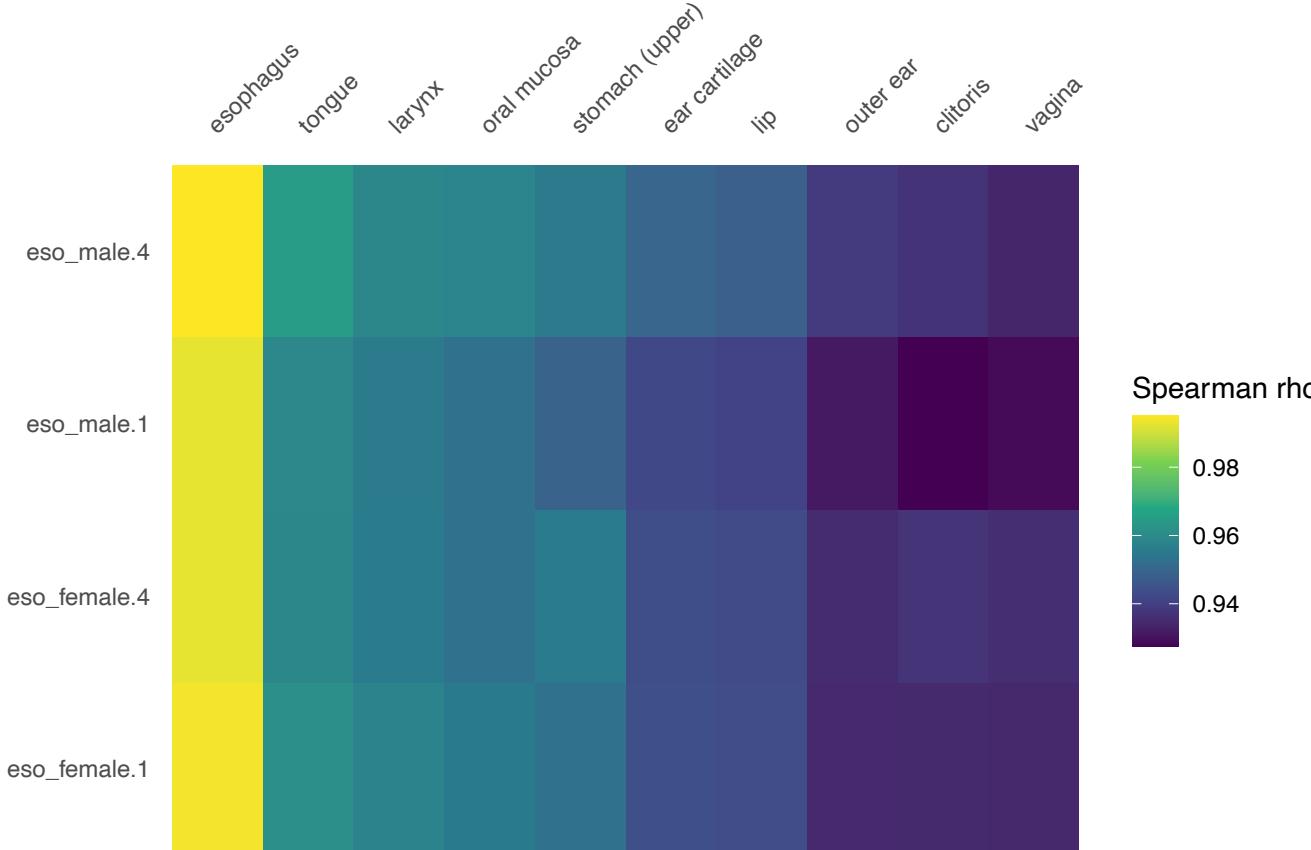
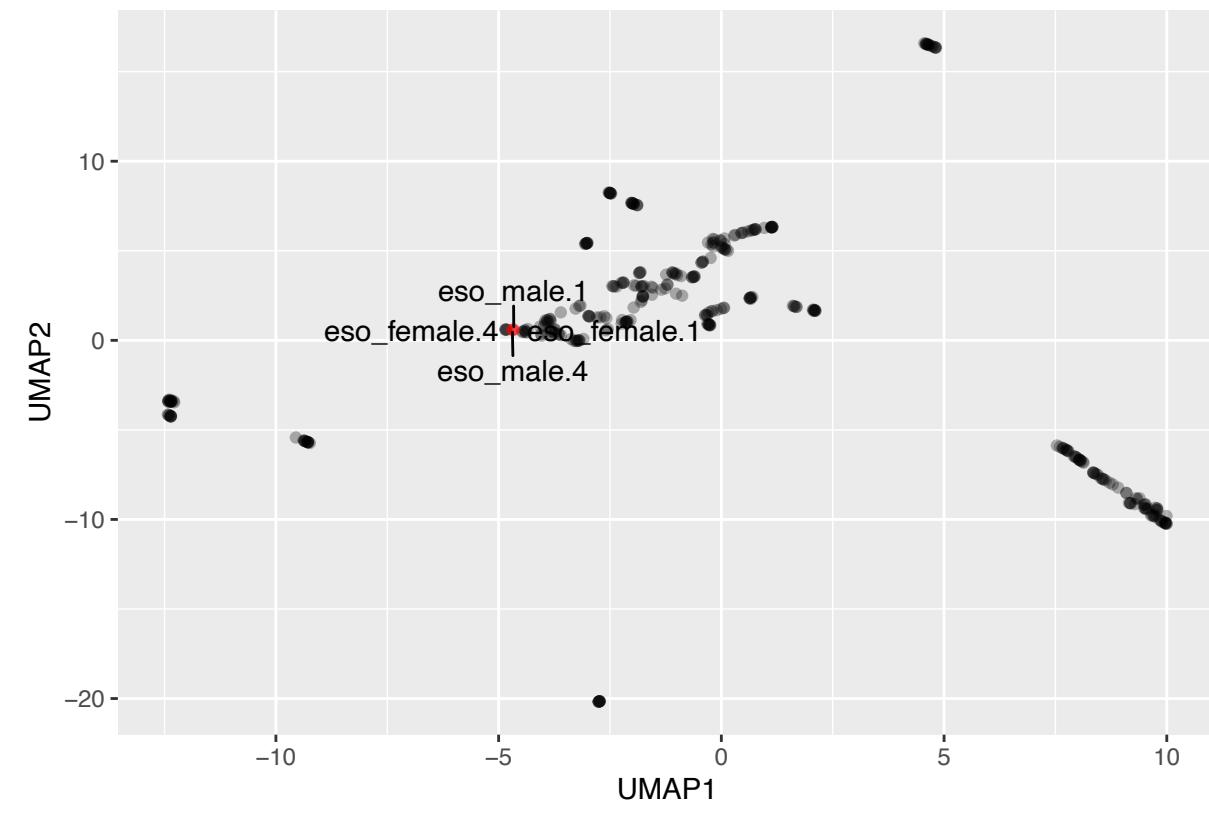
epididymis, UMAP: TMM expression values

epi_male.1
epi_male.4

esophagus, PCA: TMM expression values

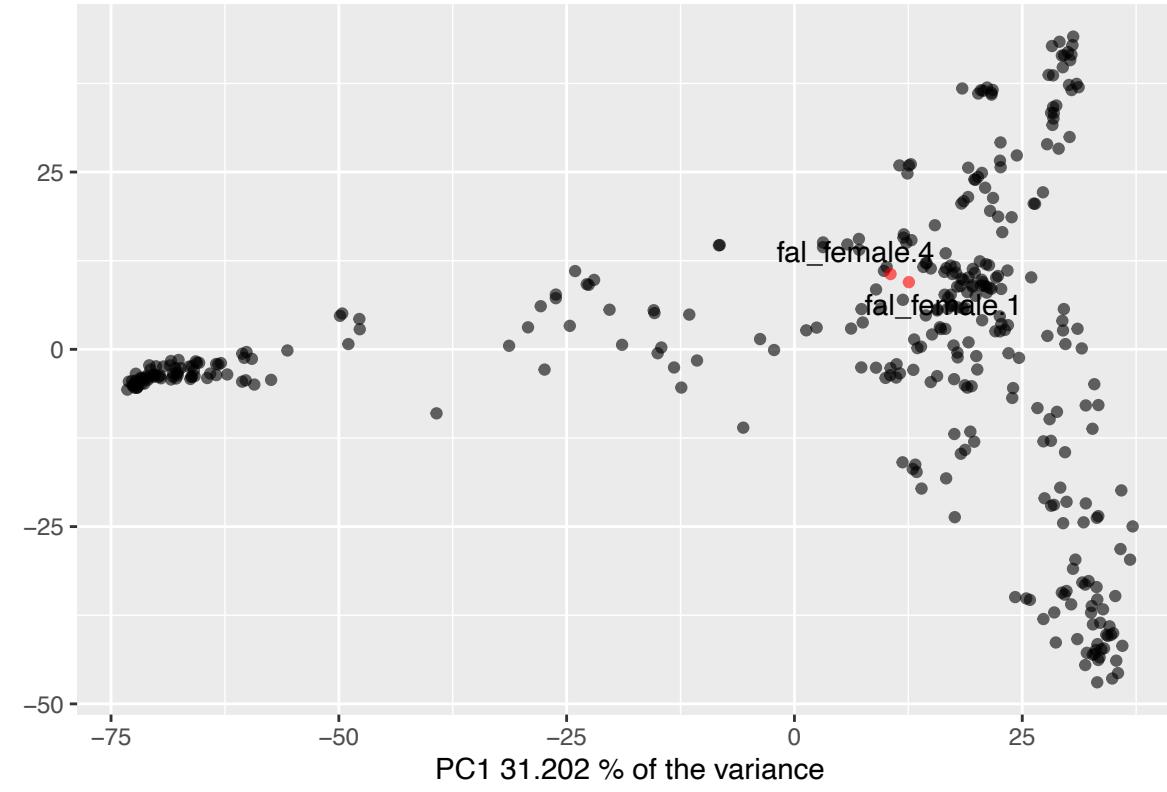


esophagus, UMAP: TMM expression values

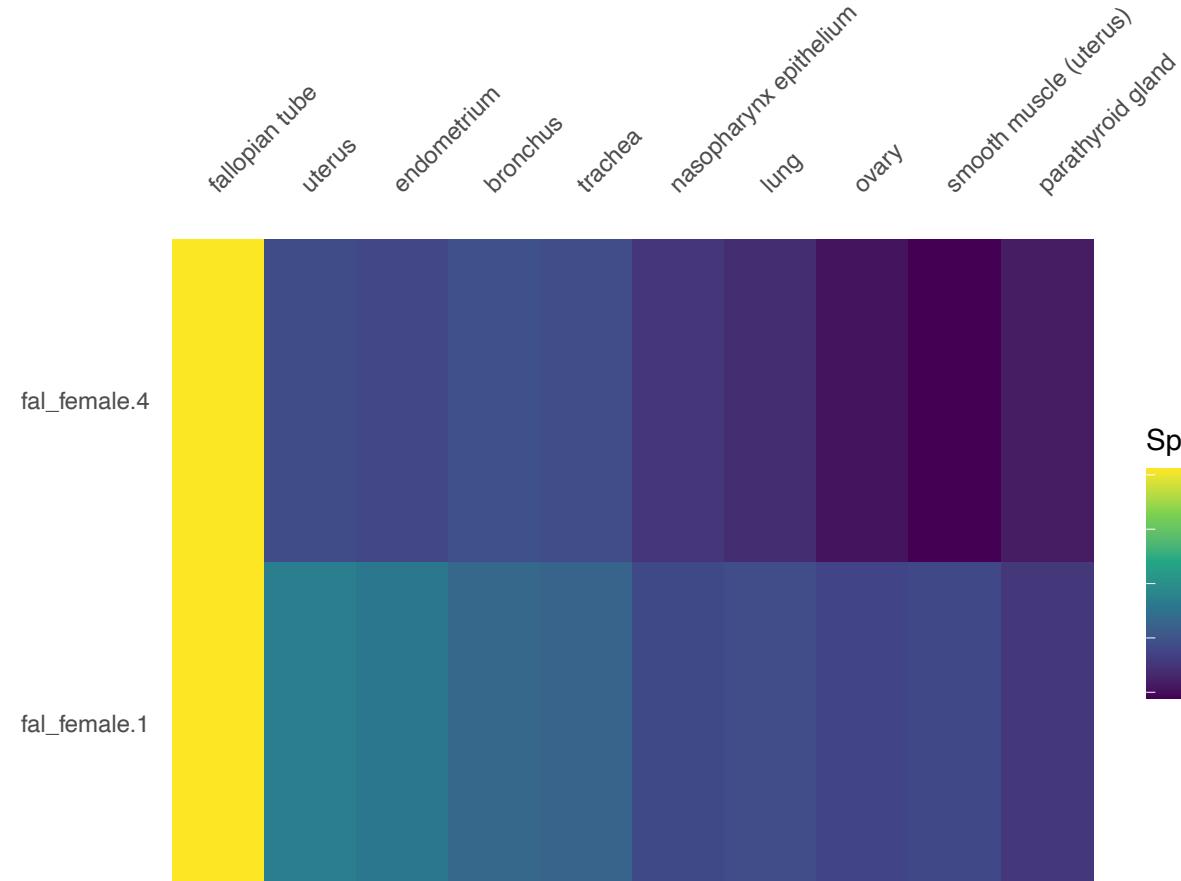


fallopian tube, PCA: TMM expression values

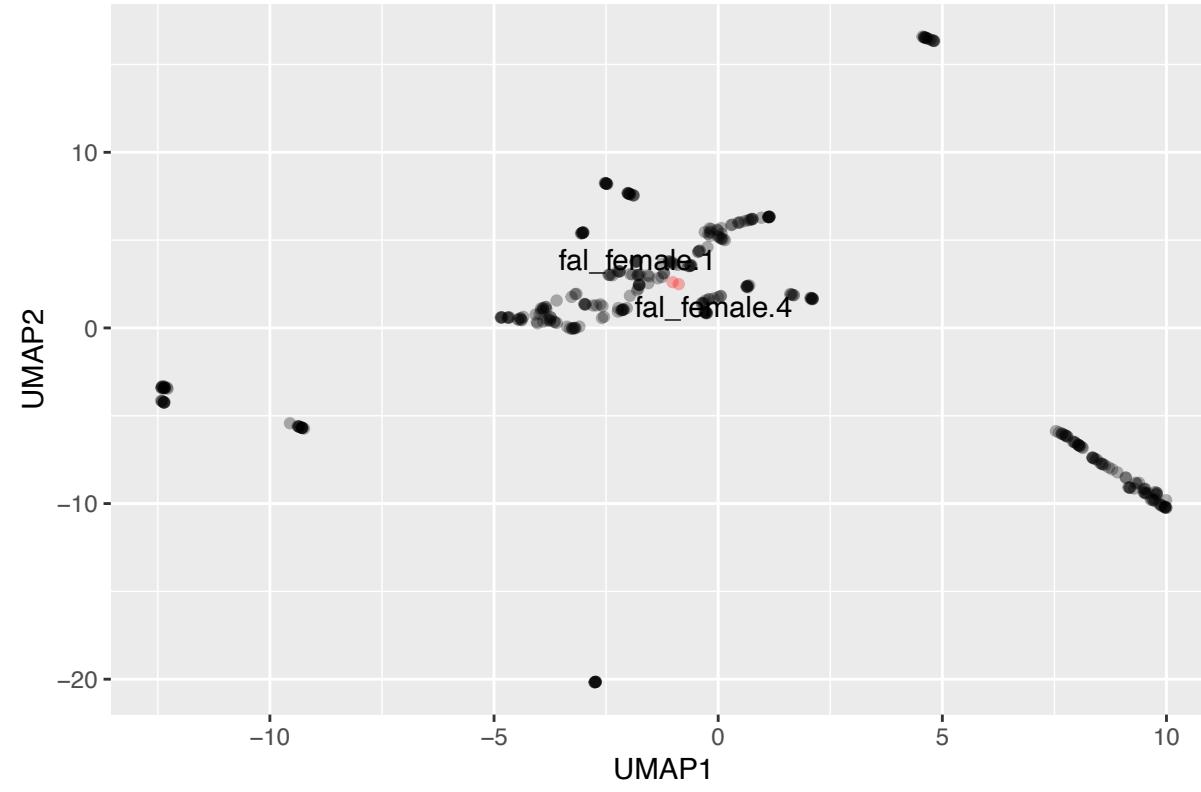
PC2 9.077 % of the variance



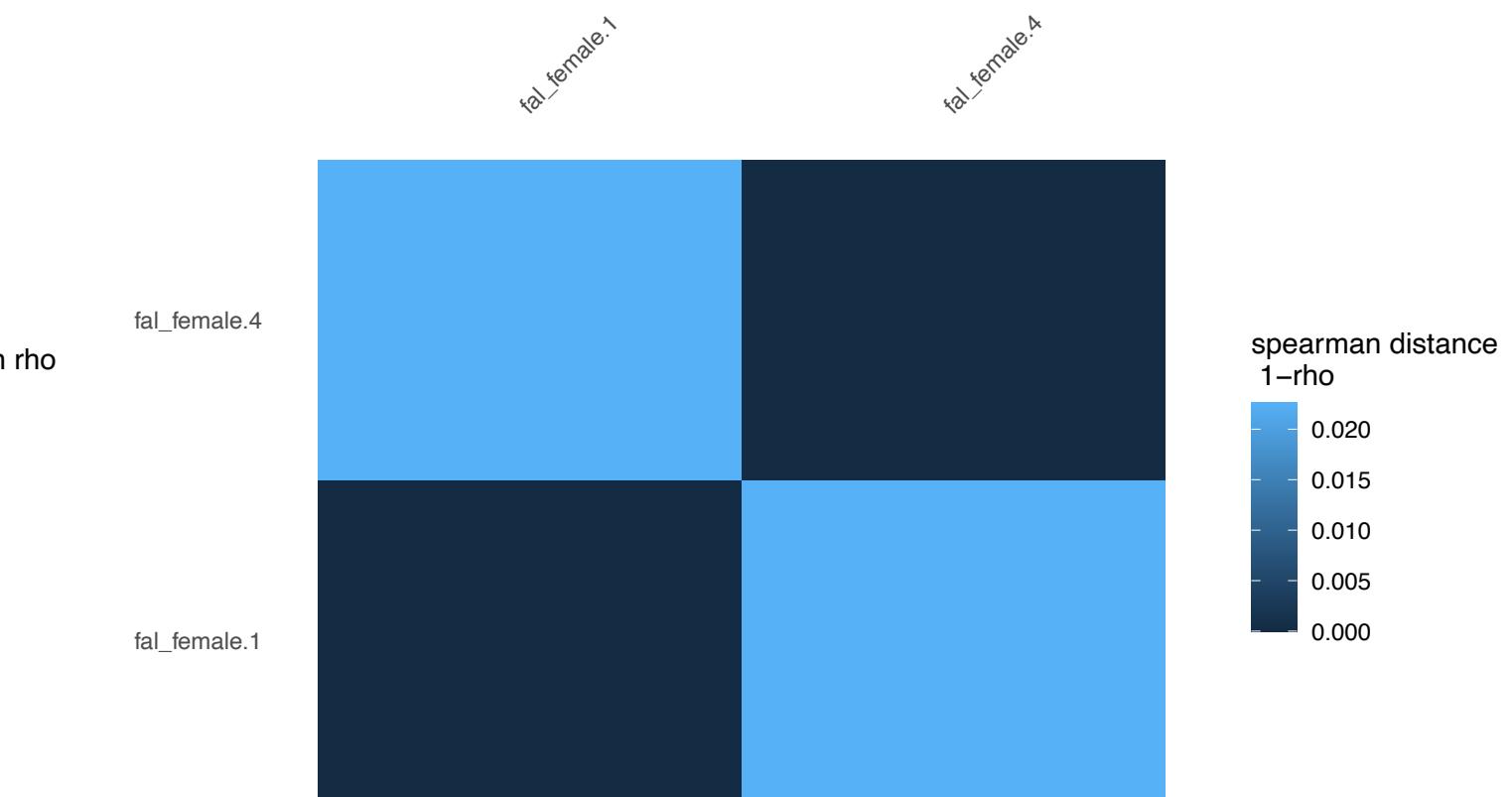
Tissue group to sample correlation



fallopian tube, UMAP: TMM expression values

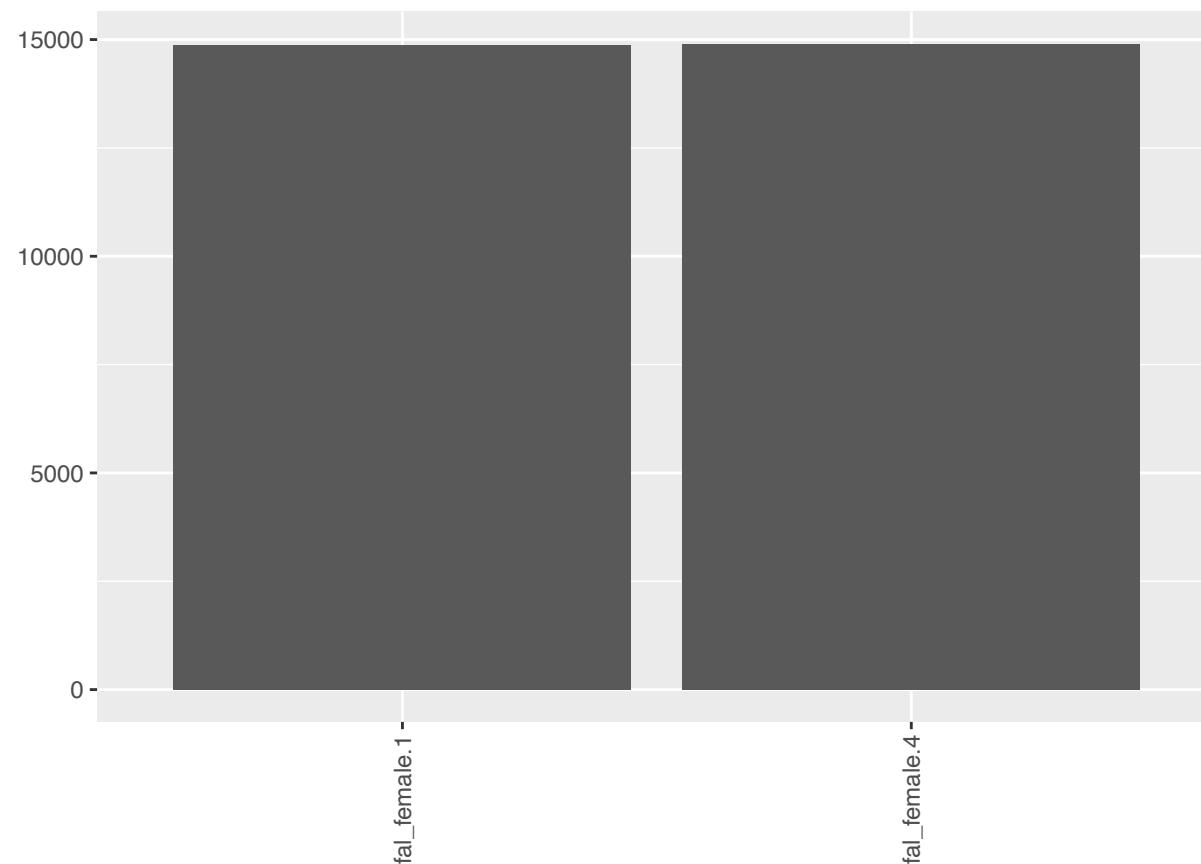


In tissue sample to sample Spearman Distance

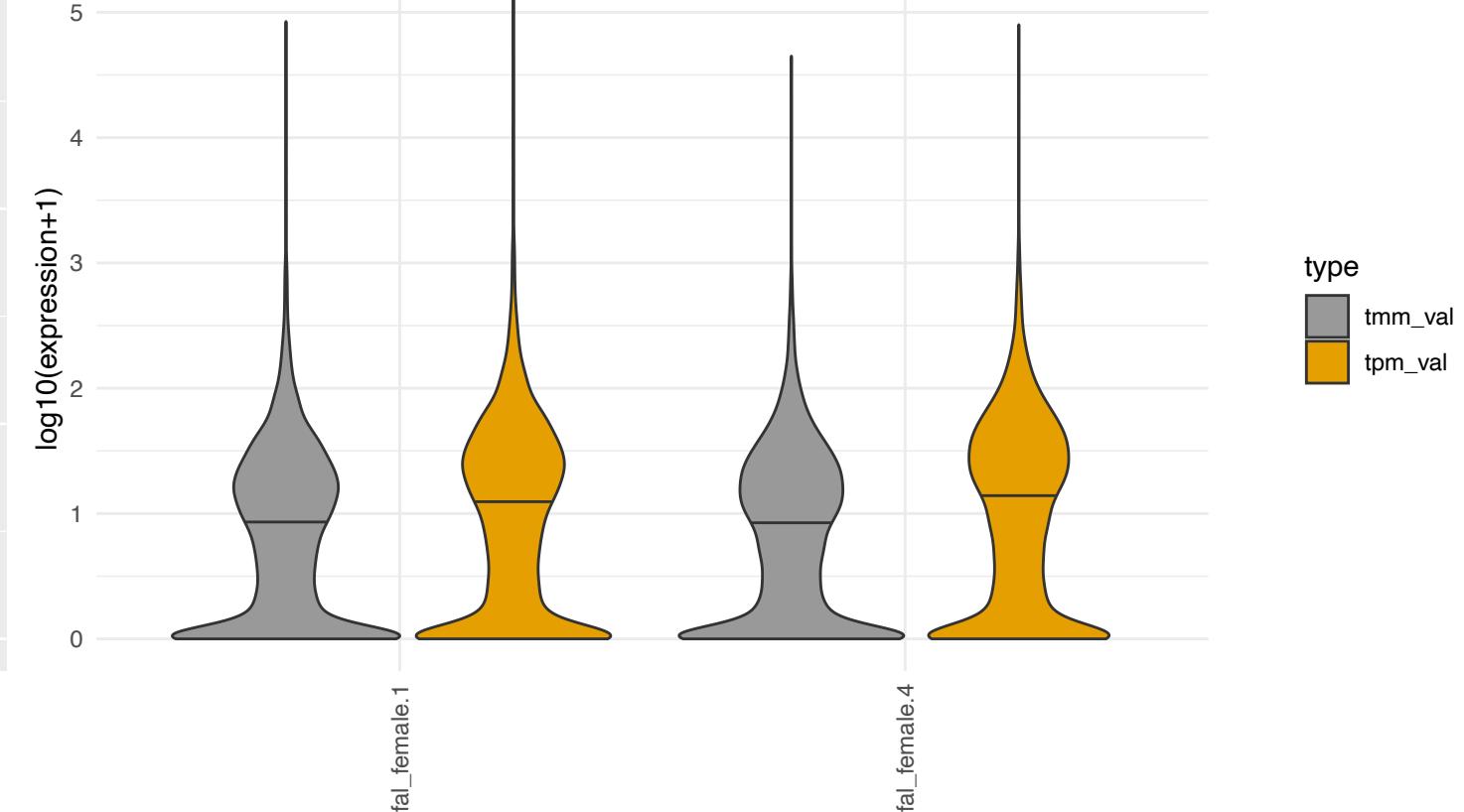


fallopian tube

n(genes) >= 1 TMM

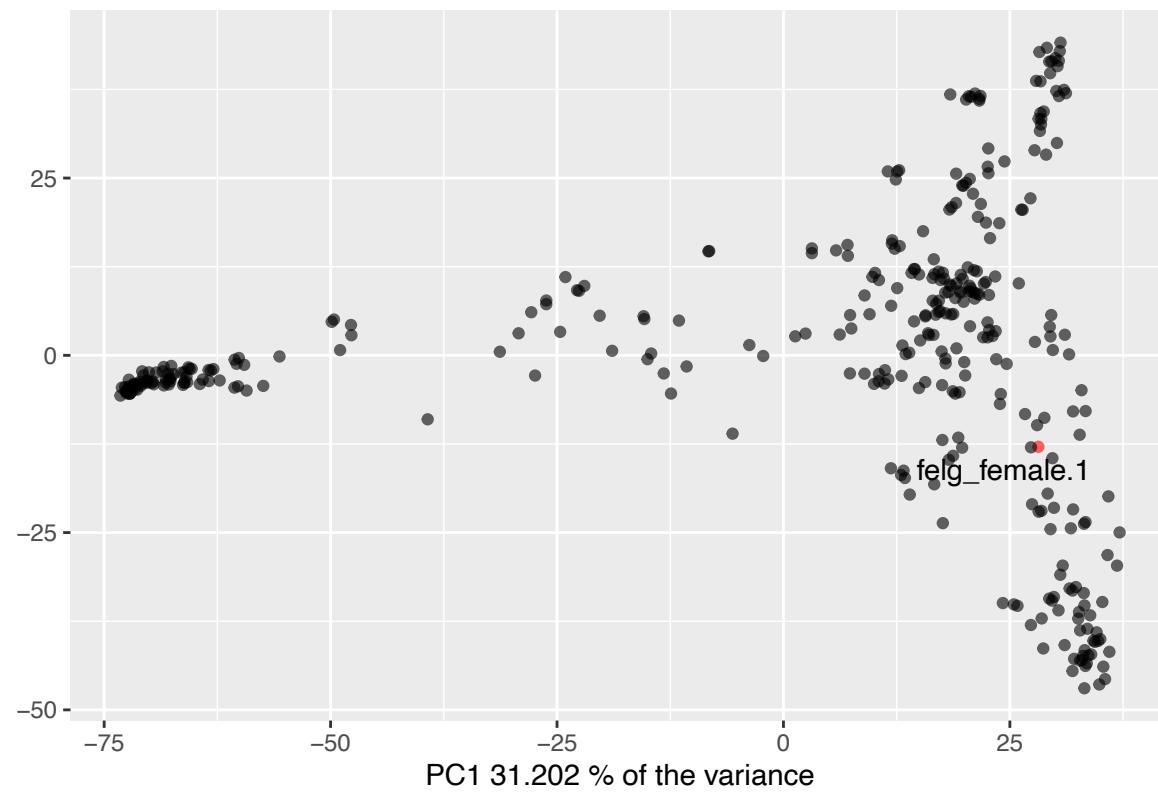


fallopian tube



female preputial gland, PCA: TMM expression values

PC2 9.077 % of the variance



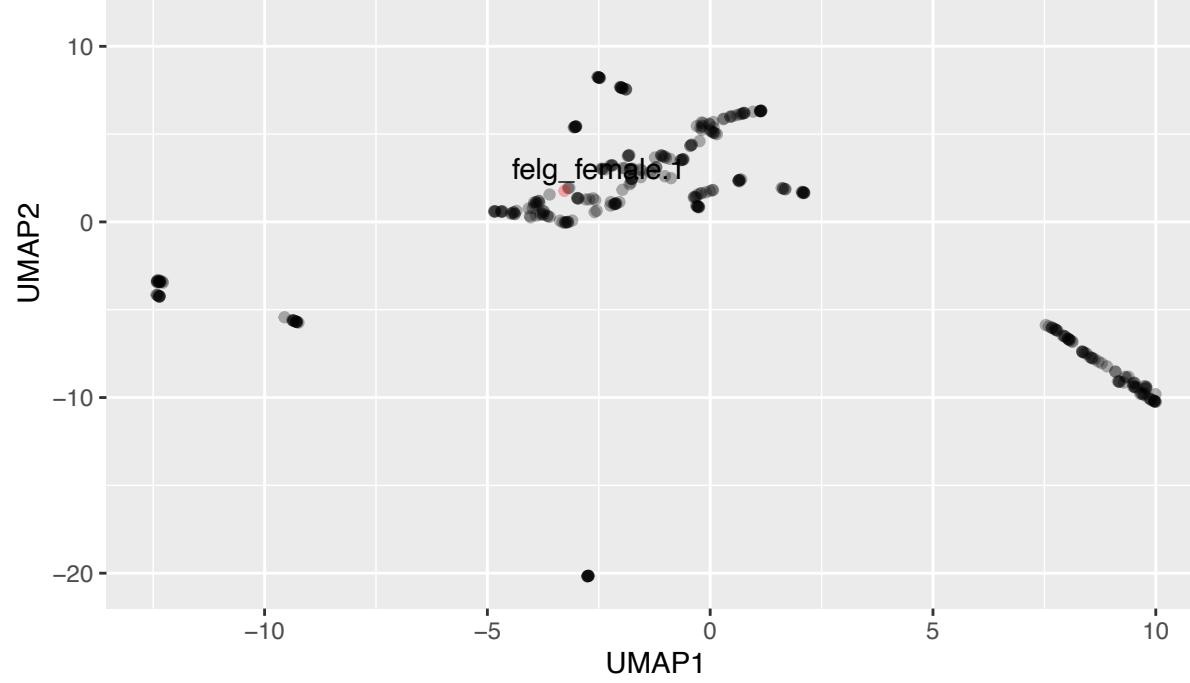
Tissue group to sample correlation

female preputial gland
male preputial gland
clitoris
breast
stomach (upper)
outer ear
vagina
cervix
esophagus
pleura

feli_female.1



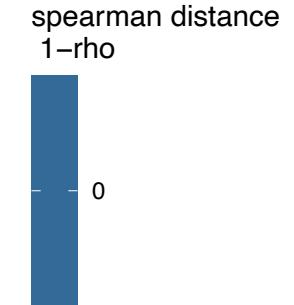
female preputial gland, UMAP: TMM expression values



In tissue sample to sample Spearman Distance

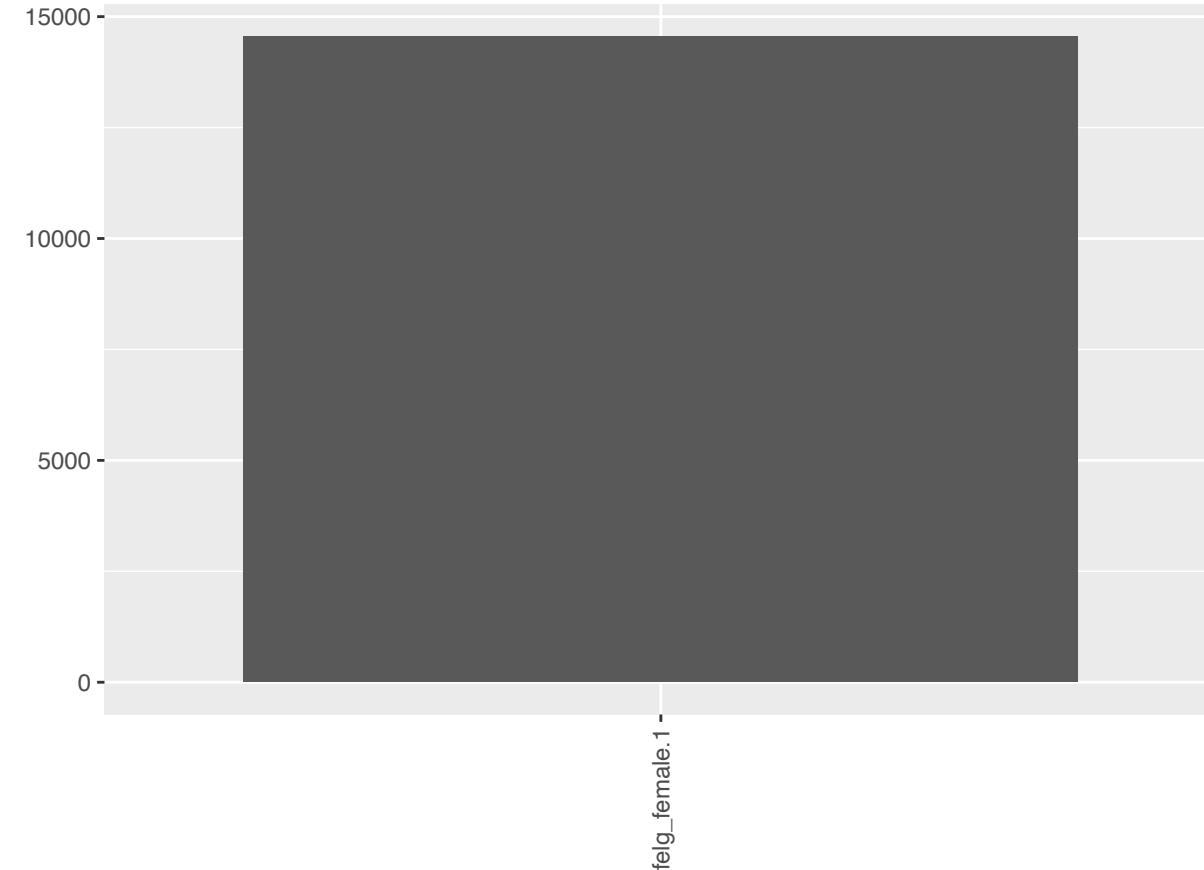
feli_female.1

feli_female.1



female preputial gland

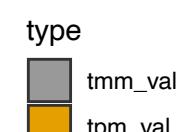
n(genes) >= 1 TMM



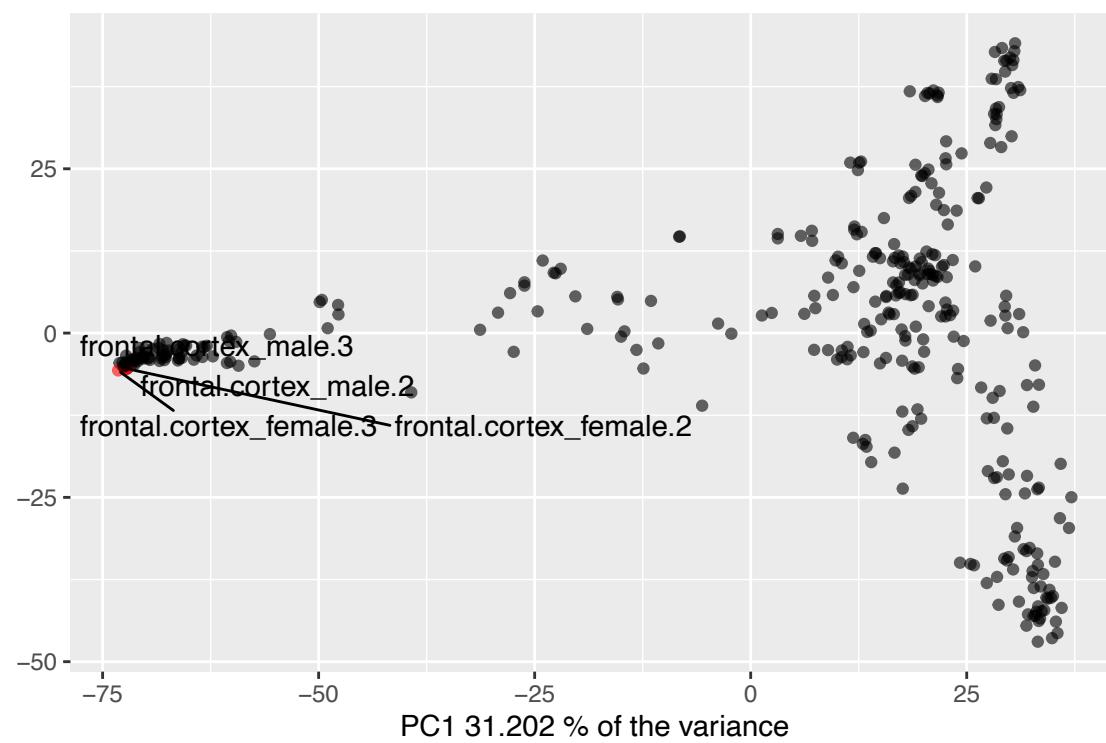
female preputial gland

log10(expression+1)

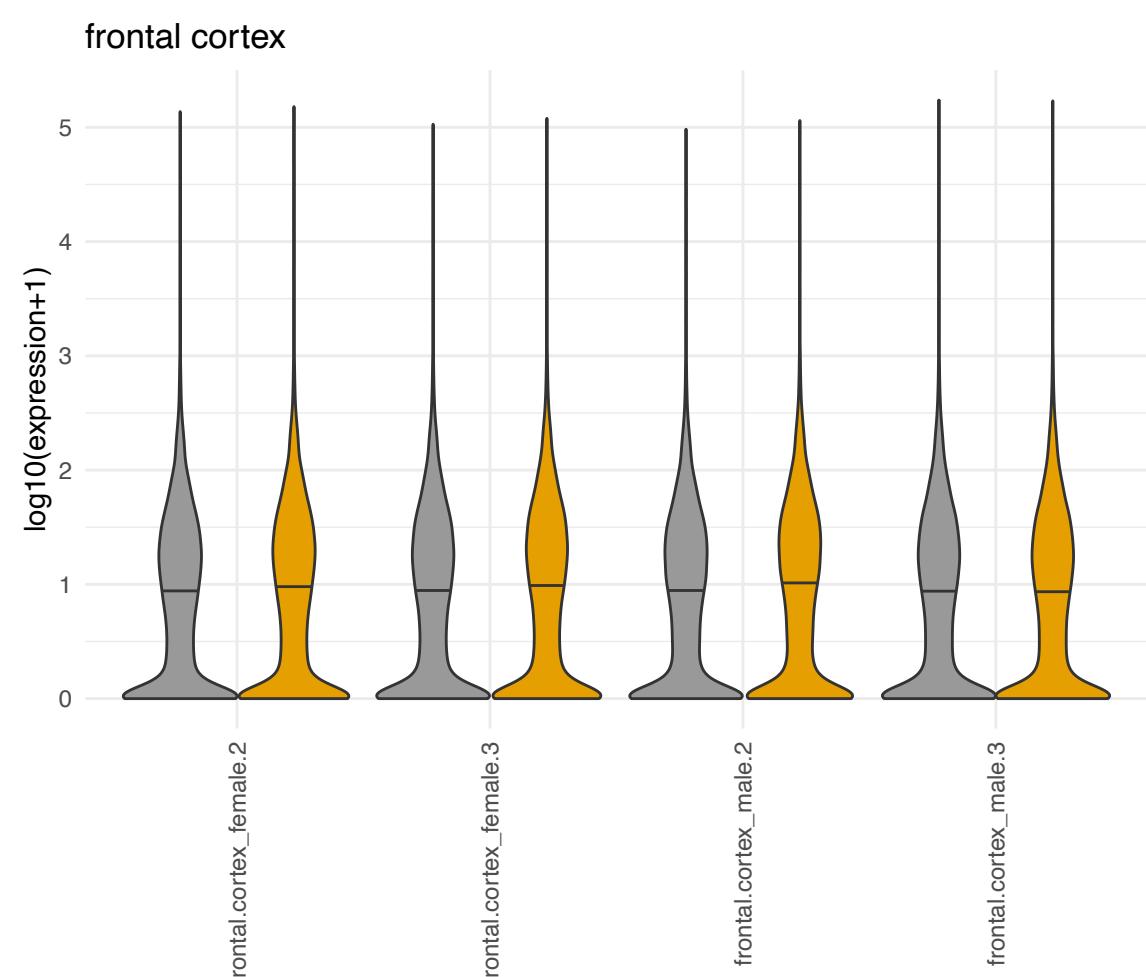
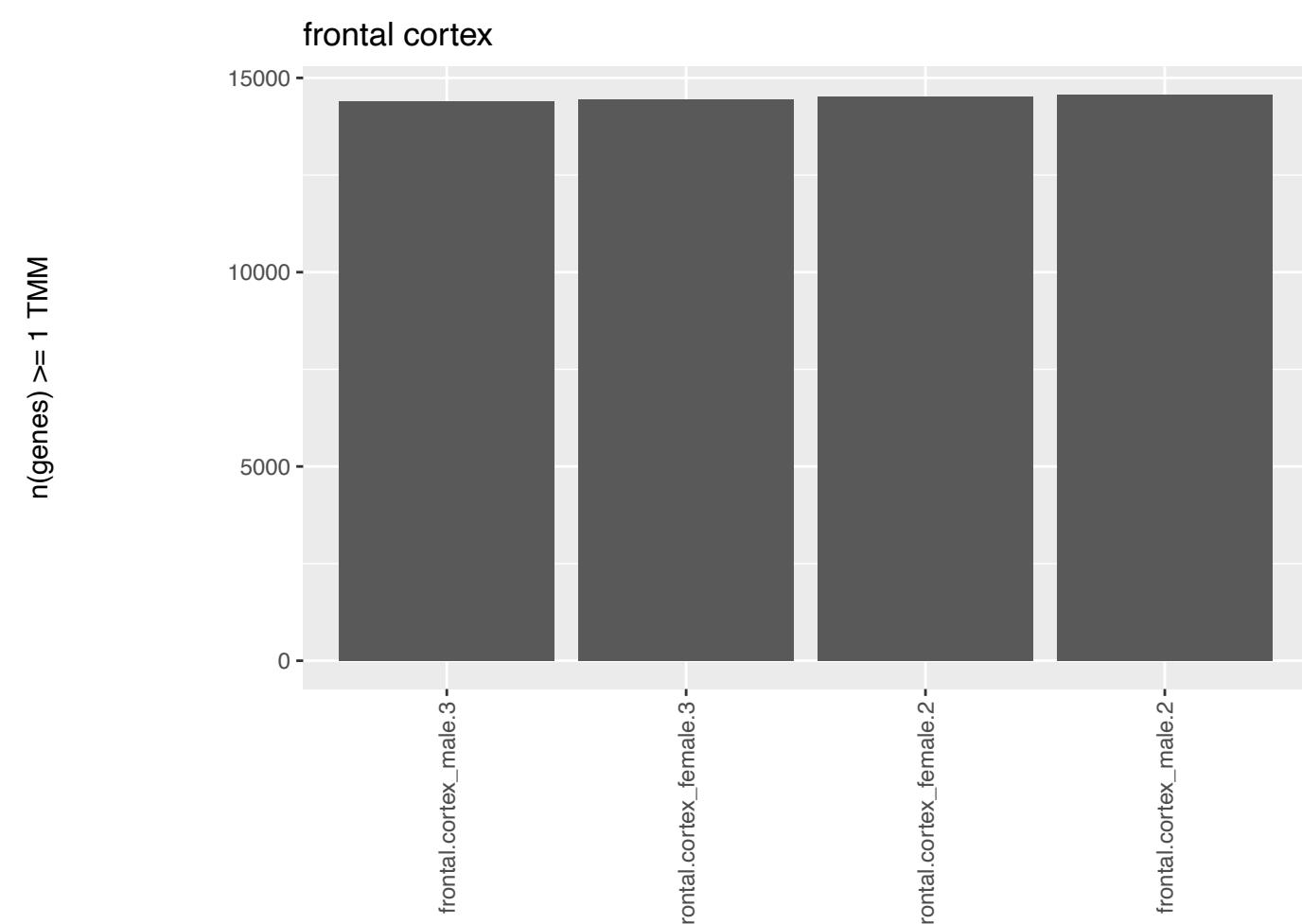
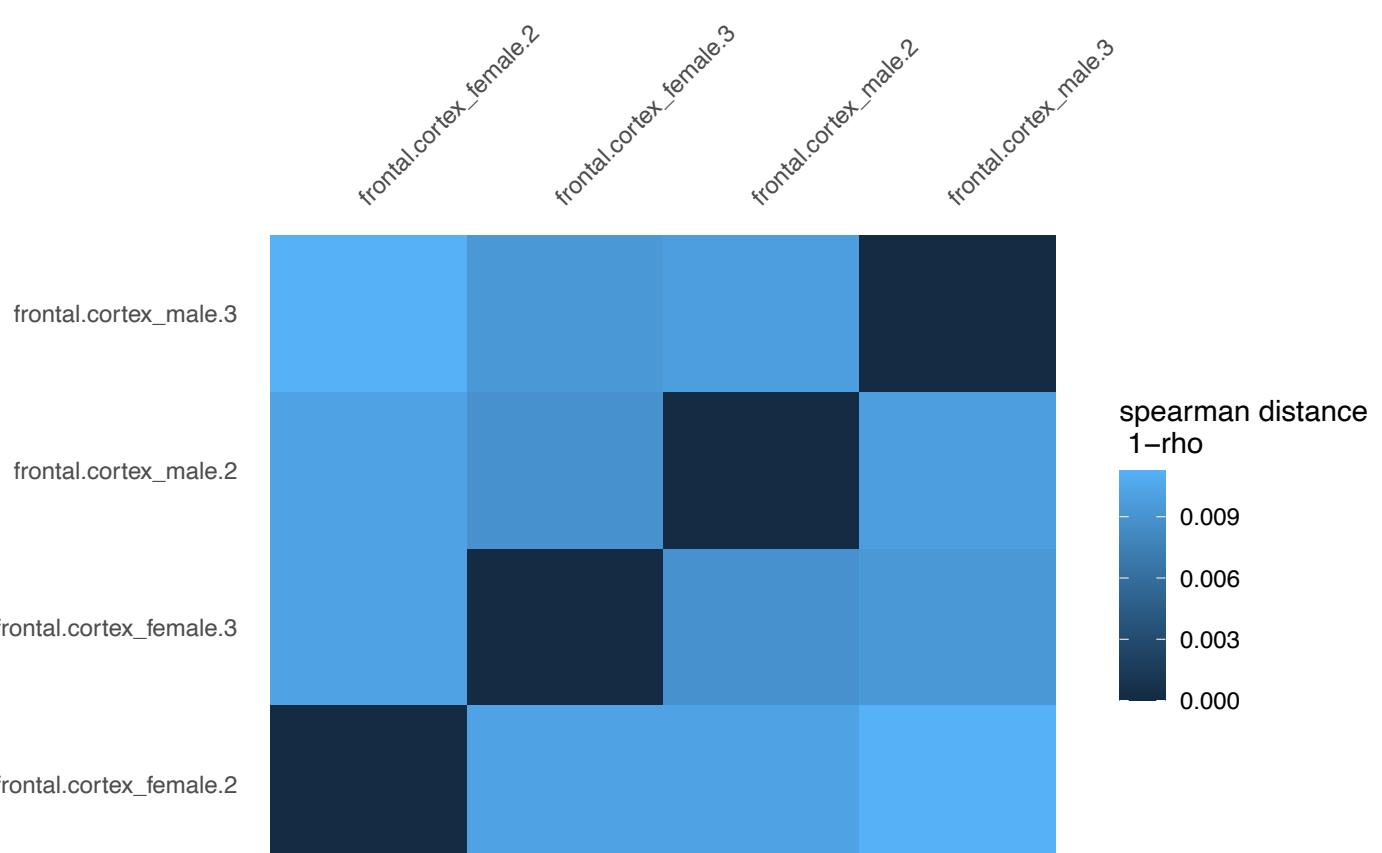
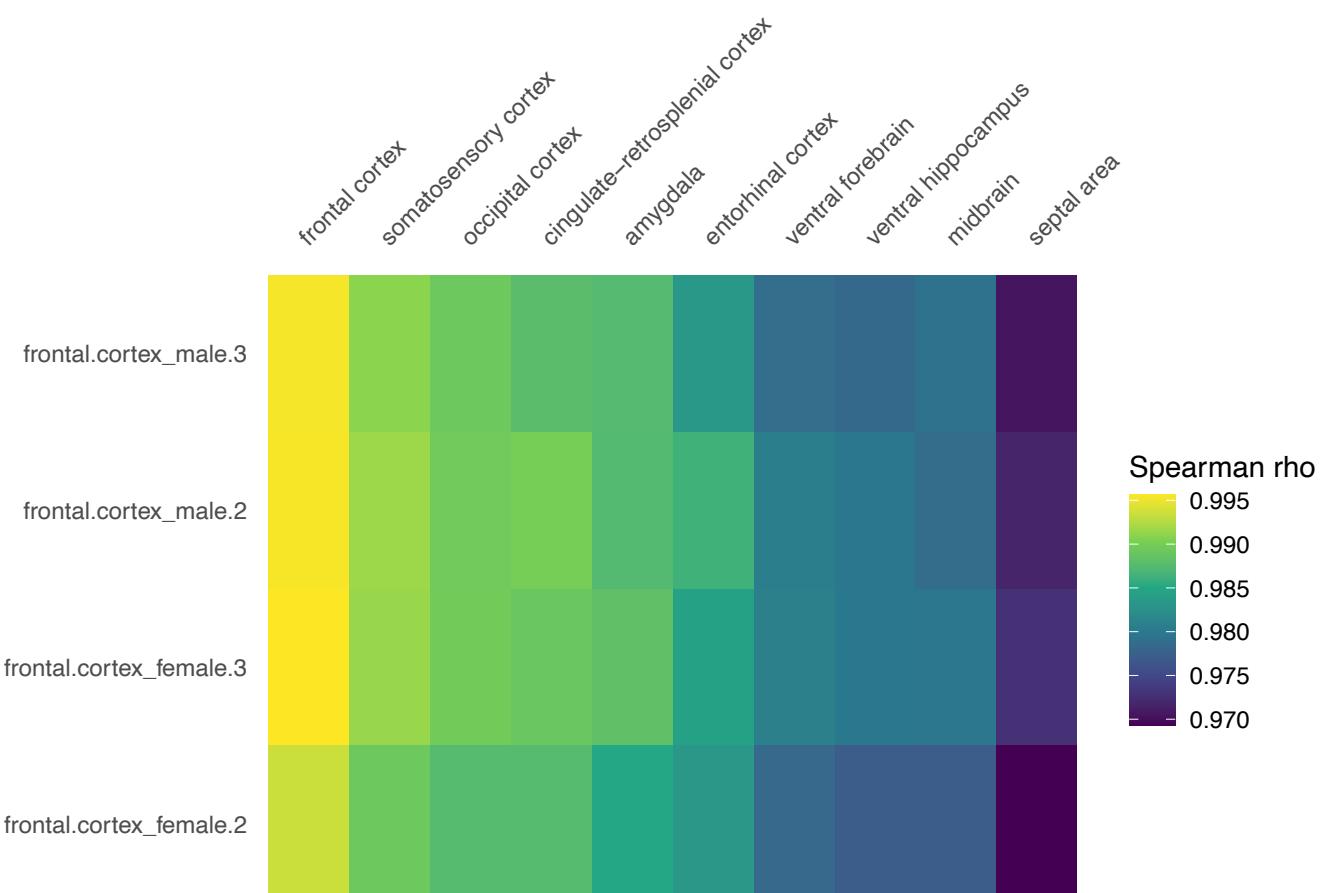
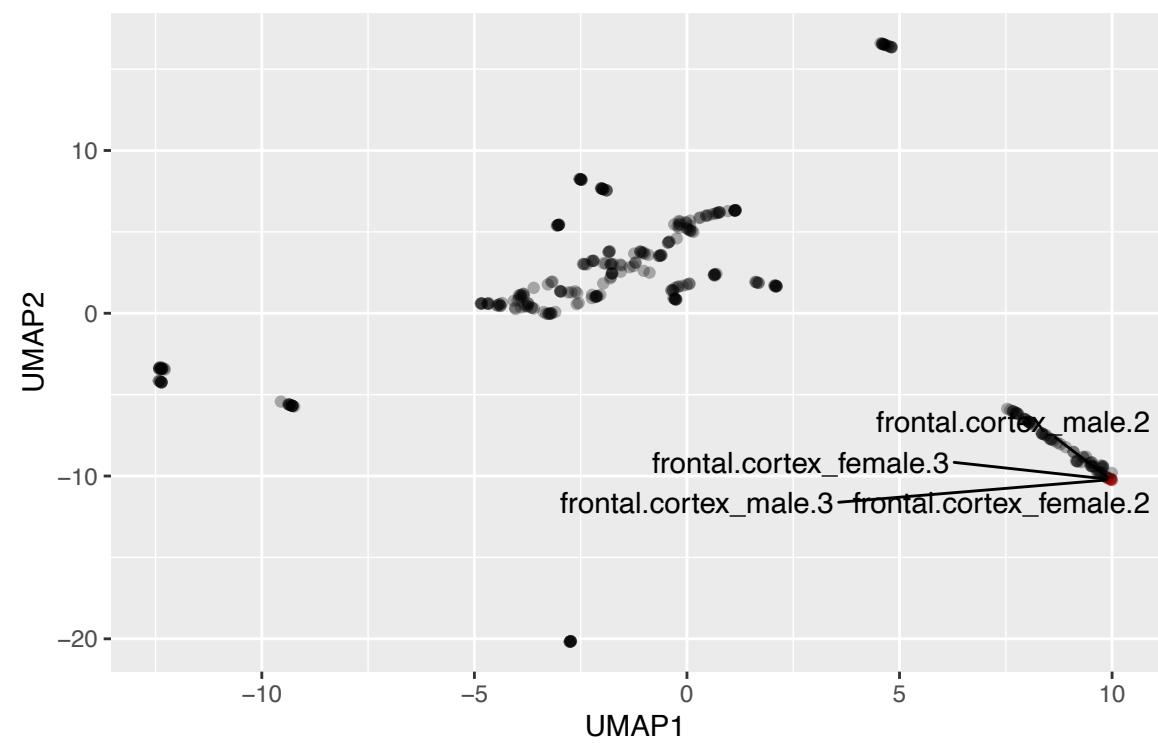
feli_female.1



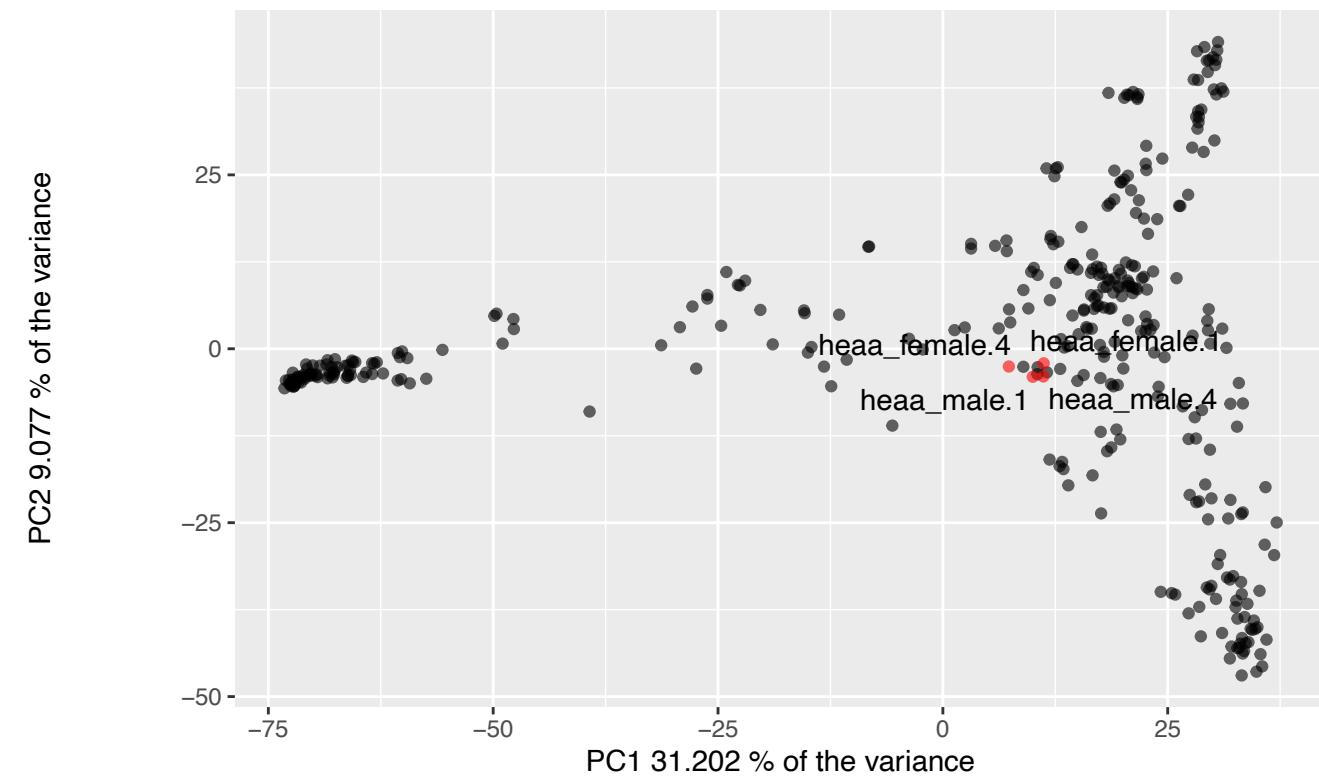
frontal cortex, PCA: TMM expression values



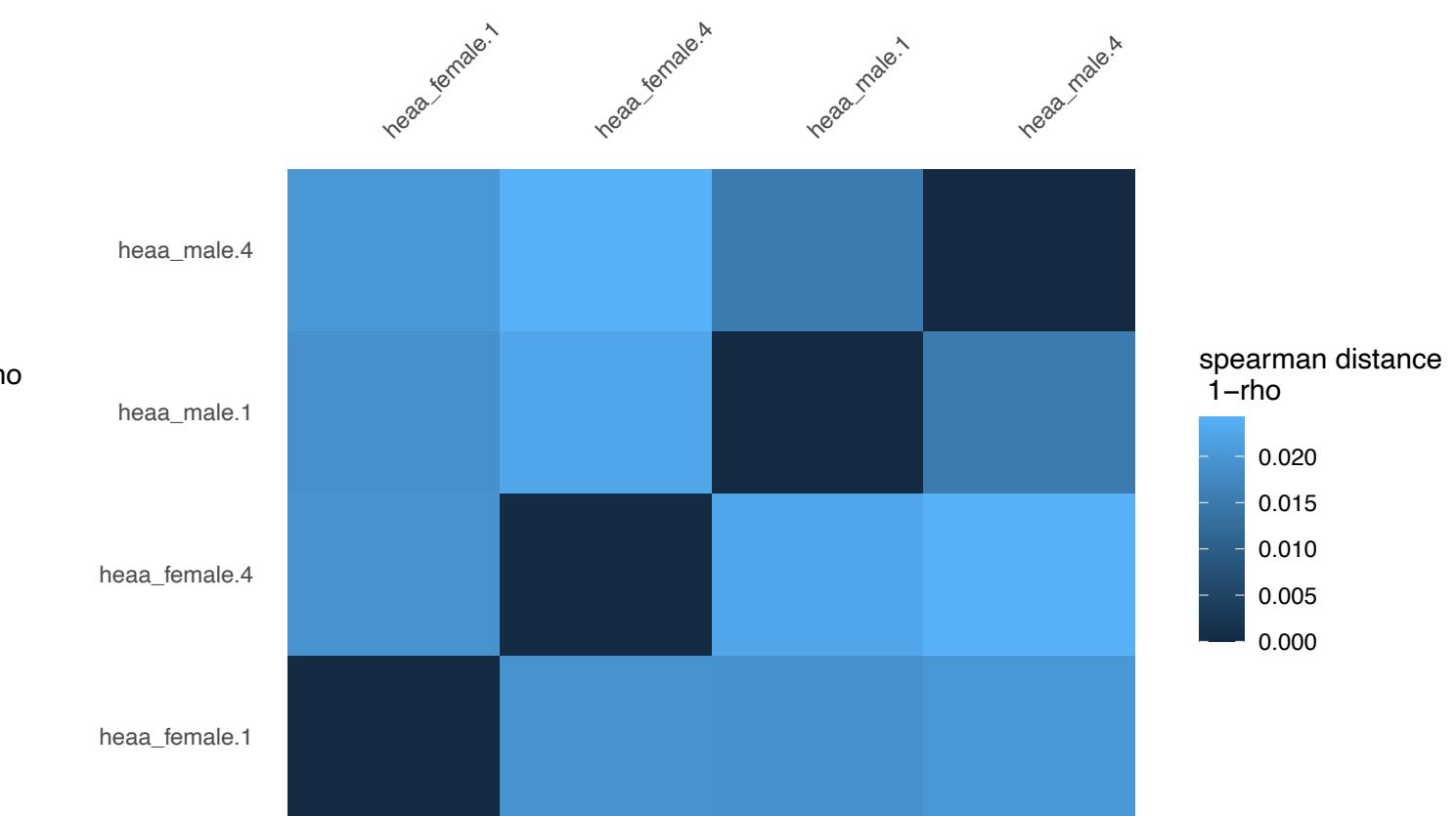
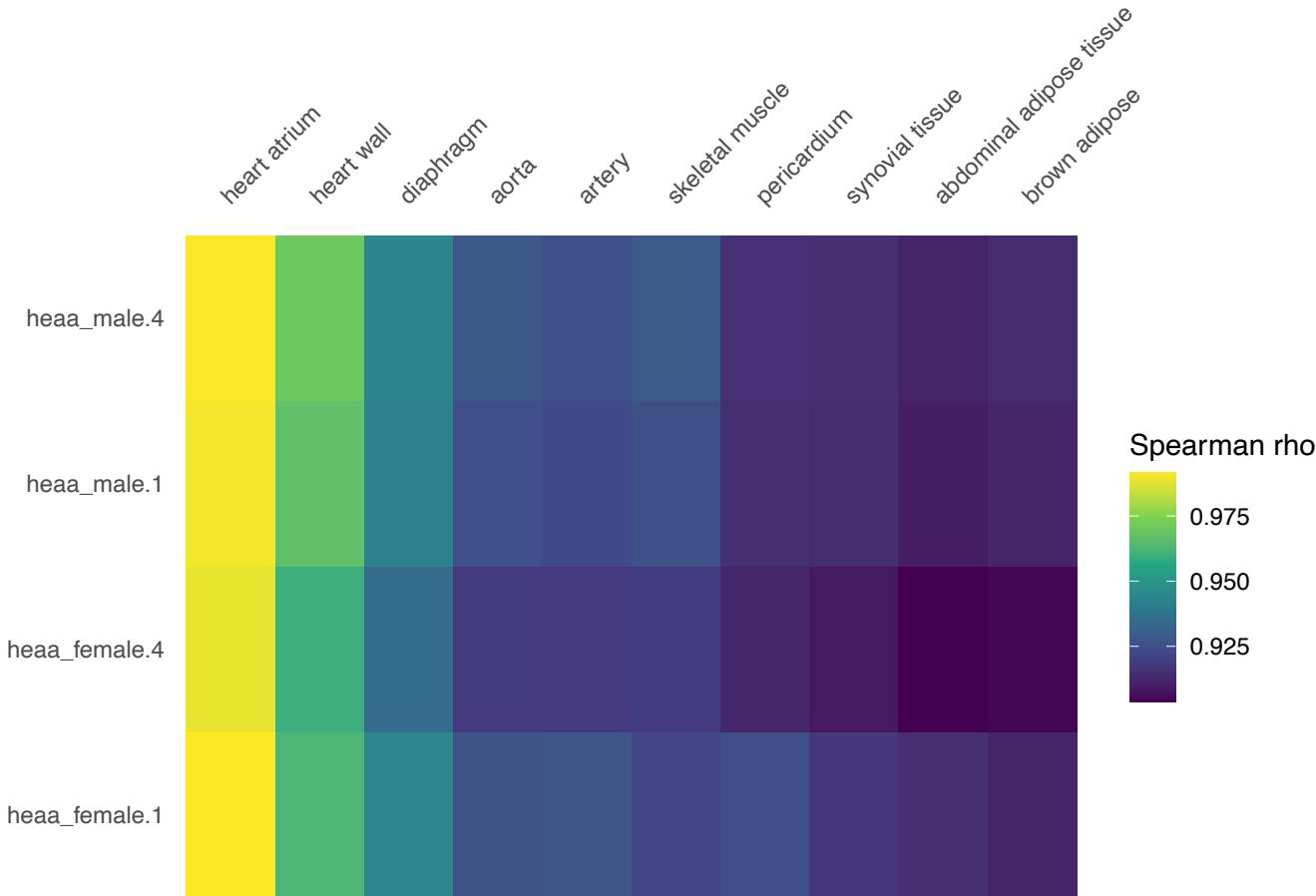
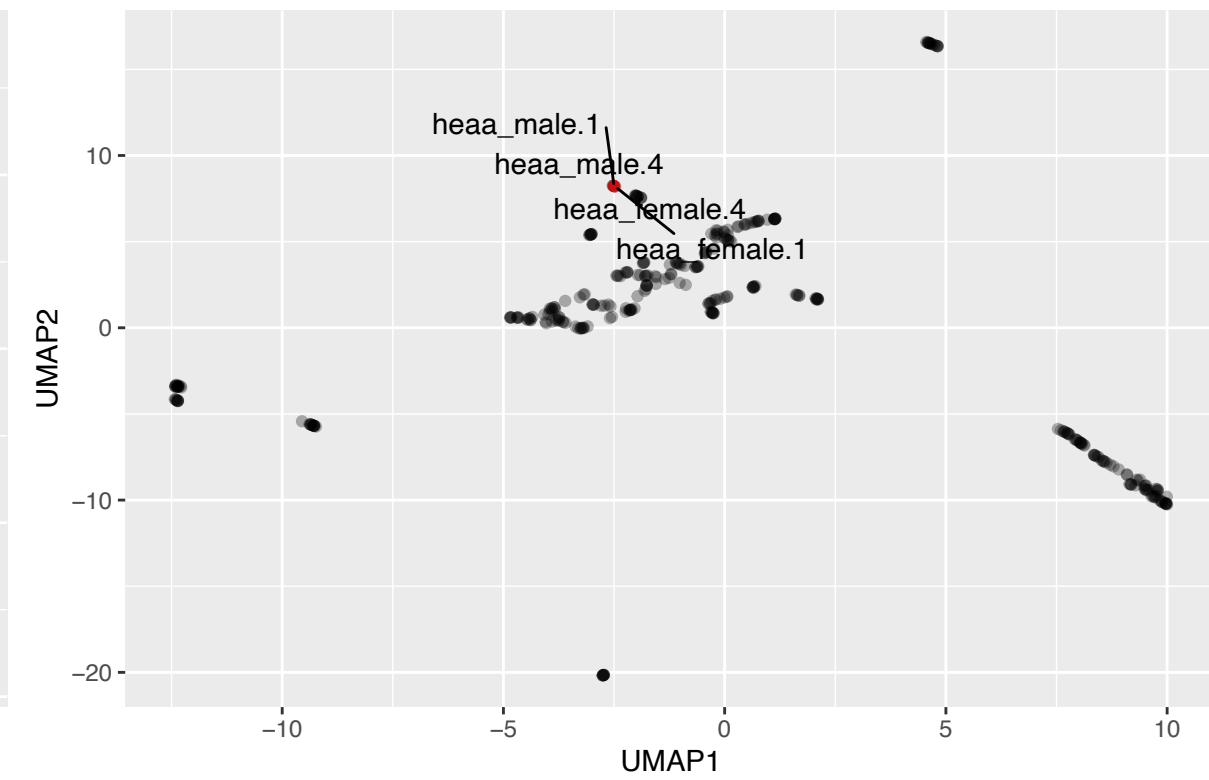
frontal cortex, UMAP: TMM expression values



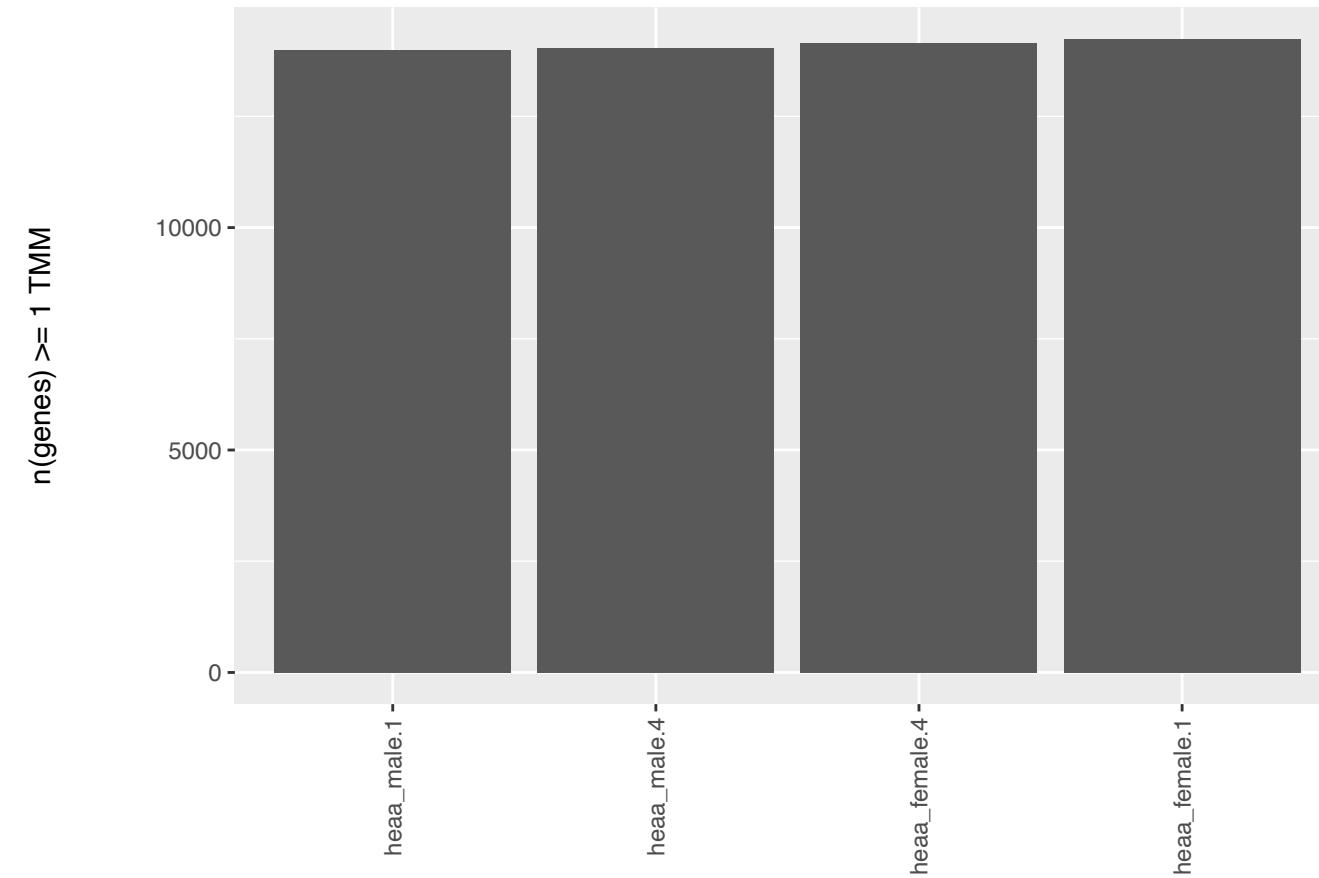
heart atrium, PCA: TMM expression values



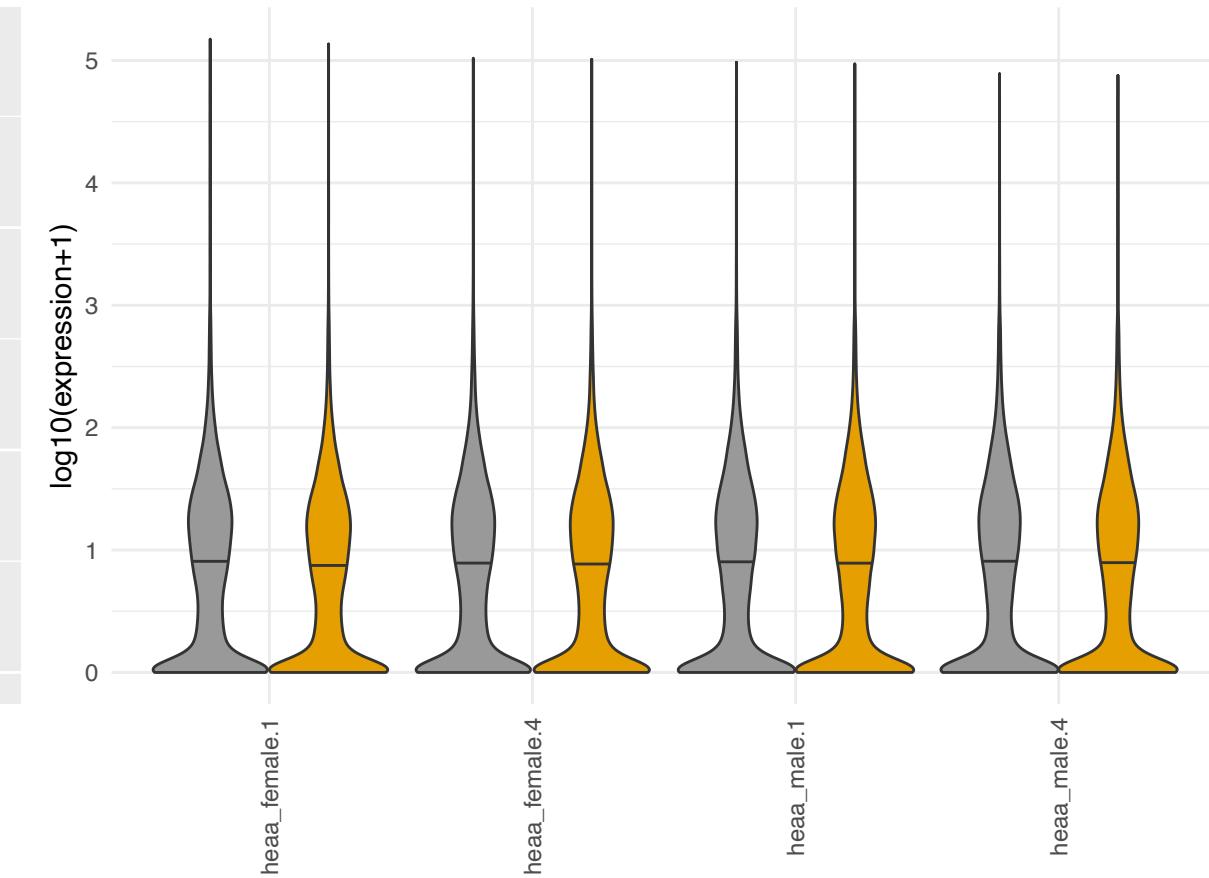
heart atrium, UMAP: TMM expression values



heart atrium

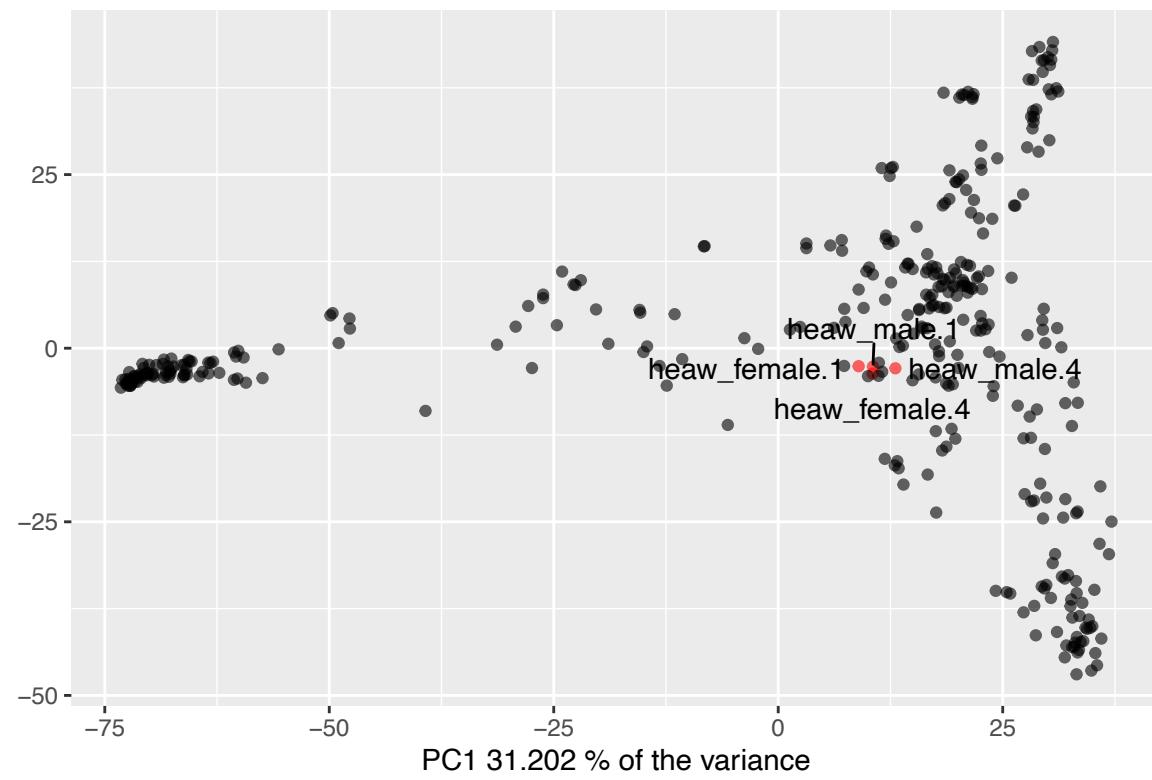


heart atrium



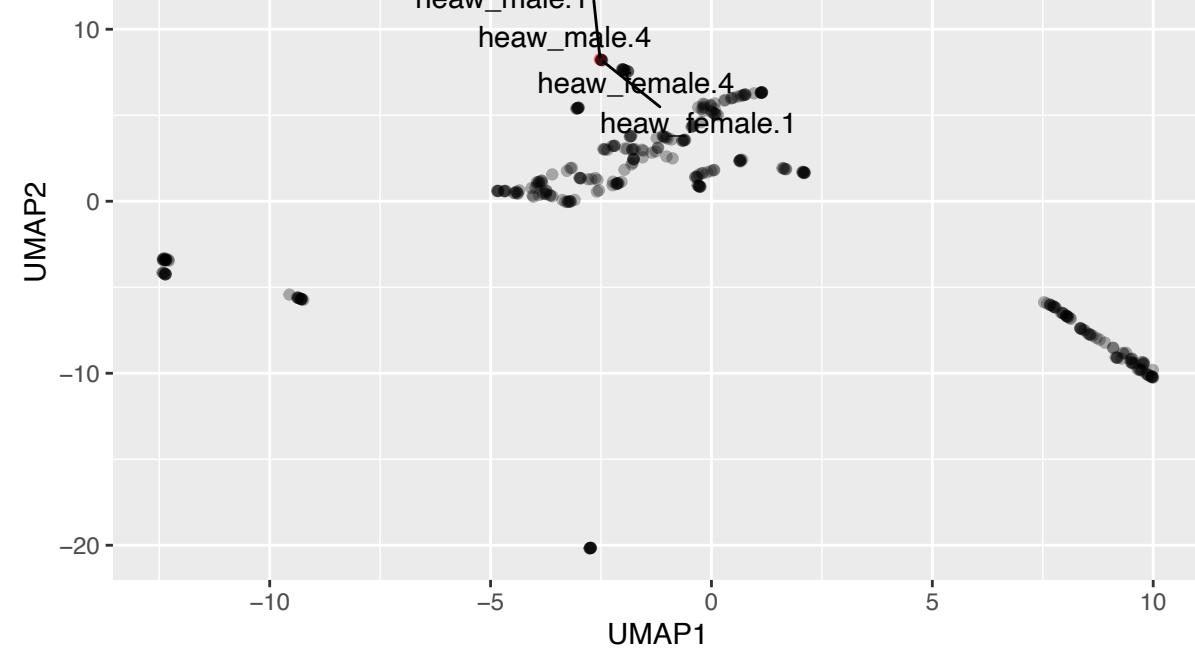
heart wall, PCA: TMM expression values

PC2 9.077 % of the variance

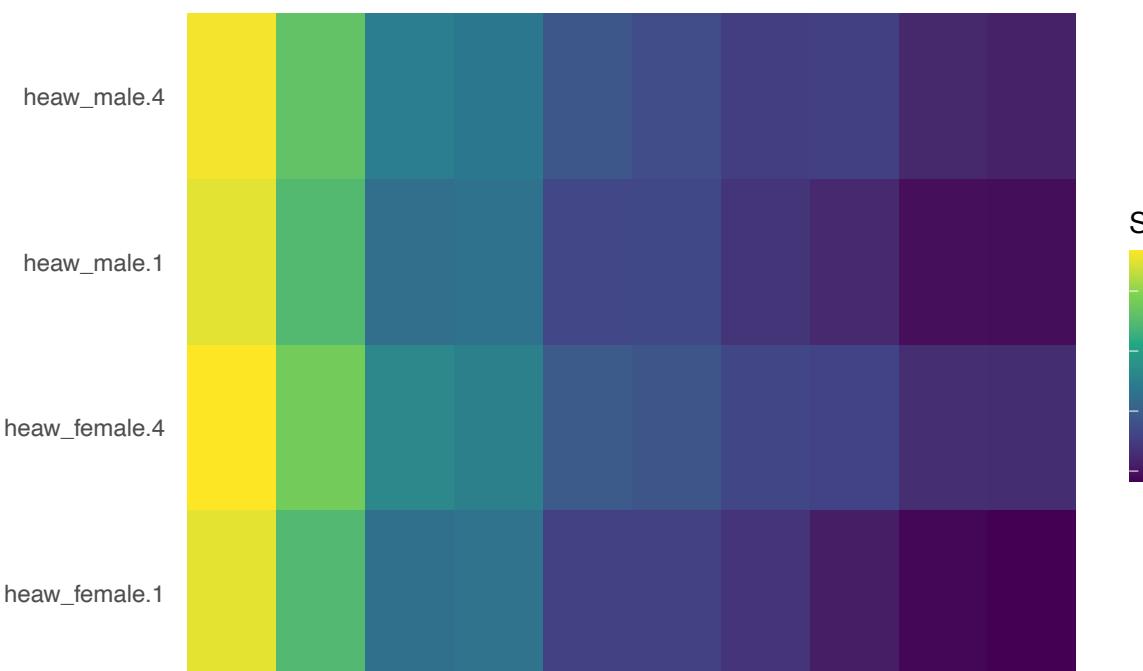


heart wall, UMAP: TMM expression values

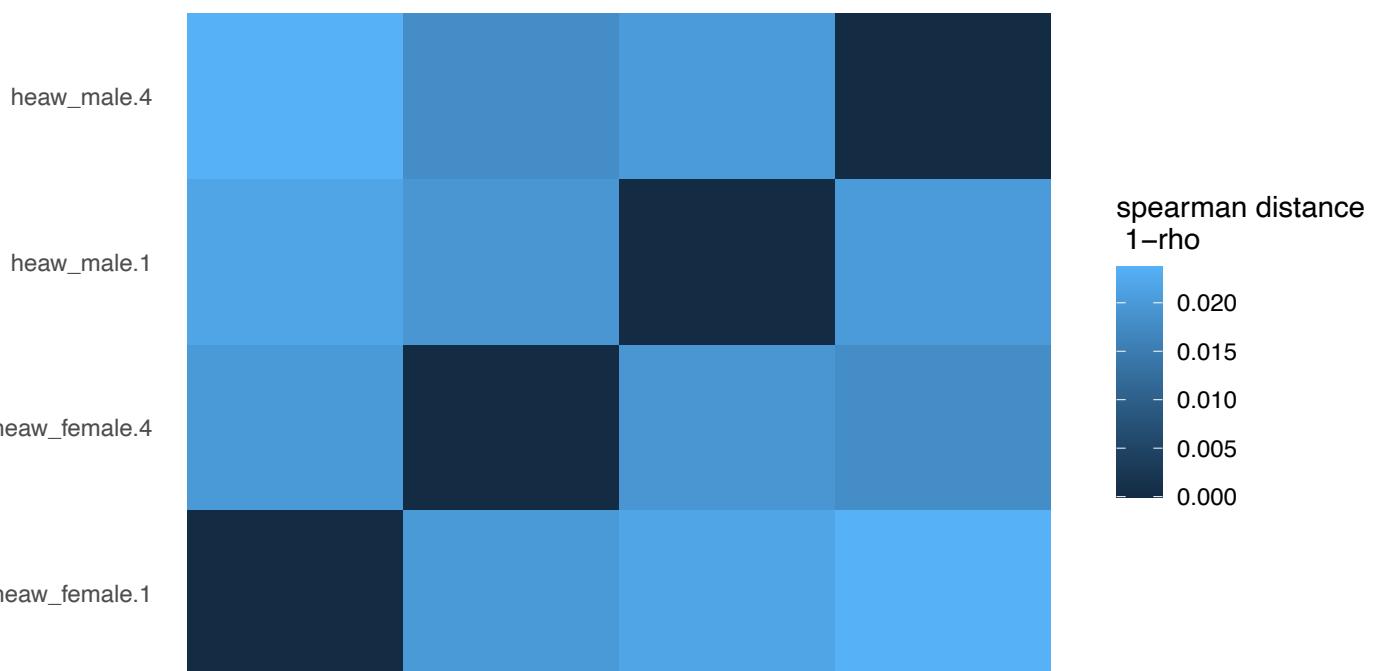
UMAP2



heart wall
heart atrium
diaphragm
skeletal muscle
aorta
brown adipose
vagus nerve
artery
abdominal adipose tissue
synovial tissue

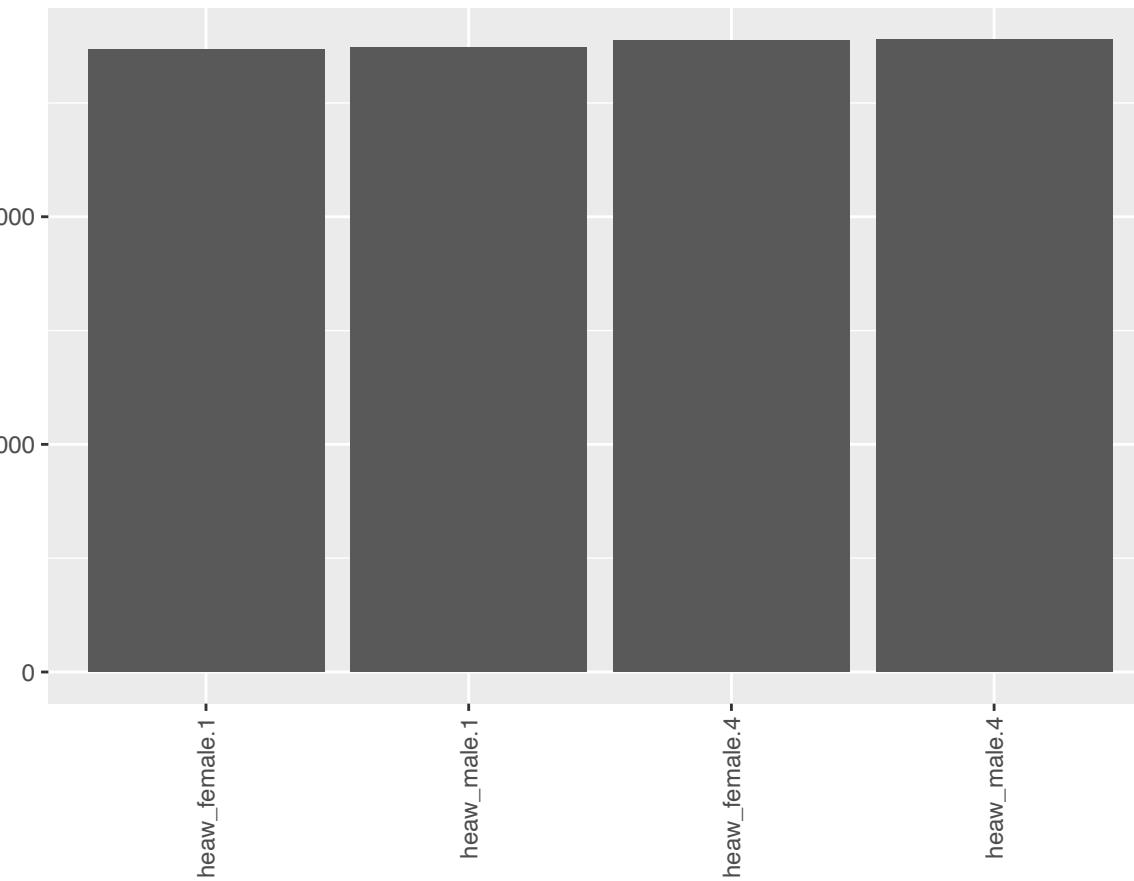


heaw_male.4
heaw_male.1
heaw_female.4
heaw_female.1



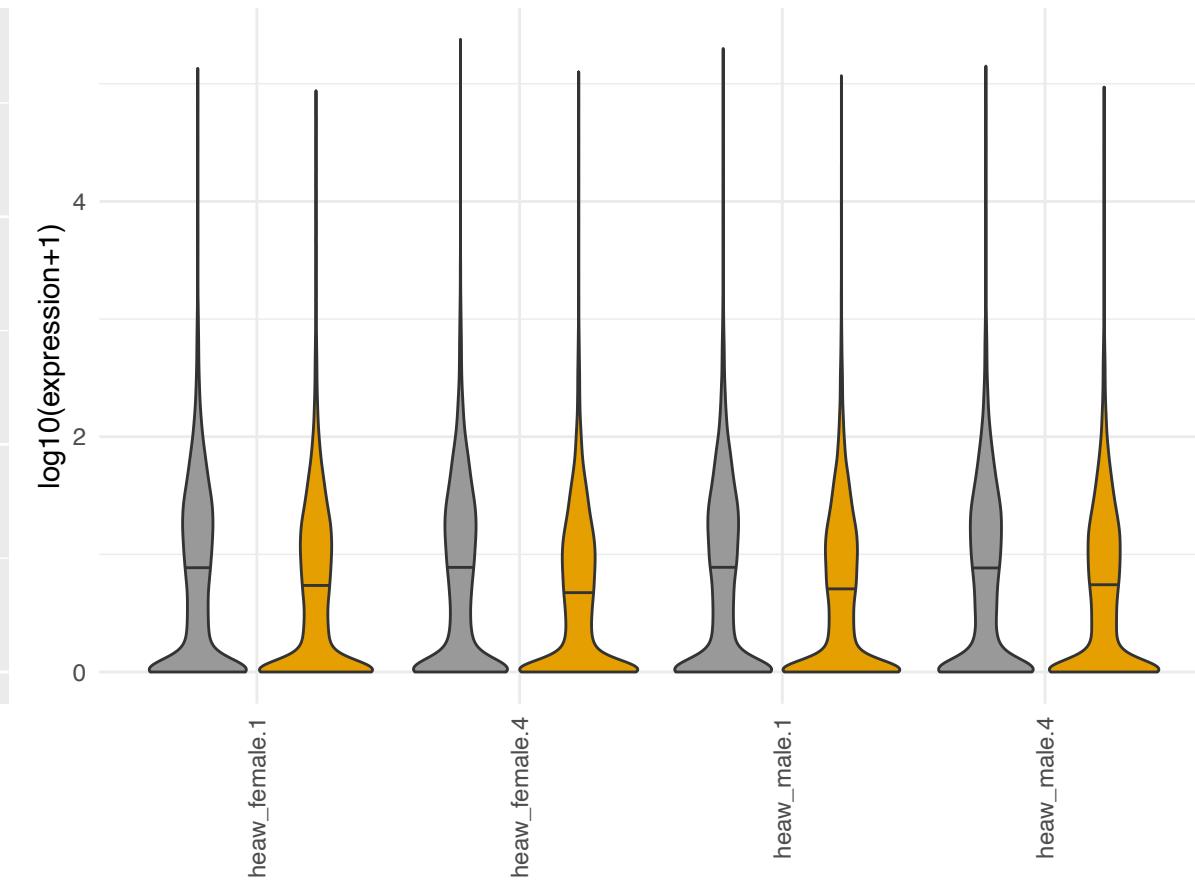
heart wall

n(genes) >= 1 TMM

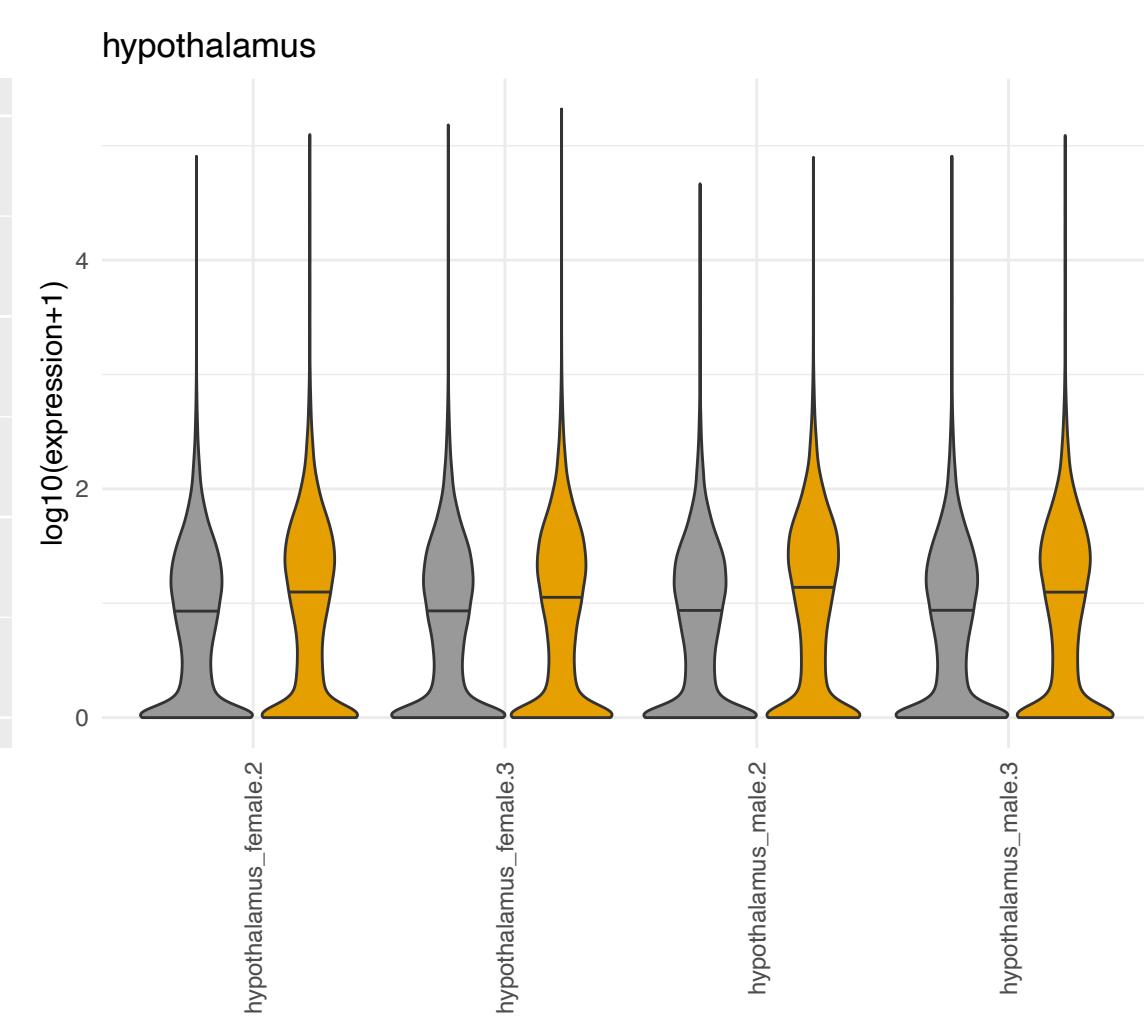
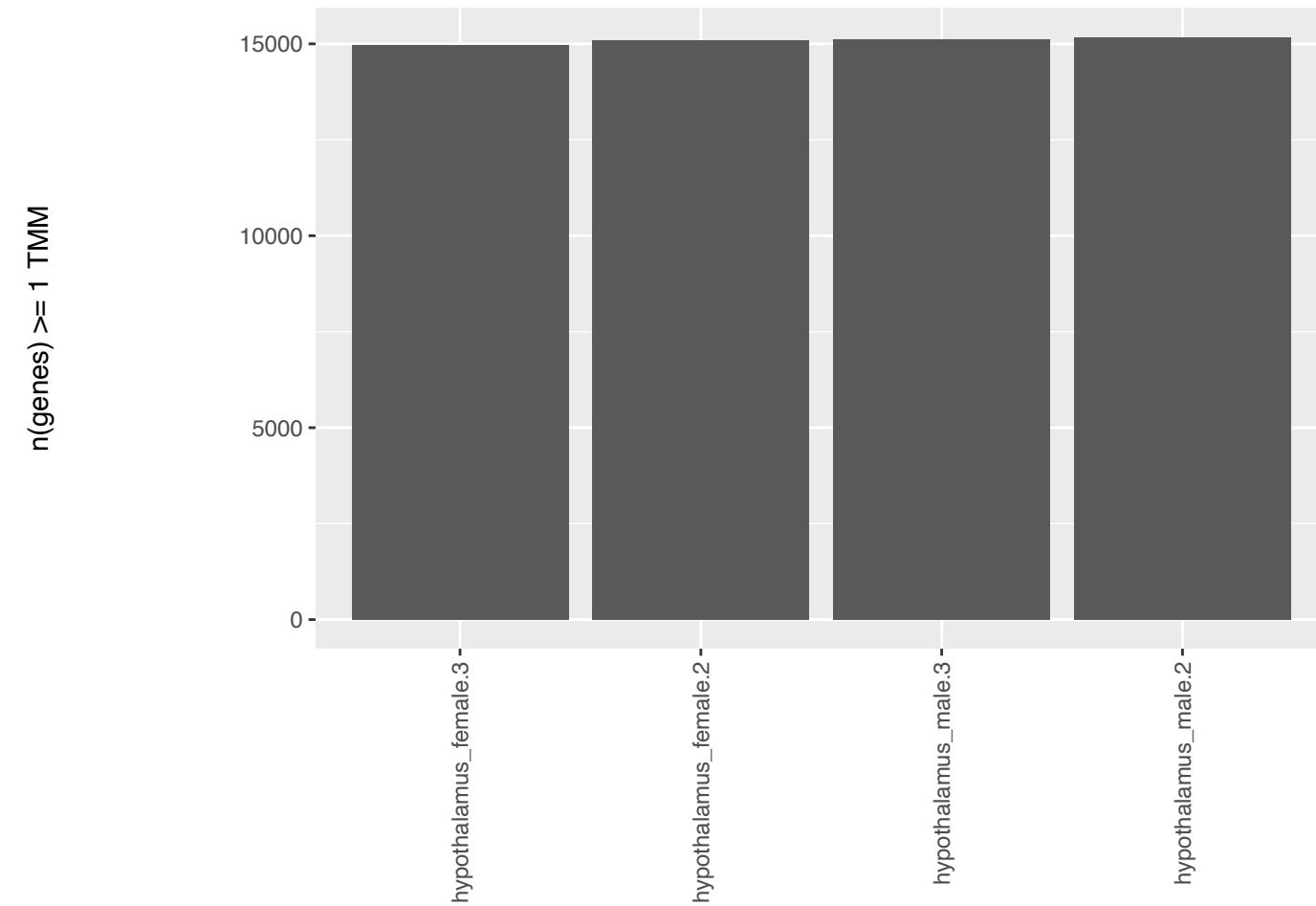
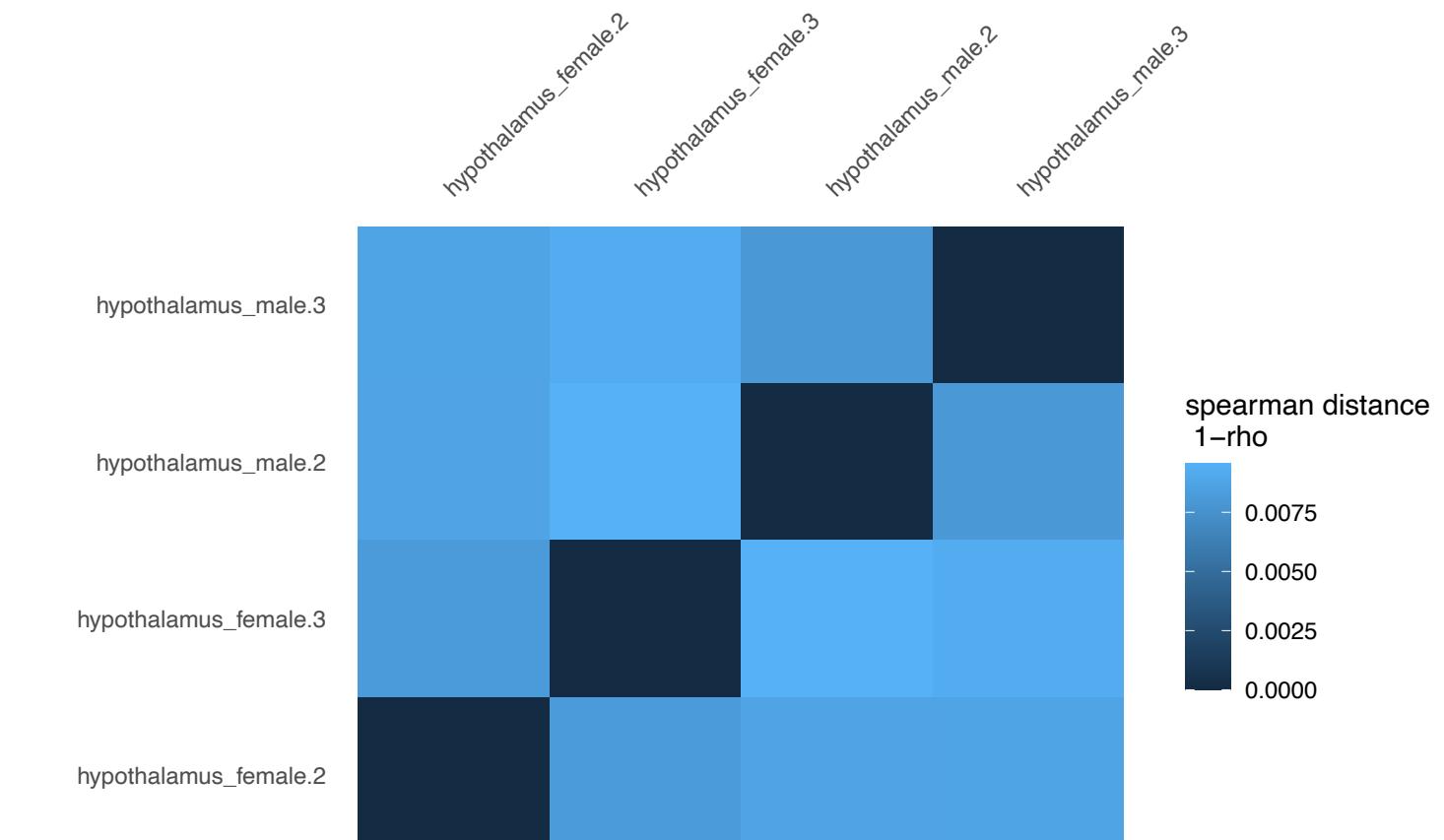
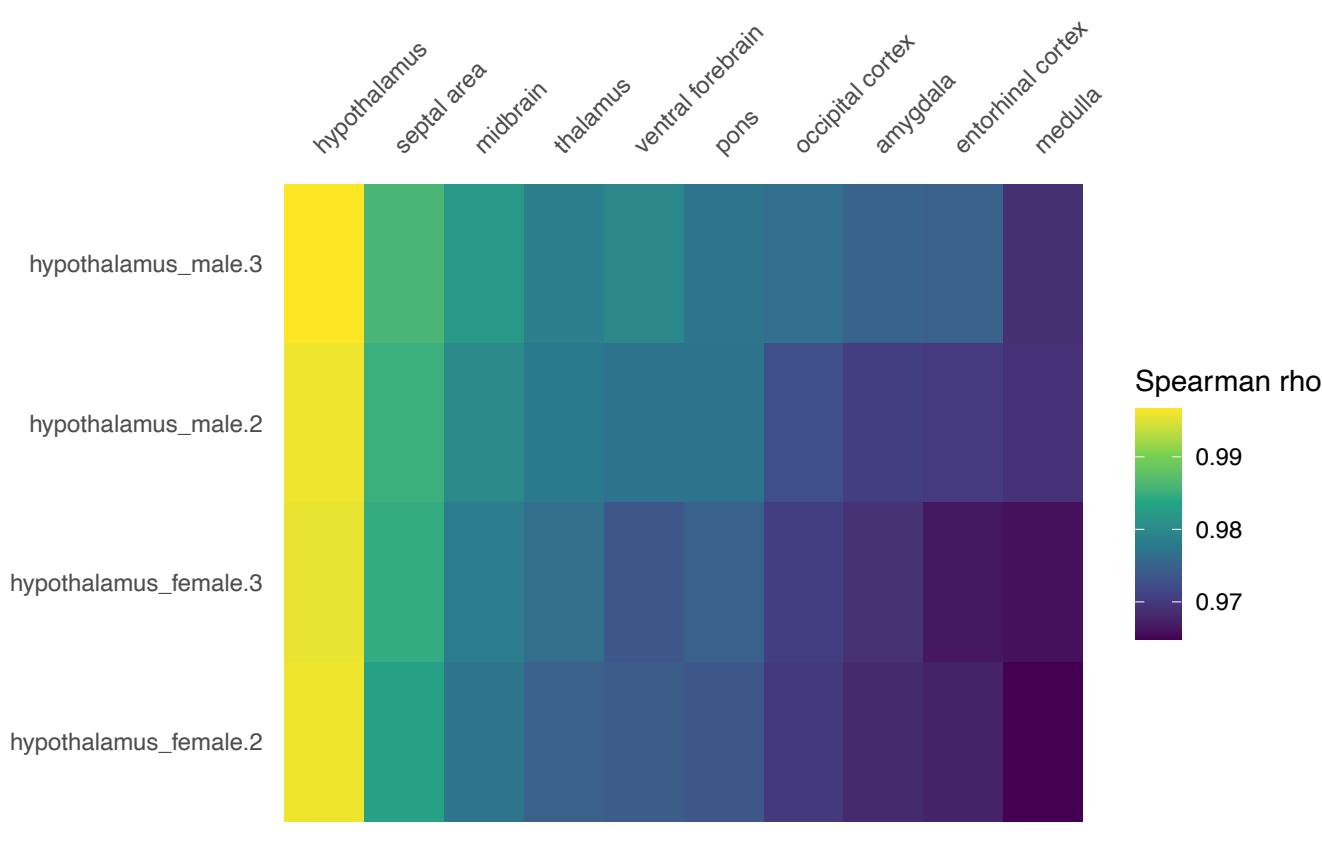
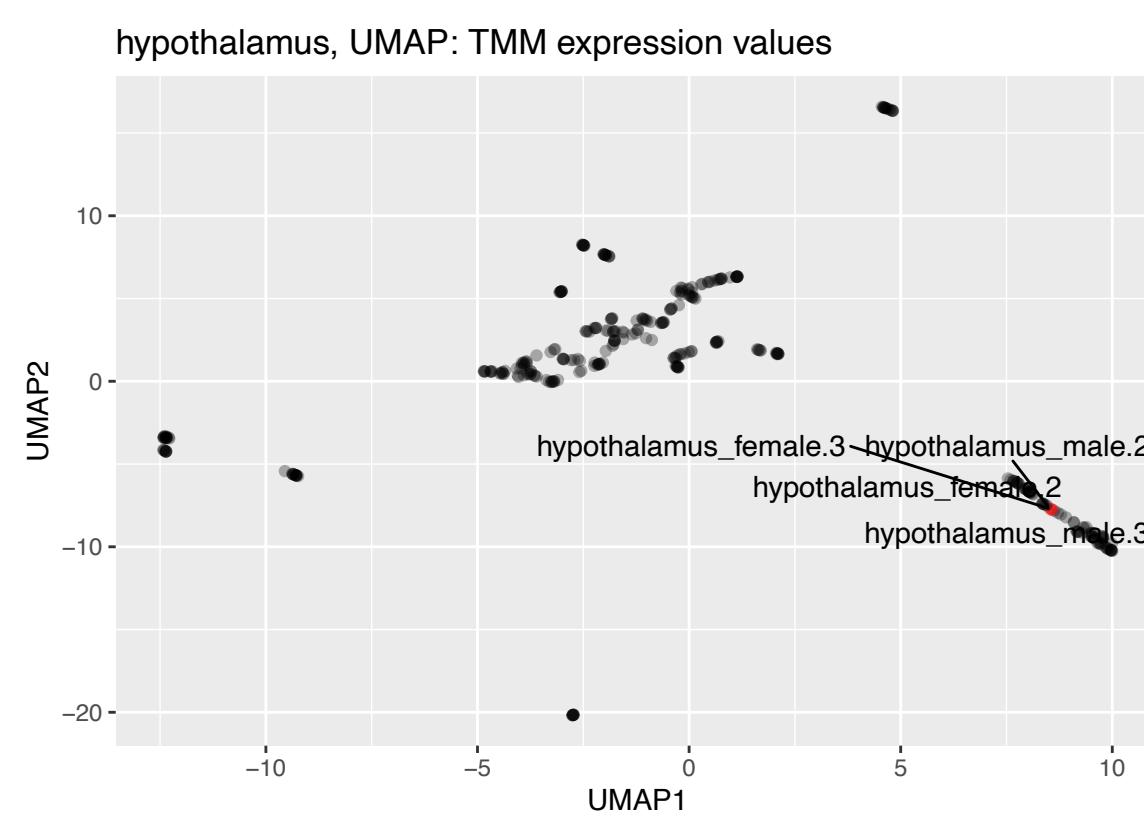
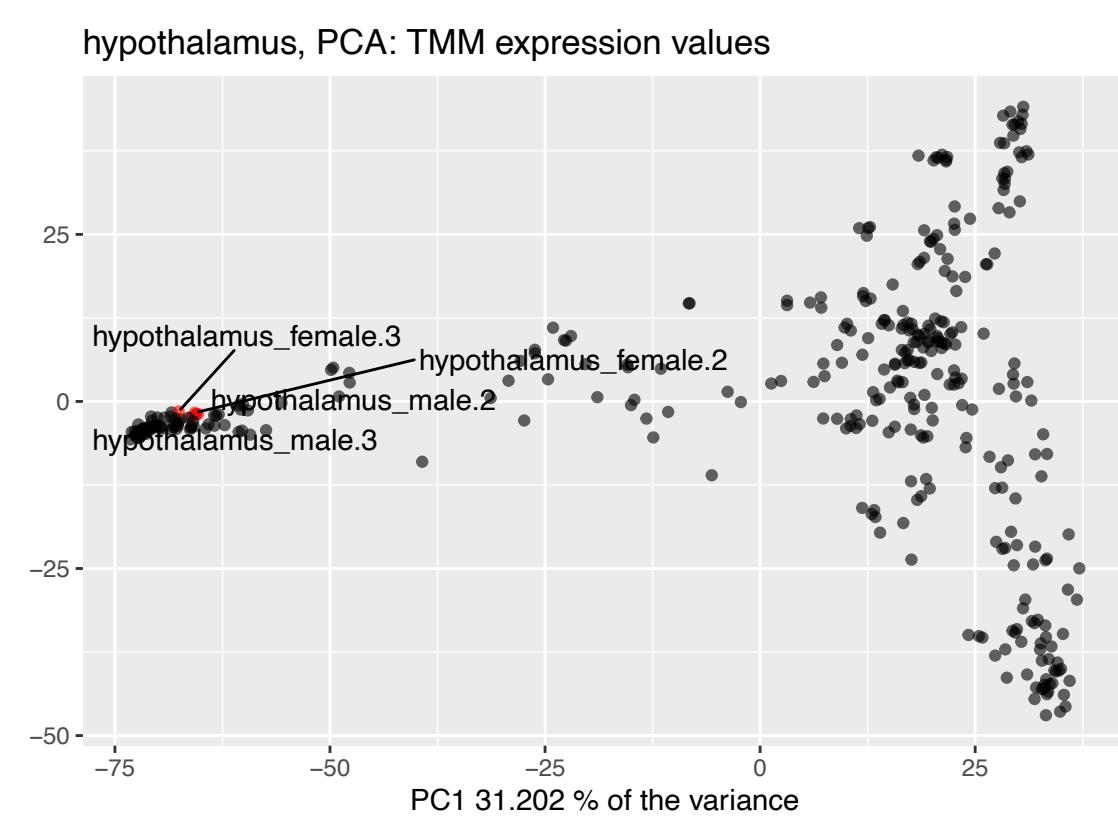


heart wall

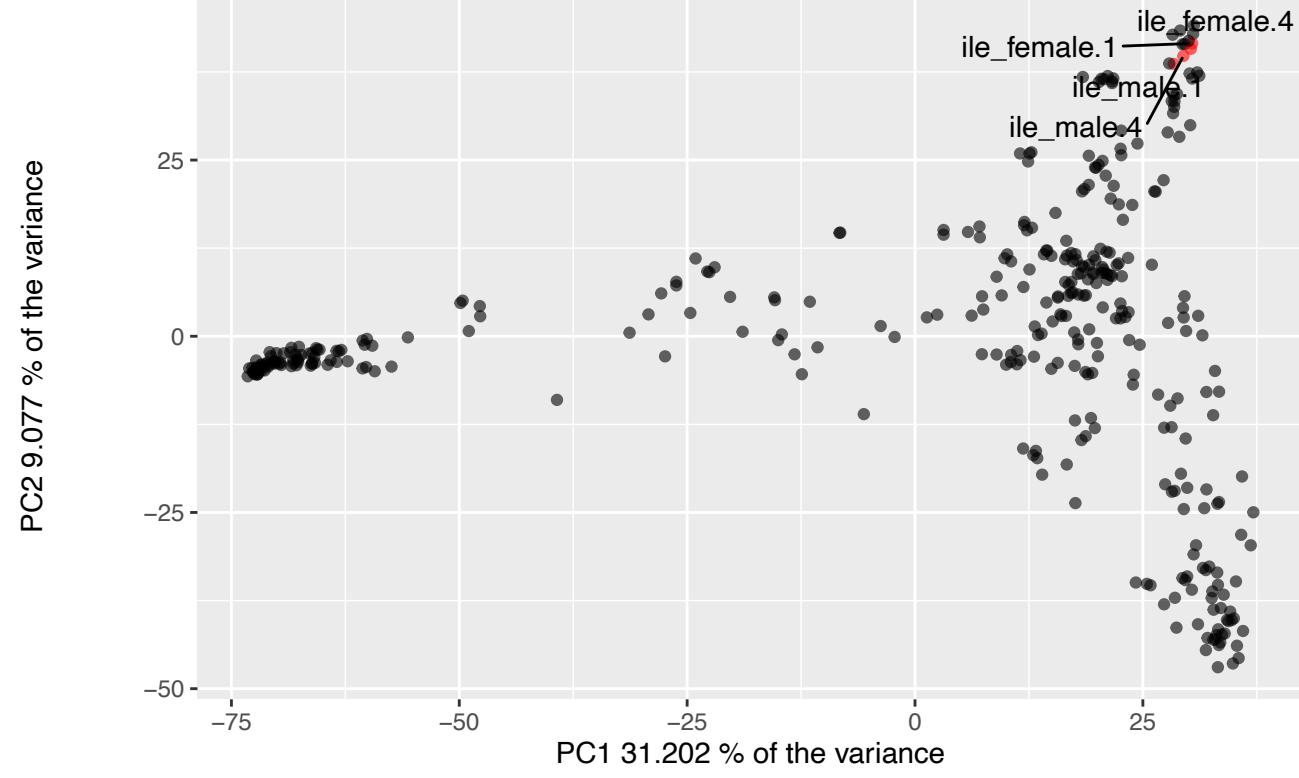
log10(expression+1)



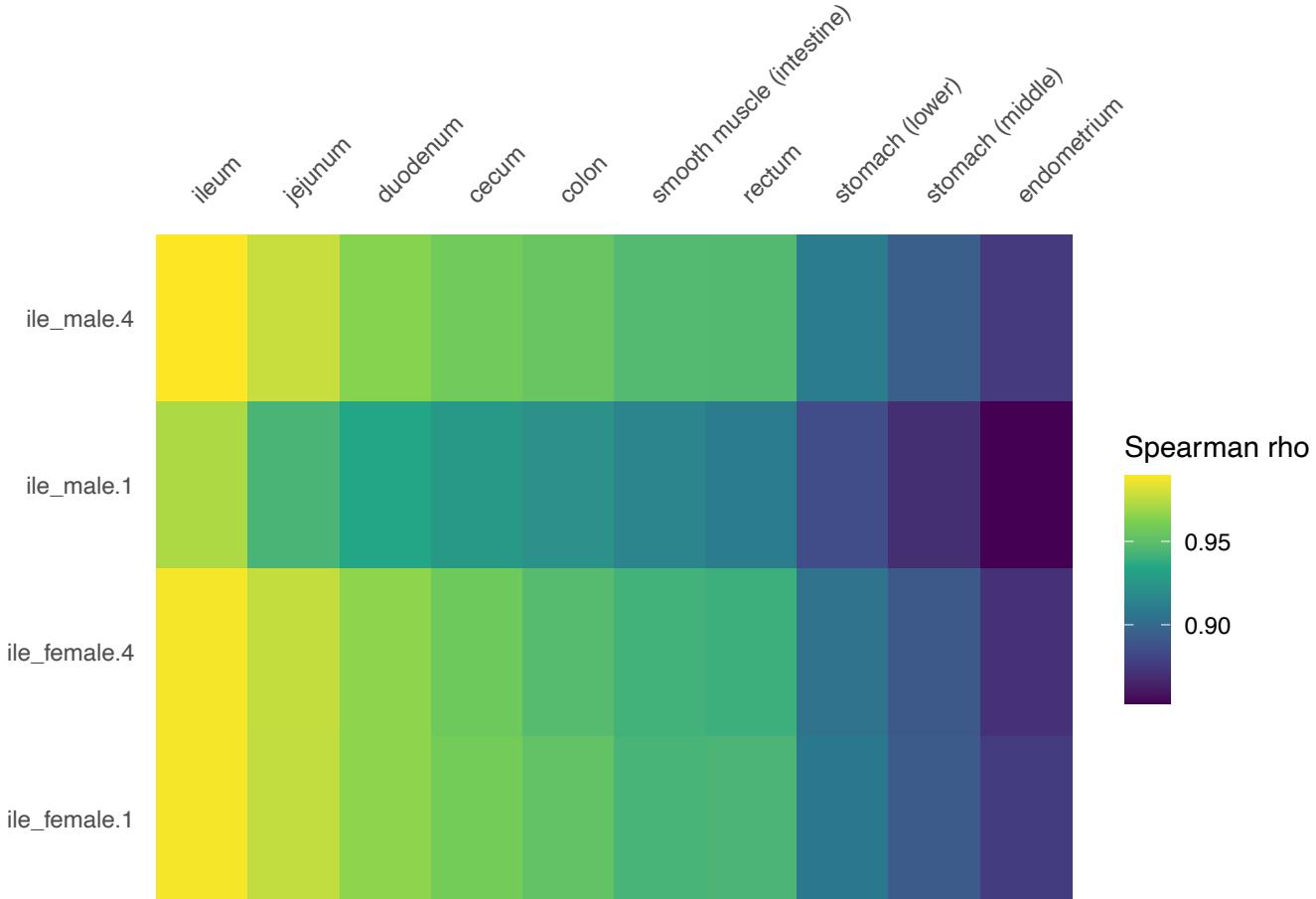
PC2 9.077 % of the variance



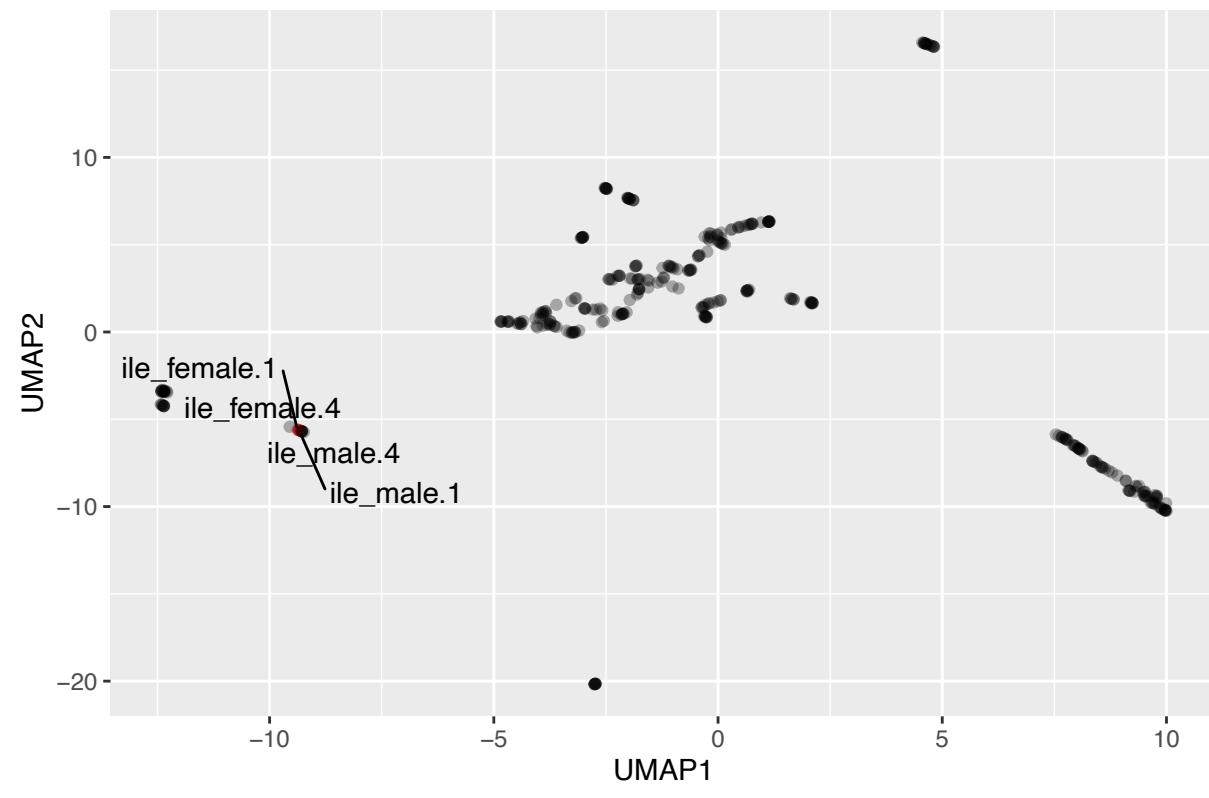
ileum, PCA: TMM expression values



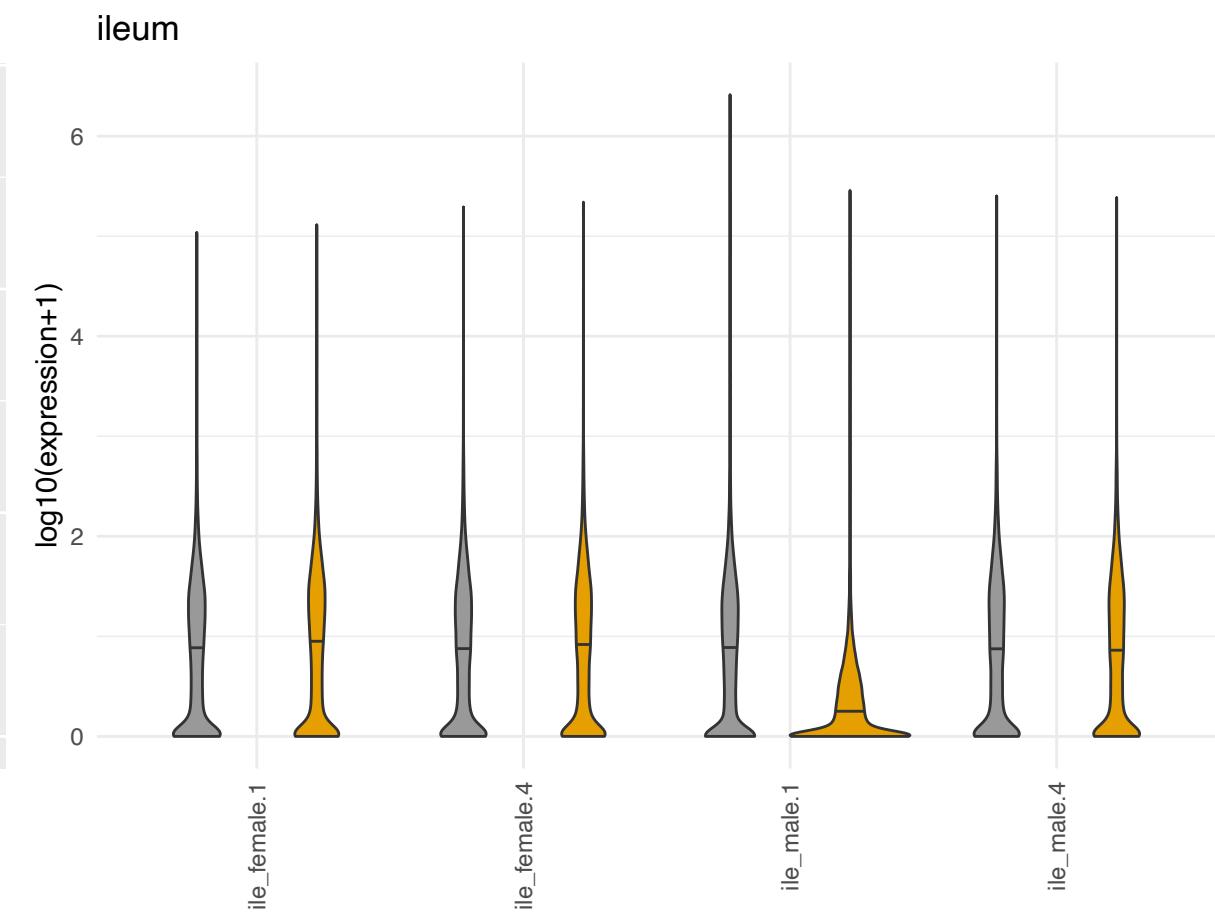
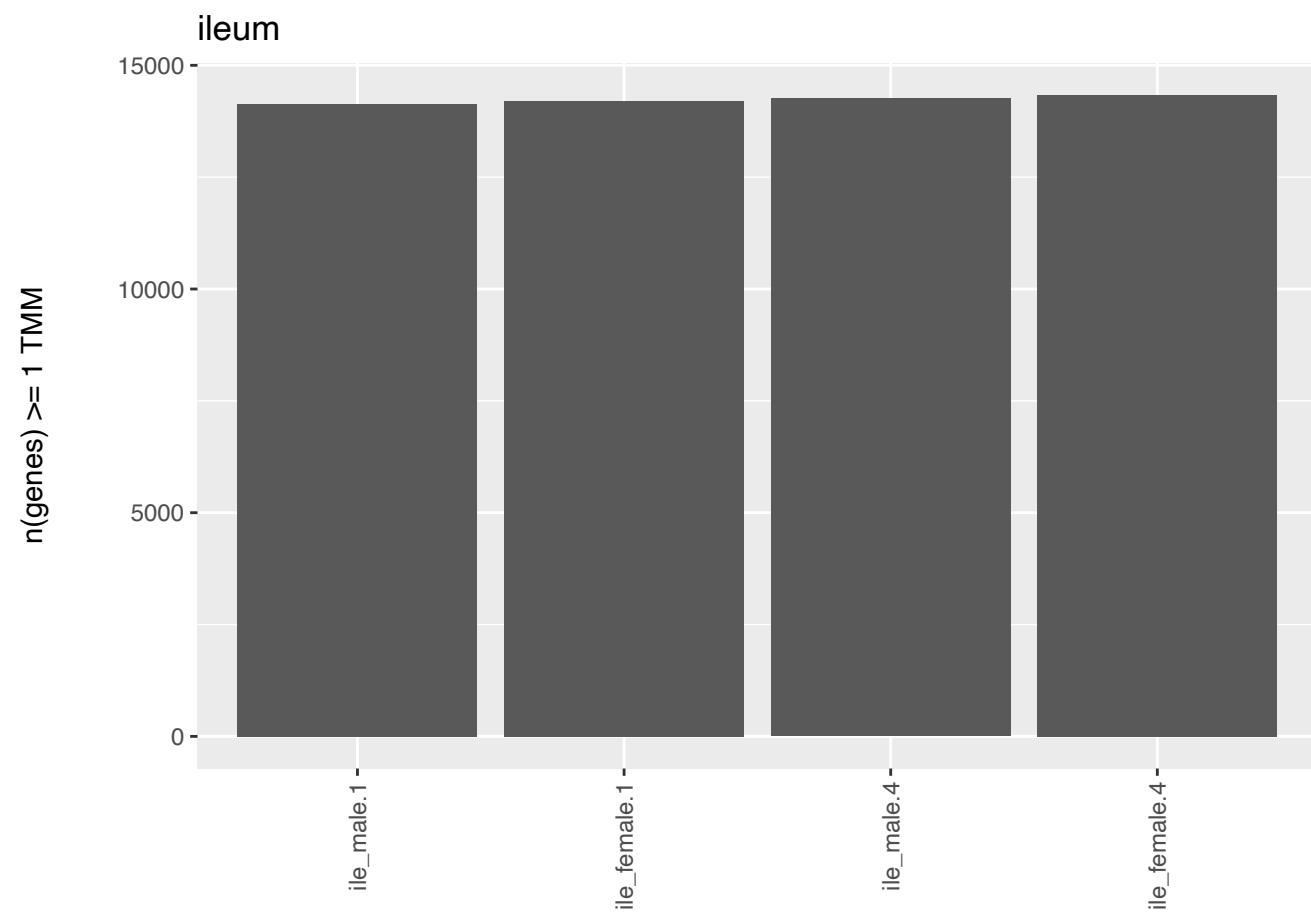
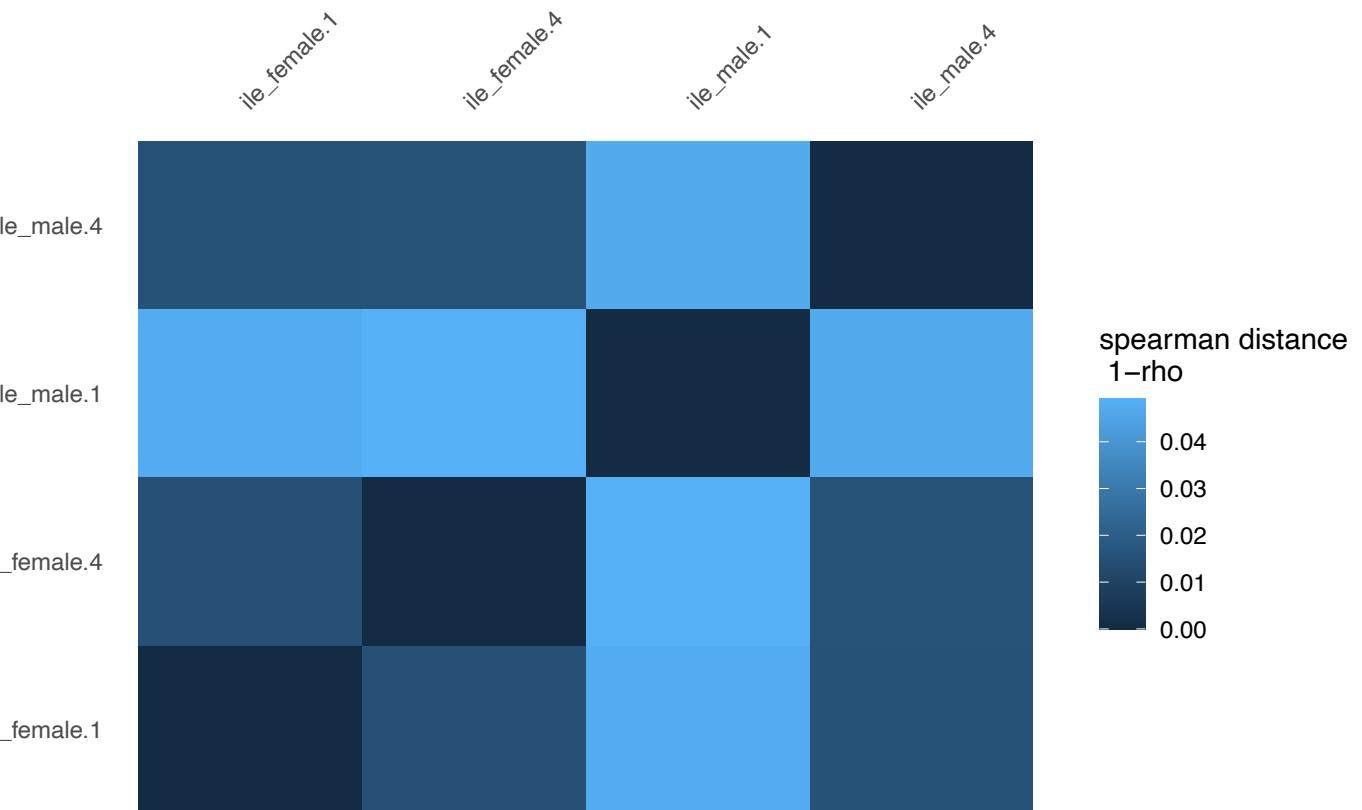
Tissue group to sample correlation



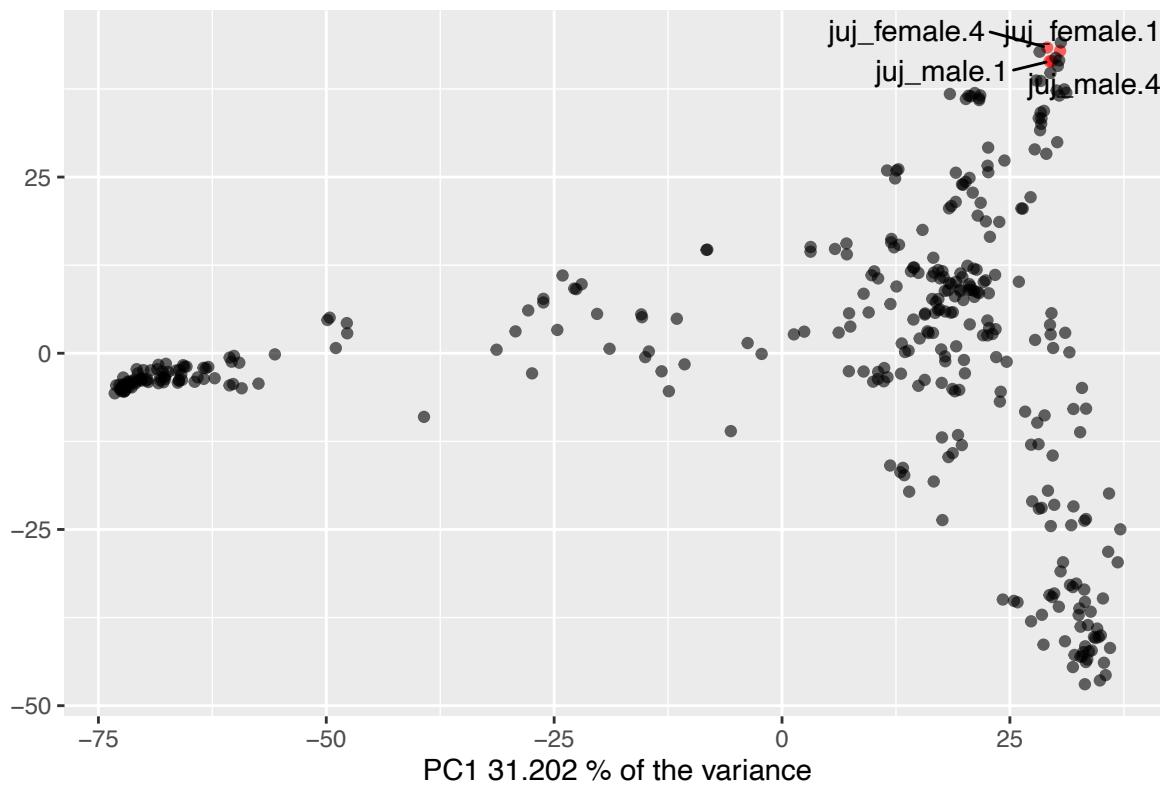
ileum, UMAP: TMM expression values



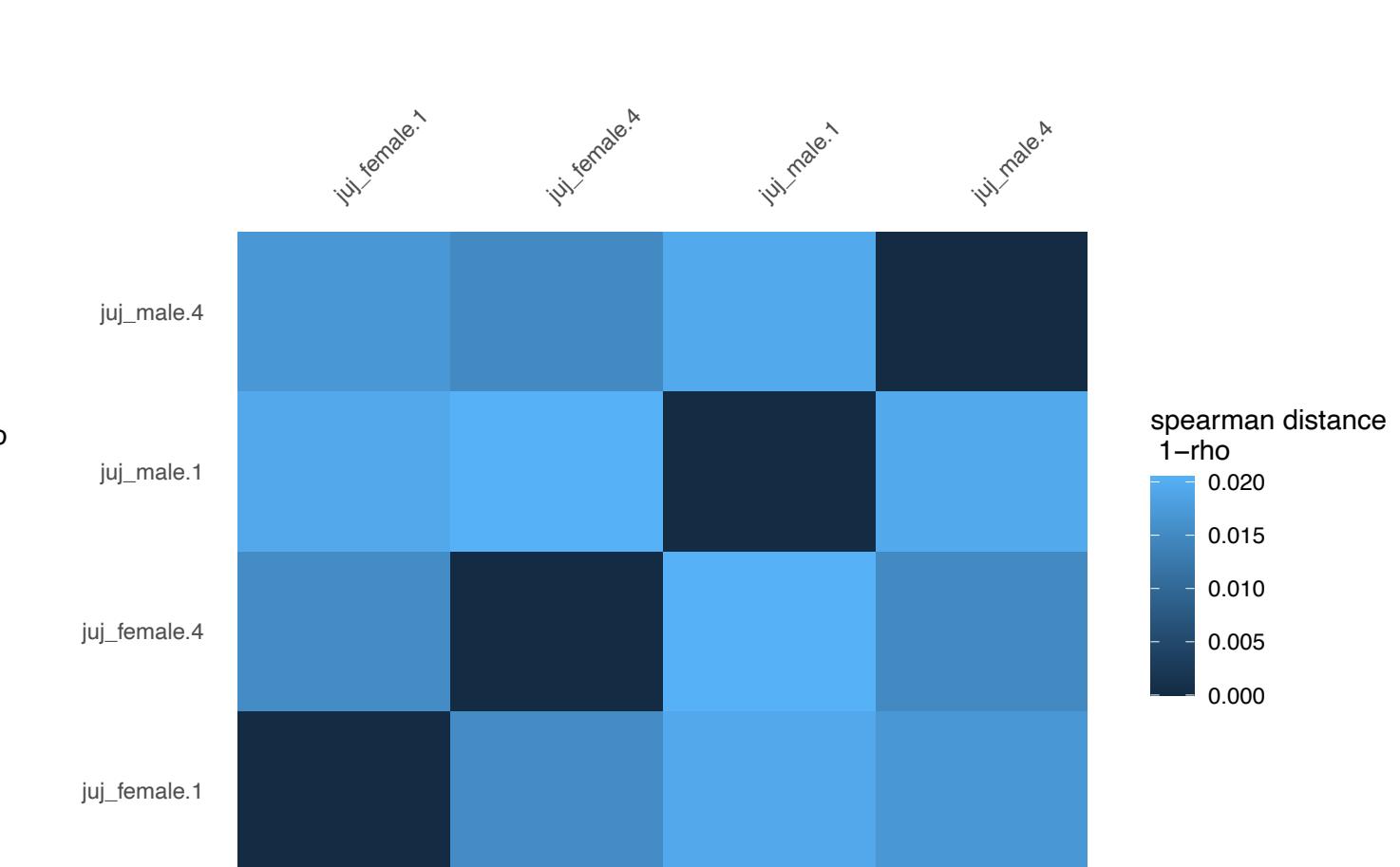
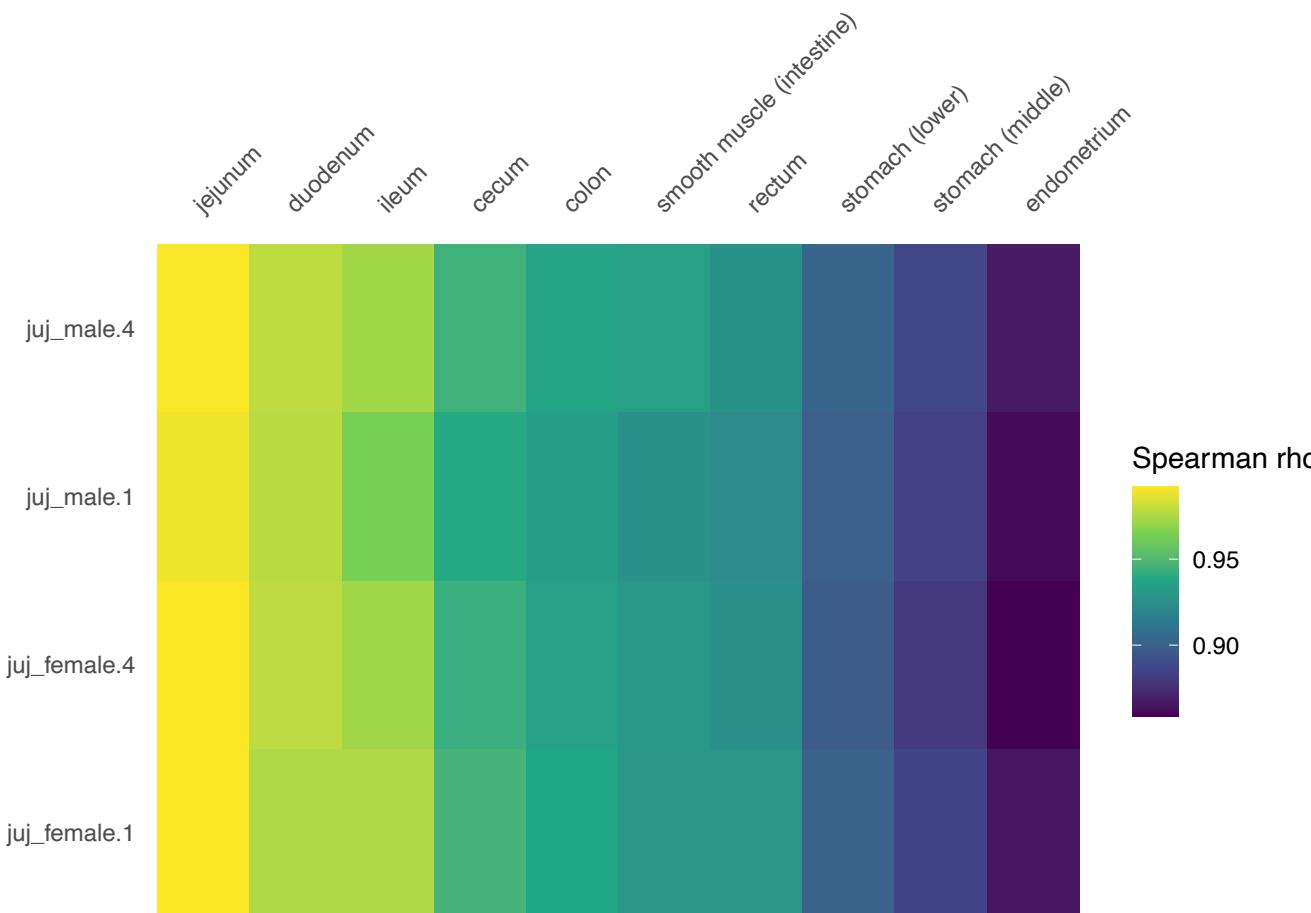
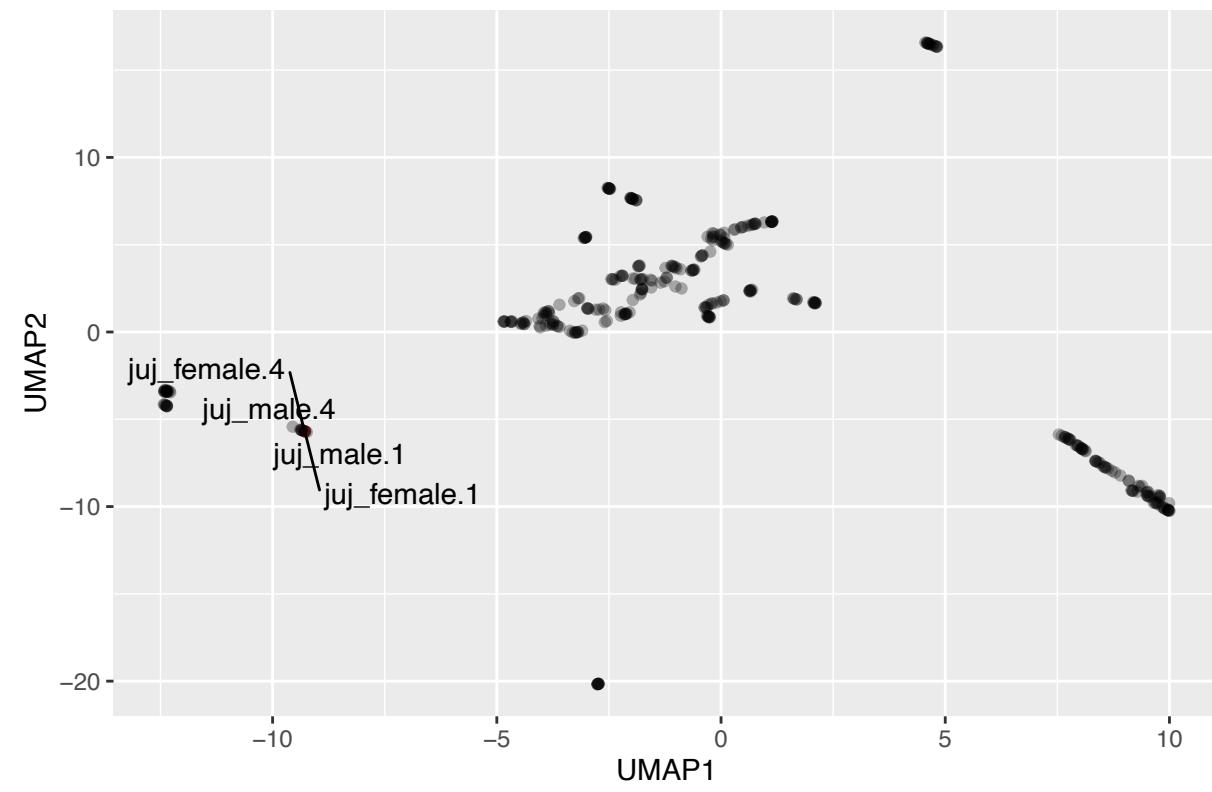
In tissue sample to sample Spearman Distance



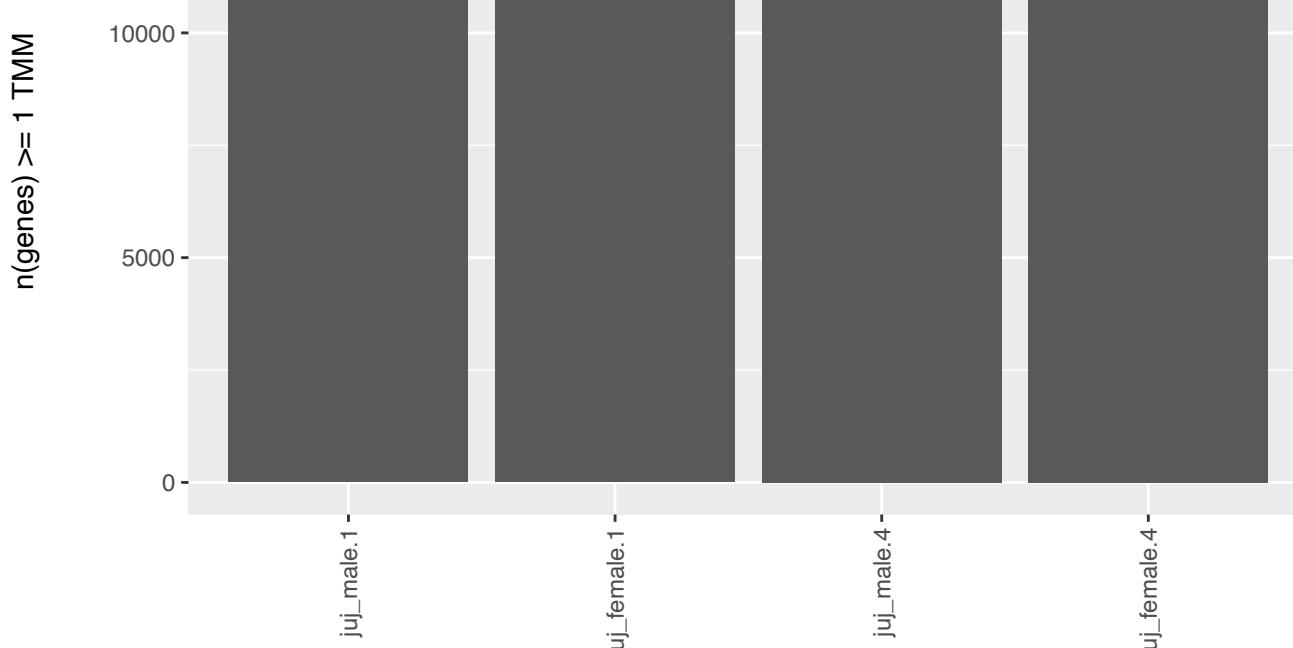
jejunum, PCA: TMM expression values



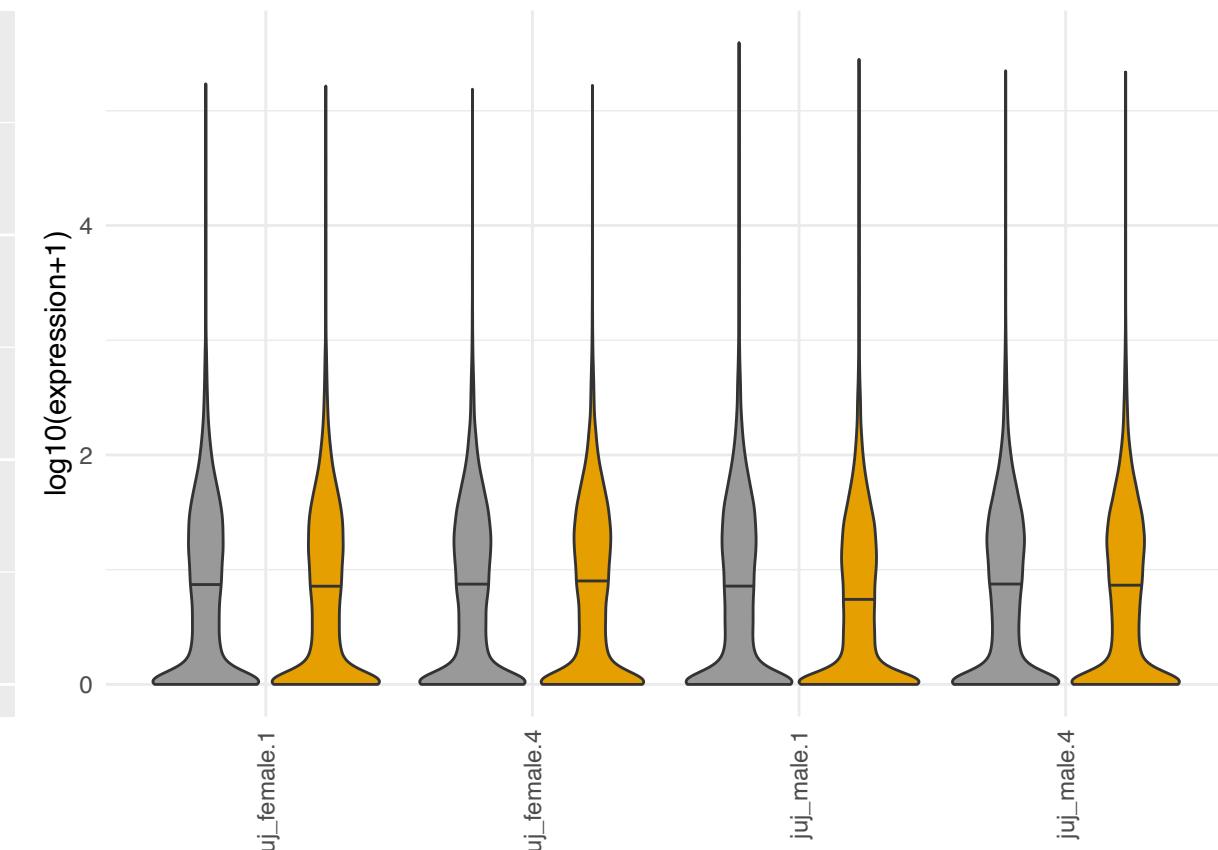
jejunum, UMAP: TMM expression values



jejunum

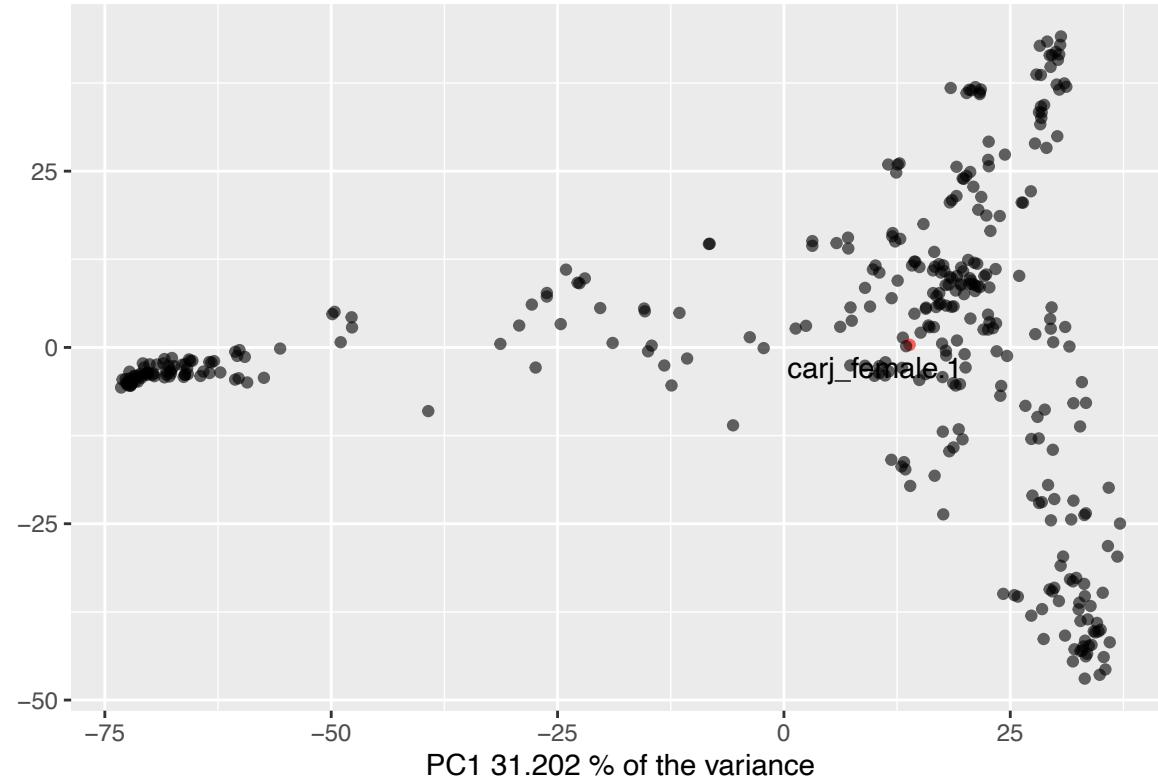


jejunum



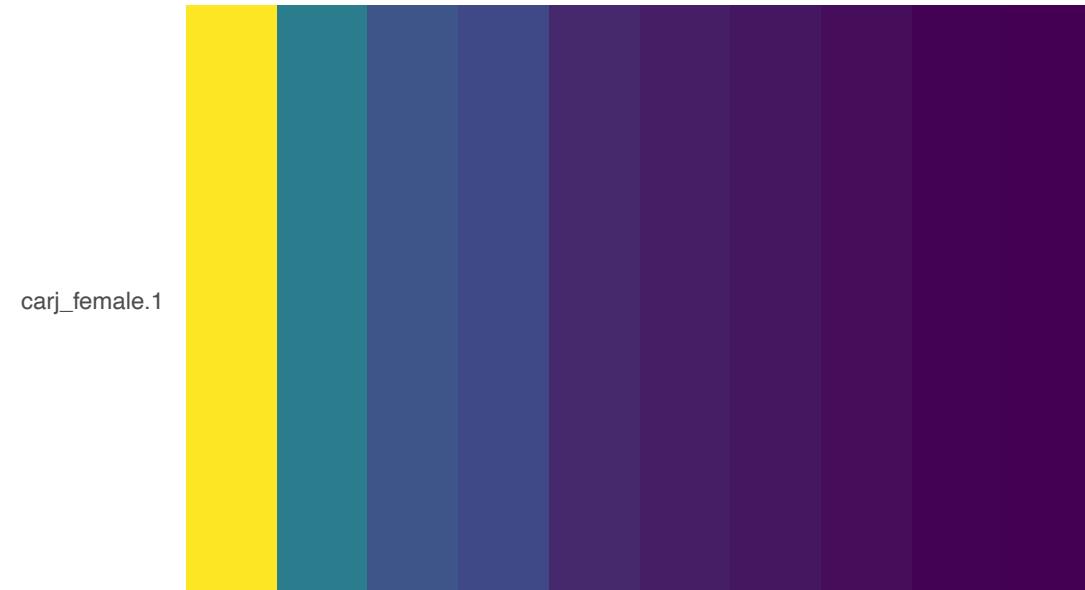
joint cartilage, PCA: TMM expression values

PC2 9.077 % of the variance



Tissue group to sample correlation

joint cartilage
synovial tissue
dura mater
artery
penis
vein
aorta
smooth muscle (uterus)
pleura
pericardium



Spearman rho
1.00
0.98
0.96
0.94
0.92

carj_female.1

In tissue sample to sample Spearman Distance

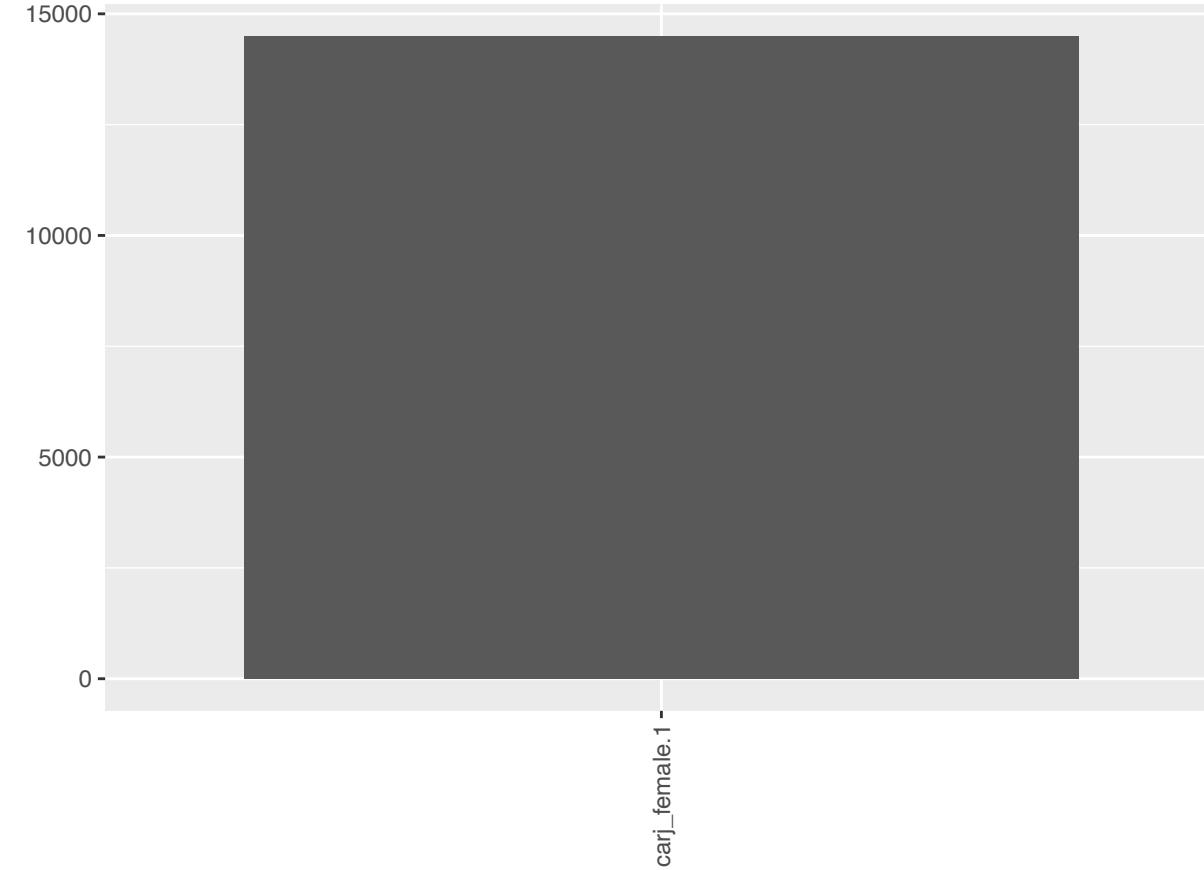
carj_female.1



spearman distance
1-rho
0

joint cartilage

n(genes) >= 1 TMM



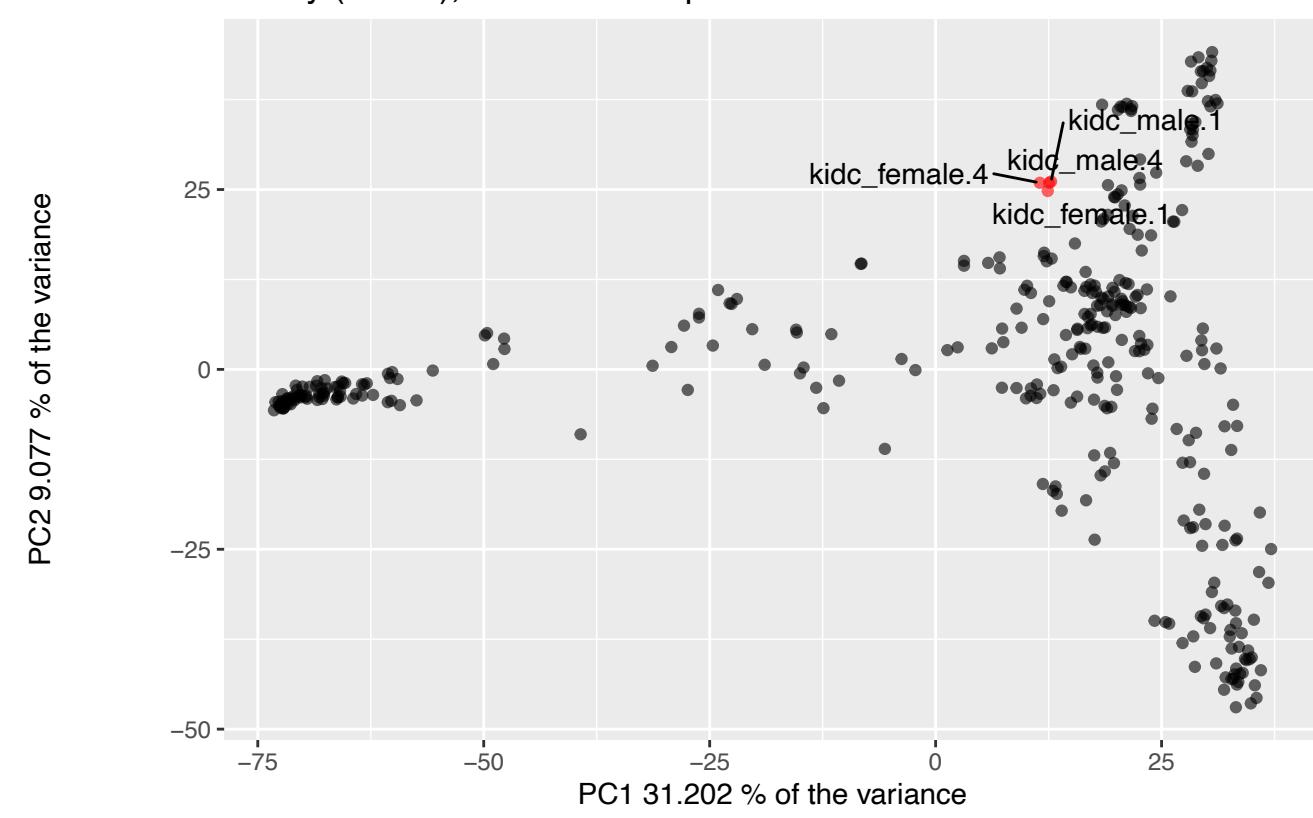
joint cartilage

log10(expression+1)

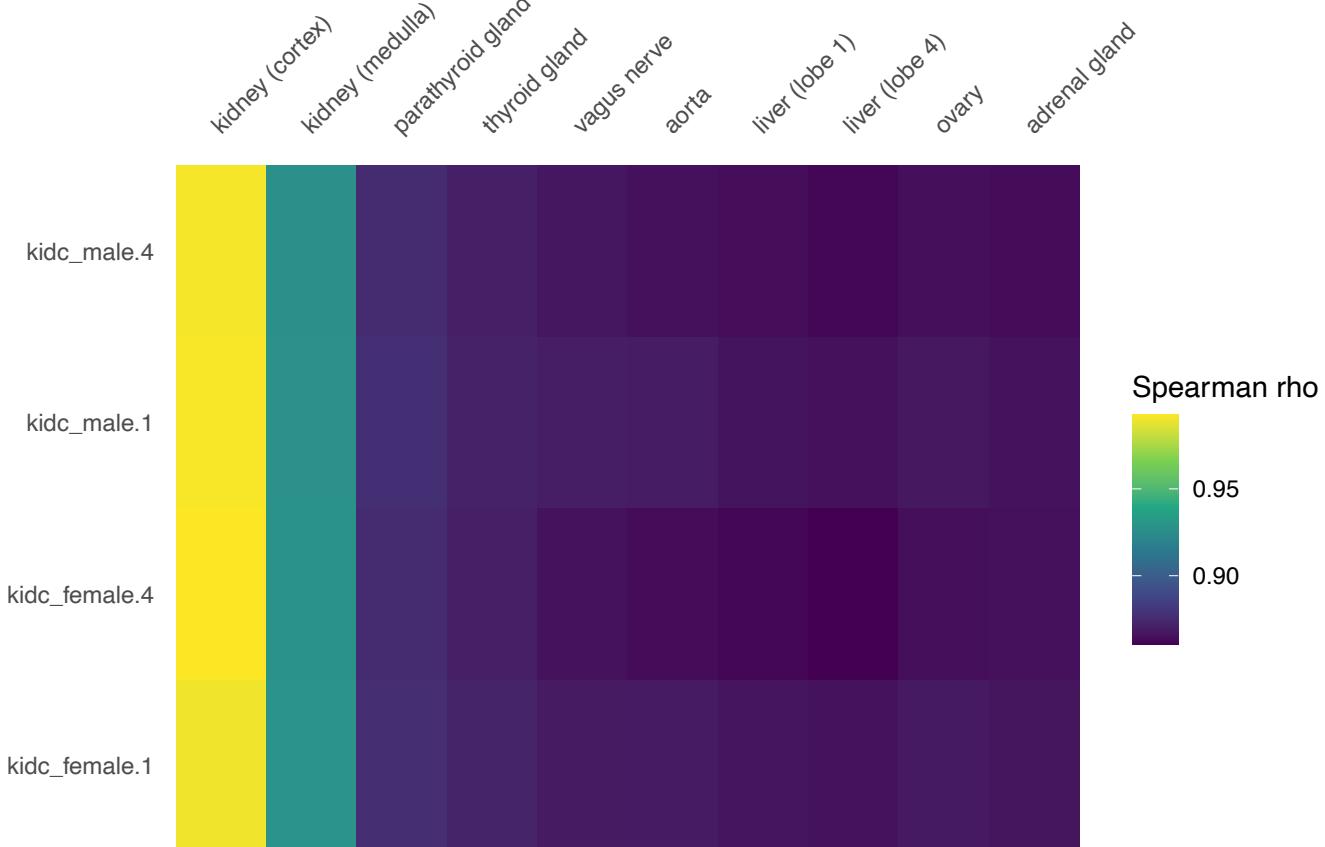
carj_female.1

type
tmm_val
tpm_val

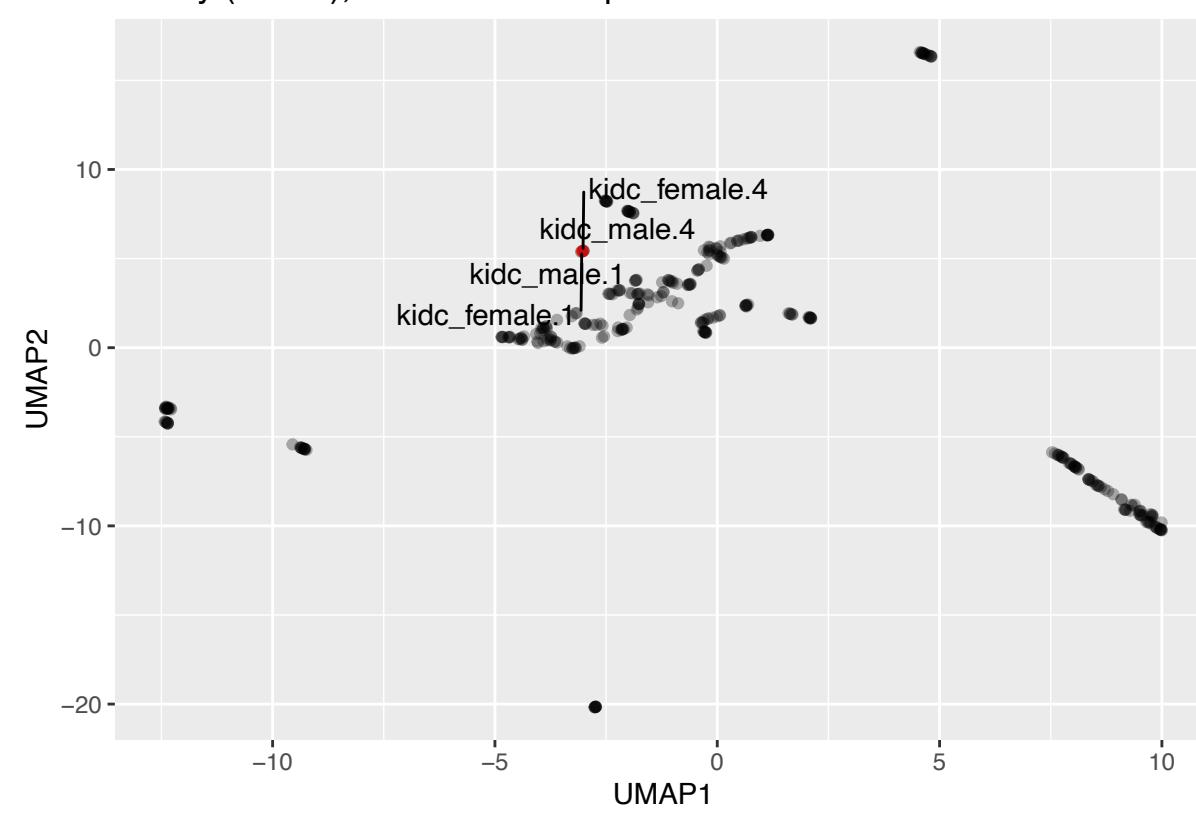
kidney (cortex), PCA: TMM expression values



