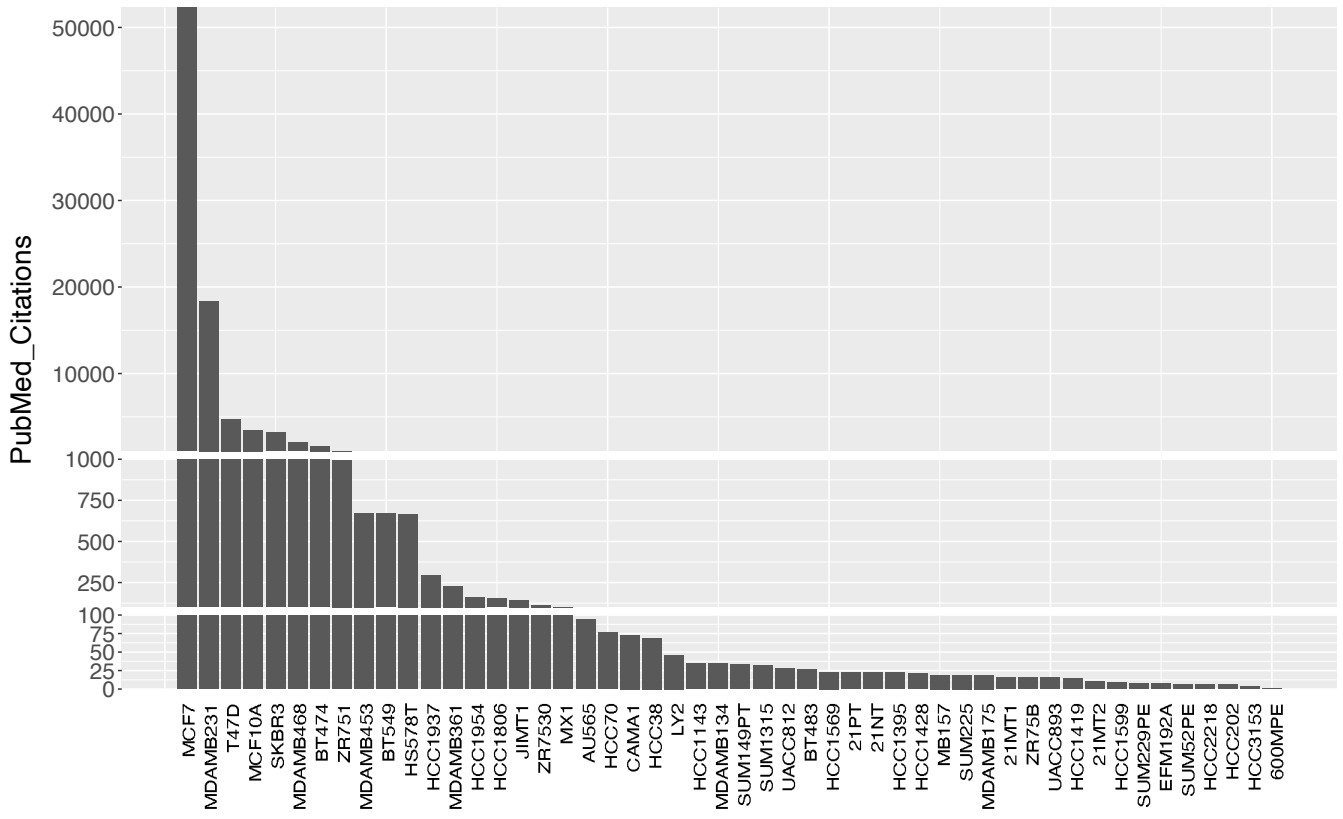# Figure S1



# Figure S2

