G3viz: an R package to interactively visualize genetic mutation data using a lollipop-diagram

```r
# Retrieve TP53 mutation data of the MSK-IMPACT study from the cBioPortal server
mutation.dat <- getMutationsFromCbioportal("msk_impact_2017", "TP53")
#> Found study msk_impact_2017
#> Found mutation data set msk_impact_2017_mutations
#> 10945 cases in this study

# Using the `nature2` chart theme
chart.options <- g3Lollipop.theme(theme.name = "nature2",
                                  title.text = "TP53 gene mutation (MSK-IMPACT)",
                                  y.axis.label = "# of TP53 mutations",
                                  legend.title = "Mutation Class")

# Render g3viz lollipop diagram
g3Lollipop(mutation.dat,
           gene.symbol = "TP53",
           btn.style = "blue",
           plot.options = chart.options,
           output.filename = "TP53_MSK_IMPACT_mutation")
#> Factor is set to Mutation_Class
```

save as SVG   **save as PNG**