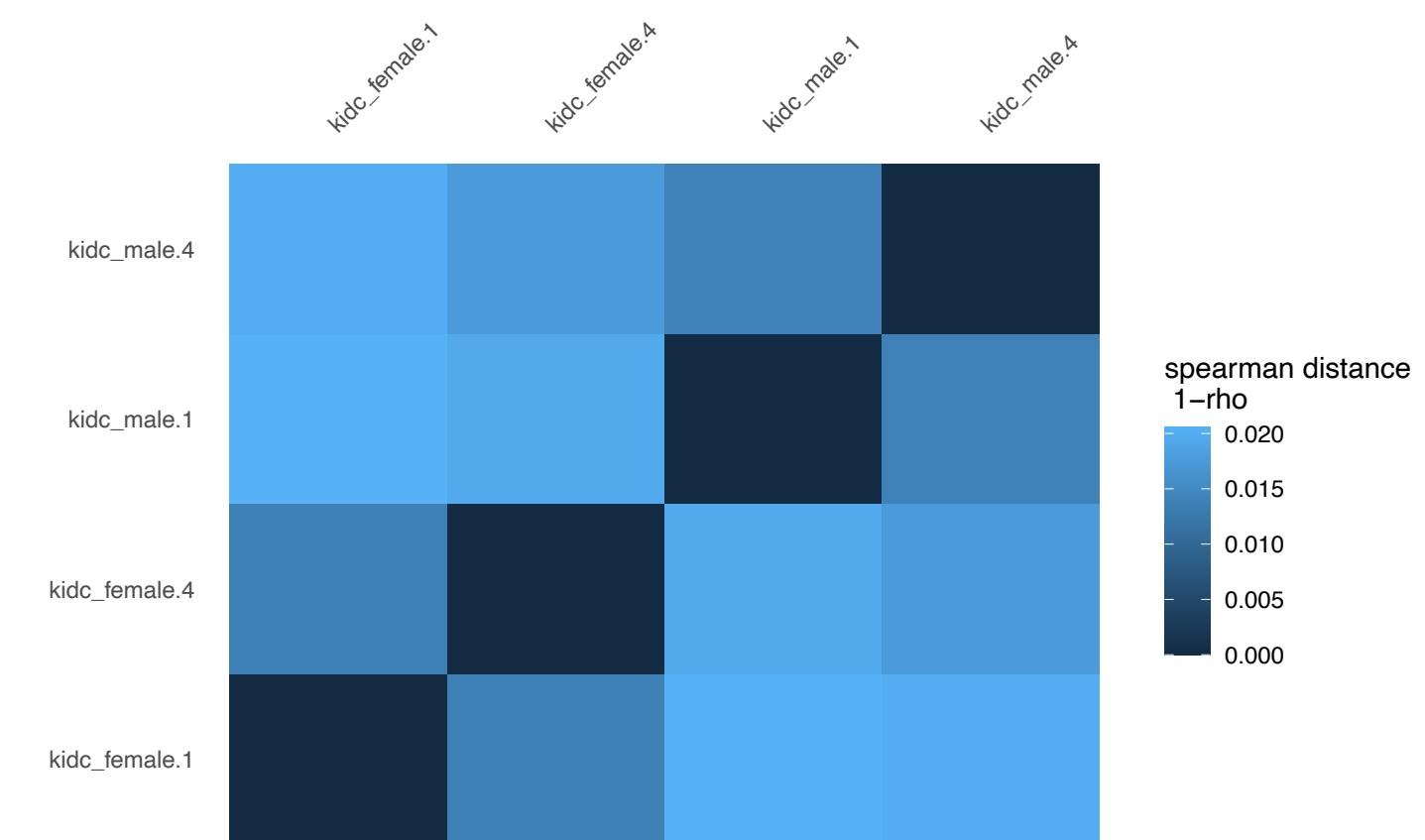
Tissue group to sample correlation



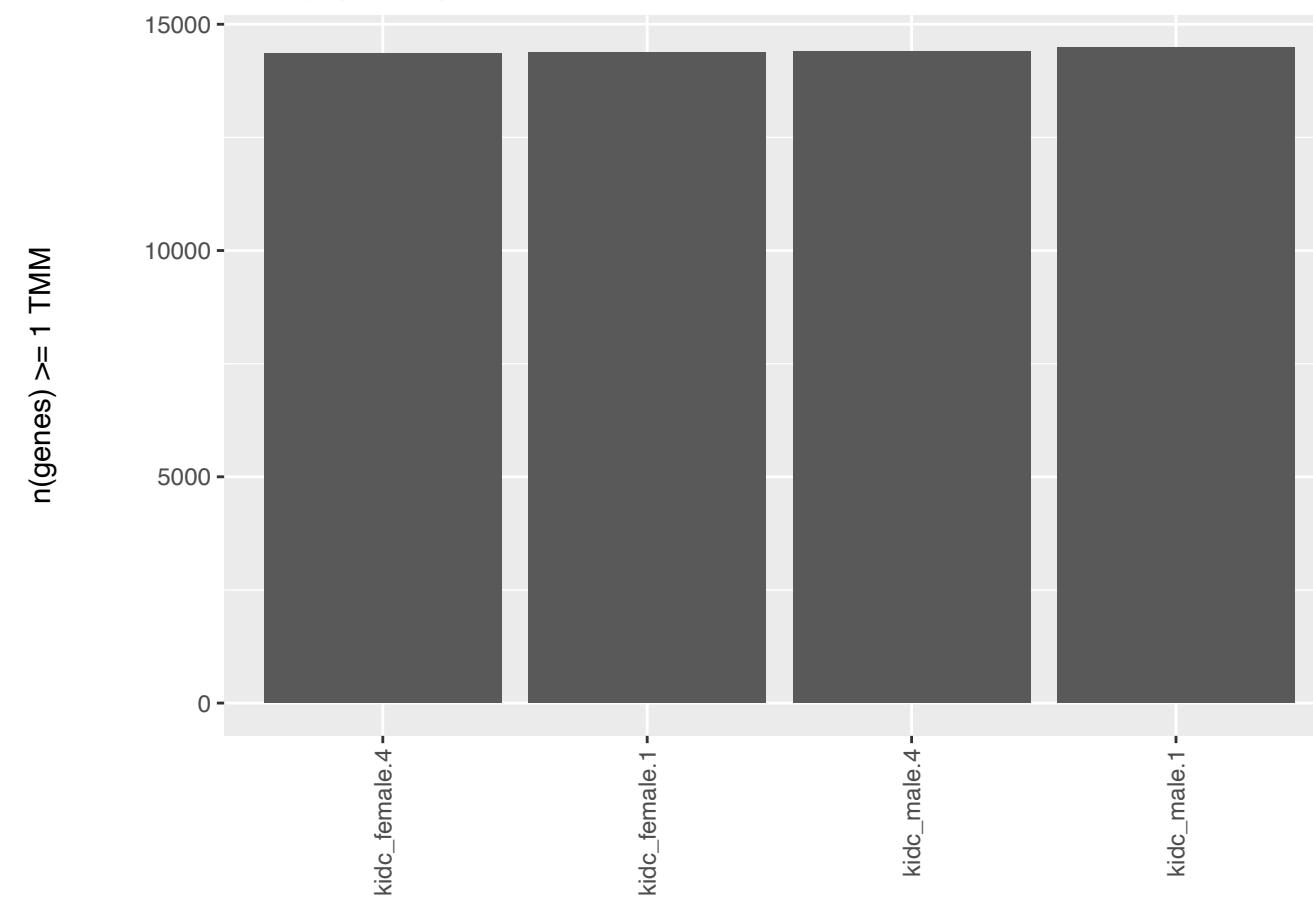
kidney (cortex), UMAP: TMM expression values



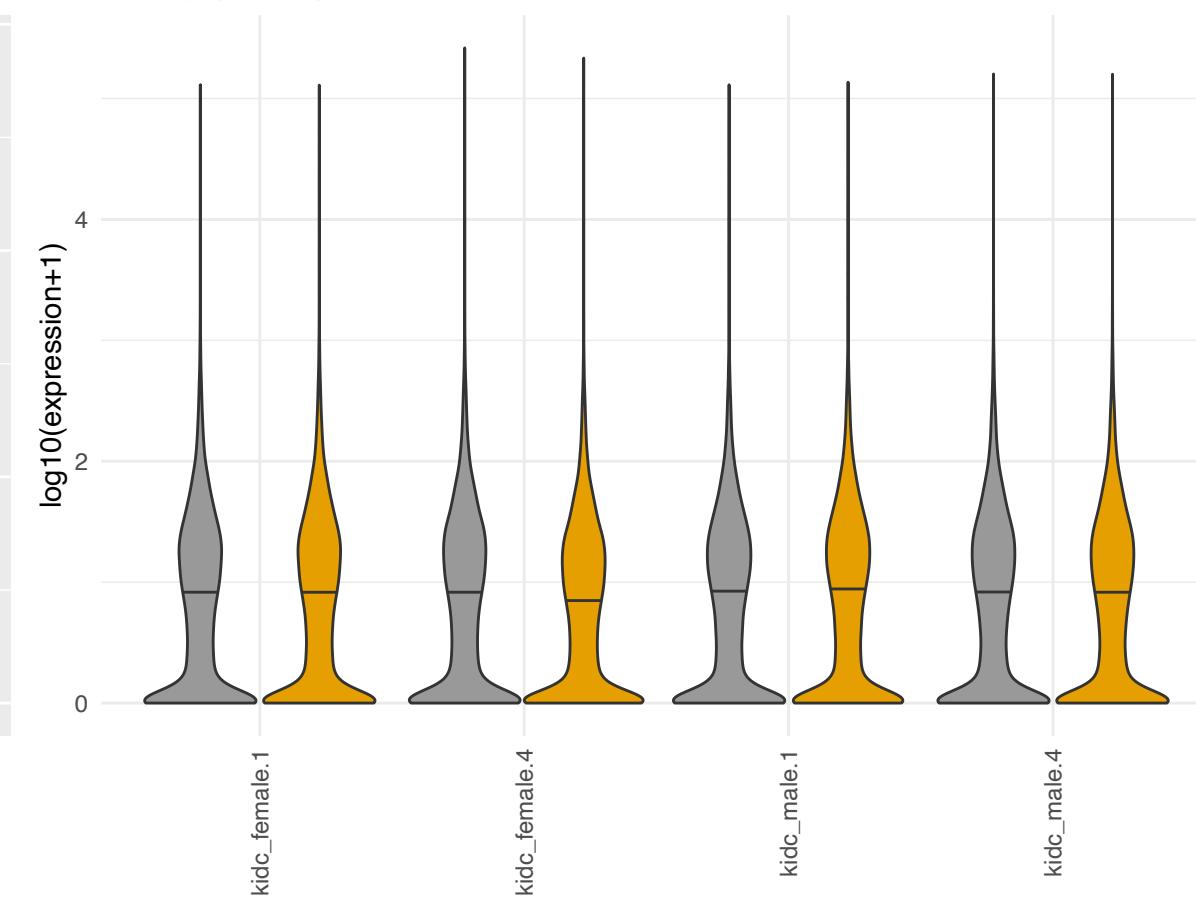
In tissue sample to sample Spearman Distance

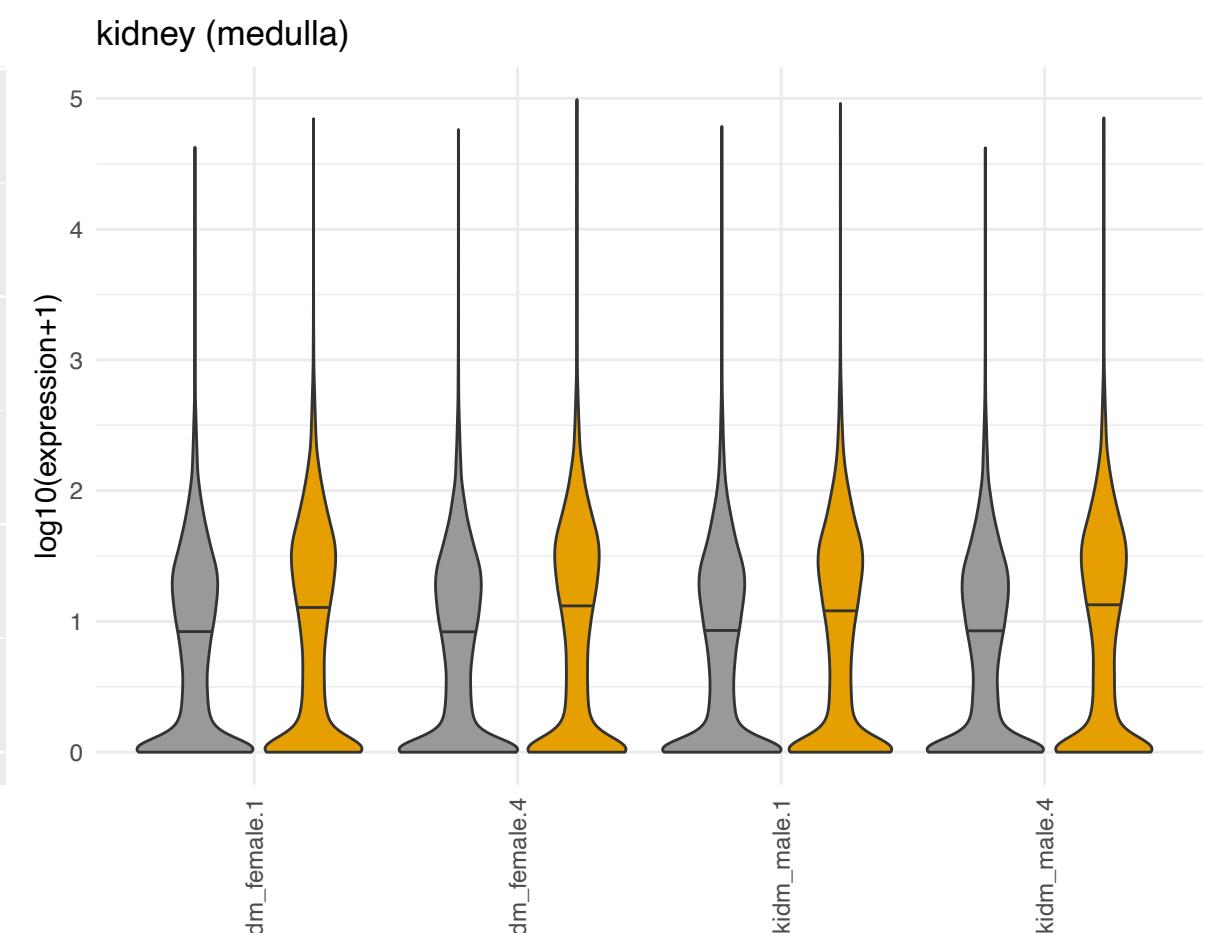
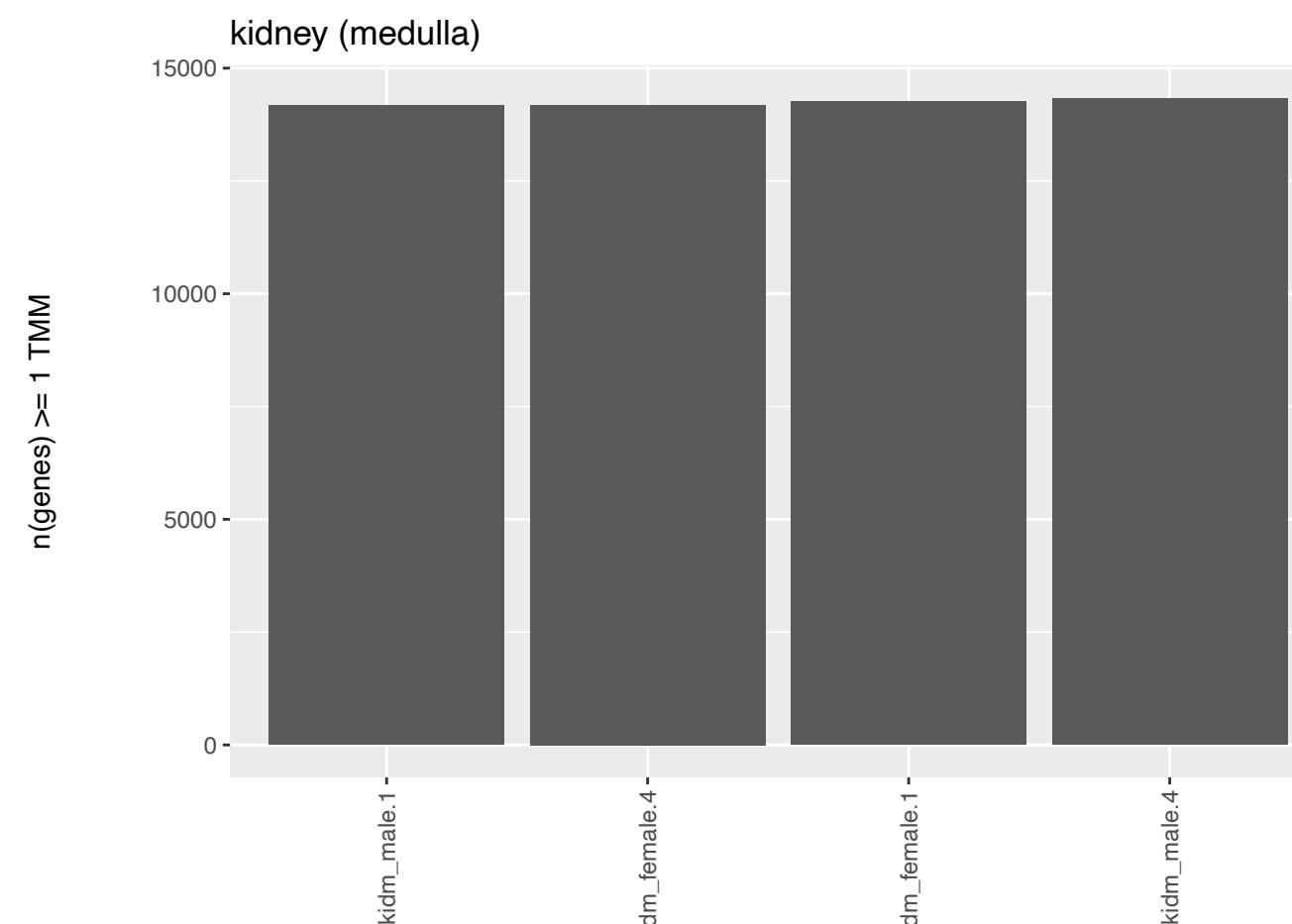
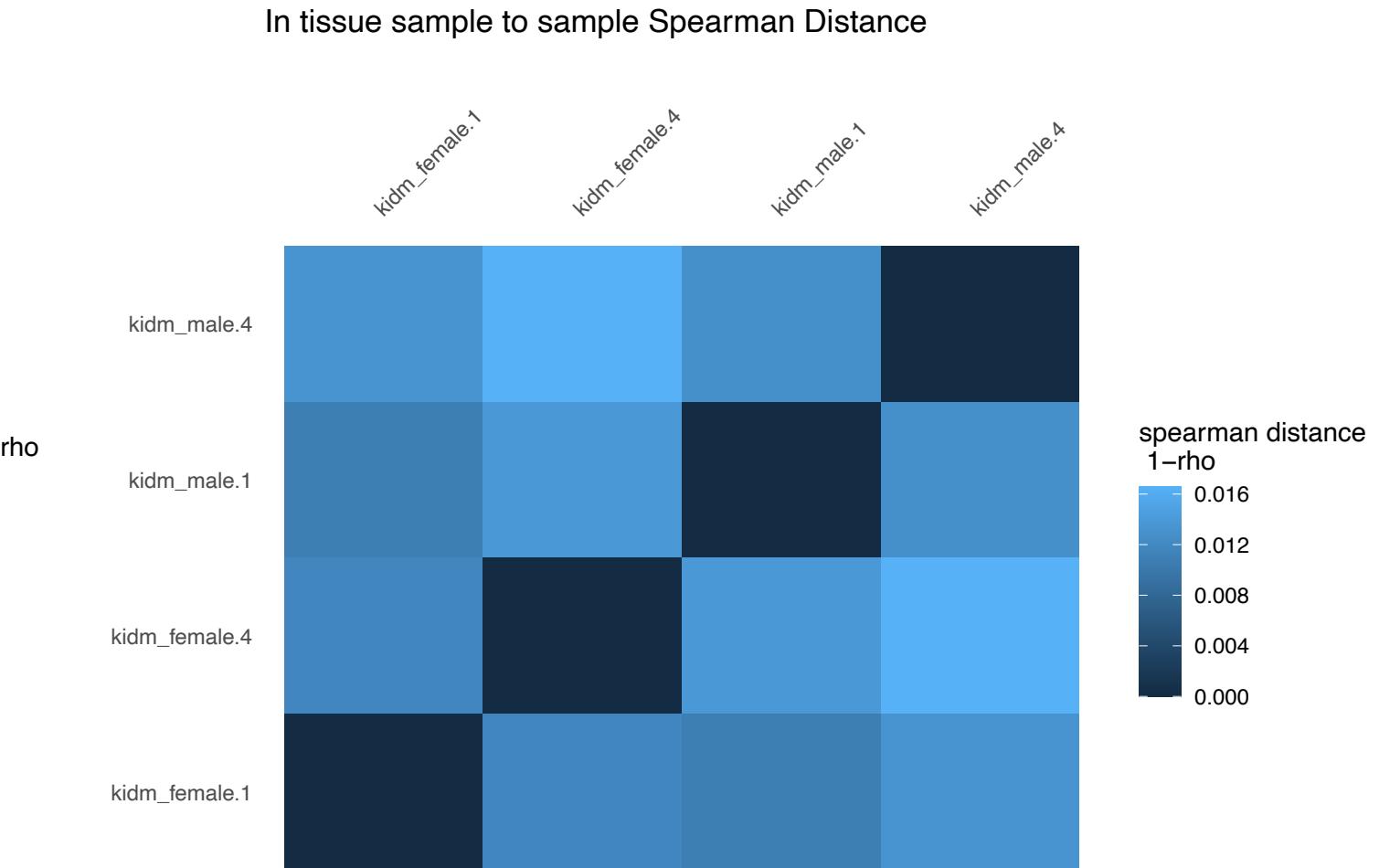
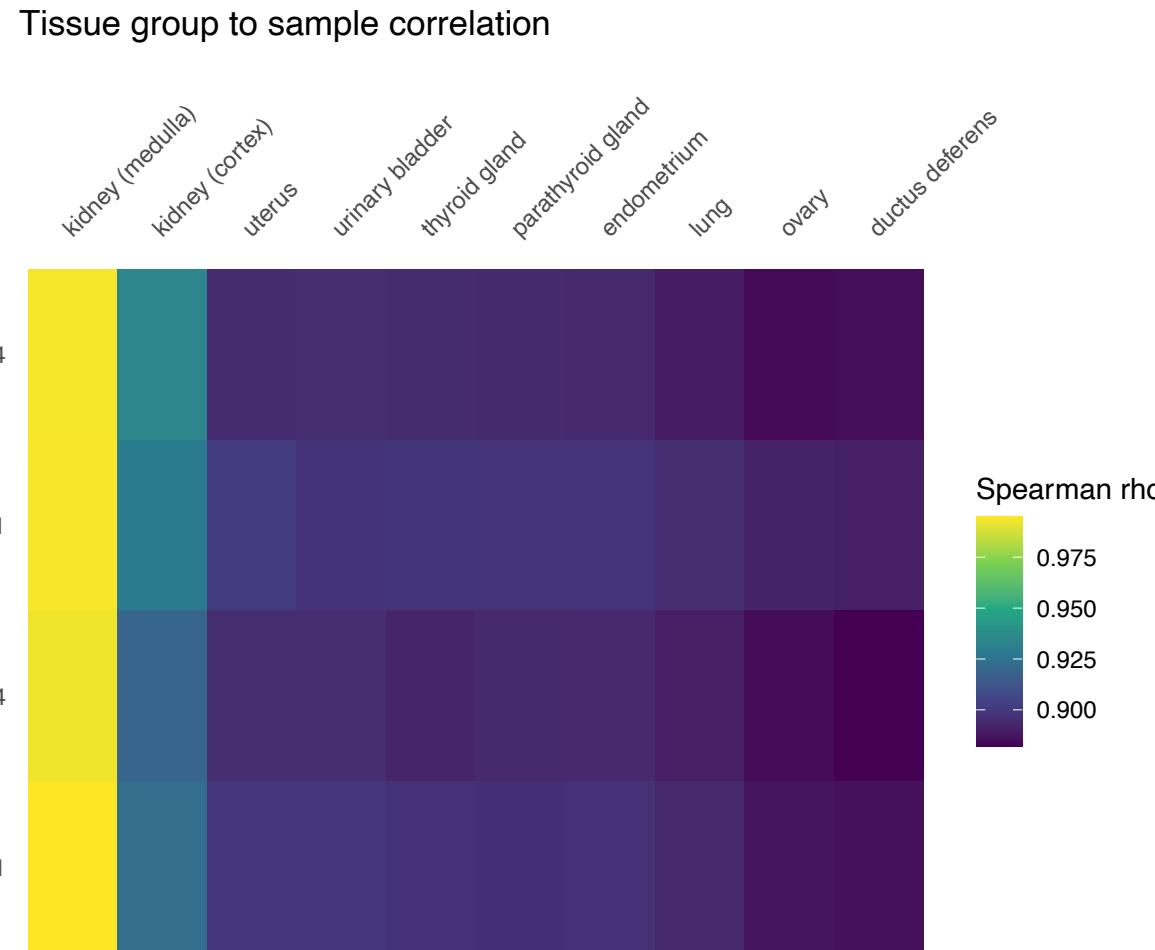
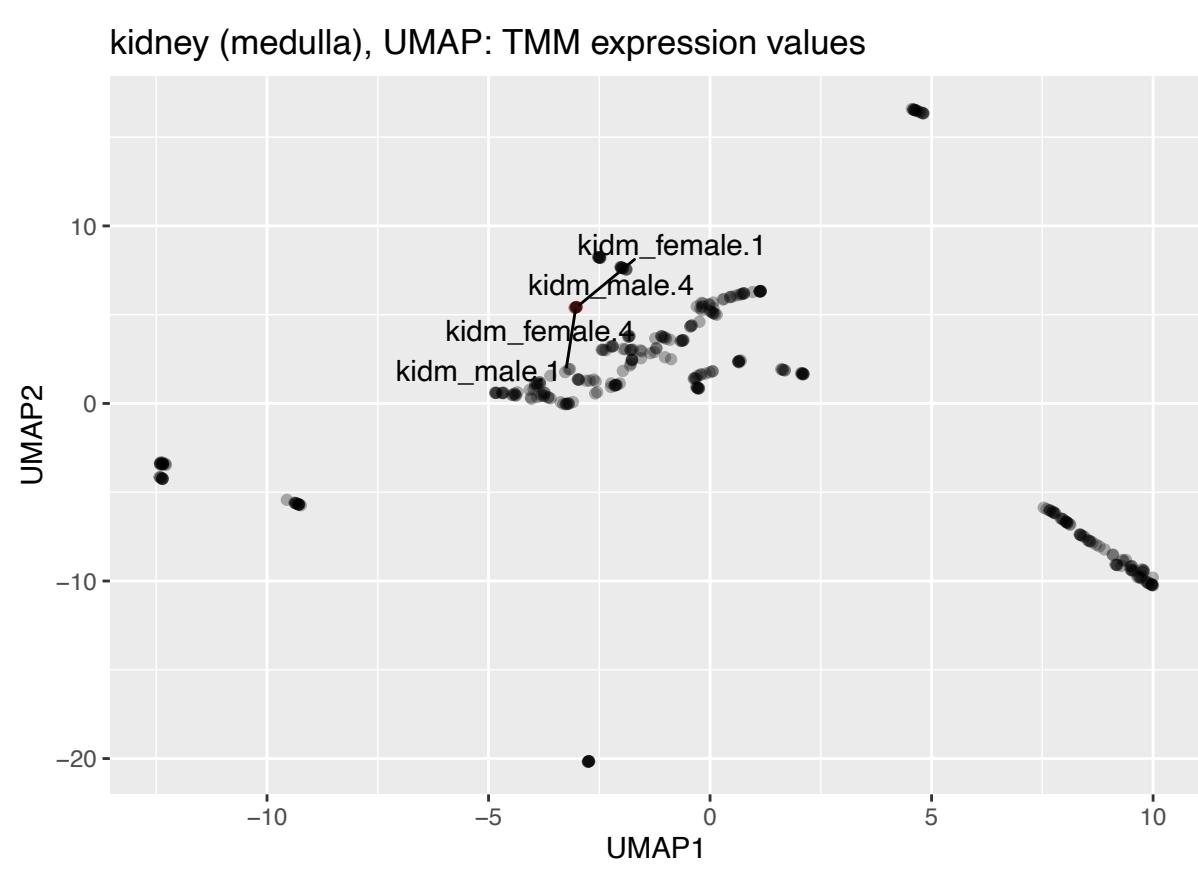
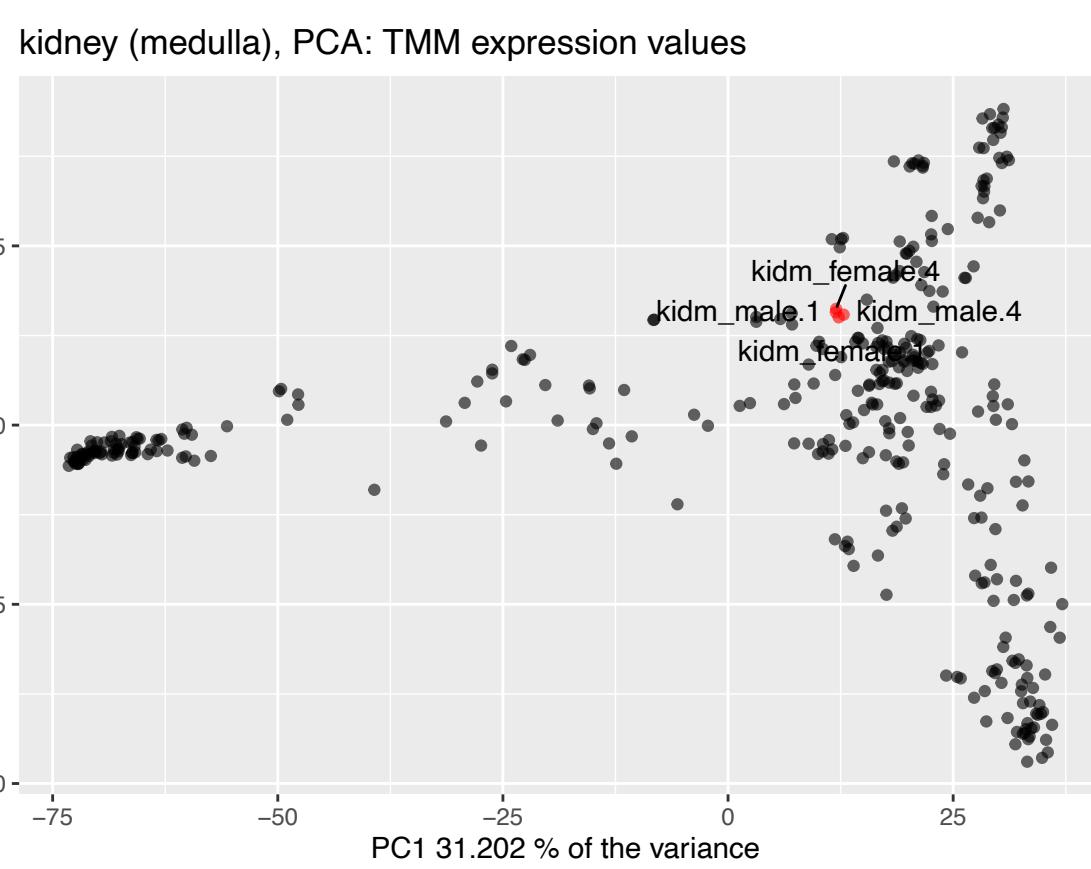


kidney (cortex)

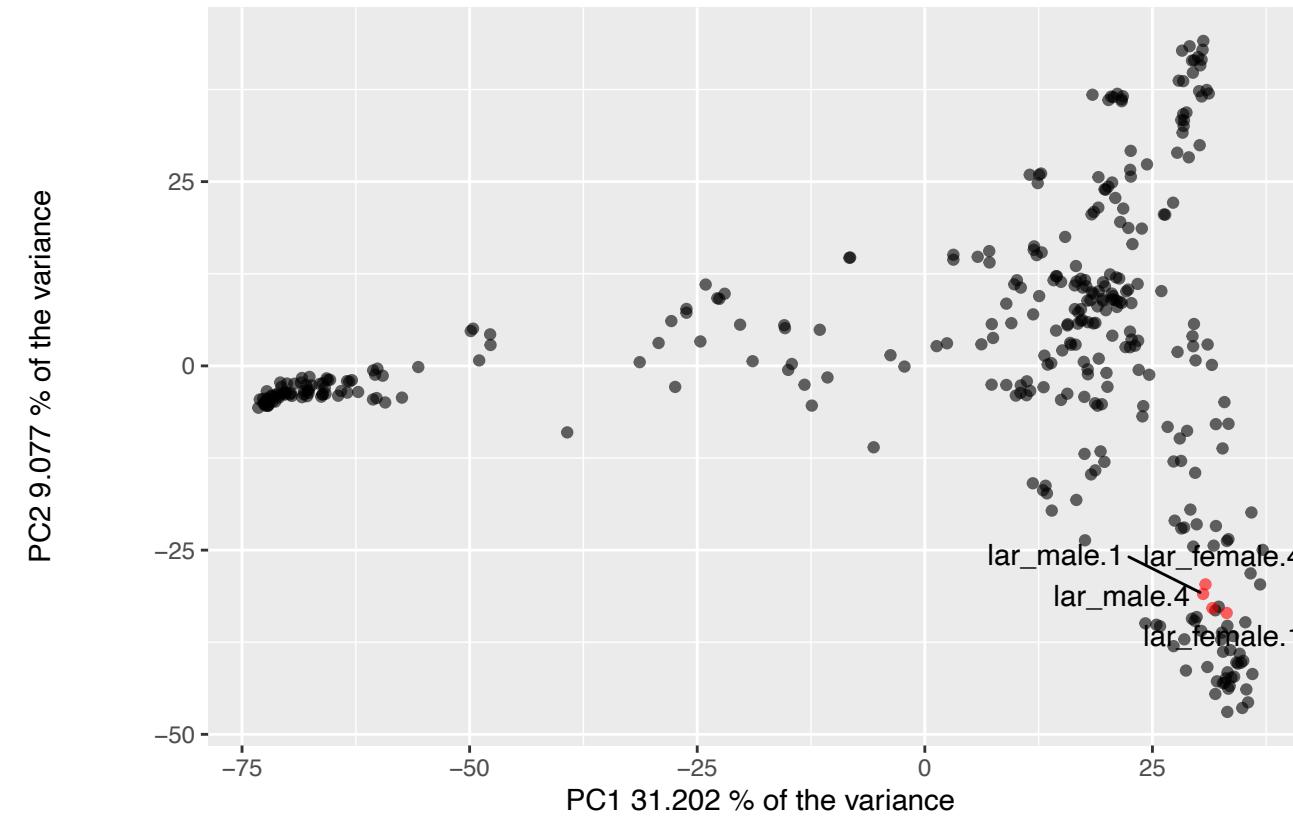


kidney (cortex)





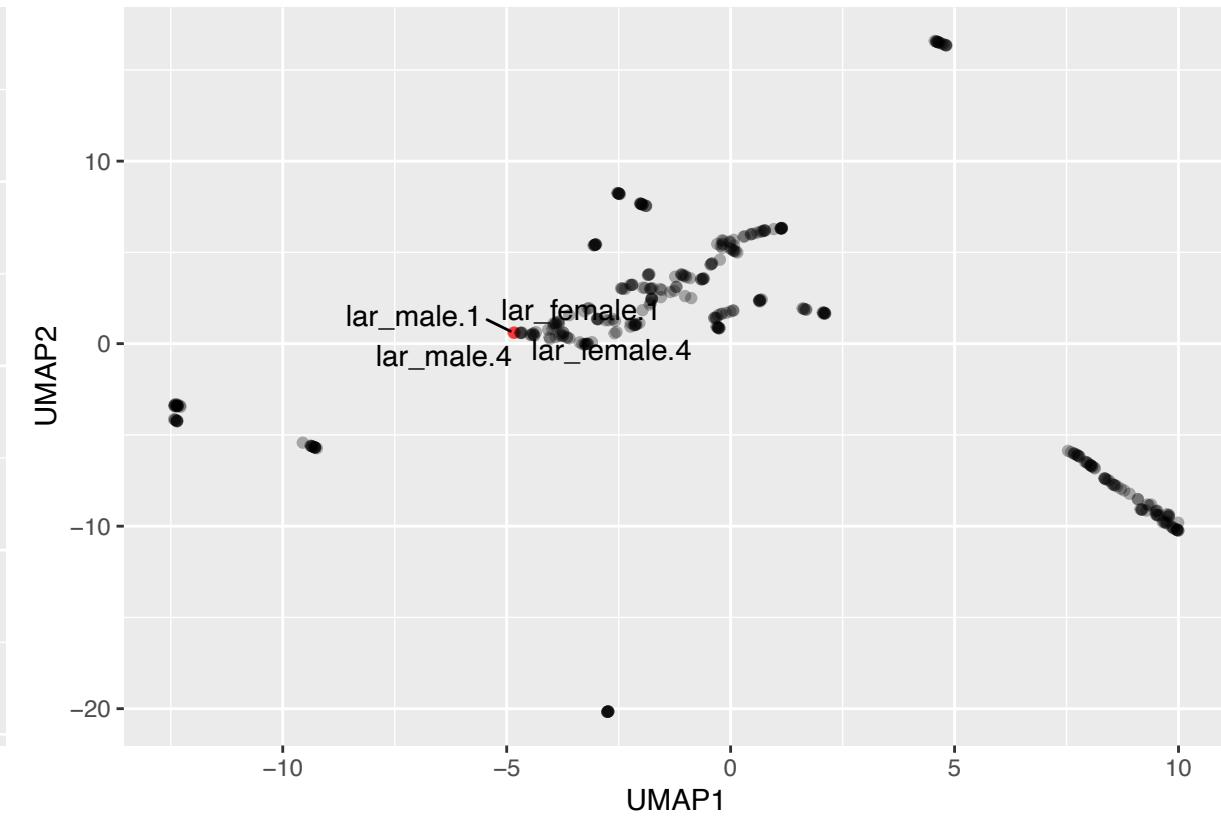
larynx, PCA: TMM expression values



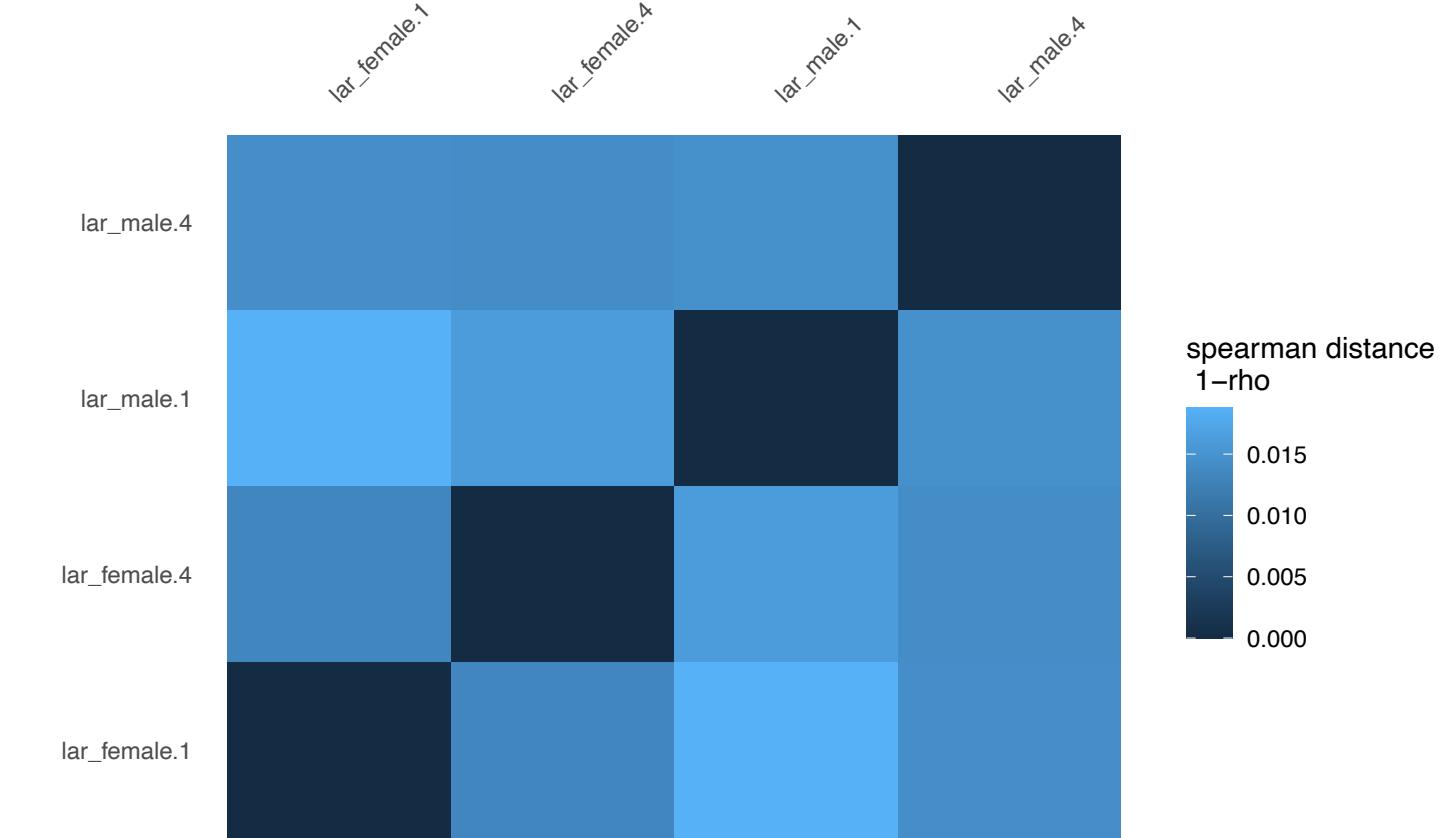
Tissue group to sample correlation



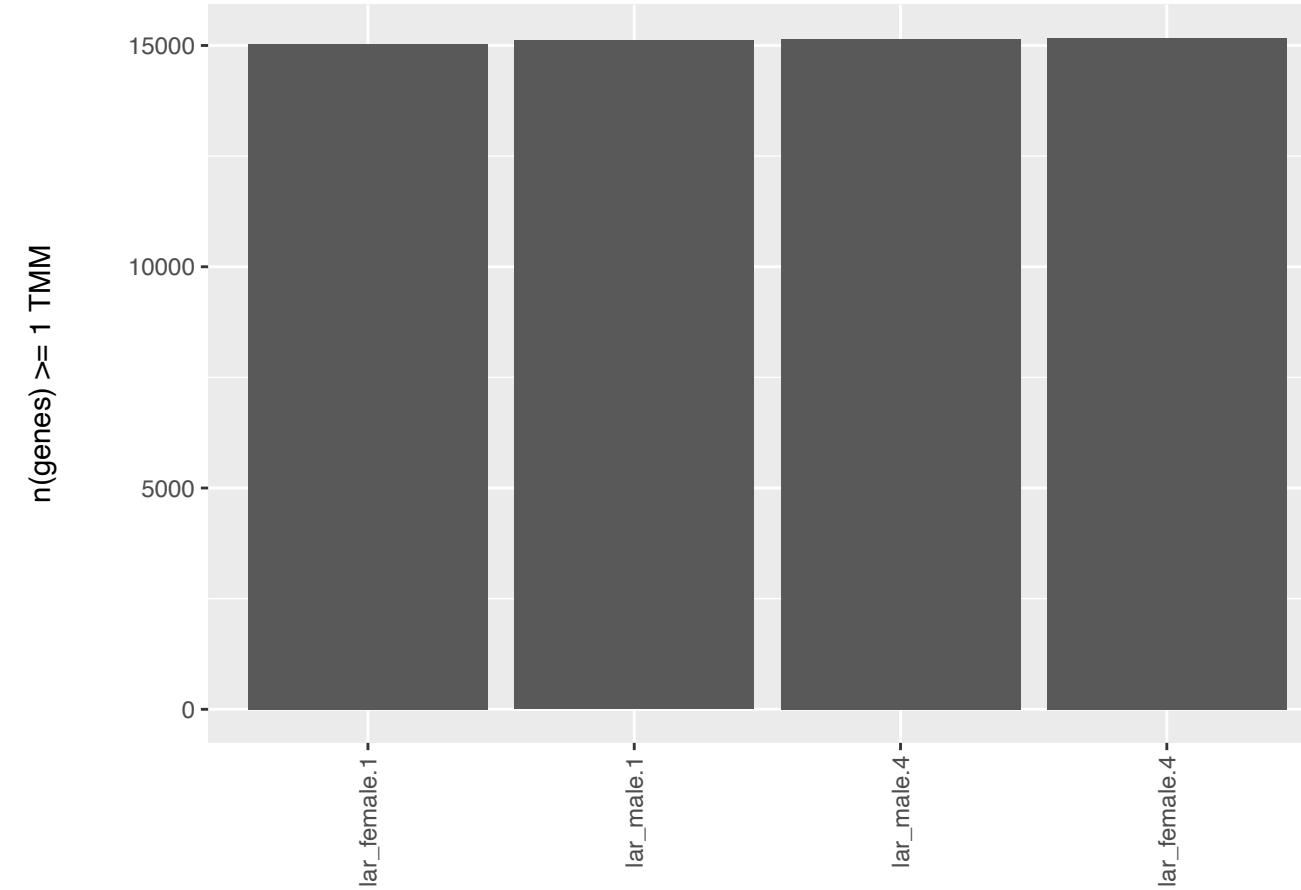
larynx, UMAP: TMM expression values



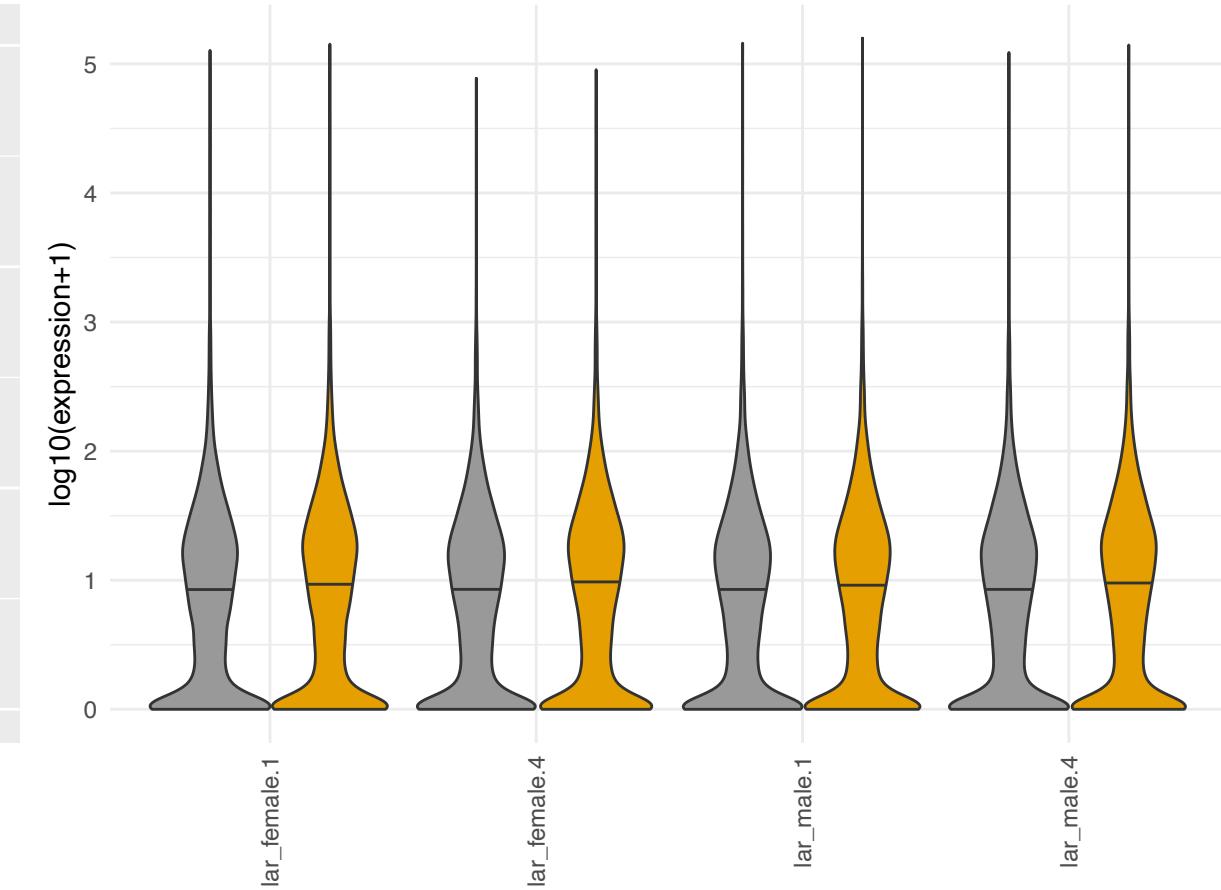
In tissue sample to sample Spearman Distance



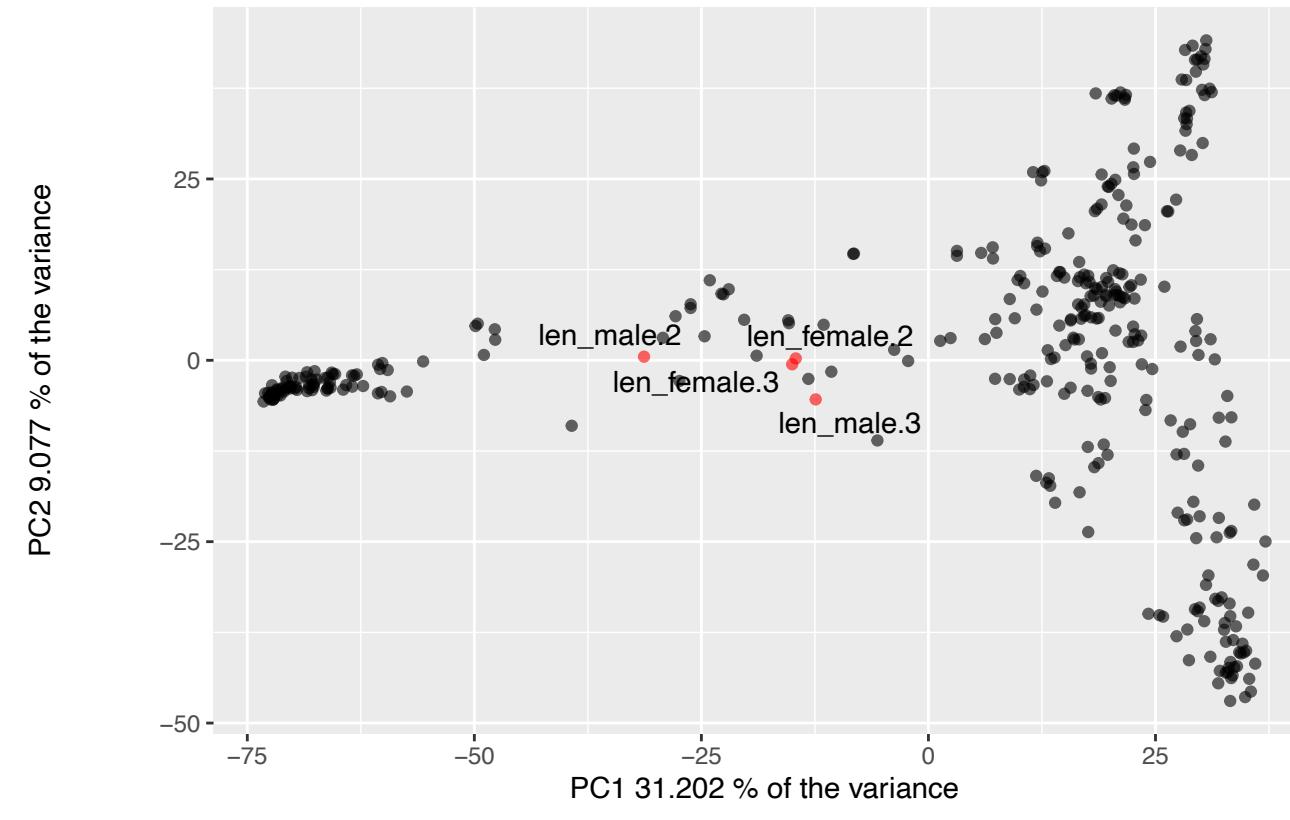
larynx



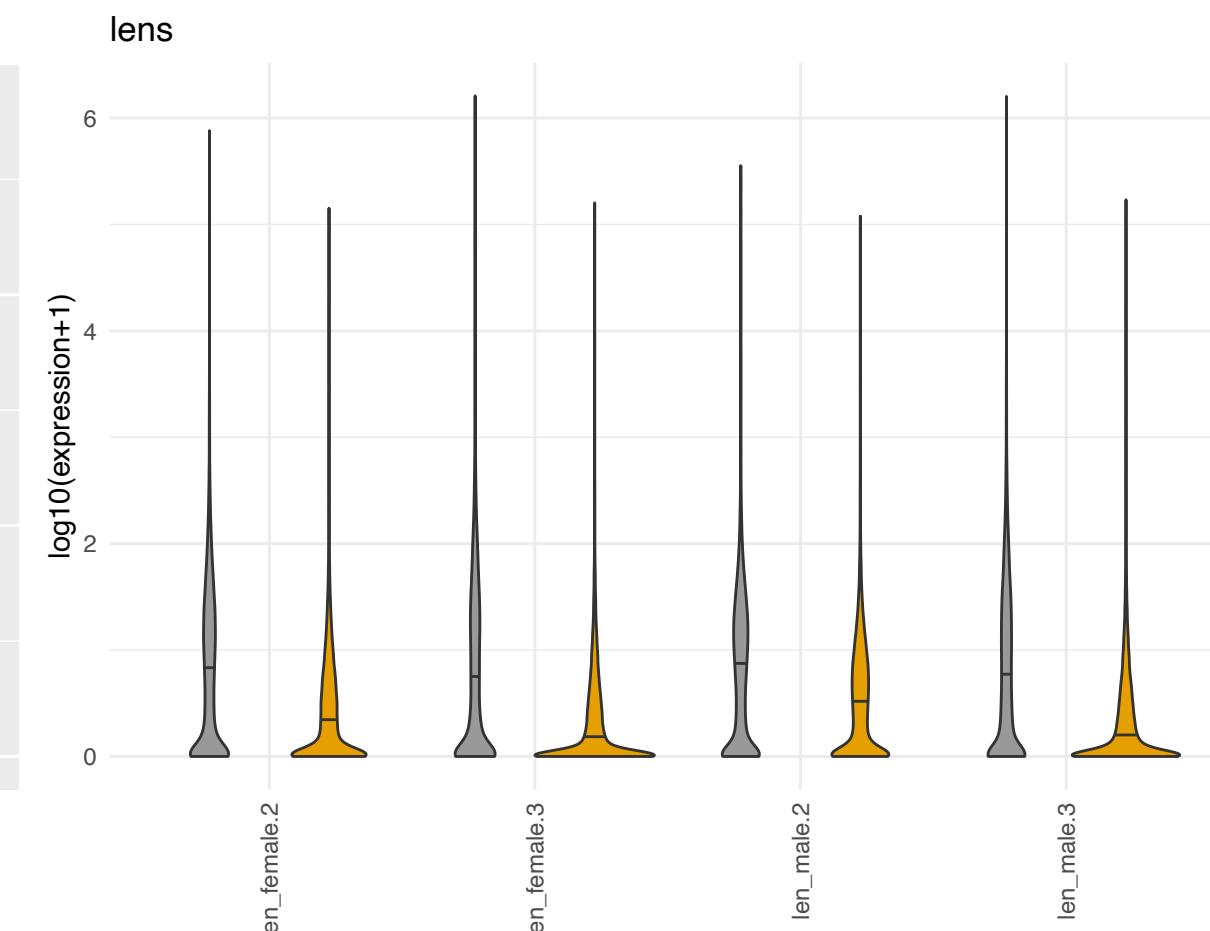
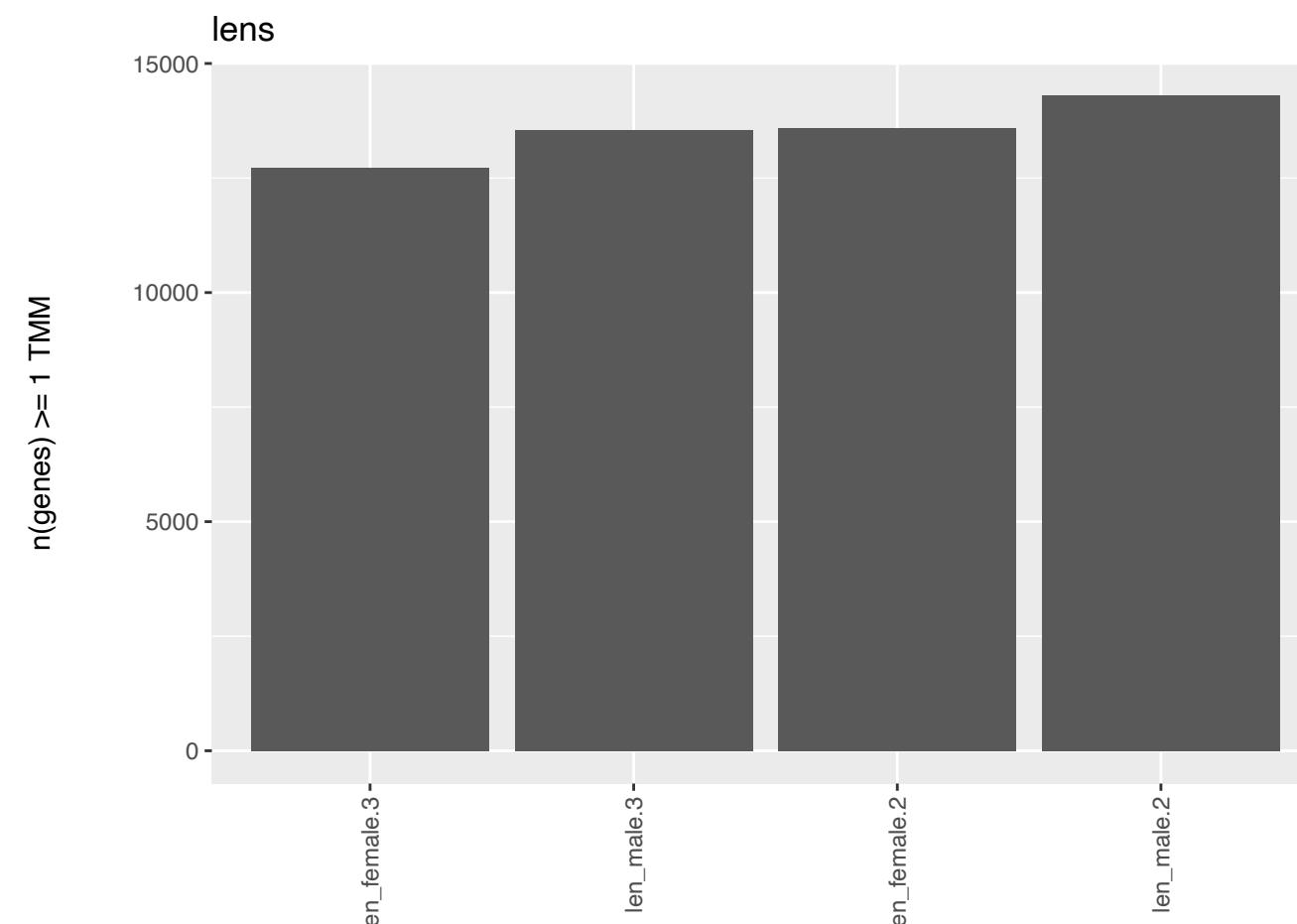
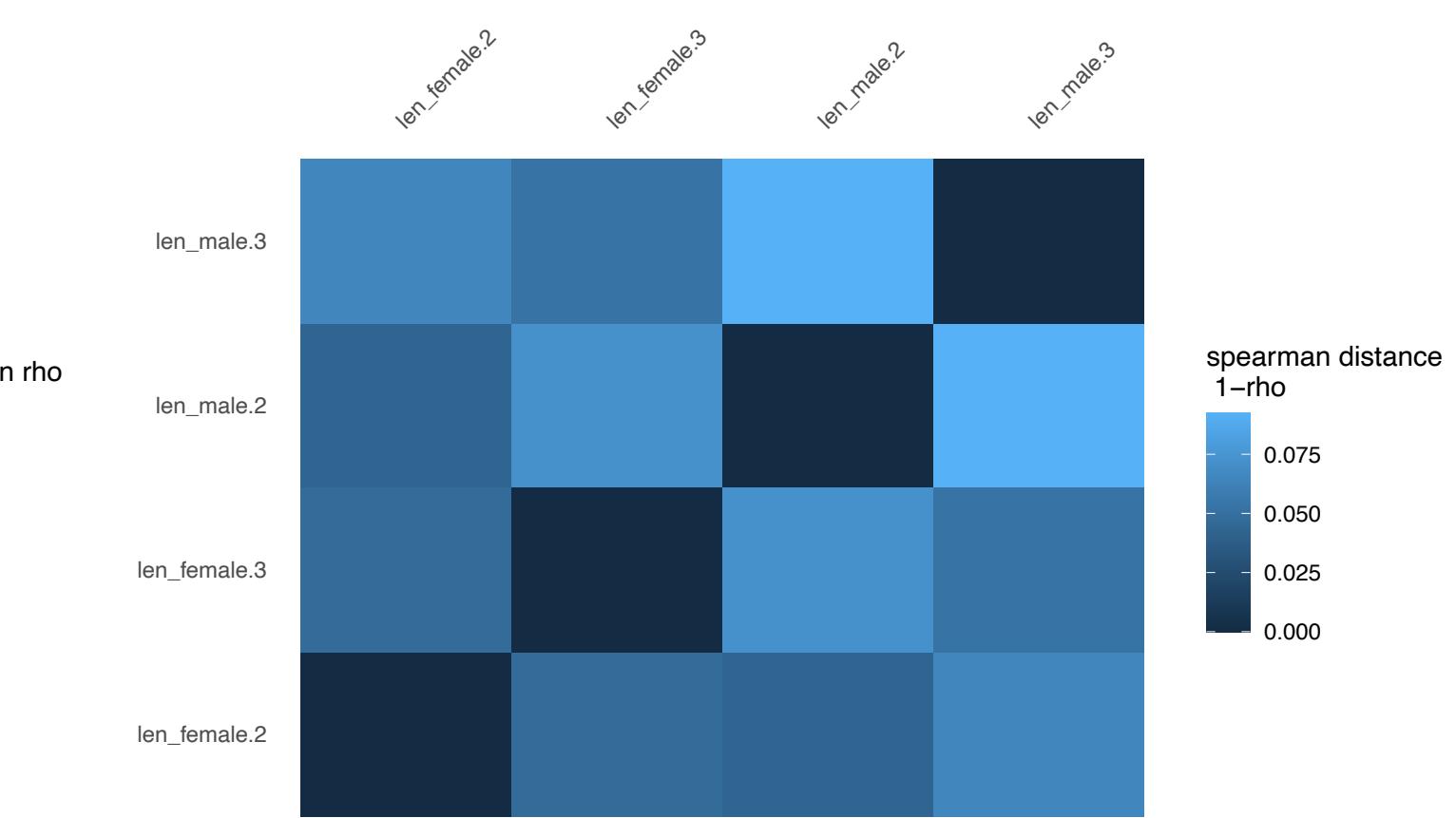
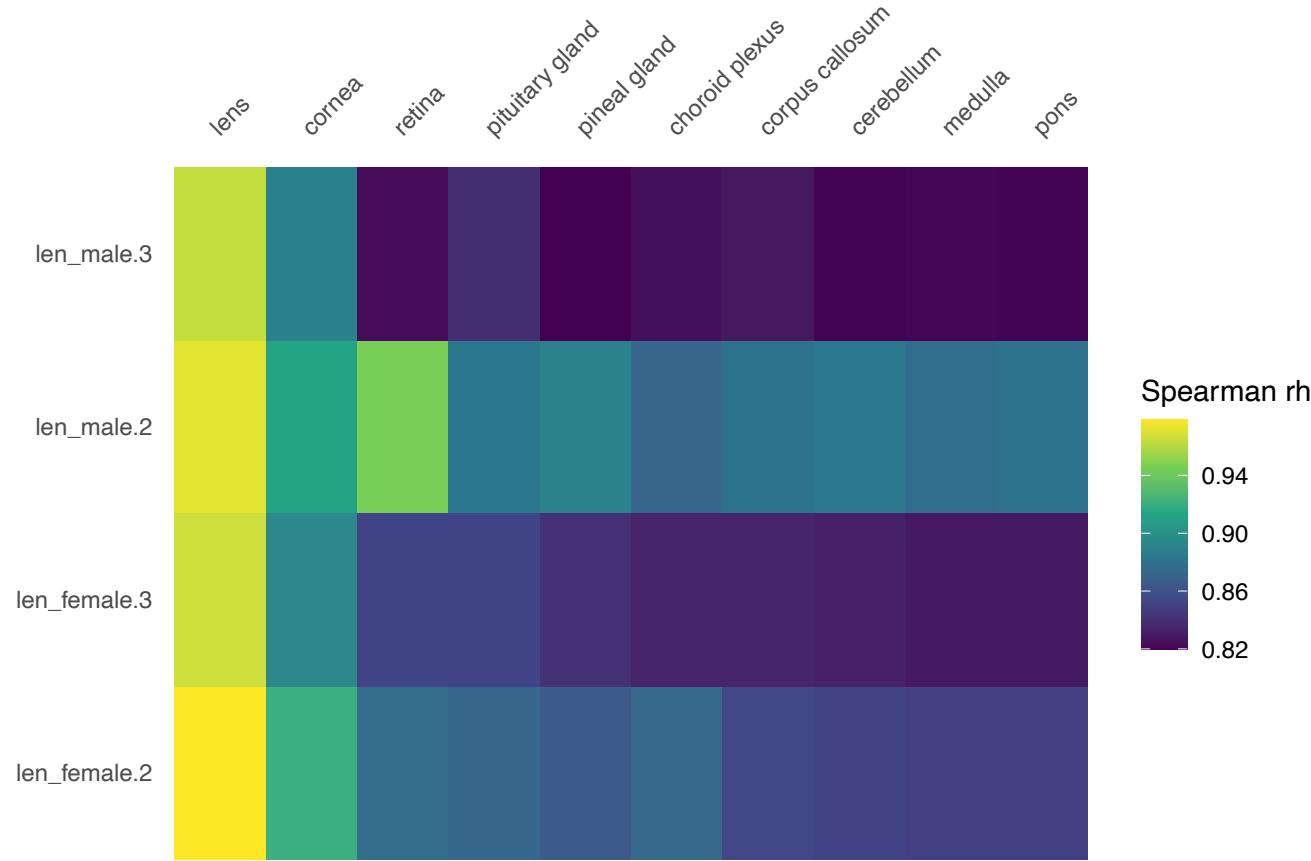
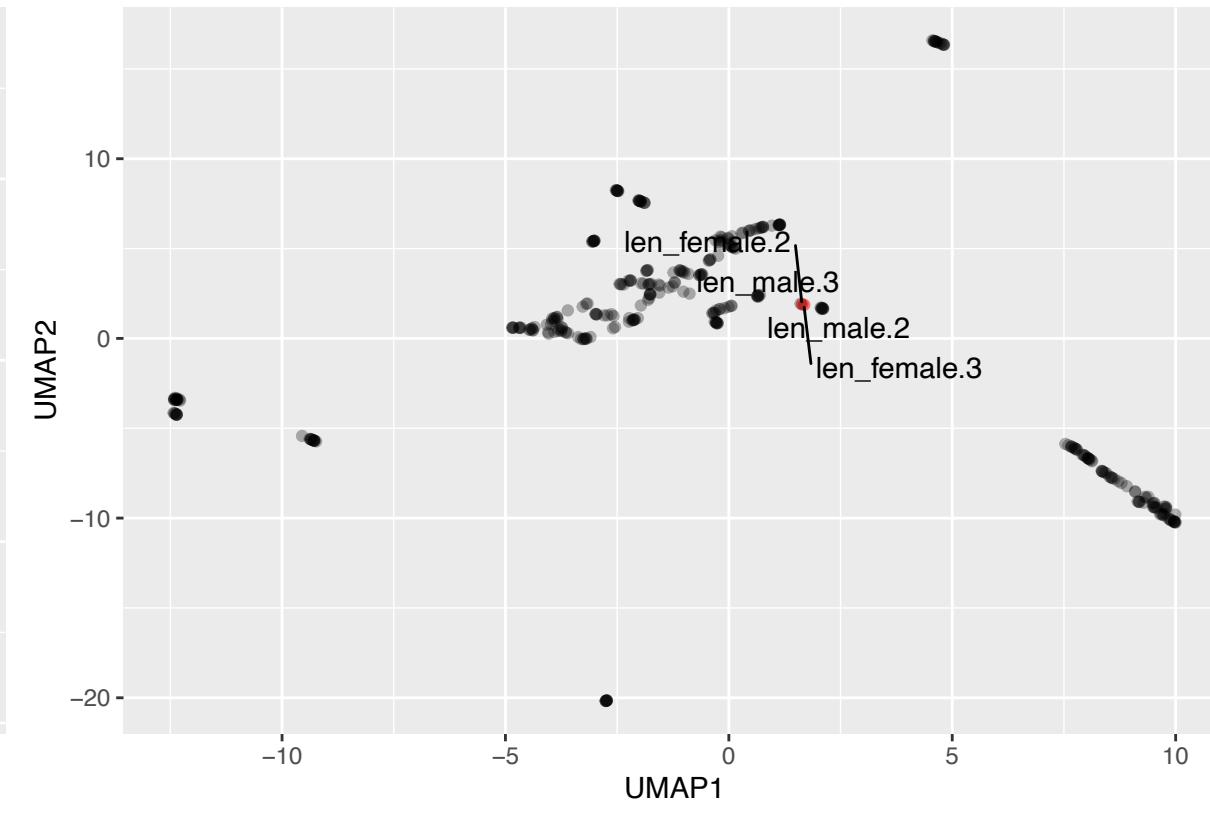
larynx



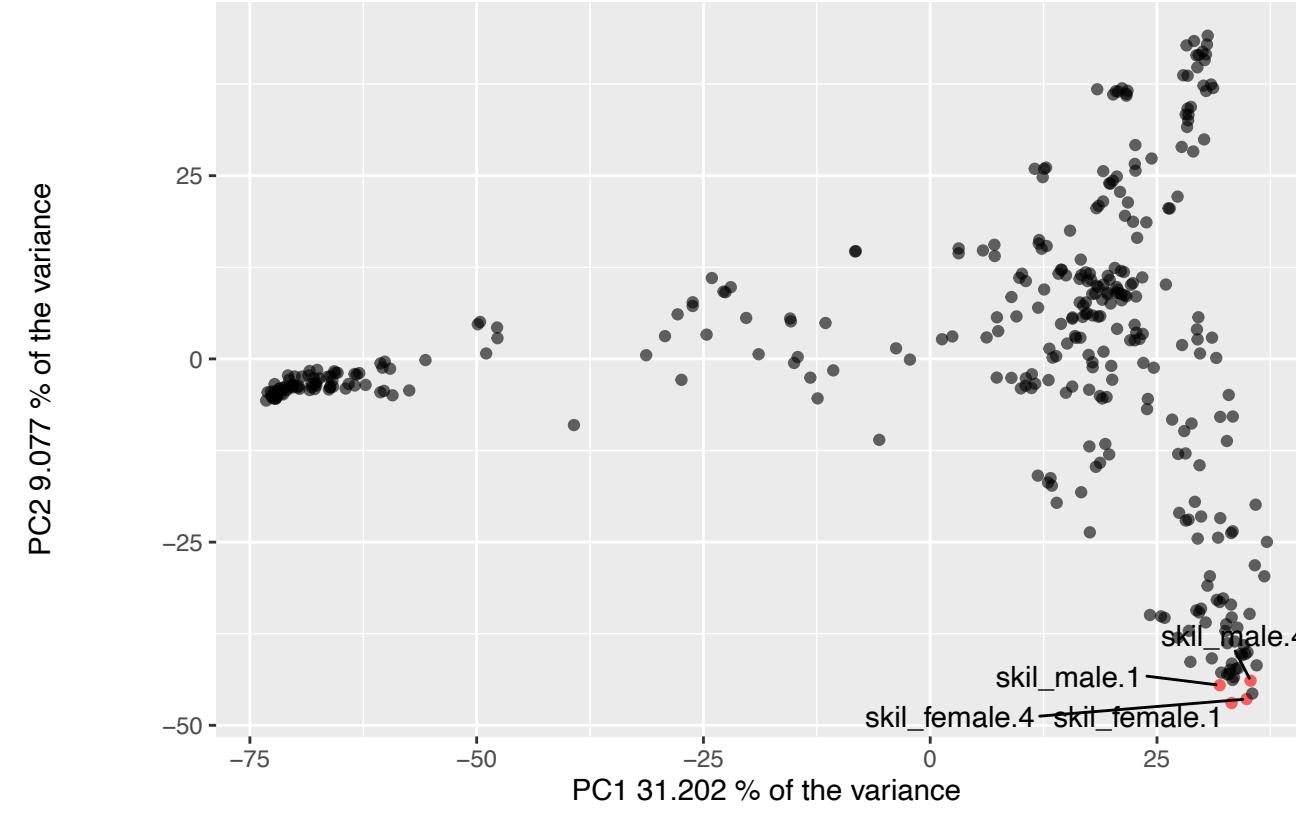
lens, PCA: TMM expression values



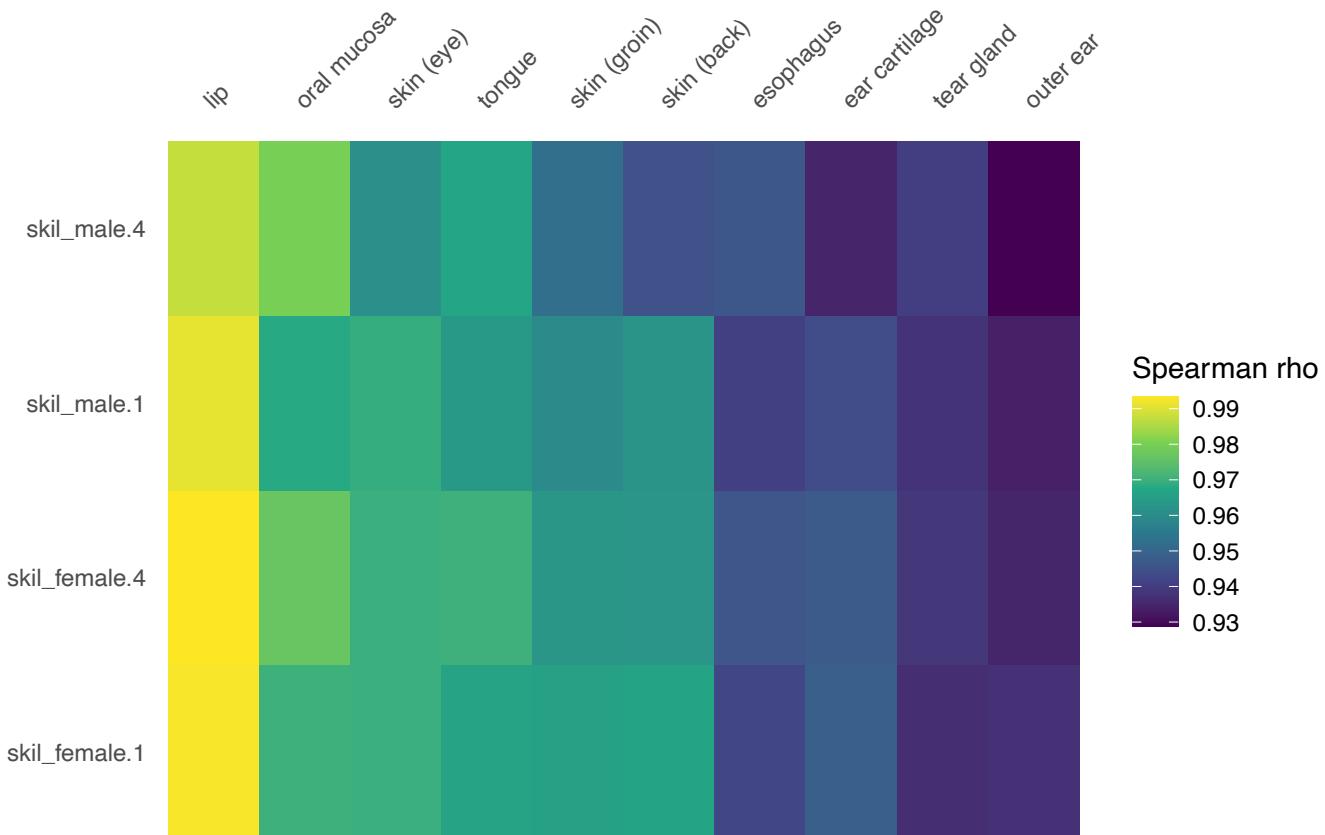
lens, UMAP: TMM expression values



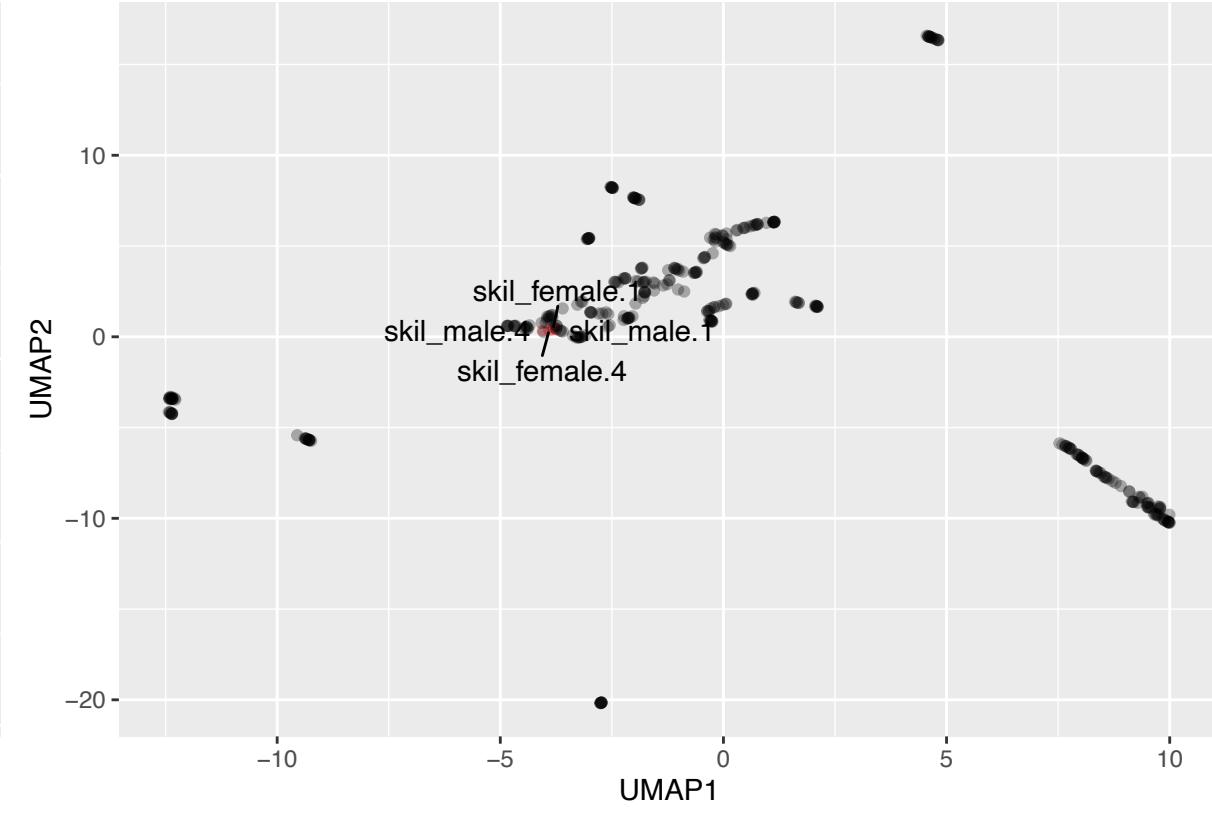
lip, PCA: TMM expression values



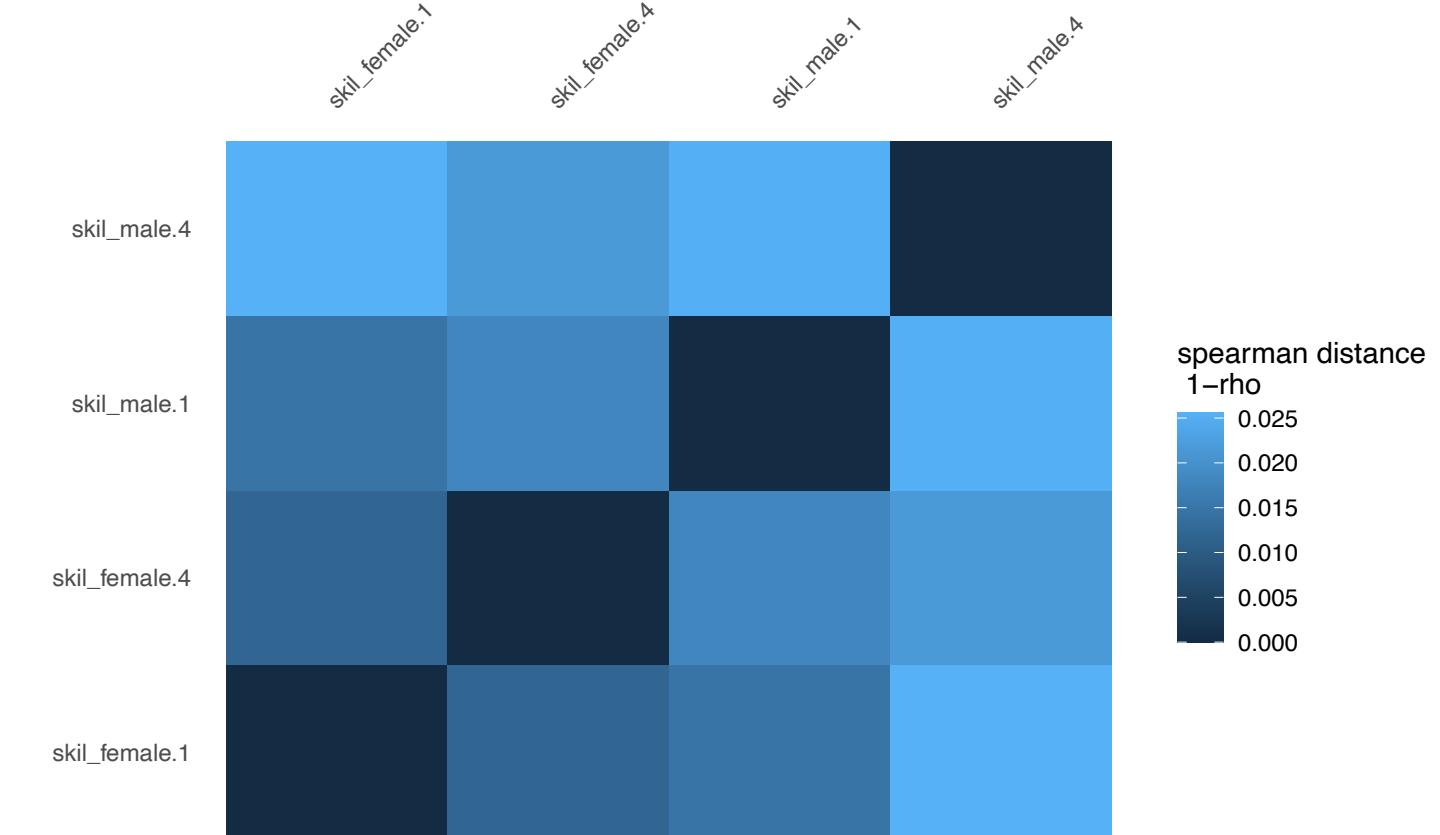
Tissue group to sample correlation



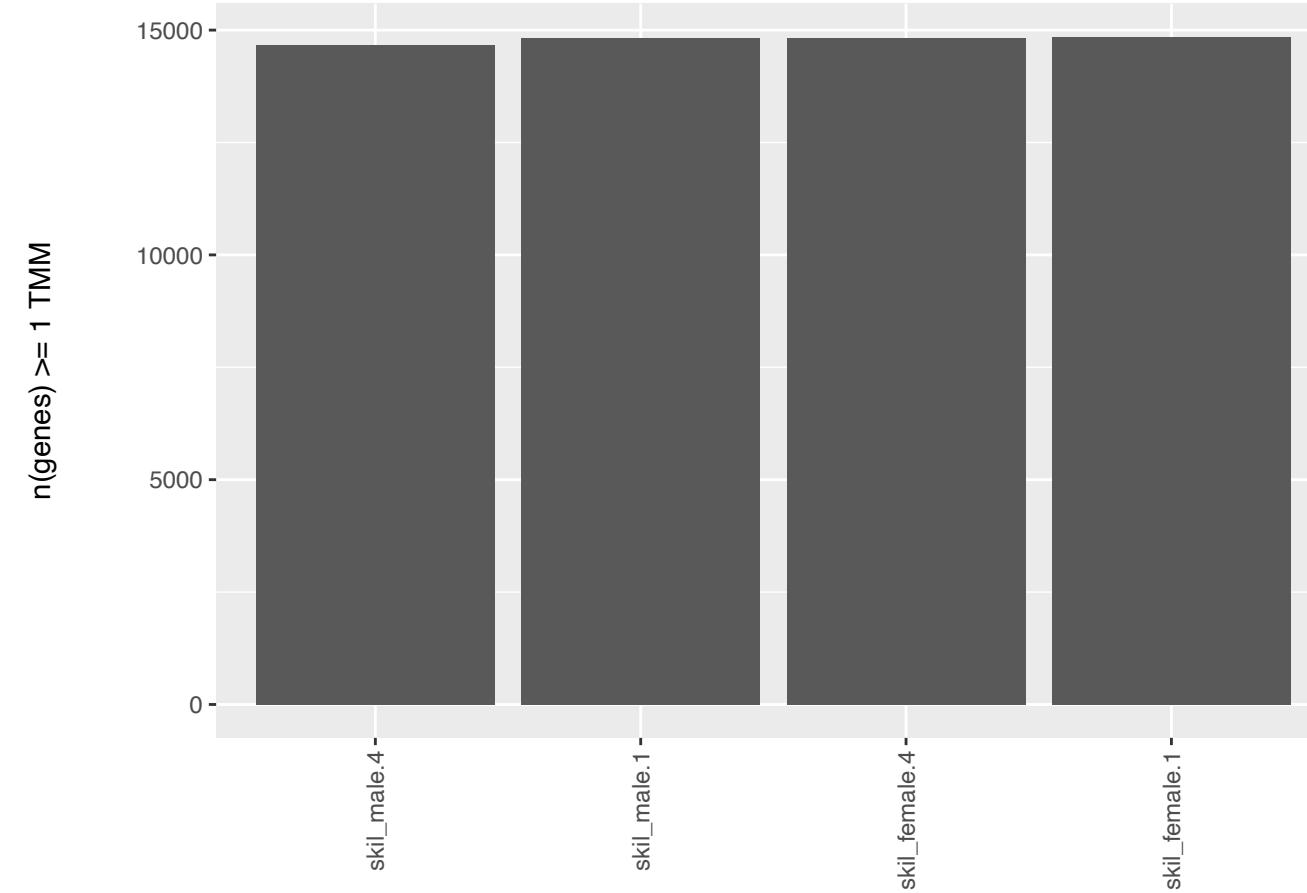
lip, UMAP: TMM expression values



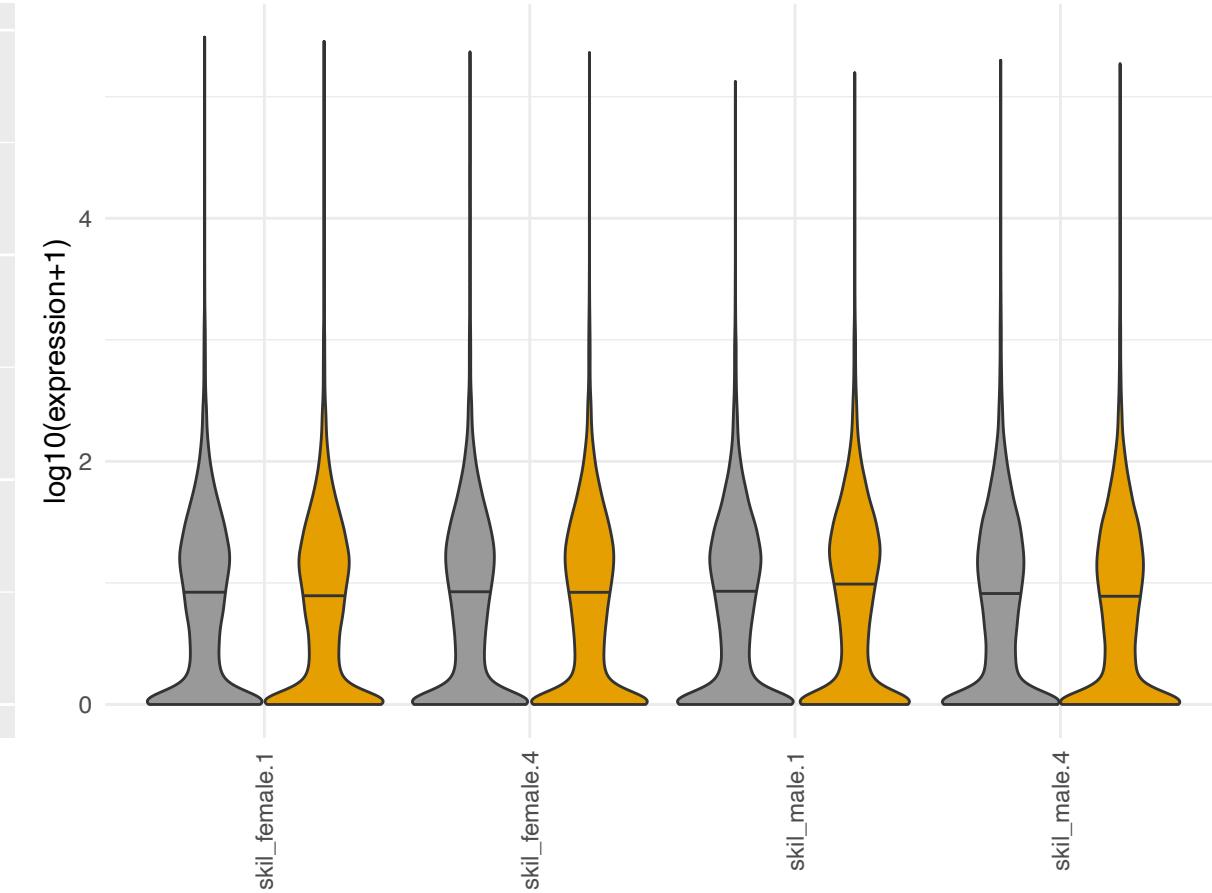
In tissue sample to sample Spearman Distance



lip

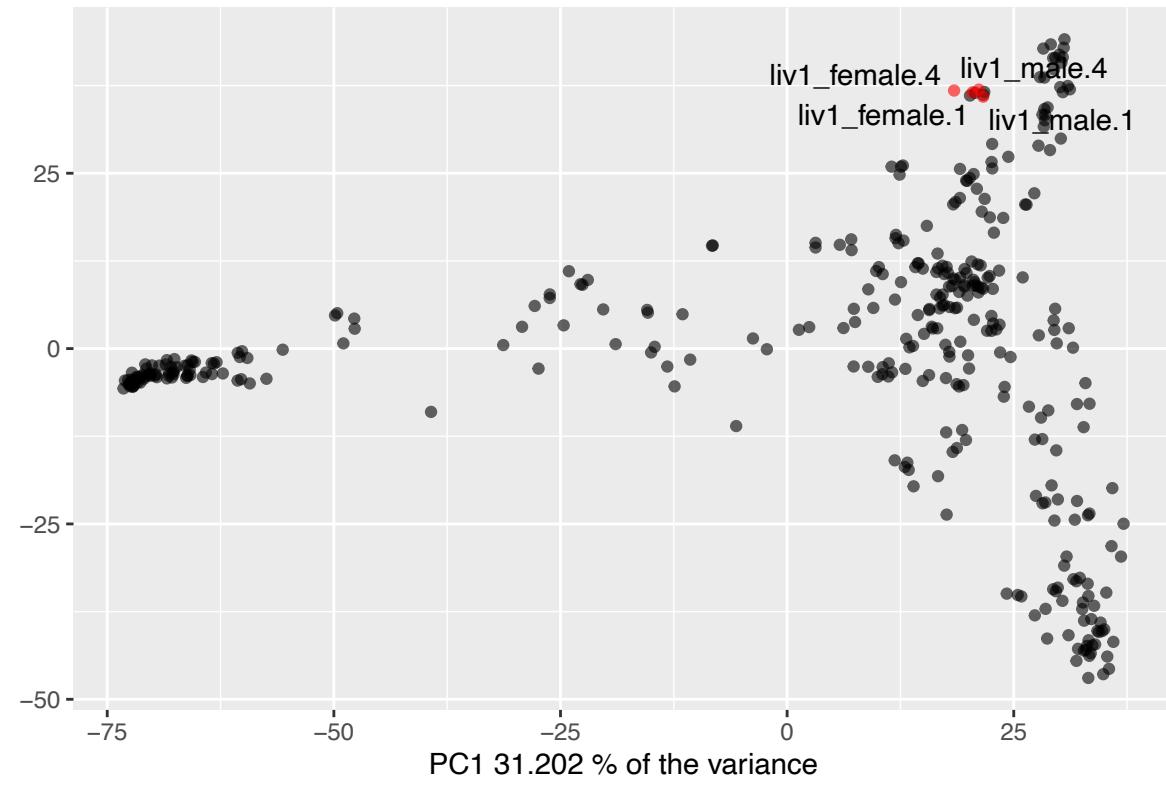


lip

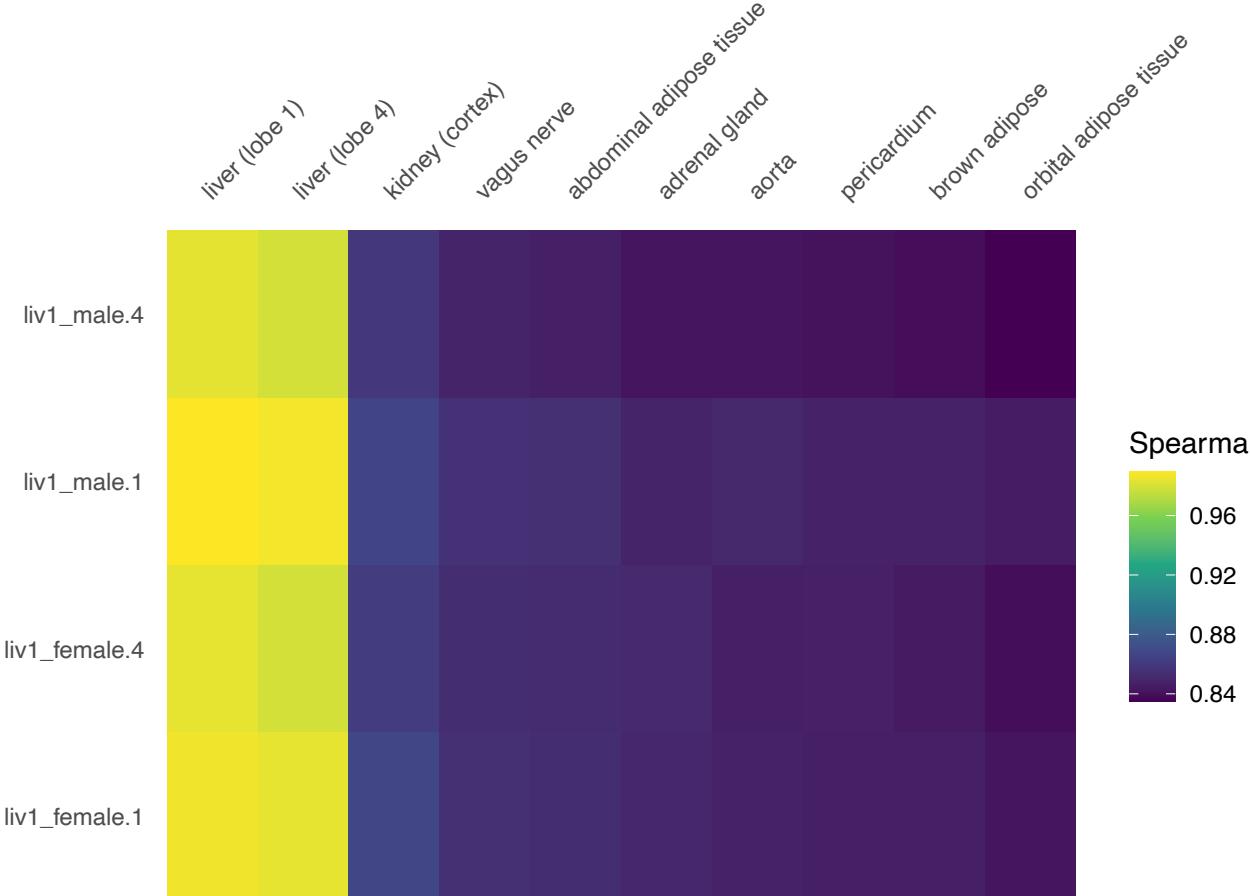


liver (lobe 1), PCA: TMM expression values

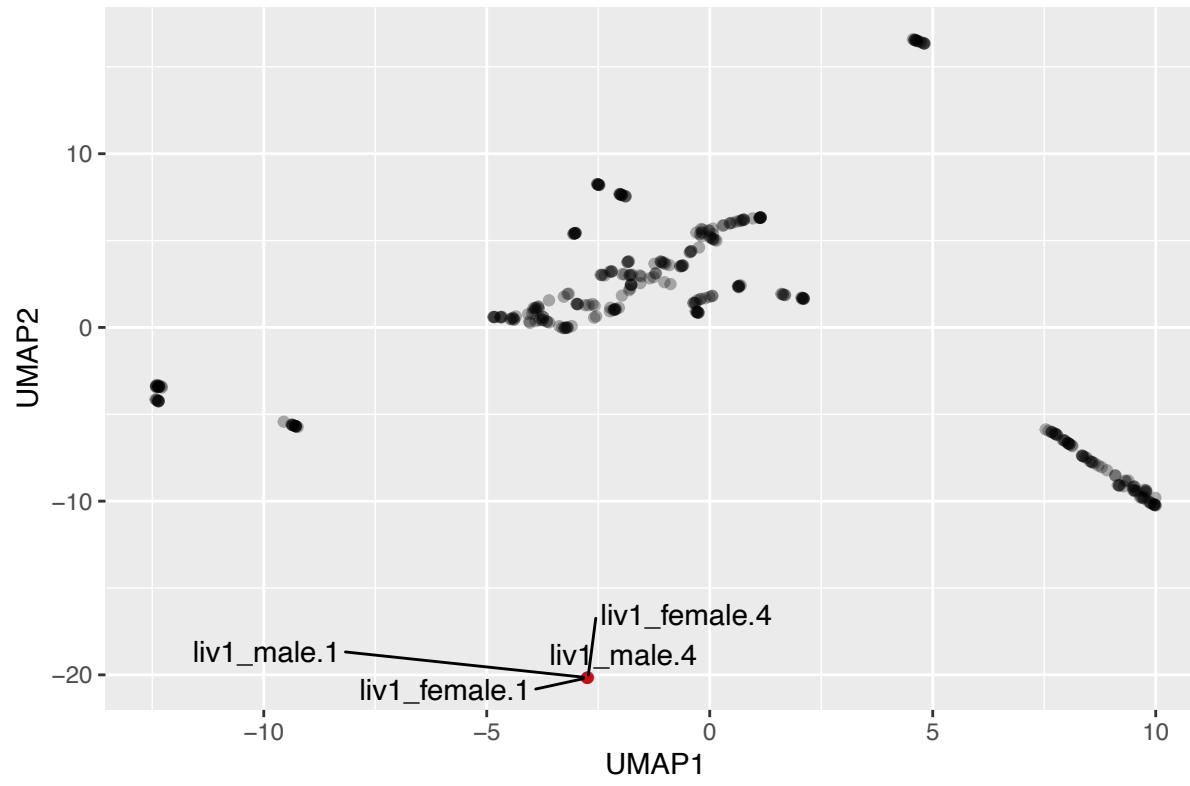
PC2 9.077 % of the variance



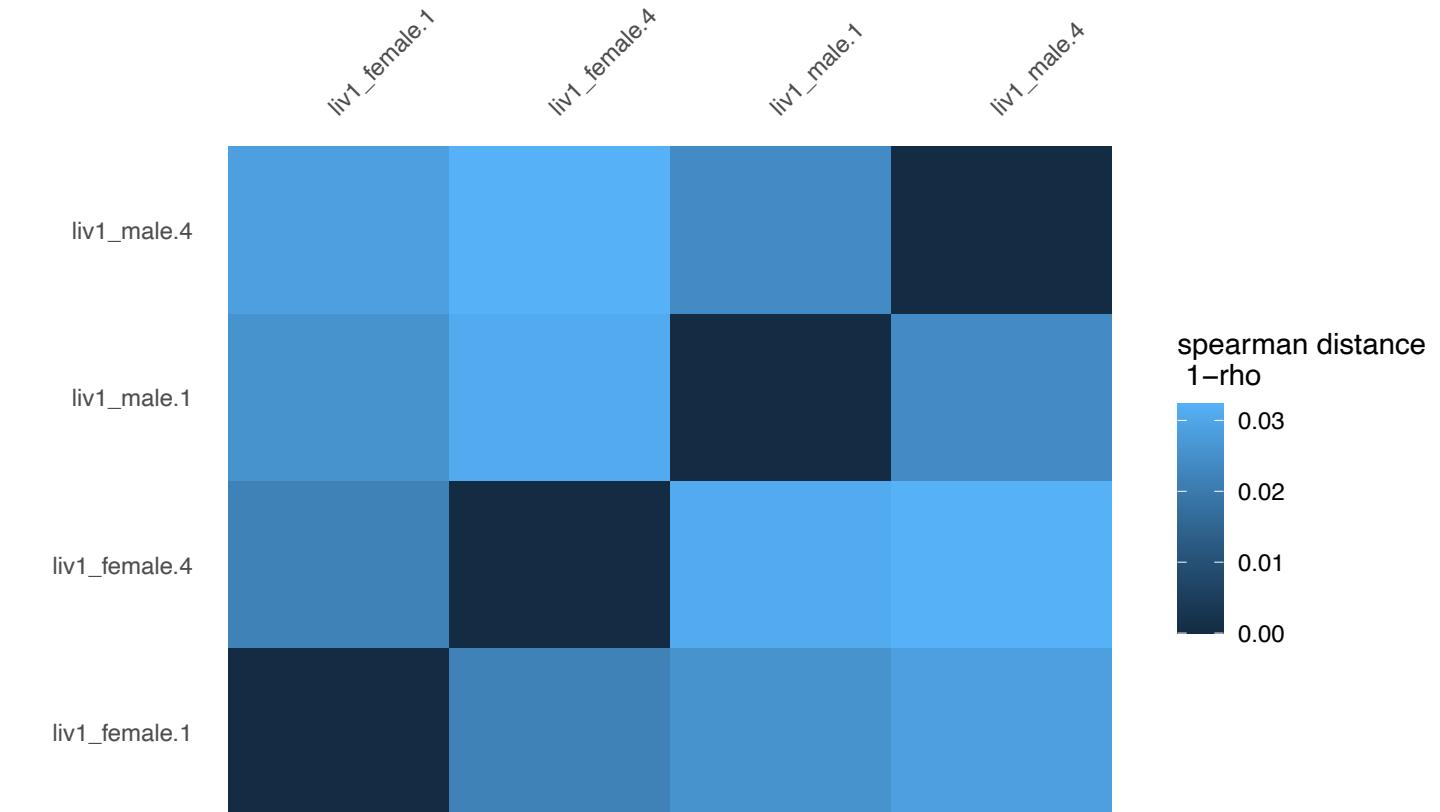
Tissue group to sample correlation



liver (lobe 1), UMAP: TMM expression values

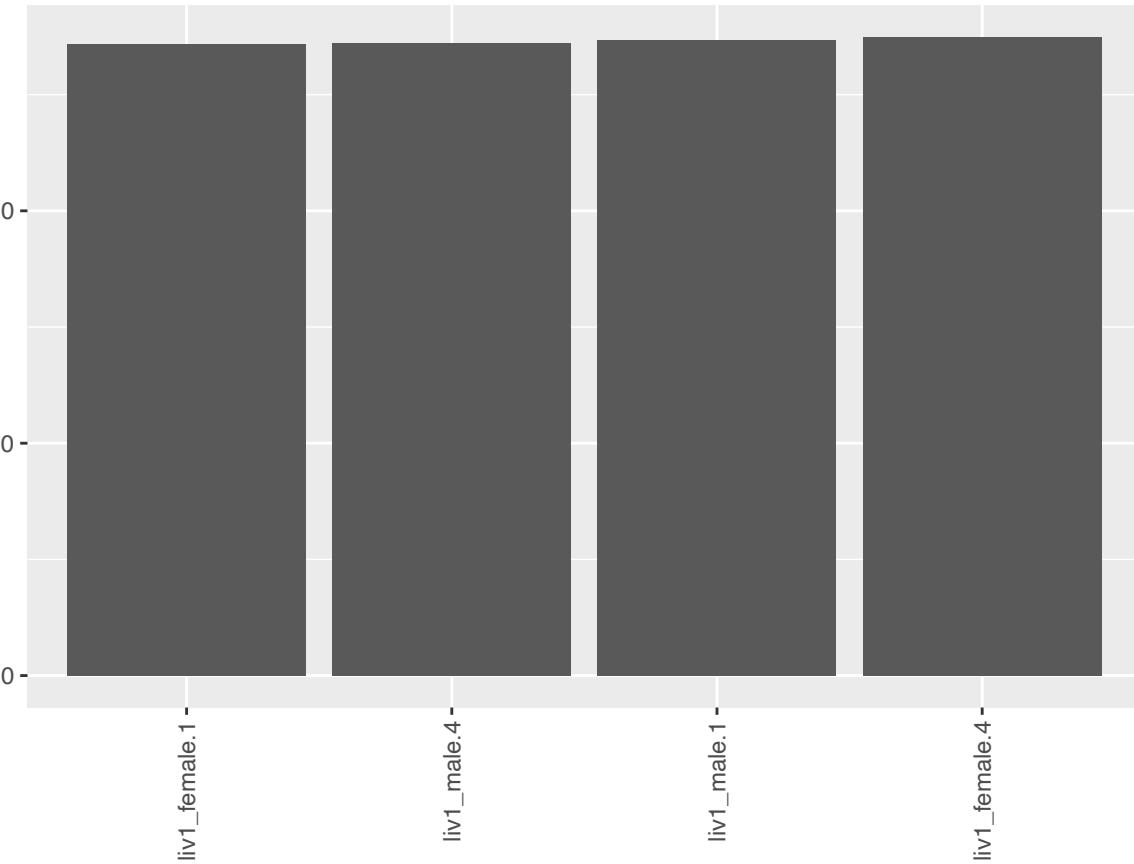


In tissue sample to sample Spearman Distance

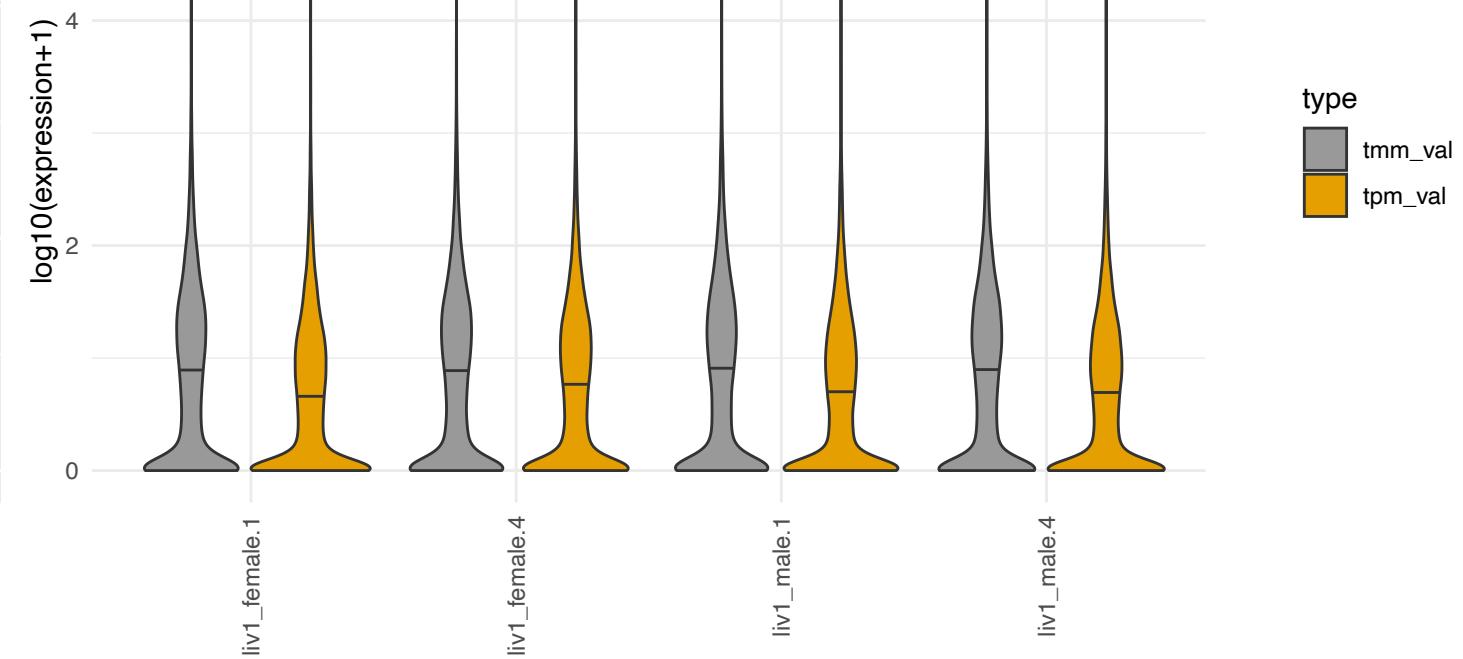


liver (lobe 1)

n(genes) >= 1 TMM

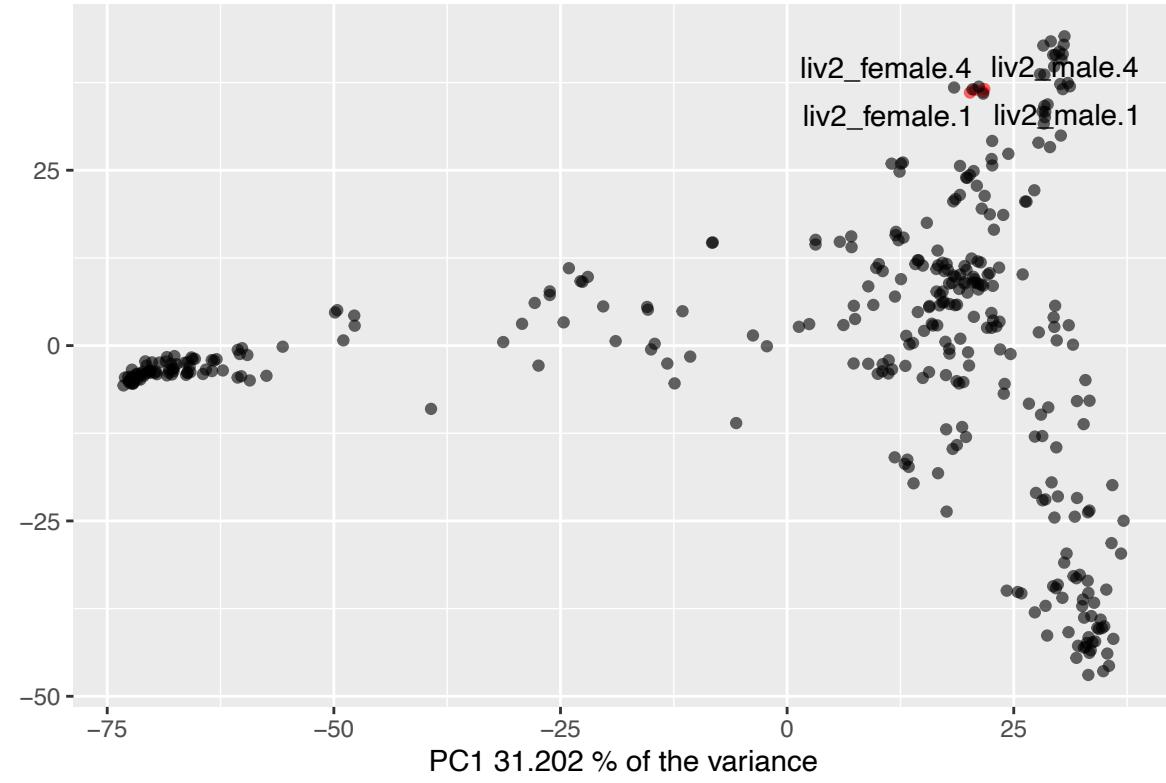


liver (lobe 1)

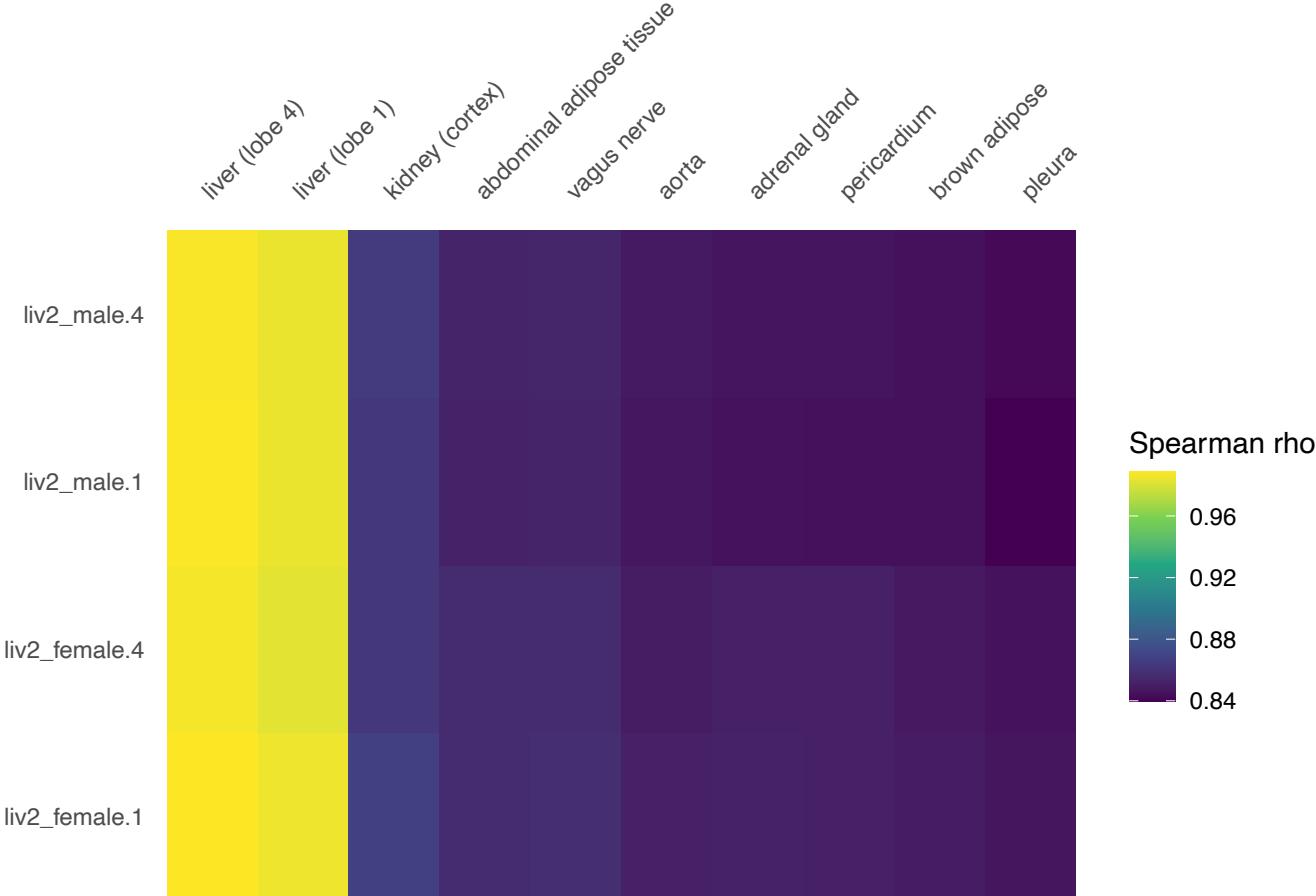


liver (lobe 4), PCA: TMM expression values

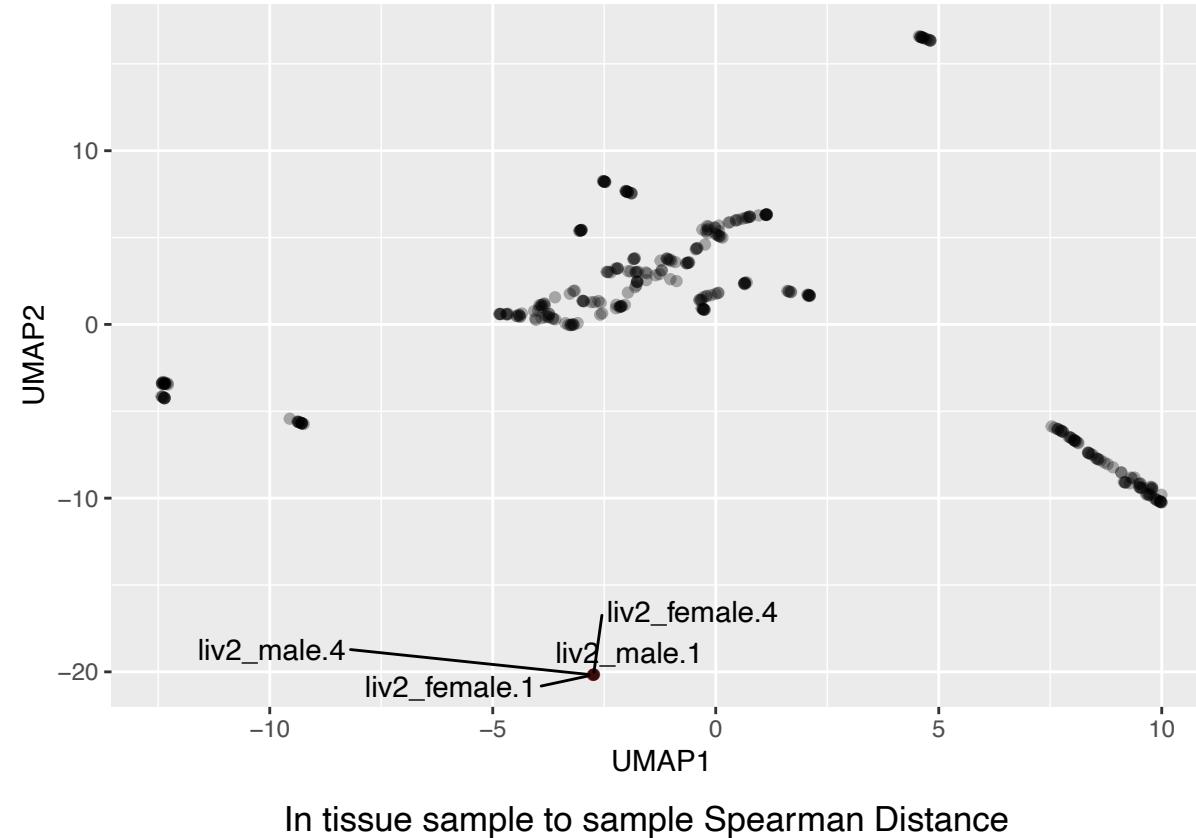
PC2 9.077 % of the variance



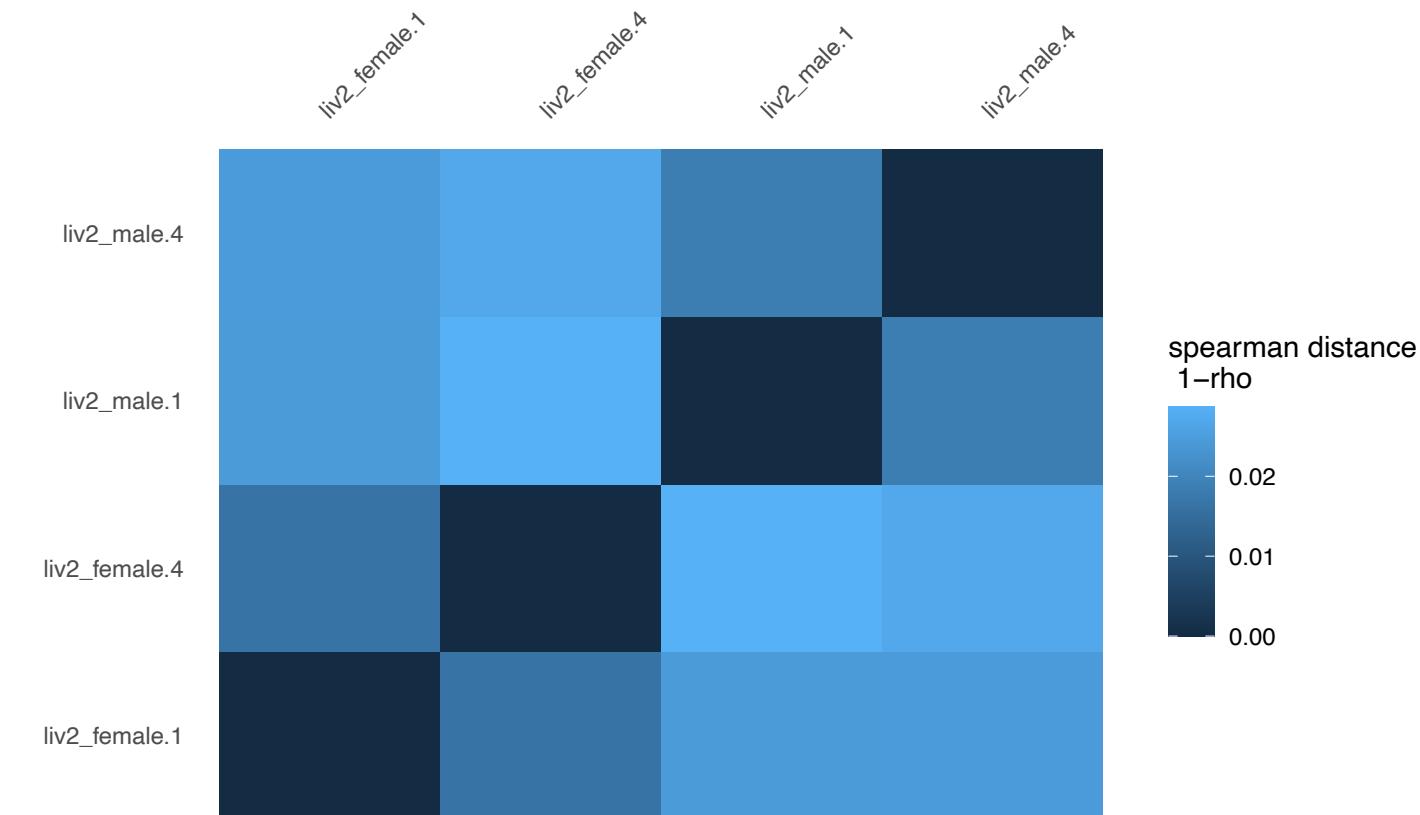
Tissue group to sample correlation



liver (lobe 4), UMAP: TMM expression values

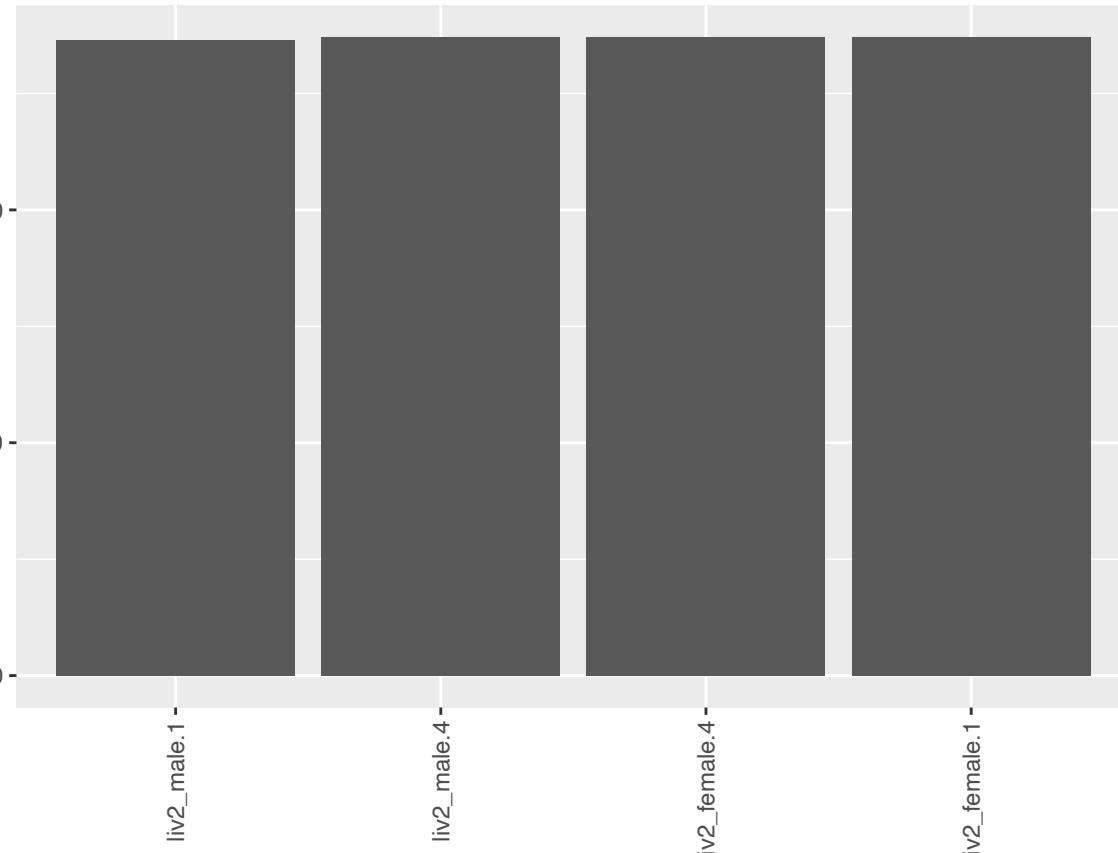


In tissue sample to sample Spearman Distance

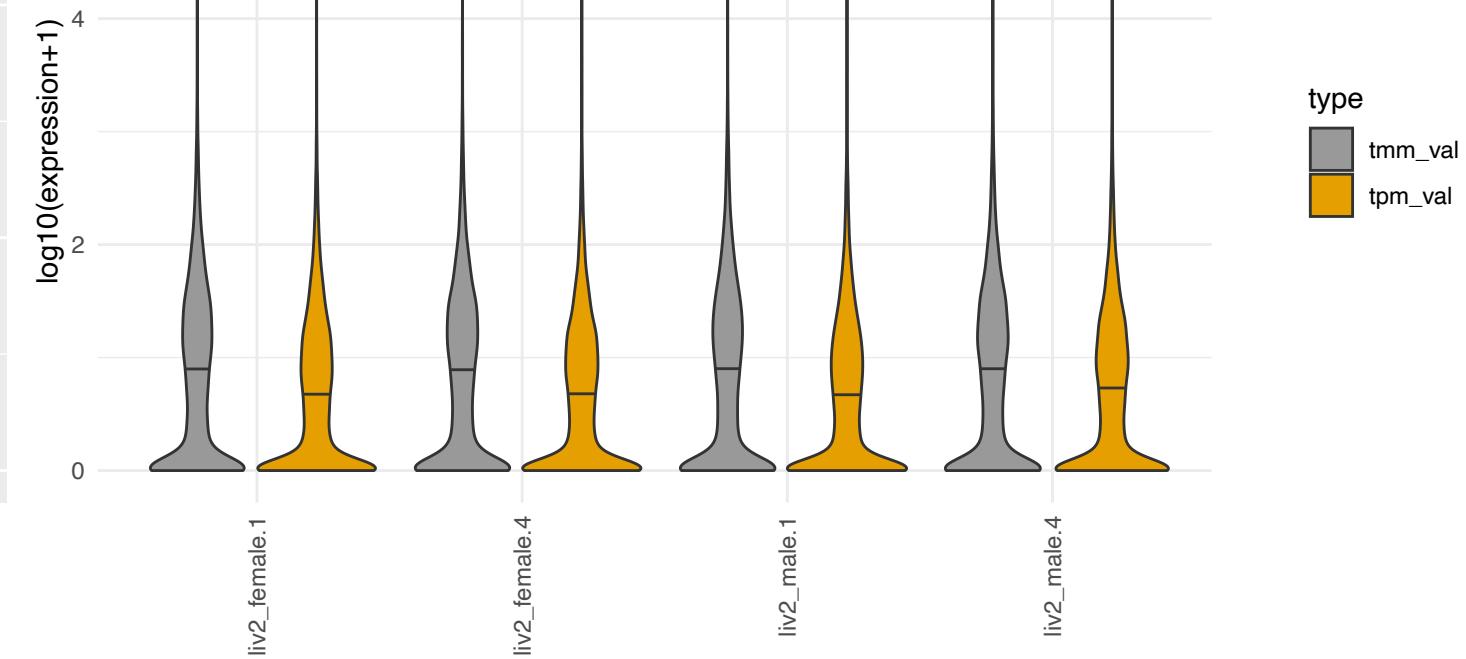


liver (lobe 4)

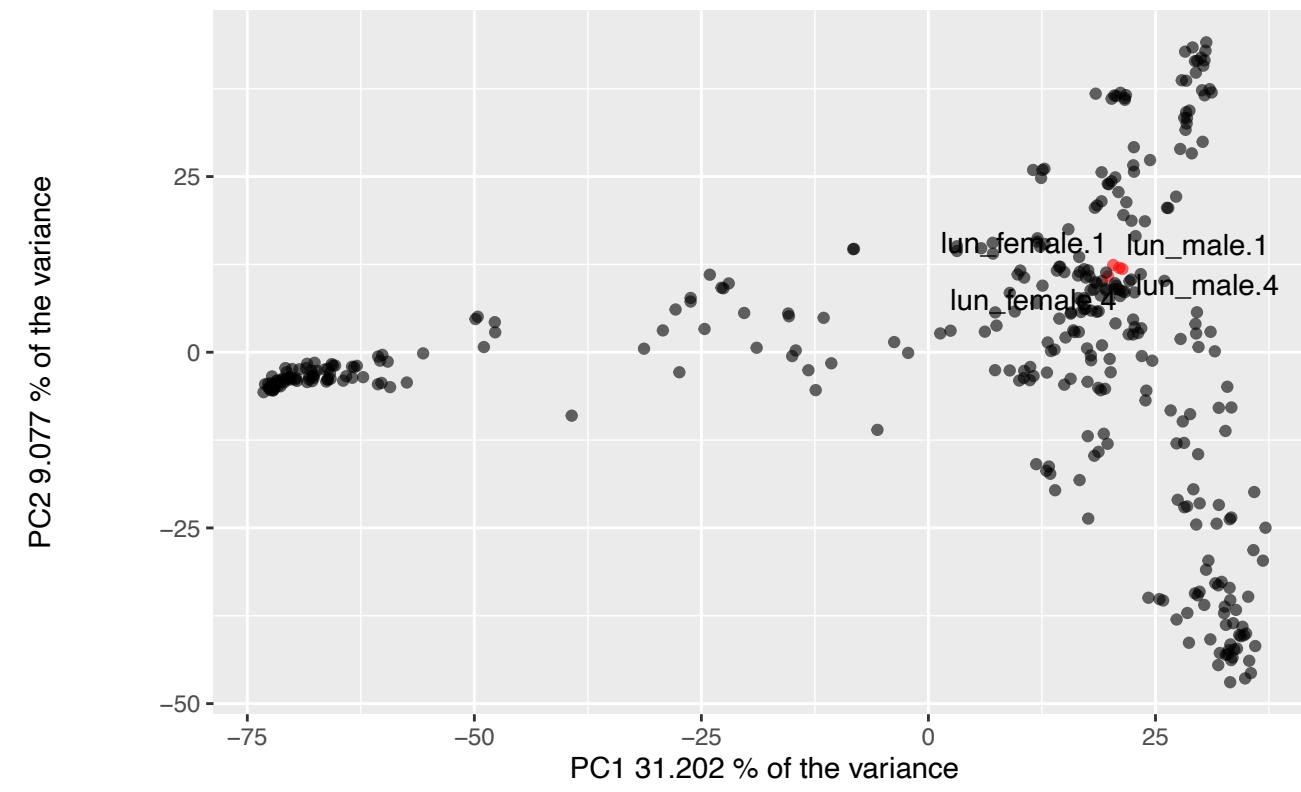
n(genes) >= 1 TMM



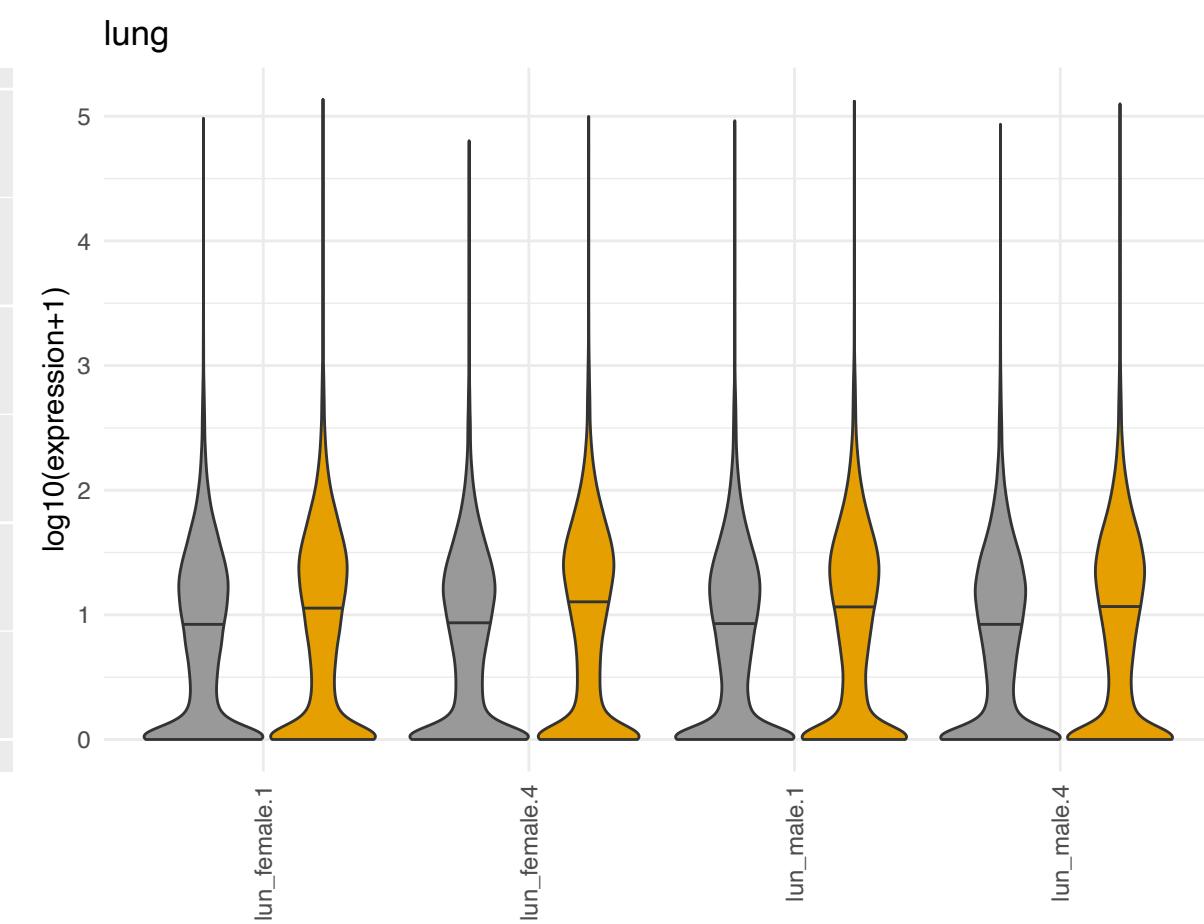
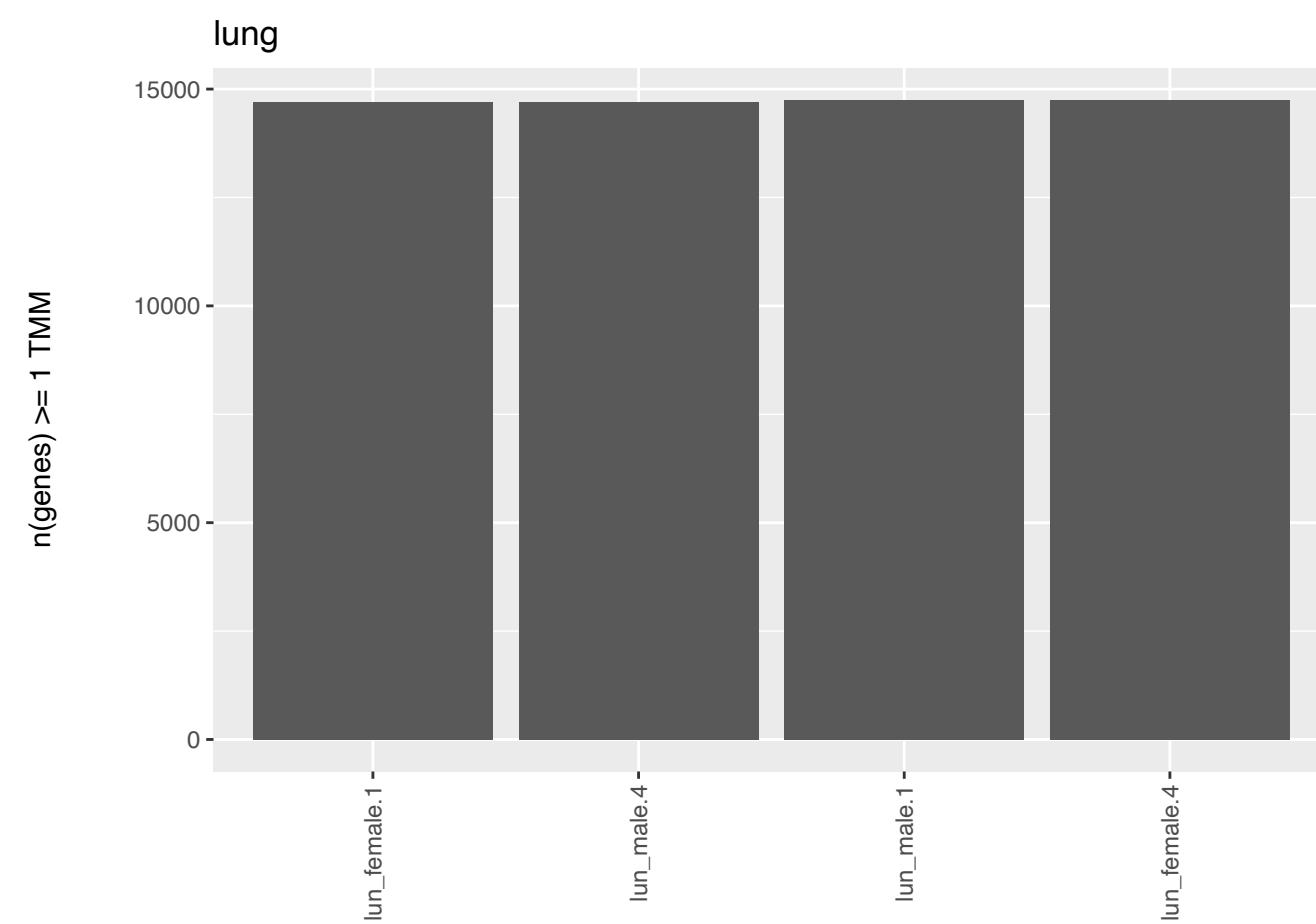
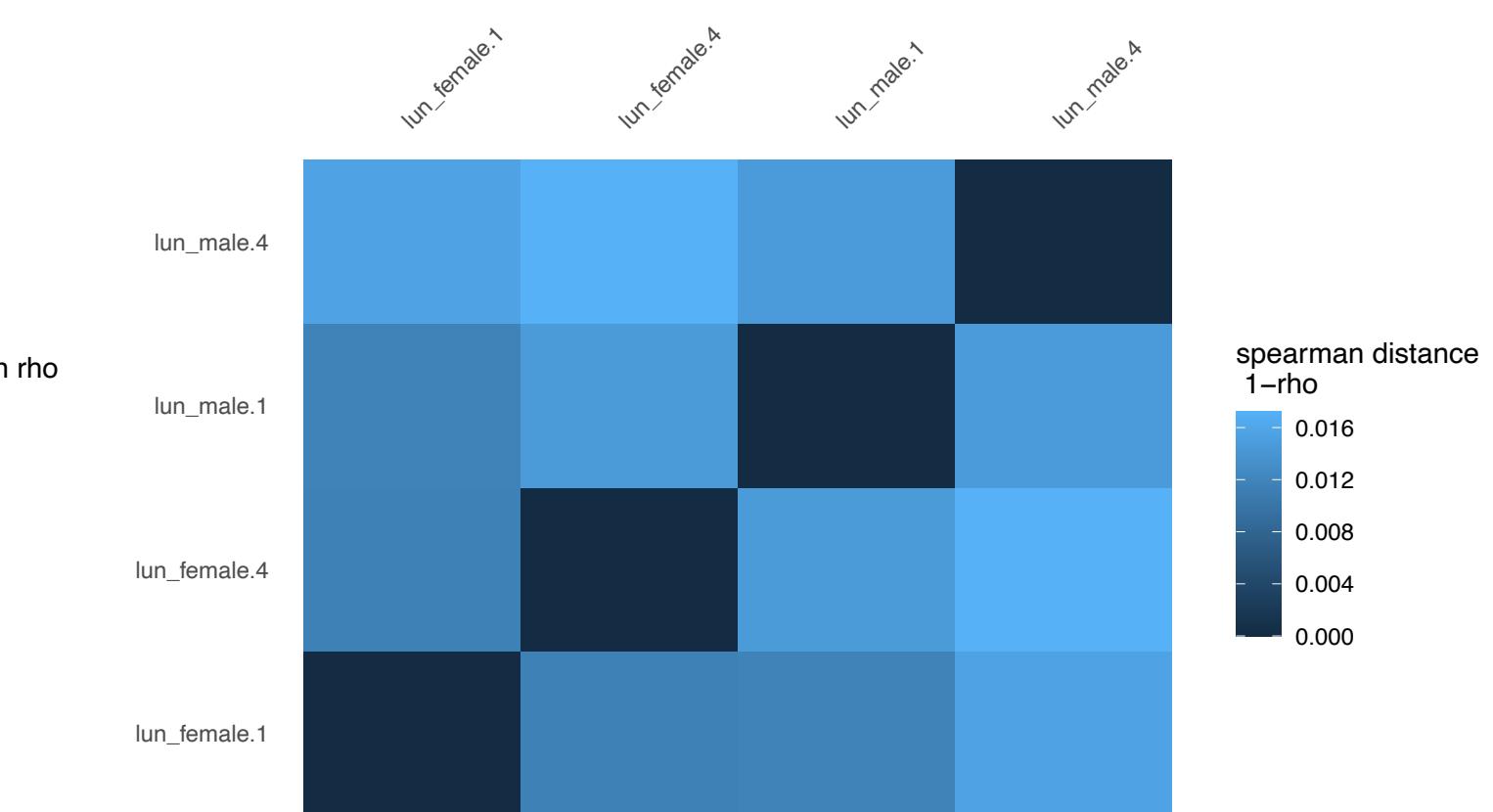
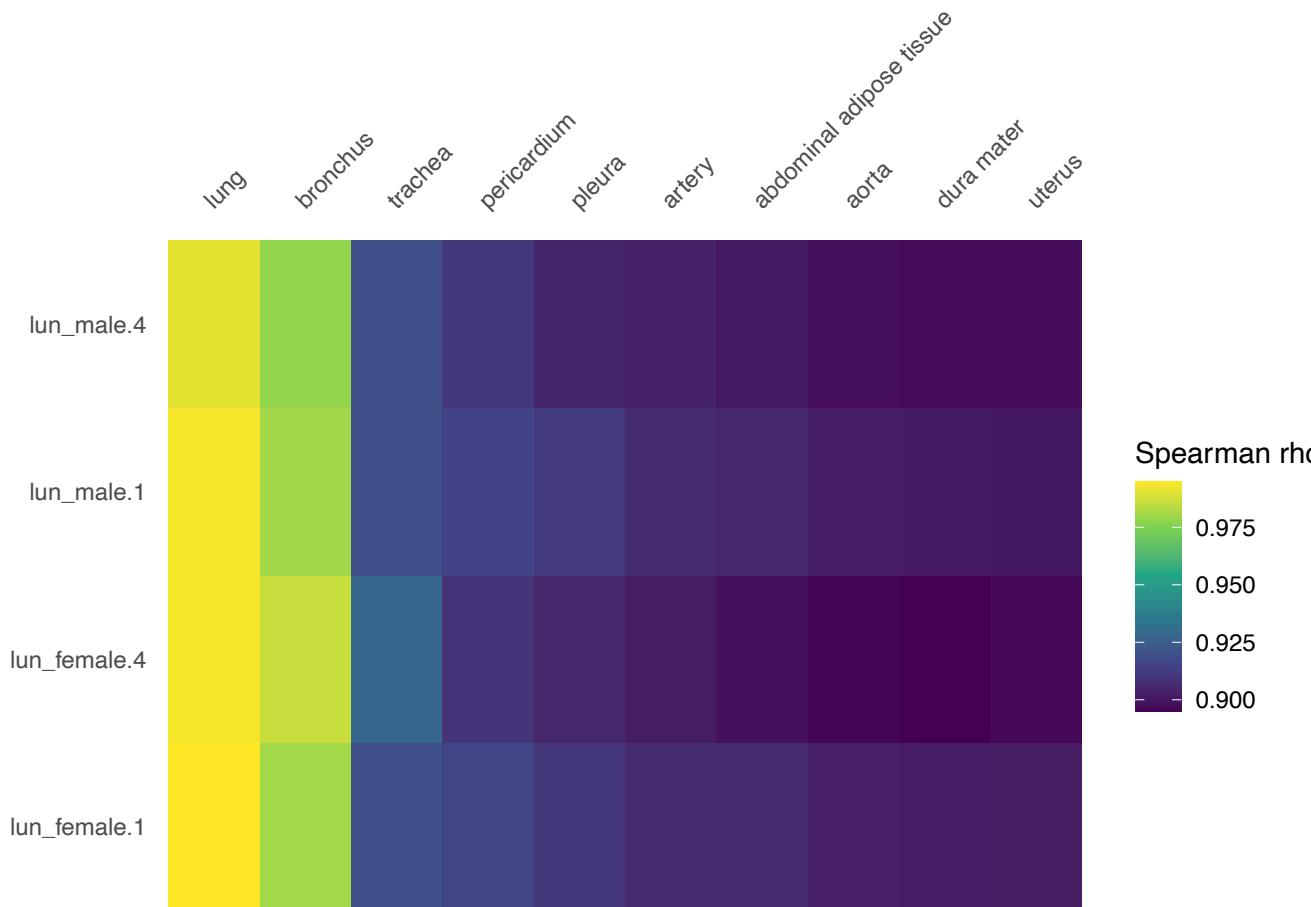
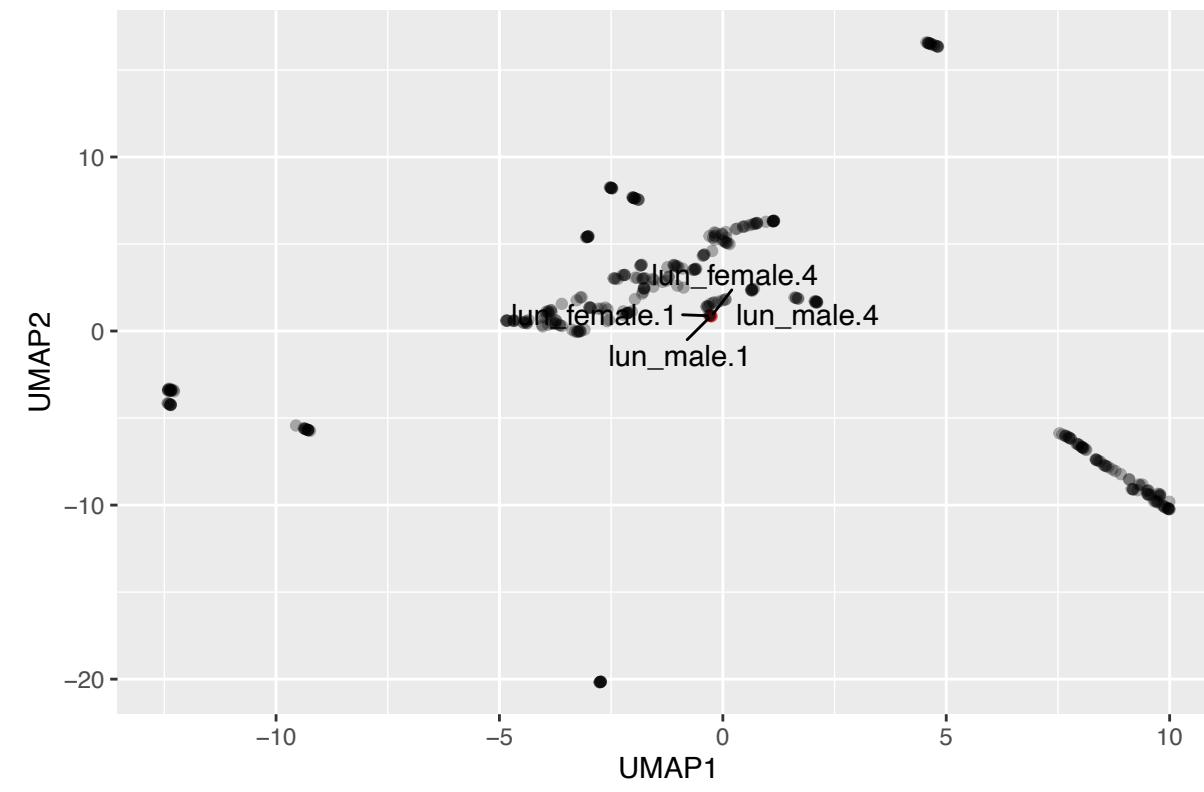
liver (lobe 4)



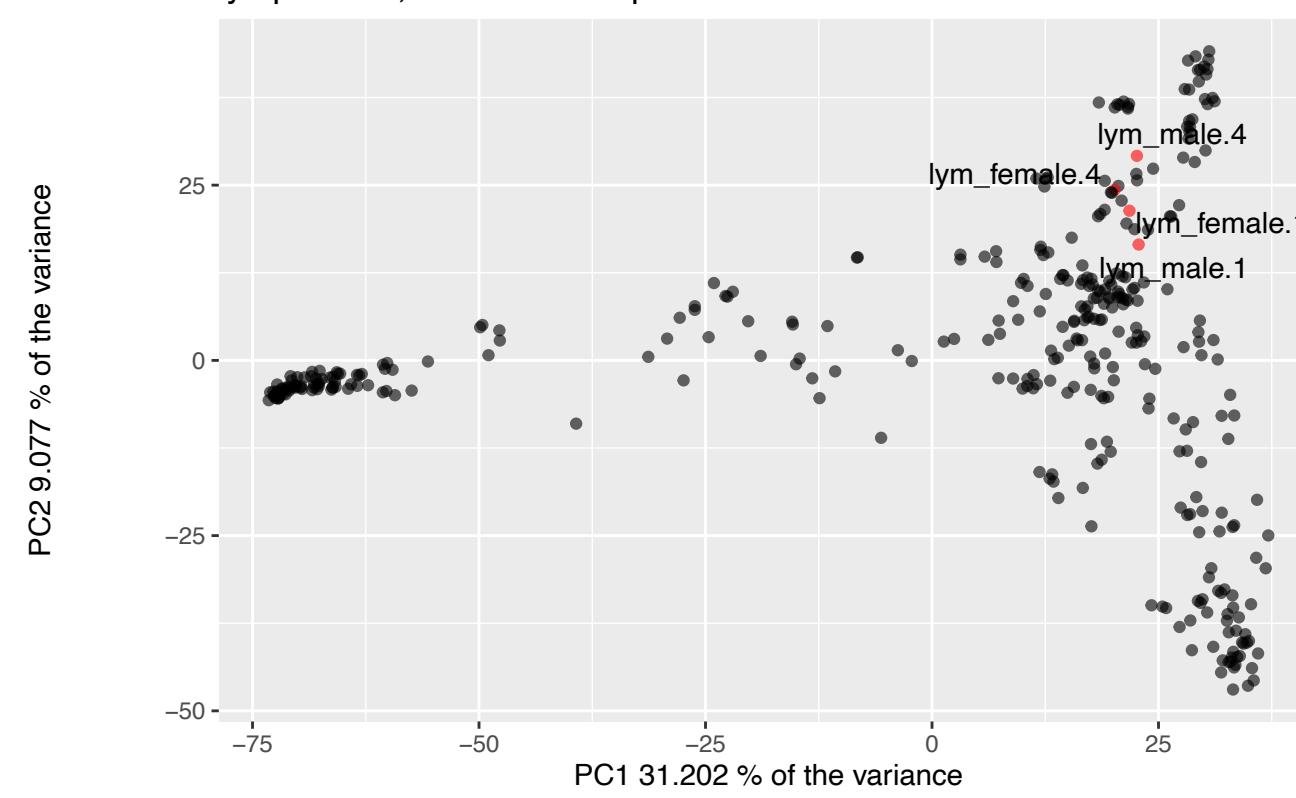
lung, PCA: TMM expression values



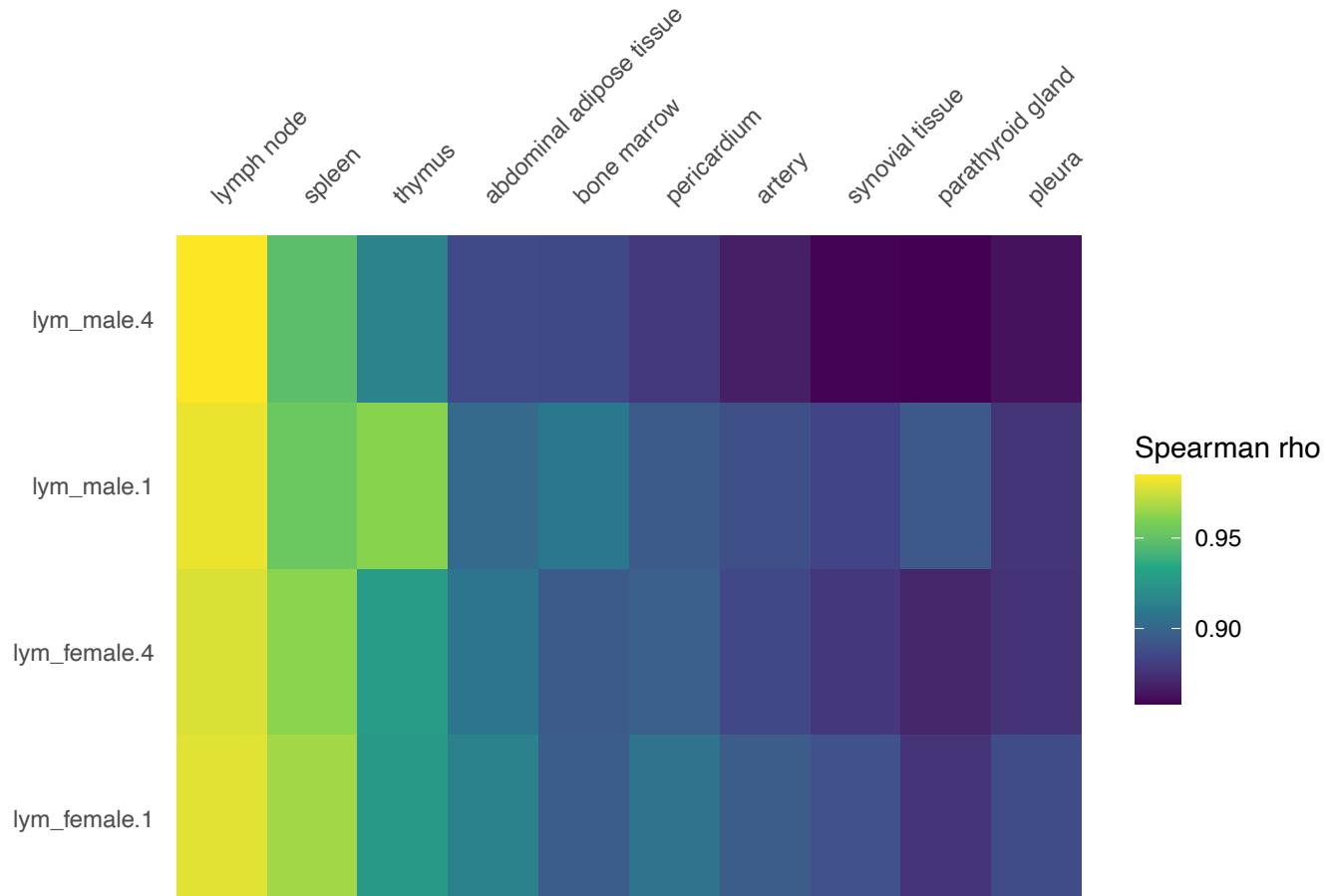
lung, UMAP: TMM expression values



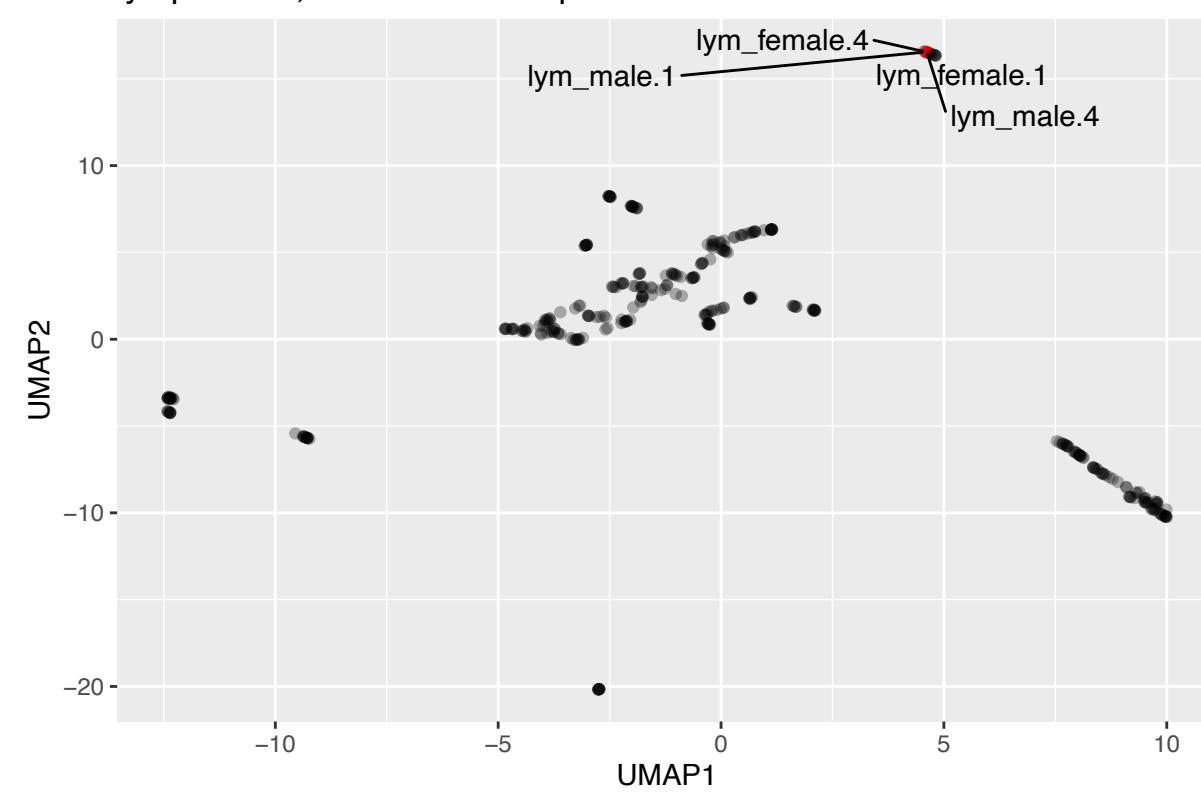
lymph node, PCA: TMM expression values



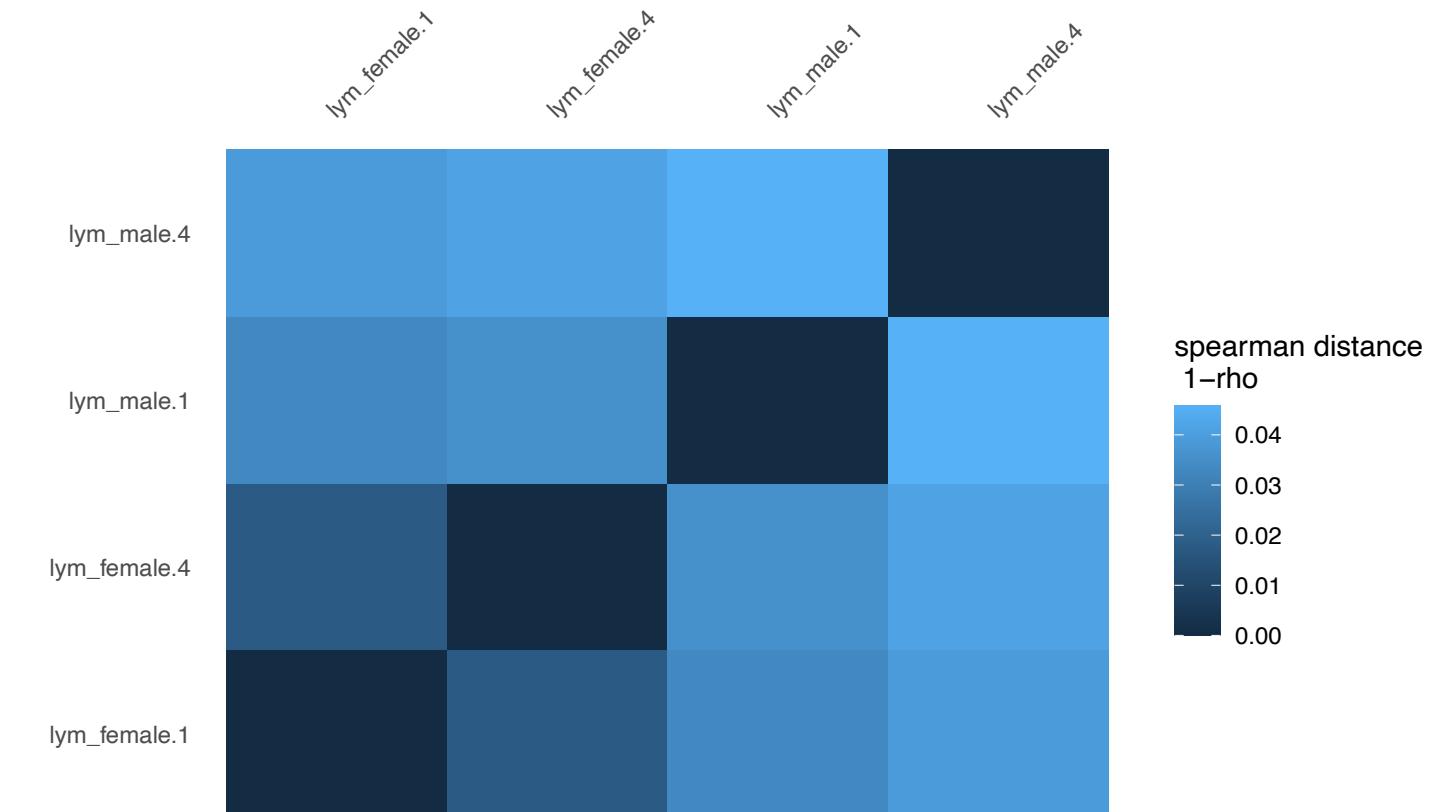
Tissue group to sample correlation



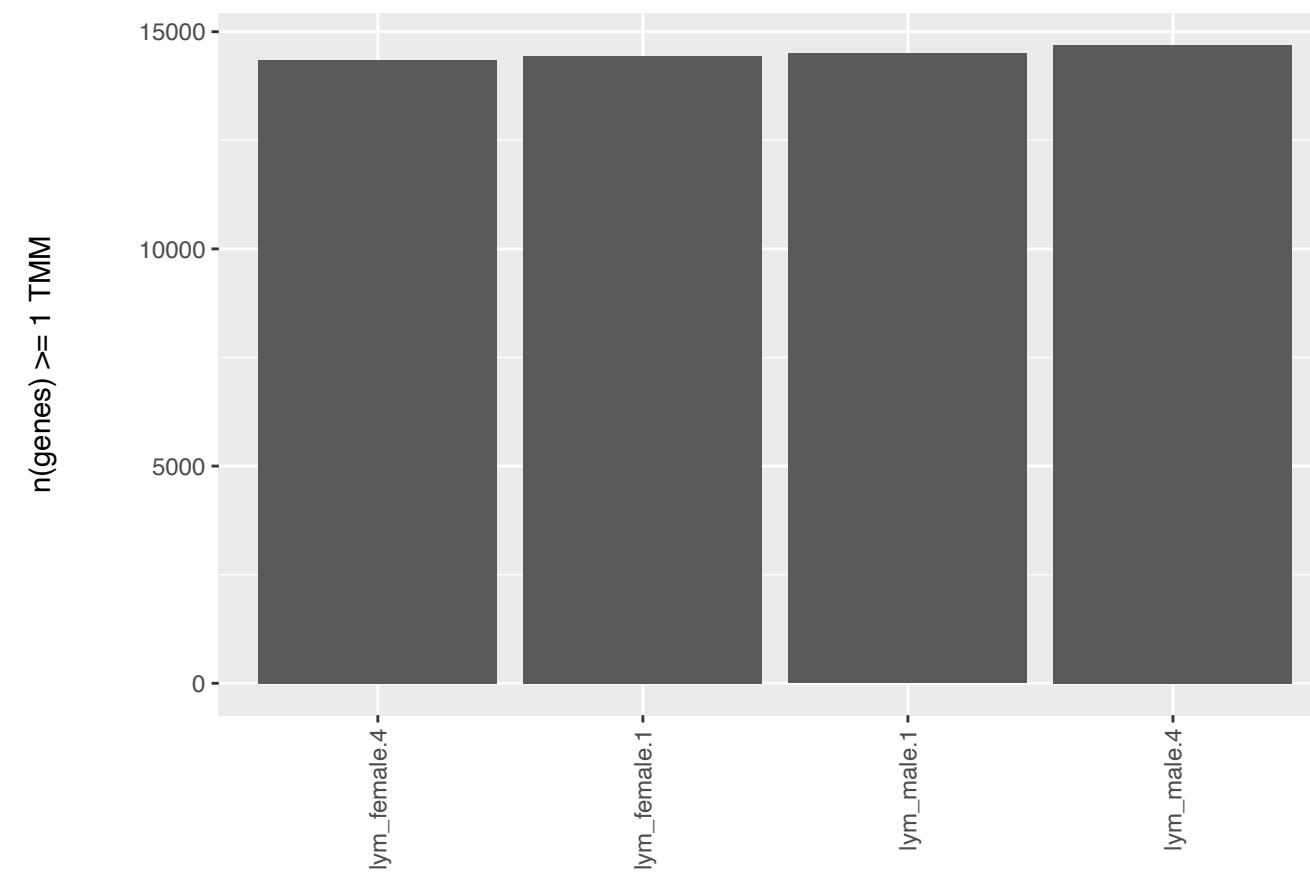
lymph node, UMAP: TMM expression values



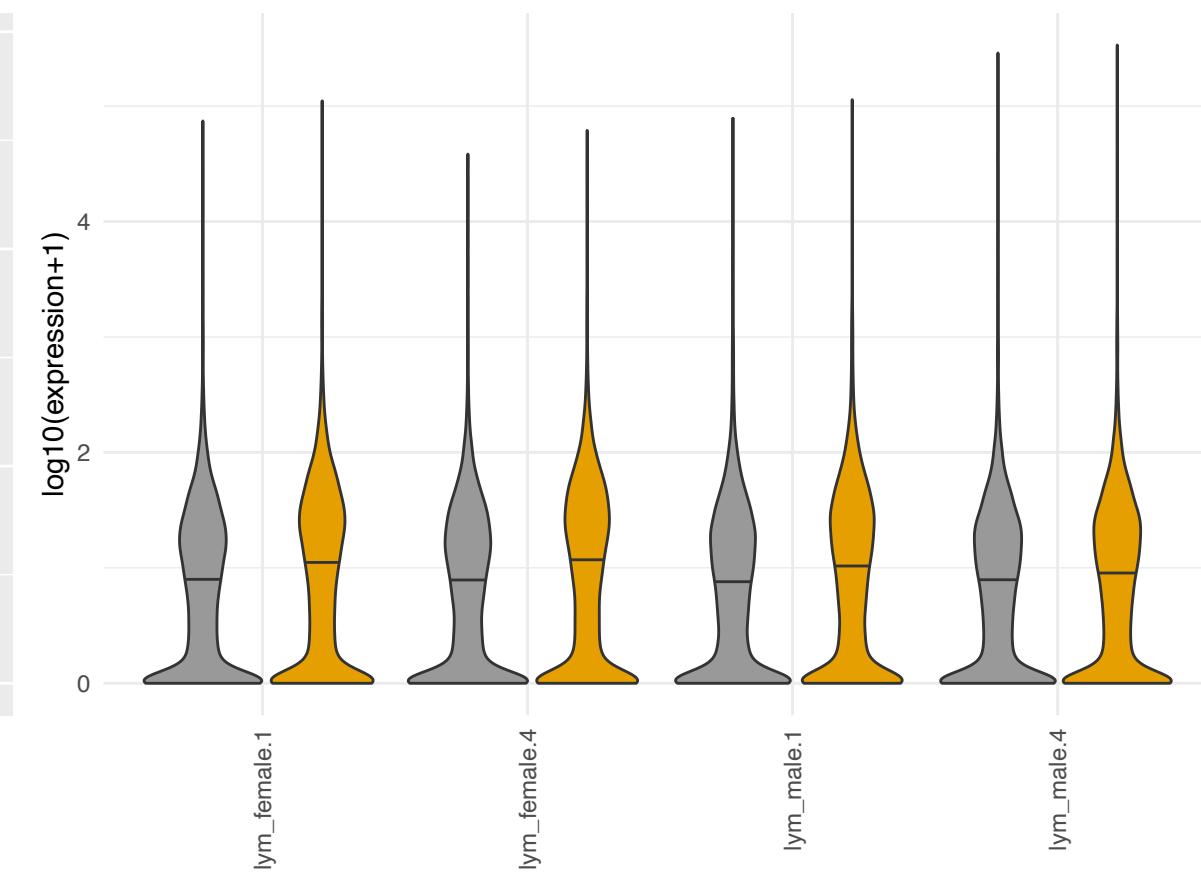
In tissue sample to sample Spearman Distance



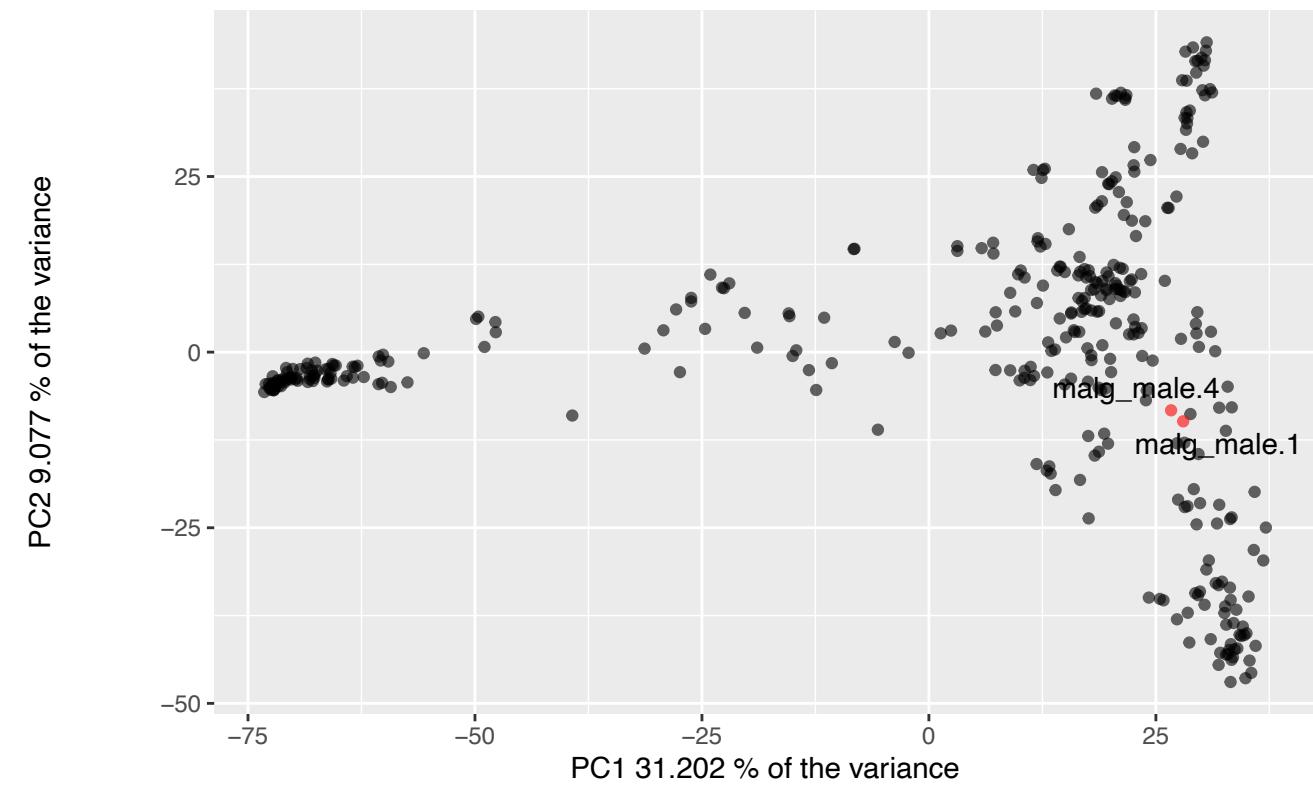
lymph node



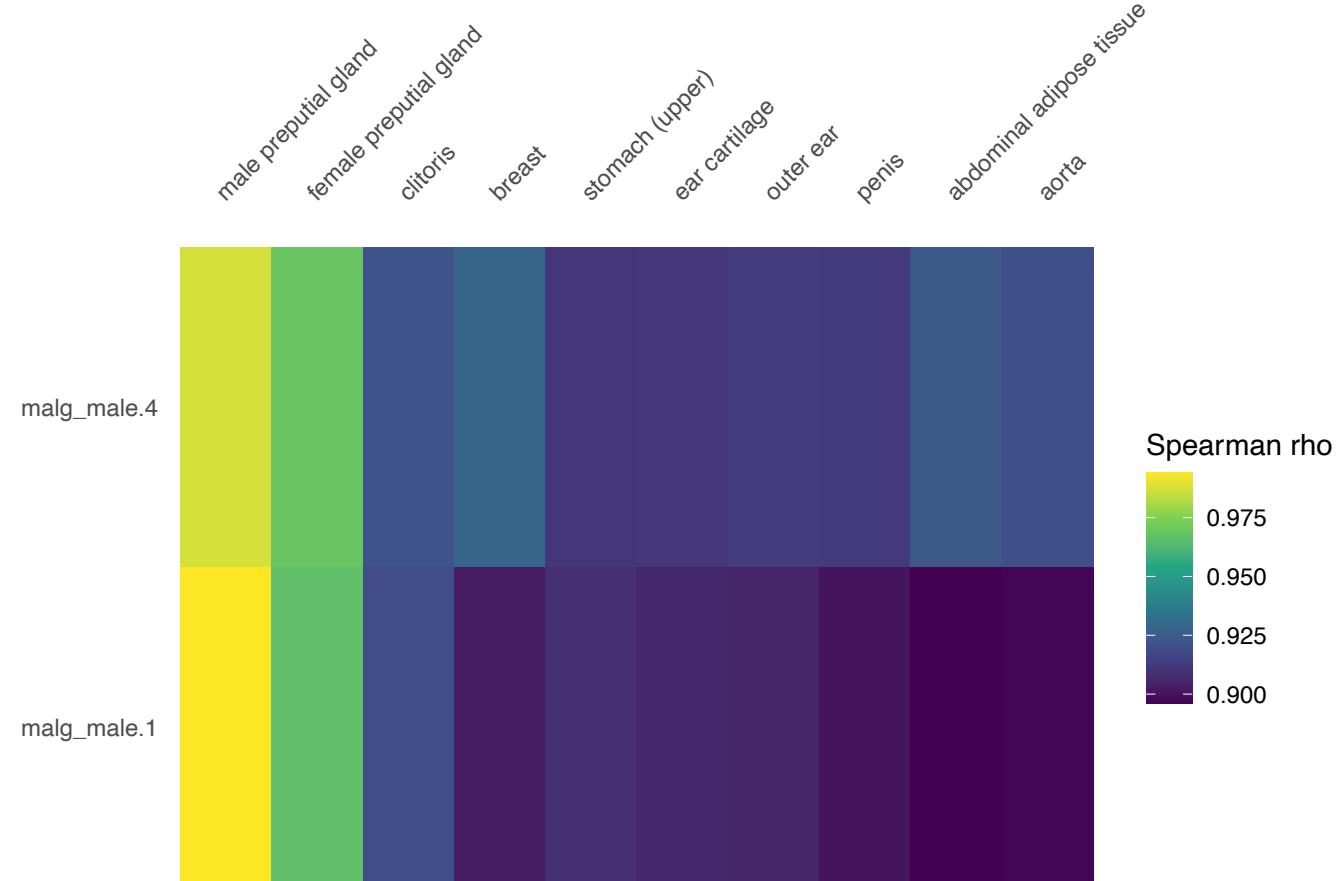
lymph node



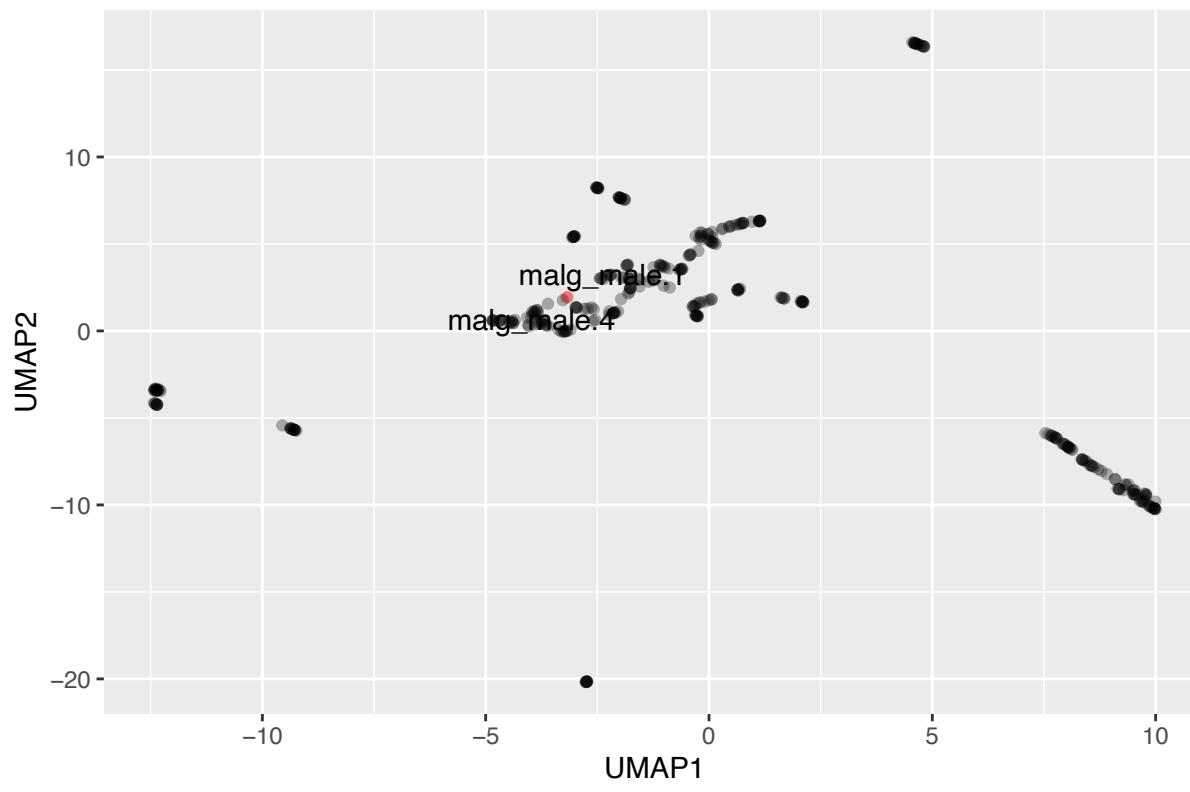
male preputial gland, PCA: TMM expression values



