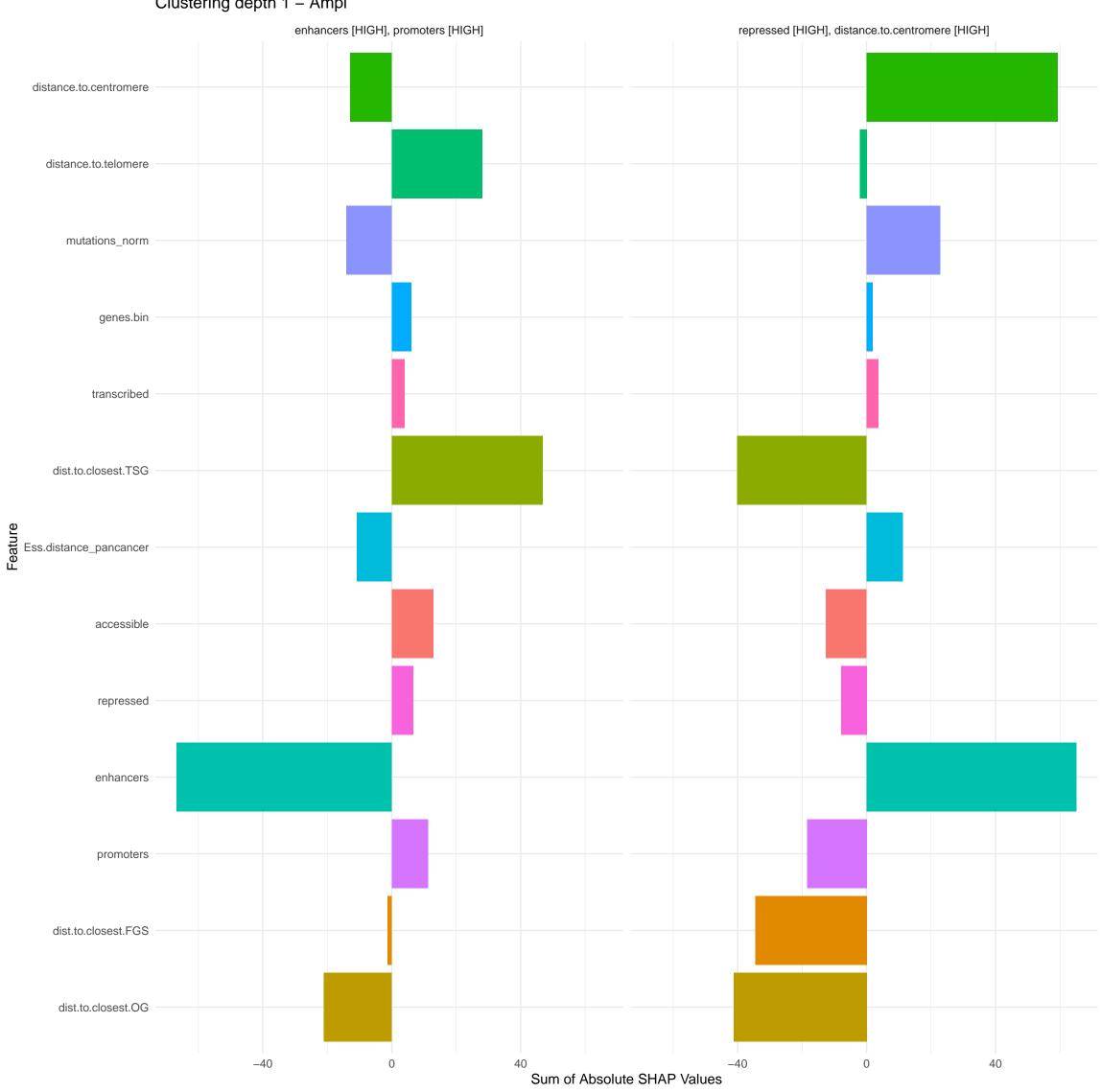
