# PCA_plotting_corrected_July2023
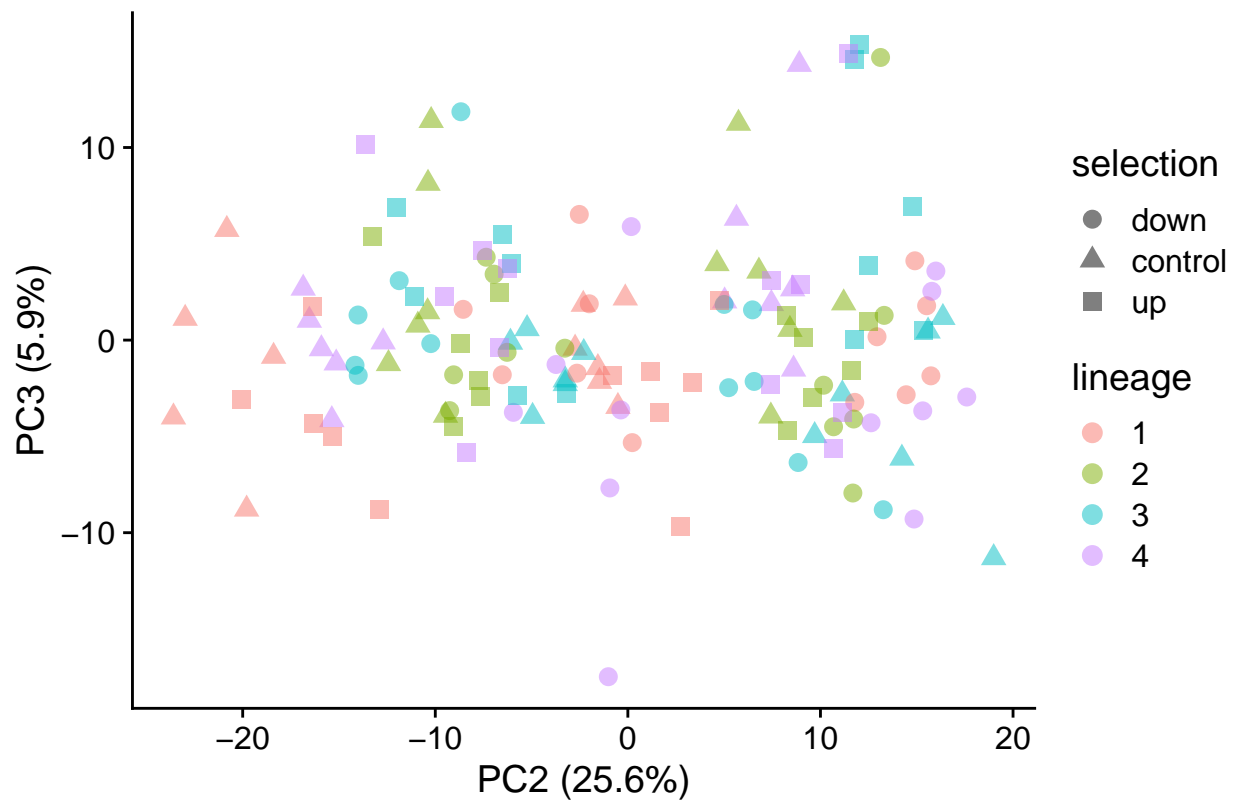
2023-07-19

PC 1 vs 2 and 2 vs 3, 500 genes

```
pca_1v2_500 <- plot_pca(vsd, PC_x = 1, PC_y = 2,
                  color_by = "lineage", shape_by = "selection",
                  n_feats = 500, #number of genes
                  scale_feats = FALSE, # we have already scaled these
                  point_rel_size = 3,
                  point_alpha = 0.5)
```
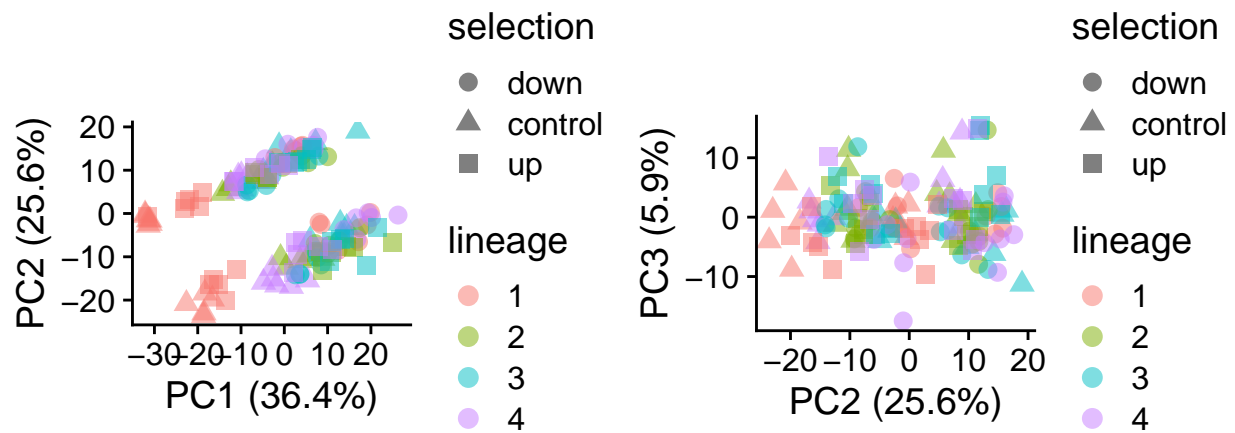


```
pca_2v3_500 <- plot_pca(vsd, PC_x = 2, PC_y = 3,
                  color_by = "lineage", shape_by = "selection",
                  n_feats = 500, #number of genes
                  scale_feats = FALSE, # we have already scaled these
                  point_rel_size = 3,
                  point_alpha = 0.5)
```
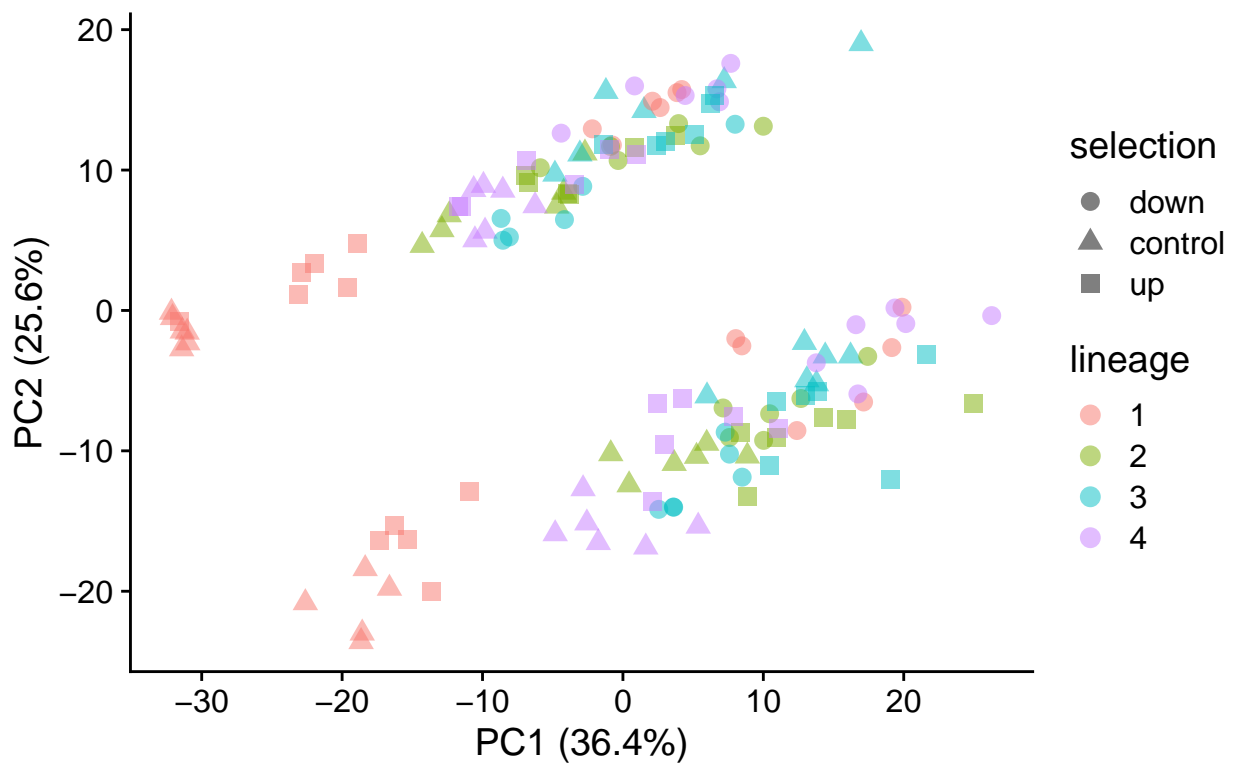
```
plot_grid(pca_1v2_500$plot, pca_2v3_500$plot,
          nrow = 1, ncol = 2,
          labels = c("A)", "B)"))
```
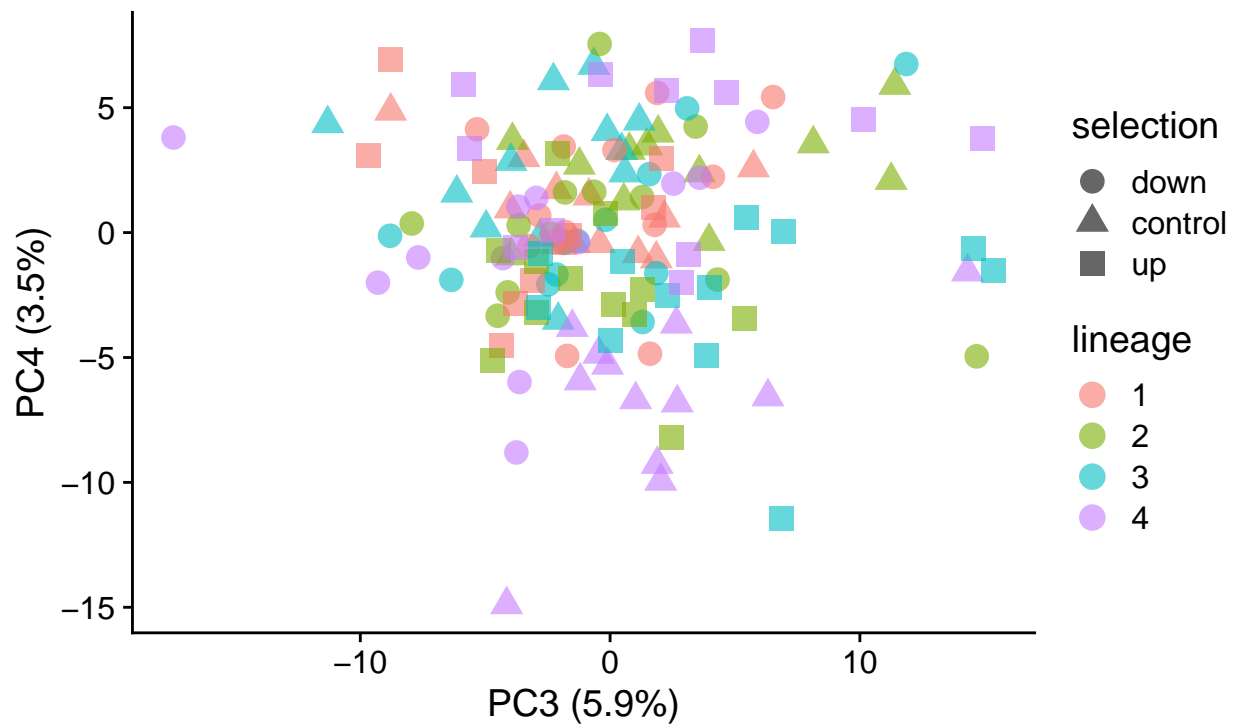
A)
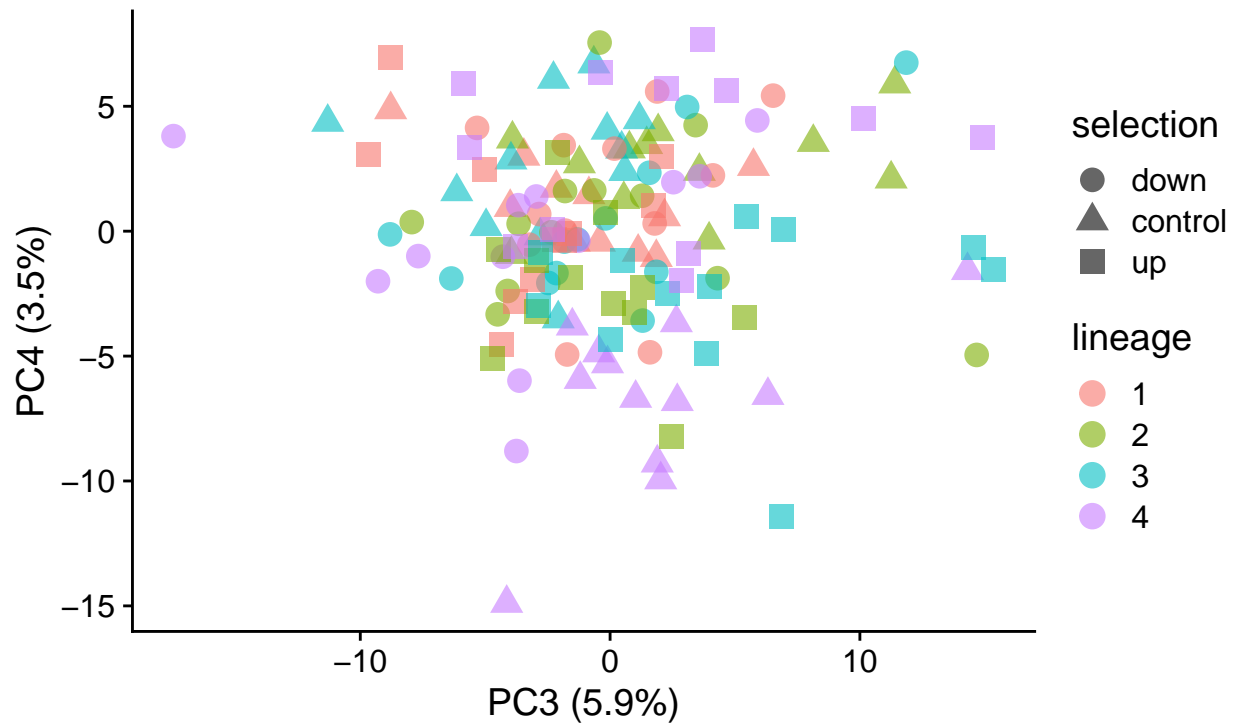
B)

