Increase upon intron region deletion (intronic–intronic pairs) — % Intron regions with phenotype vs Cutoff for calling intron region phenotype (fraction of significant pairs). Legend: Intron regions in fitness genes (red); Intron regions in non-fitness genes (blue). Annotations: 0.3; Only 'clean' guide pairs; Only intron regions with min. 2 informative guide pairs; Requiring min. 2 pairs with increase; 2.6%; 0.3%

Increase upon single cut (intronic–intergenic pairs) — % Intron regions with phenotype vs Cutoff for calling intron region phenotype (fraction of significant pairs). Annotations: 0.3; T12_NT:T0; Only intron regions with min. 2 informative guide pairs; Requiring min. 2 pairs with increase; 0%

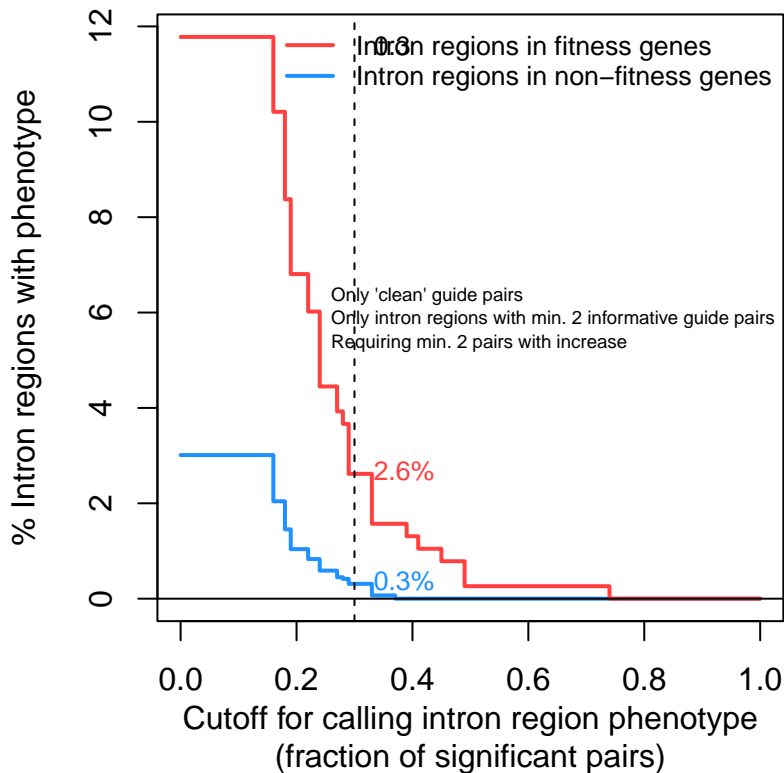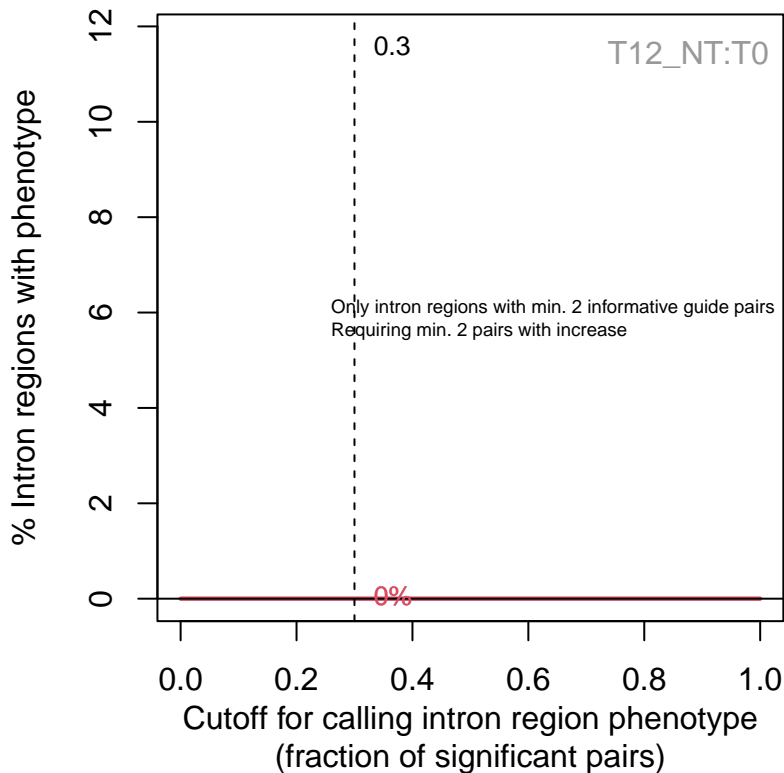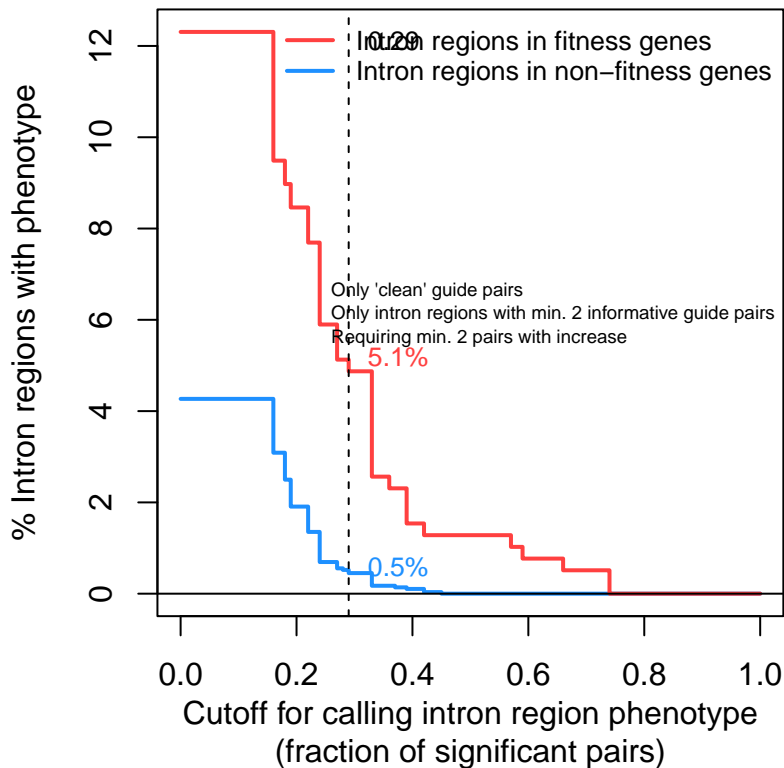**Increase upon intron region deletion (intronic–intronic pairs)**

Increase upon single cut (intronic–intergenic pairs)

Left plot:
- Y-axis: % Intron regions with phenotype
- X-axis: Cutoff for calling intron region phenotype (fraction of significant pairs)
- 0.29
- Intron regions in fitness genes
- Intron regions in non-fitness genes
- Only 'clean' guide pairs
- Only intron regions with min. 2 informative guide pairs
- Requiring min. 2 pairs with increase
- 5.1%
- 0.5%

Right plot:
- Y-axis: % Intron regions with phenotype
- X-axis: Cutoff for calling intron region phenotype (fraction of significant pairs)
- 0.29
- T18_NT:T0
- Only intron regions with min. 2 informative guide pairs
- Requiring min. 2 pairs with increase
- 0%