Brief overview on how to start exploring **functionality**

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Work Flow

- Download bkg genes: https://www.ensembl.org/info/data/ftp/index.html

- Results overview in FUMA

  – https://fuma.ctglab.nl/snp2gene

  – Input file: GWASresults.txt

- Variant Effect Prediction in Ensembl

  – https://www.ensembl.org/Multi/Tools/VEP

  – Input file (significant SNPs): Map.selected.rs

  – Output file (Functional Info): Select 'Gene' column

- Enrichment analysis

  – https://fuma.ctglab.nl/gene2func

  – Input files: GENES from significant SNPs ('Gene' column from VEP)

  - Background genes from the specie (Canis_familiaris.bkg_genes)