

FT_RGC

Proportion of subcategory in observed novel isoforms

100%
75
50
25
0

alt_left_site_known
alt_left_site_novel
alt_right_site_known
alt_right_site_novel
alternative_polya_site_left
alternative_polya_site_right
alternative_structure_known
alternative_structure_novel
correct_polya_site_left
correct_polya_site_right
exon_detach_known
exon_detach_novel
exon_elongation_left
exon_elongation_right
exon_gain_known
exon_gain_novel
exon_merge_known
exon_merge_novel
exon_misalignment
exon_skipping_known
exon_skipping_novel
exon_intron_flanking_left
exon_intron_flanking_right
extra_intron_known
extra_intron_novel
fake_micro_intron_retention
fake_terminal_exon_left
fake_terminal_exon_right
ism
incomplete_intron_retention_left
incomplete_intron_retention_right
intron_alternation_known
intron_alternation_novel
intron_migration
intron_retention
intron_shift
ism_left
ism_right
major_exon_elongation_left
major_exon_elongation_right
mono_exon_match
mutually_exclusive_exons_known
mutually_exclusive_exons_novel
terminal_exon_misalignment_left
terminal_exon_misalignment_right
terminal_exon_shift_known
terminal_exon_shift_novel
terminal_site_match_left
terminal_site_match_left_precise
terminal_site_match_right
terminal_site_match_right_precise

Subcategories

21.3%

22.2%

17.1%

19.1%

18.8%

24.4%

21.5%

20.9%