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# #

**#SCRIPT : Detection of MNVs using VCF file & VEP**

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**#### Bash Script ####**

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### Files

# General

VCF="[VCF file .gz]"

# For VEP

FASTA="[FASTA file]"

GTF="[VCF file]"

cache="[Cache Version]"

species="[Species Name]"

**### 1) Generation of VEP file**

# → To accelerate the analysis, VEP is used in offline mode (--offline) and with a GTF produced in the lab.

# The --everything and --total\_length parameters are used to provide access to the SIFT information and the position of the SNP in the cDNA,

# CDS and protein in the format: "Position/Length".

vep \

--offline \

--species ${species} \

--cache \

--fasta ${FASTA} \

--gtf ${GTF} \

--cache\_version ${cache} \

-i ${VCF} \

-o VEP\_results.txt \

--everything \

--total\_length

VEP="VEP\_results.txt"

**### 2) Reduction of the VEP file**

# → Selection of consequences in the coding regions.

grep -v "#" $VEP | grep -P "missense\_variant|start\_lost|stop\_gained|stop\_lost|stop\_retained\_variant|synonymous\_variant" > 0b\_consSelected.vep

# → Generation of a VEP file of reduced size to facilitate and accelerate the calculations.

# The columns kept are : ($1) Uploaded variation - as chromosome\_start\_alleles

# ($5) Feature

# ($7) Consequence

# ($10) Position in protein

# ($11) Amino acid change

# ($12) Codon change

# (a) Strand

grep -v "#" 0b\_consSelected.vep | awk '{

match($14, /STRAND=-1|STRAND=1/)

a = substr($14,RSTART,RLENGTH)

print $1"\t"$5"\t"$7"\t"$10"\t"$11"\t"$12"\t"a

}' | sed "s/STRAND=//g"> 0c\_consSelected\_reduced.vep

**### 3) Reduction of the VCF file**

# → List of SNP from the VCF file with the same format as VEP

# i.e. ($1) Uploaded variation - as chromosome\_start\_alleles

zgrep -v "#" $VCF | awk -F "\t" '{

print $1"\_"$2"\_"$4"/"$5

}' > 1\_VCF\_SNPid.list

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**#### R Script ####**

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**### 4) Extraction of the SNP present by 2 or 3 in a same codon**

## Definition of the working directory

setwd("")

## Imporation of file

# Vep File

VEP <- read.delim("0b\_consSelected.vep", dec=".", stringsAsFactors = FALSE, header = FALSE)

colnames(VEP) <- c("Uploaded\_variation", "Location", "Allele", "Gene", "Feature", "Feature\_type", "Consequence", "cDNA\_position", "CDS\_position", "Protein\_position",

"Amino\_acids", "Codons", "Existing\_variation", "Extra")

VEP <- VEP[match(unique(VEP$Location), VEP$Location), ]

# VCF File

VCF <- scan("1\_VCF\_SNPid.list", what = "character")

## Creation of a codon ID [TranscriptID\_proteinPosition]

idCodonCreation <- function(x){

return(paste0(x["Feature"], "\_", x["Protein\_position"]))

}

VEP$codonID <- apply(VEP, 1, idCodonCreation)

## Selection of Codon with MNV

# Only duplicated ID are kept

# supposing the presence of two or three SNPs within the same codon

VEPpop <- VEP[VEP$Uploaded\_variation %in% VCF, ]

duplicatedCodon <- as.data.frame(table(VEPpop$codonID))

duplicatedCodon <- duplicatedCodon[duplicatedCodon$Freq >1, ]

print(table(duplicatedCodon$Freq))

res <- VEPpop[VEPpop$codonID %in% duplicatedCodon$Var1, 1]

# List of SNP in MNV

write(res, paste0("1\_VCF\_MNVid.list"))

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**#### Bash Script ####**

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**### 5) Extraction of the information contained in the VCF file**

## for each SNP of the previous list

# → Use of the ID format ($1) Uploaded variation - as chromosome\_start\_alleles

zgrep -v "#" $VCF | awk '{

print $0"\t"$1"\_"$2"\_"$4"/"$5

}' | grep -f 1\_VCF\_MNVid.list > 2\_VCF\_MNVid.vcf

**### 6) Extraction of SNP only phased**

zgrep -v "#" 2\_VCF\_MNVid.vcf | grep "|" > 3\_VCF\_MNVid\_phased.vcf

**### 7) Extraction of the necessary information : 1) ID / 2) phase**

grep -v "#" 3\_VCF\_MNVid\_phased.vcf | awk -F "\t" '{

for (i = 0; i < NF; i++ ){

match($i, /.\|.:.[^:]\*/)

a = substr($i,RSTART,RLENGTH)

array[a] = a

}

printf "%s ",$NF

for (a in array){

printf "%s ",a

}

printf "\n"

delete array

}' | sed "s/1\/0//g" | sed "s/0\/0//g" | sed "s/1\/1//g" | sed "s/0\/1//g" | sed "s/\.\/\.//g" > 4\_VCF\_MNVid\_minimalPhaseInfo.txt

