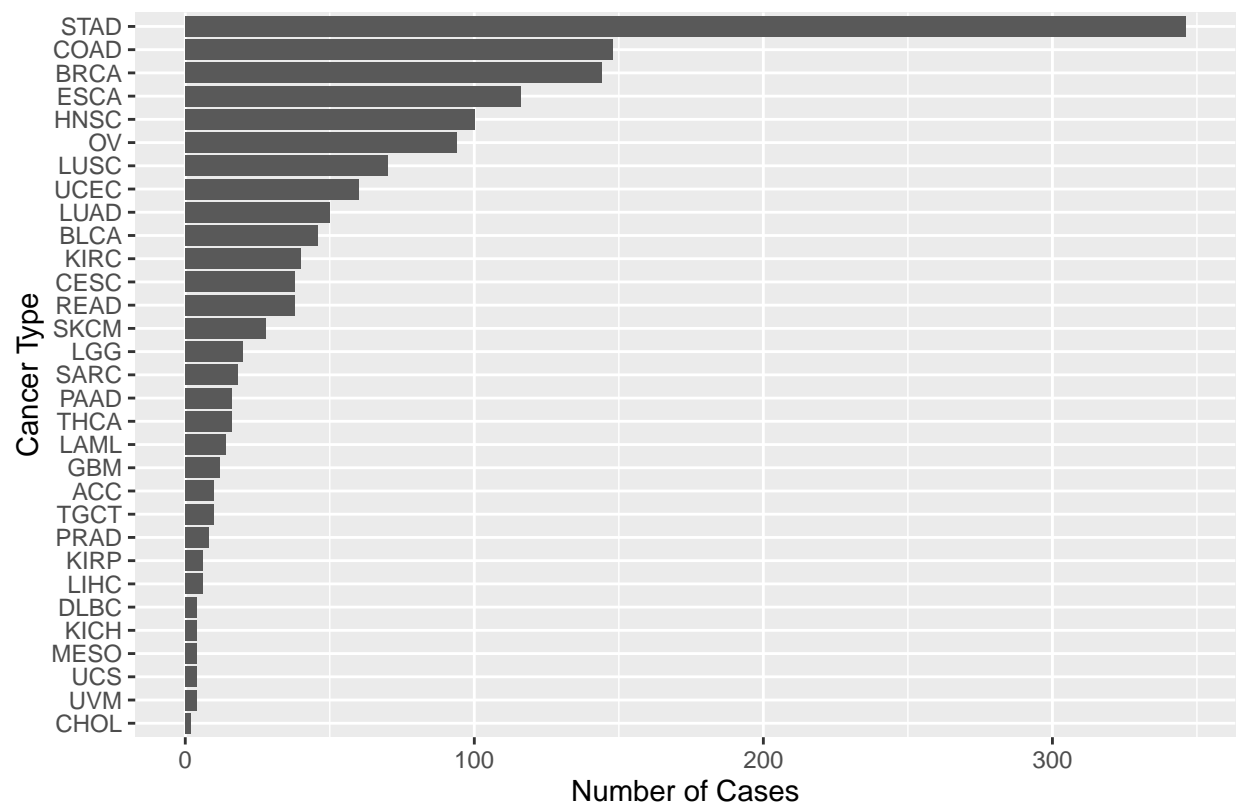
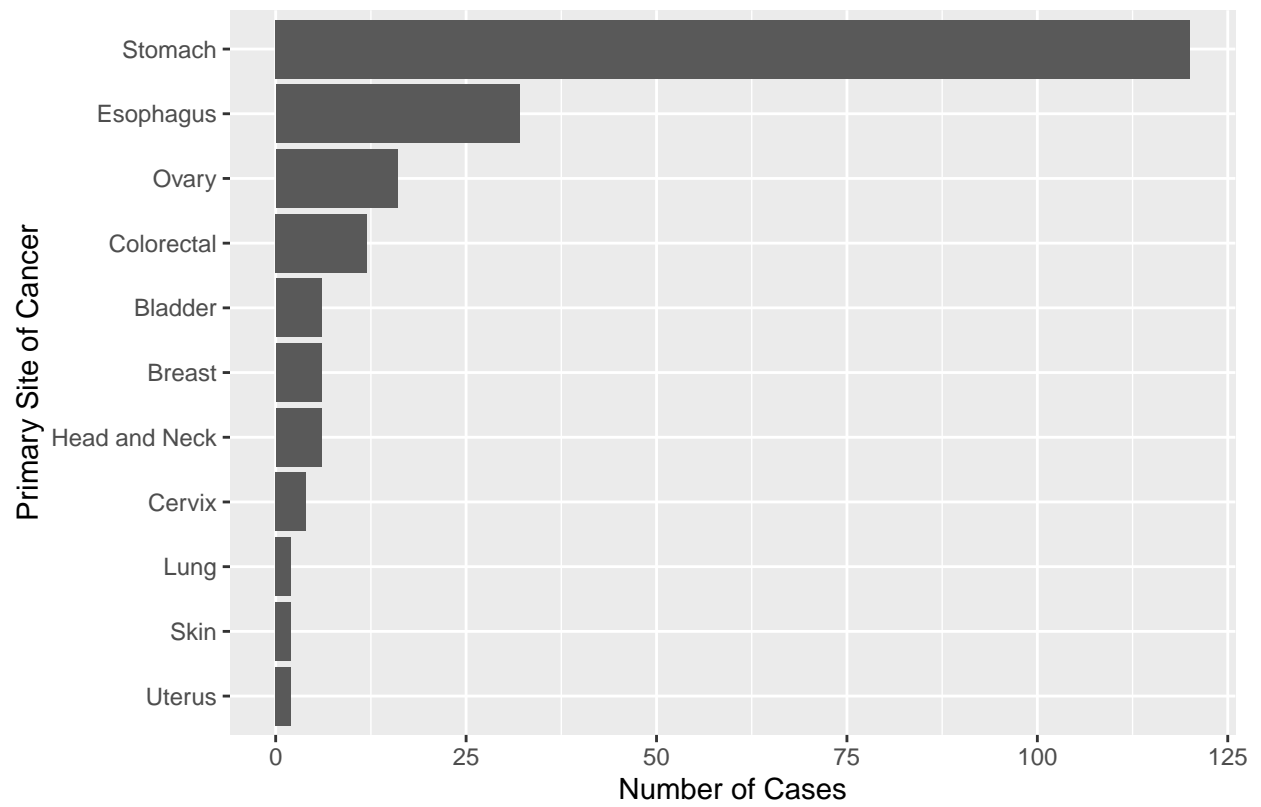


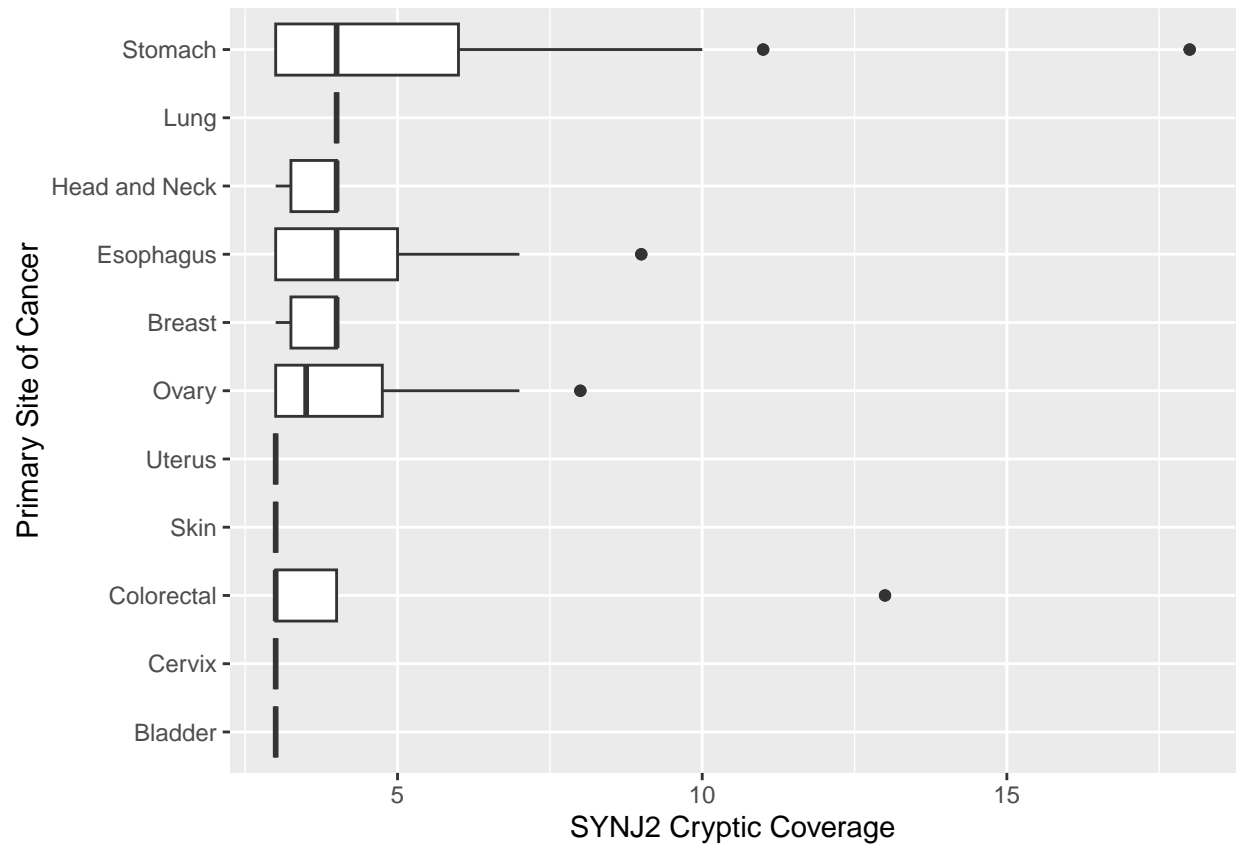
SYNJ2_analysis

Querying for cryptic and annotated SYNJ2 reads

