

analysis

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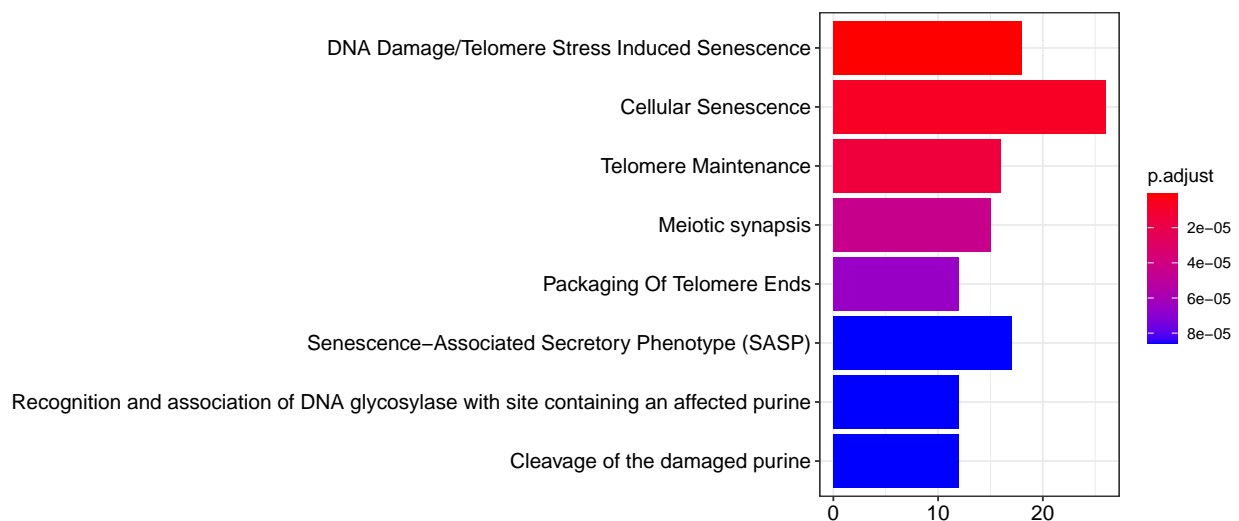
14 July, 2020

1000 genes that have high variability in tumor and normal

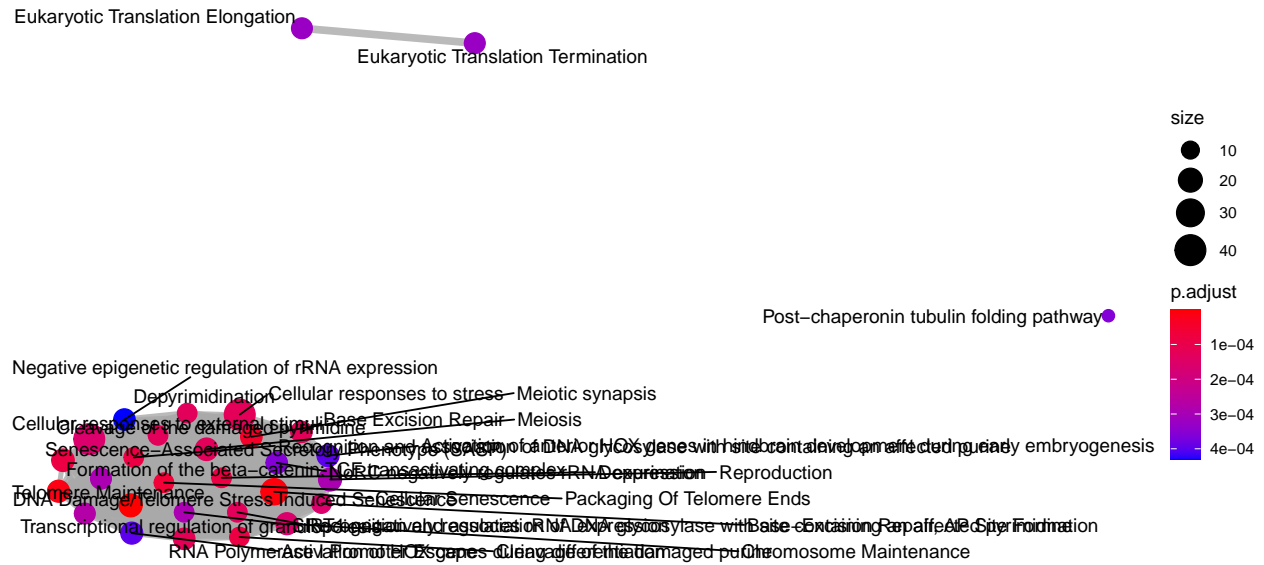
```
as.data.frame(gene_gsea_upper_right) %>%  
  select(ID, Description) %>%  
  as_tibble()
```

```
## # A tibble: 114 x 2  
##   ID          Description  
##   <chr>      <chr>  
## 1 R-HSA-25595~ DNA Damage/Telomere Stress Induced Senescence  
## 2 R-HSA-25595~ Cellular Senescence  
## 3 R-HSA-157579 Telomere Maintenance  
## 4 R-HSA-12216~ Meiotic synapsis  
## 5 R-HSA-171306 Packaging Of Telomere Ends  
## 6 R-HSA-25595~ Senescence-Associated Secretory Phenotype (SASP)  
## 7 R-HSA-110330 Recognition and association of DNA glycosylase with site containi-  
## 8 R-HSA-110331 Cleavage of the damaged purine  
## 9 R-HSA-73927  Depurination  
## 10 R-HSA-73772 RNA Polymerase I Promoter Escape  
## # ... with 104 more rows
```

```
barplot(gene_gsea_upper_right)
```



```
emapplot(gene_gsea_upper_right)
```

