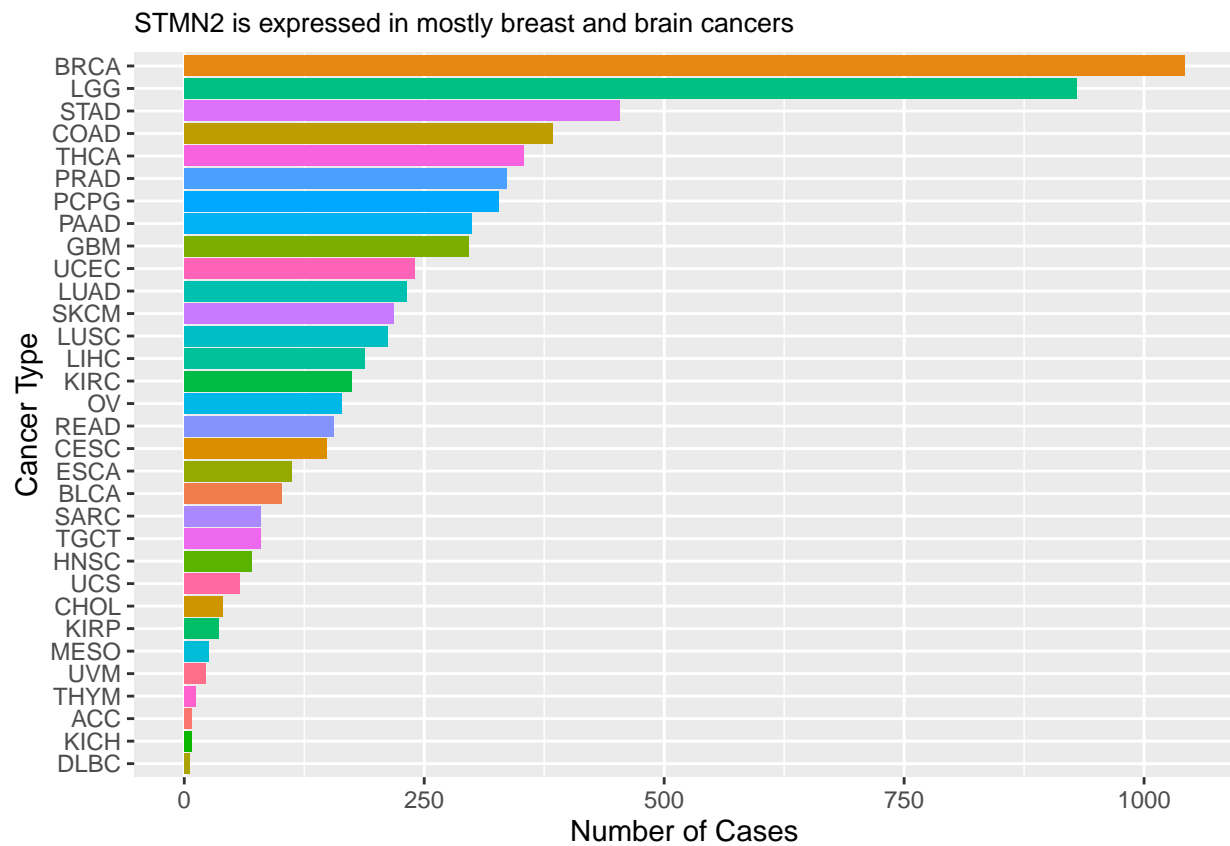


# Clinical, gene and mutation data of cancers with cryptic STMN2 events

## Cancers with STMN2 expression

```
STMN2_clinical |>
  ggplot(aes(x = fct_rev(fct_infreq(cancer_type)))) +
  geom_bar(aes(fill = cancer_type)) +
  coord_flip() +
  labs(
    x = "Cancer Type",
    y = "Number of Cases",
    title = "STMN2 is expressed in mostly breast and brain cancers"
  ) +
  theme(legend.position = "none", plot.title = element_text(size=10))
```