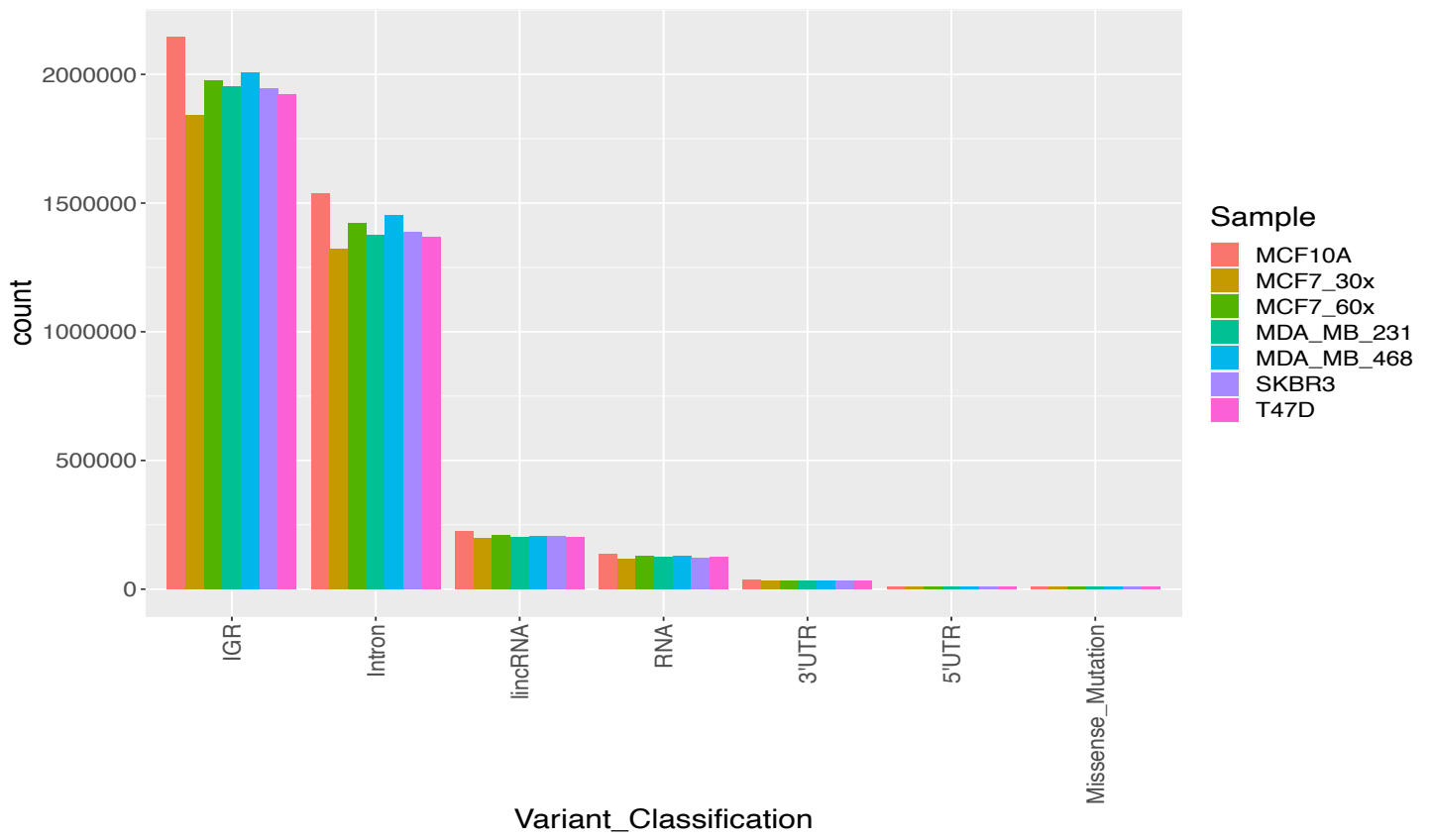Figure S3

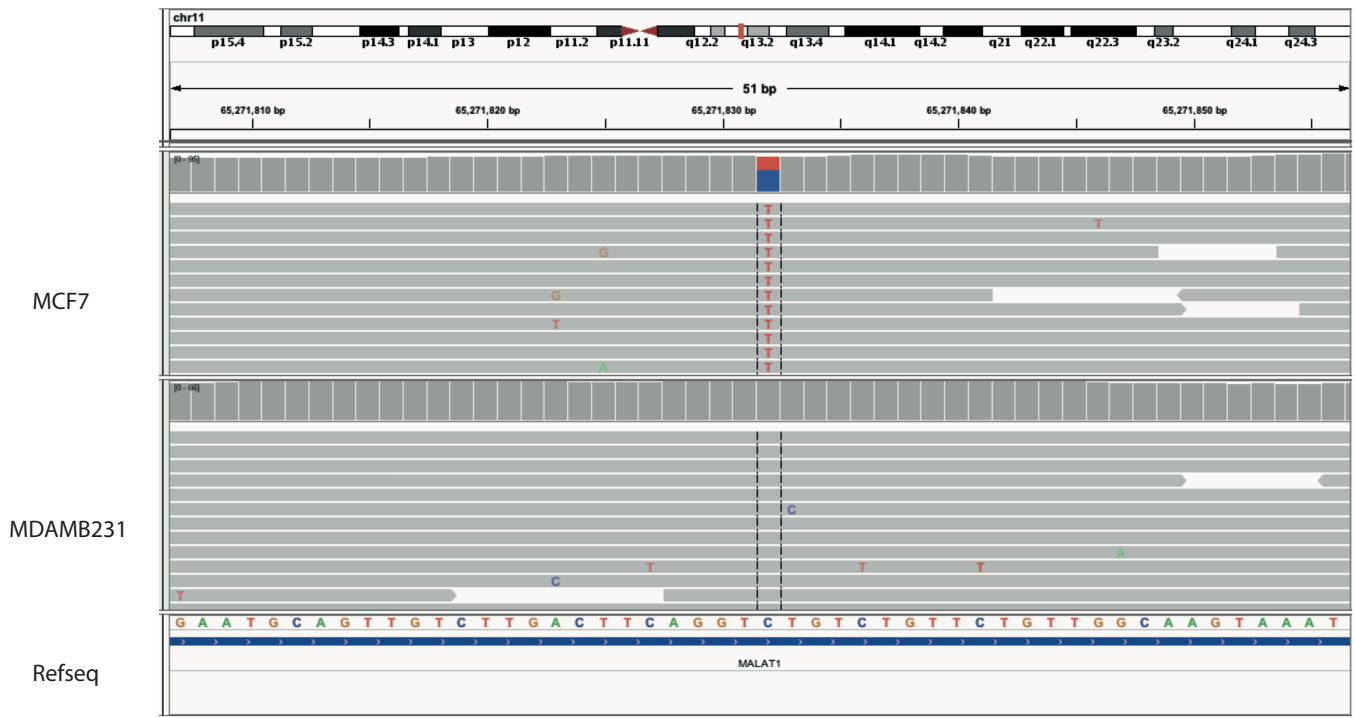