```
gene_name = "SYNJ2" snapcount_coords_cryptic = "chr6:158017291-158019983" snapcount_coords_annotated = "chr6:158017291-158028755" strand_code = "+"
```

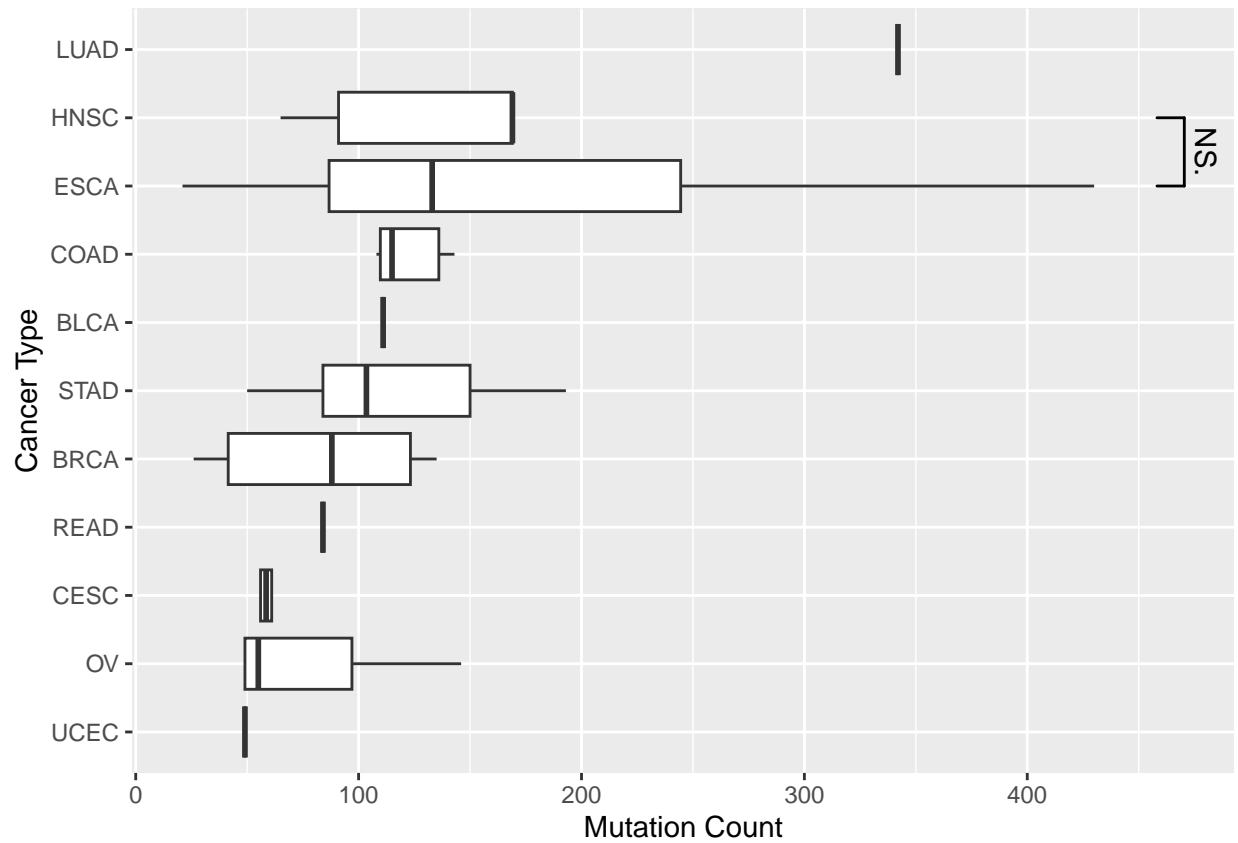






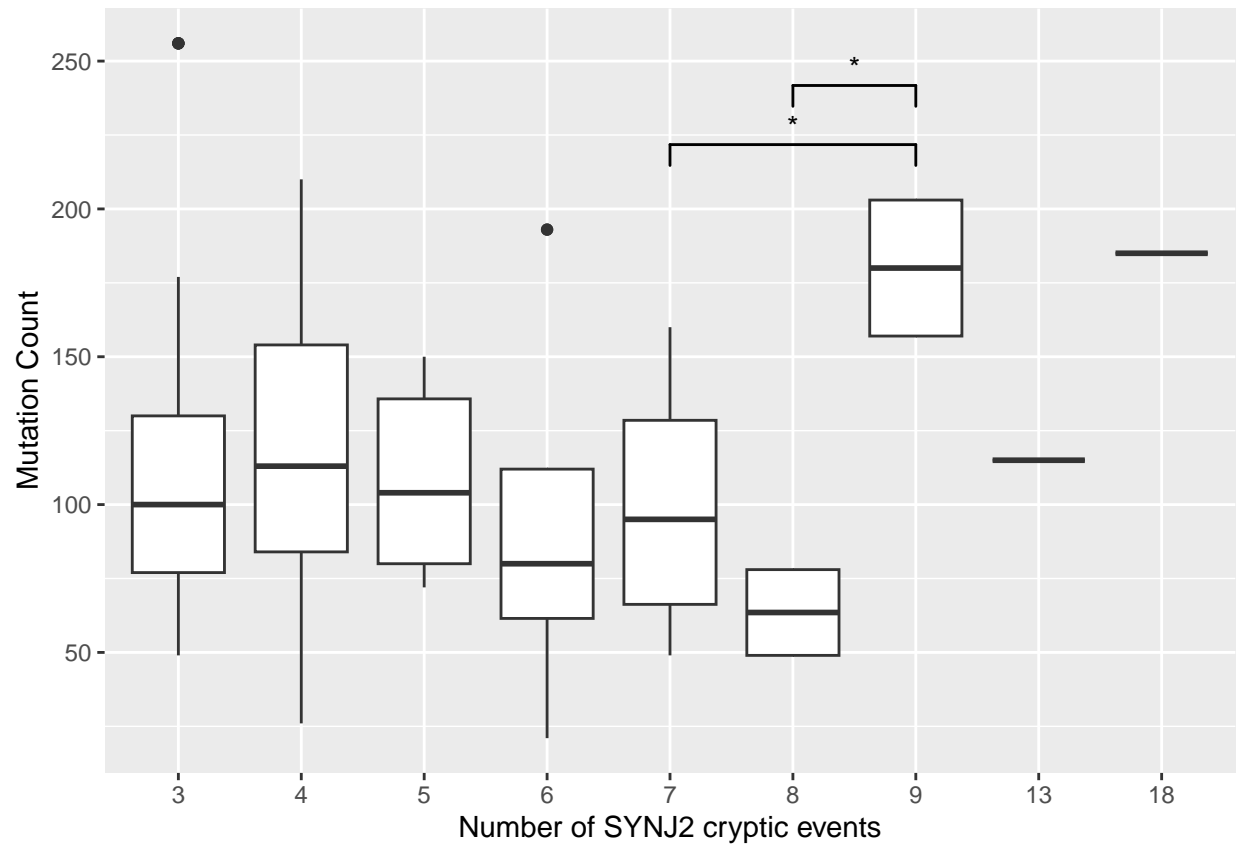
```
## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'mutation_count = .Primitive("as.double")(mutation_count)'.