PC 3 vs 4, 500 genes

```
pca_3v4_500 <- plot_pca(vsd, PC_x = 3, PC_y = 4,
                    color_by = "lineage", shape_by = "selection",
                    n_feats = 500, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 4,
                    point_alpha = 0.6)
```
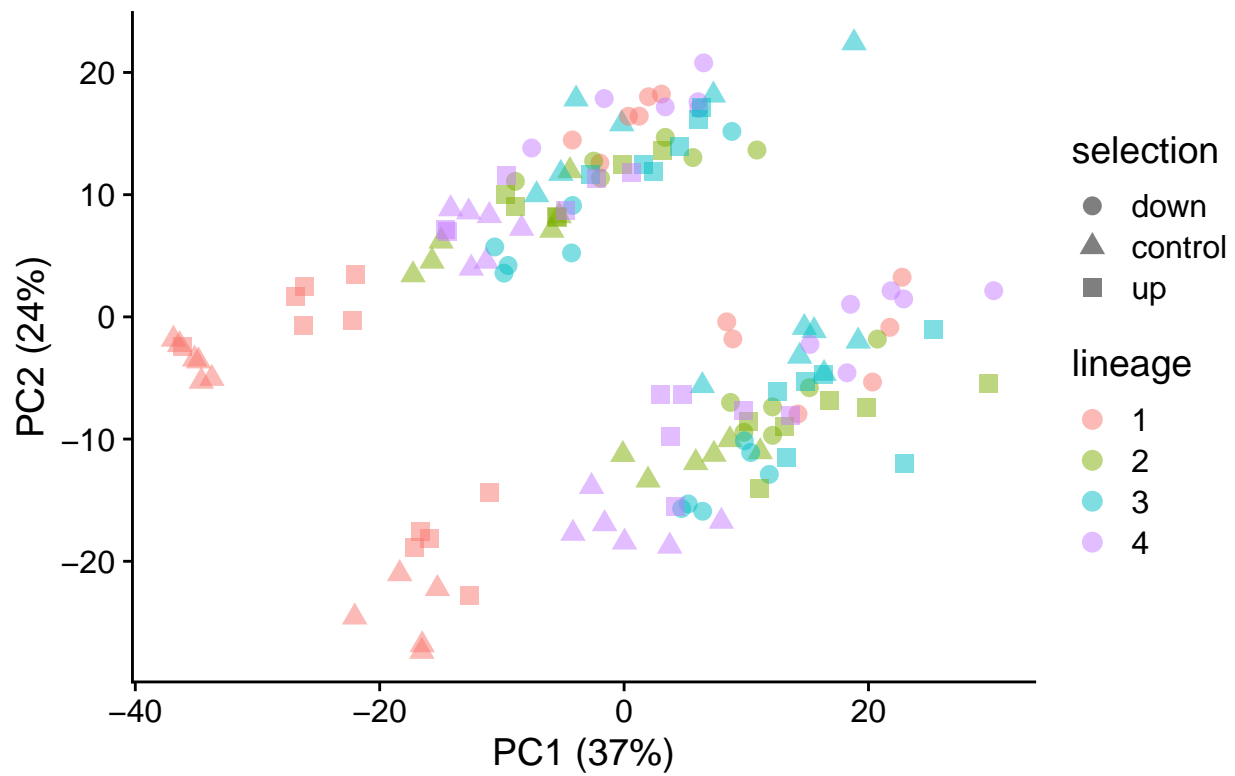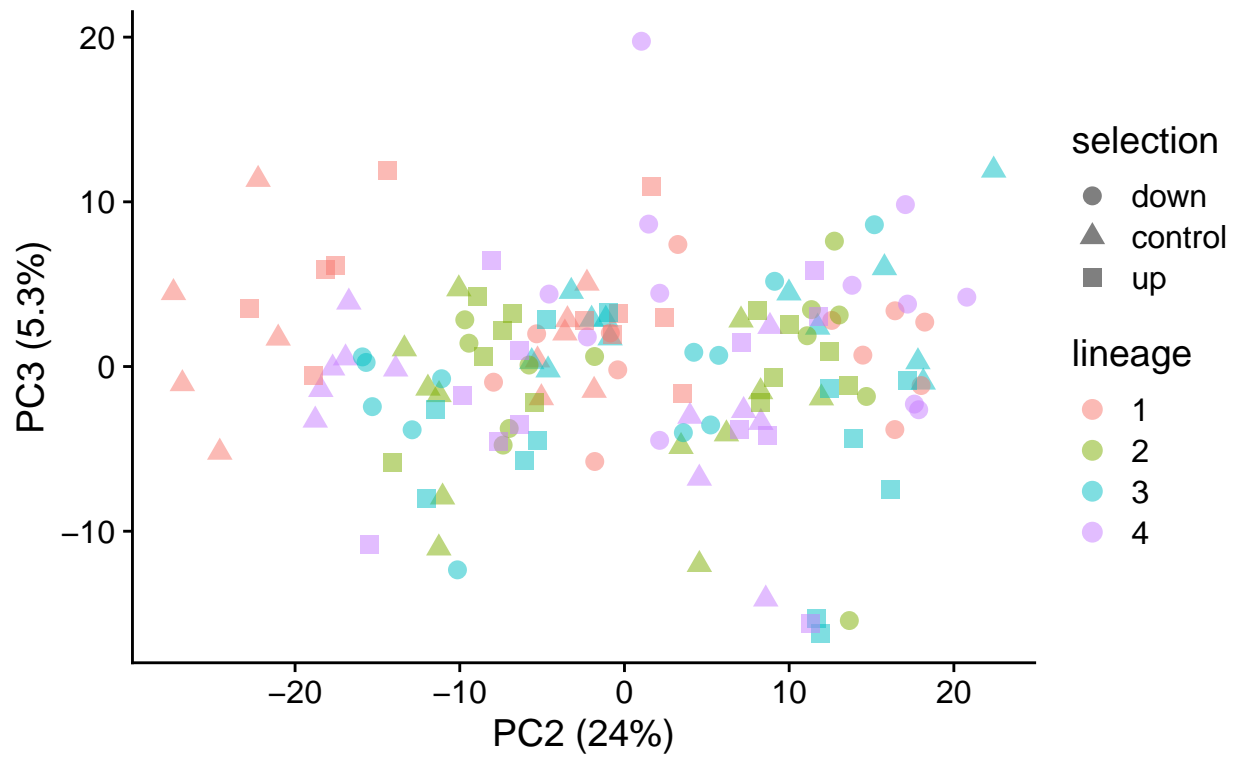


```
pca_3v4_500$plot
```

