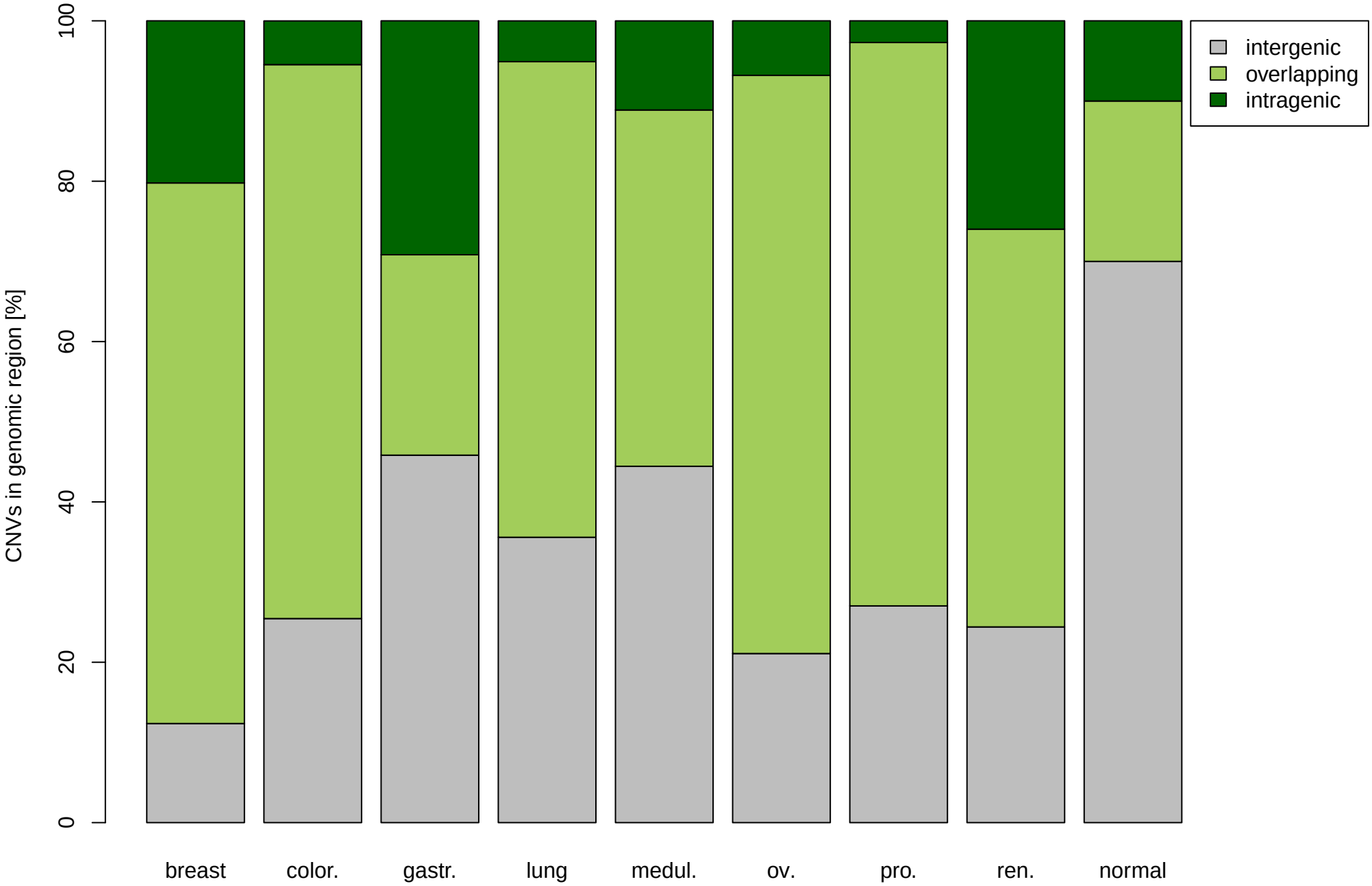
CNVs in genomic region [%]
0
20
40
60
80
100
breast
color.
gastr.
lung
medul.
ov.
pro.
ren.
normal
intergenic
overlapping
intragenic