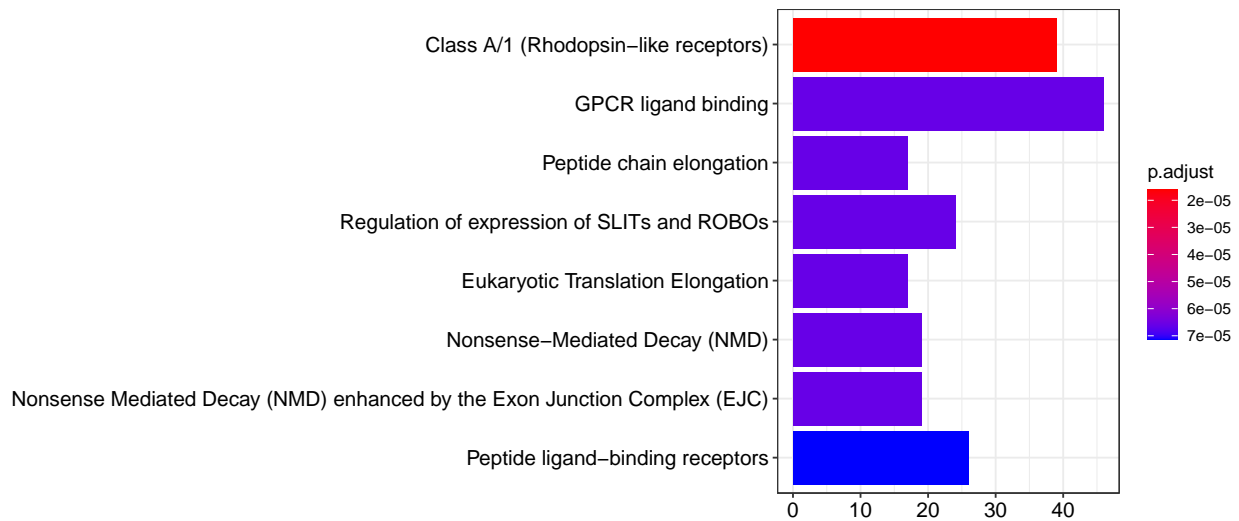


1000 genes that have low variability in tumor and normal

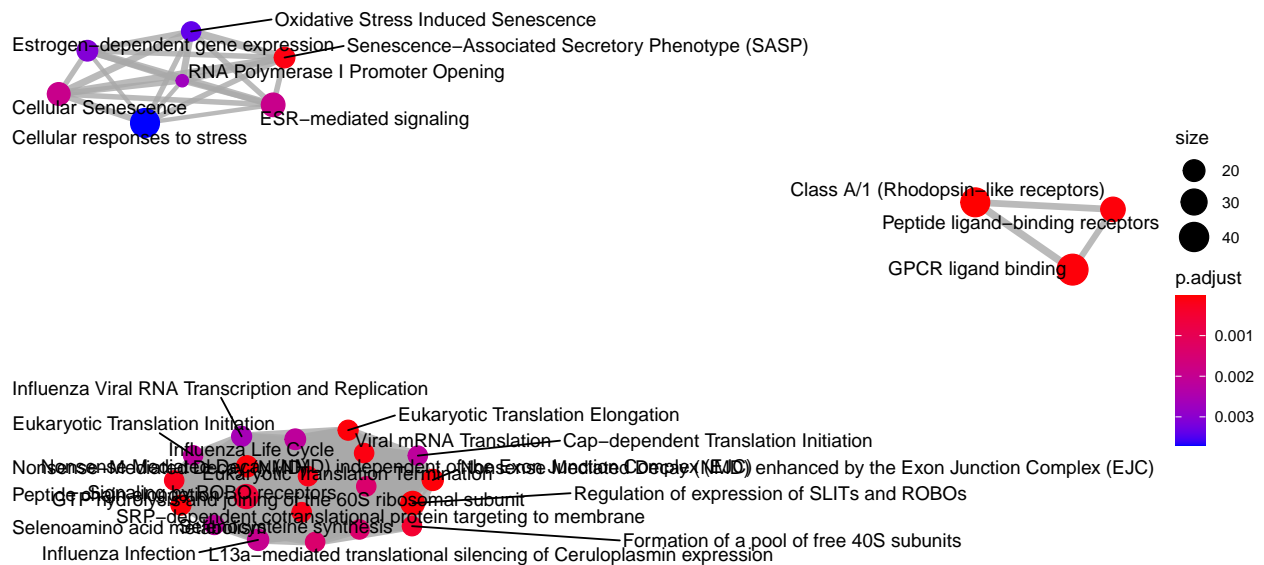
```
as.data.frame(gene_gsea_upper_left) %>%
  select(ID, Description) %>%
  as_tibble()
```

```
## # A tibble: 59 x 2
##   ID          Description
##   <chr>      <chr>
## 1 R-HSA-373076 Class A/1 (Rhodopsin-like receptors)
## 2 R-HSA-500792 GPCR ligand binding
## 3 R-HSA-156902 Peptide chain elongation
## 4 R-HSA-90105~ Regulation of expression of SLITs and ROBOs
## 5 R-HSA-156842 Eukaryotic Translation Elongation
## 6 R-HSA-927802 Nonsense-Mediated Decay (NMD)
## 7 R-HSA-975957 Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Com-
## 8 R-HSA-375276 Peptide ligand-binding receptors
## 9 R-HSA-25595~ Senescence-Associated Secretory Phenotype (SASP)
## 10 R-HSA-192823 Viral mRNA Translation
## # ... with 49 more rows
```

```
barplot(gene_gsea_upper_left)
```



```
emapplot(gene_gsea_upper_left)
```



1000 where variability is higher for tumor than in normal

```
as.data.frame(gene_gsea_lower_right) %>%
  select(ID, Description) %>%
  as_tibble()
```