PC 1 vs 2 and 2 vs 3, 1000 genes

```
pca_1v2_1000 <- plot_pca(vsd, PC_x = 1, PC_y = 2,
                color_by = "lineage", shape_by = "selection",
                n_feats = 1000, #number of genes
                scale_feats = FALSE, # we have already scaled these
                point_rel_size = 3,
                point_alpha = 0.5)
```
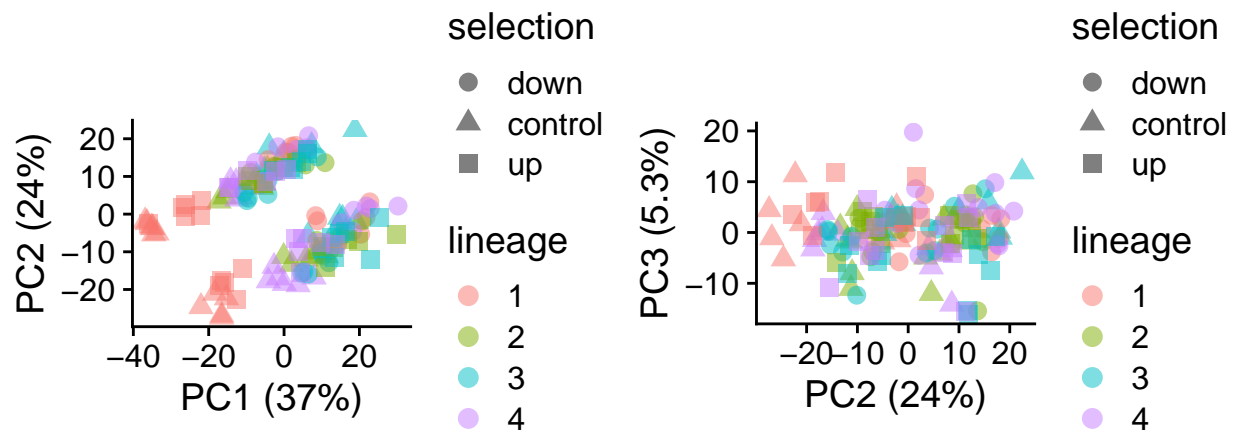
```
pca_2v3_1000 <- plot_pca(vsd, PC_x = 2, PC_y = 3,
                color_by = "lineage", shape_by = "selection",
                n_feats = 1000, #number of genes
                scale_feats = FALSE, # we have already scaled these
                point_rel_size = 3,
                point_alpha = 0.5)
```

```
plot_grid(pca_1v2_1000$plot, pca_2v3_1000$plot,
          nrow = 1, ncol = 2,
          labels = c("A)", "B)"))
```

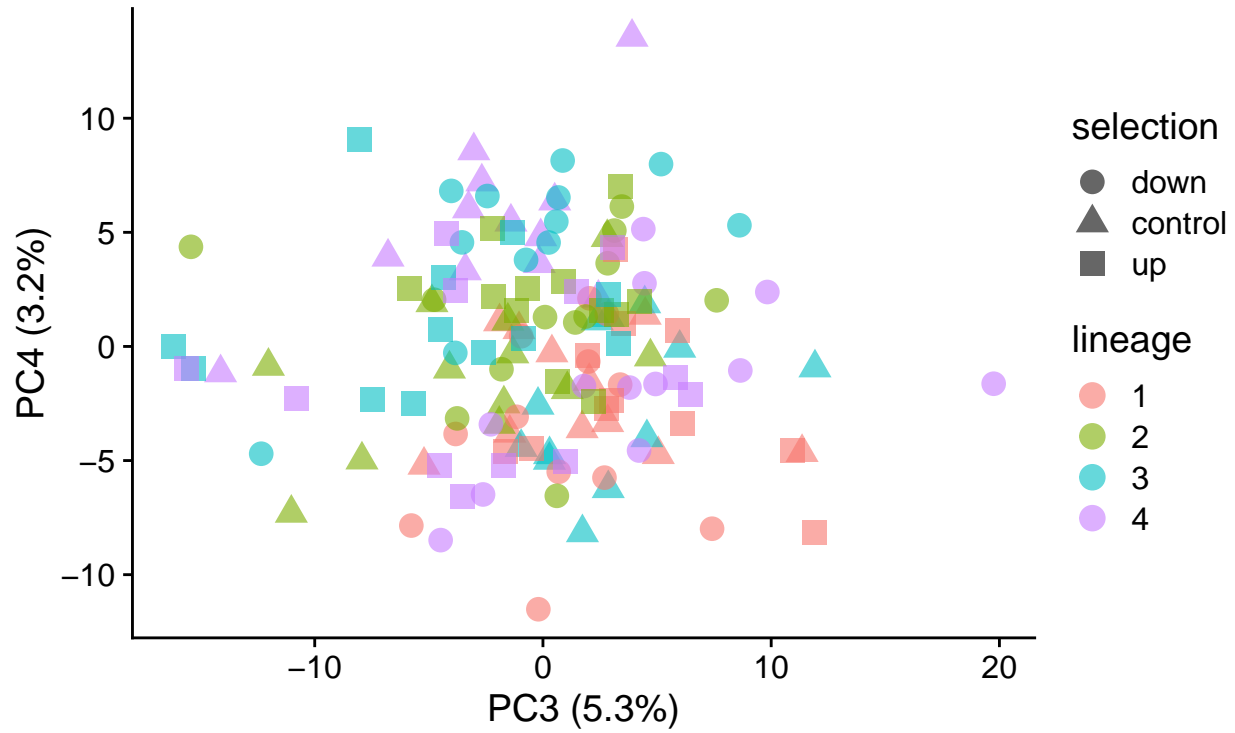**A)**   **B)**
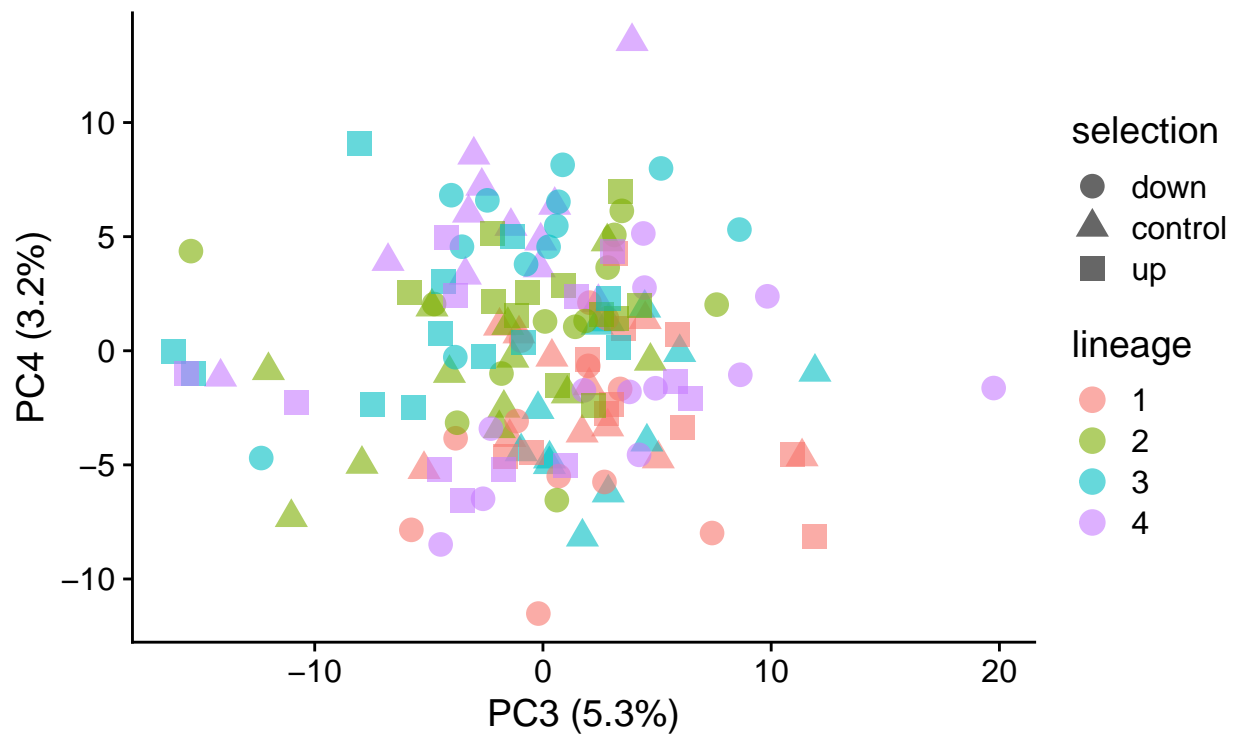

PC 3 vs 4, 1000 genes

```
pca_3v4_1000 <- plot_pca(vsd, PC_x = 3, PC_y = 4,
                         color_by = "lineage", shape_by = "selection",
```

```
n_feats = 1000, #number of genes
scale_feats = FALSE, # we have already scaled these
point_rel_size = 4,
point_alpha = 0.6)
```
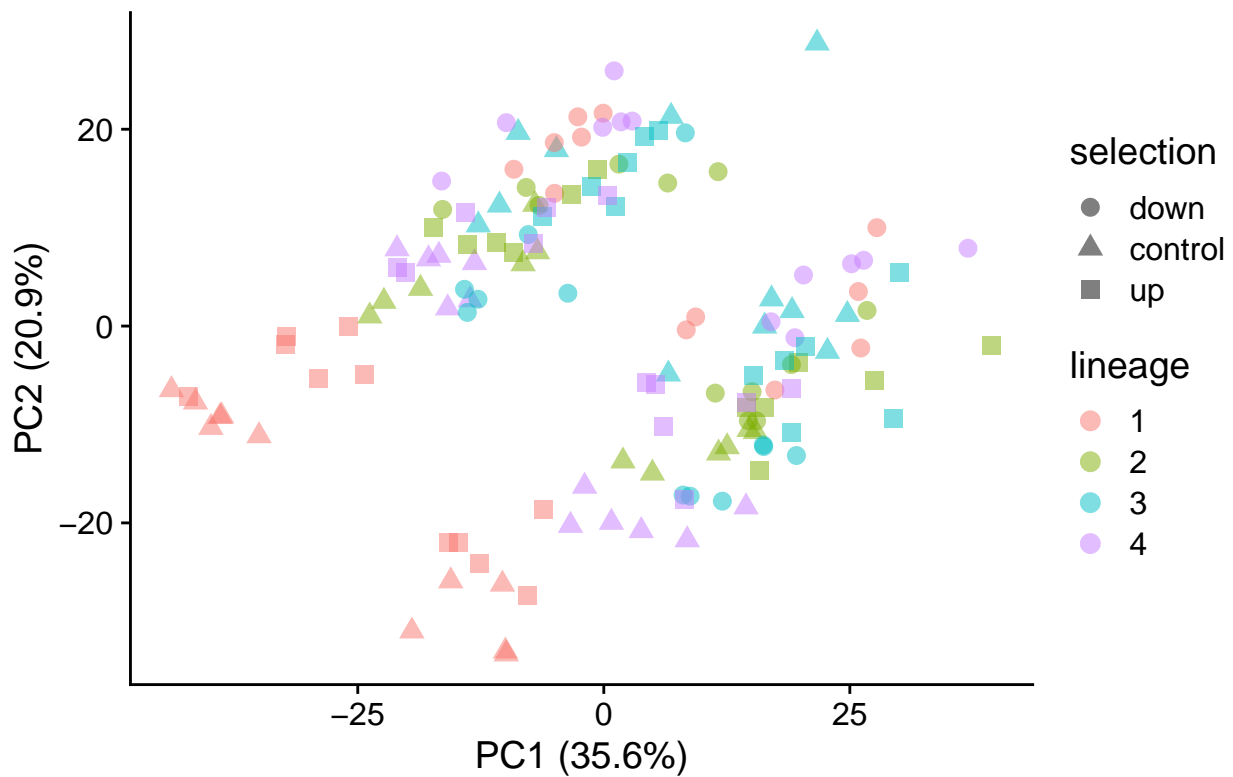