# Figure S4
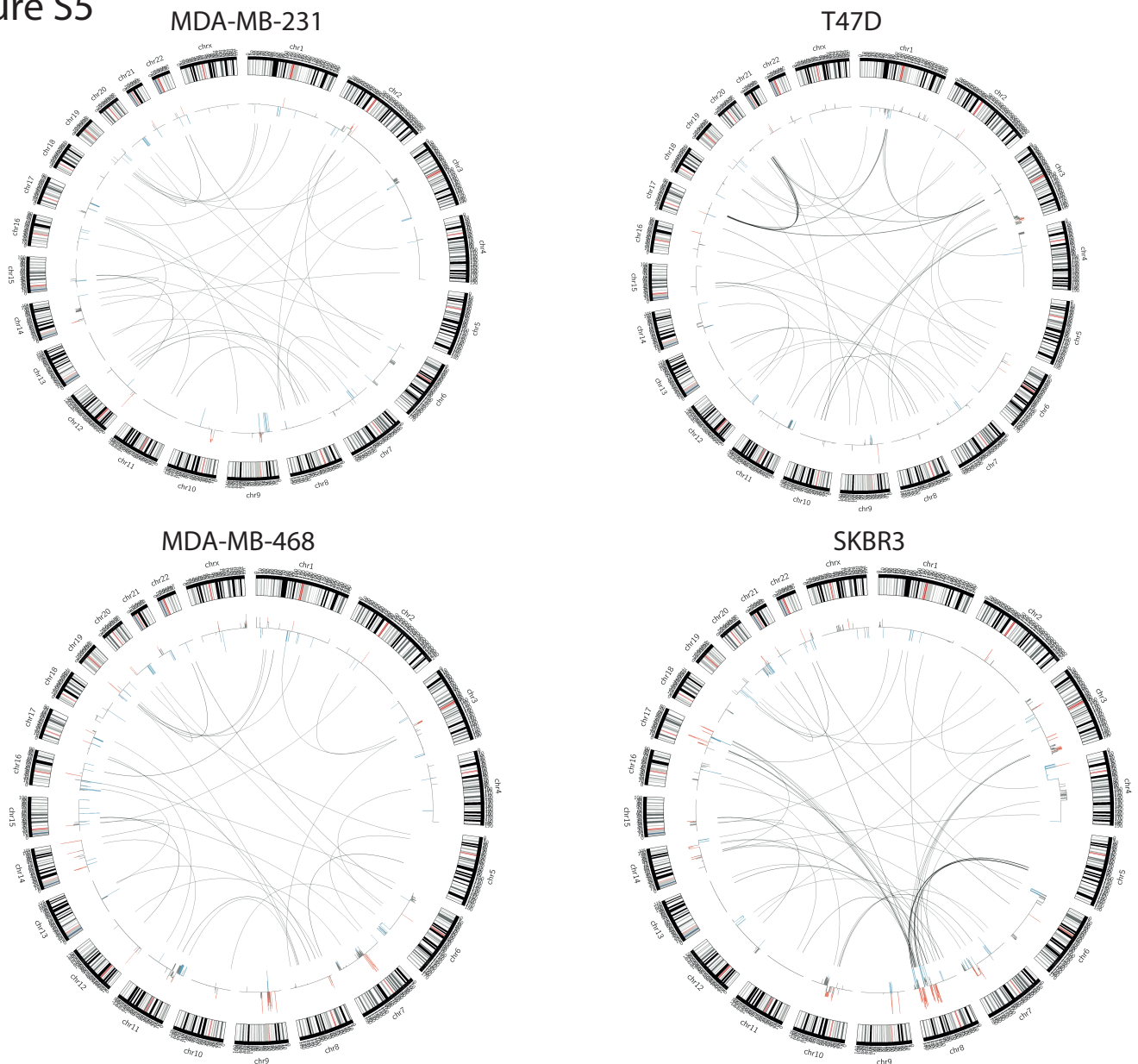