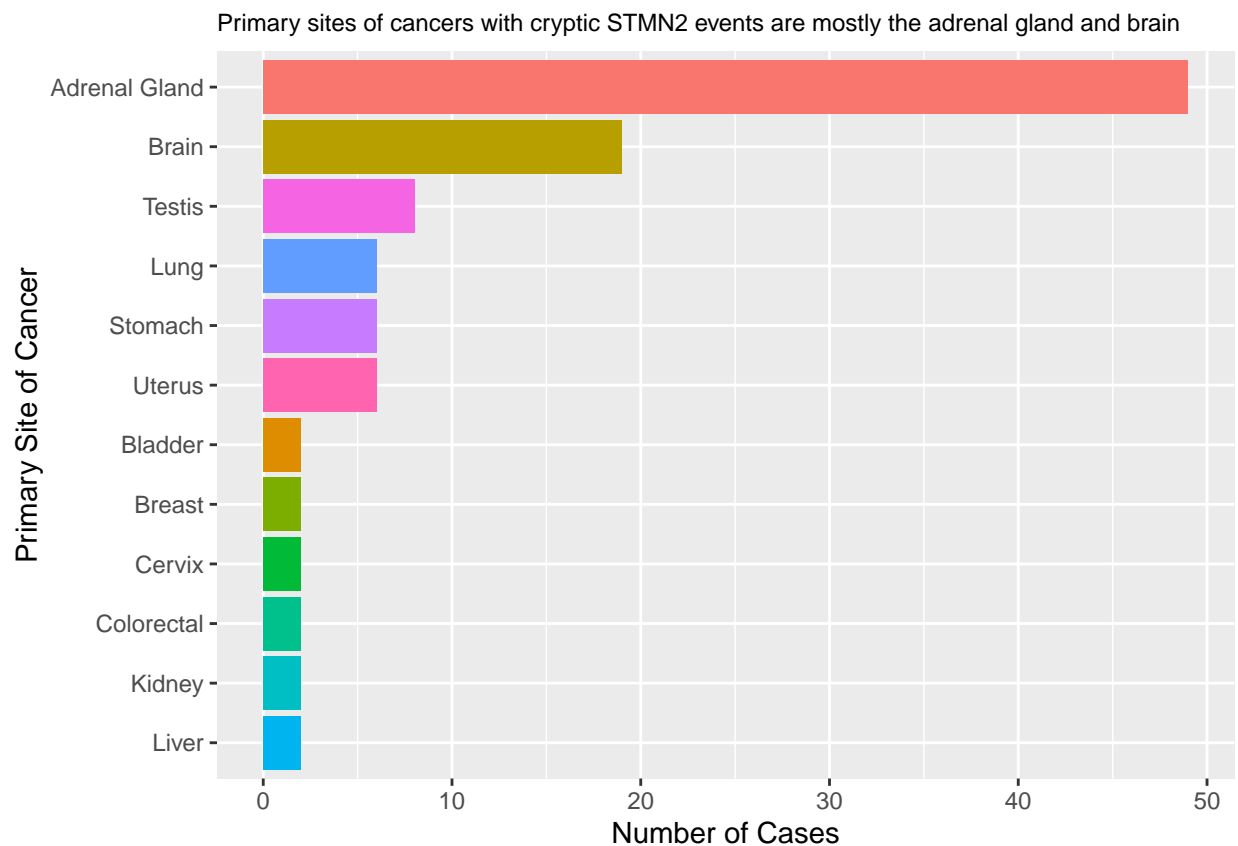
**Figure 1:** STMN2 events are found mostly in breast and brain cancer patients. BRCA = breast cancer; LGG = low-grade gliomas (brain tumours)

## Cancers with cryptic STMN2 expression

```
STMN2_clinical_jir_cryptic <- STMN2_clinical_jir |>
  filter(STMN2_cryptic_coverage > 2)
```

### Primary sites of cancers

```
STMN2_clinical_jir_cryptic |>
  drop_na() |>
  ggplot(aes(x = fct_rev(fct_infreq(gdc_primary_site)))) +
  geom_bar(aes(fill = gdc_primary_site)) +
  coord_flip() +
  labs(
    x = "Primary Site of Cancer",
    y = "Number of Cases",
    title =
      "Primary sites of cancers with cryptic STMN2 events are mostly the adrenal gland and brain"
  ) +
  theme(legend.position = "none", plot.title = element_text(size=9))
```