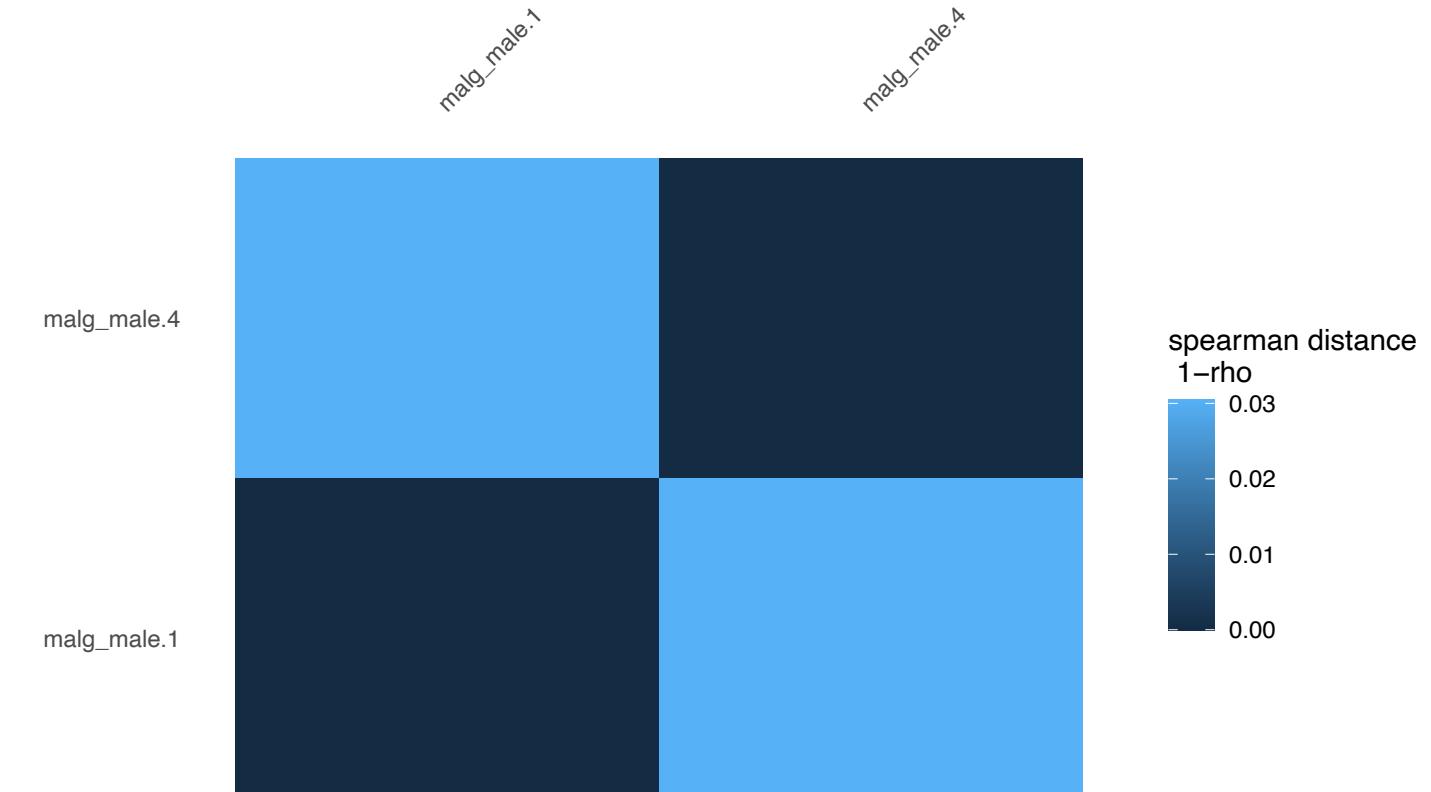
Tissue group to sample correlation



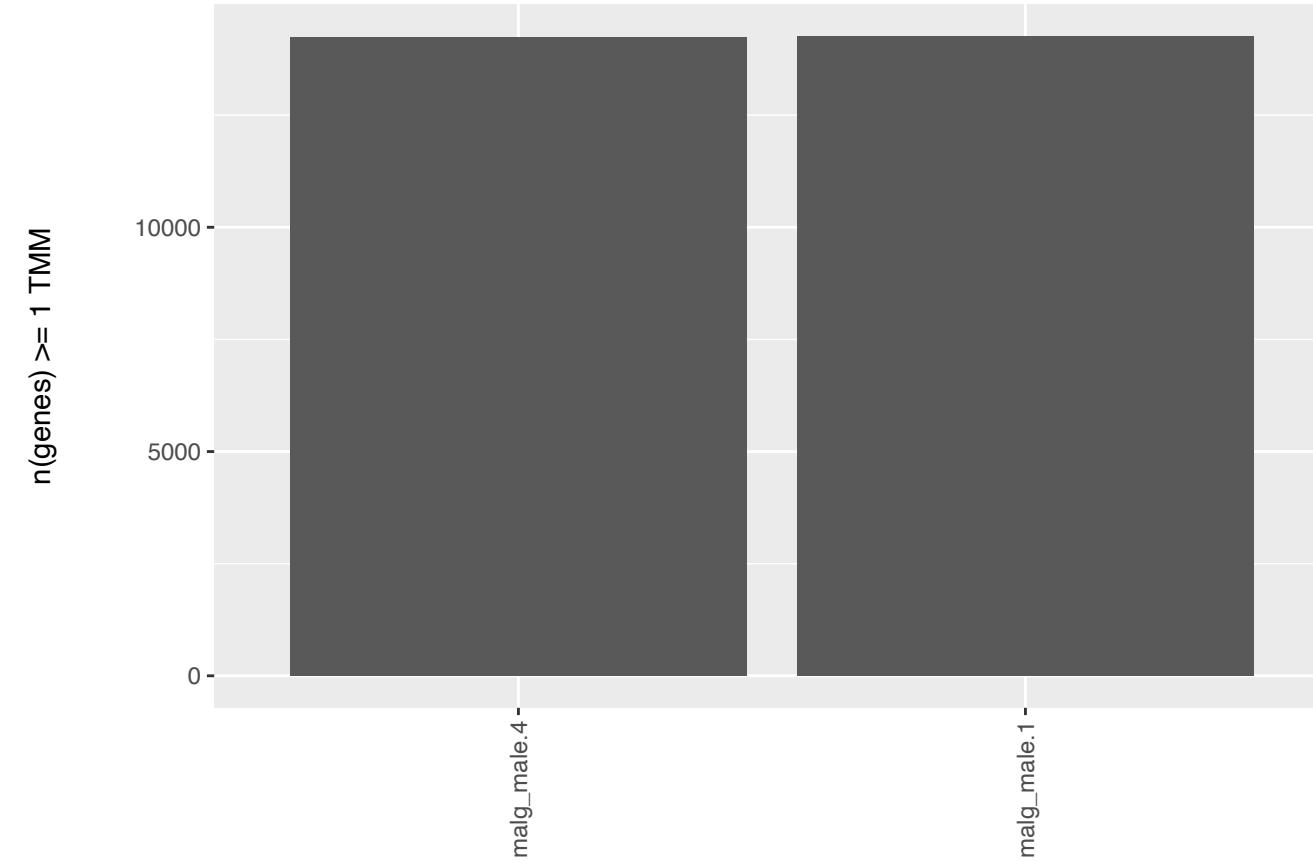
male preputial gland, UMAP: TMM expression values



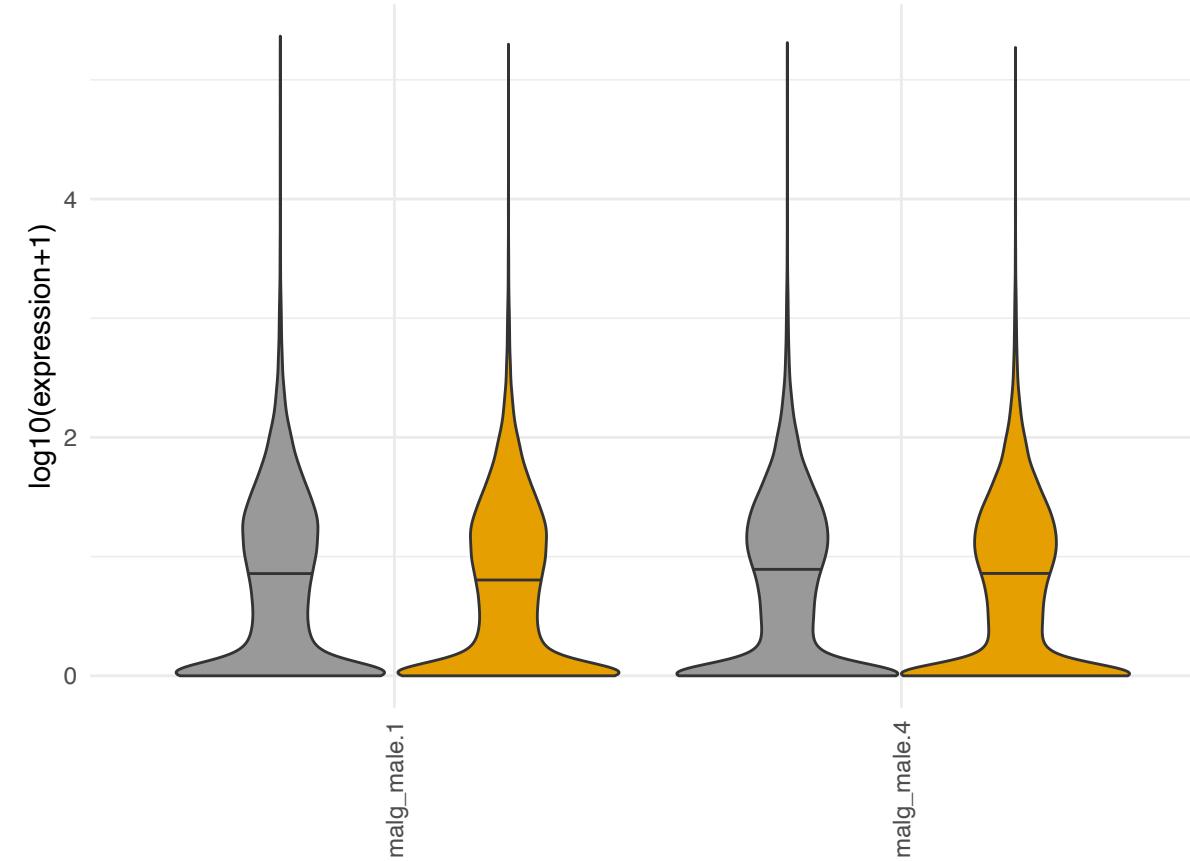
In tissue sample to sample Spearman Distance



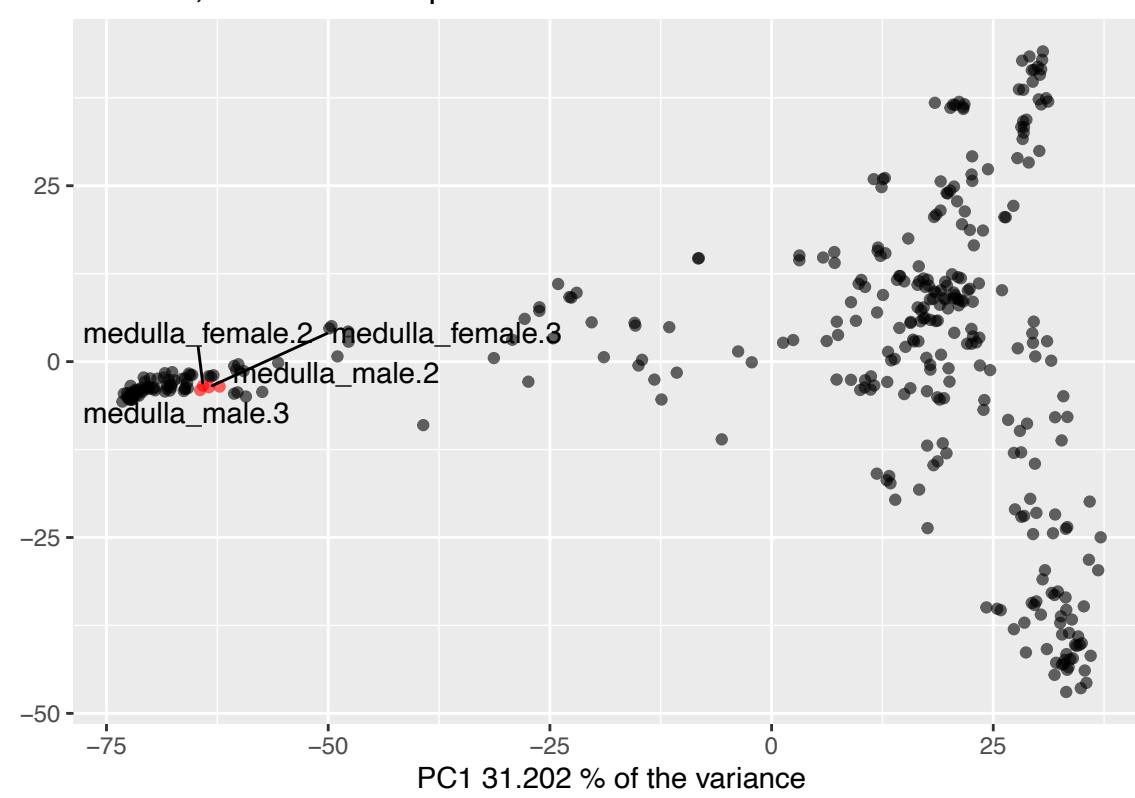
male preputial gland



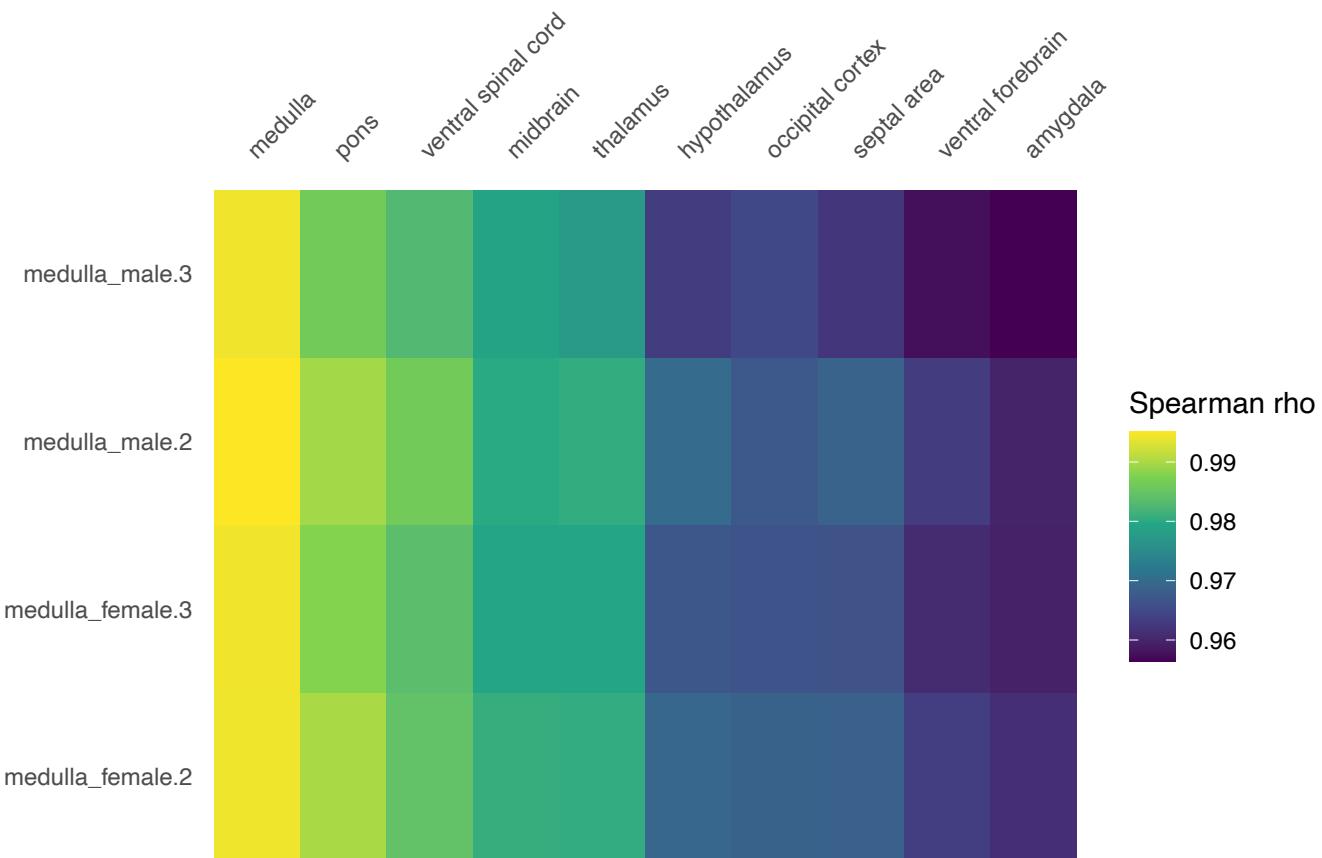
male preputial gland



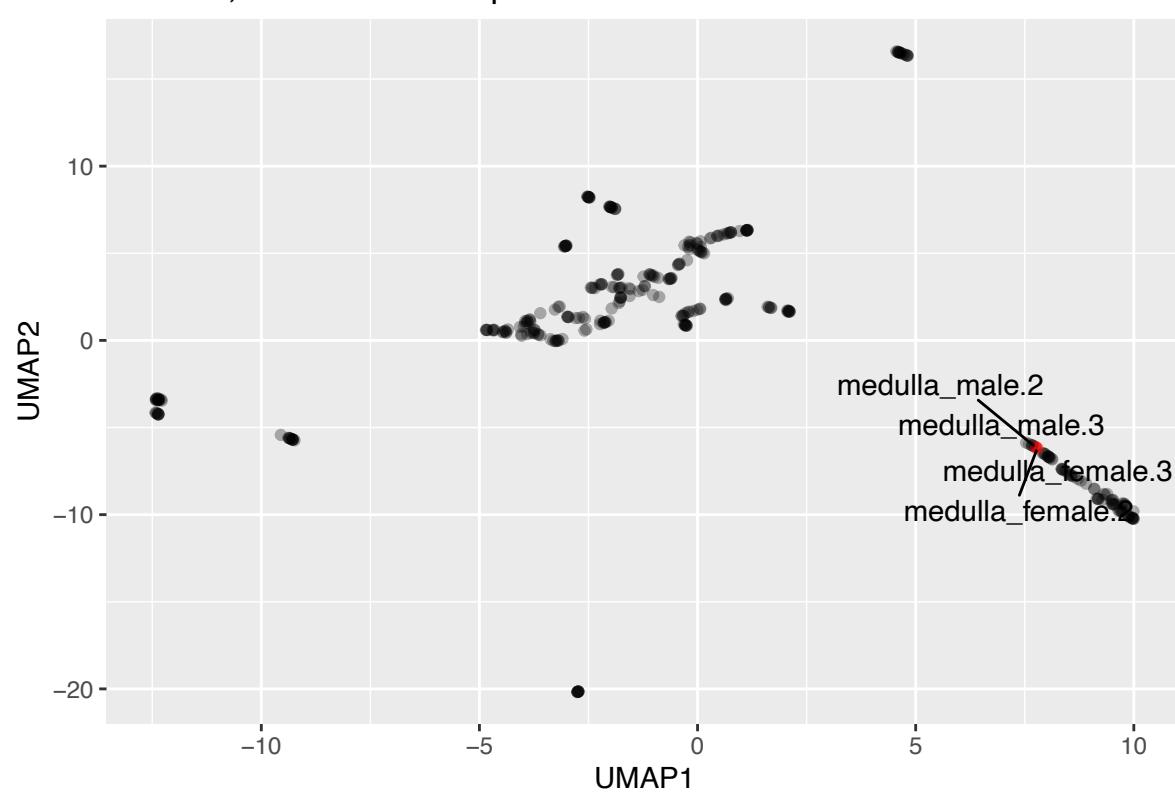
medulla, PCA: TMM expression values



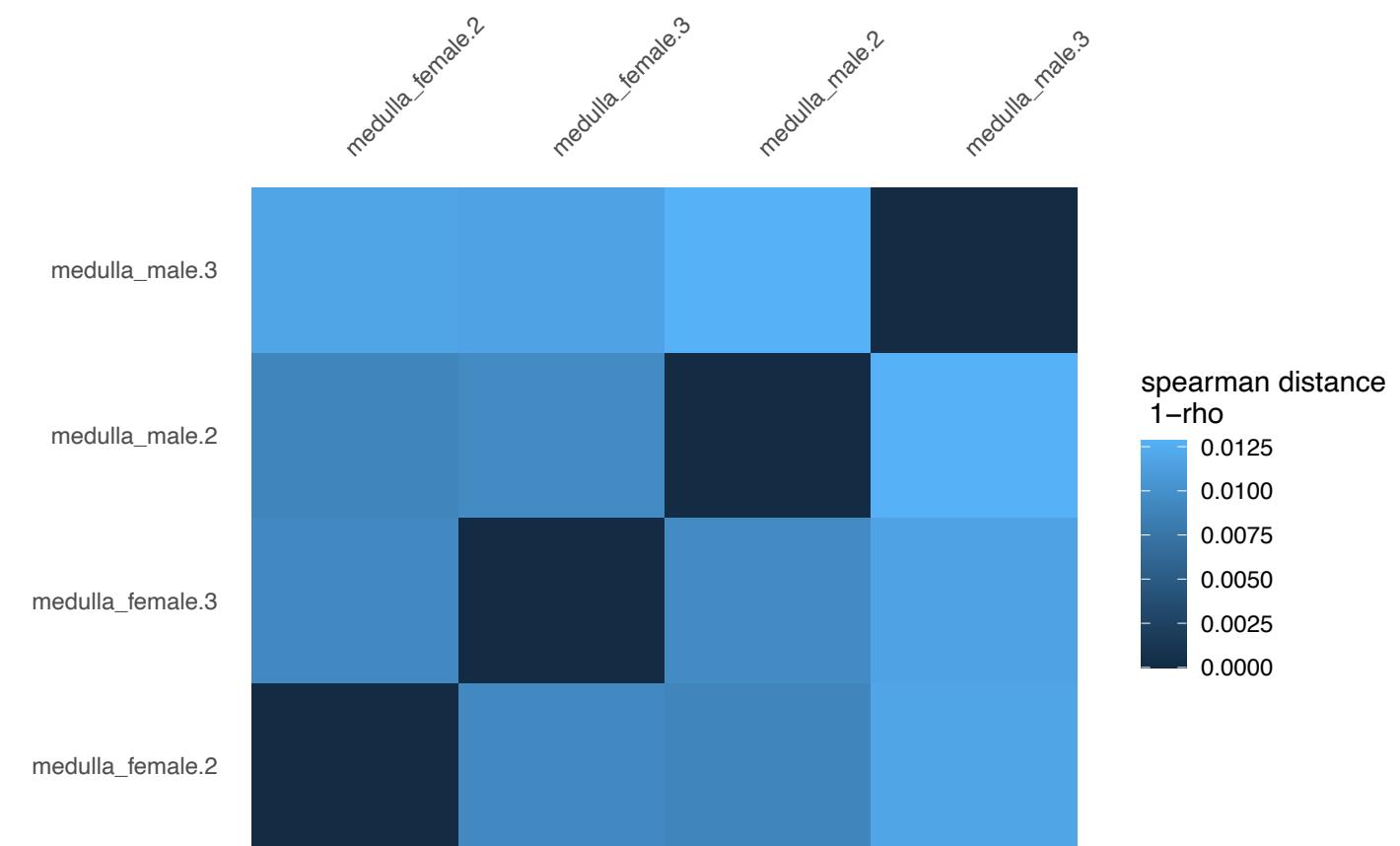
Tissue group to sample correlation



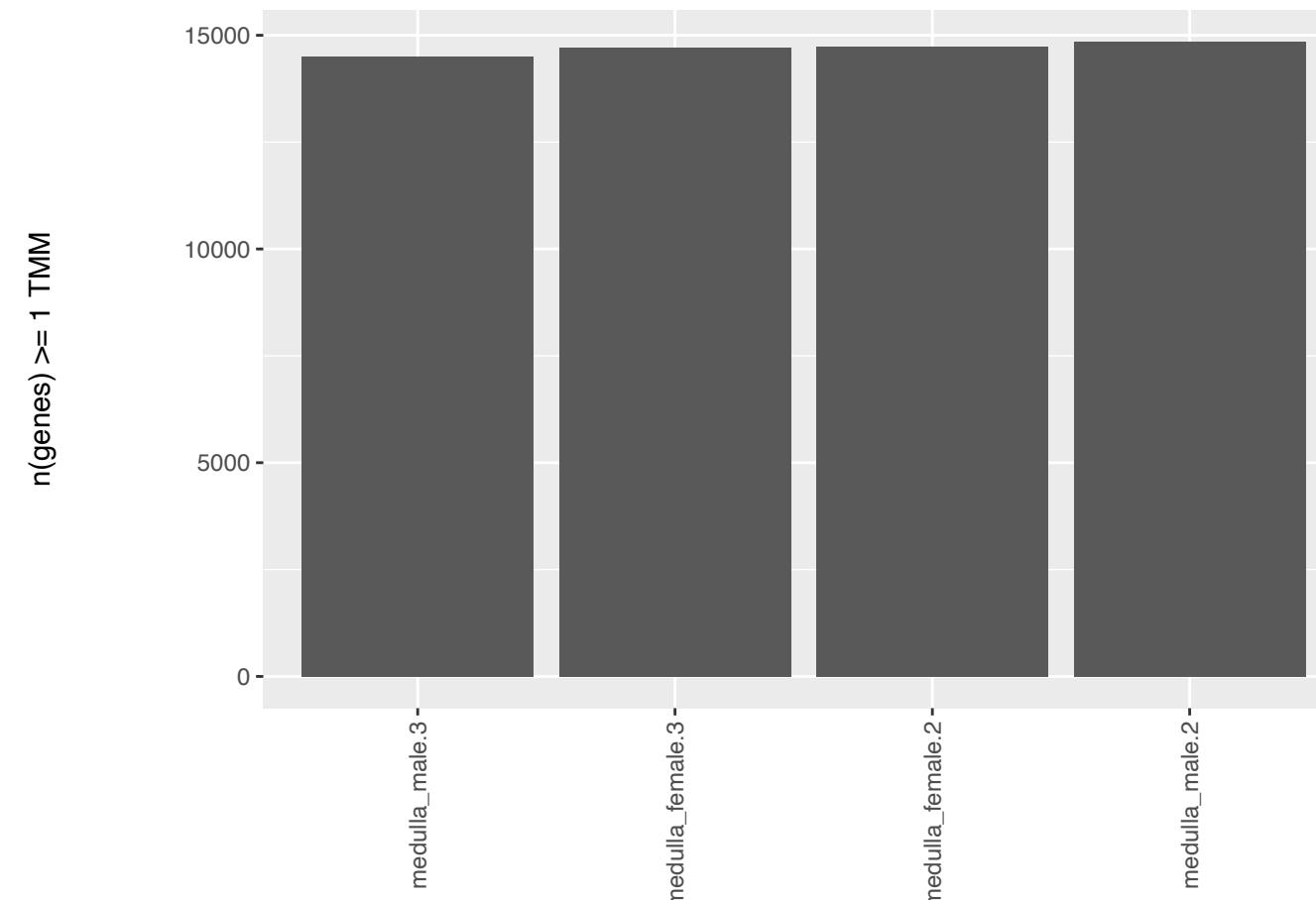
medulla, UMAP: TMM expression values



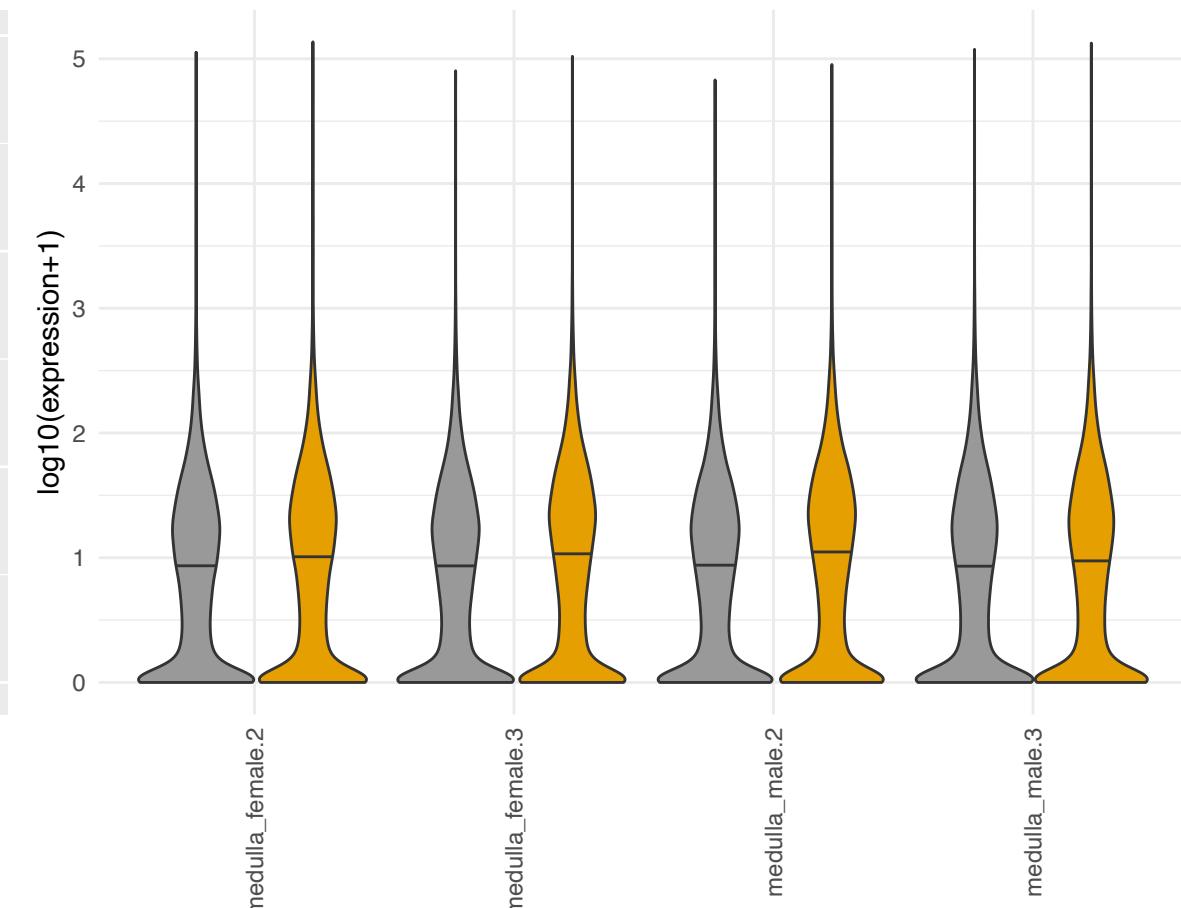
In tissue sample to sample Spearman Distance



medulla

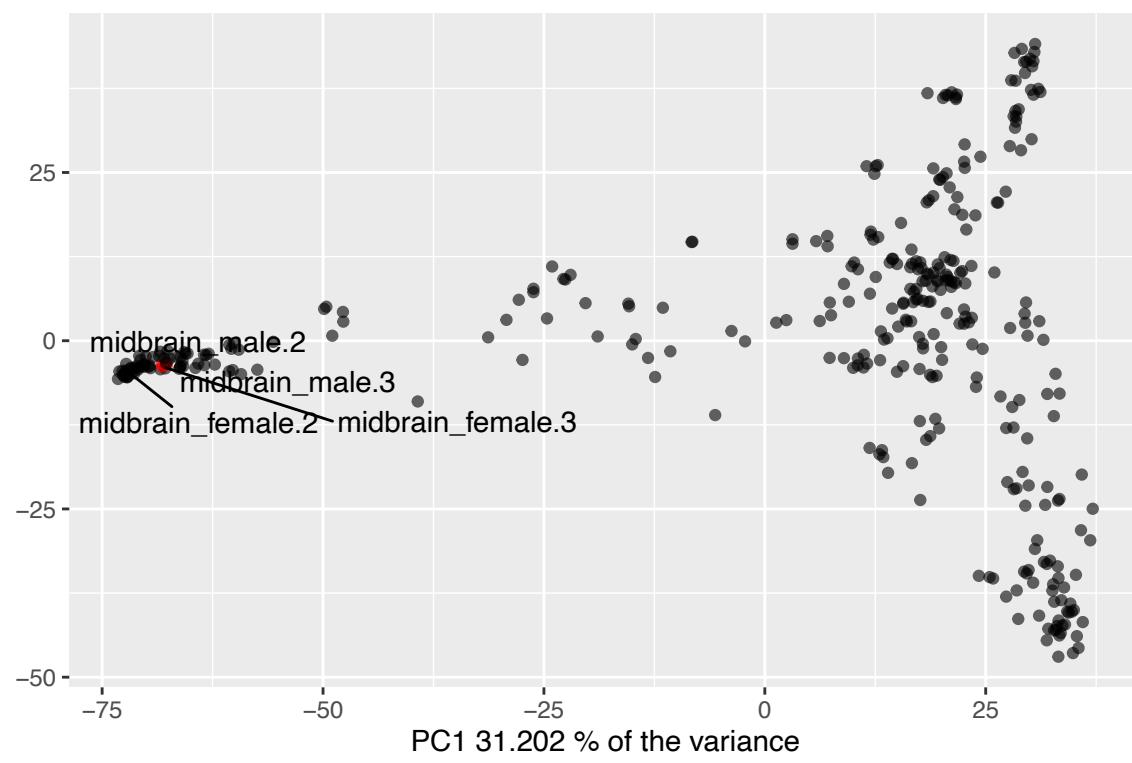


medulla

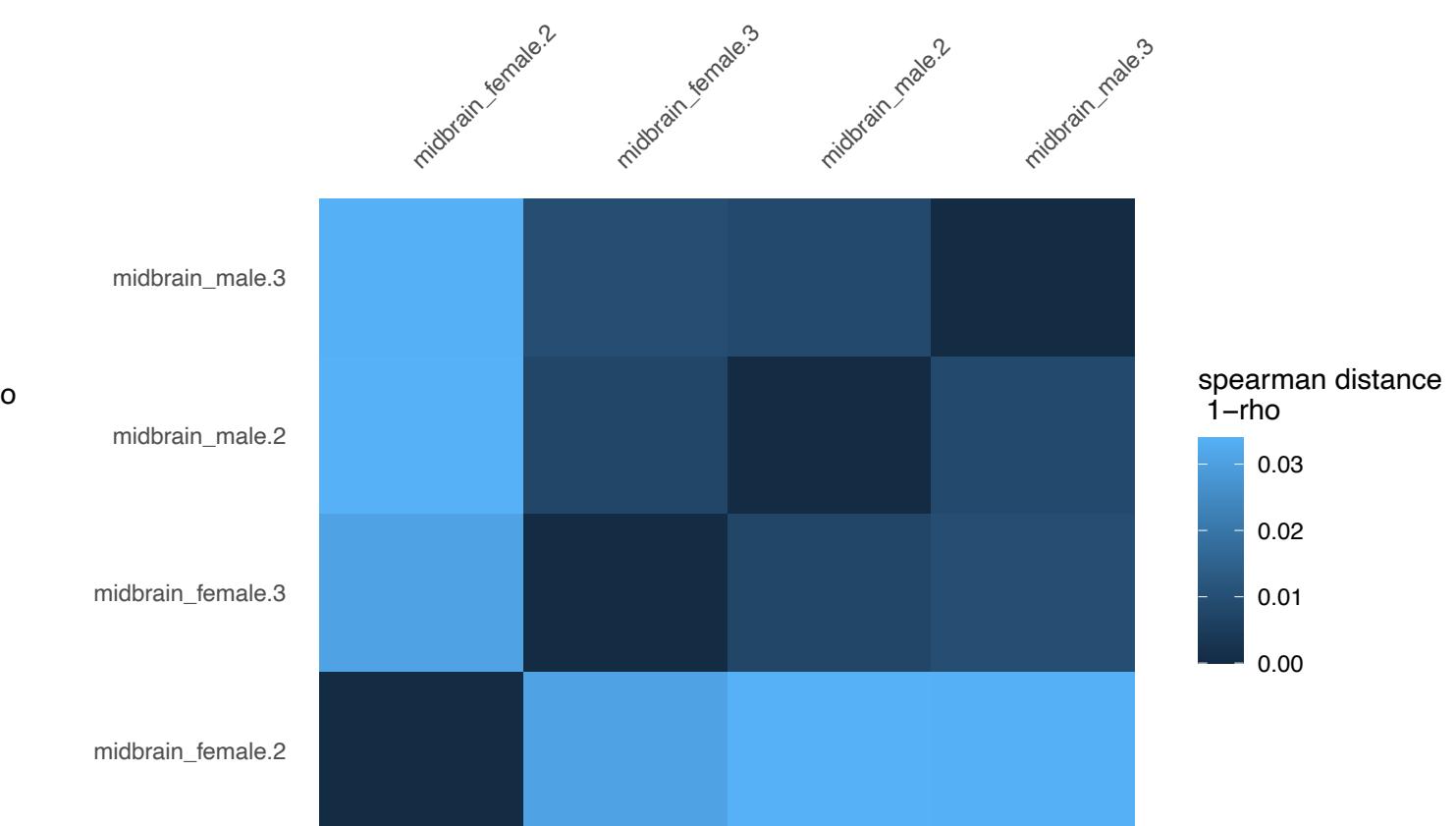
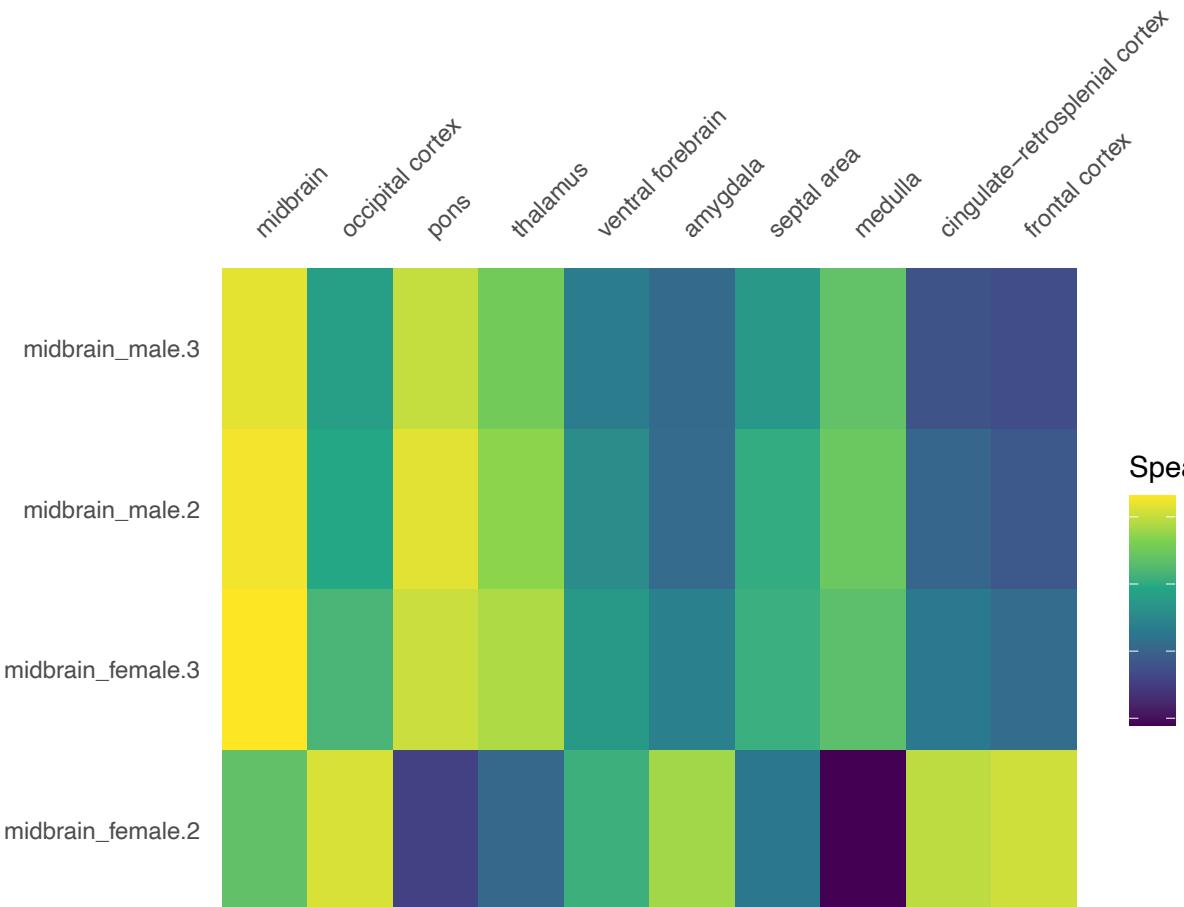
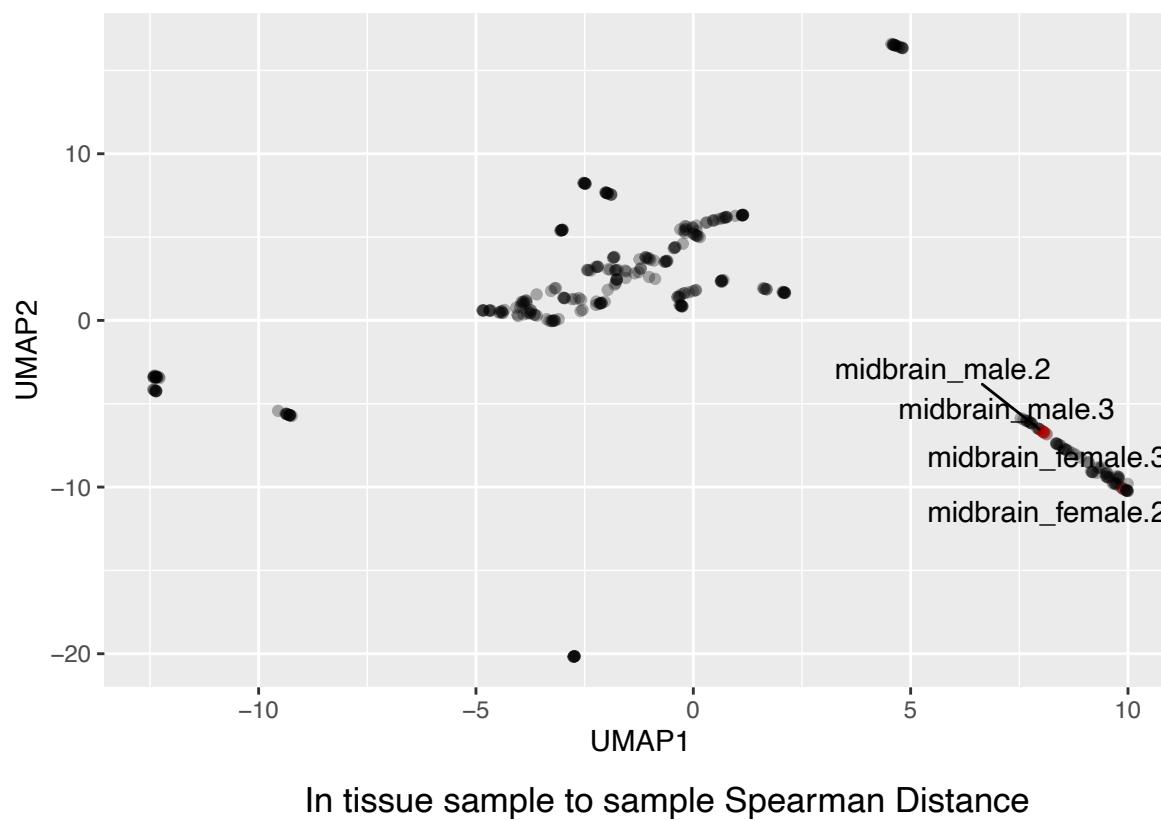


midbrain, PCA: TMM expression values

PC2 9.077 % of the variance

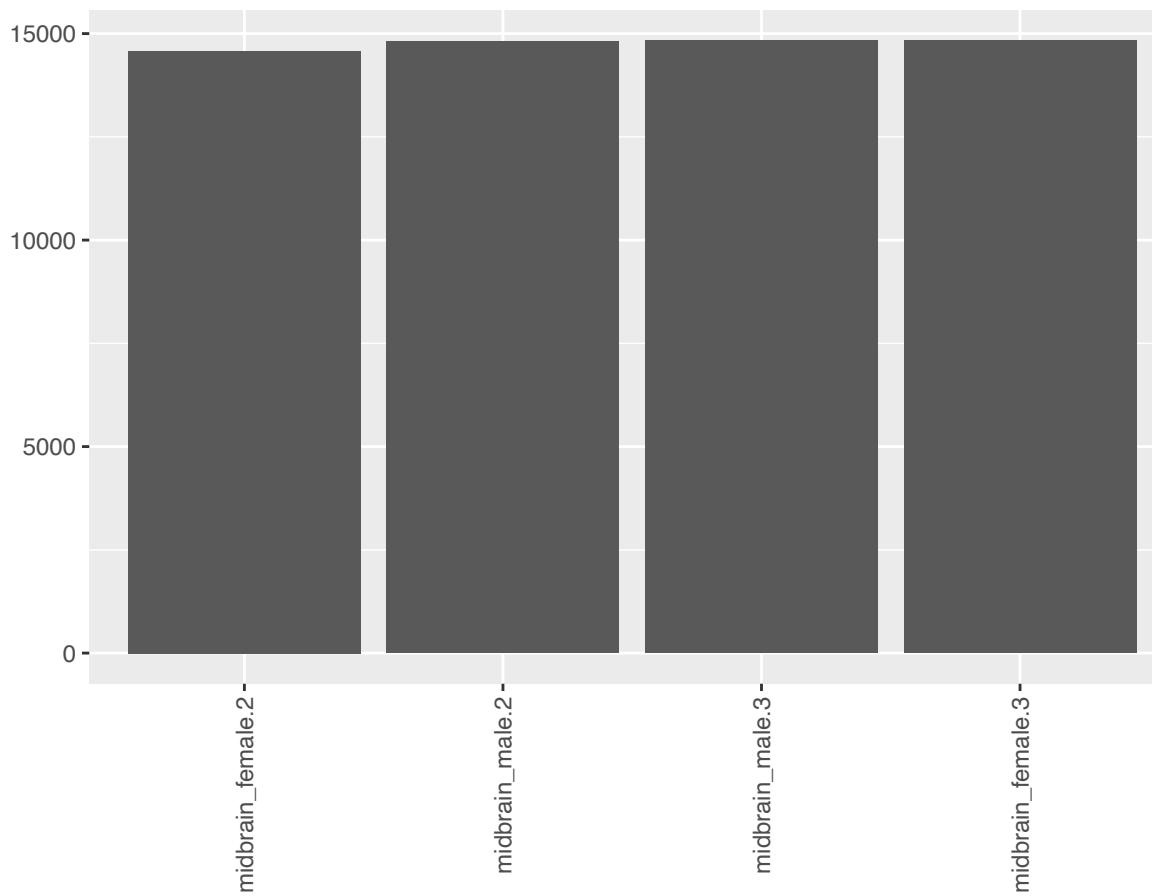


midbrain, UMAP: TMM expression values

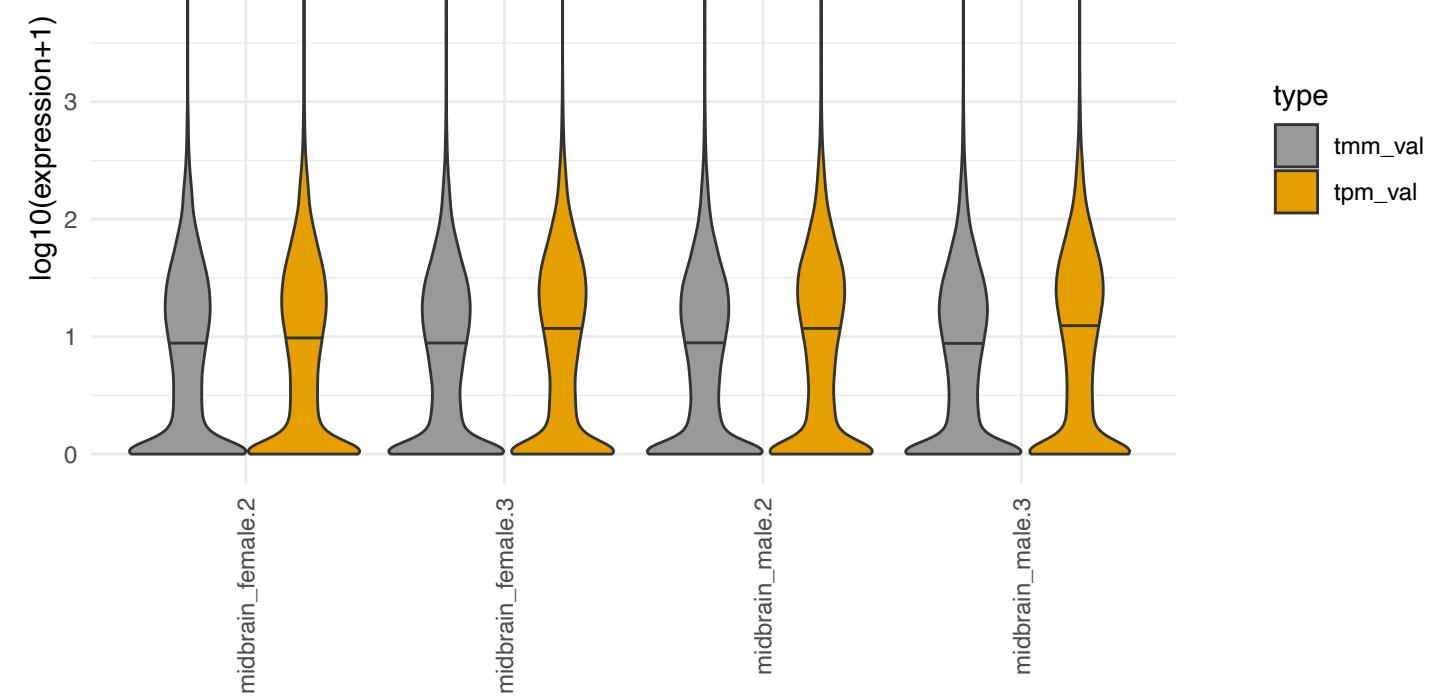


midbrain

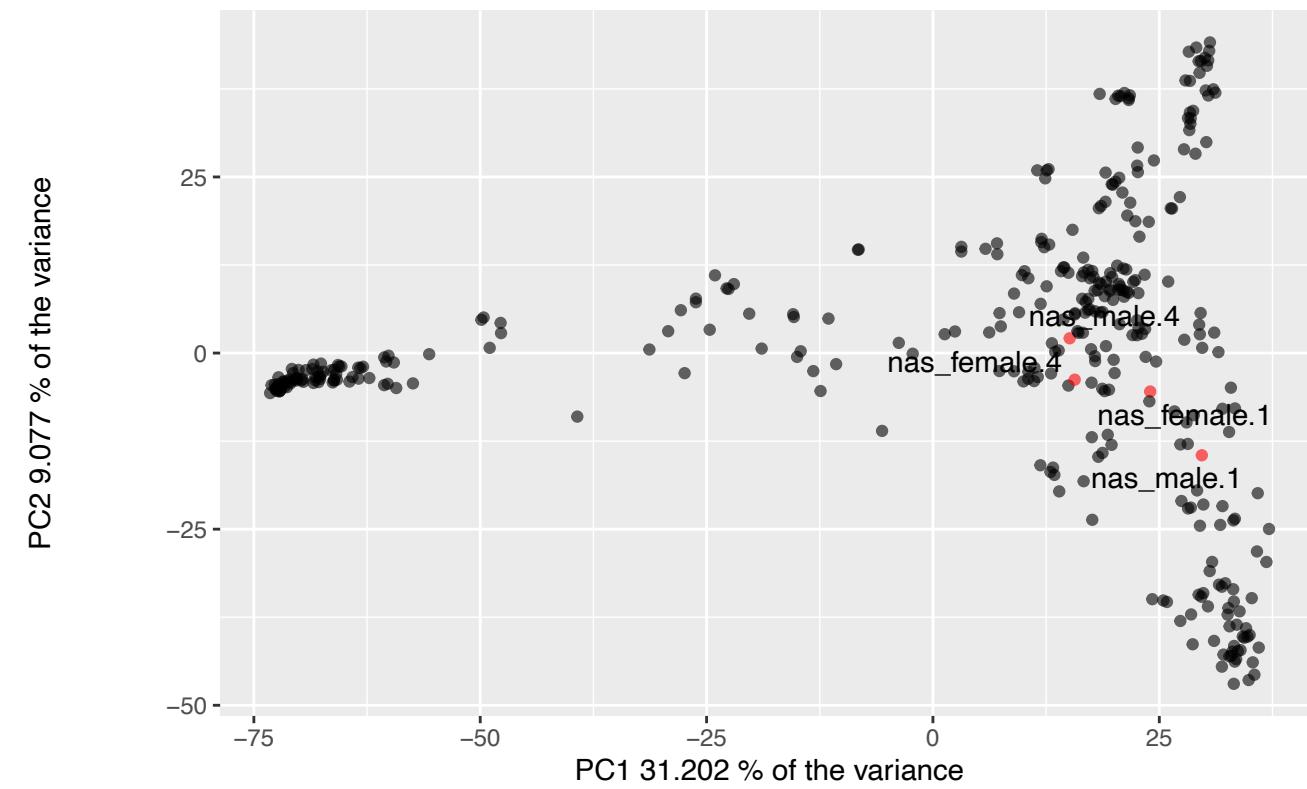
n(genes) >= 1 TMM



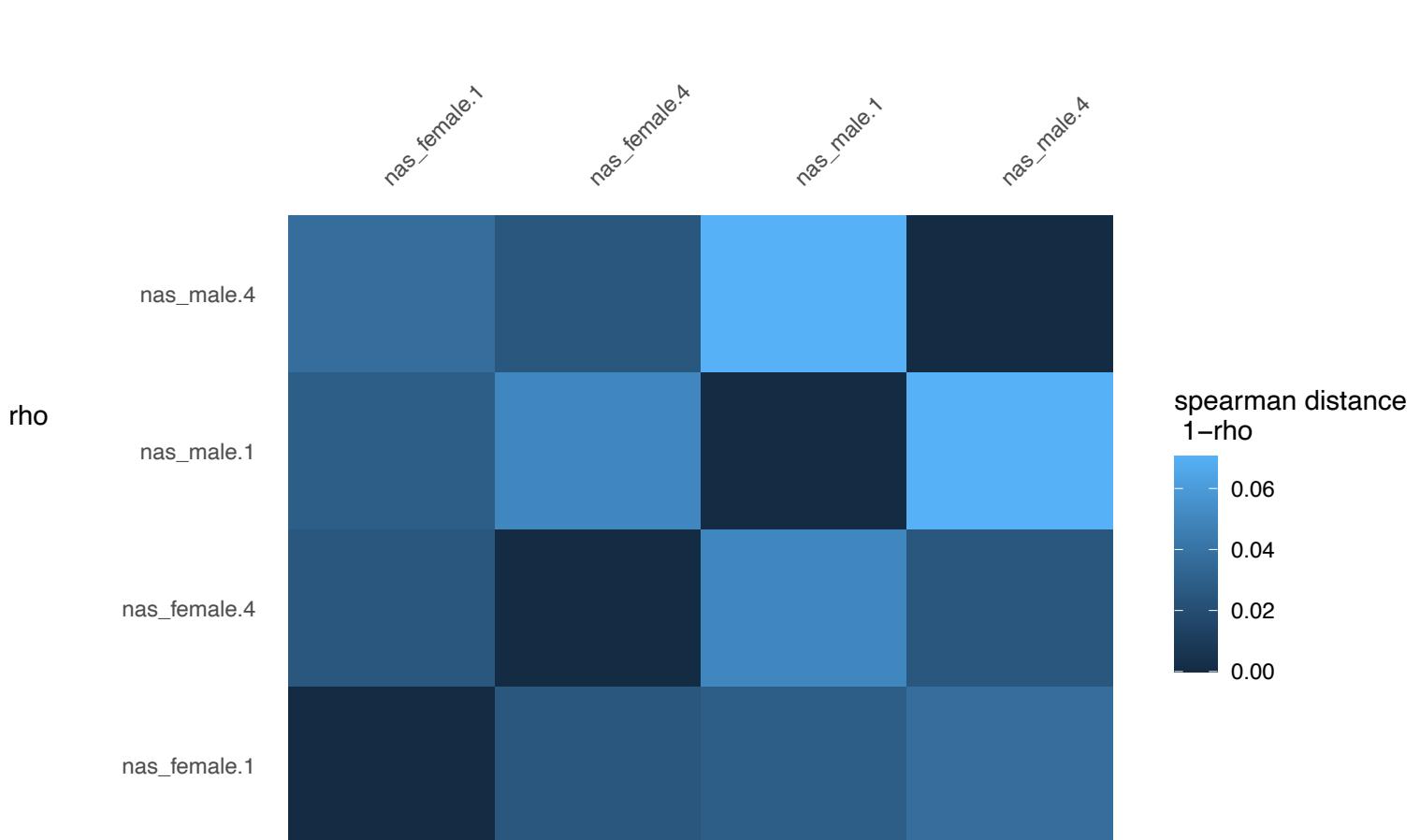
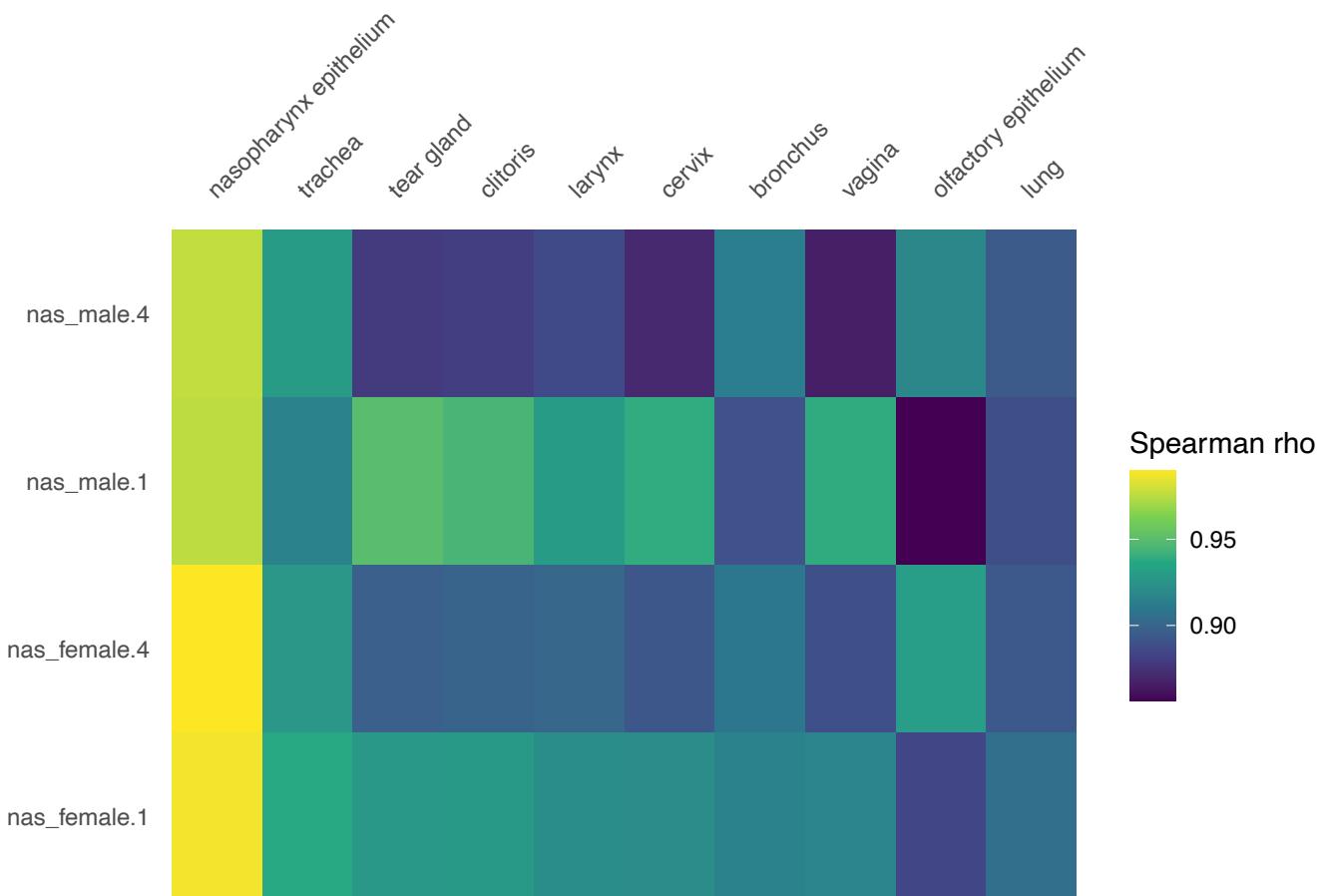
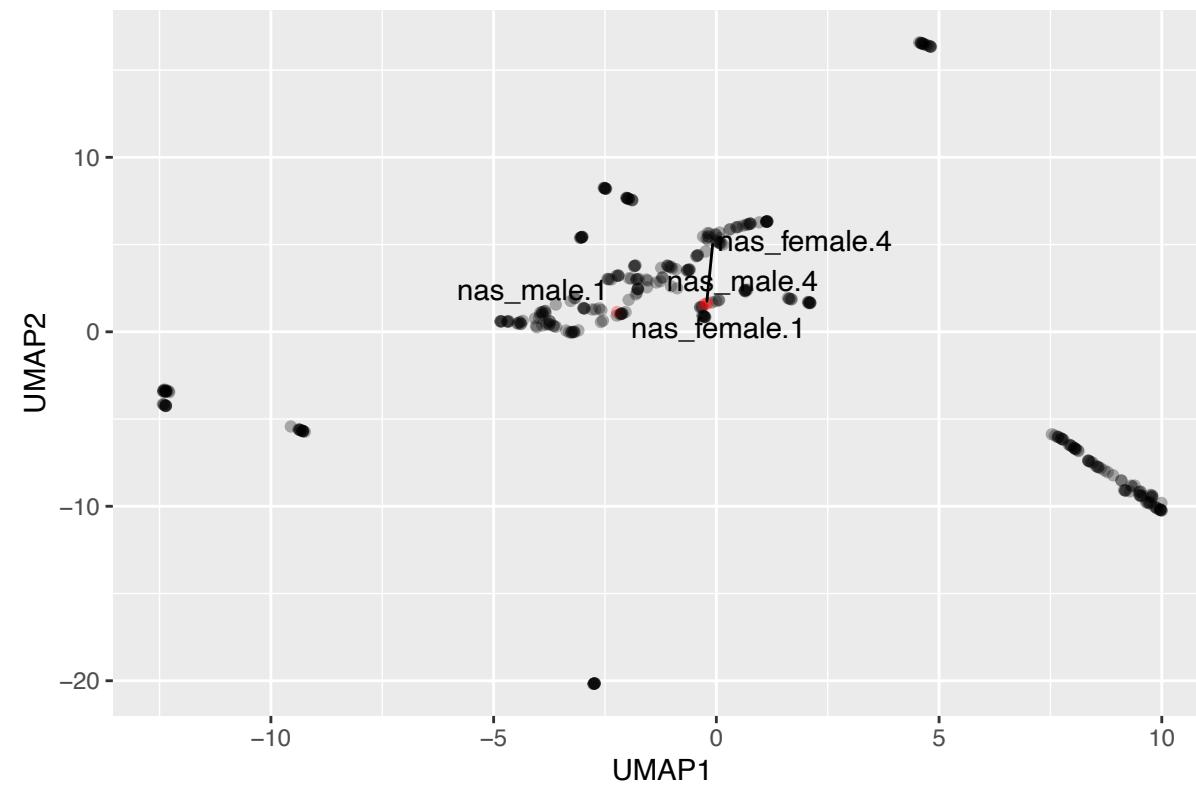
midbrain



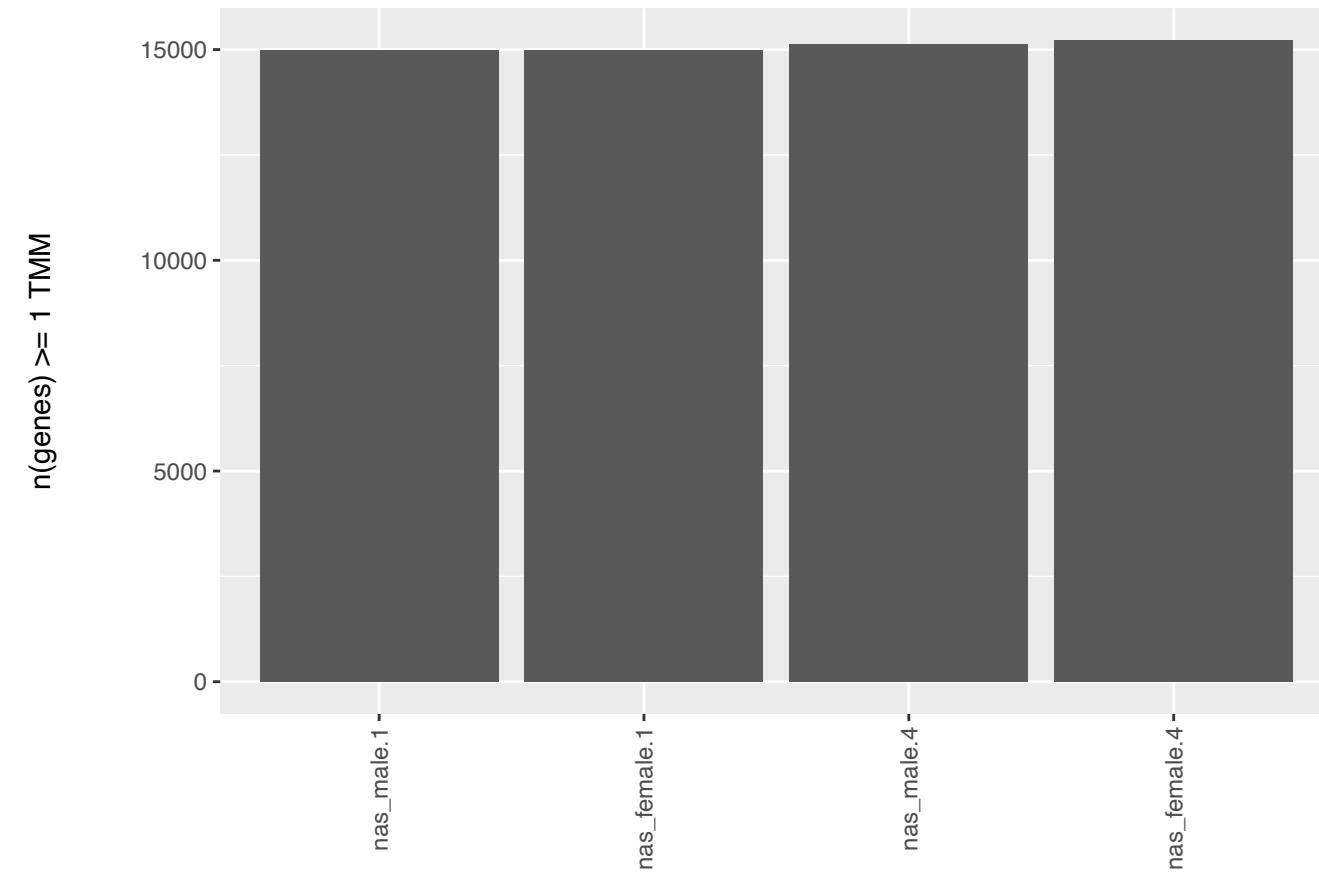
nasopharynx epithelium, PCA: TMM expression values



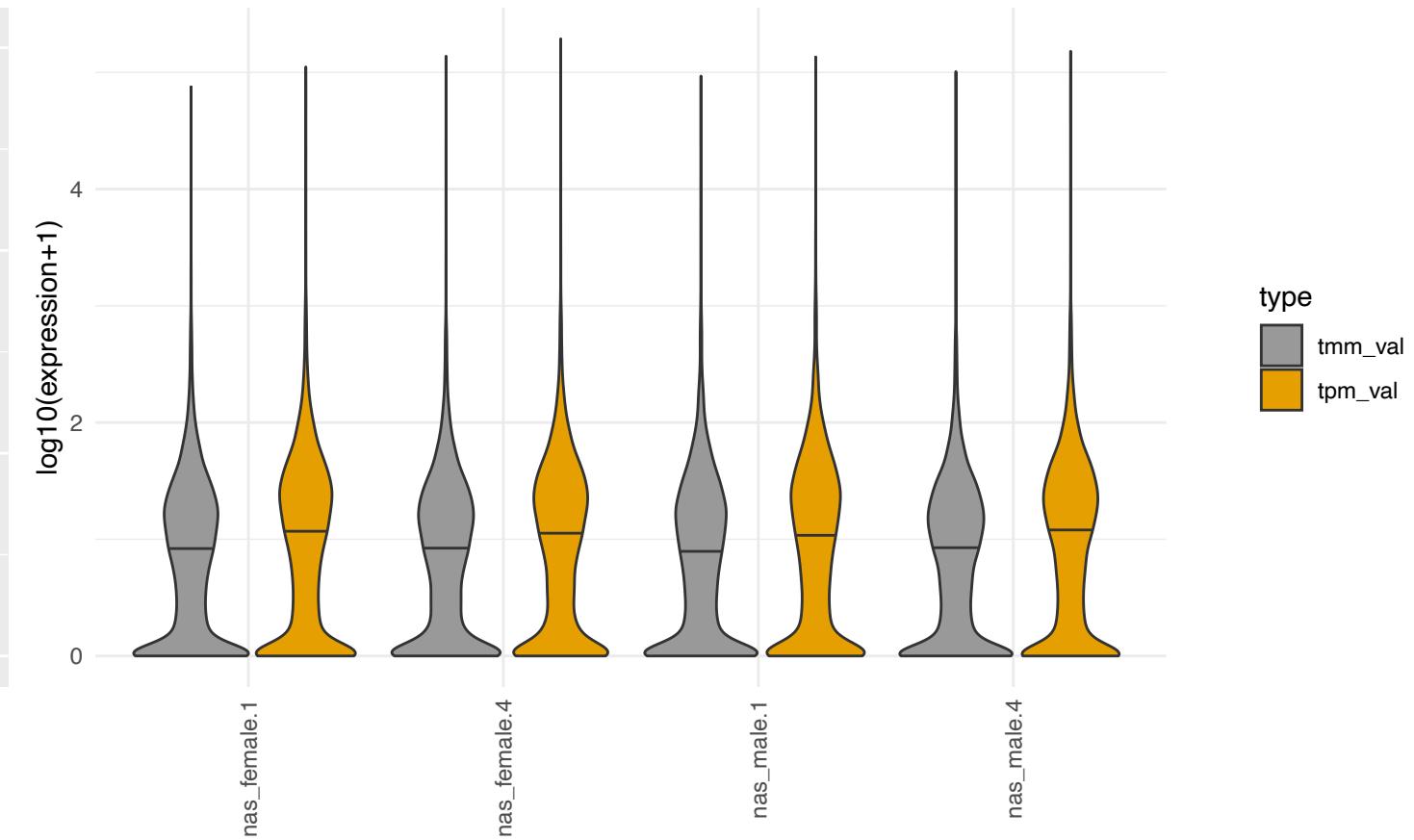
nasopharynx epithelium, UMAP: TMM expression values



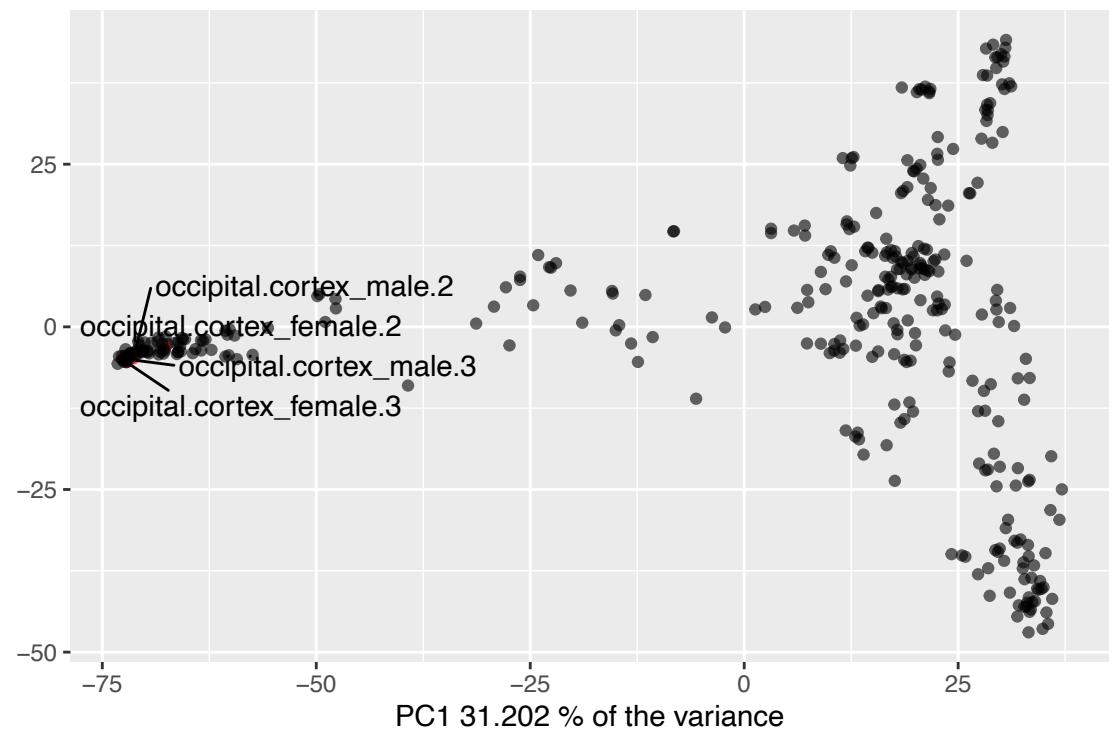
nasopharynx epithelium



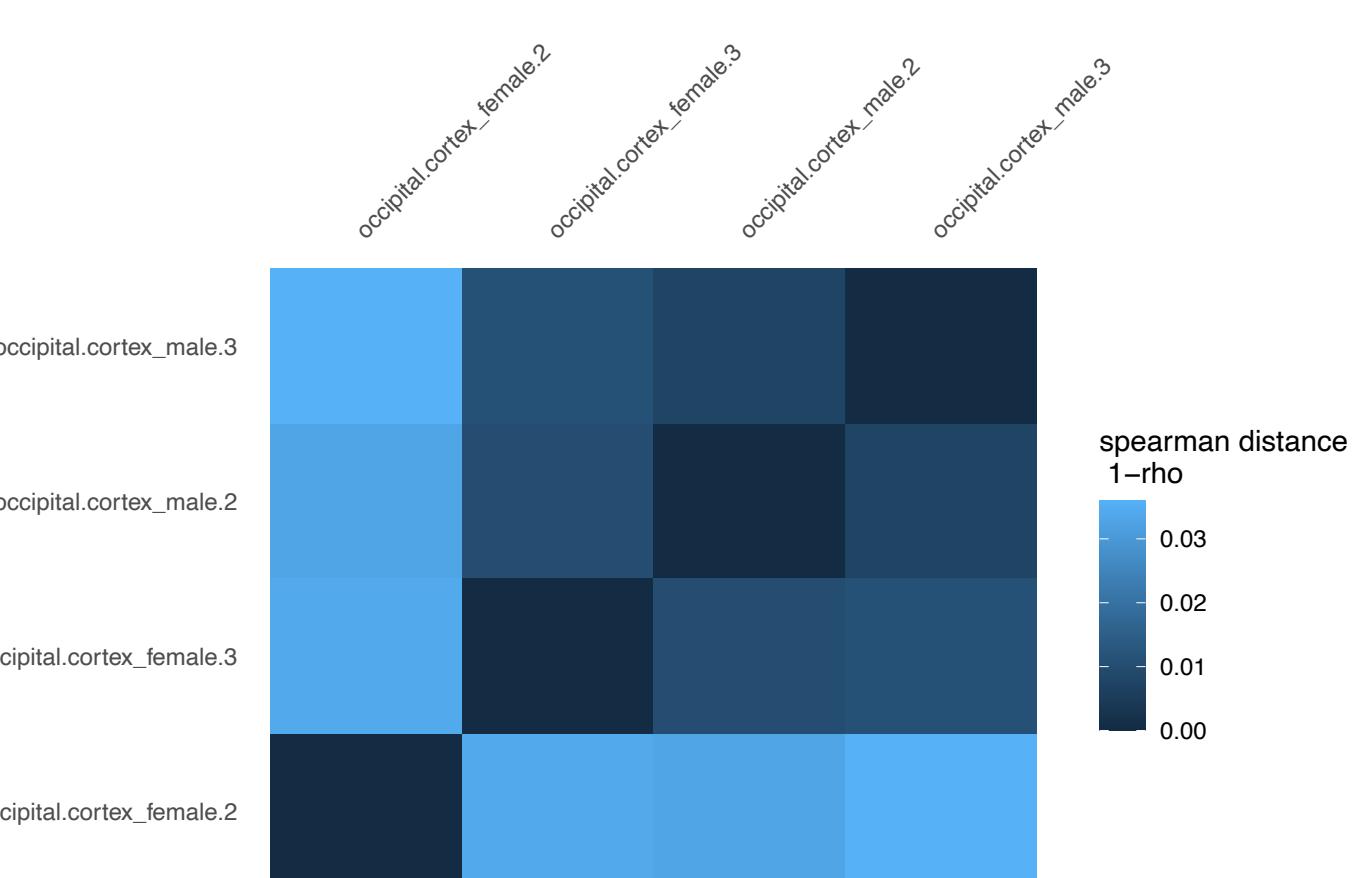
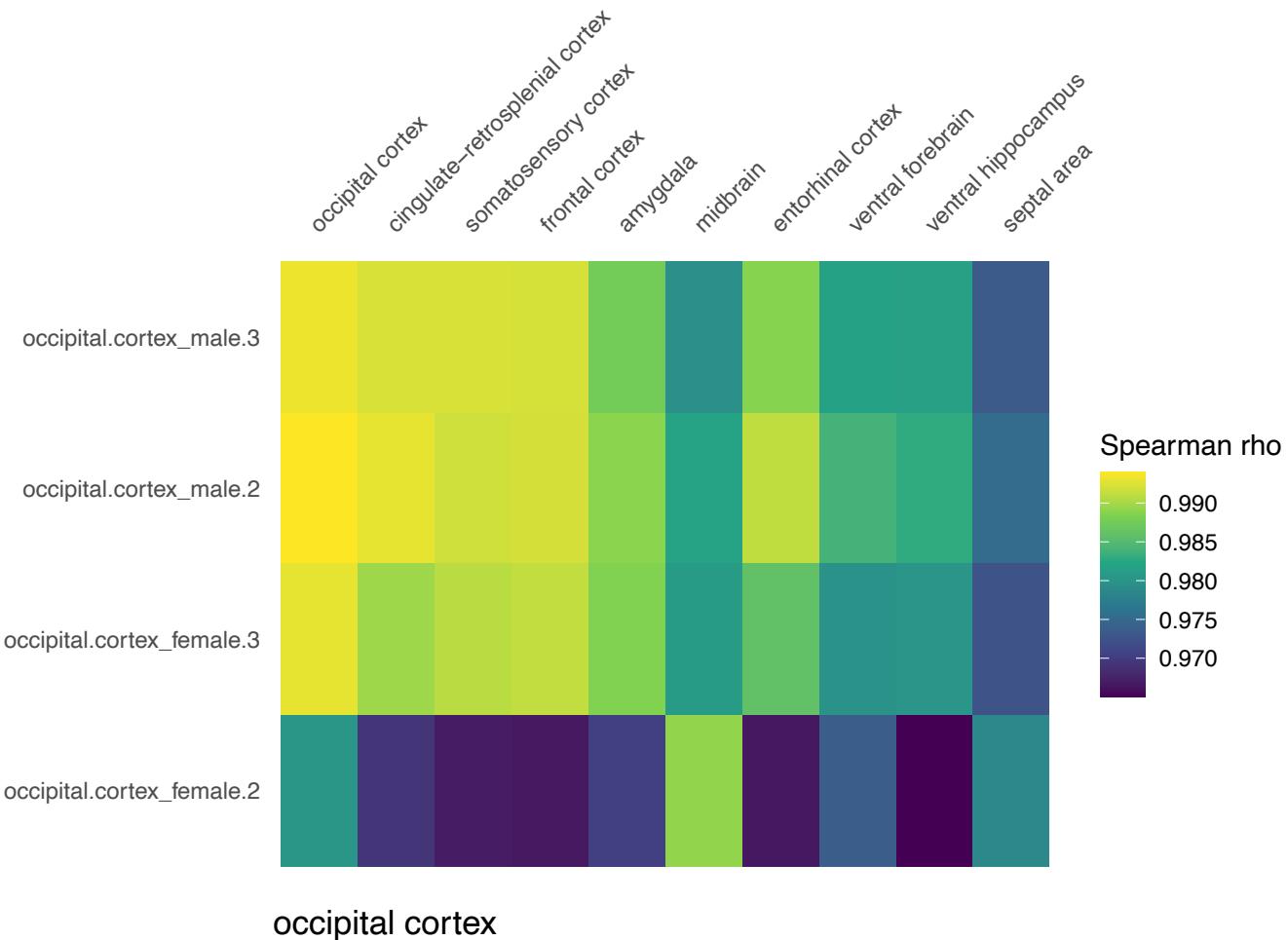
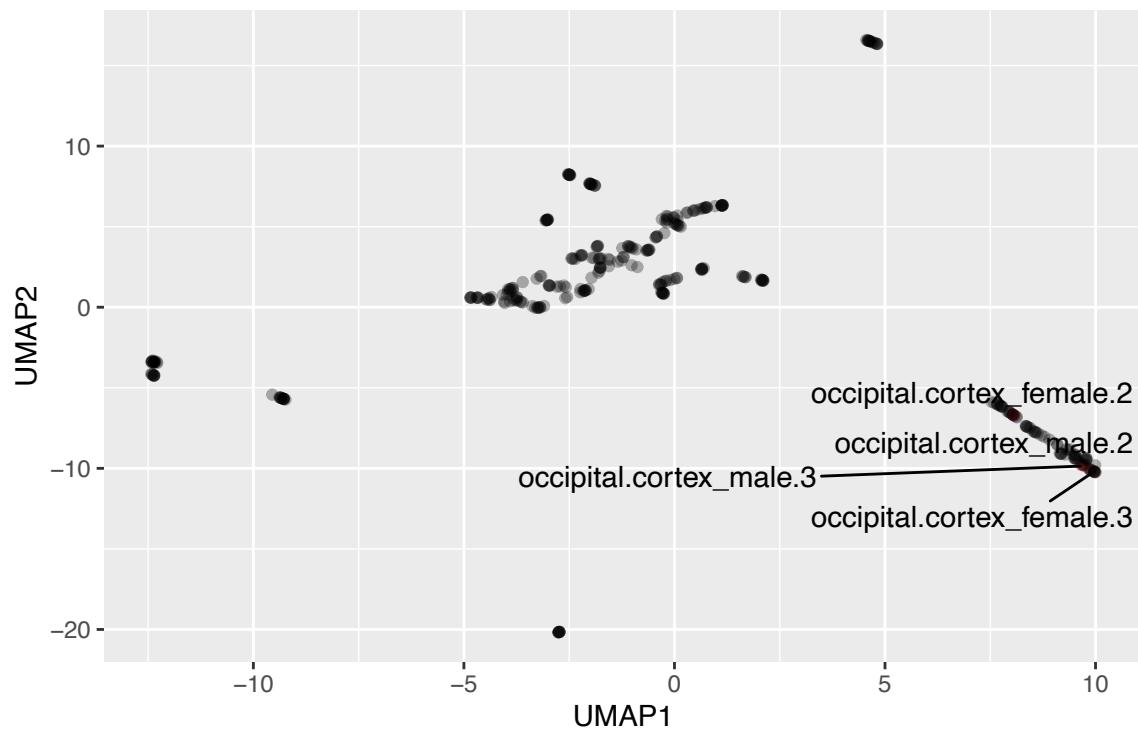
nasopharynx epithelium



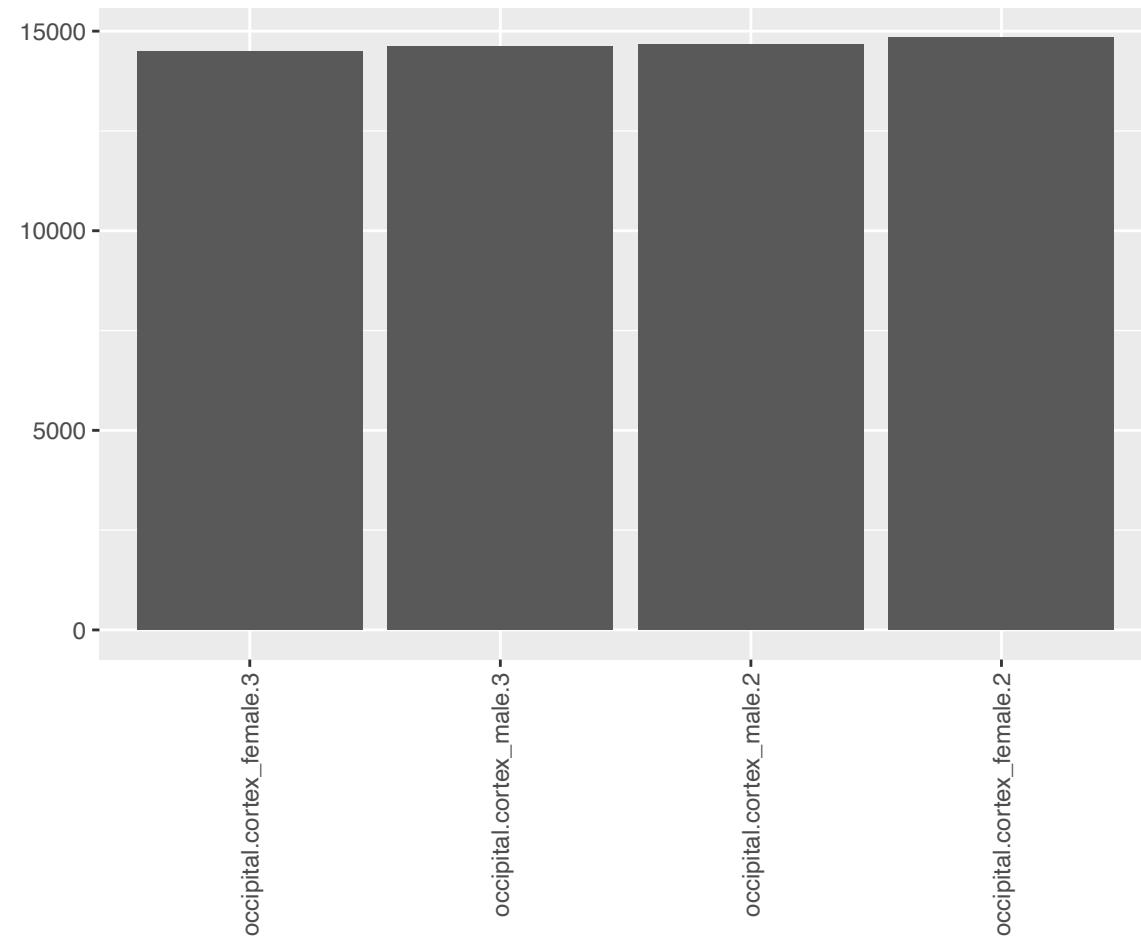
occipital cortex, PCA: TMM expression values



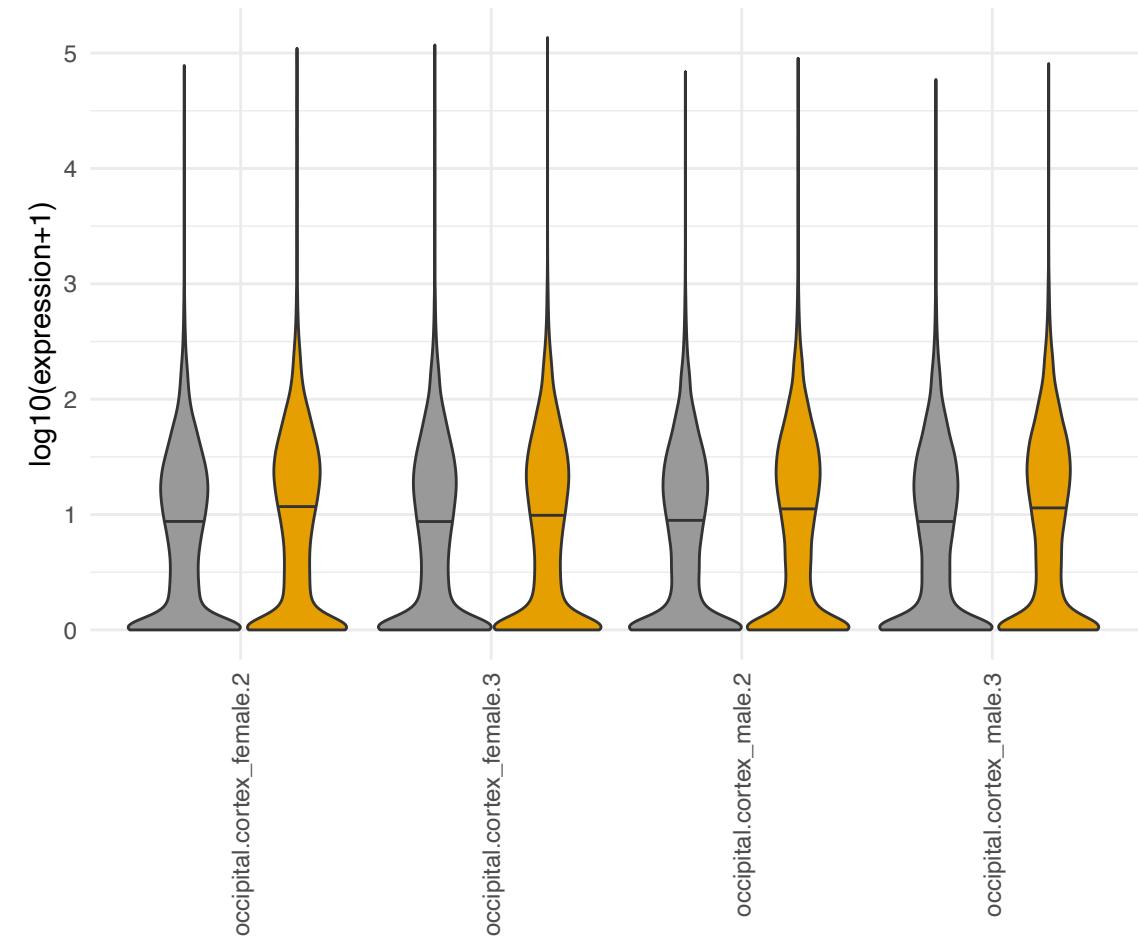
occipital cortex, UMAP: TMM expression values



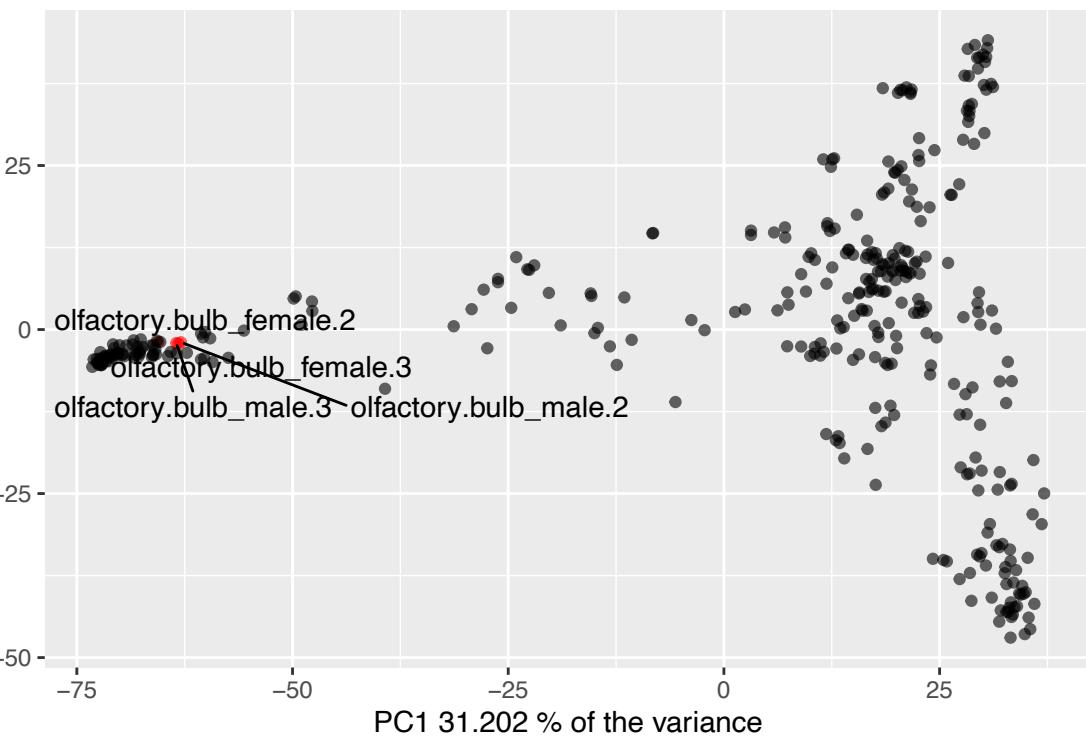
occipital cortex



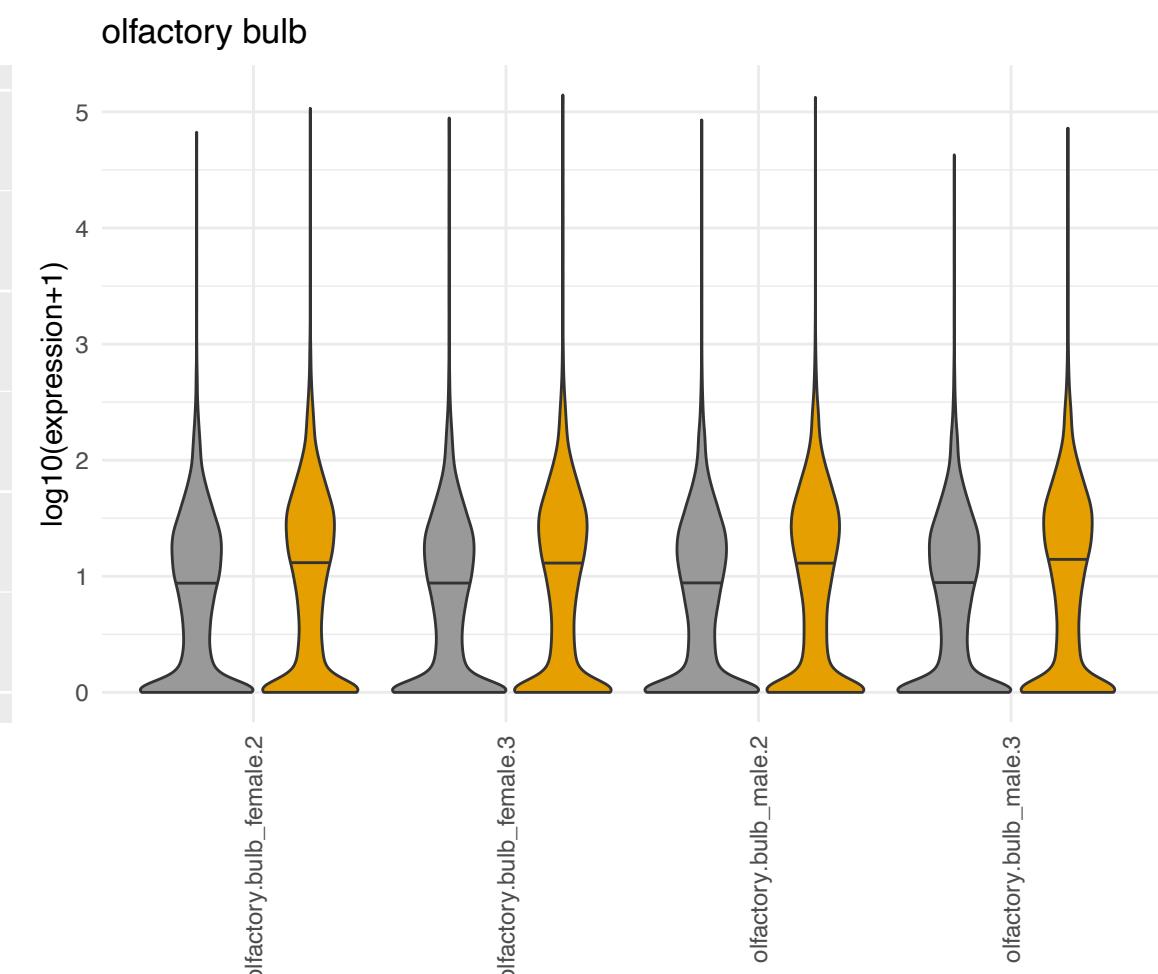
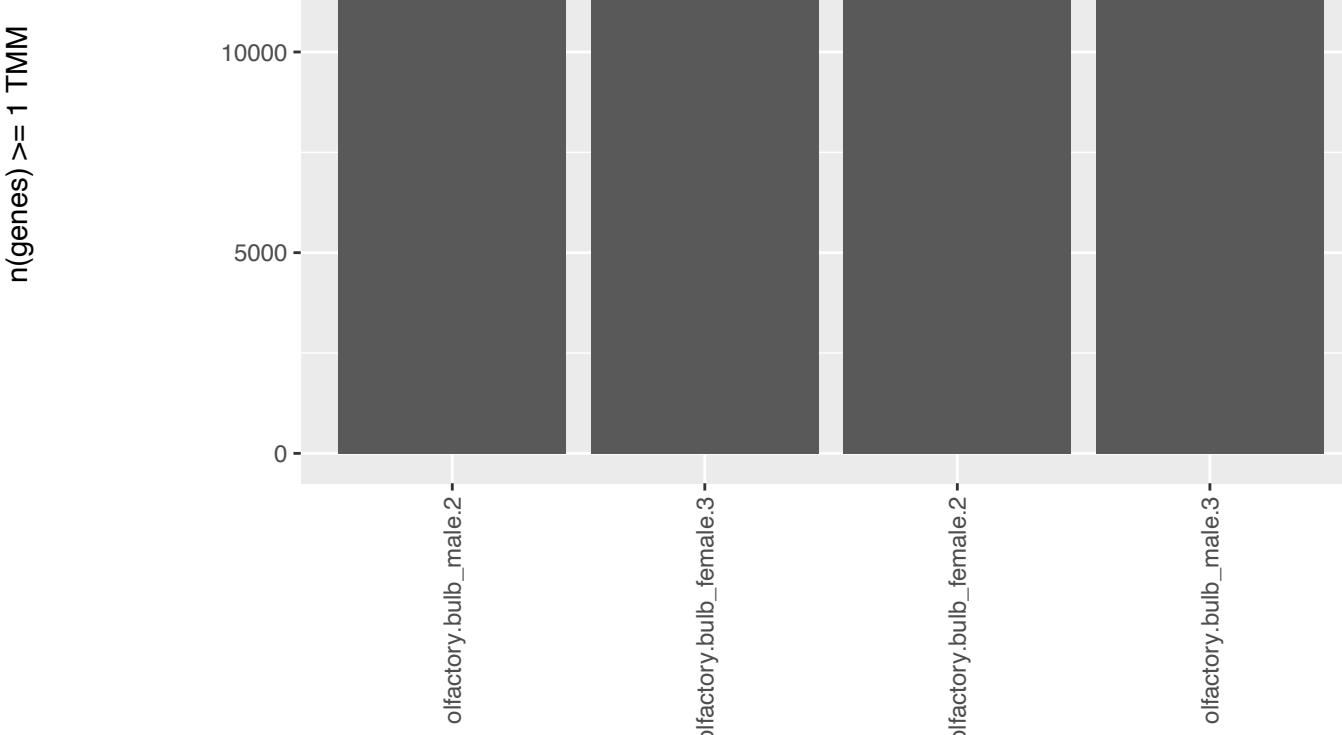
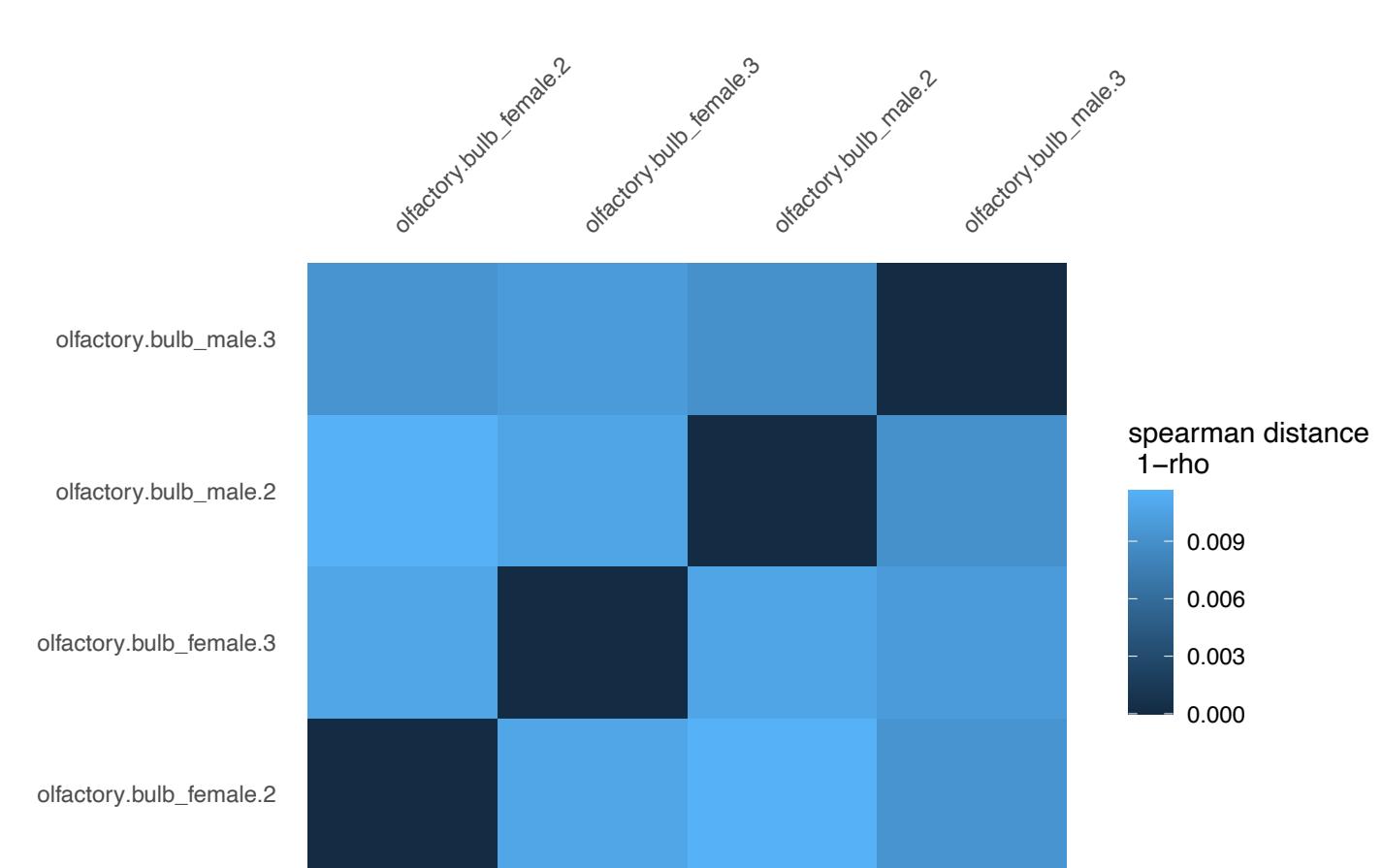
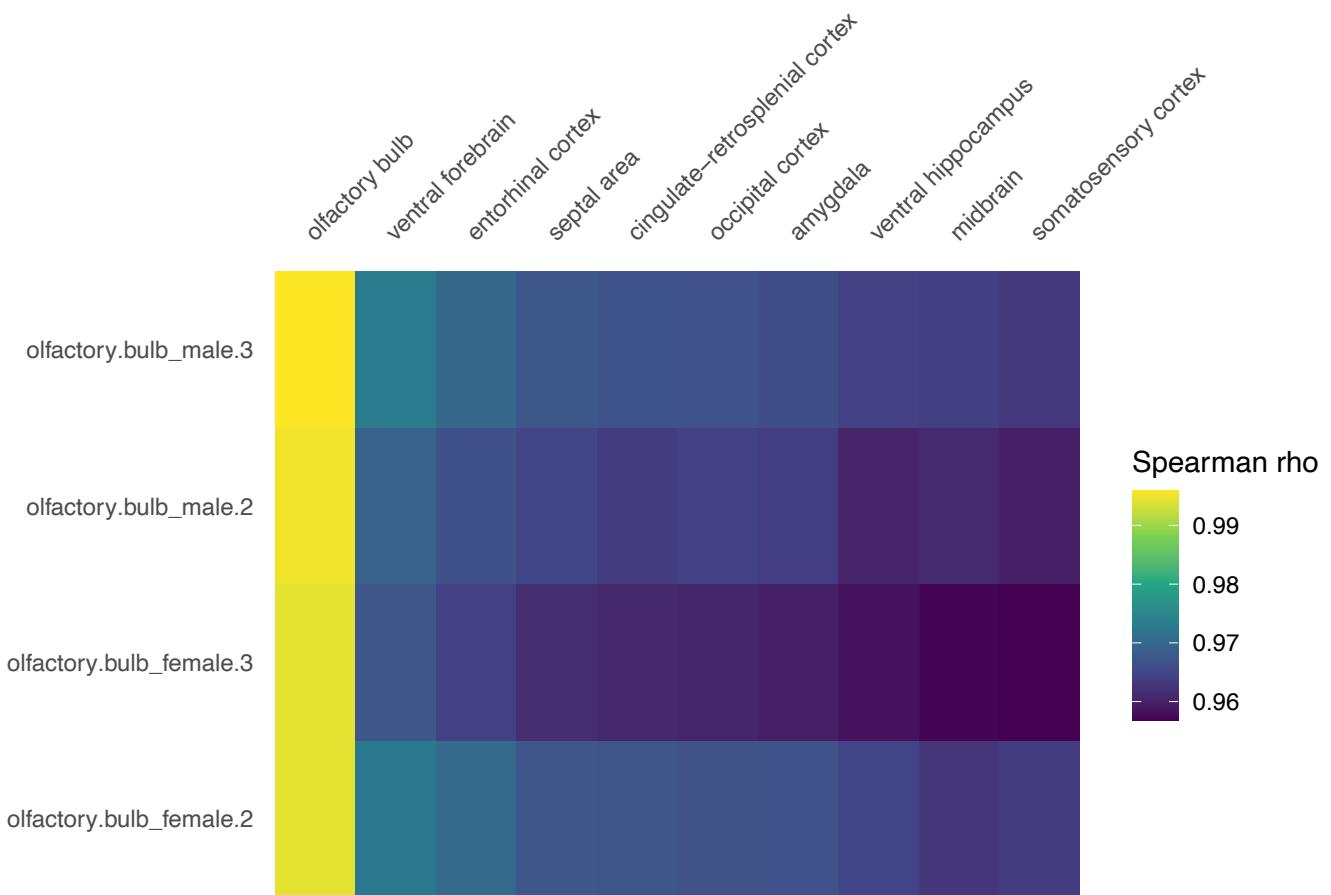
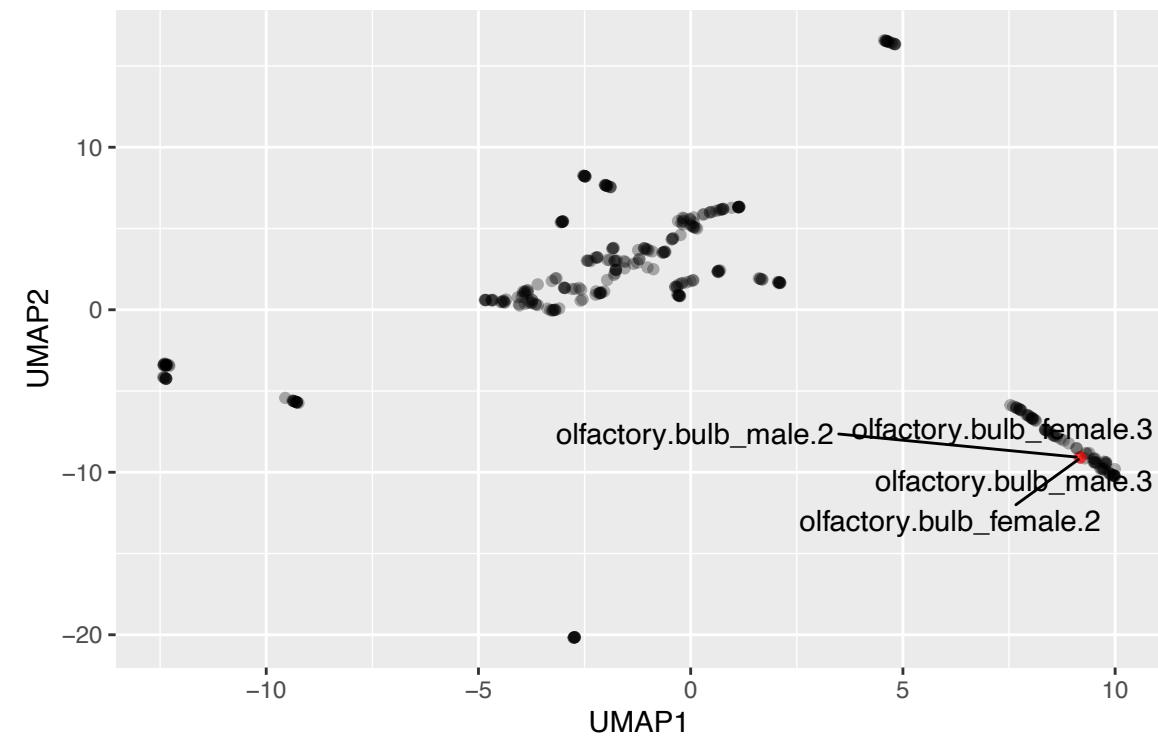
occipital cortex



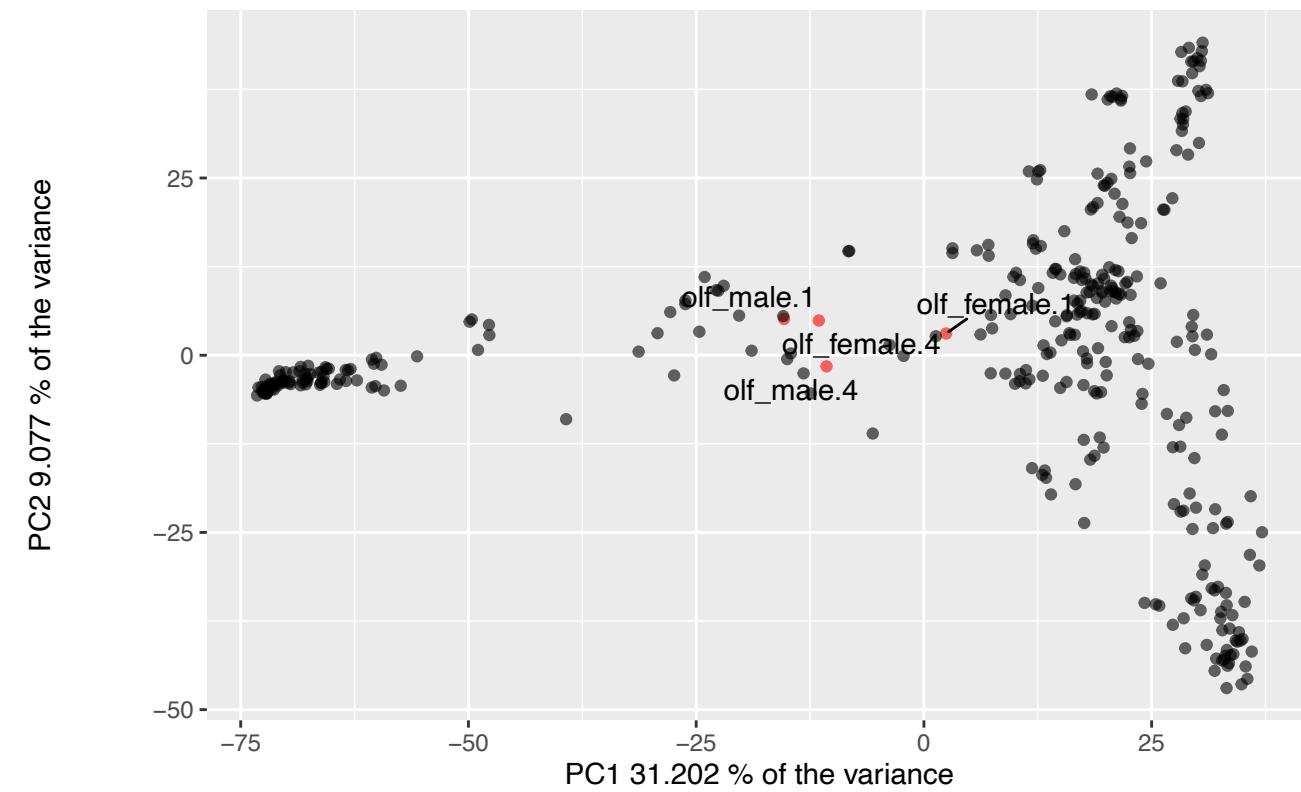
olfactory bulb, PCA: TMM expression values



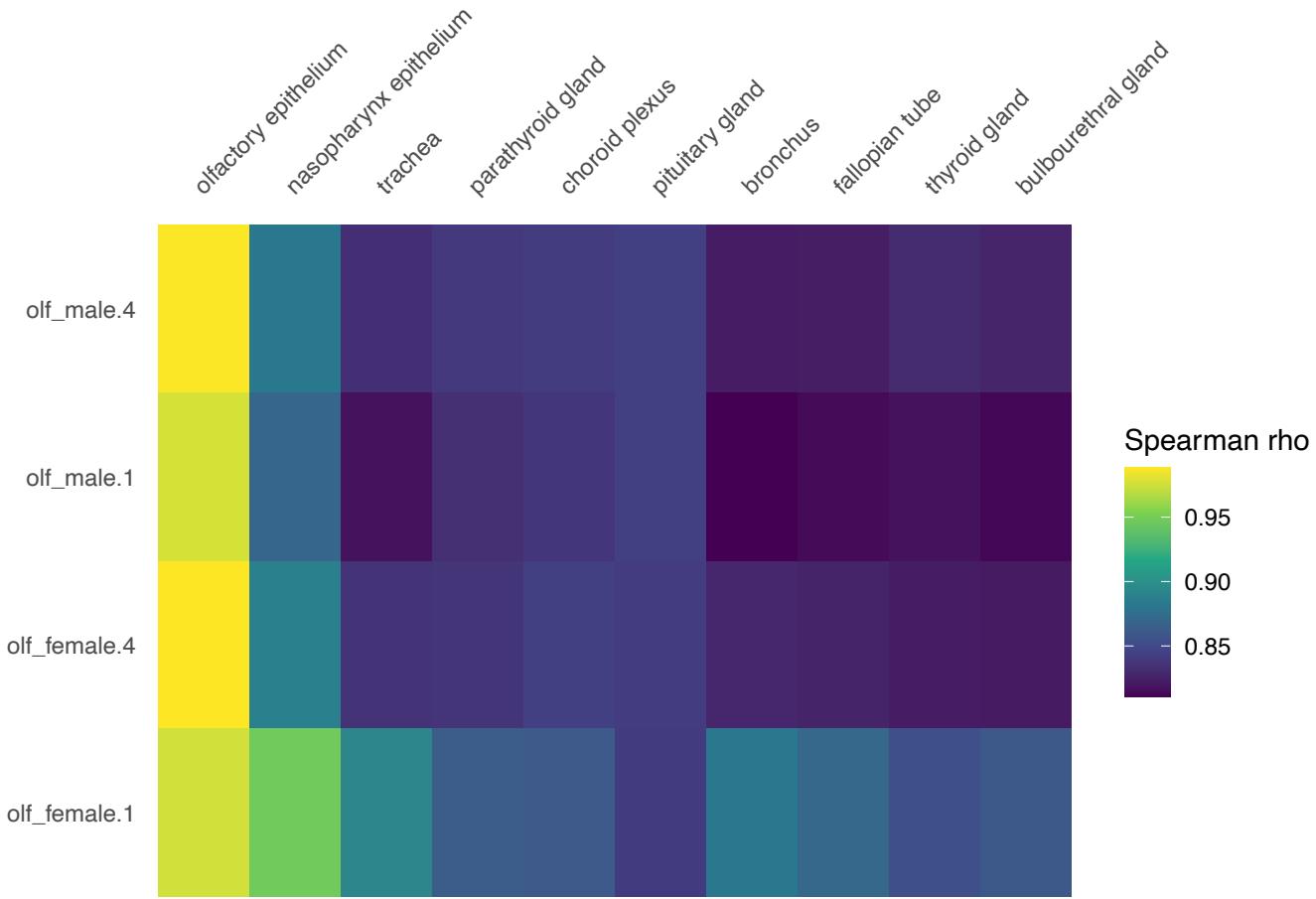
olfactory bulb, UMAP: TMM expression values



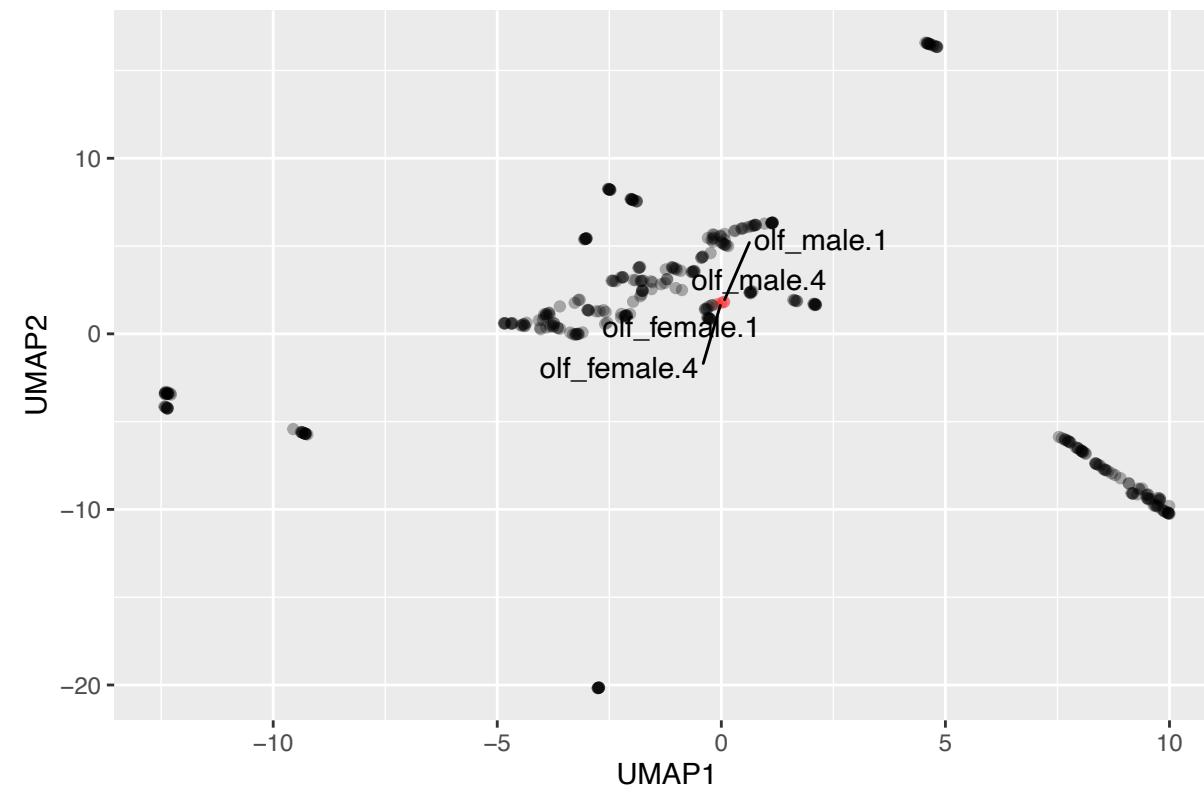
olfactory epithelium, PCA: TMM expression values



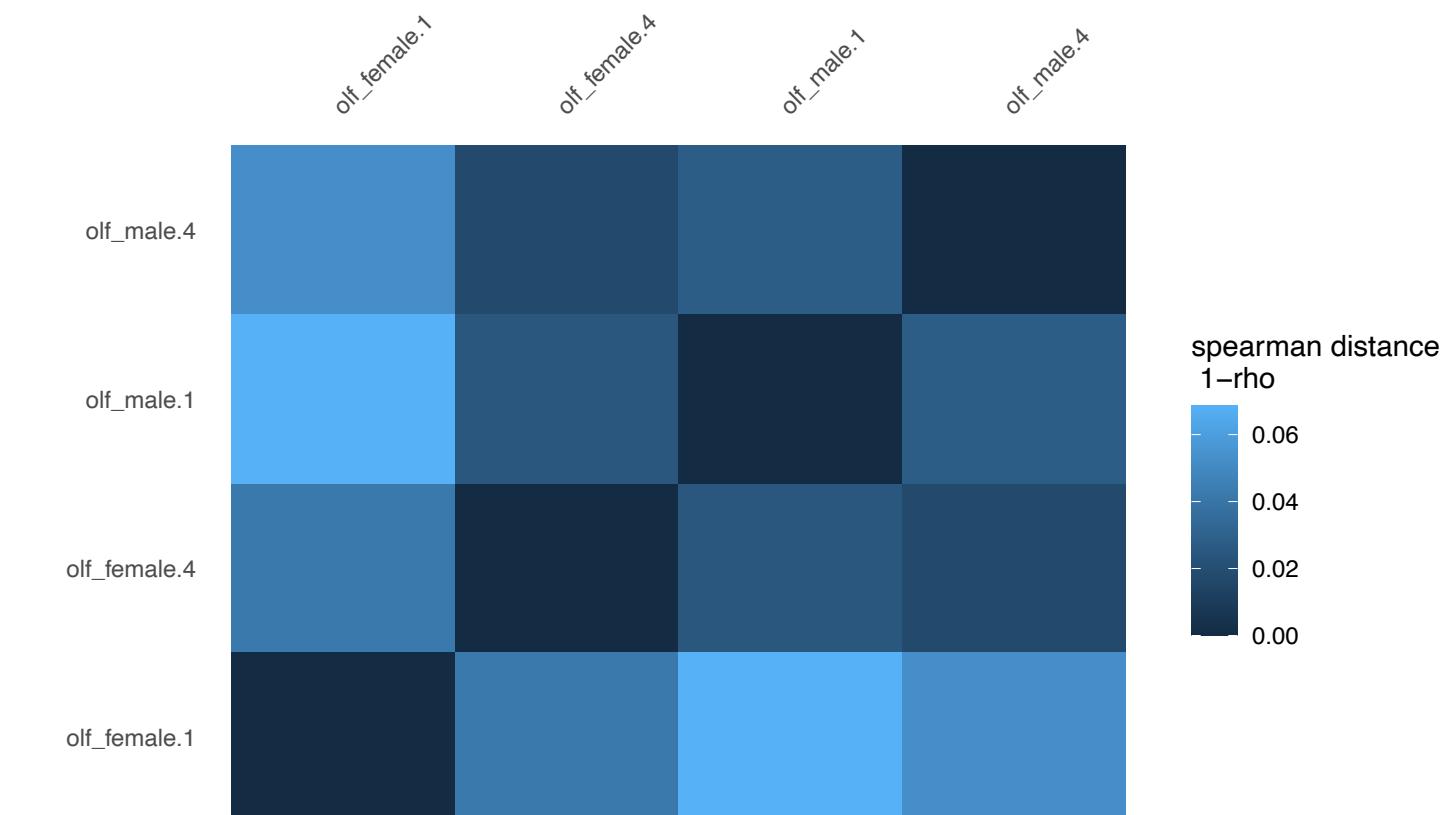
Tissue group to sample correlation



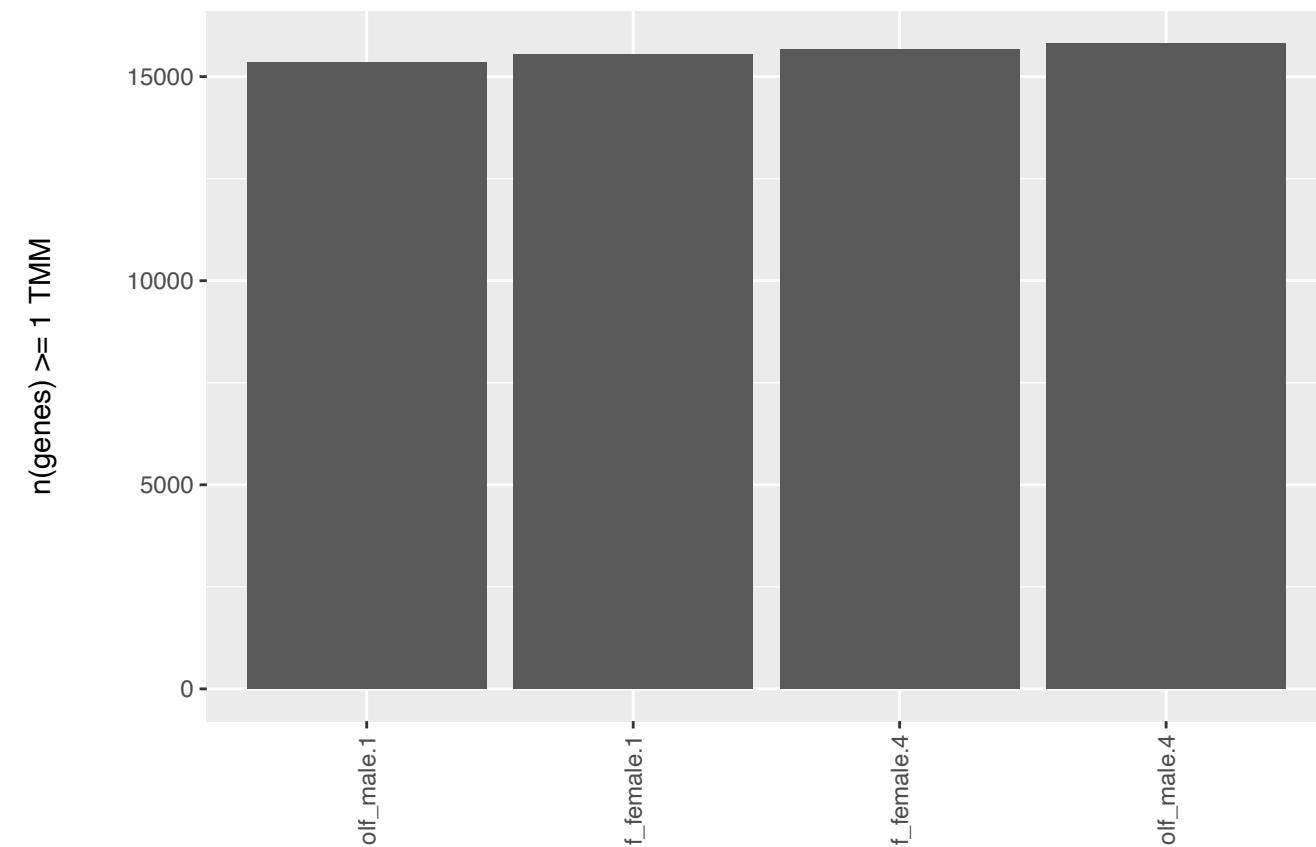
olfactory epithelium, UMAP: TMM expression values



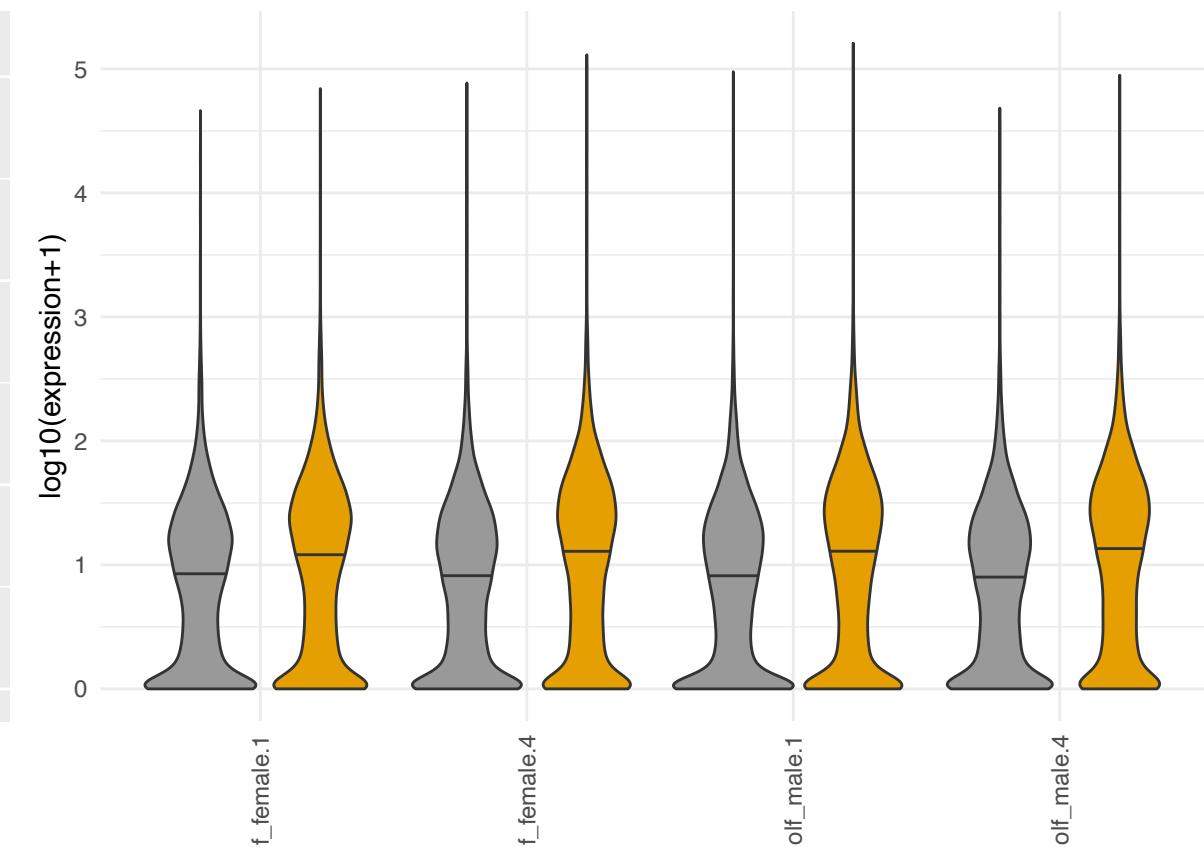
In tissue sample to sample Spearman Distance



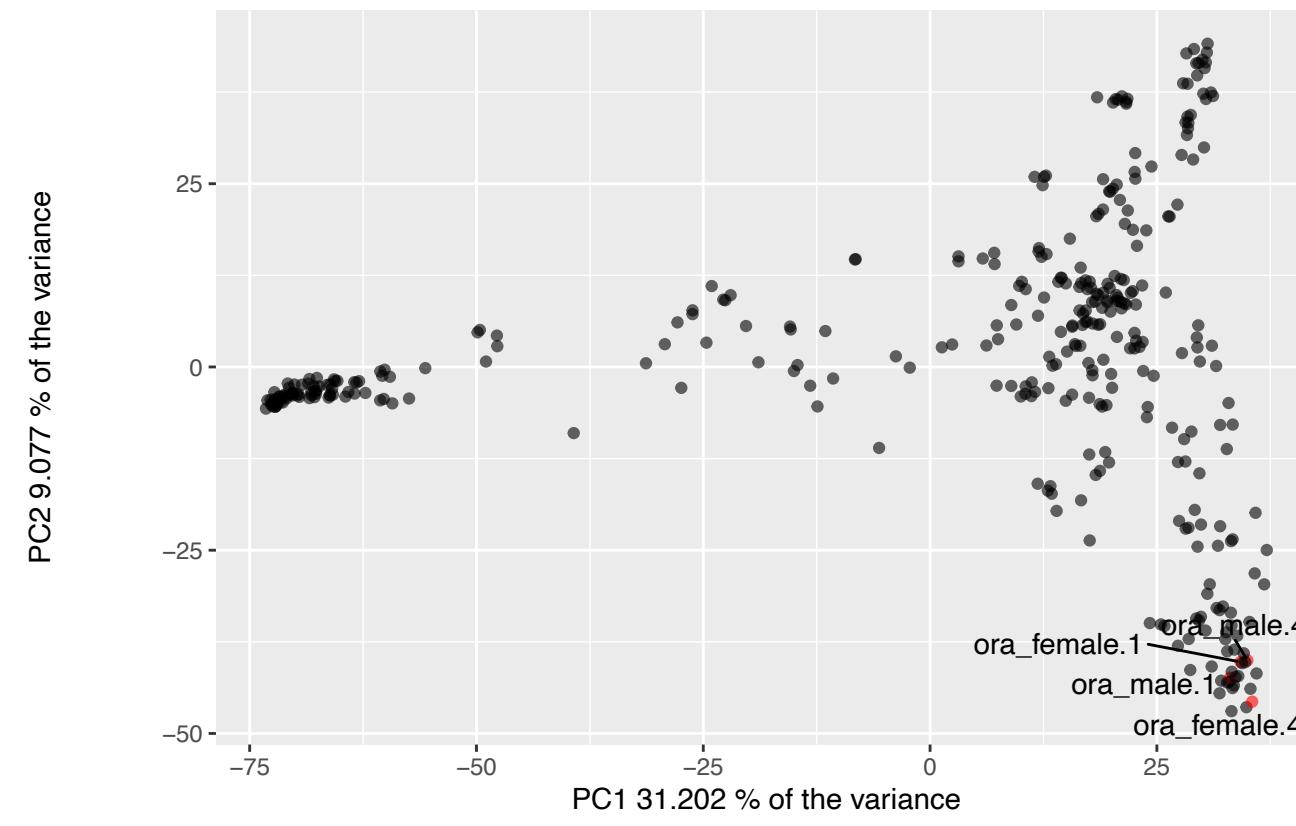
olfactory epithelium



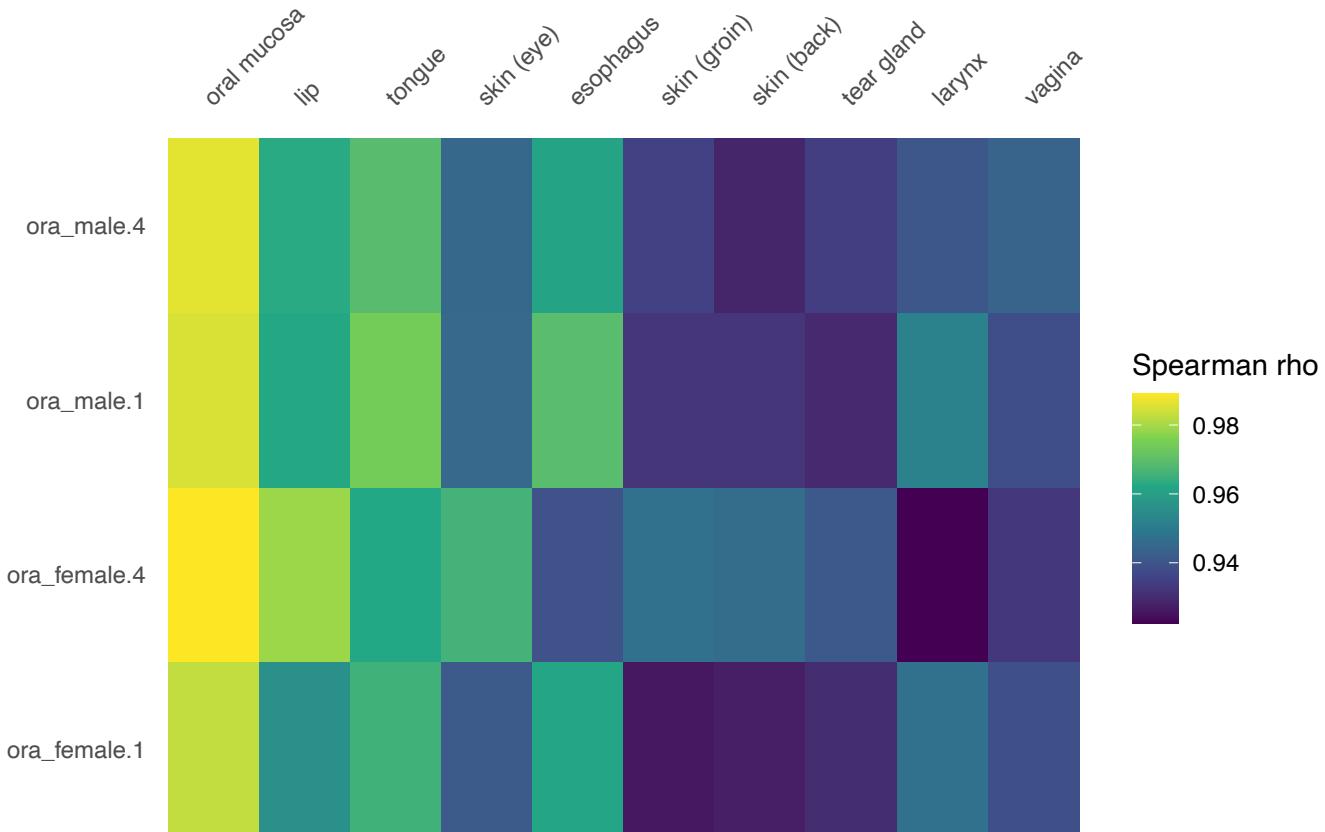
olfactory epithelium



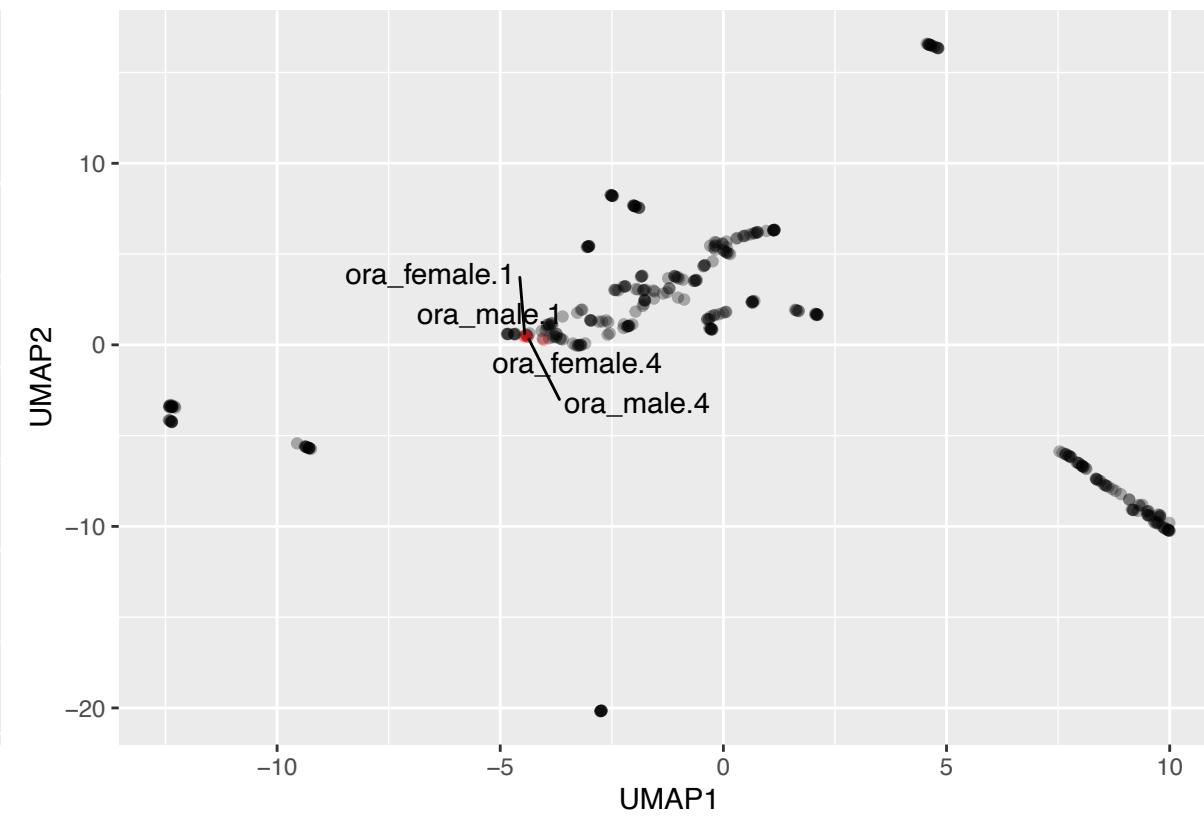
oral mucosa, PCA: TMM expression values



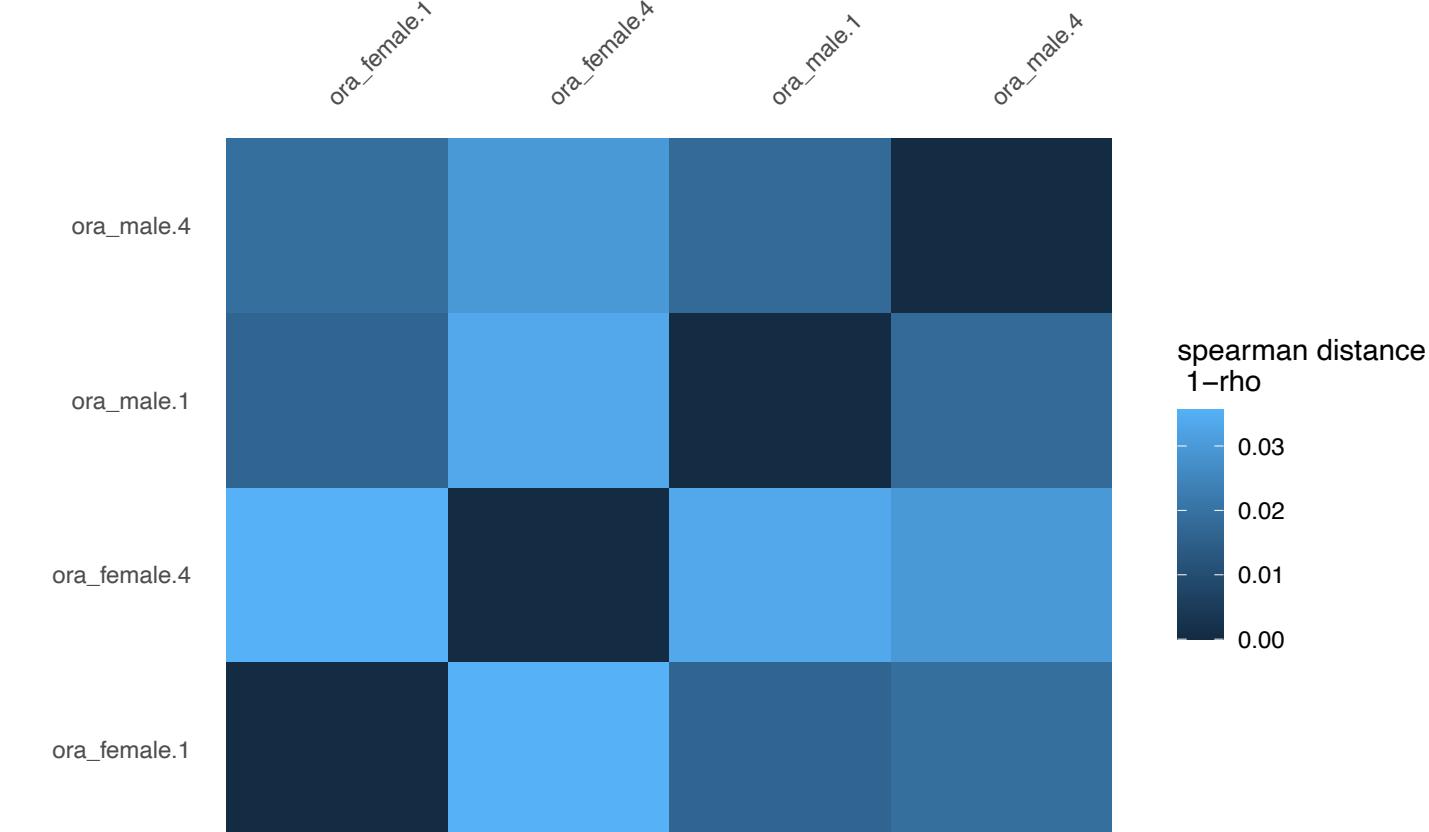
Tissue group to sample correlation



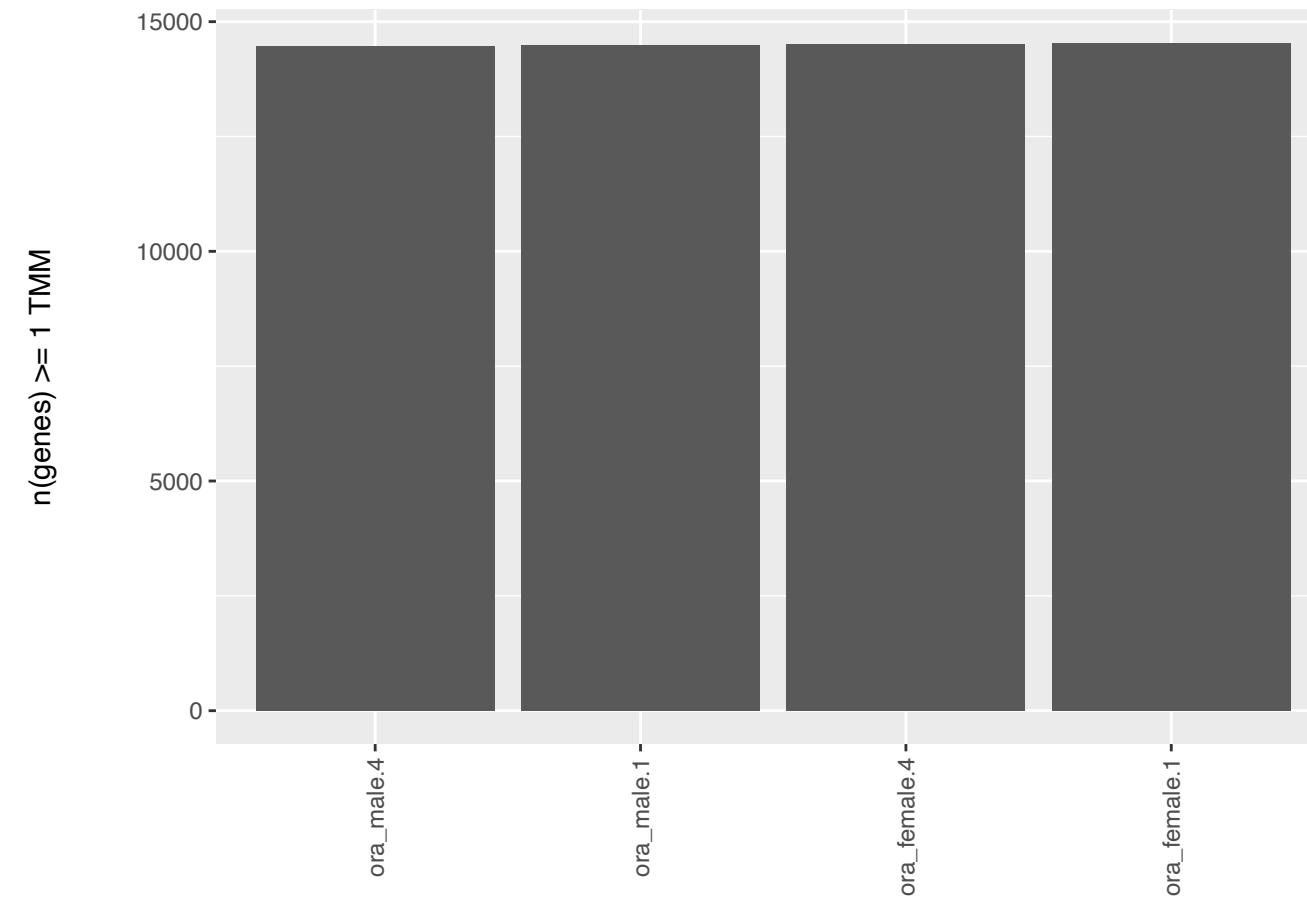
oral mucosa, UMAP: TMM expression values



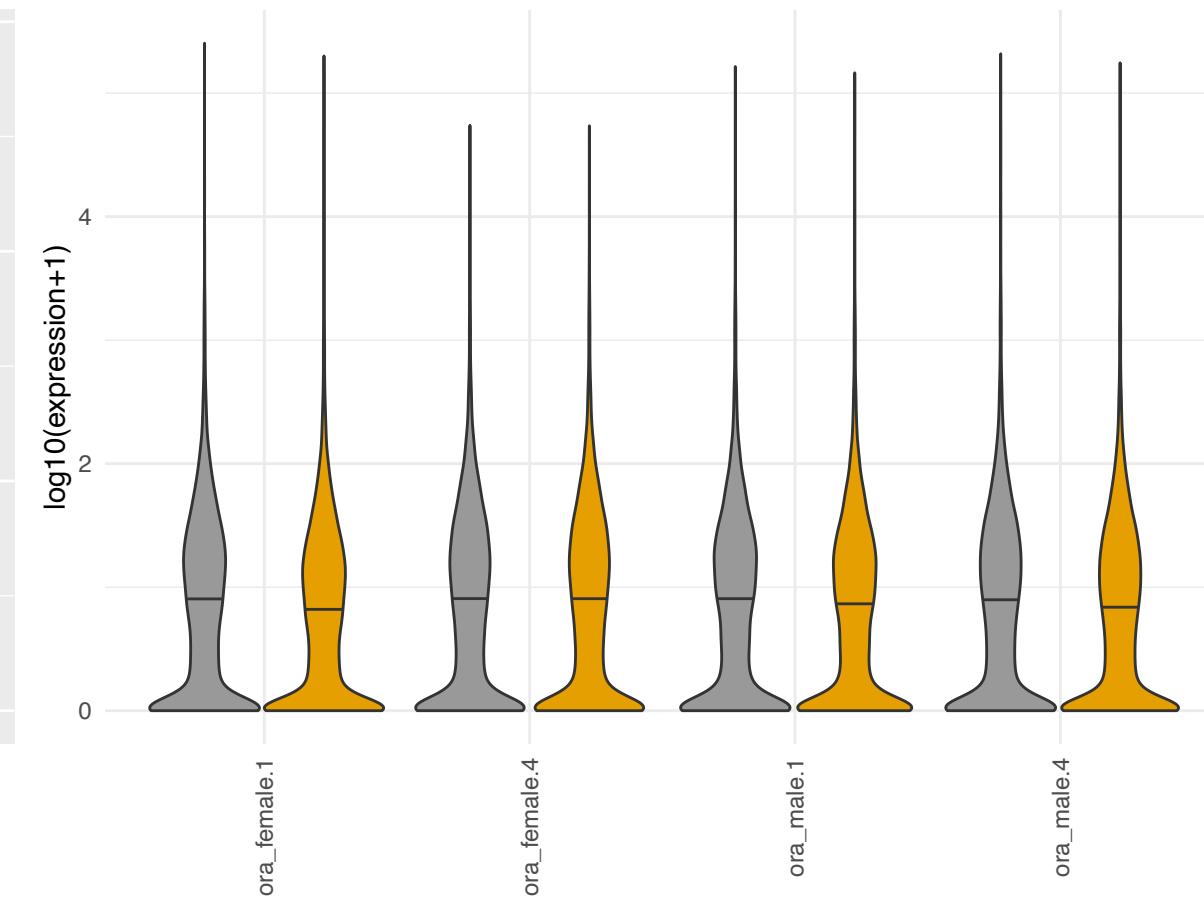
In tissue sample to sample Spearman Distance



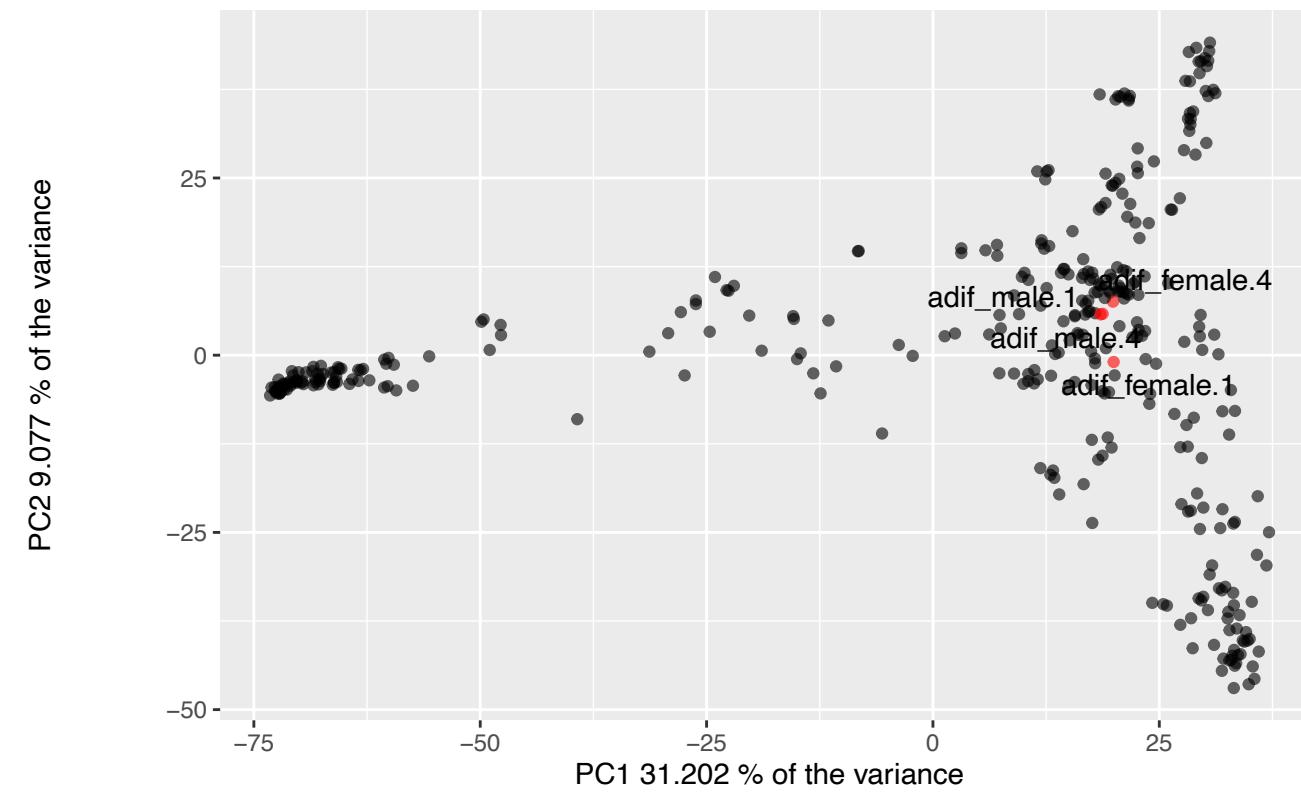
oral mucosa



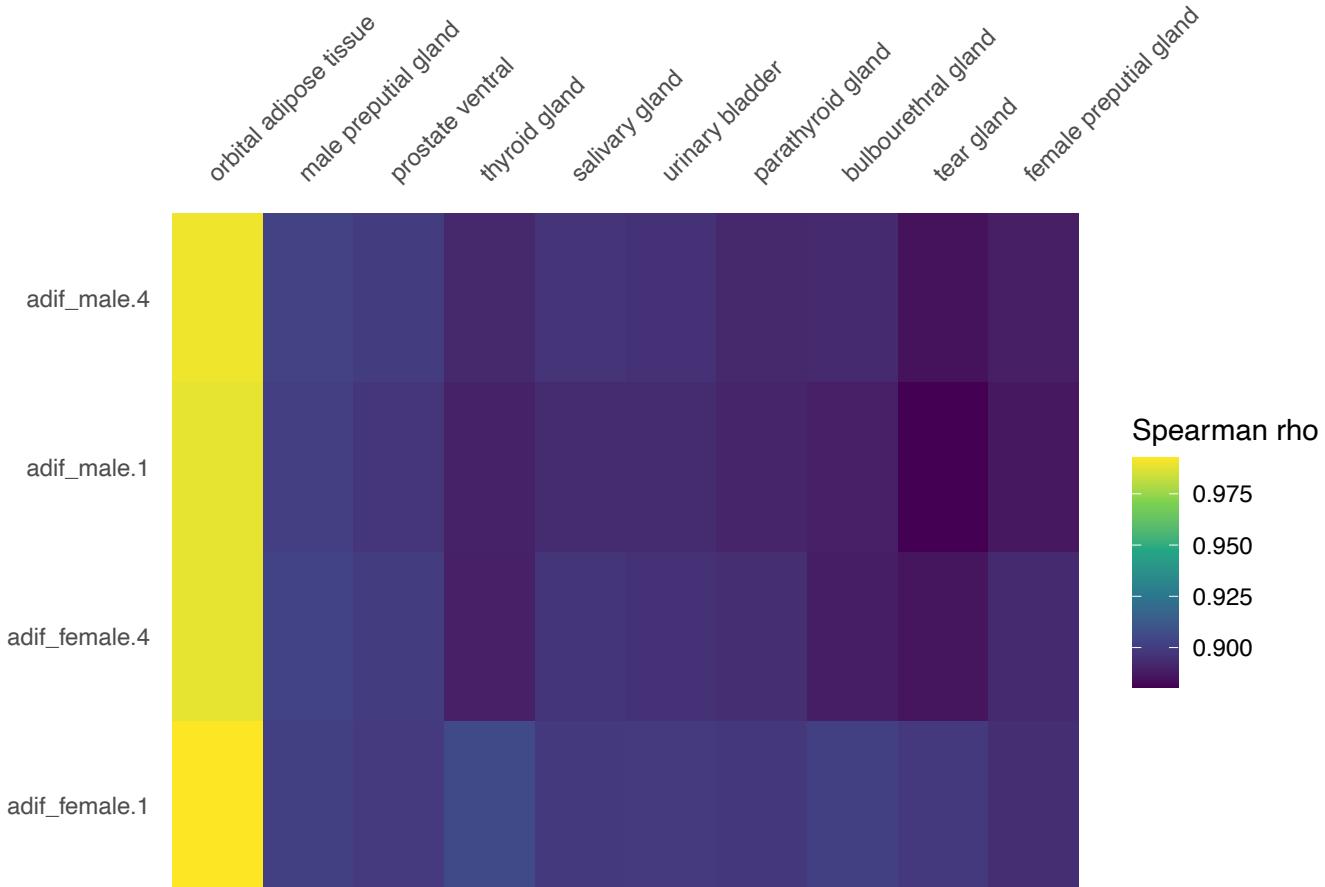
oral mucosa



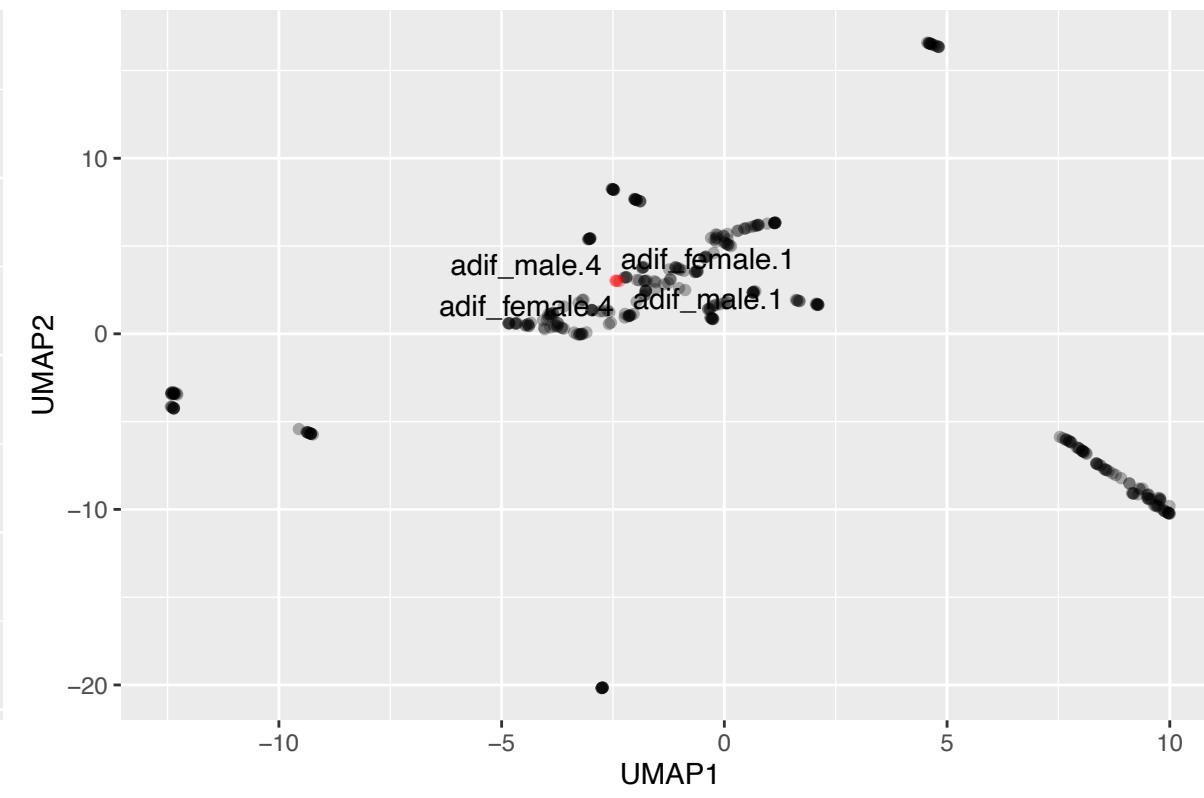
orbital adipose tissue, PCA: TMM expression values



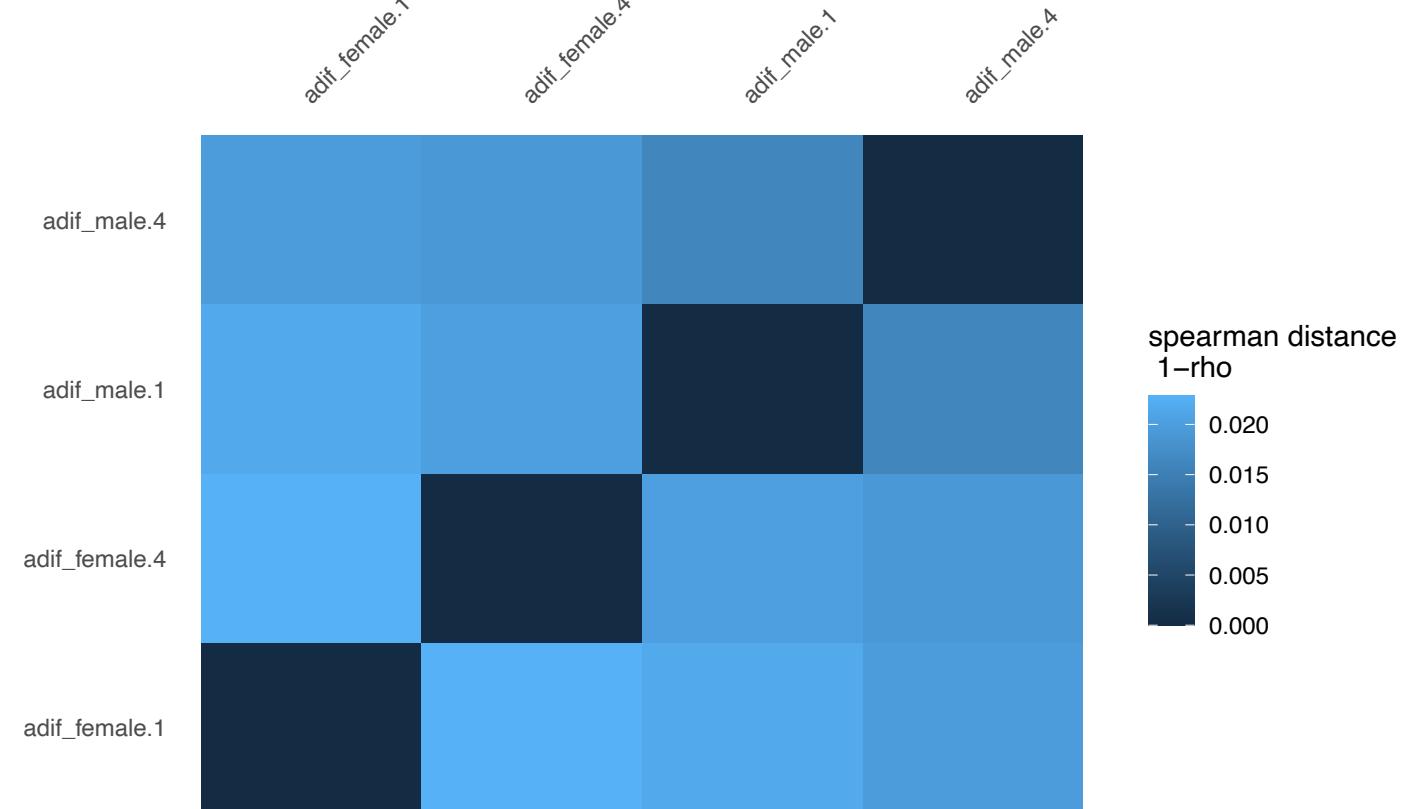
Tissue group to sample correlation



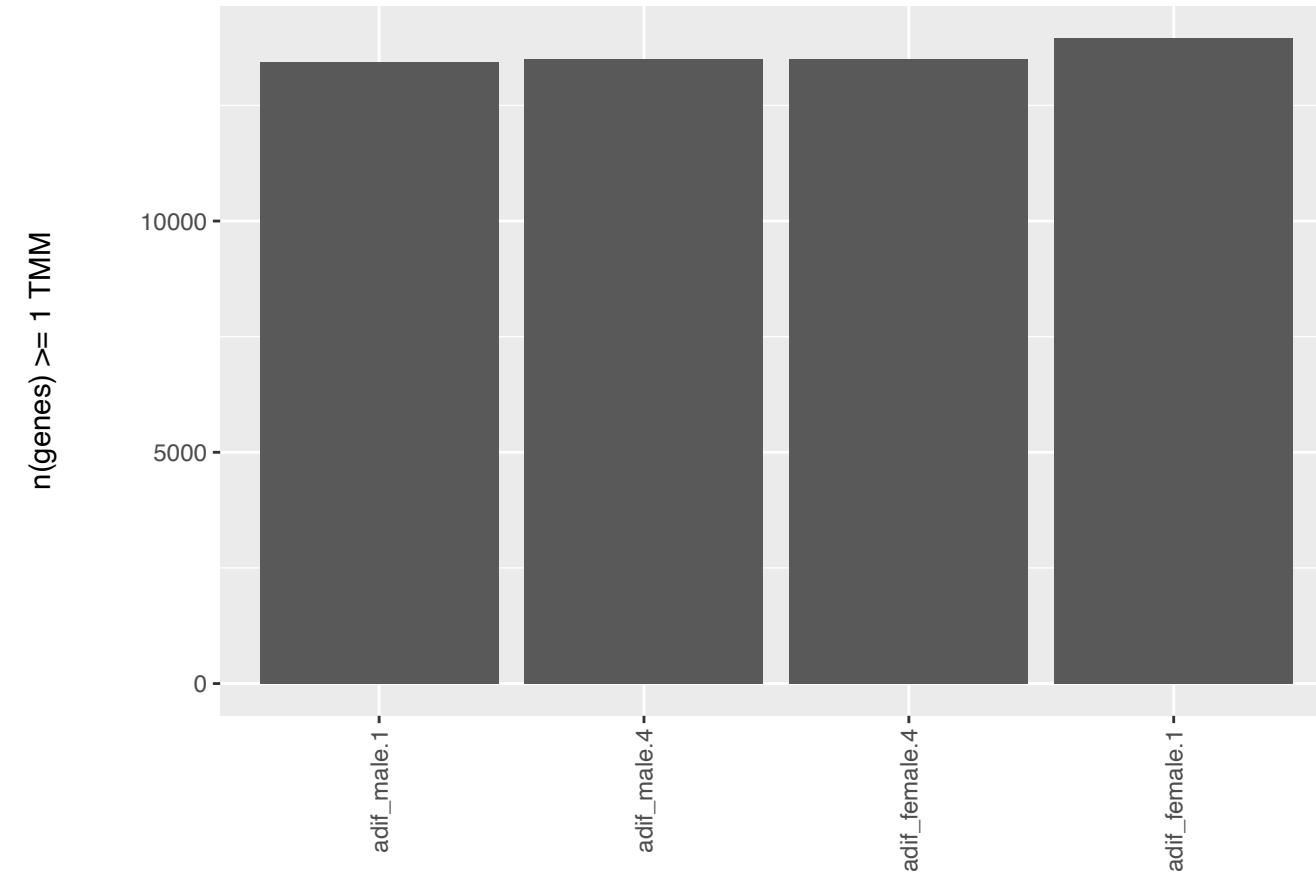
orbital adipose tissue, UMAP: TMM expression values



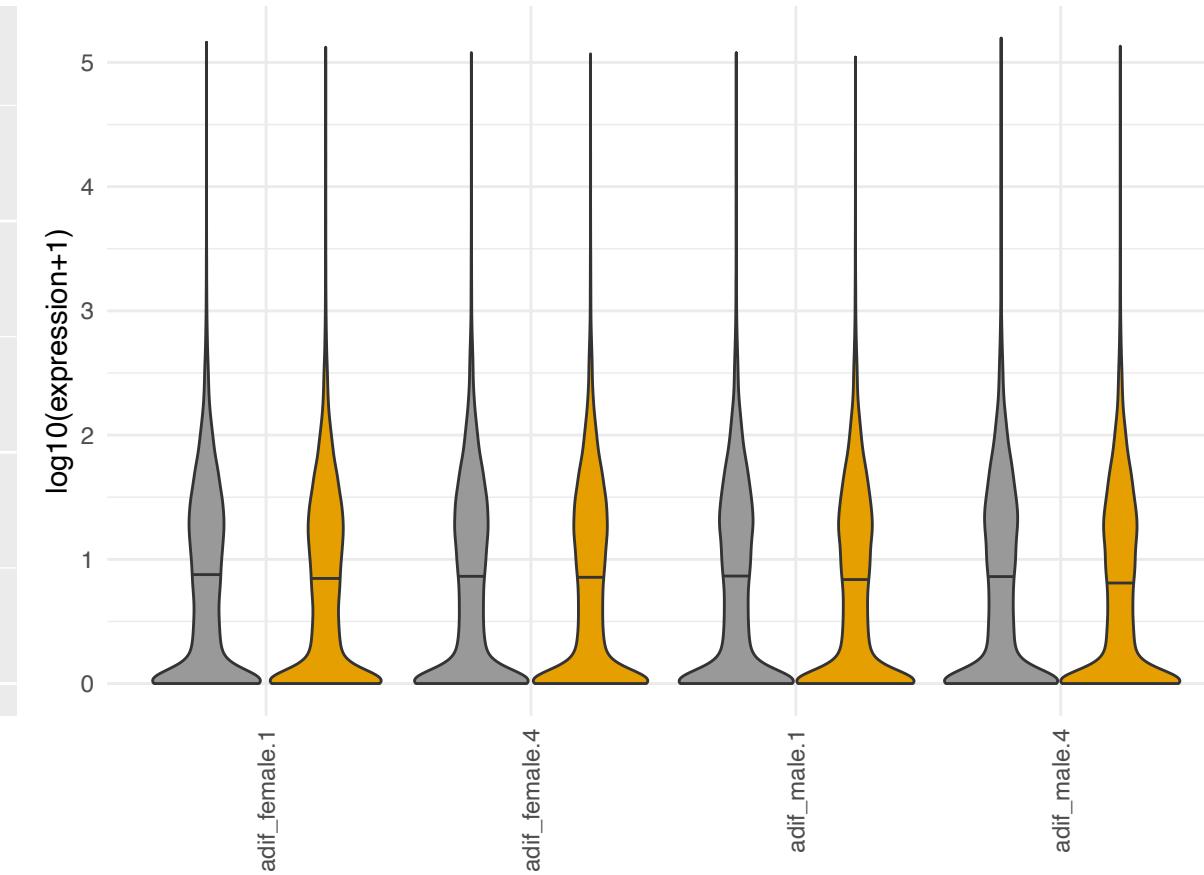
In tissue sample to sample Spearman Distance