## Caused by warning:
## ! NAs introduced by coercion

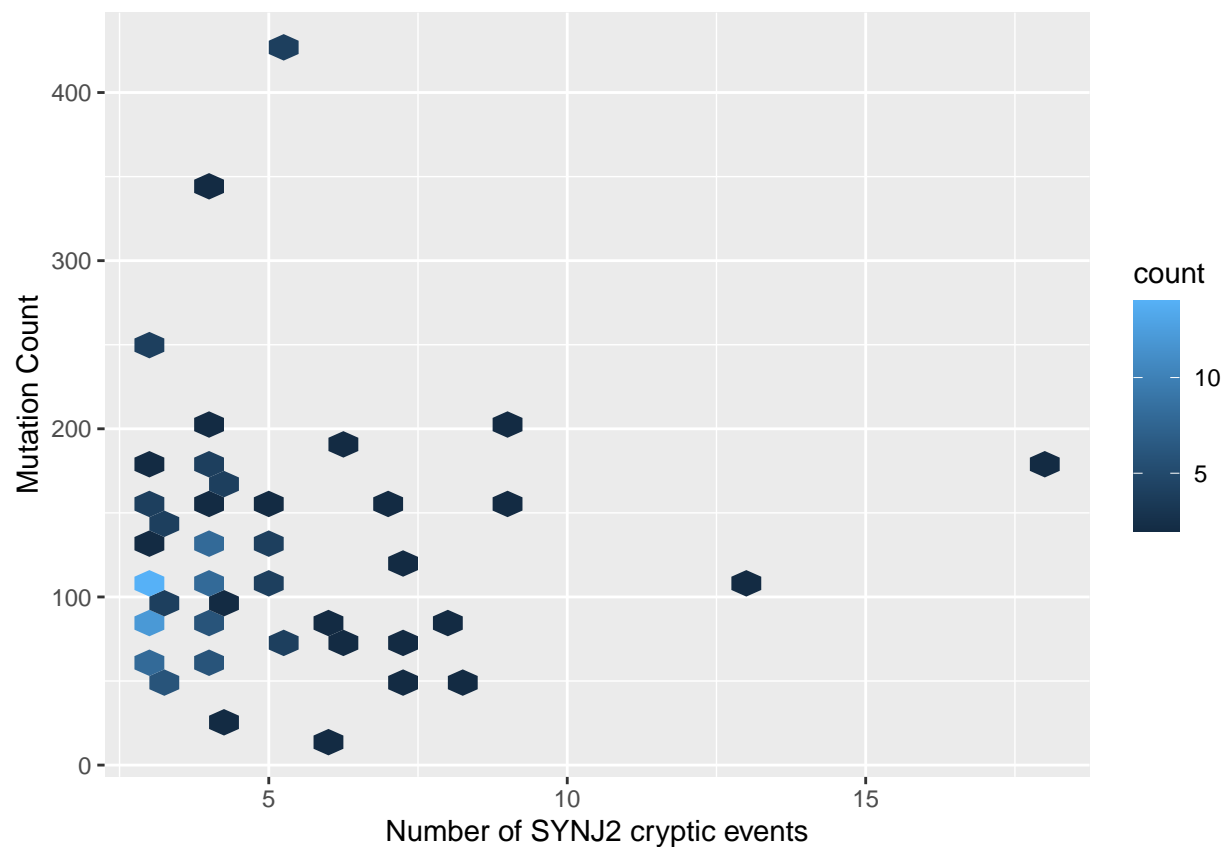
## Warning in wilcox.test.default(c(203, 203, 72, 72, 72, 72, 95, 95, 92, 92, :
## cannot compute exact p-value with ties
```



```
## Warning in wilcox.test.default(c(160, 160, 49, 49, 118, 118, 72, 72), c(203, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(78, 78, 49, 49), c(203, 203, 157, 157)):
## cannot compute exact p-value with ties
```

