Comp	name	usage	icon
geom	$geom_rect$	rectangle	
	${\rm geom_segment}$	segment	- —
	geom_chevron	chevron	1
	$geom_arrow$	arrow	** ·······
	$geom_arch$	arches	$\Lambda \subseteq \Lambda$
	geom_bar	bar	
	$geom_alignmer$	ntgene structure	
stat	$stat_aggregate$	$\begin{array}{c} {\rm aggregation~in~sliding~win-} \\ {\rm dow} \end{array}$	
	$stat_coverage$	coverage for reads	
	$stat_gene$	gene structure	
	stat_identity	identity mode	_= =
	$stat_mismatch$	mismatch summary for variants	
	$stat_stepping$	stepping levels	
	stat_table	tabulate ranges	-
coord	linear	default linear but facet by chromosomes space	शिष्ट
	genome	put everything on genome coordiante	
	truncate	compact view by cutting	1
	gaps	gaps	for a
layout	default	normal layout	
	karyogram	karyogram layout	
	circle	circular layout	G
faceting formula		formula based faceting	644 444 44- 864
	ranges	ranges based faceting	
scale	not extended	ggplot2 default	

Table 1: Components of the basic grammar of graphics, with the extensions available in ggbio.

object	usage	icon
GRanges	Genomic intervals	
GRangesList	Genomic interval list	
IRanges	intervals	
Gapped Alignments	gapped alignments	
BamFile	alignemnts files	
character	for flat files	
Rle/RleList	atomic vector	
TranscriptDb	gene structure	
VCF		A C T G

Table 2: Formal data model and their default graphics