**### 8) Extraction of PID for each SNP**

cat 3\_VCF\_MNVid\_phased.vcf | awk -F '\t' '

BEGIN{

c=0;}

{split($9,test,":");

if (test[6] == "PID") c=6;

if (test[7] == "PID") c=7;

printf "%s ",$NF;

for (i = 10; i < NF; i++ ){

split($i,a,":")

printf "%s ",a[c]}

printf "\n"

}' > 4\_idAndPhases.tsv

**### 8) Extraction of the VCF header**

zgrep "#C" $VCF > 4\_headerVCF.txt

**### 9) New consequences for MNV with 2 SNP**

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**#### R Script ####**

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### Definition of the working directory

setwd("")

### Librabries

library(stringr)

library(Biostrings)

### Importing files

# VEP

vep <- read.delim(file = "0c\_consSelected\_reduced.vep", header = F, sep = "\t", stringsAsFactors = F)

colnames(vep) <- c("id", "transcript", "consequence", "posAA", "AA", "codon", "strand")

# VCF

vcf <- read.delim(file="4\_VCF\_MNVid\_minimalPhaseInfo.txt", header = F, stringsAsFactors = F)

# For annotation

# /!This file depends on the GTF file used. It is to be generated upstream.

# Its structure is as follows :

# gnId tpId

# ENSGALG00000031626 ENSGALT00000065662

# ENSGALG00000031626 ENSGALT00000081419

geneTranscript <- read.delim("", header = T, stringsAsFactors = F)

### Script

## Creation of a dataframe with : 1) ID 2) phased

vcfToDF <- function(x){

idAndphases <- unlist(str\_split(x, " "))

idAndphases <- idAndphases[!(idAndphases == "")]

return(c(idAndphases[1], paste0(idAndphases[2:length(idAndphases)], collapse = "$") ))

}

vcf <- data.frame(t(apply(vcf, 1, vcfToDF)), stringsAsFactors = F)

colnames(vcf) <- c("id", "phases")

# Addition of VEP info

res <- merge(vcf, vep, by.x = "id", by.y = "id")

# Creation of an ID (transcript\_posAA) which permits to detect MNVd

res$transcriptID <- apply(res[, c("transcript", "posAA")], 1, function(x){return(paste0(x, collapse = "\_"))})

transcriptID <- unique(res$transcriptID)

table(table(res$transcriptID))

## Importation of the PID for each SNP

idAndPhases <- read.delim("4\_idAndPhases.tsv", header = F, sep = " ", stringsAsFactors = F)

## Treatment of the VCF header

# Parse the header and rename to consider

# individuals and not sample

# ex : RpRm\_livr\_001 & RpRm\_adip\_001 → RpRm\_001

header <- scan("4\_headerVCF.txt", what = "character")

partToKeep <- header[1:9]

partToWork <- header[10:length(header)]

# Depends on the naming, specific to each laboratory

naming <- function(x){

spl <- str\_split(x, "\_", simplify = T)

pop <- spl[1]

num <- paste0(str\_split(spl[3], "\\.", simplify = T)[8:9], collapse = ".")

num <- num[length(num)]

name <- paste0(pop, "\_", num)

}

partToWork <- unlist(lapply(partToWork, naming))

# Number of individuals per pop

table(str\_sub(unique(partToWork), 1, 4))

# Function to calculate the new consequence considering

# the two SNPs phased

newConsequencesFor2SNP <- function(x){

## Subset of the info corresponding to the IDtranscript

df <- res[res$transcriptID == x, ]

# Test1 : MNV = 2 ?

test1 <- 0

test2 <- 0

if (nrow(df) == 2){test1 <- 1}

## If test OK, we continue

if (test1 == 1){

# Test2 : Are they phased ?

test2 <- 0

# a) Direct link of phased ?

toFind <- str\_replace(paste0(unlist(str\_split(df[1, "id"], "\_"))[2:3], collapse = "\_"), "/", "\_")

# We eliminate the case 1/0 (Not the same haplotype)

toFind2 <- paste0("0\\|1:", toFind)

toFind3 <- paste0("1\\|1:", toFind)

# Phase with both cases

if (sum(grepl(toFind2, df$phases)) == 2 | sum(grepl(toFind3, df$phases)) == 2){

test2 <- 1

}

if (test2 != 1){

# b) phased by an intermediate ?

# We test if a phase of the first SNP is in the 2 SNP

## SNP1

allPhases <- df[1, "phases"]