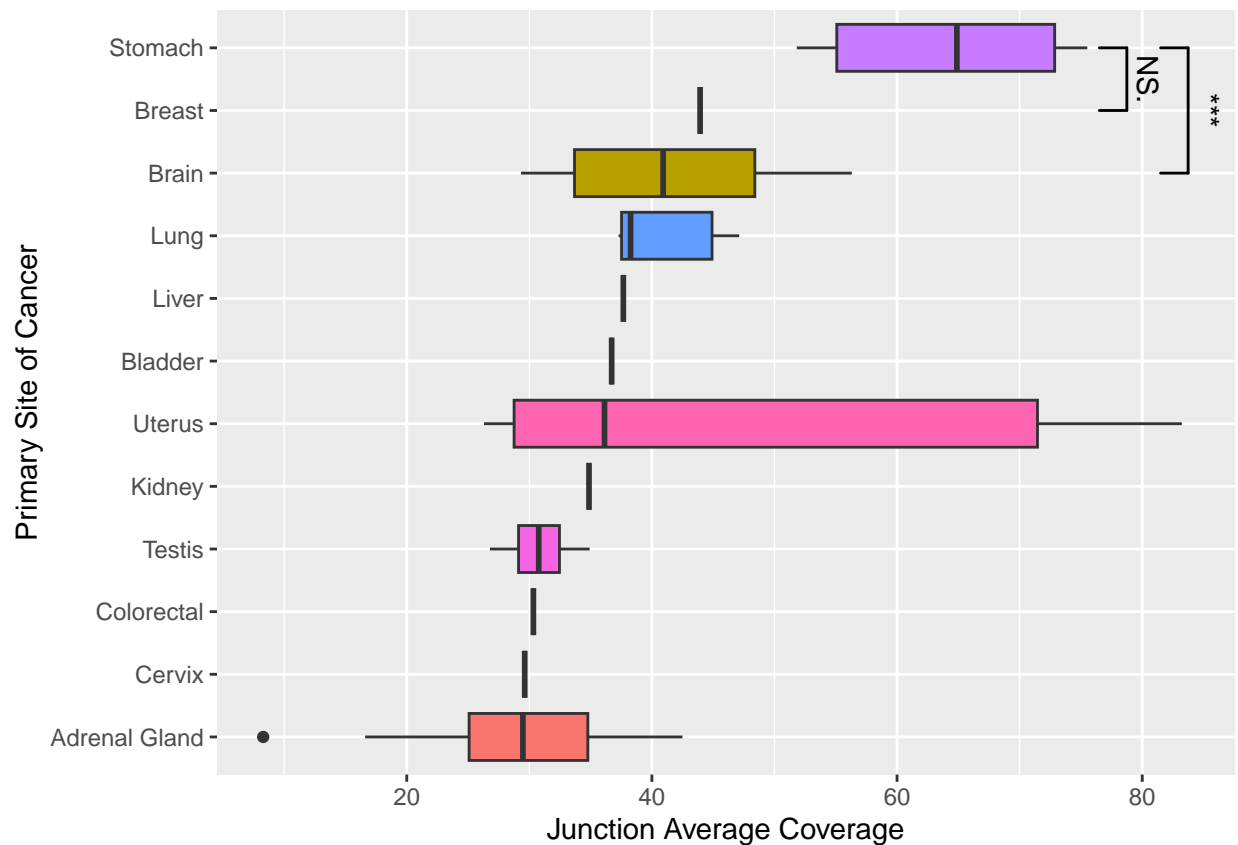
**Figure 2:** Cryptic STMN2 events are found mostly in the adrenal gland and brain.

Interestingly, Figure 2 shows that cryptic STMN2 expression is low in the breast. Comparing this to Figure

1, this shows that the STMN2 events expressed in breast cancers may be mostly annotated non-cryptic events.