`pca_3v4_1000$plot`
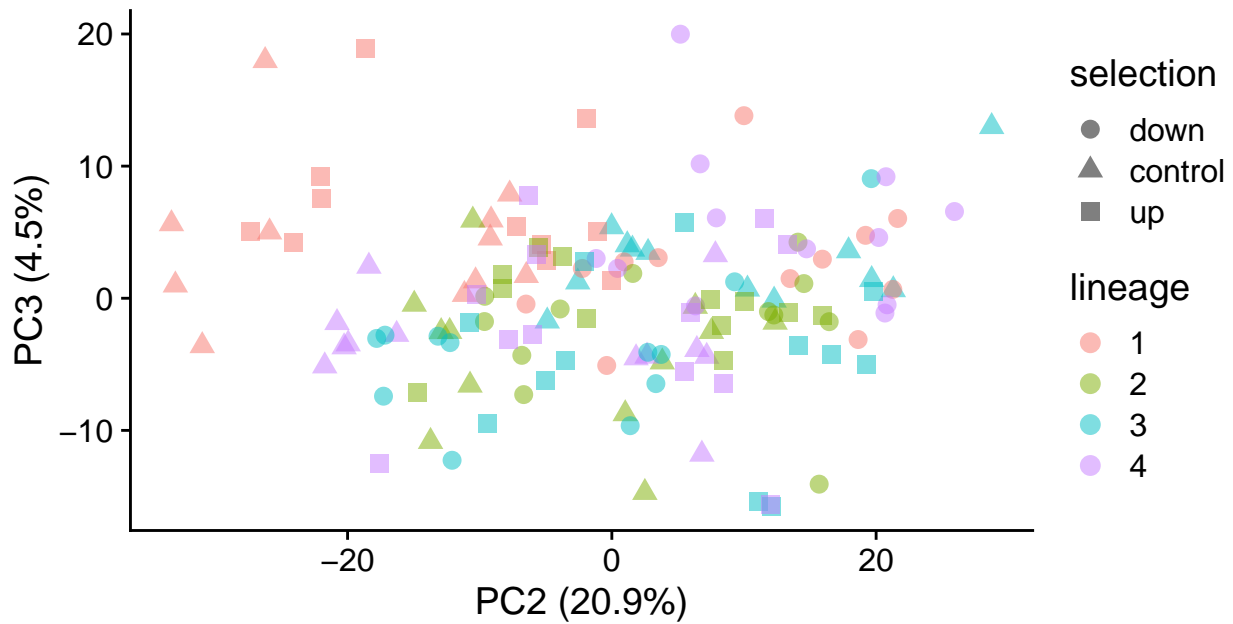
PC 1 vs 2 and 2 vs 3, 5000 genes

```
pca_1v2_5000 <- plot_pca(vsd, PC_x = 1, PC_y = 2,
                color_by = "lineage", shape_by = "selection",
                n_feats = 5000, #number of genes
                scale_feats = FALSE, # we have already scaled these
                point_rel_size = 3,
                point_alpha = 0.5)
```



```
pca_2v3_5000 <- plot_pca(vsd, PC_x = 2, PC_y = 3,
                color_by = "lineage", shape_by = "selection",
                n_feats = 5000, #number of genes
                scale_feats = FALSE, # we have already scaled these
                point_rel_size = 3,
                point_alpha = 0.5)
```
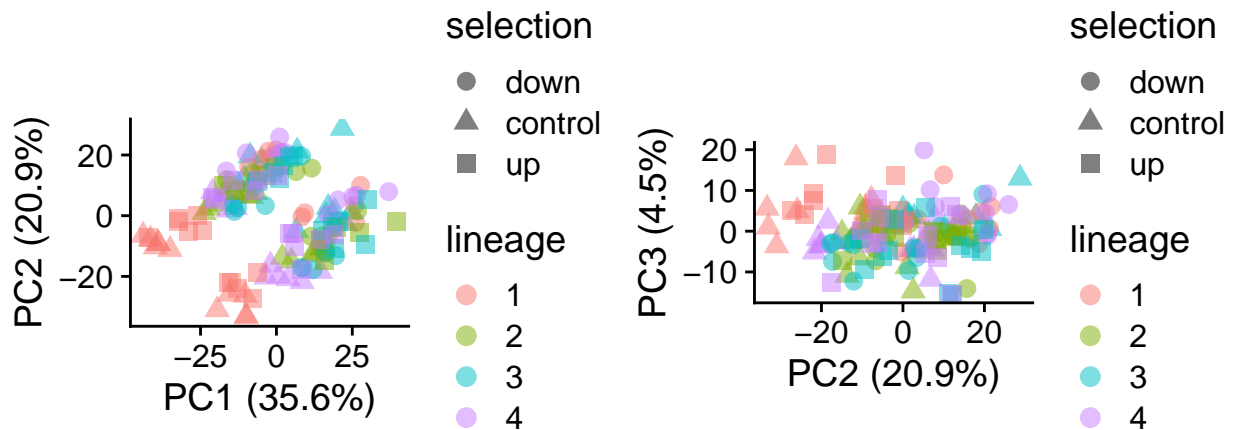
```
plot_grid(pca_1v2_5000$plot, pca_2v3_5000$plot,
          nrow = 1, ncol = 2,
          labels = c("A)", "B)"))
```

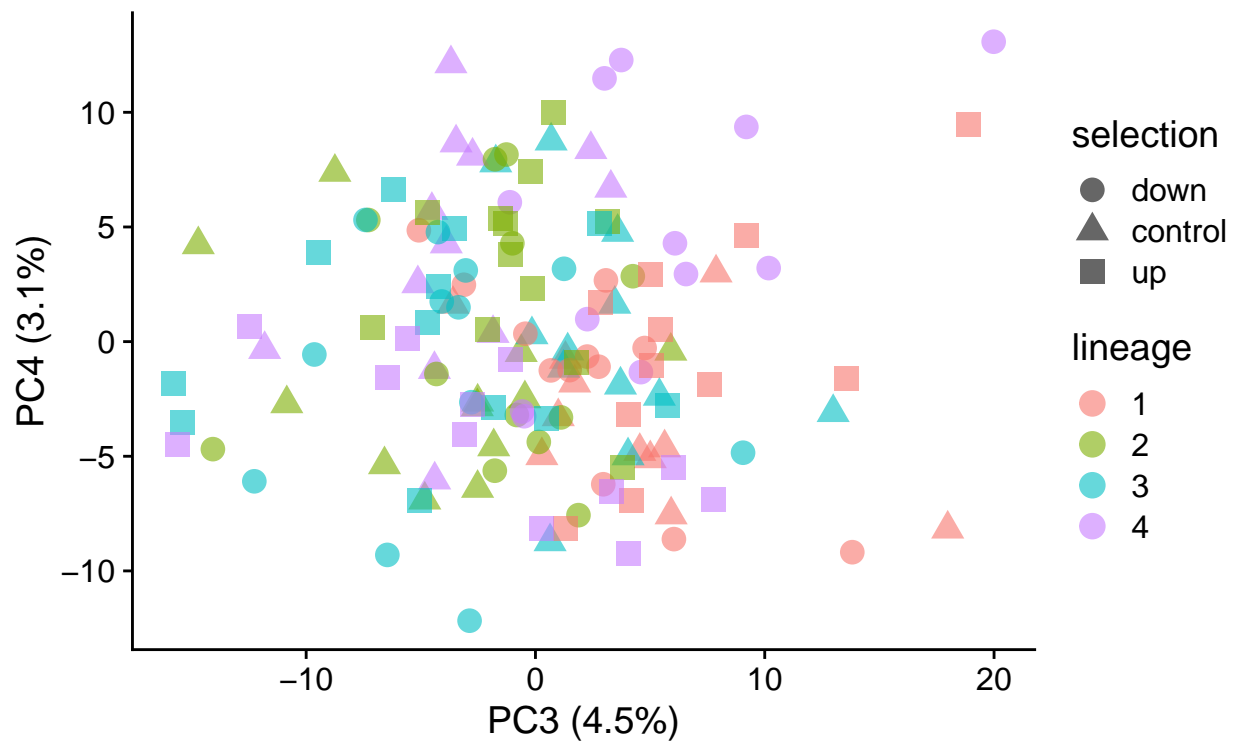**A)**   **B)**
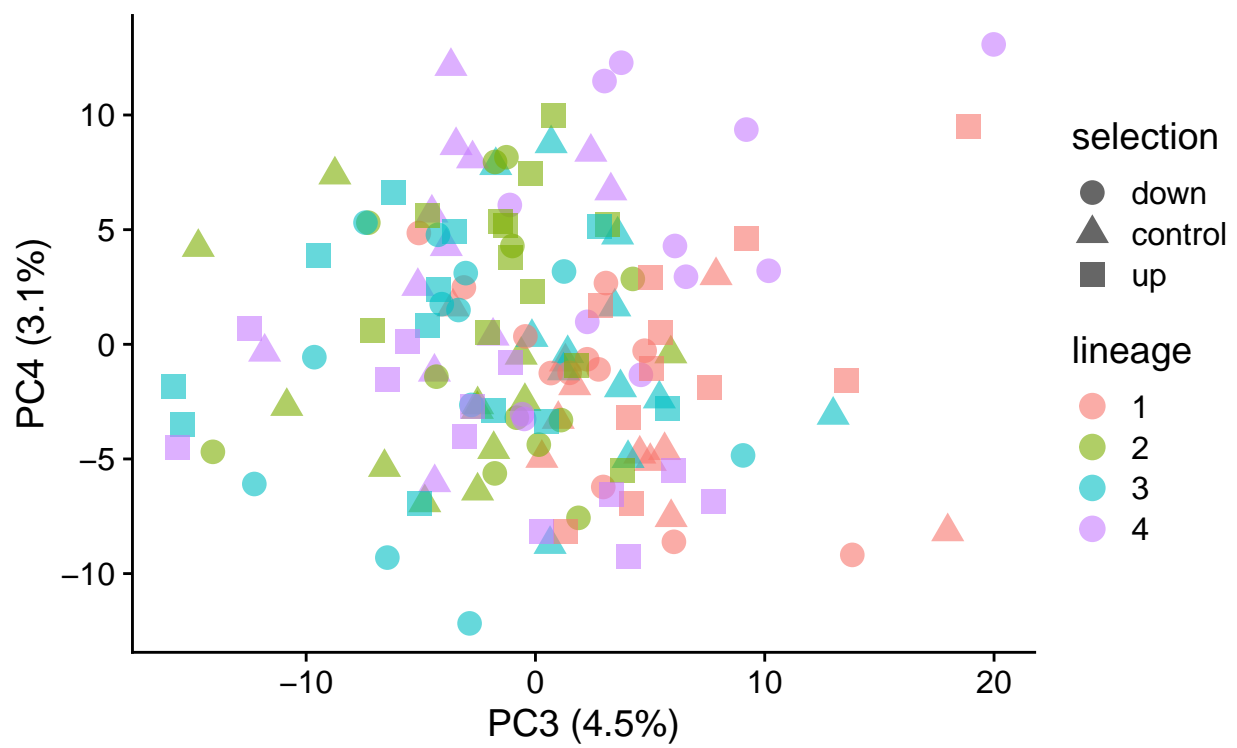