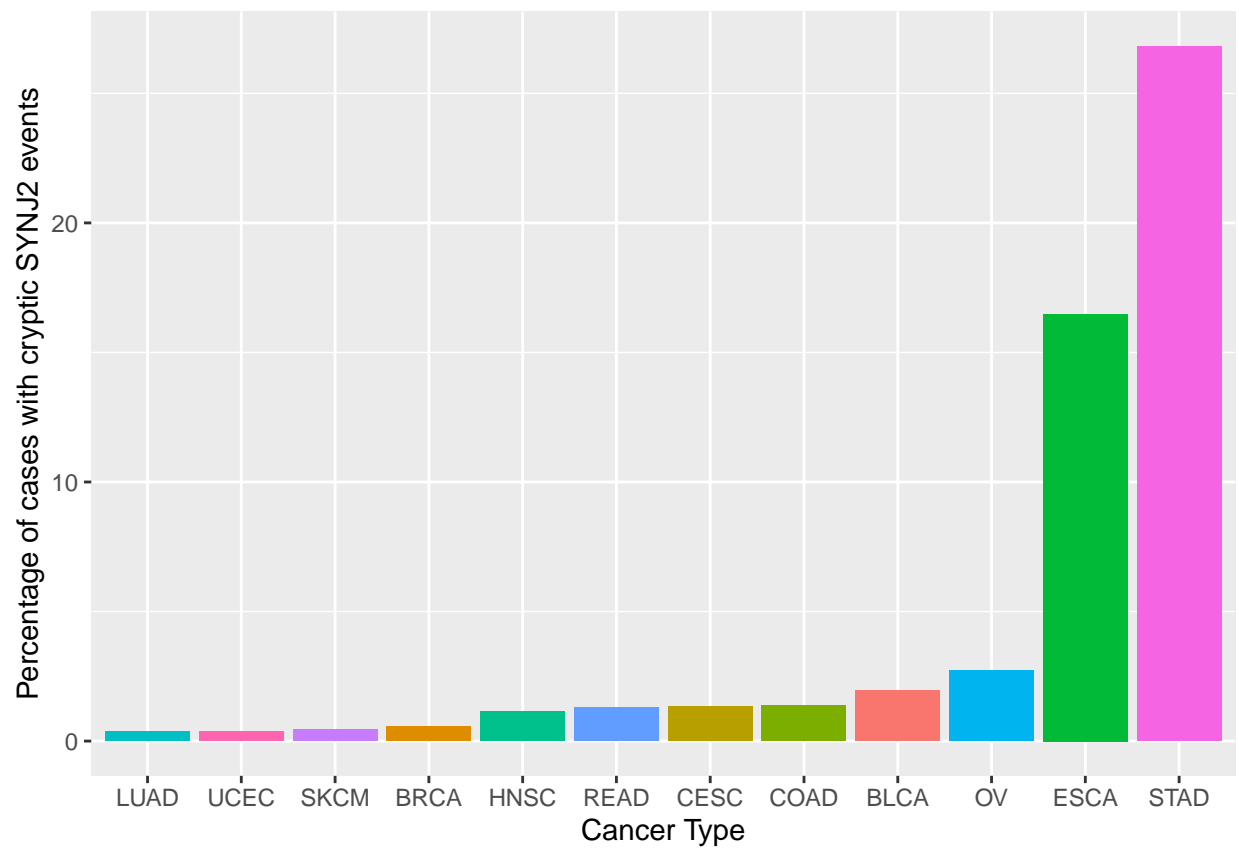


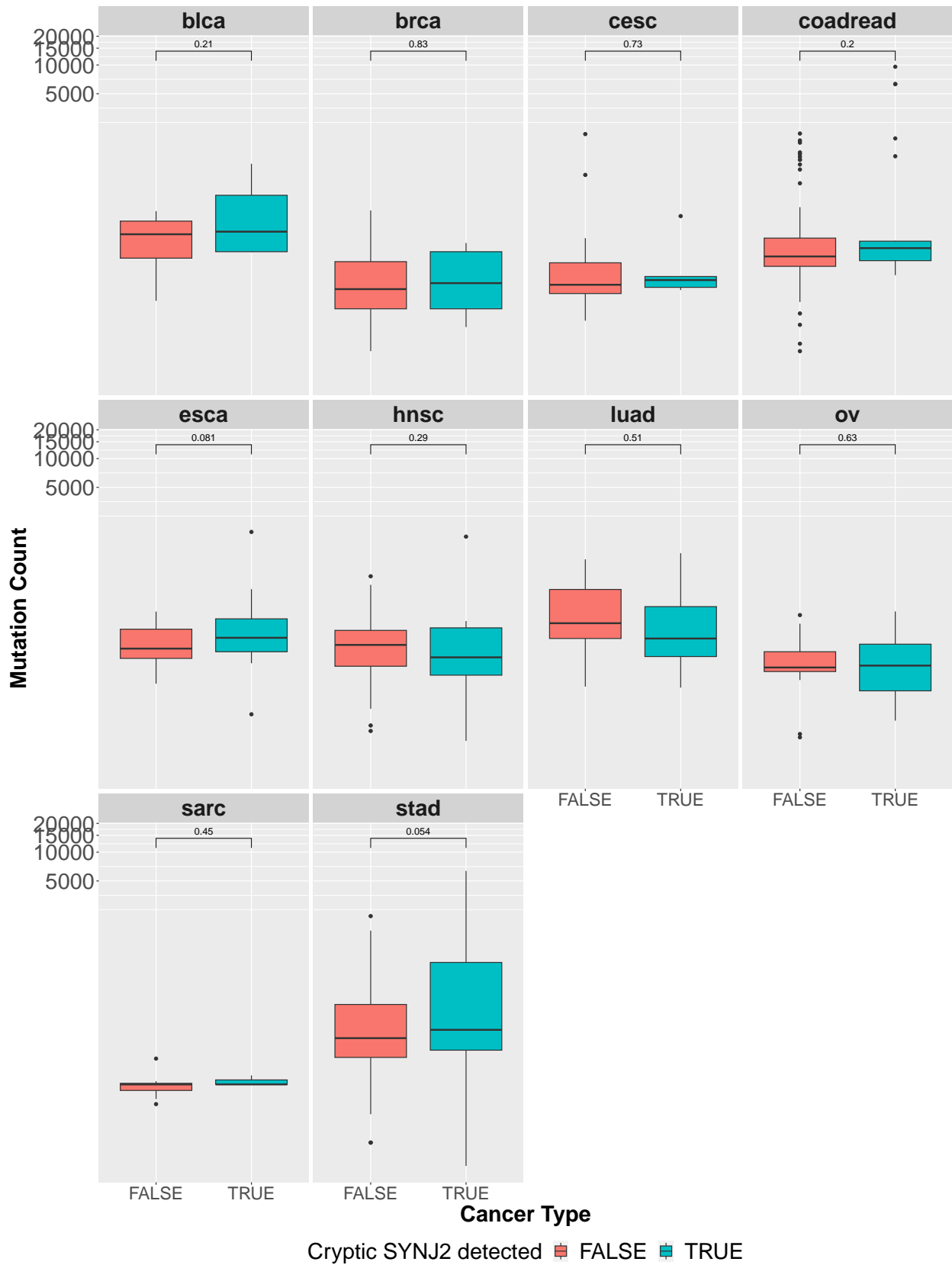


Mutational burden

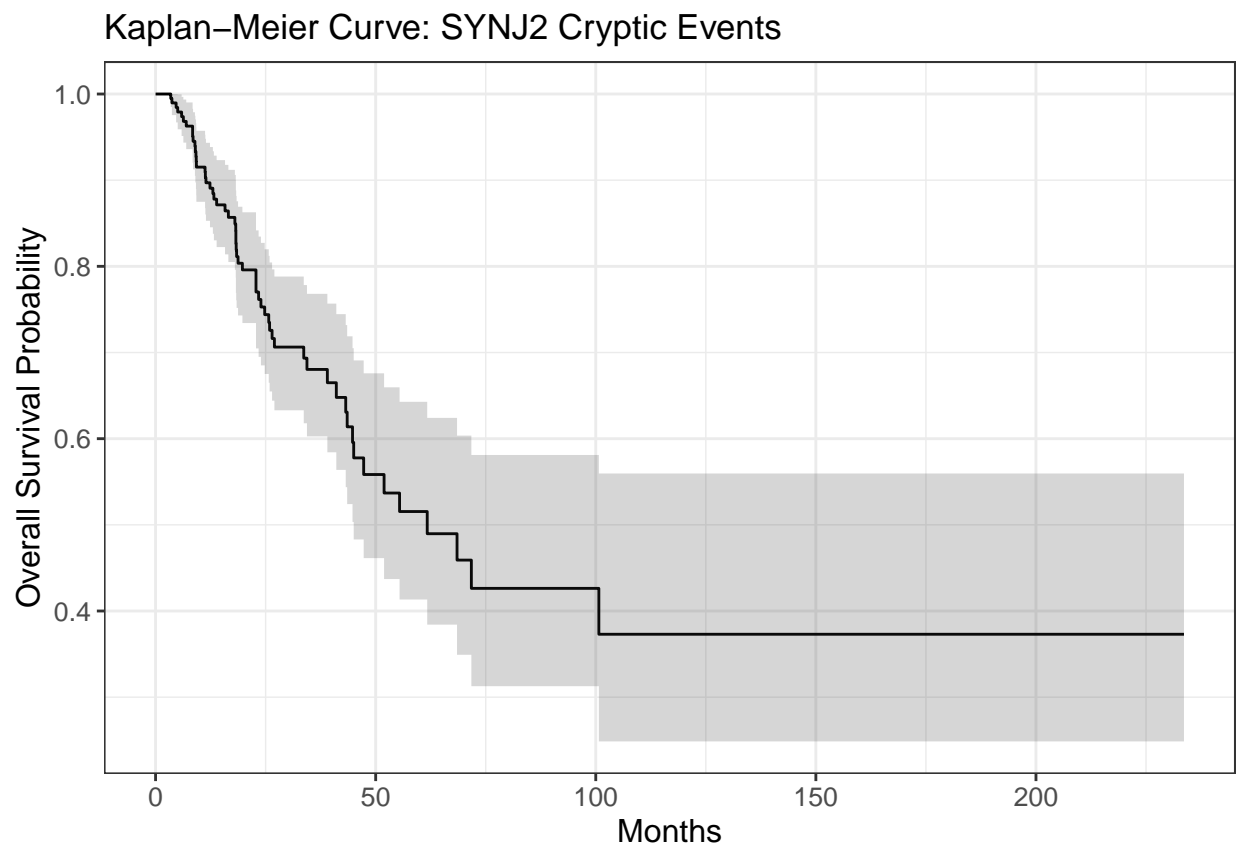
cancer_abbrev	total_mutations	total_mutations_cryptic	percent_with_cryptic
STAD	147953	48240	32.6049489
ESCA	25631	5248	20.4752058
BLCA	99709	2514	2.5213371
OV	36093	902	2.4990995
SKCM	325852	4342	1.3325068
HNSC	74994	806	1.0747526
BRCA	84230	498	0.5912383
COAD	165465	732	0.4423896