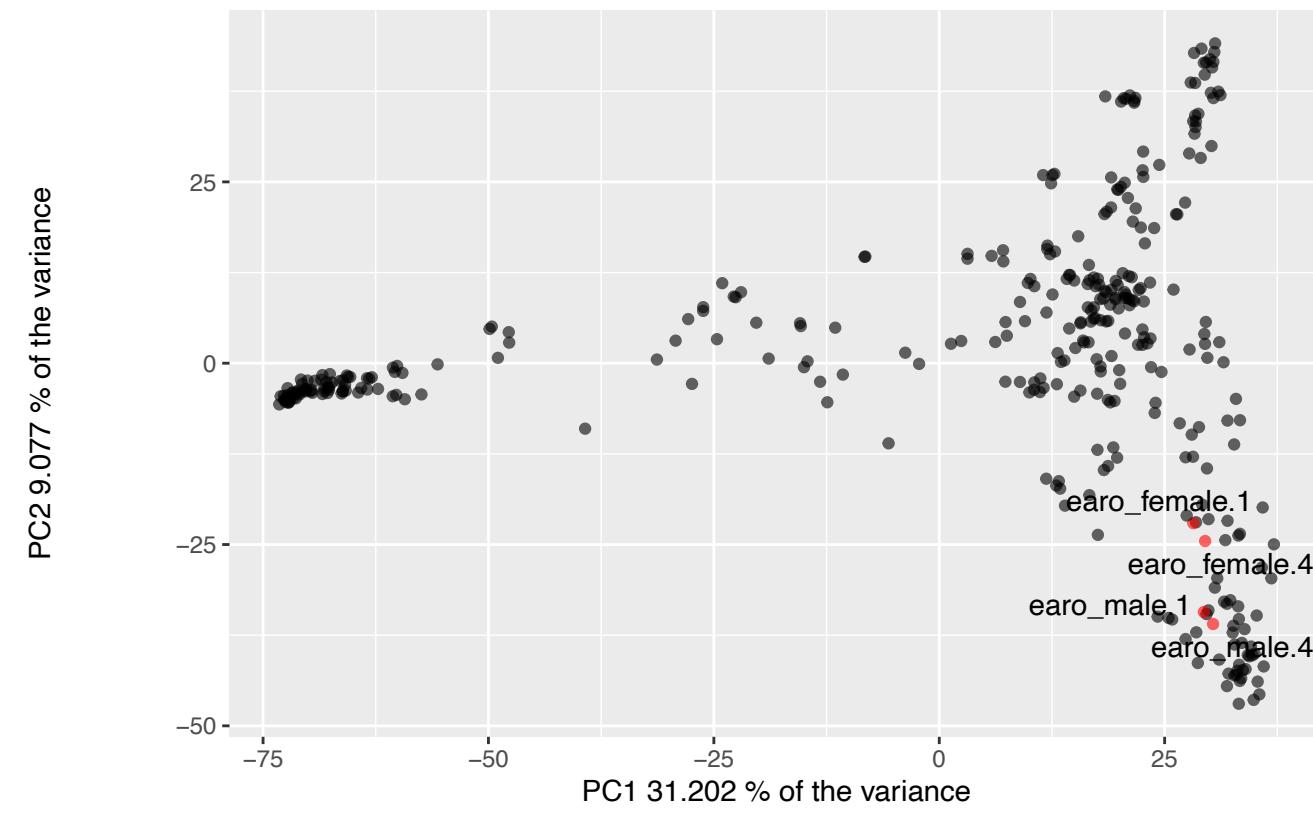
orbital adipose tissue



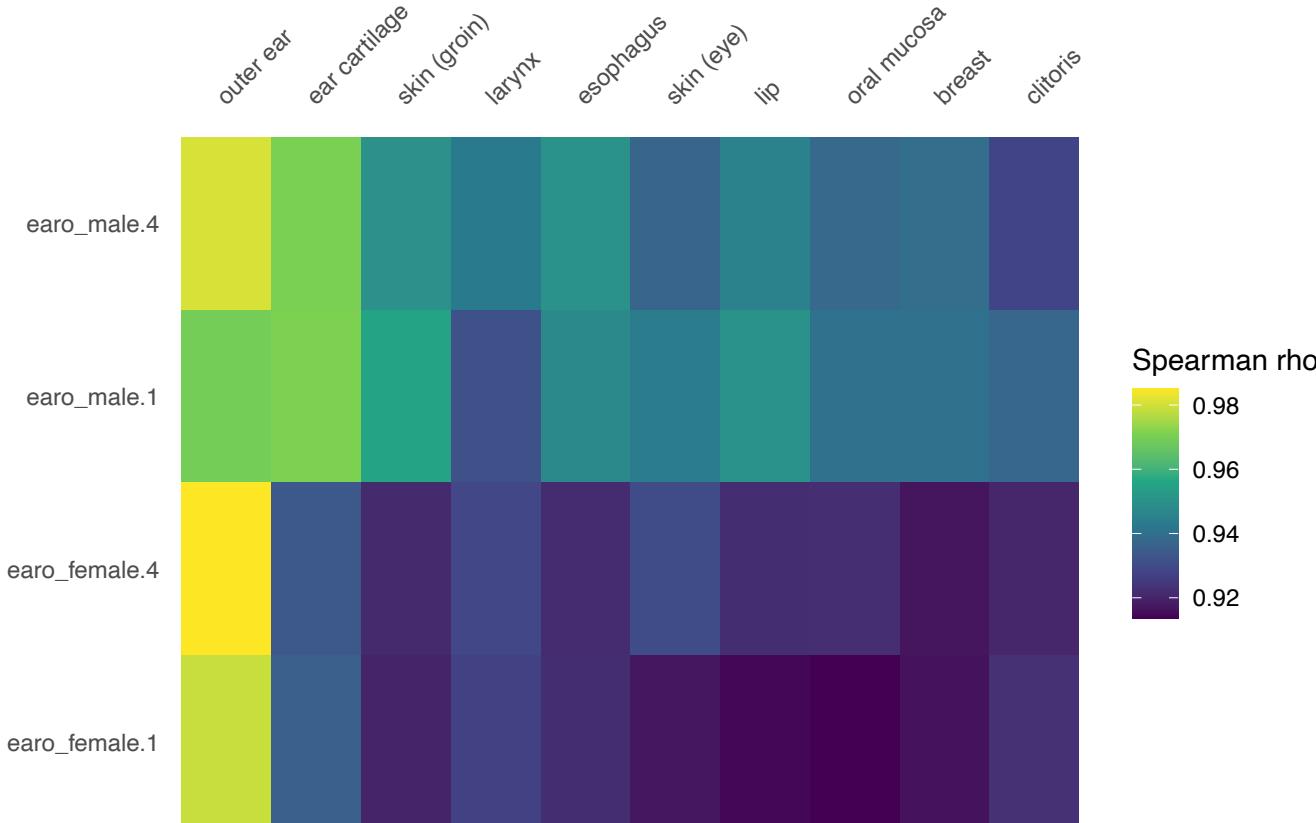
orbital adipose tissue



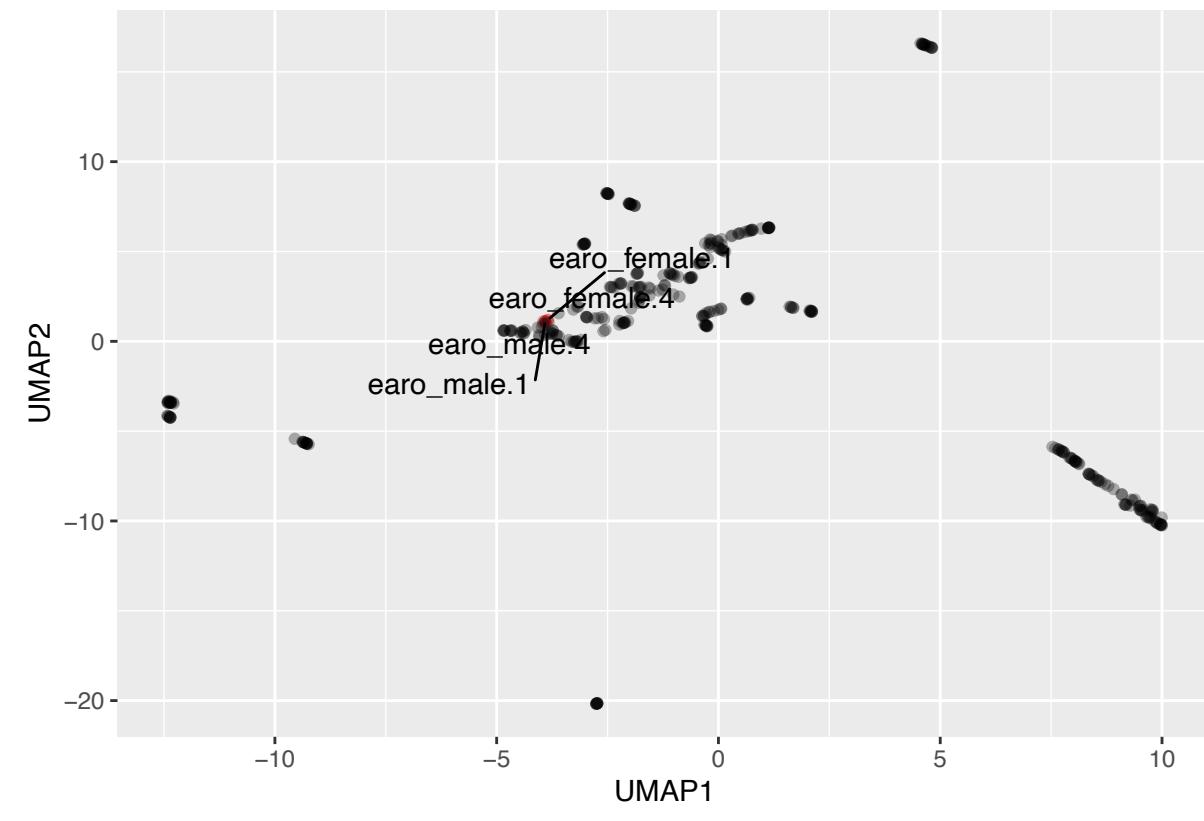
outer ear, PCA: TMM expression values



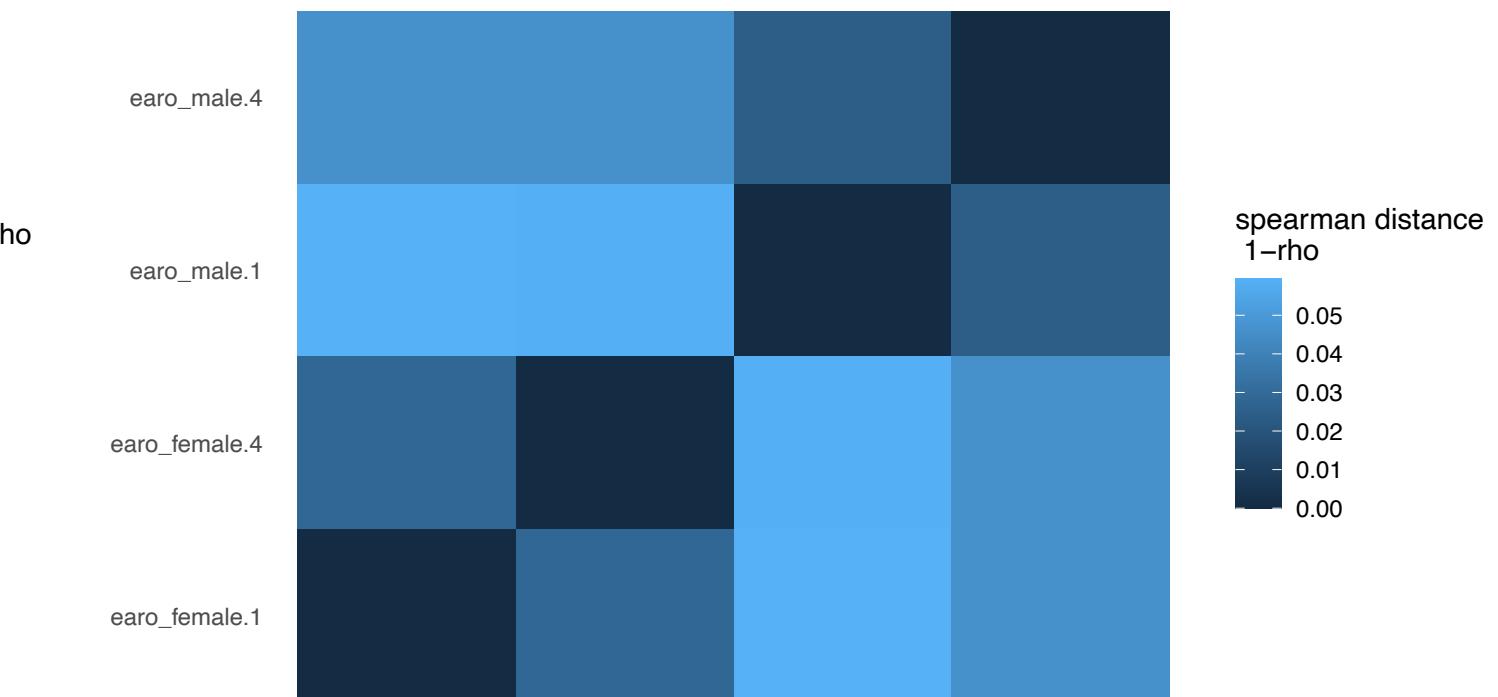
Tissue group to sample correlation



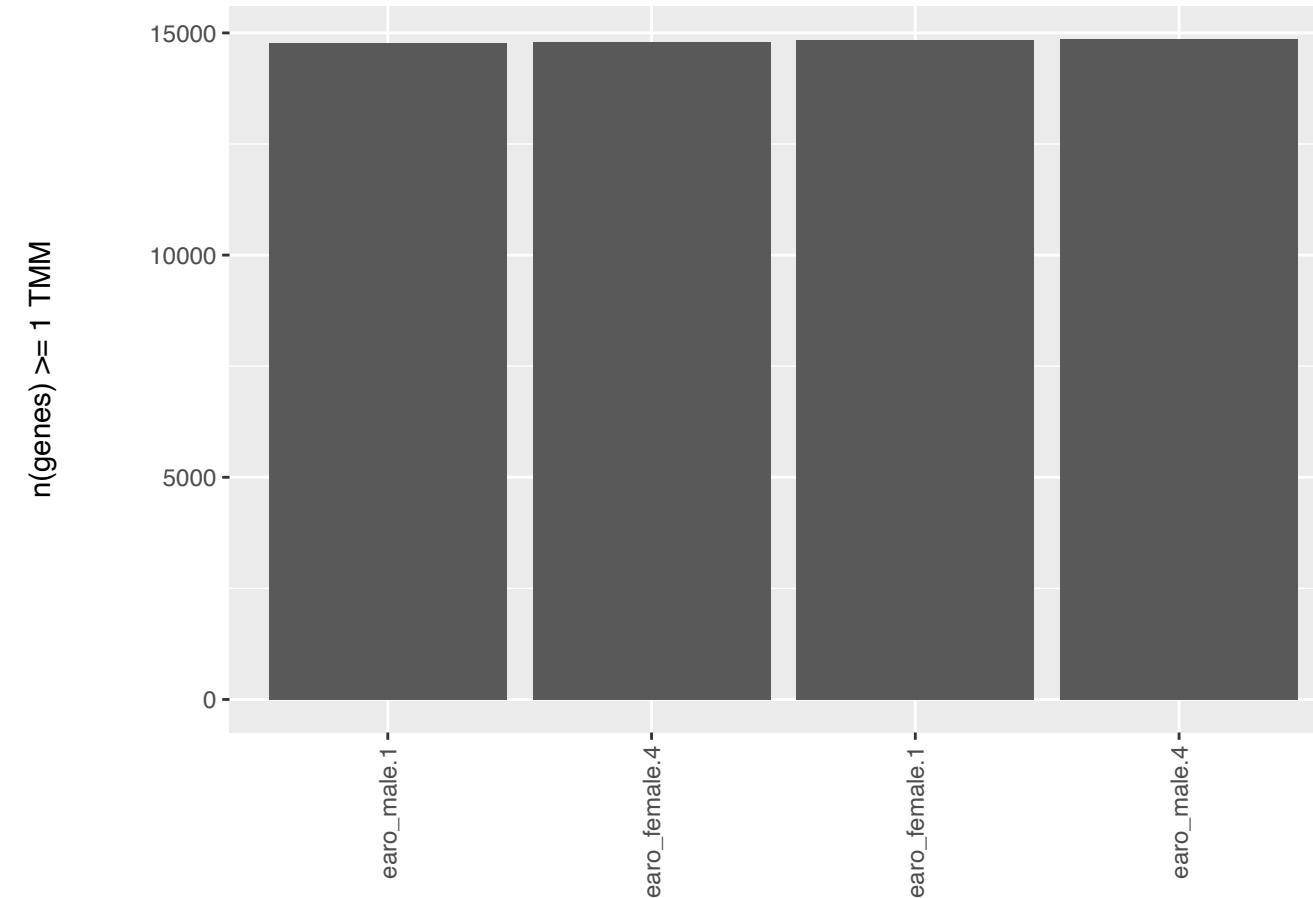
outer ear, UMAP: TMM expression values



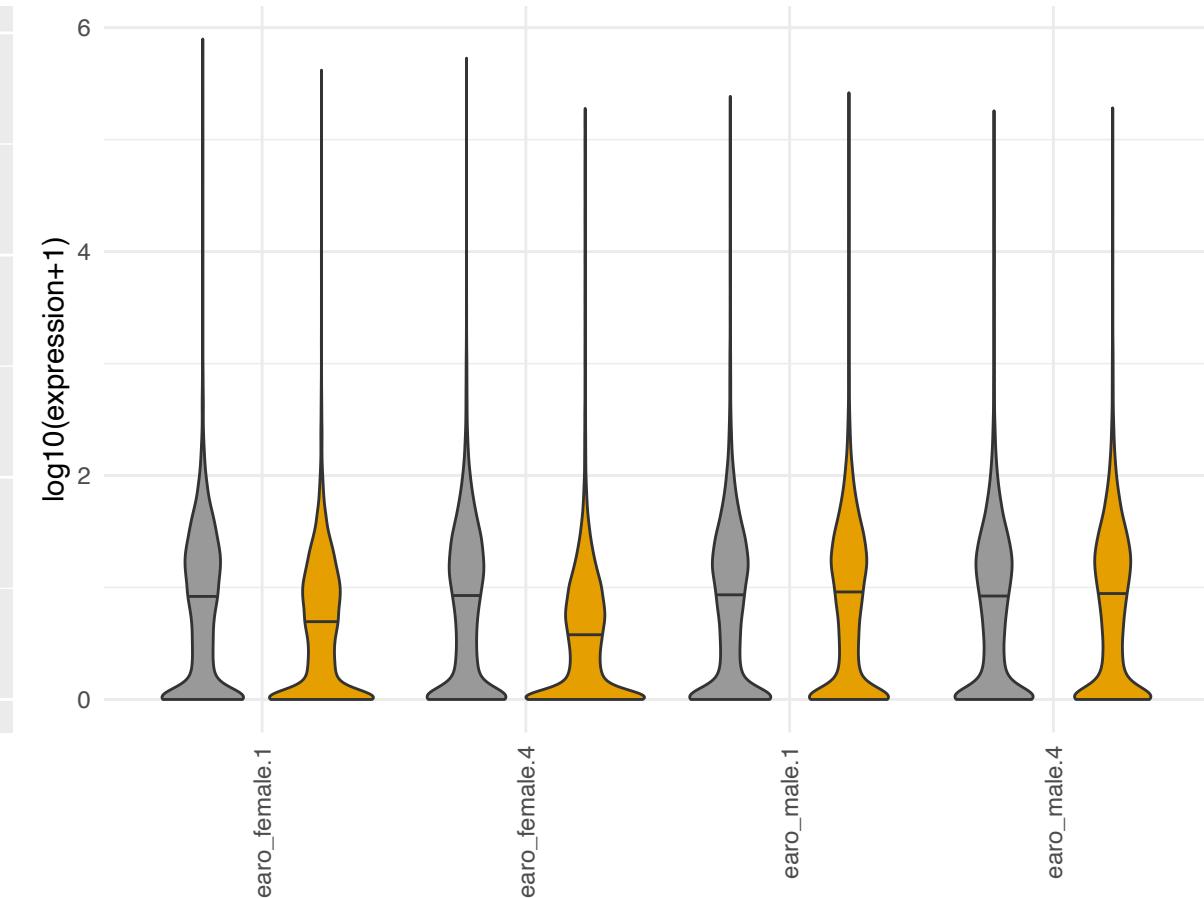
earo_female.1
earo_female.4
earo_male.1
earo_male.4



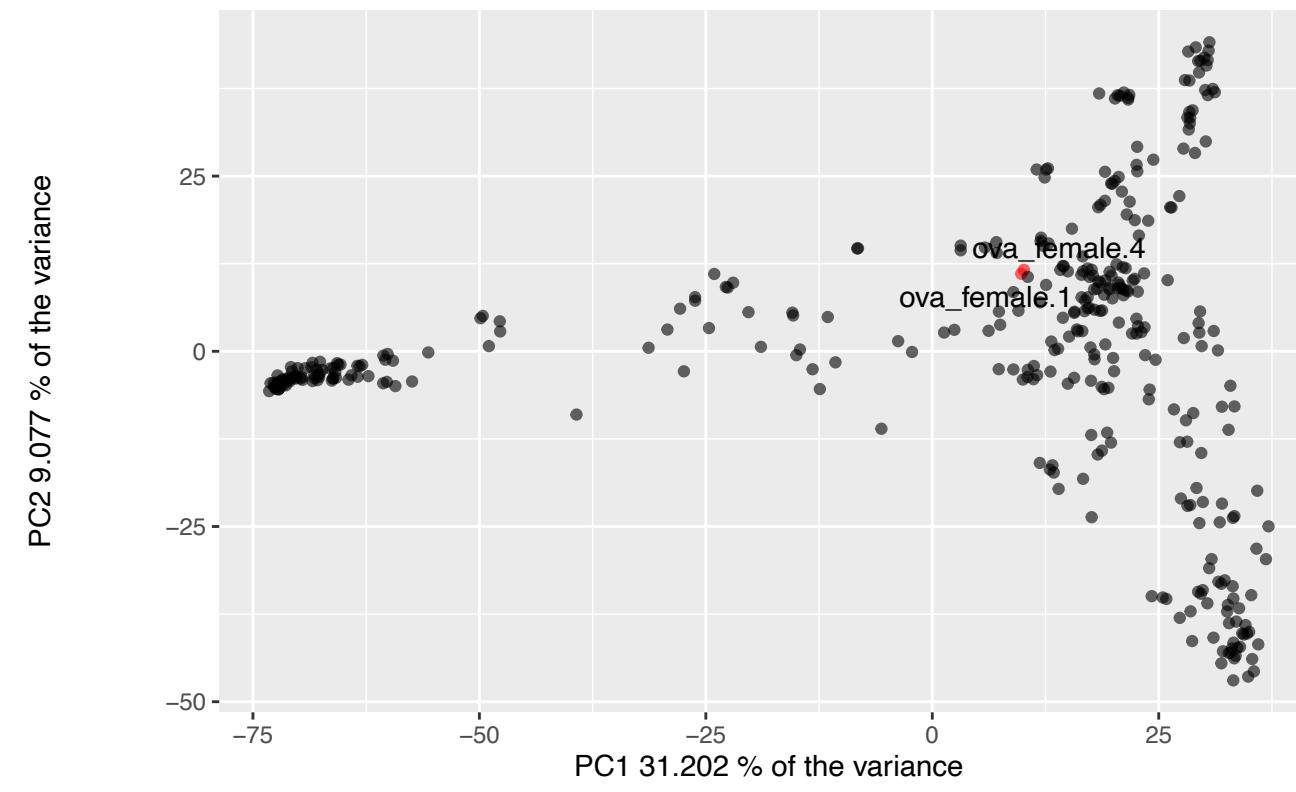
outer ear



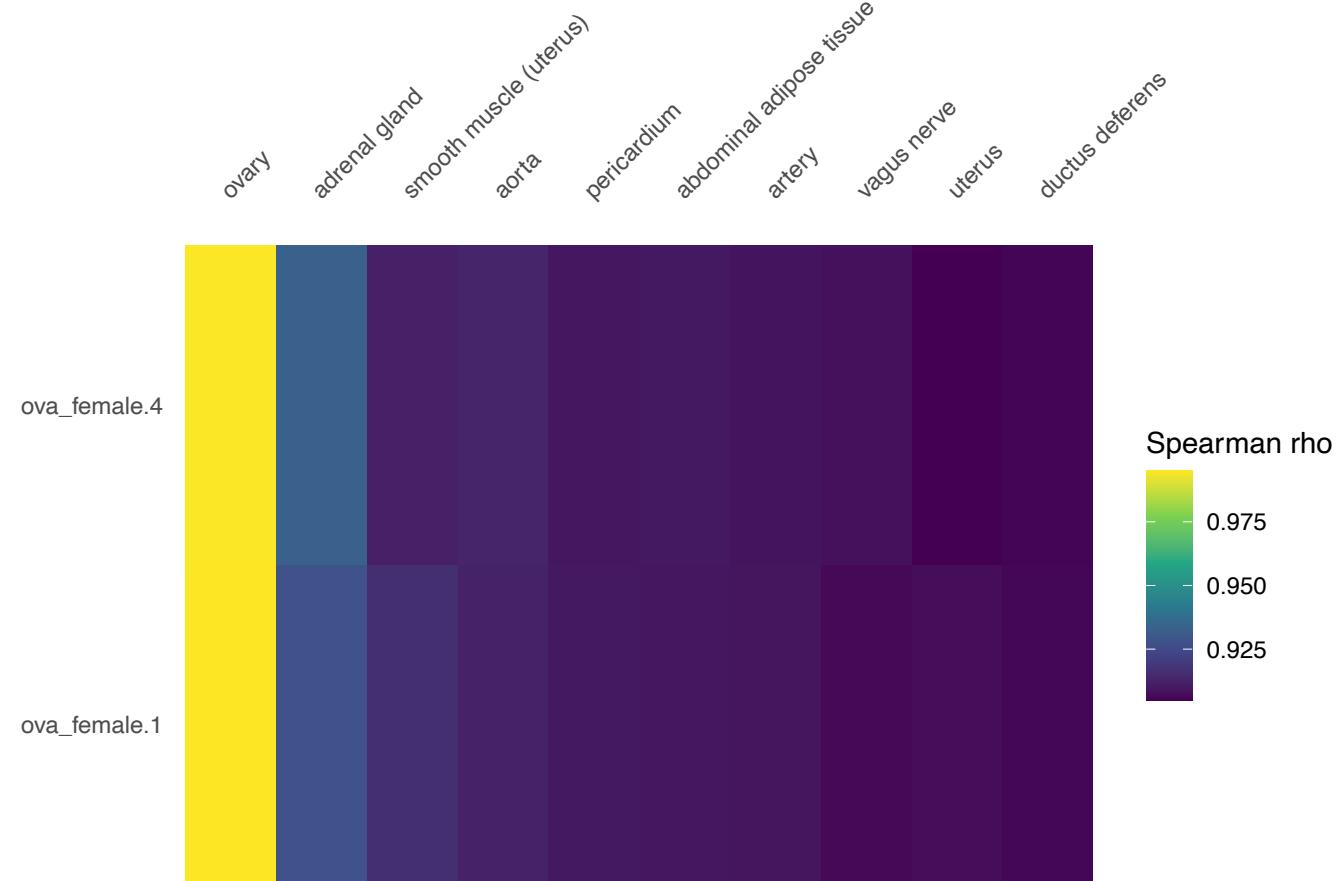
outer ear



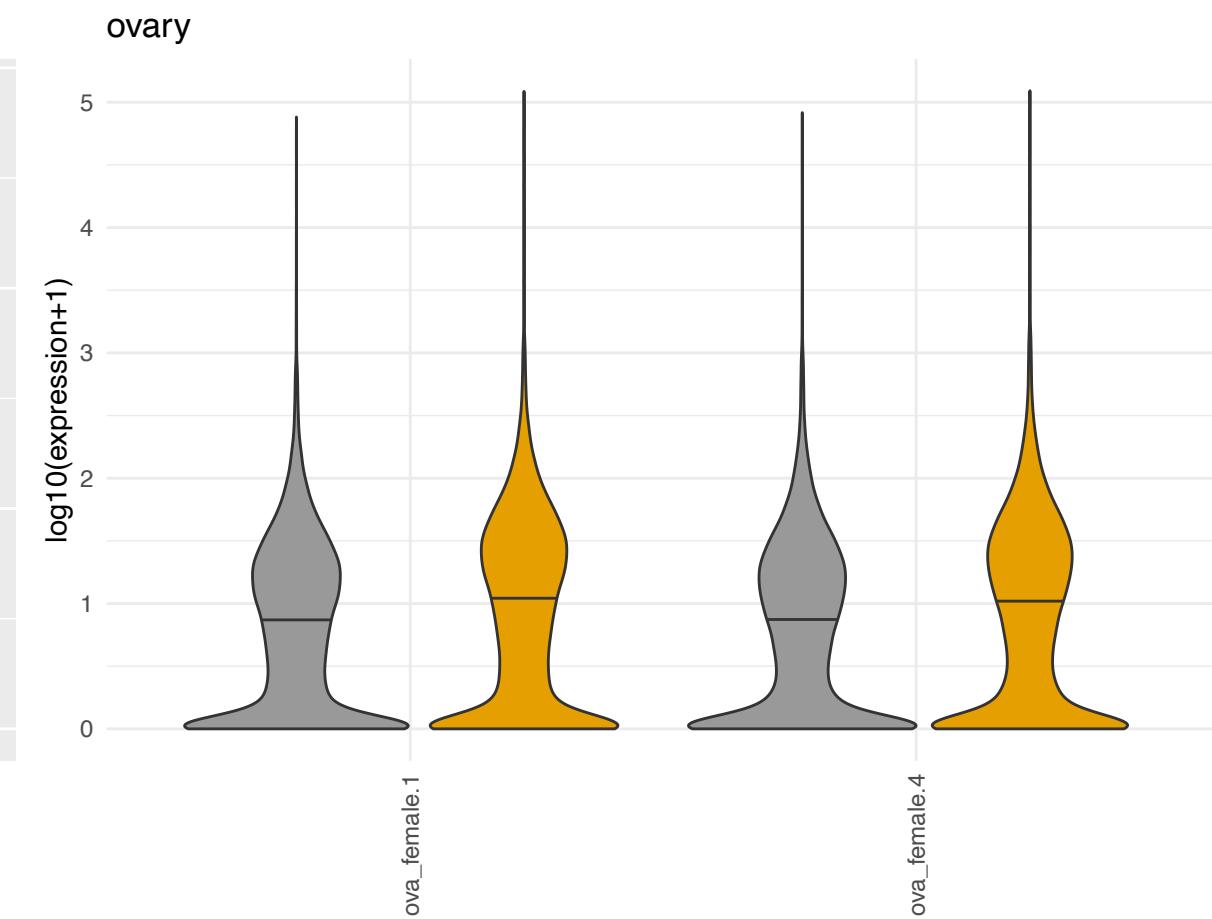
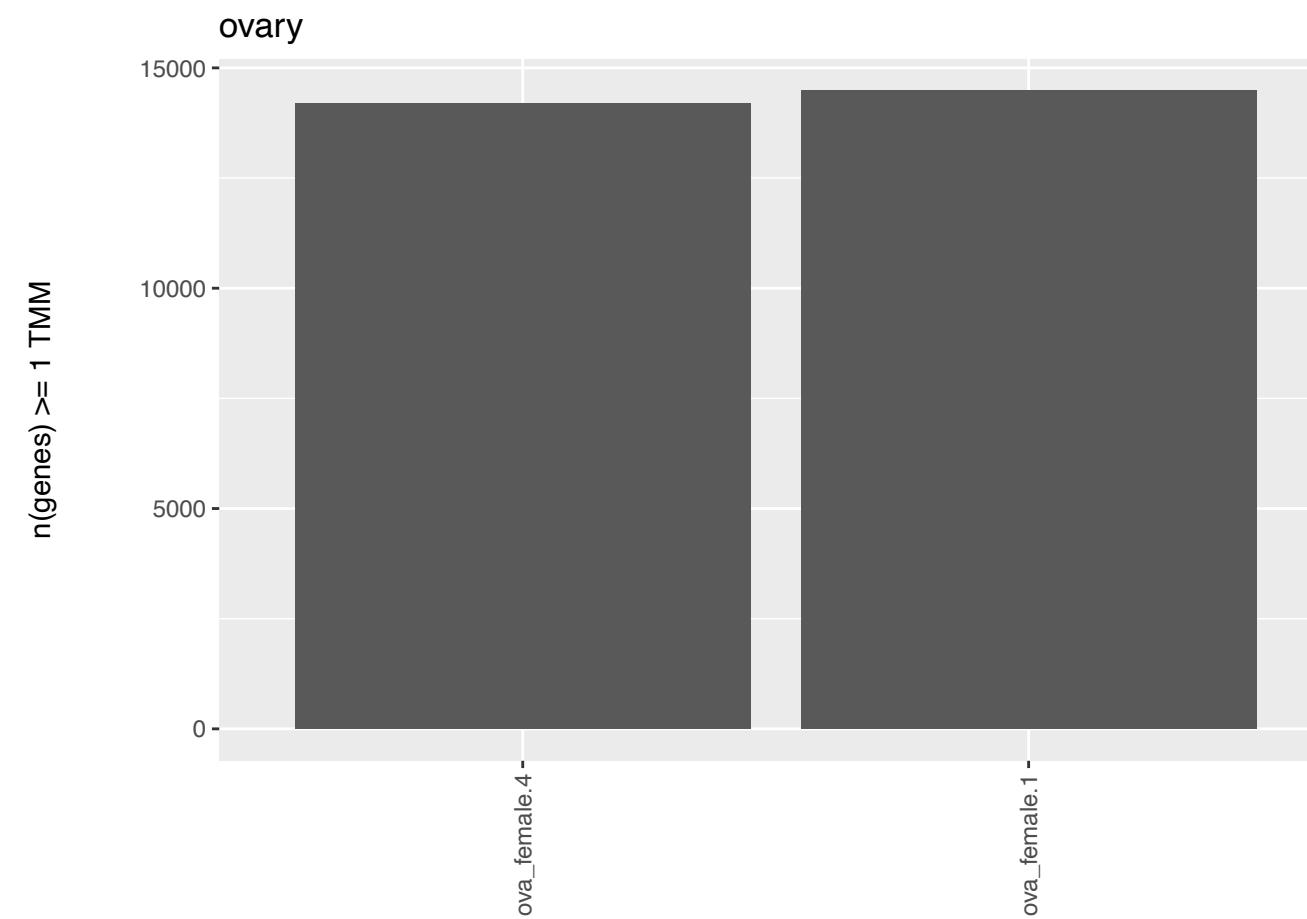
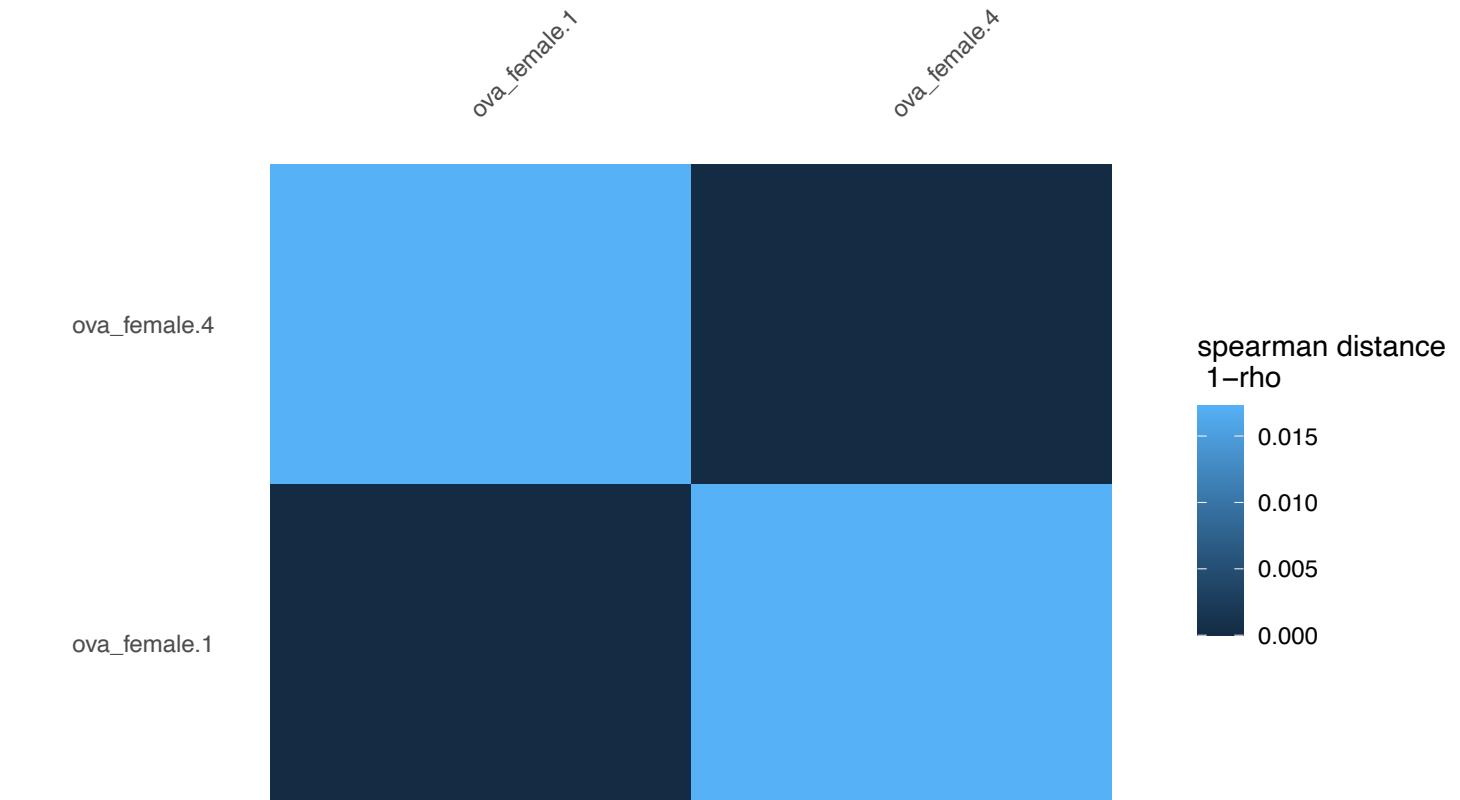
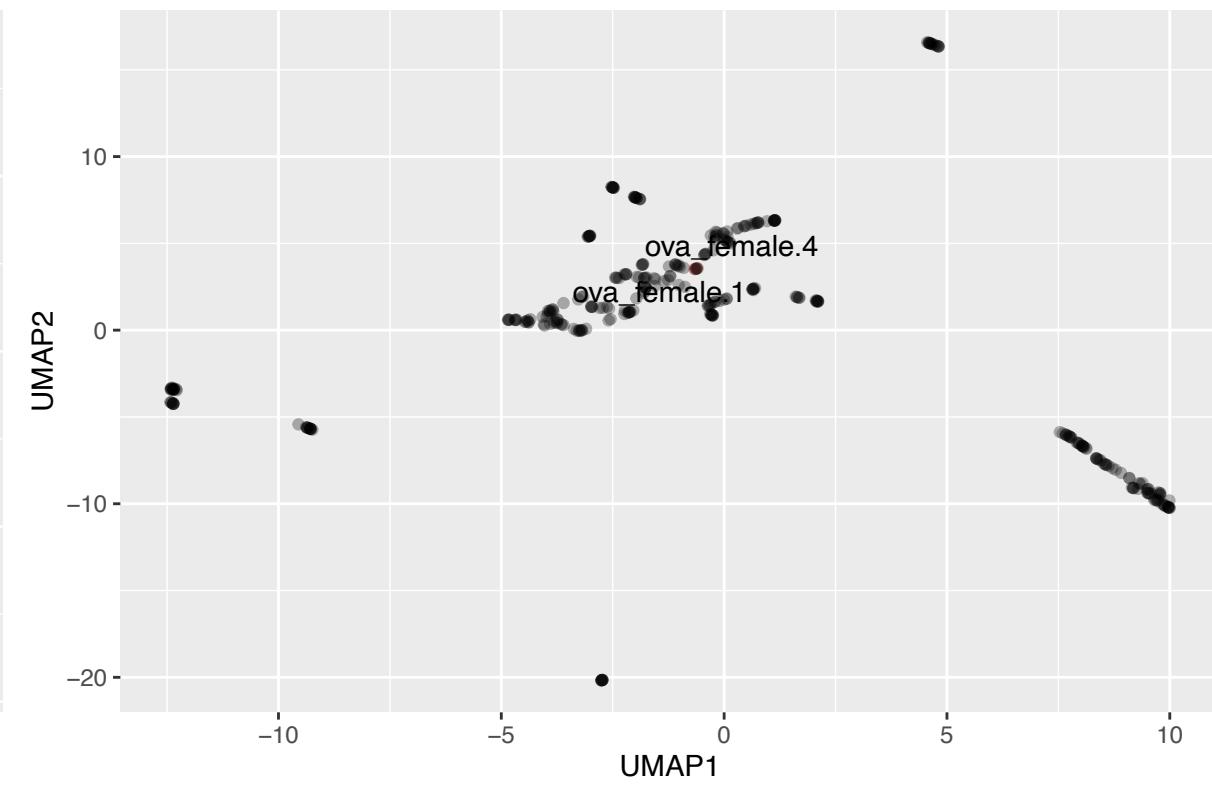
ovary, PCA: TMM expression values

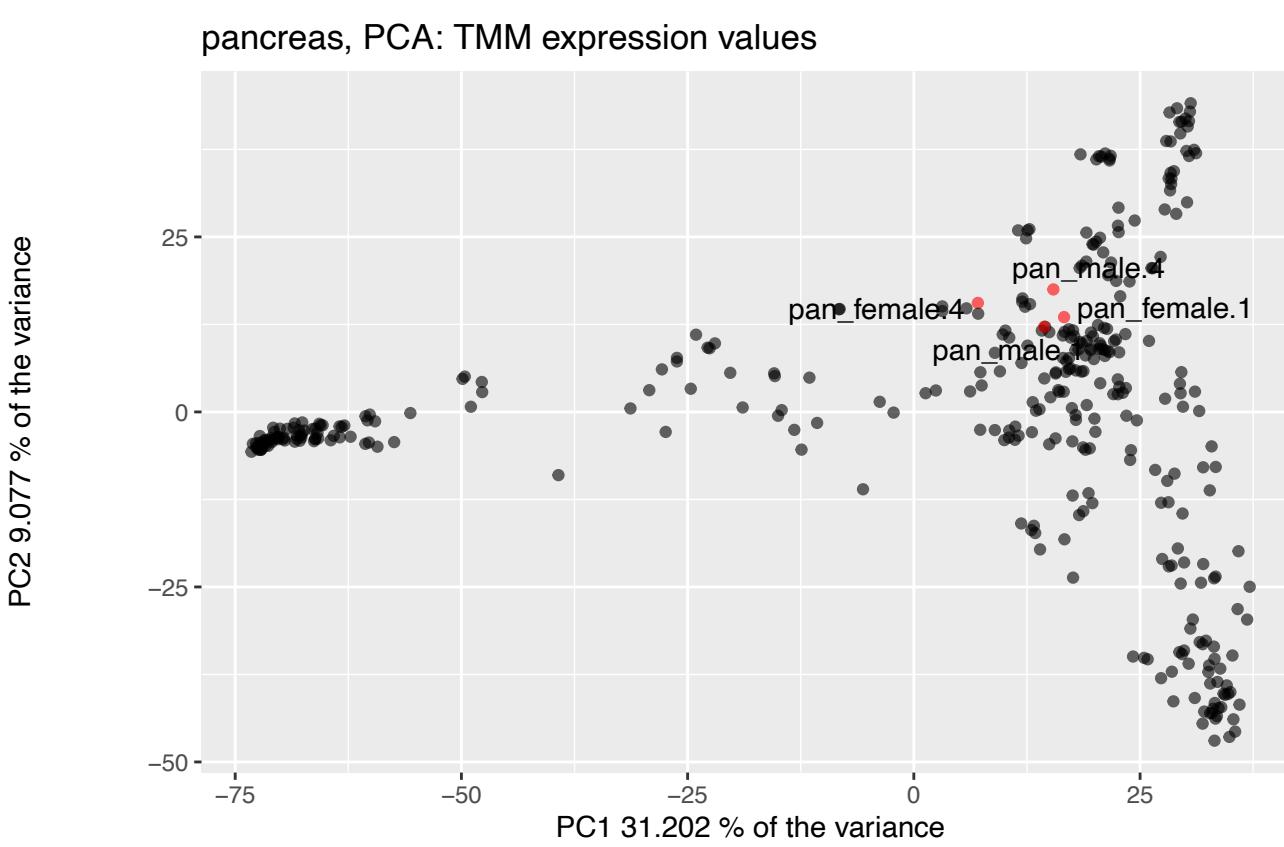


Tissue group to sample correlation

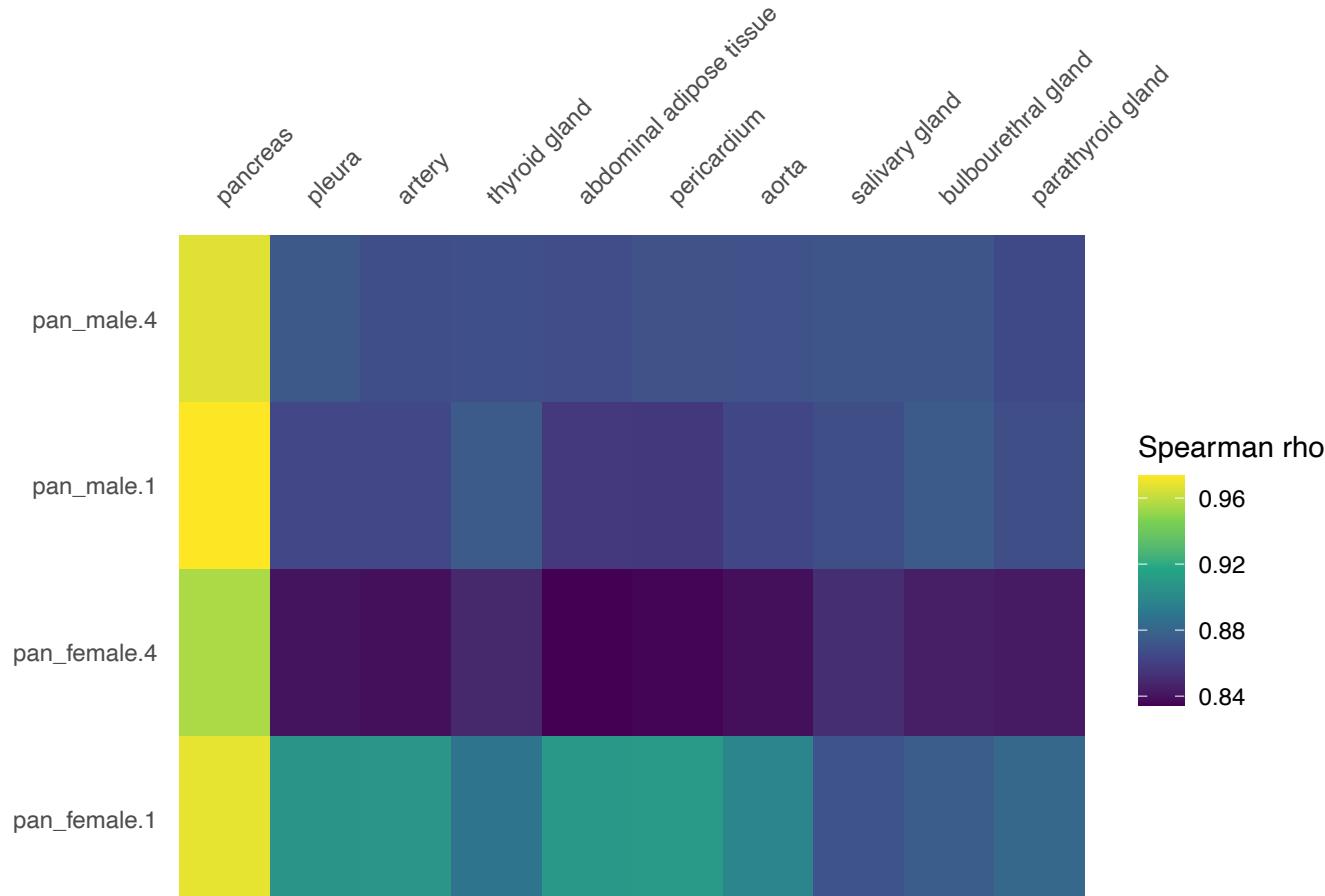


ovary, UMAP: TMM expression values

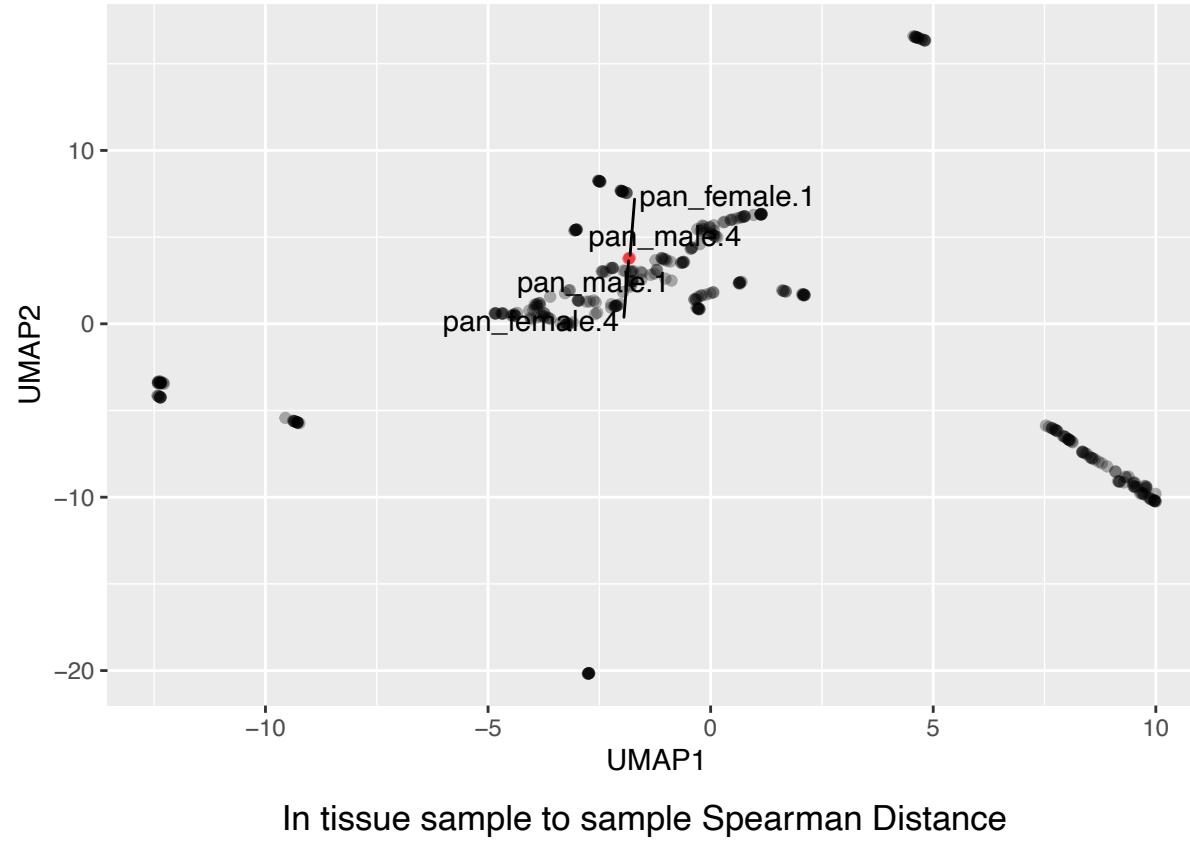




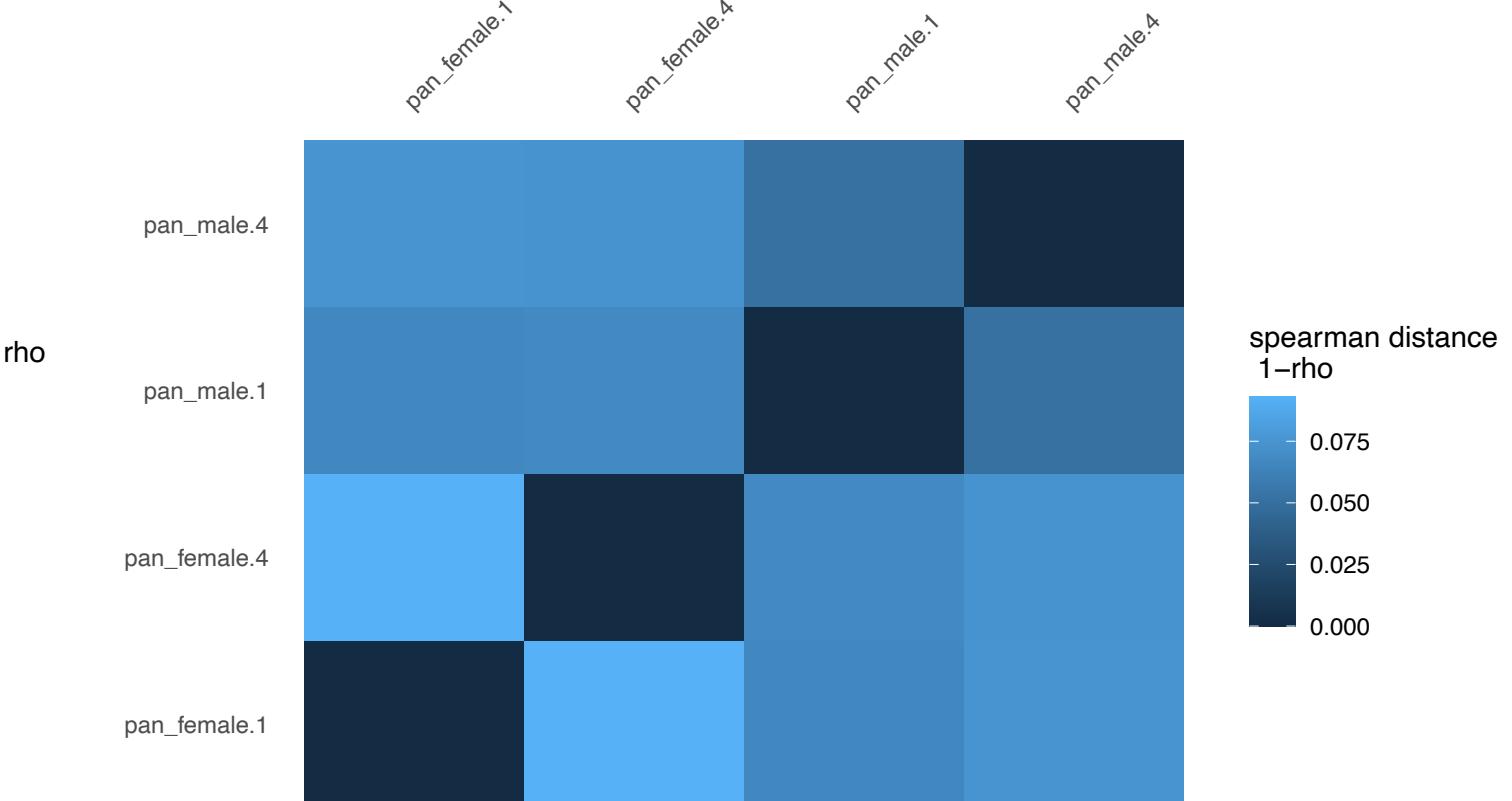
Tissue group to sample correlation



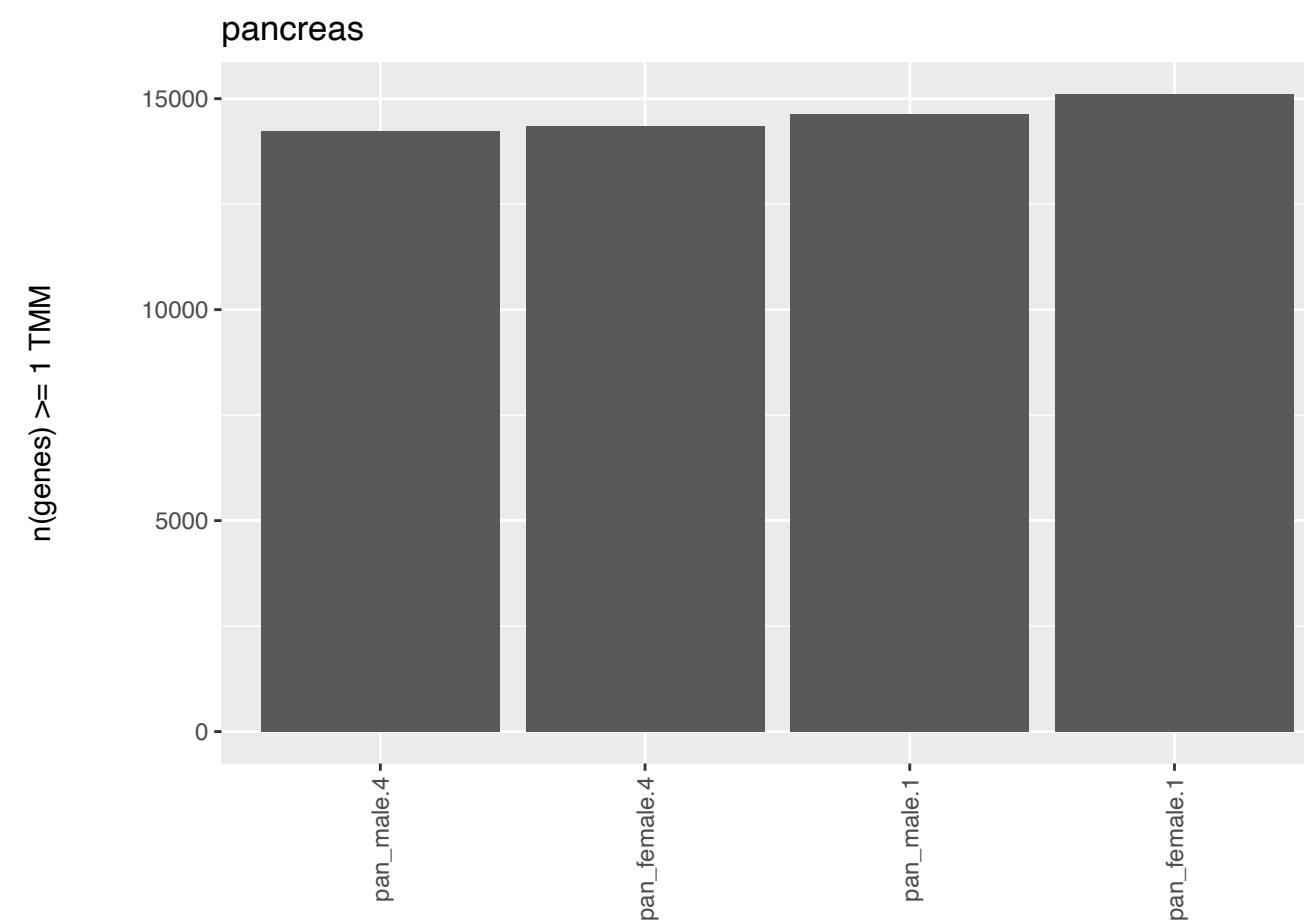
pancreas, UMAP: TMM expression value



In tissue sample to sample Spearman Distance



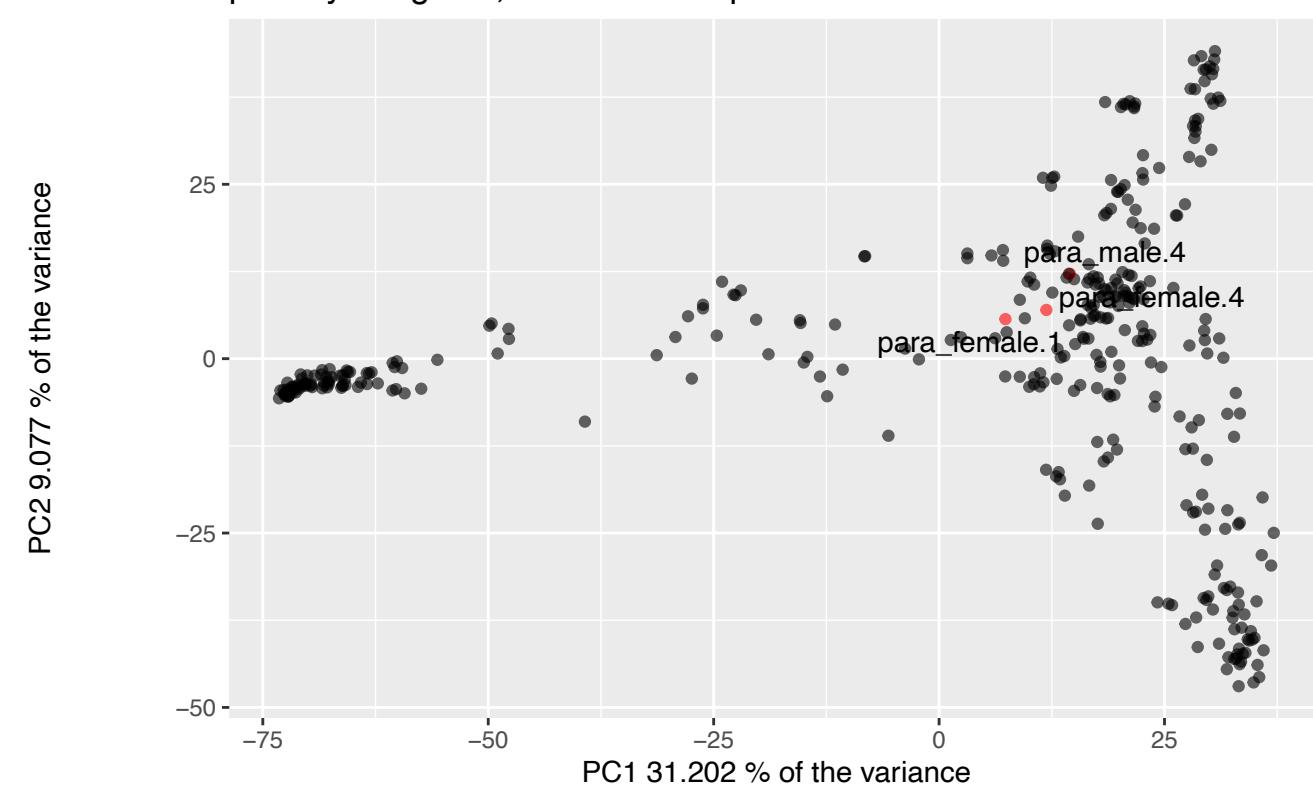
pancreas



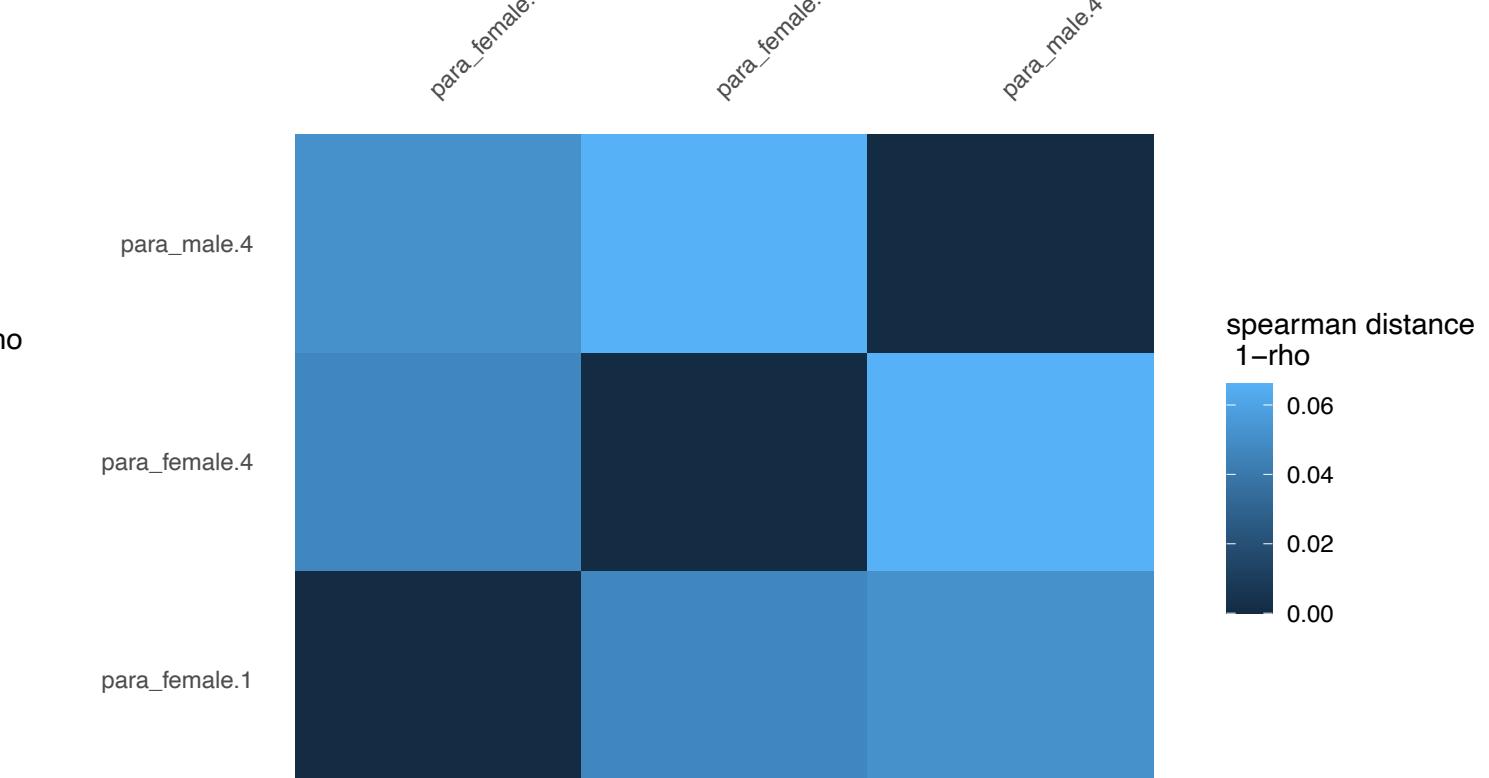
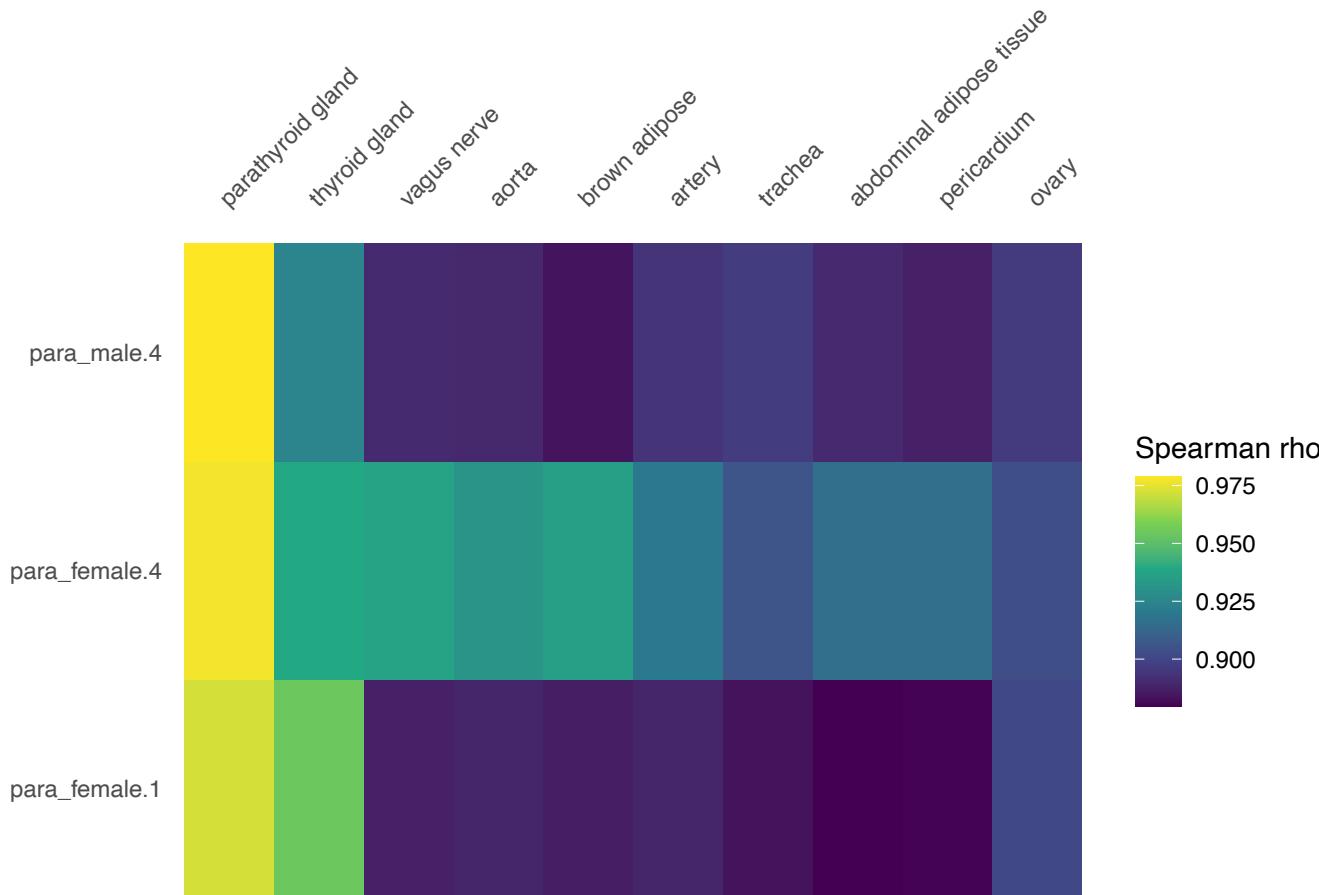
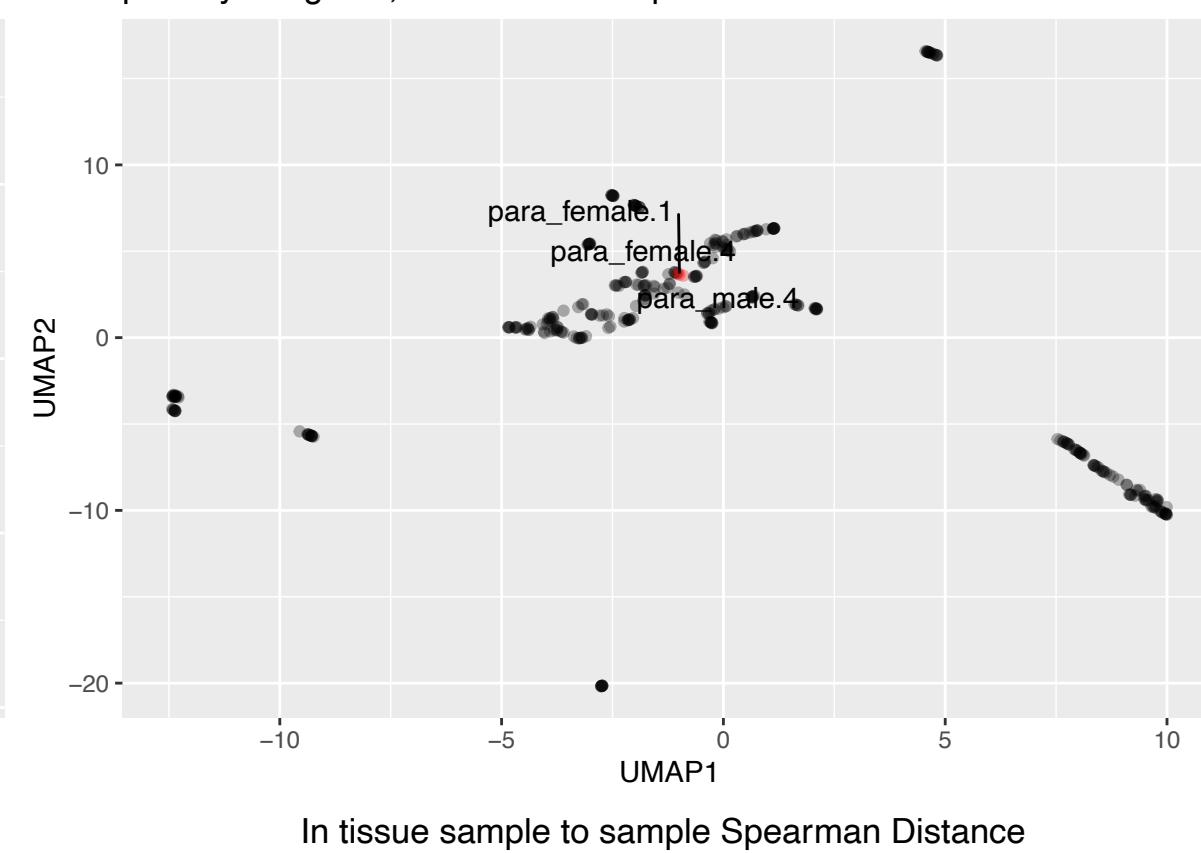
pancreas

This violin plot displays the distribution of gene expression levels across different samples. The y-axis represents the logarithmic expression value, ranging from 0 to 6. The x-axis lists six samples: pan_female.1, pan_female.4, pan_male.1, and pan_male.4. Each sample is represented by a dark grey violin, which shows the density of expression values. A small orange segment at the top of each violin indicates the median expression level. The plots show that most samples have a median expression near zero, with one notable exception: pan_female.1, which has a significantly higher median expression than the others.

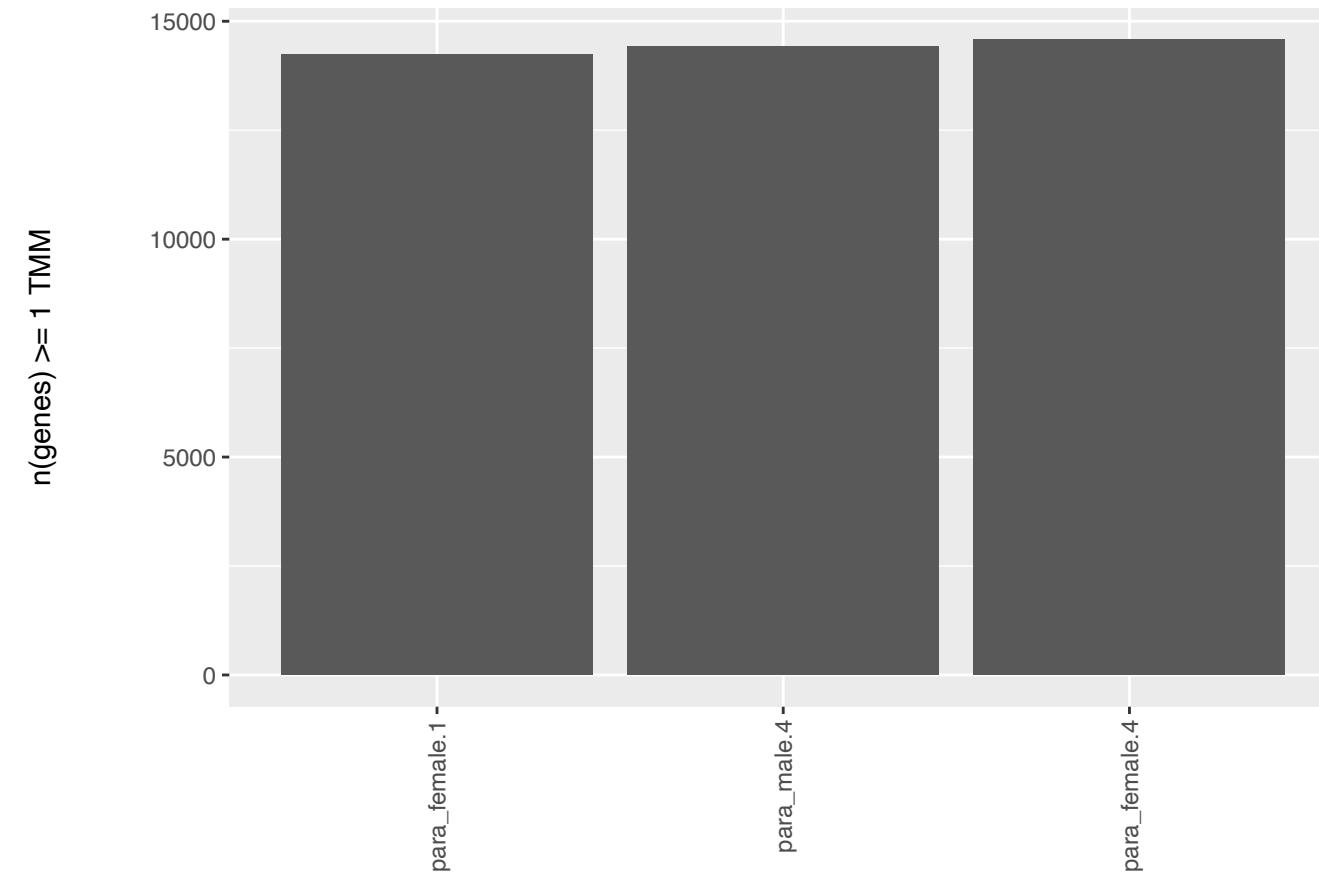
parathyroid gland, PCA: TMM expression values



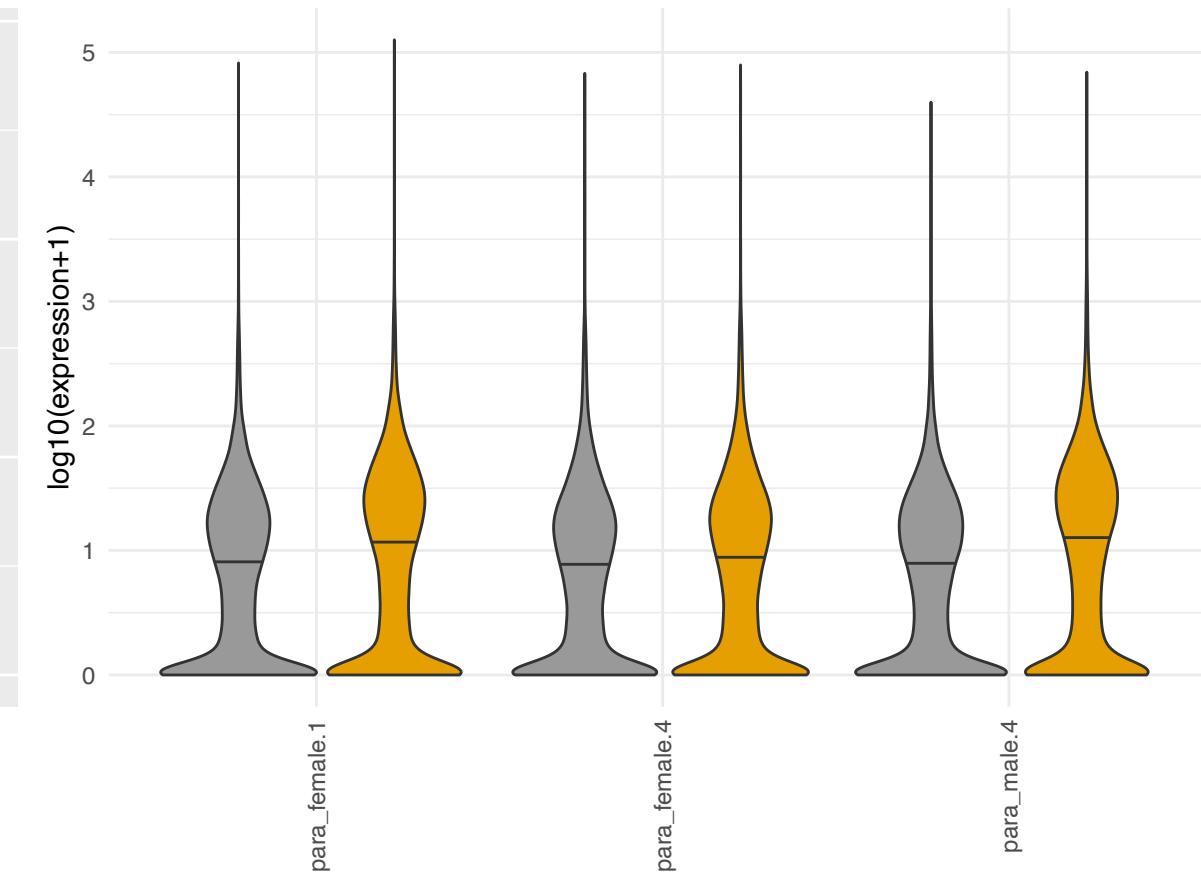
parathyroid gland, UMAP: TMM expression values



parathyroid gland

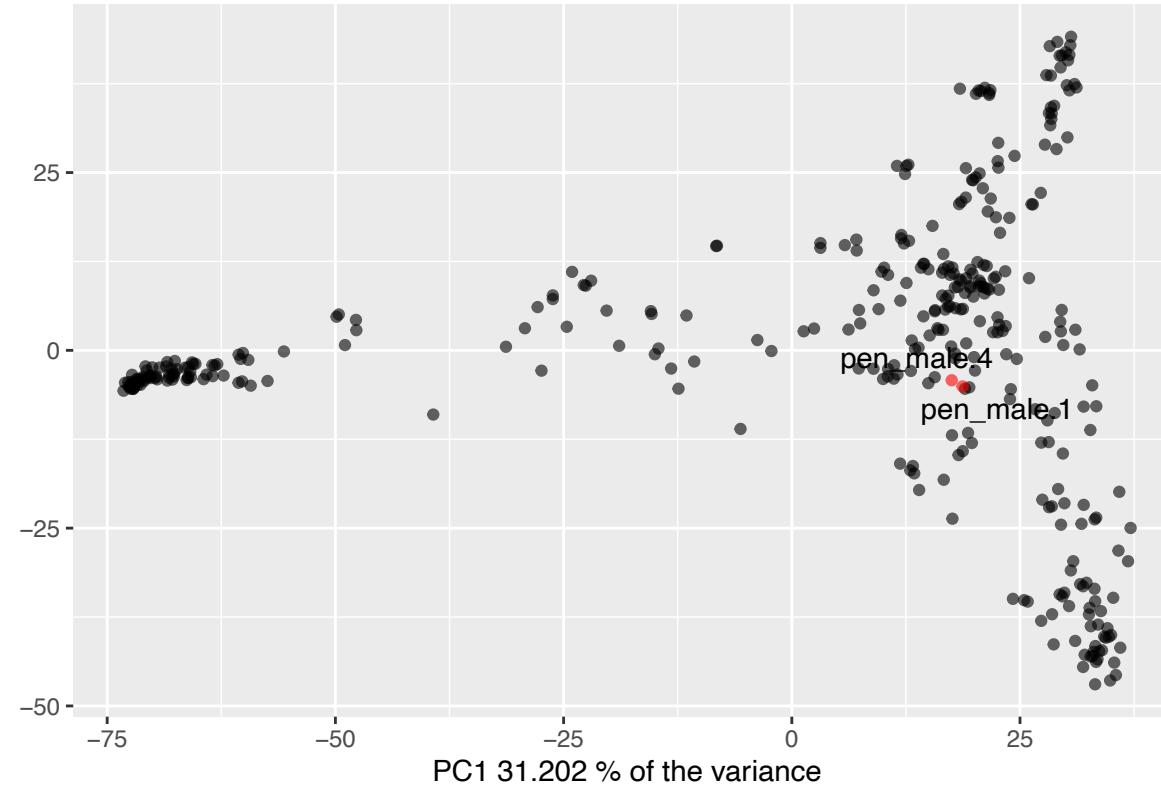


parathyroid gland

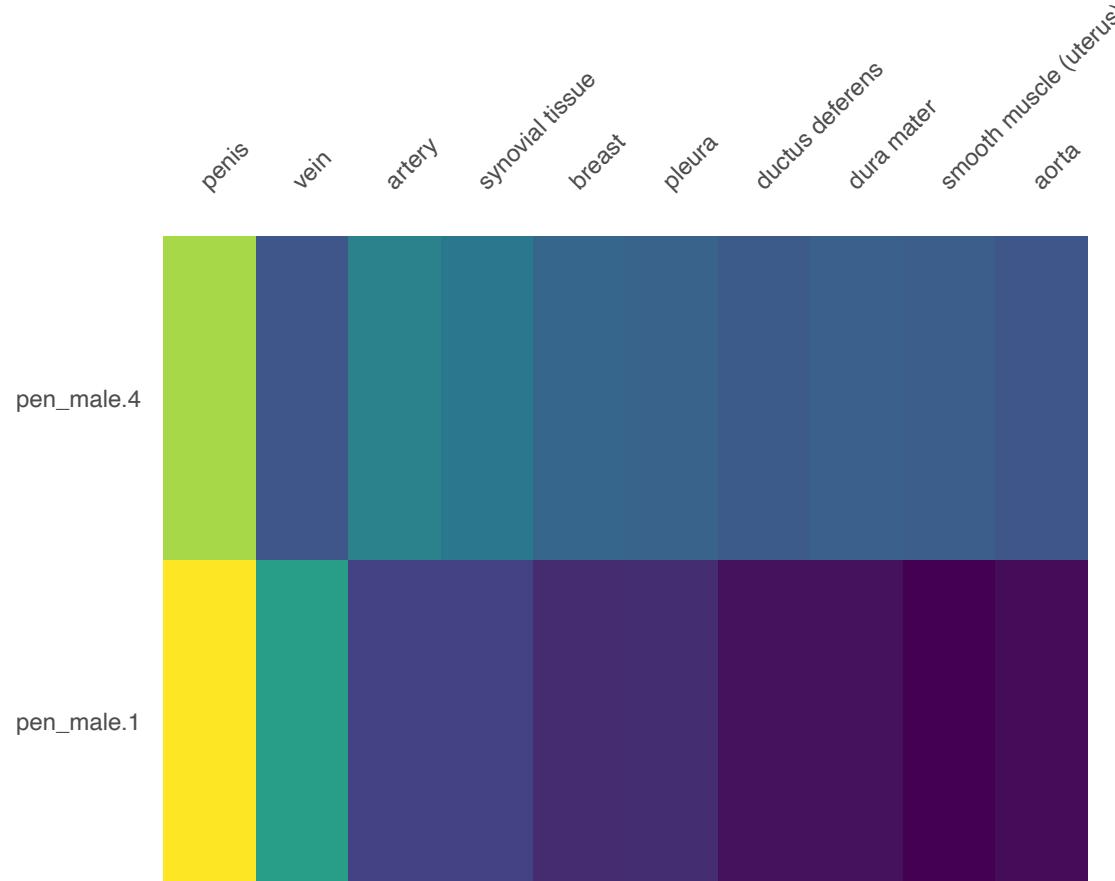


penis, PCA: TMM expression values

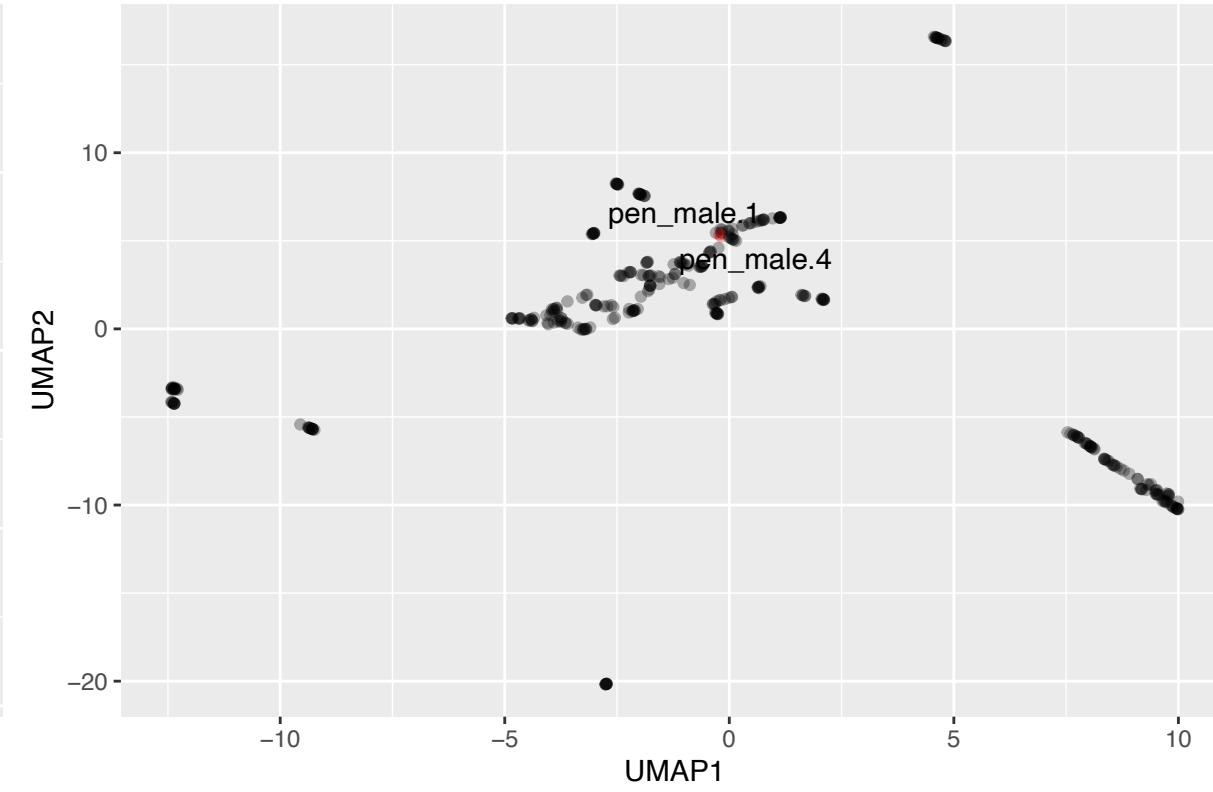
PC2 9.077 % of the variance



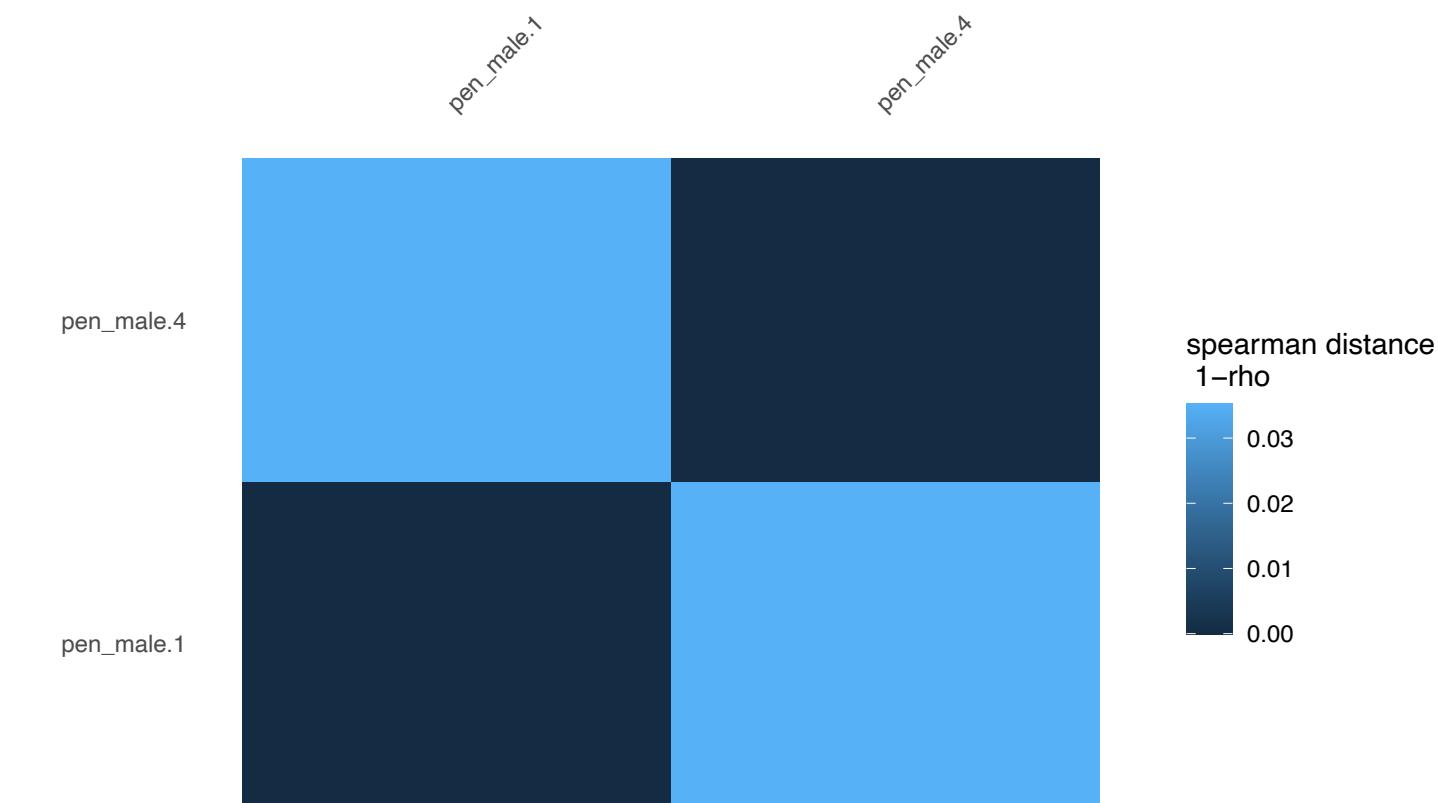
Tissue group to sample correlation



penis, UMAP: TMM expression values

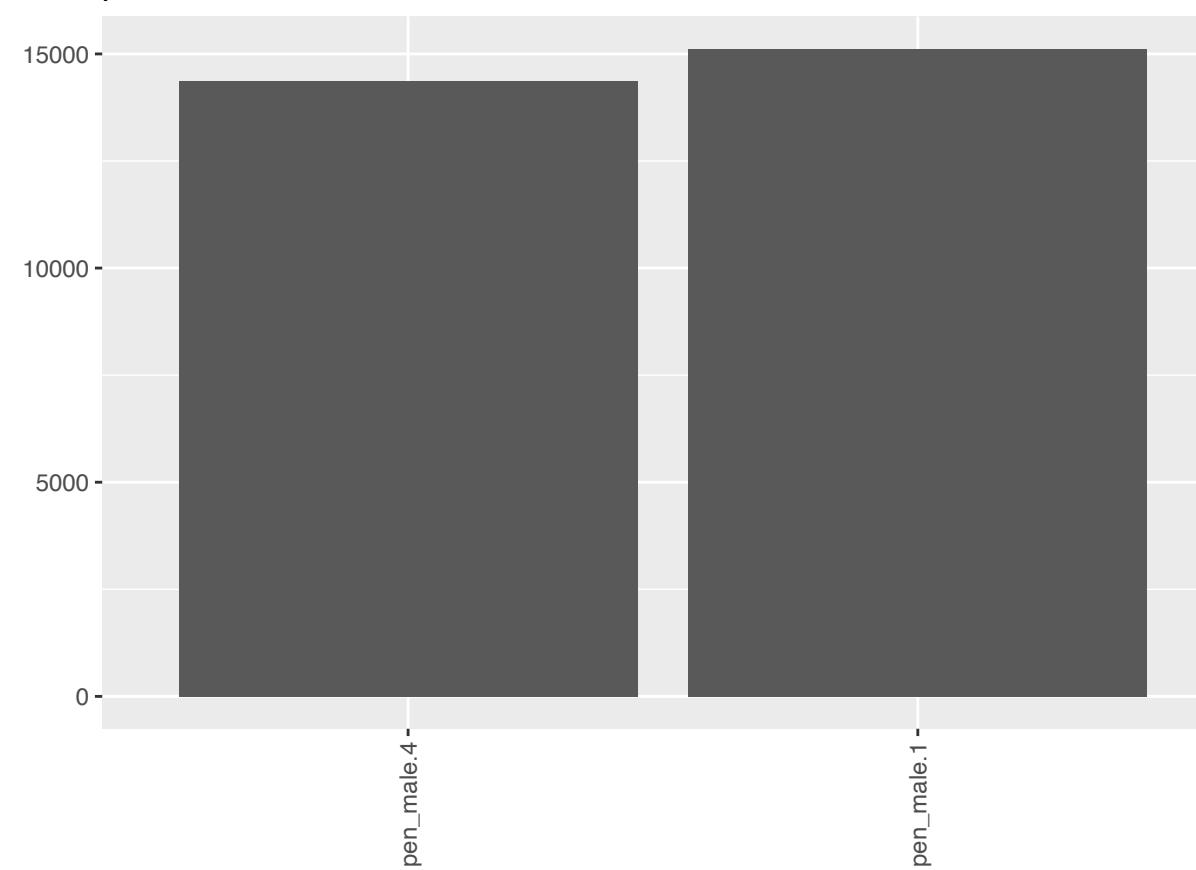


In tissue sample to sample Spearman Distance

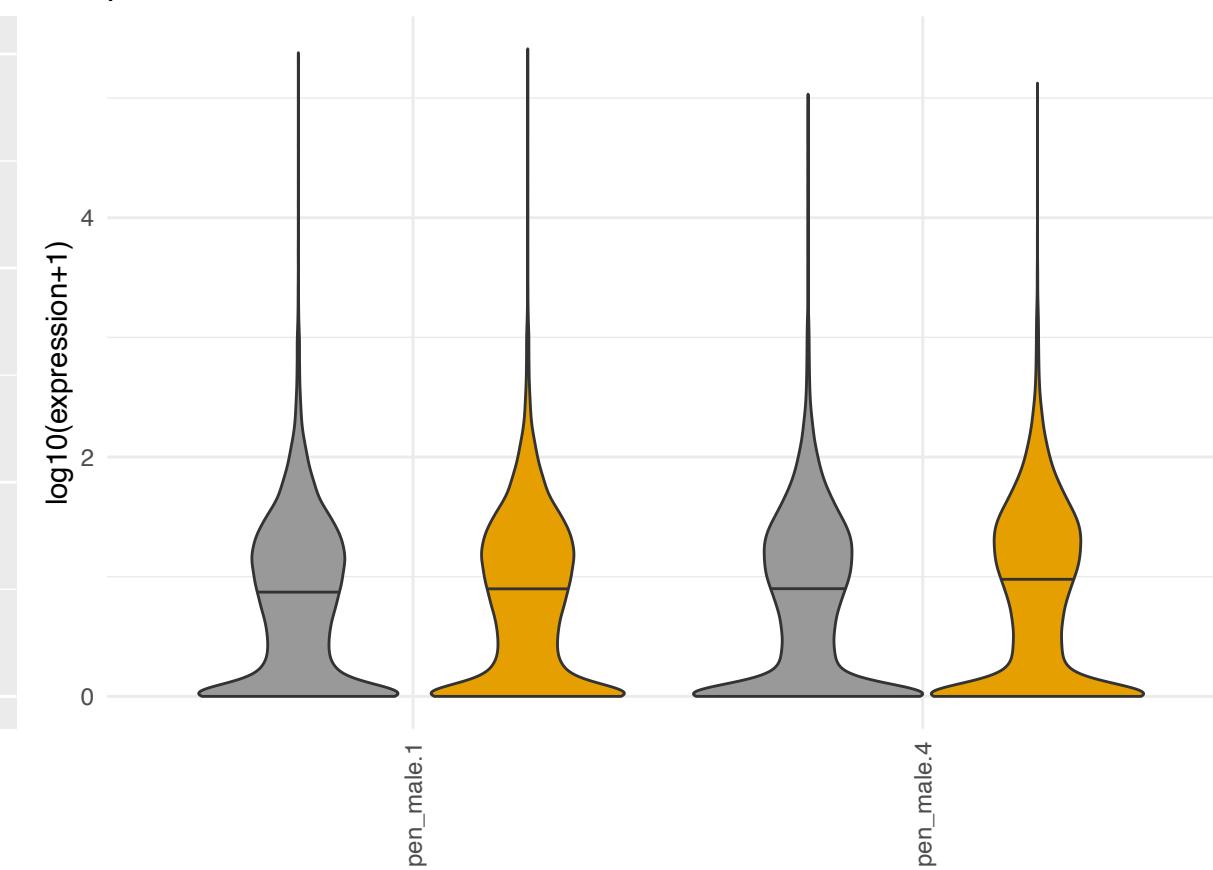


penis

n(genes) >= 1 TMM

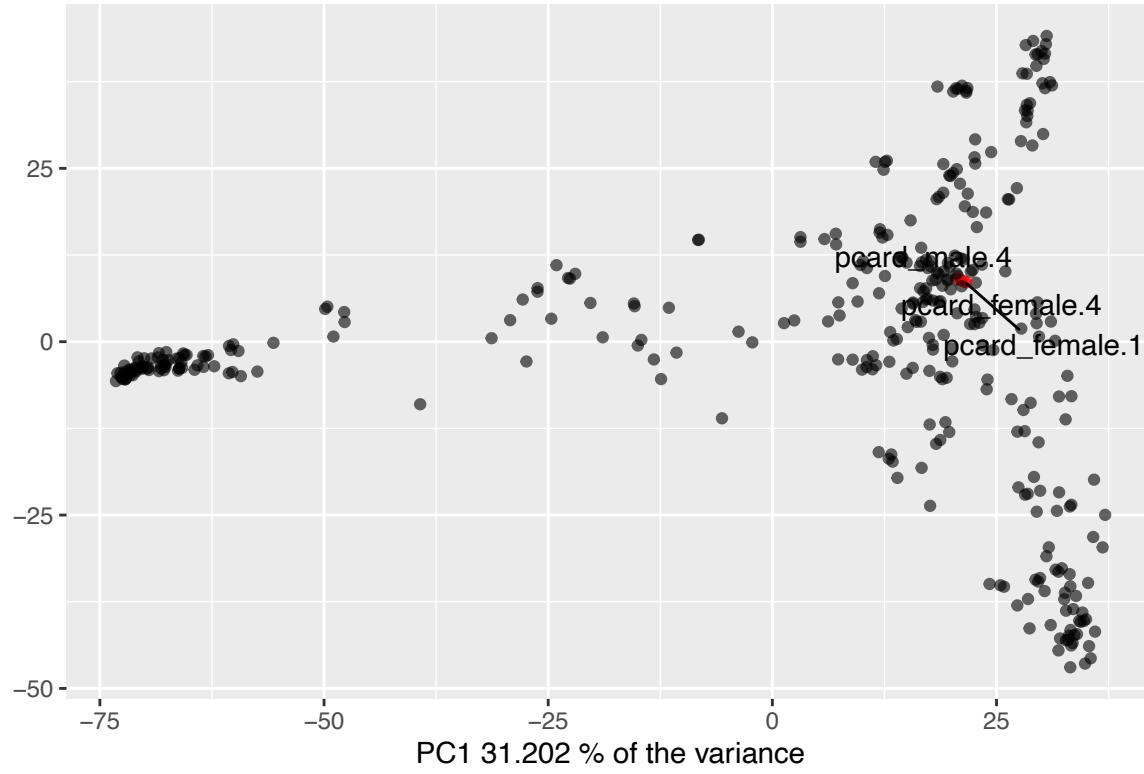


penis



pericardium, PCA: TMM expression values

PC2 9.077 % of the variance

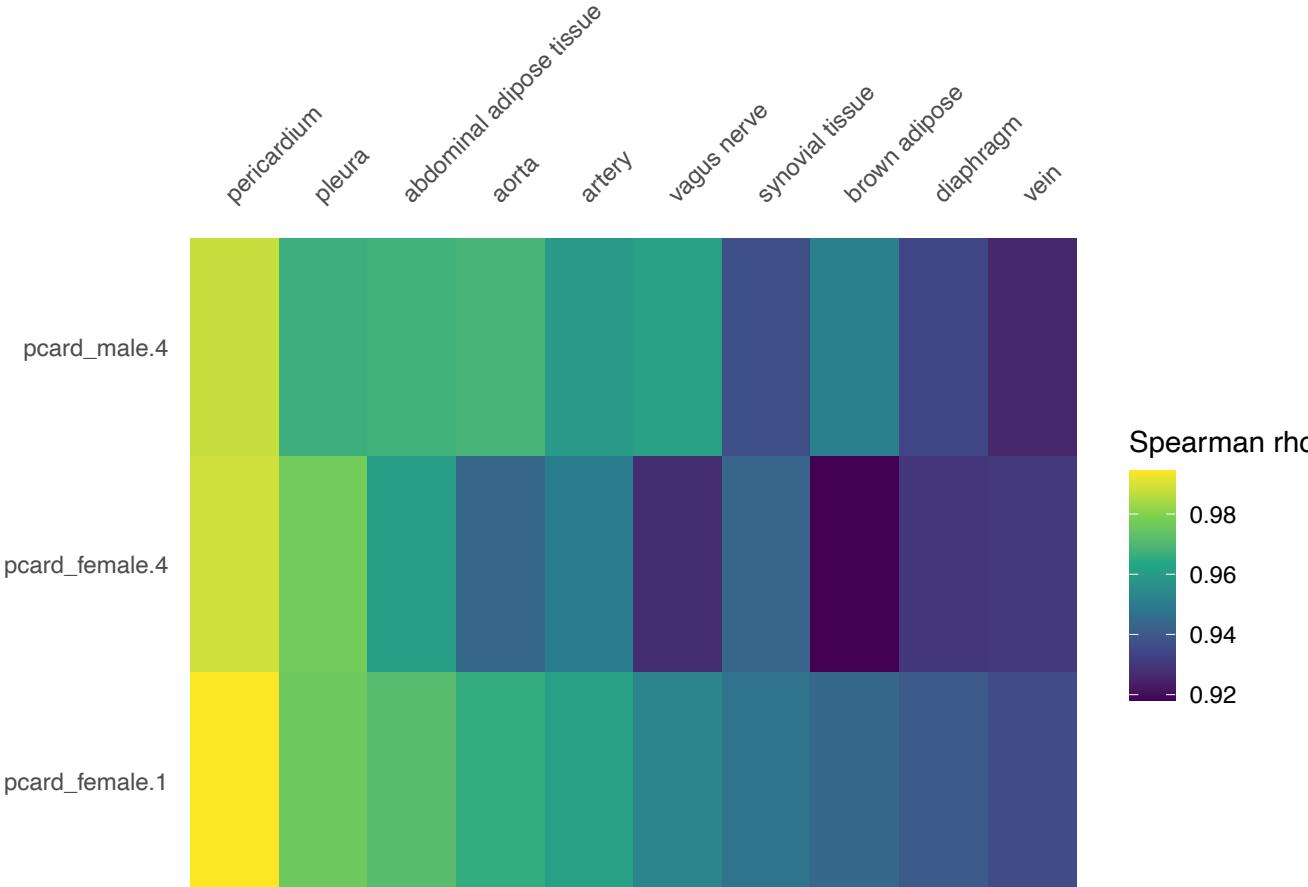
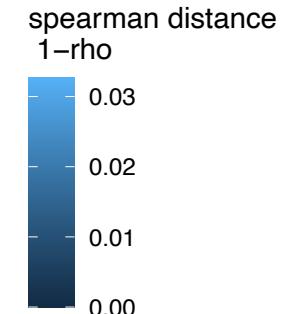


pericardium, UMAP: TMM expression values

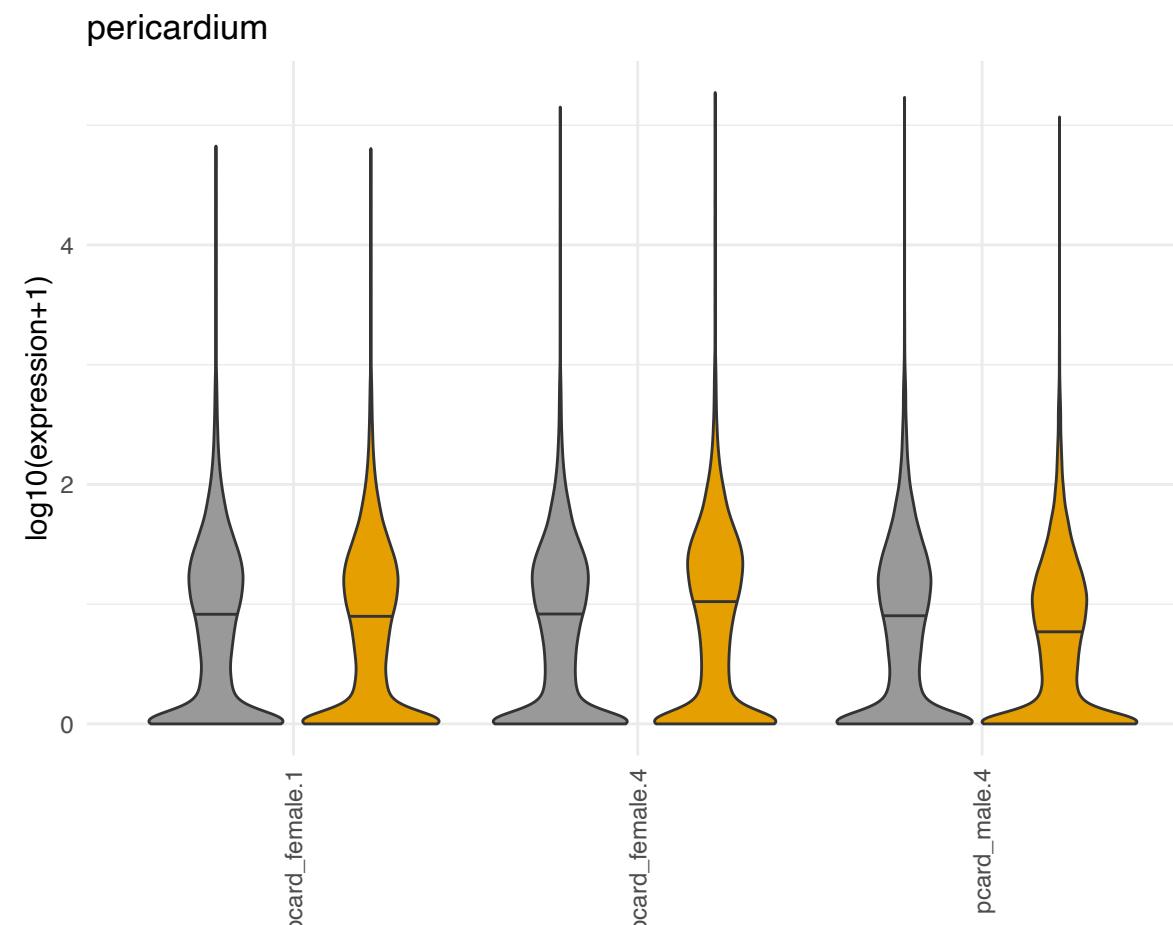
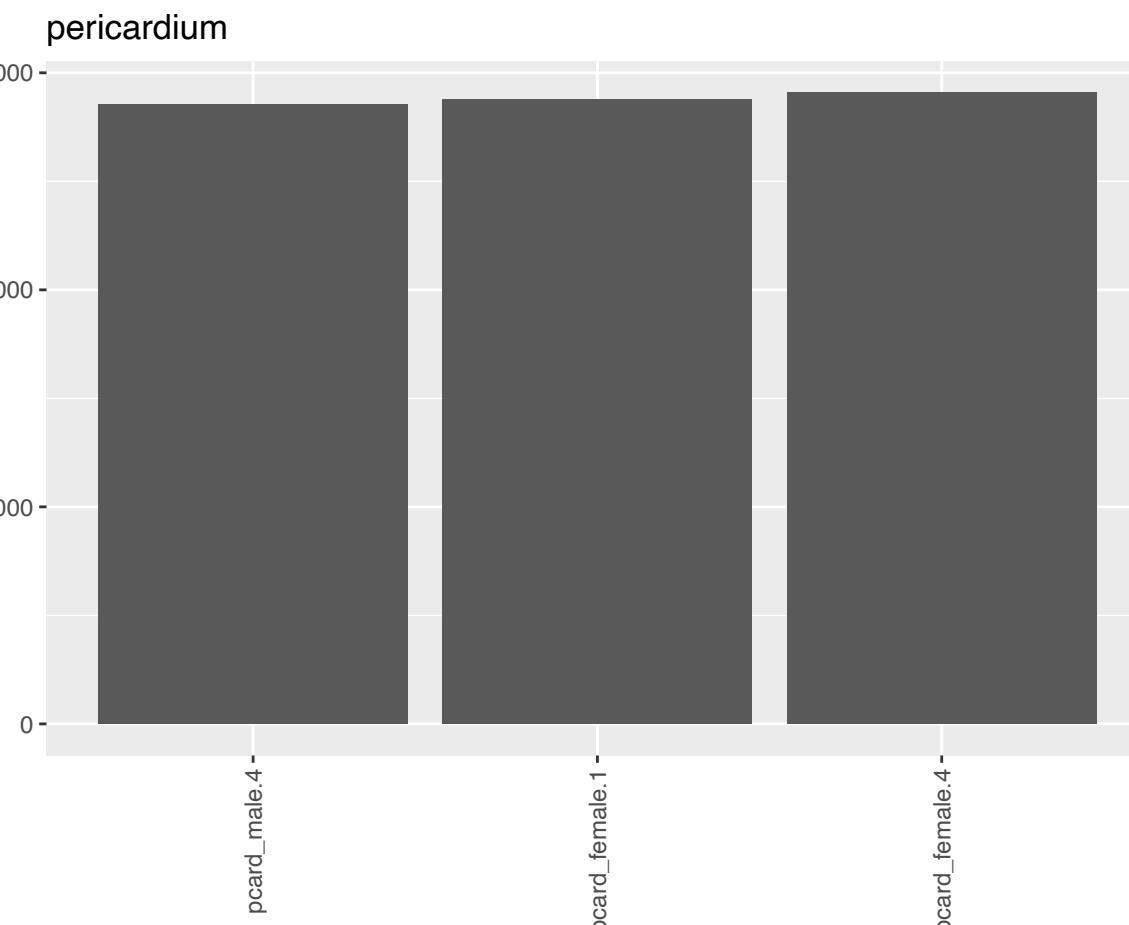
UMAP2

UMAP1

In tissue sample to sample Spearman Distance

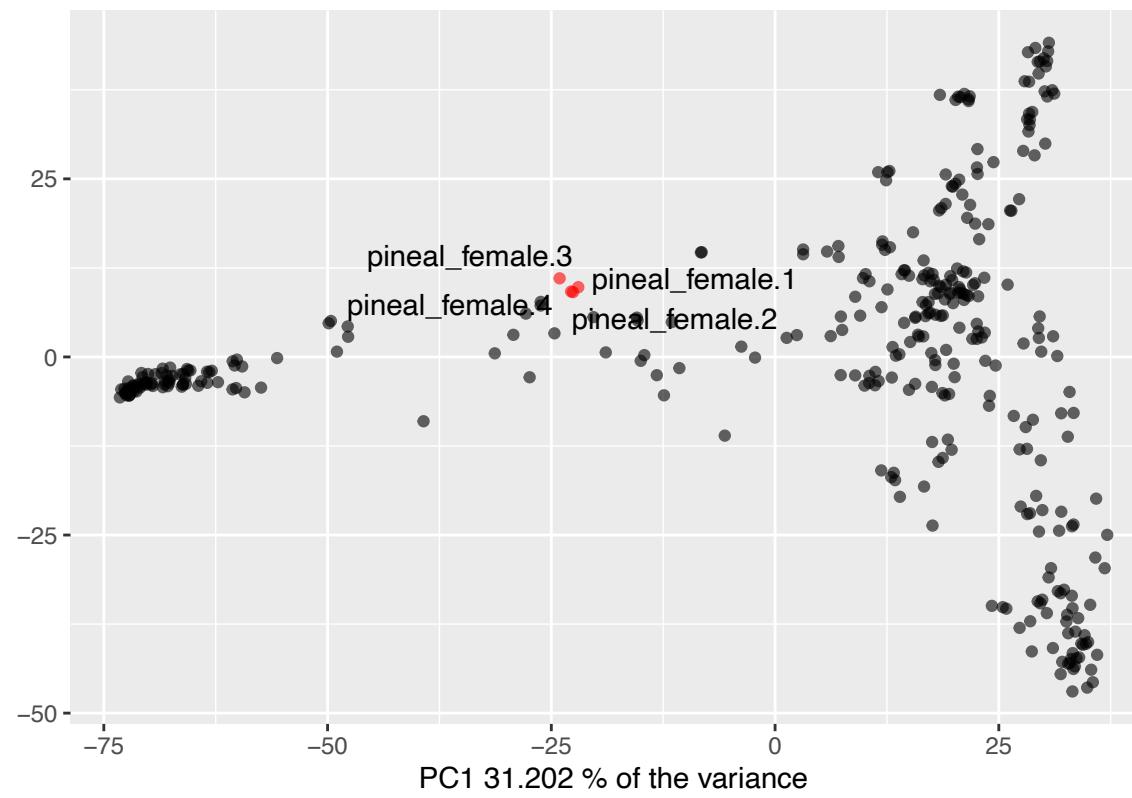
pcard_female.1
pcard_female.4
pcard_male.4pcard_male.4
pcard_female.4
pcard_female.1

n(genes) >= 1 TMM

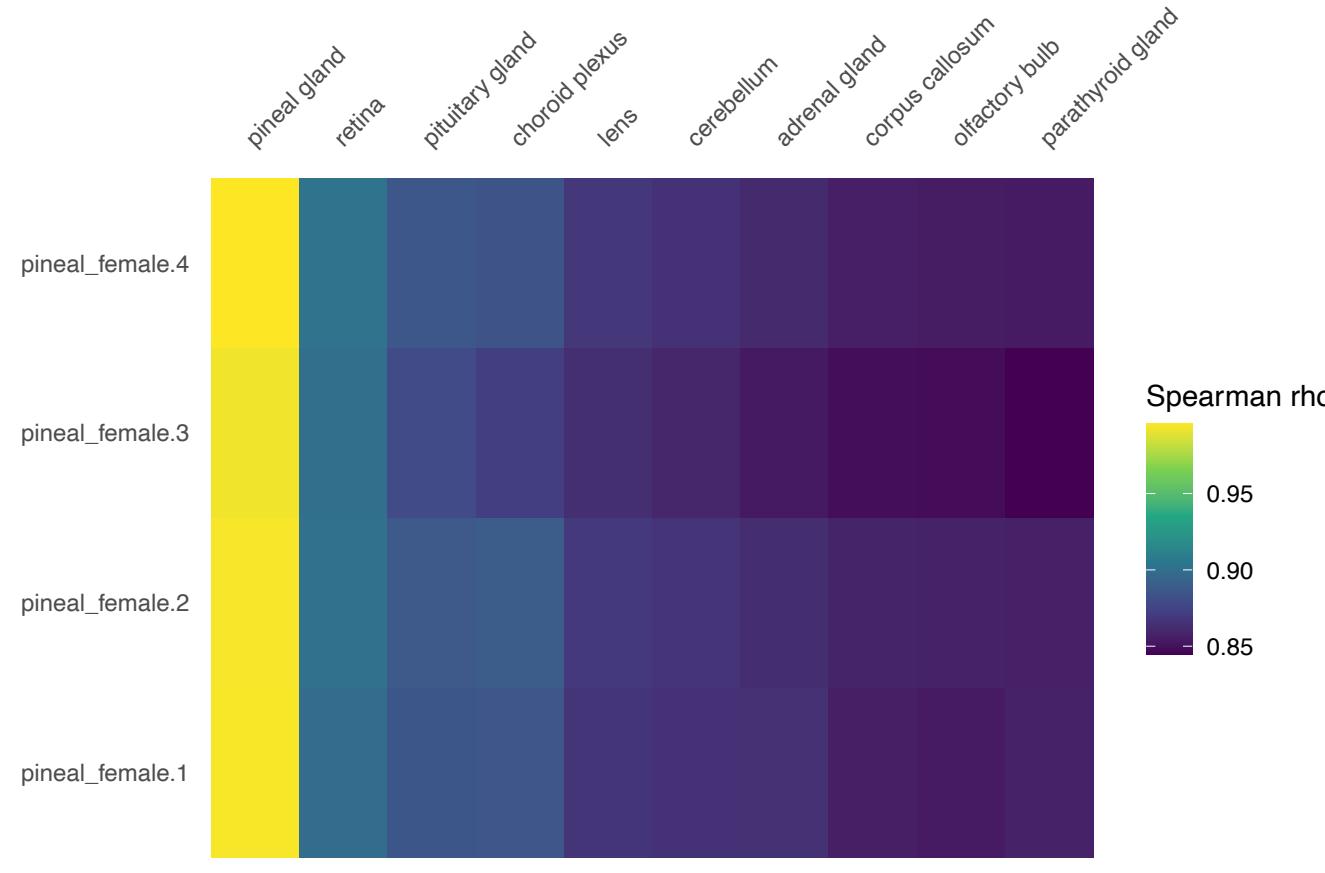


pineal gland, PCA: TMM expression values

PC2 9.077 % of the variance

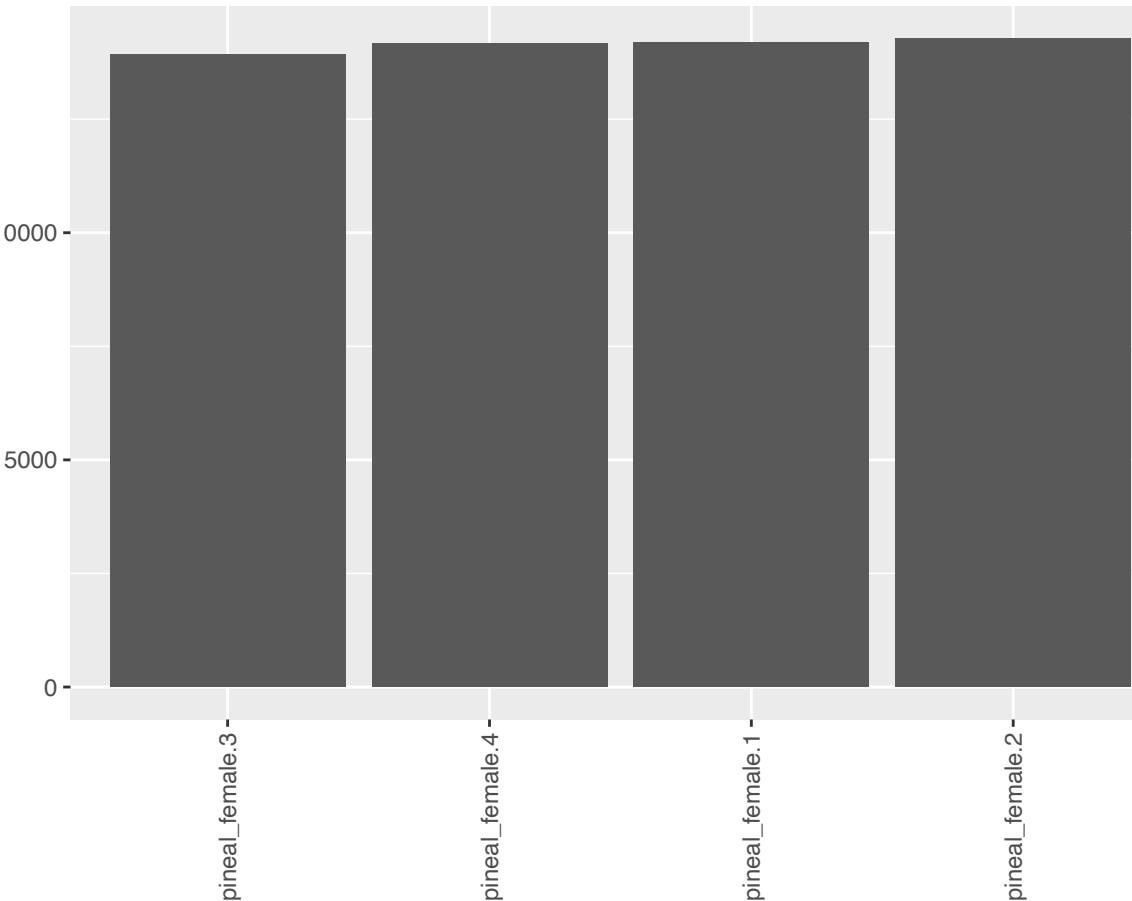


Tissue group to sample correlation

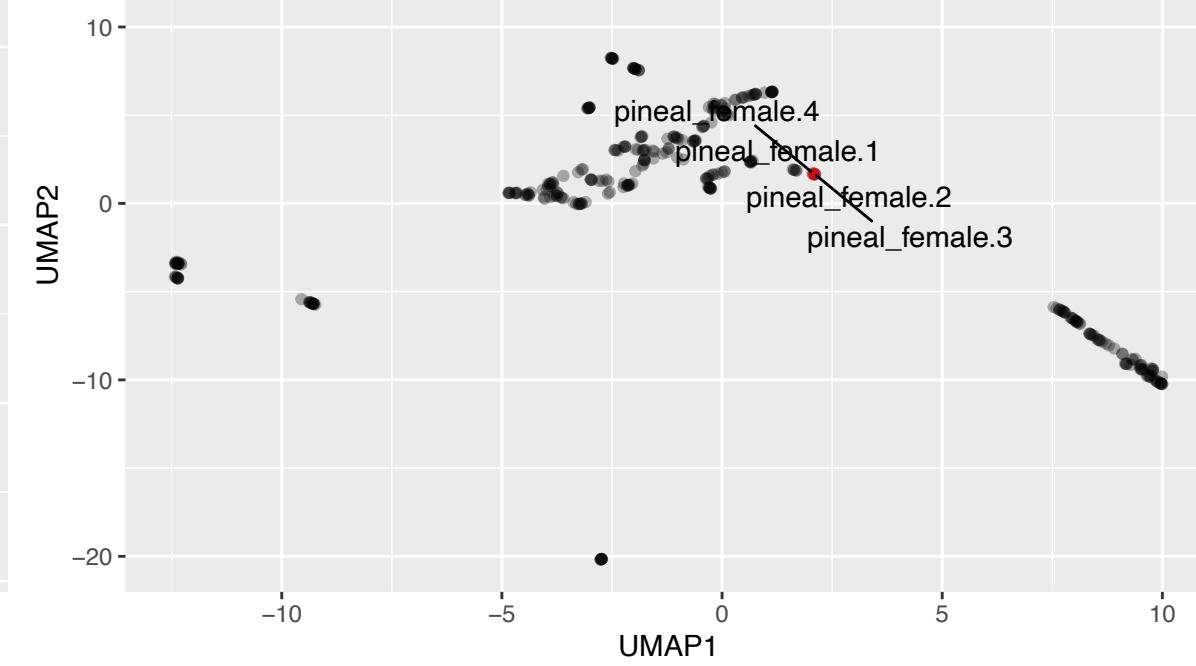


pineal gland

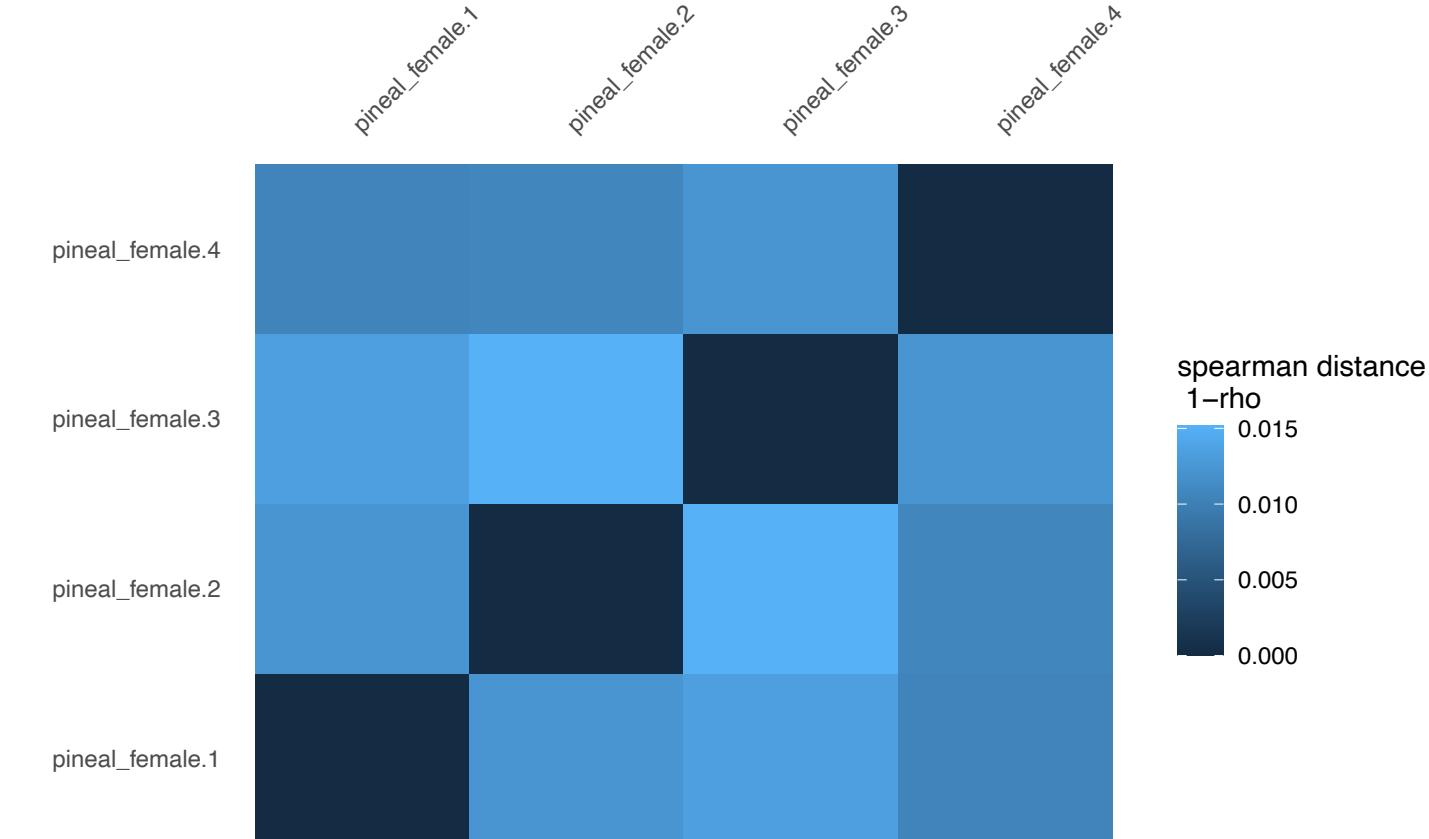
n(genes) >= 1 TMM



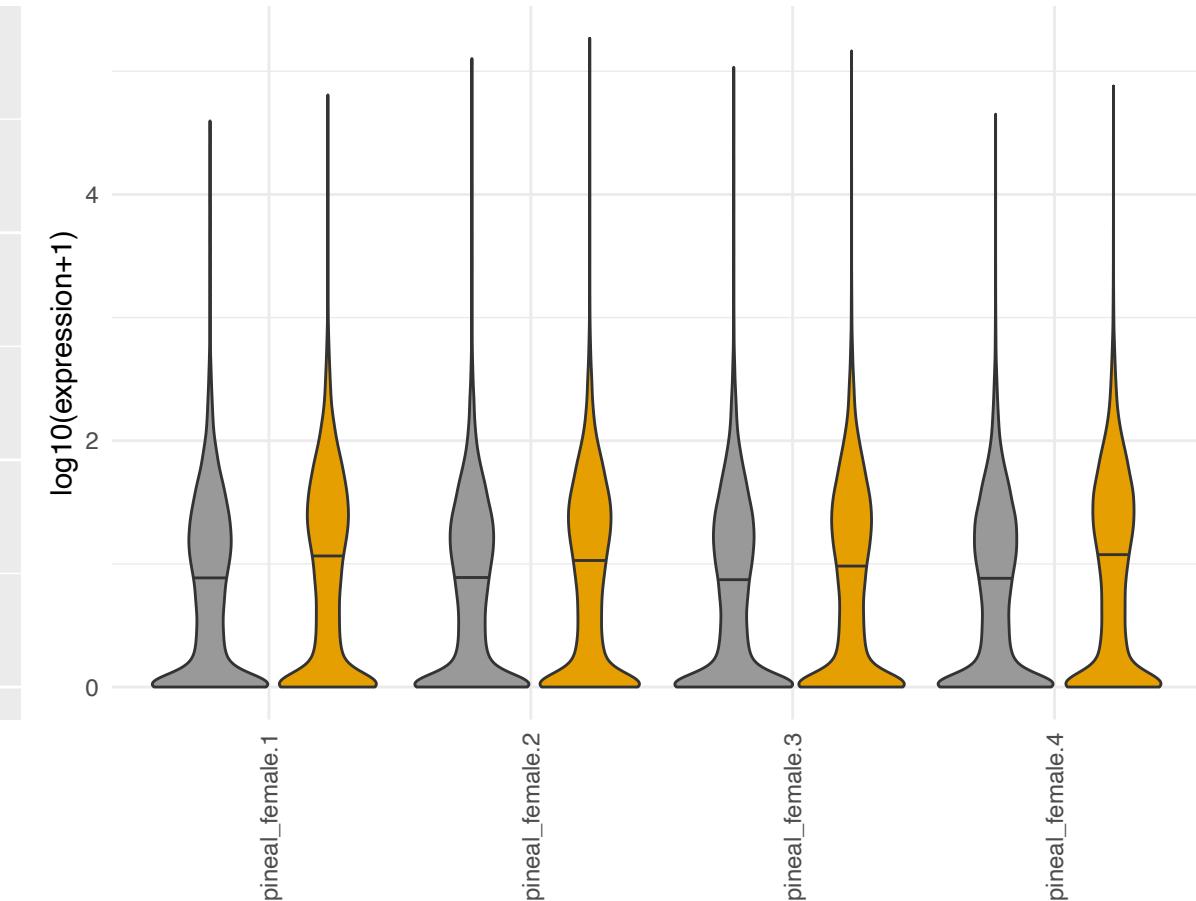
pineal gland, UMAP: TMM expression values



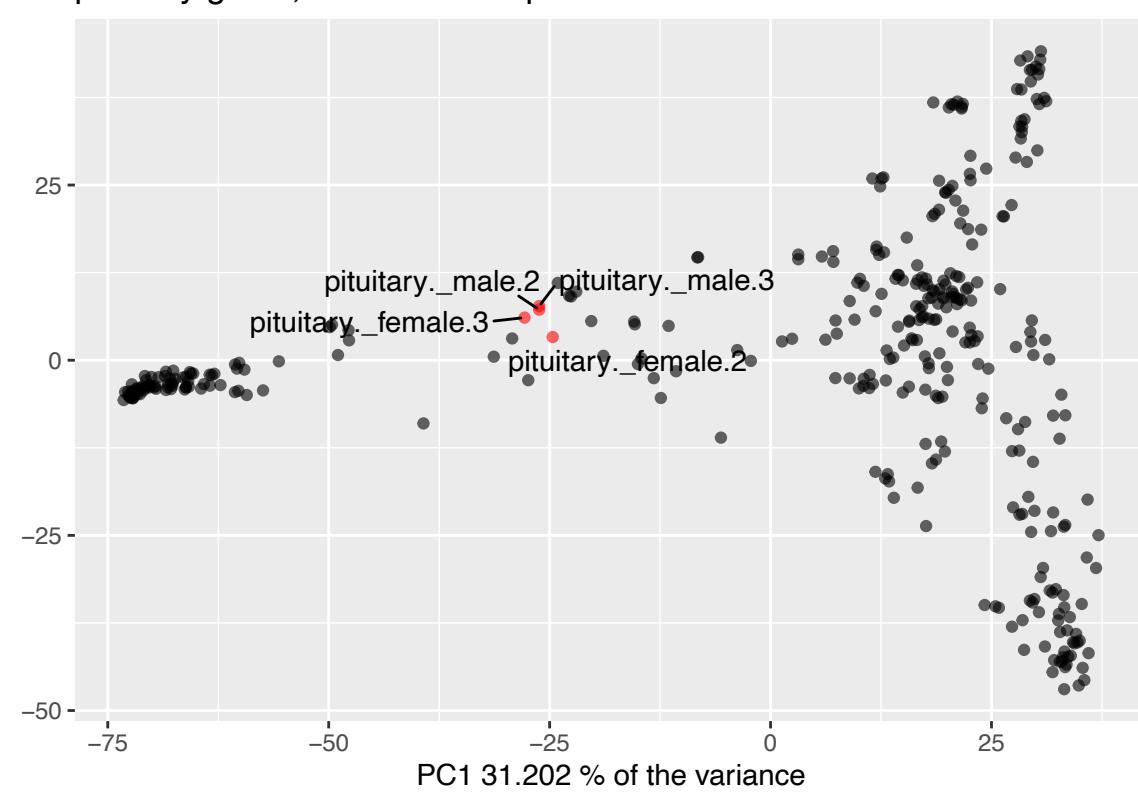
In tissue sample to sample Spearman Distance



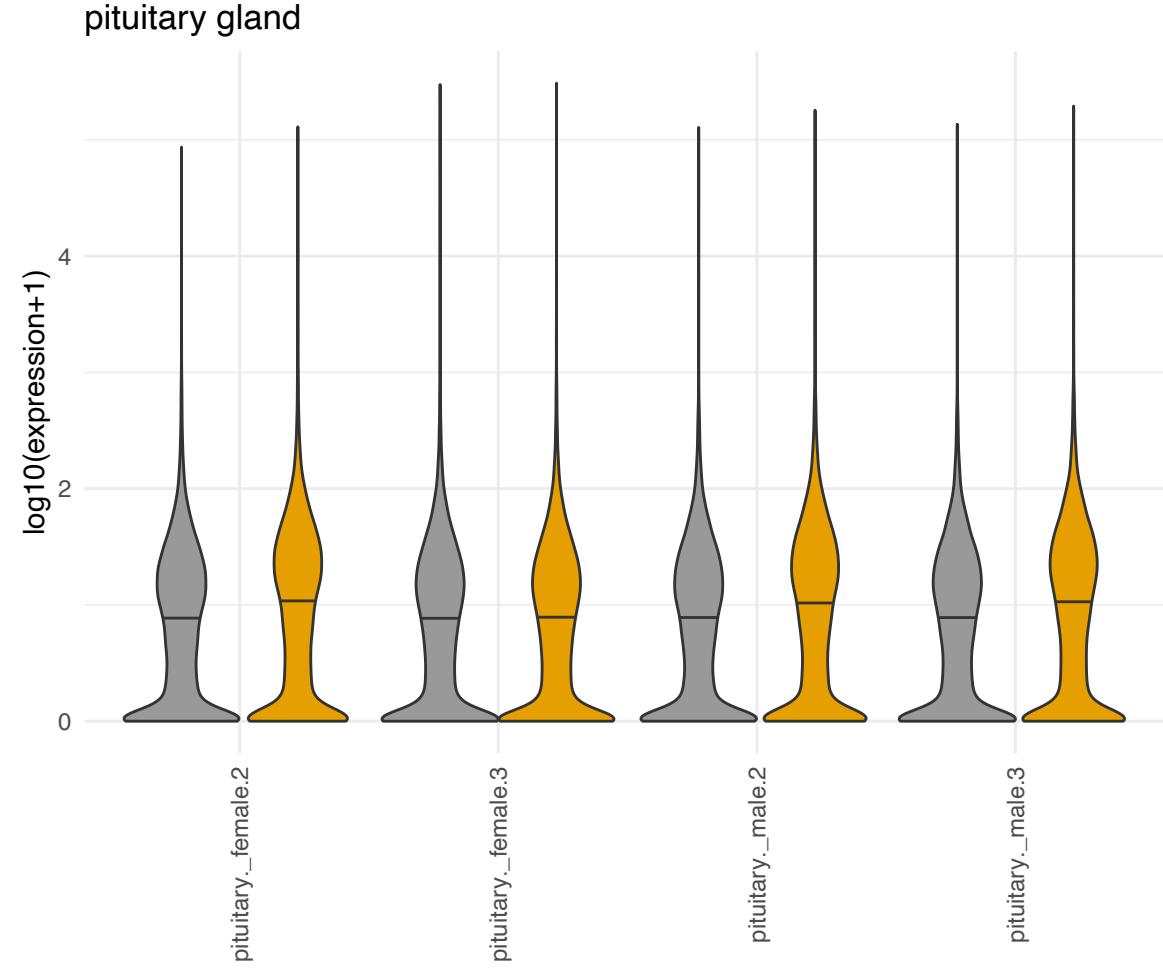
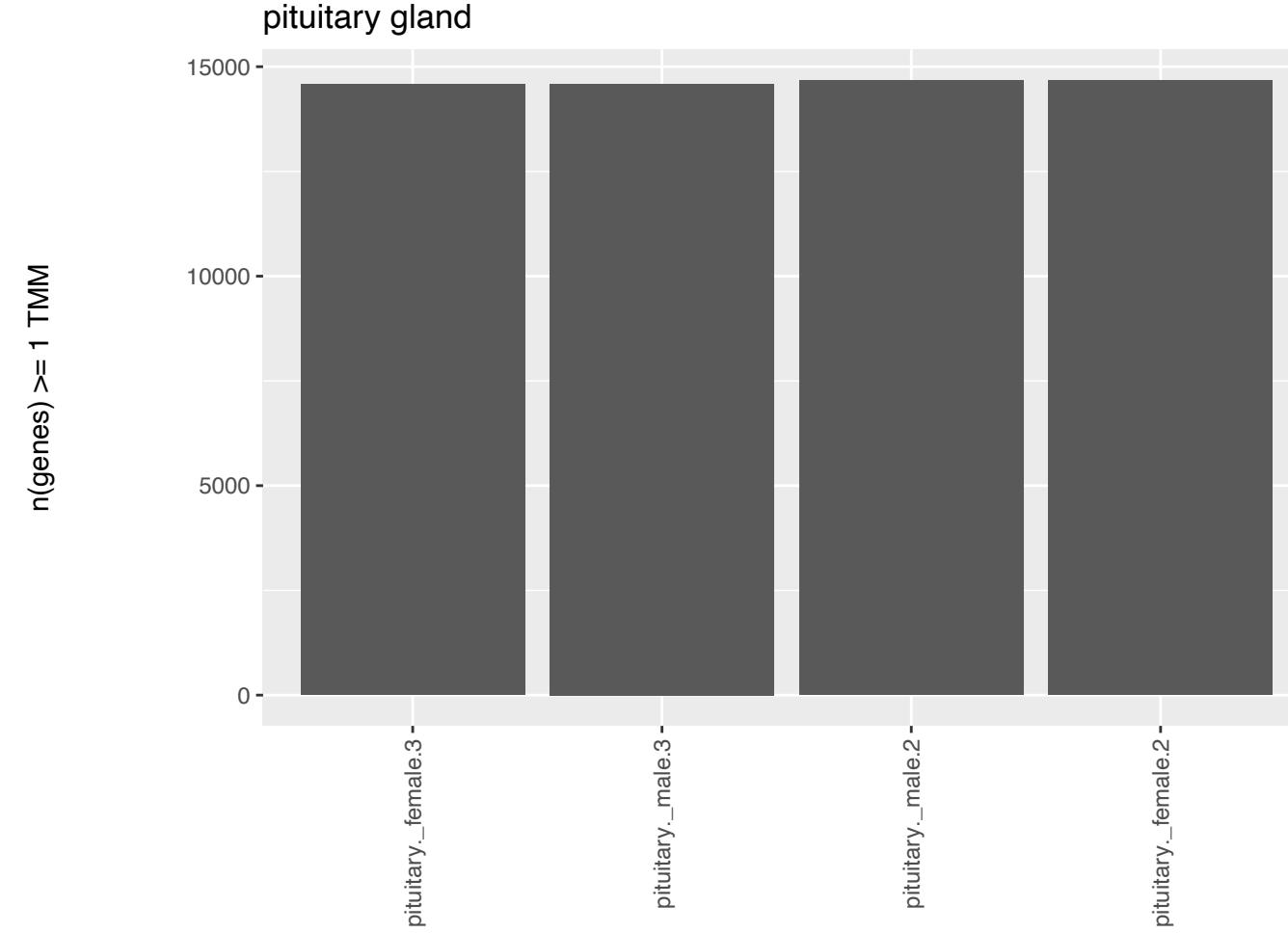
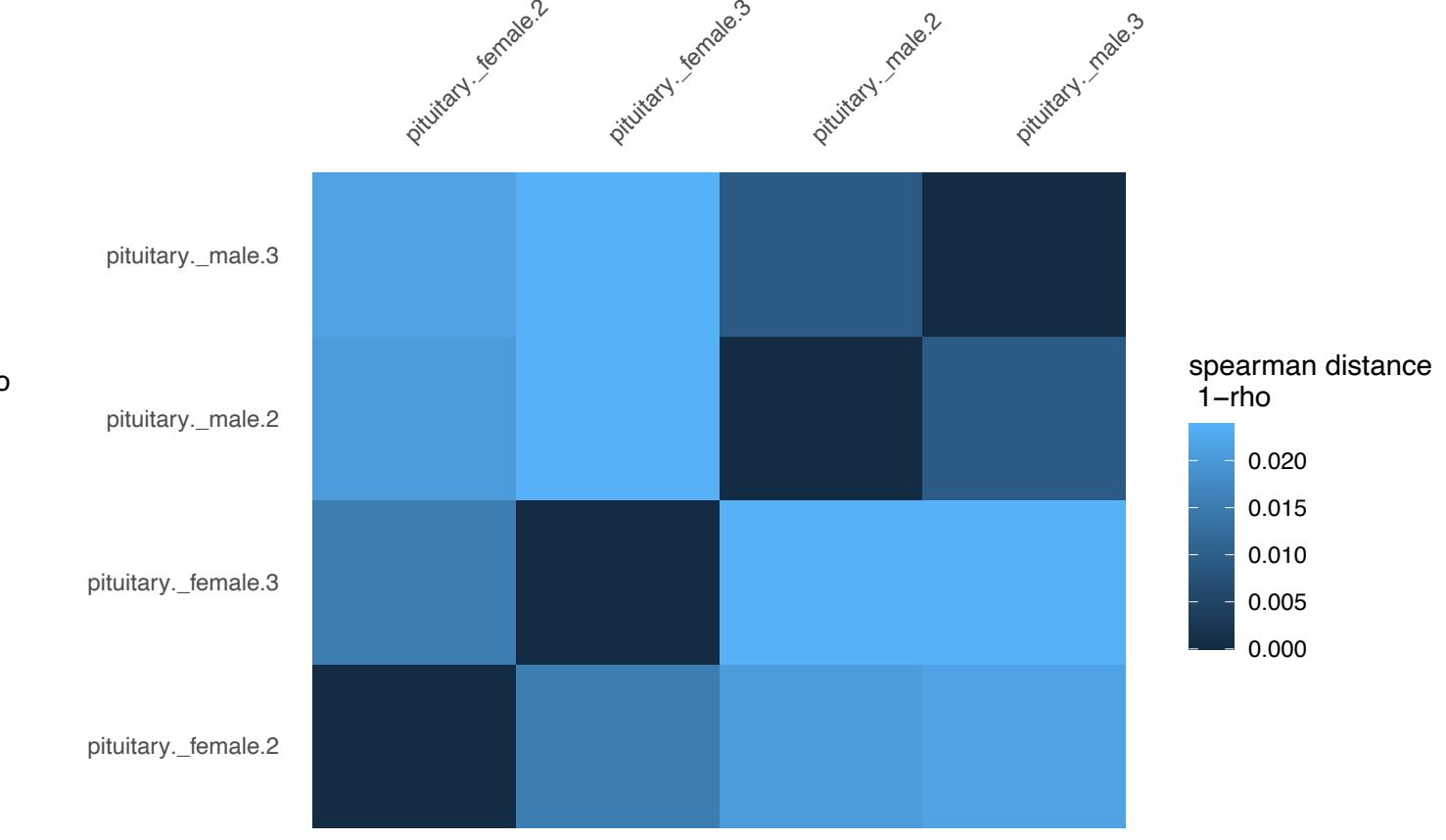
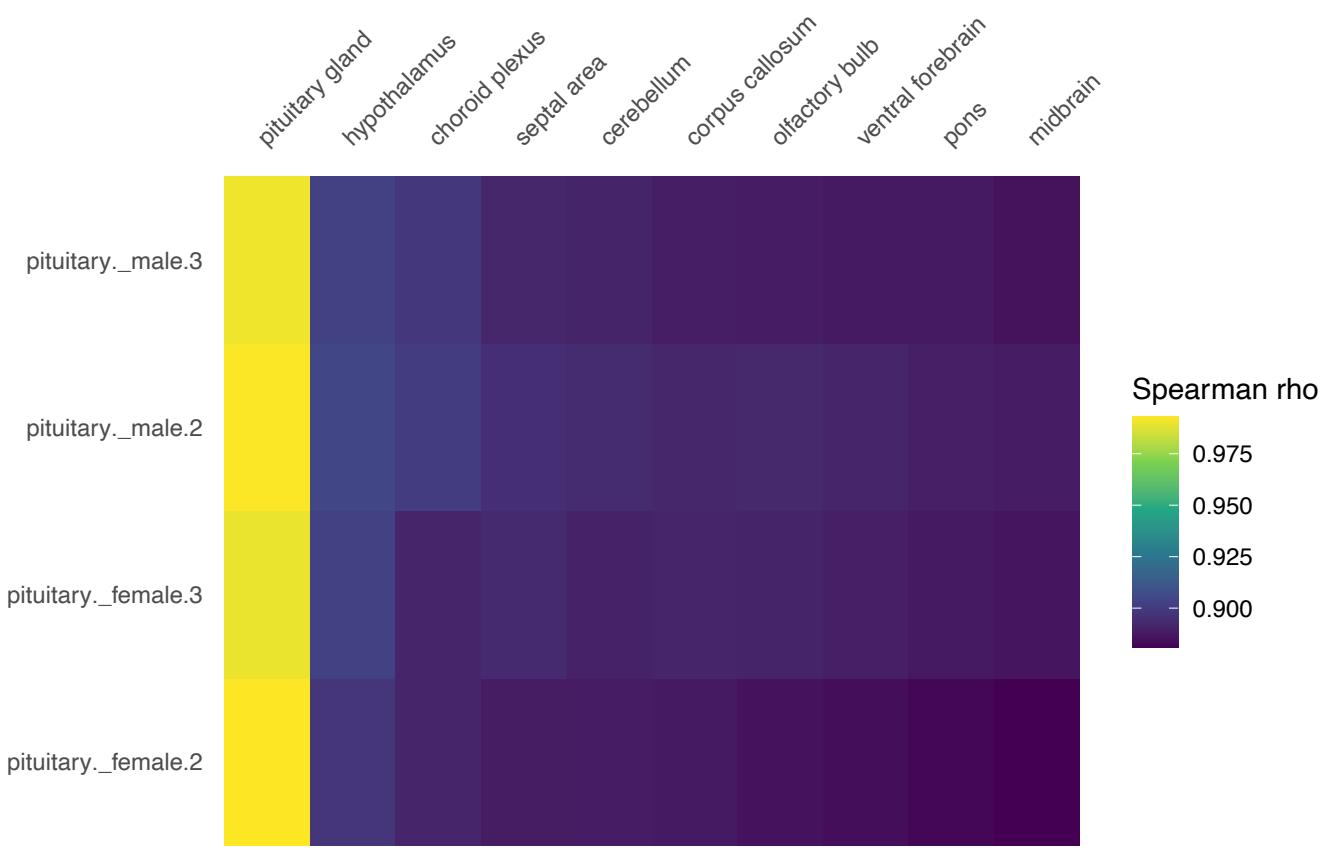
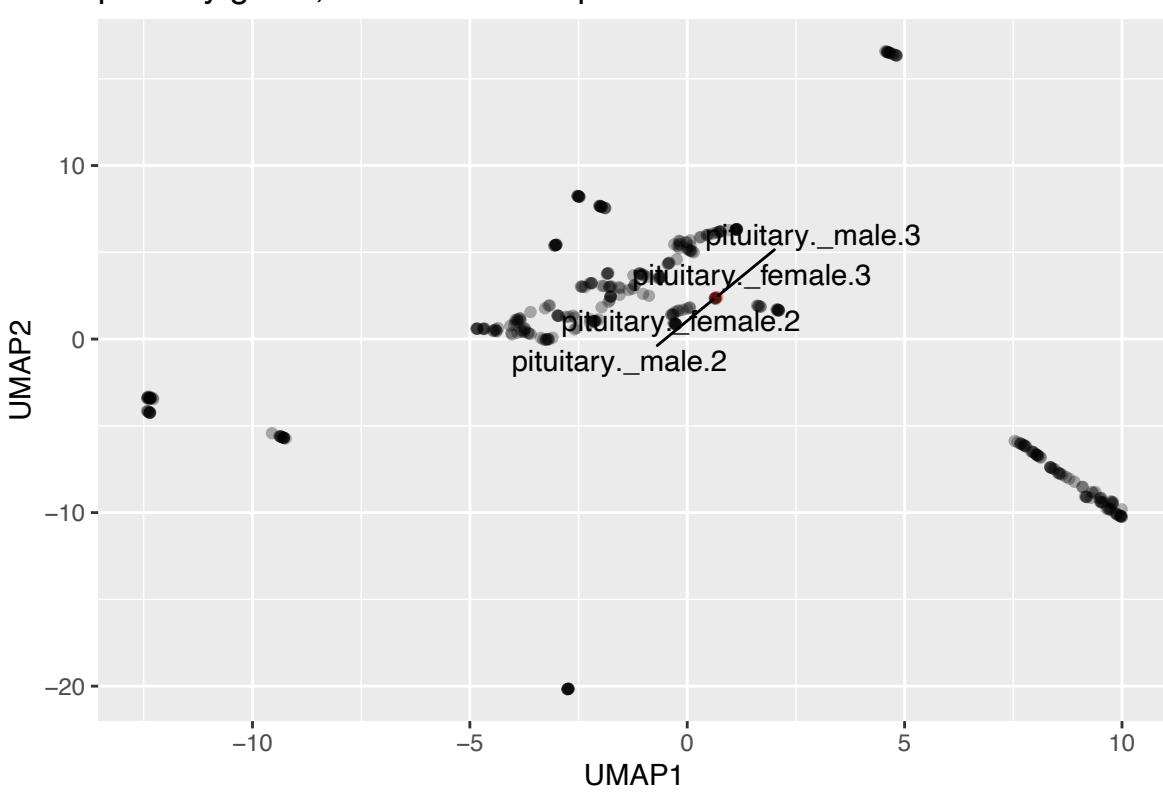
pineal gland



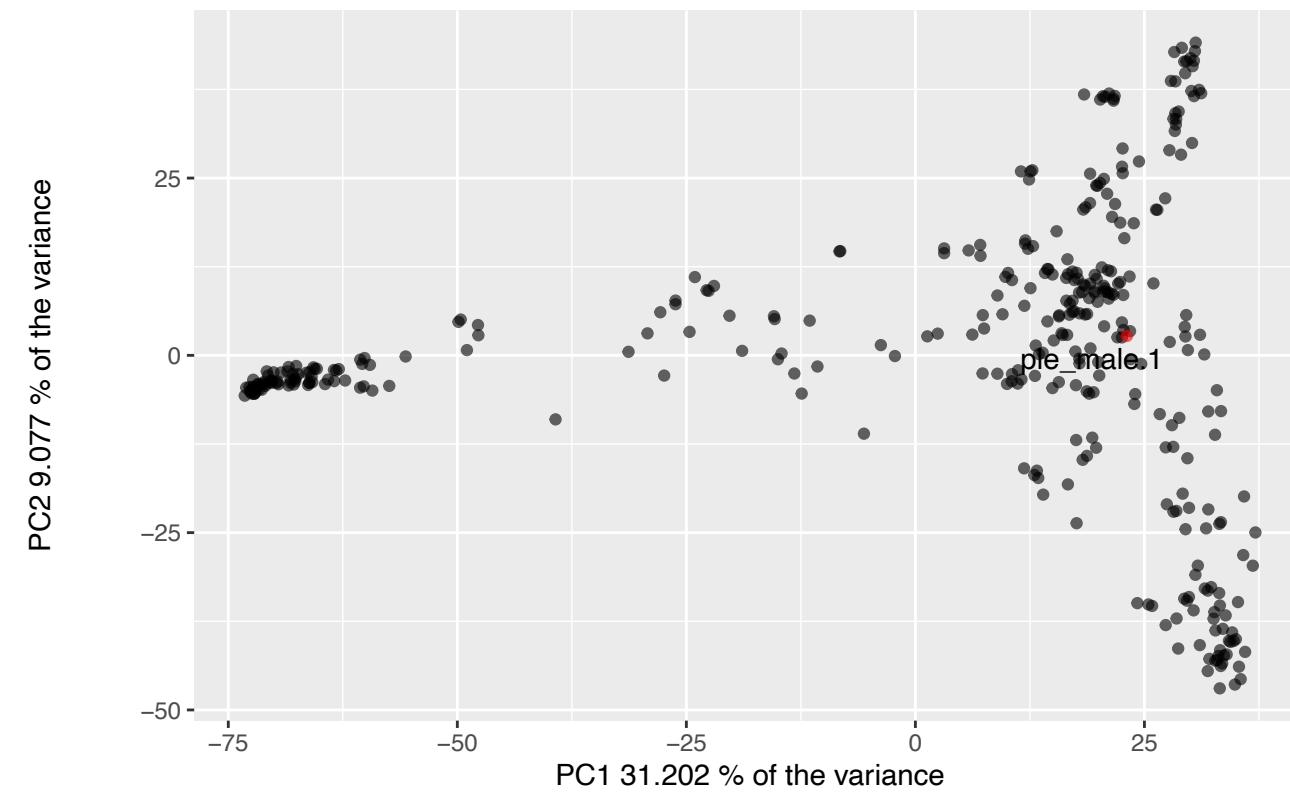
pituitary gland, PCA: TMM expression values



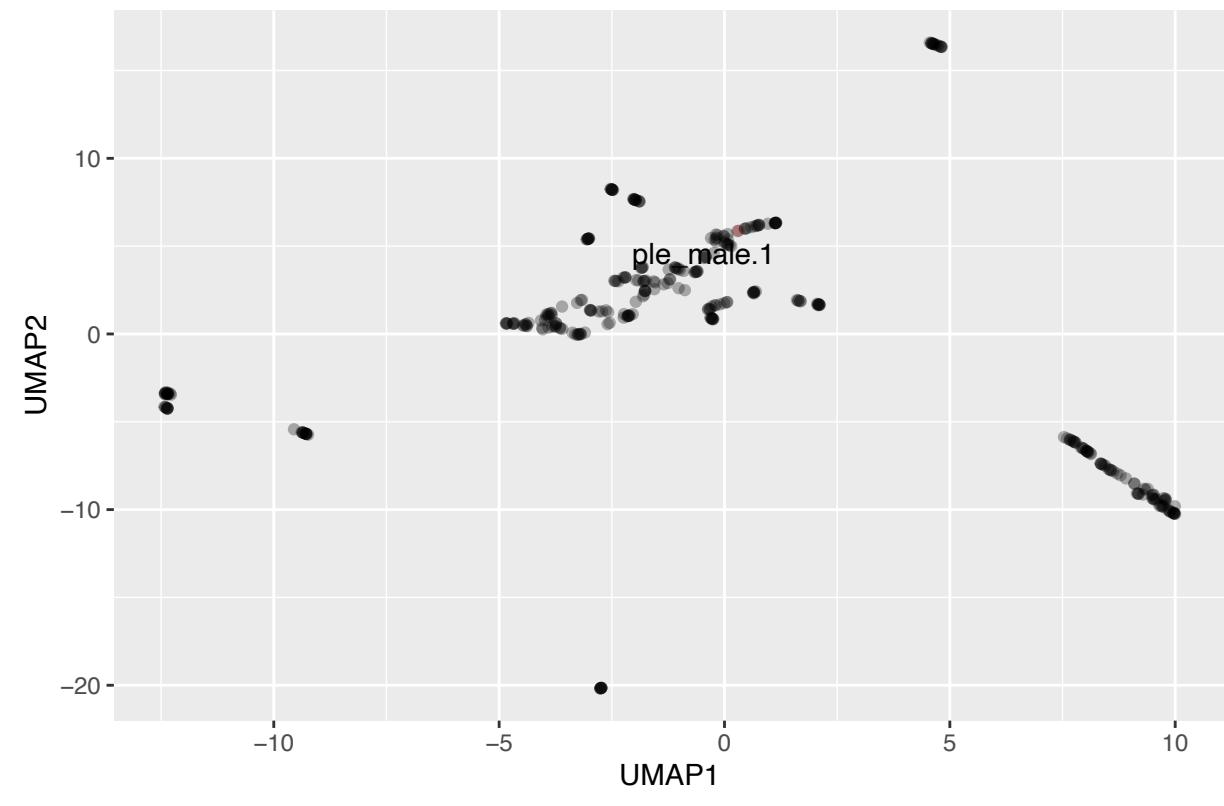
pituitary gland, UMAP: TMM expression values



pleura, PCA: TMM expression values



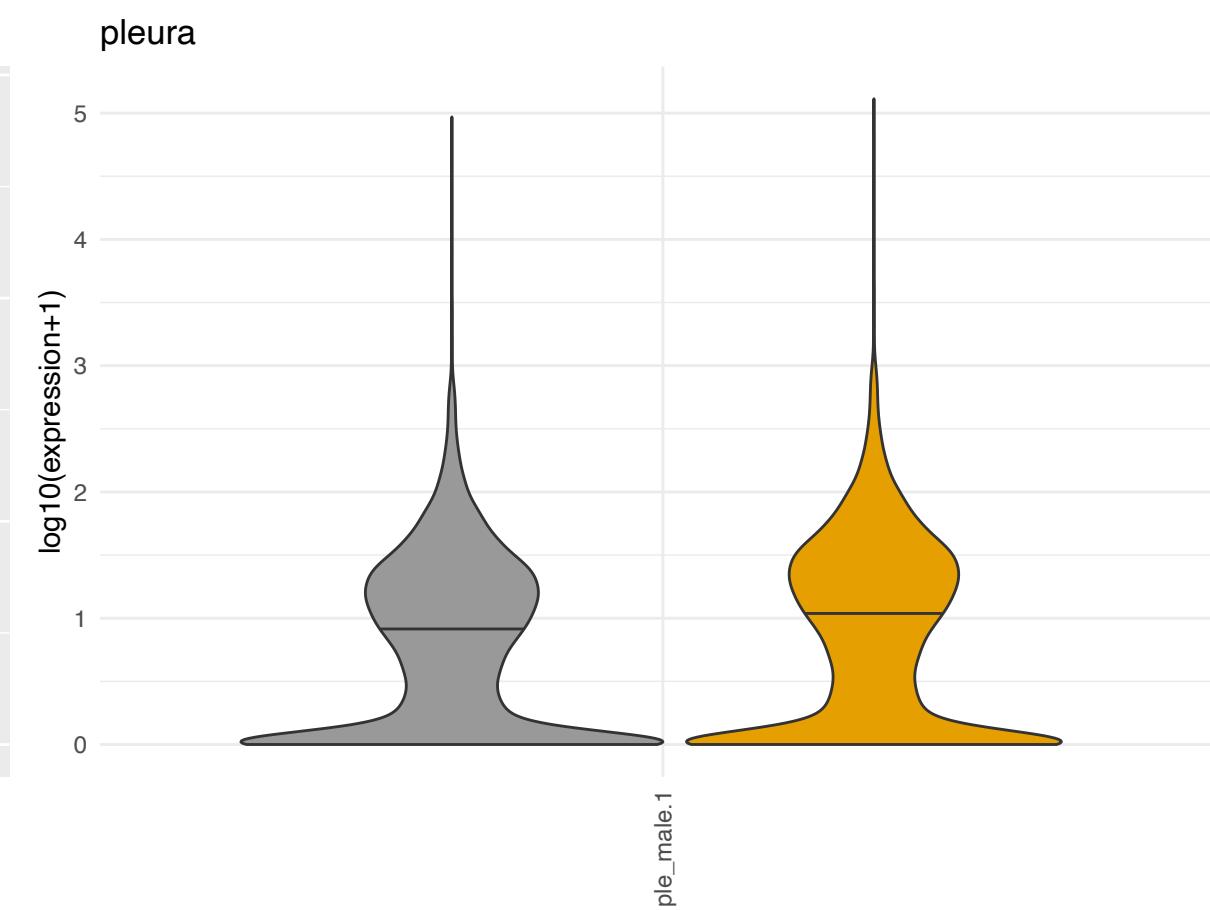
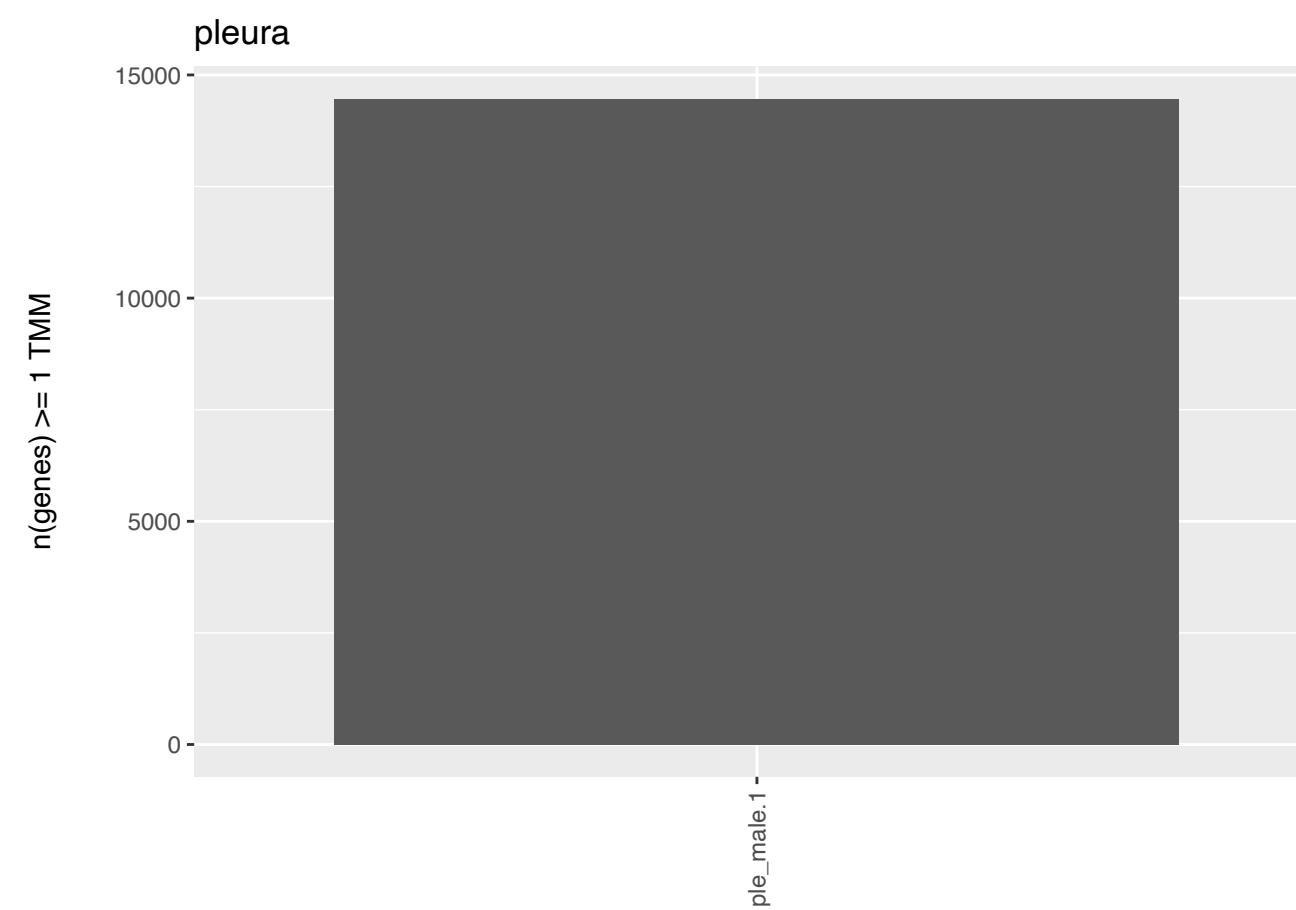
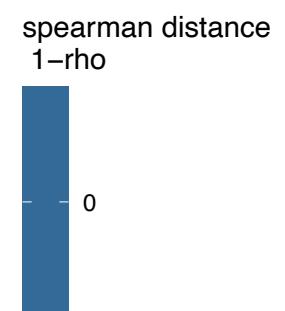
pleura, UMAP: TMM expression values



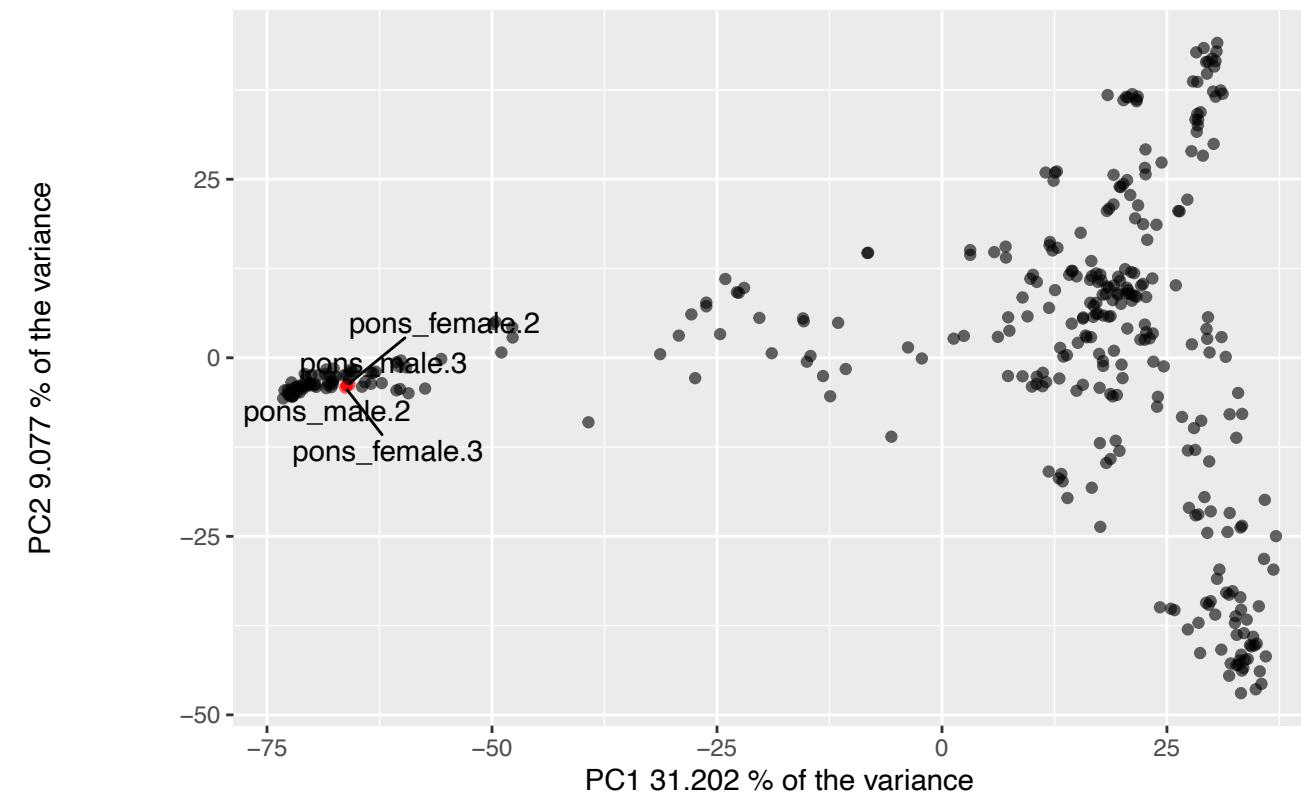
pleura pericardium abdominal adipose tissue artery aorta synovial tissue breast diaphragm vagus nerve penis