### Cryptic STMN2 junction coverage in different sites of cancers

```
STMN2_clinical_jir_cryptic |>
  drop_na() |>
  filter(cgc_primary_site != "") |>
  ggplot(aes(x = junction_avg_coverage, y = fct_reorder(gdc_primary_site,
                                                         junction_avg_coverage, median))) +
  geom_boxplot(aes(fill = gdc_primary_site)) +
  labs(
    x = "Junction Average Coverage",
    y = "Primary Site of Cancer",
  ) +
  theme(legend.position = "none", plot.title = element_text(size=10)) +
  geom_signif(comparisons = list(c("Stomach", "Breast"), c("Stomach", "Brain")),
             map_signif_level = TRUE,
             y_position = c(75, 80))
```



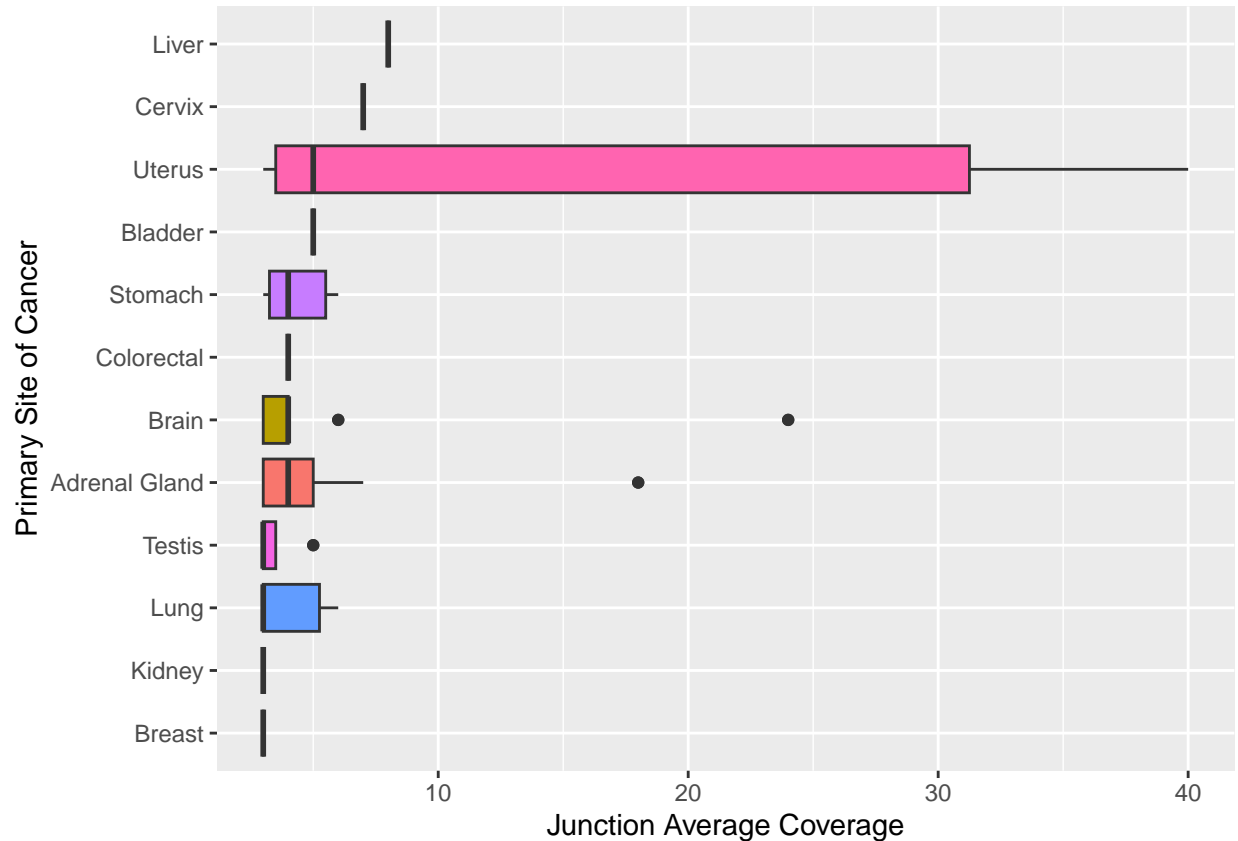
**Figure 3:** Stomach and breast cancers are the most deeply sequenced.

```
STMN2_clinical_jir_cryptic |>
  drop_na() |>
```

```

filter(cgc_primary_site != "") |>
ggplot(aes(x = STMN2_cryptic_coverage,
           y = fct_reorder(gdc_primary_site, STMN2_cryptic_coverage, median))) +
geom_boxplot(aes(fill = gdc_primary_site)) +
labs(
  x = "Junction Average Coverage",
  y = "Primary Site of Cancer",
) +
theme(legend.position = "none", plot.title = element_text(size=10))

```



On average, cancers in the stomach and breast have the greatest number of reads supporting cryptic STMN2 events. Cancers of the brain have significantly fewer reads supporting cryptic events.