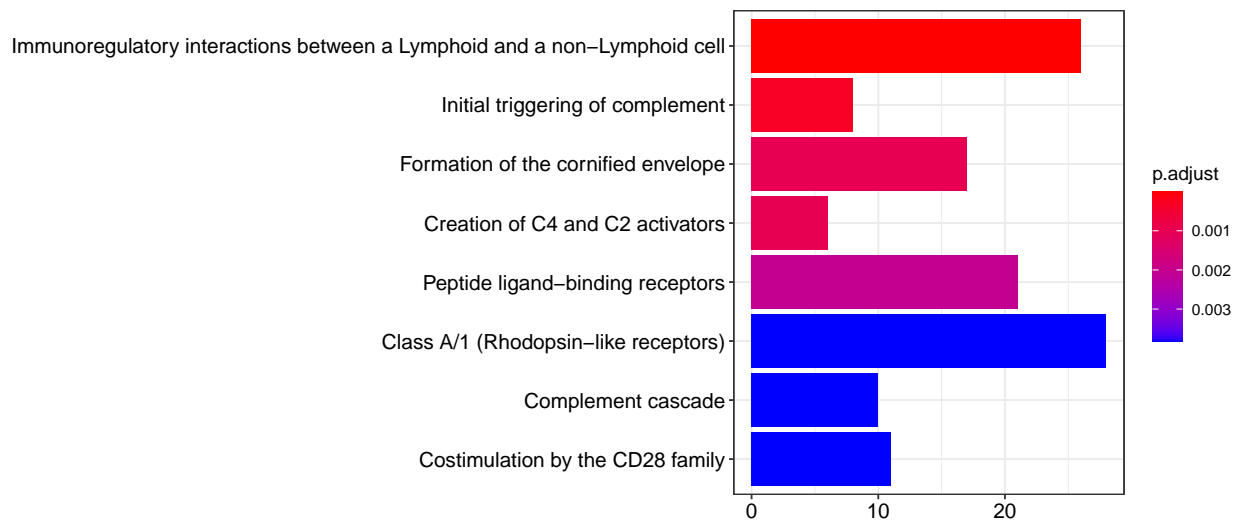
```
## # A tibble: 15 x 2
##   ID           Description
##   <chr>        <chr>
## 1 R-HSA-198933 Immunoregulatory interactions between a Lymphoid and a non-Lymp~
## 2 R-HSA-166663 Initial triggering of complement
```

```

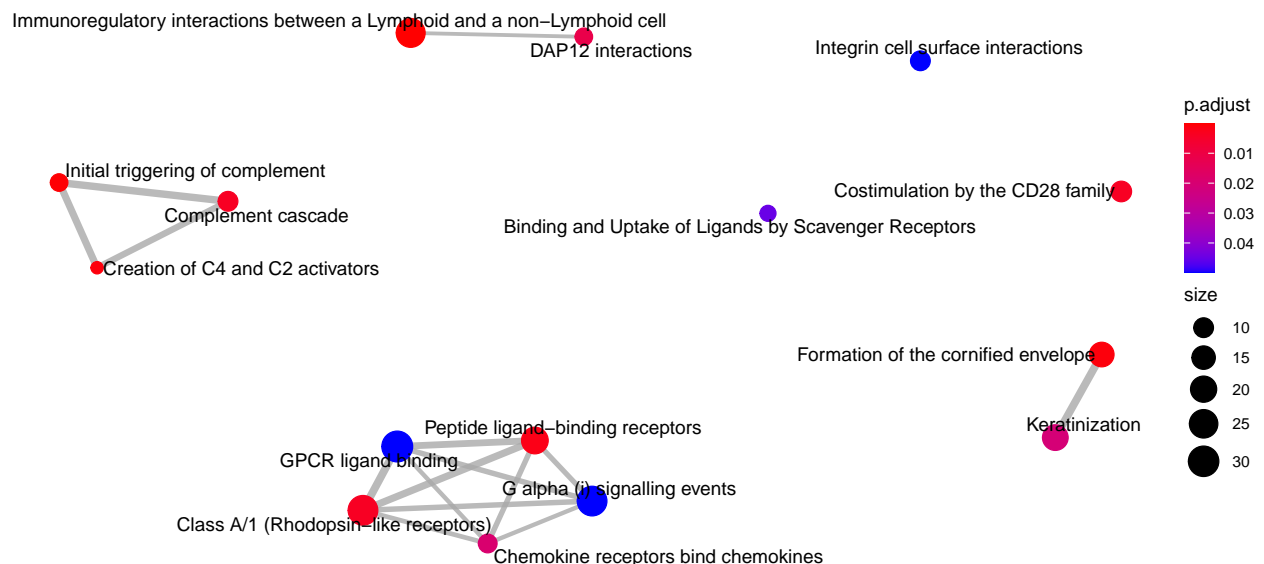
## 3 R-HSA-68093~ Formation of the cornified envelope
## 4 R-HSA-166786 Creation of C4 and C2 activators
## 5 R-HSA-375276 Peptide ligand-binding receptors
## 6 R-HSA-373076 Class A/1 (Rhodopsin-like receptors)
## 7 R-HSA-166658 Complement cascade
## 8 R-HSA-388841 Costimulation by the CD28 family
## 9 R-HSA-21721~ DAP12 interactions
## 10 R-HSA-380108 Chemokine receptors bind chemokines
## 11 R-HSA-68055~ Keratinization
## 12 R-HSA-21737~ Binding and Uptake of Ligands by Scavenger Receptors
## 13 R-HSA-418594 G alpha (i) signalling events
## 14 R-HSA-500792 GPCR ligand binding
## 15 R-HSA-216083 Integrin cell surface interactions

