

Supplementary Information for

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

Table S1. Default mapping table between *Mutation Type* (a.k.a., *Variant Classification*) to *Mutation Class* in g3viz

Mutation_Type	Mutation_Class	Short_Name
Inframe		
In_Frame_Del	Inframe	IF del
In_Frame_Ins	Inframe	IF ins
Silent	Inframe	Silent
Targeted_Region	Inframe	IF
Missense		
Missense_Mutation	Missense	Missense
Truncating		
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
Other		
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