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

Default mapping table between variant classification and mutation class

Mutation\_Type

Mutation\_Class

Short\_Name

In\_Frame\_Del

Inframe

IF del

In\_Frame\_Ins

Inframe

IF ins

Silent

Inframe

Silent

Targeted\_Region

Inframe

IF

Missense\_Mutation

Missense

Missense

Frame\_Shift

Truncating

FS

Frame\_Shift\_Del

Truncating

FS del

Frame\_Shift\_Ins

Truncating

FS ins

Nonsense\_Mutation

Truncating

Nonsense

Nonstop\_Mutation

Truncating

Nonstop

Splice\_Region

Truncating

Splice

Splice\_Site

Truncating

Splice

3’Flank

Other

3’Flank

3’UTR

Other

3’UTR

5’Flank

Other

5’Flank

5’UTR

Other

5’UTR

De\_novo\_Start\_InFrame

Other

de\_novo\_start\_inframe

De\_novo\_Start\_OutOfFrame

Other

de\_novo\_start\_outofframe

Fusion

Other

Fusion

IGR

Other

IGR

Intron

Other

Intron

lincRNA

Other

lincRNA

RNA

Other

RNA

Start\_Codon\_Del

Other

Nonstart

Start\_Codon\_Ins

Other

start\_codon\_ins

Start\_Codon\_SNP

Other

Nonstart

Translation\_Start\_Site

Other

TSS

Unknown

Other

Unknown