

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

STMN2 junction coverage

Overall STMN2 junction coverage in different cancer sites

```
## Warning in wilcox.test.default(c(64.8789804967288, 64.8789804967288,  
## 51.8185835185835, : cannot compute exact p-value with ties
```

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```

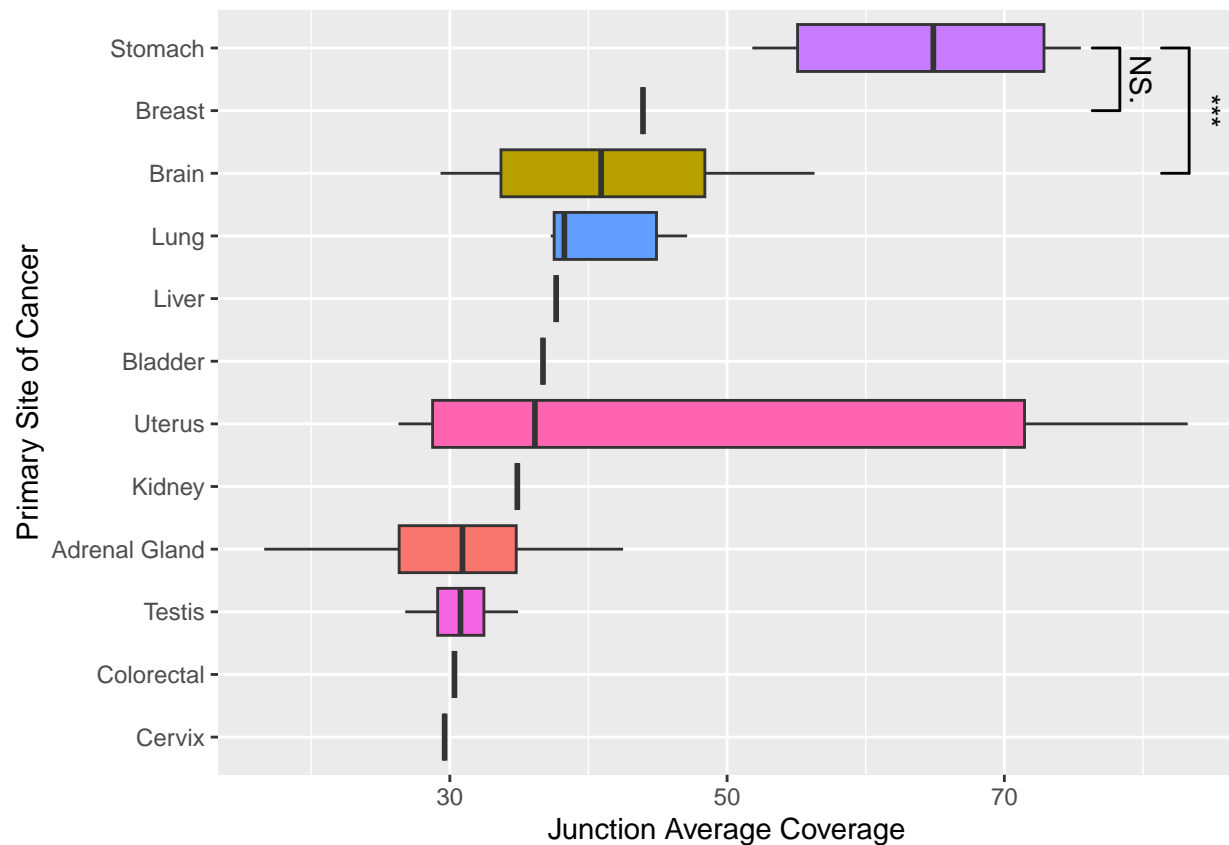


Figure 1: Stomach and breast cancers are the most deeply sequenced in general.

Cryptic STMN2 junction coverage in different cancer sites

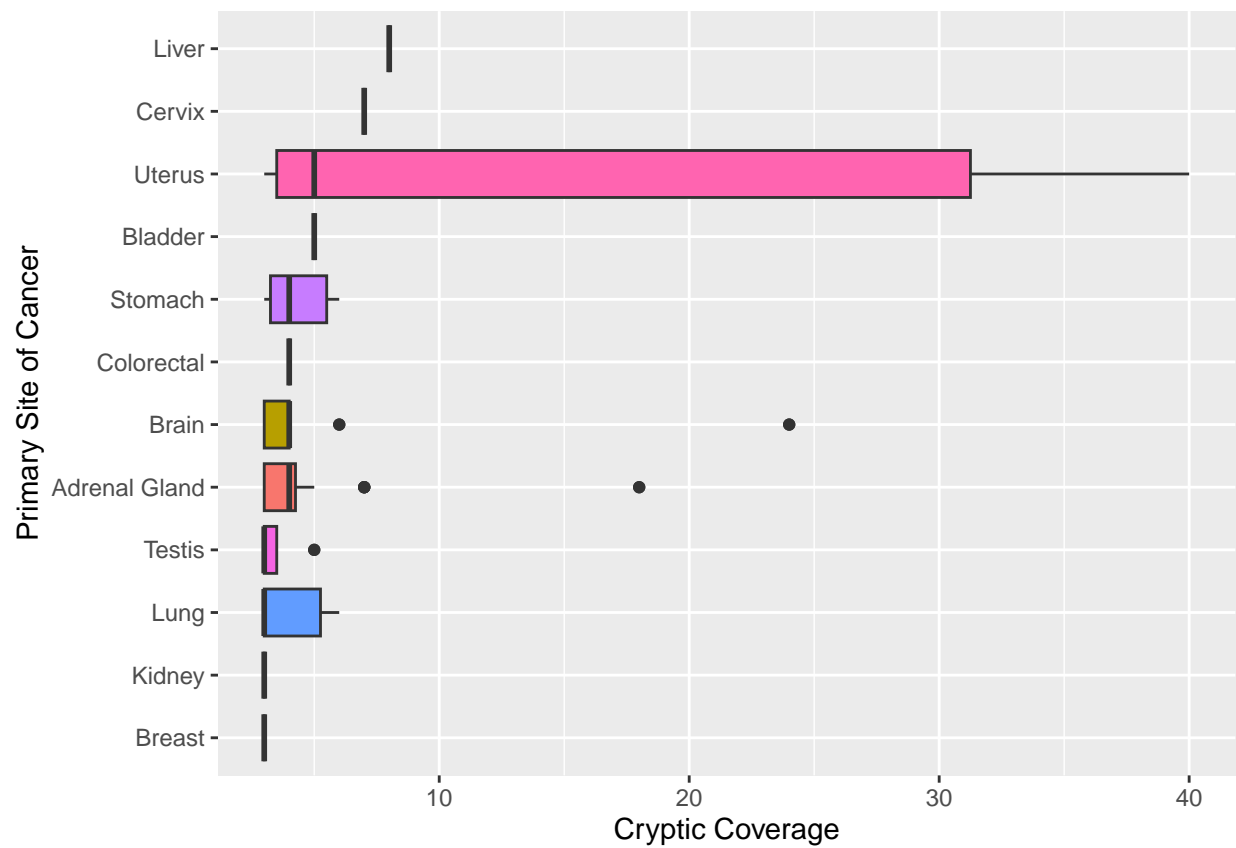


Figure 2:

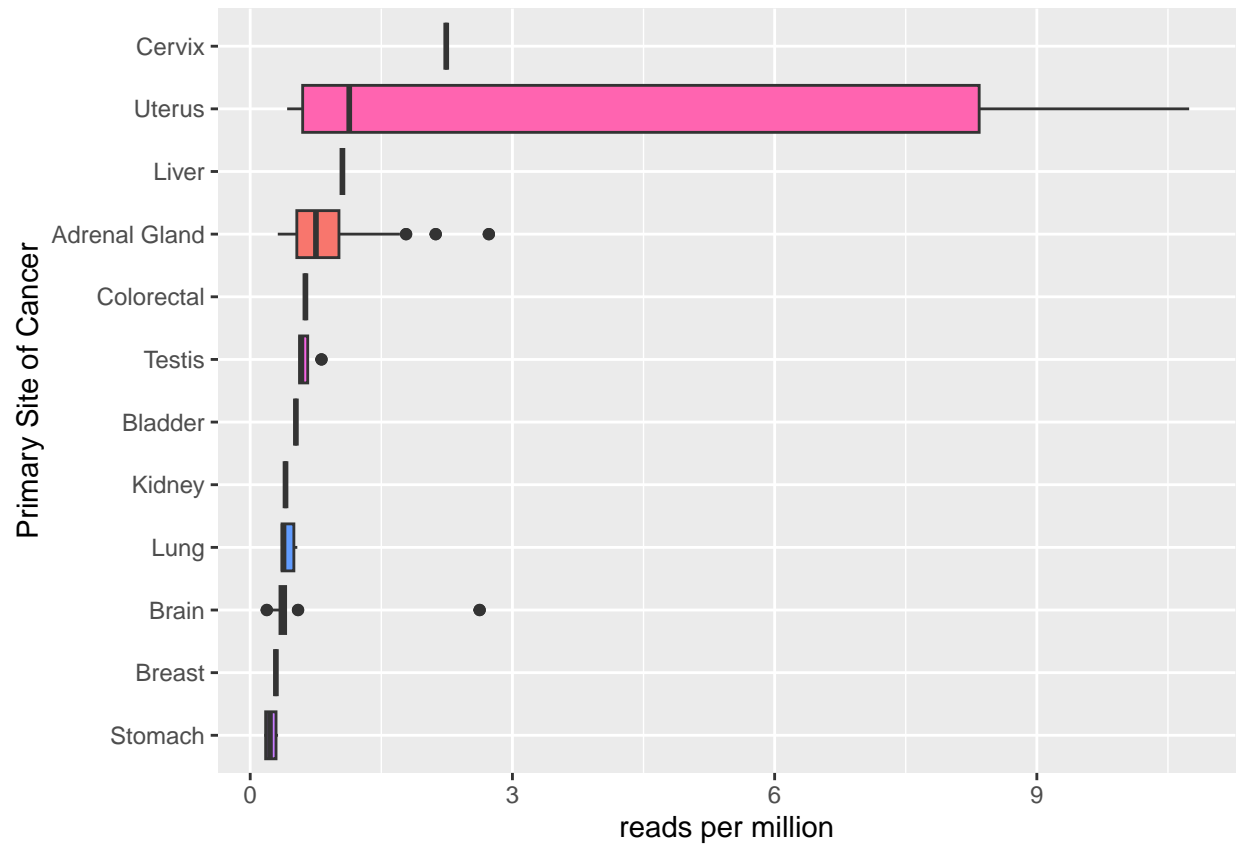


Figure 3:

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.