### Which cancers have the most cryptic STMN2 events?

Table 1: Breast and brain cancers have high cryptic STMN2 expression.

cancer__type	n	percent
Pheochromocytoma and Paraganglioma	49	0.4622642
Glioblastoma Multiforme	15	0.1415094
Testicular Germ Cell Tumors	8	0.0754717
Stomach Adenocarcinoma	6	0.0566038

cancer_type	n	percent
Brain Lower Grade Glioma	4	0.0377358
Lung Squamous Cell Carcinoma	4	0.0377358
Uterine Corpus Endometrial Carcinoma	4	0.0377358
Bladder Urothelial Carcinoma	2	0.0188679
Breast Invasive Carcinoma	2	0.0188679
Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma	2	0.0188679
Kidney Renal Clear Cell Carcinoma	2	0.0188679
Liver Hepatocellular Carcinoma	2	0.0188679
Lung Adenocarcinoma	2	0.0188679
Rectum Adenocarcinoma	2	0.0188679
Uterine Carcinosarcoma	2	0.0188679

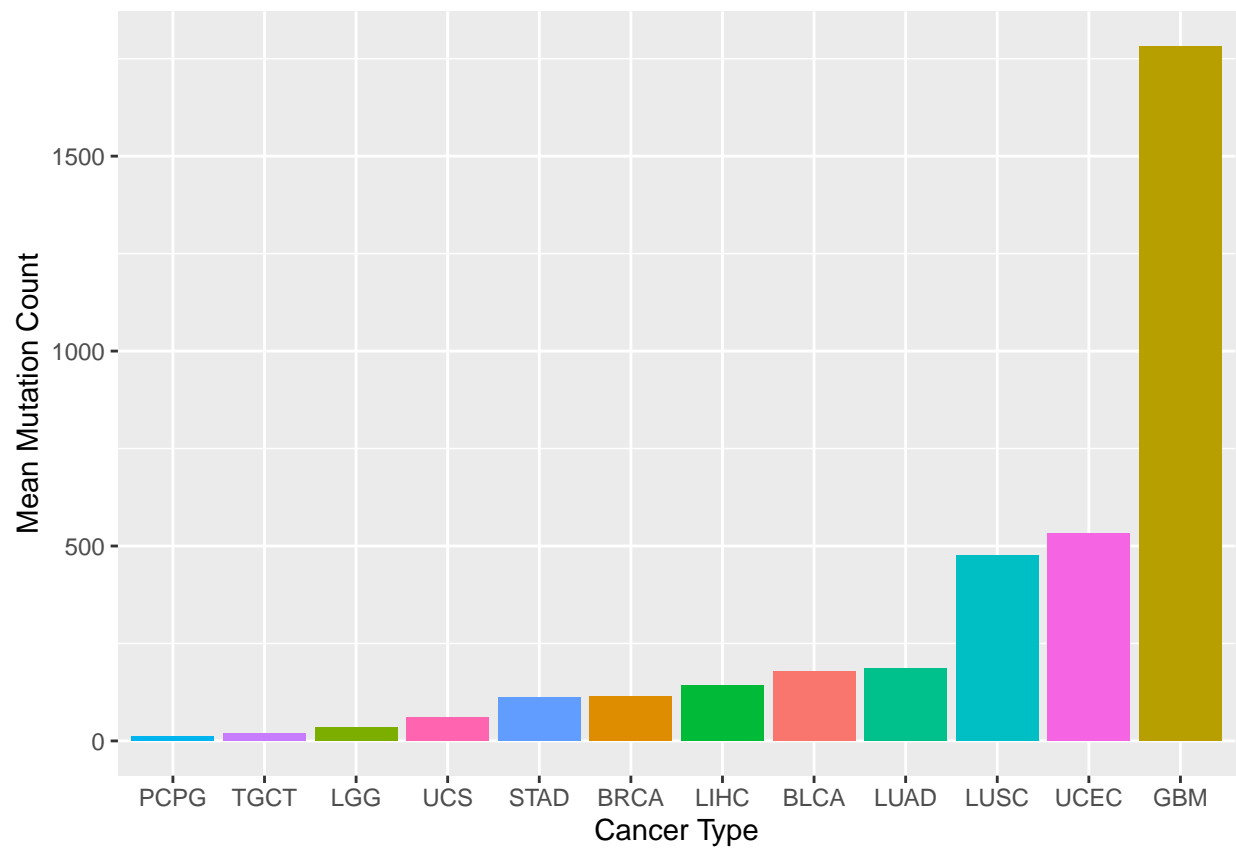
## Where are the cancers with cryptic STMN2 events located?