# Figure S5

# Figure S6

## MCF7

**MSigDB Perturbation**

-log10(Binomial p value)

| | | | | | | | | | | | |
|0|5|10|15|20|25|30|35|40|45|50|

Genes within amplicon 20q12-q13 identified in 191 breast tumours — **53.52**
Genes within amplicon 17q21-q25 identified in 191 breast tumours — **21.68**
Cluster 6: selected luminal genes clustered across breast tumours — **10.56**

## T47D

**MSigDB Perturbation**

-log10(Binomial p value)

| | | | | | | | | | | | |
|0|2|4|6|8|10|12|14|16|18|20|

Genes within amplicon 20q12-q13 identified in 191 breast tumours — **20.11**
Genes within amplicon 17q21-q25 identified in 191 breast tumours — **14.12**
Cluster 6: selected luminal genes clustered across breast tumours — **10.51**
Genes up-regulated with HEMGN in the TLX1 Tet on iEBHX15-4 cells — **10.23**

## SKBR3

**MSigDB Perturbation**

-log10(Binomial p value)

| | | | | | | | |
|0|2|4|6|8|10|12|14|

Genes within amplicon 8q23-q24 identified in 191 breast tumours — **14.53**
Genes down-regulated in HFK cells in response to UVB irradiation — **9.20**
Genes with putative STAT5 — **5.08**
Genes up-regulated by IL2 — **4.89**
Angiogenic markers down-regulated in HV (Kaposi's sarcoma herpes virus) — **4.87**
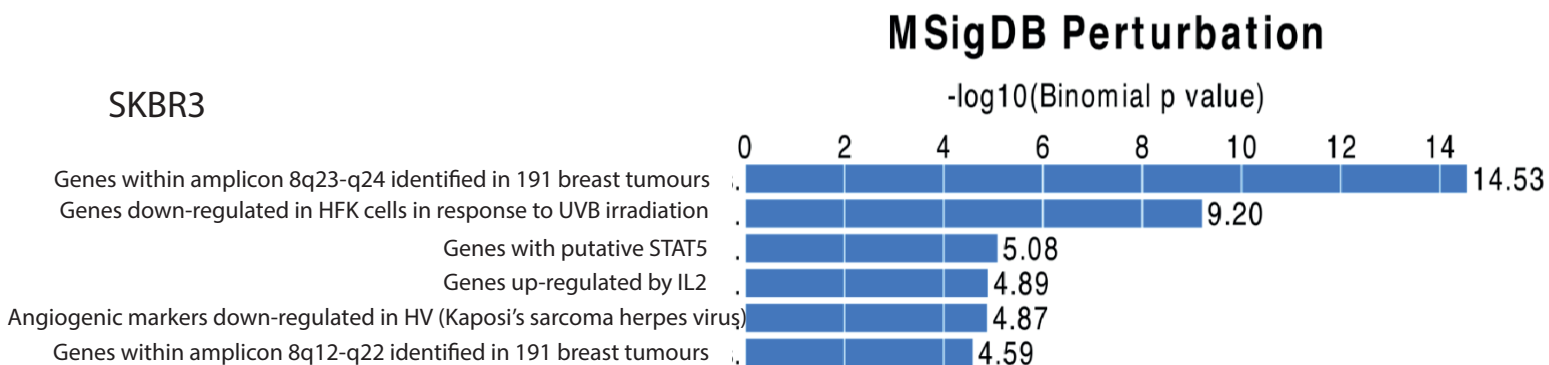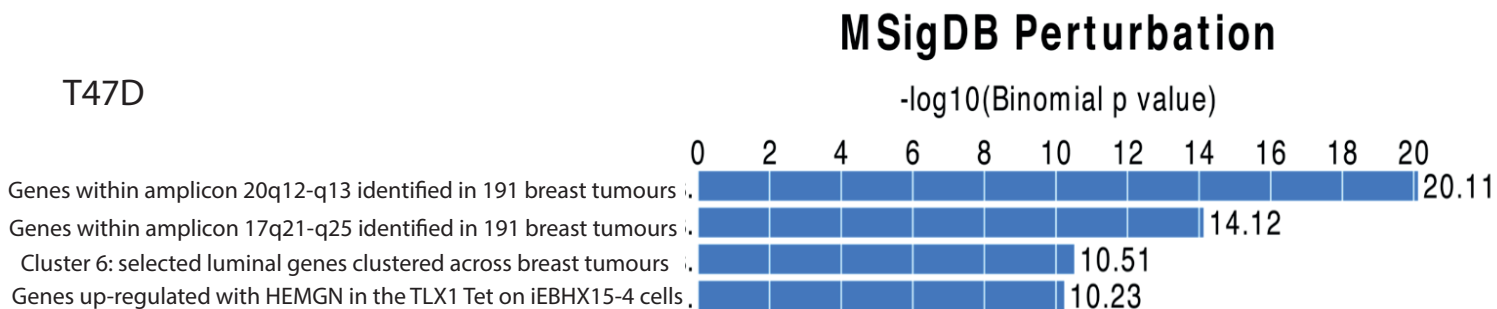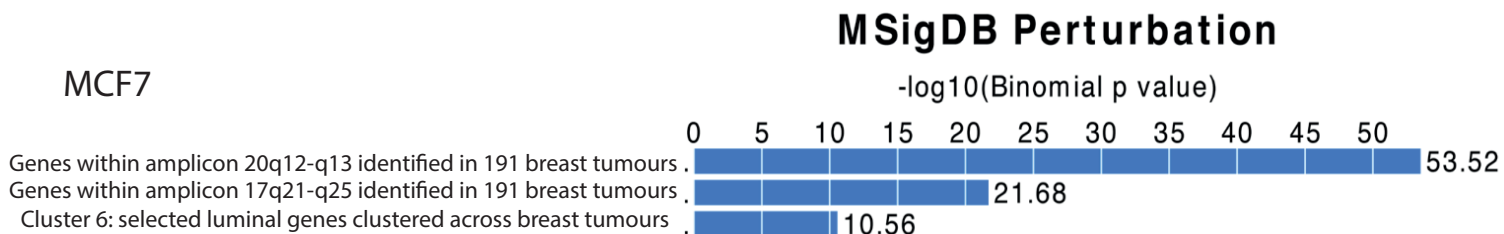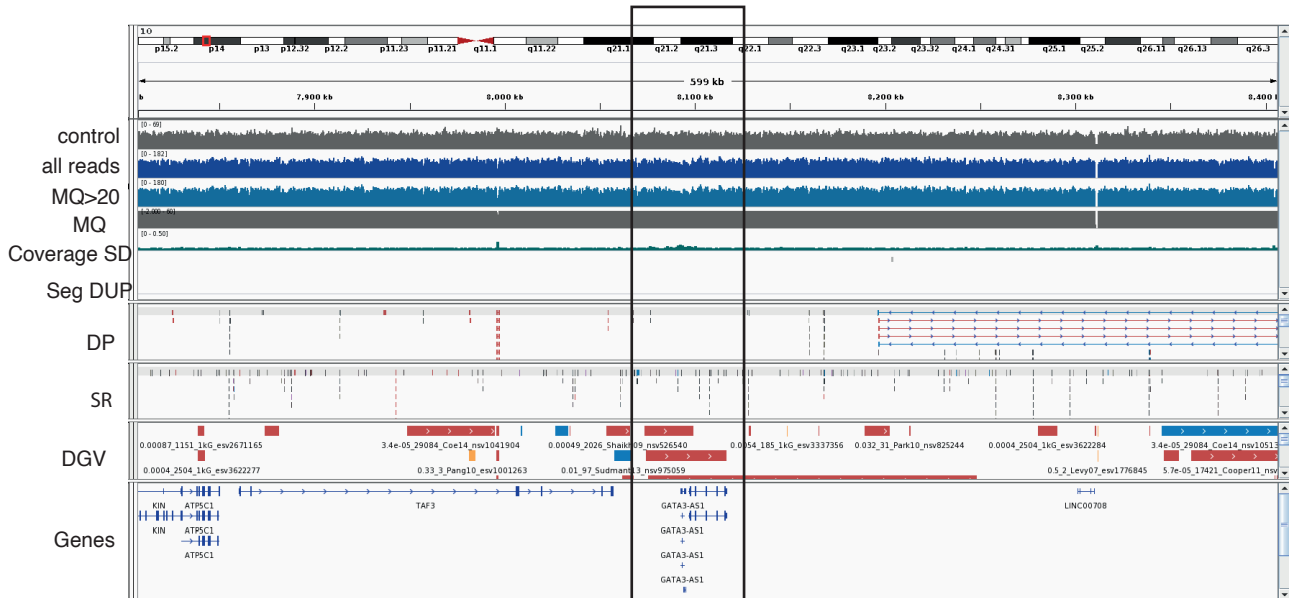Genes within amplicon 8q12-q22 identified in 191 breast tumours — **4.59**