Cancers of the cervix, uterus and liver have the greatest cryptic coverage. However, there is only one data value for cancers of the cervix and liver.

Cryptic STMN2 Expression

Cancers with STMN2 events (in general)

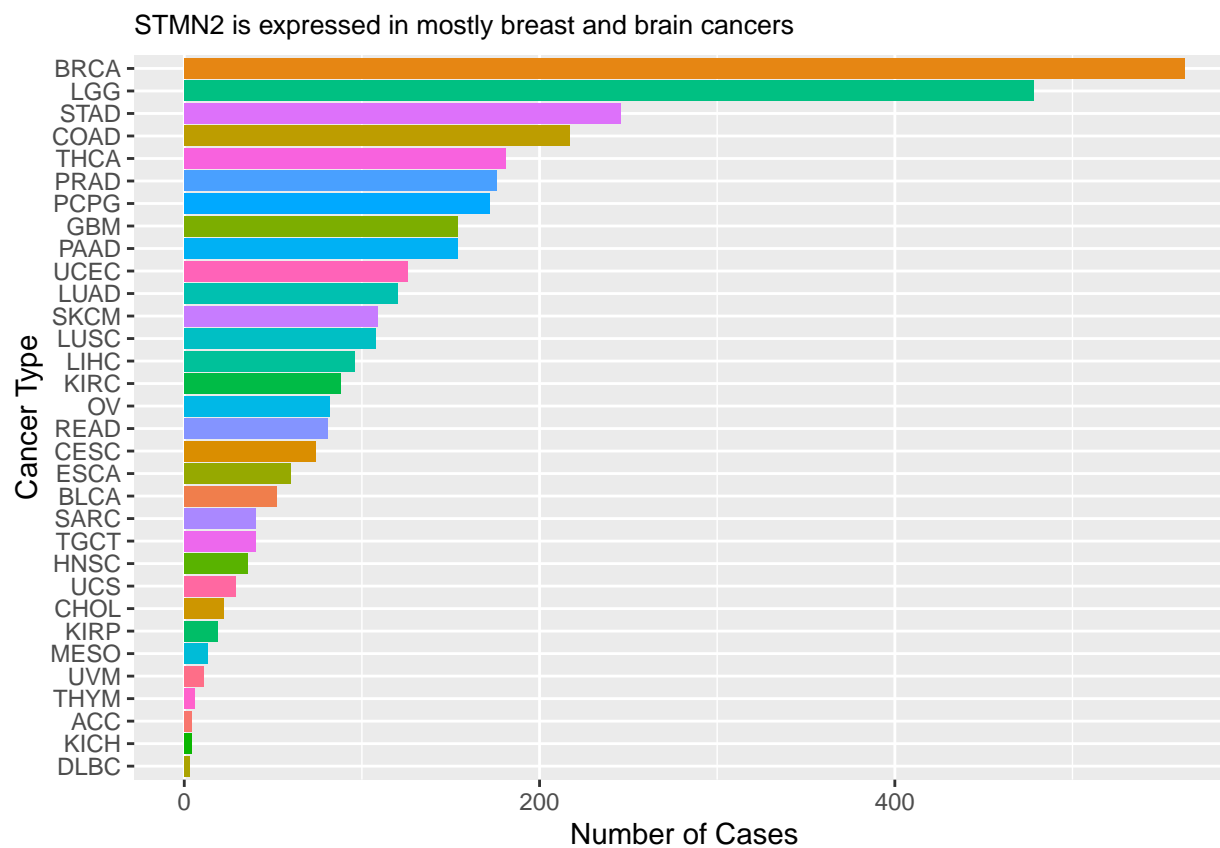
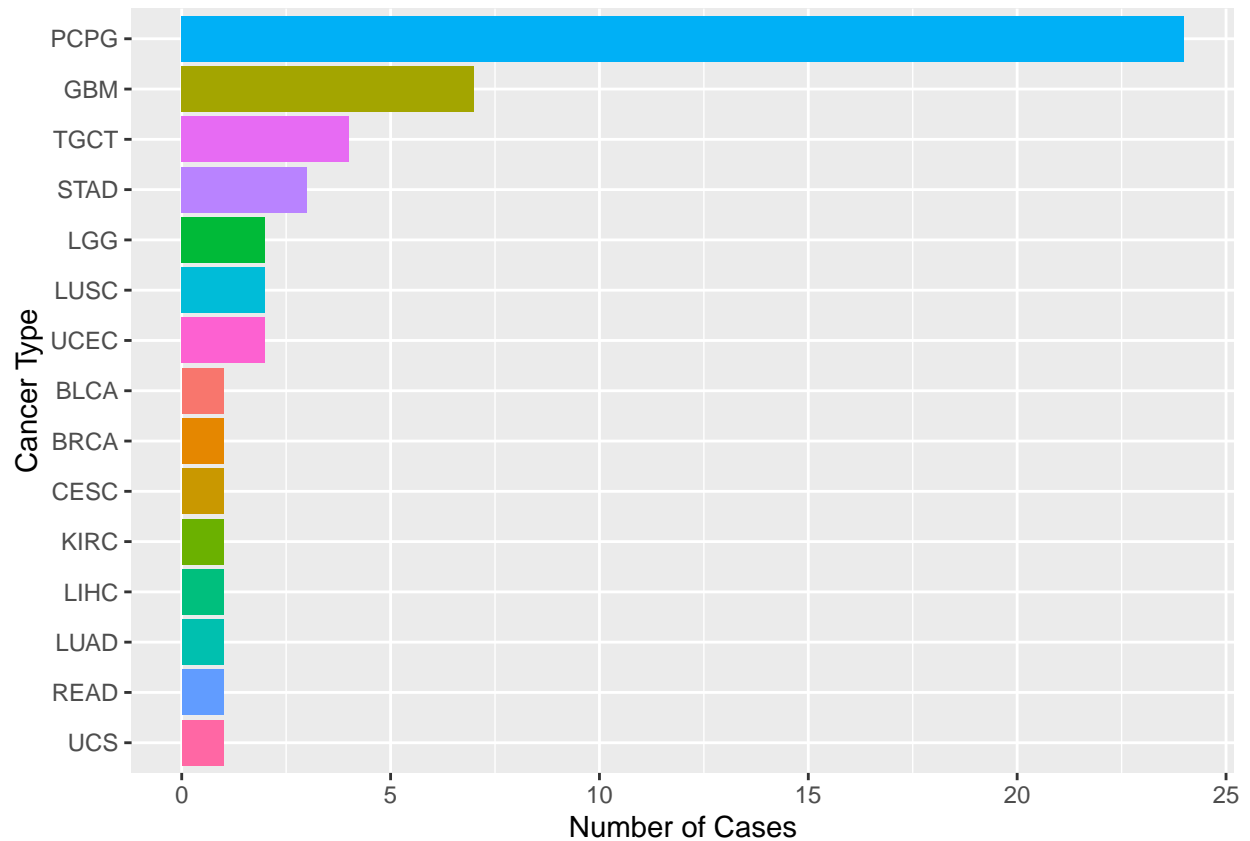


Figure 4: STMN2 events are found mostly in breast and brain cancer patients.