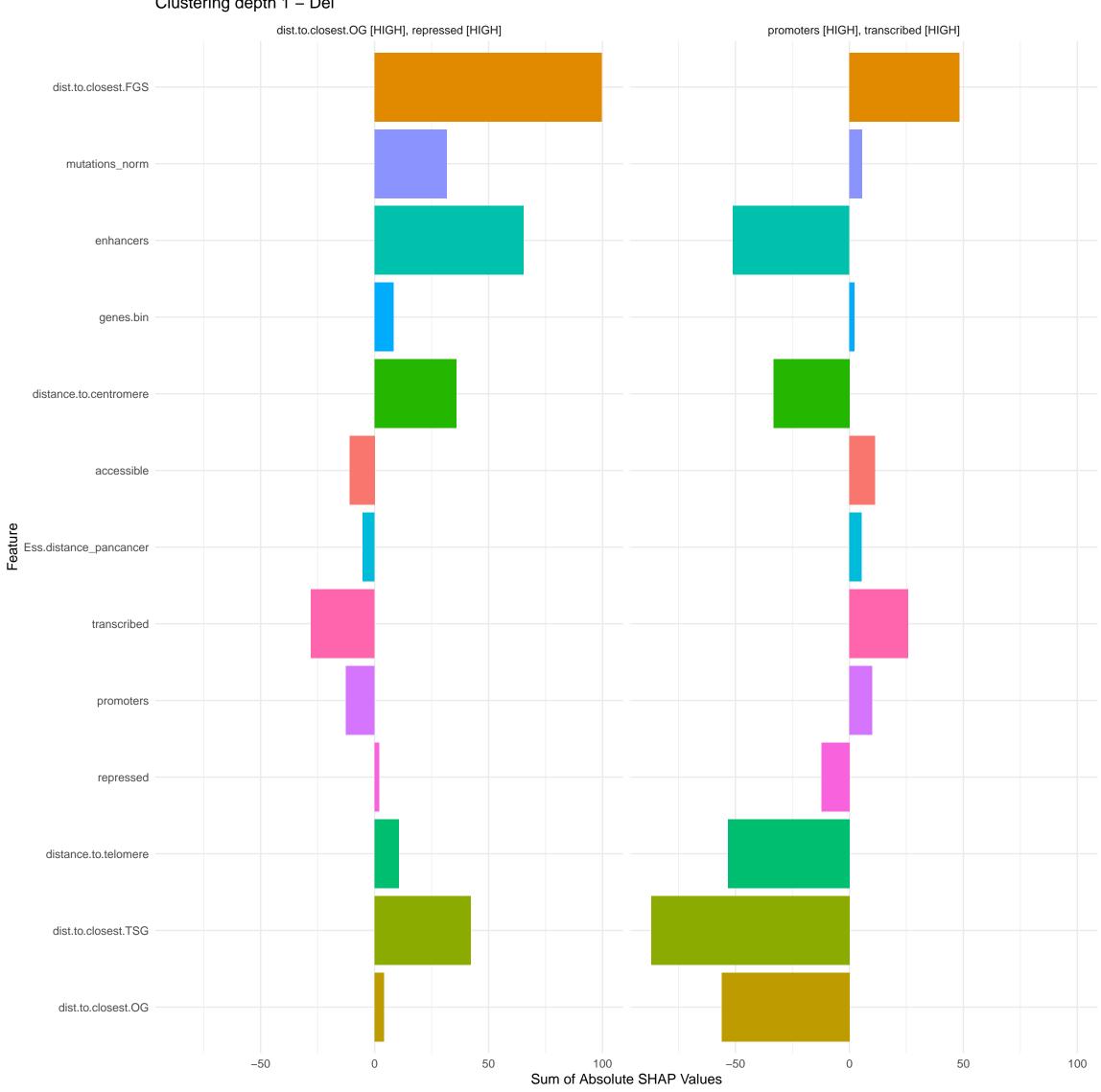
Clustering depth 1 – Ampl



