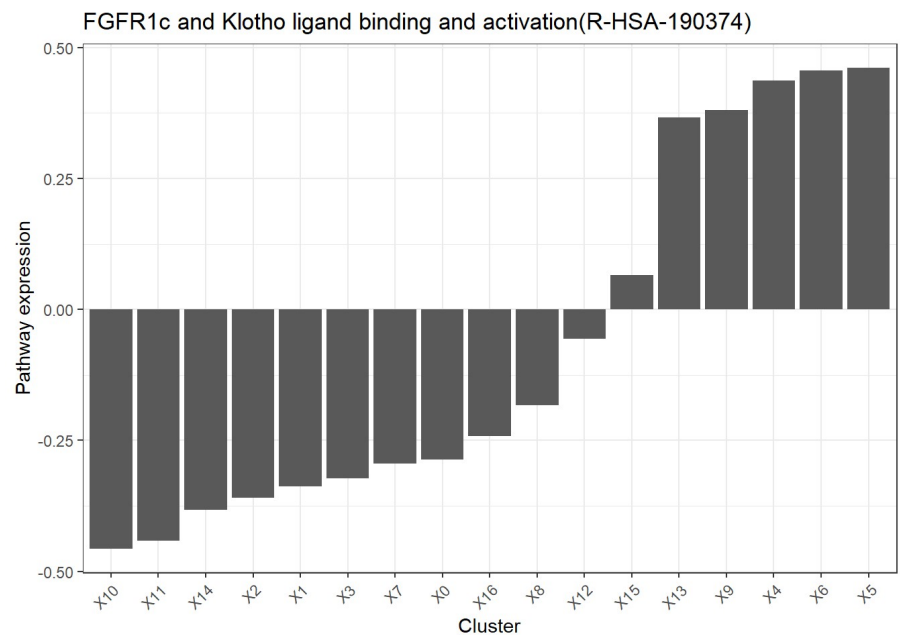


```
## R-HSA-390522 7.248471e-02 0.0883873016 0.015902595
## R-HSA-927802 2.016349e-01 0.2174535010 0.015818620
## R-HSA-975957 2.016349e-01 0.2174535010 0.015818620
## R-HSA-168643 1.074199e-01 0.1229019000 0.015481957
## R-HSA-5654738 7.126211e-02 0.0864816246 0.015219512
## R-HSA-202403 9.067312e-02 0.1058737000 0.015200578
## R-HSA-5621481 1.194739e-01 0.1342092000 0.014735295
## R-HSA-5358351 8.073733e-02 0.0944054100 0.013668082
## R-HSA-5610787 9.041418e-02 0.1035509100 0.013136728
## R-HSA-6804756 5.275690e-02 0.0658172372 0.013060336
## R-HSA-9758274 6.294461e-02 0.0756277184 0.012683111
## R-HSA-8948751 1.019816e-01 0.1141148052 0.012133202
## R-HSA-5218859 8.488693e-02 0.0967008966 0.011813962
## R-HSA-5357956 9.881083e-02 0.1103047658 0.011493934
## R-HSA-75893 9.500284e-02 0.1051410115 0.010138168
## R-HSA-5357905 9.809594e-02 0.1070763325 0.008980396
```

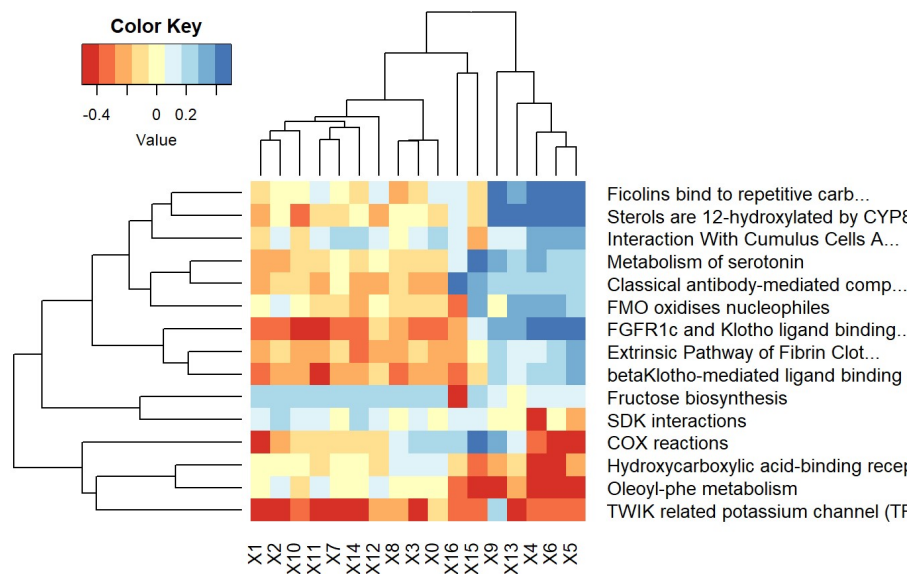
Pathways of interest:

```
plot_gsva_pathway(Reactome_pathways_object[[1]], pathway_id = rownames(Reactome_pathways_object[[3]])[1])
```



Same pathways showed as a heatmap:

```
plot_gsva_heatmap(Reactome_pathways_object[[1]], max_pathways = 15)
```



Relevant pathways based on user's list:

```
relevant_pathways <- c("R-HSA-983170", "R-HSA-388841", "R-HSA-2132295", "R-HS
A-983705", "R-HSA-5690714")
plot_gsva_heatmap(Reactome_pathways_object[[1]],
  pathway_ids = relevant_pathways,
  dendrogram = "col",
  scale = "row", # scale for each pathway
  key = FALSE,
  lwid=c(0.1,4))
```