Table 2: Cancers with cryptic STMN2 events are found primarily in the adrenal gland and brain

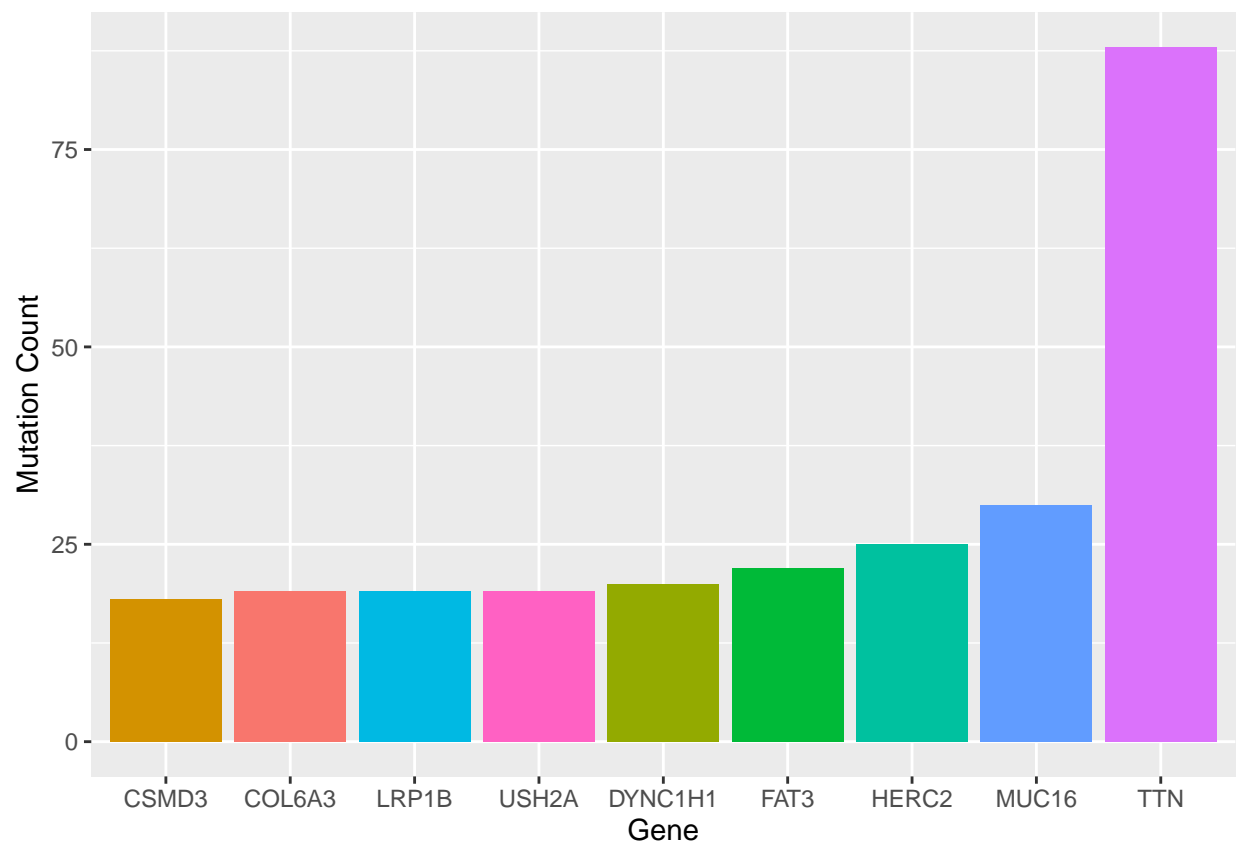
gdc_primary_site	n	percent
Adrenal Gland	49	0.4622642
Brain	19	0.1792453
Testis	8	0.0754717
Lung	6	0.0566038
Stomach	6	0.0566038
Uterus	6	0.0566038
Bladder	2	0.0188679
Breast	2	0.0188679
Cervix	2	0.0188679
Colorectal	2	0.0188679
Kidney	2	0.0188679
Liver	2	0.0188679