# Figure S7

## FOXA1- 8 copies, focal amplification



## GATA3, broad gain, 4 copies



## ESR1, partial gain
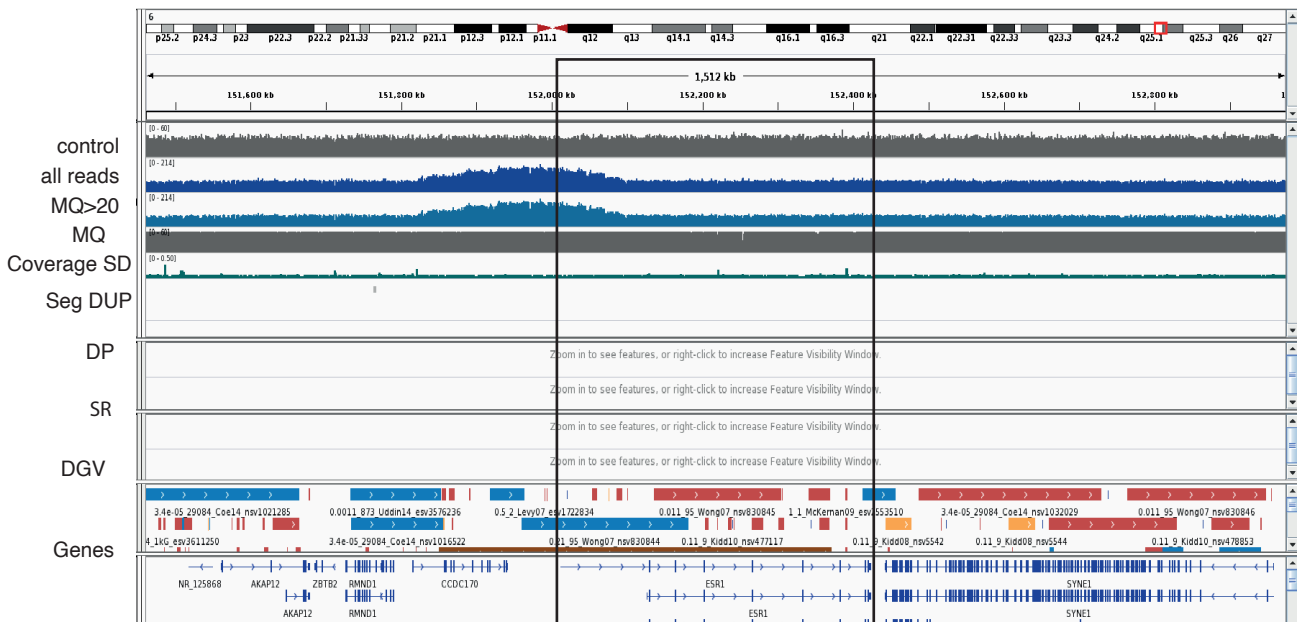