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 =
      "Cryptic STMN2 events are found mostly in cancers of the adrenal gland and brain"
  ) +
  theme(legend.position = "none", plot.title = element_text(size=9))
```

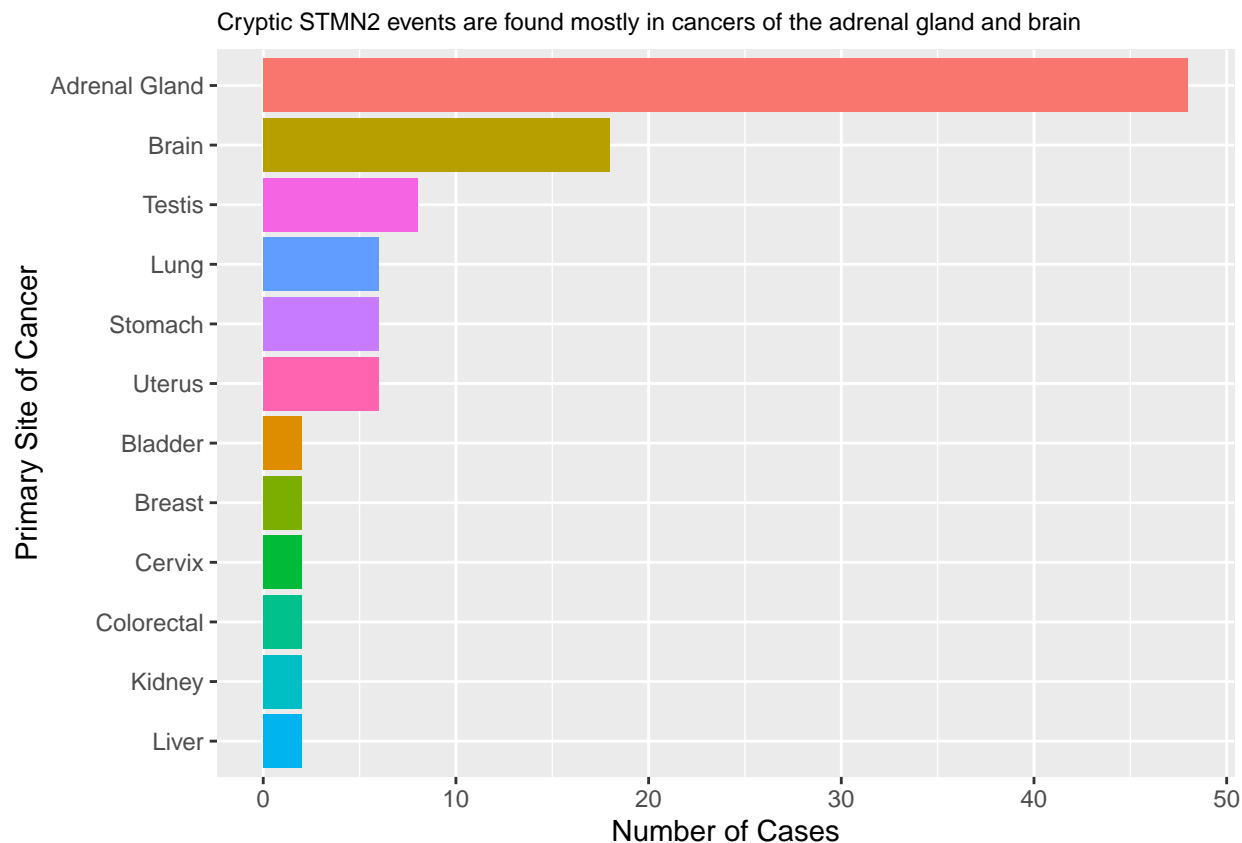


Figure 5: Cryptic STMN2 events are found mostly in the adrenal gland and brain.

Interestingly, Figure 5 shows that cryptic STMN2 expression is low in the breast. Comparing this to Figure 4, this shows that the STMN2 events expressed in breast cancers may be mostly annotated non-cryptic events.

Which cancers have the most cryptic STMN2 events?

Fraction of each cancer with cryptic STMN2 expression

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

cancer	n	percent
Pheochromocytoma and Paranganglioma	48	0.4615385
Glioblastoma Multiforme	14	0.1346154
Testicular Germ Cell Tumors	8	0.0769231
Stomach Adenocarcinoma	6	0.0576923
Brain Lower Grade Glioma	4	0.0384615
Lung Squamous Cell Carcinoma	4	0.0384615
Uterine Corpus Endometrial Carcinoma	4	0.0384615
Bladder Urothelial Carcinoma	2	0.0192308
Breast Invasive Carcinoma	2	0.0192308
Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma	2	0.0192308
Kidney Renal Clear Cell Carcinoma	2	0.0192308
Liver Hepatocellular Carcinoma	2	0.0192308

cancer	n	percent
Lung Adenocarcinoma	2	0.0192308
Rectum Adenocarcinoma	2	0.0192308
Uterine Carcinosarcoma	2	0.0192308

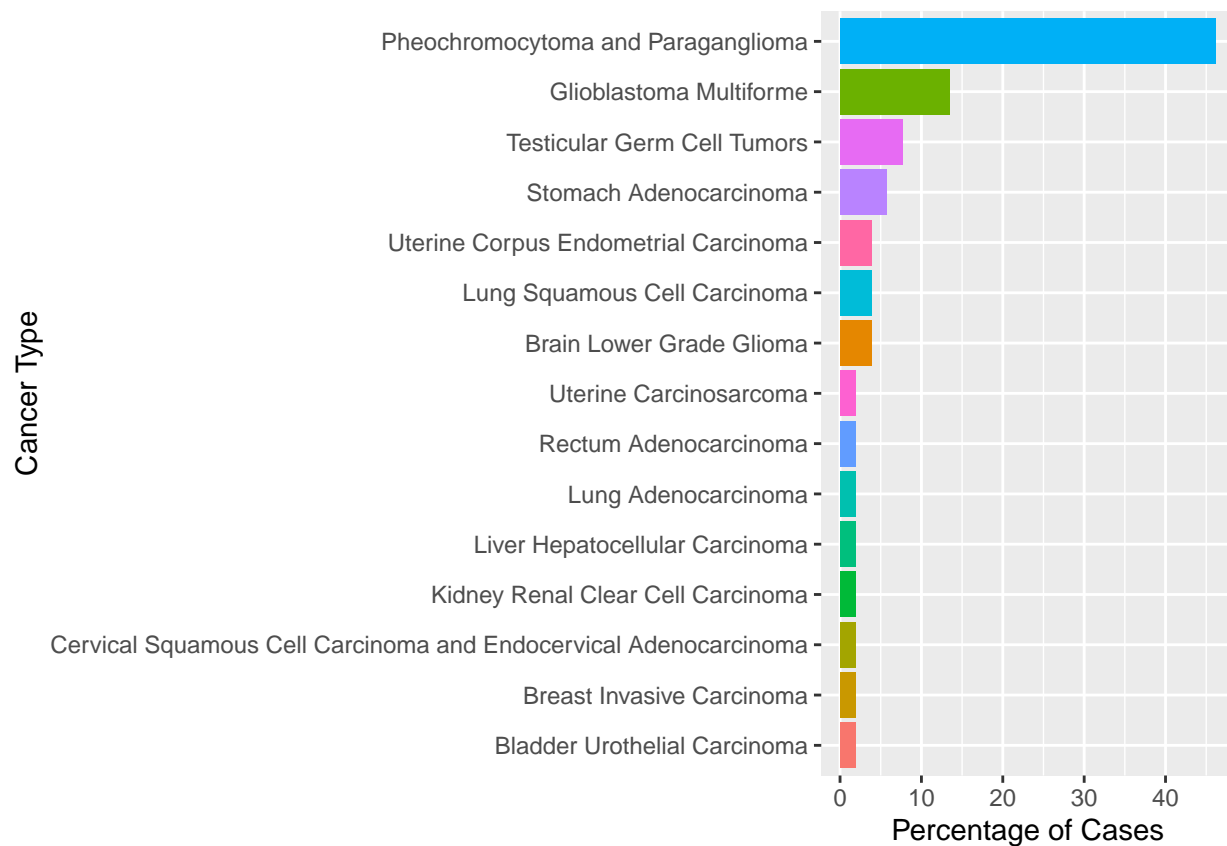


Figure 6:

Where are the cancers with cryptic STMN2 events located?

Fraction of cases with STMN2 events in cancer sites

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

gdc_primary_site	n	percent
Adrenal Gland	48	0.4615385
Brain	18	0.1730769
Testis	8	0.0769231
Lung	6	0.0576923
Stomach	6	0.0576923
Uterus	6	0.0576923
Bladder	2	0.0192308
Breast	2	0.0192308
Cervix	2	0.0192308

gdc_primary_site	n	percent
Colorectal	2	0.0192308
Kidney	2	0.0192308
Liver	2	0.0192308

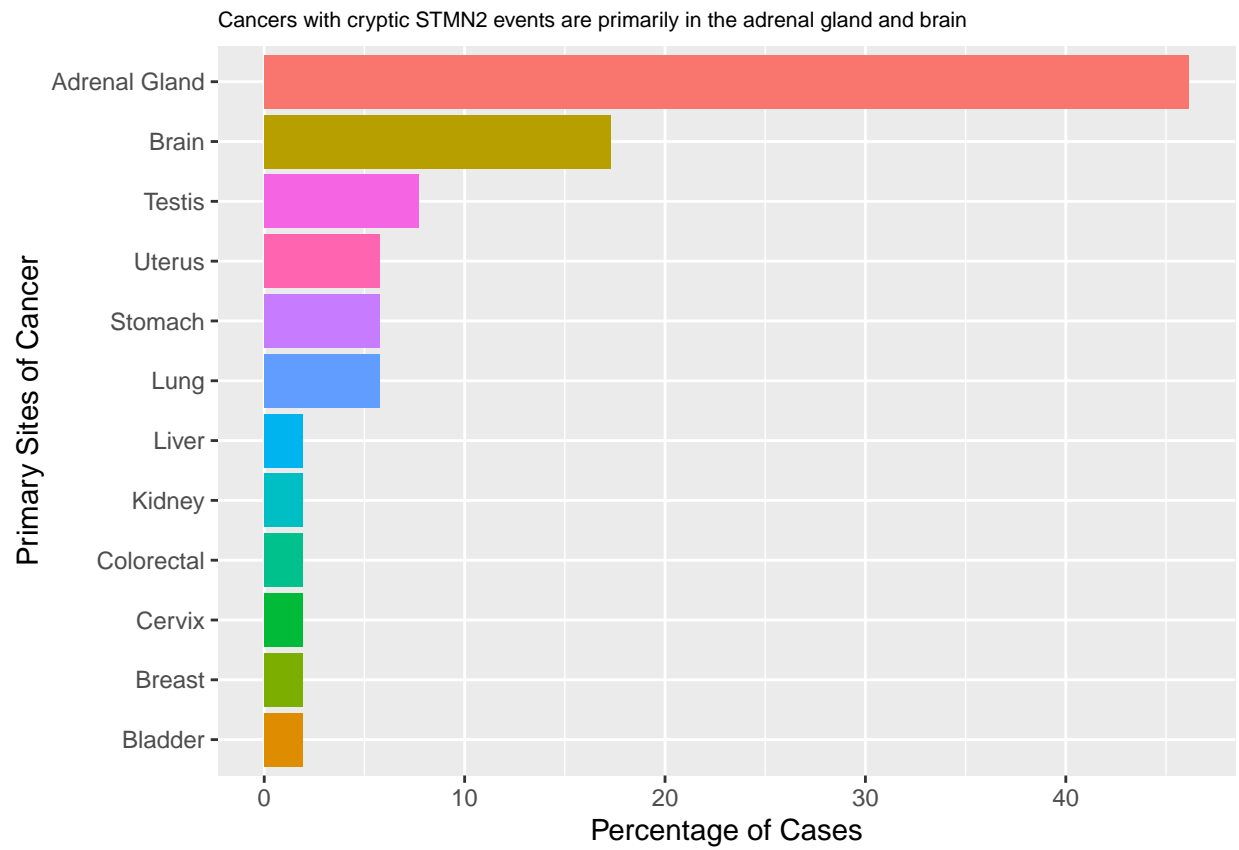


Figure 7:

TCGA/cBioPortal Clinical Data

Mutation Counts

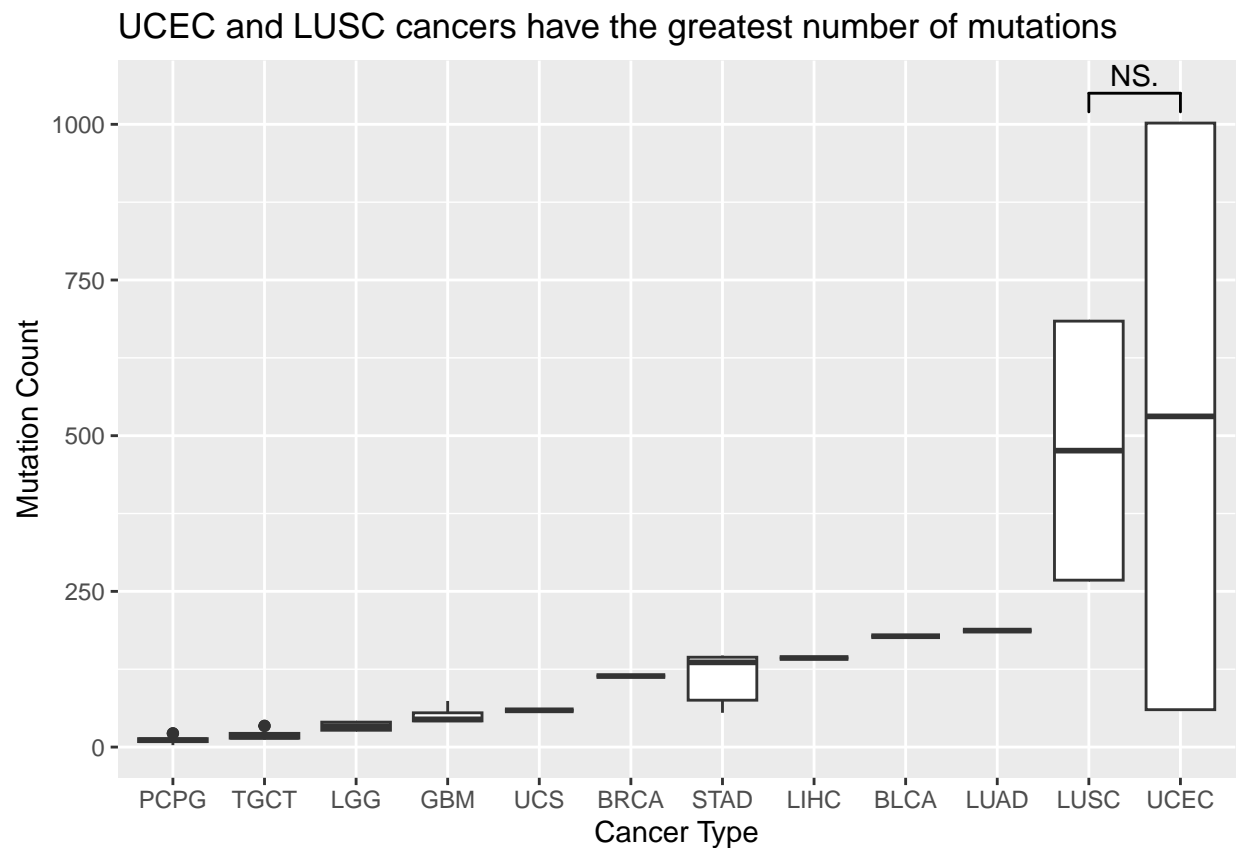


Figure 8: Among cancer patients with STMN2 cryptic expression, uterine corpus endometrial carcinoma (UCEC) has the greatest number of mutations.

Mutational burden