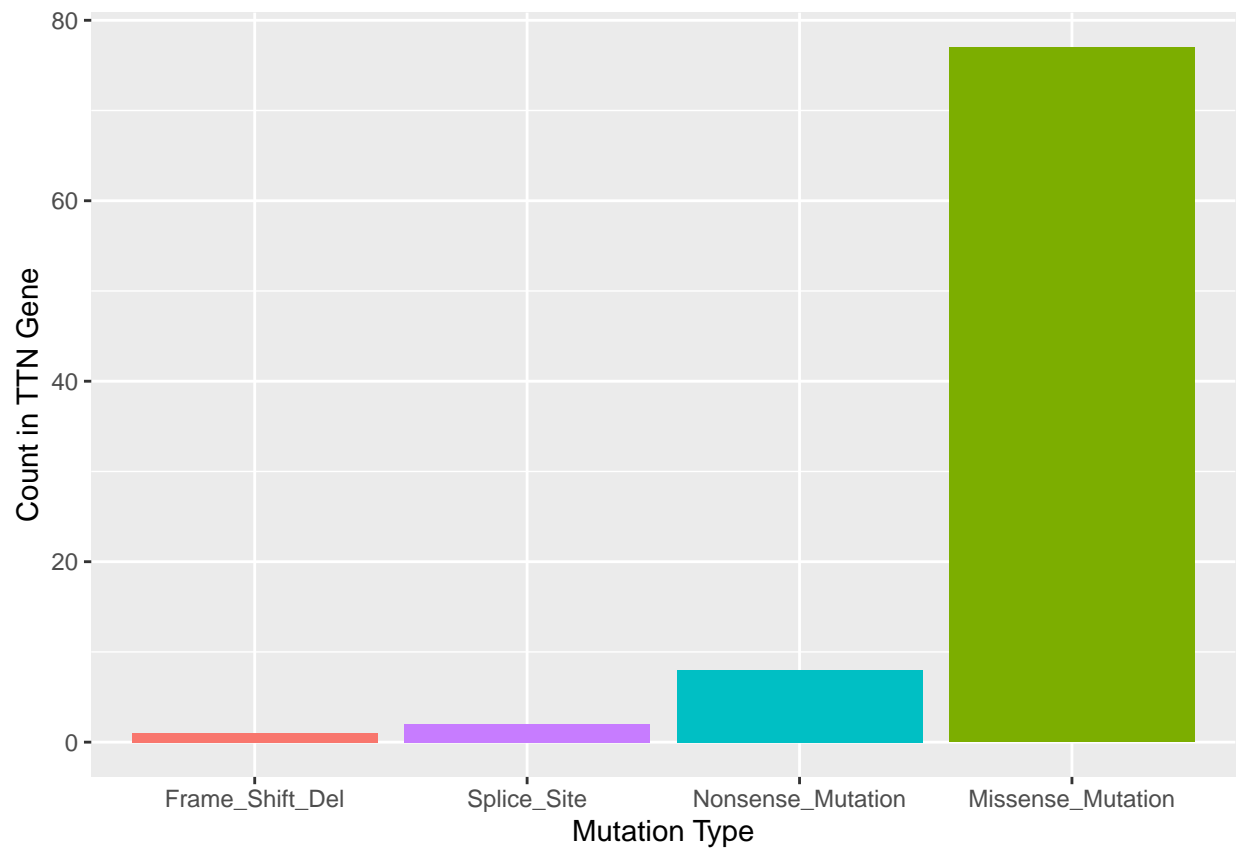
# TCGA Clinical Data

## Mutation Counts



Mutation Data of one patient





TCGA biolinks