PC 3 vs 4, 5000 genes

```
pca_3v4_5000 <- plot_pca(vsd, PC_x = 3, PC_y = 4,
                 color_by = "lineage", shape_by = "selection",
                 n_feats = 5000, #number of genes
                 scale_feats = FALSE, # we have already scaled these
                 point_rel_size = 4,
                 point_alpha = 0.6)
```
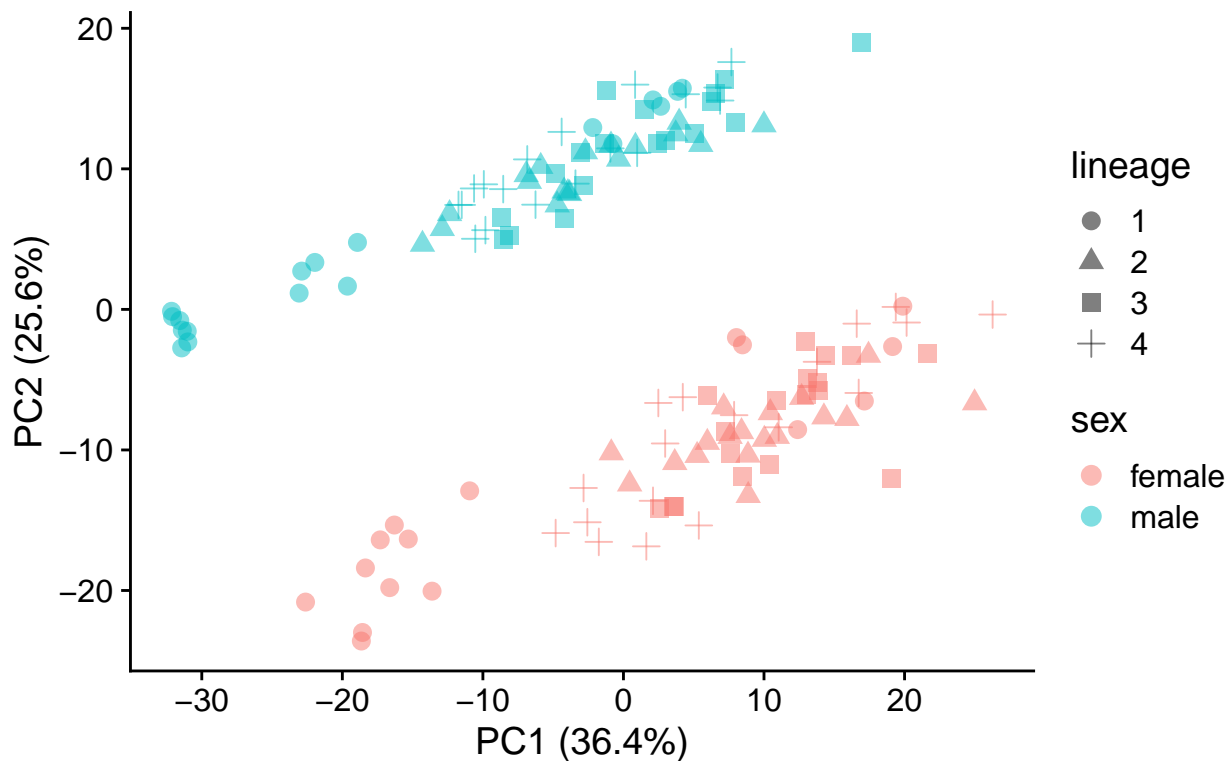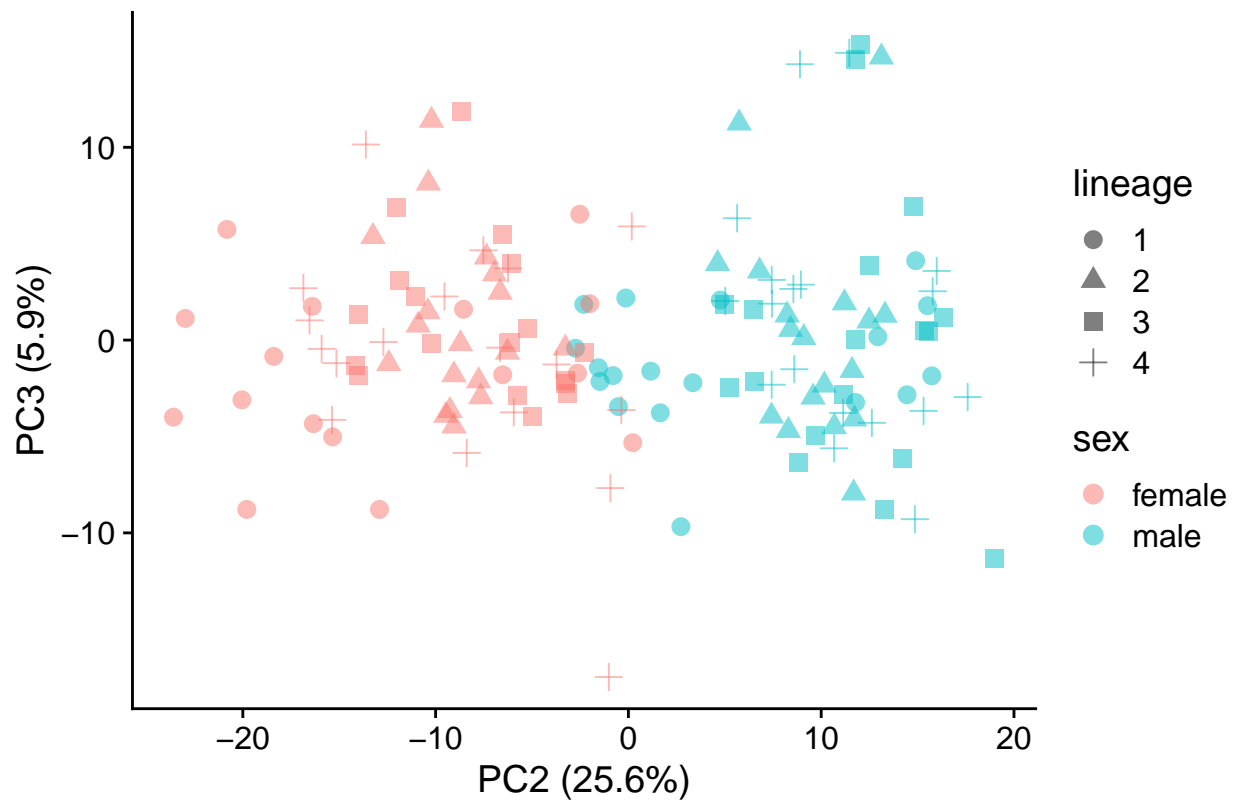
pca_3v4_5000$plot

Now colouring by sex and shape by lineage

Sex & Lineage PC 1 vs 2 and 2 vs 3, 500 genes

```r
sex_pca_1v2_500 <- plot_pca(vsd, PC_x = 1, PC_y = 2,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 500, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 3,
                    point_alpha = 0.5)
```



```r
sex_pca_2v3_500 <- plot_pca(vsd, PC_x = 2, PC_y = 3,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 500, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 3,
                    point_alpha = 0.5)
```
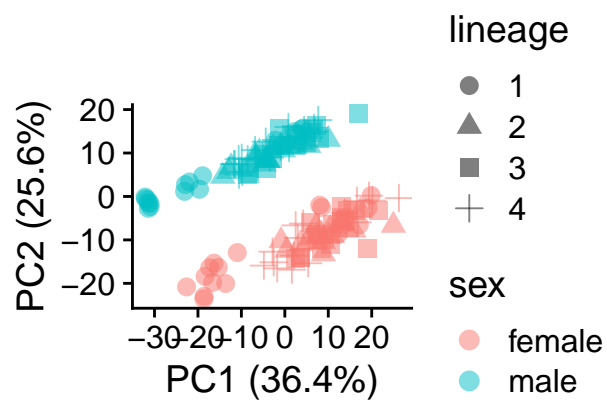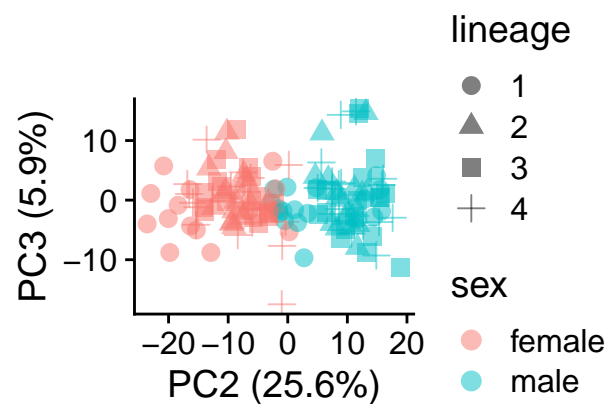
```
plot_grid(sex_pca_1v2_500$plot, sex_pca_2v3_500$plot,
          nrow = 1, ncol = 2,
          labels = c("A)", "B)"))
```