```
total_mutations_each_cancer <- cBio_clinical |>
  drop_na(Mutation.Count) |>
  filter(grepl("^\\d+$", Mutation.Count)) |>
  group_by(cancer_abbrev) |>
  summarise(total_mutations = sum(as.numeric(Mutation.Count)))

total_mutations_each_cancer_with_cryptic <- STMN2_cryptic_cBio |>
  drop_na(mutation_count) |>
  filter(mutation_count < 2500) |>
  group_by(cancer_abbrev) |>
  summarise(total_mutations_cryptic = sum(mutation_count))

mutations_each_cancer_general_vs_cryptic <- total_mutations_each_cancer |>
  left_join(total_mutations_each_cancer_with_cryptic, by=c("cancer_abbrev")) |>
```

```
mutate(percent_with_cryptic = (total_mutations_cryptic/total_mutations)*100)  
#16% of all mutations in LGG cancer are in cases with STMN2 cryptic events
```

Fraction of each cancer that has cryptic STMN2 events

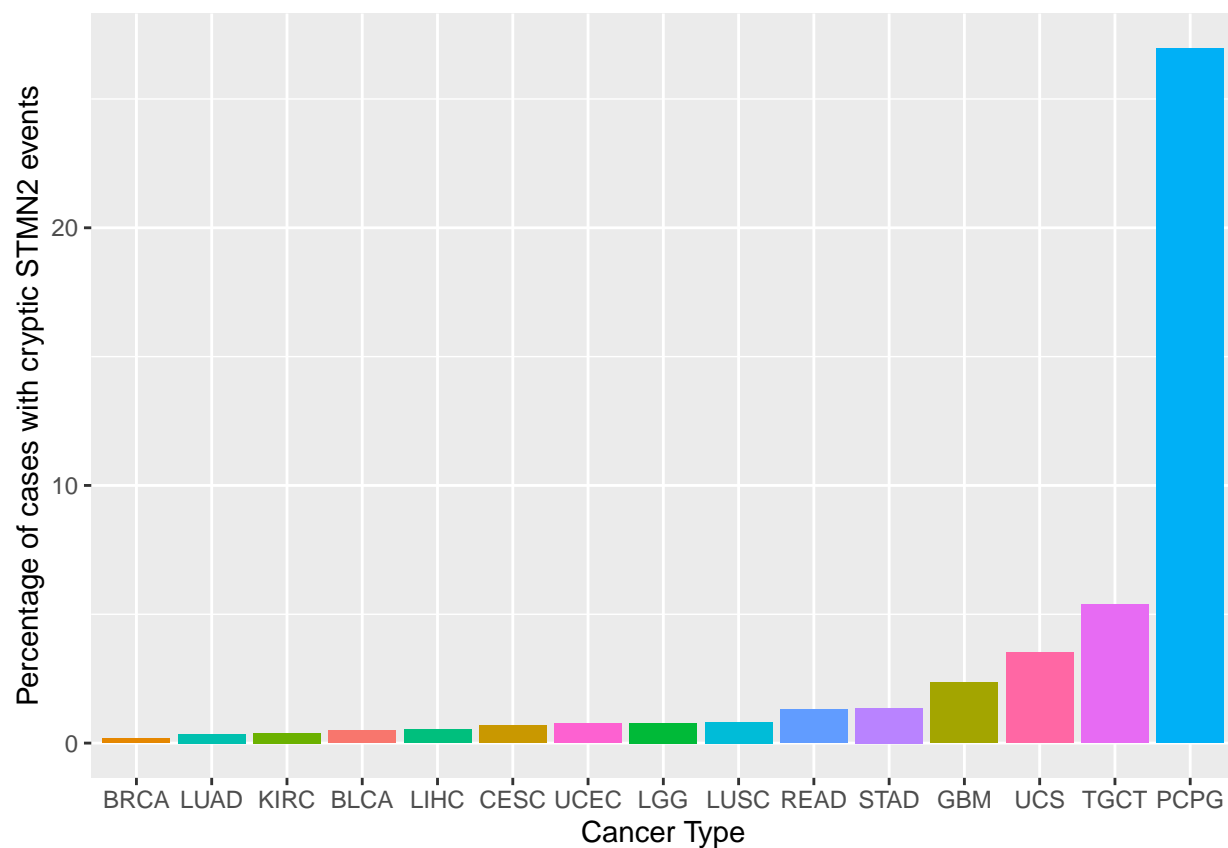
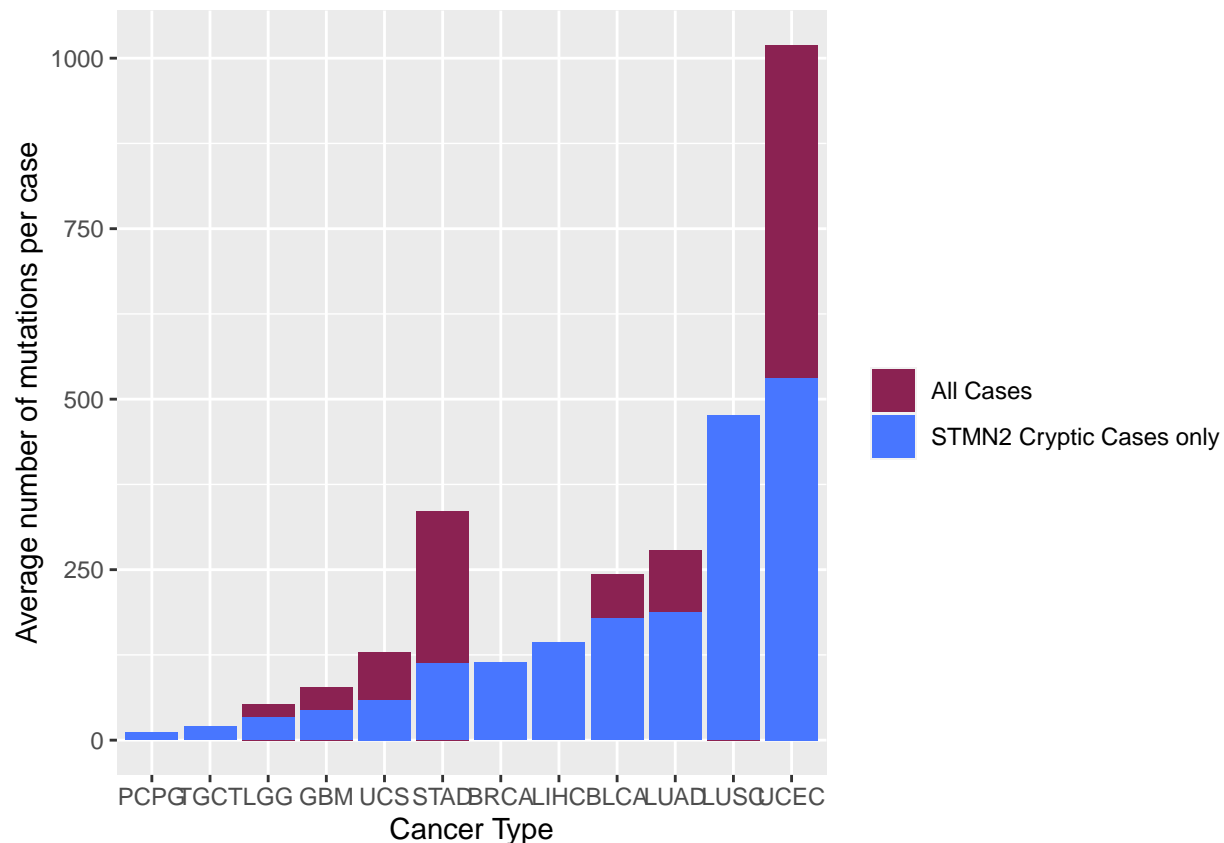


Figure 9:



```
## Warning in left_join(cBio_clinical, STMN2_clinical_jir, by = c("case_submitter_id")): Detected an un
## i Row 25 of 'x' matches multiple rows in 'y'.
## i Row 590 of 'y' matches multiple rows in 'x'.
## i If a many-to-many relationship is expected, set 'relationship =
##   "many-to-many"' to silence this warning.

## Warning: Expected 1 pieces. Additional pieces discarded in 14659 rows [1, 2, 3, 4, 5, 6,
## 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...].

## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'mutation_count = as.numeric(mutation_count)'.
## Caused by warning:
## ! NAs introduced by coercion

## Warning: Computation failed in 'stat_signif()'
## Caused by error in 'if (scales$x$map(comp[1]) == data$group[1] | manual) ...':
## ! missing value where TRUE/FALSE needed
```

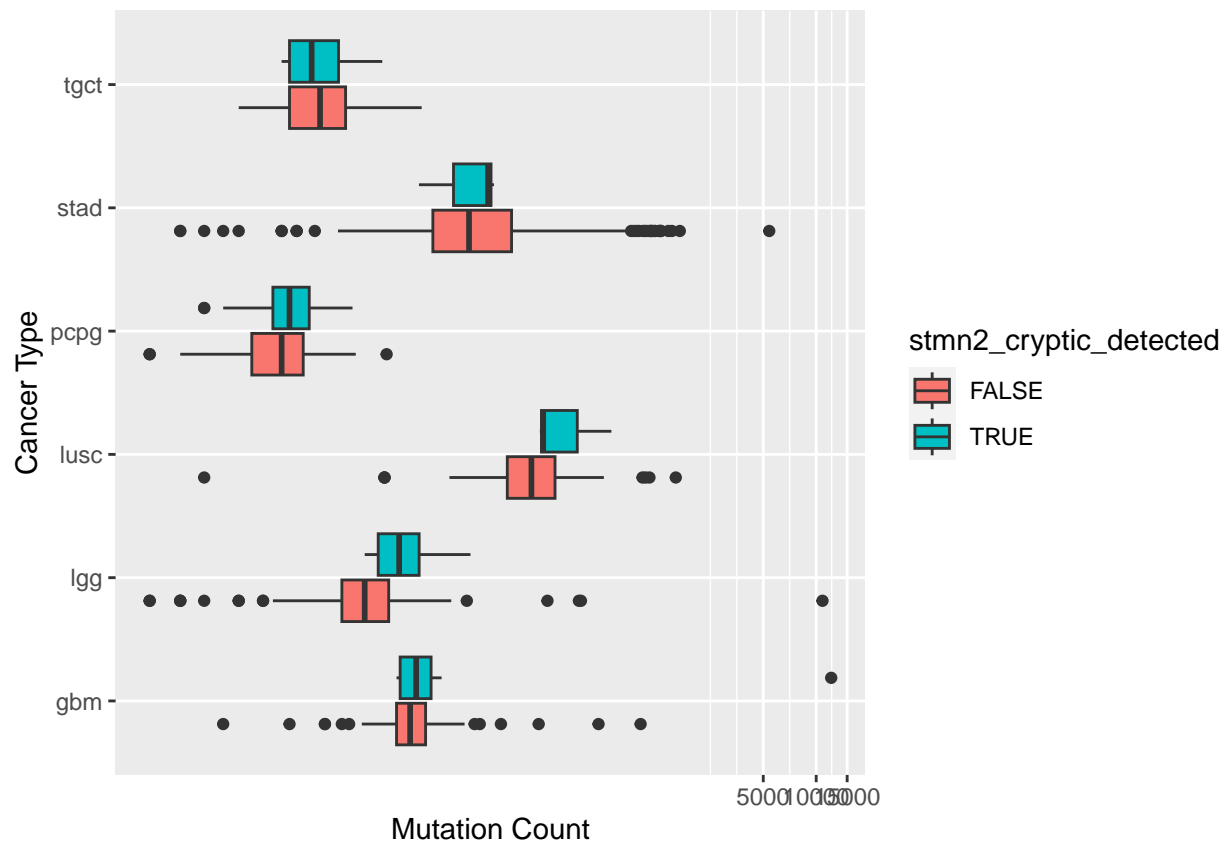


Figure 10:

Survival Comparisons

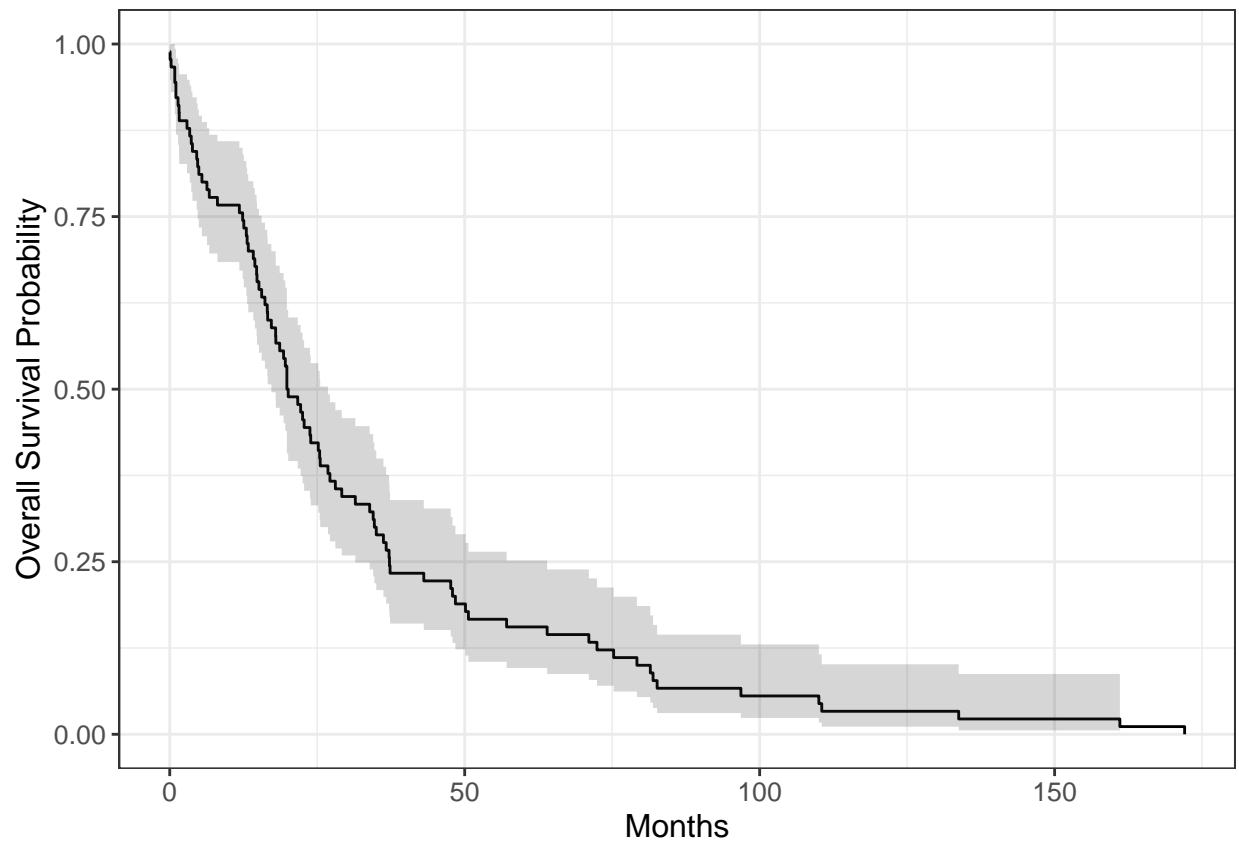


Figure 11:

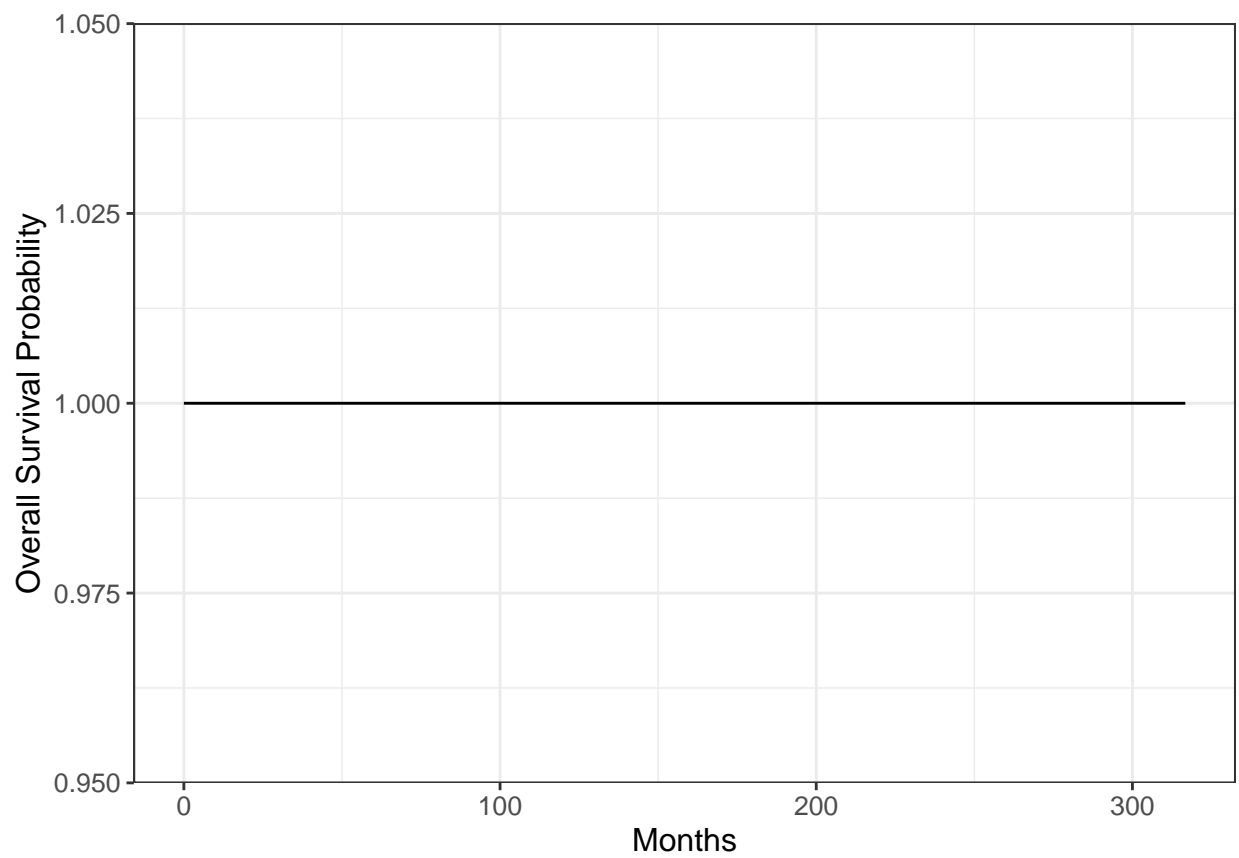


Figure 12:

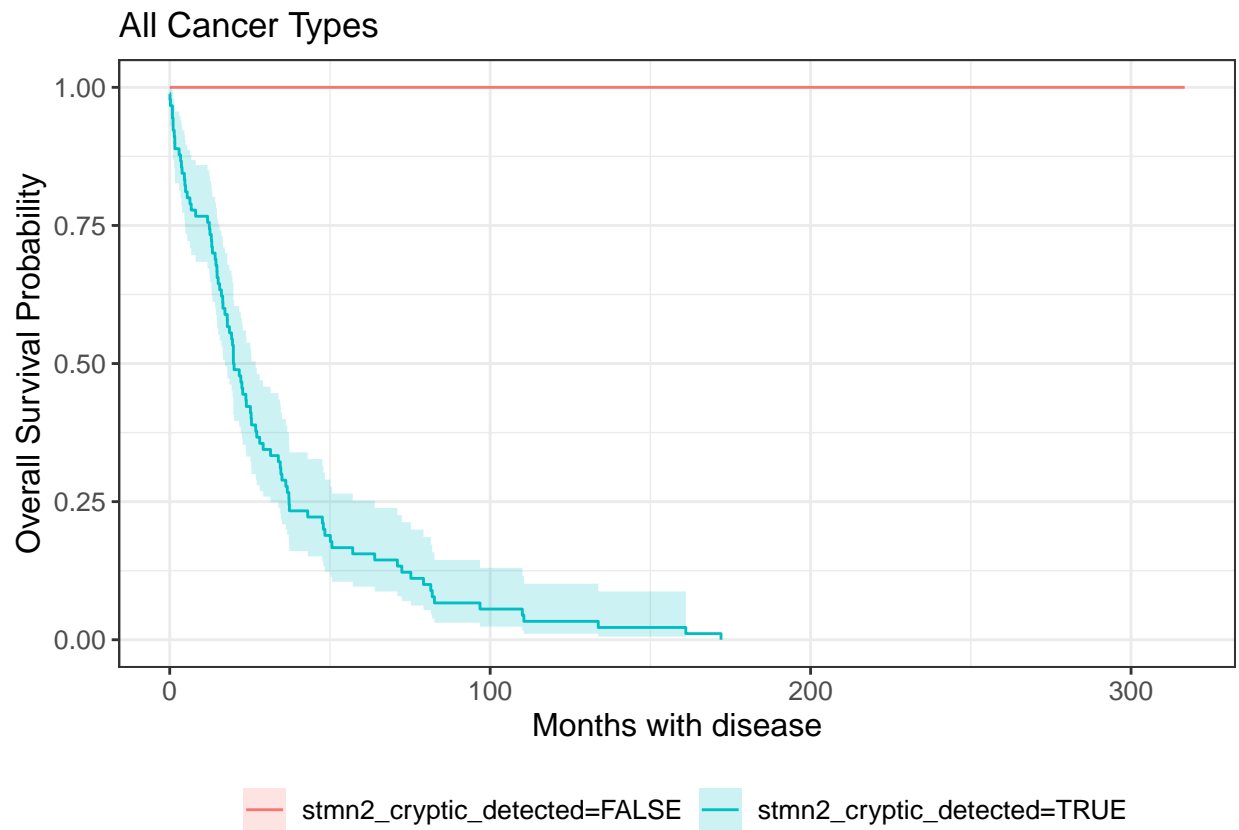


Figure 13:

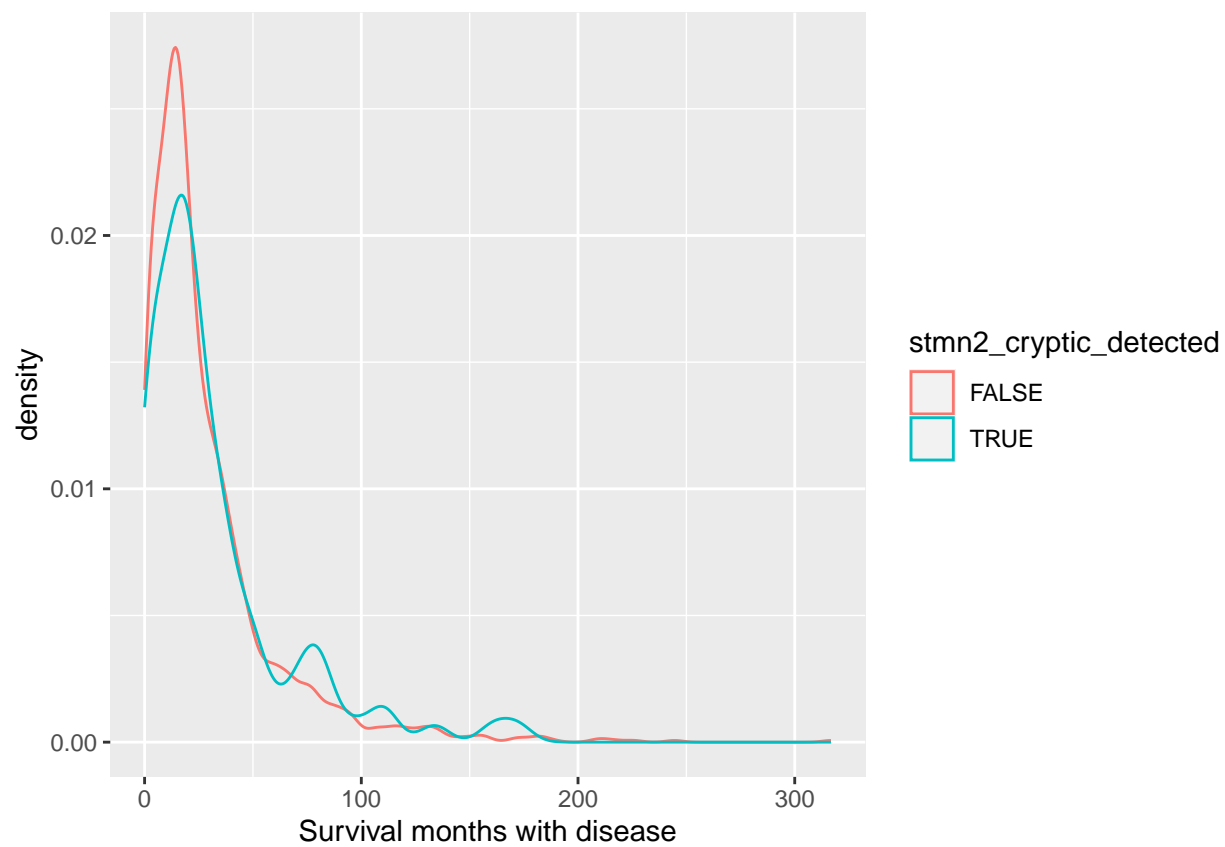


Figure 14:

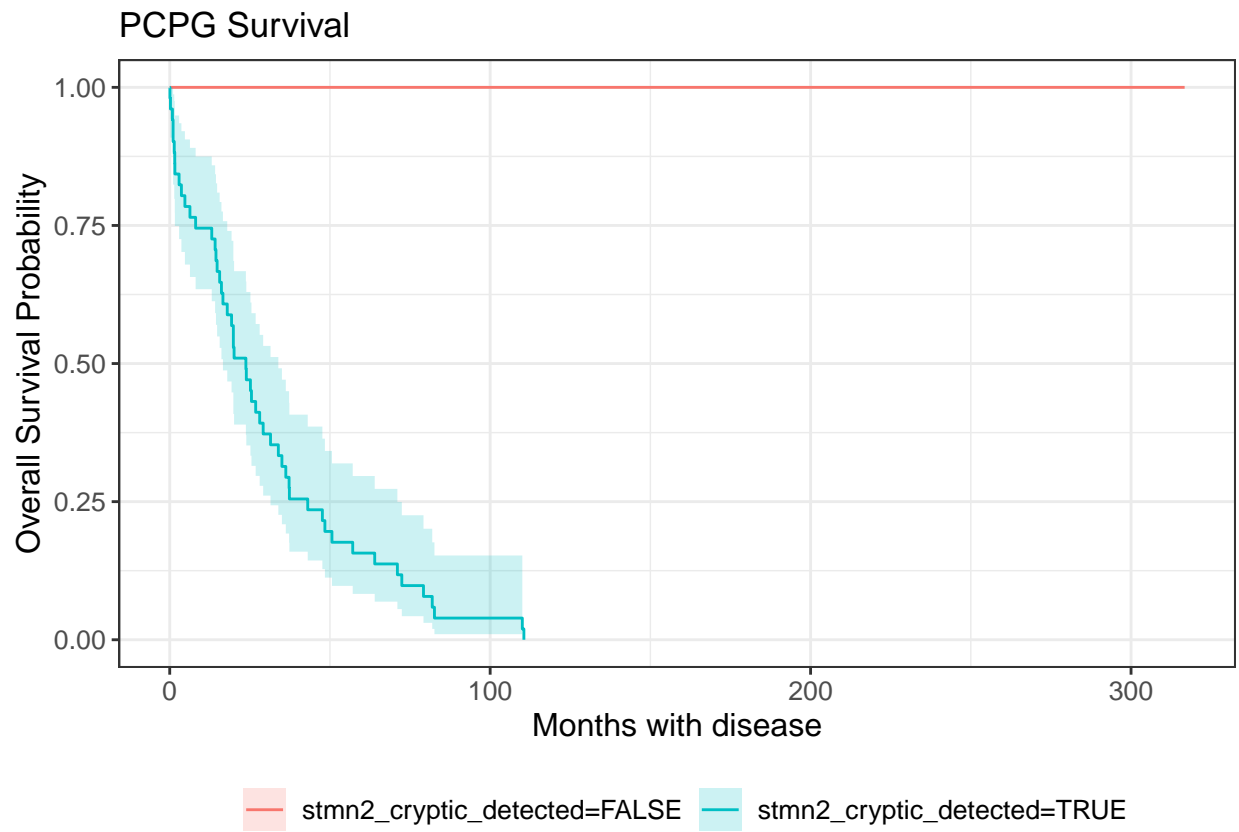


Figure 15:

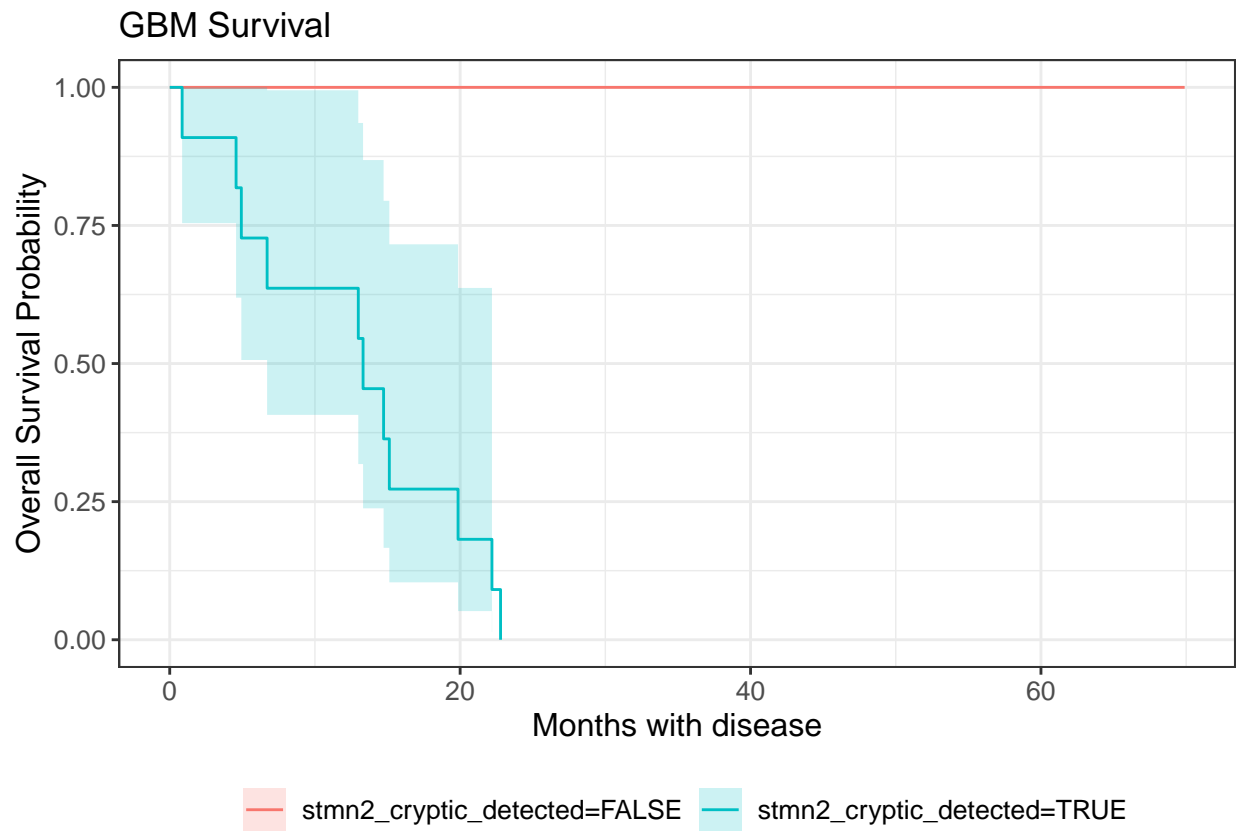


Figure 16:

Mutation Data of one patient

STMN2 cryptic expression

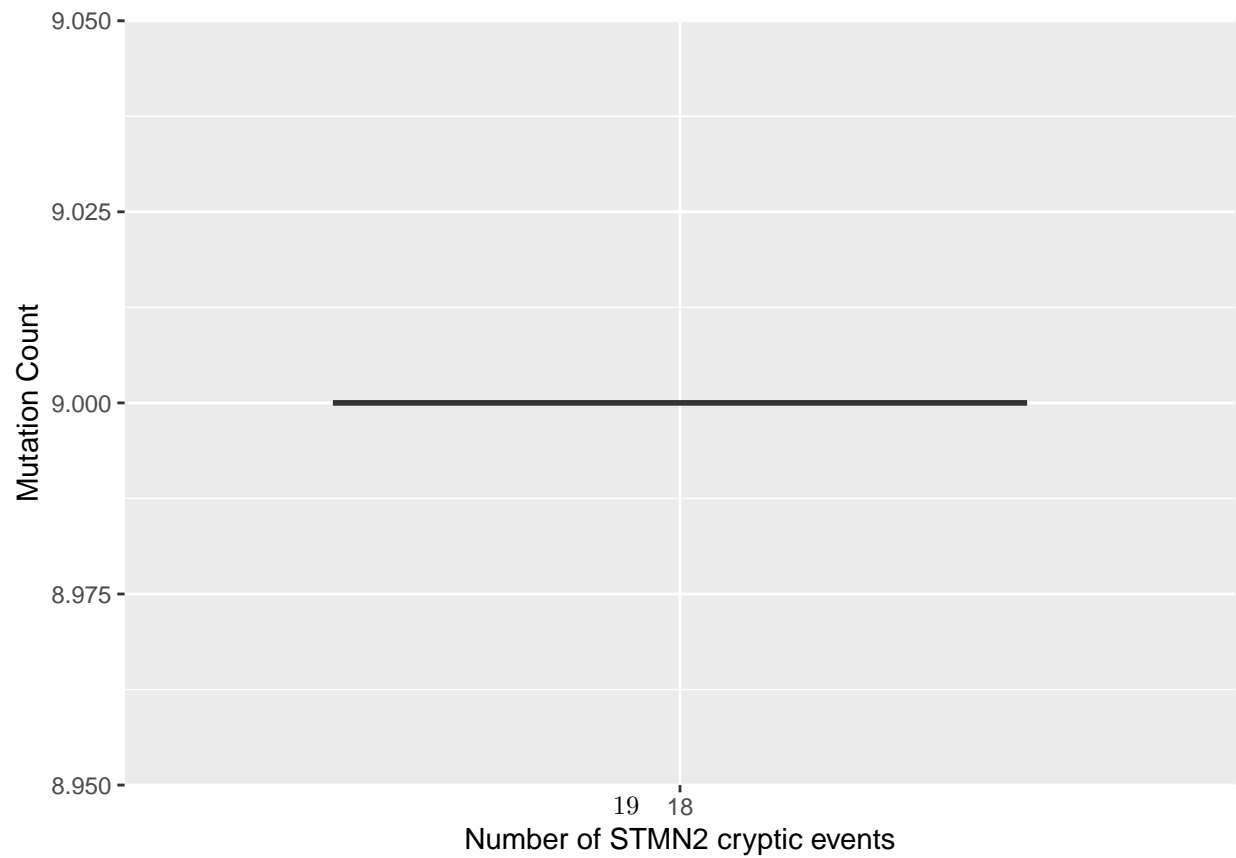
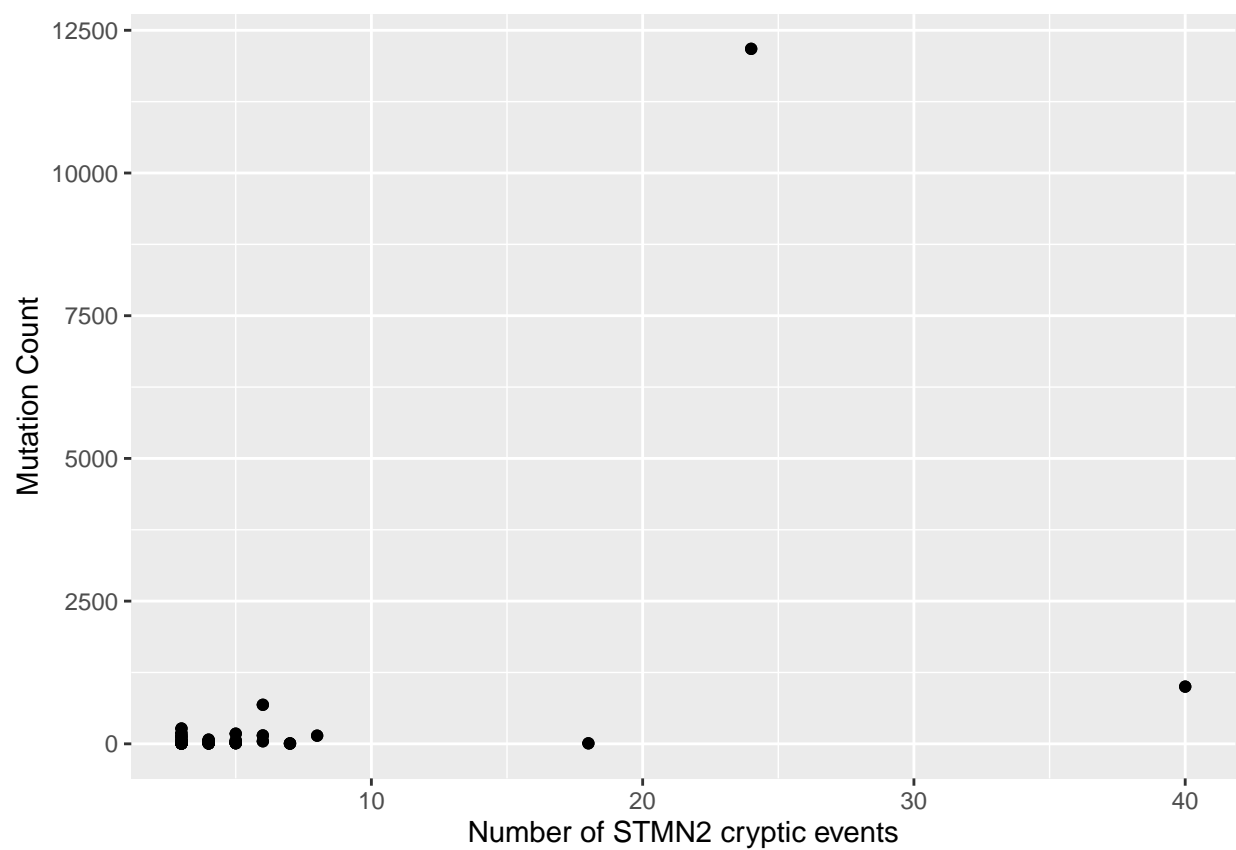