```

```
barplot(gene_gsea_lower_right)
```



```
emapplot(gene_gsea_lower_right)
```

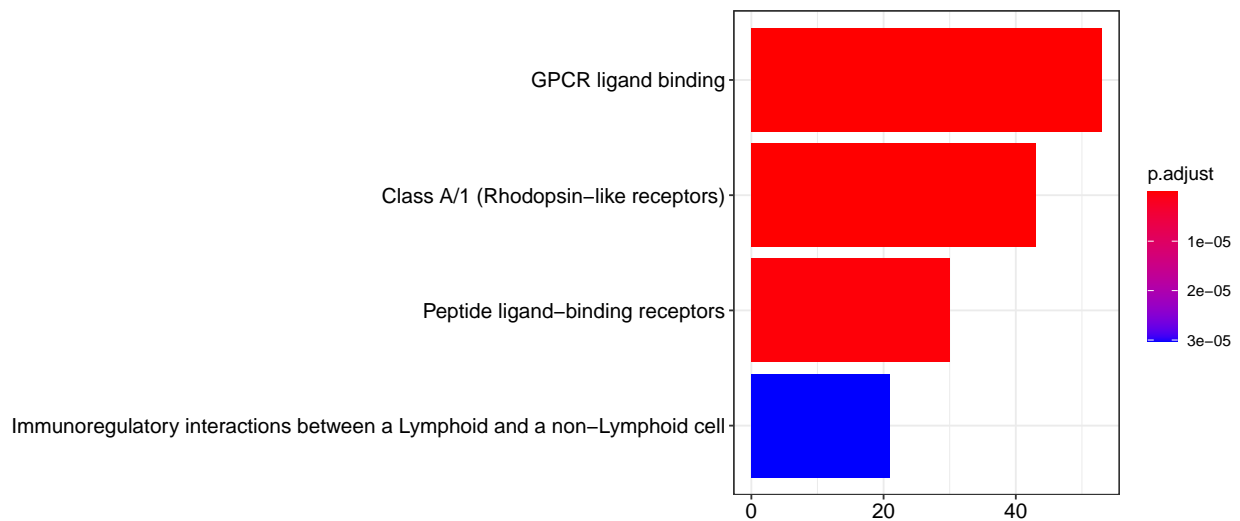


1000 where variability is higher for normal than in tumor

```
as.data.frame(gene_gsea_lower_left) %>%  
  select(ID, Description) %>%  
  as_tibble()
```

```
## # A tibble: 4 x 2  
##   ID           Description  
##   <chr>        <chr>  
## 1 R-HSA-500792 GPCR ligand binding  
## 2 R-HSA-373076 Class A/1 (Rhodopsin-like receptors)  
## 3 R-HSA-375276 Peptide ligand-binding receptors  
## 4 R-HSA-198933 Immunoregulatory interactions between a Lymphoid and a non-Lymph-
```

```
barplot(gene_gsea_lower_left)
```



```
emapplot(gene_gsea_lower_left)
```

Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell