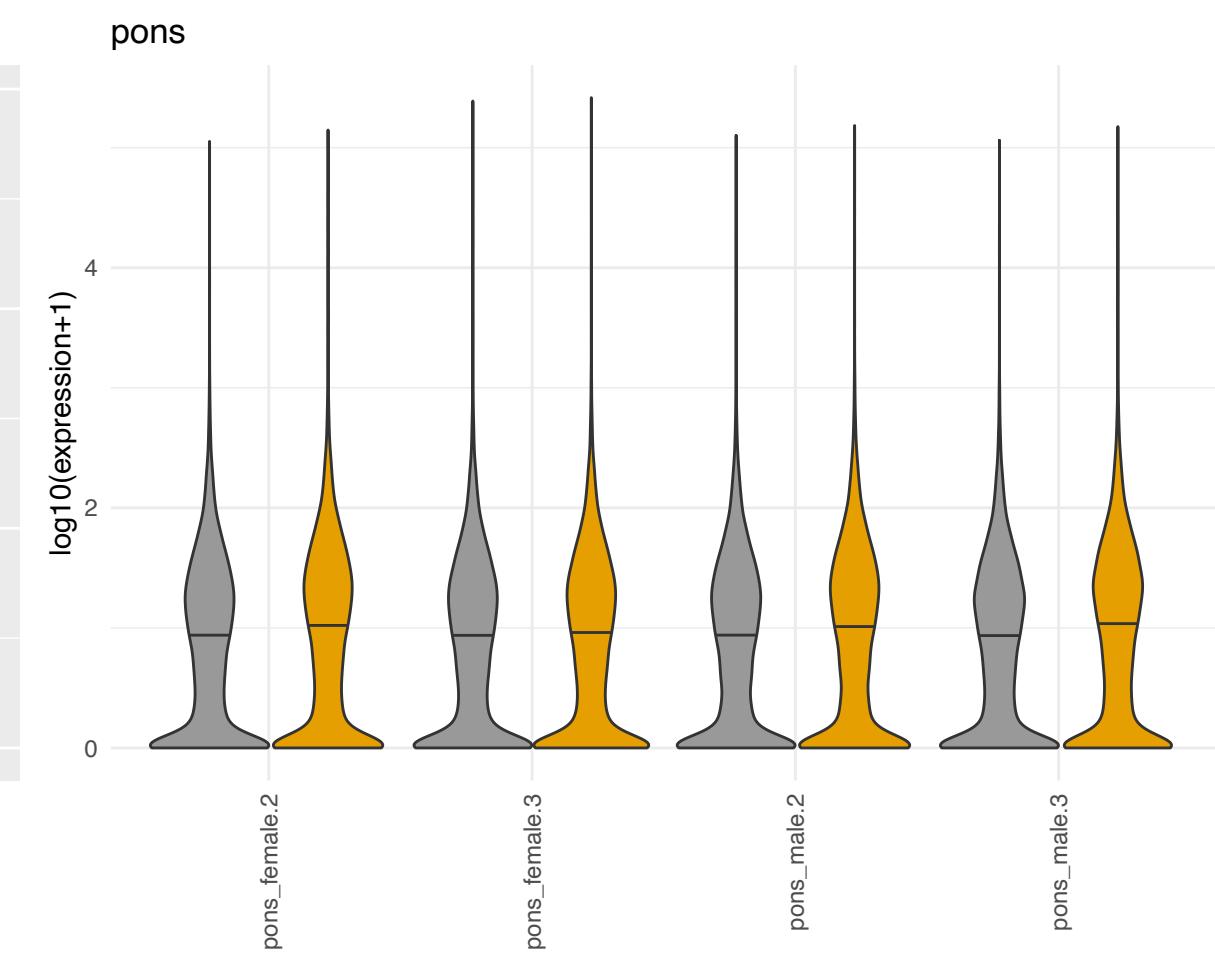
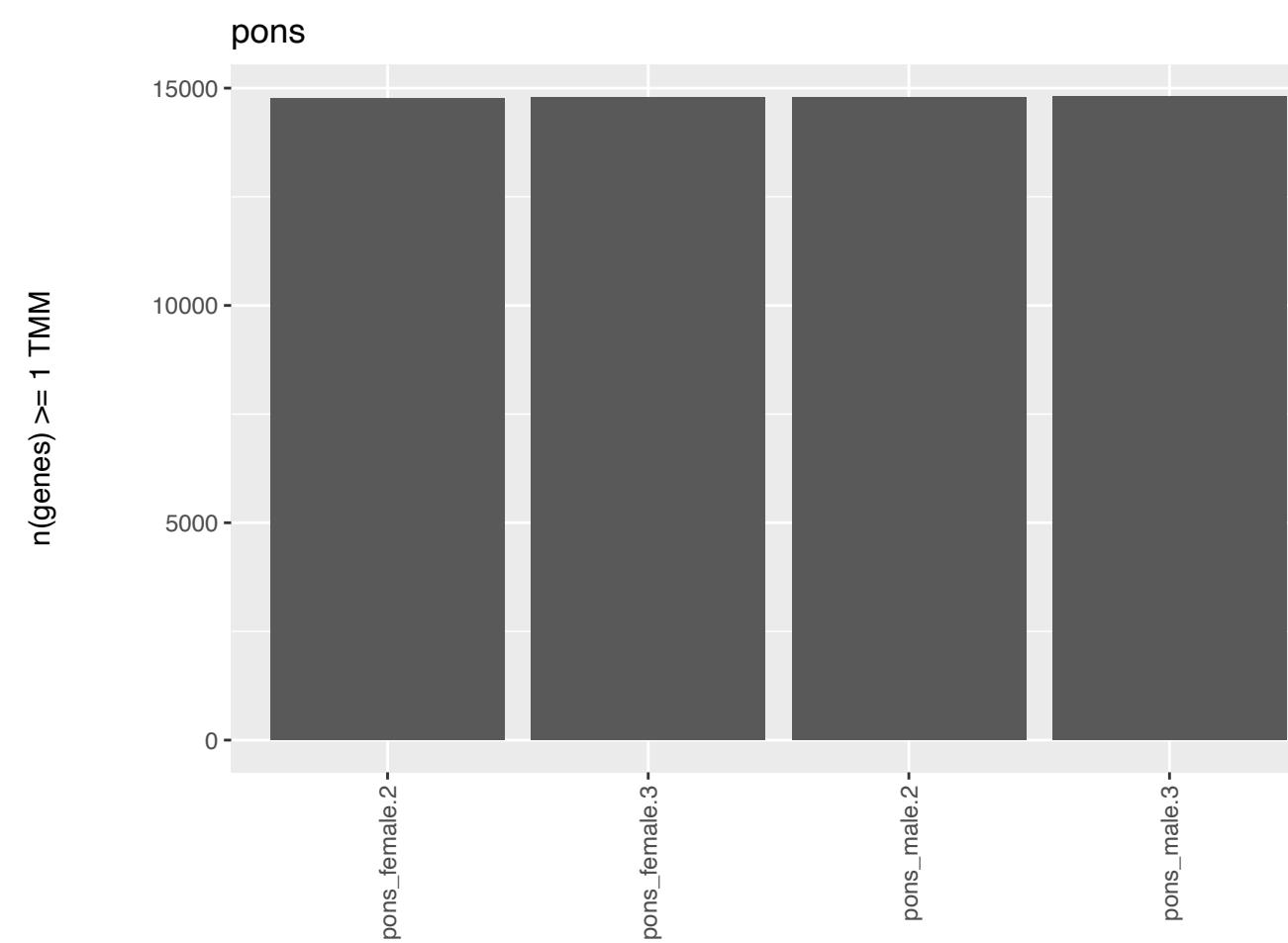
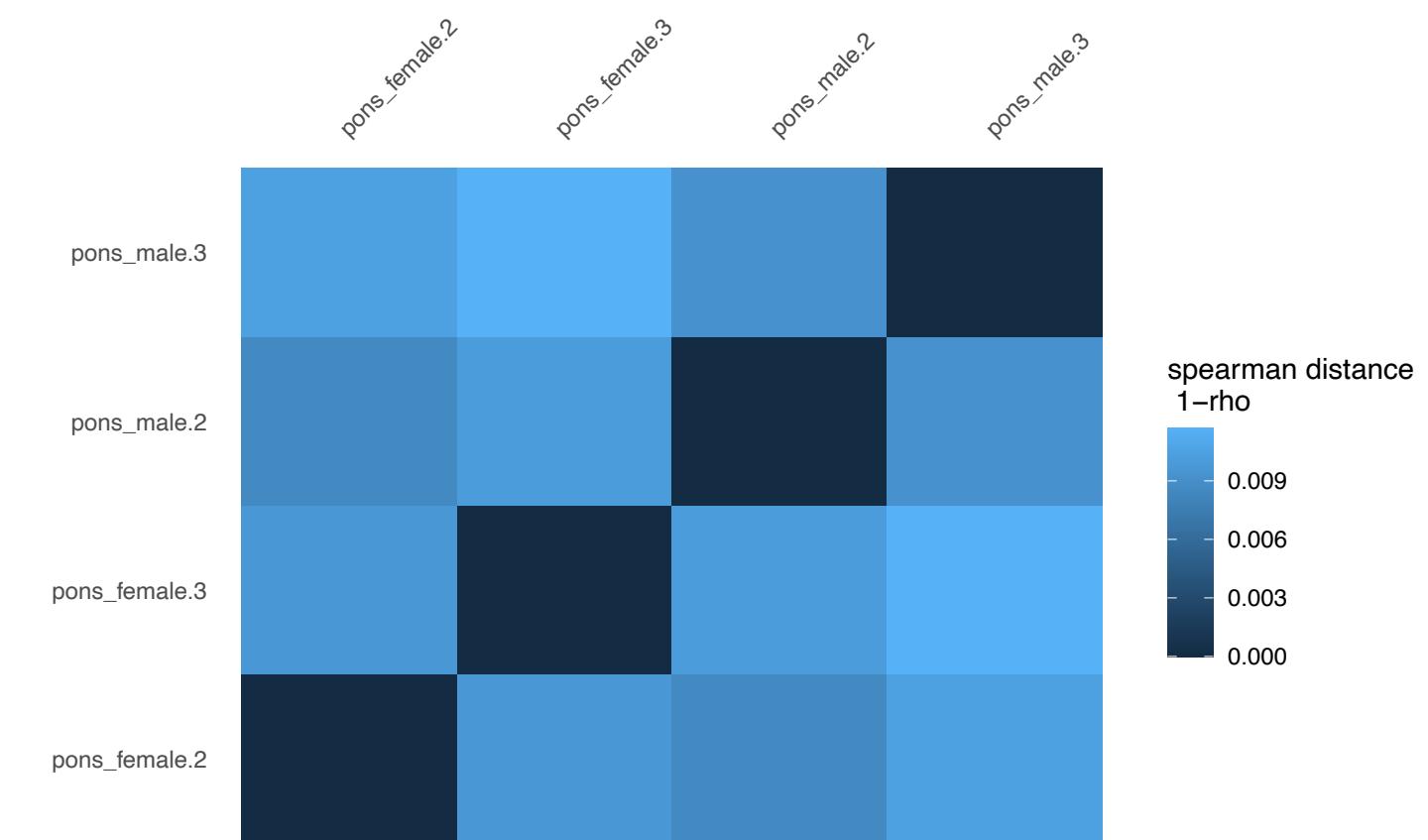
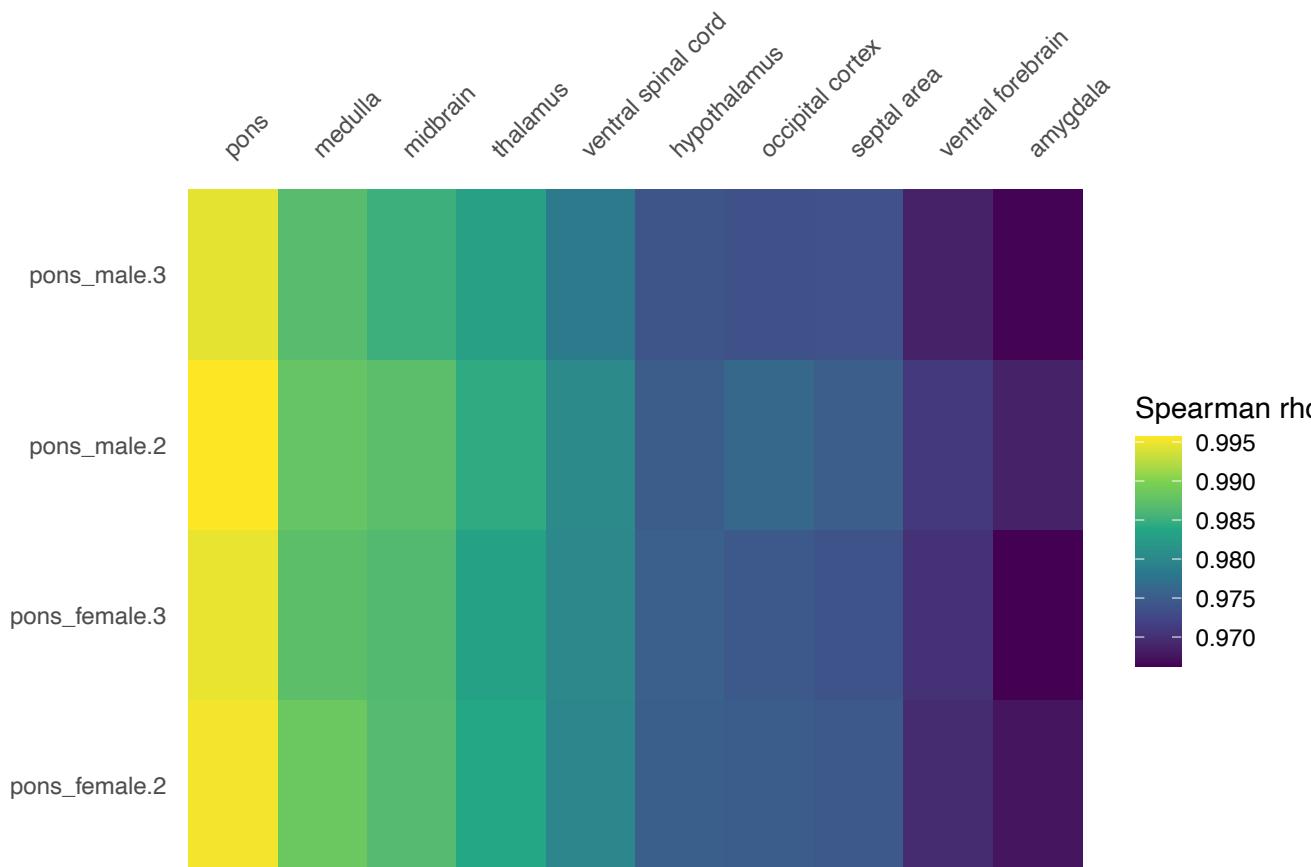
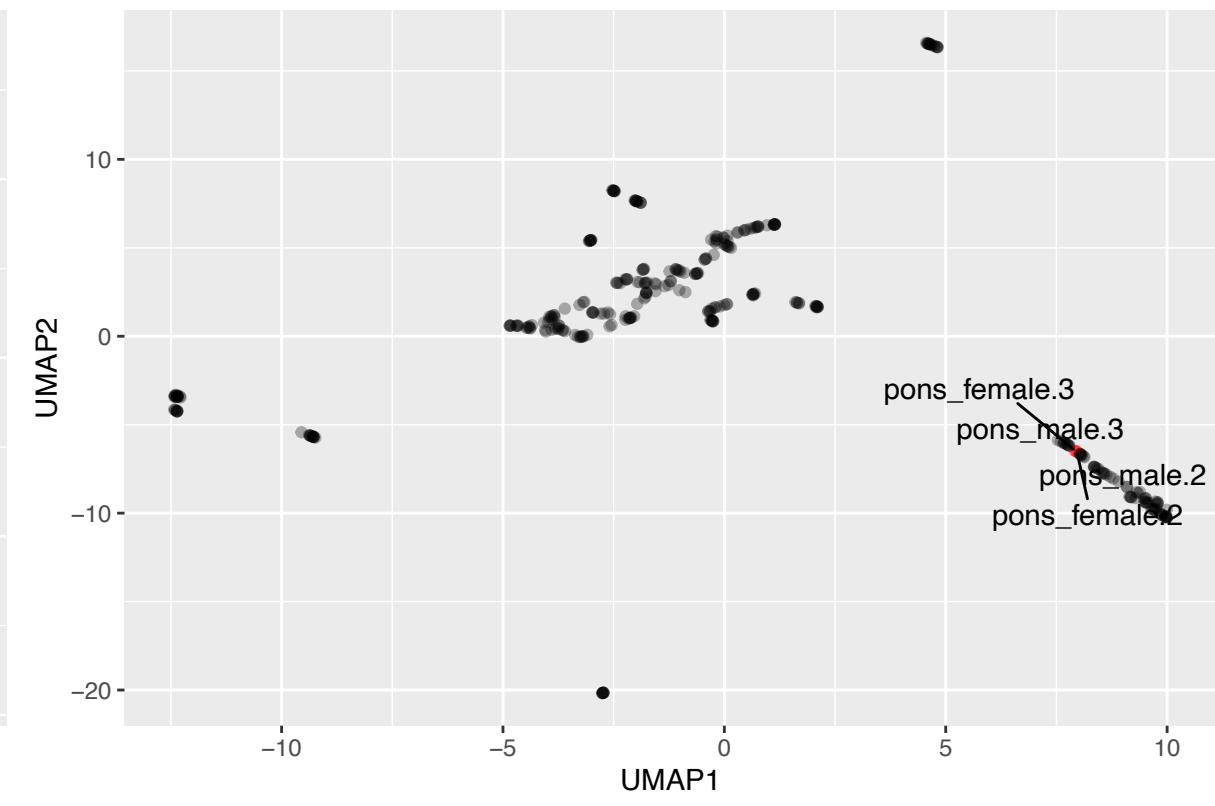
ple_male.1



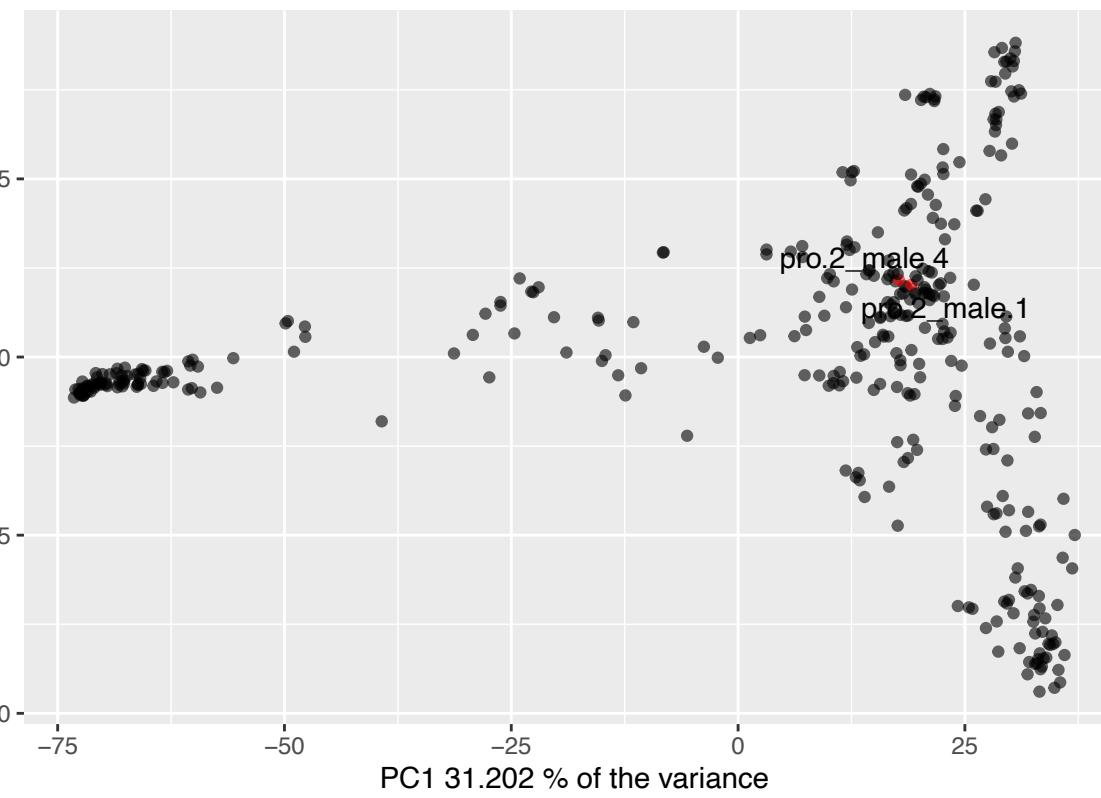
pons, PCA: TMM expression values



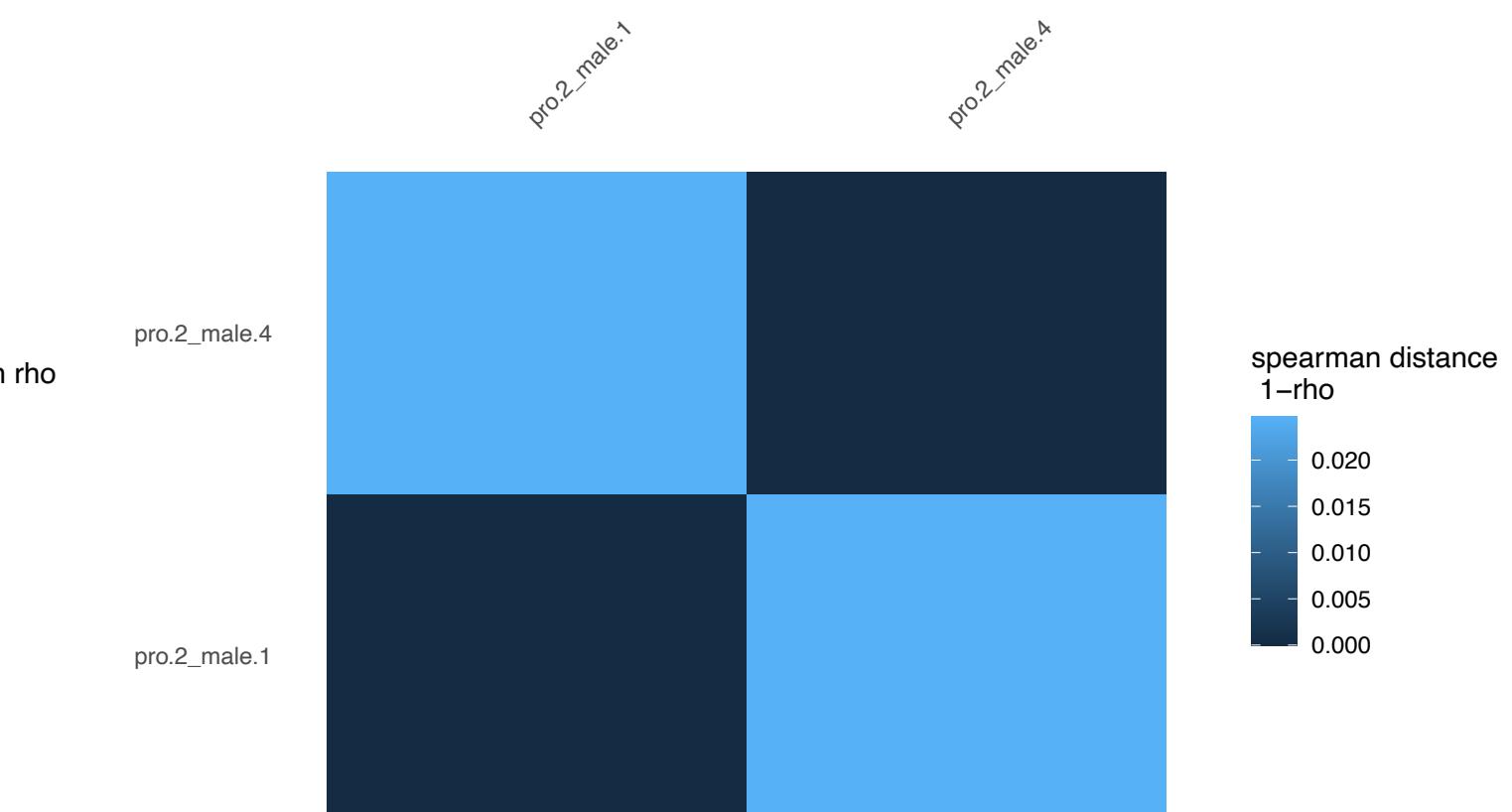
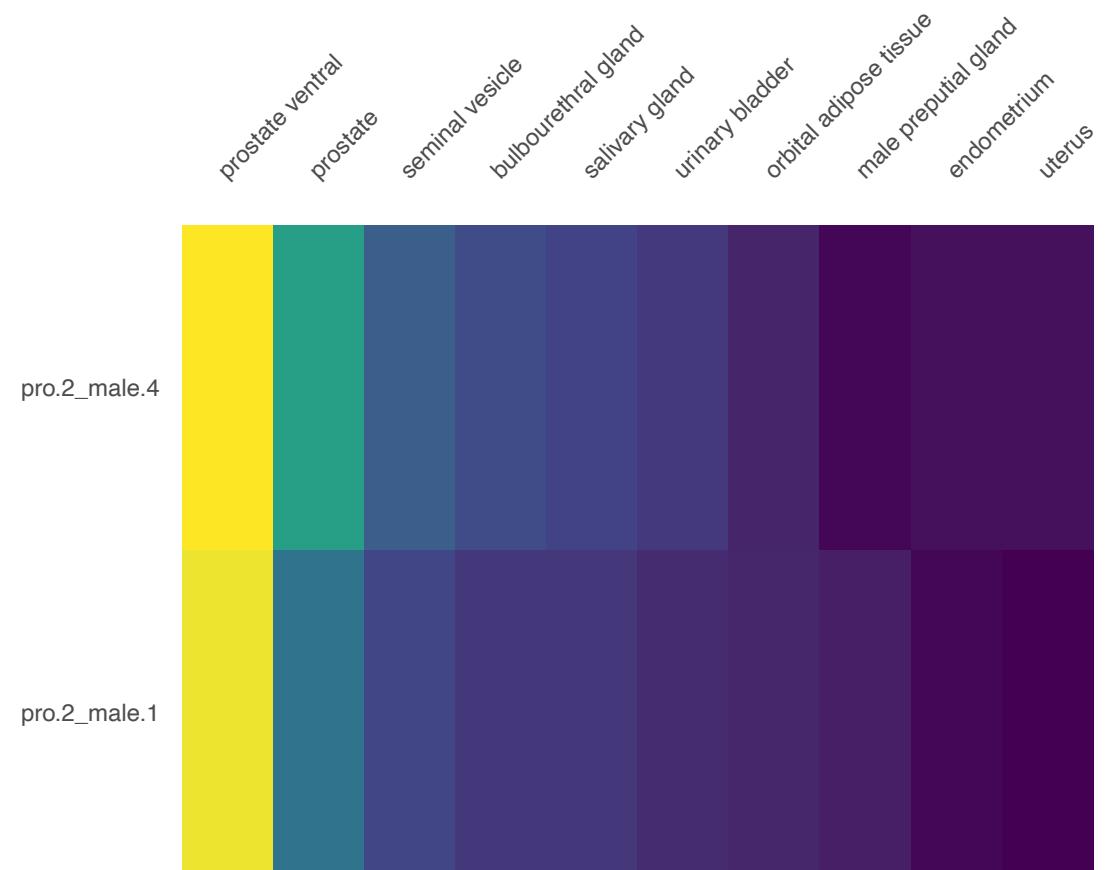
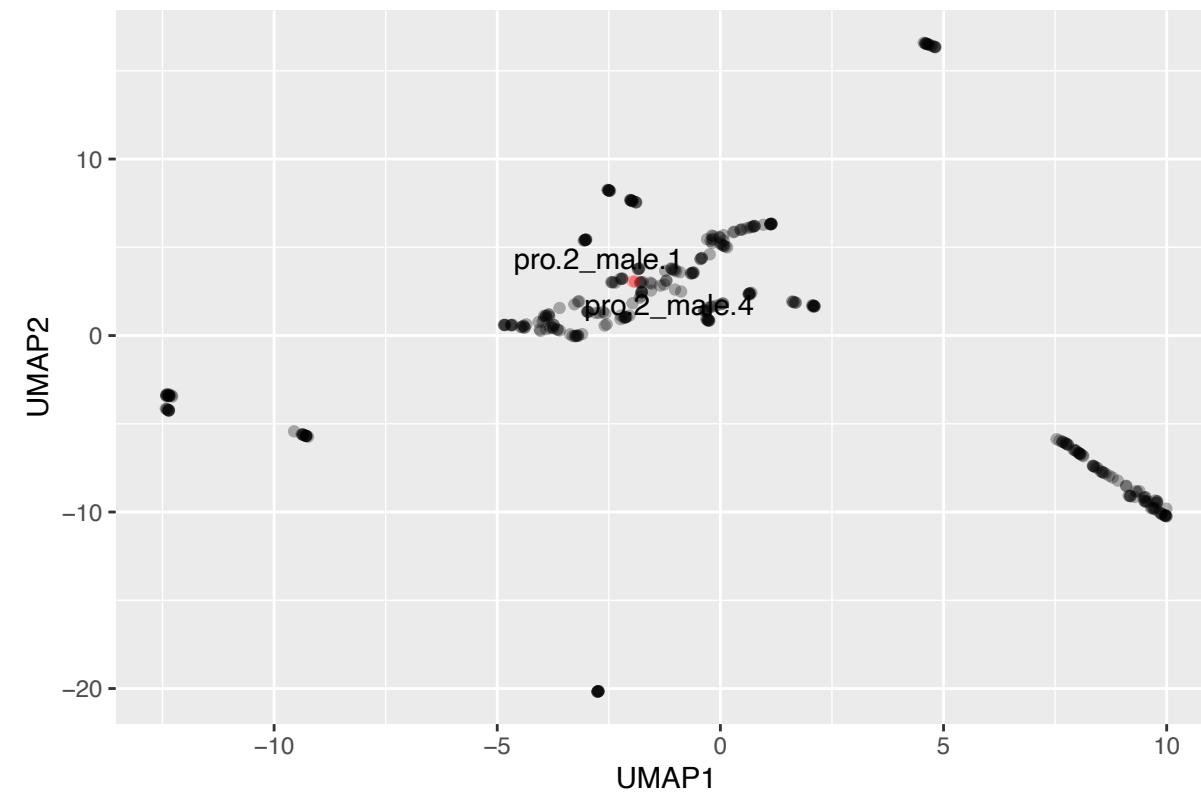
pons, UMAP: TMM expression values



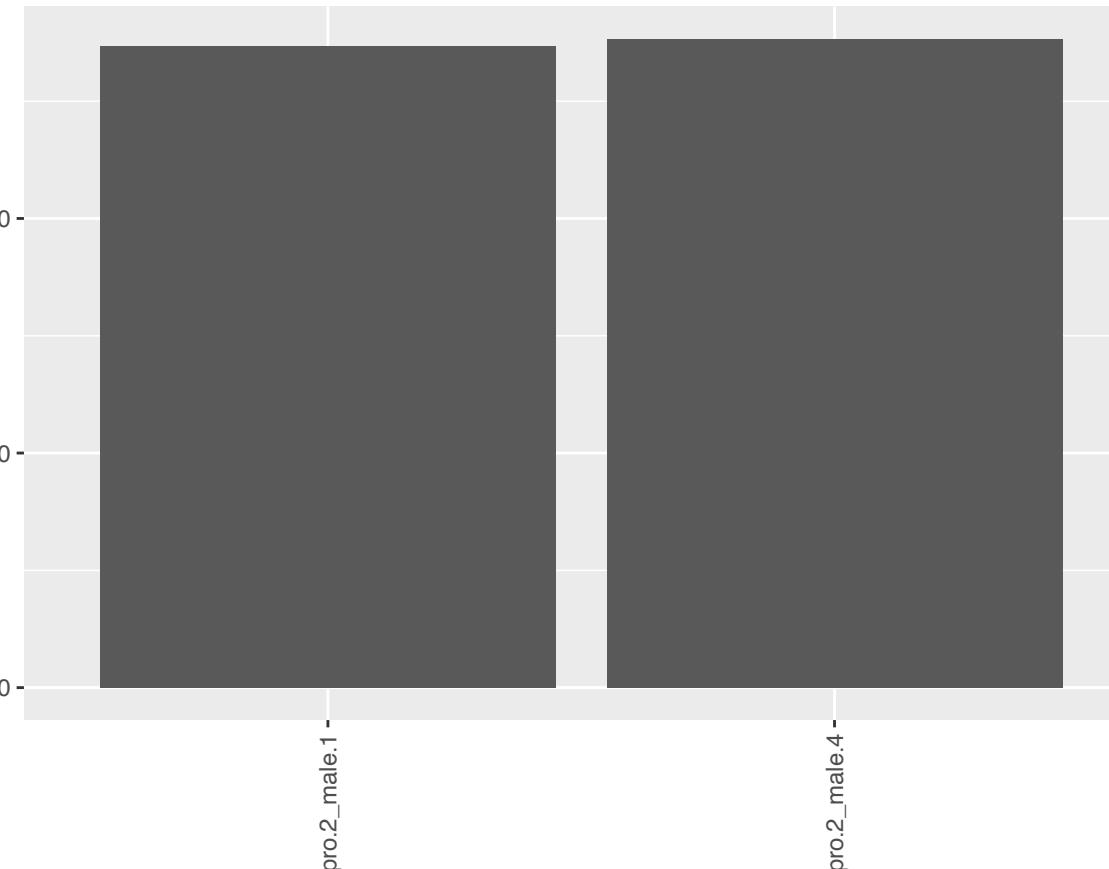
prostate ventral, PCA: TMM expression values



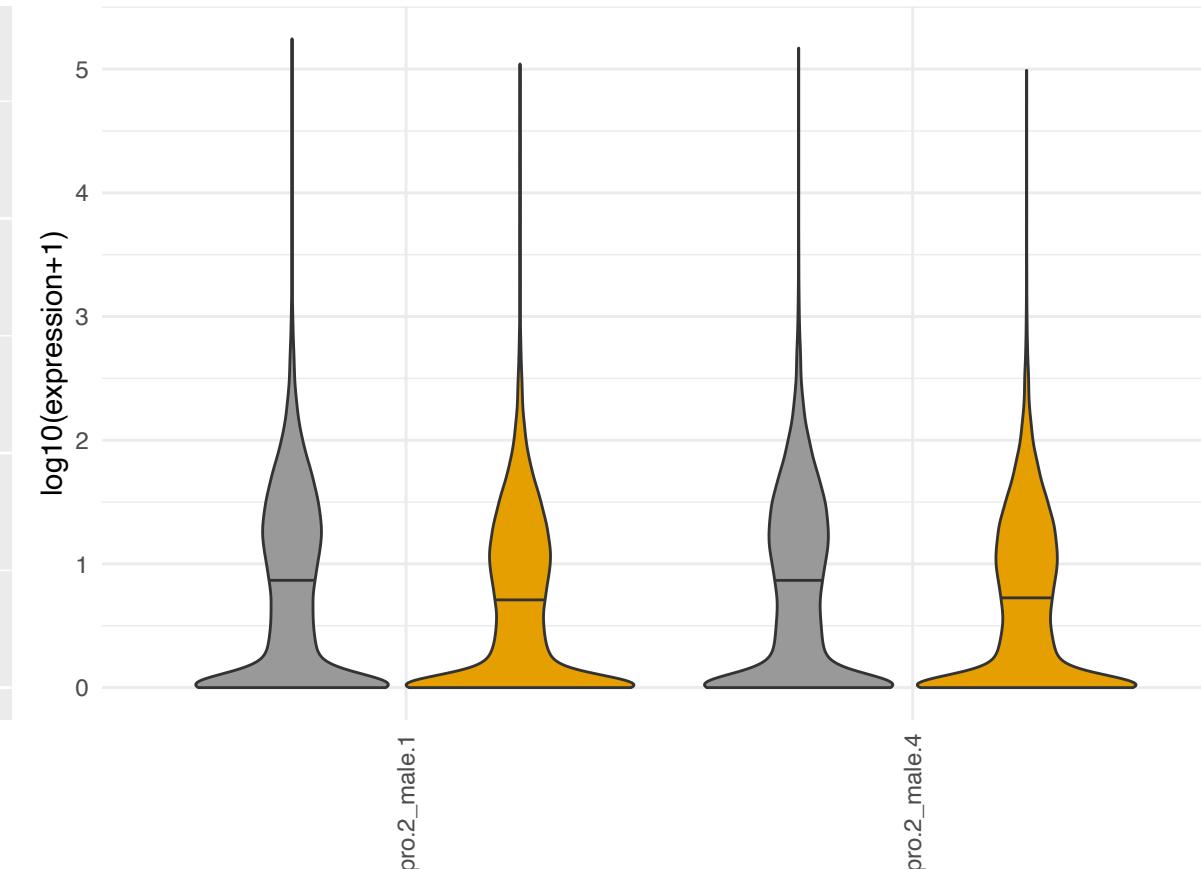
prostate ventral, UMAP: TMM expression values



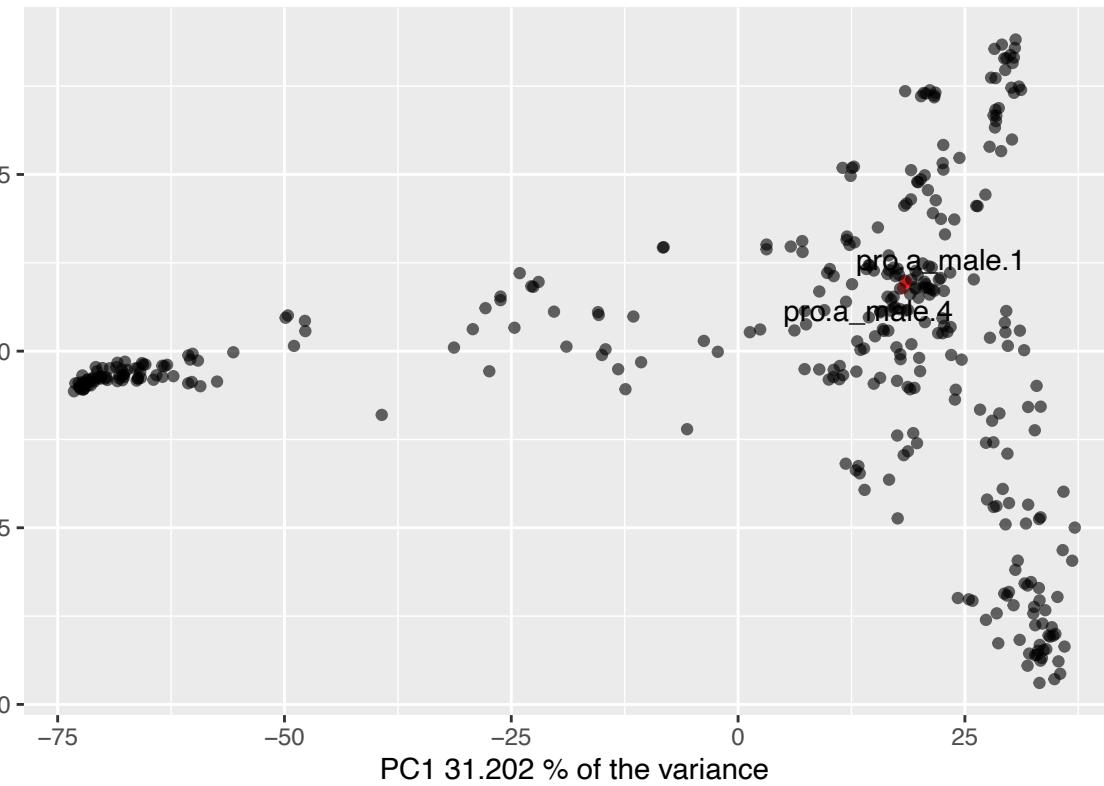
prostate ventral



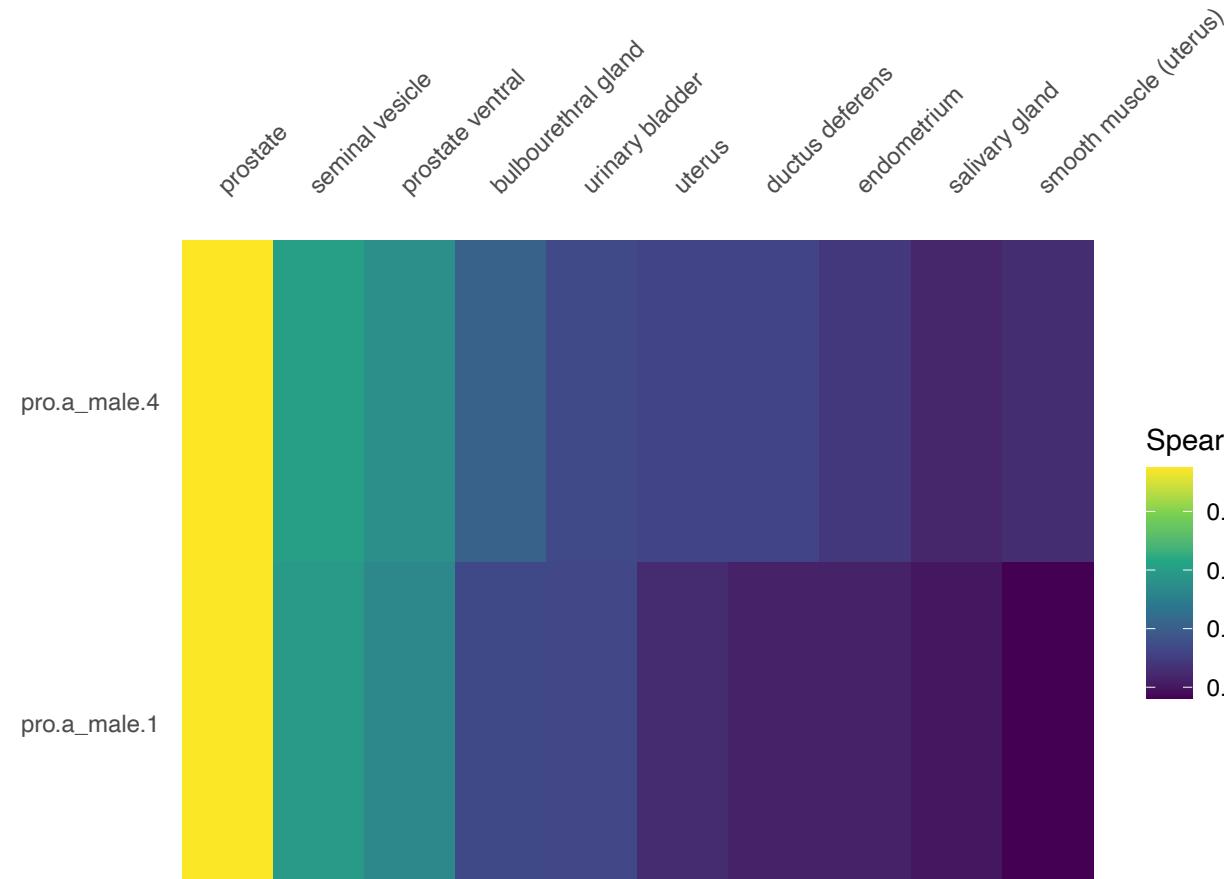
prostate ventral



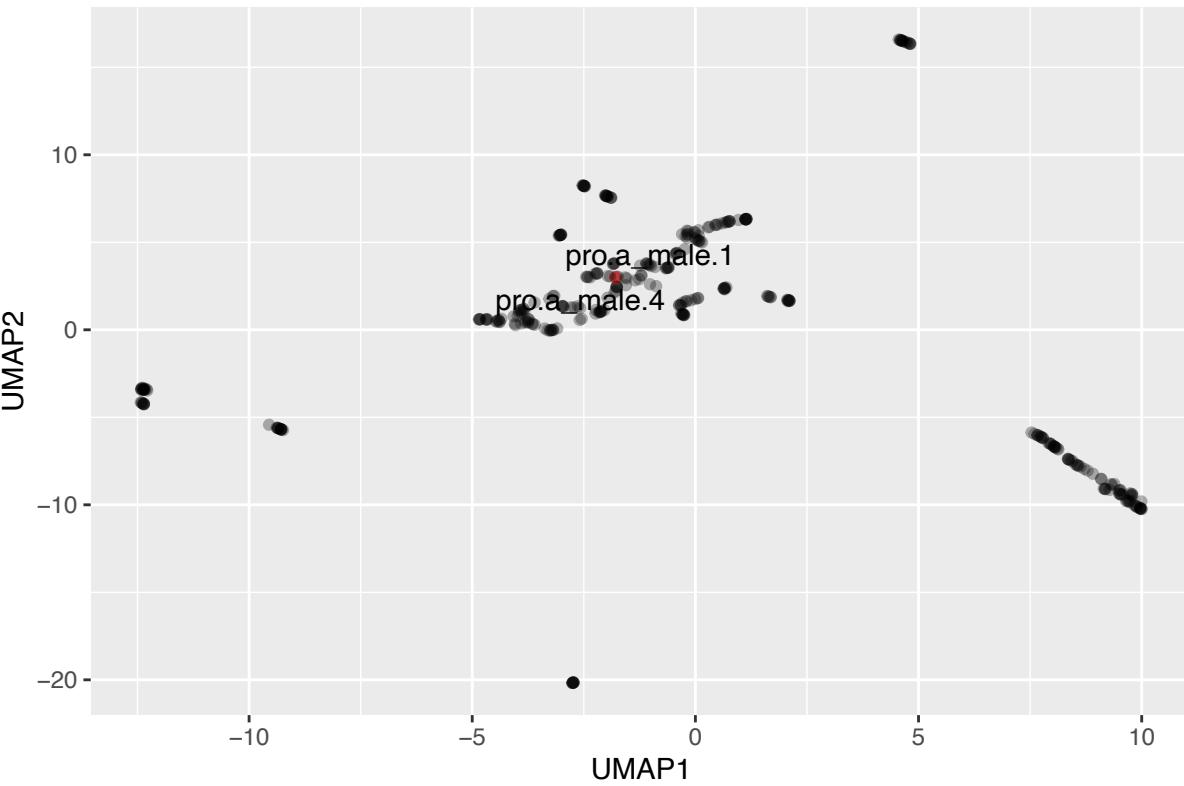
prostate, PCA: TMM expression values



Tissue group to sample correlation

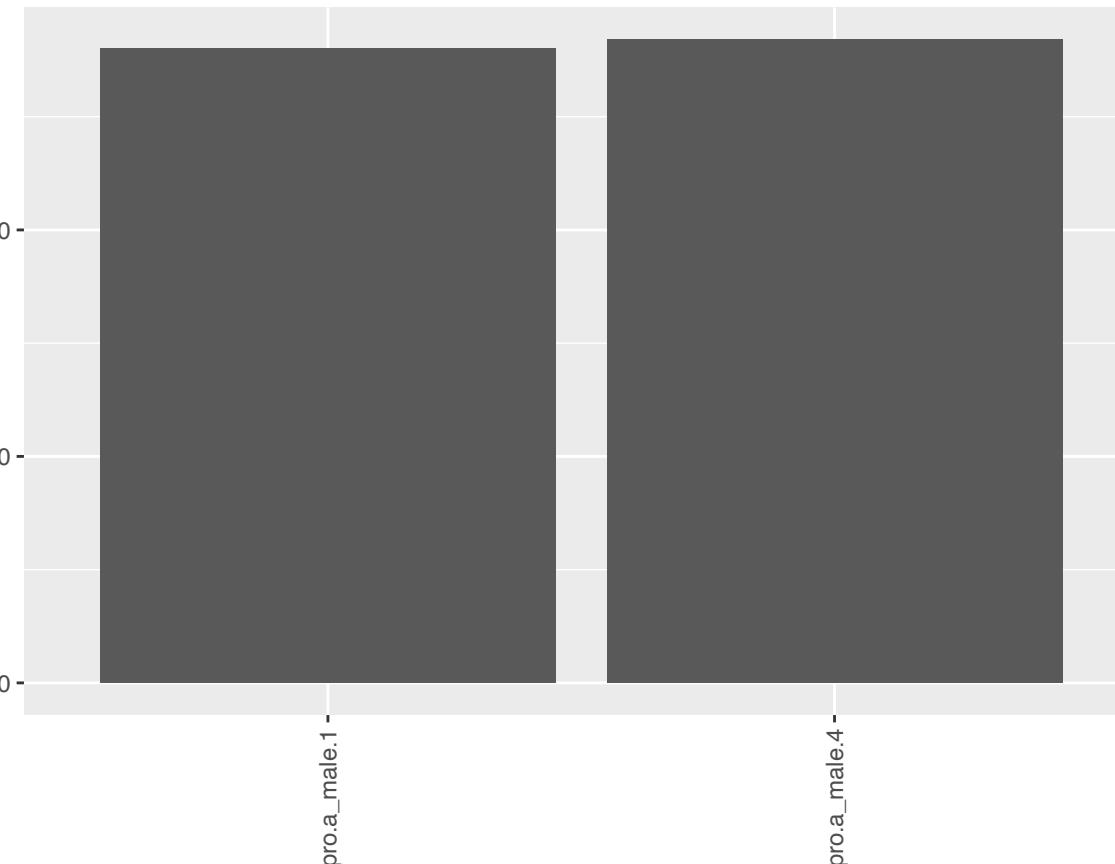


prostate, UMAP: TMM expression values

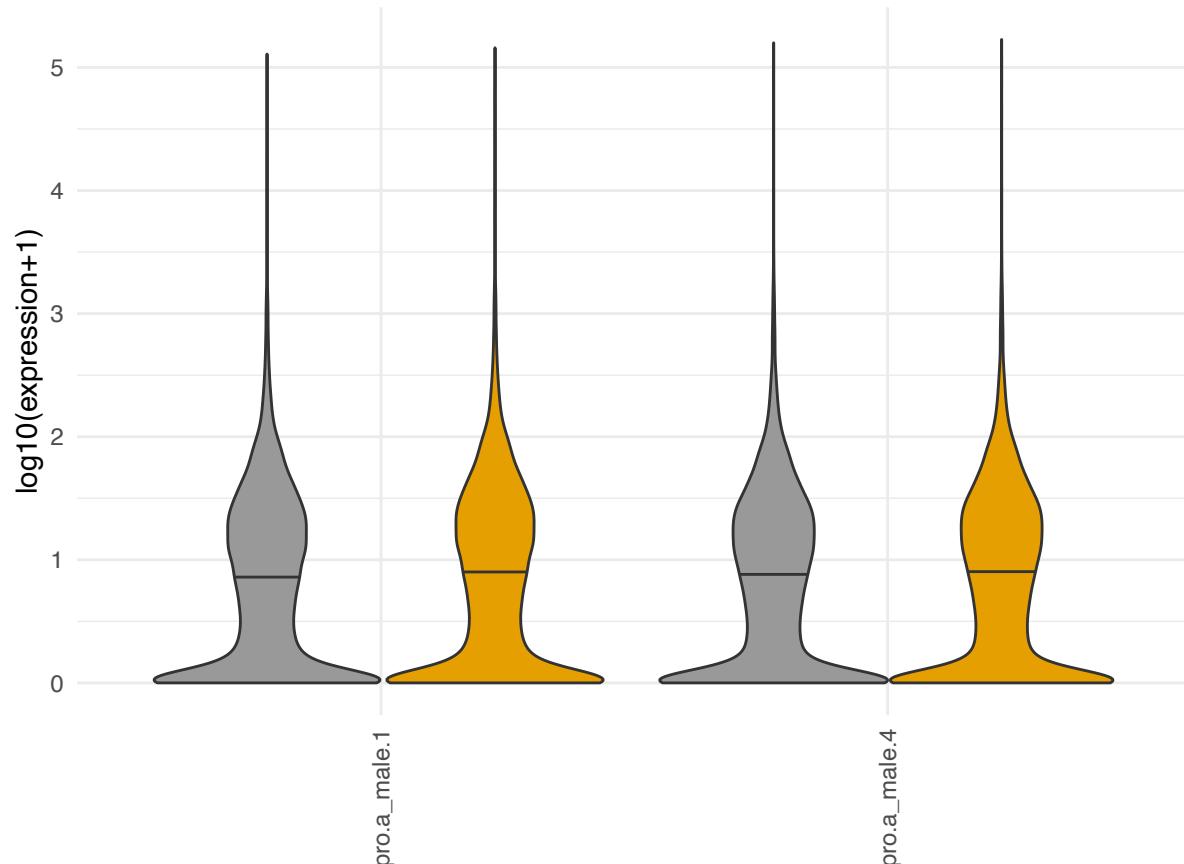


pro.a_male.1
pro.a_male.4

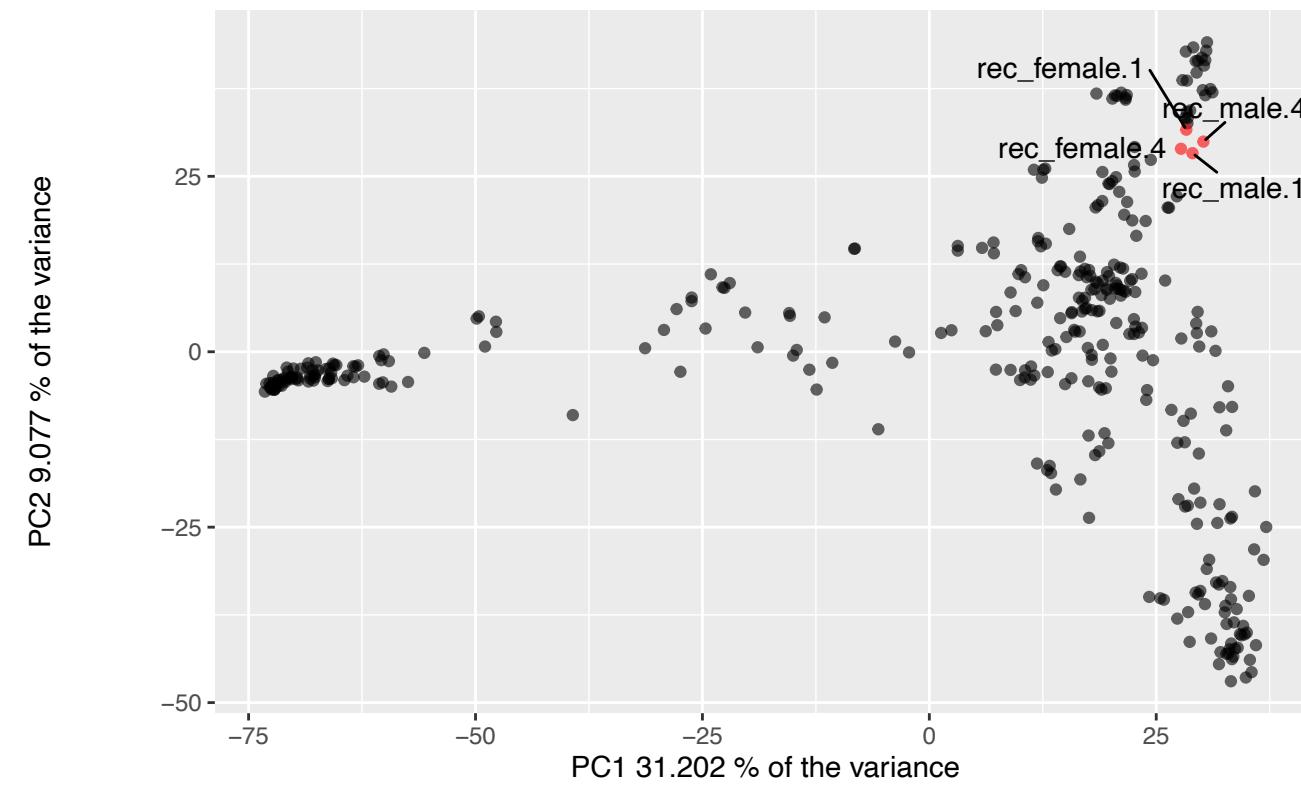
prostate



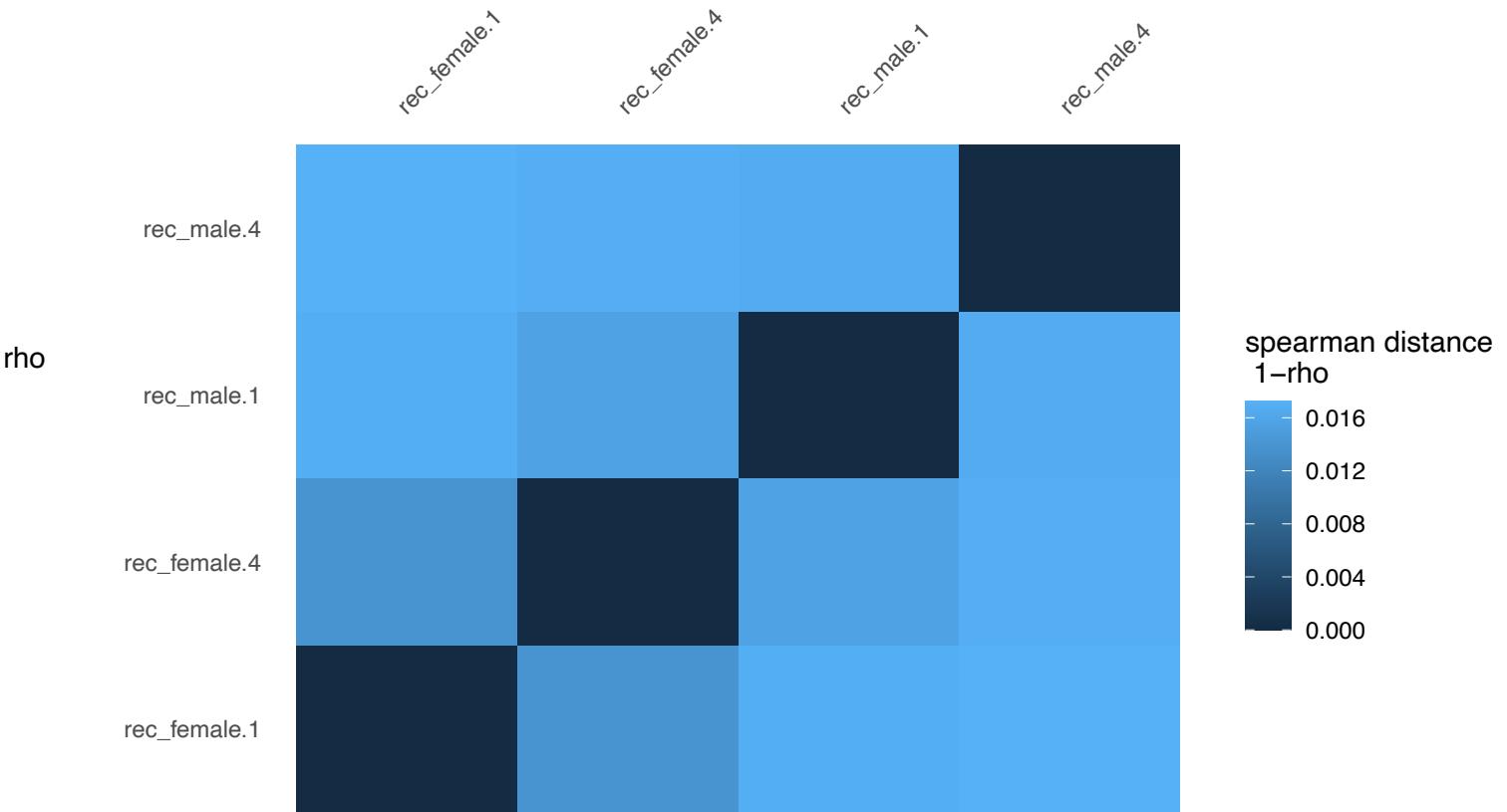
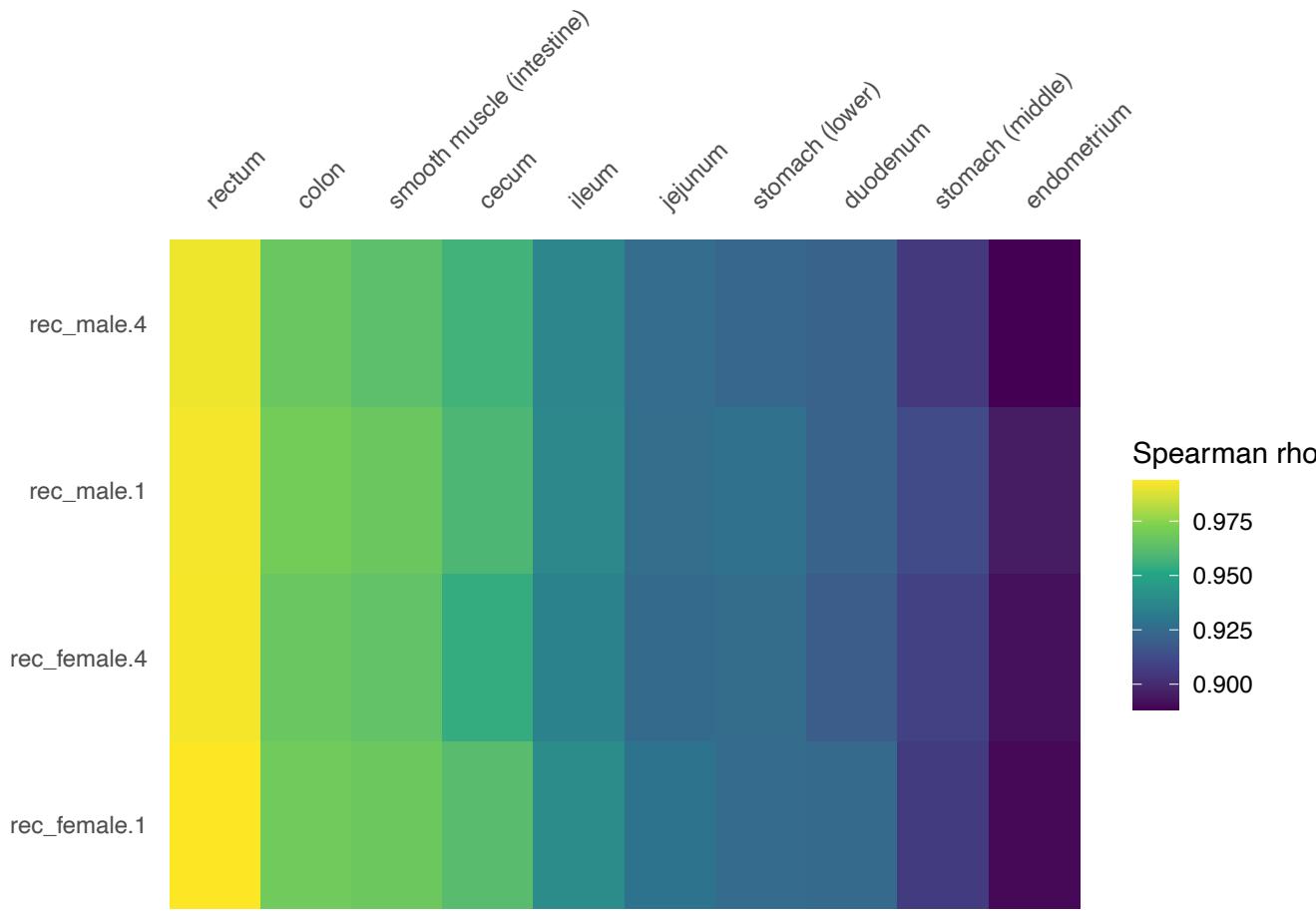
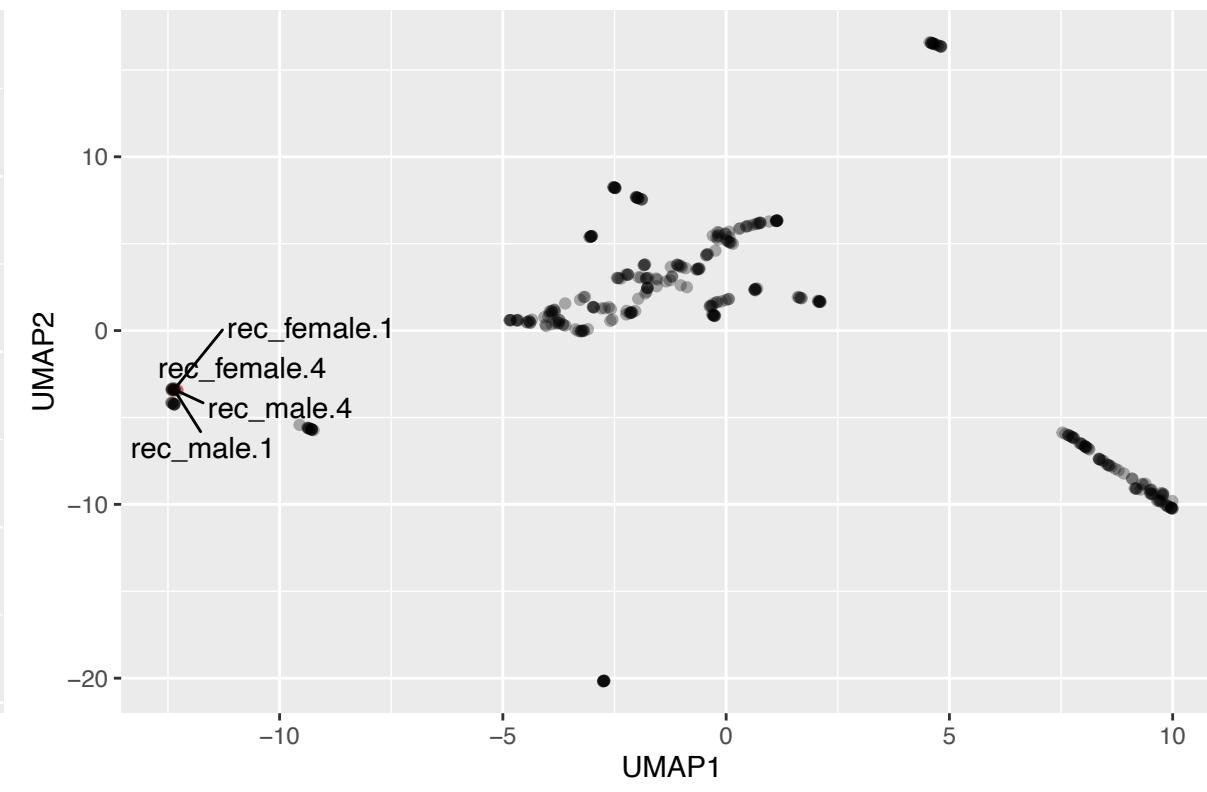
prostate



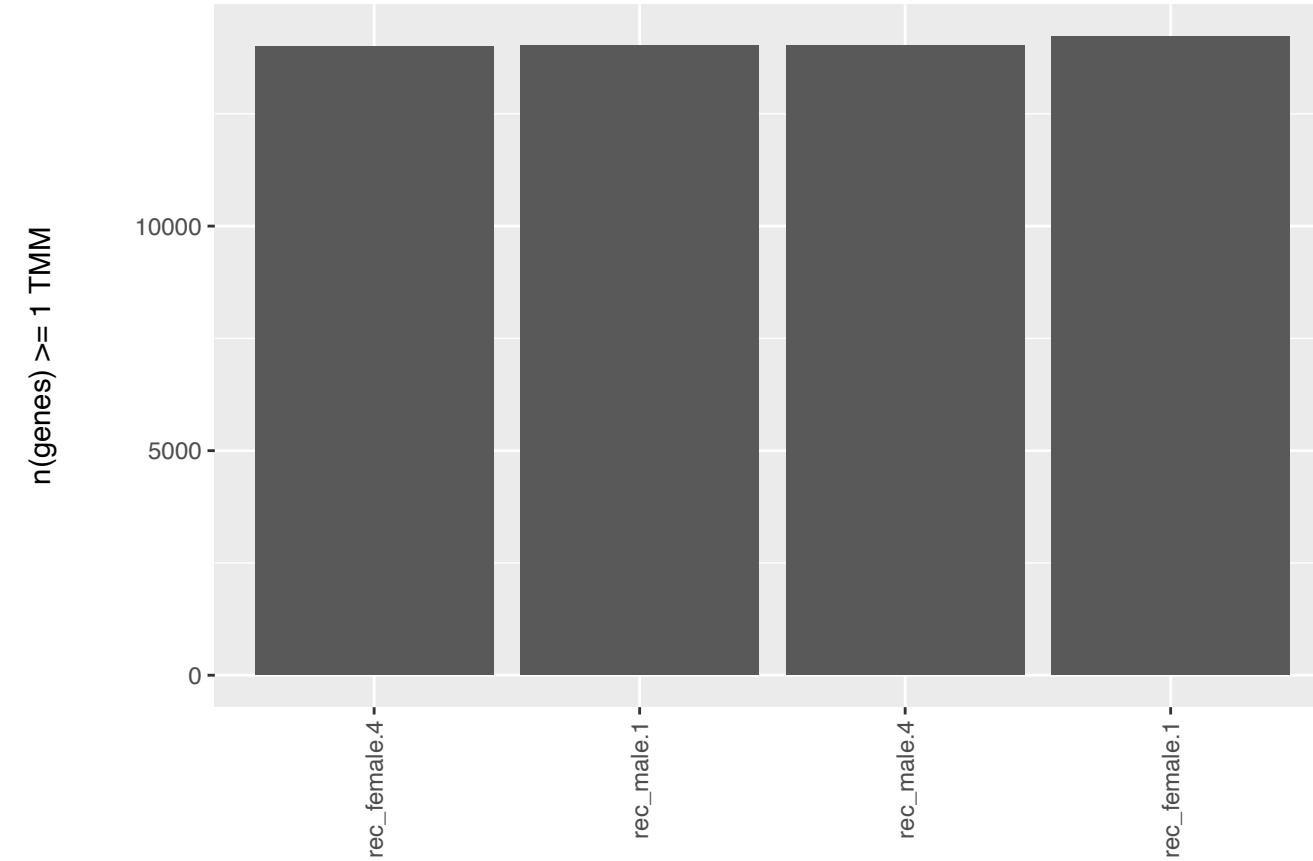
rectum, PCA: TMM expression values



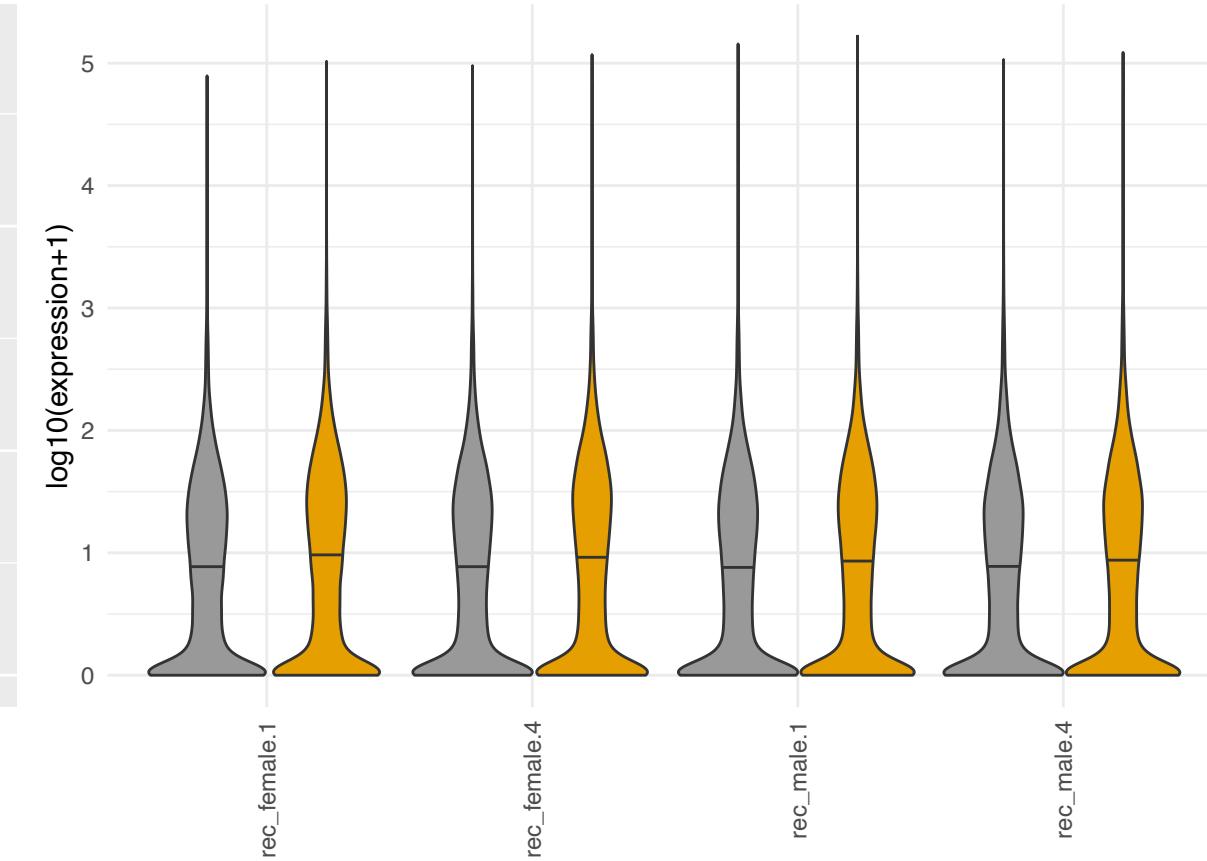
rectum, UMAP: TMM expression values



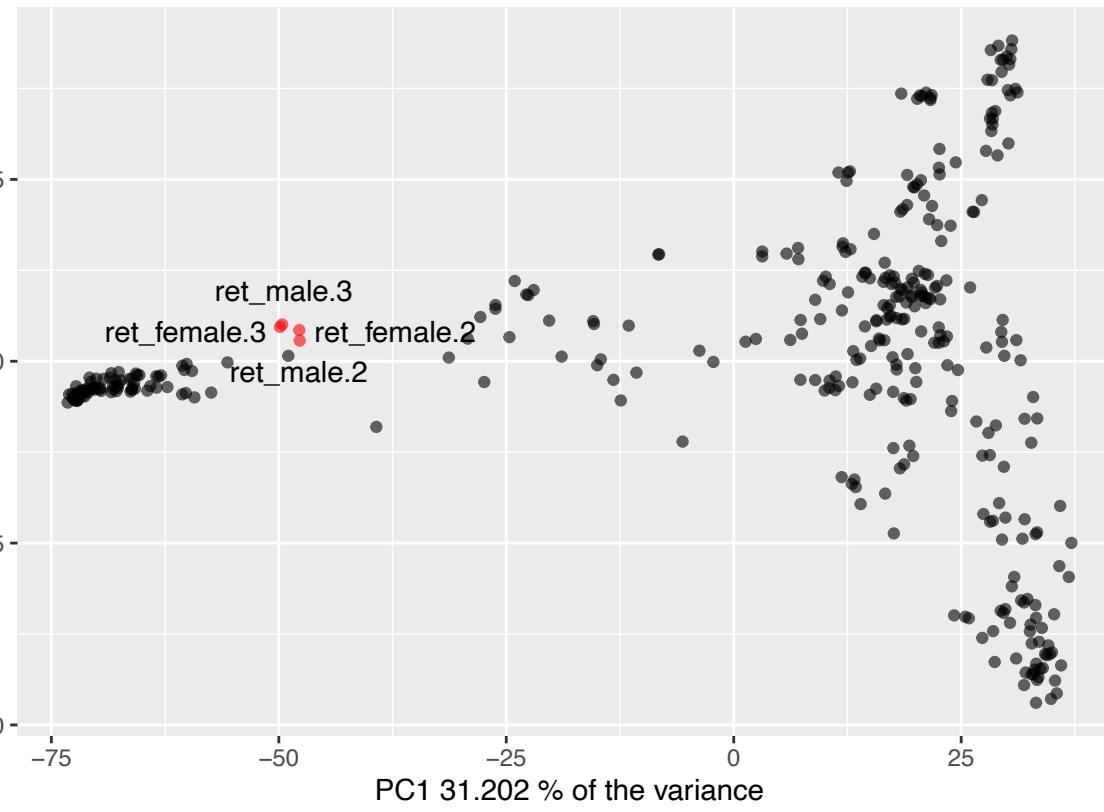
rectum



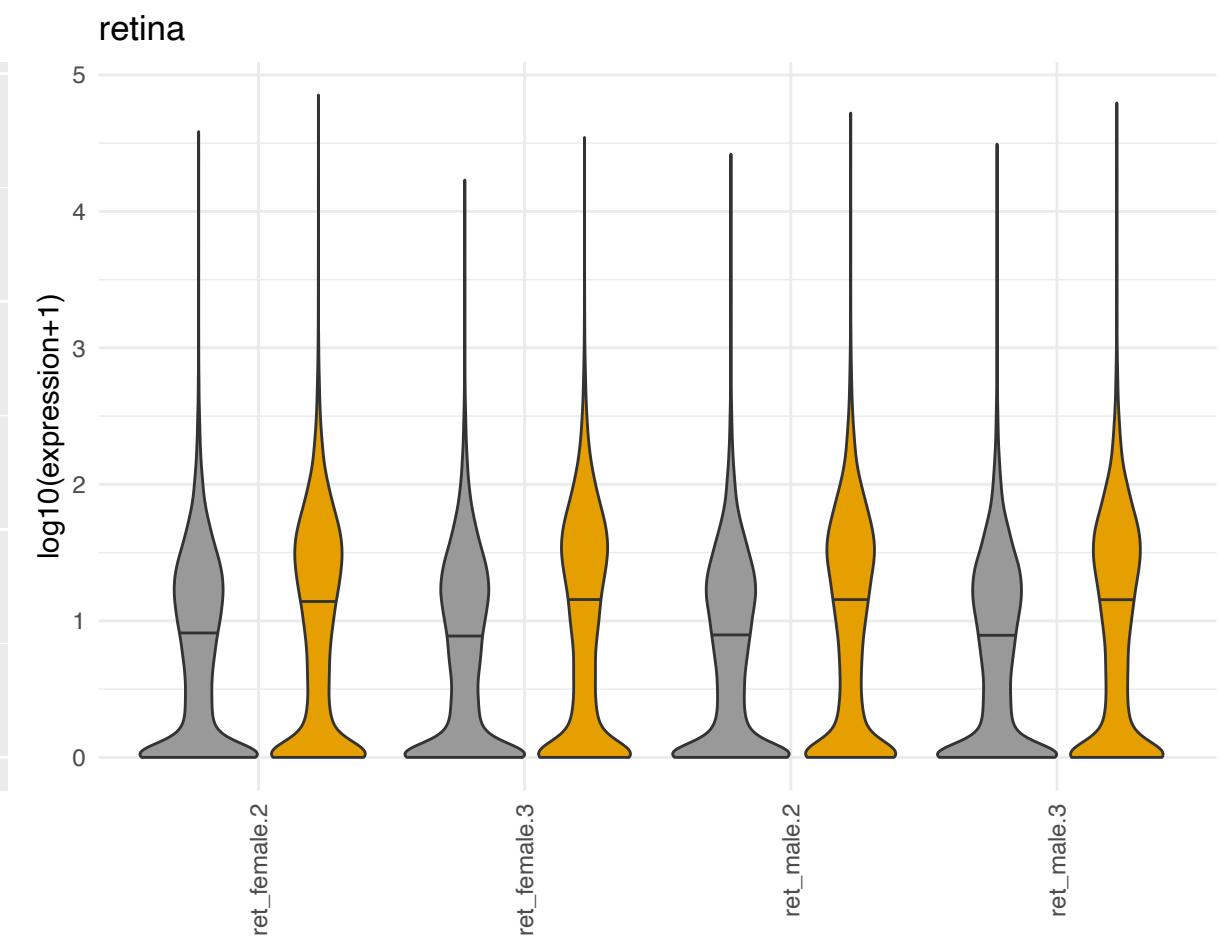
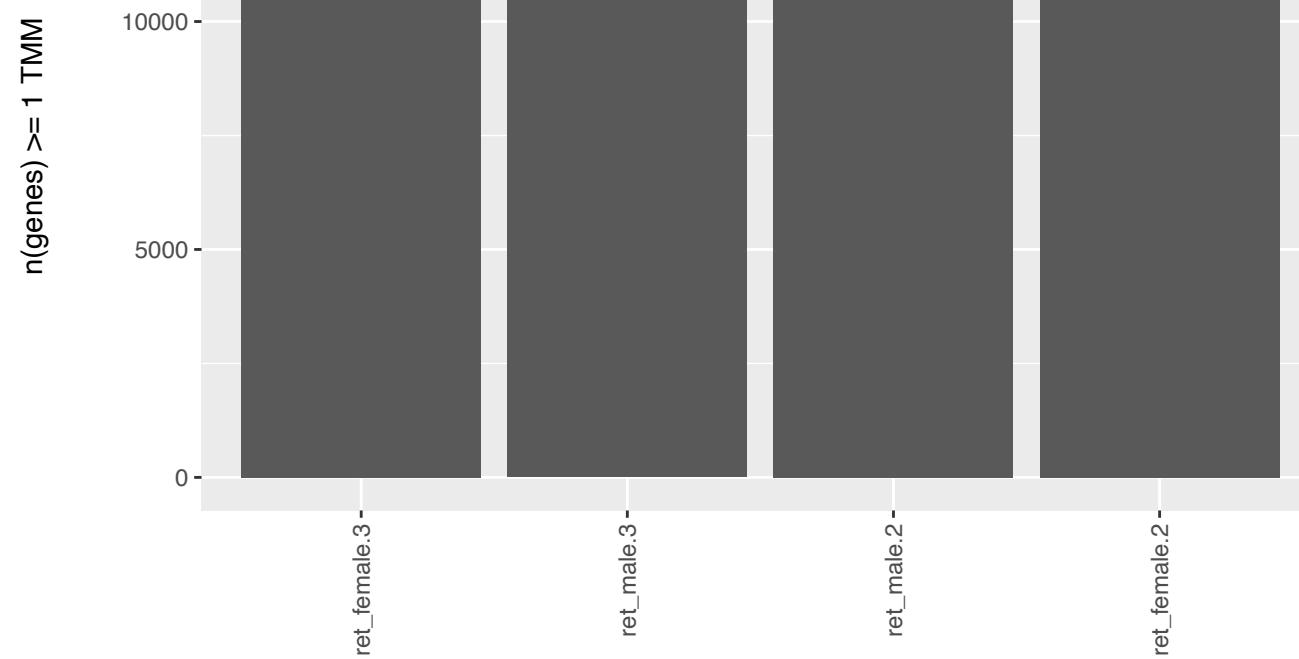
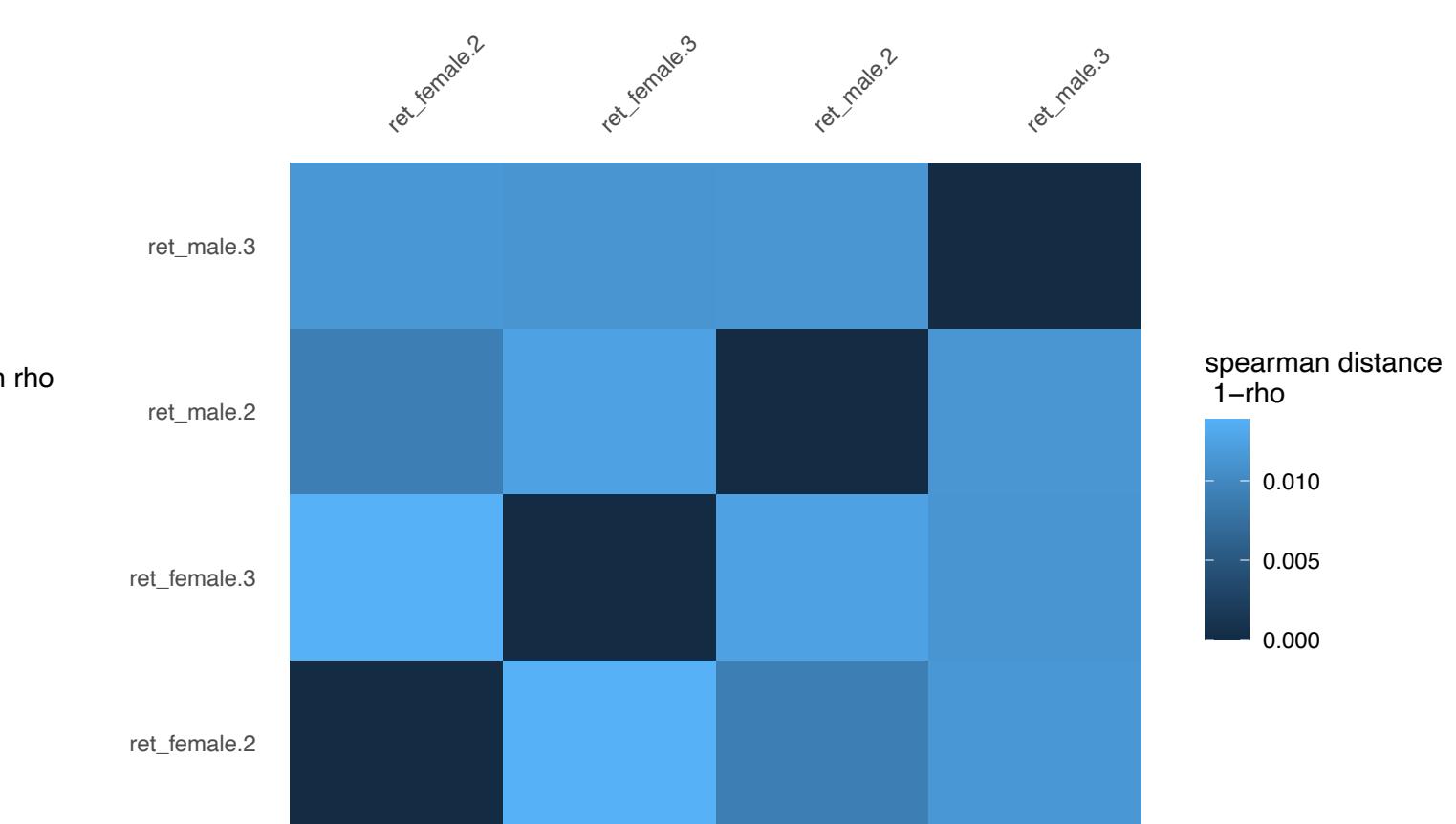
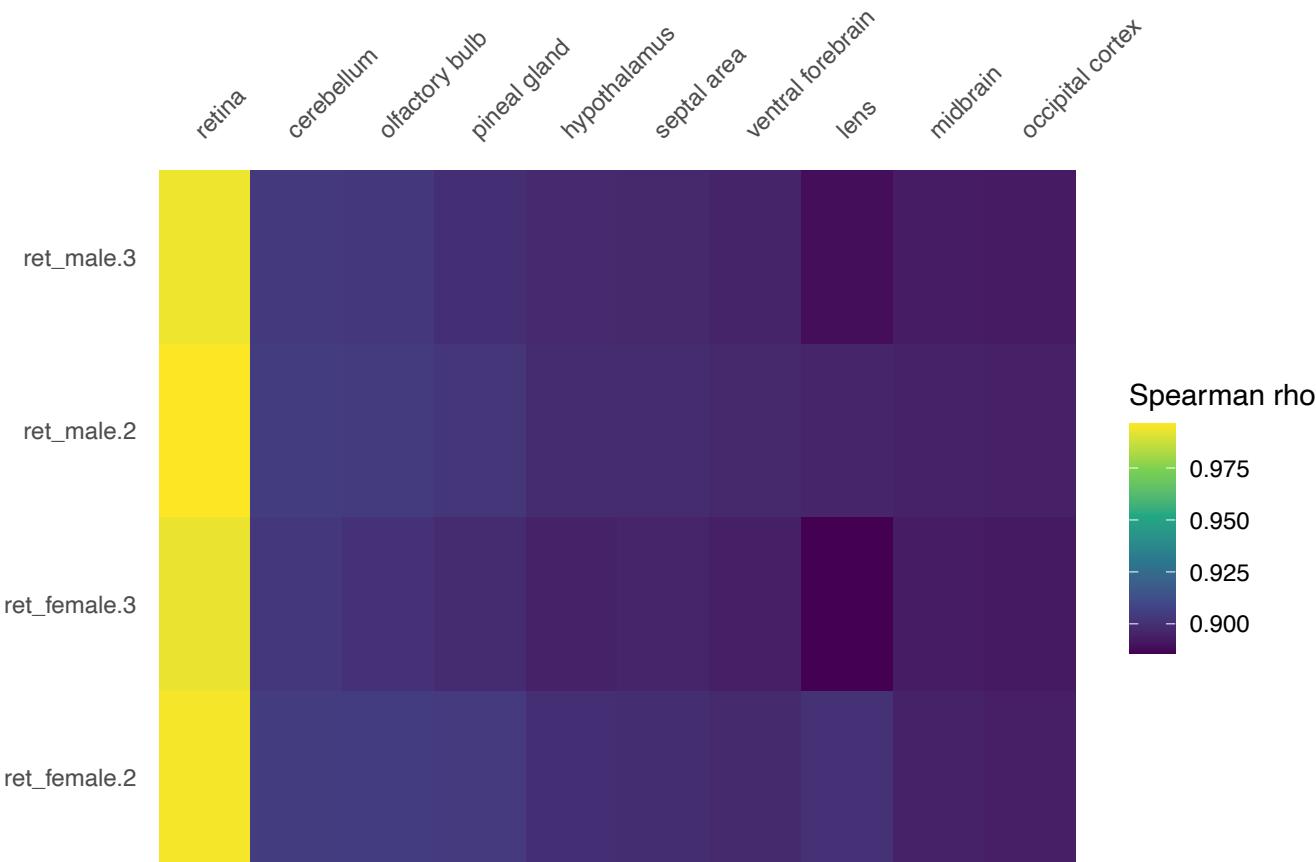
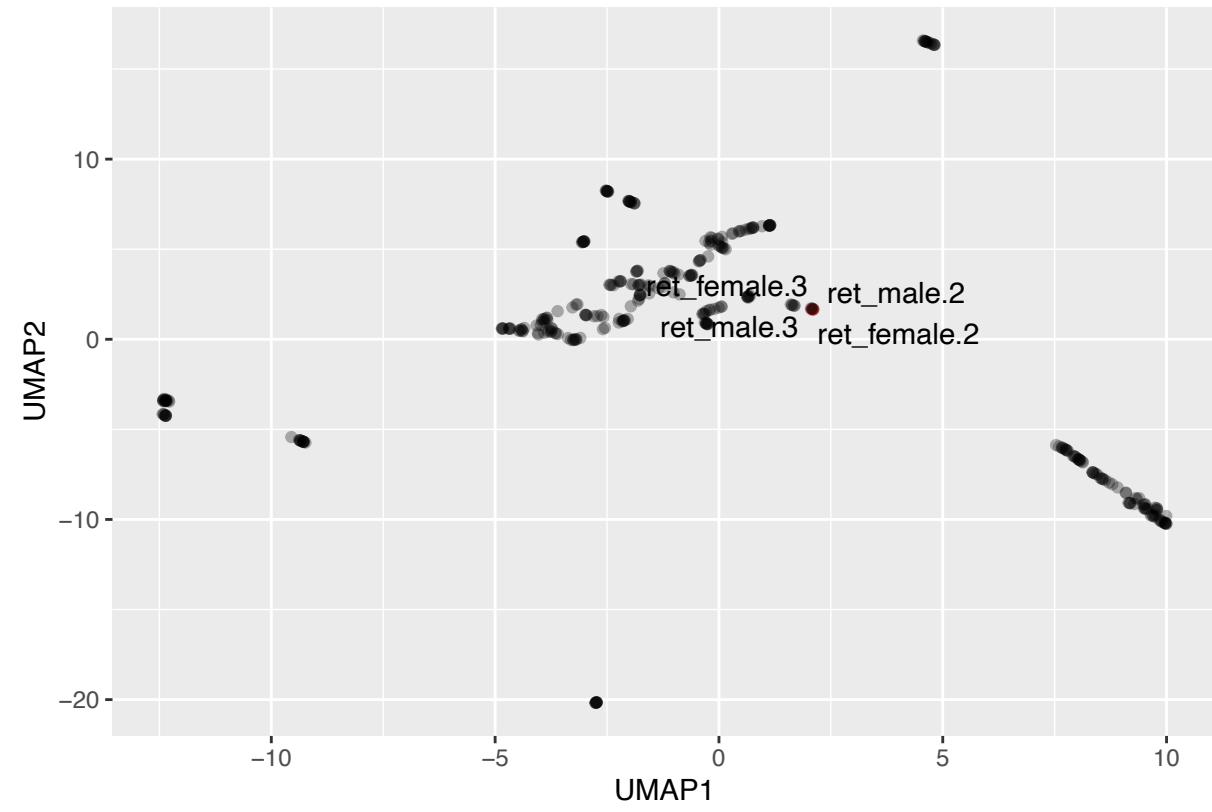
rectum



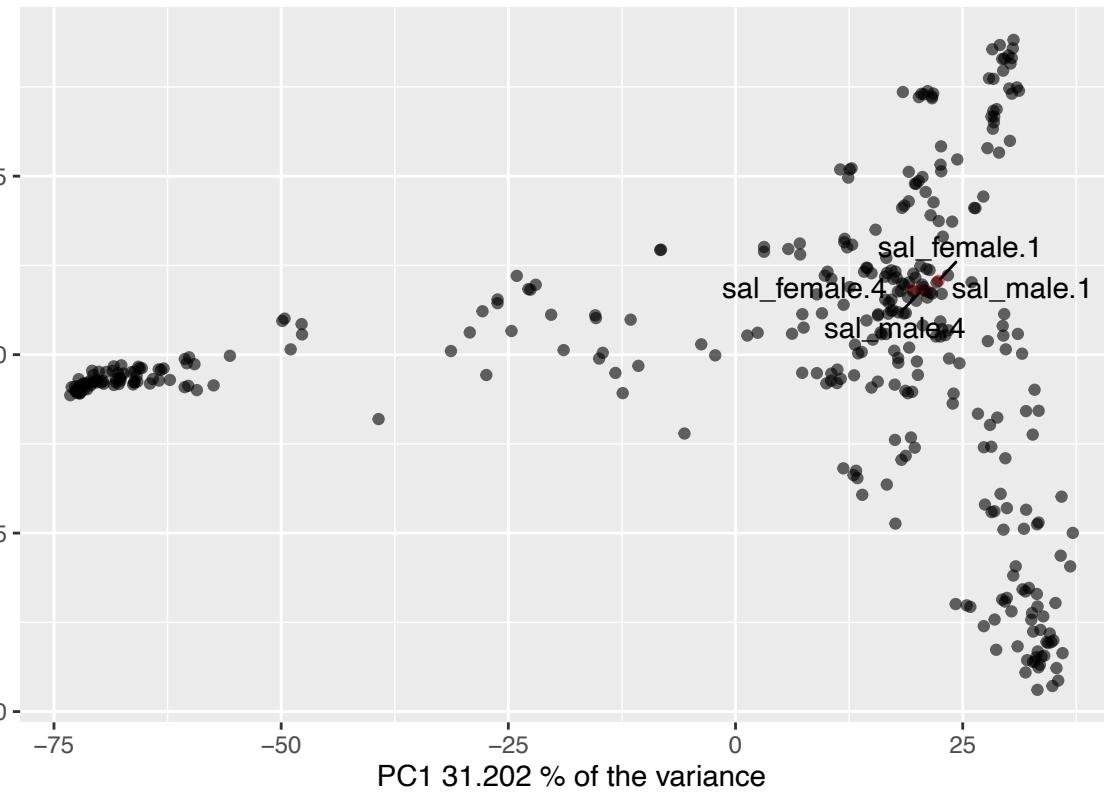
retina, PCA: TMM expression values



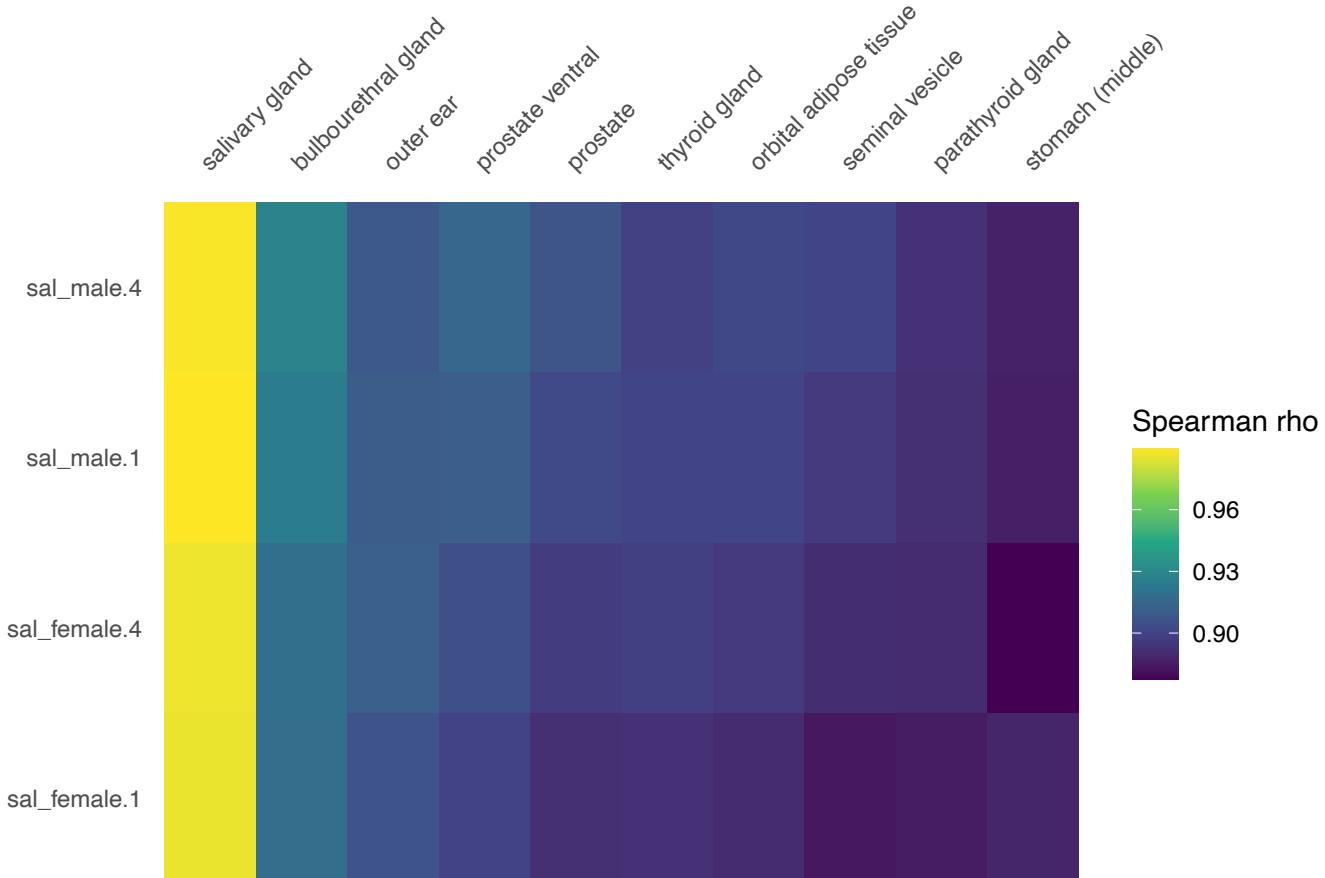
retina, UMAP: TMM expression values



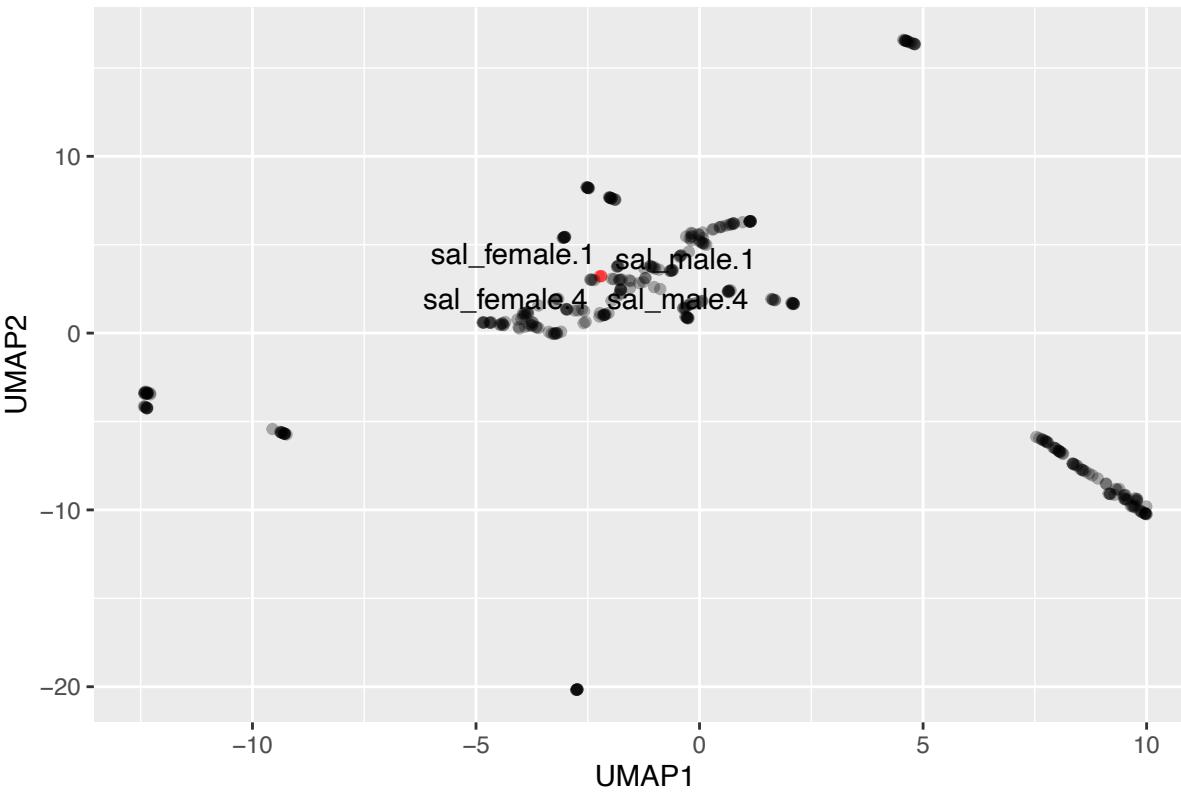
salivary gland, PCA: TMM expression values



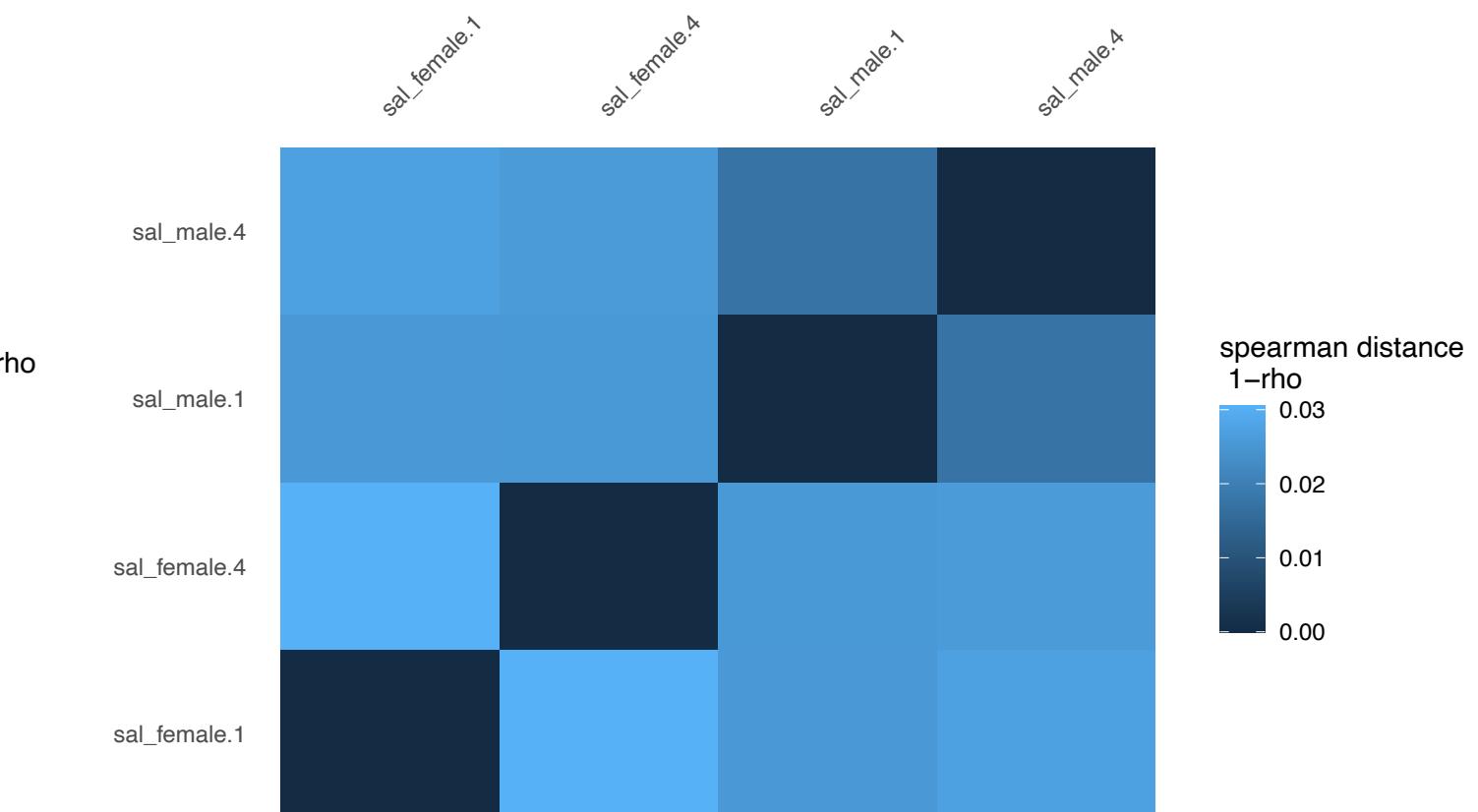
Tissue group to sample correlation



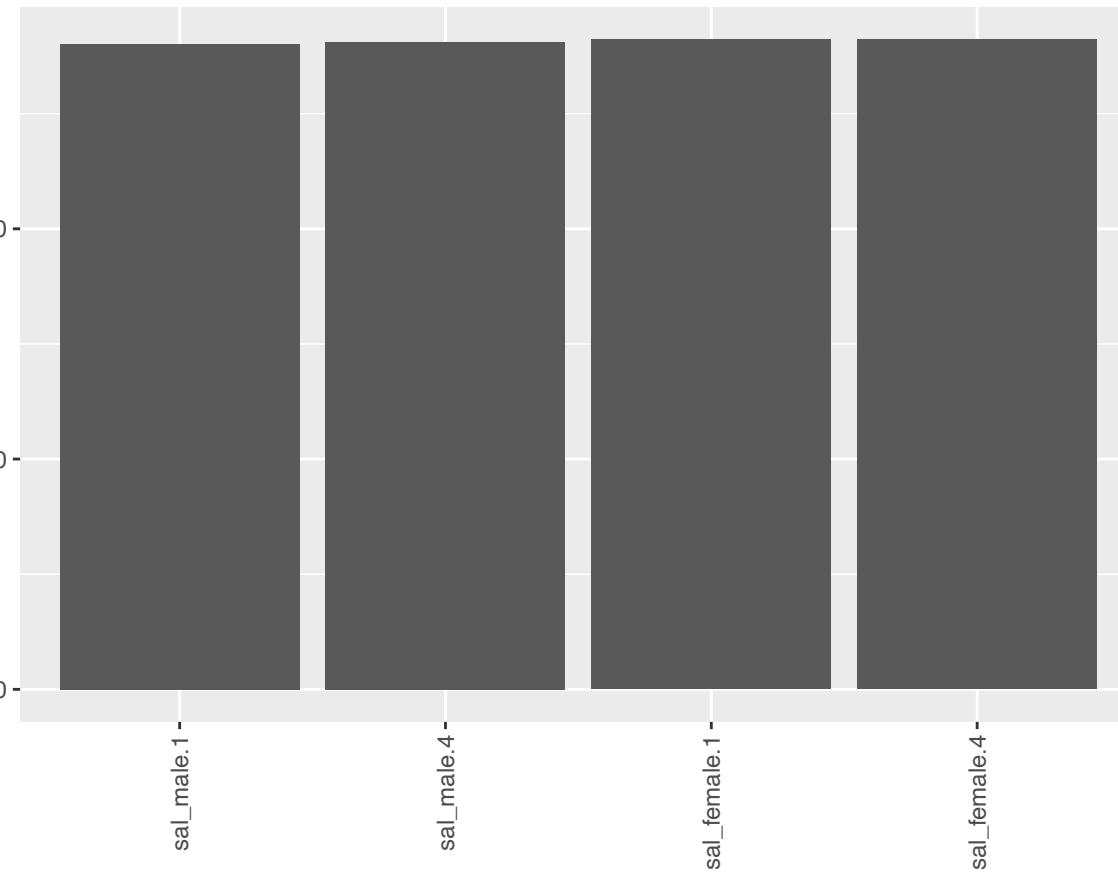
salivary gland, UMAP: TMM expression values



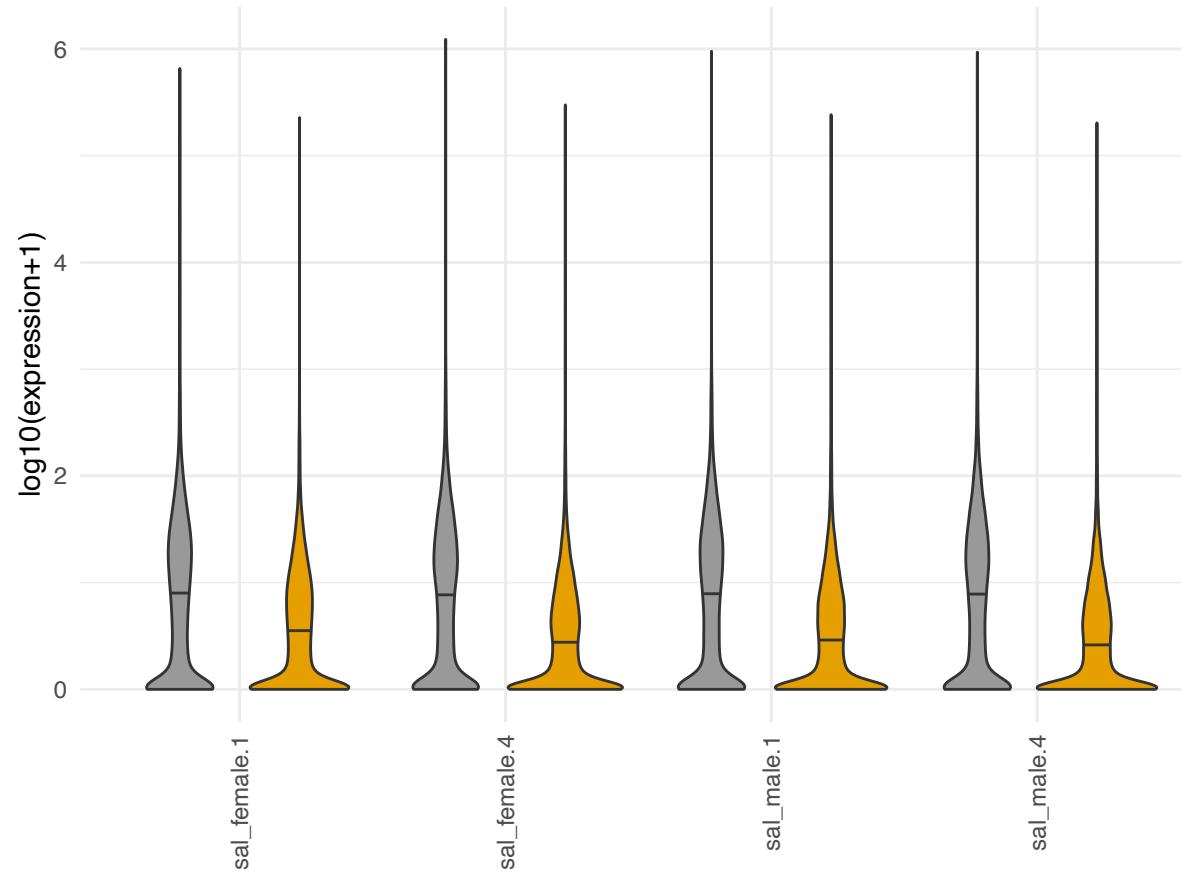
In tissue sample to sample Spearman Distance



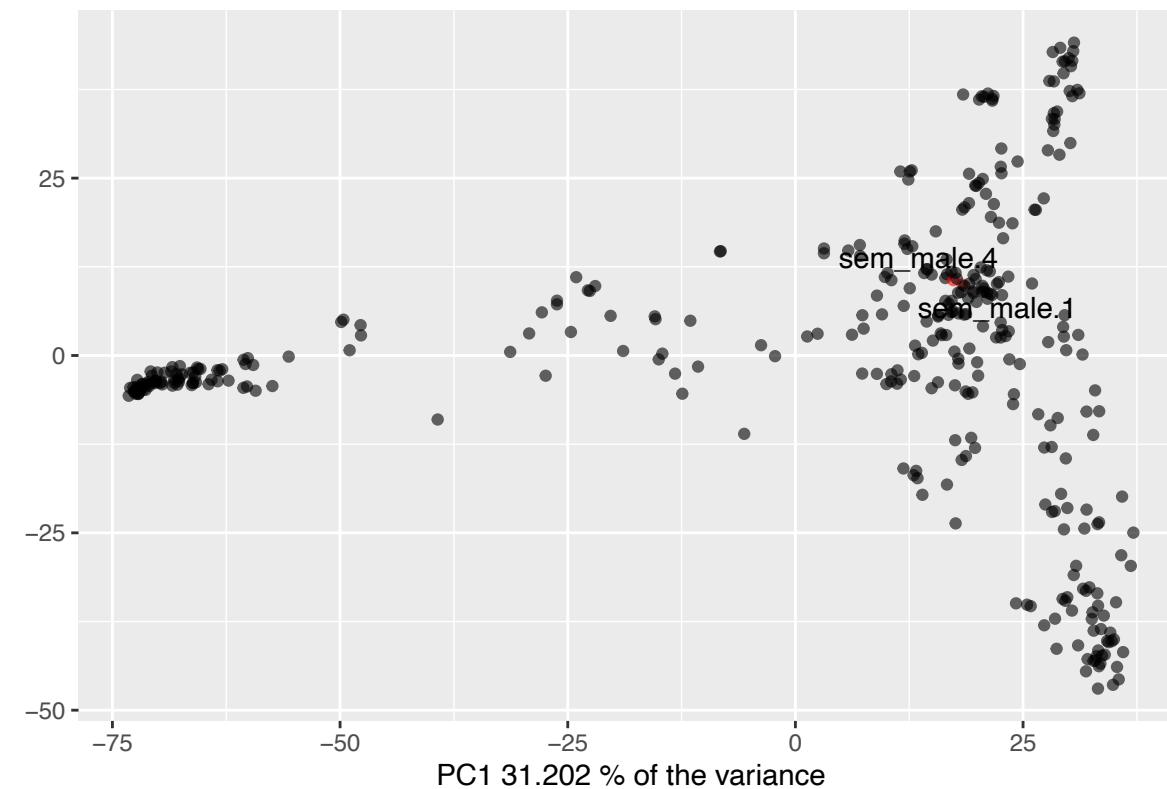
salivary gland



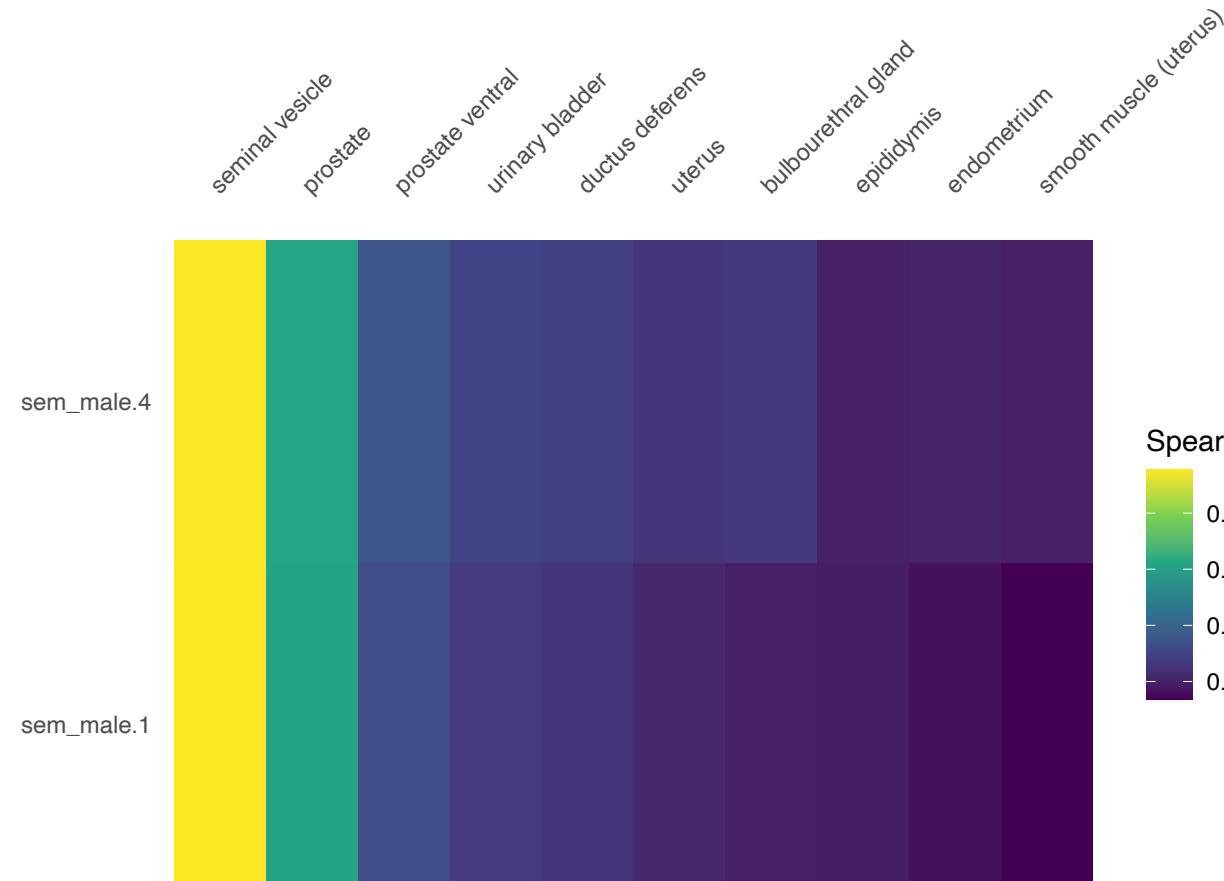
salivary gland



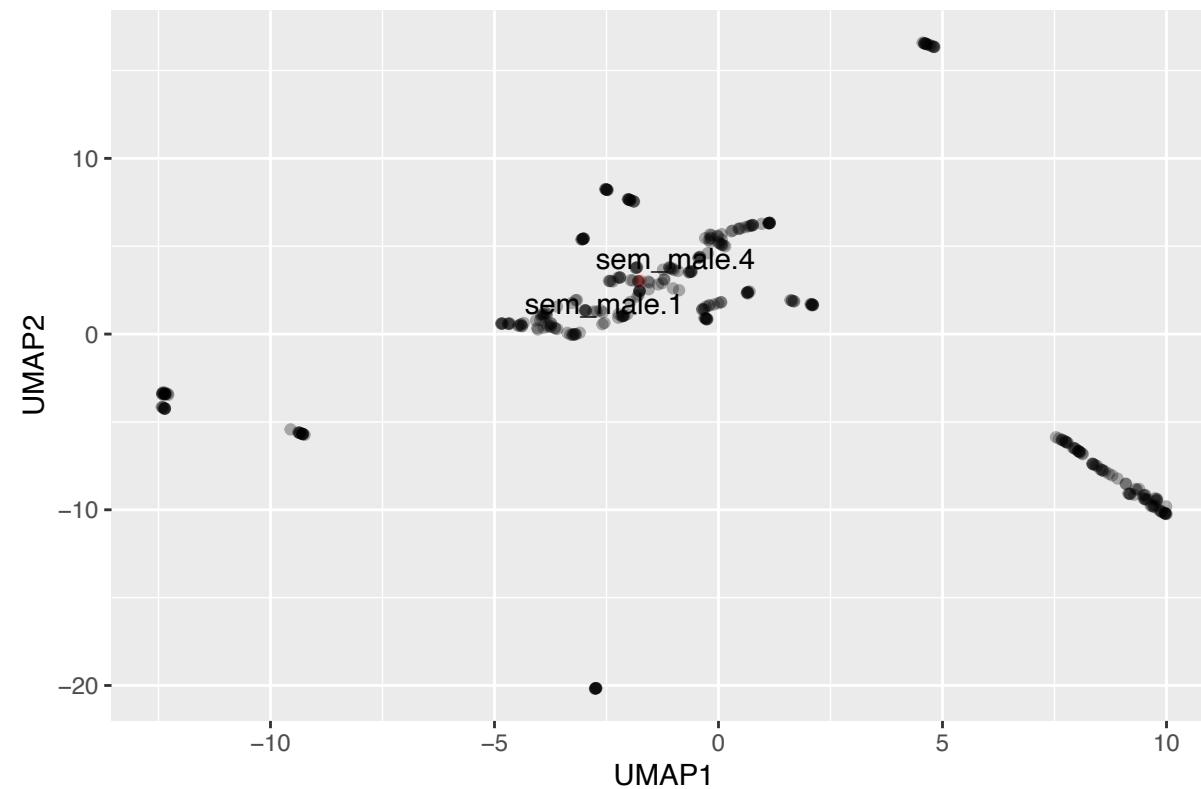
seminal vesicle, PCA: TMM expression values



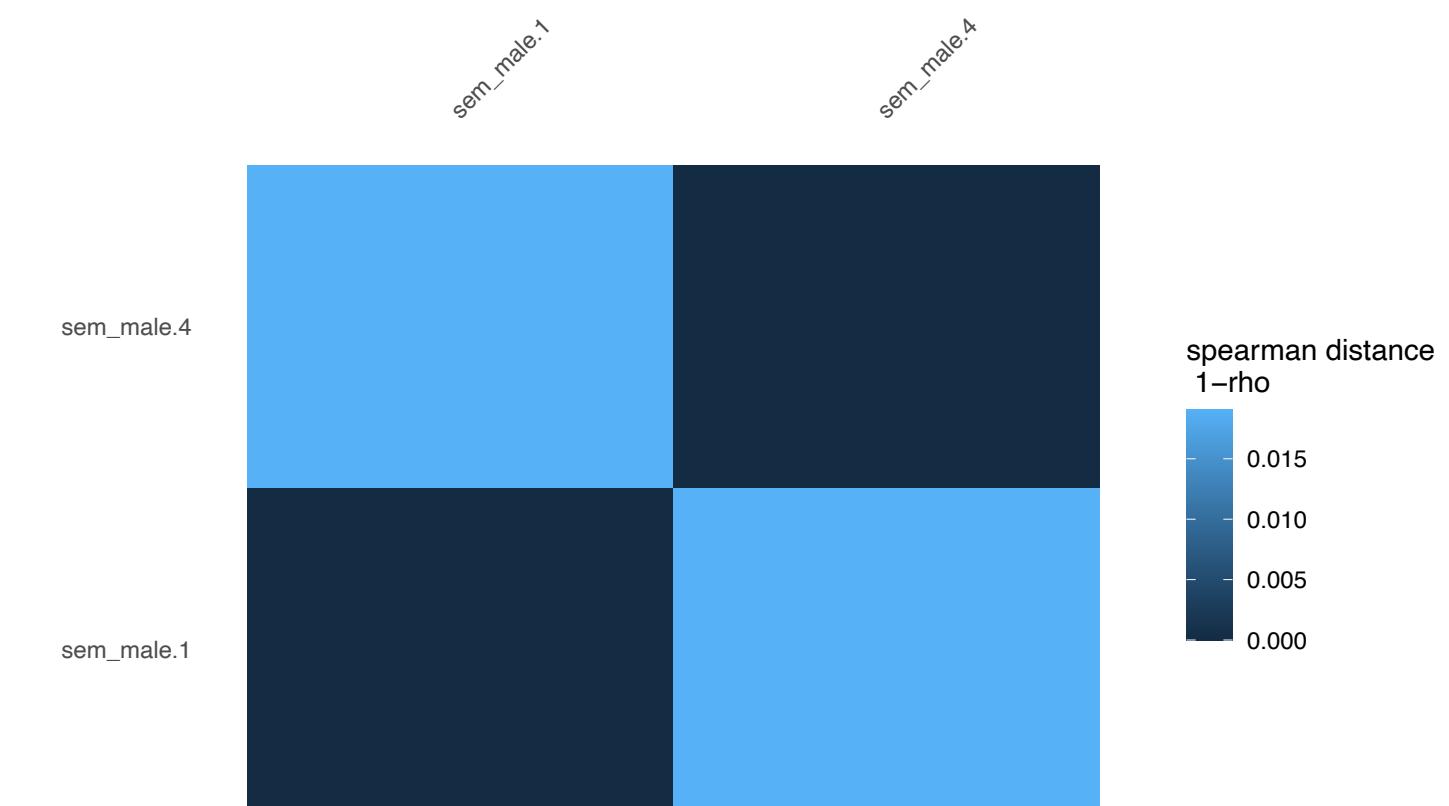
Tissue group to sample correlation



seminal vesicle, UMAP: TMM expression values



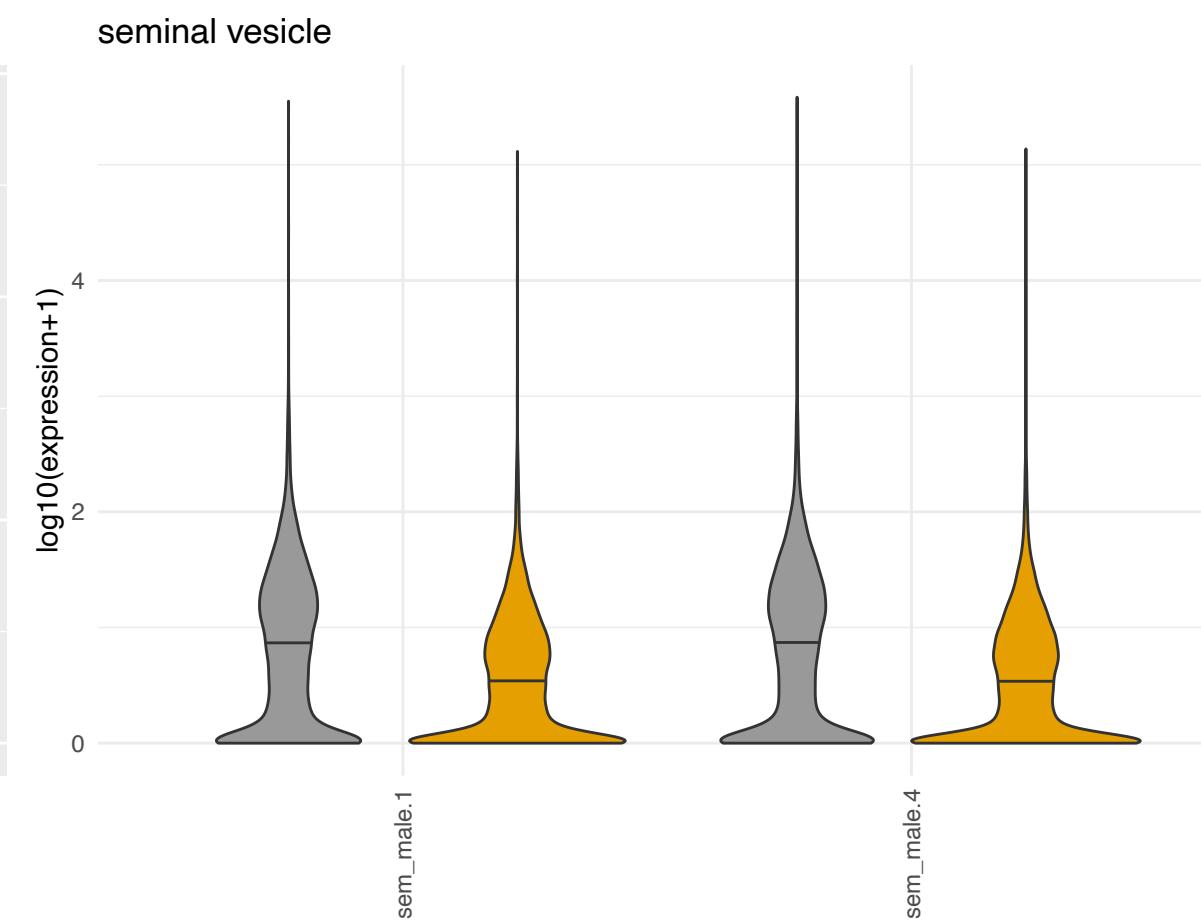
In tissue sample to sample Spearman Distance



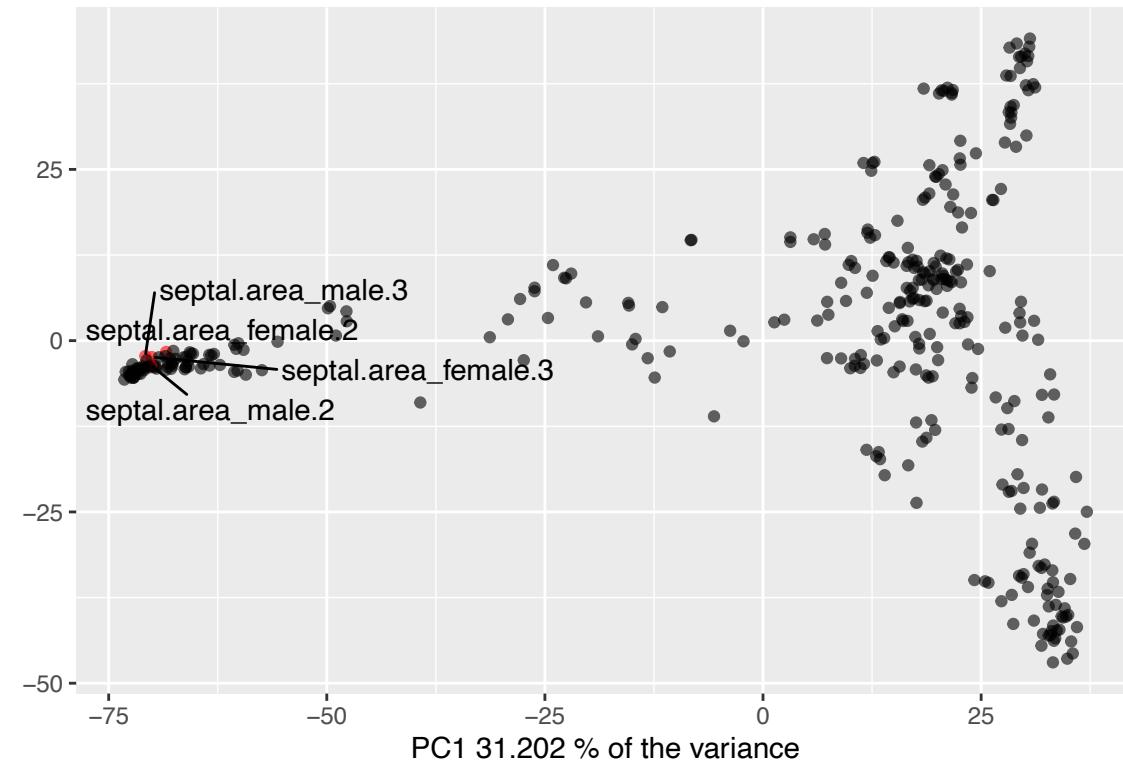
seminal vesicle



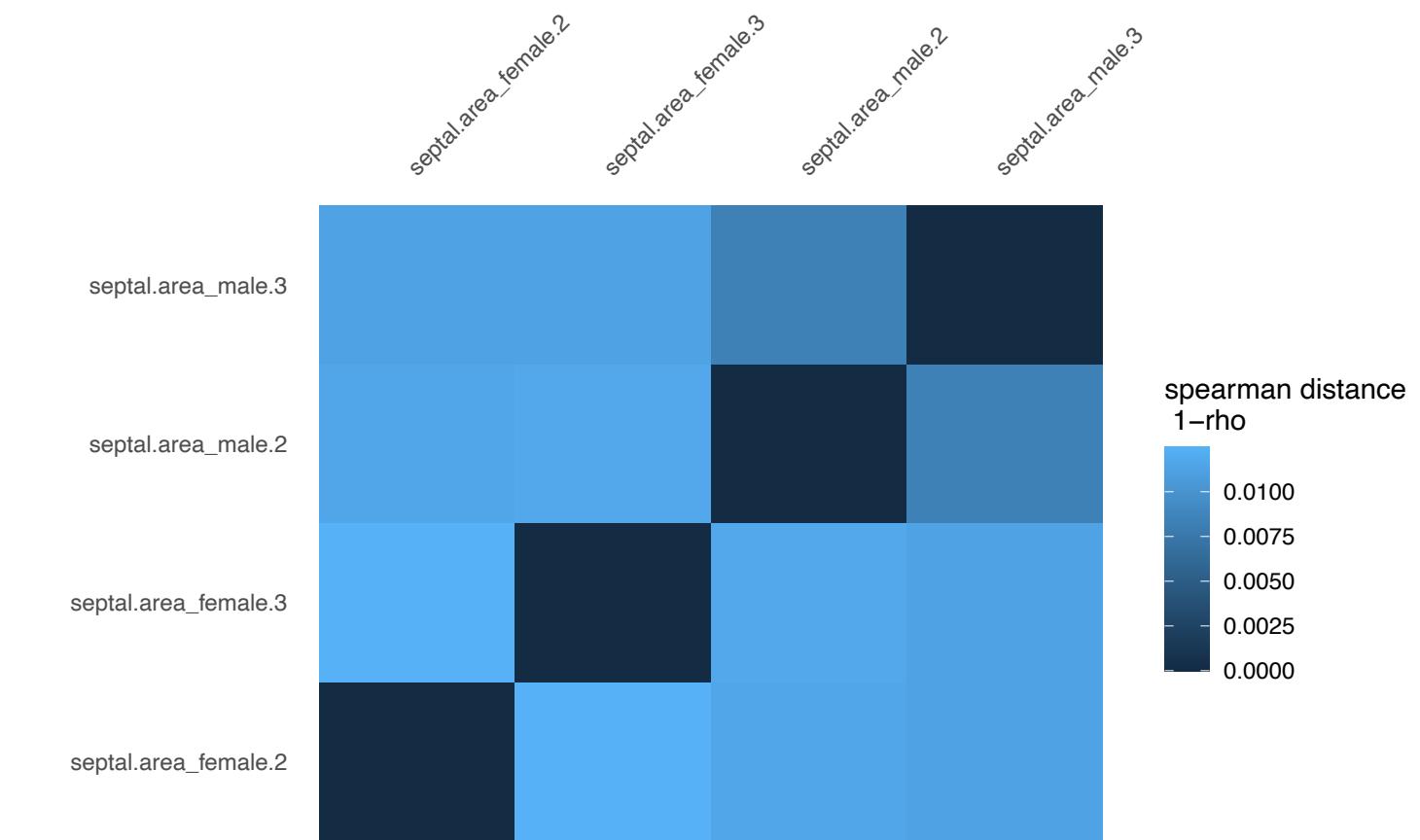
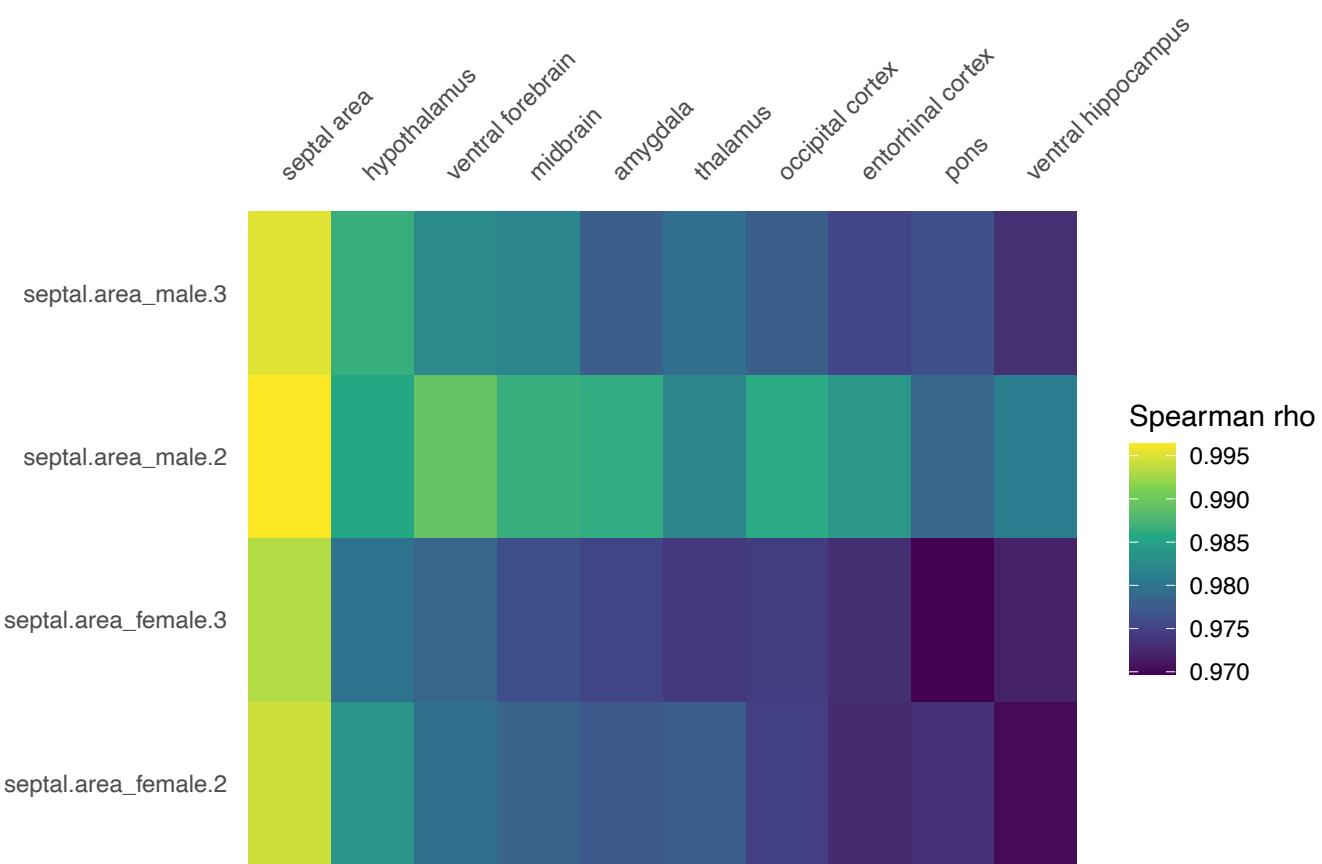
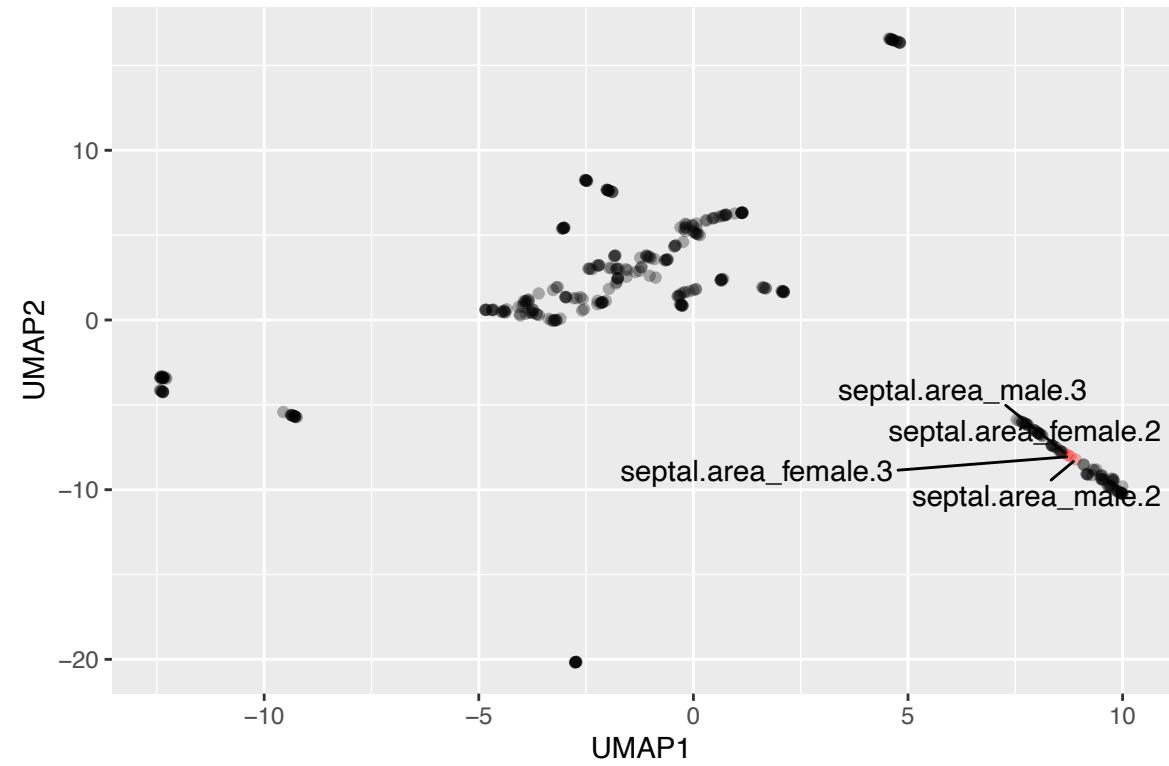
seminal vesicle



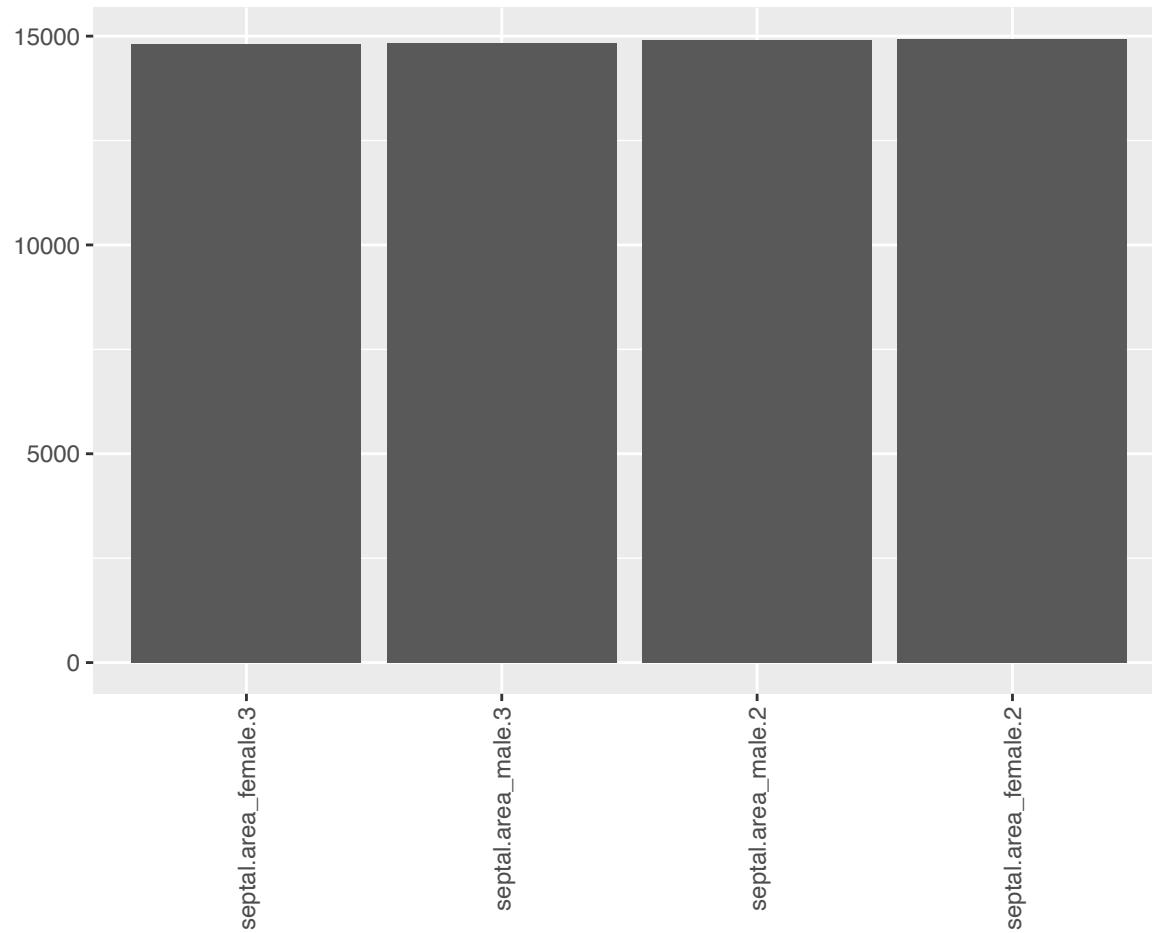
septal area, PCA: TMM expression values



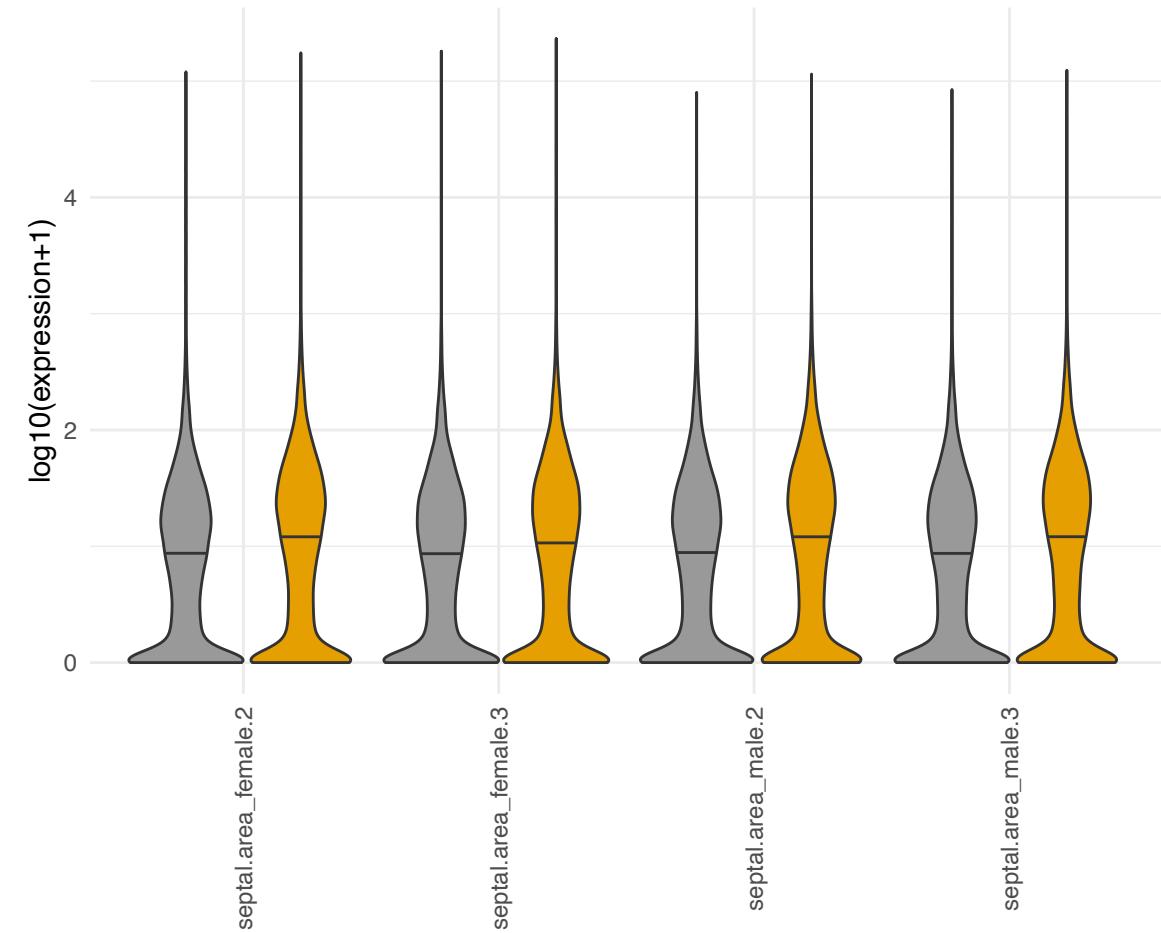
septal area, UMAP: TMM expression values



septal area

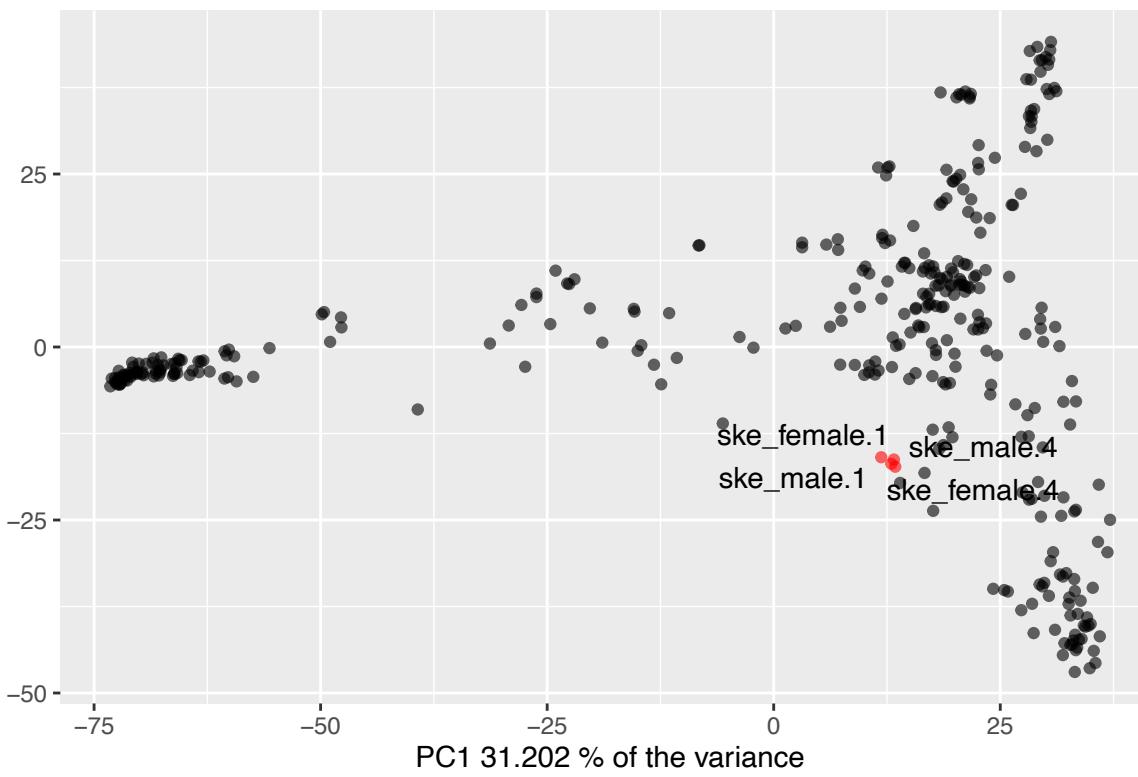


septal area

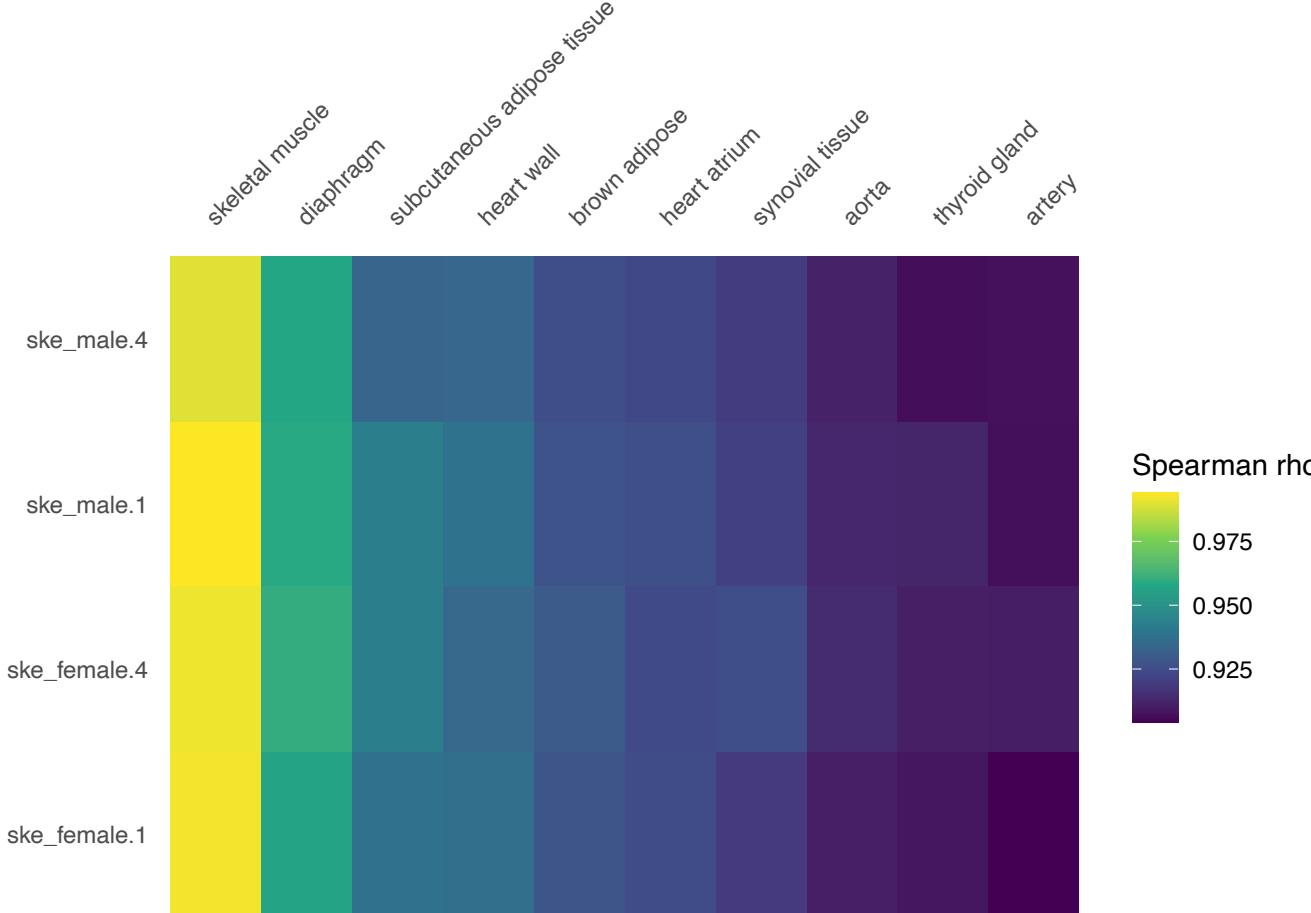


skeletal muscle, PCA: TMM expression values

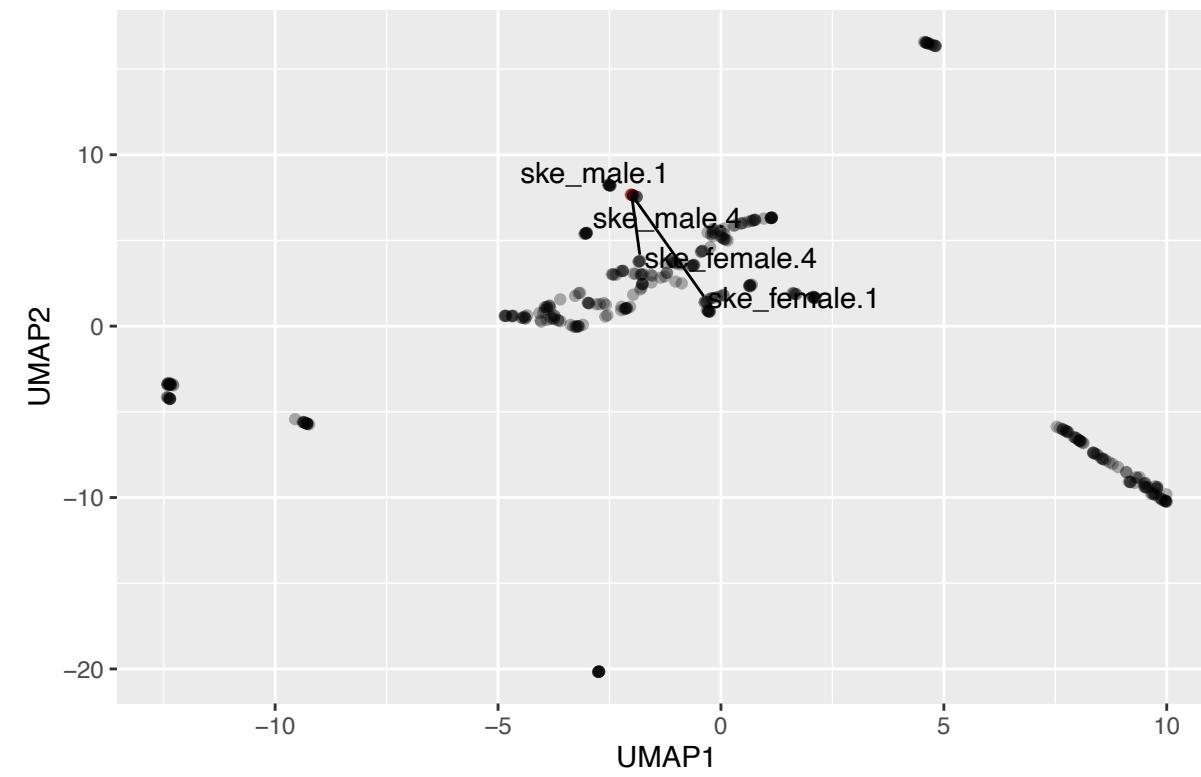
PC2 9.077 % of the variance



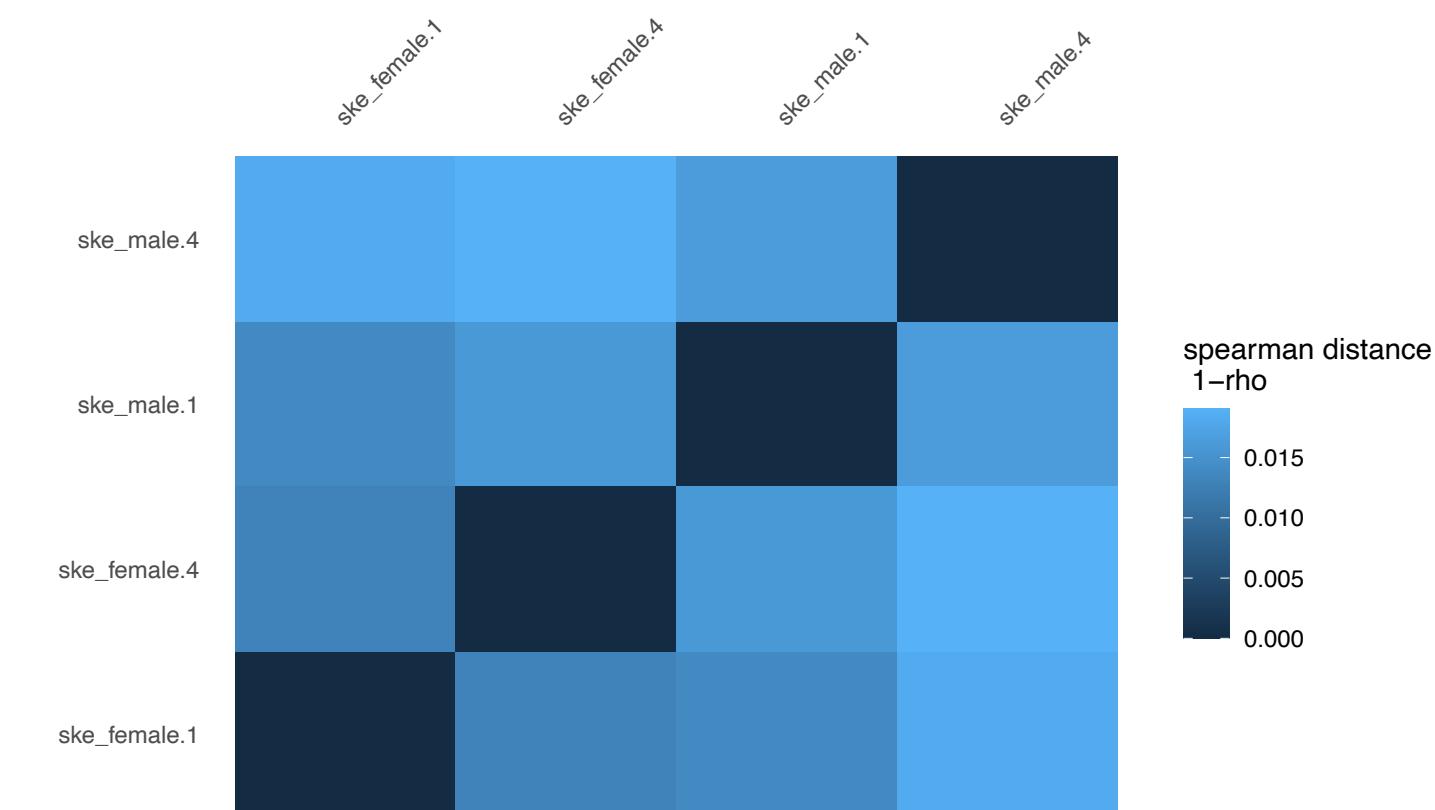
Tissue group to sample correlation



skeletal muscle, UMAP: TMM expression values

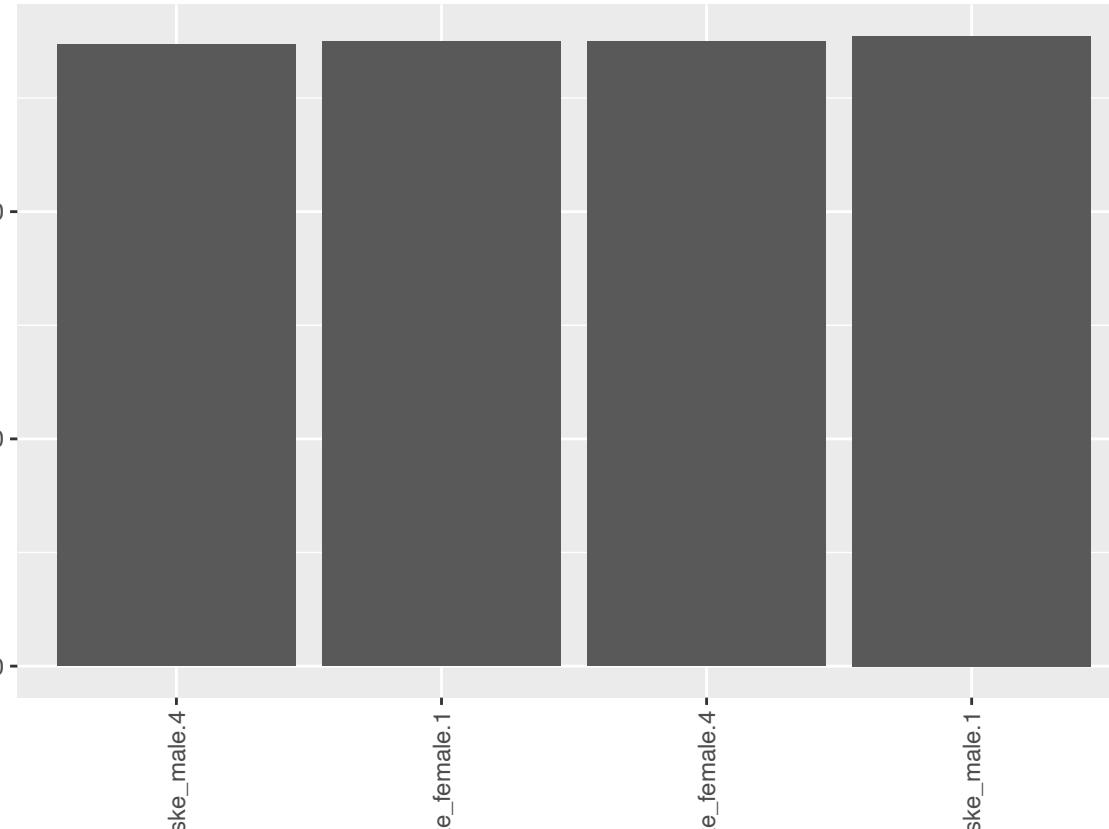


In tissue sample to sample Spearman Distance



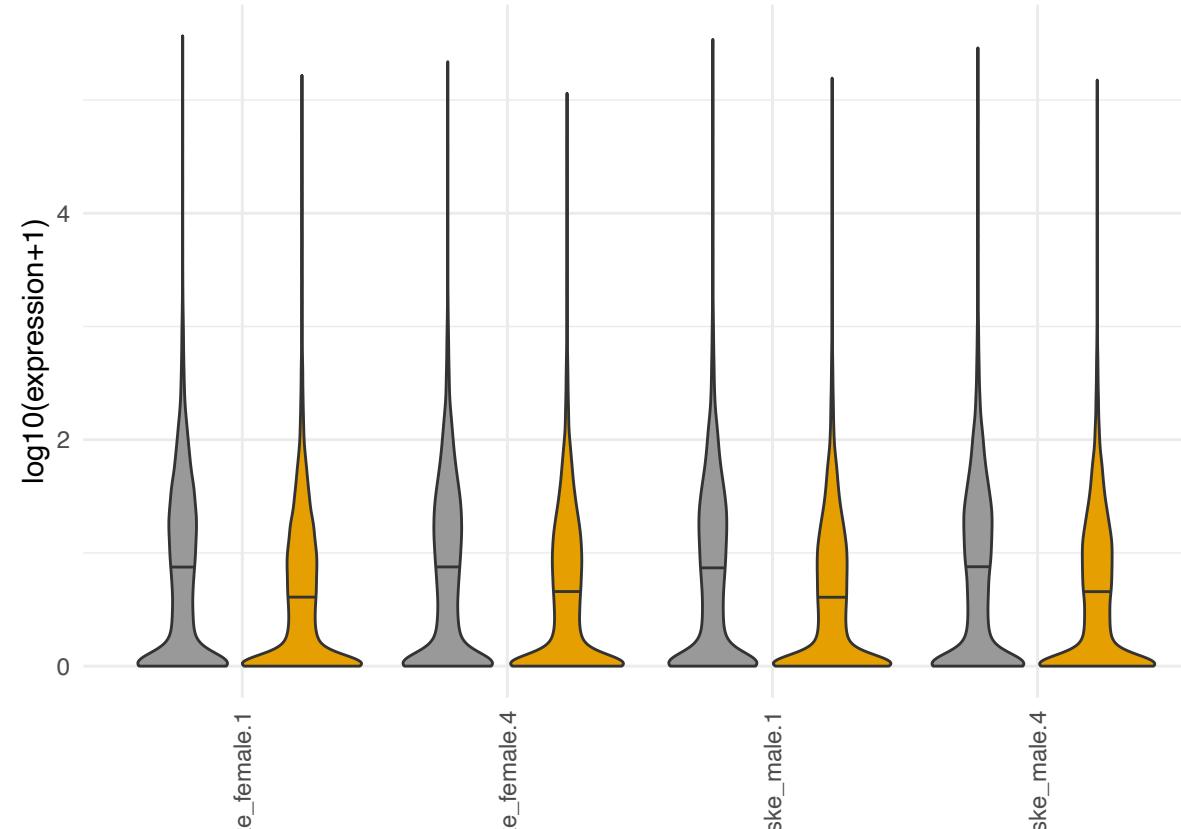
skeletal muscle

n(genes) >= 1 TMM

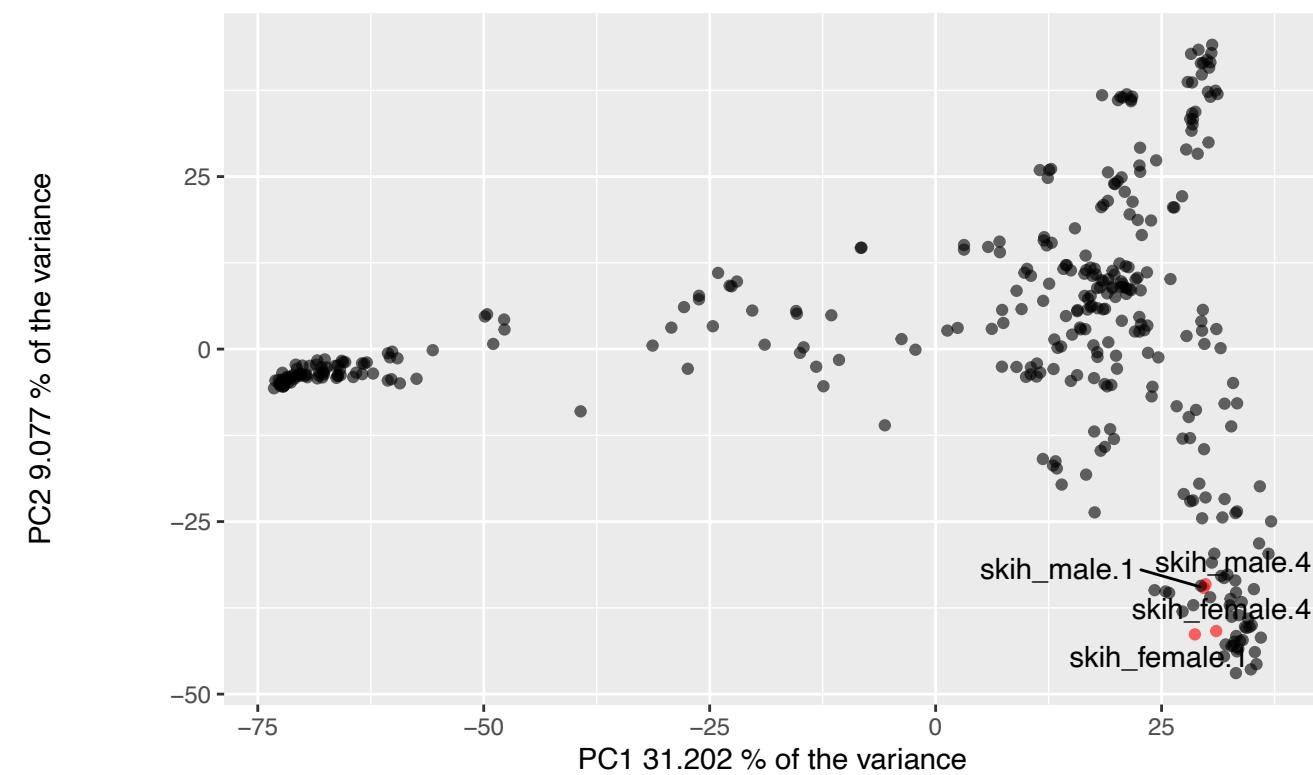


skeletal muscle

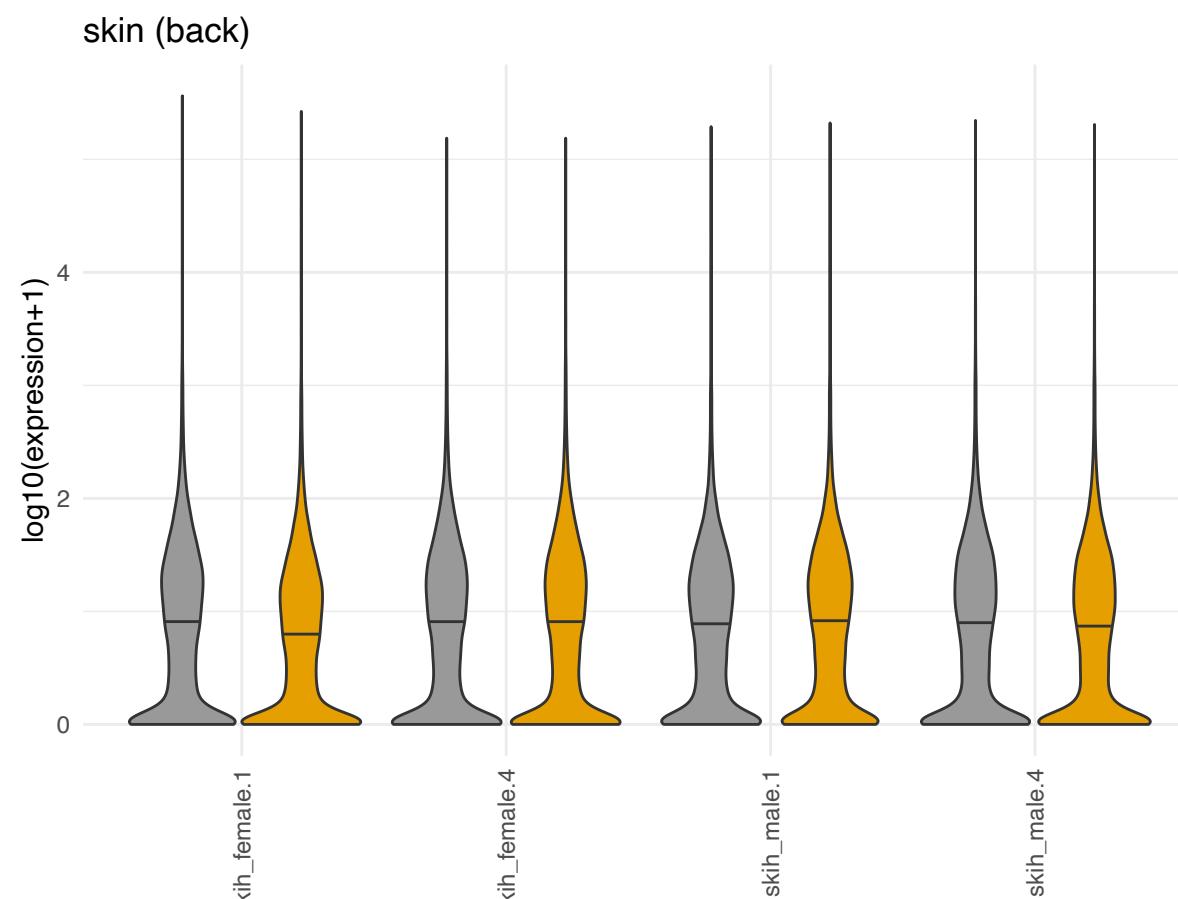
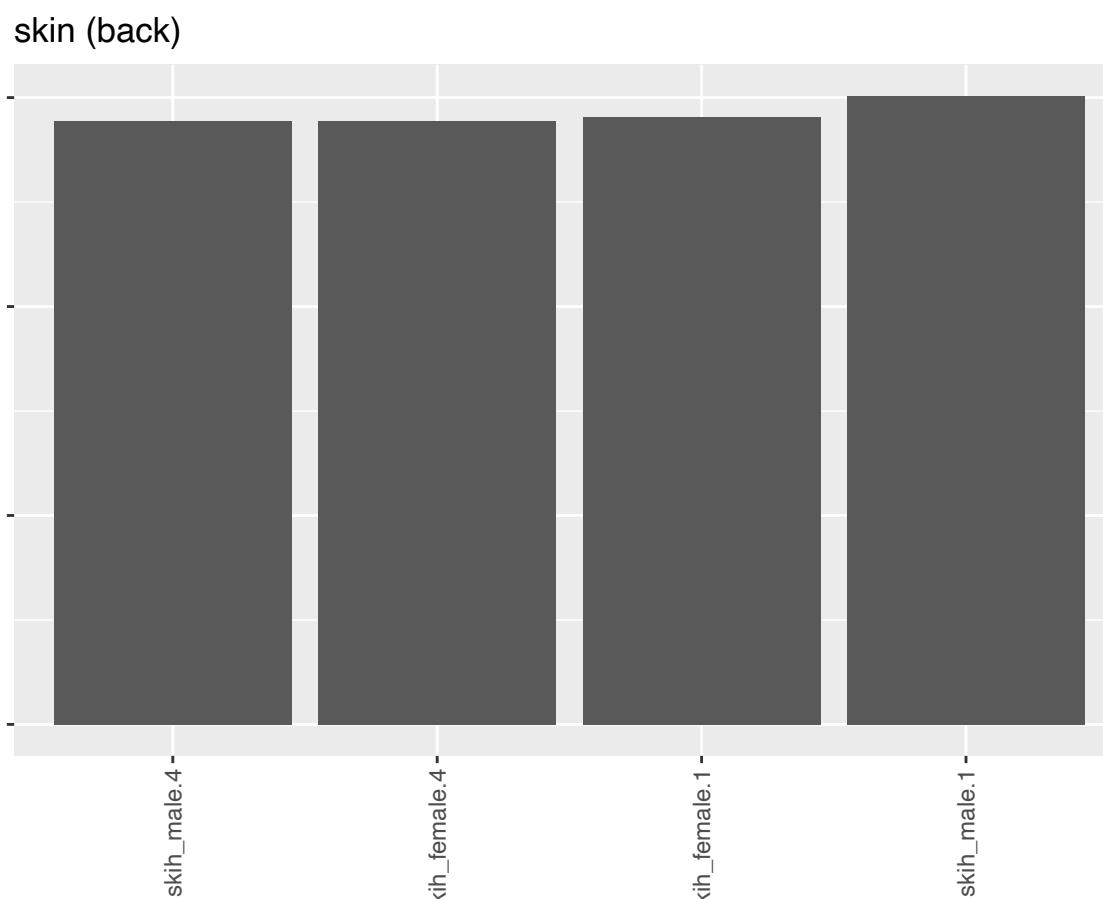
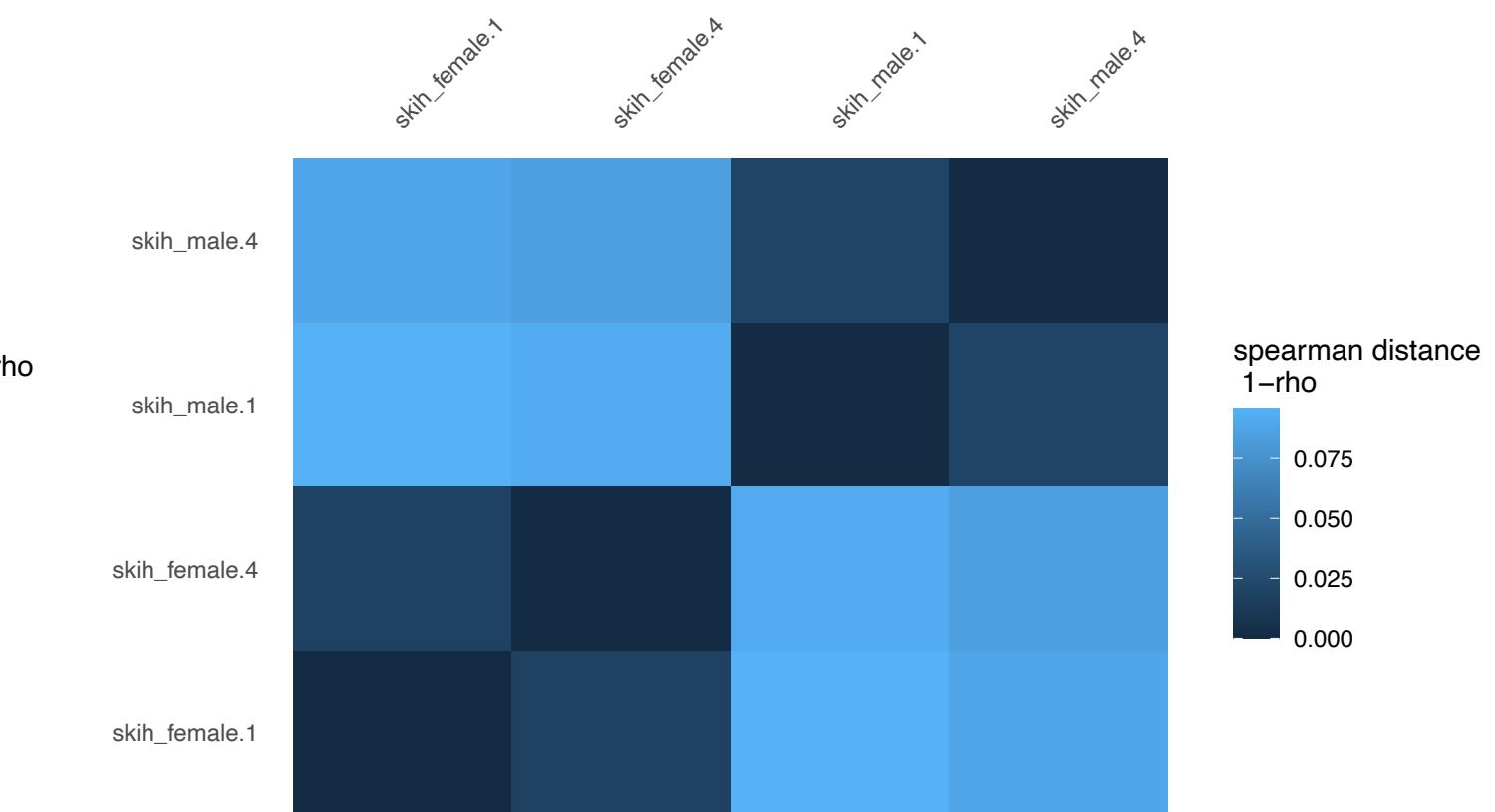
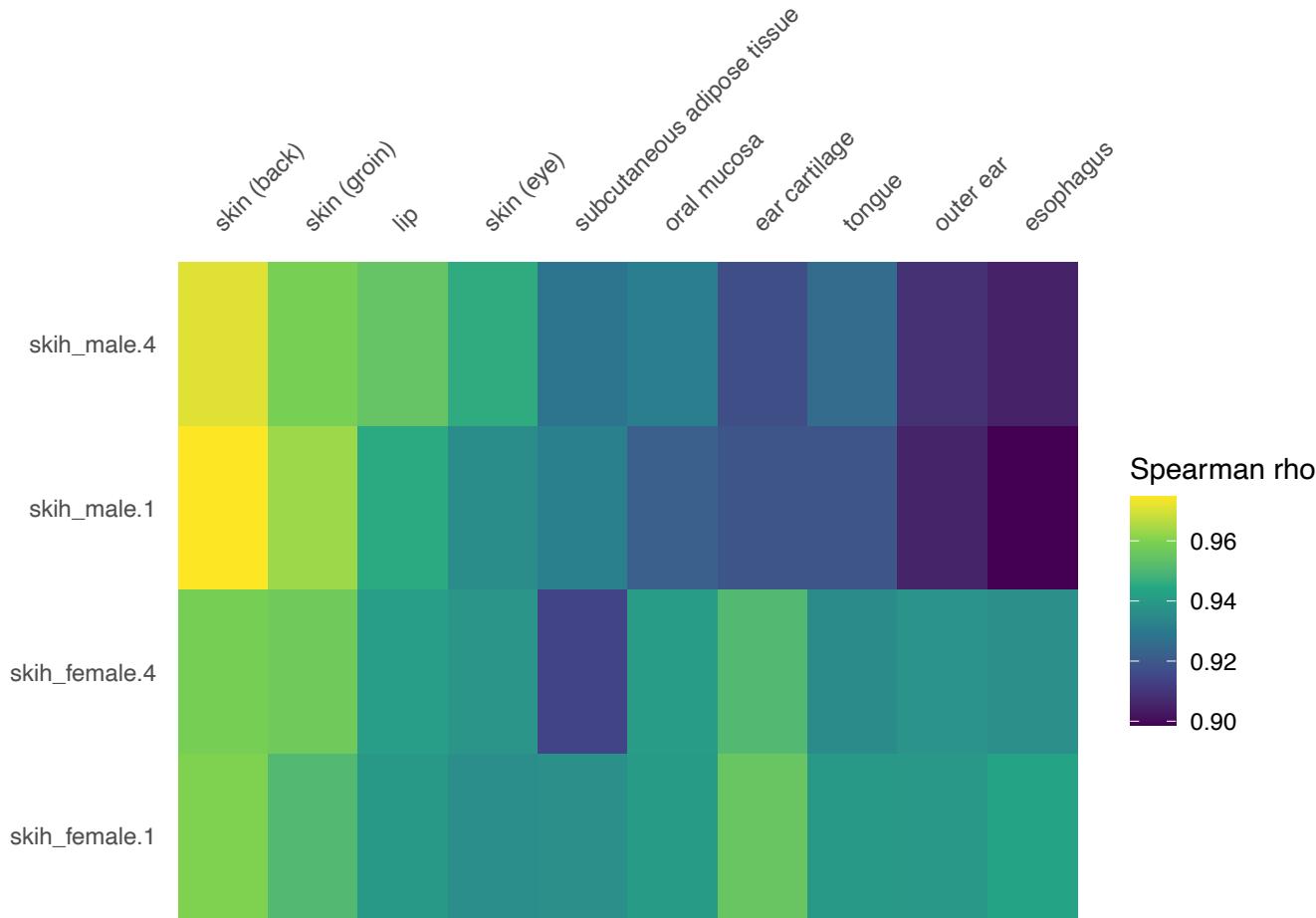
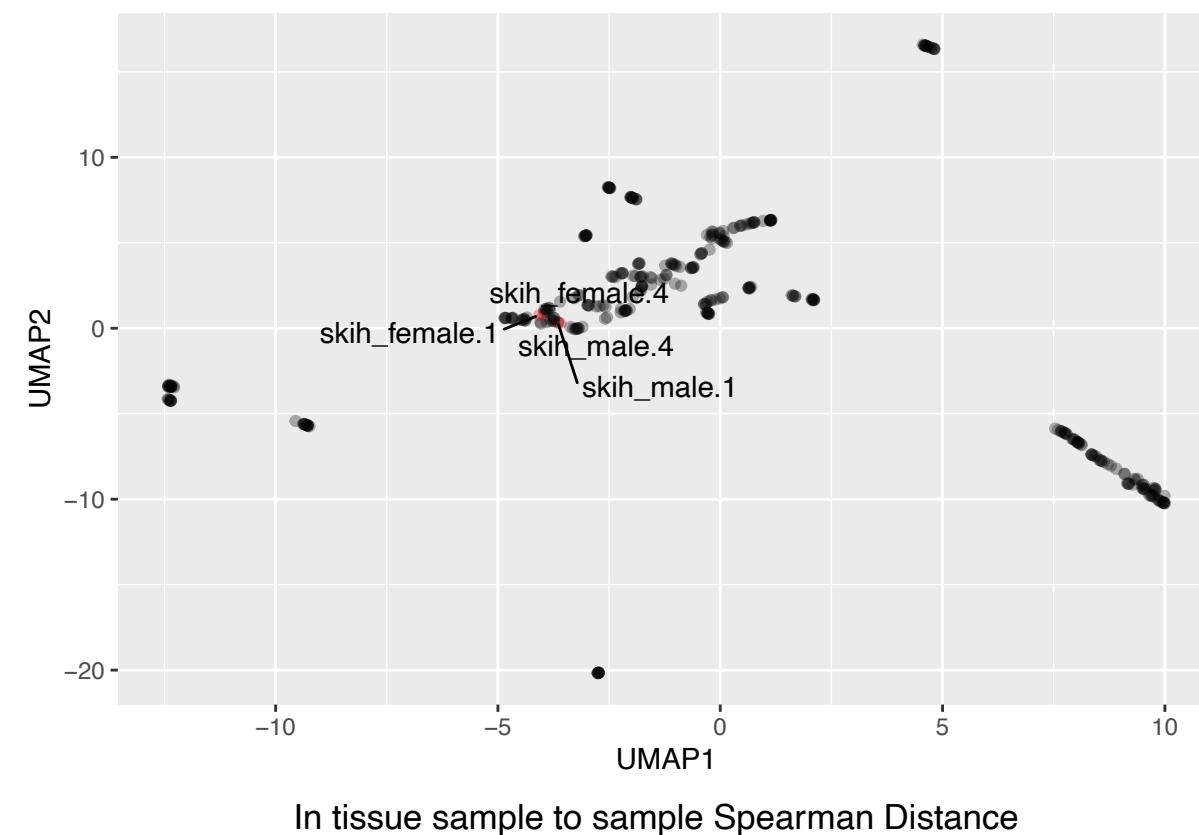
log10(expression+1)