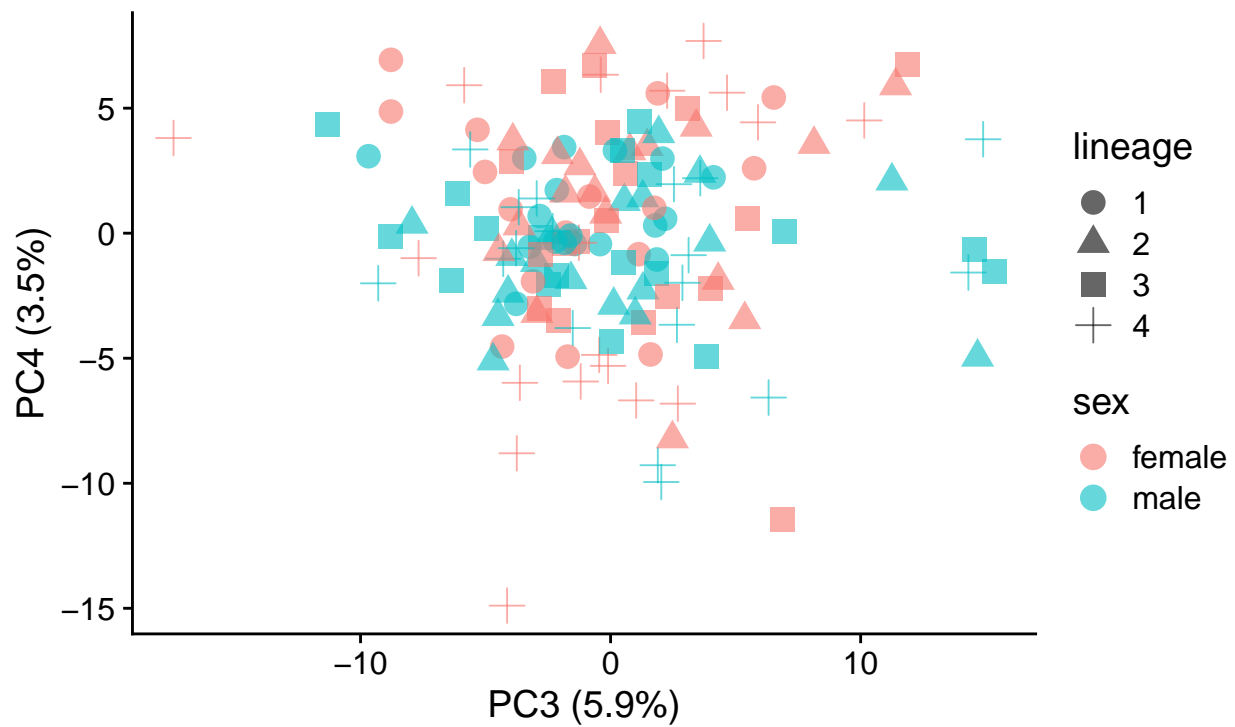**A)**   **B)**
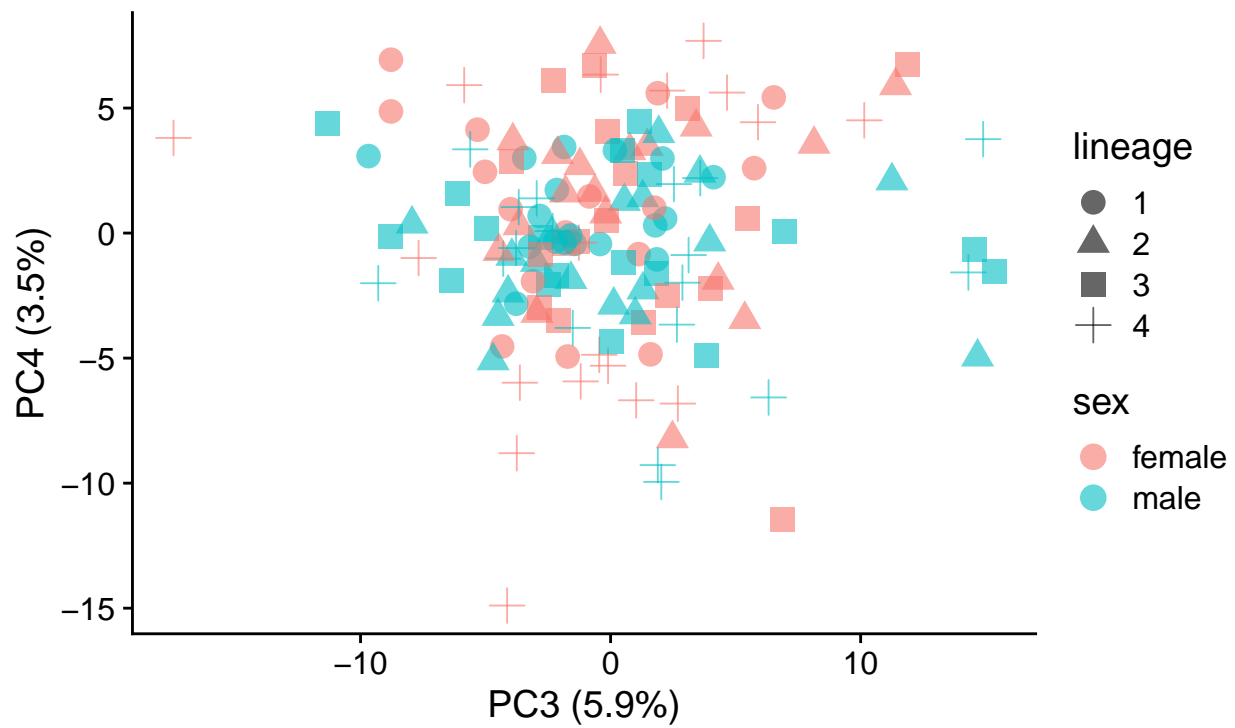

Sex & Lineage PC 3 vs 4, 500 genes

```
sex_pca_3v4_500 <- plot_pca(vsd, PC_x = 3, PC_y = 4,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 500, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 4,
                    point_alpha = 0.6)
```



```
sex_pca_3v4_500$plot
```