Figure 17: There is no correlation between number of STMN2 cryptic events and number of mutations.

Cancer Driver Genes

Mutations in each cancer gene

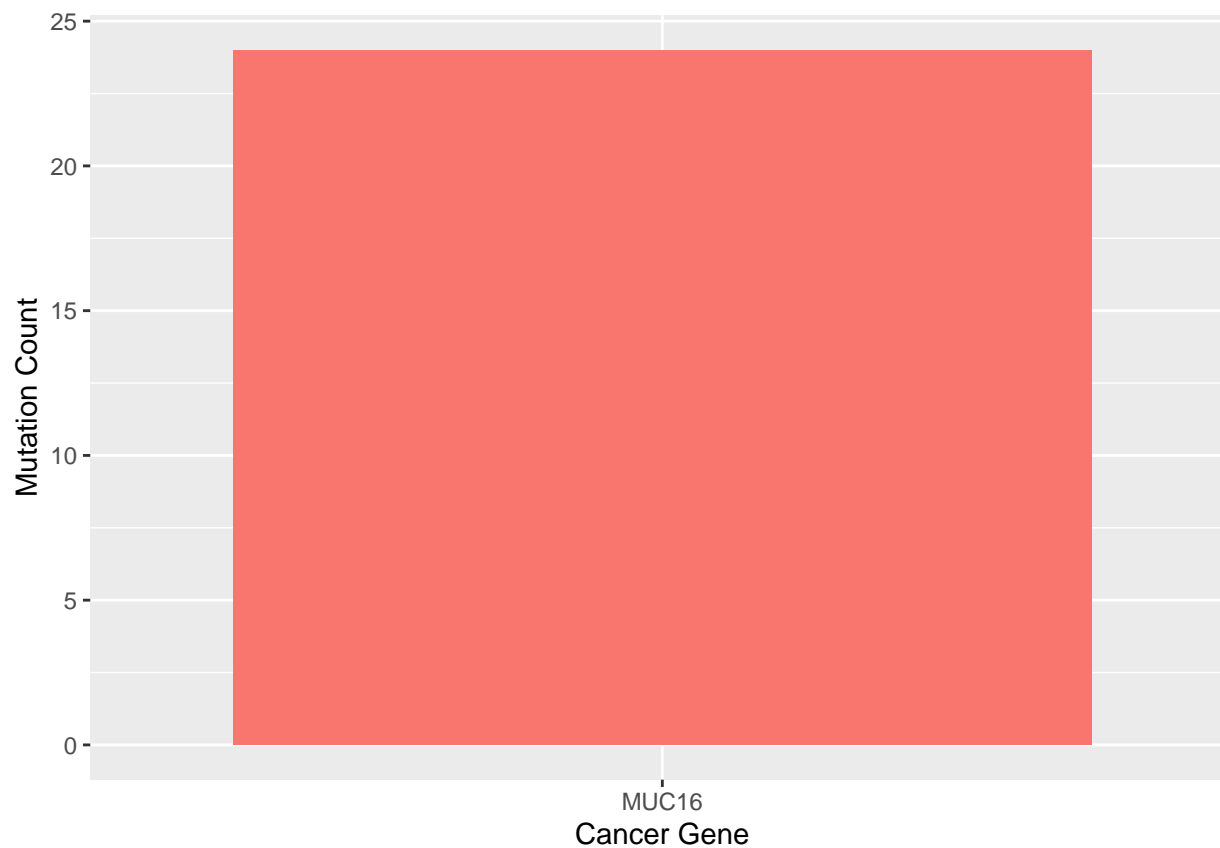


Figure 18: Ovarian cancer gene MUC16 has the greatest number of mutations.

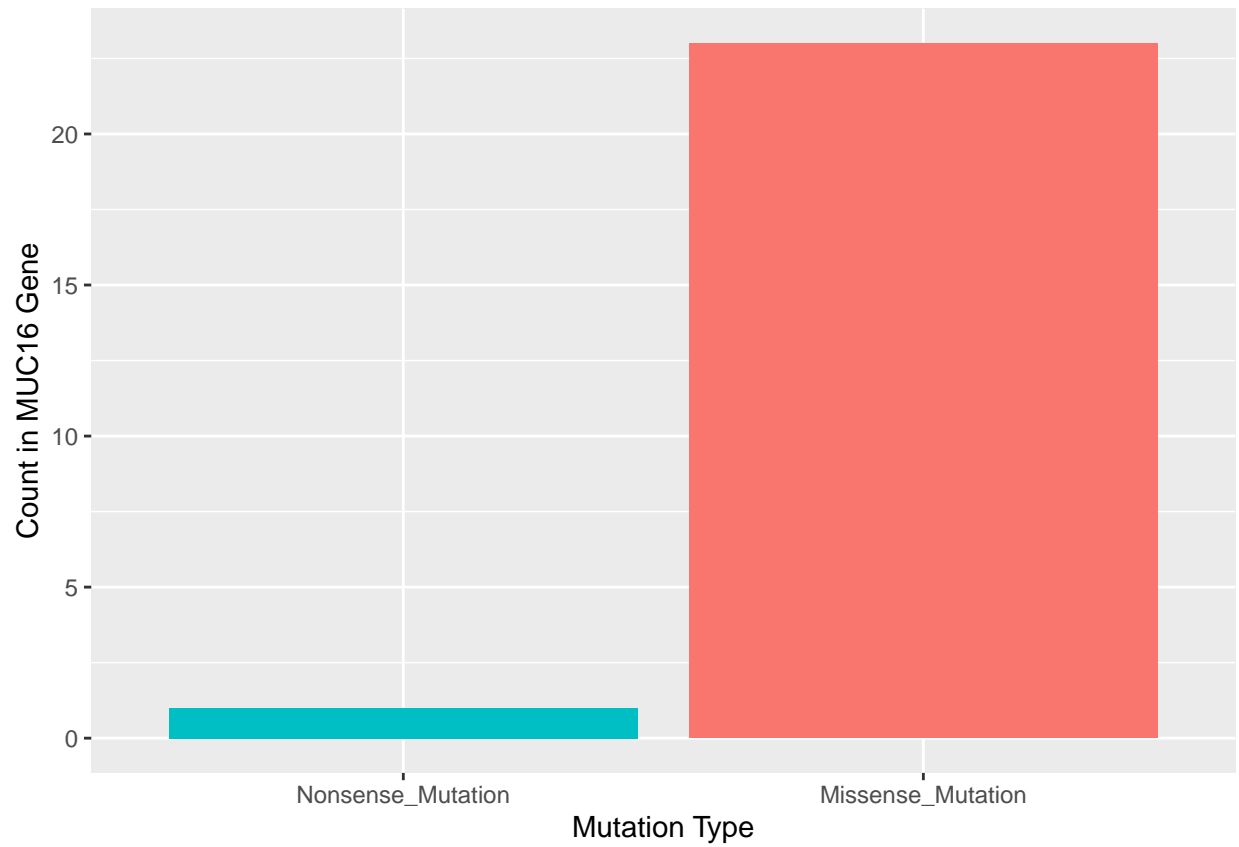


Figure 19: Ovarian cancer gene MUC16 has mostly missense mutations.

Types of cancer genes

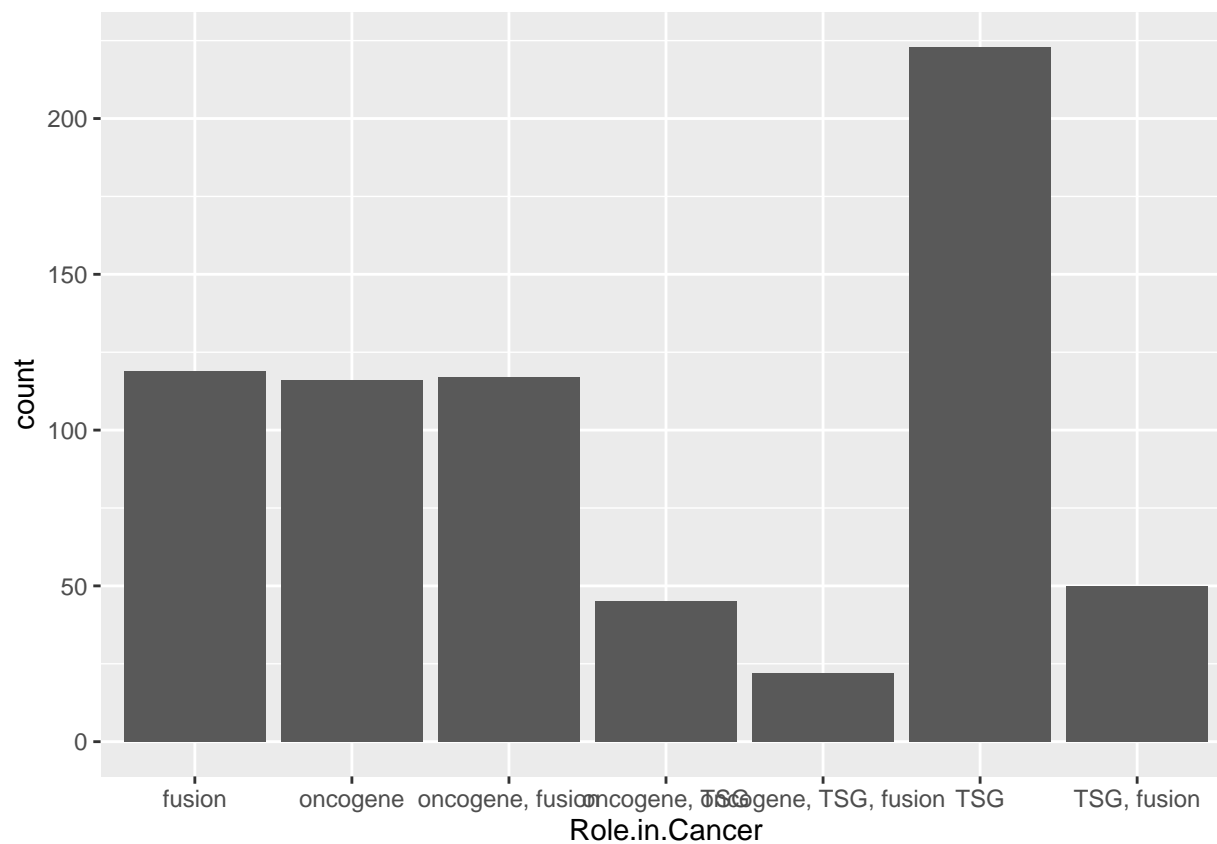


Table 3: 45% of cancer genes with cryptic STMN2 expression are tumour suppressor genes.

TSG	n	percent
no	394	0.5367847
yes	340	0.4632153

Table 4: 39% of cancer genes with cryptic STMN2 expression are oncogenes.

oncogene	n	percent
no	434	0.5912807
yes	300	0.4087193

Table 5: 44% of cancer genes with cryptic STMN2 expression are gene fusions.

fusion	n	percent
no	426	0.5803815

fusion	n	percent
yes	308	0.4196185

TCGA biolinks