Clustering depth 1 – Del



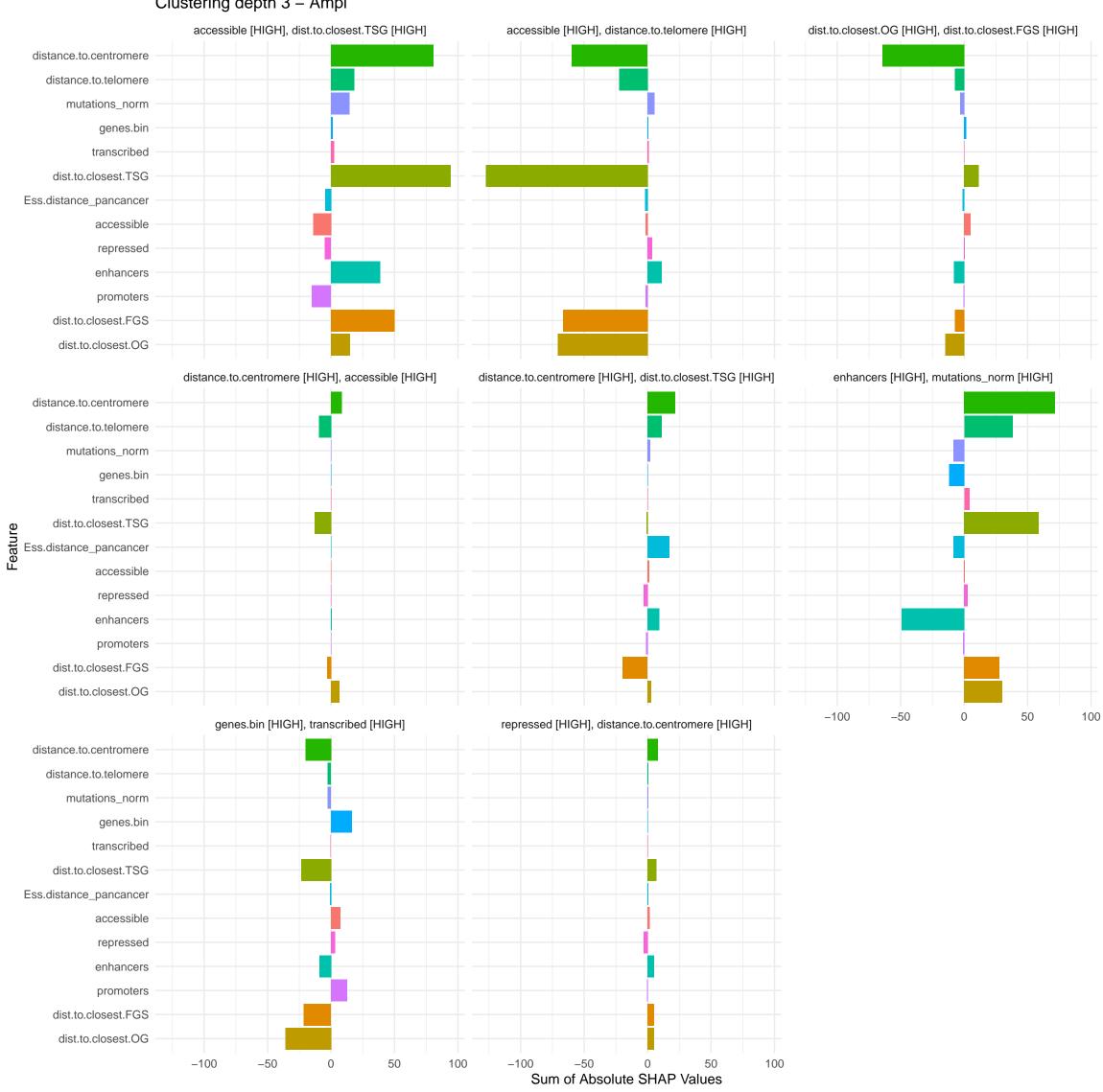
Clustering depth 2 – Ampl



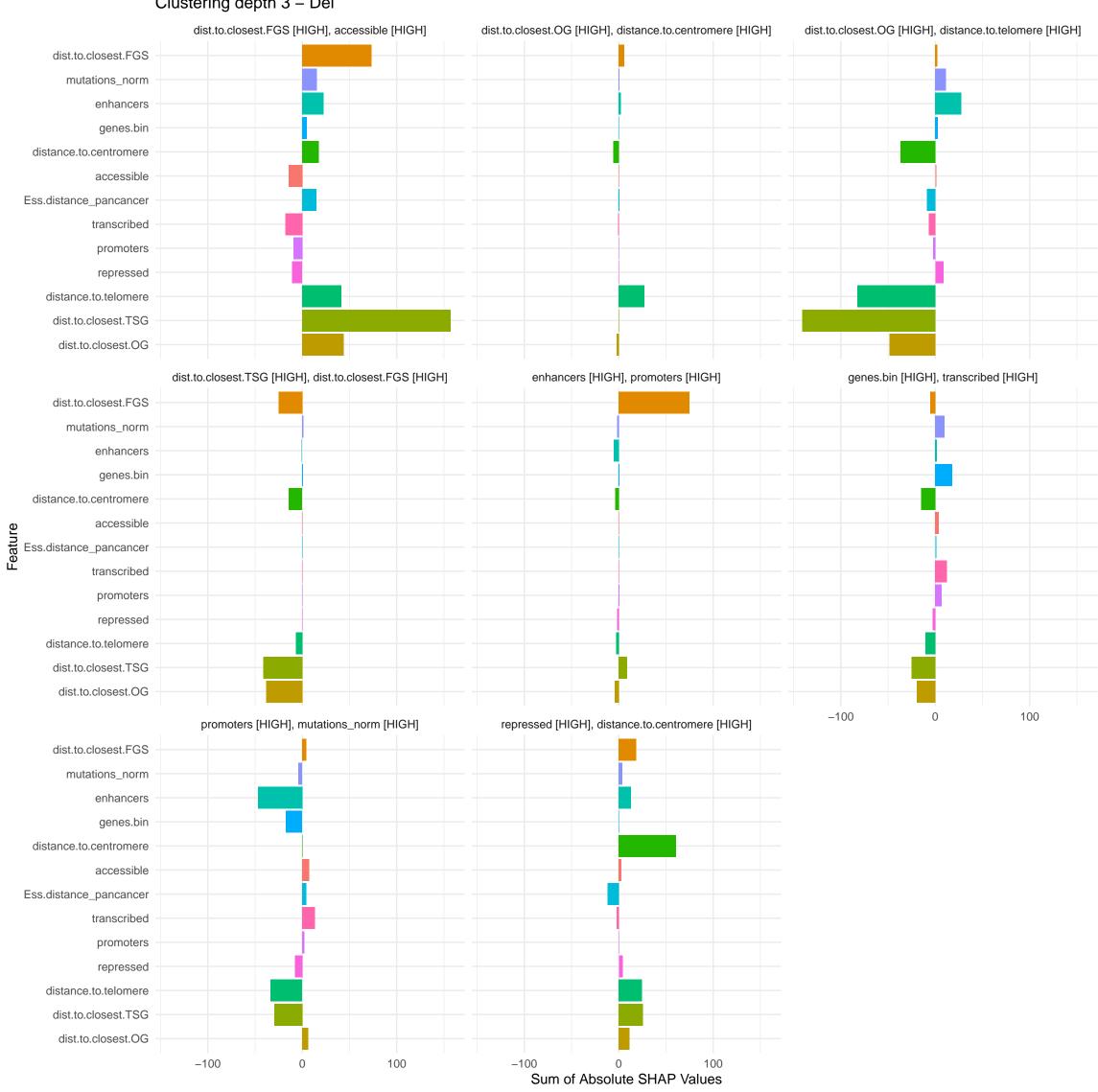
Clustering depth 2 – Del



Clustering depth 3 – Ampl



Clustering depth 3 - Del



## Clustering depth 4 - Ampl accessible [HIGH], dist.to.closest.FGS [HIGH] accessible [HIGH], distance.to.centromere [HIGH] accessible [HIGH], Ess.distance\_pancancer [HIC closest.FGS [HIGH], distance.to.centromere [HIGH], ess.distance.to.centromere [HIG distance.to.centromere distance.to.telomere mutations\_norm genes.bin transcribed dist.to.closest.TSG Ess.distance\_pancancer accessible repressed enhancers promoters dist.to.closest.FGS dist.to.closest.OG to.closest.OG [HIGH], dist.to.closest.FGS [HIL to.closest.OG [HIGH], dist.to.closest.TSG [HIL o.closest.TSG [HIGH], distance.to.telomere [H stance.to.centromere [HIGH], accessible [HIG distance.to.centromere distance.to.telomere mutations\_norm genes.bin transcribed dist.to.closest.TSG Ess.distance\_pancancer accessible repressed enhancers promoters dist.to.closest.FGS dist.to.closest.OG Feature ce.to.centromere [HIGH], dist.to.closest.OG [I stance.to.centromere [HIGH], repressed [HIGI enhancers [HIGH], promoters [HIGH] genes.bin [HIGH], transcribed [HIGH] distance.to.centromere distance.to.telomere mutations\_norm genes.bin transcribed dist.to.closest.TSG Ess.distance\_pancancer accessible repressed enhancers promoters dist.to.closest.FGS dist.to.closest.OG $mutations\_norm\ [HIGH],\ transcribed\ [HIGH]\quad pressed\ [HIGH],\ distance.to.centromere\ [HIGI^{-75}]$ -50 -25 25 mutations\_norm [HIGH], accessible [HIGH] distance.to.centromere distance.to.telomere mutations\_norm genes.bin transcribed dist.to.closest.TSG Ess.distance\_pancancer accessible repressed enhancers promoters dist.to.closest.FGS dist.to.closest.OG

25

-75

Sum of Absolute SHAP Values

-50

0

25

0

-50

-25

25

-75

-50

-25

## Clustering depth 4 – Del accessible [HIGH], dist.to.closest.FGS [HIGH] accessible [HIGH], enhancers [HIGH] >losest.FGS [HIGH], Ess.distance\_pancancer o.closest.TSG [HIGH], distance.to.telomere [H dist.to.closest.FGS mutations\_norm enhancers genes.bin distance.to.centromere accessible Ess.distance\_pancancer transcribed promoters