Sex & Lineage PC 1 vs 2 and 2 vs 3, 1000 genes

```
sex_pca_1v2_1000 <- plot_pca(vsd, PC_x = 1, PC_y = 2,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 1000, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 3,
                    point_alpha = 0.5)
```
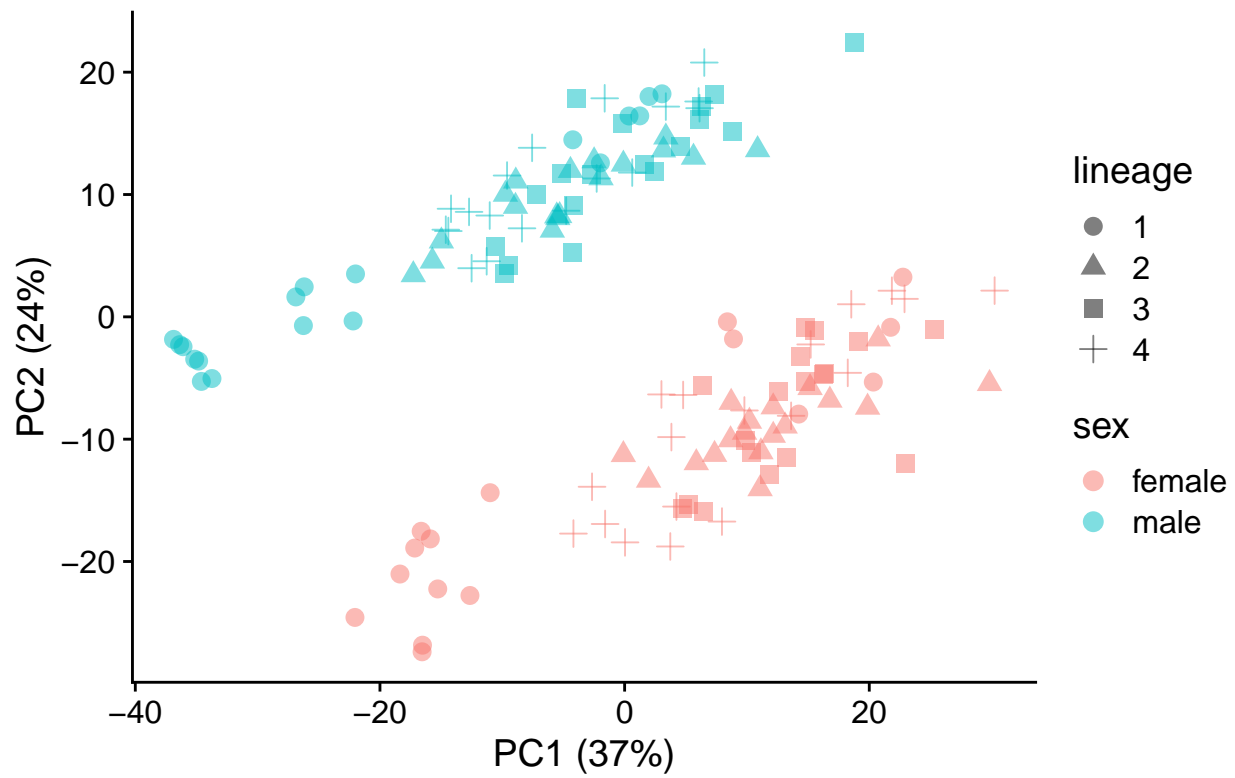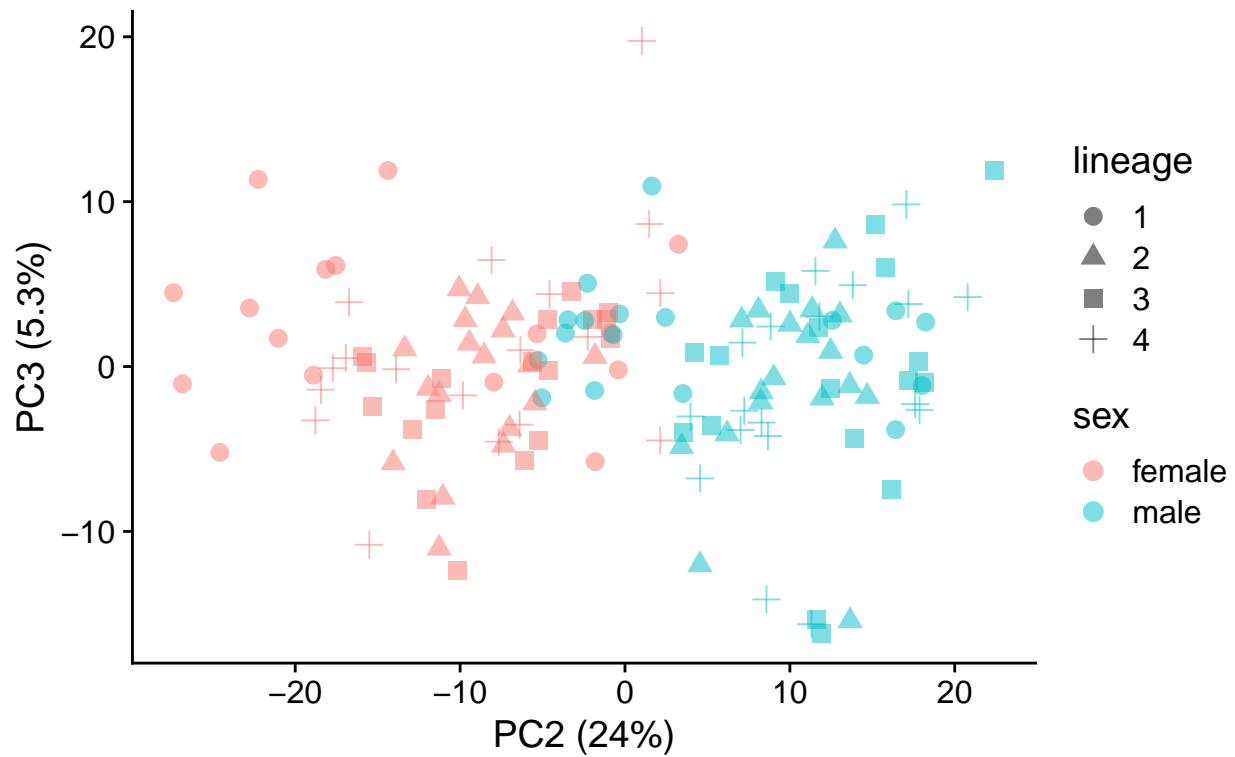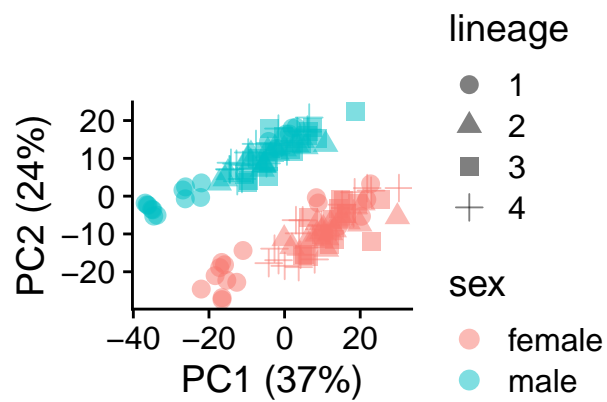
```
sex_pca_2v3_1000 <- plot_pca(vsd, PC_x = 2, PC_y = 3,
                  color_by = "sex", shape_by = "lineage",
                  n_feats = 1000, #number of genes
                  scale_feats = FALSE, # we have already scaled these
                  point_rel_size = 3,
                  point_alpha = 0.5)
```

```
plot_grid(sex_pca_1v2_1000$plot, sex_pca_2v3_1000$plot,
          nrow = 1, ncol = 2,
          labels = c("A)", "B)"))
```
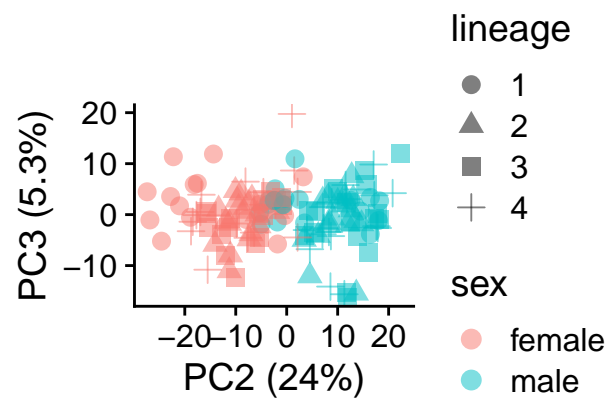
A)   **B)**
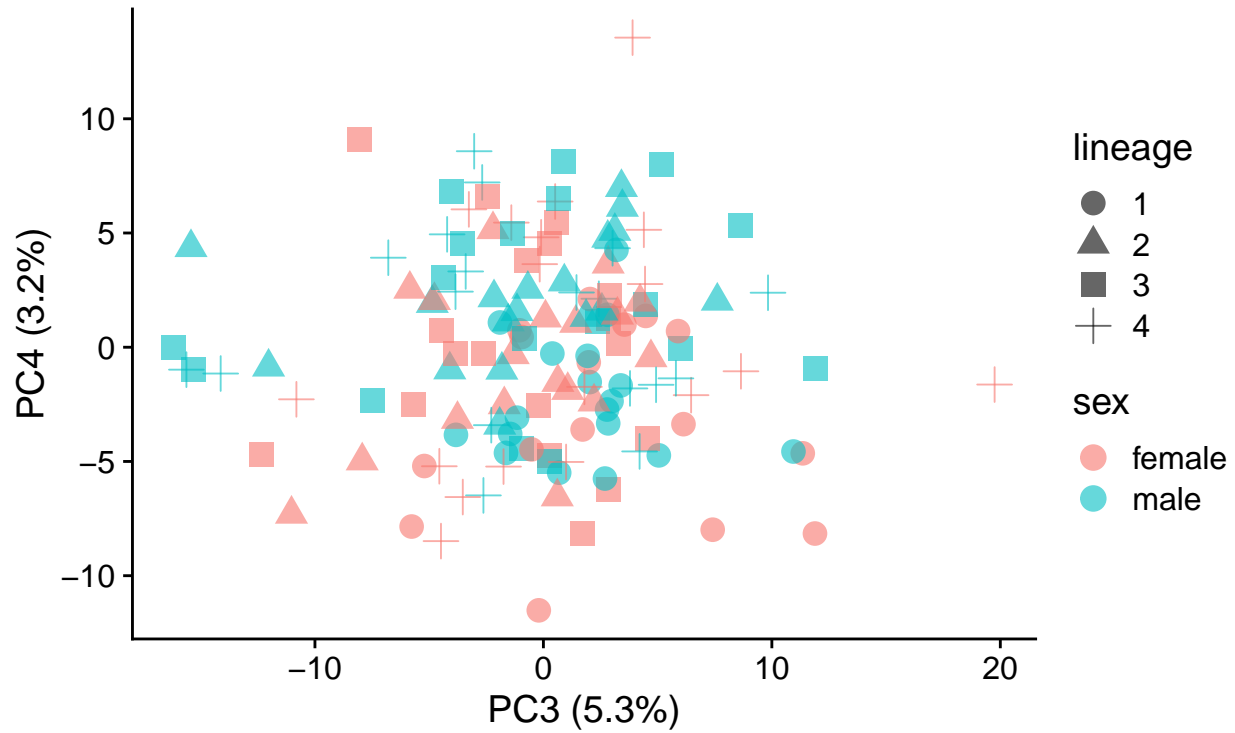

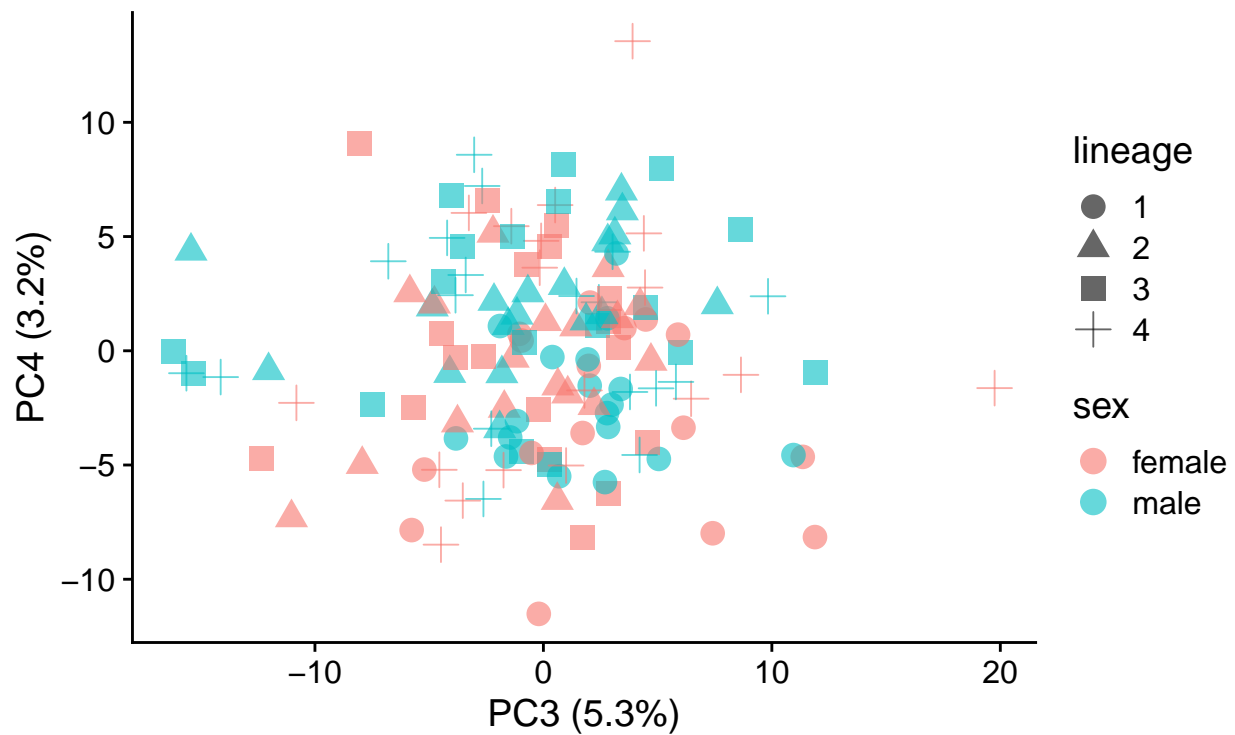Sex & Lineage PC 3 vs 4, 1000 genes

```
sex_pca_3v4_1000 <- plot_pca(vsd, PC_x = 3, PC_y = 4,
                    color_by = "sex", shape_by = "lineage",
```

```
n_feats = 1000, #number of genes
scale_feats = FALSE, # we have already scaled these
point_rel_size = 4,
point_alpha = 0.6)
```



```
sex_pca_3v4_1000$plot
```