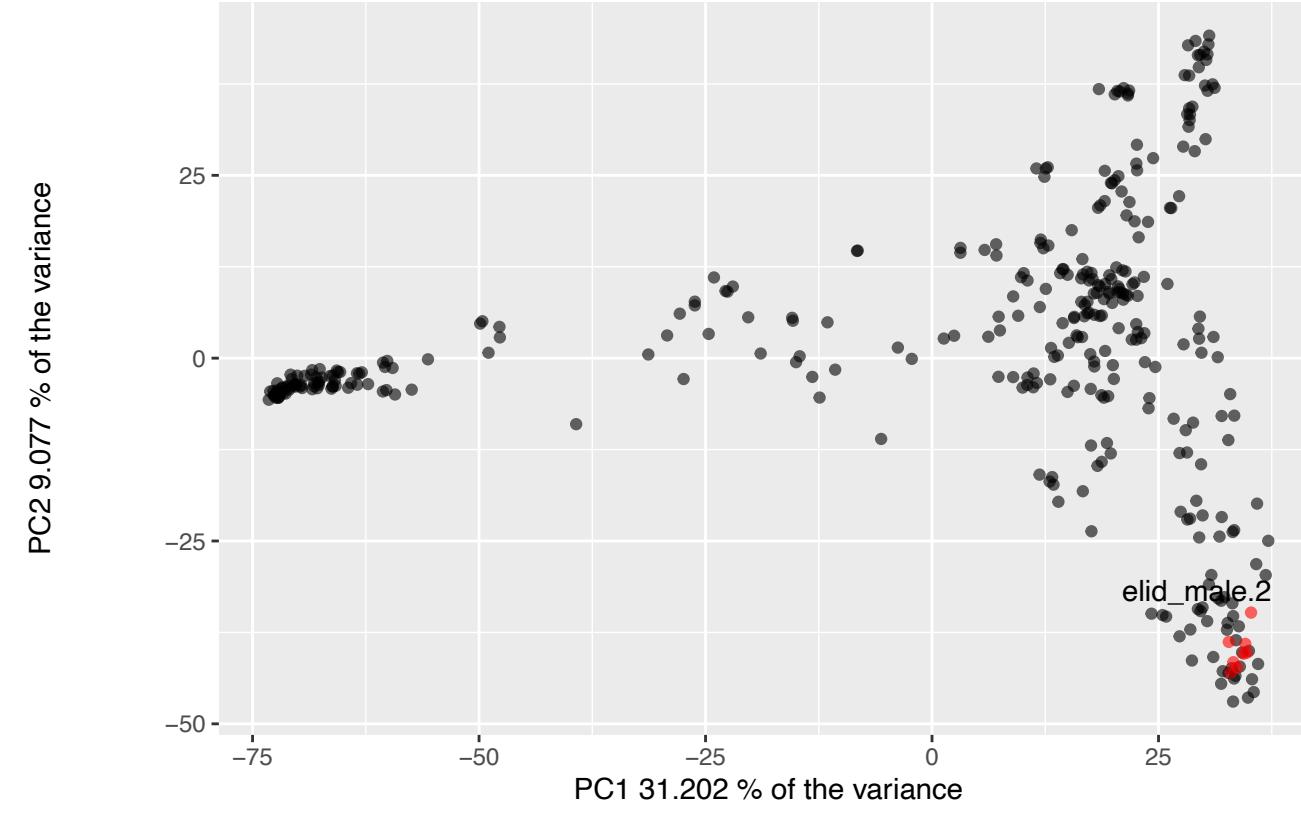
skin (back), PCA: TMM expression values



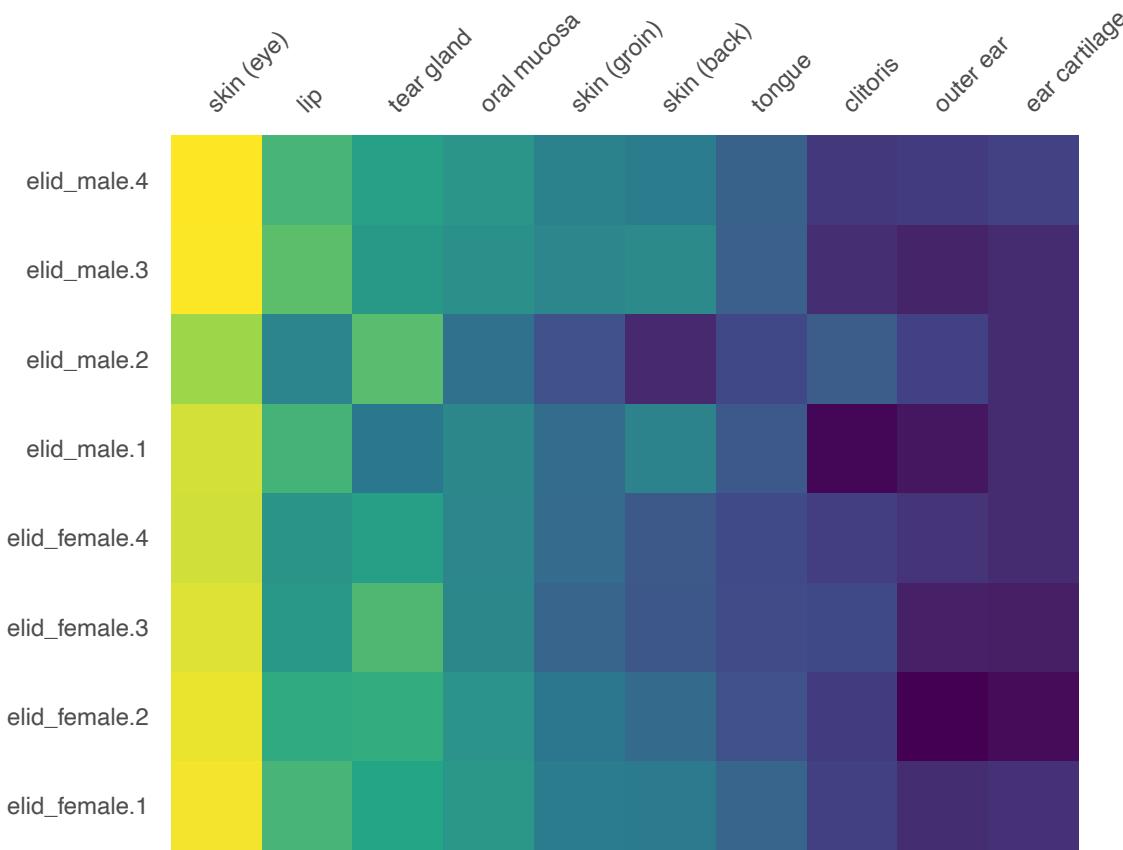
skin (back), UMAP: TMM expression values



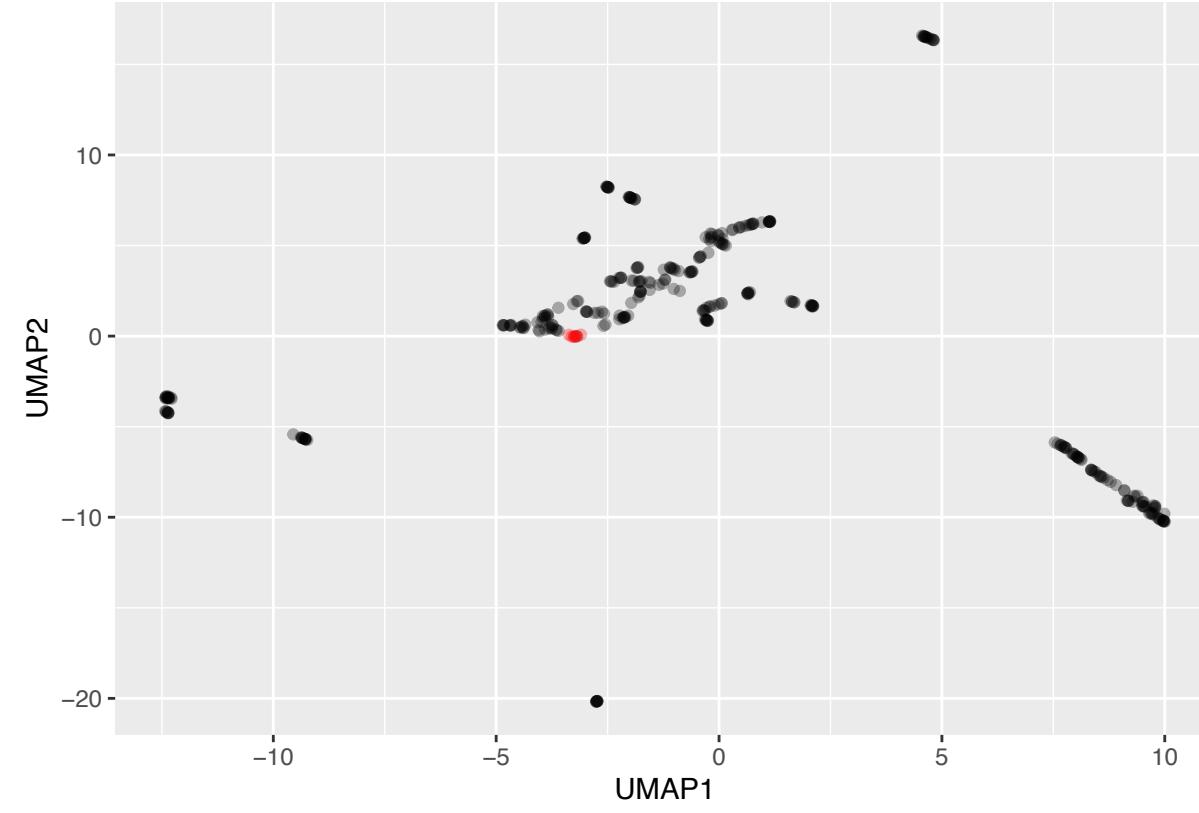
skin (eye), PCA: TMM expression values



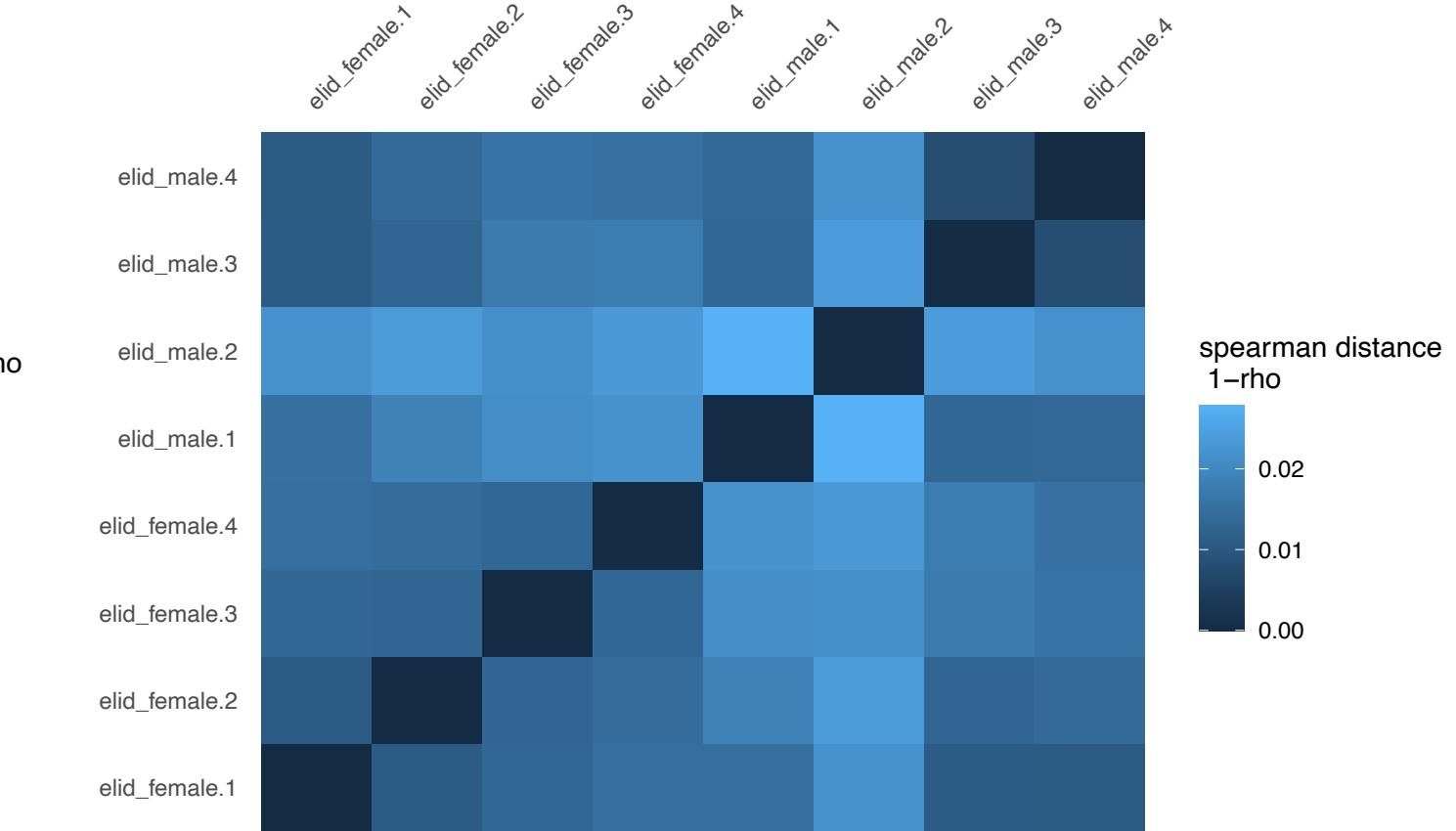
Tissue group to sample correlation



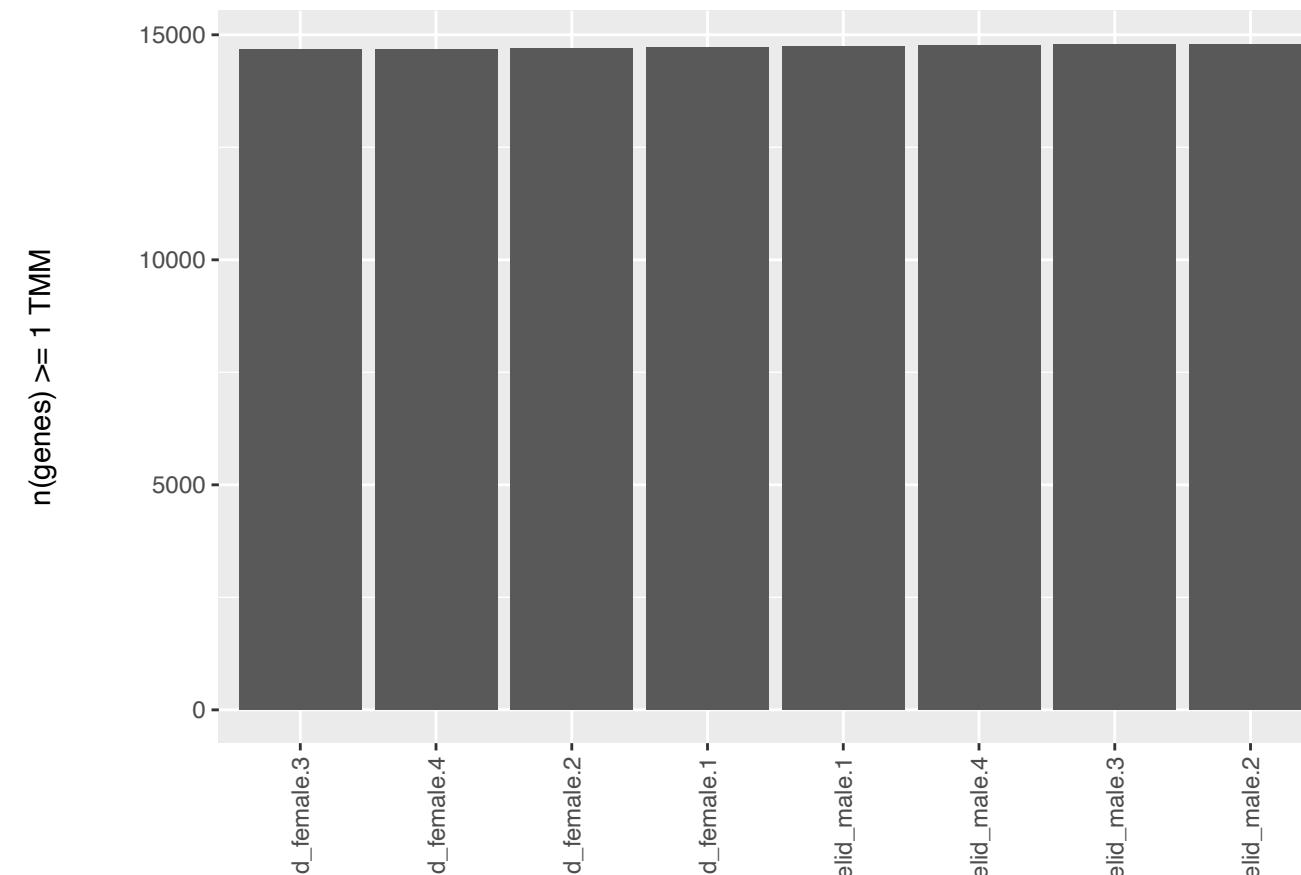
skin (eye), UMAP: TMM expression values



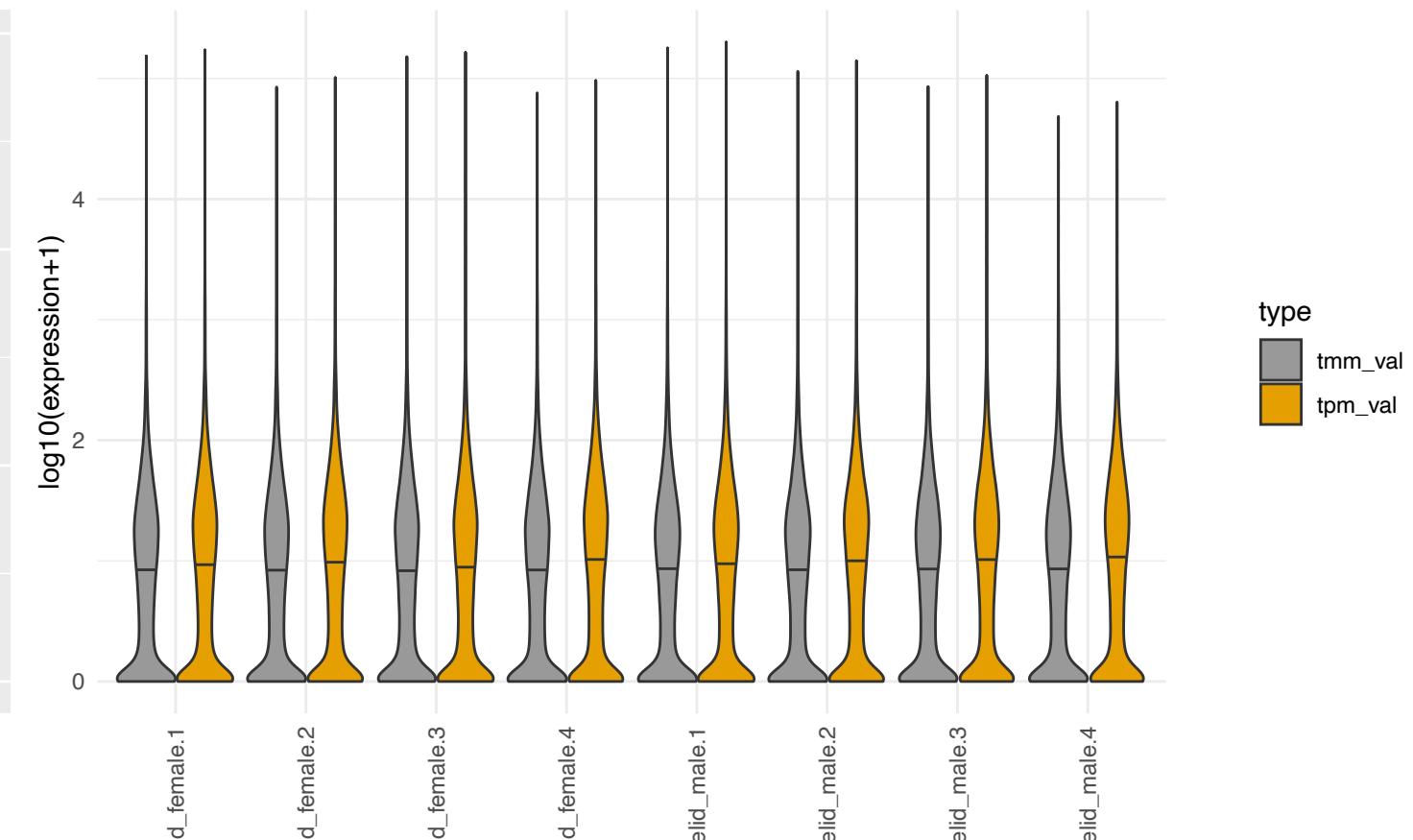
In tissue sample to sample Spearman Distance



skin (eye)

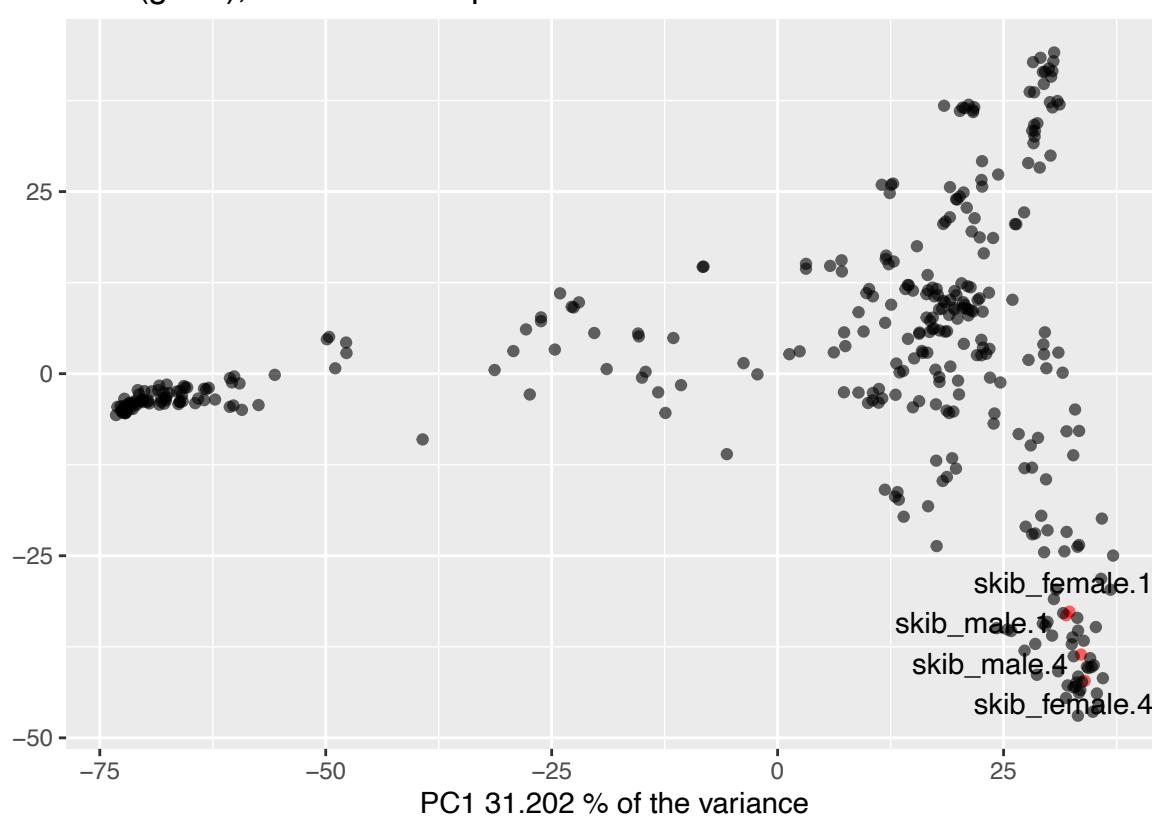


skin (eye)

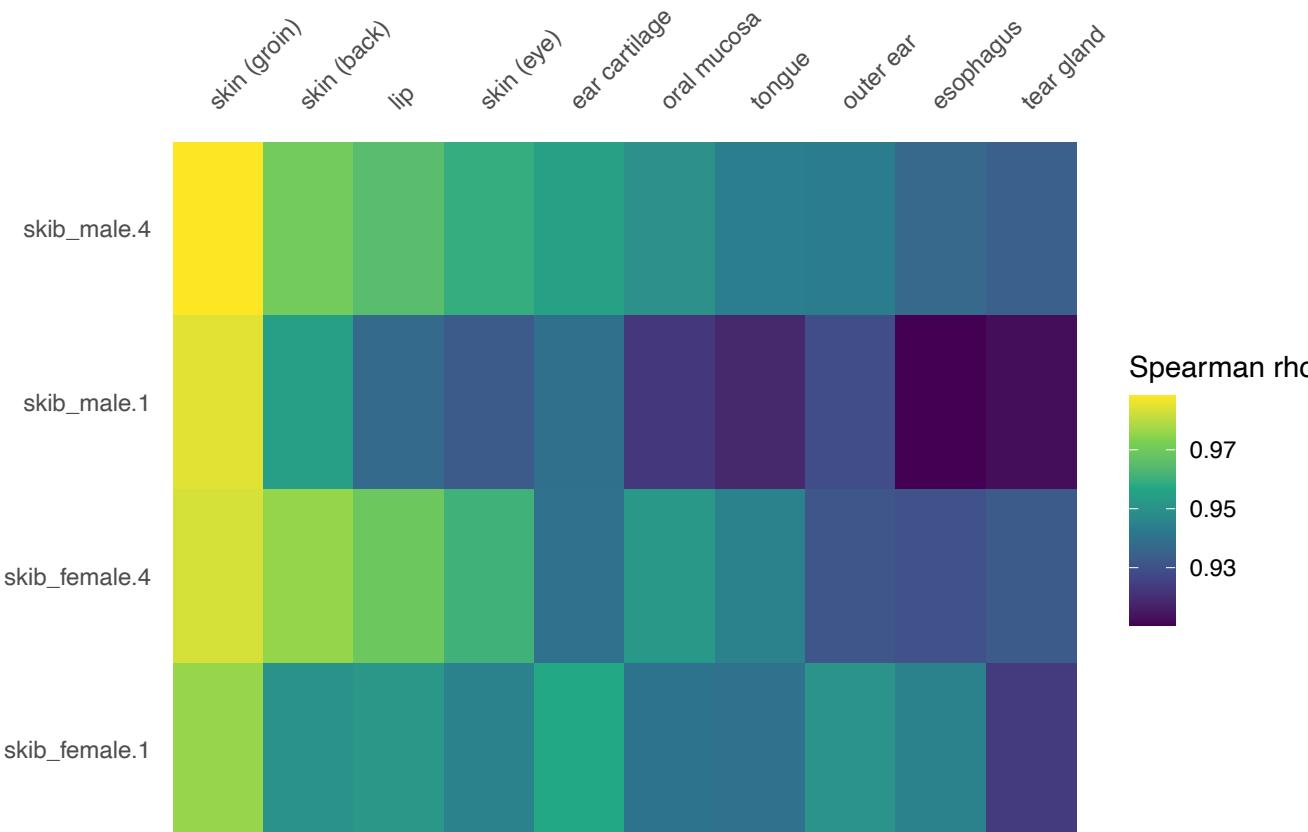


skin (groin), PCA: TMM expression values

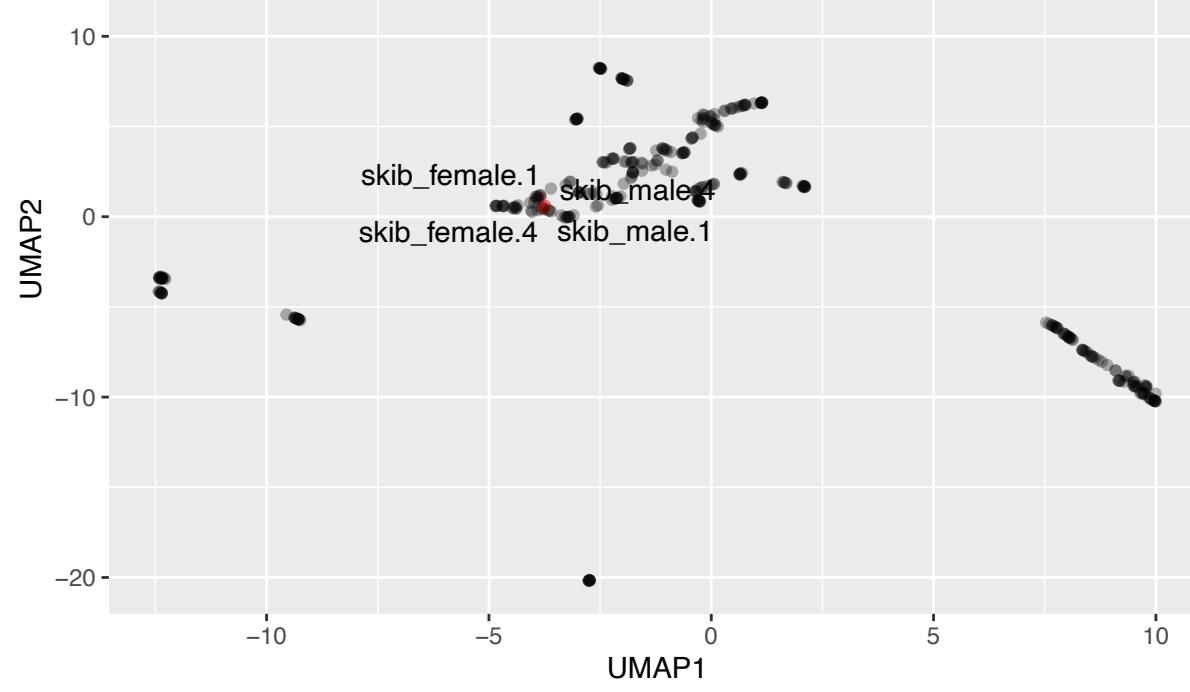
PC2 9.077 % of the variance



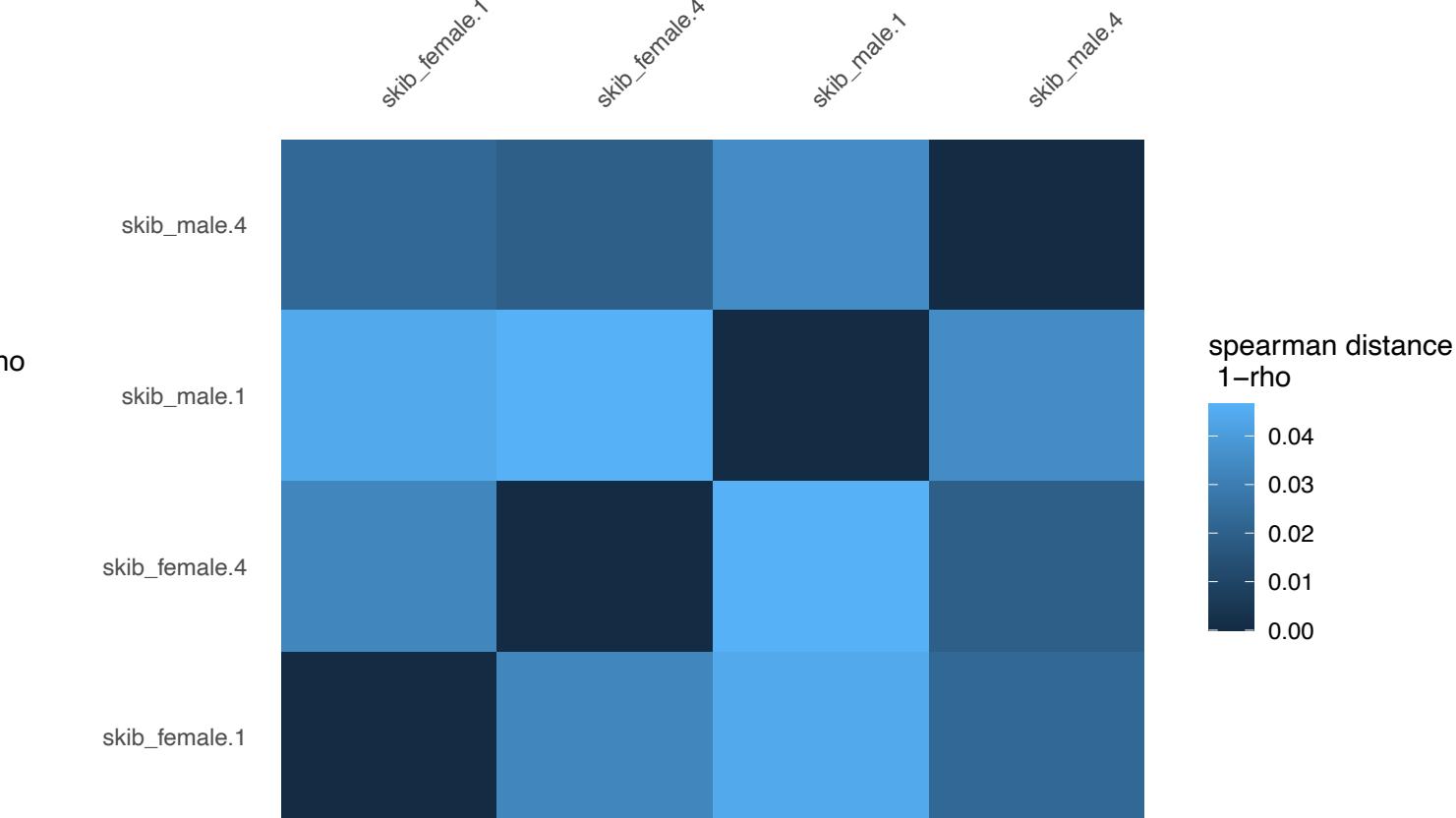
Tissue group to sample correlation



skin (groin), UMAP: TMM expression values

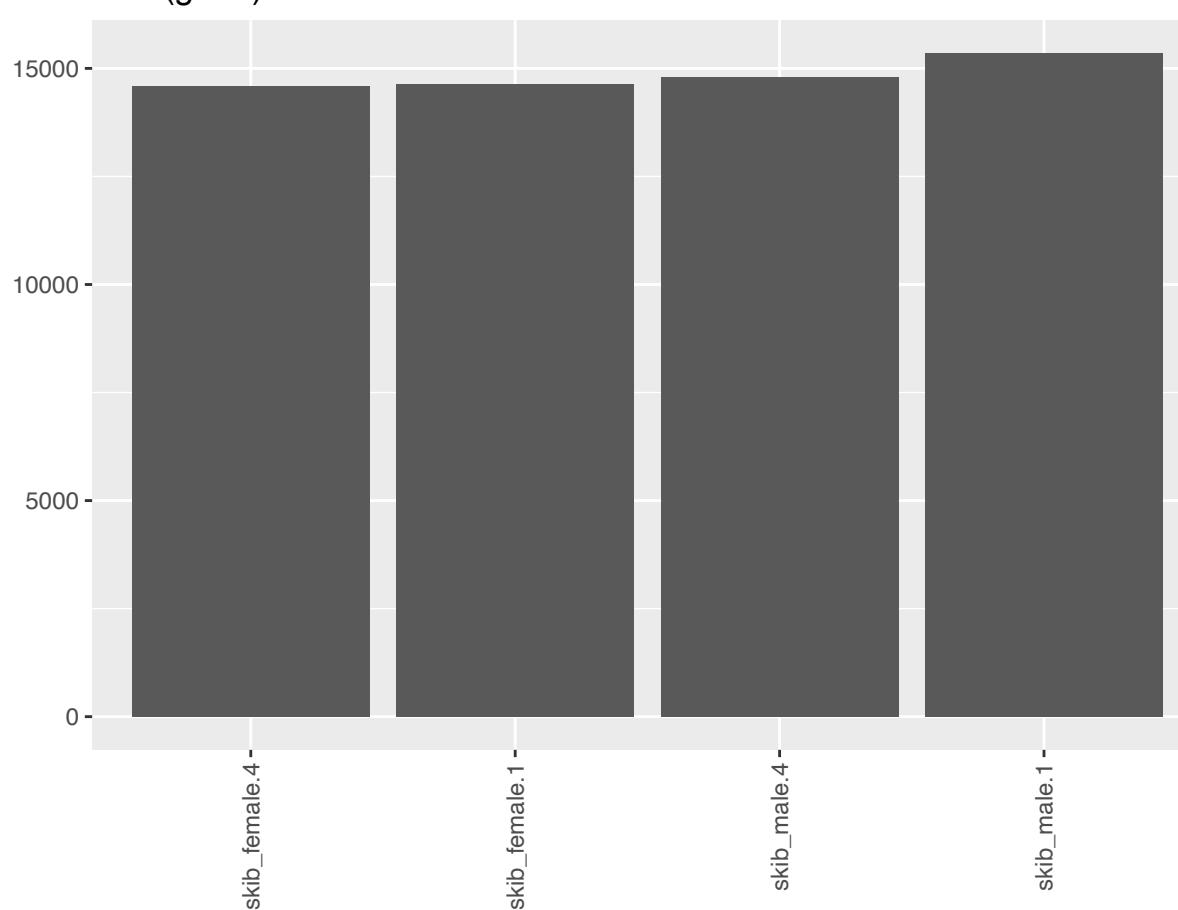


In tissue sample to sample Spearman Distance

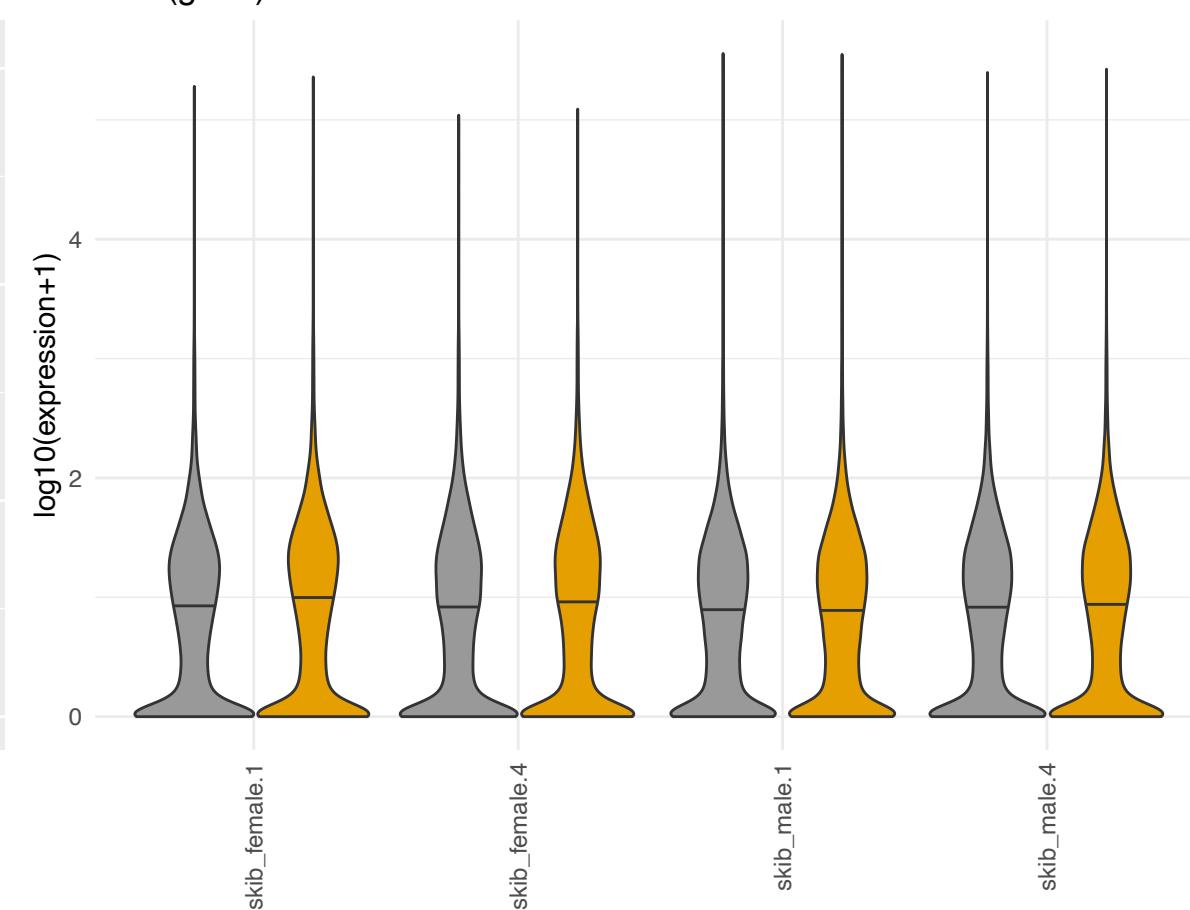


skin (groin)

n(genes) >= 1 TMM

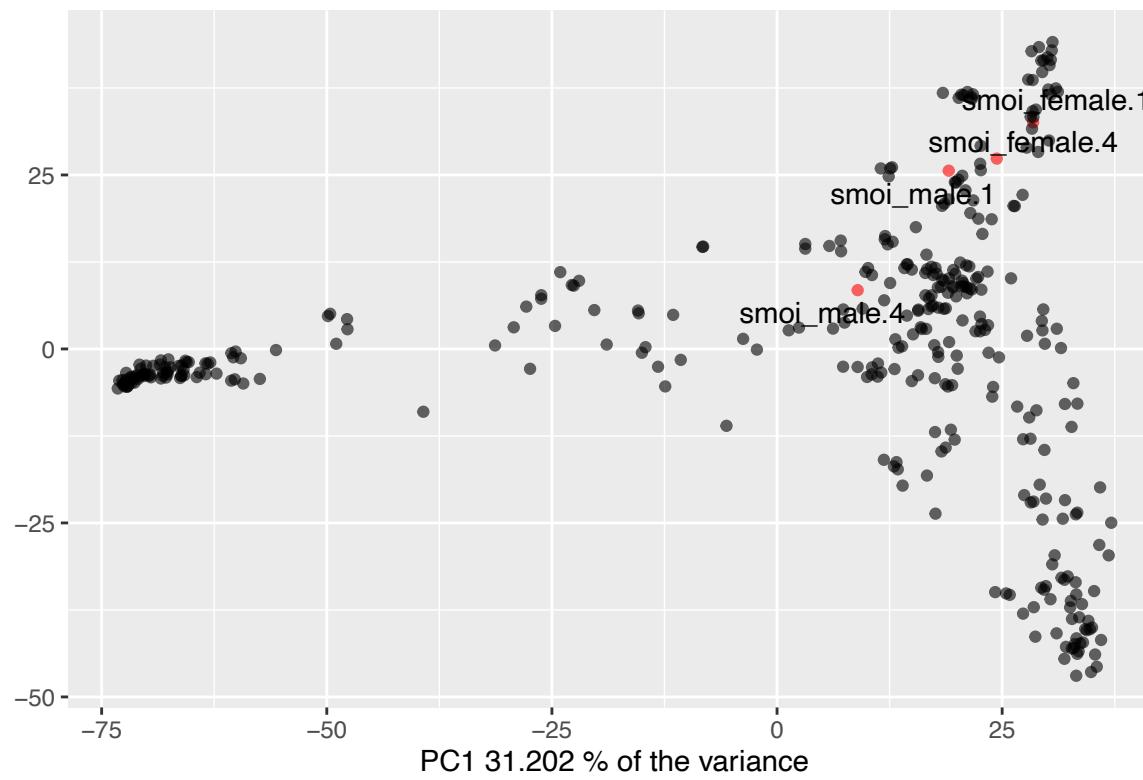


skin (groin)

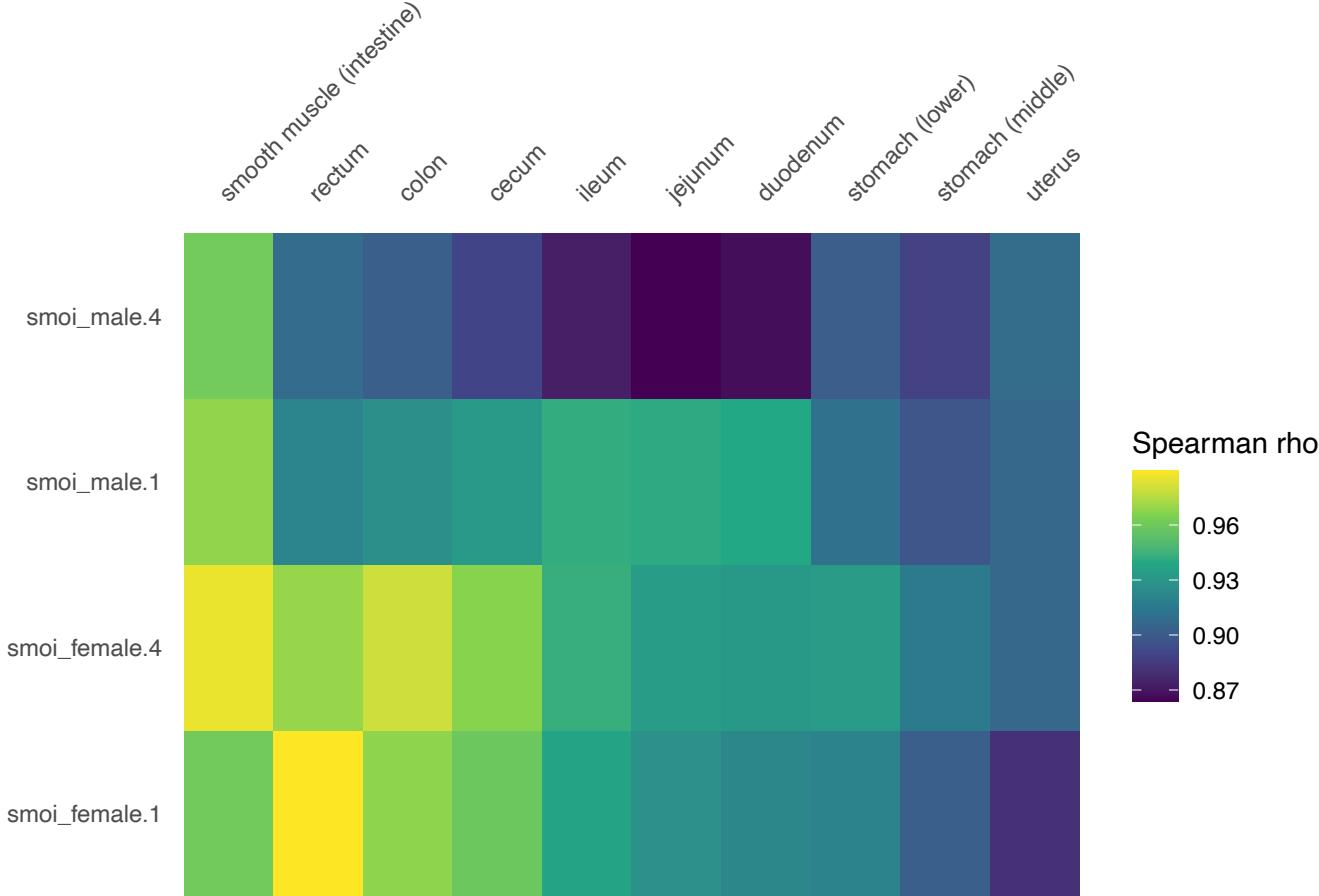
log₁₀(expression+1)

smooth muscle (intestine), PCA: TMM expression values

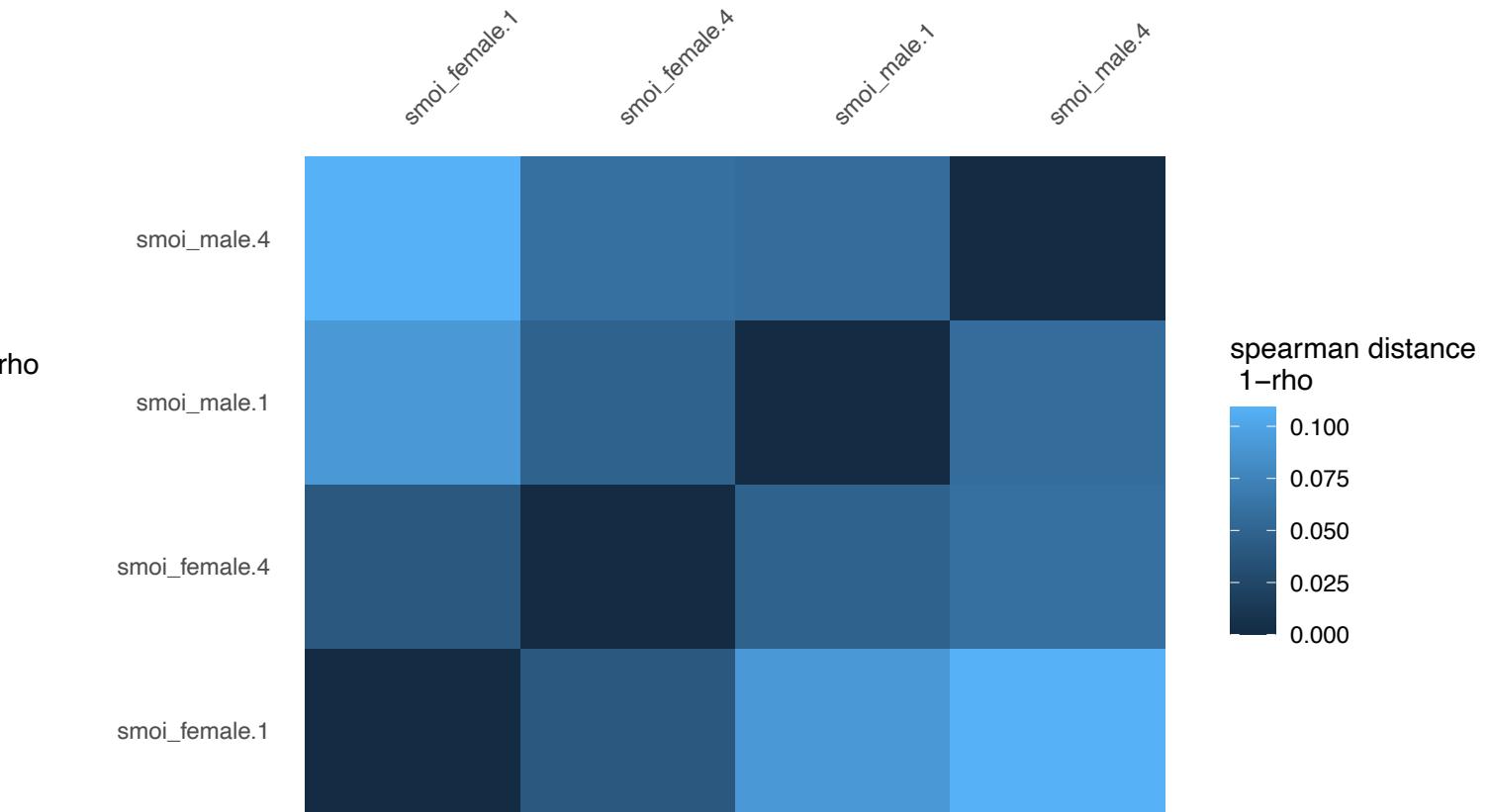
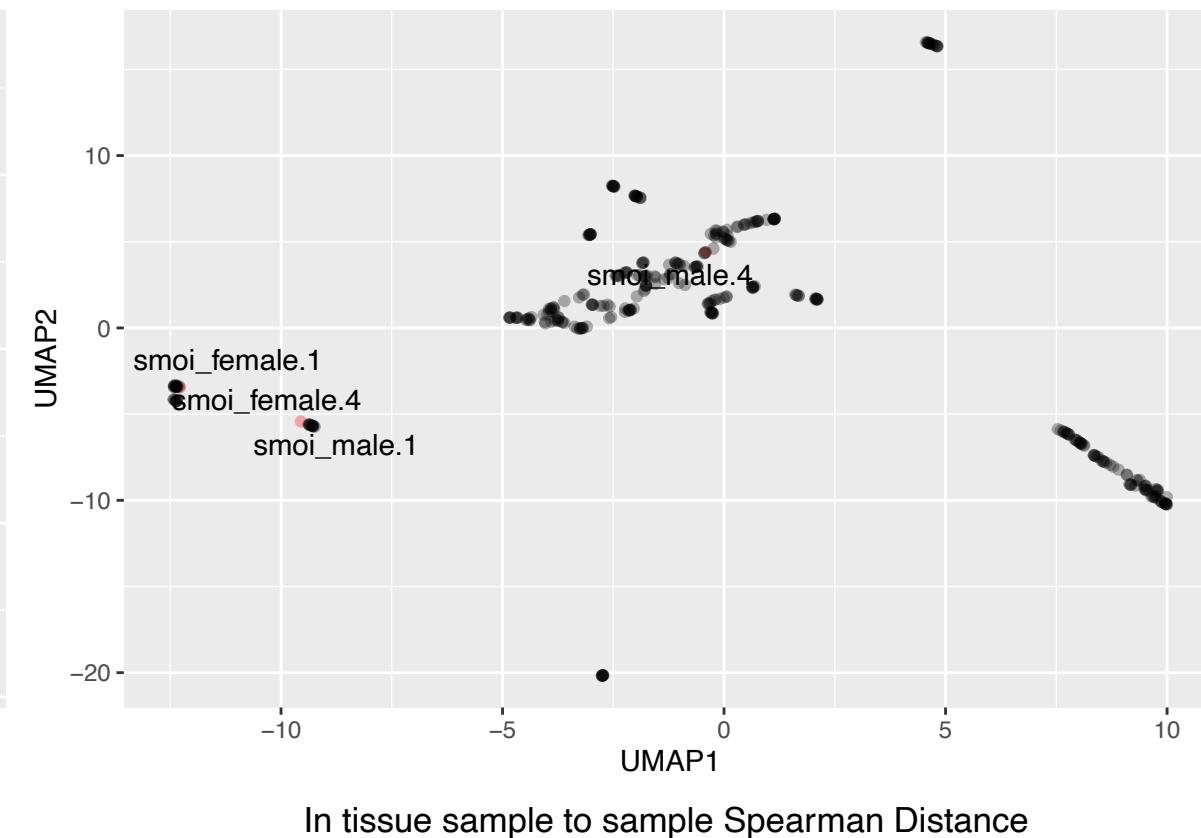
PC2 9.077 % of the variance



Tissue group to sample correlation

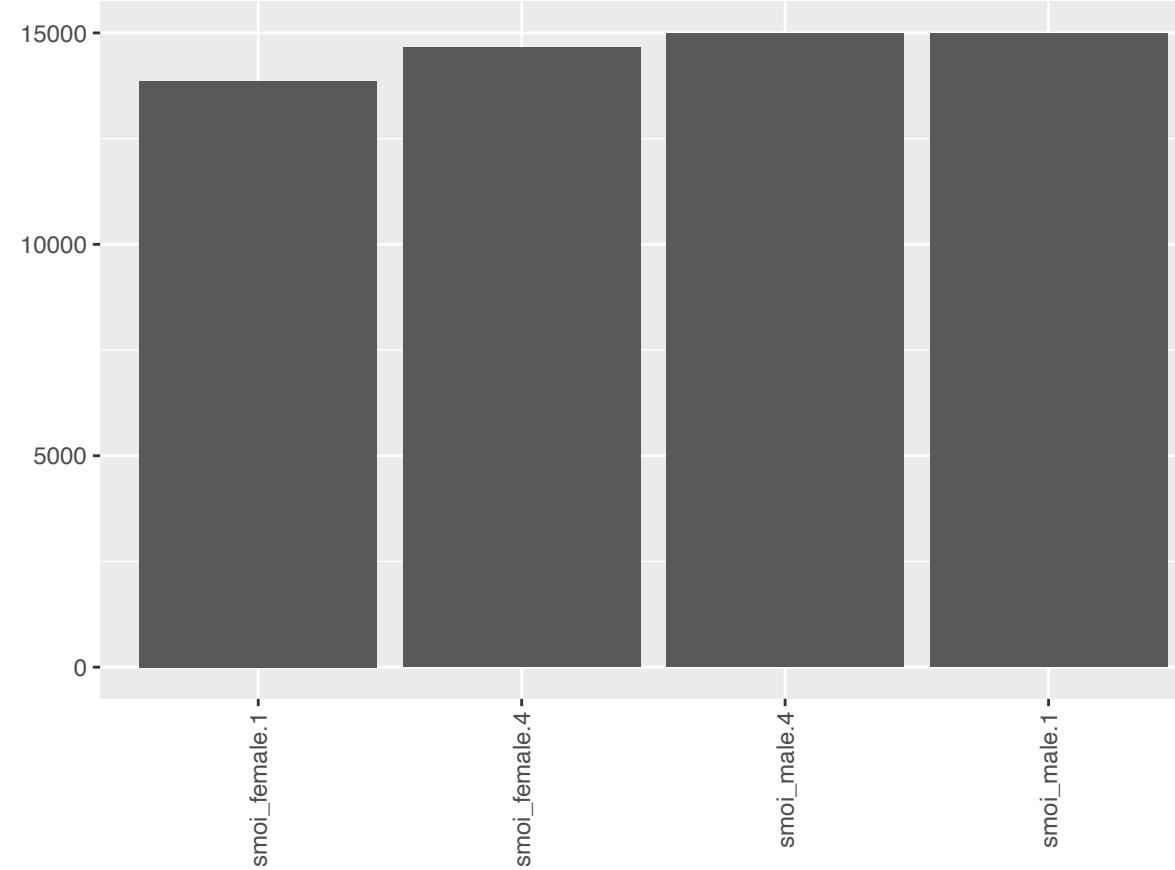


smooth muscle (intestine), UMAP: TMM expression values

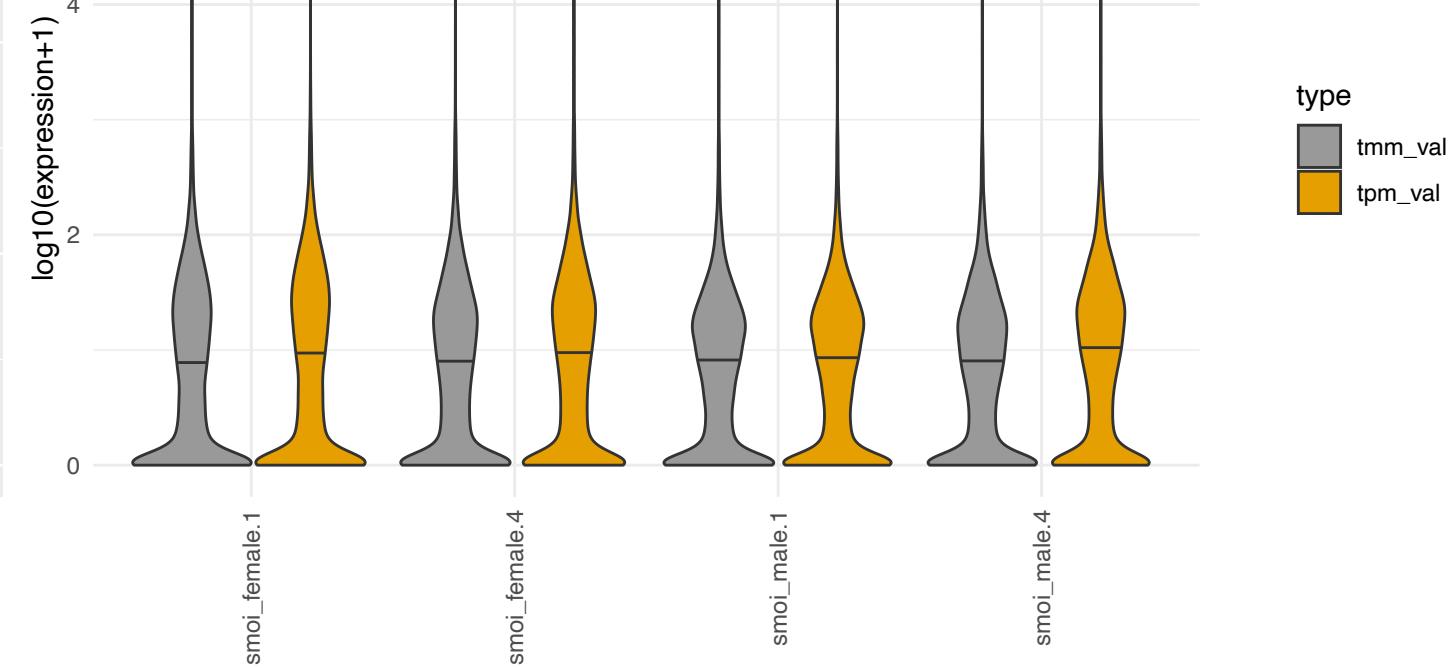


smooth muscle (intestine)

n(genes) >= 1 TMM

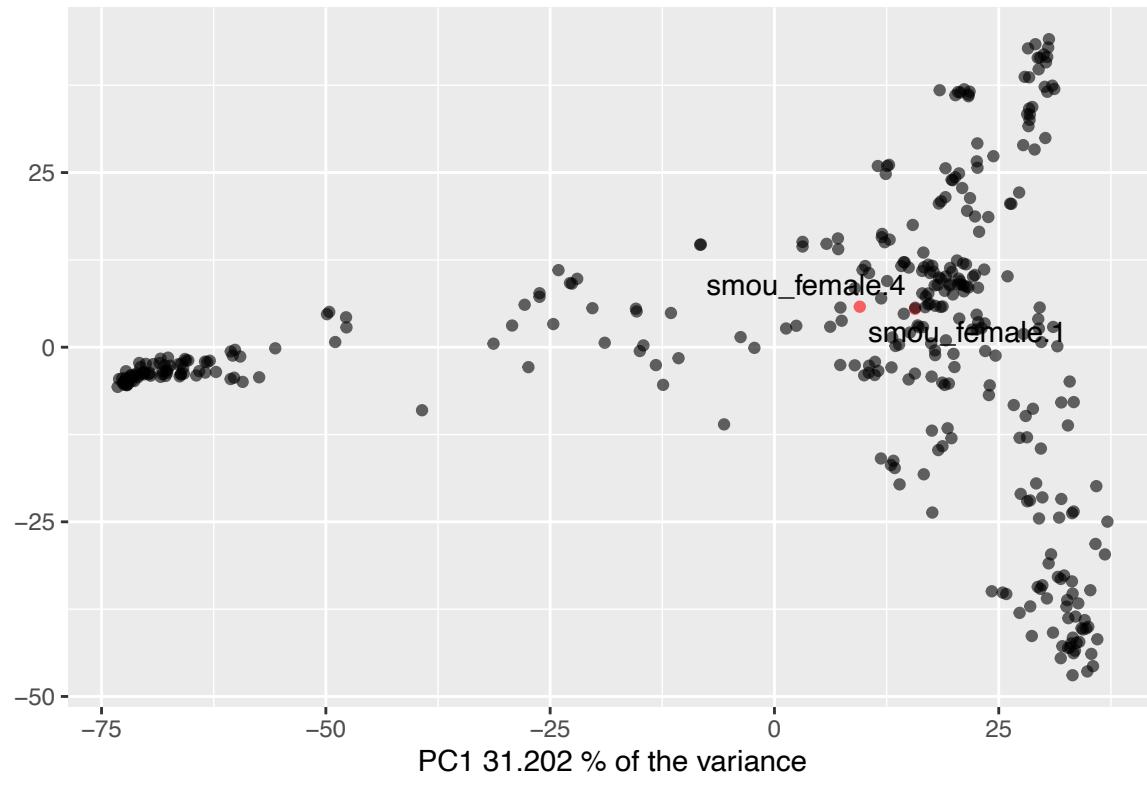


smooth muscle (intestine)

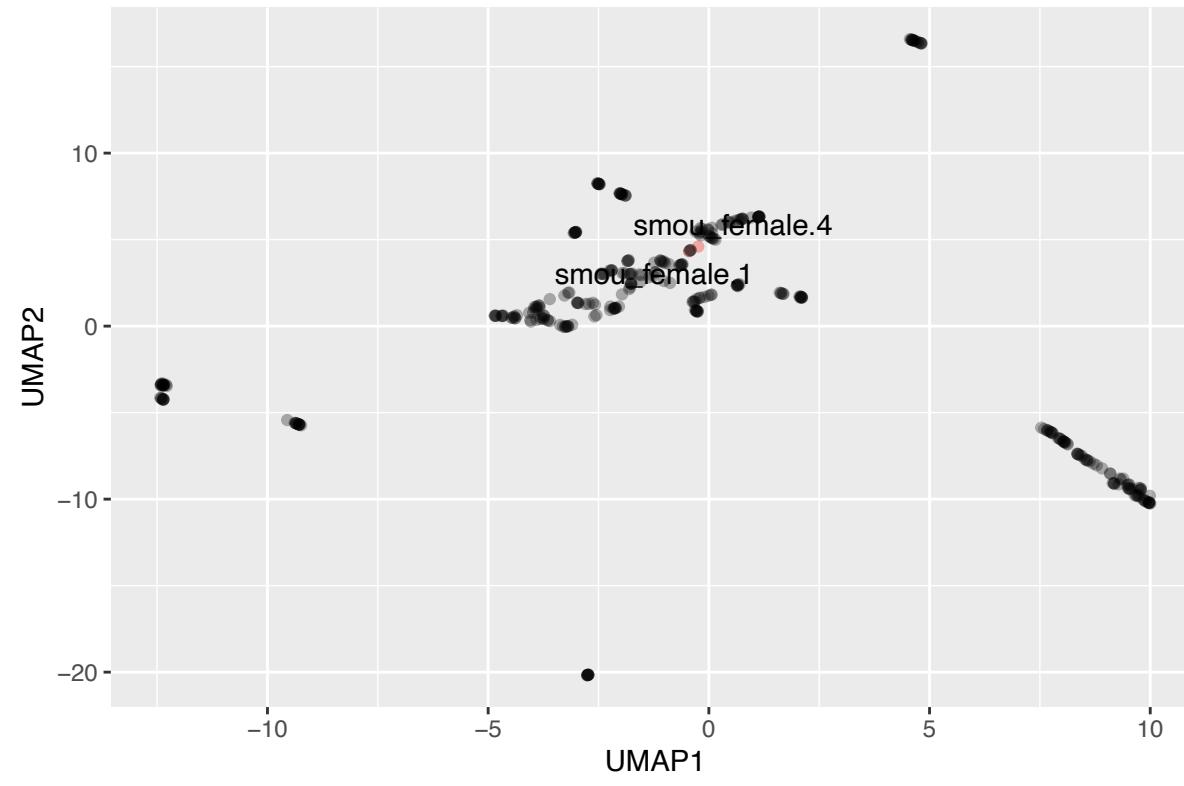


smooth muscle (uterus), PCA: TMM expression values

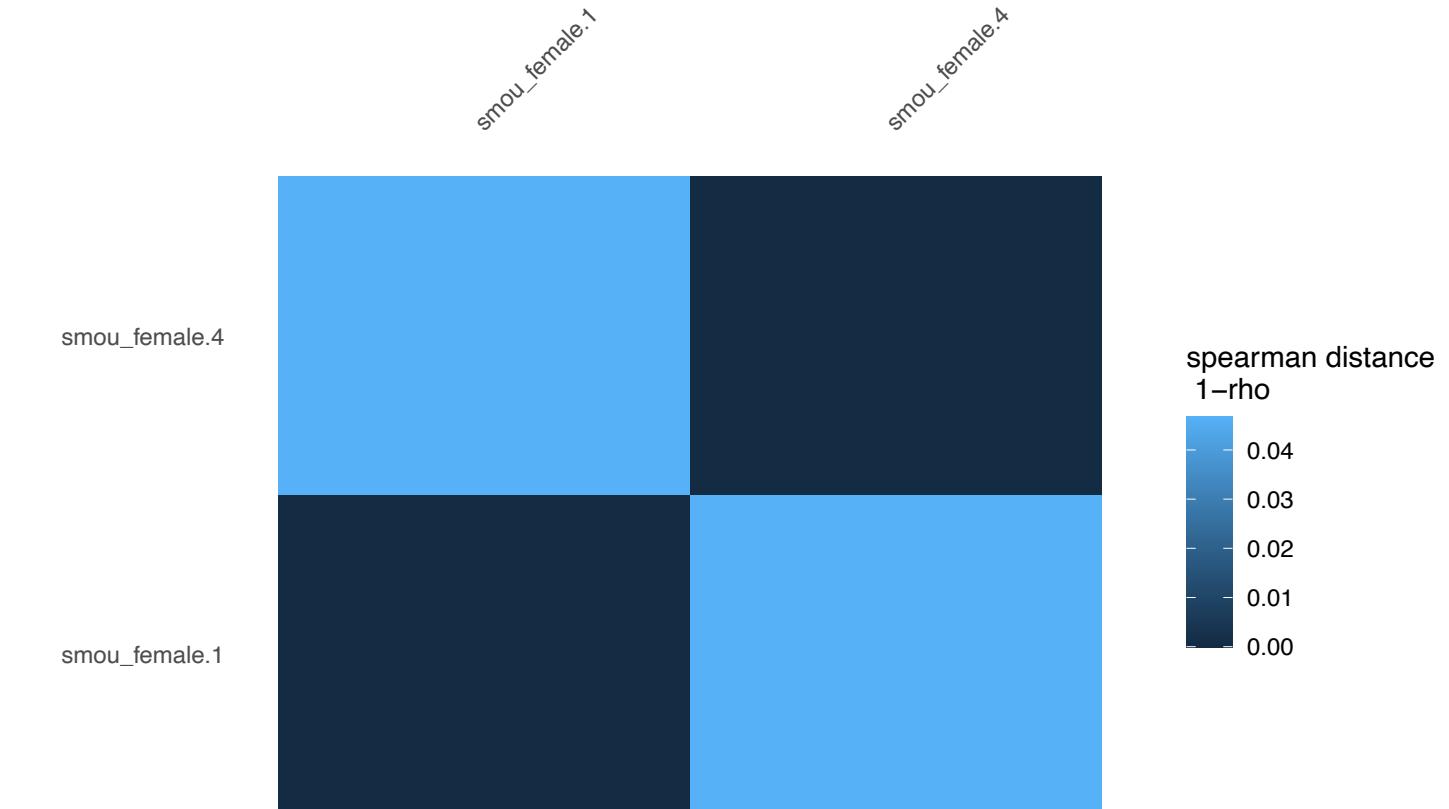
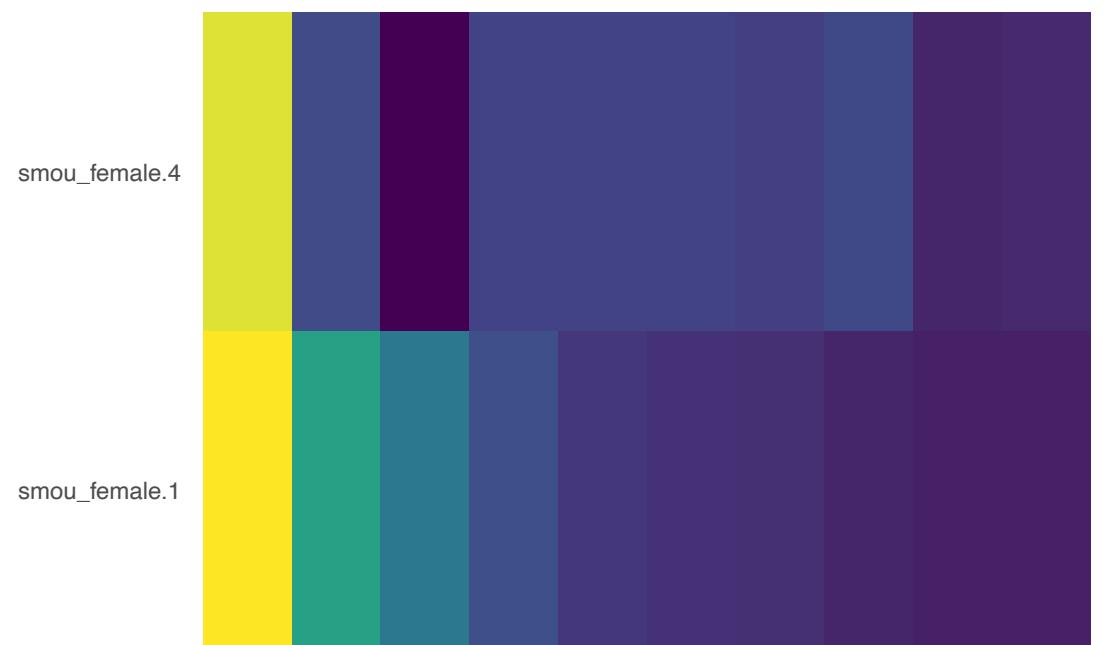
PC2 9.077 % of the variance



smooth muscle (uterus), UMAP: TMM expression values

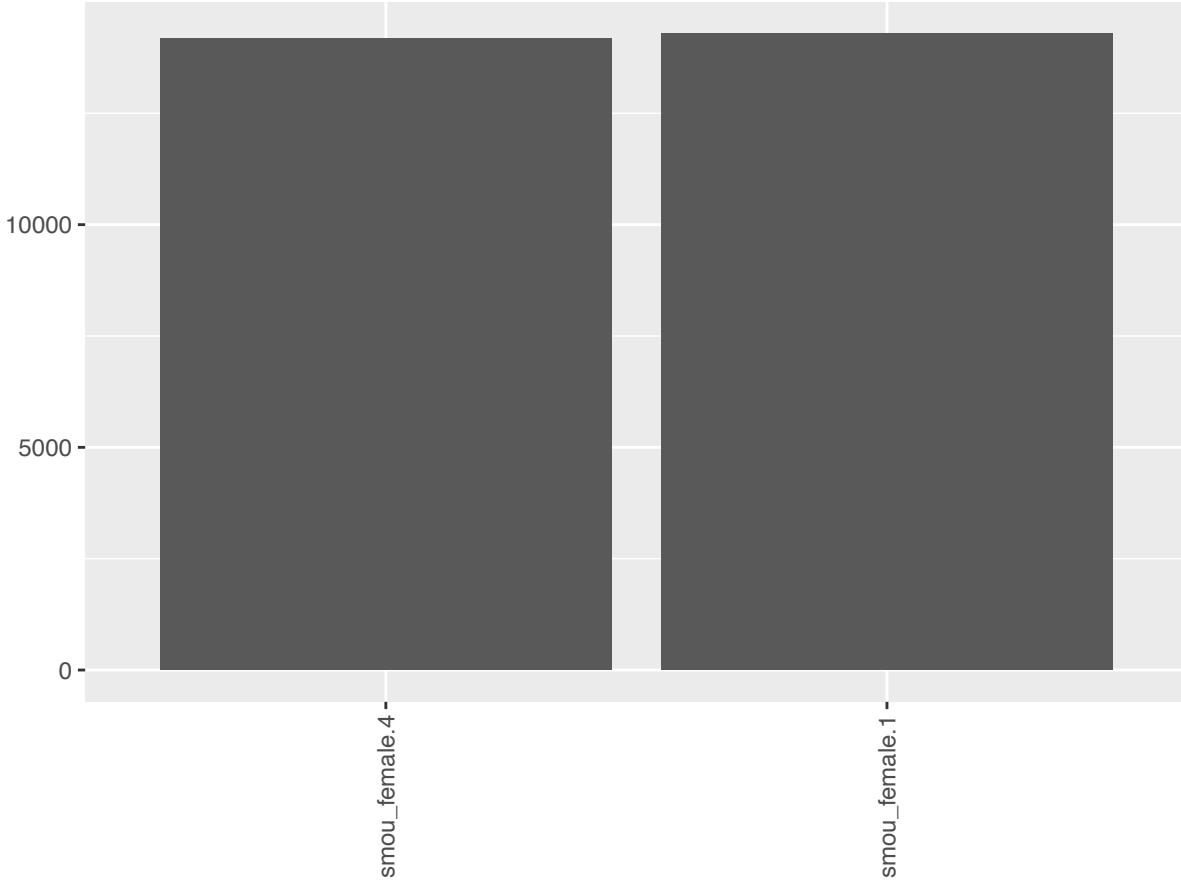


smooth muscle (uterus)
uterus
endometrium
ductus deferens
penis
artery
synovial tissue
dura mater
breast
pleura

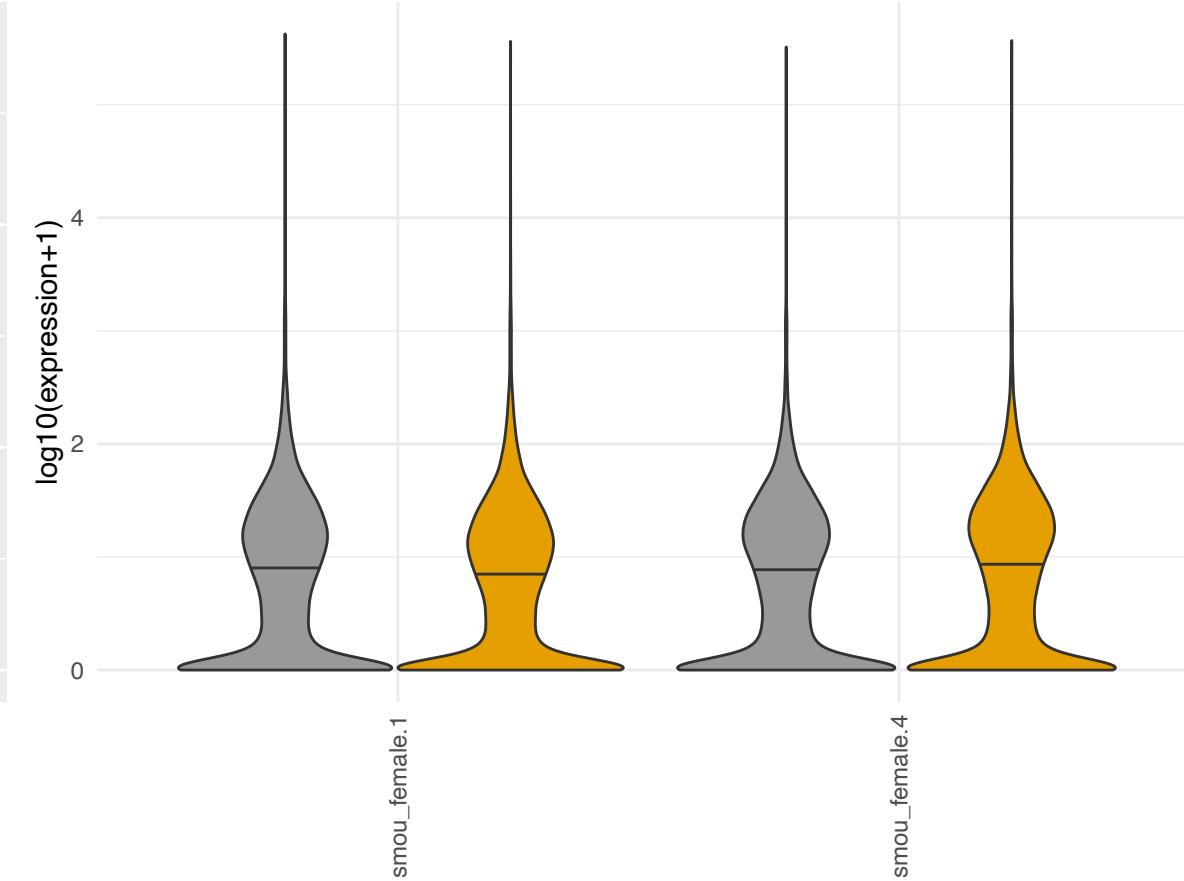


smooth muscle (uterus)

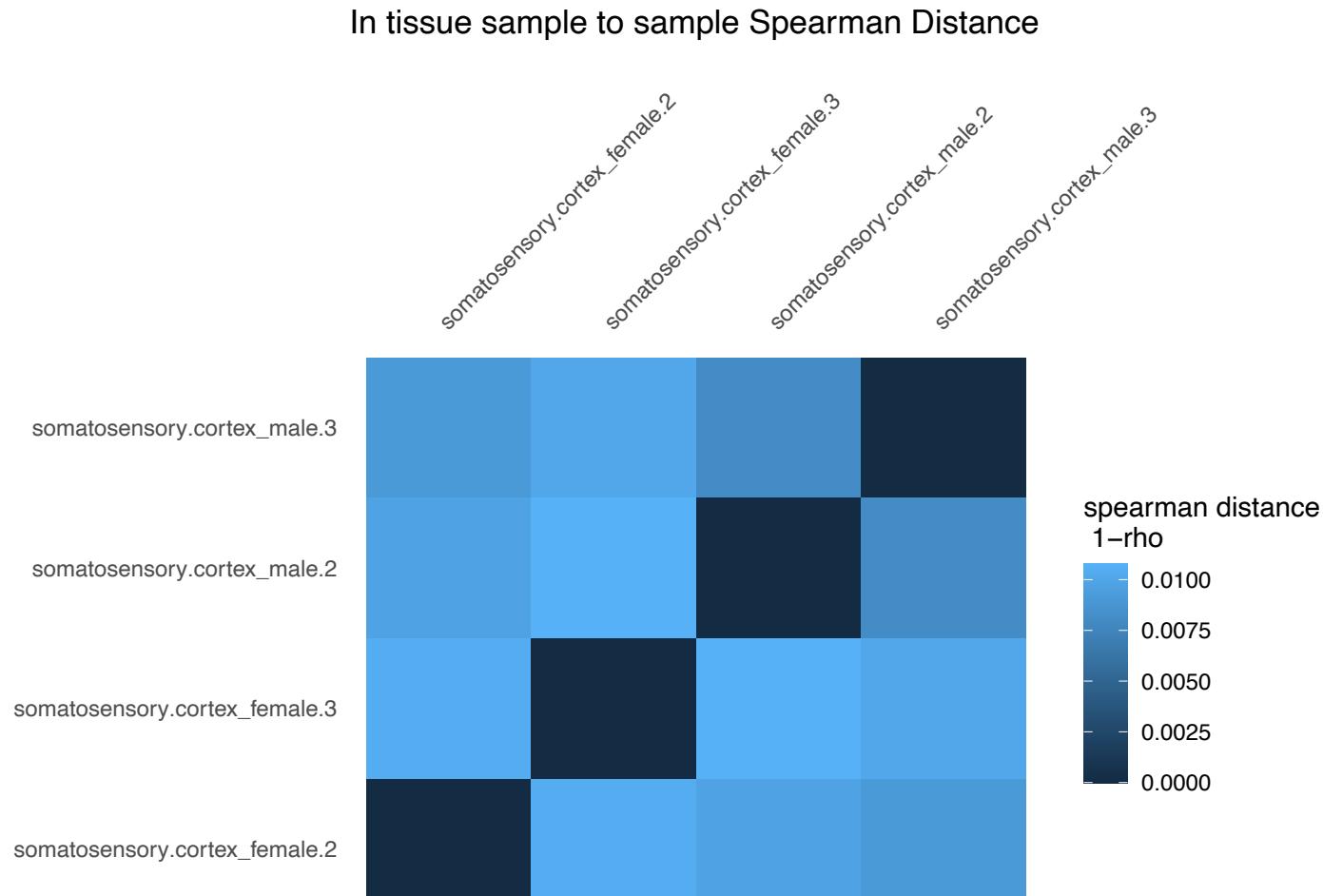
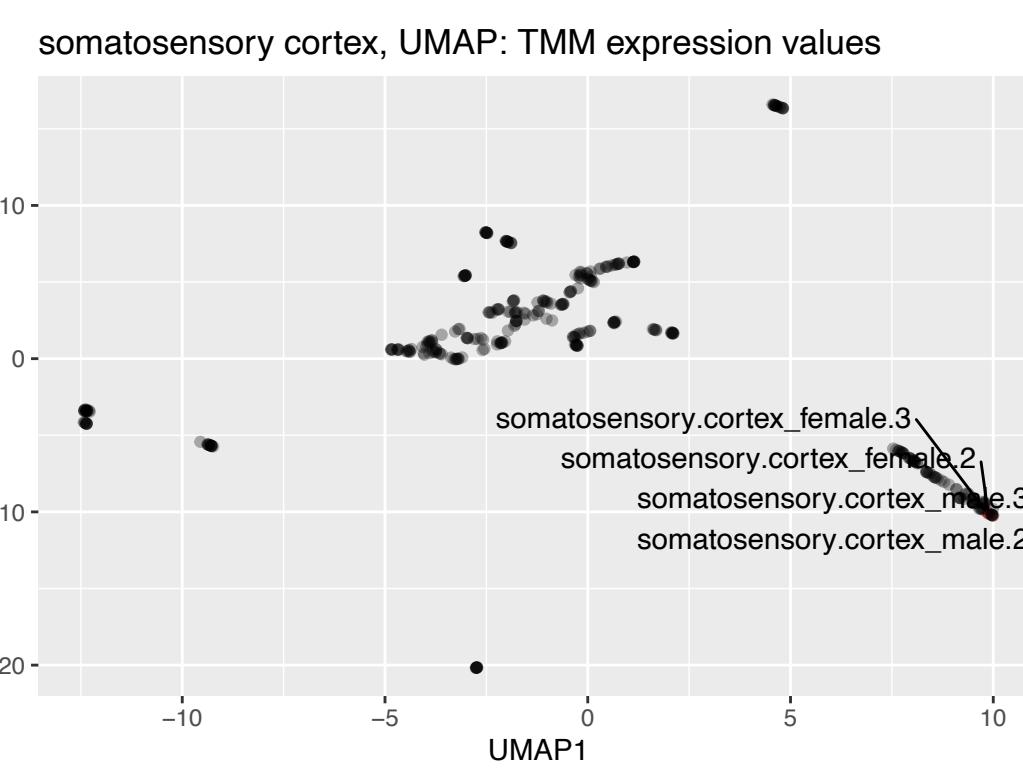
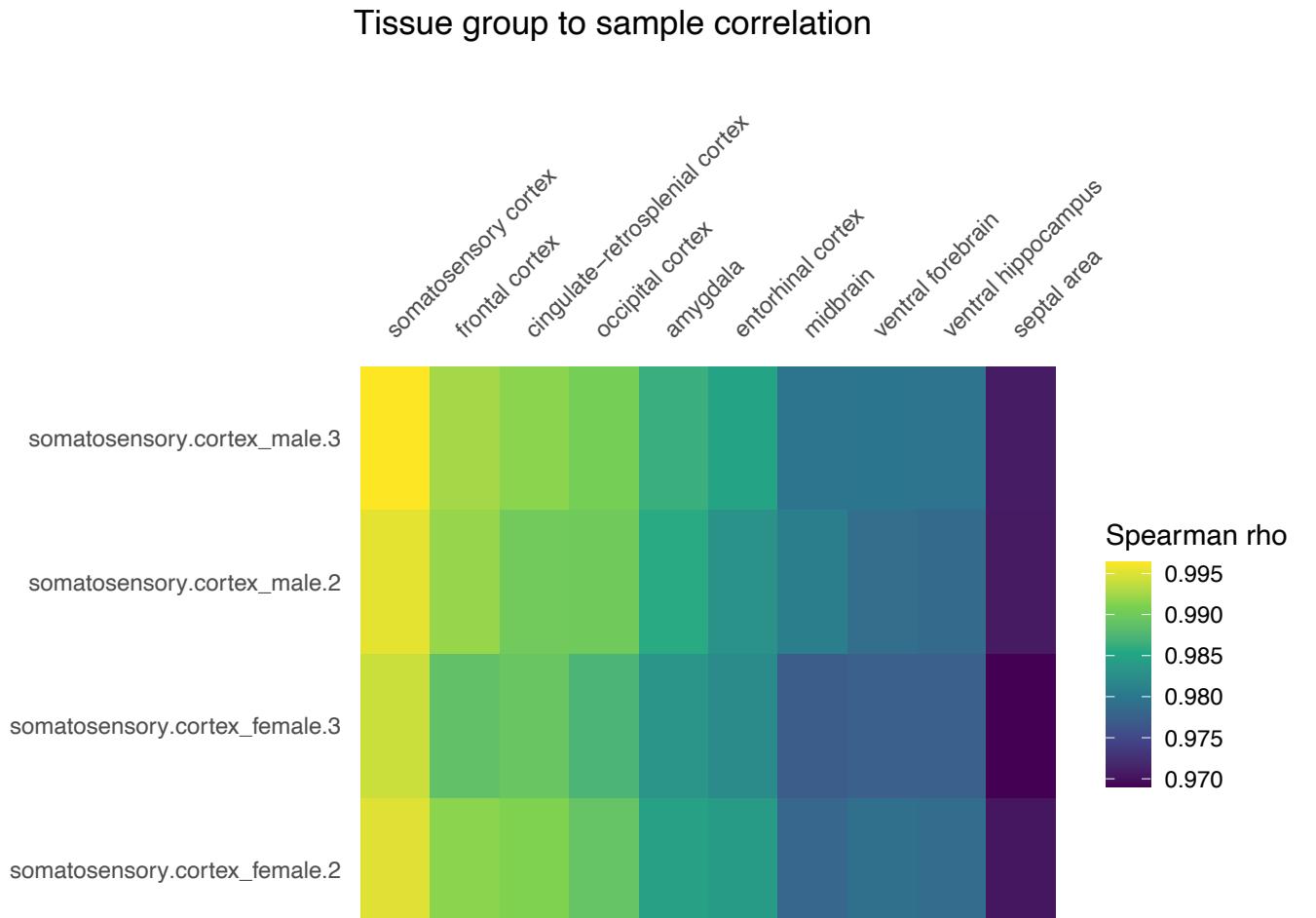
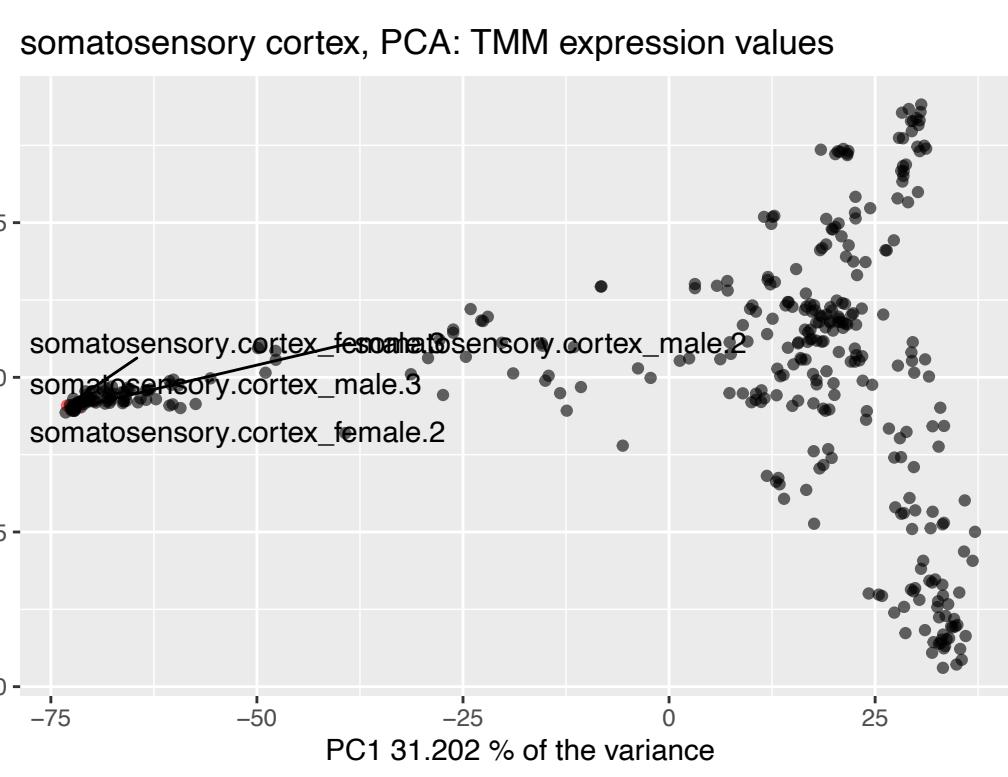
n(genes) >= 1 TMM



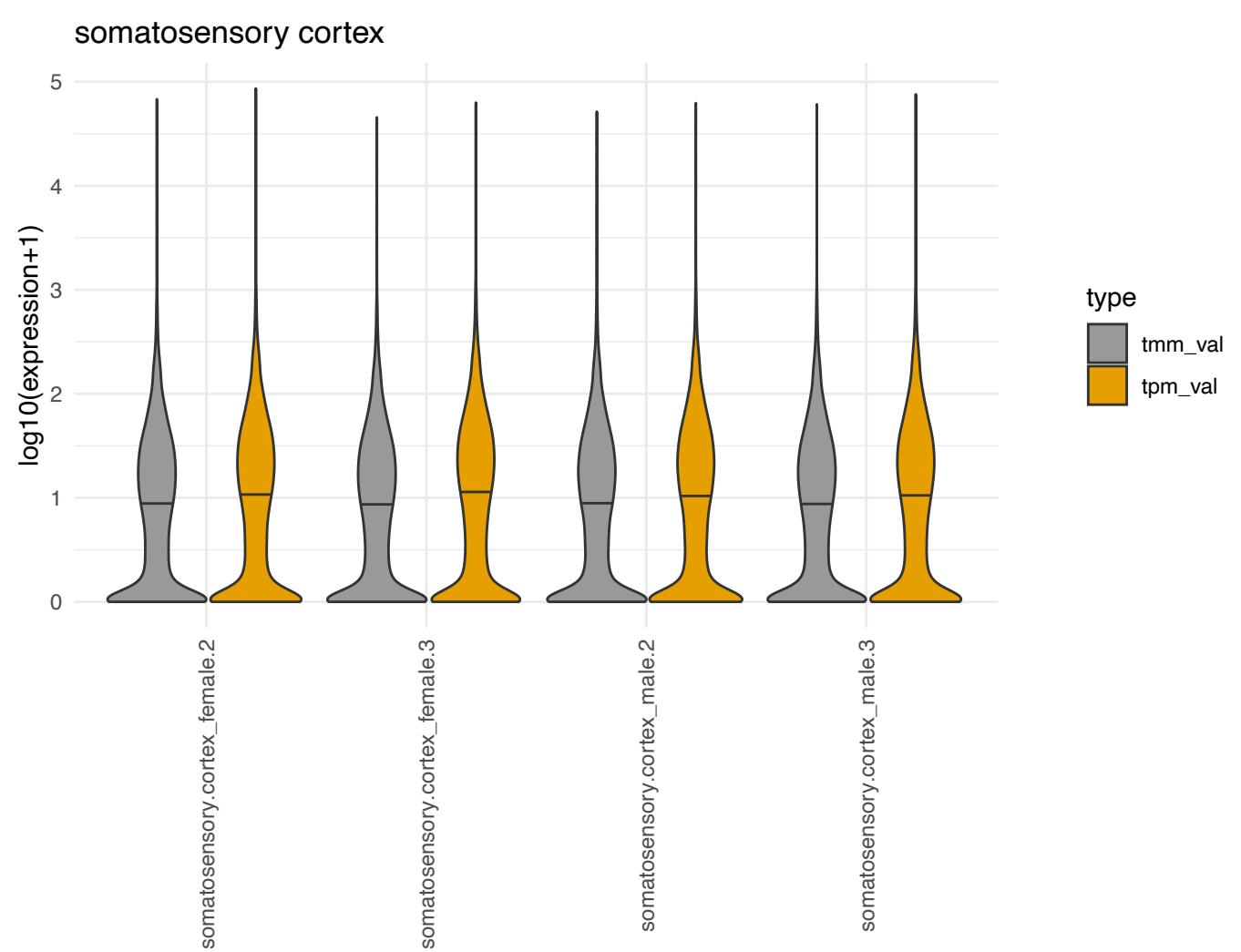
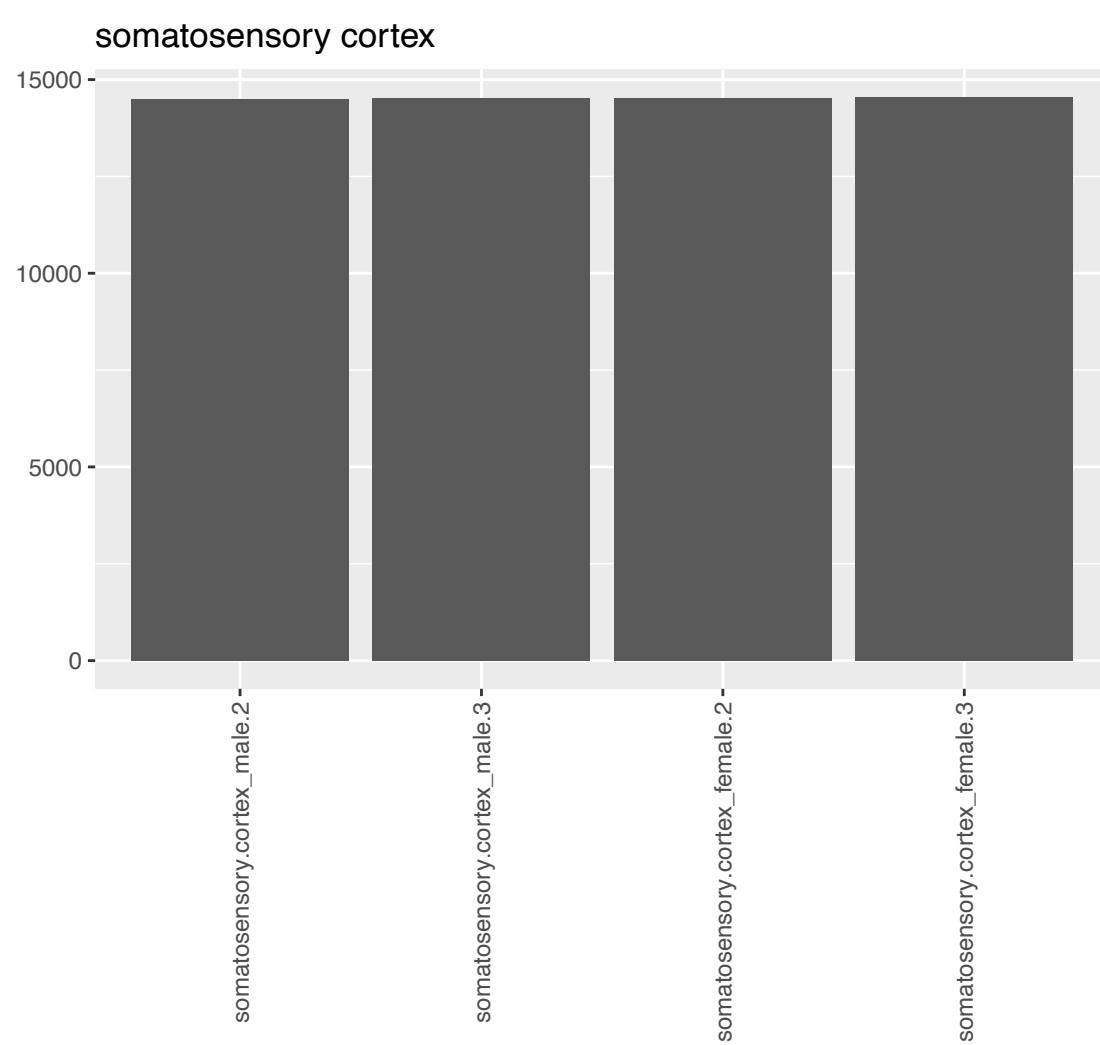
smooth muscle (uterus)



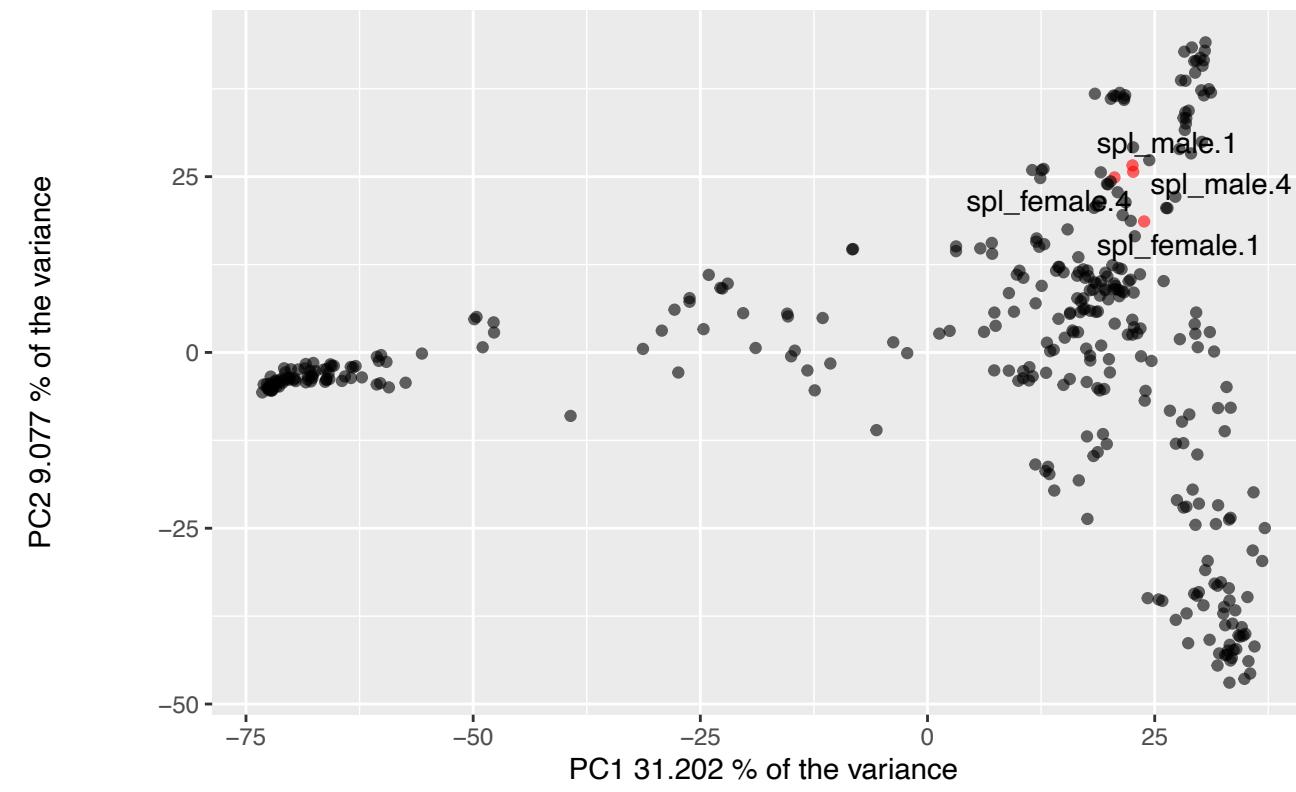
PC2 9.077 % of the variance



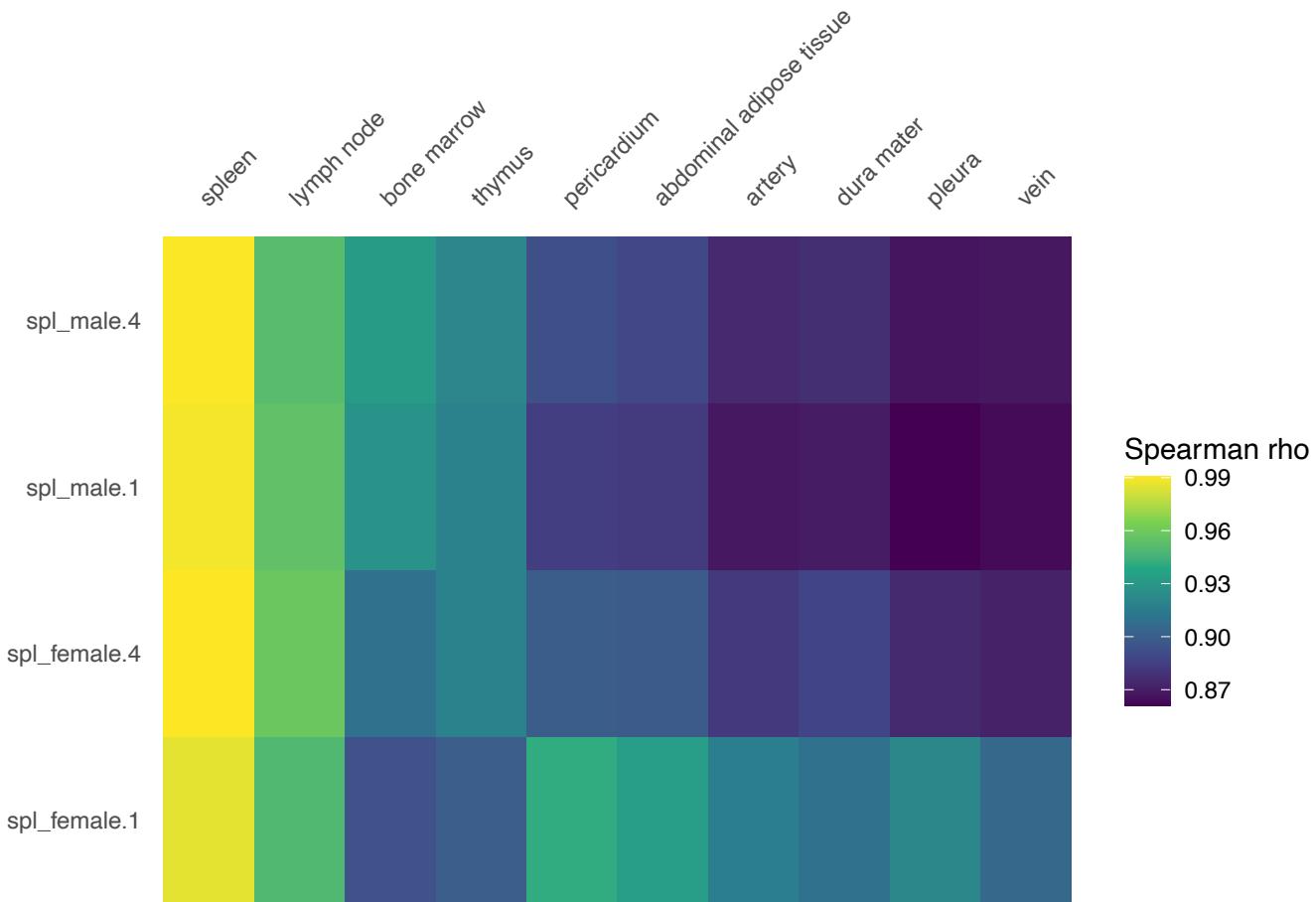
n(genes) >= 1 TMM



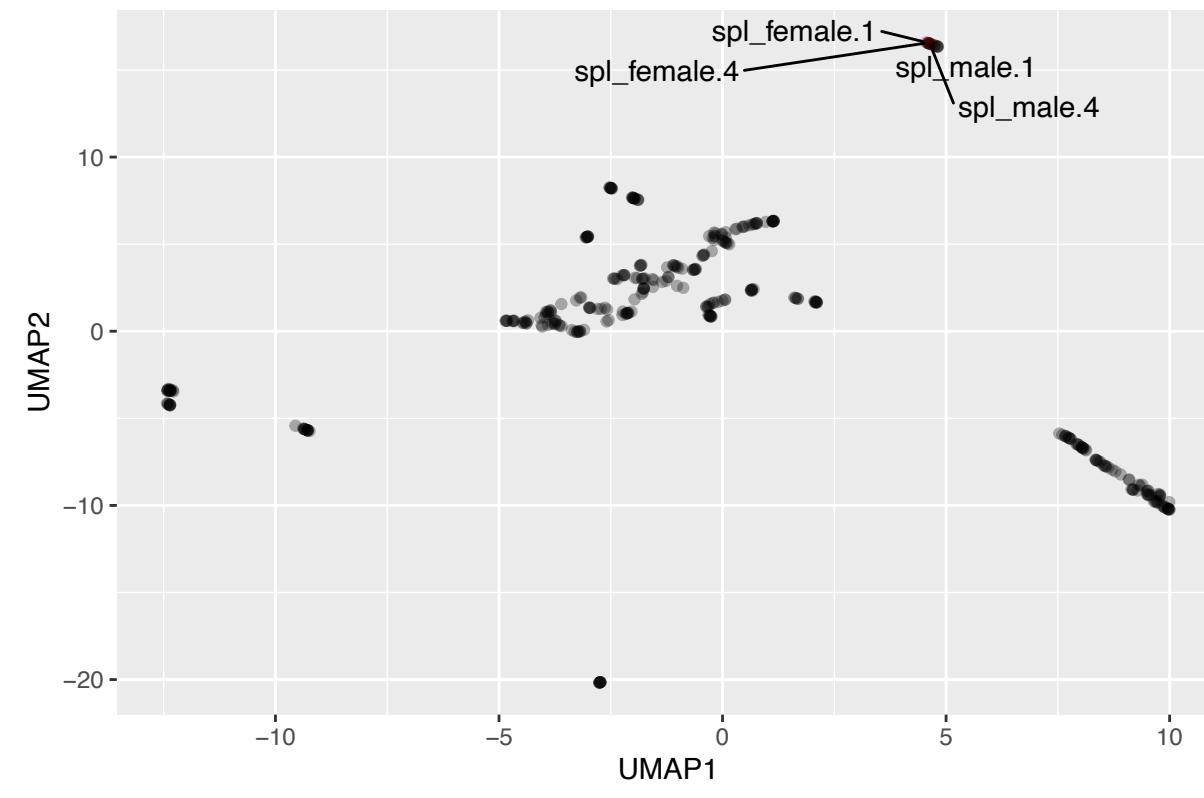
spleen, PCA: TMM expression values



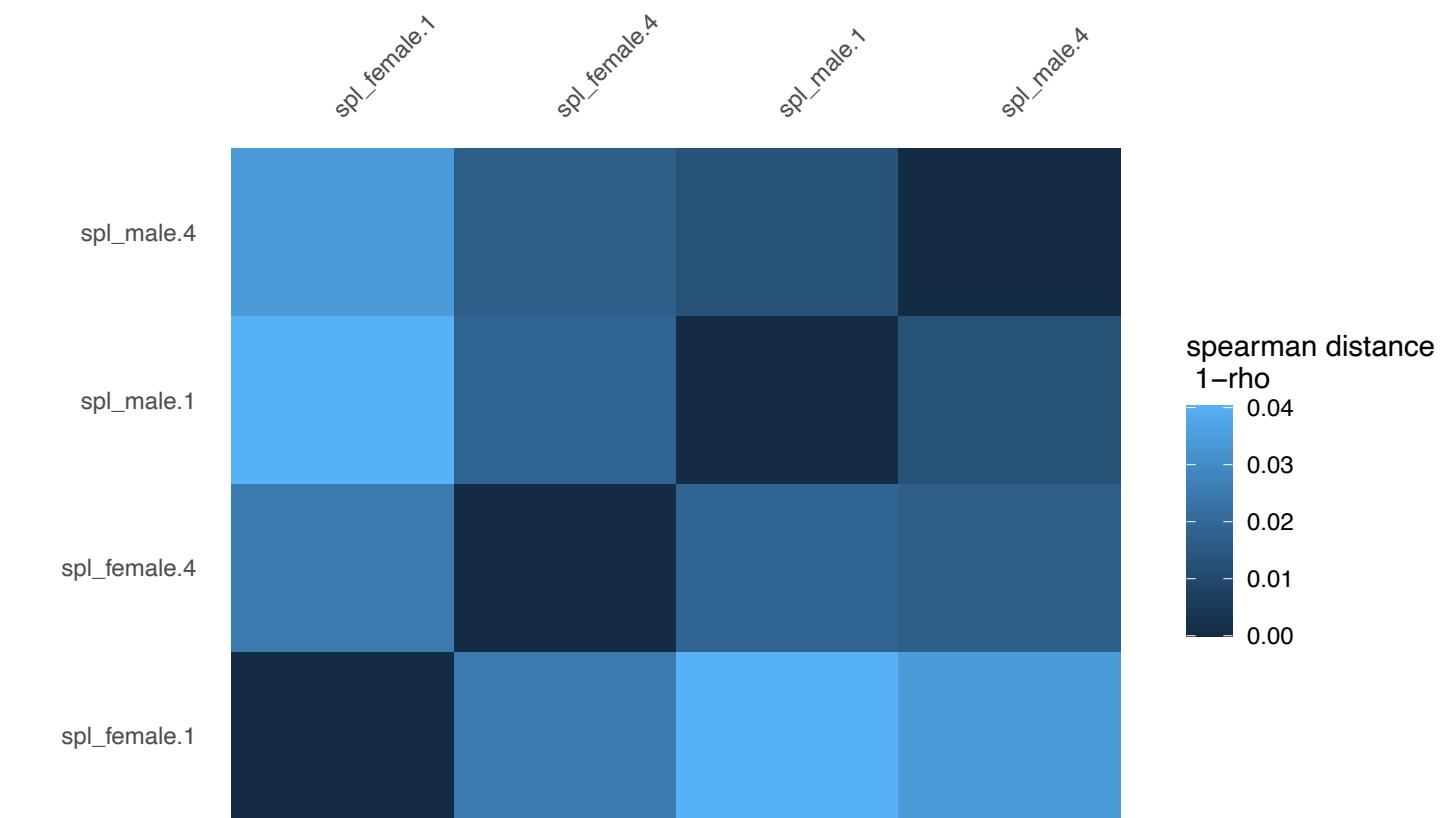
Tissue group to sample correlation



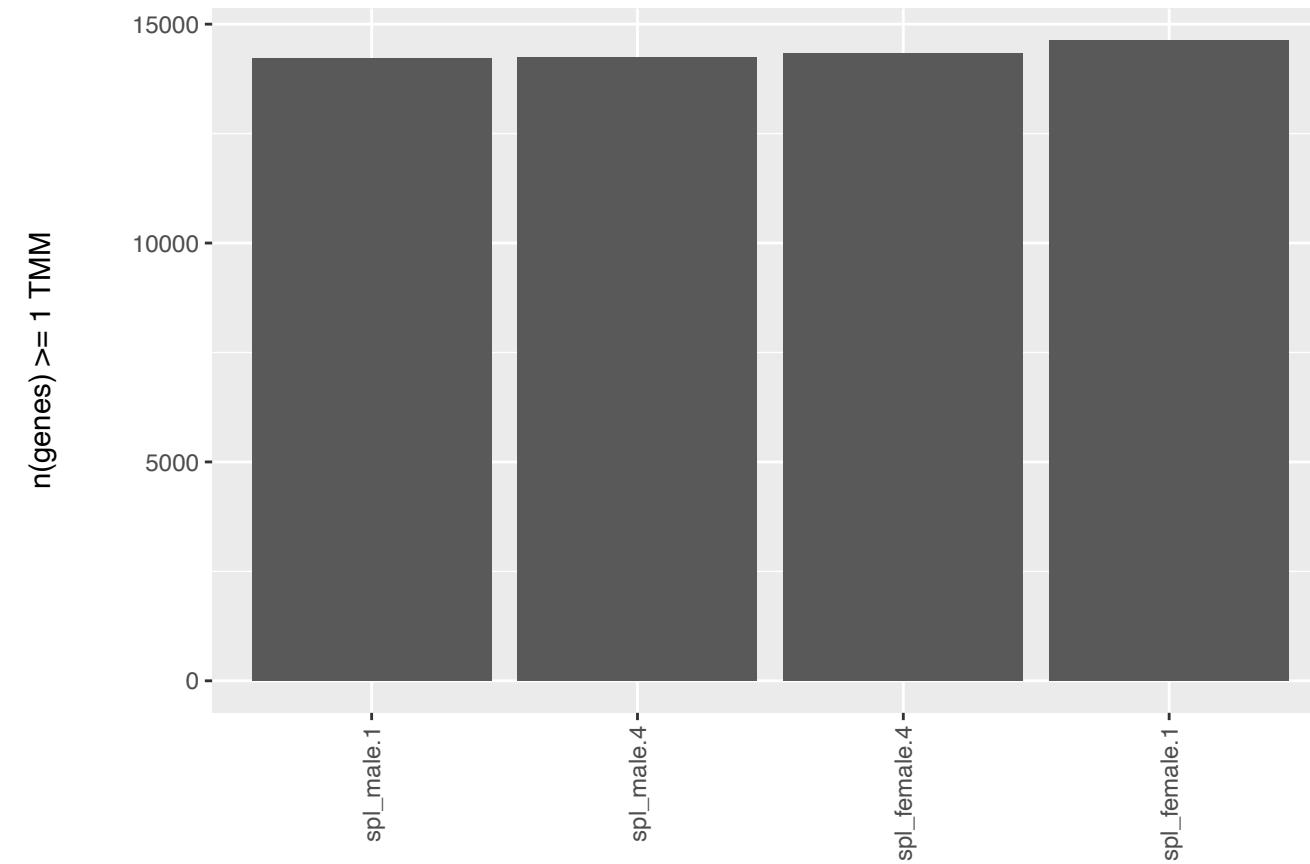
spleen, UMAP: TMM expression values



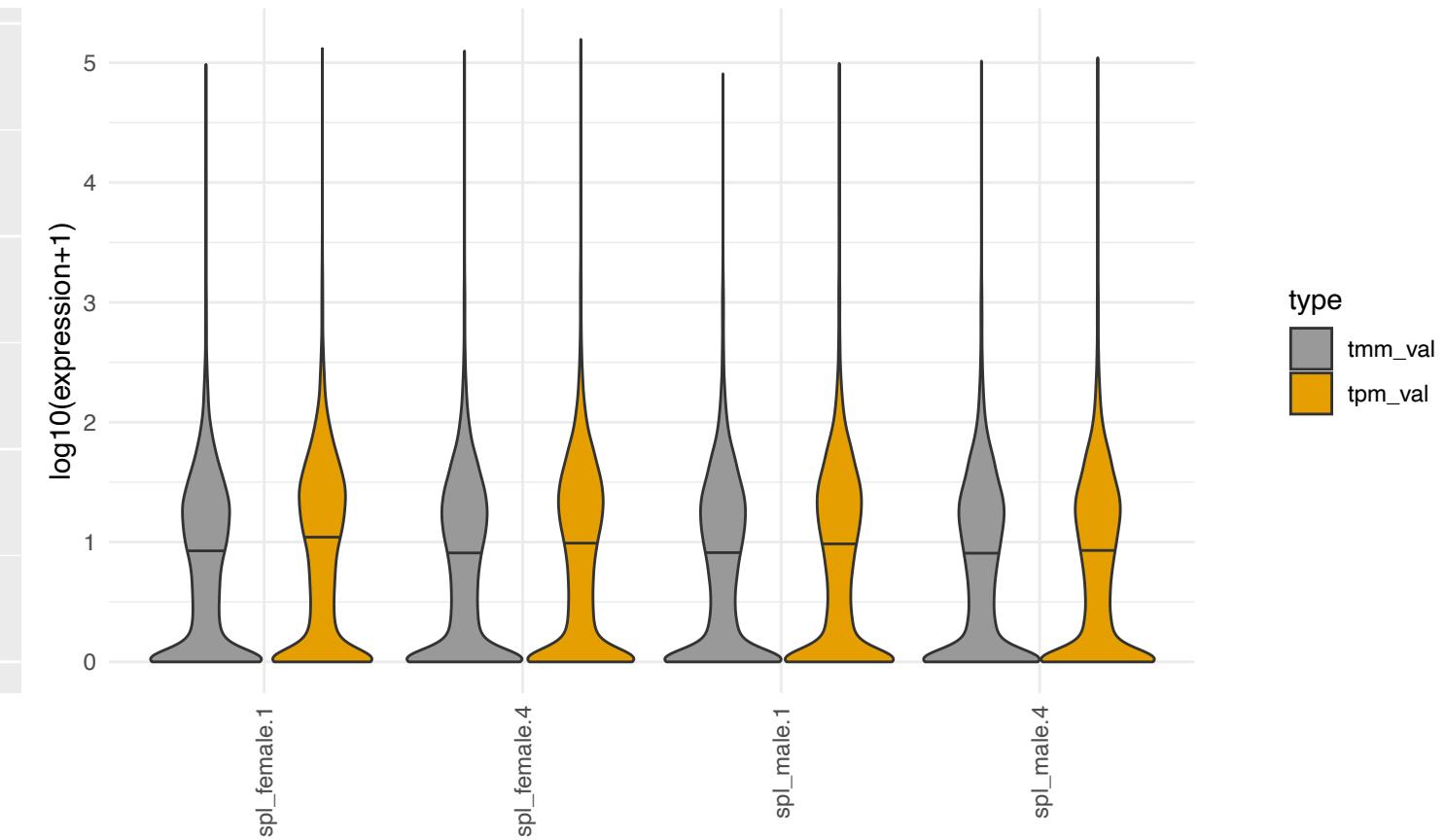
In tissue sample to sample Spearman Distance



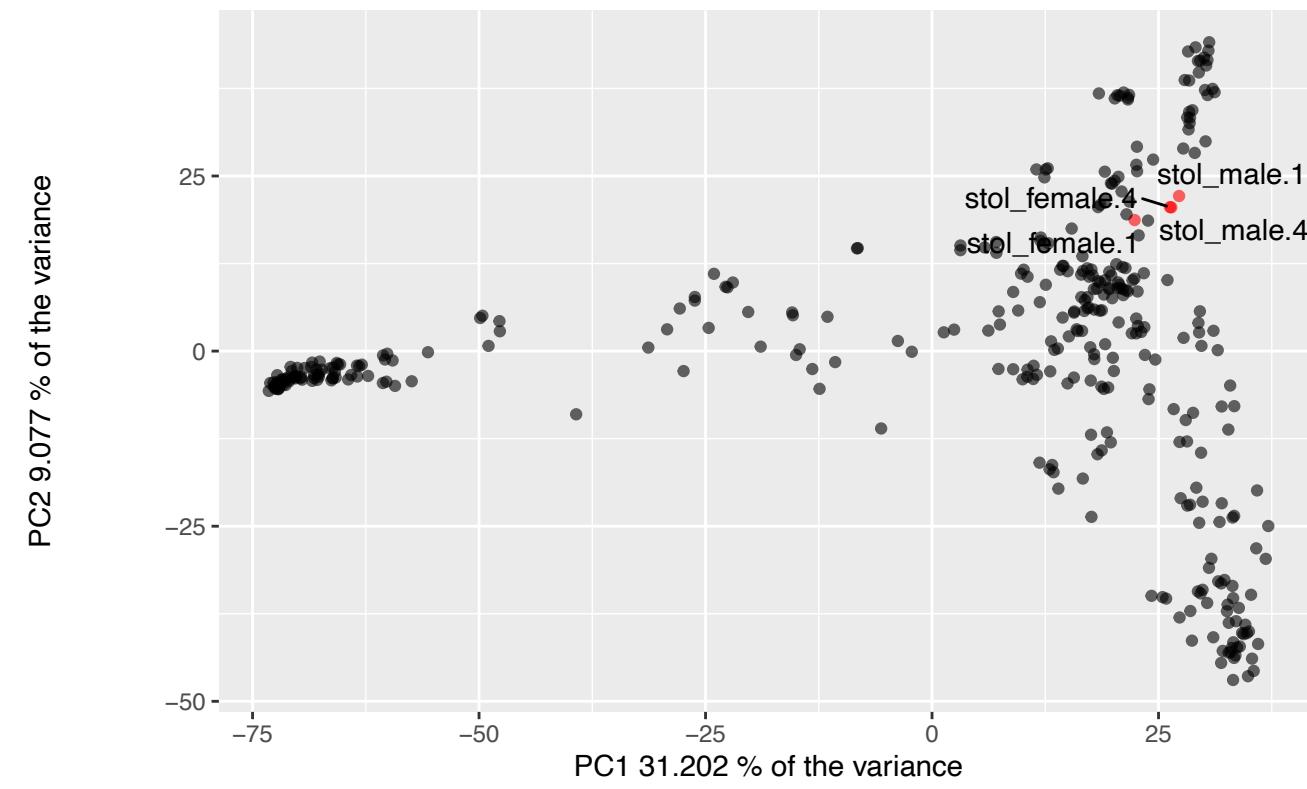
spleen



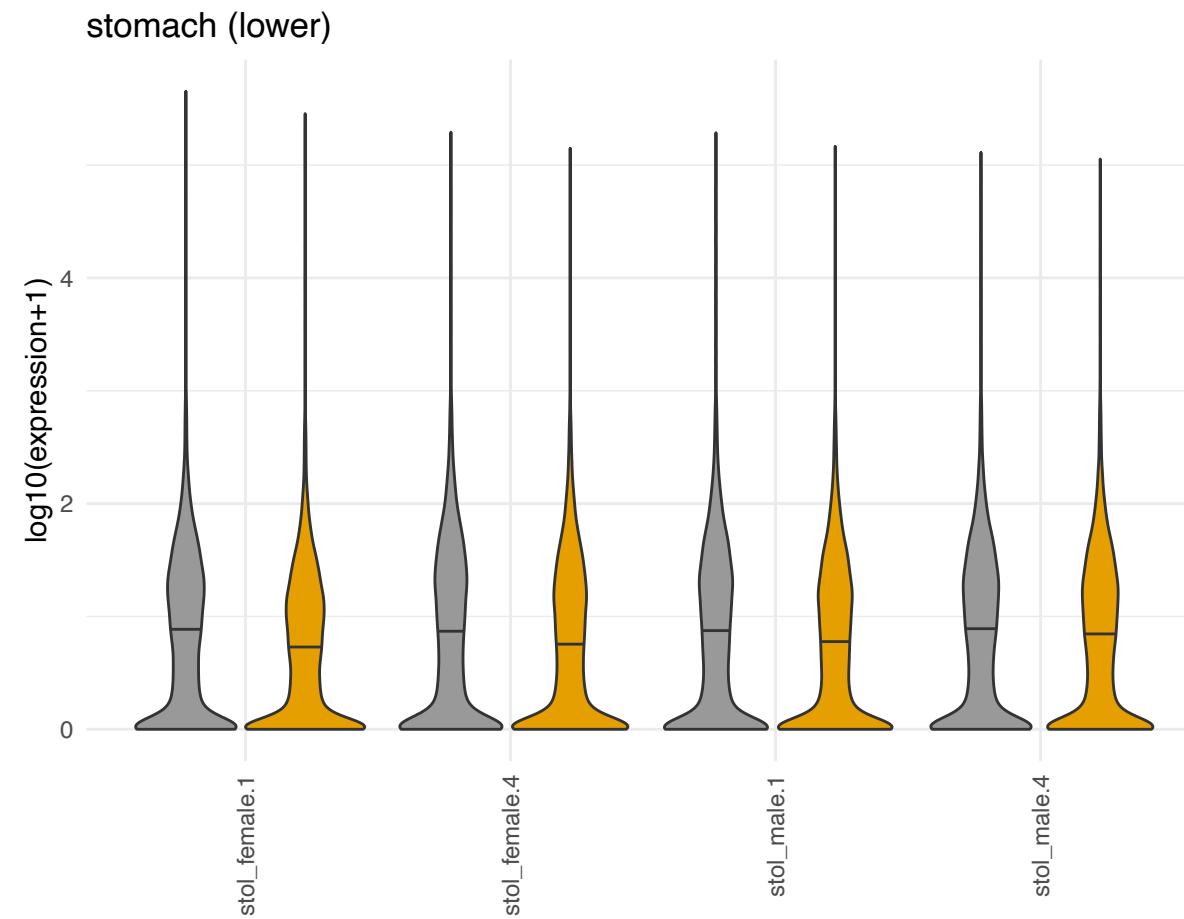
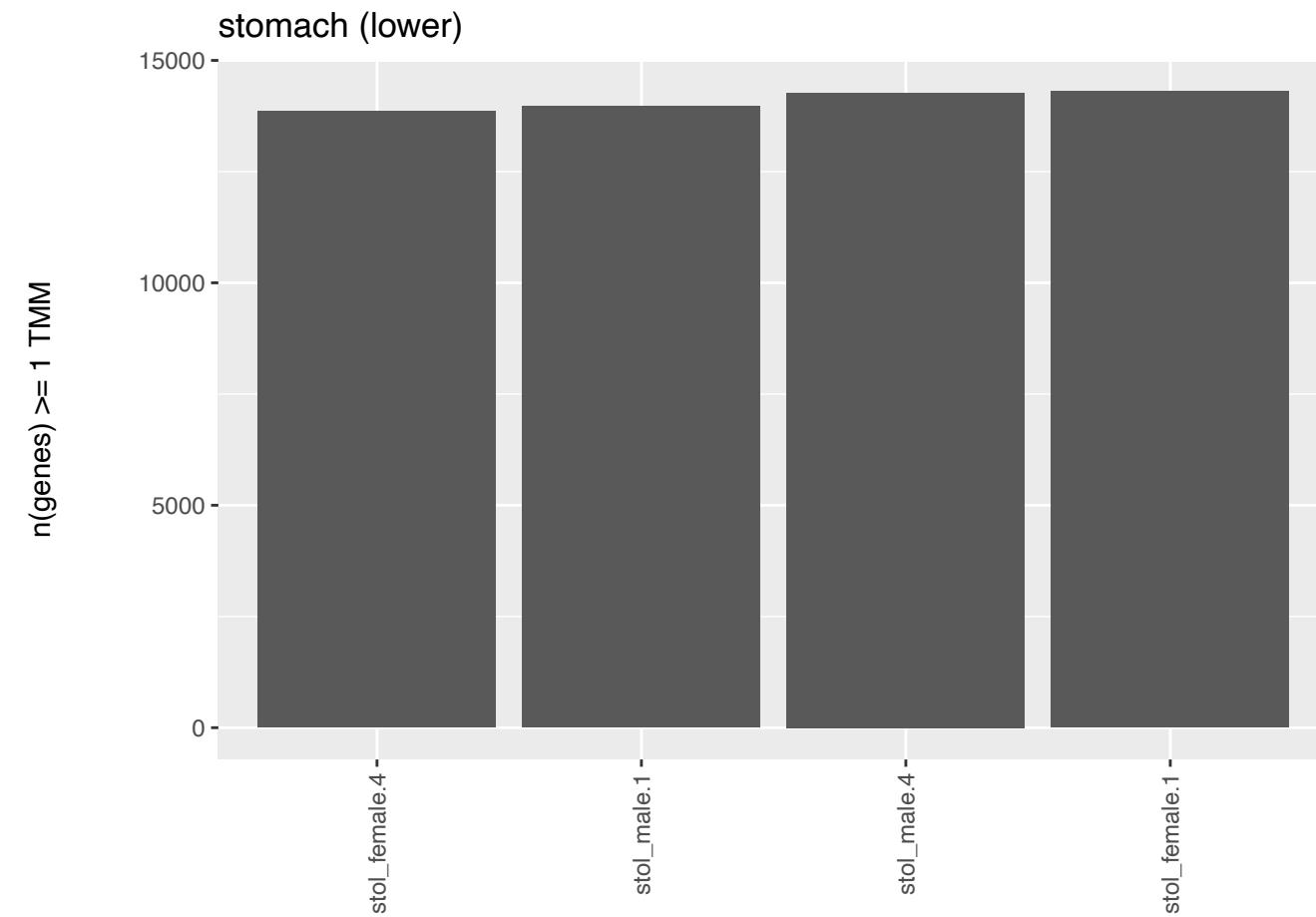
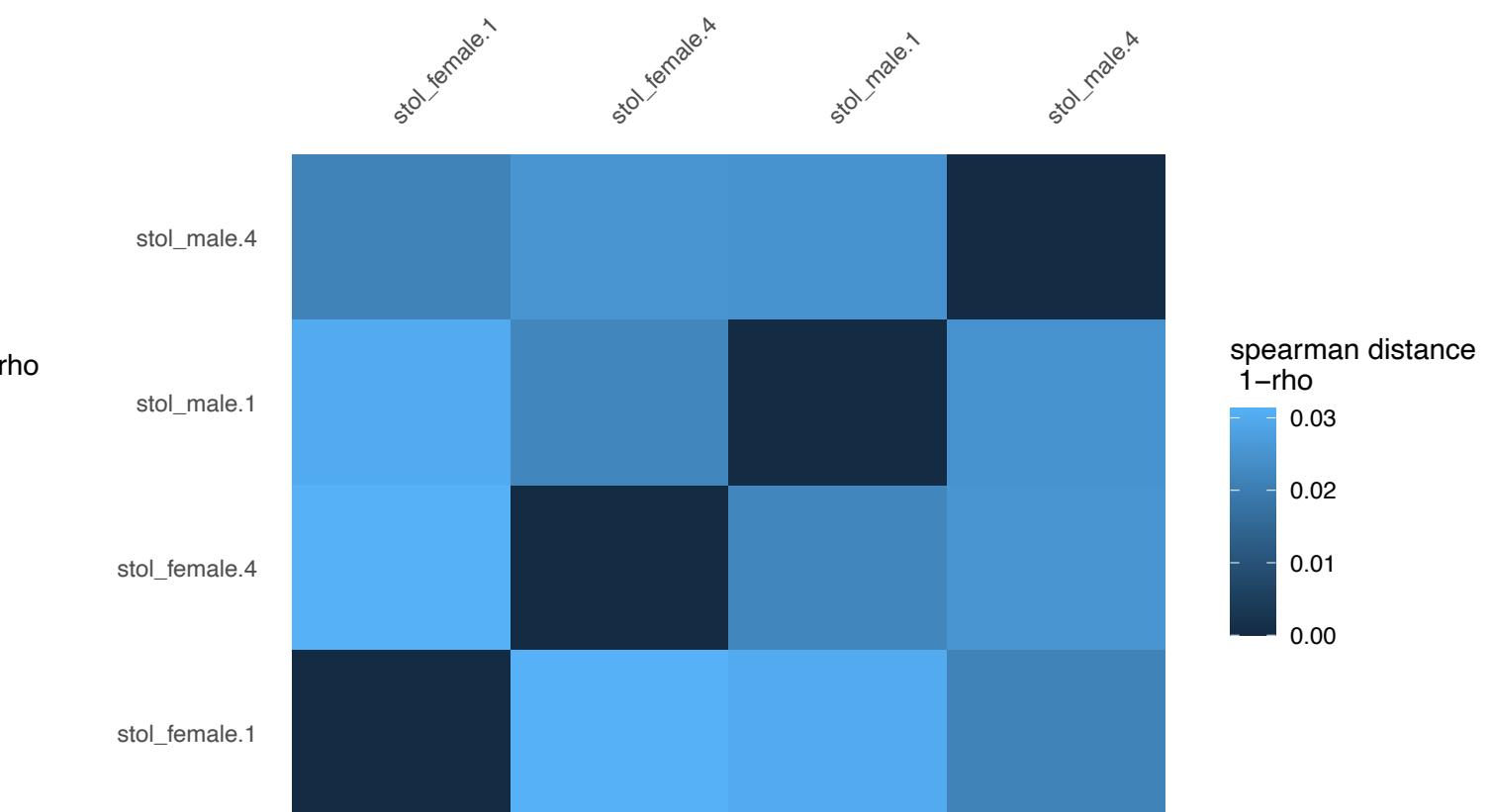
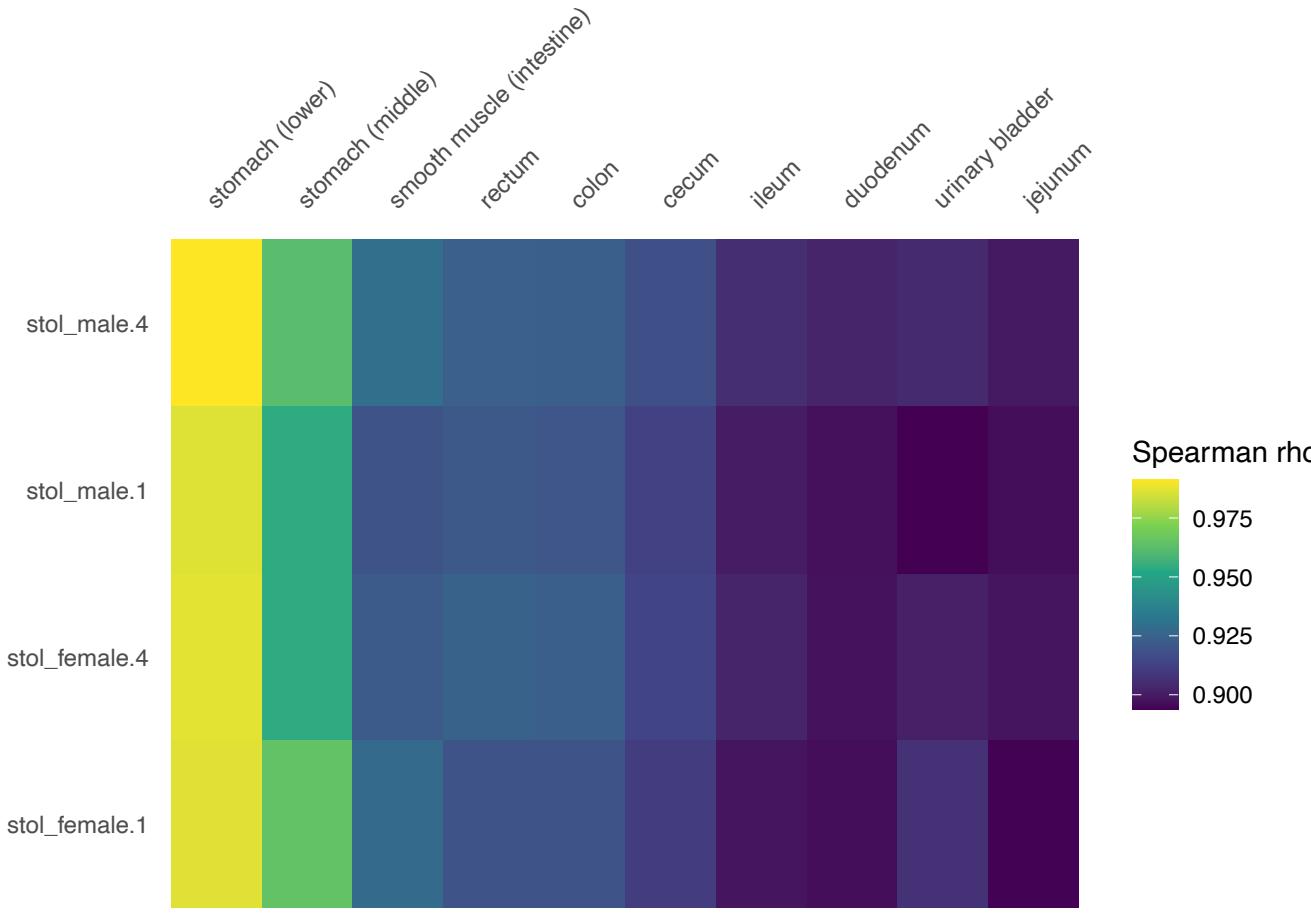
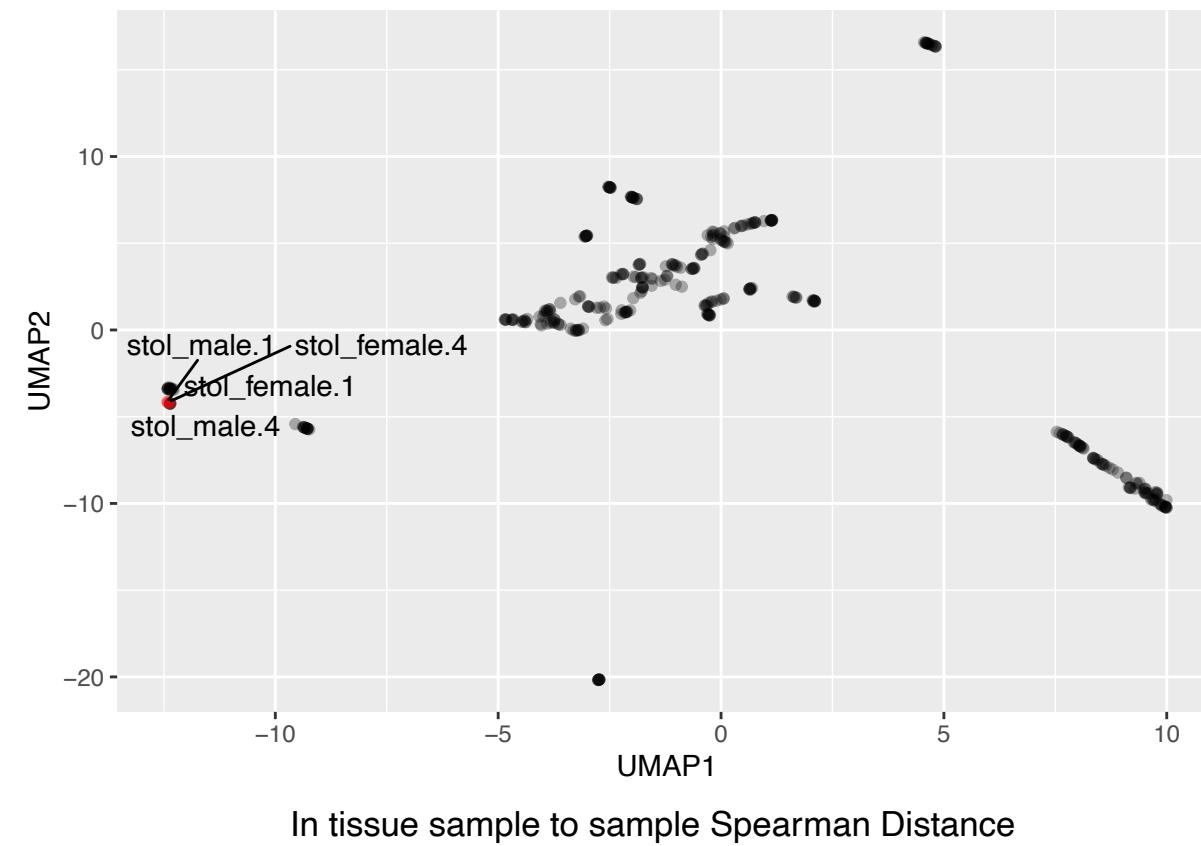
spleen



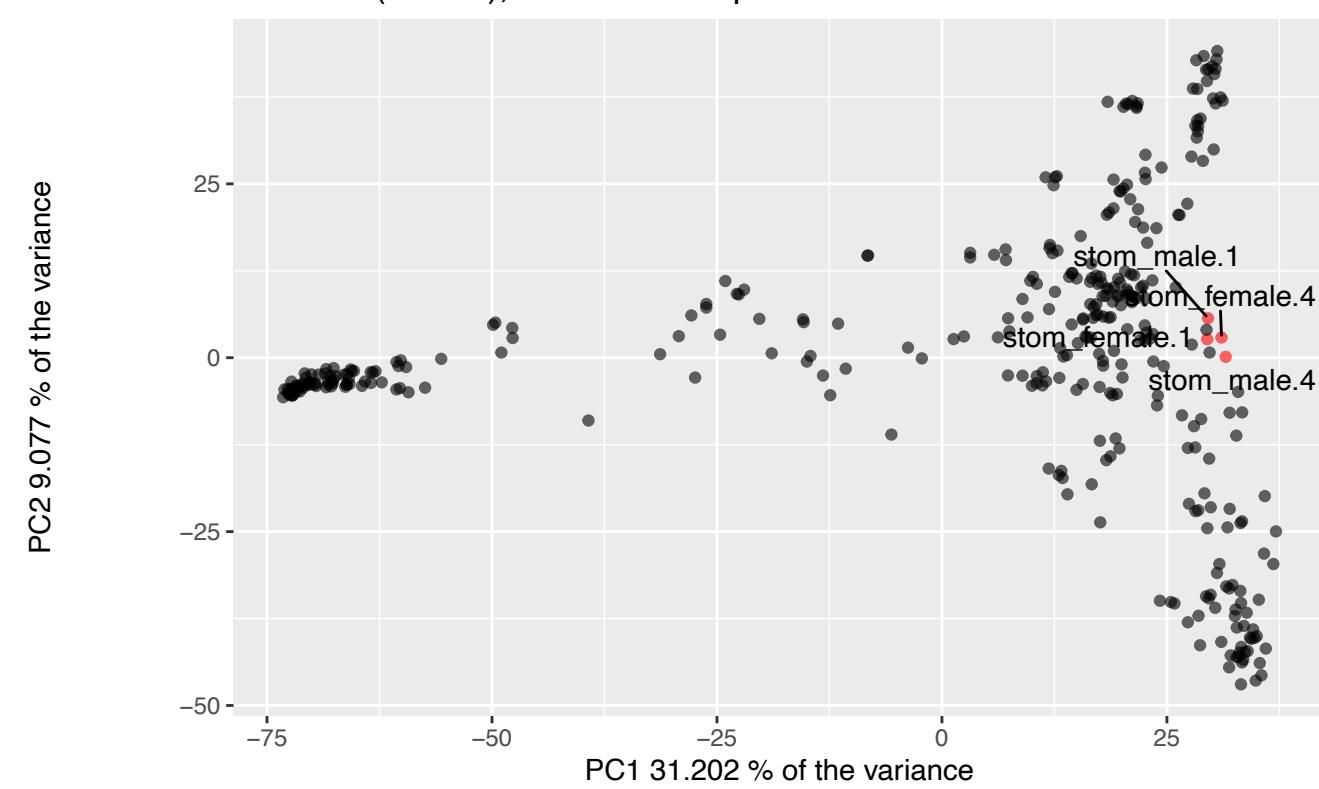
stomach (lower), PCA: TMM expression values



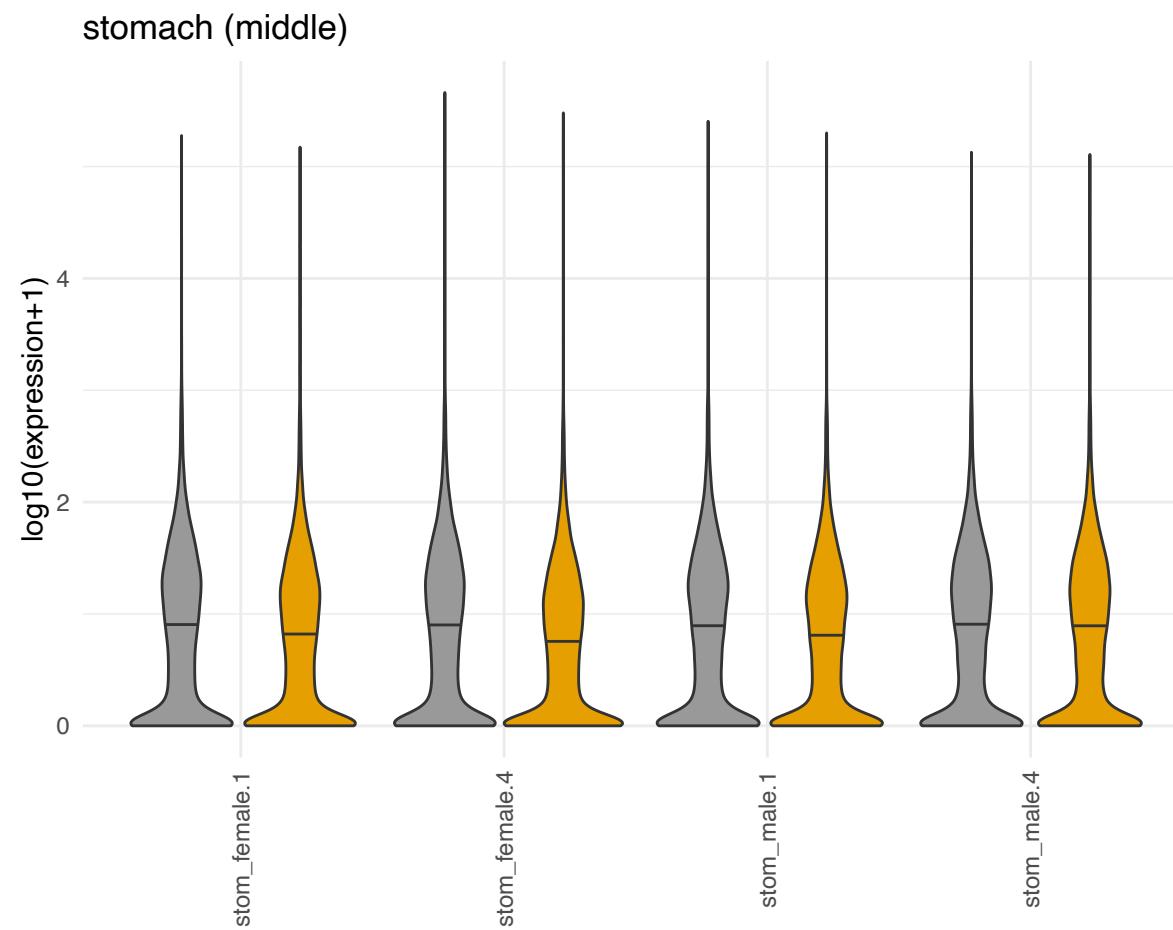
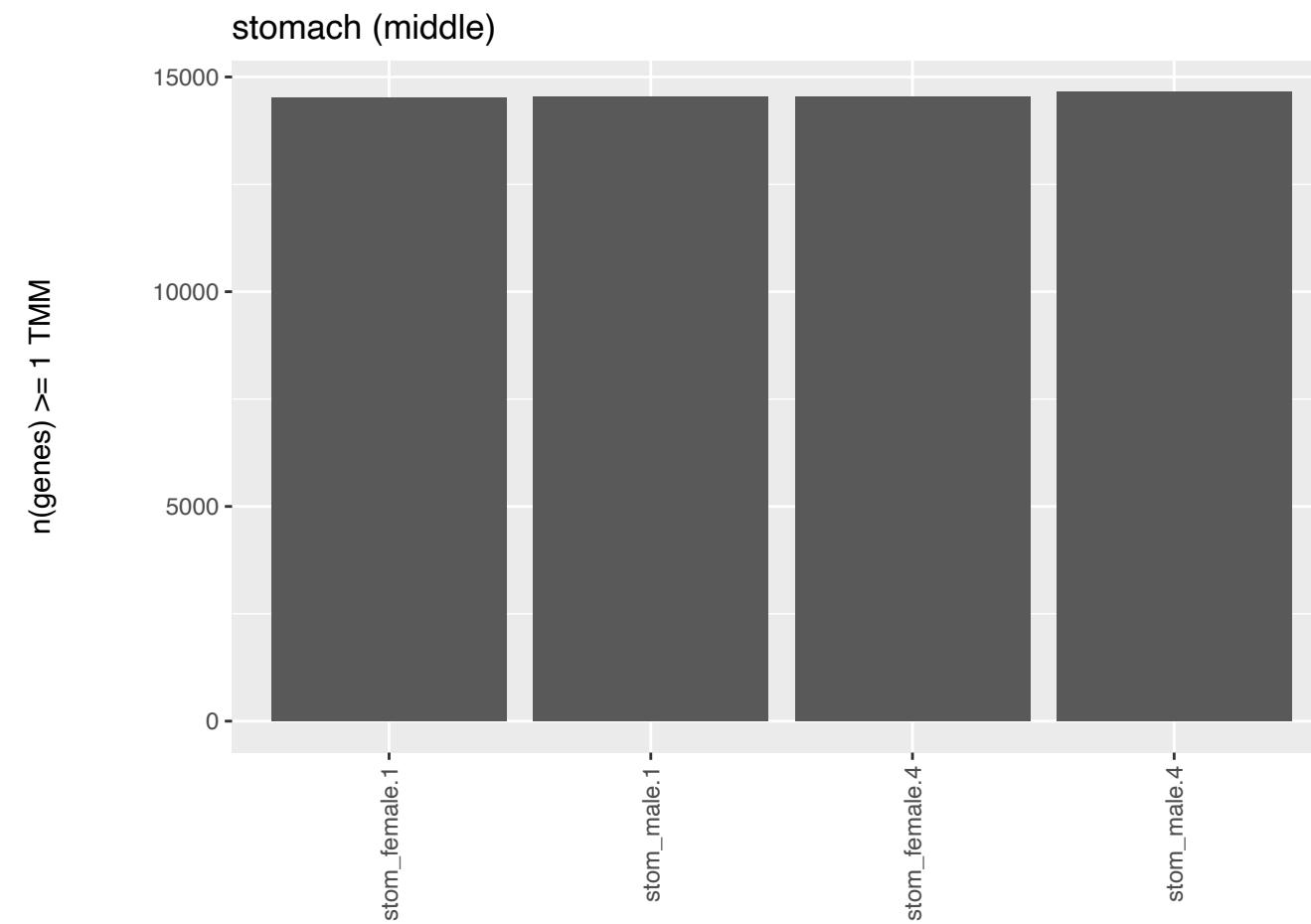
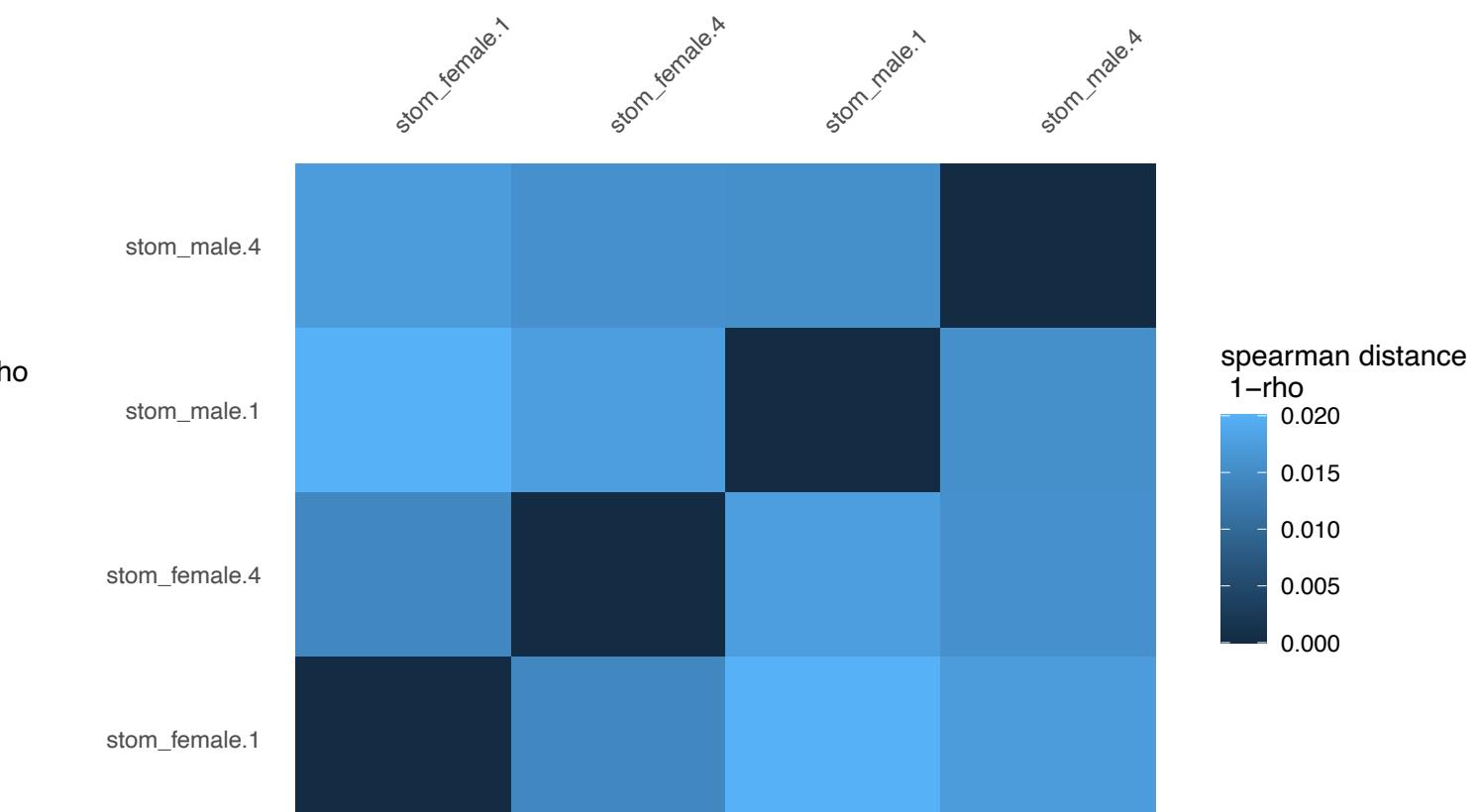
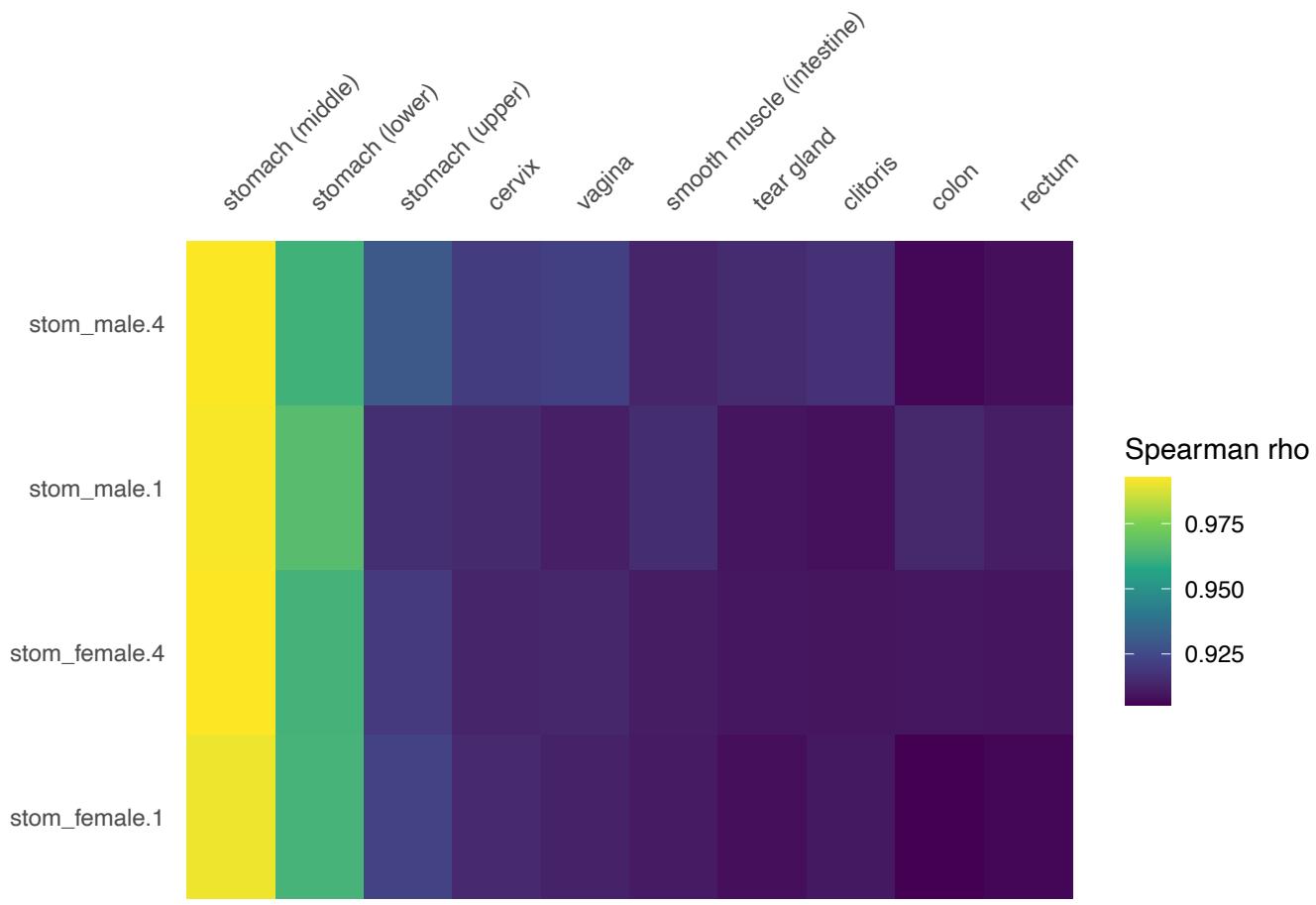
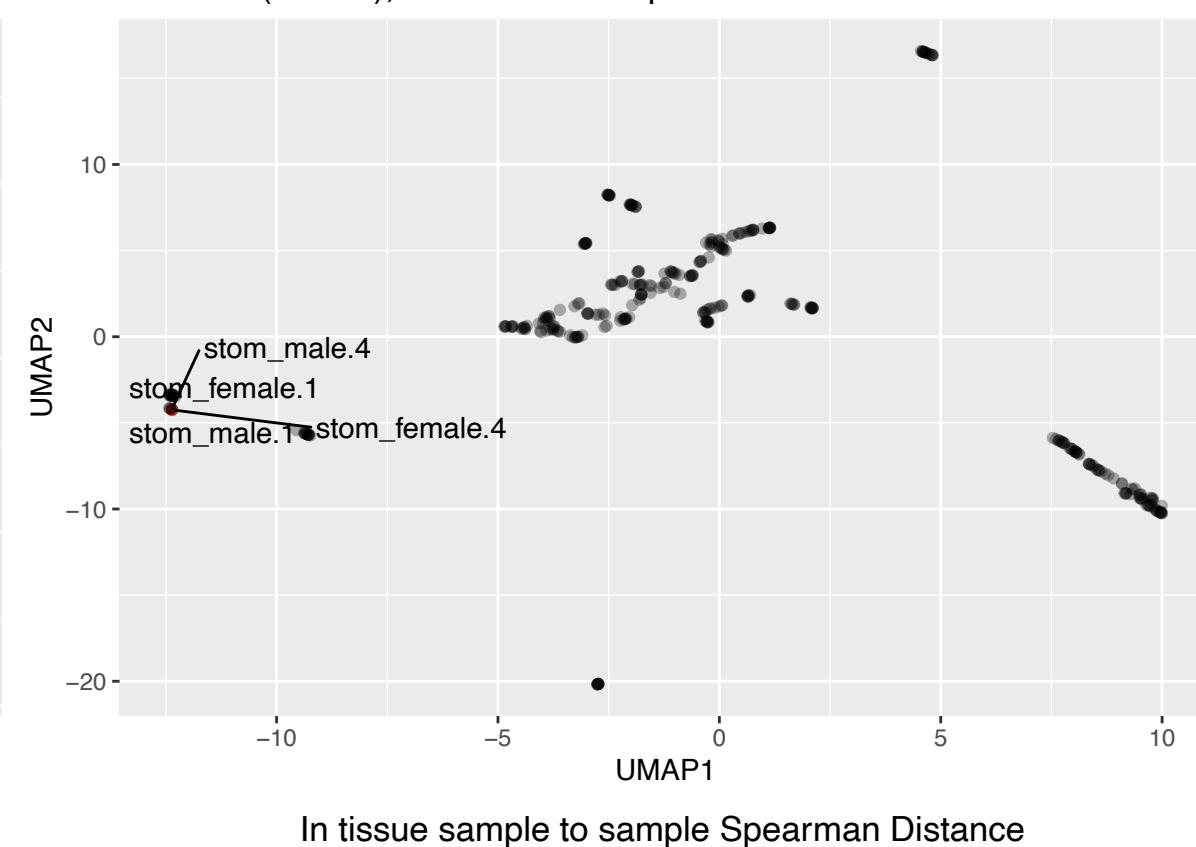
stomach (lower), UMAP: TMM expression values



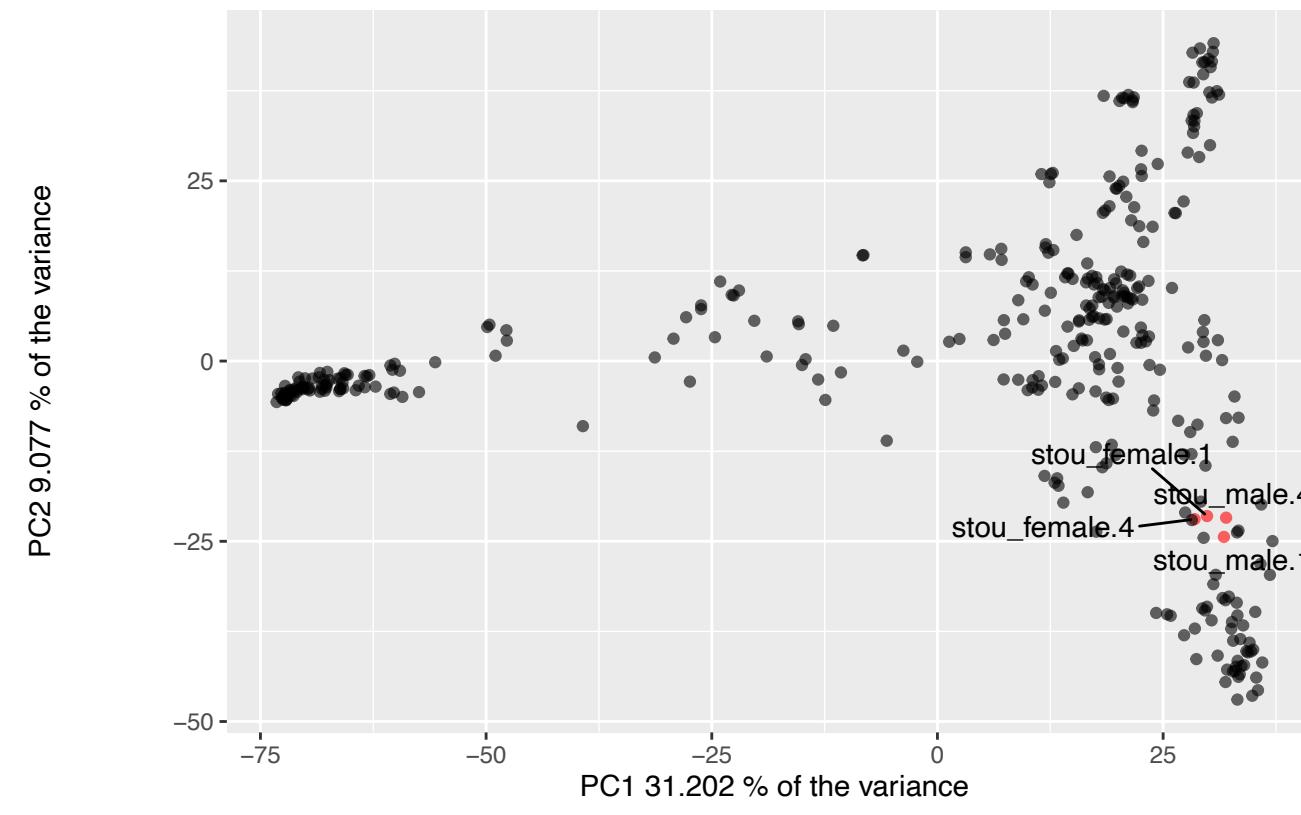
stomach (middle), PCA: TMM expression values



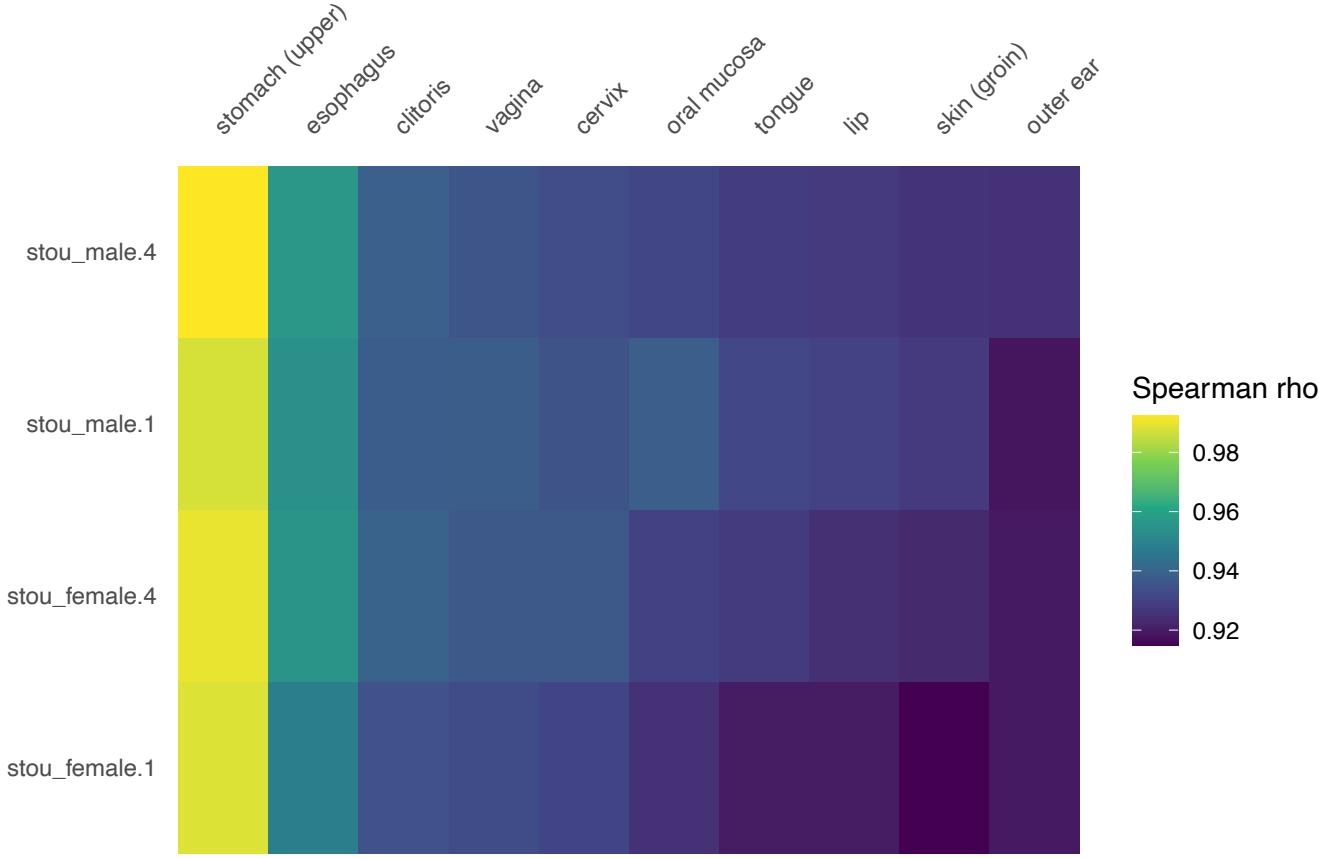
stomach (middle), UMAP: TMM expression values