LUAD	157145	684	0.4352668
CESC	56054	234	0.4174546
READ	43274	168	0.3882239
UCEC	538960	98	0.0181832

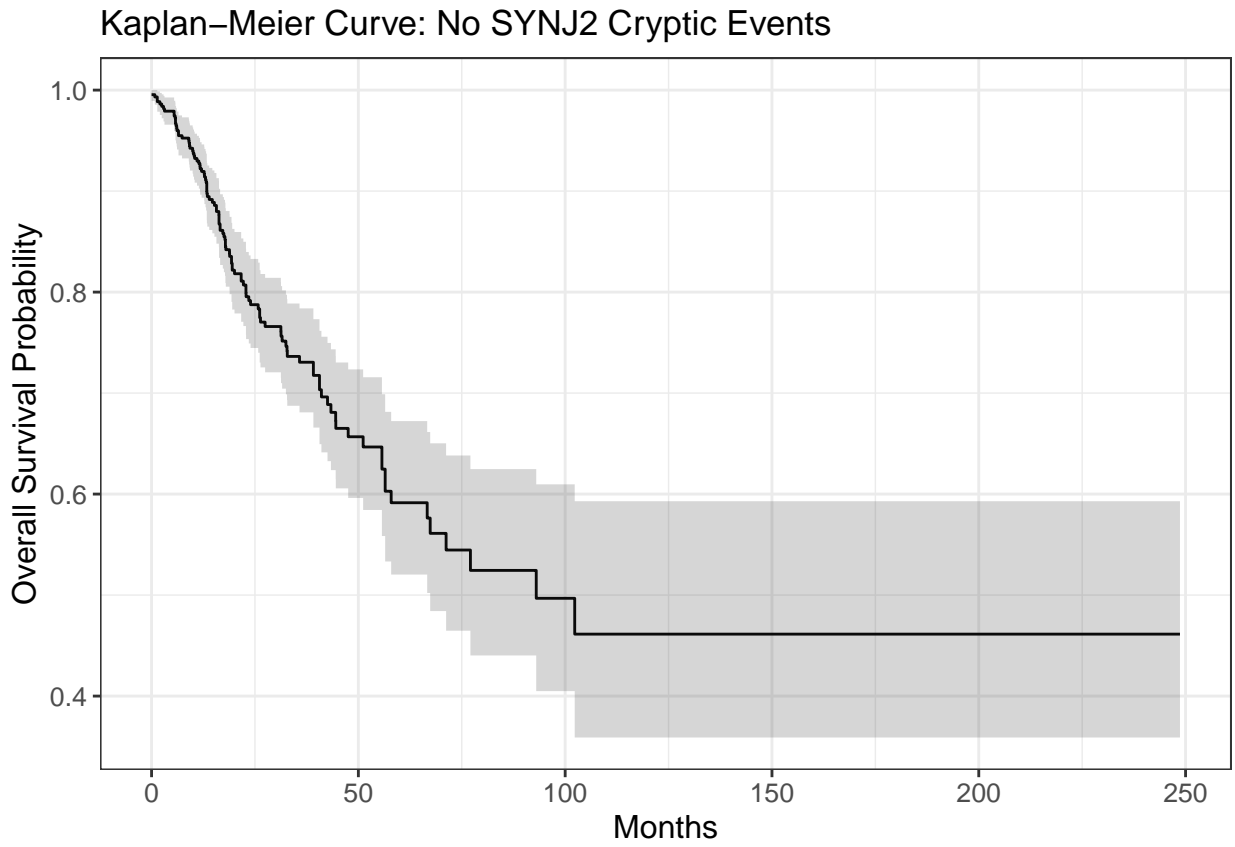
Fraction of each cancer that has cryptic STMN2 events



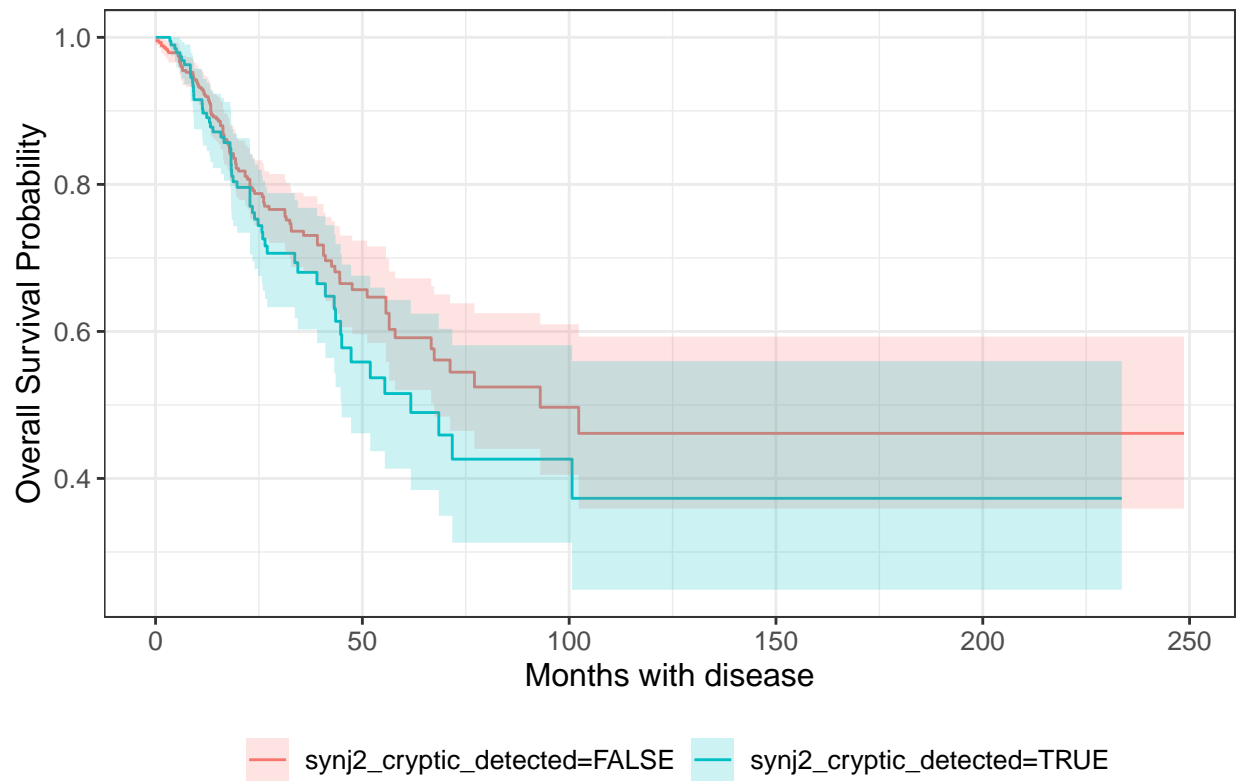


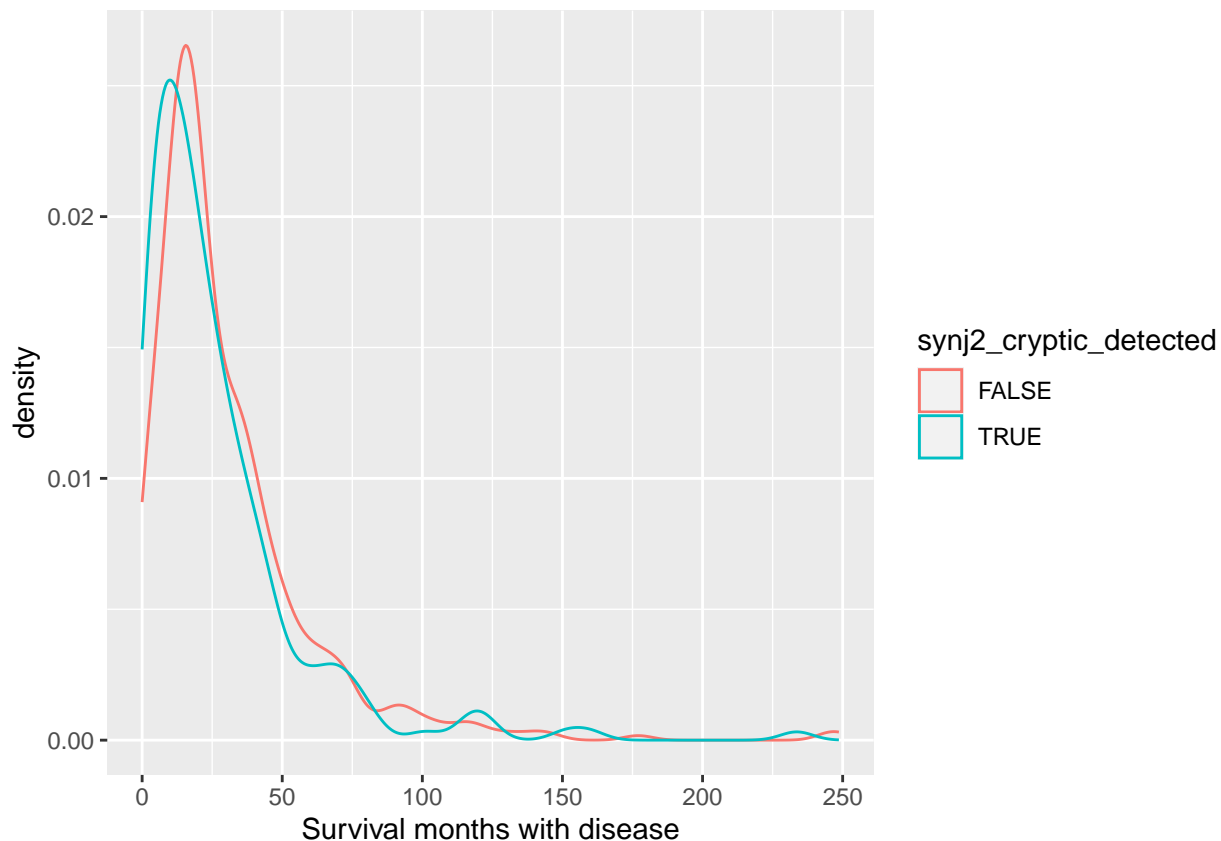
Survival Comparisons





Kaplan–Meier Curve: All Cancer Types (SYNJ2)





Comparing Aneuploidy cancer-by-cancer

```
## Warning: Expected 1 pieces. Additional pieces discarded in 11916 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: 'aneuploidy_score = as.numeric(aneuploidy_score)'.
## Caused by warning:
## ! NAs introduced by coercion
```

```
## Warning in wilcox.test.default(c(25, 25, 25, 16, 19, 2), c(19, 15, 15, 6, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(3, 8, 4, 18, 1), c(11, 6, 21, 3, 5, 23, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(25, 8, 8, 24, 23, 7, 9, 4, 26, 26, 6, 6, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(4, 13, 7, 5, 4, 11, 14, 14, 9, 9, 10, 10, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(3, 16, 22, 15, 9, 13), c(24, 24, 24, 24, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(20, 7, 4, 7, 20, 12, 8, 21, 27, 7, 19, :
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(6, 7, 7), c(4, 4, 15, 14, 8, 16, 7, 7, :
## cannot compute exact p-value with ties
```