Figure S8

# Figure S9



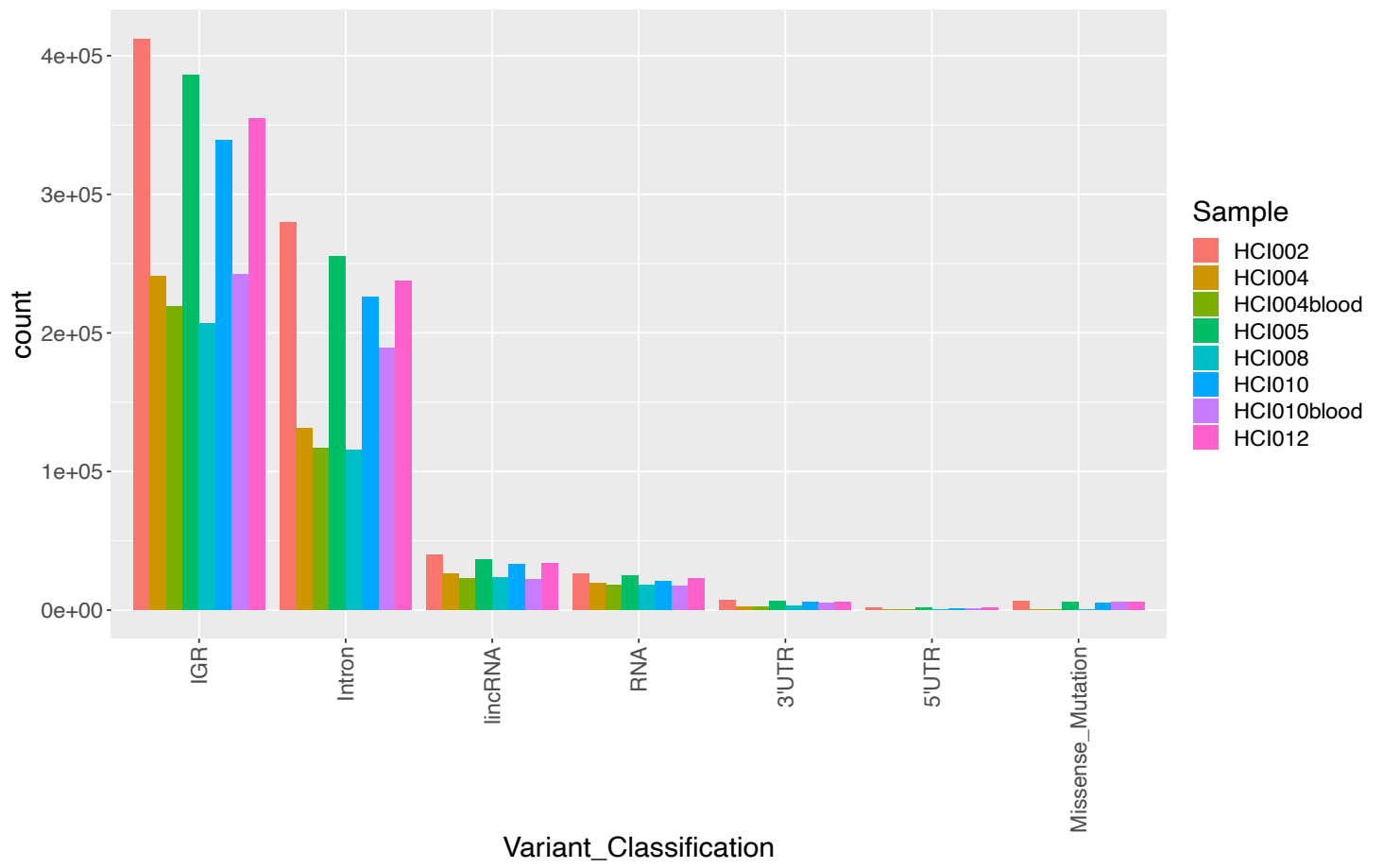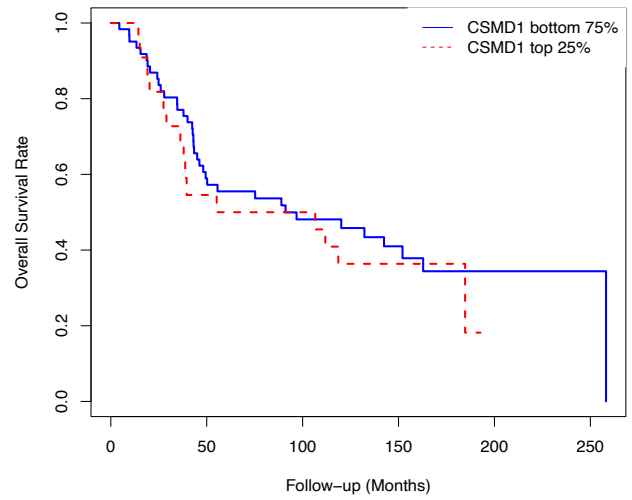**Survival of CSMD1 in METABRIC1 Basal ( p = 0.834 )**