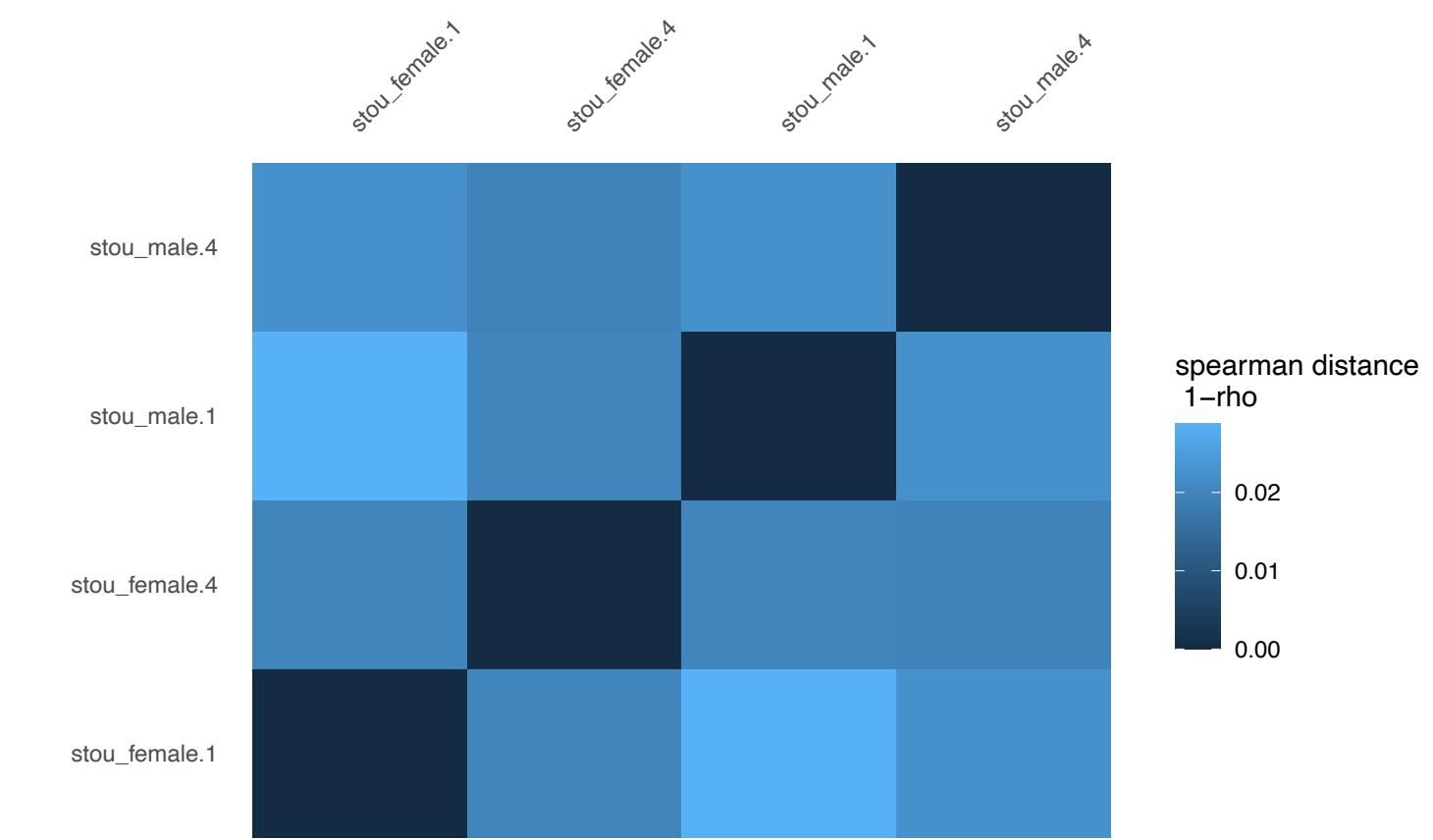
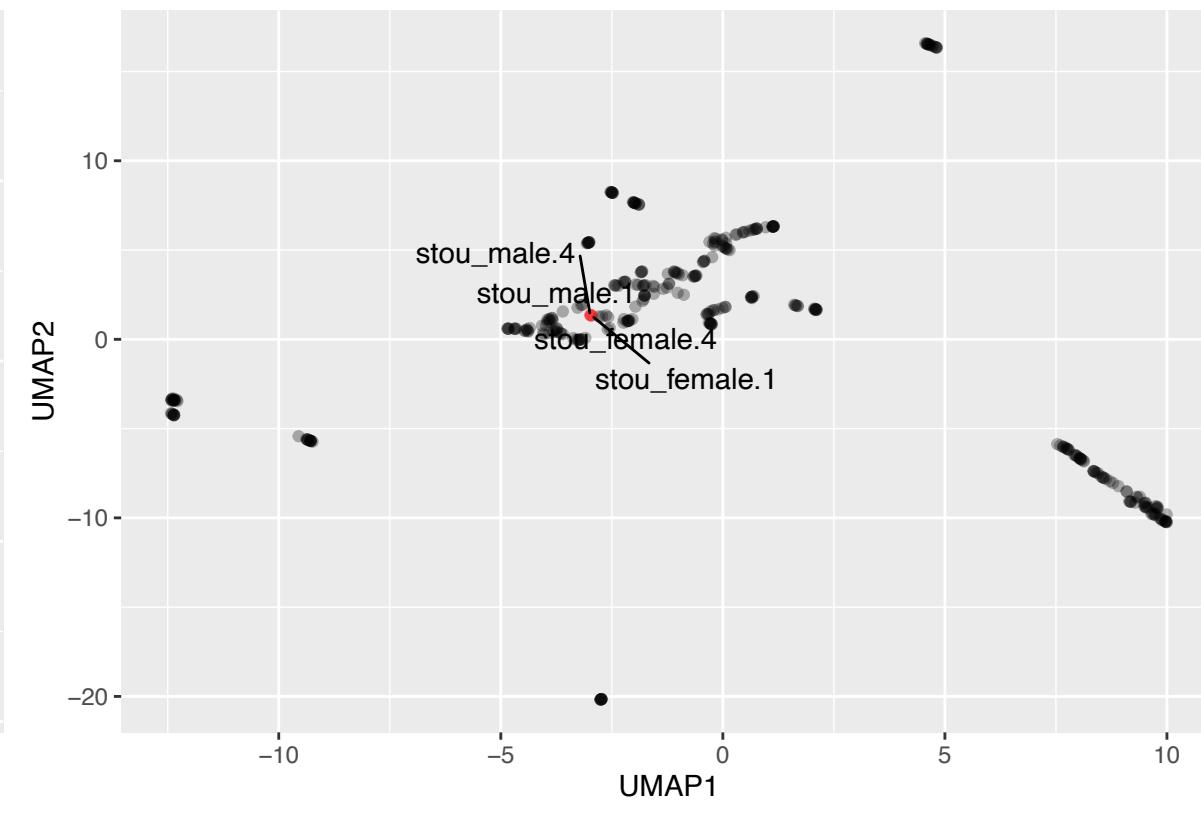
stomach (upper), PCA: TMM expression values



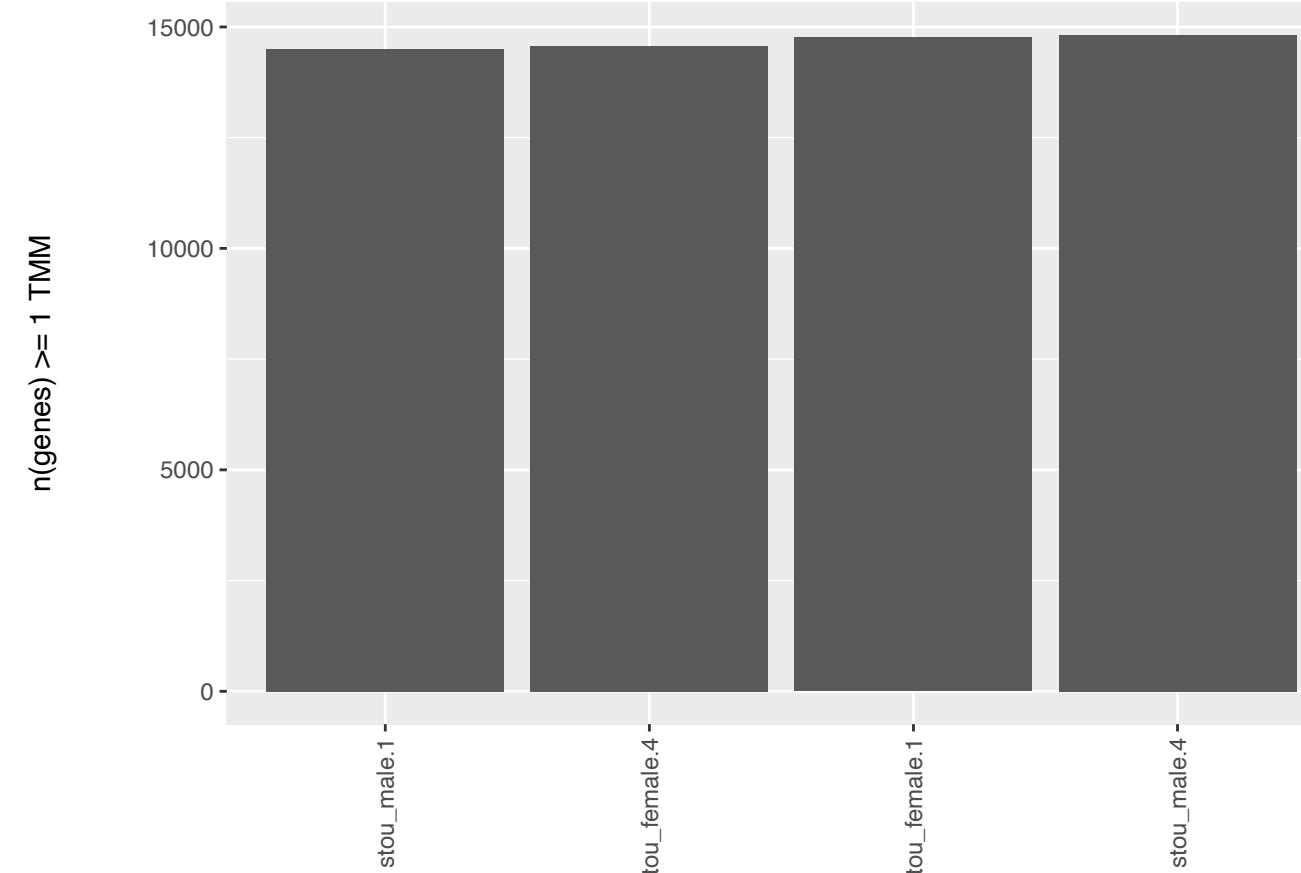
Tissue group to sample correlation



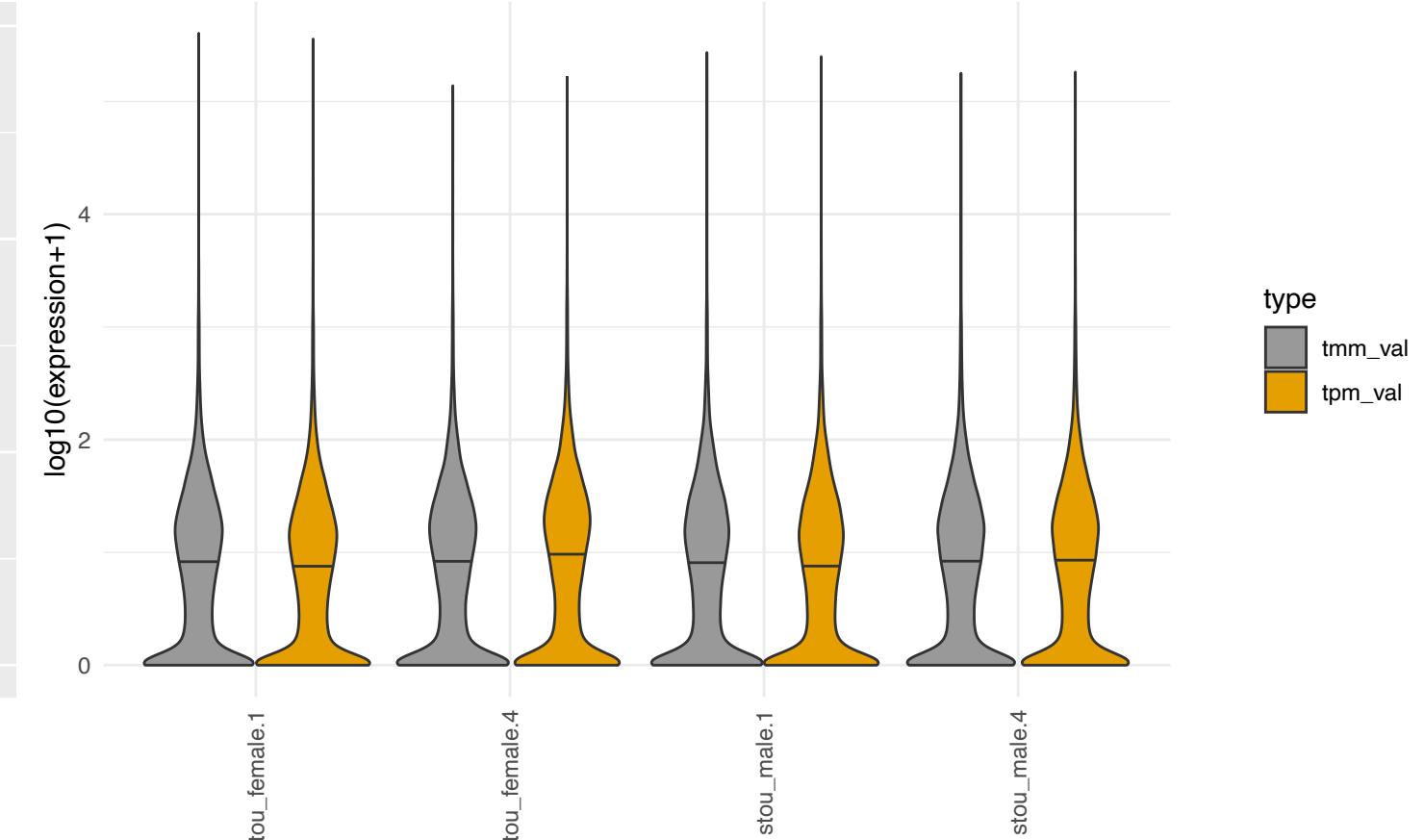
stomach (upper), UMAP: TMM expression values



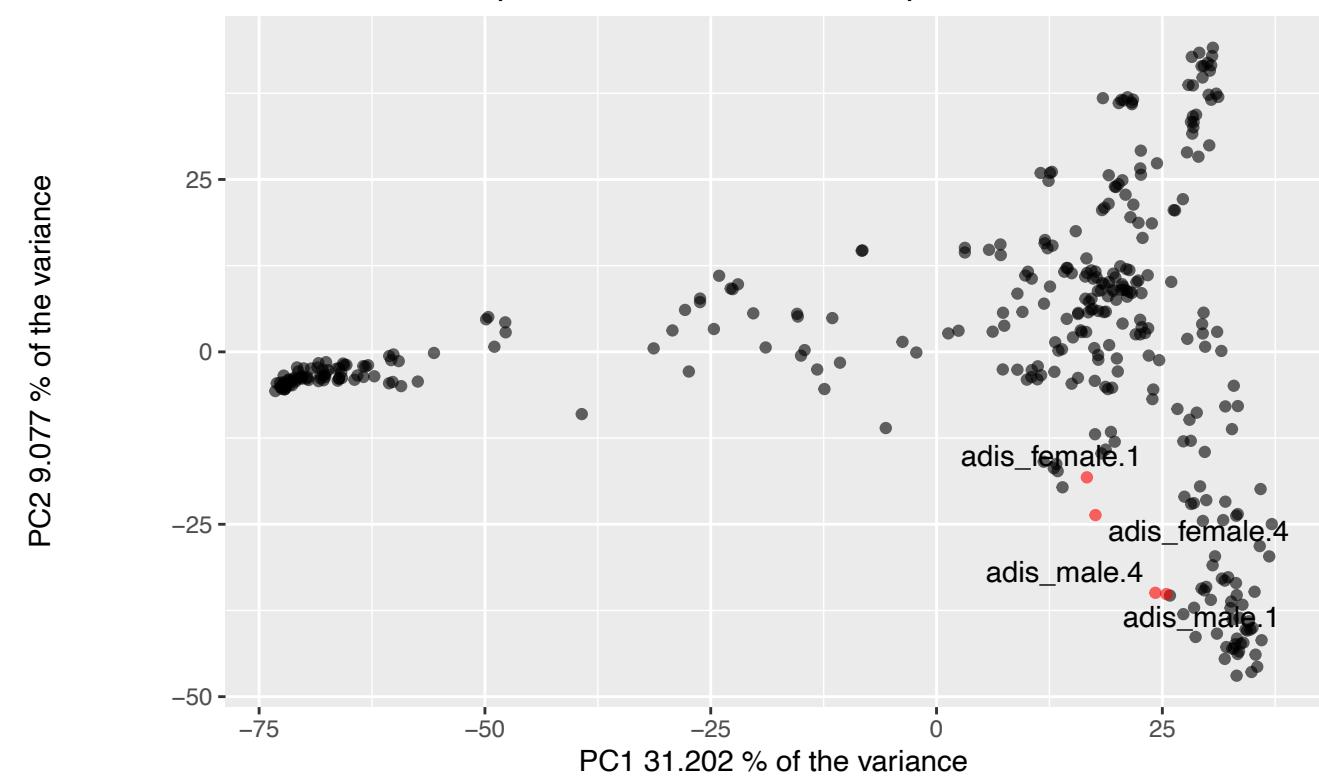
stomach (upper)



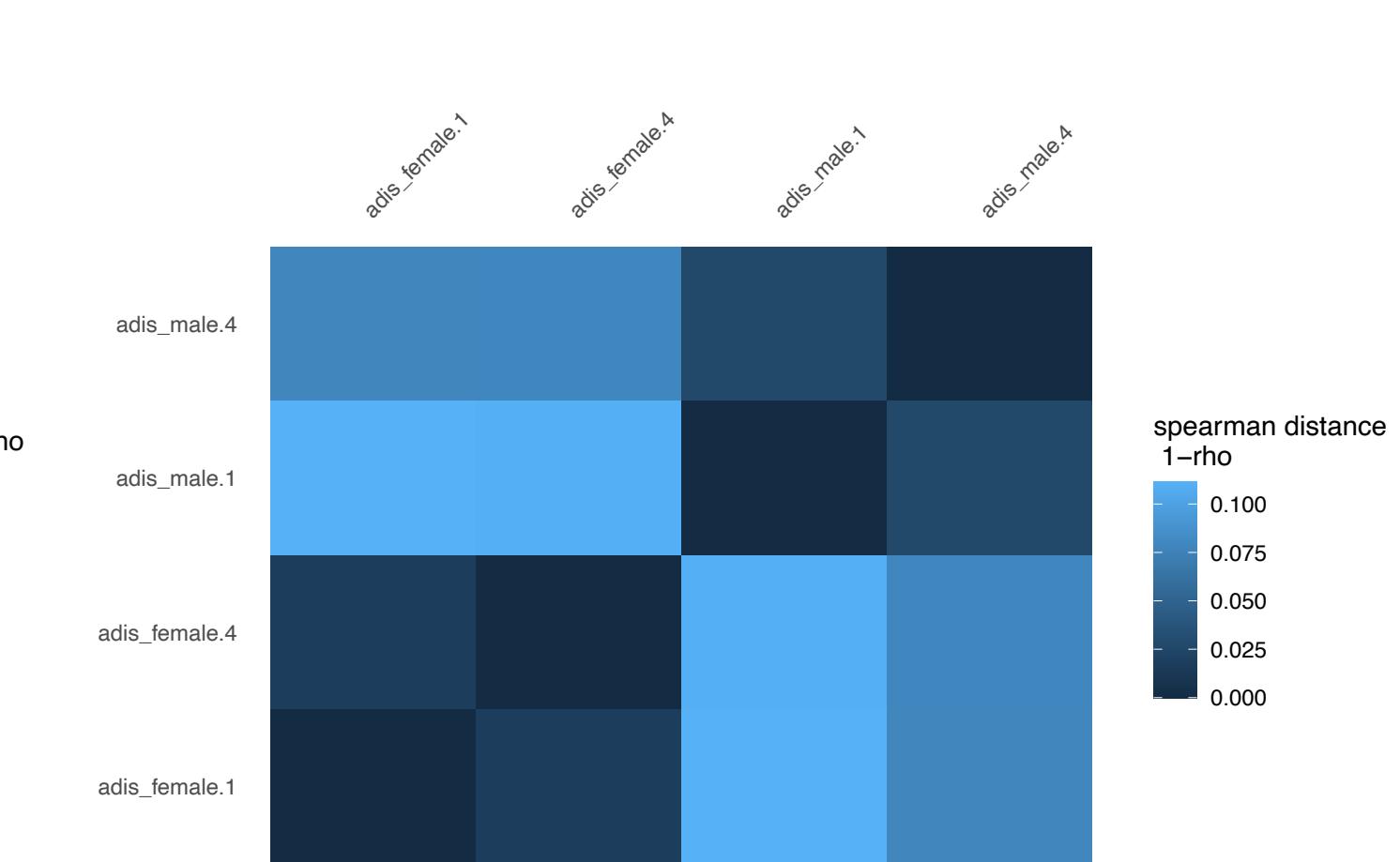
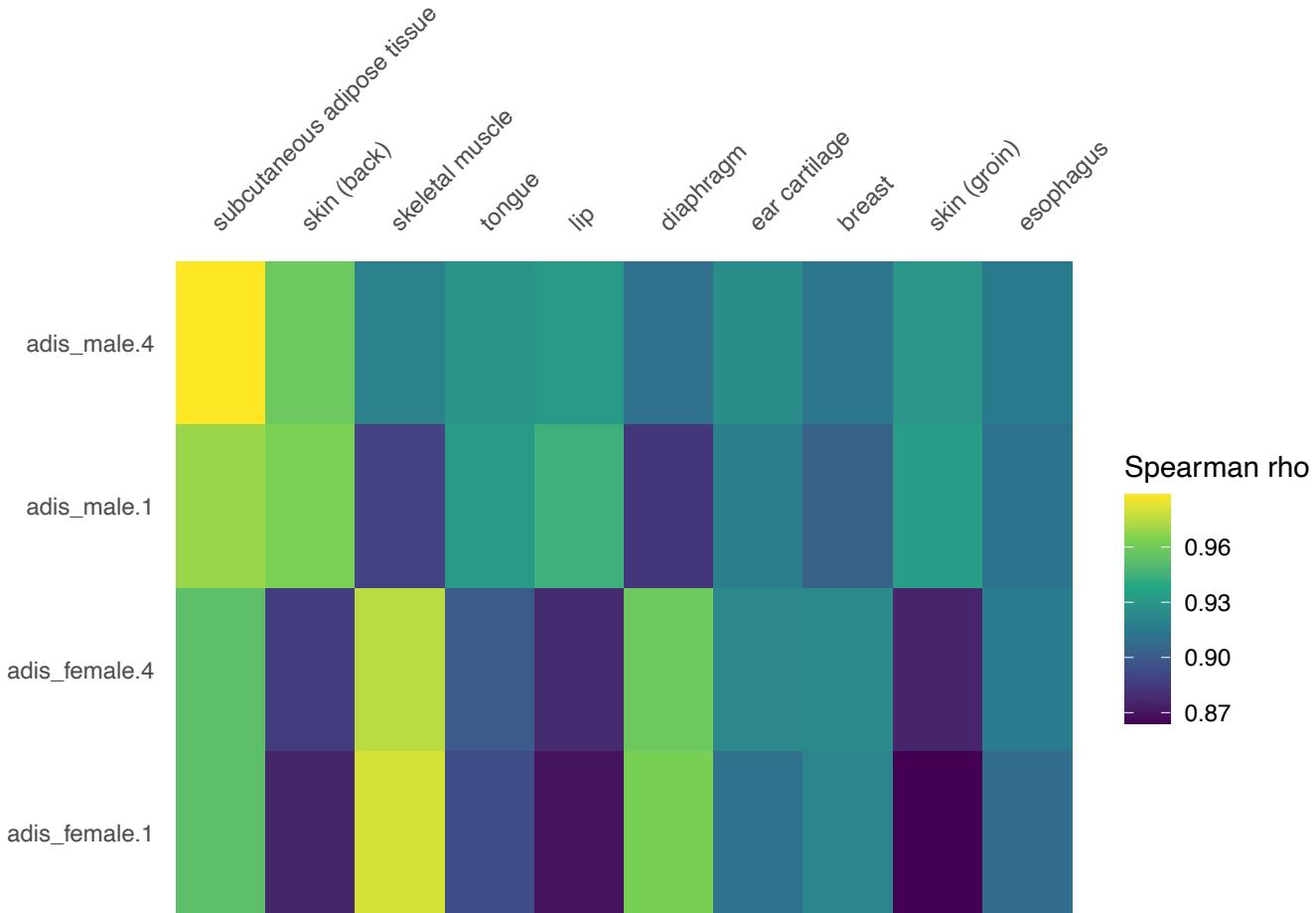
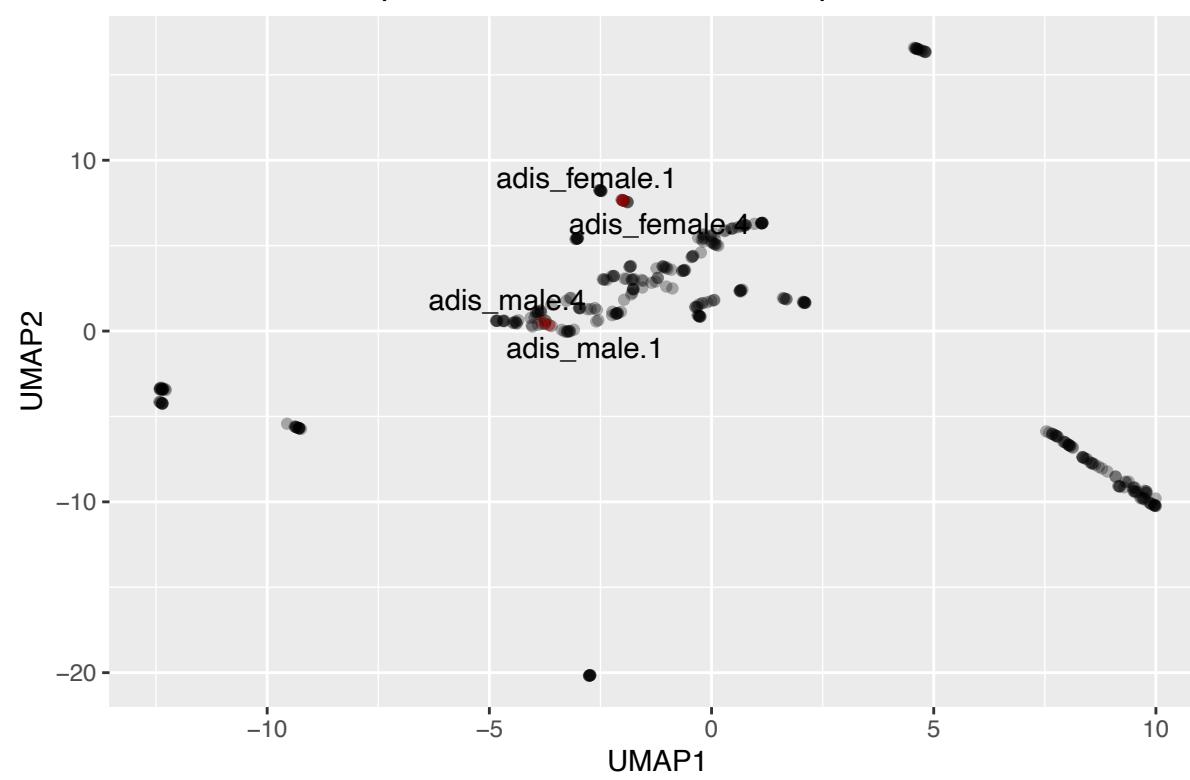
stomach (upper)



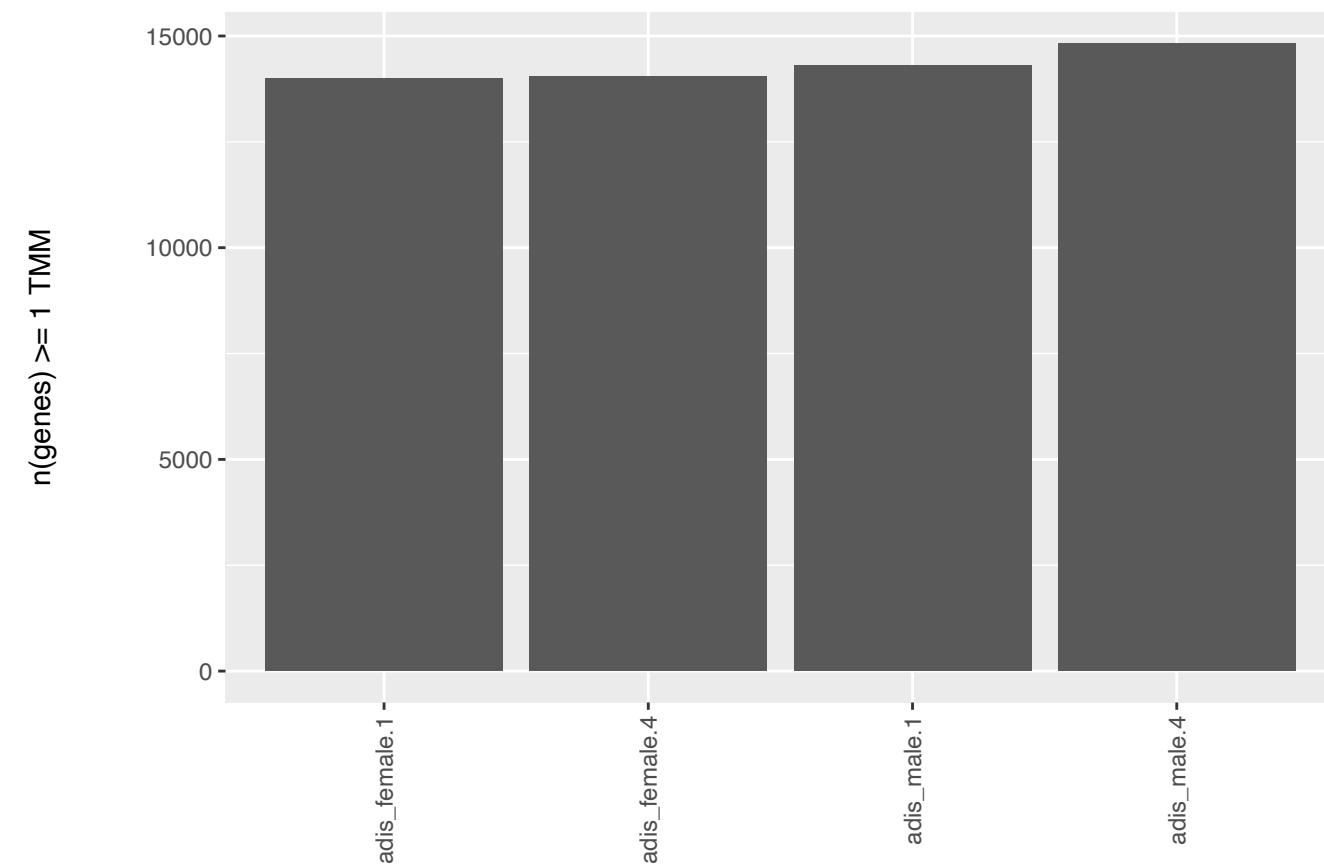
subcutaneous adipose tissue, PCA: TMM expression values



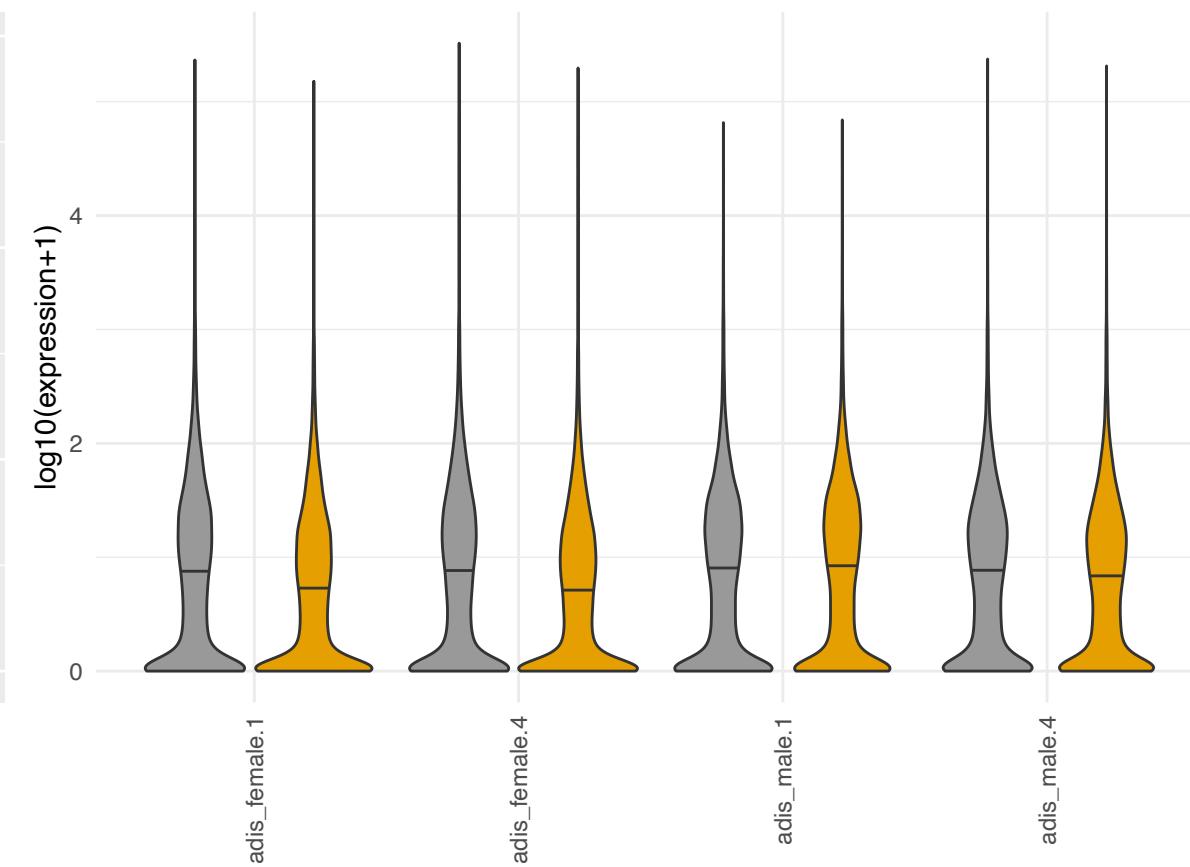
subcutaneous adipose tissue, UMAP: TMM expression values



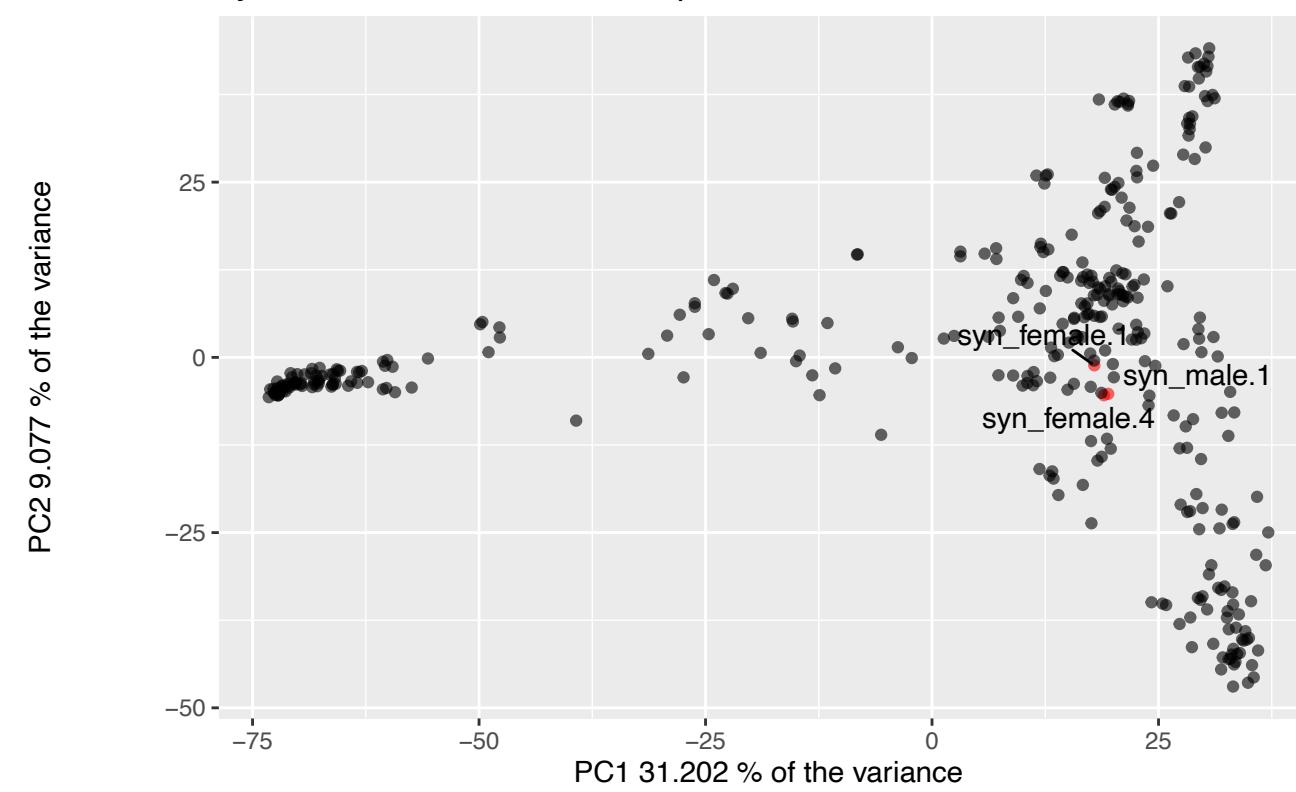
subcutaneous adipose tissue



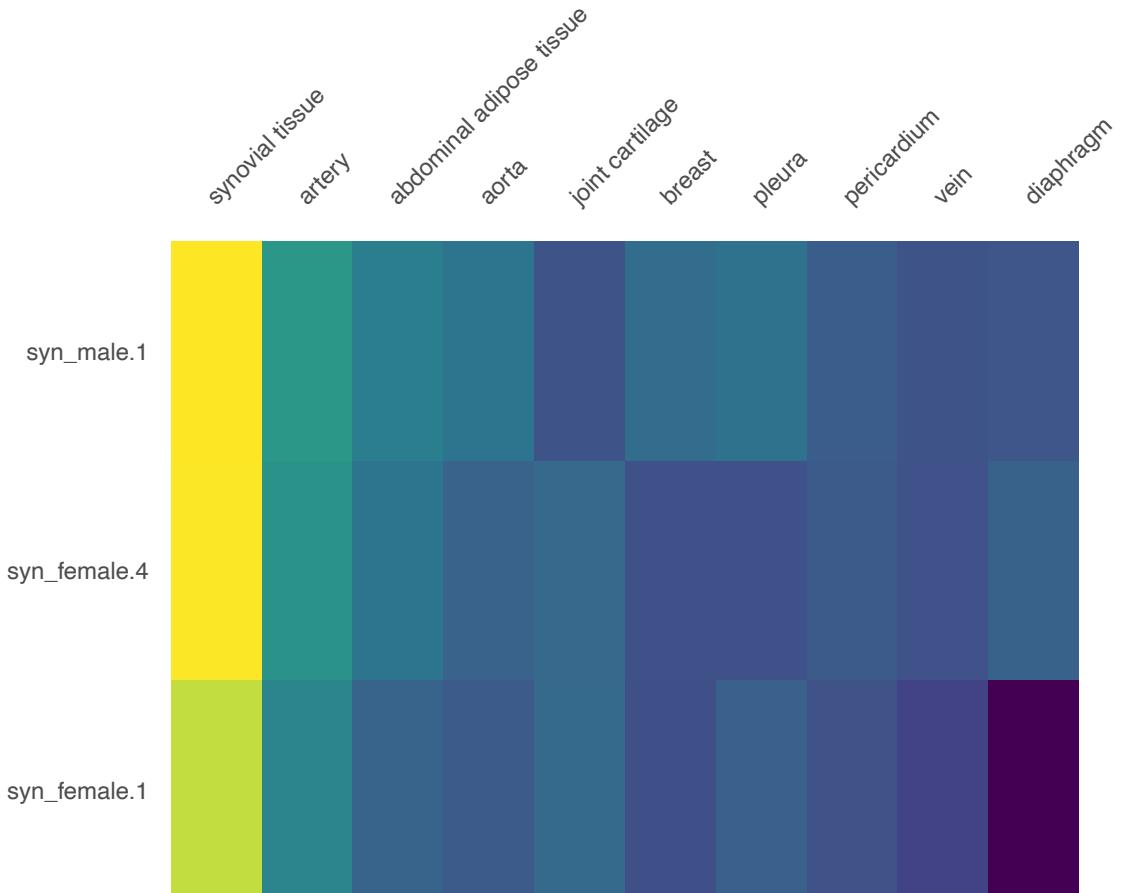
subcutaneous adipose tissue



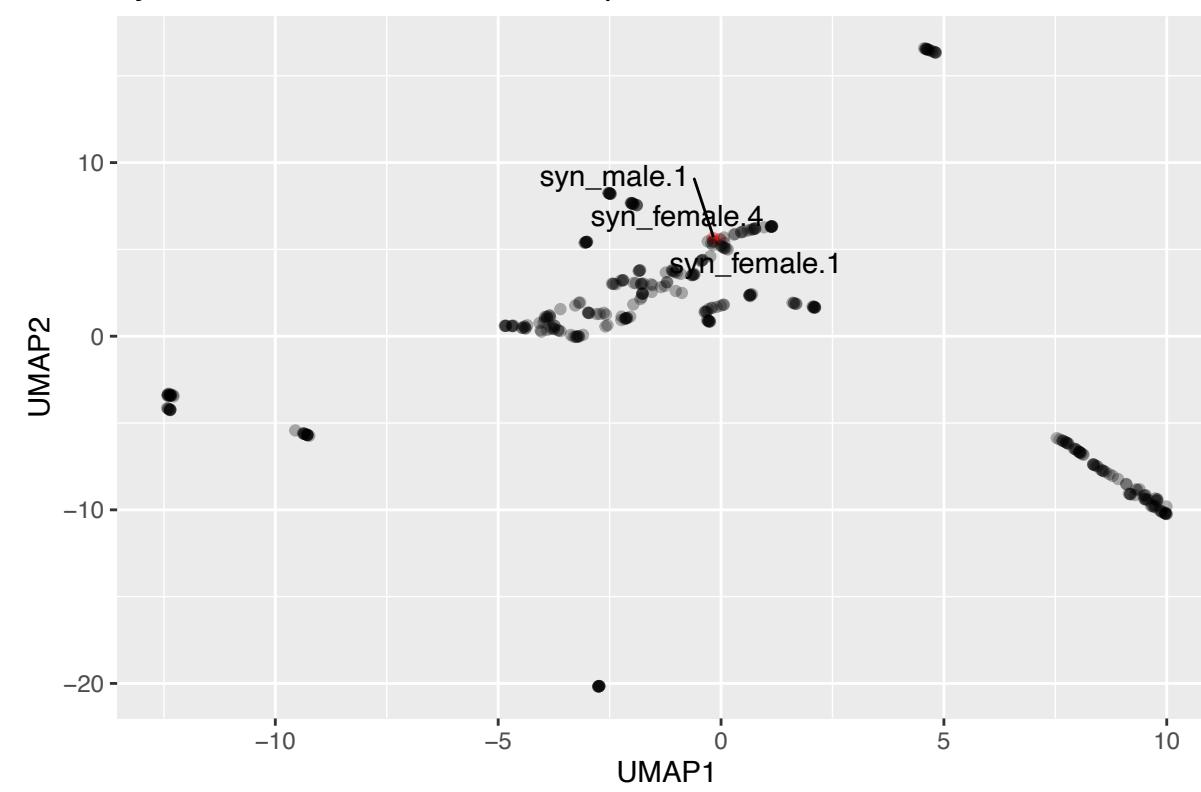
synovial tissue, PCA: TMM expression values



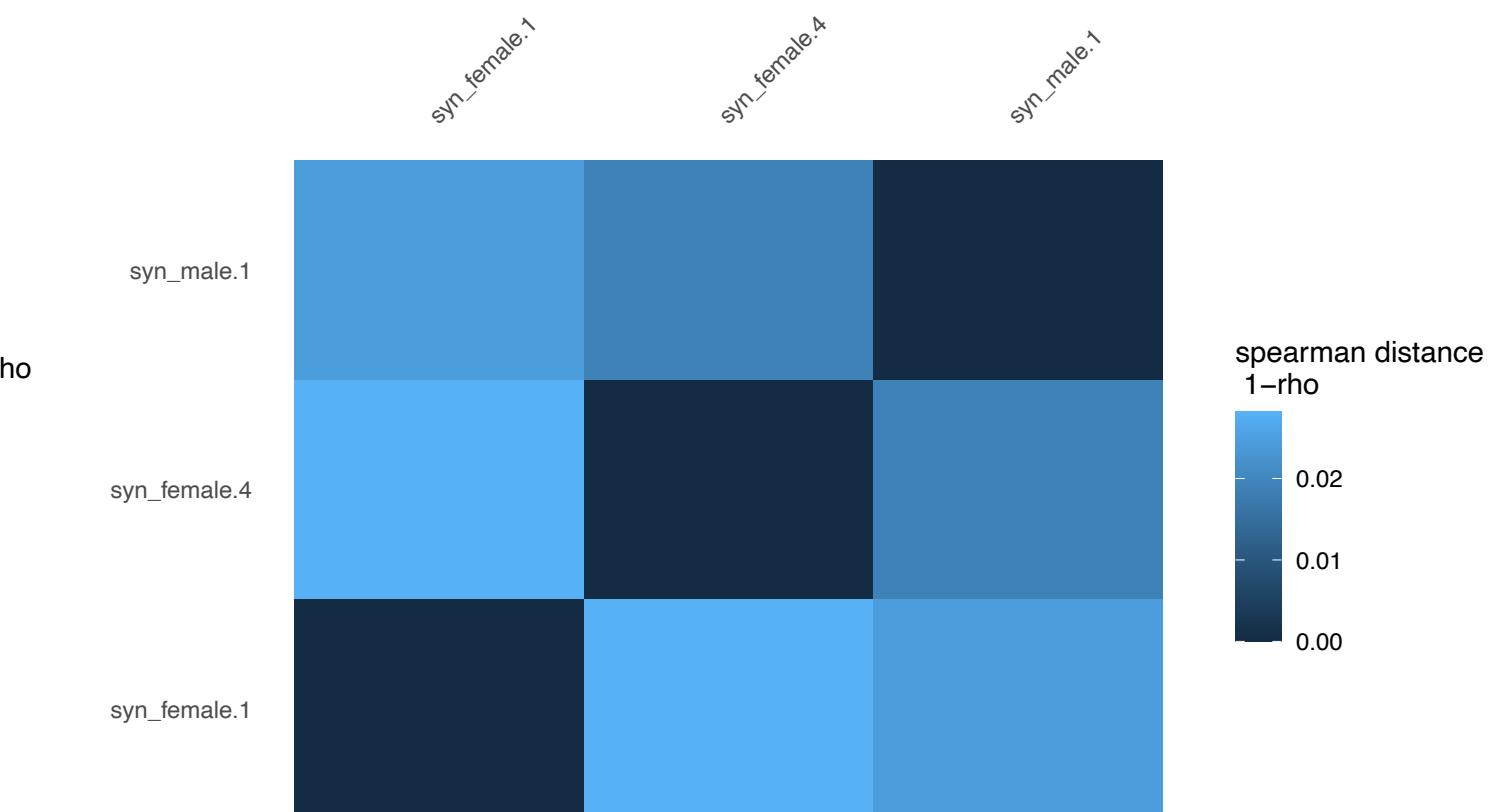
Tissue group to sample correlation



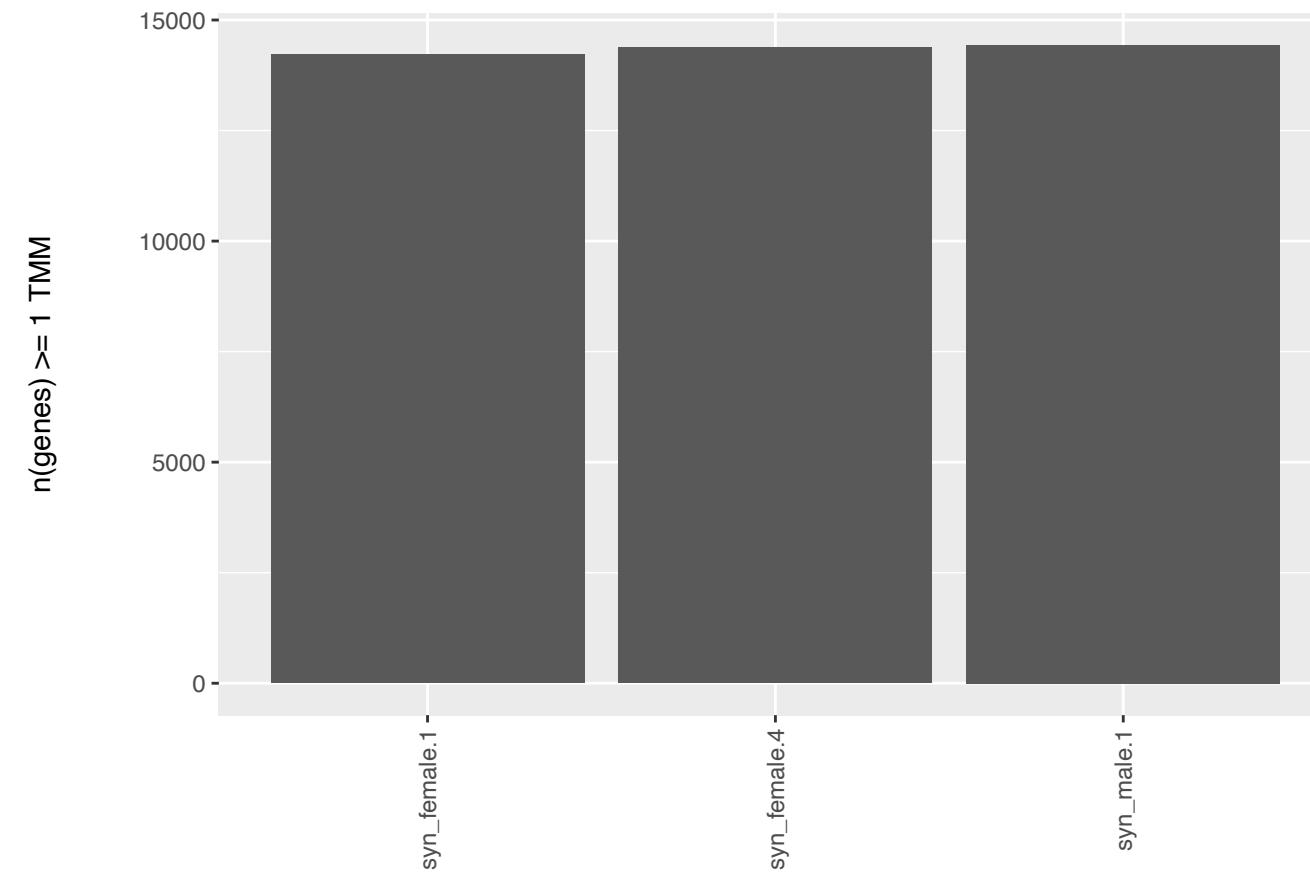
synovial tissue, UMAP: TMM expression values



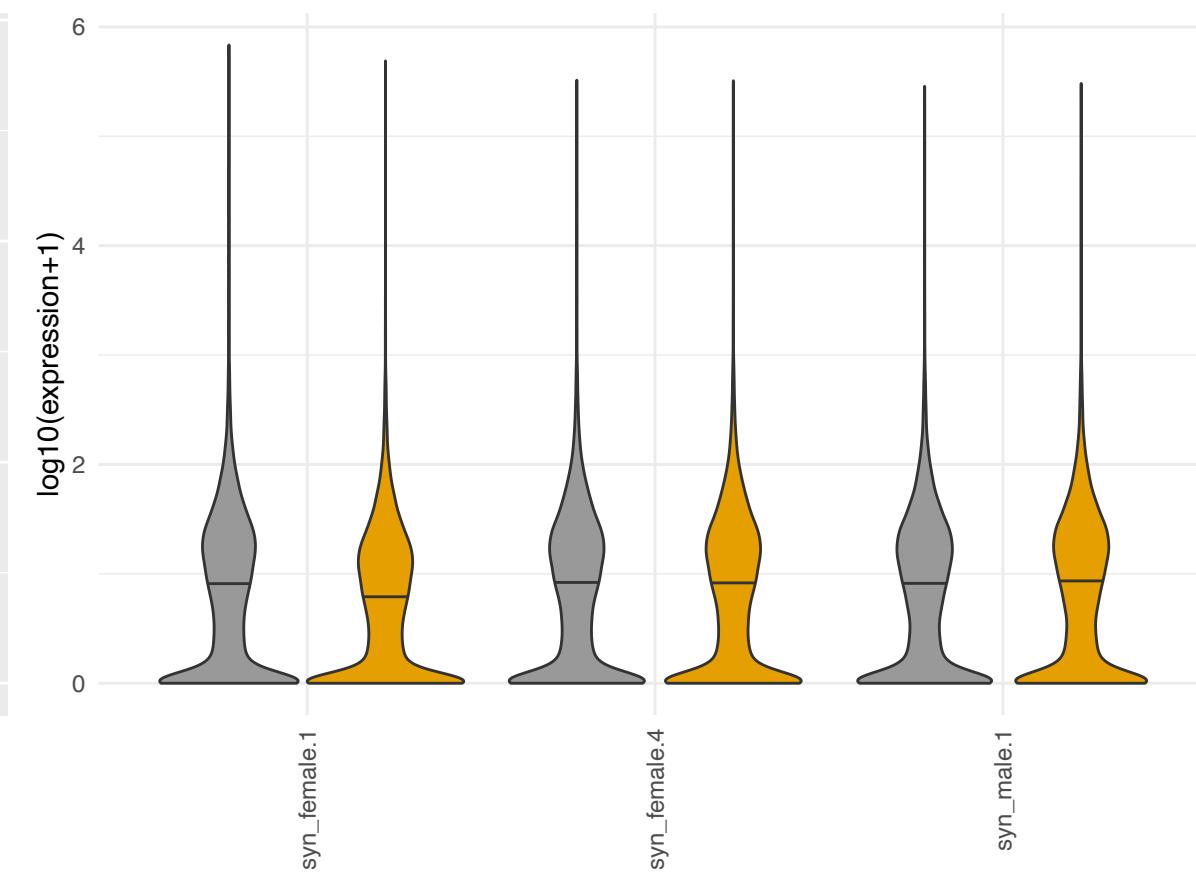
In tissue sample to sample Spearman Distance



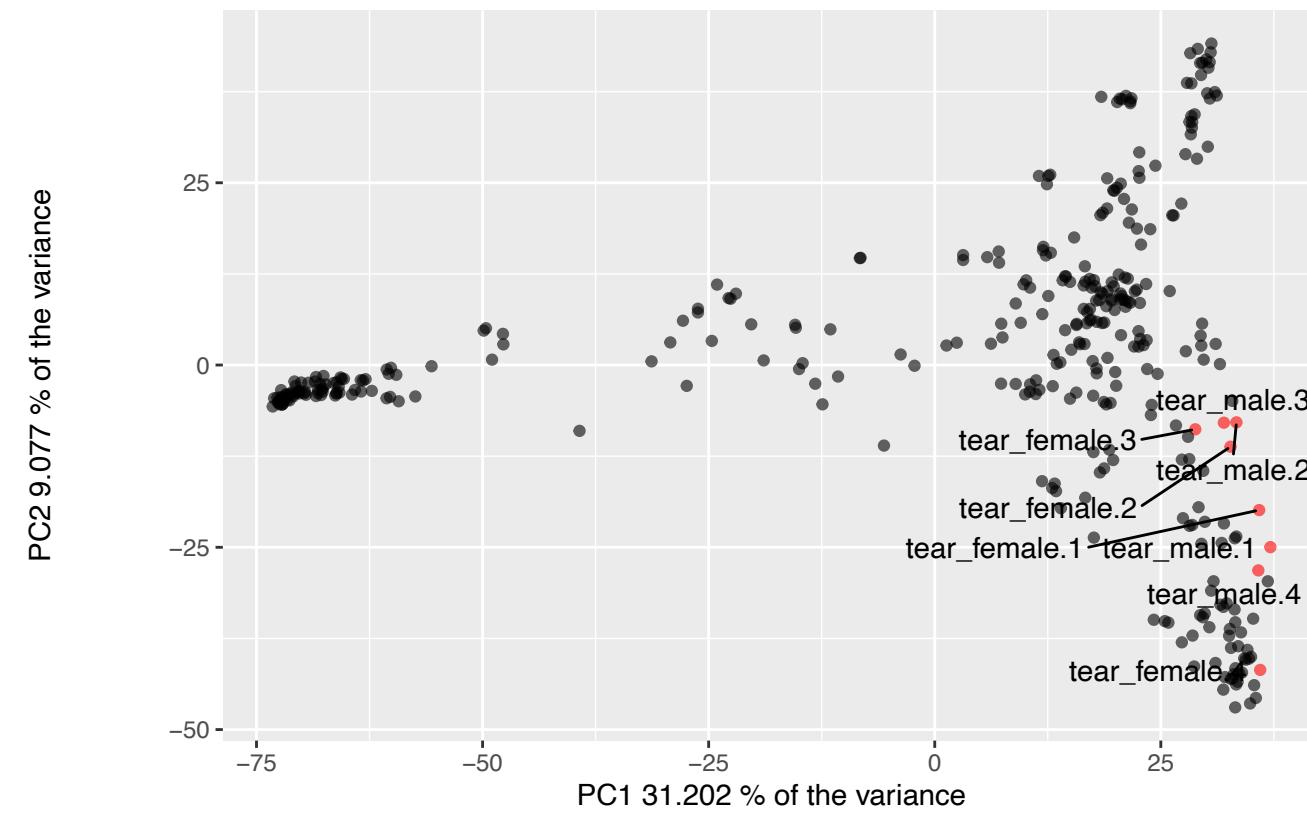
synovial tissue



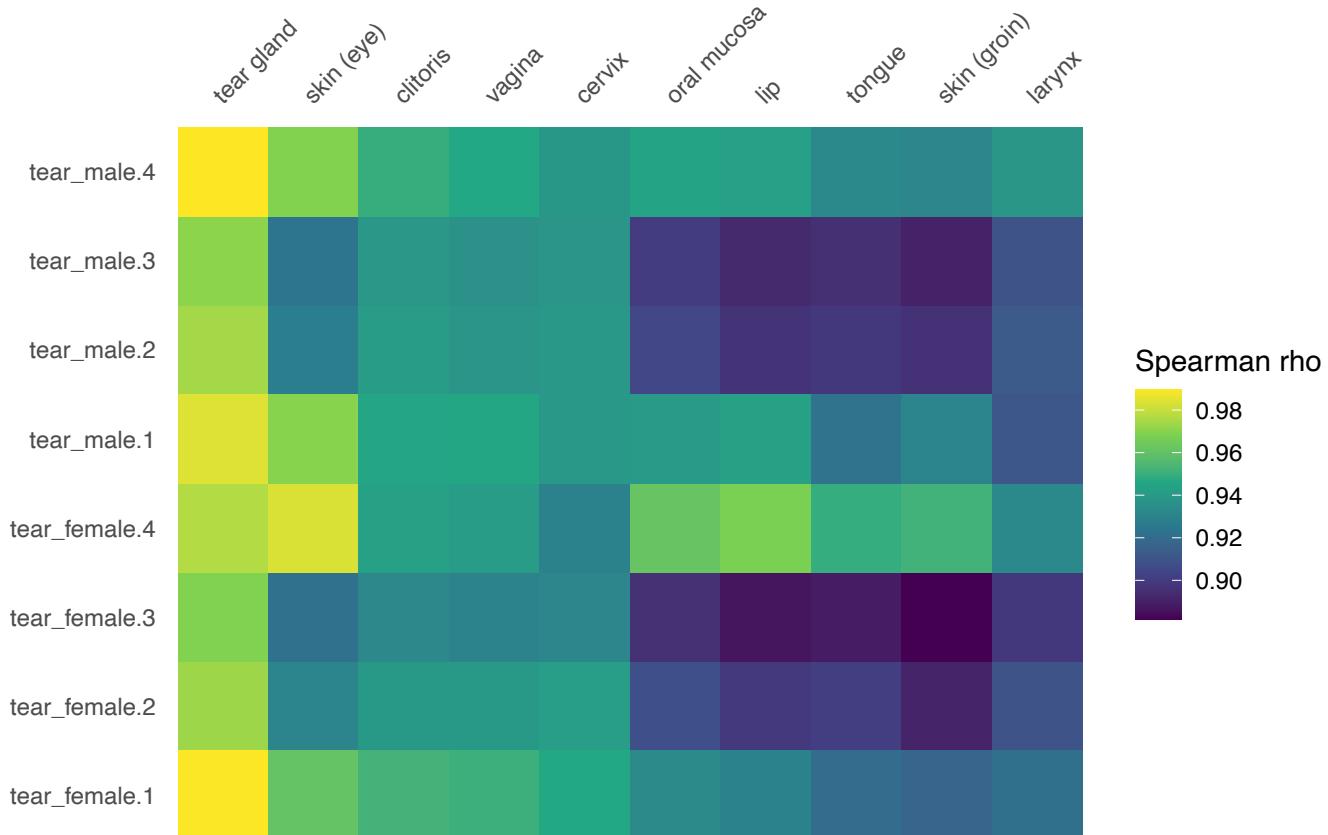
synovial tissue



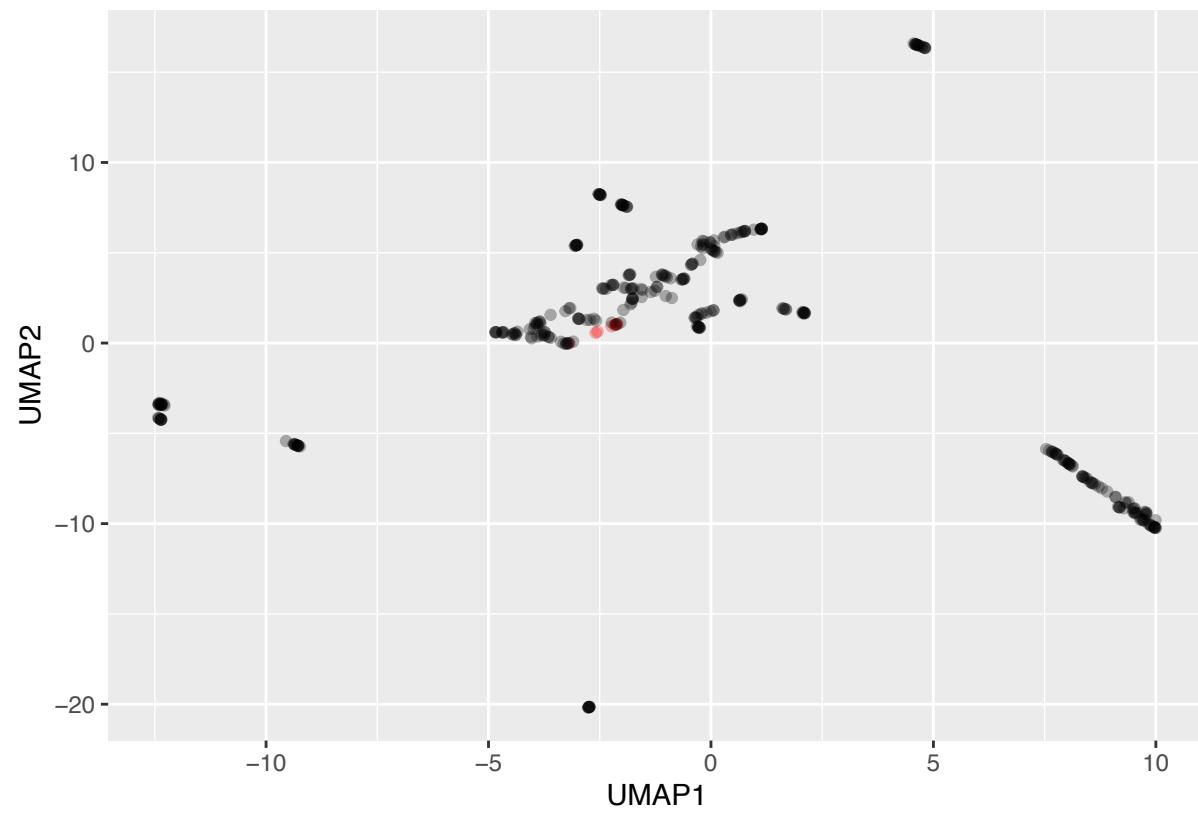
tear gland, PCA: TMM expression values



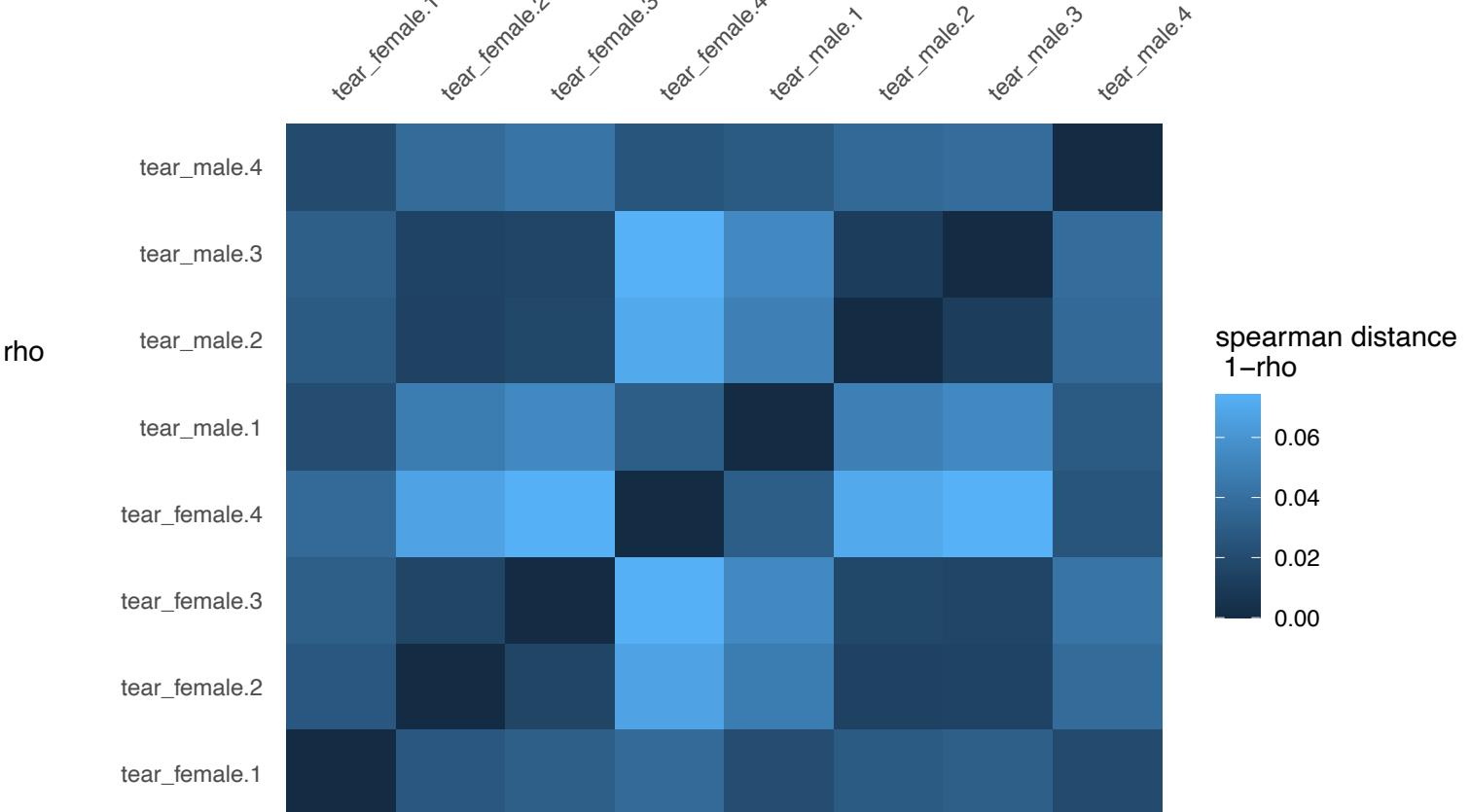
Tissue group to sample correlation



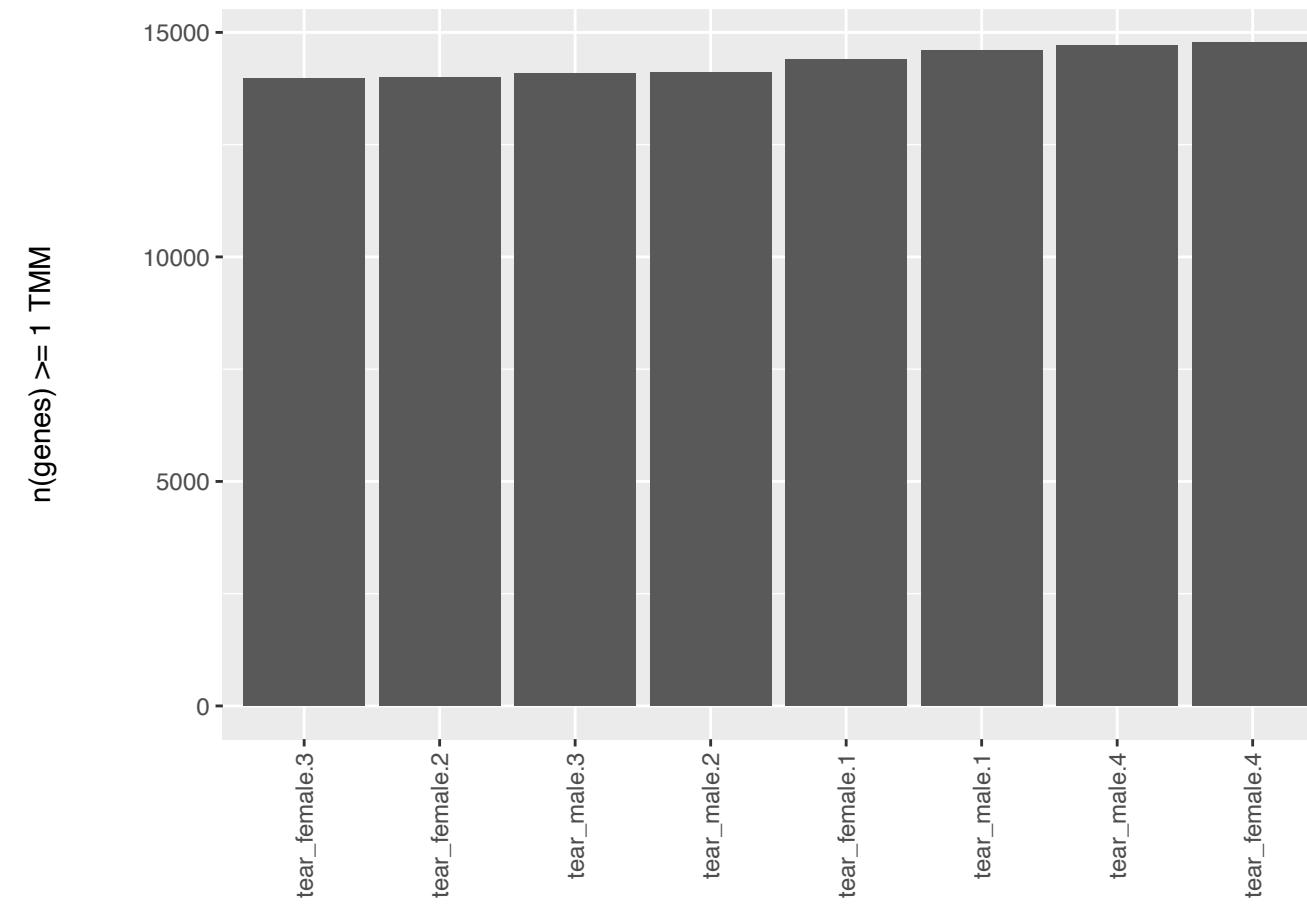
tear gland, UMAP: TMM expression values



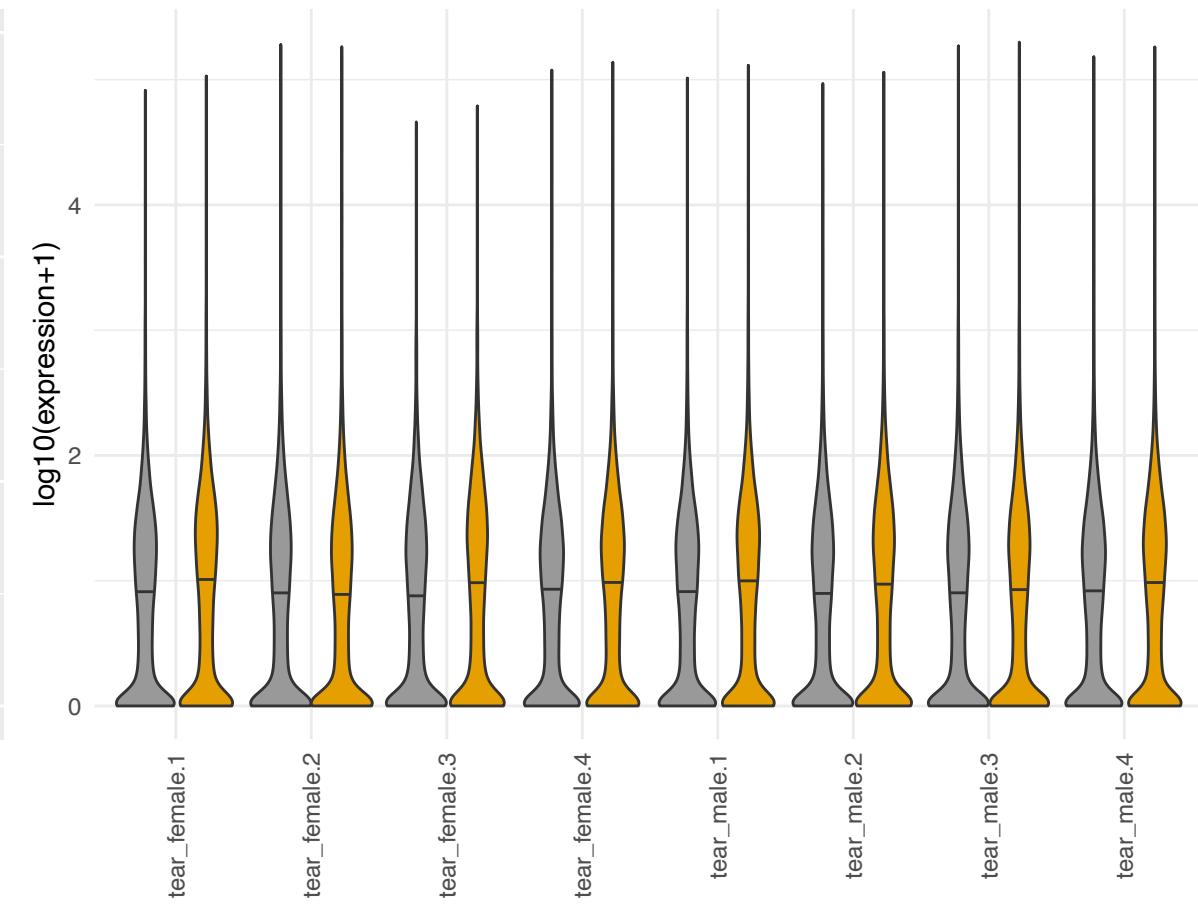
In tissue sample to sample Spearman Distance



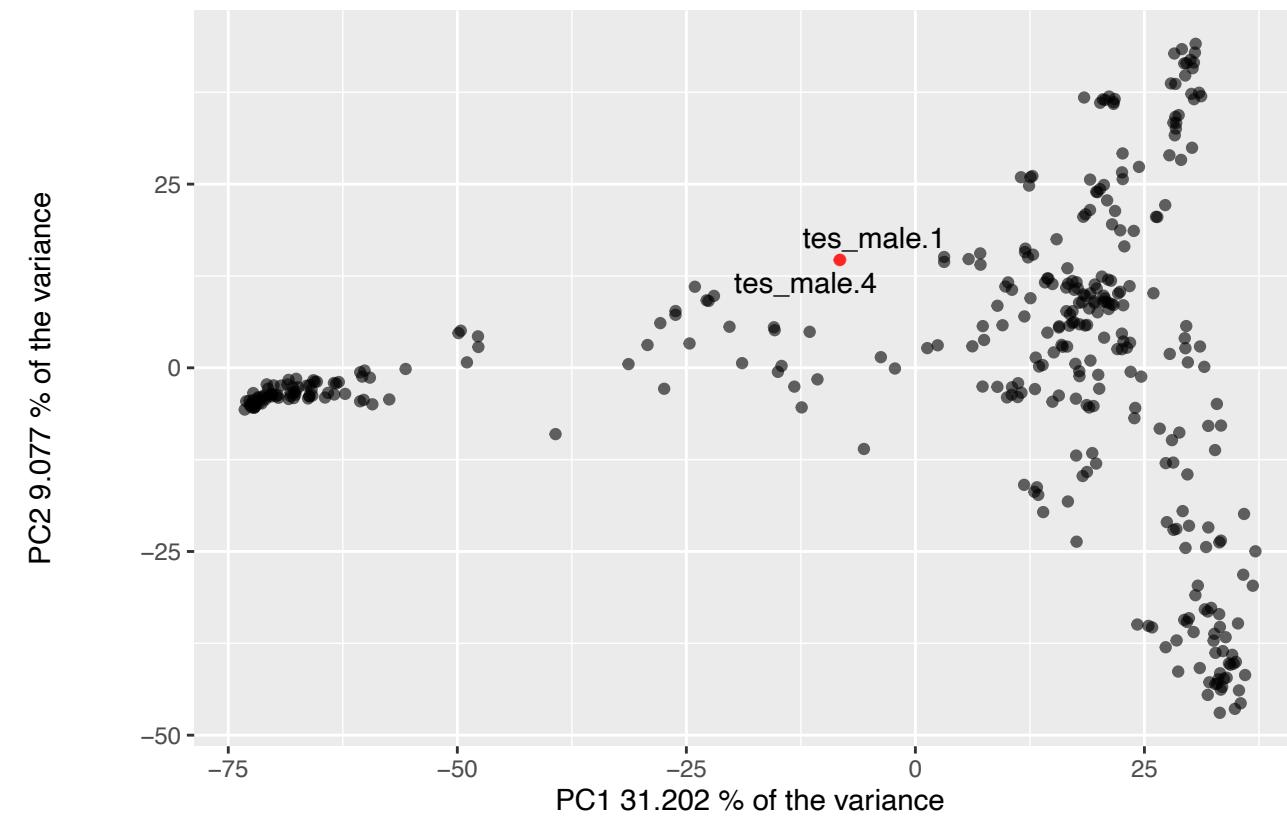
tear gland



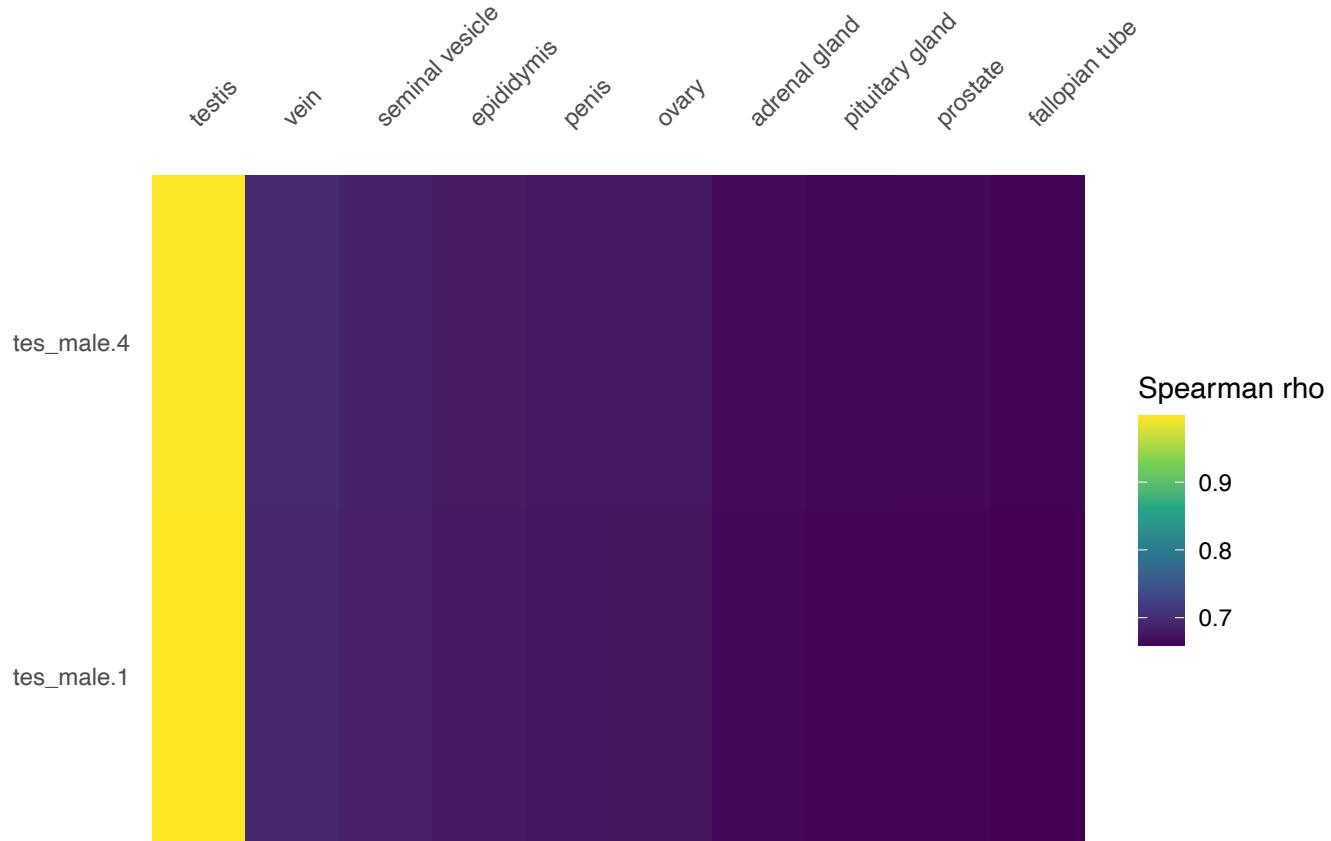
tear gland



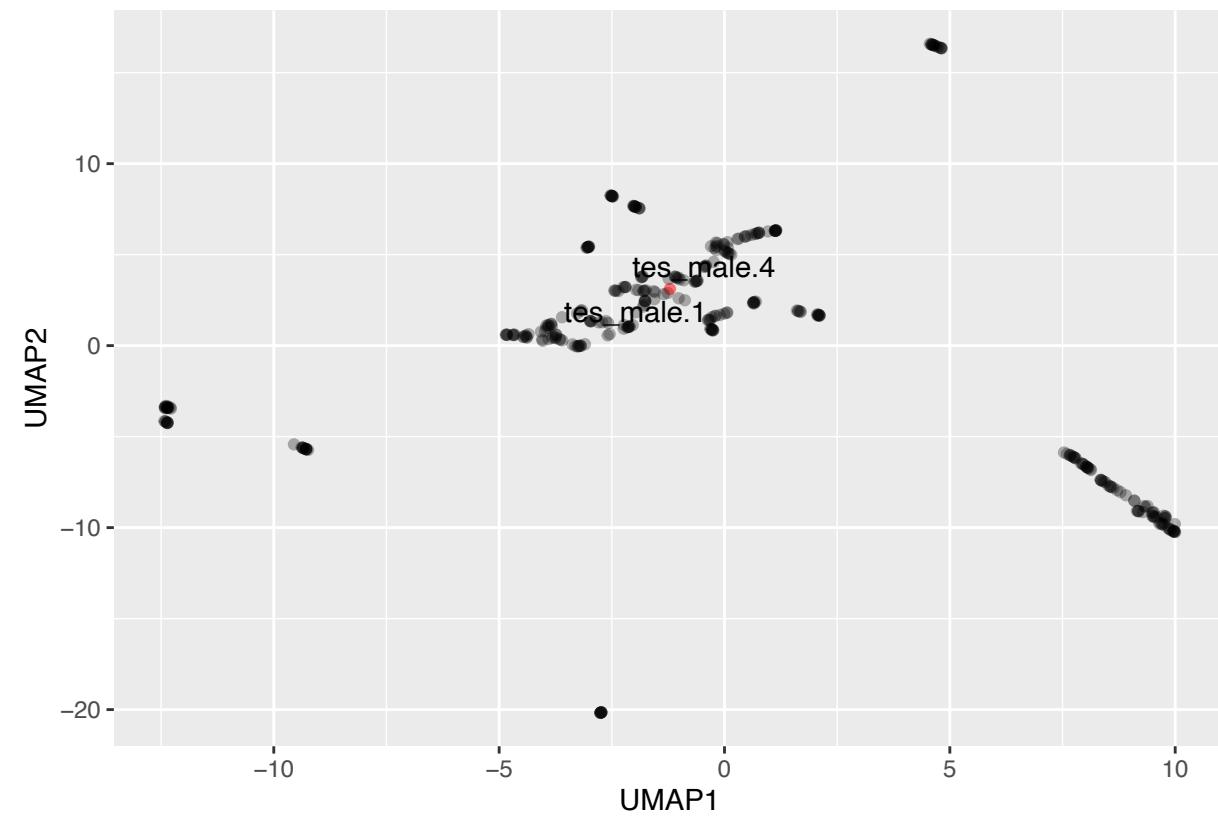
testis, PCA: TMM expression values



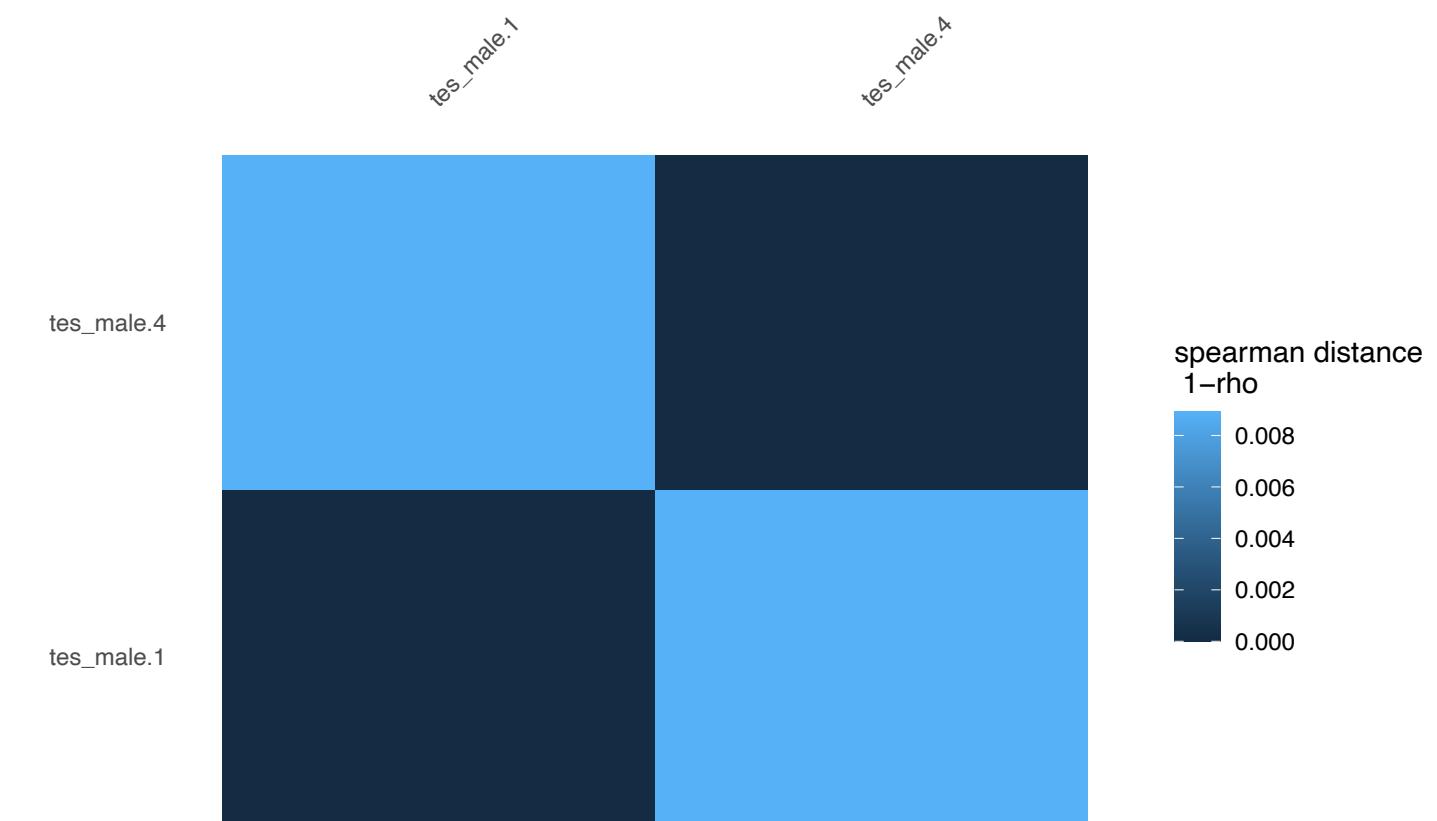
Tissue group to sample correlation



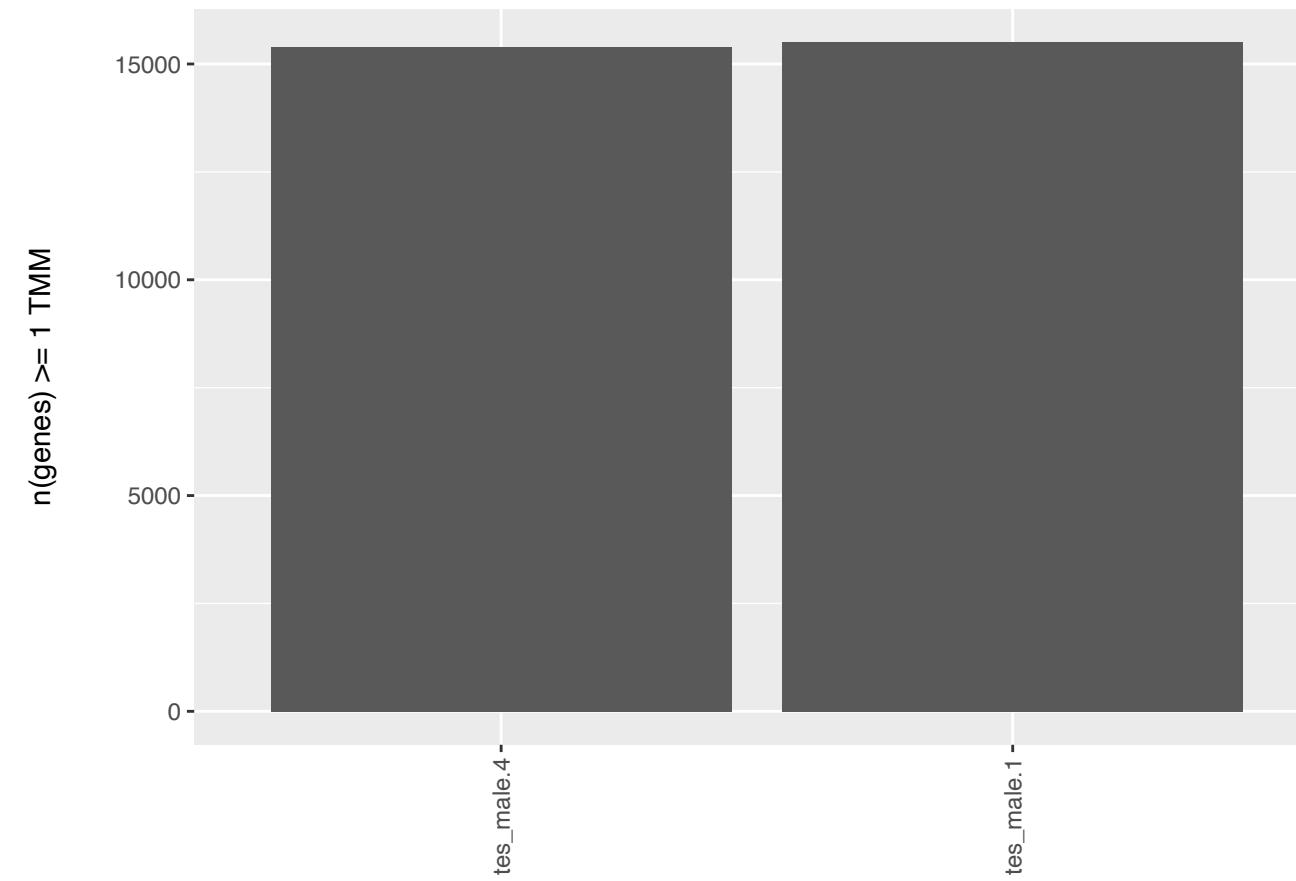
testis, UMAP: TMM expression values



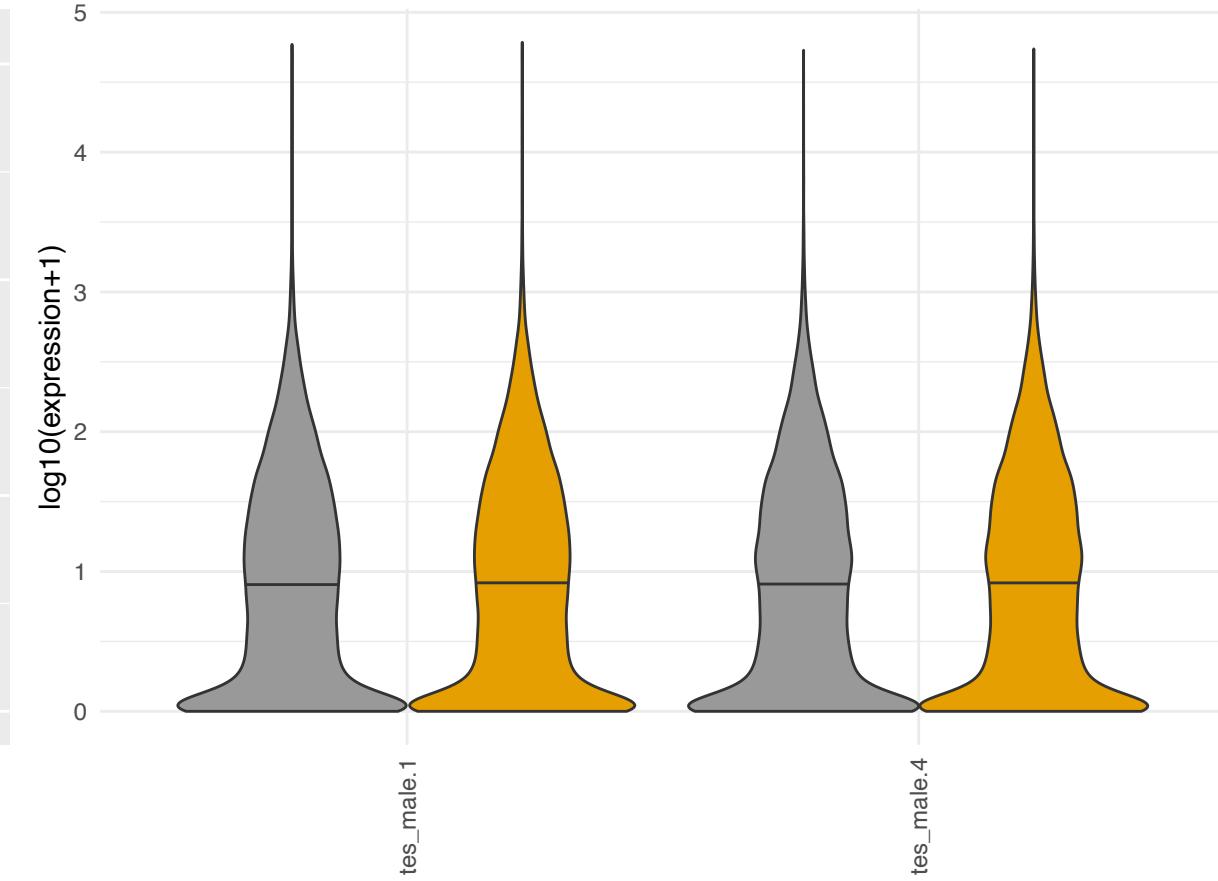
In tissue sample to sample Spearman Distance



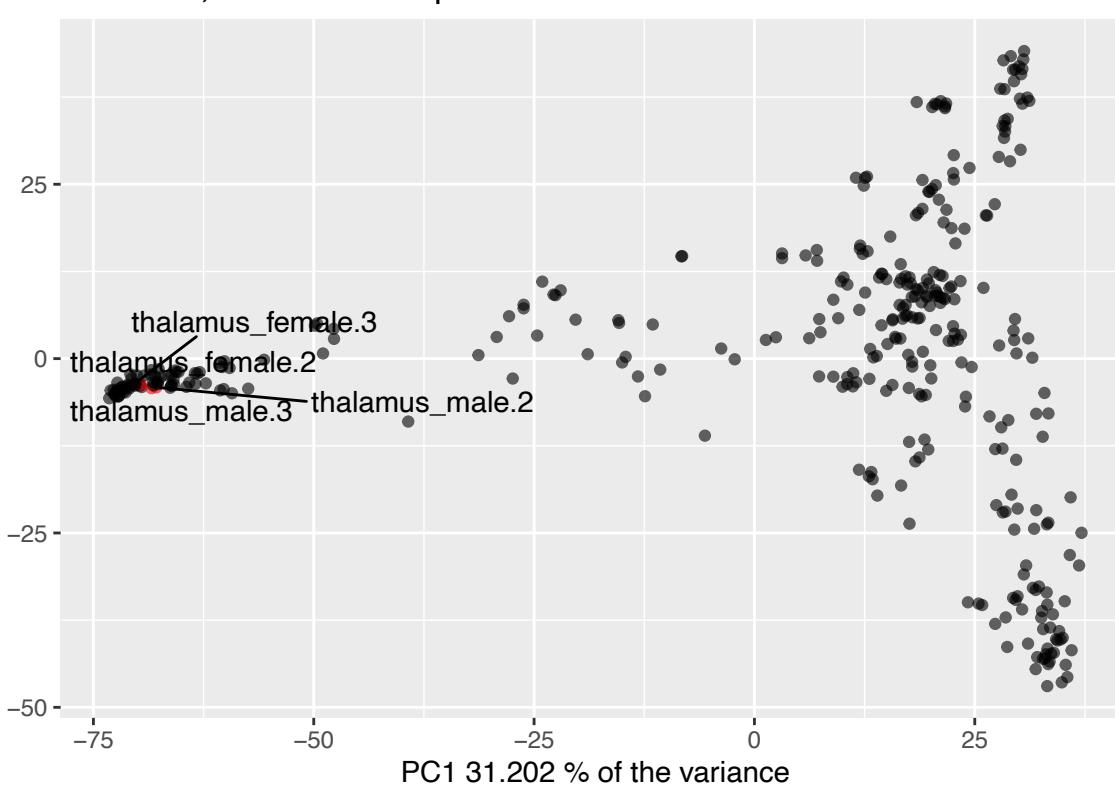
testis



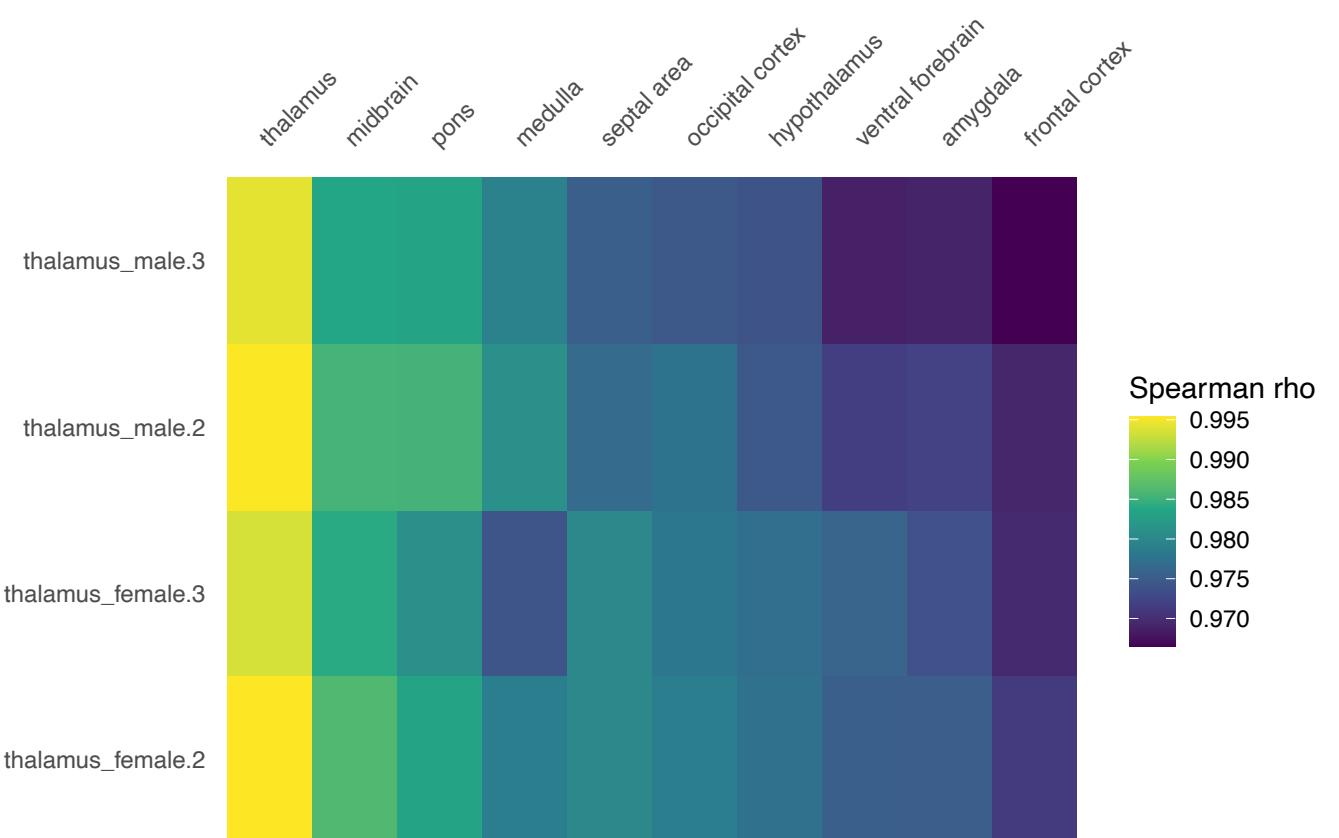
testis



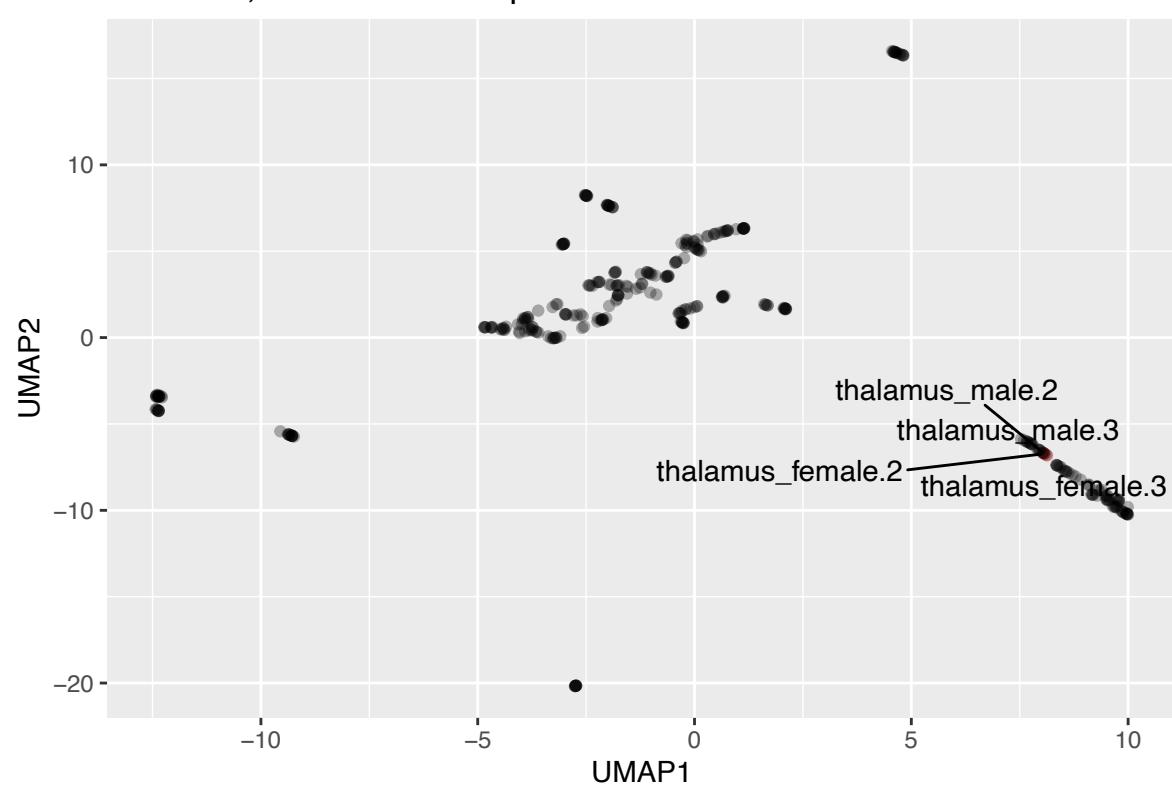
thalamus, PCA: TMM expression values



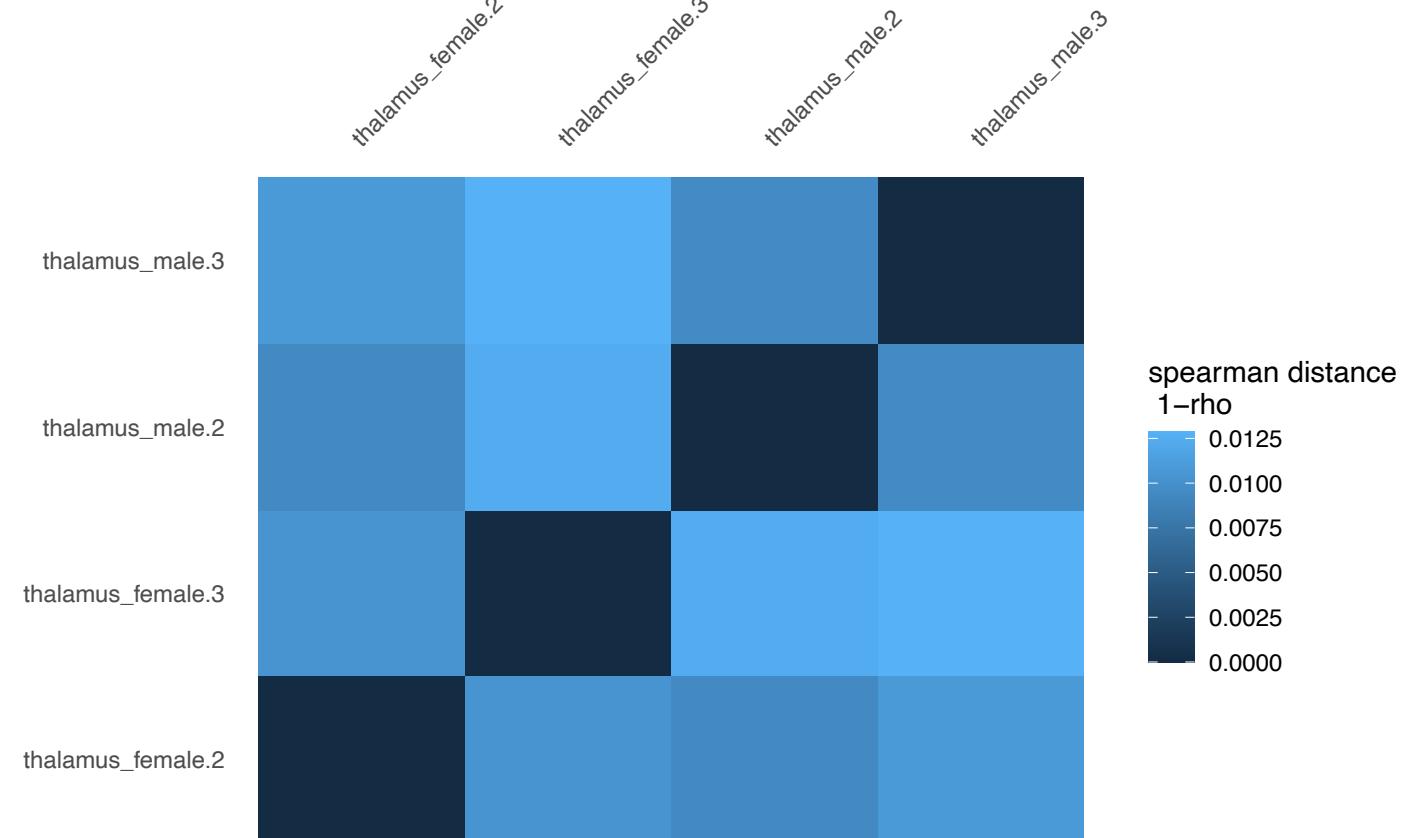
Tissue group to sample correlation



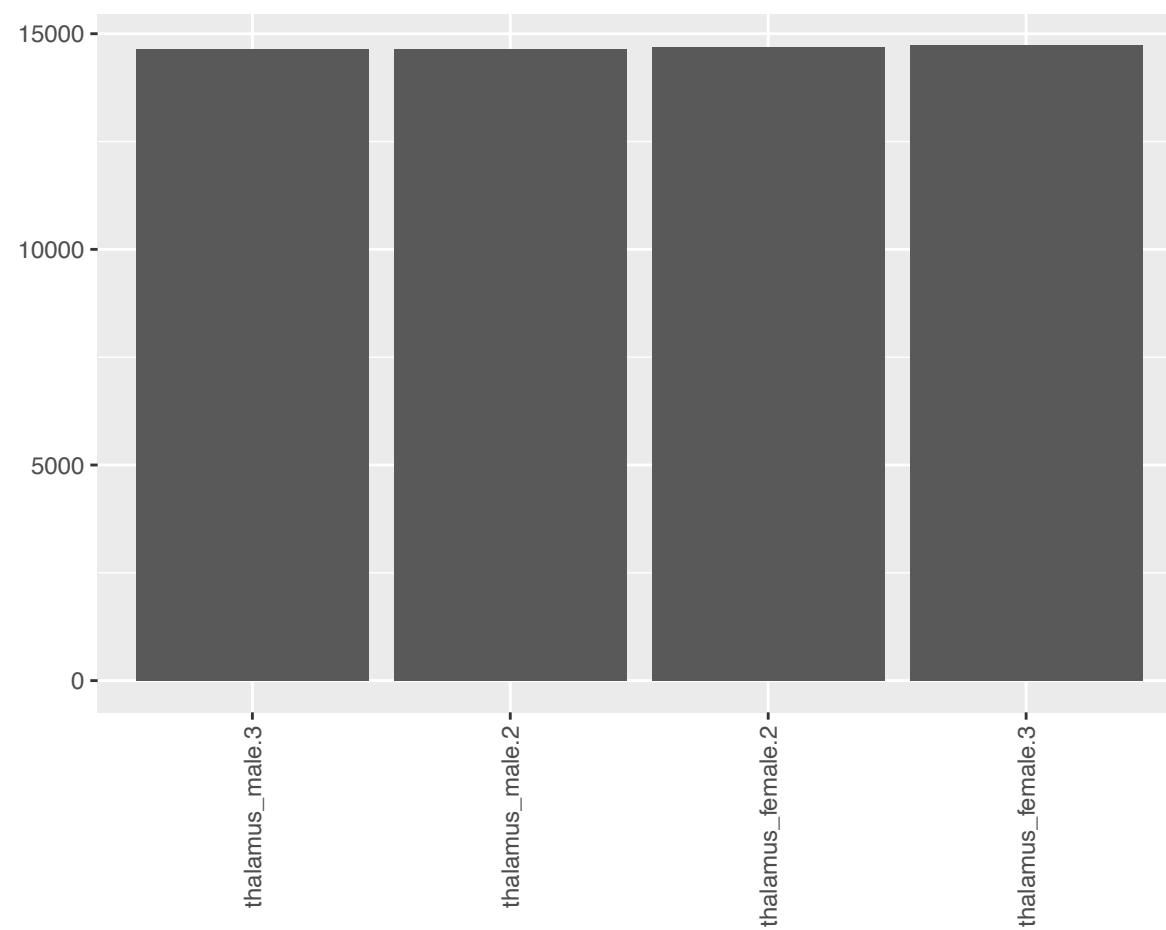
thalamus, UMAP: TMM expression values



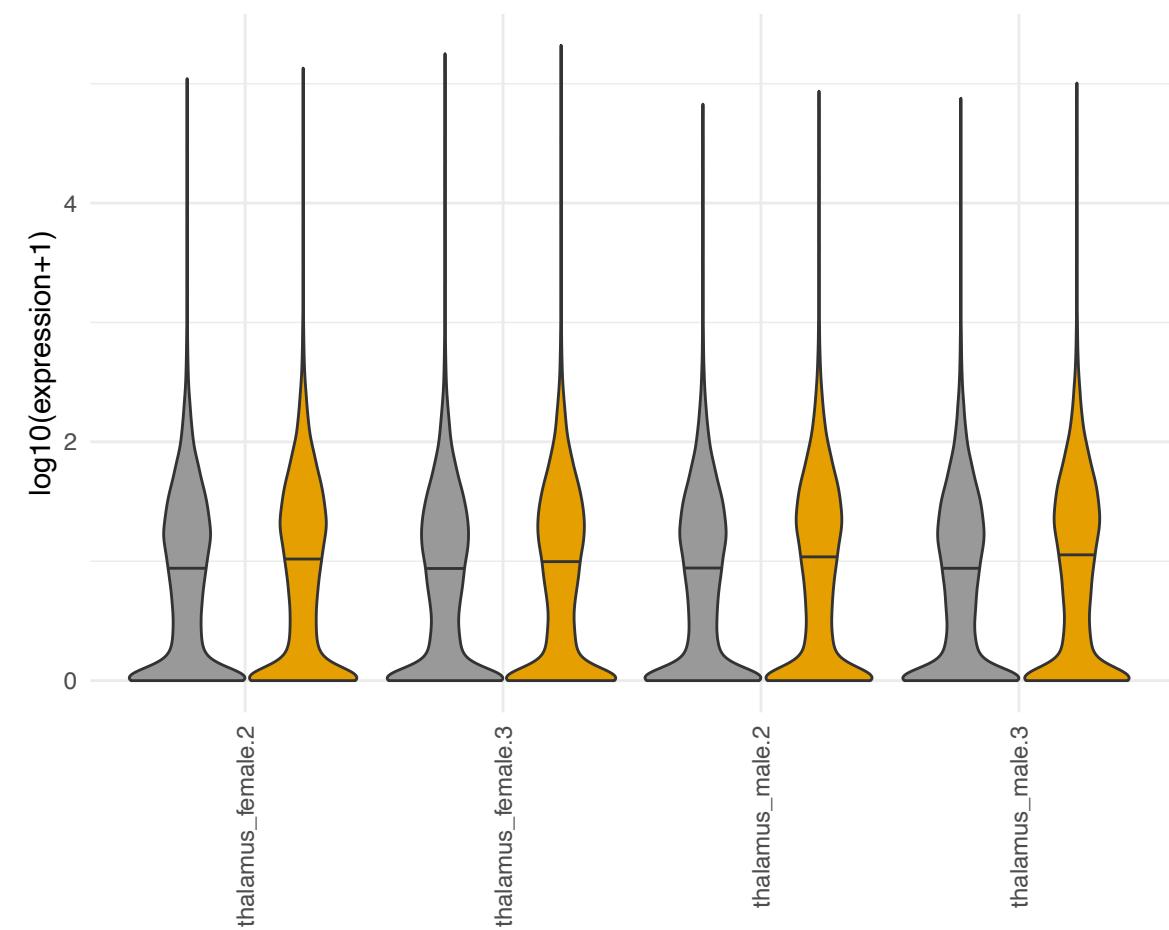
In tissue sample to sample Spearman Distance



thalamus

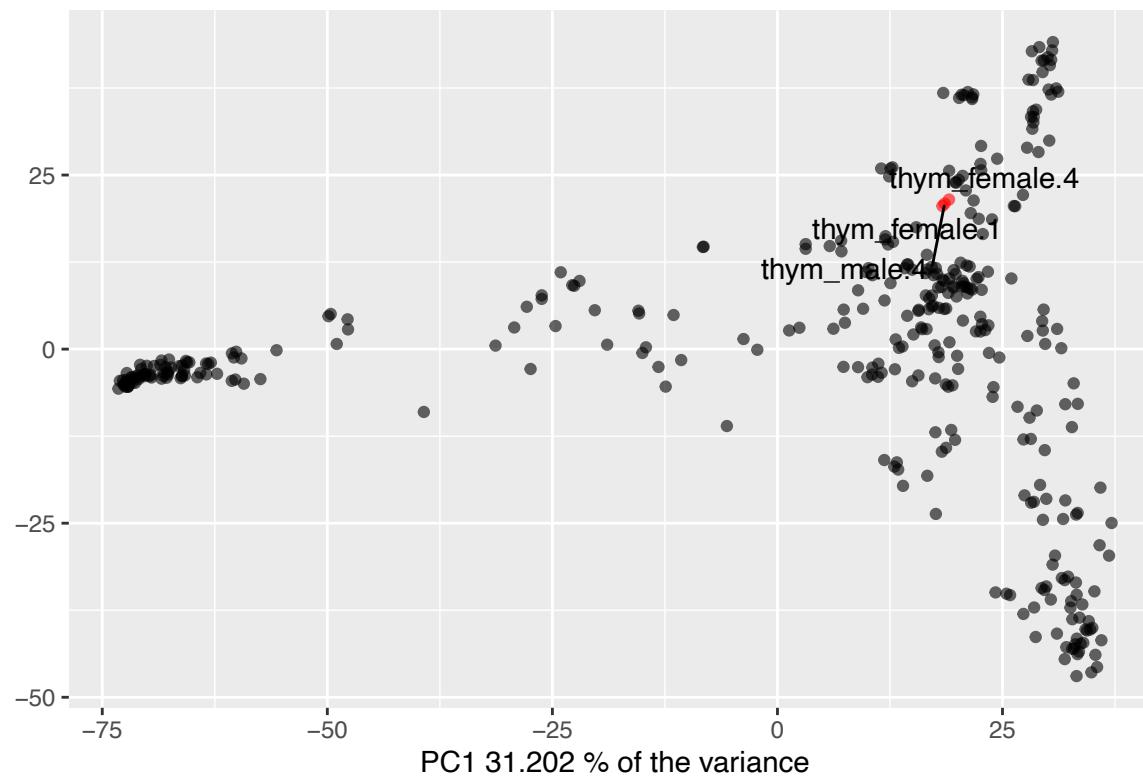


thalamus

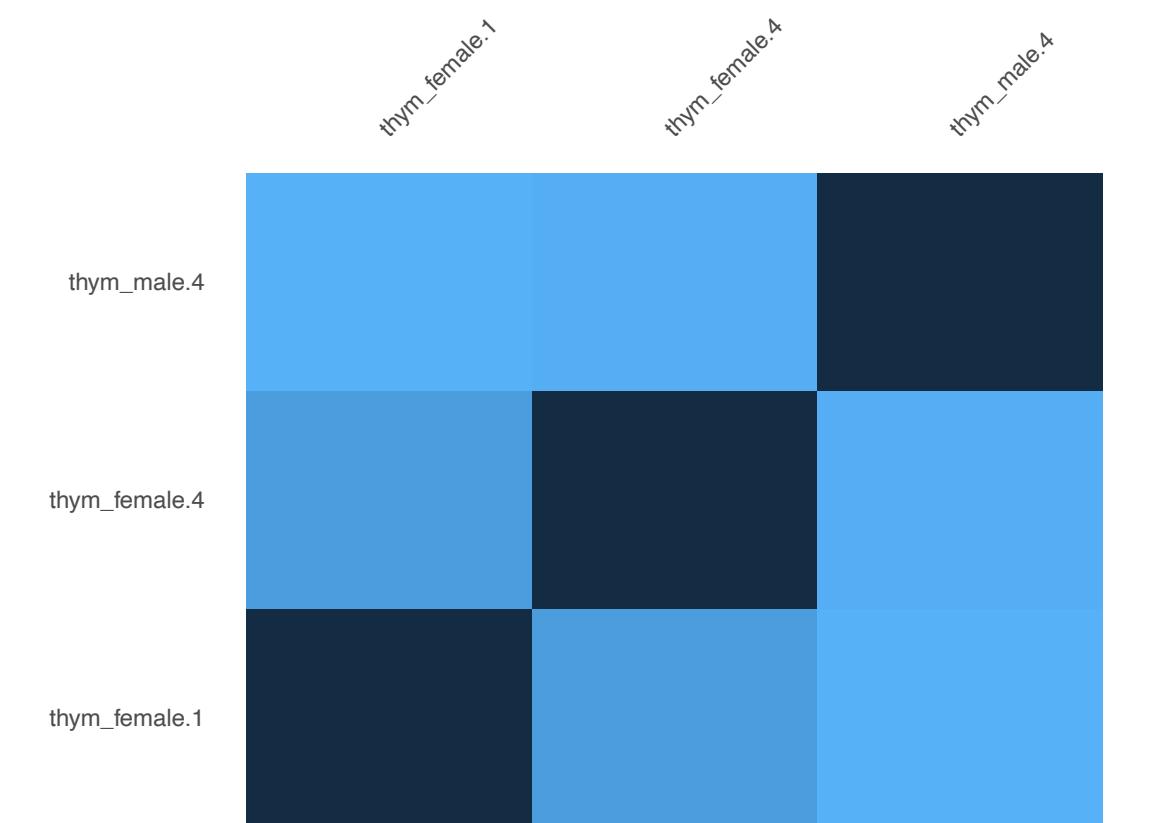
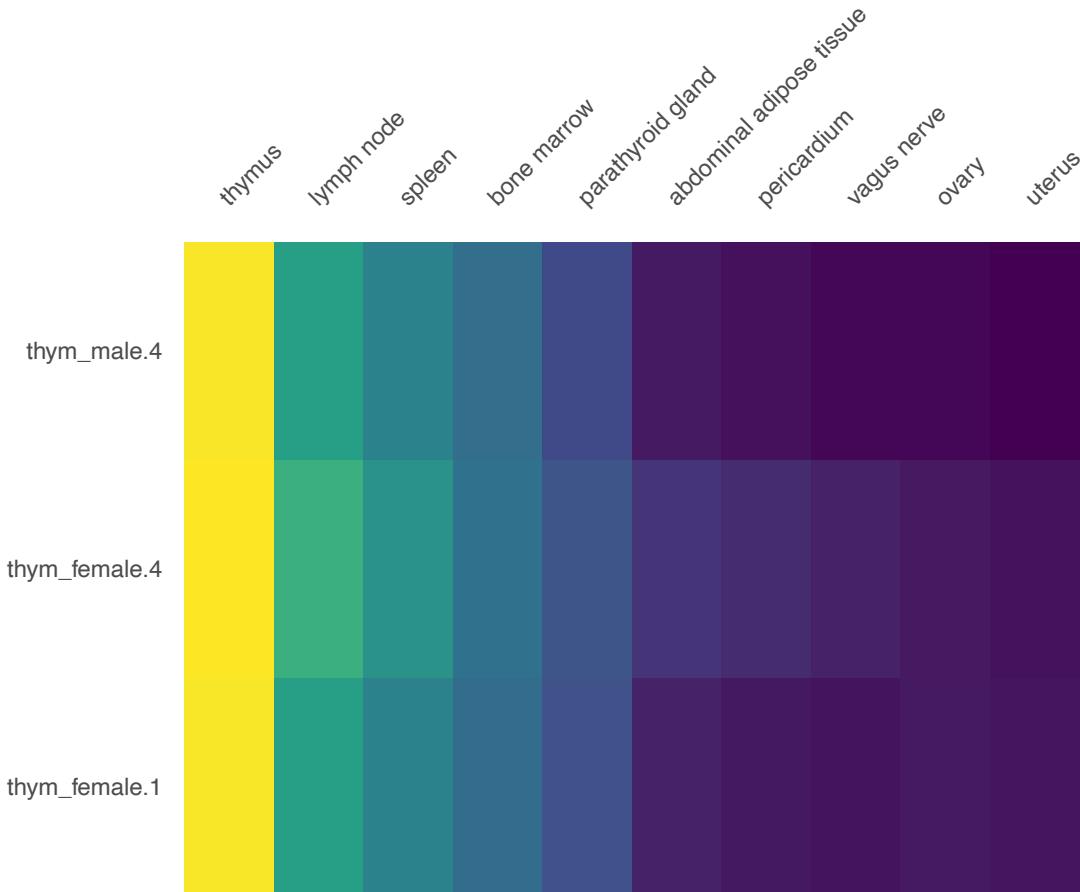
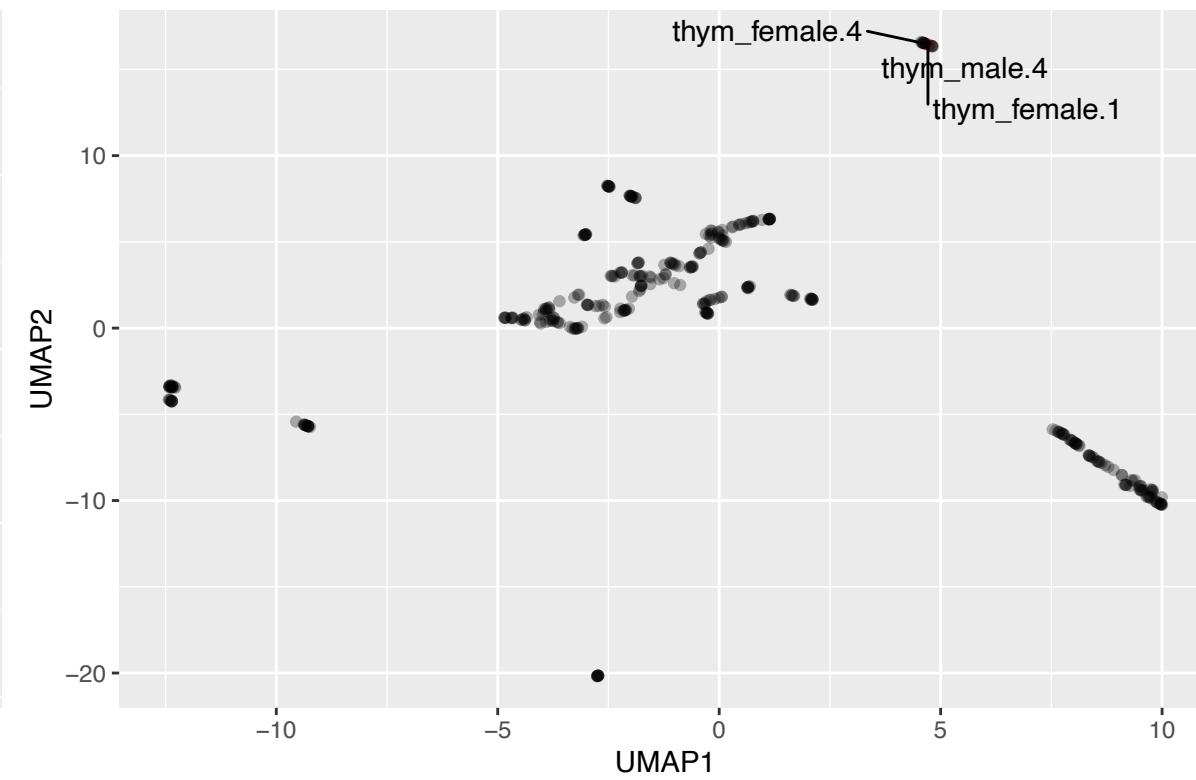


thymus, PCA: TMM expression values

PC2 9.077 % of the variance

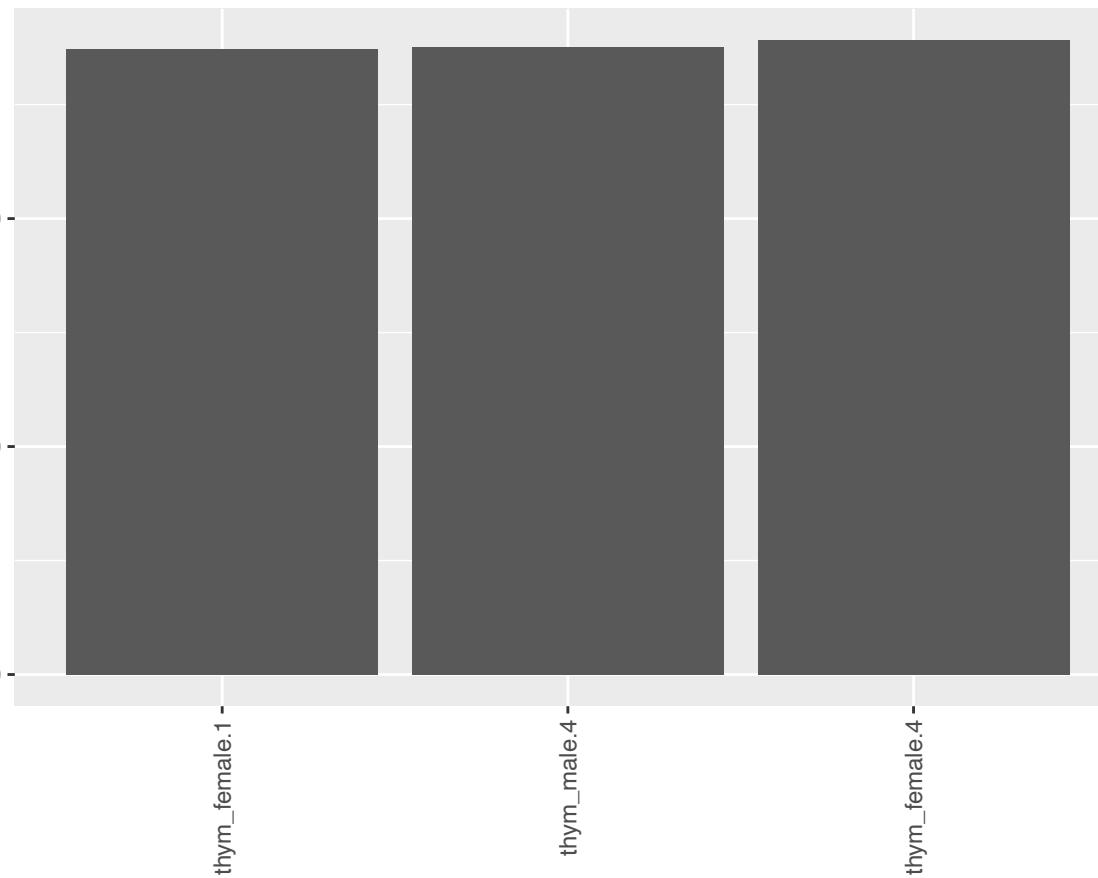


thymus, UMAP: TMM expression values

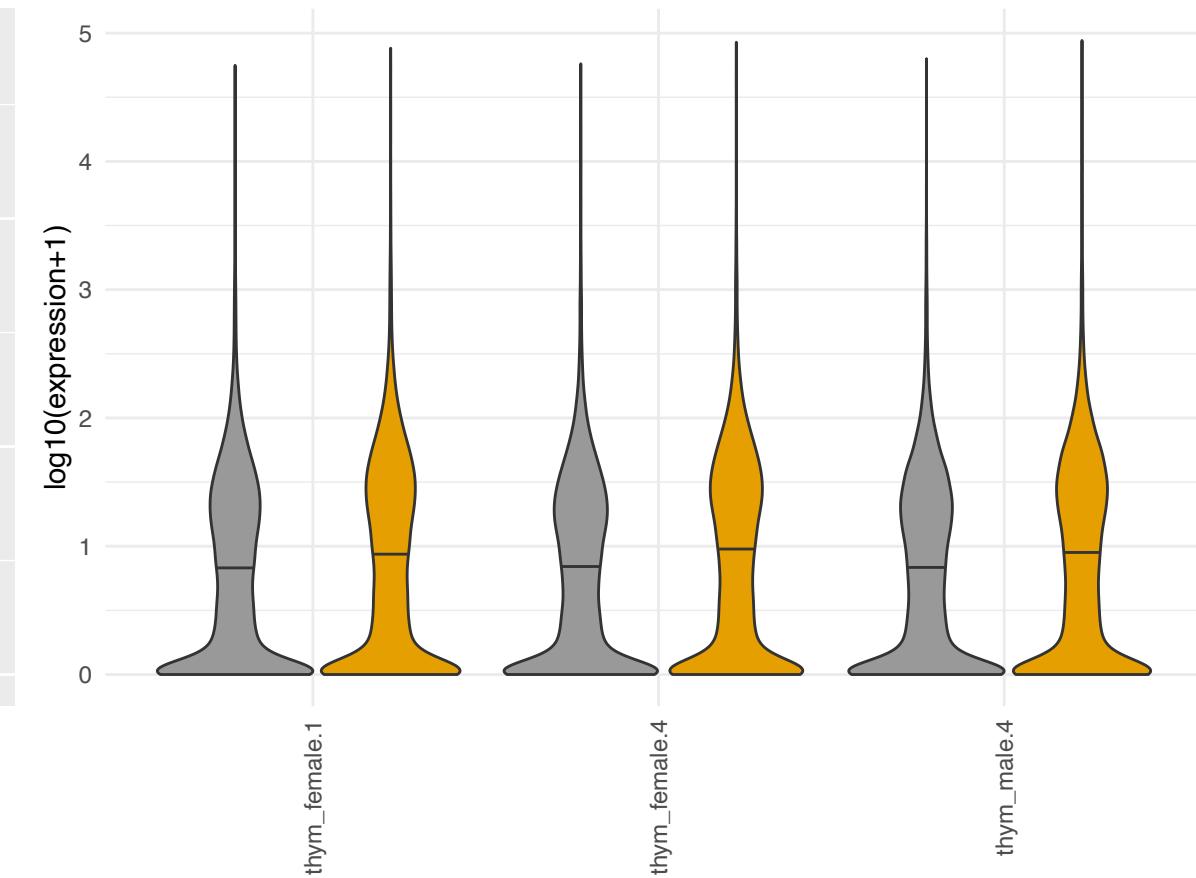


thymus

n(genes) >= 1 TMM

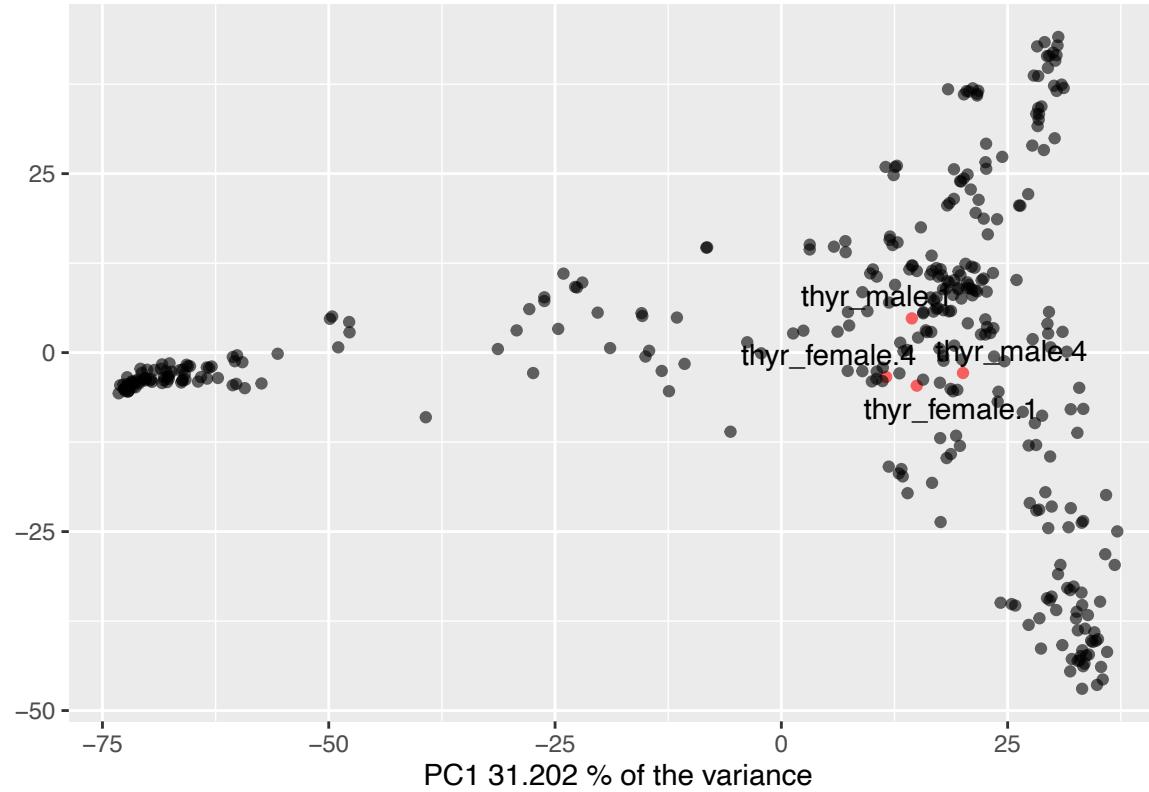


thymus

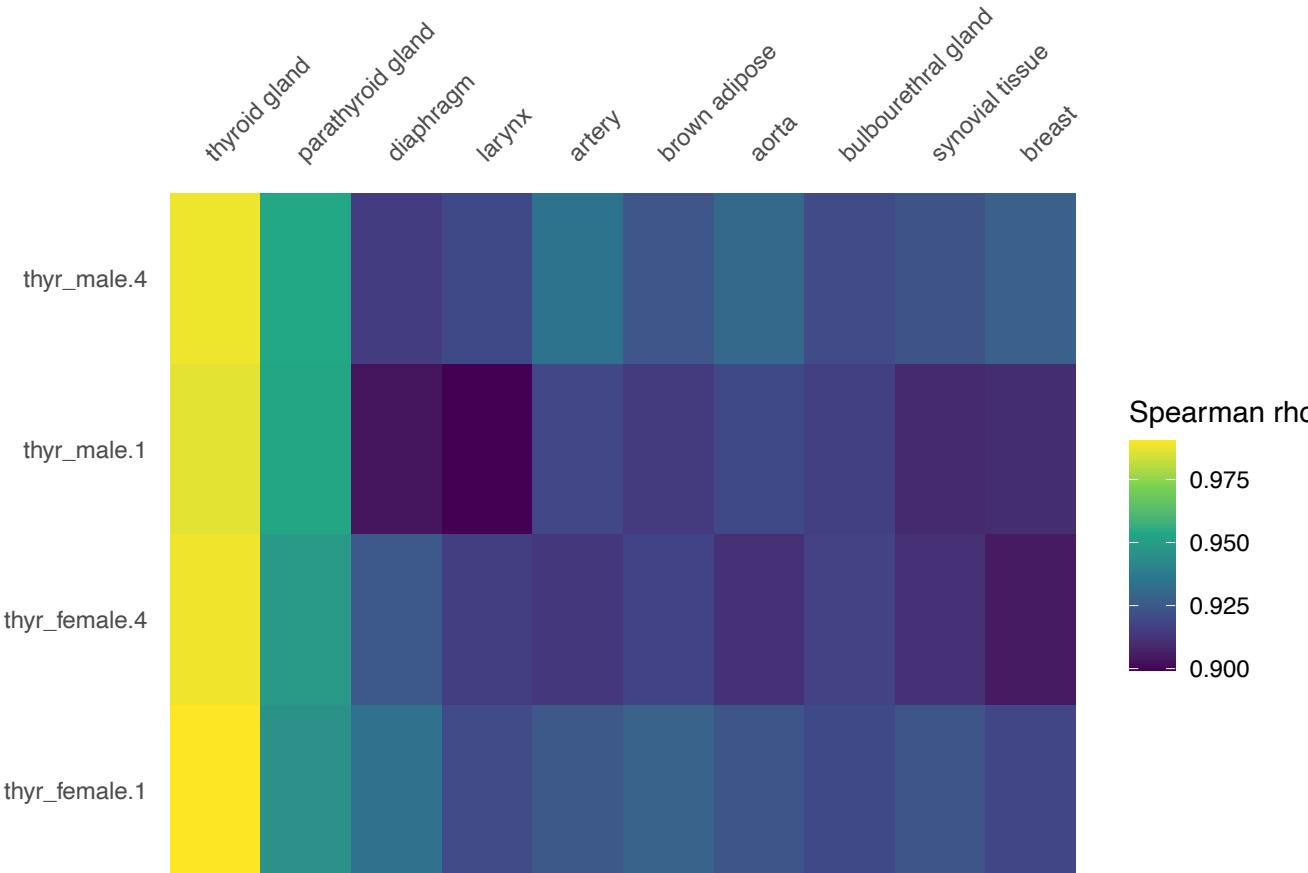


thyroid gland, PCA: TMM expression values

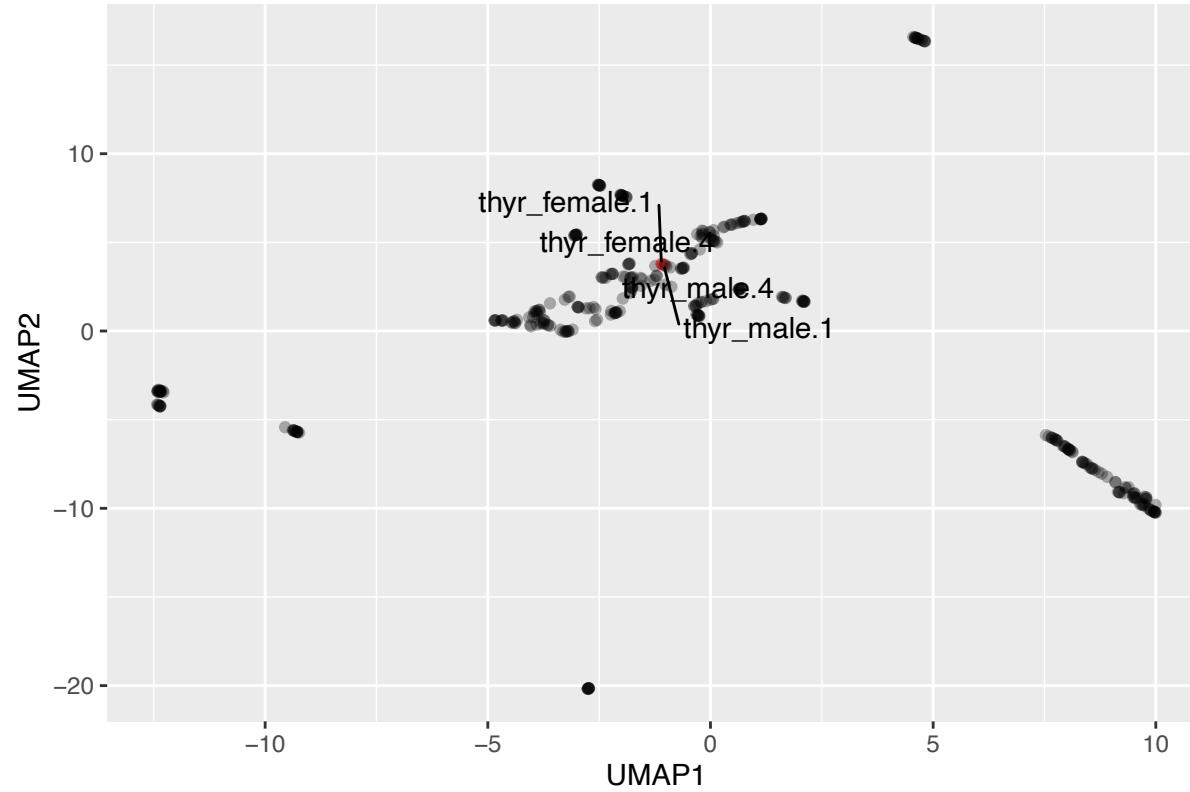
PC2 9.077 % of the variance



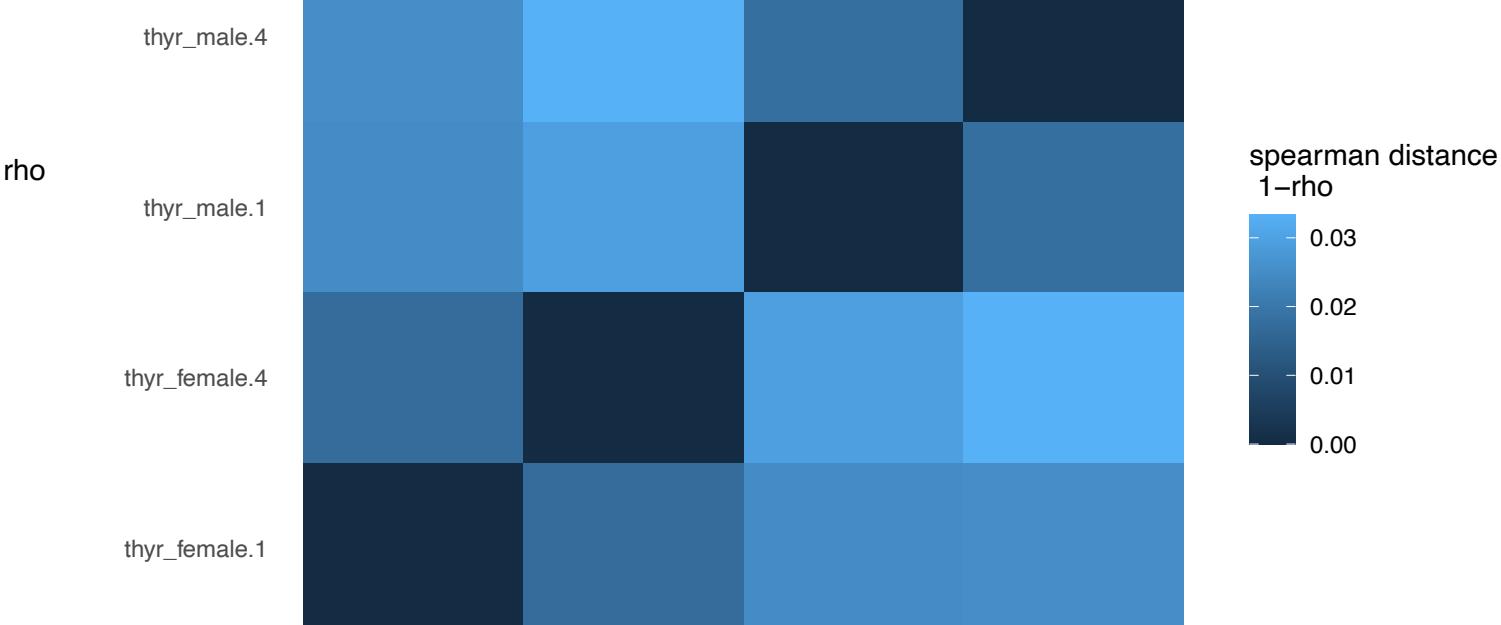
Tissue group to sample correlation



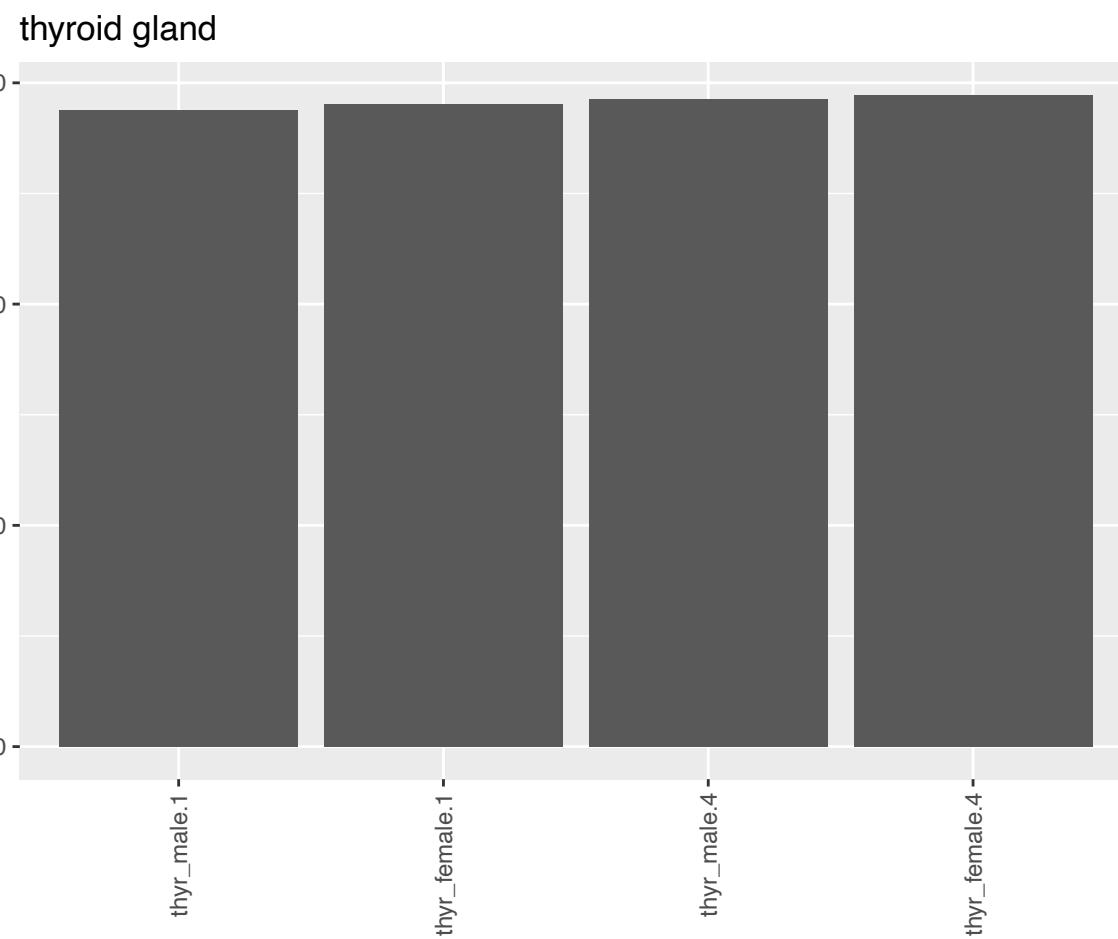
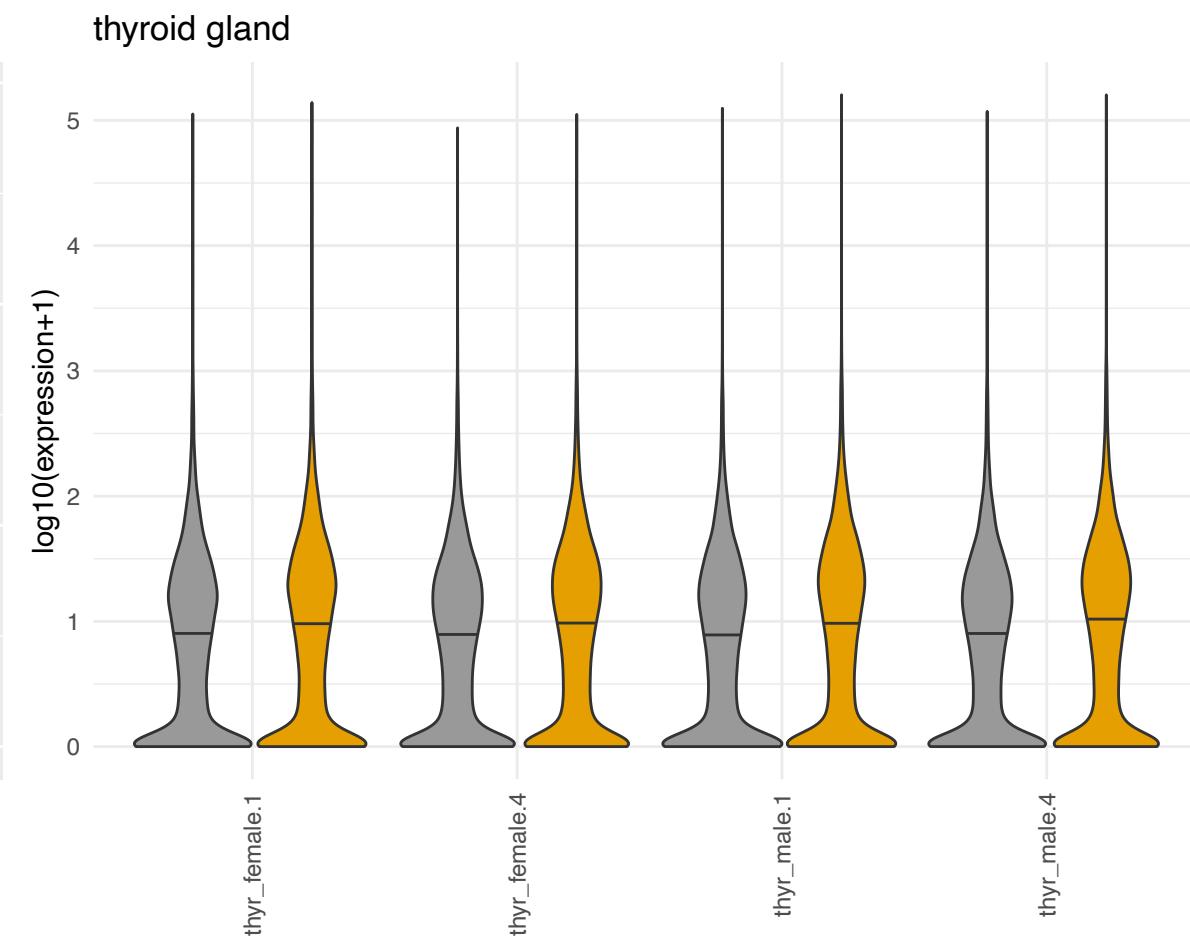
thyroid gland, UMAP: TMM expression values



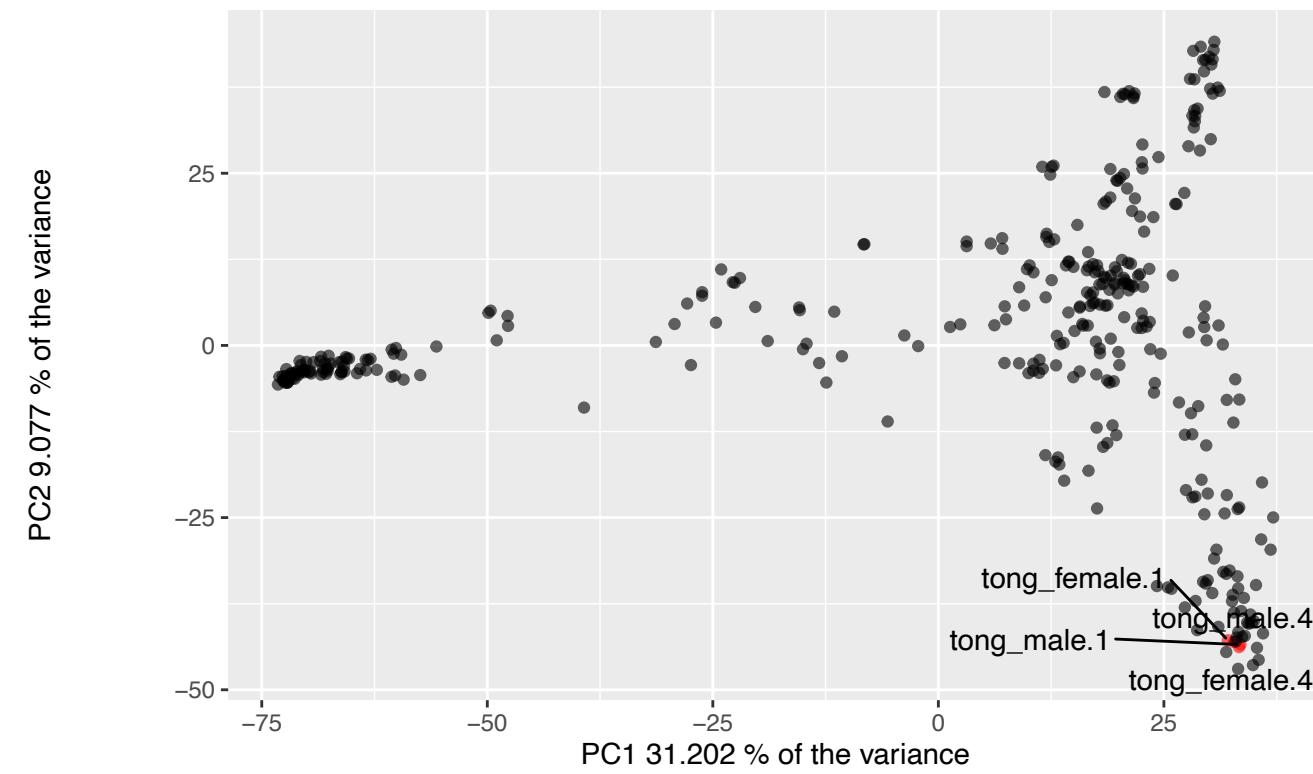
thy_r_female.1, thy_r_female.4, thy_r_male.1, thy_r_male.4



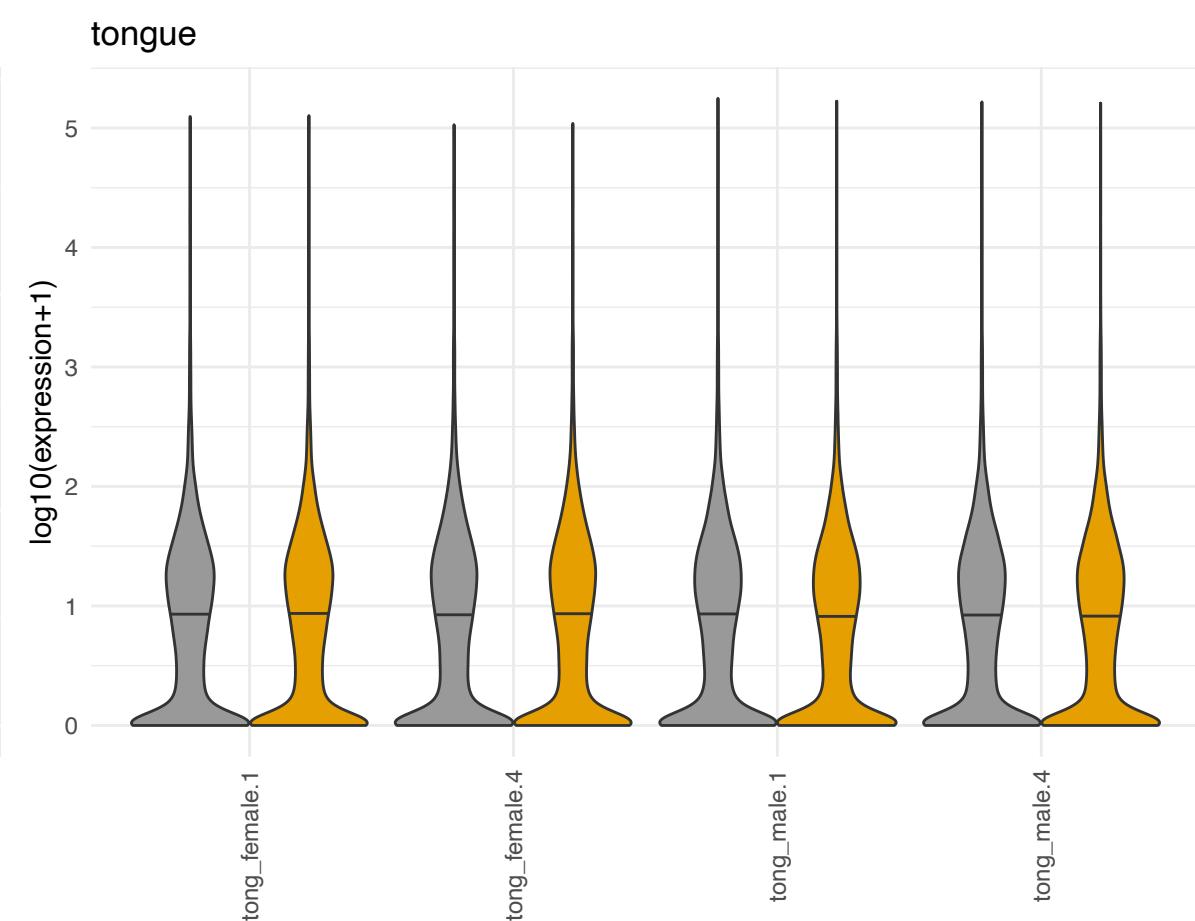
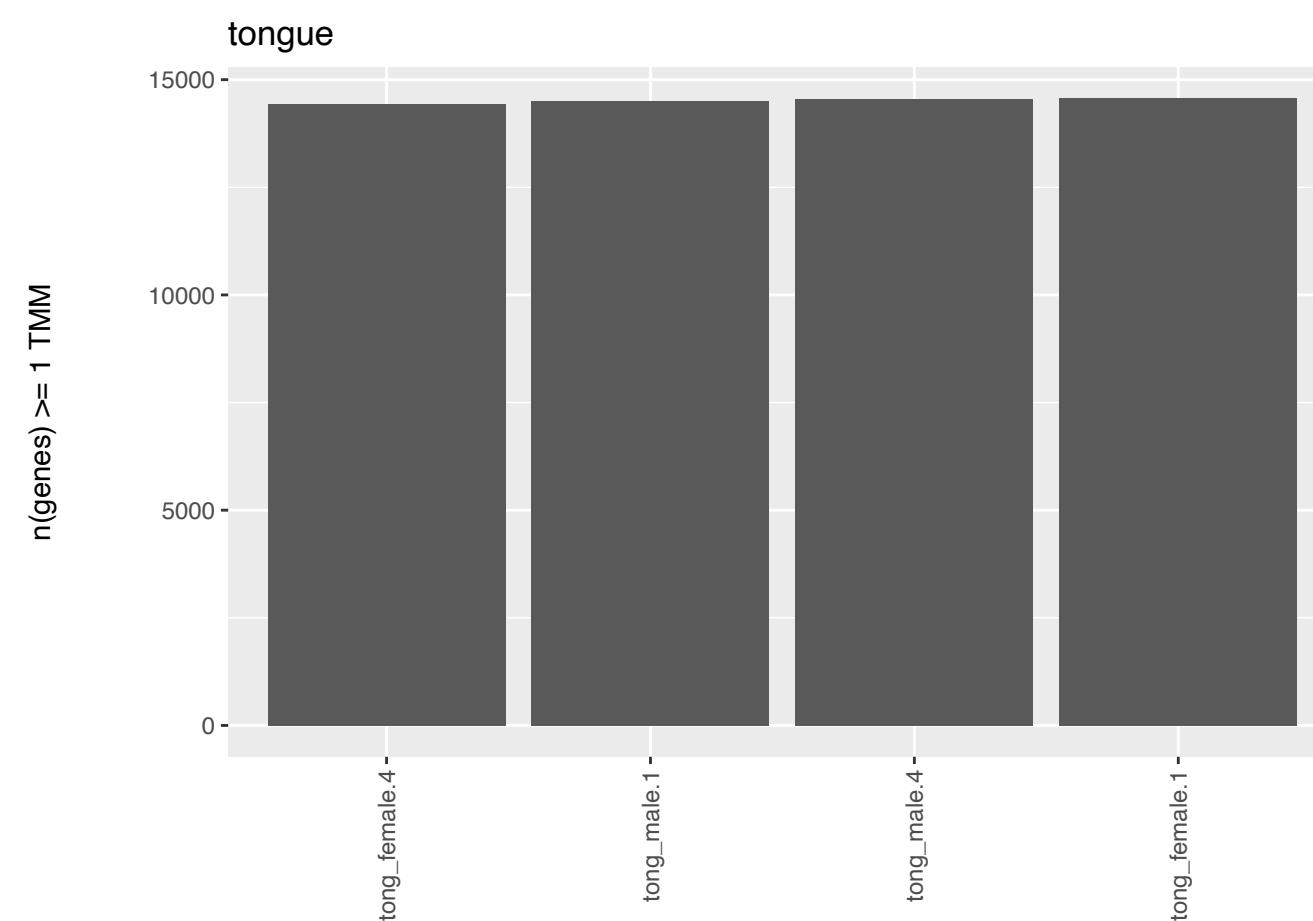
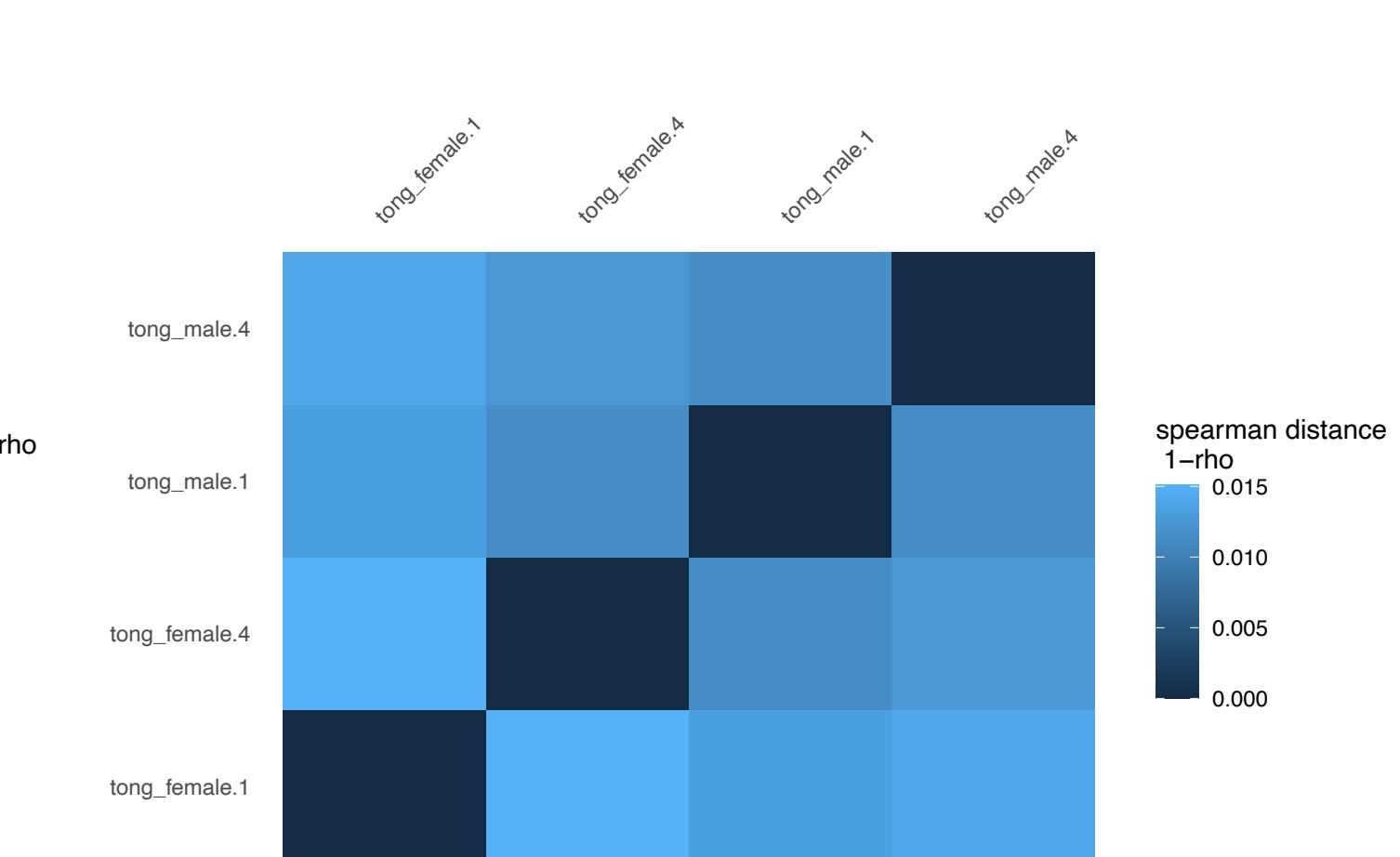
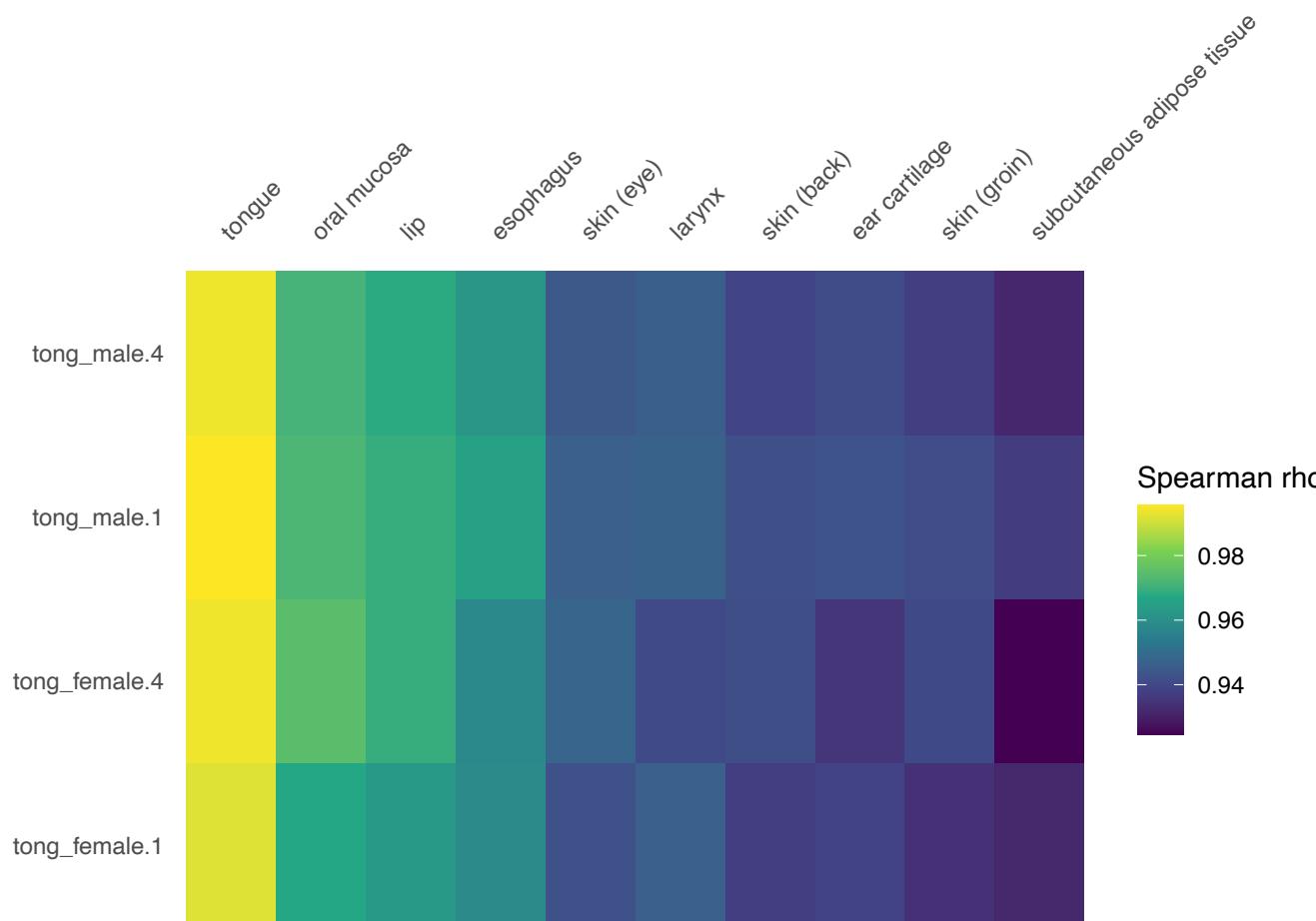
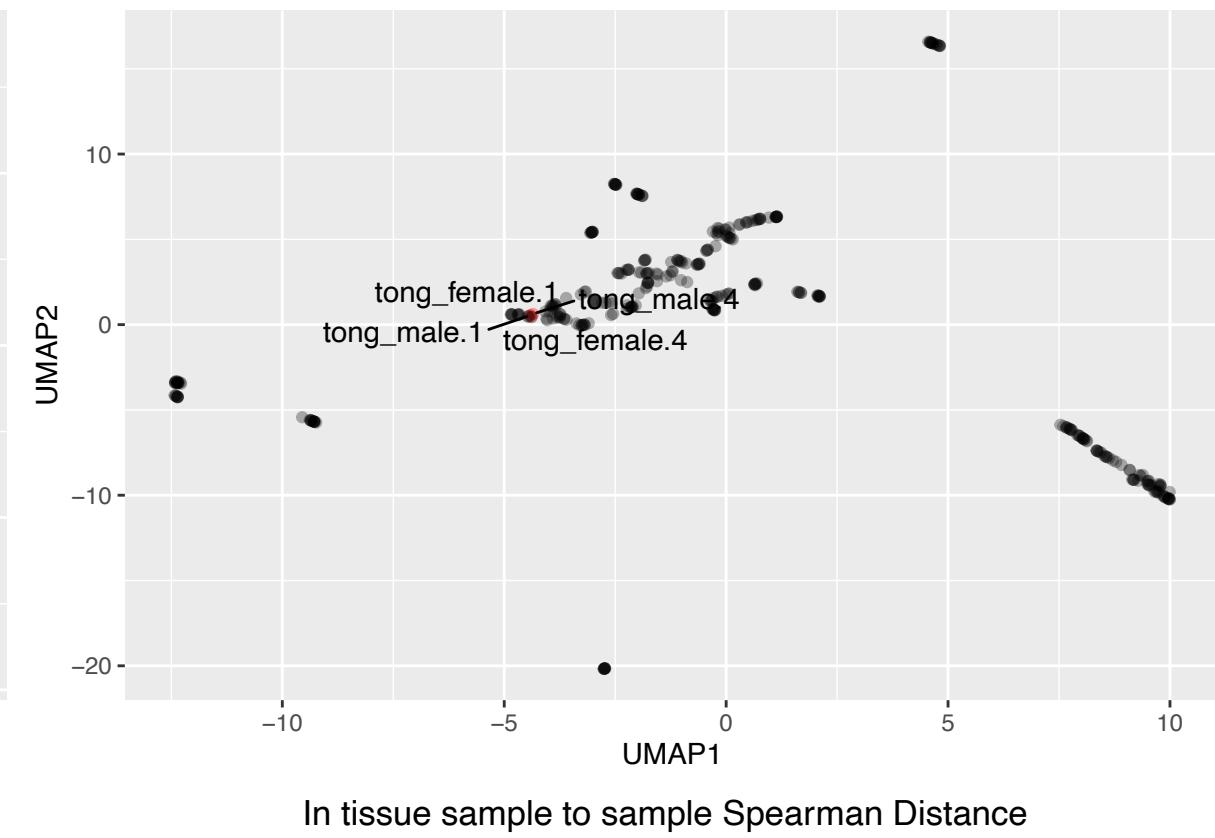
n(genes) >= 1 TMM