Sex & Lineage PC 1 vs 2 and 2 vs 3, 5000 genes

```
sex_pca_1v2_5000 <- plot_pca(vsd, PC_x = 1, PC_y = 2,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 5000, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 3,
                    point_alpha = 0.5)
```
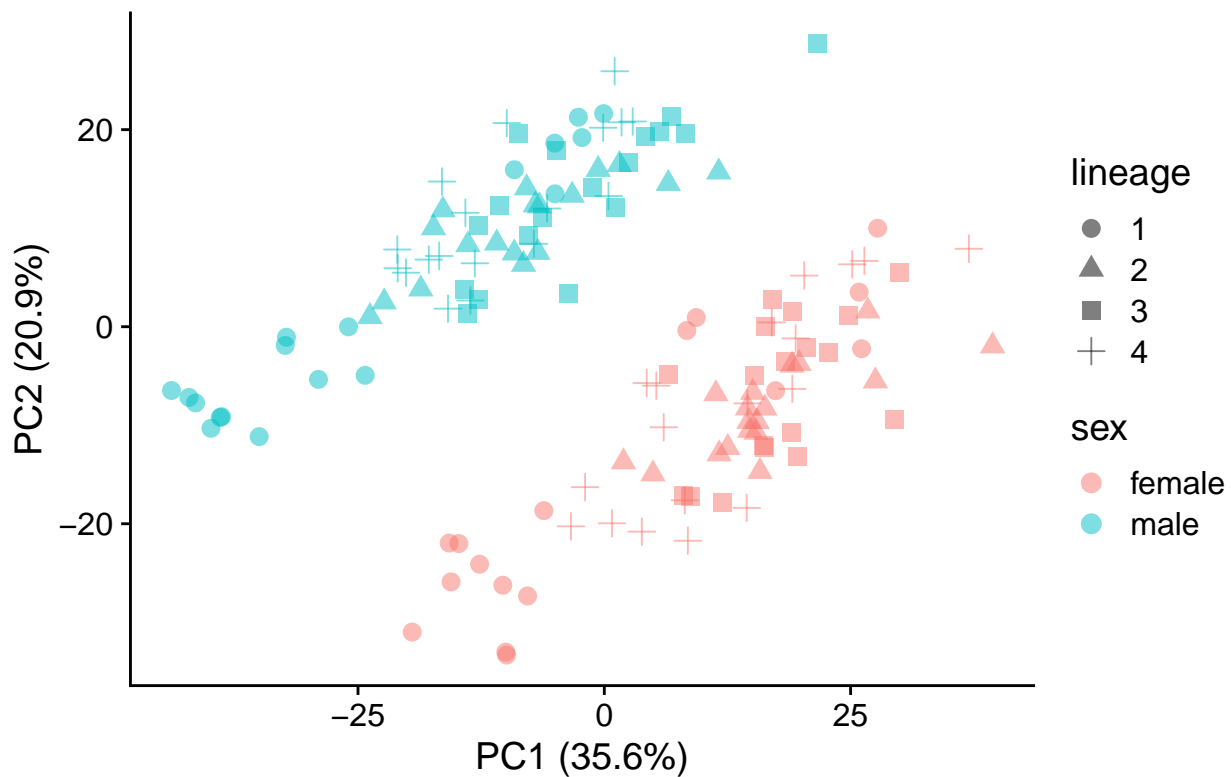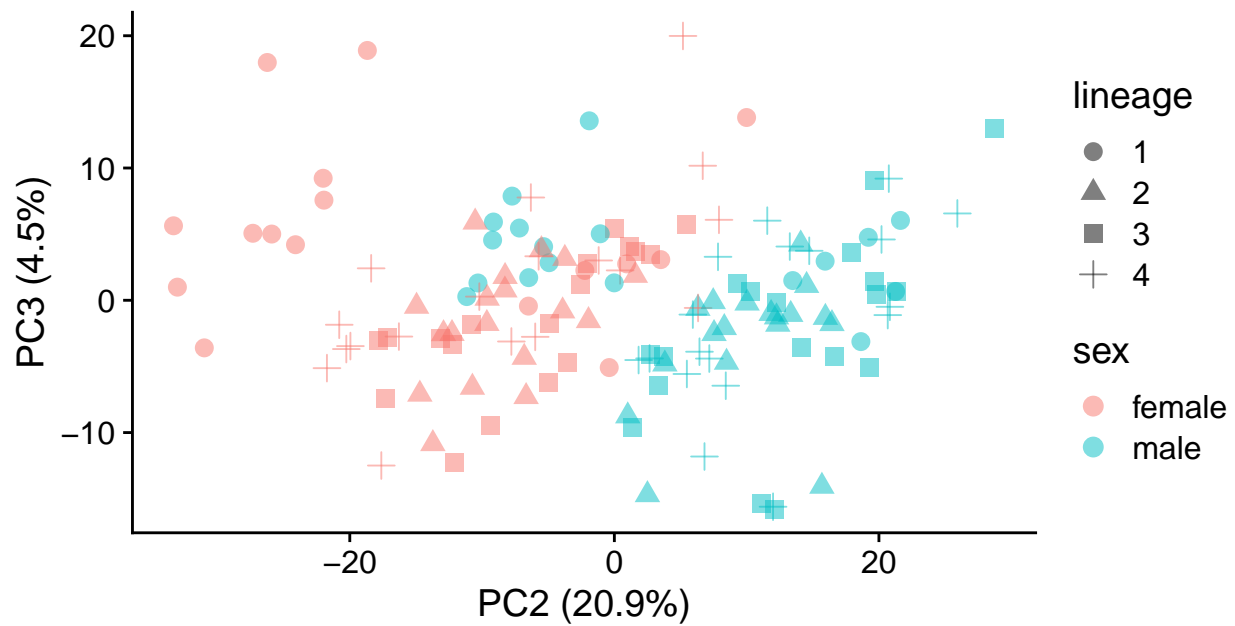

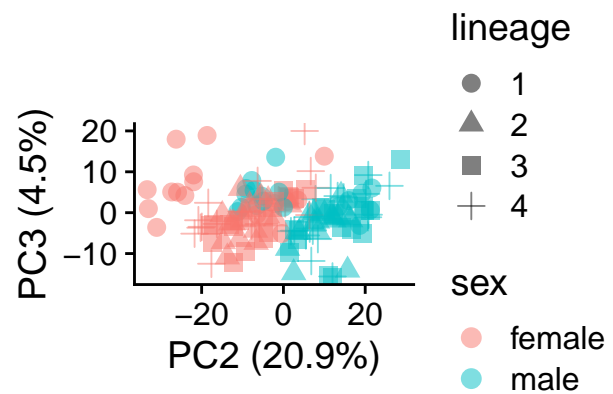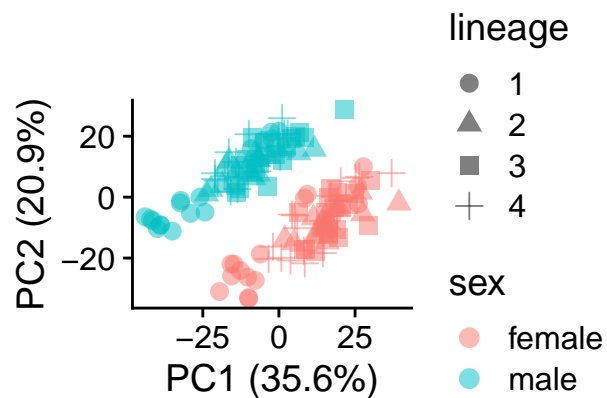```
sex_pca_2v3_5000 <- plot_pca(vsd, PC_x = 2, PC_y = 3,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 5000, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 3,
                    point_alpha = 0.5)
```

```
plot_grid(sex_pca_1v2_5000$plot, sex_pca_2v3_5000$plot,
          nrow = 1, ncol = 2,
          labels = c("A)", "B)"))
```
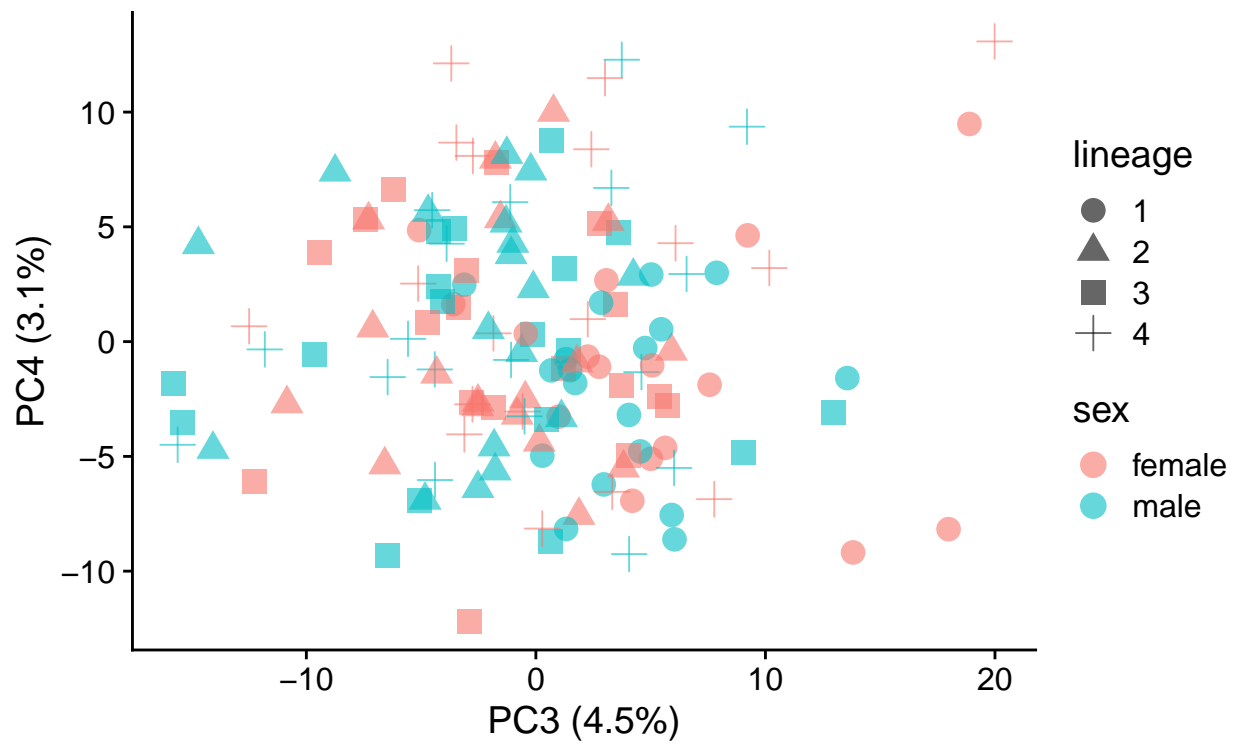
**A)**                                    **B)**



Sex & Lineage PC 3 vs 4, 5000 genes

```
sex_pca_3v4_5000 <- plot_pca(vsd, PC_x = 3, PC_y = 4,
                    color_by = "sex", shape_by = "lineage",
                    n_feats = 5000, #number of genes
                    scale_feats = FALSE, # we have already scaled these
                    point_rel_size = 4,
                    point_alpha = 0.6)
```

sex_pca_3v4_5000$plot