Distal intergenic regions (31.8%)

5'- or 3'- proximal regions (31.8%)

5' or 3'UTR (1.13%)

span (13.68%)

non-first coding exon (12.53%)

1st coding exon (2.17%)

non-first Intron (7.12%)

1st Intron (3.12%)

Multiples (12.8%)