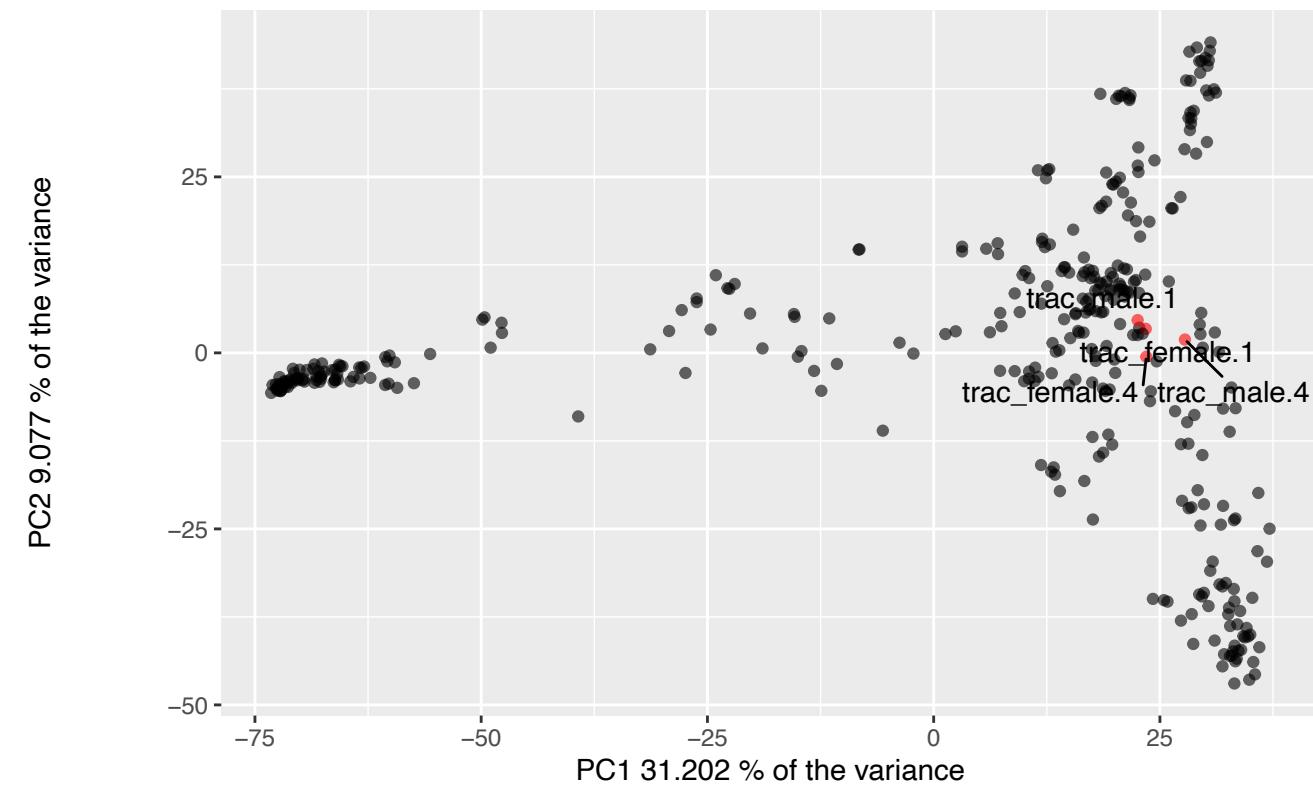
tongue, PCA: TMM expression values



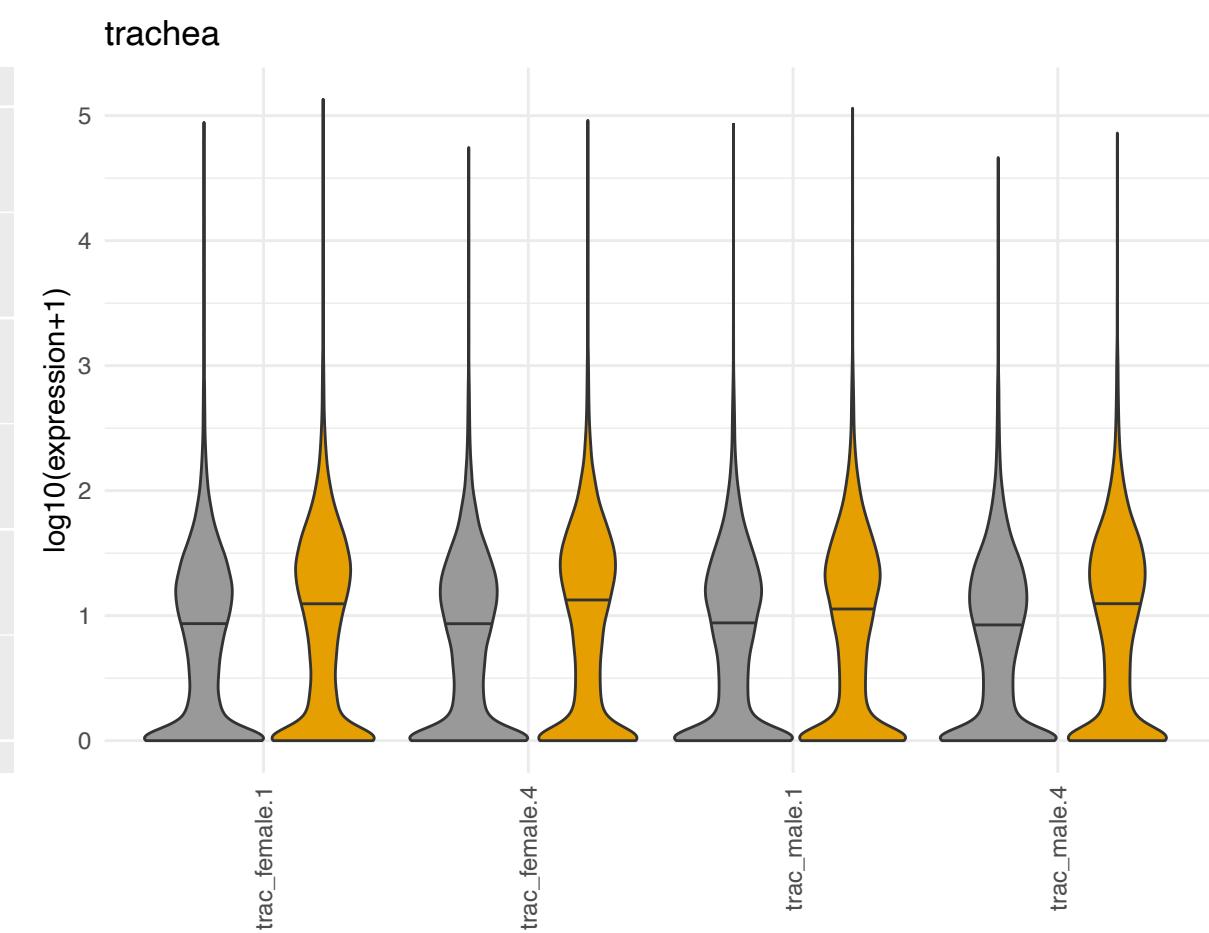
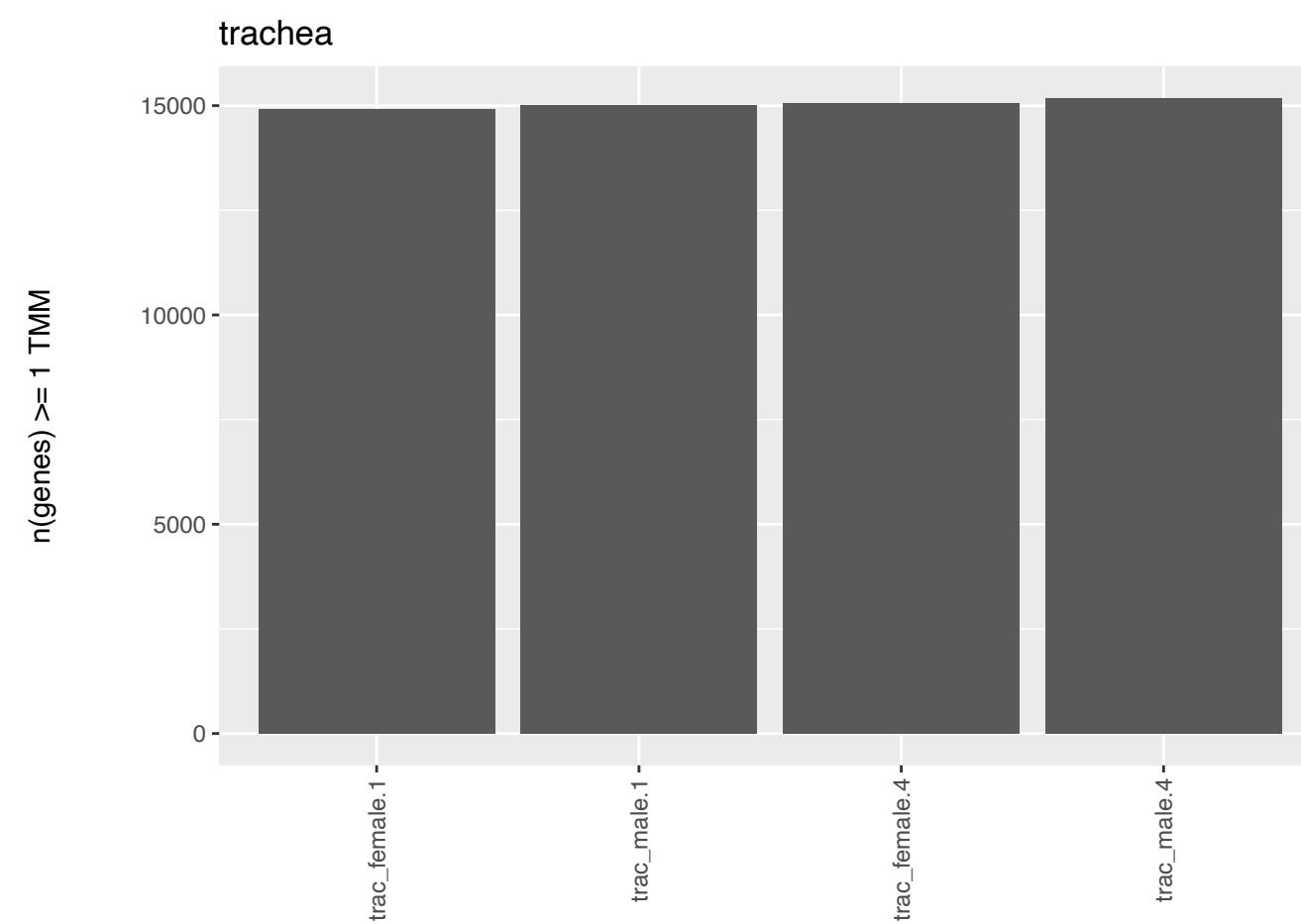
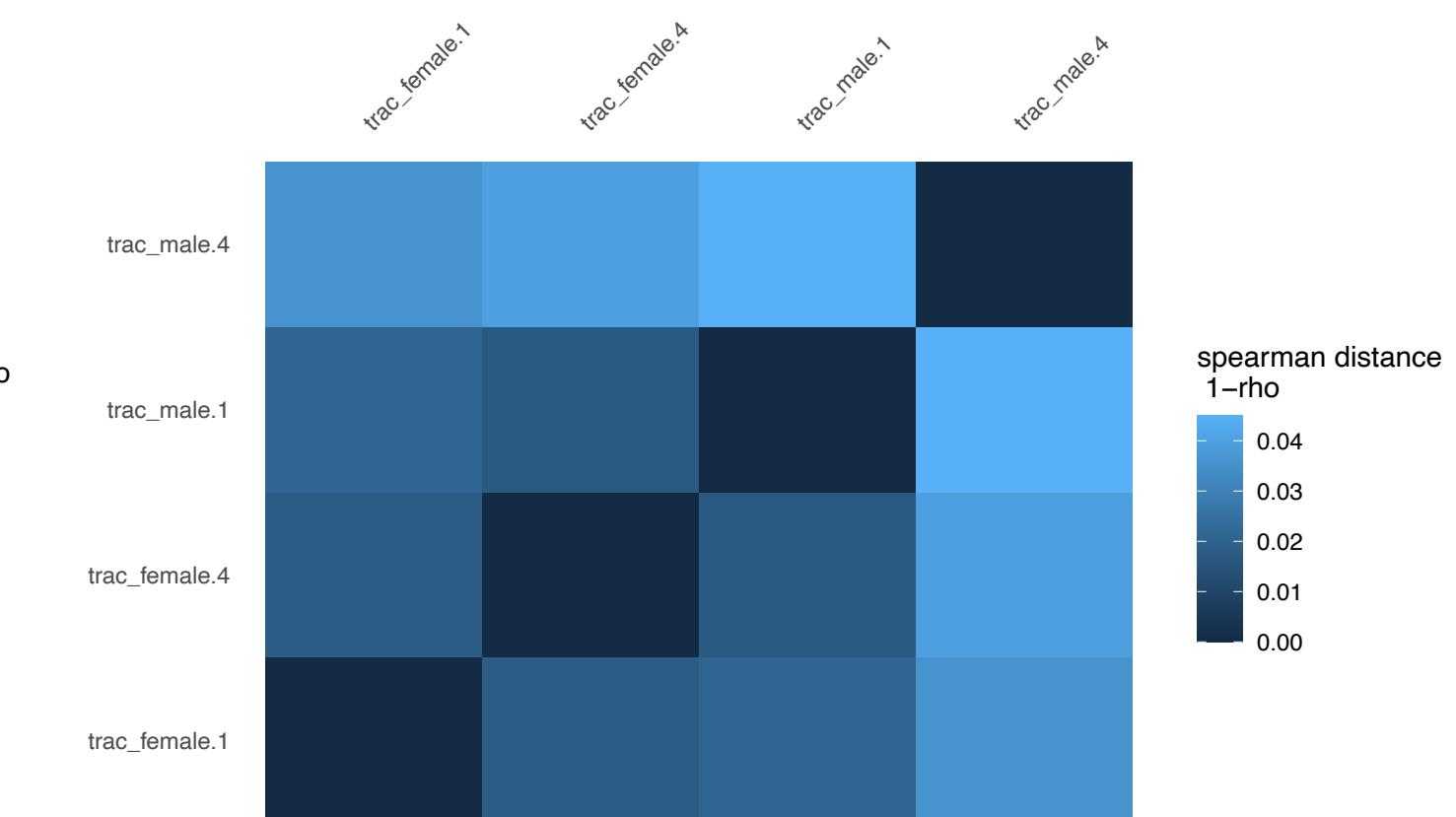
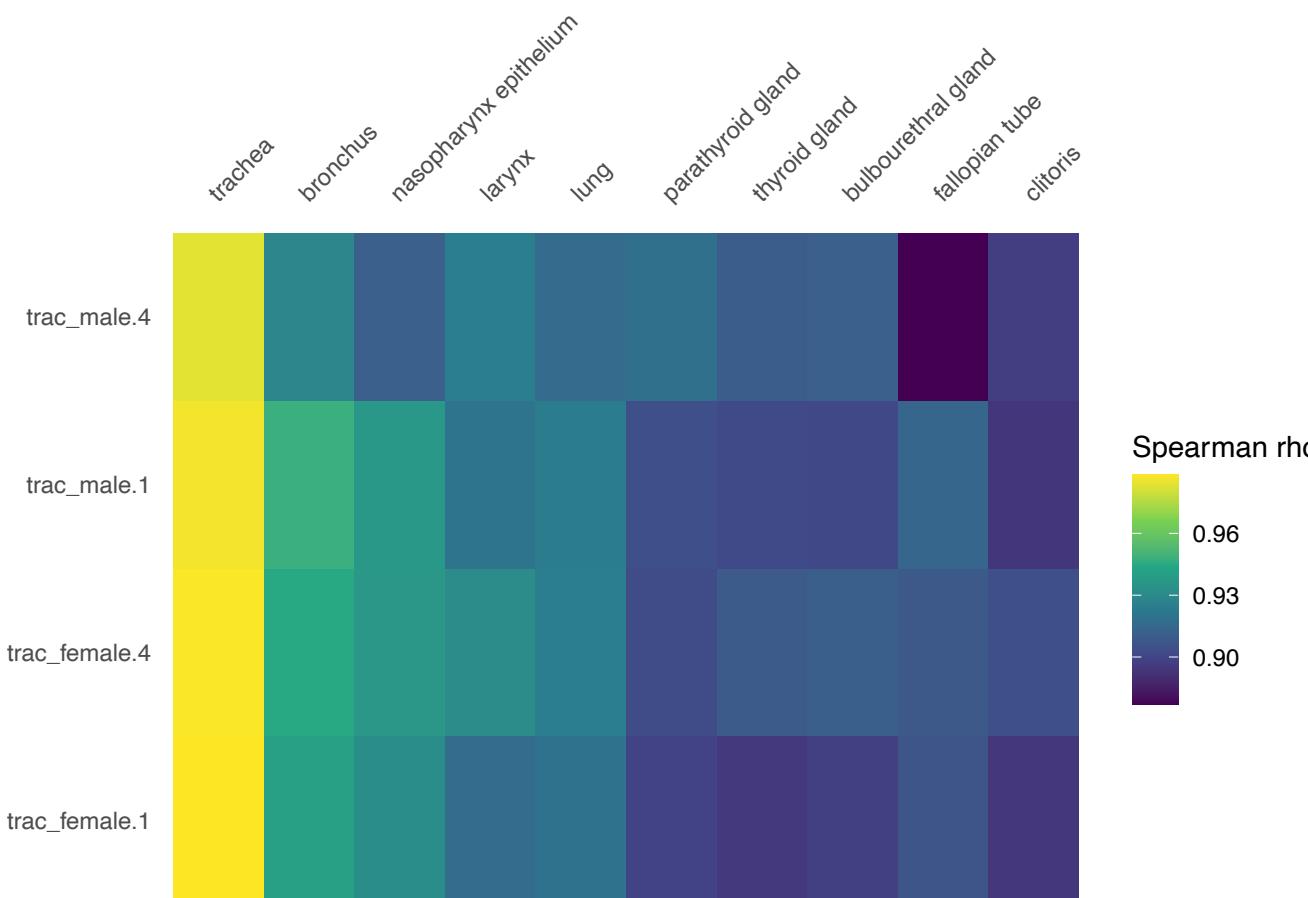
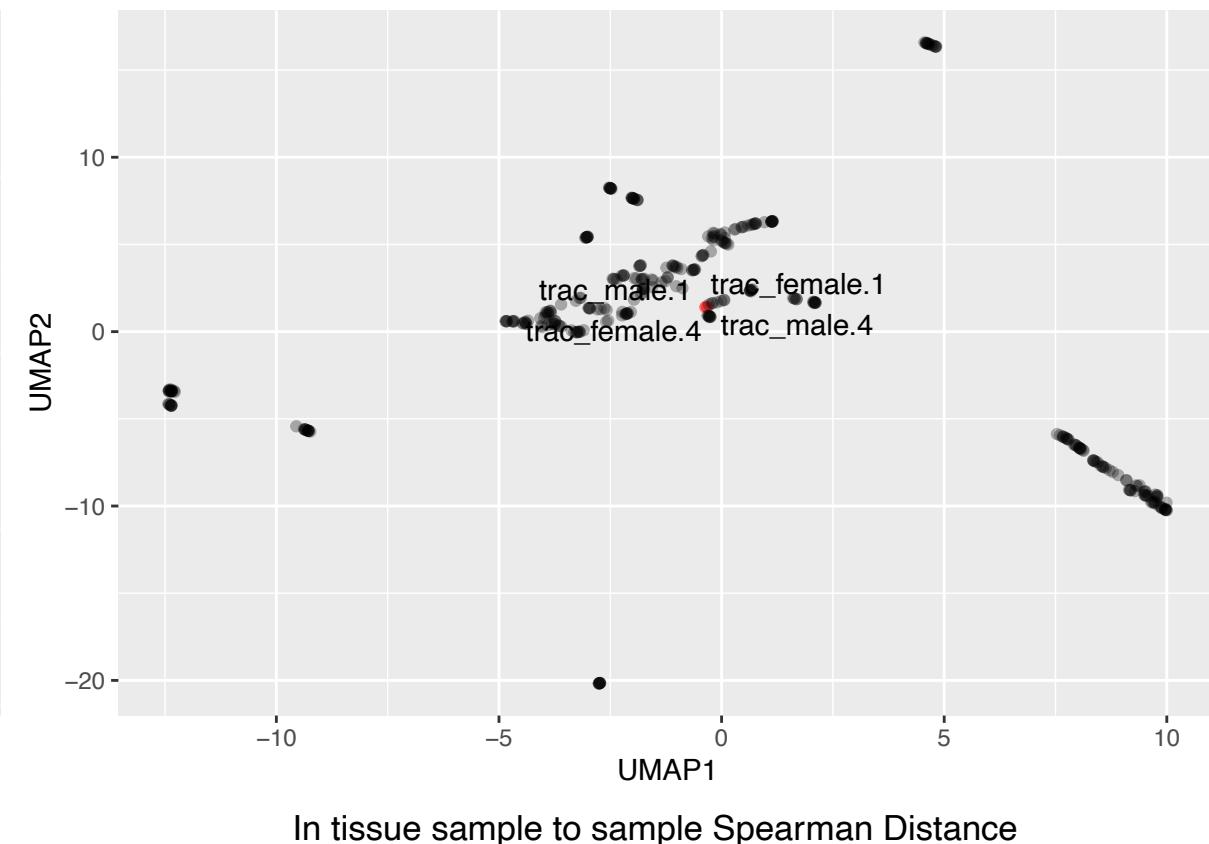
tongue, UMAP: TMM expression values



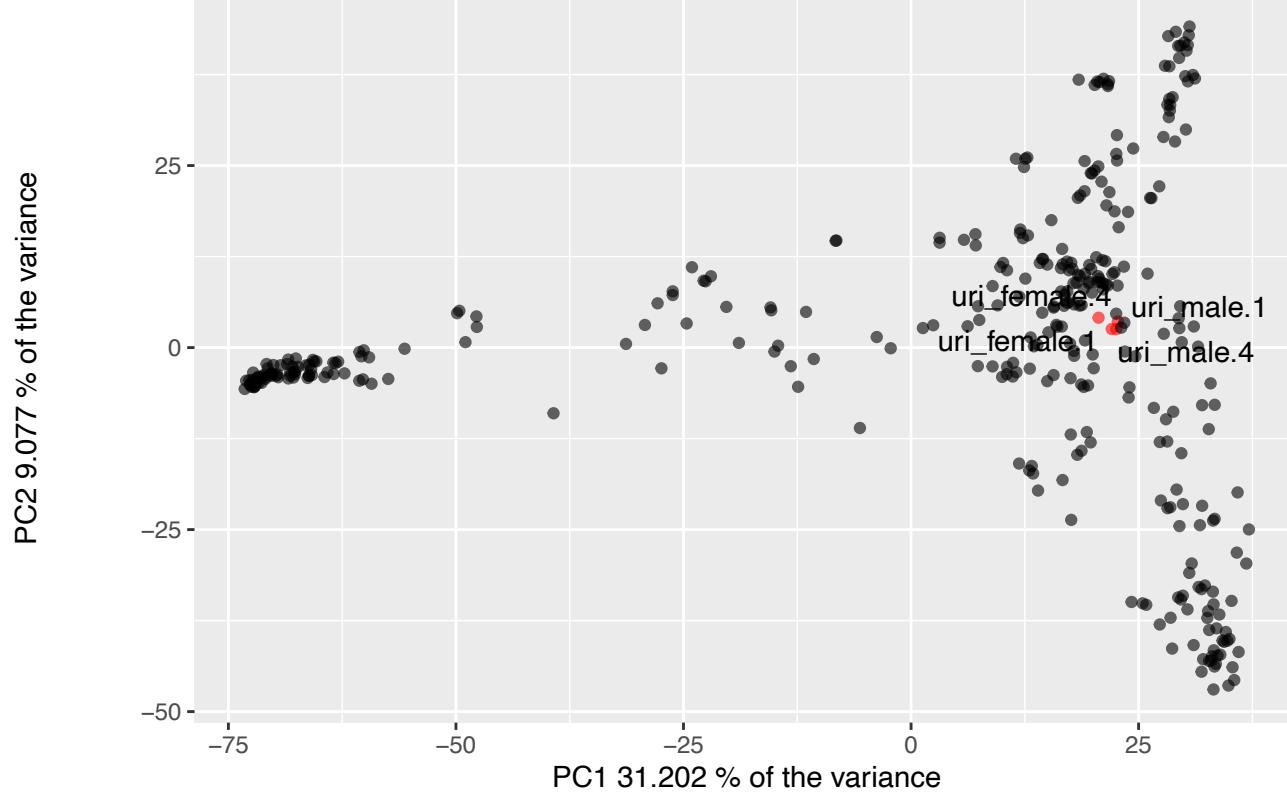
trachea, PCA: TMM expression values



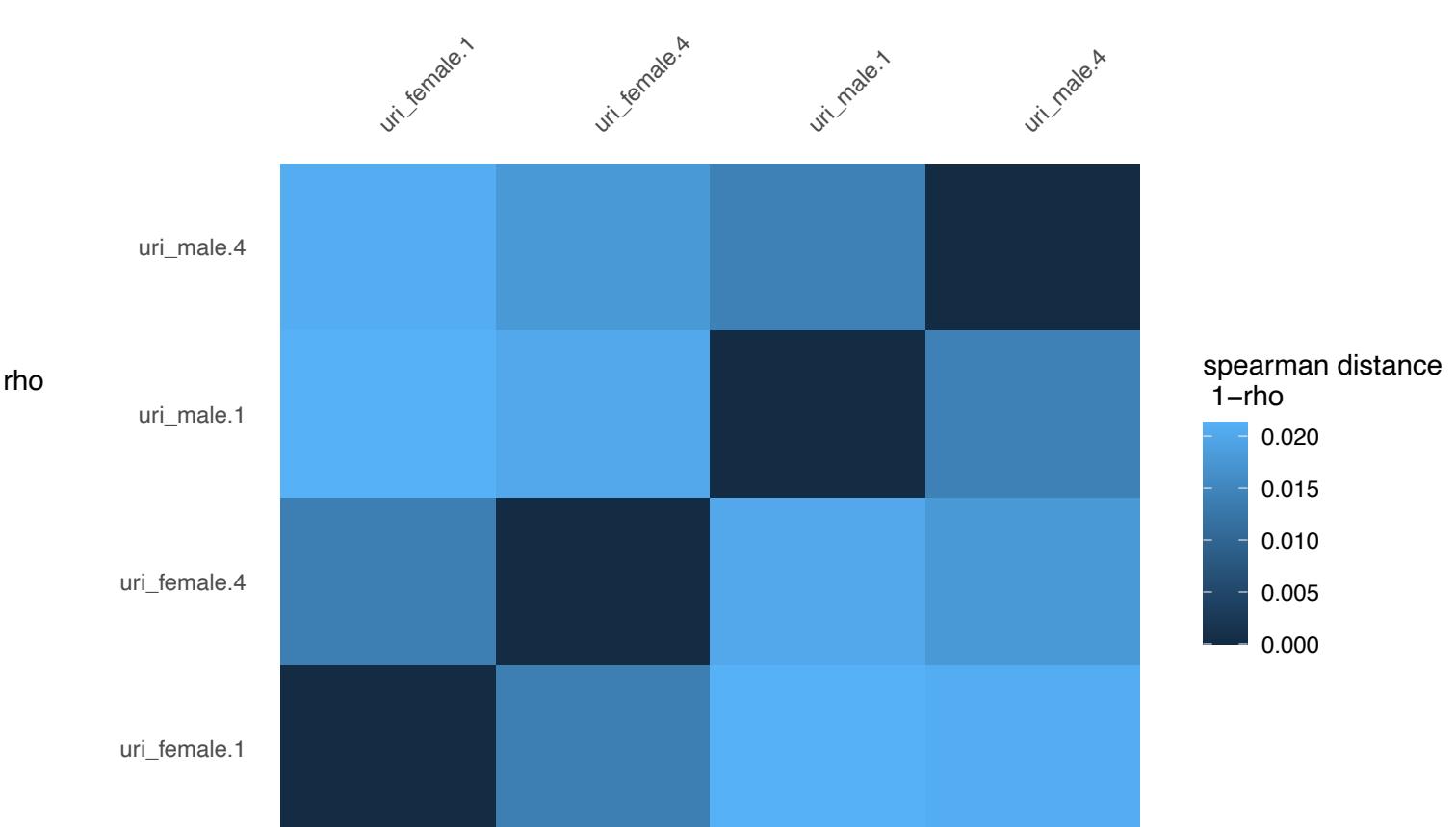
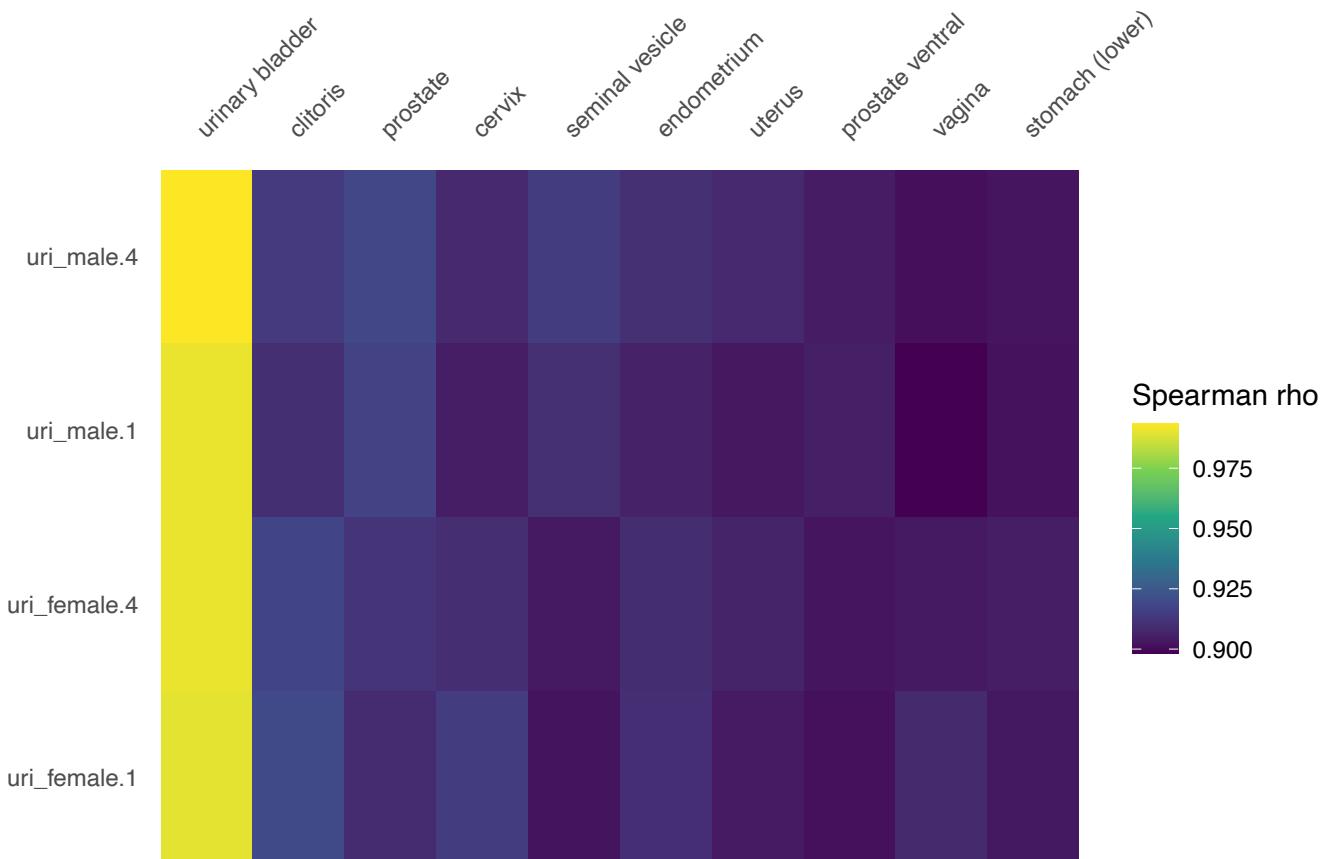
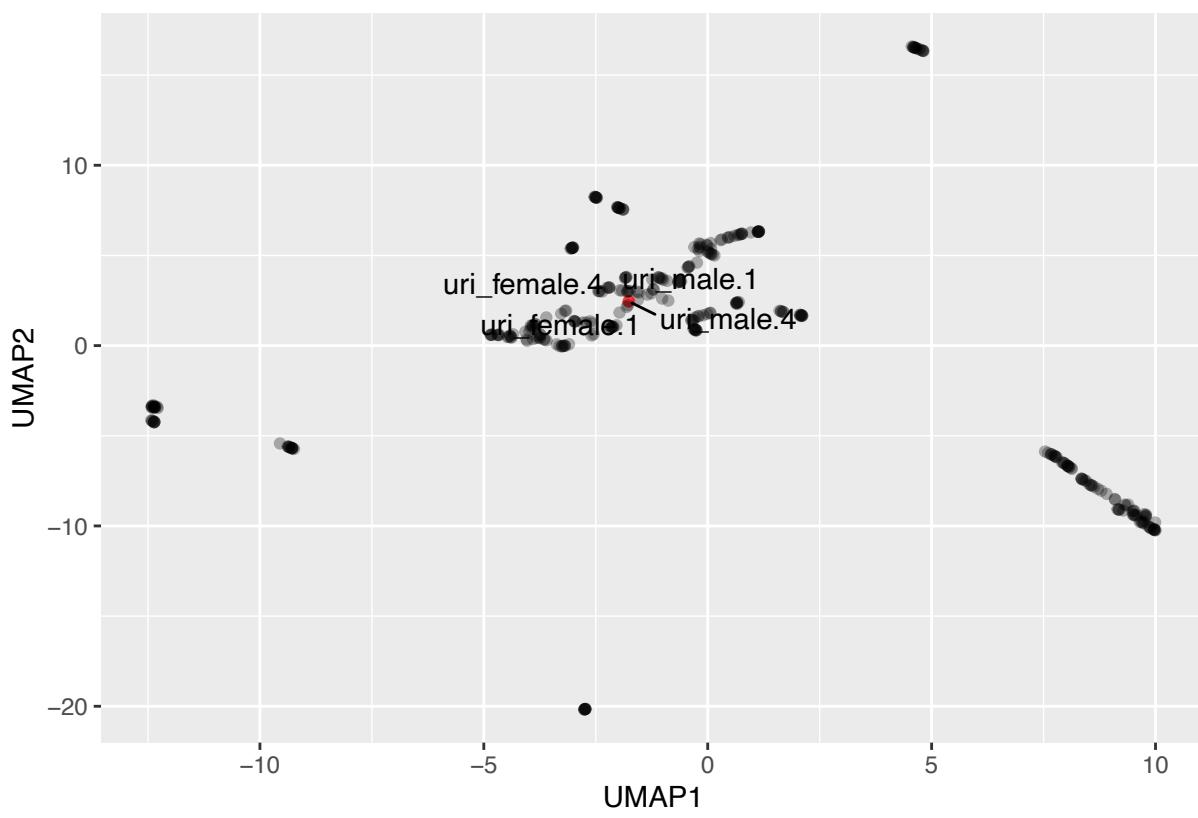
trachea, UMAP: TMM expression values



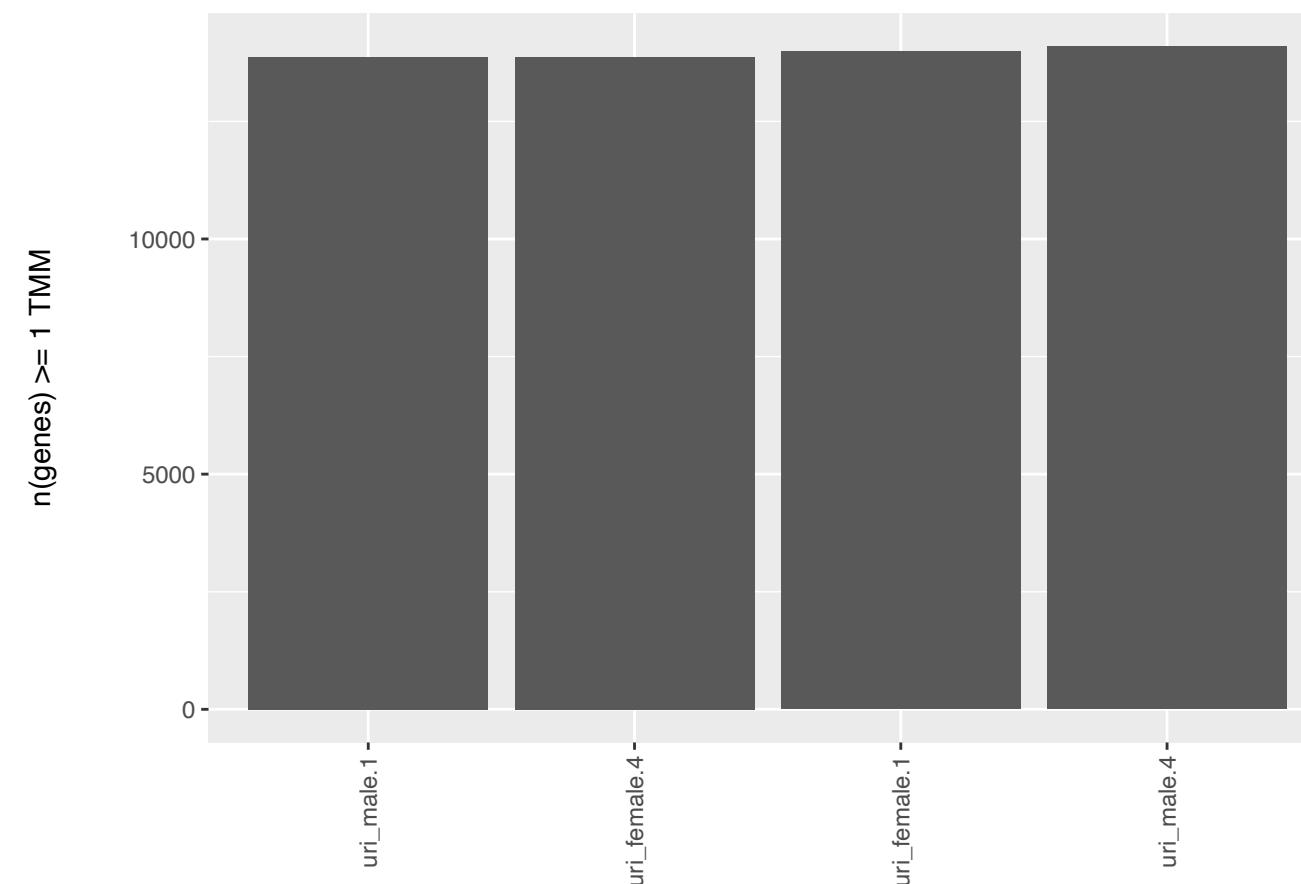
urinary bladder, PCA: TMM expression values



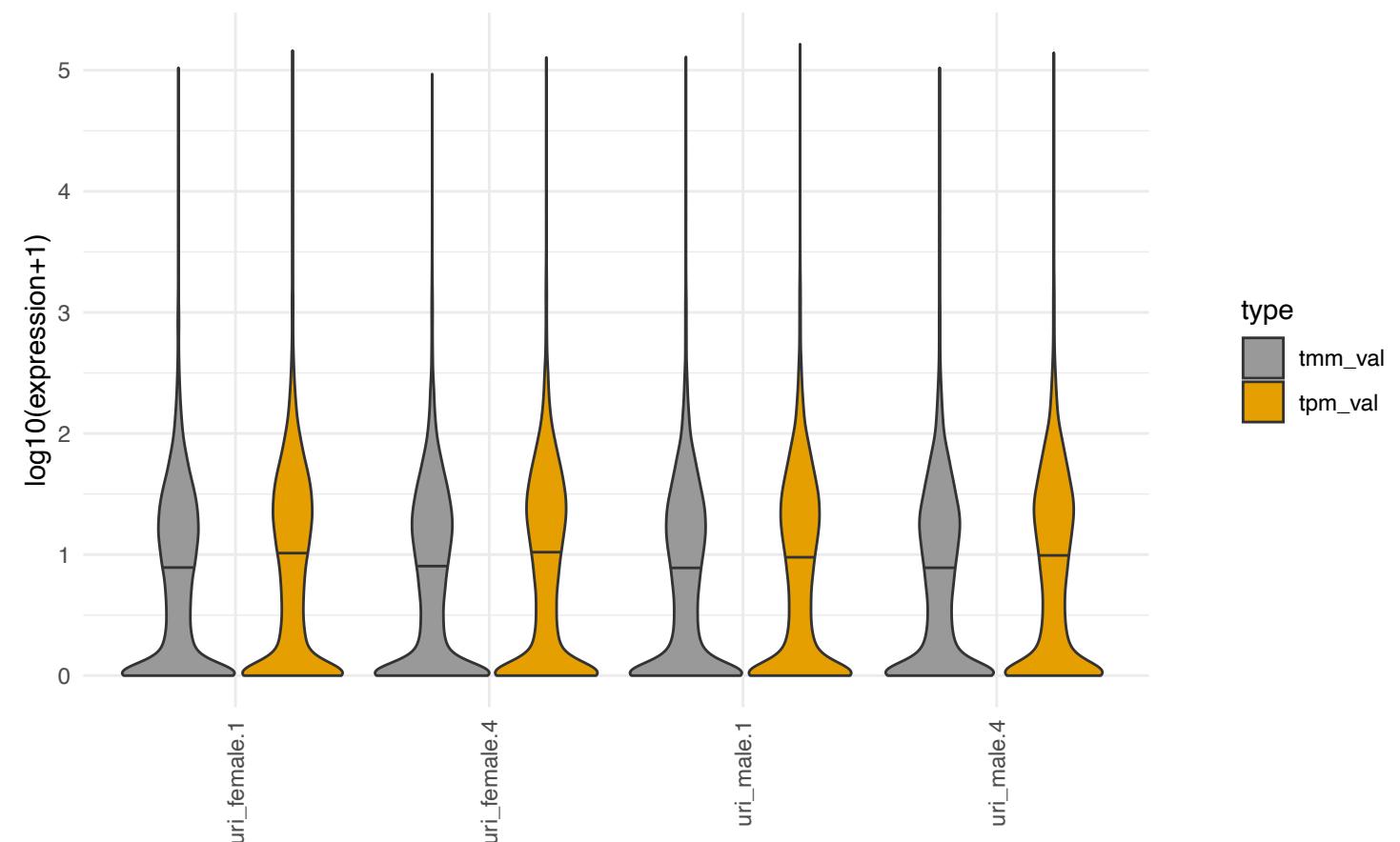
urinary bladder, UMAP: TMM expression values



urinary bladder

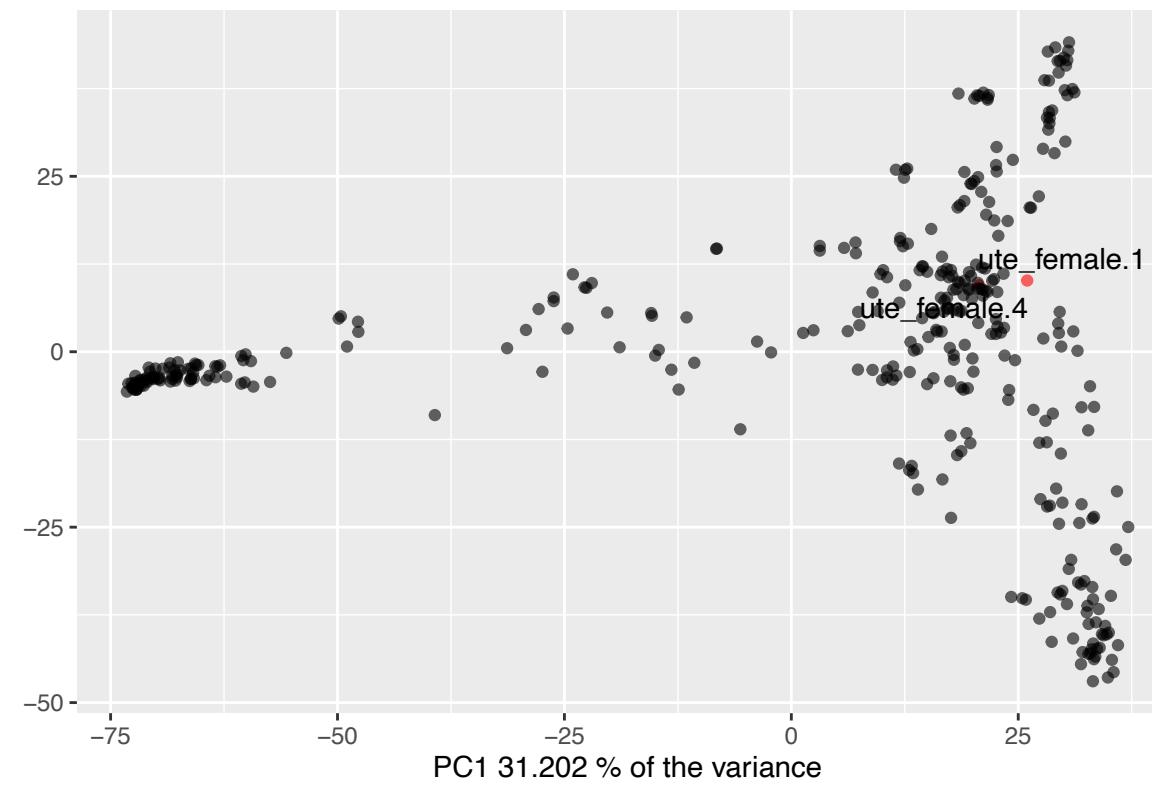


urinary bladder

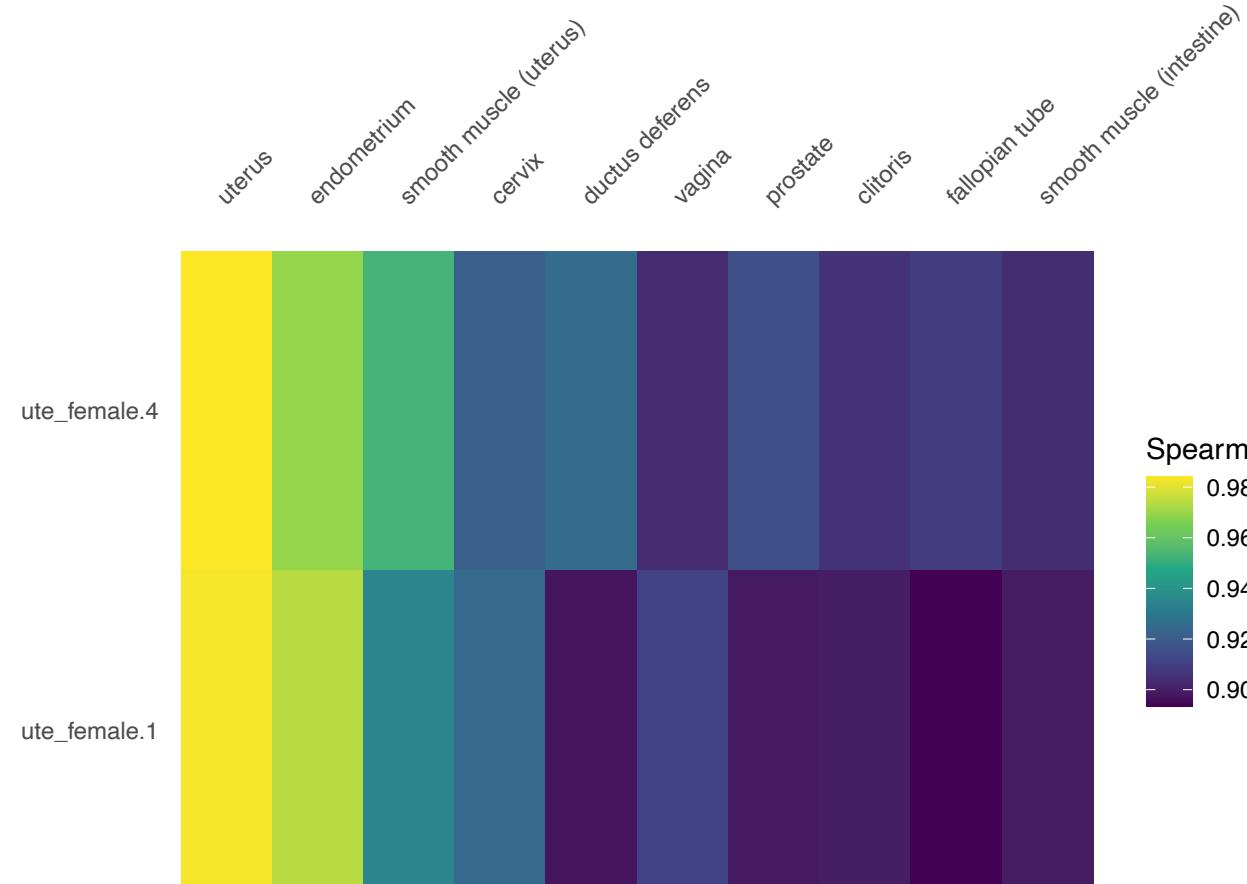


uterus, PCA: TMM expression values

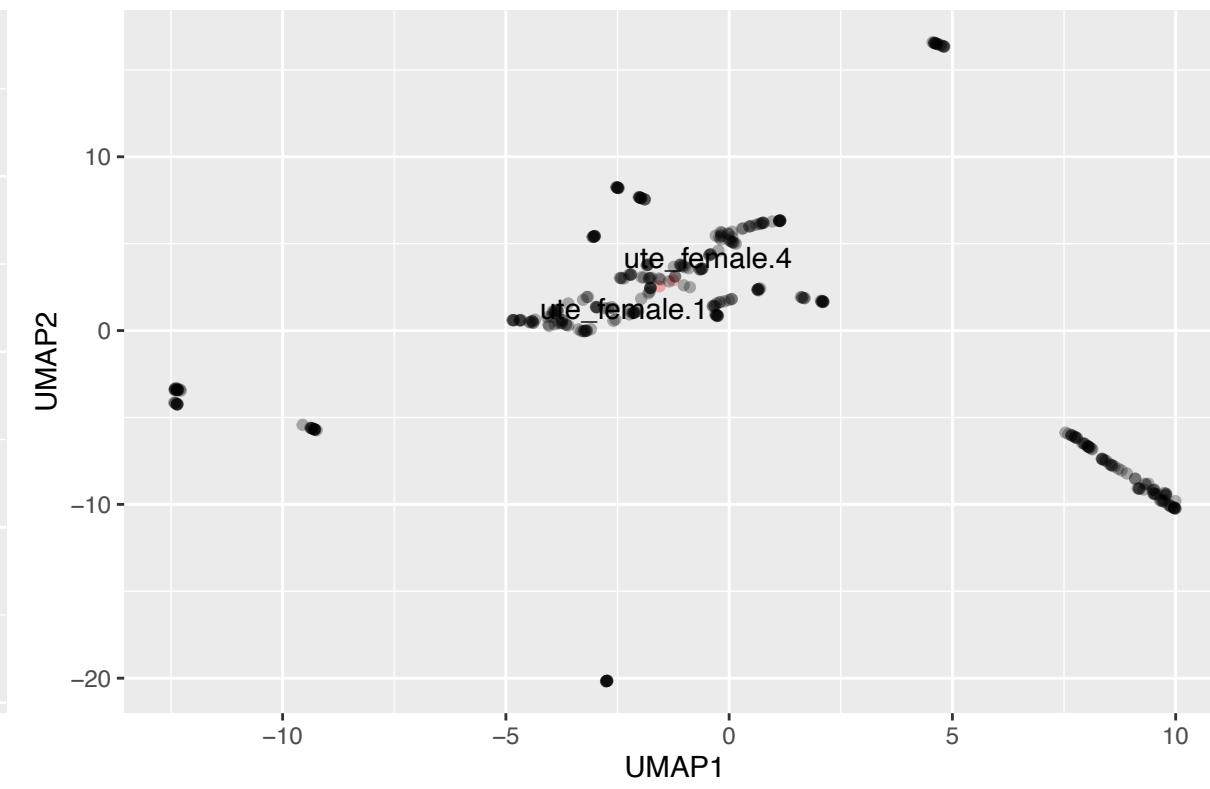
PC2 9.077 % of the variance



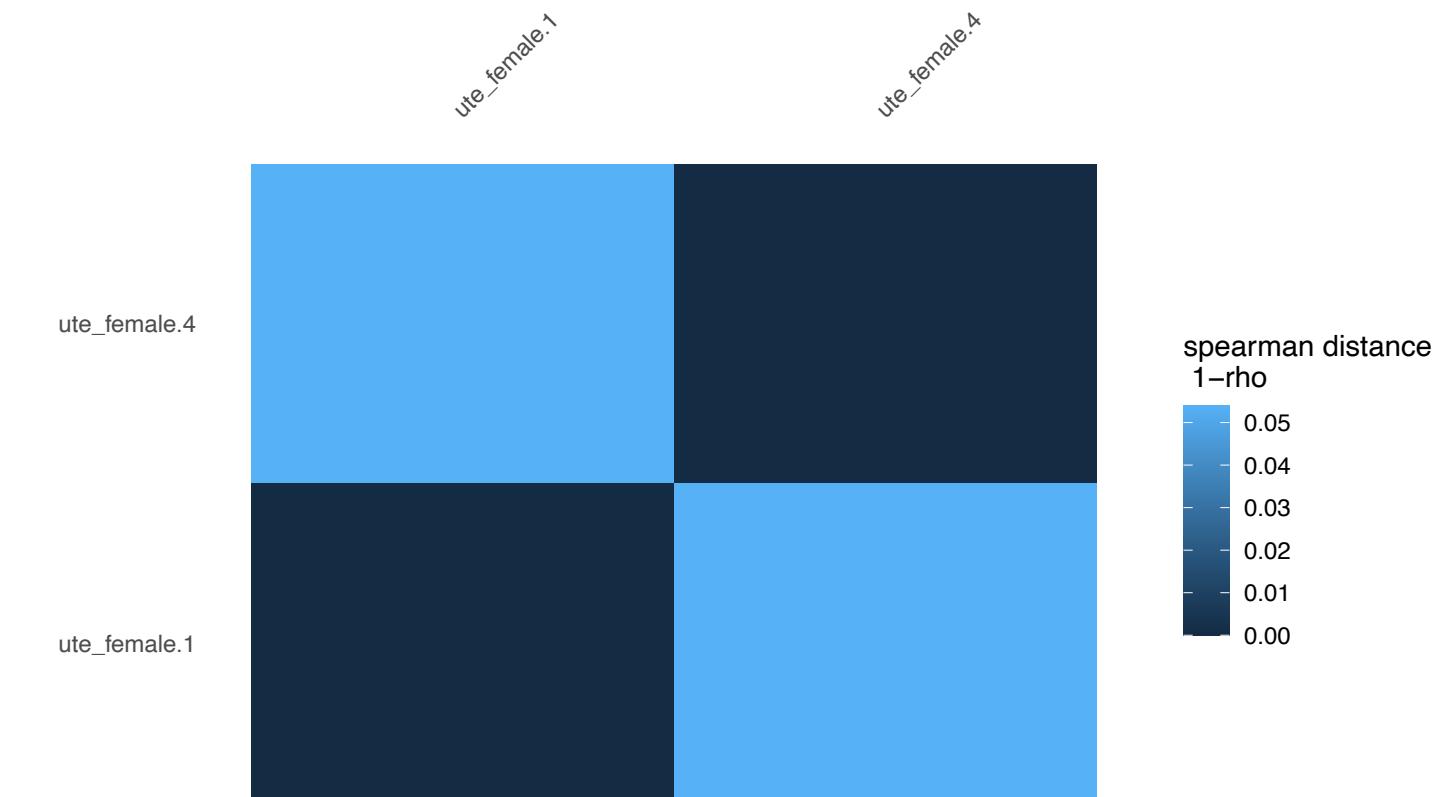
Tissue group to sample correlation



uterus, UMAP: TMM expression values

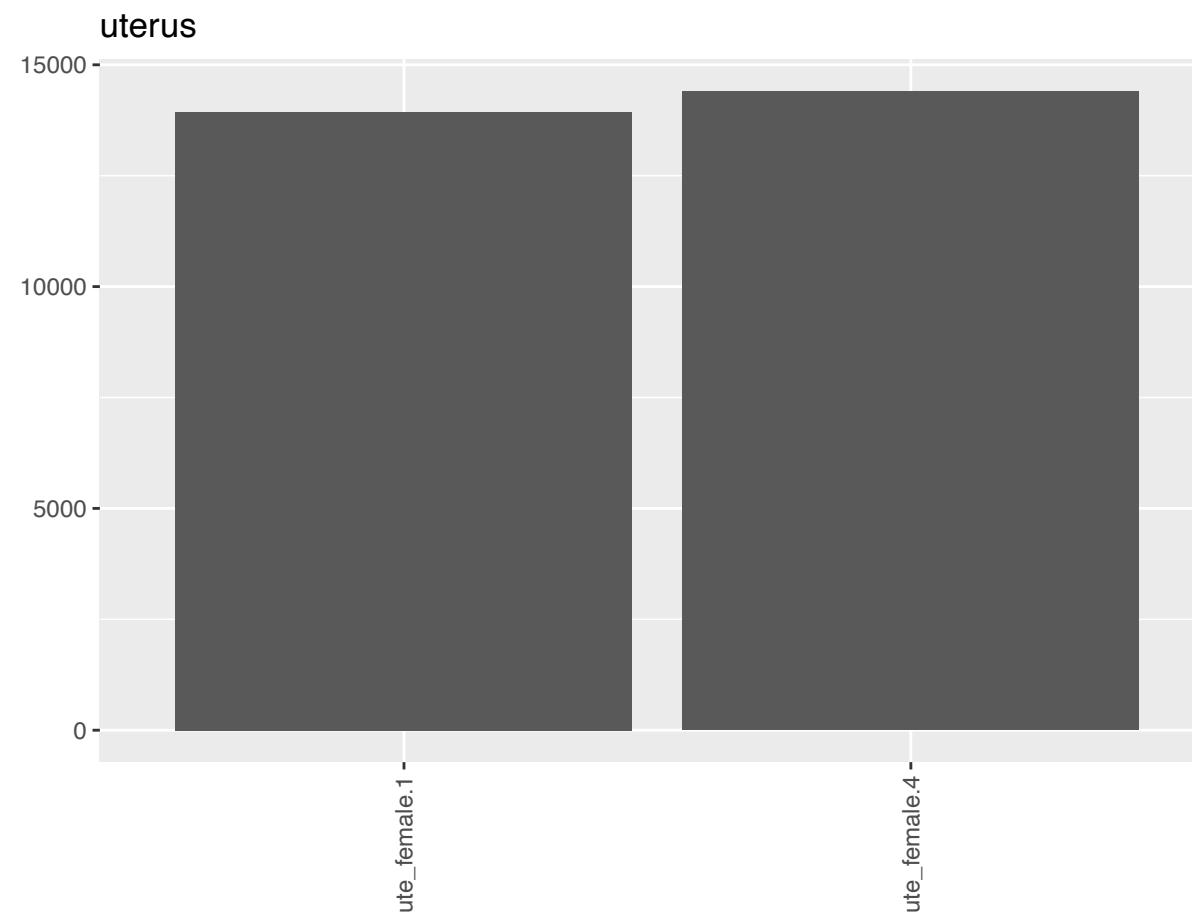


In tissue sample to sample Spearman Distance

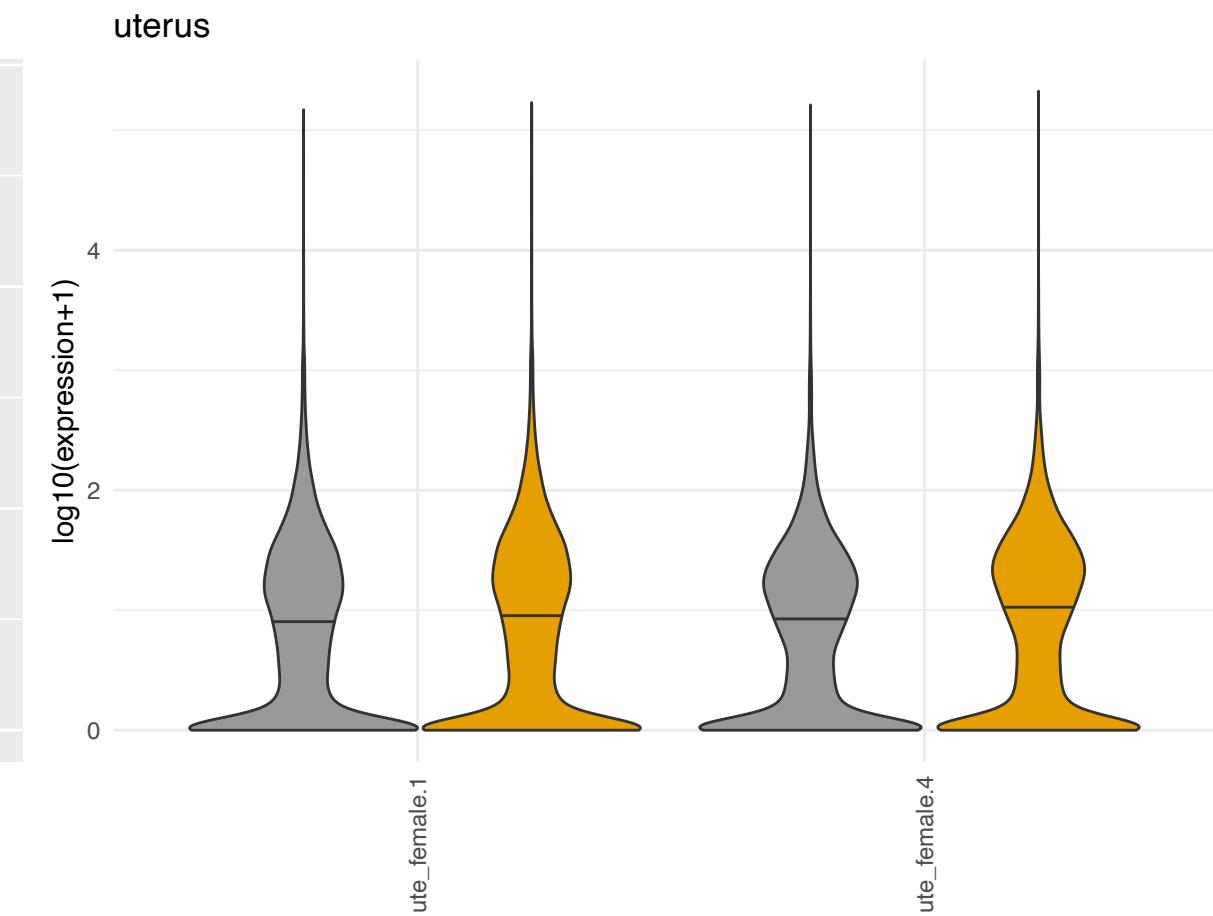


uterus

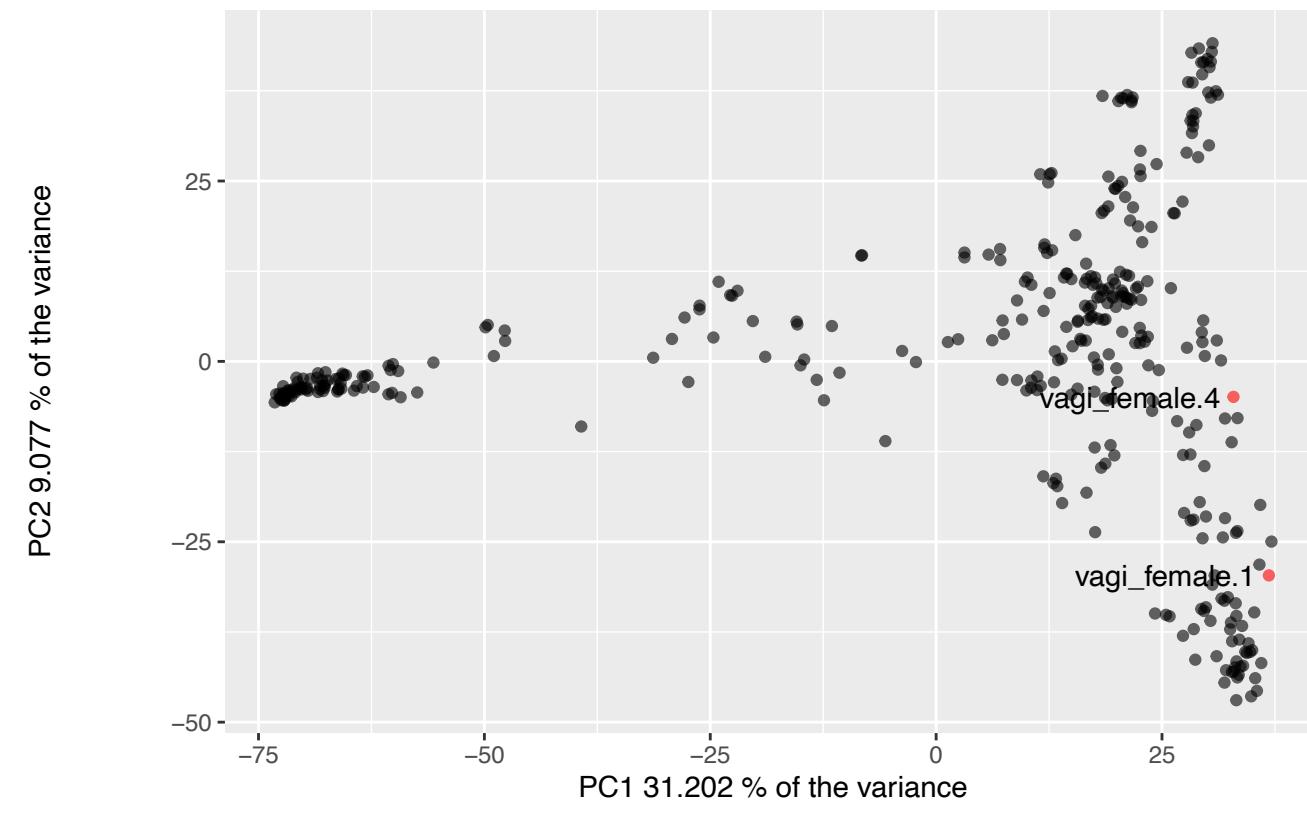
n(genes) >= 1 TMM



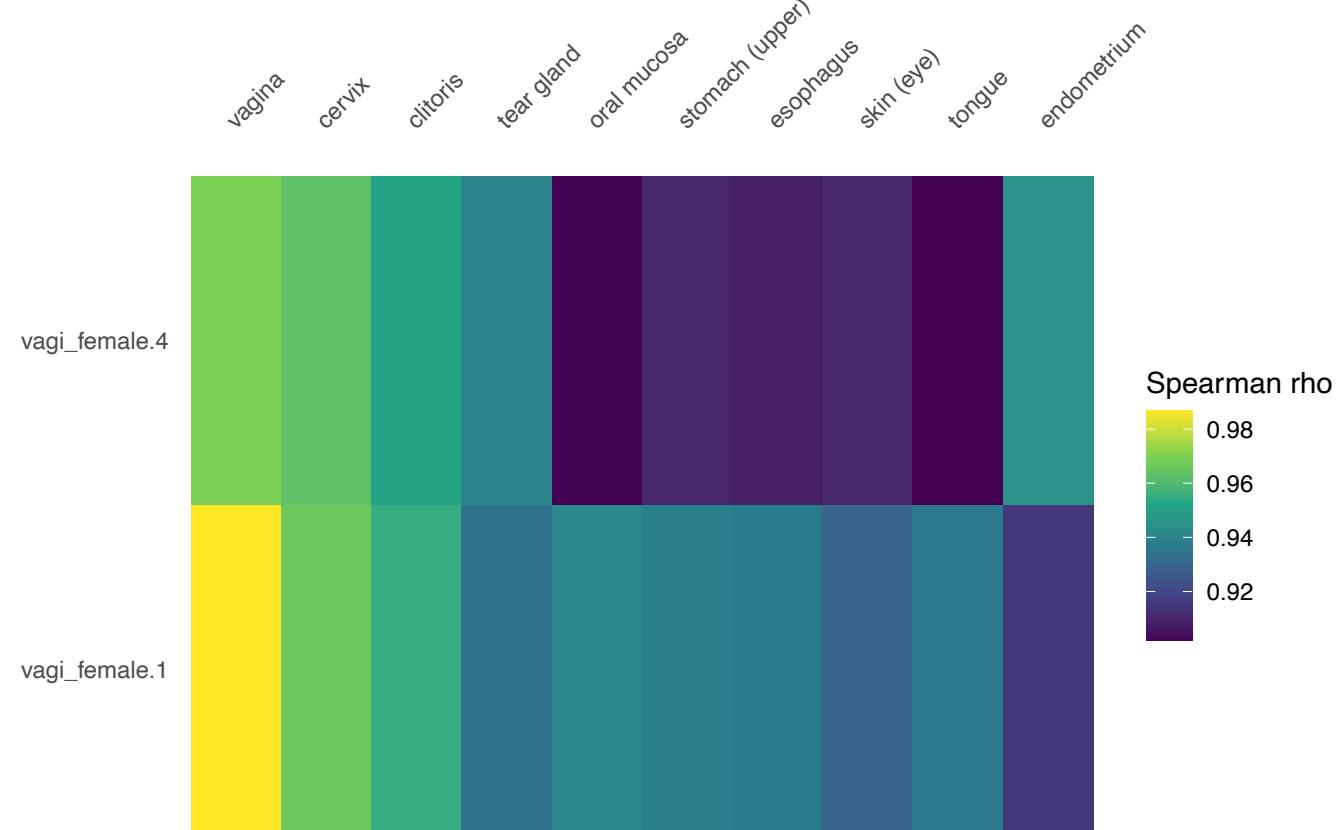
uterus

 $\log_{10}(\text{expression}+1)$ 

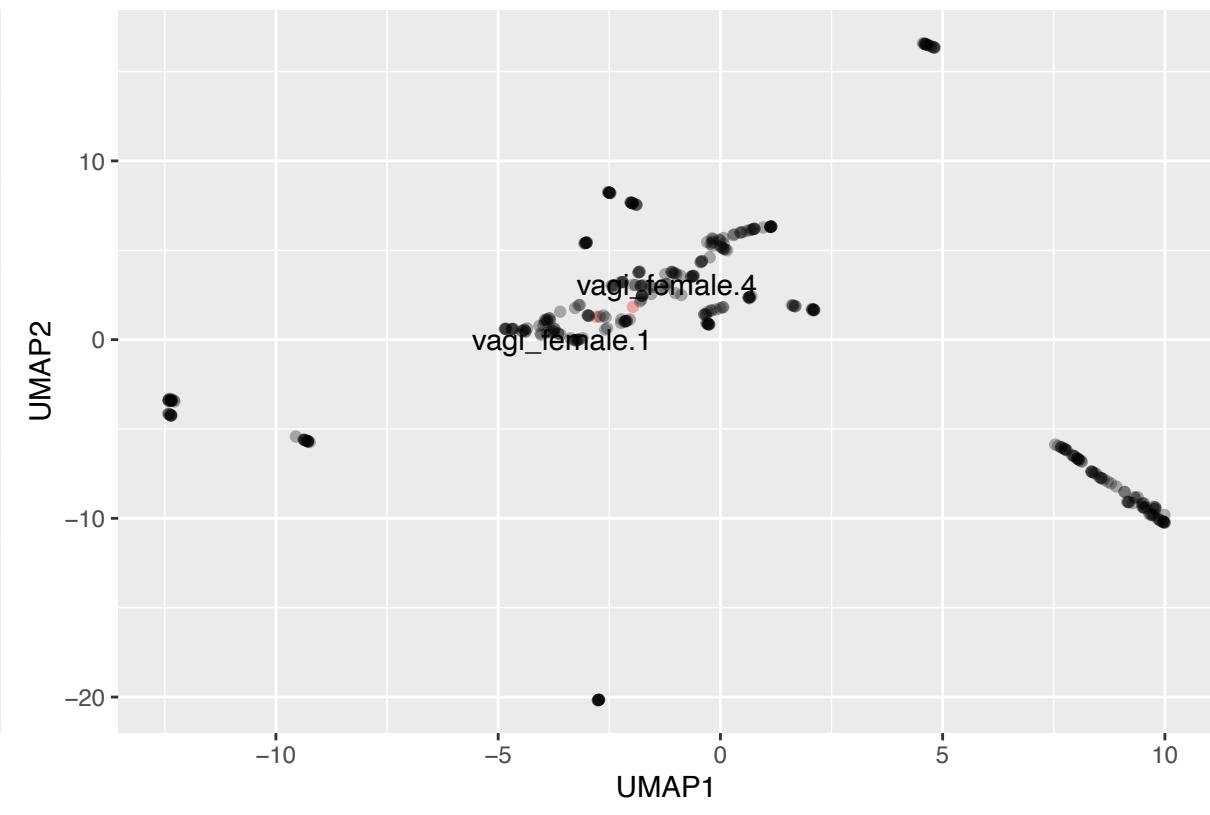
vagina, PCA: TMM expression values



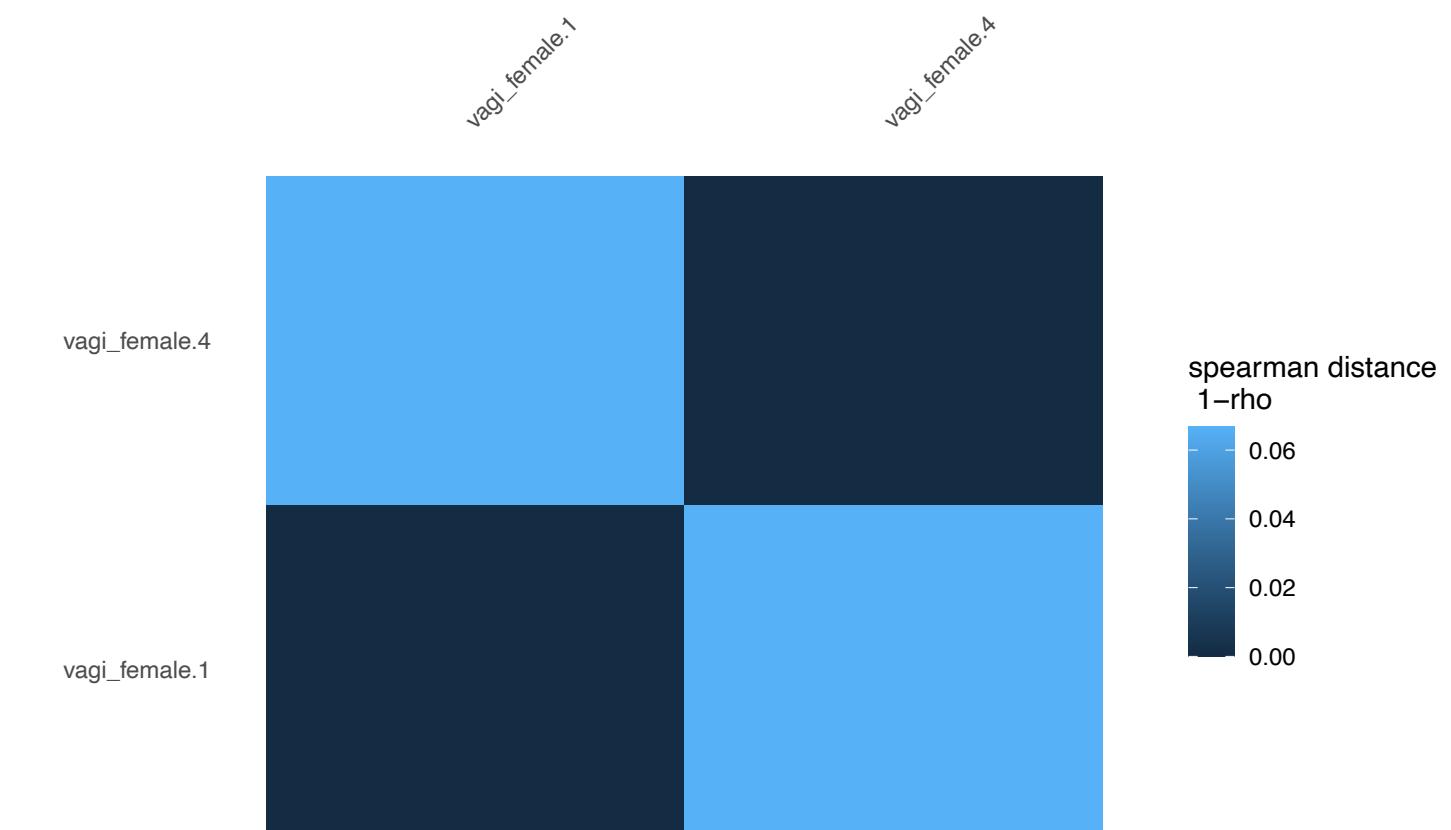
Tissue group to sample correlation



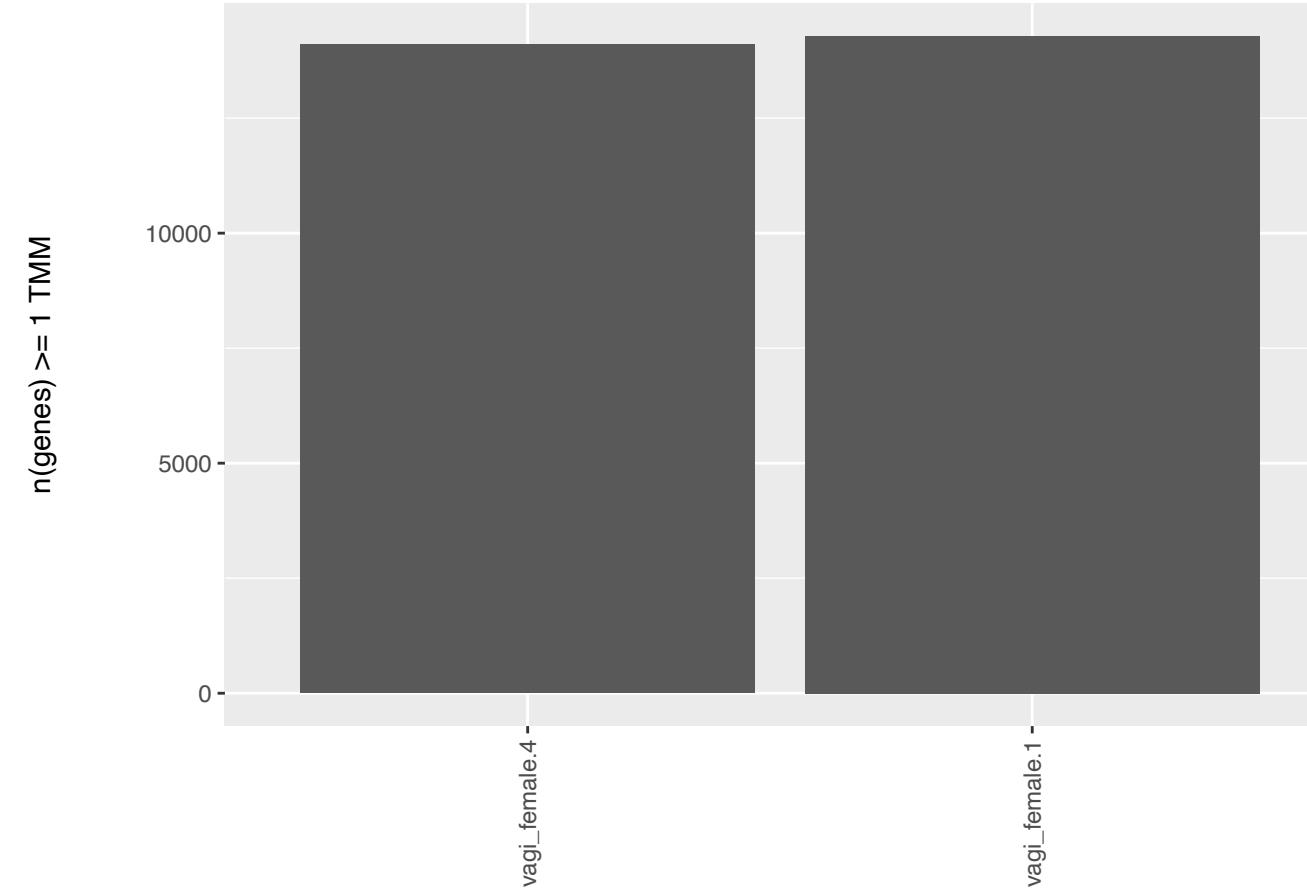
vagina, UMAP: TMM expression values



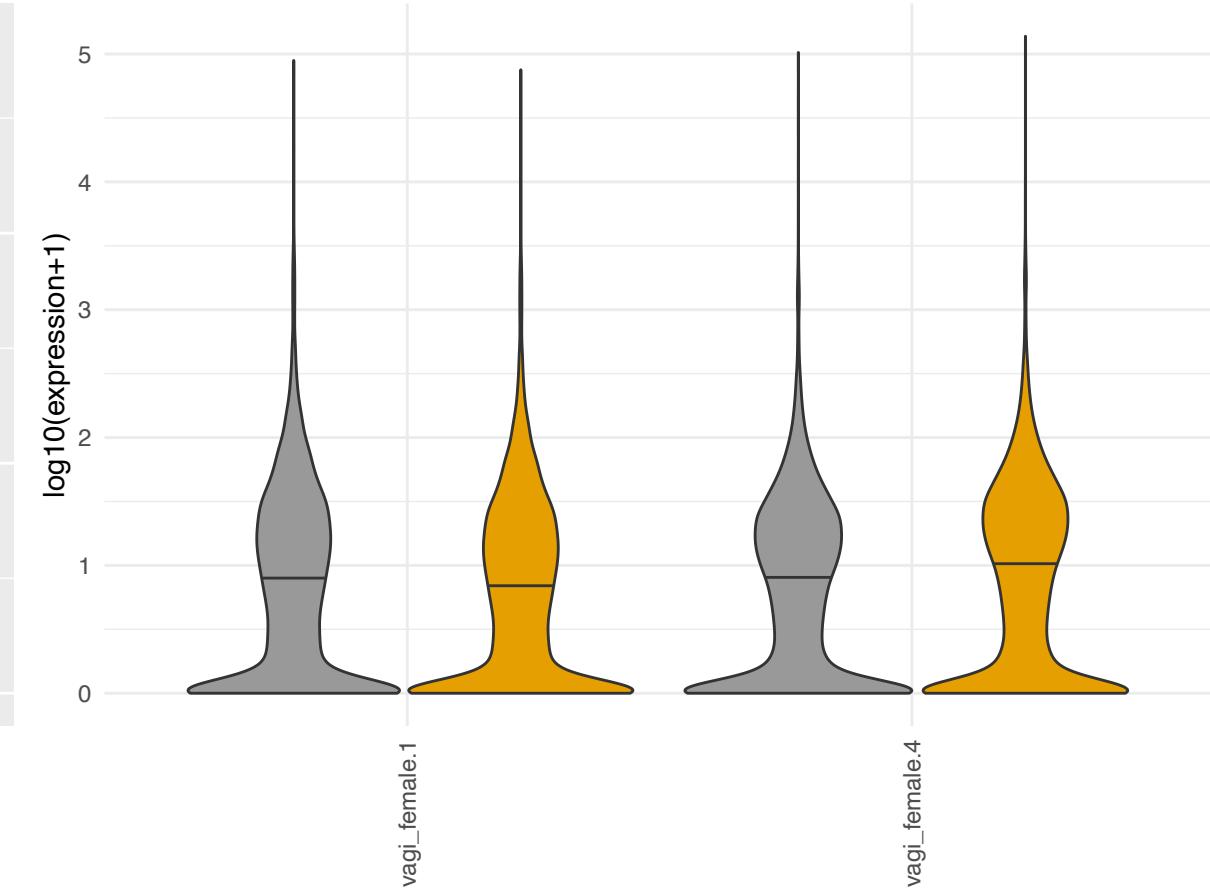
In tissue sample to sample Spearman Distance



vagina

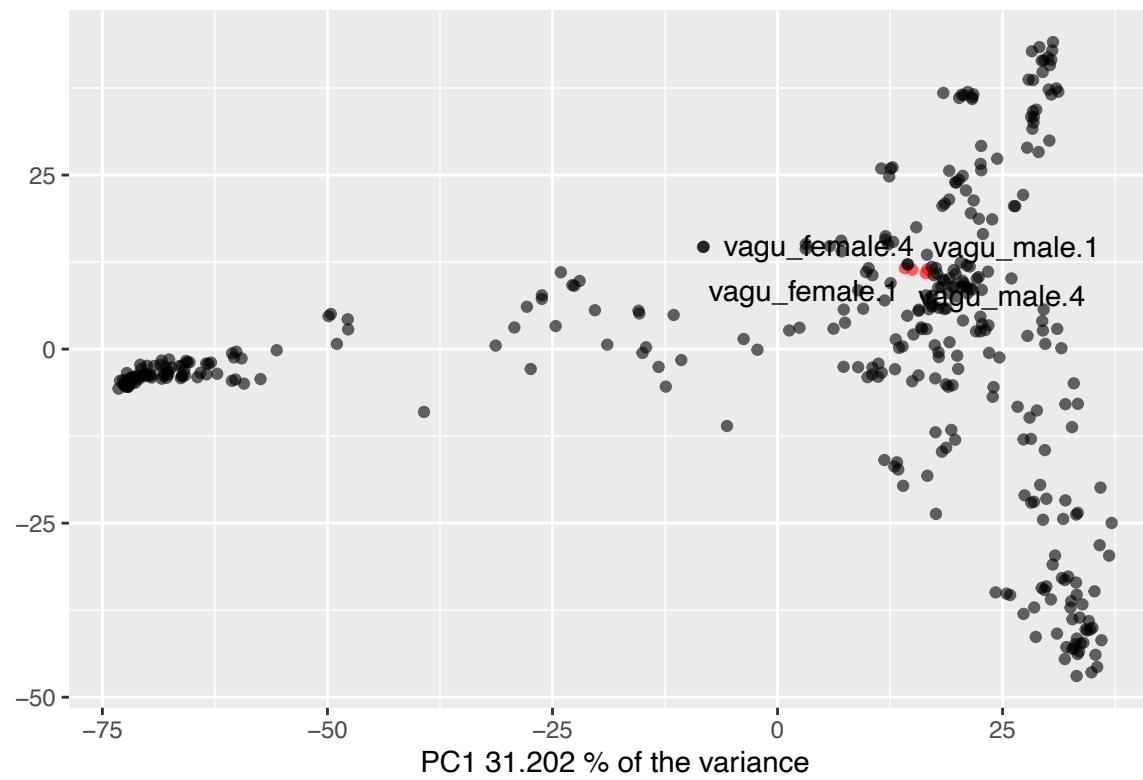


vagina

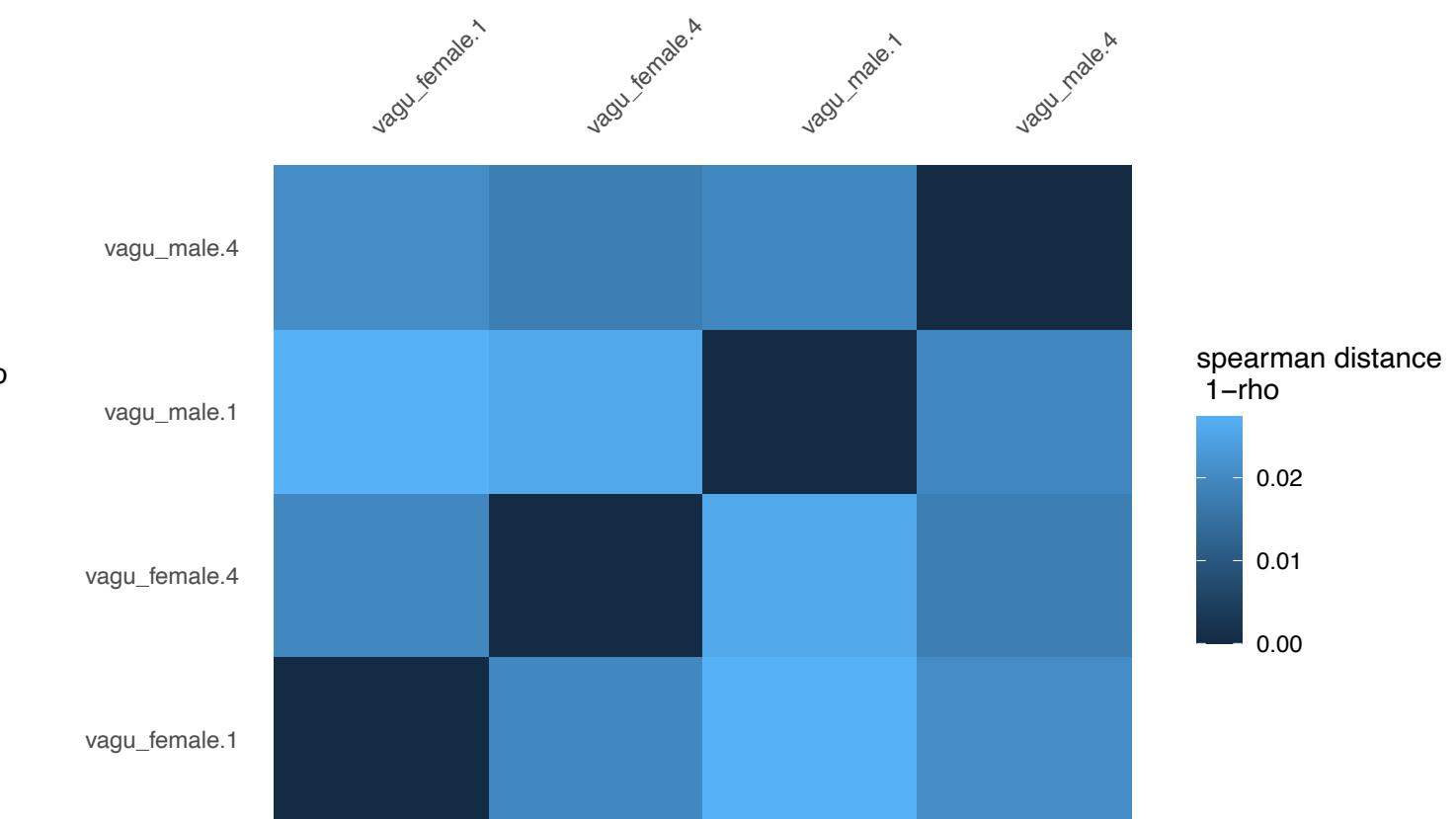
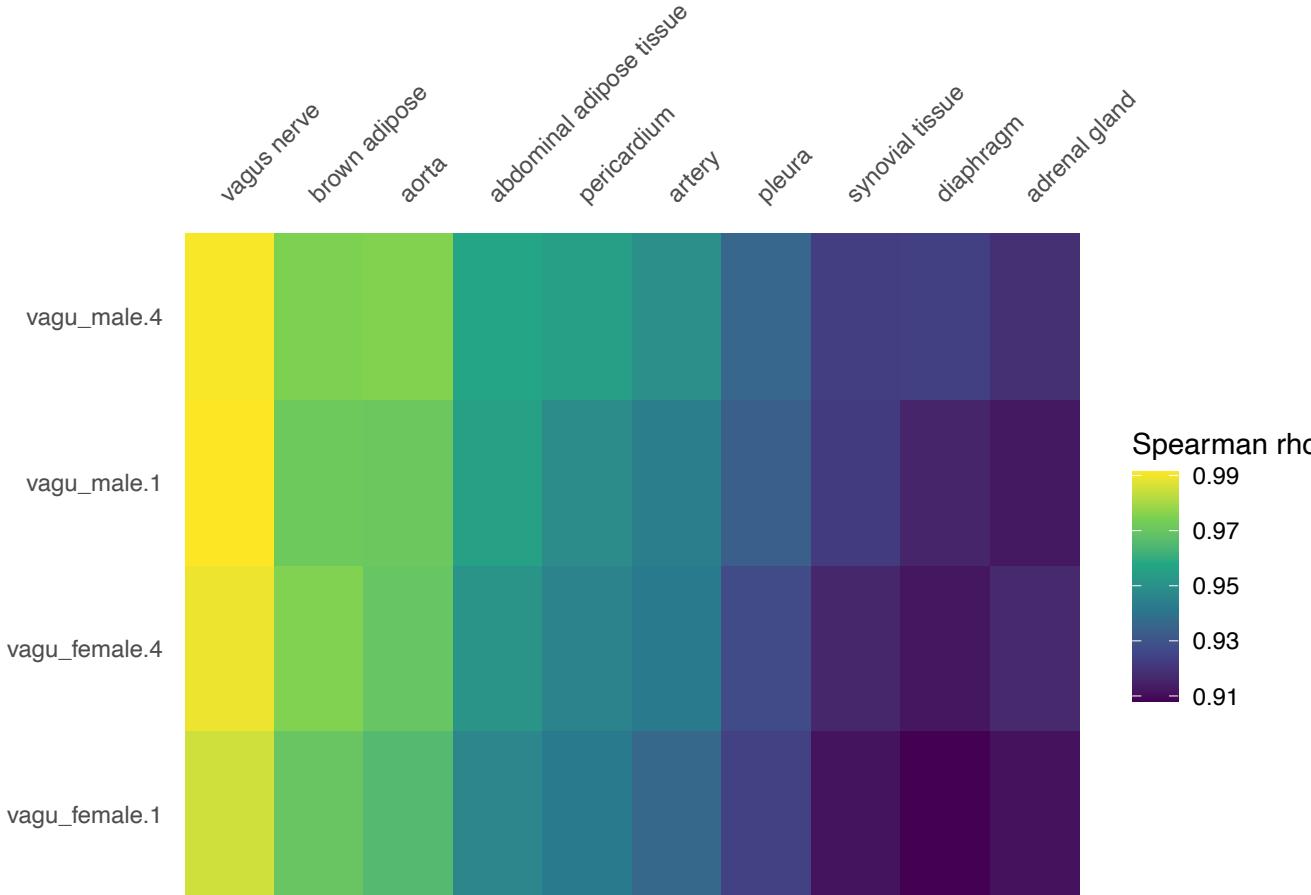
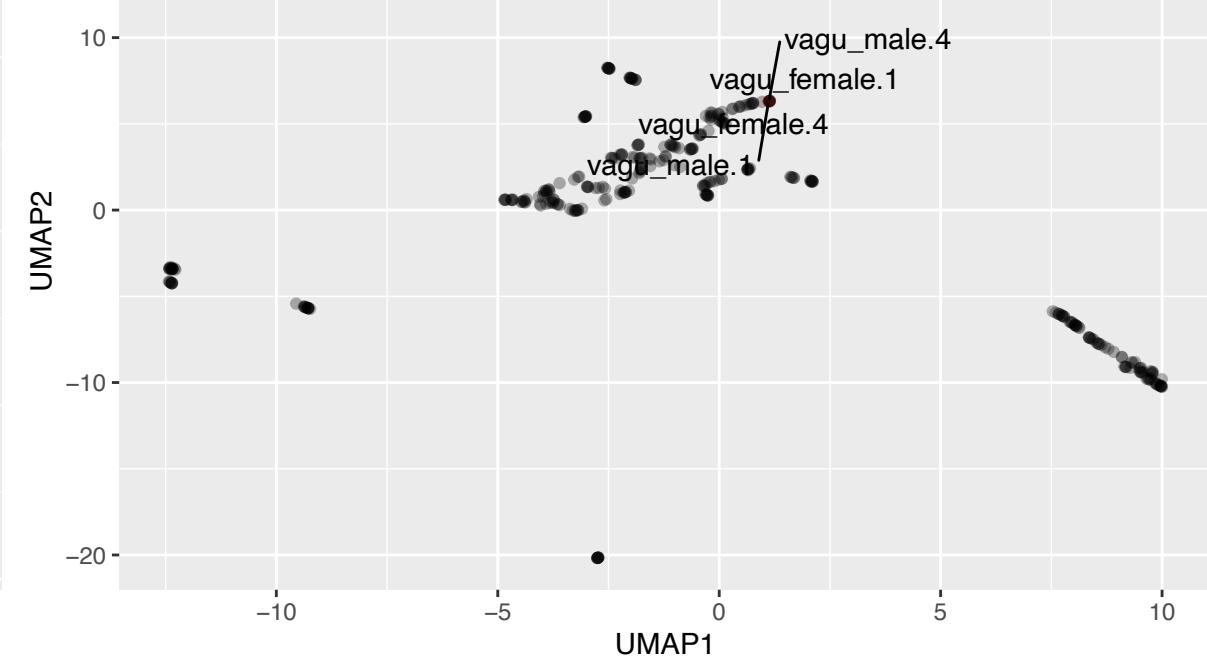


vagus nerve, PCA: TMM expression values

PC2 9.077 % of the variance

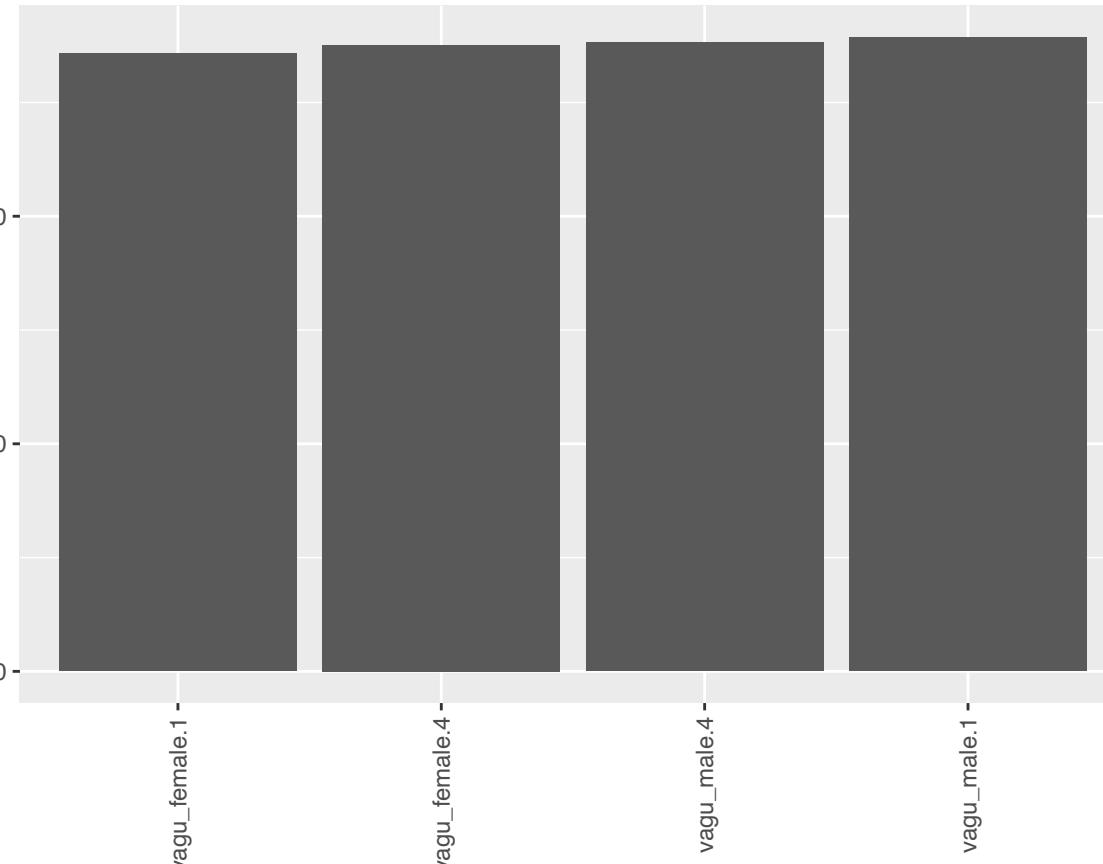


vagus nerve, UMAP: TMM expression values

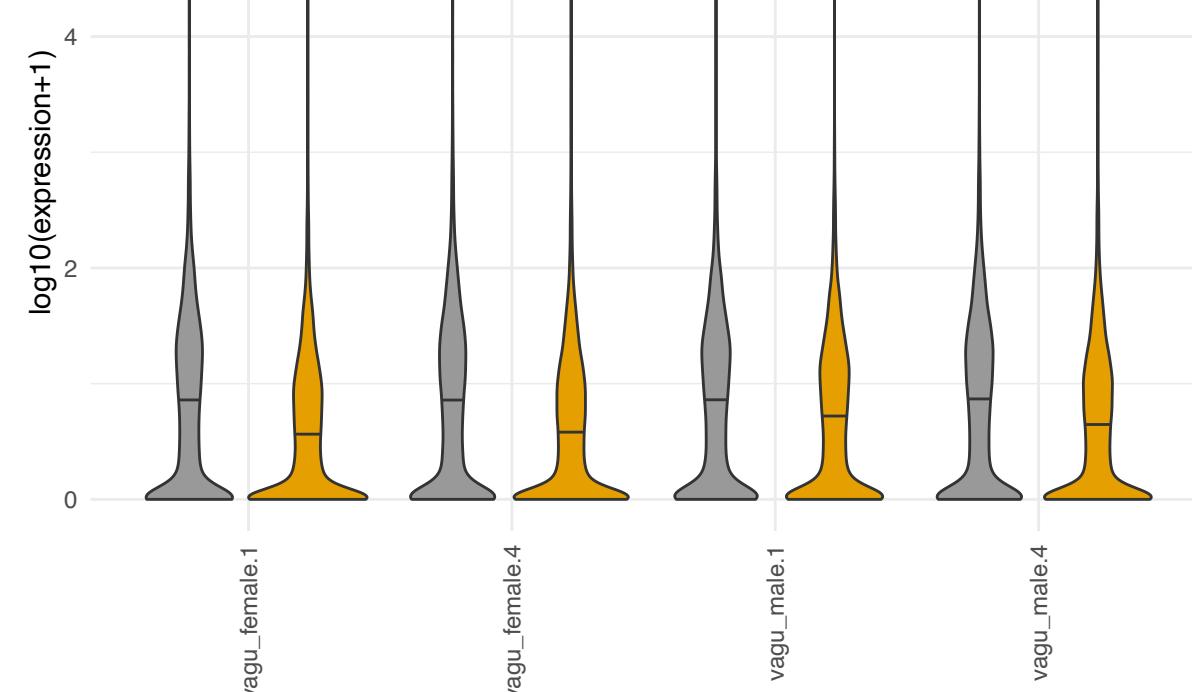


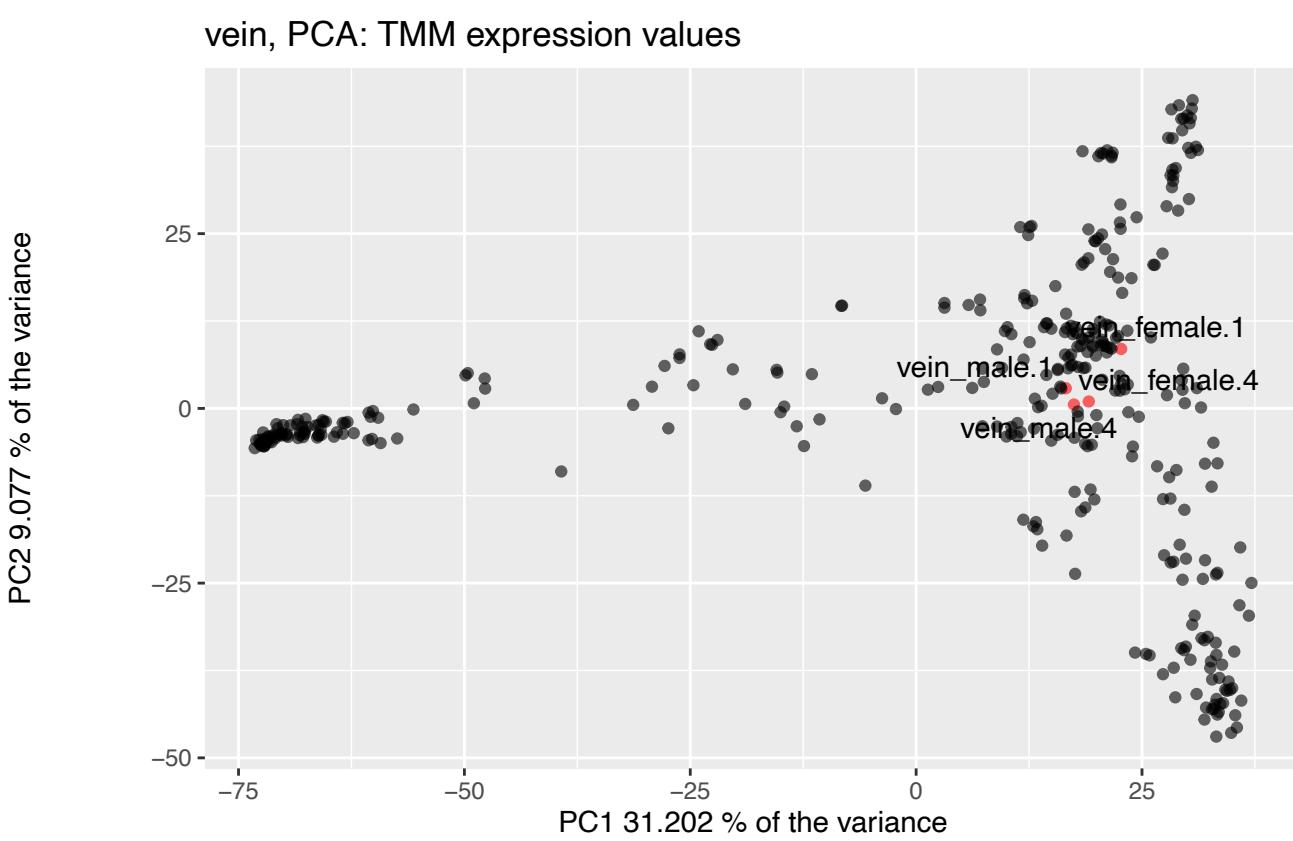
vagus nerve

n(genes) >= 1 TMM

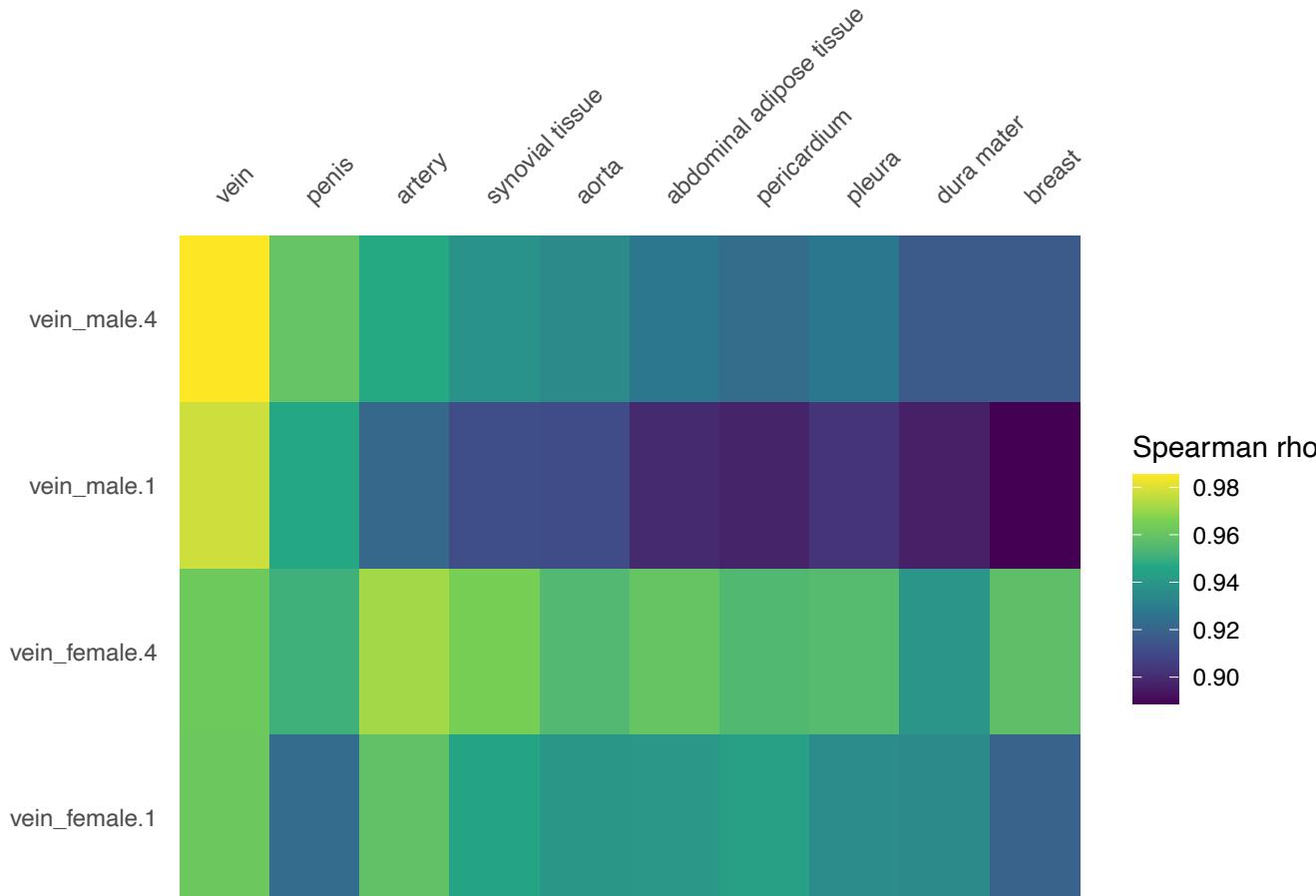


vagus nerve

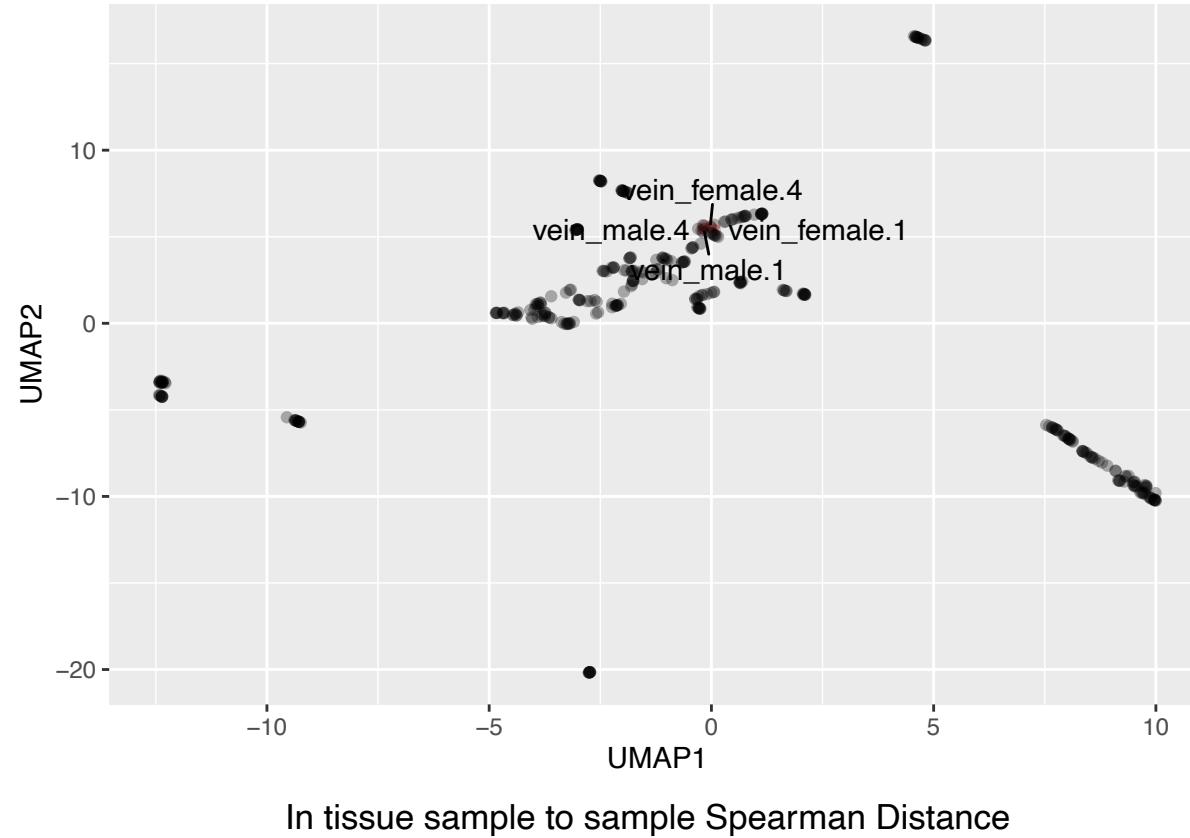




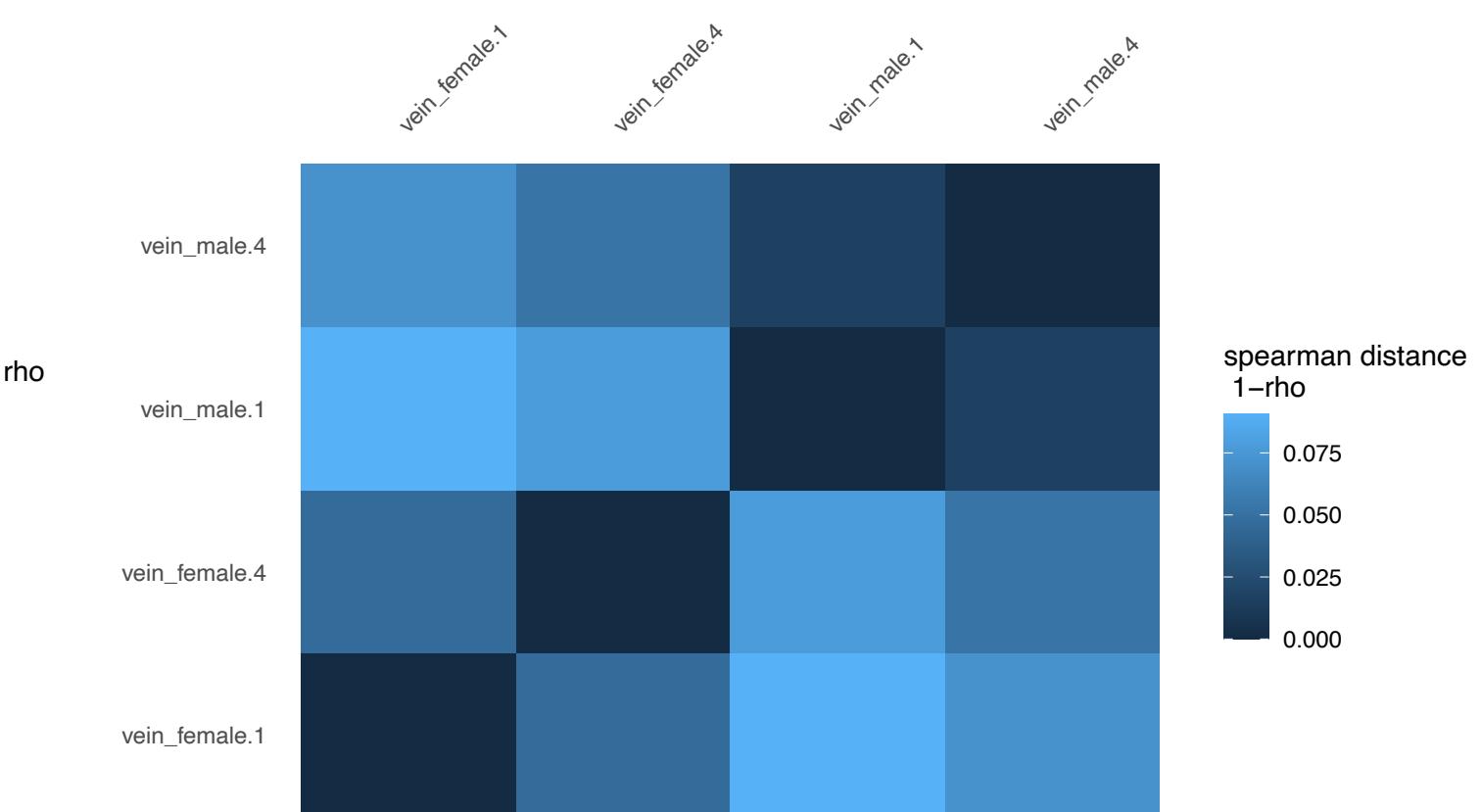
Tissue group to sample correlation



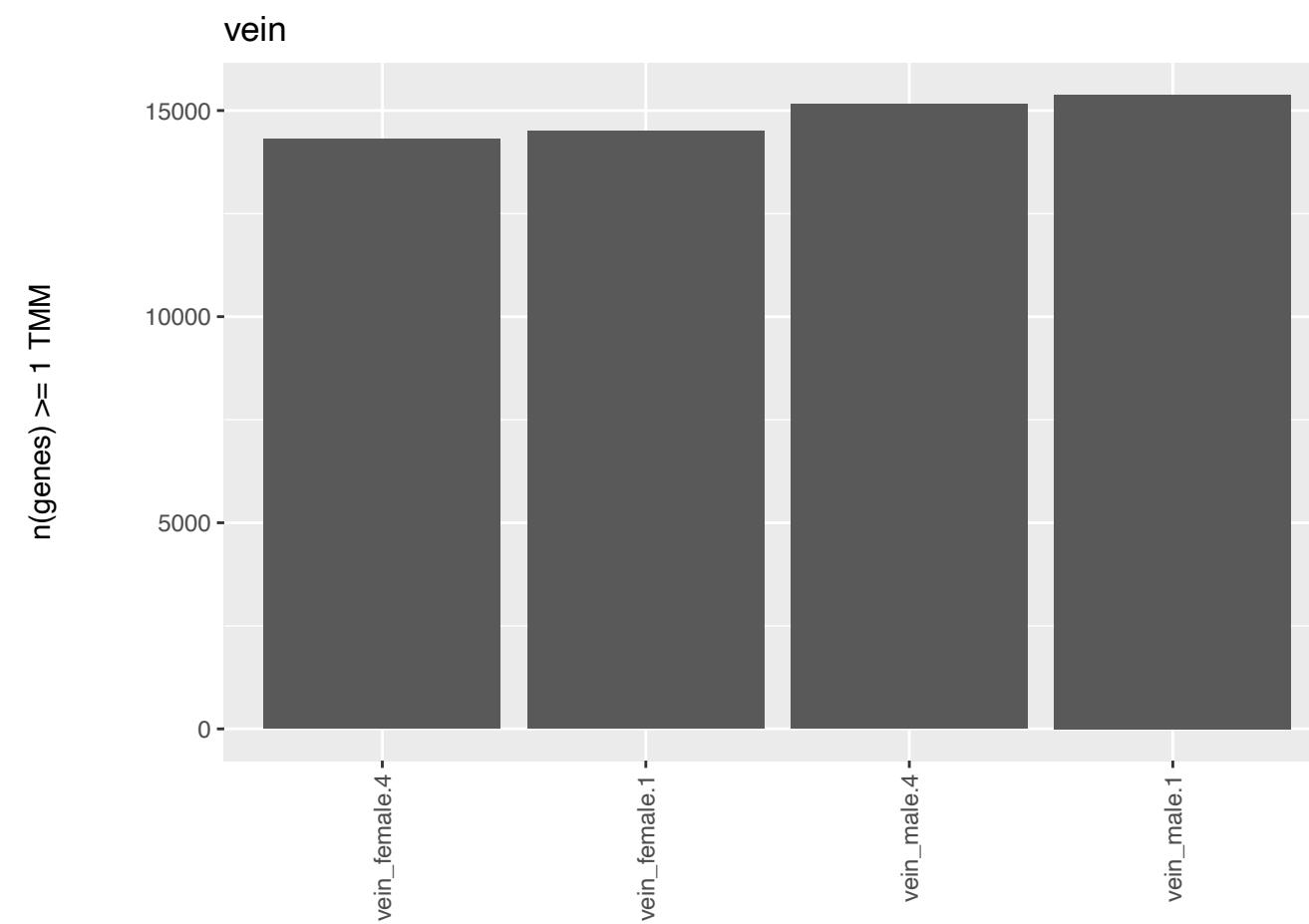
vein, UMAP: TMM expression values



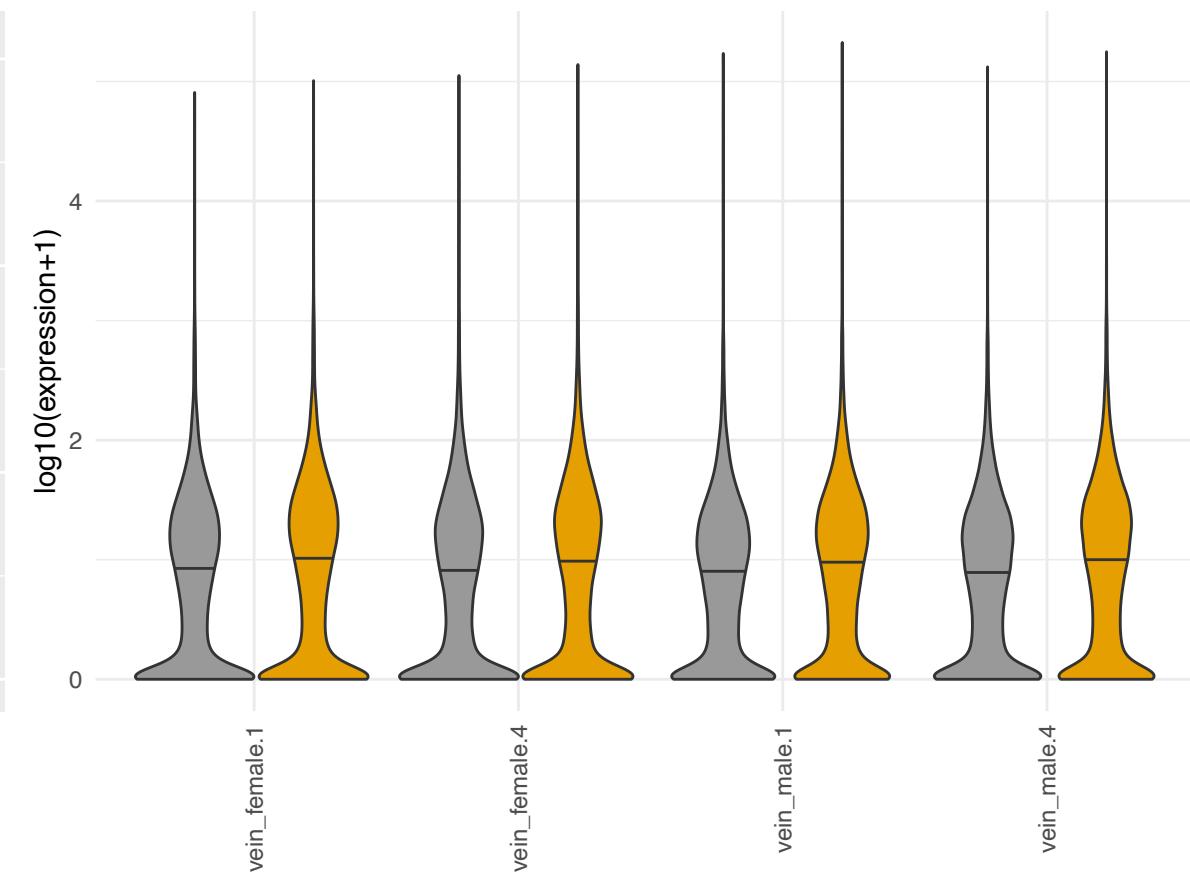
In tissue sample to sample Spearman Distance



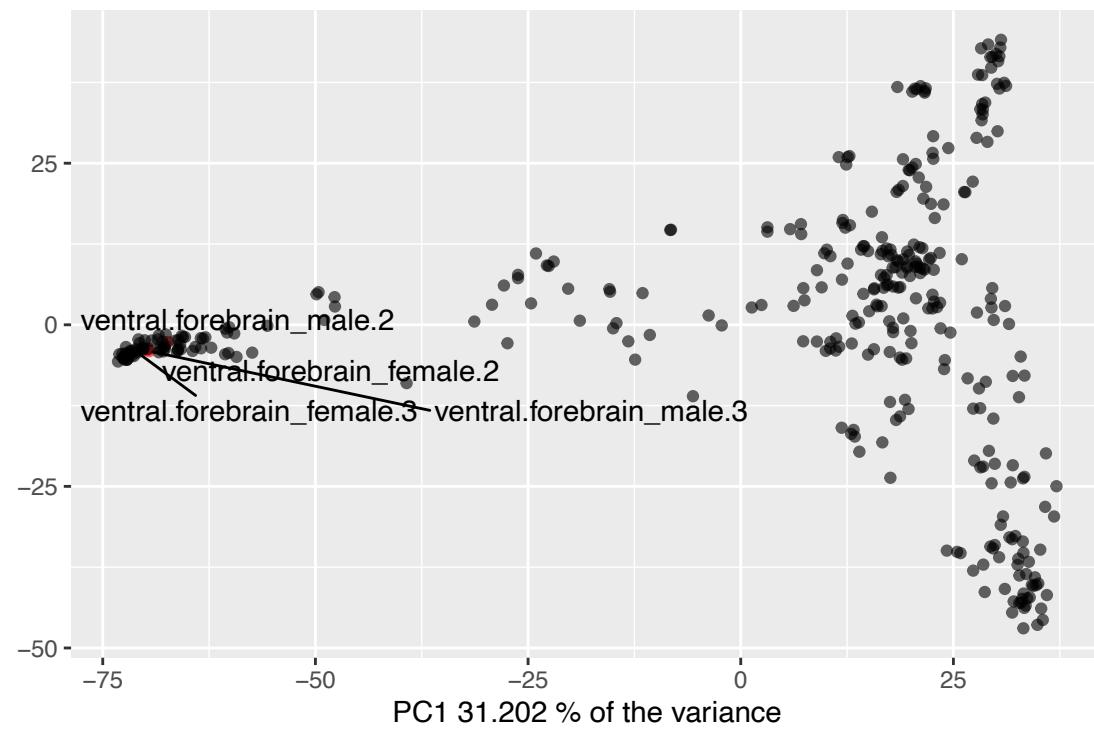
vein



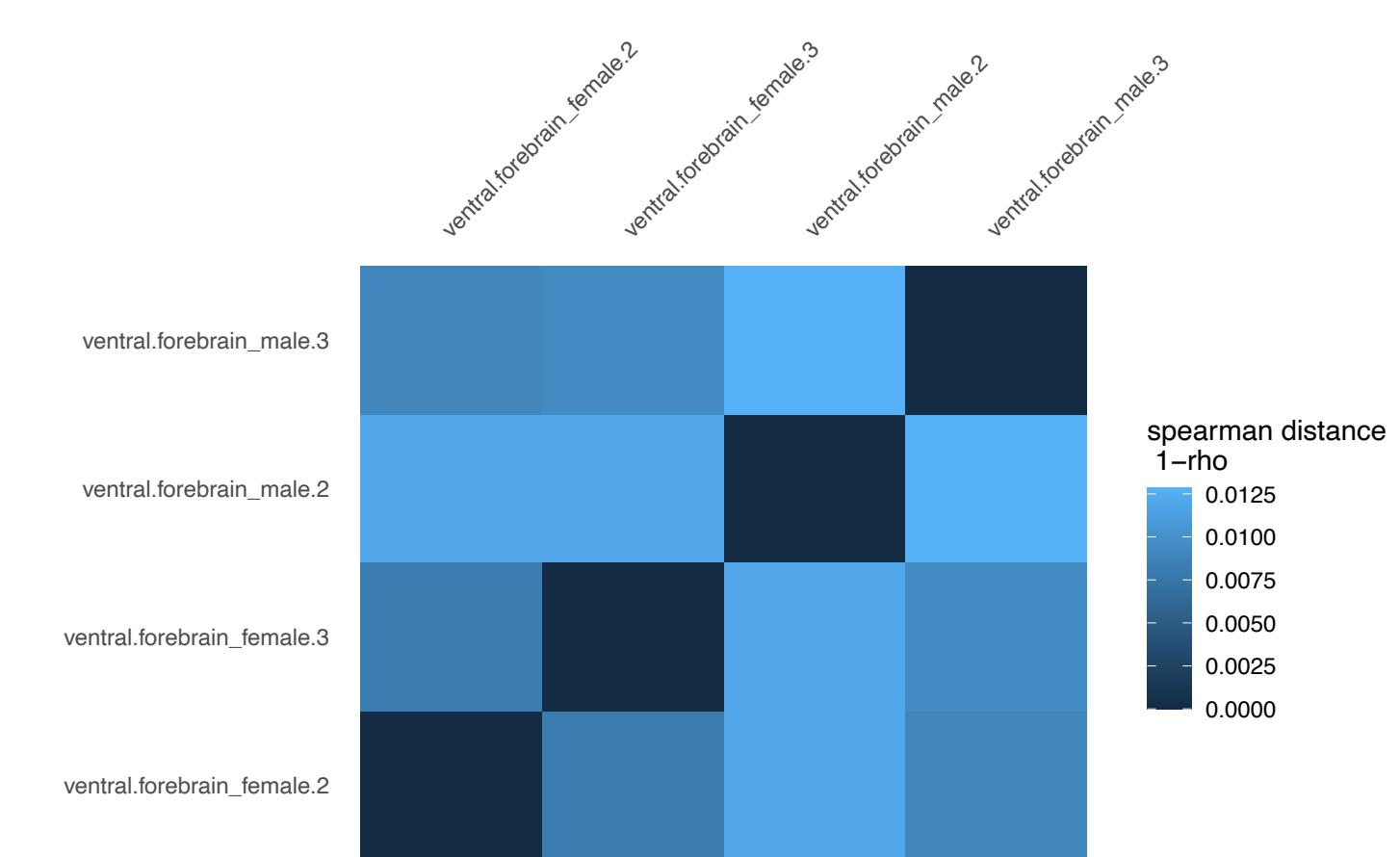
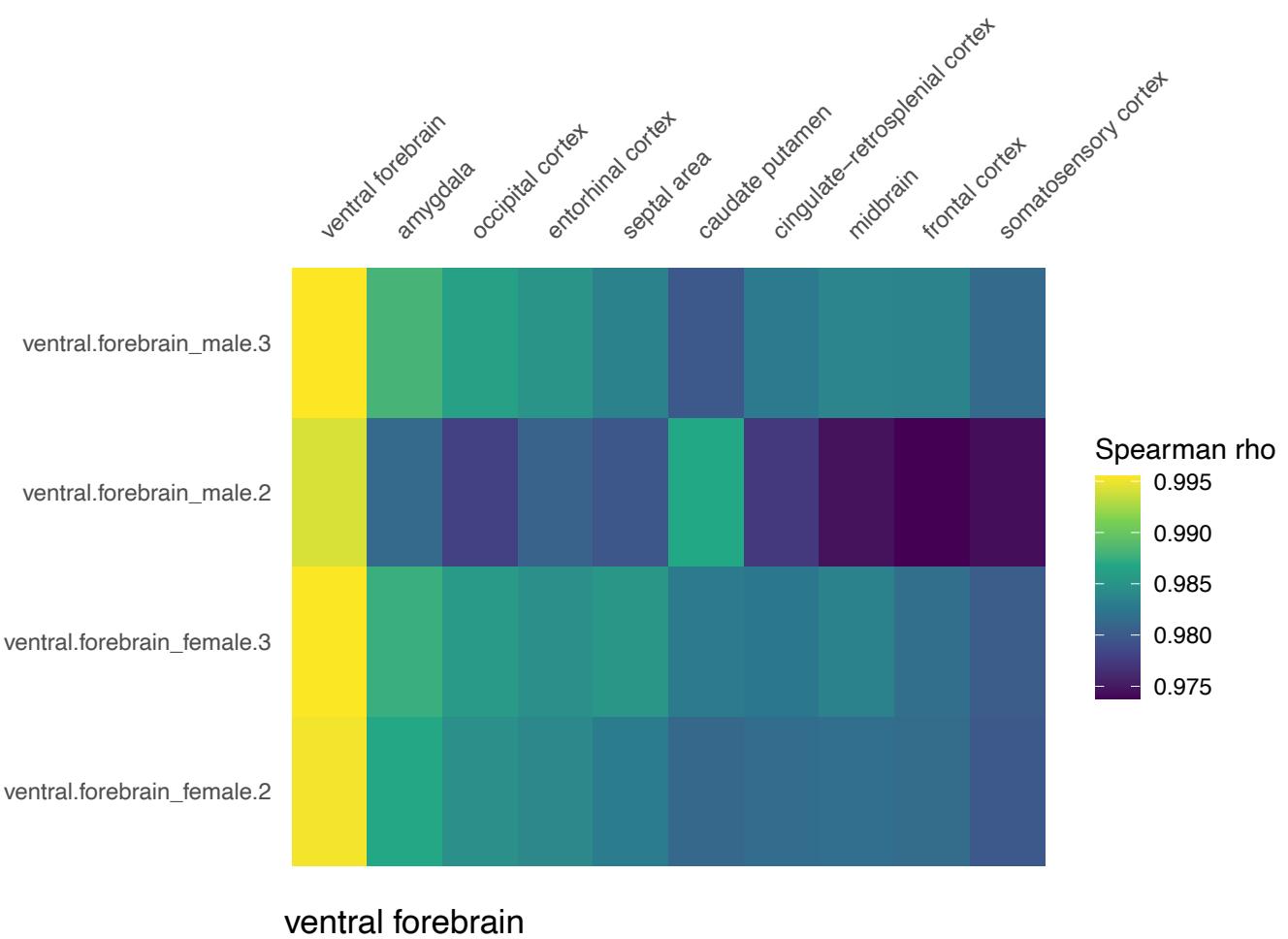
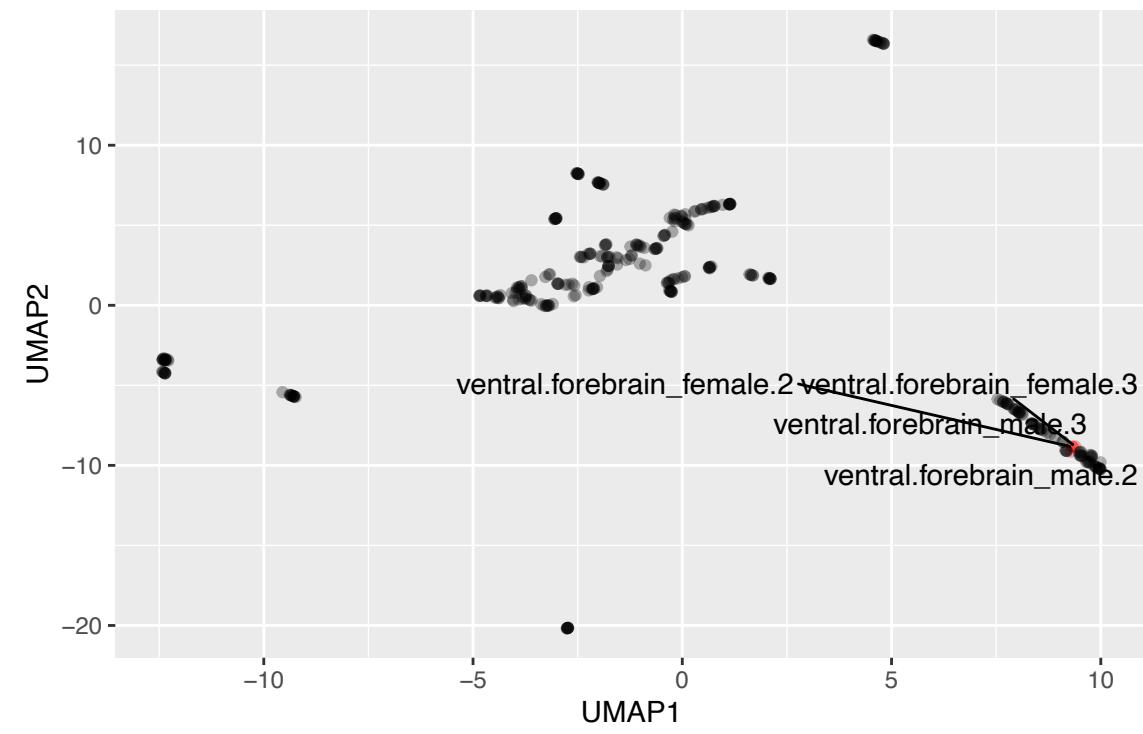
vein



ventral forebrain, PCA: TMM expression values

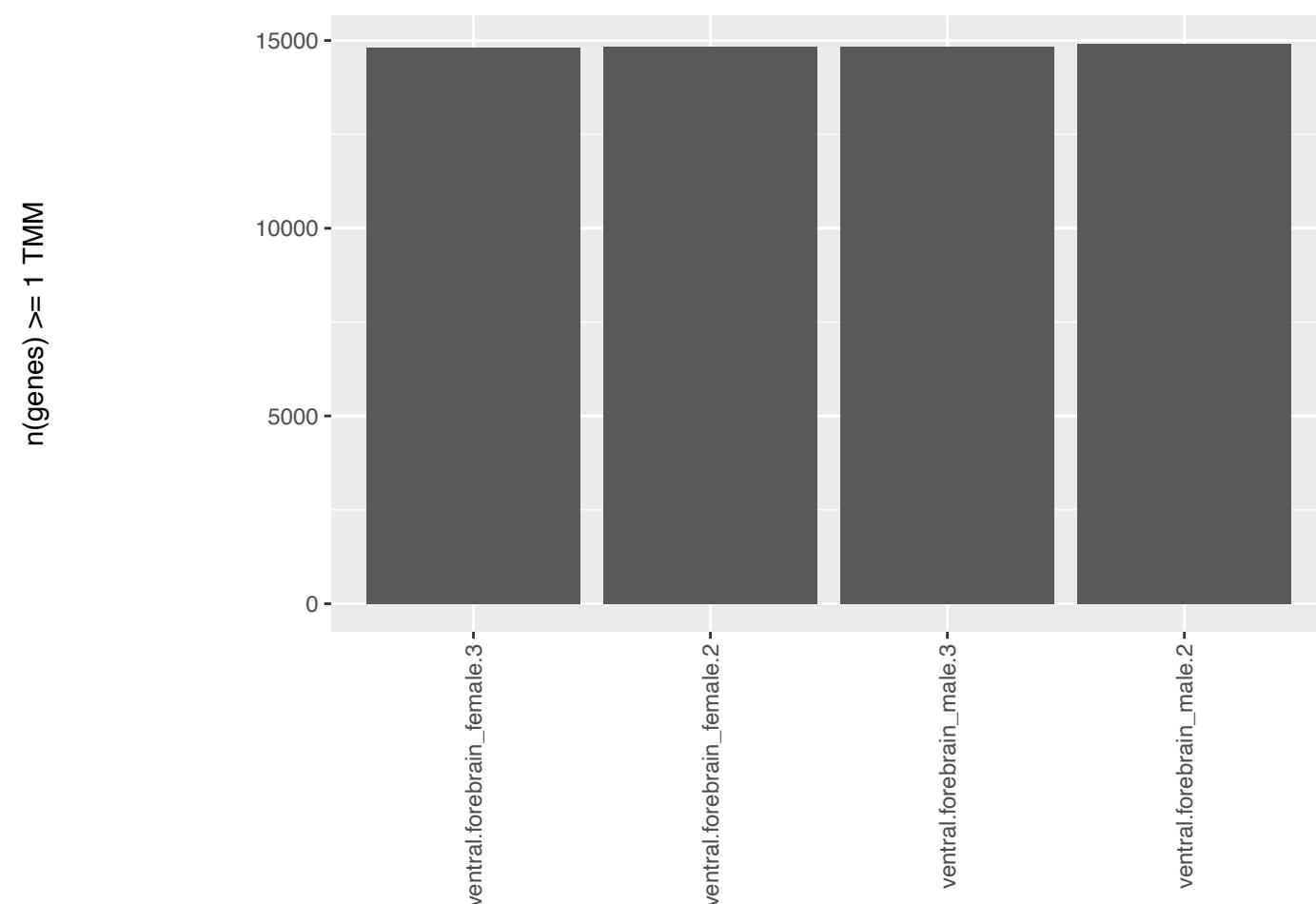


ventral forebrain, UMAP: TMM expression values

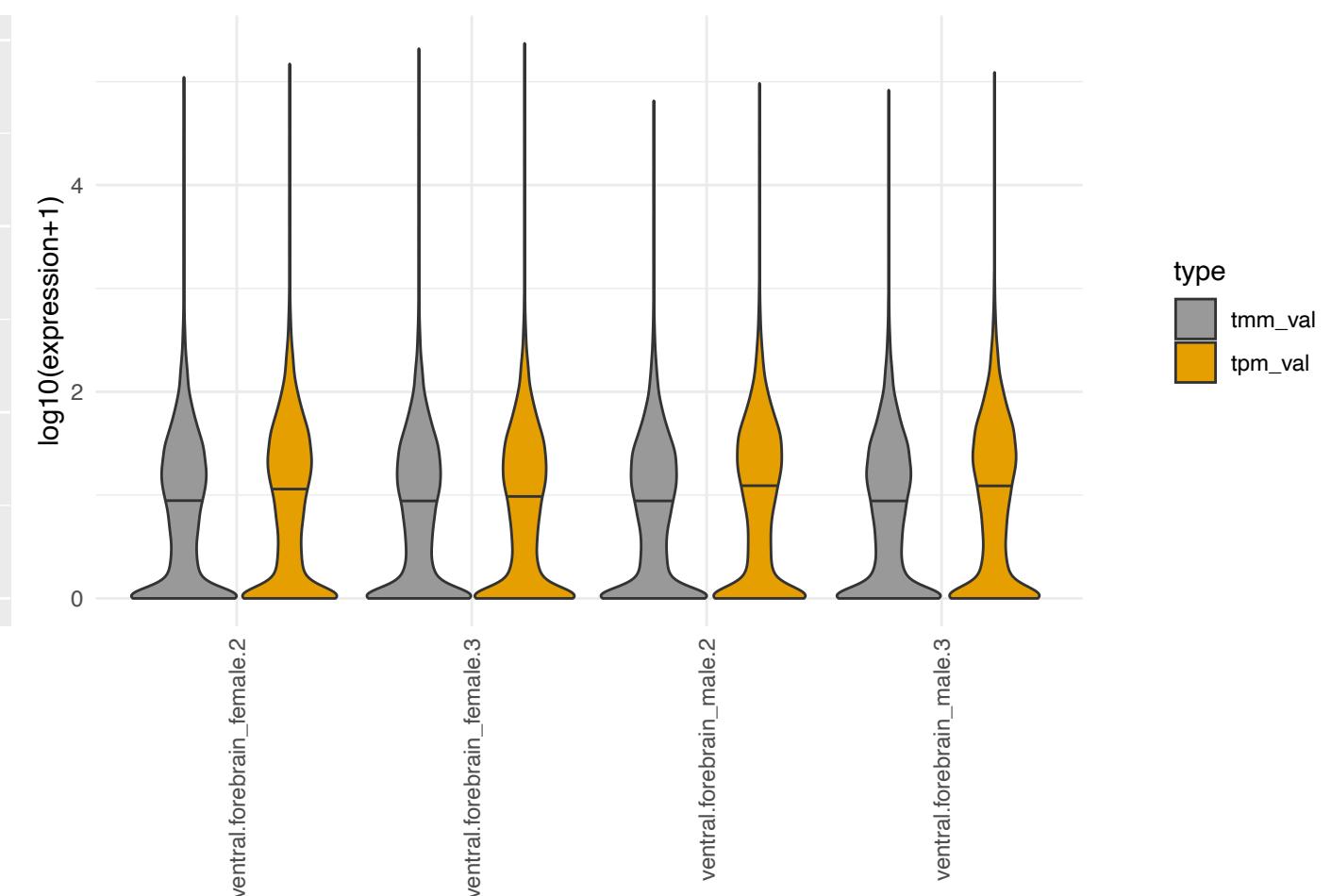


PC2 9.077 % of the variance

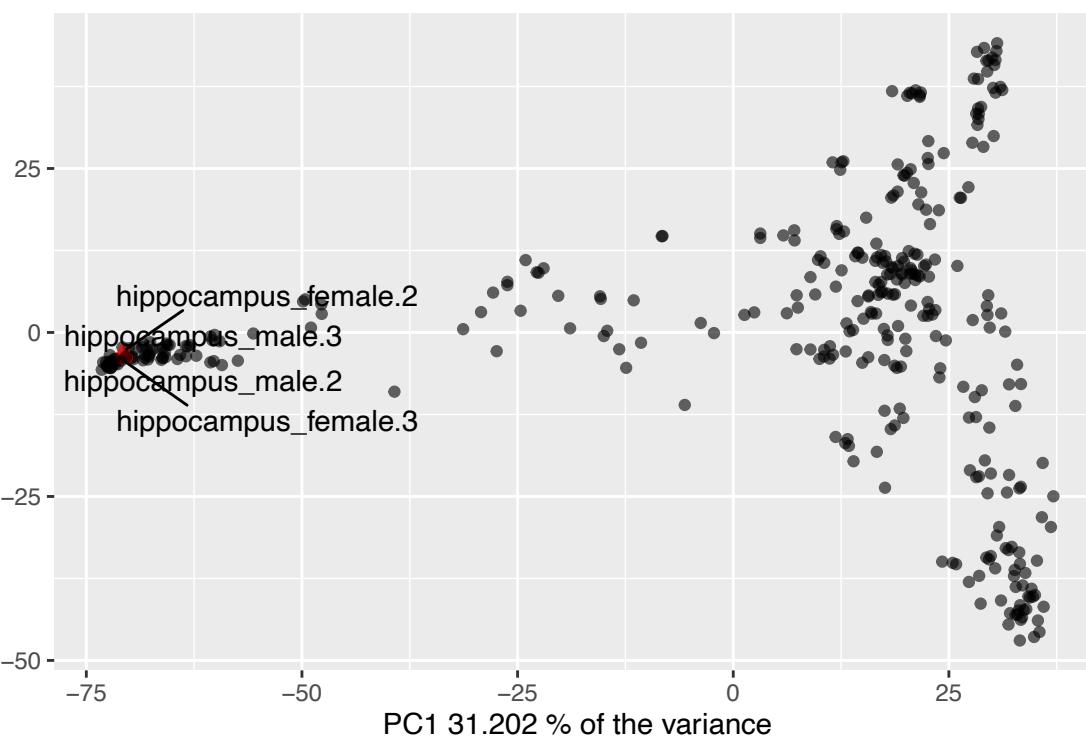
n(genes) >= 1 TMM



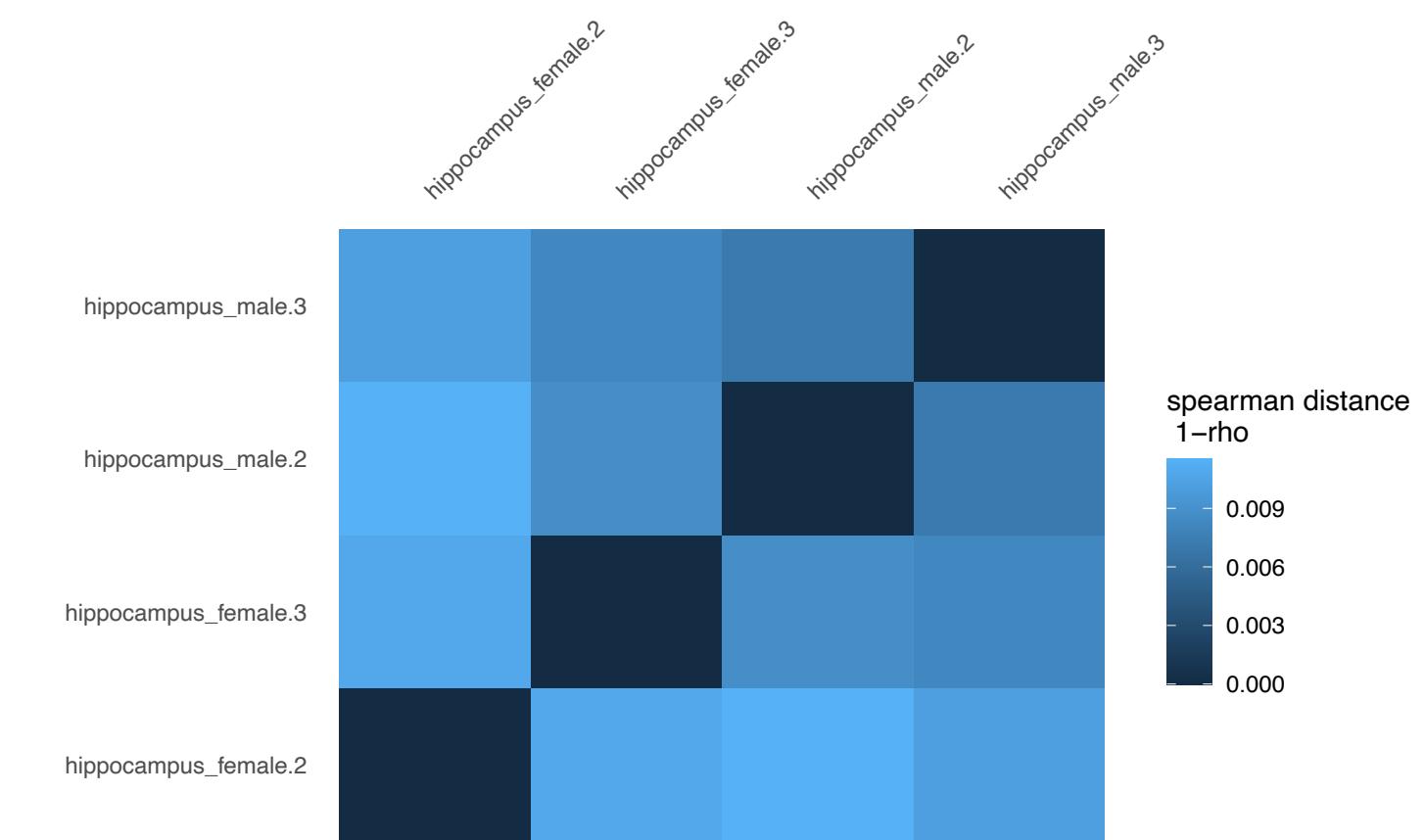
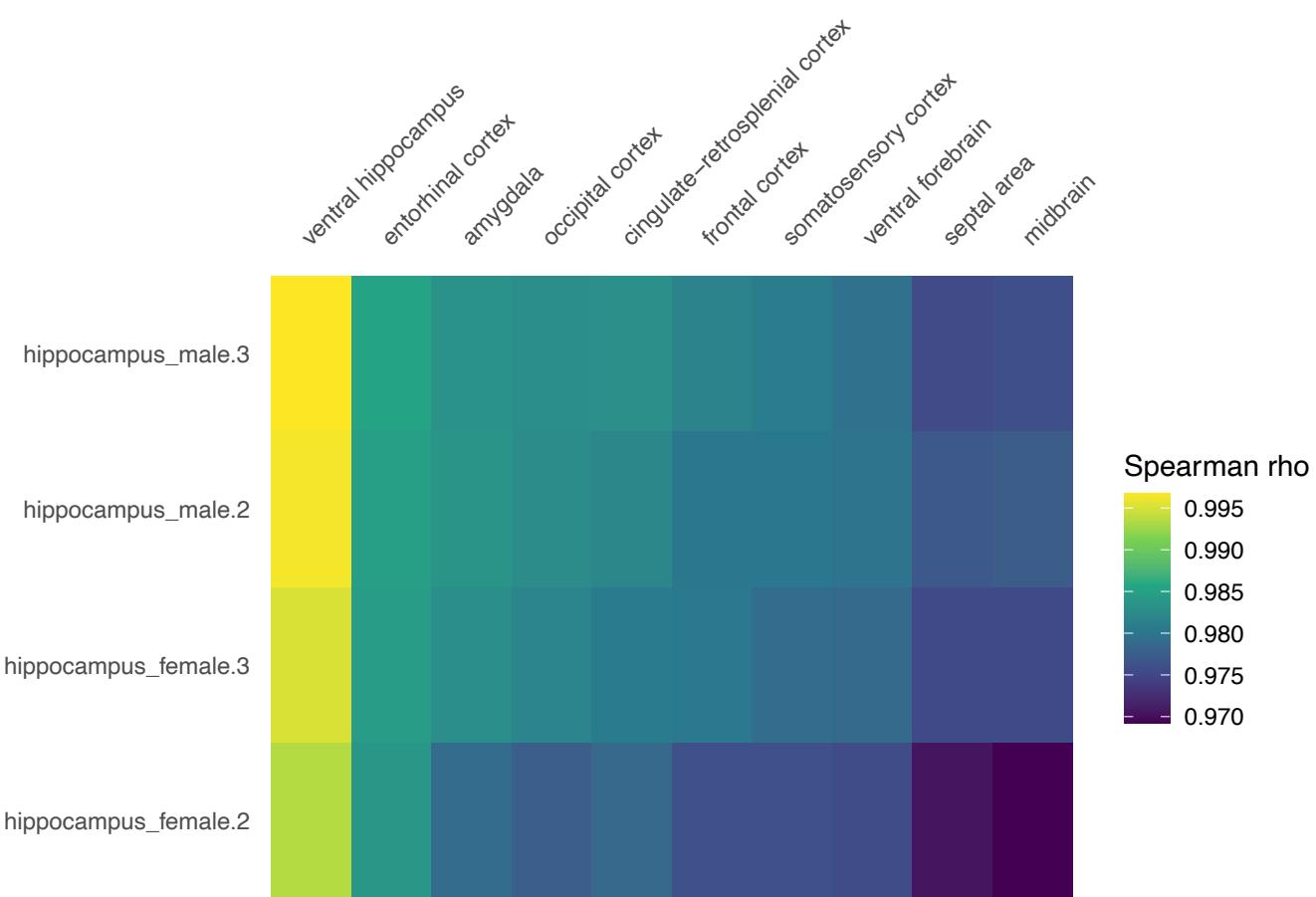
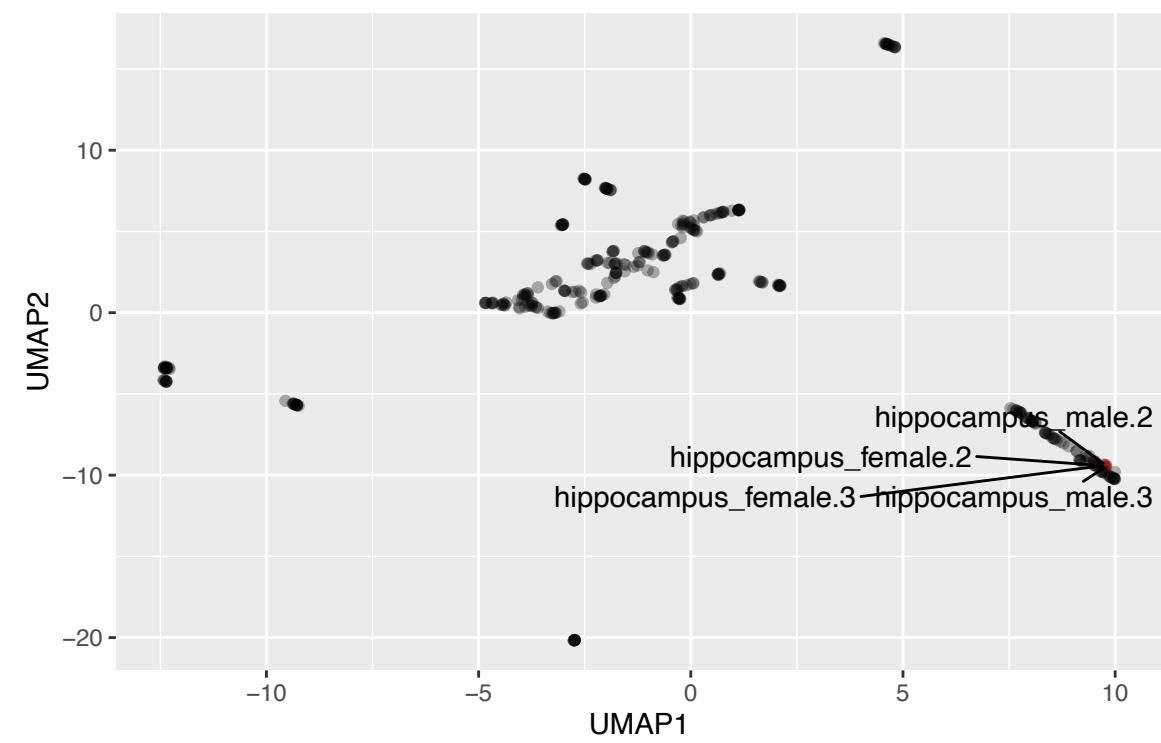
ventral forebrain



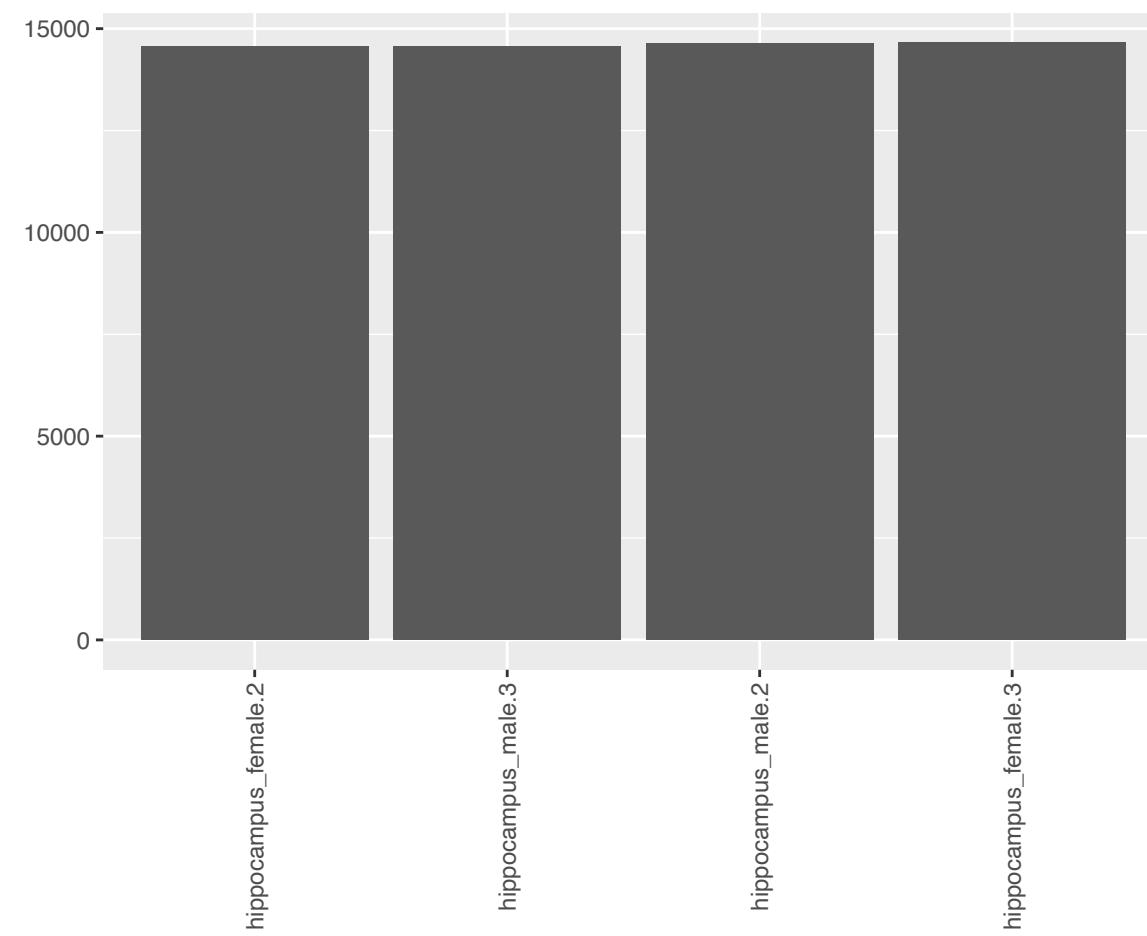
ventral hippocampus, PCA: TMM expression values



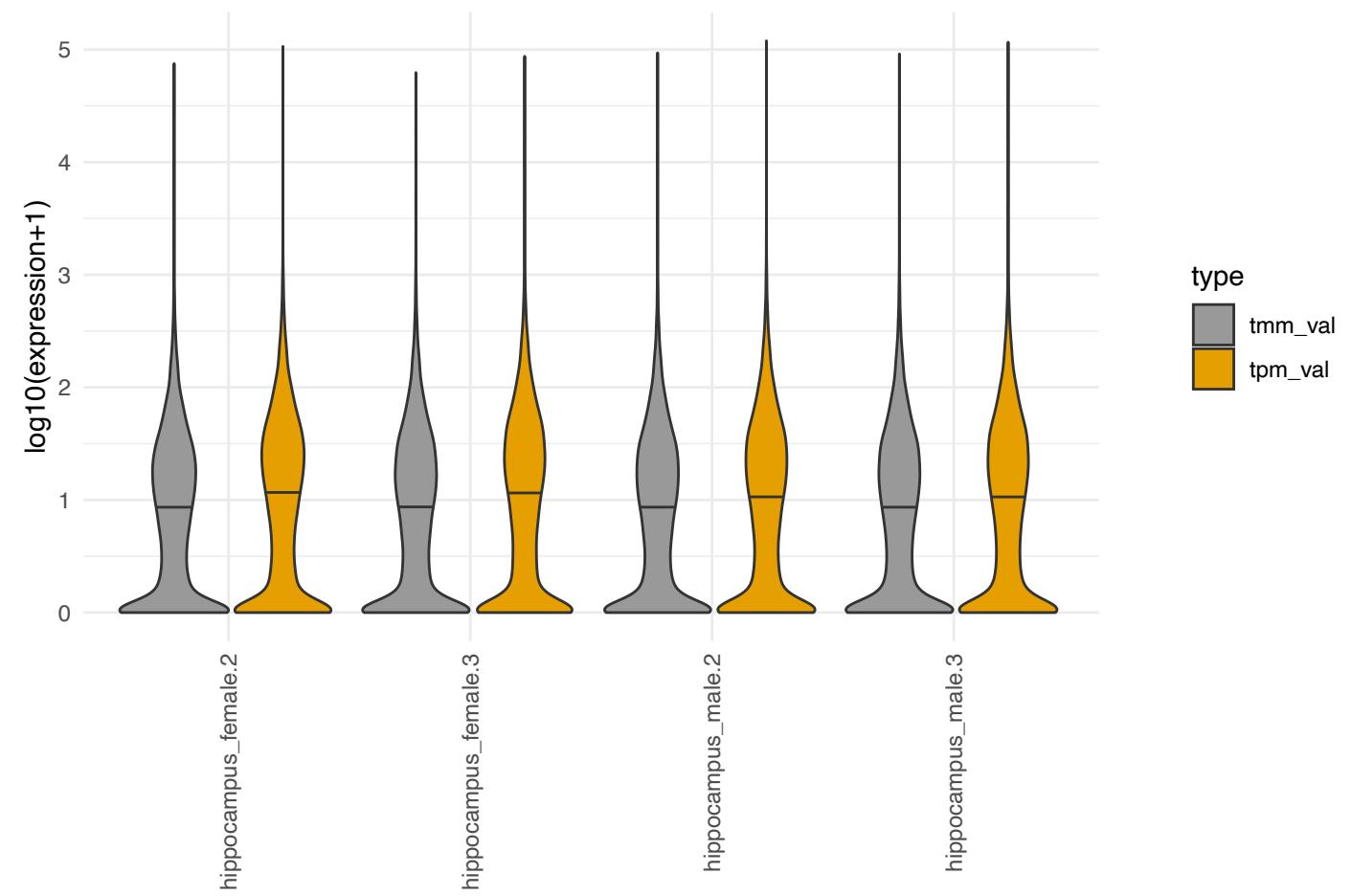
ventral hippocampus, UMAP: TMM expression values



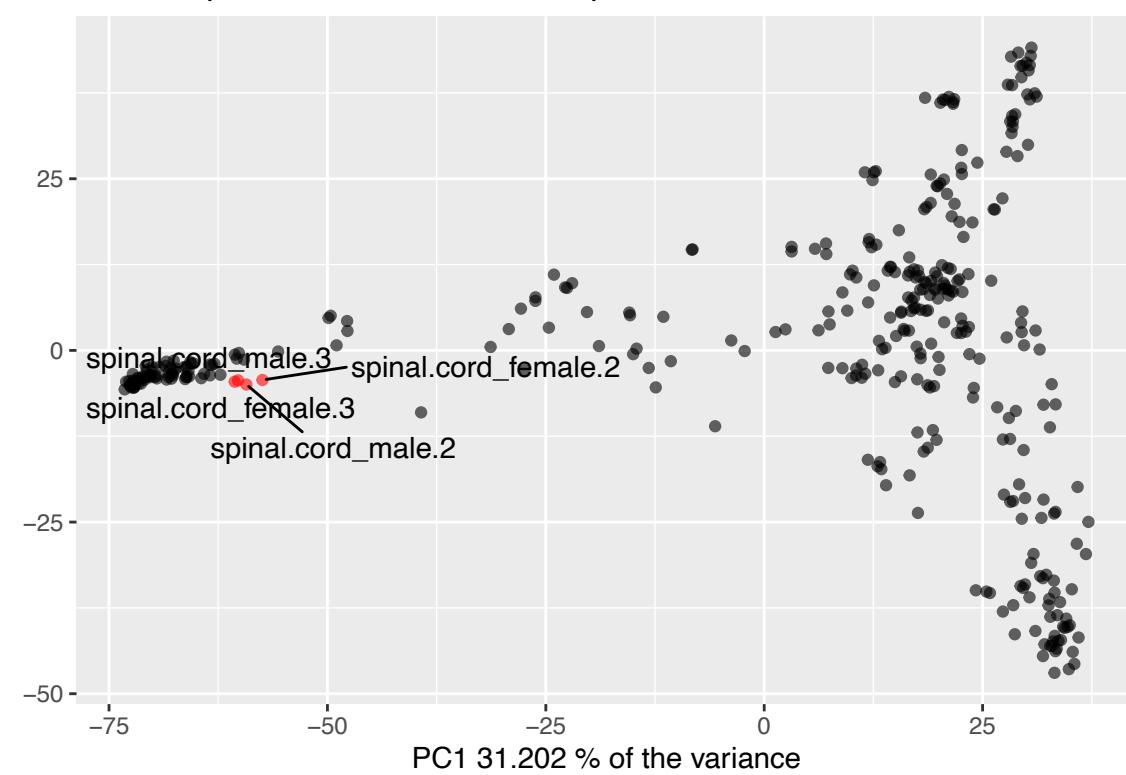
ventral hippocampus



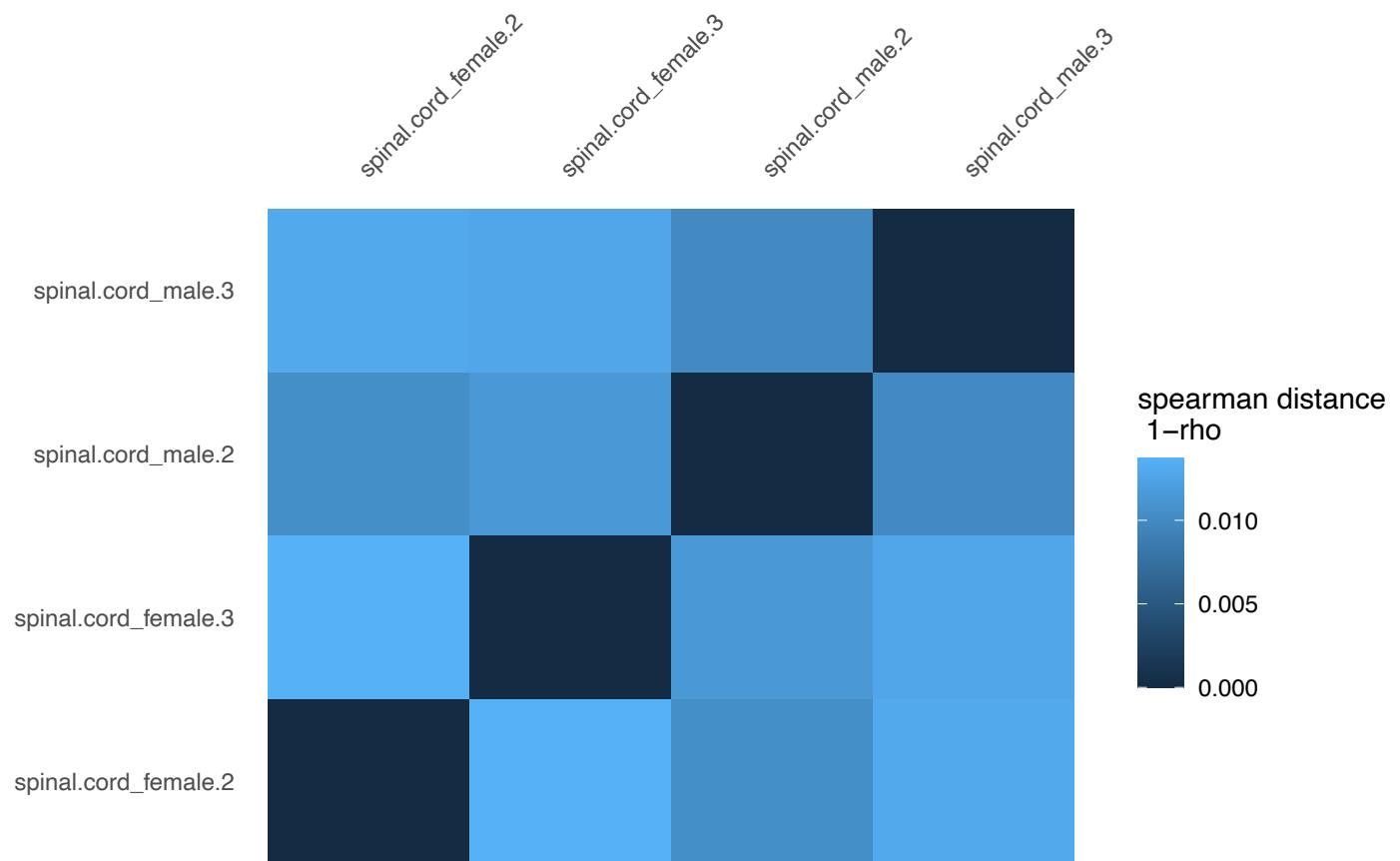
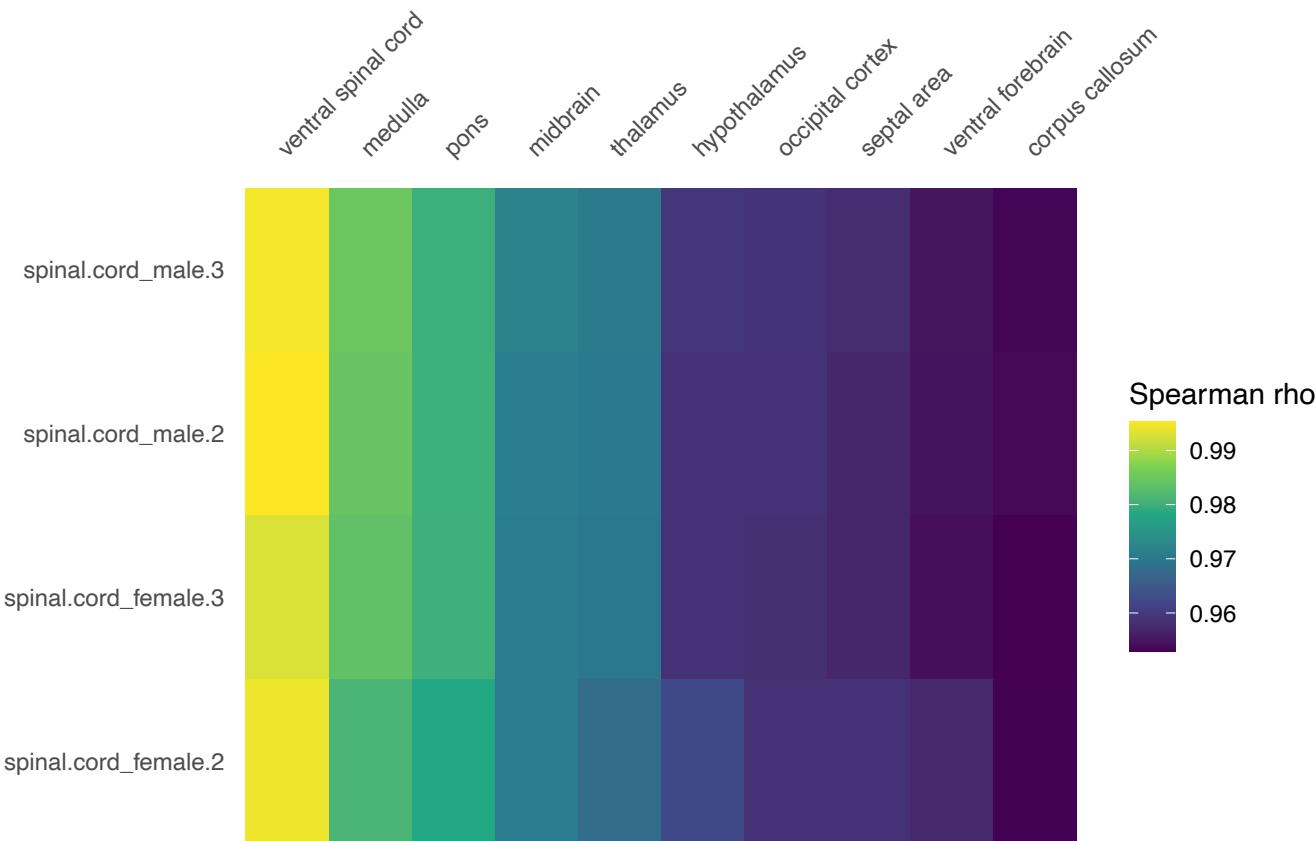
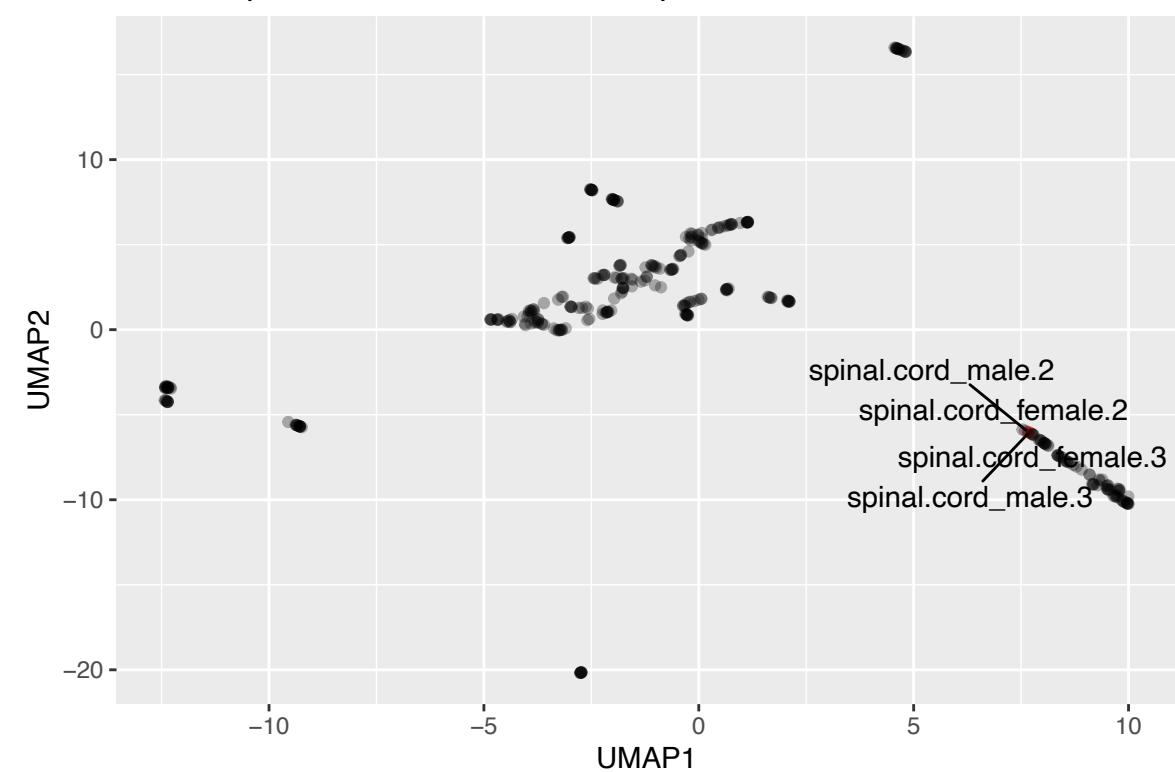
ventral hippocampus



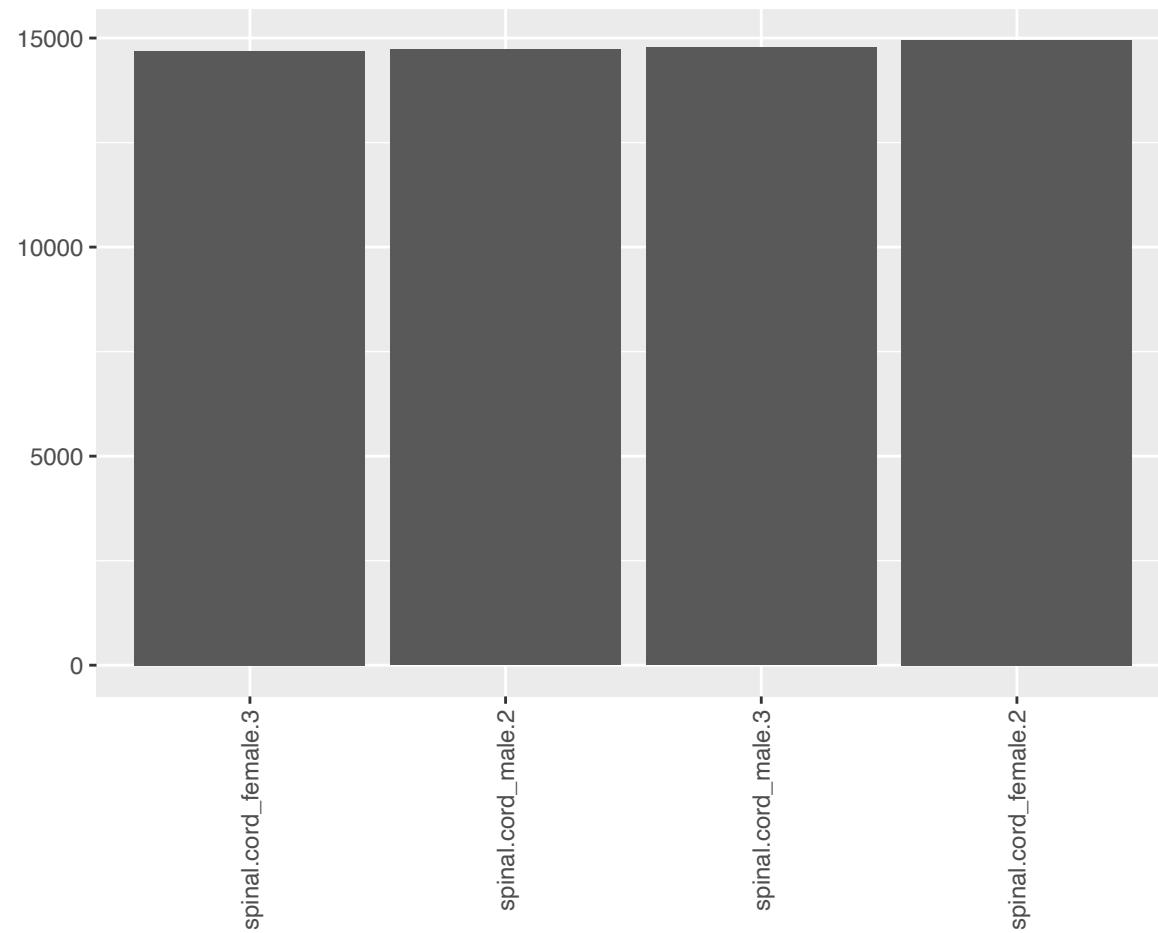
ventral spinal cord, PCA: TMM expression values



ventral spinal cord, UMAP: TMM expression values



ventral spinal cord



ventral spinal cord