repressed distance.to.telomere dist.to.closest.TSG dist.to.closest.OG ce.to.centromere [HIGH], dist.to.closest.OG [I stance.to.centromere [HIGH], repressed [HIGI Ince.to.telomere [HIGH], dist.to.closest.OG [H enhancers [HIGH], promoters [HIGH] dist.to.closest.FGS mutations\_norm enhancers genes.bin distance.to.centromere accessible Ess.distance\_pancancer transcribed promoters repressed distance.to.telomere dist.to.closest.TSG dist.to.closest.OG Feature genes.bin [HIGH], promoters [HIGH] stations\_norm [HIGH], dist.to.closest.OG [HIG mutations\_norm [HIGH], transcribed [HIGH] pressed [HIGH], distance.to.centromere [HIGH] dist.to.closest.FGS mutations\_norm enhancers genes.bin distance.to.centromere accessible Ess.distance\_pancancer transcribed promoters repressed distance.to.telomere dist.to.closest.TSG dist.to.closest.OG -100-100 -100transcribed [HIGH], genes.bin [HIGH] dist.to.closest.FGS mutations\_norm enhancers genes.bin distance.to.centromere accessible Ess.distance\_pancancer transcribed promoters repressed distance.to.telomere dist.to.closest.TSG dist.to.closest.OG -100 Sum of Absolute SHAP Values