

ensembl_ids and genomic_context of a variant

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Packages

rs137931178 as an example

I have checked **rs137931178**.

HCG23 and **LOC105379657** are available in the `ensembl_ids` segment although none of them is in the `genomic_context` segment.

```
rs137931178 <- gwasrapidd::get_variants(variant_id = "rs137931178")

unique_genes_of_rs137931178_in_genomic_context <- unique(rs137931178@genomic_contexts$gene_name)

unique_genes_of_rs137931178_in_ensembl_ids <- unique(rs137931178@ensembl_ids$gene_name)

genes_of_genomic_context_of_rs137931178_not_in_ensembl_ids_rs137931178 <- setdiff(unique_genes_of_rs137931178, unique_genes_of_rs137931178_in_genomic_context)

print(genes_of_genomic_context_of_rs137931178_not_in_ensembl_ids_rs137931178)

## [1] "HCG23"           "LOC105379657"

genes_of_ensembl_ids_of_rs137931178_not_in_genomic_context_rs137931178 <- setdiff(unique_genes_of_rs137931178, unique_genes_of_rs137931178_in_genomic_context)

print(genes_of_ensembl_ids_of_rs137931178_not_in_genomic_context_rs137931178)

## character(0)

# rs137931178@genomic_contexts %>% dplyr::filter(gene_name == "HCG23")

# rs137931178@genomic_contexts %>% dplyr::filter(gene_name == "LOC105379657")
```