Overall Survival Rate / Follow−up (Months)

CSMD1 bottom 75%
CSMD1 top 25%
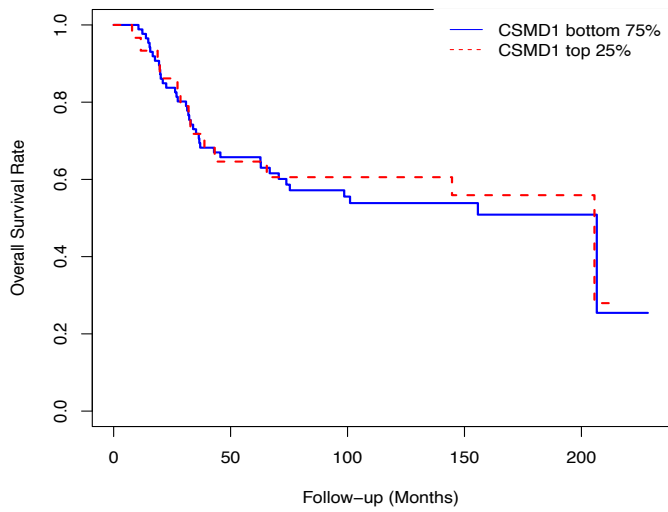
**Survival of CSMD1 in METABRIC1 Her2 ( p = 0.563 )**

Overall Survival Rate / Follow−up (Months)

CSMD1 bottom 75%
CSMD1 top 25%

**Survival of CSMD1 in METABRIC1 LumA ( p = 0.0687 )**

Overall Survival Rate / Follow−up (Months)

CSMD1 bottom 75%
CSMD1 top 25%
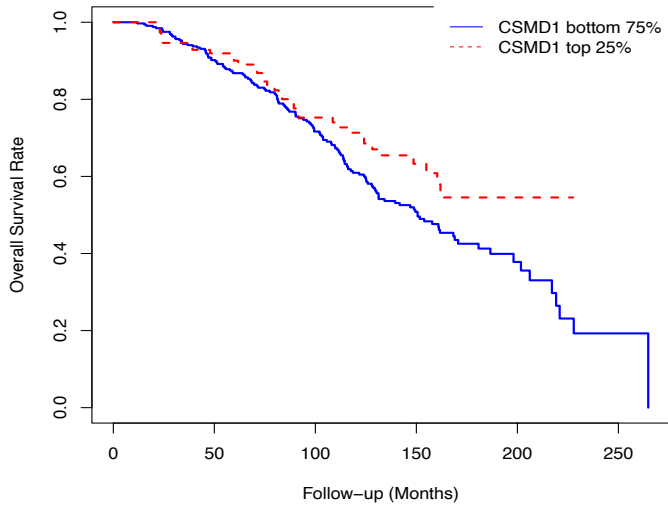
**Survival of CSMD1 in METABRIC1 LumB ( p = 0.000947 )**

Overall Survival Rate / Follow−up (Months)

CSMD1 bottom 75%
CSMD1 top 25%