# all phases

a1 <- str\_split(allPhases, "\\$",simplify = T)

# we delete phases with 1|0 → Not on the same haplotype

b1 <- a1[!grepl("1\\|0", a1, perl = F)]

## SNP2

allPhases <- df[2, "phases"]

# all phases

a2 <- str\_split(allPhases, "\\$",simplify = T)

# we delete phases with 1|0 → Not on the same haplotype

b2 <- a2[!grepl("1\\|0", a2, perl = F)]

if (T %in% (b2 %in% b1)) { test2 <- 1}

}

}

## Creation GT ( if 2 SNP and phased)

if (test1 == 1 & test2 == 1) {

#Chrom

chrom <- str\_split(df[1, 1], "\_", simplify = T)[1]

#Pos ( Default - pos of the first SNP includ in the MNV)

pos <- paste0(lapply(df[, 1 ], function(x){return(str\_split(x, "\_", simplify = T)[2])}), collapse = ";")

#MNVid

MNVid <- df[1, "transcriptID"]

# Nb of SNP

nbOfSnp <- nrow(df)

# gene

gene <- NA

# transcript

transcript <- str\_split(df[1, "transcriptID"], "\_", simplify = T)[1]

#Nb of samples

# Consider if the two SNPs are phased for the SAME indivduals

# Extract number of individuals, number of pop and the details

toExtract <- df$id

toAnalyze <- idAndPhases[match(toExtract, idAndPhases$V1), ]

toAnalyze <- rbind(toAnalyze, header)

toAnalyze <- toAnalyze[, -ncol(toAnalyze)]

toAnalyze <- toAnalyze[, (toAnalyze[1, ] != ".") & (toAnalyze[2, ] != ".")]

nbOfSamples <- 0

idIndividuals <- NA

if (is.null(ncol(toAnalyze))){

nbOfSamples <- 0

idIndividuals <- NA

} else if (ncol(toAnalyze) == 2){

if (toAnalyze[1,2] == toAnalyze[2,2]){

nbOfSamples <- 1

idIndividuals <- toAnalyze[3,2]

}

} else {

samples <- apply(toAnalyze[, 2:ncol(toAnalyze)], 2, detectionSample)

samples <- unique(samples)

if (is.na(samples)){

nbOfSamples <- 0

idIndividuals <- NA

} else {

nbOfSamples <- length(samples)

idIndividuals <- paste0(samples, collapse = ":")

}

}

# Codon of the ref seq

codonInitial <- tolower(unlist(str\_split(df$codon, "/"))[1])

# Codon of the MNV seq

codonFinal <- NULL

tmp <- unlist(lapply(df$codon, function(x){return(unlist(str\_split(x, "/"))[2])}))

for (i in 1:3){

tmp2 <- unlist(lapply(tmp, function(x){return(str\_sub(x, i, i))}))

upper <- grep("^[[:upper:]]+$", tmp2, value = T)

if (length(upper) > 0){

codonFinal <- c(codonFinal, upper)

} else {

codonFinal <- c(codonFinal, tmp2[1])

}

}

codonFinal <- paste0(codonFinal, collapse = "")

# AA identificaiton

strand <- df[1,"strand"]

AAinitial <- GENETIC\_CODE[toupper(codonInitial)]

AAfinal <- GENETIC\_CODE[toupper(codonFinal)]

transcr <- df[1, 'transcriptID']

# Calcul New cosequences

if ((AAinitial == AAfinal) & (AAfinal != "\*")){

newCons <-"synonymous\_variant"

} else if ((AAinitial == AAfinal) & (AAfinal == "\*")) {newCons <-"stop\_retained\_variant"

} else if ((AAinitial == "\*") & (AAfinal != "\*")) {newCons <-"stop\_lost"

} else if (AAfinal == "\*" & AAinitial != "\*") { newCons <-"stop\_gained"

} else if ((unlist(strsplit(unlist(strsplit(transcr,"\_"))[2], "/"))[1] == 1) & AAfinal != "M") {newCons <-"start\_lost"

} else if ((unlist(strsplit(unlist(strsplit(transcr,"\_"))[2], "/"))[1] == 1) & AAfinal == "M") {newCons <-"start\_retained\_variant"

} else if ((AAfinal %in% LETTERS) & (AAinitial %in% LETTERS) & (AAfinal != AAinitial)) {newCons <-"missense\_variant"

}

# Old consequences

oldCons <- paste0(df$consequence, collapse = "/")

return(c(chrom, pos, MNVid, nbOfSnp, gene, transcript, strand,nbOfSamples, idIndividuals, codonInitial, codonFinal, AAinitial, AAfinal, oldCons, newCons ))

}

}

print("Launch ...")

listFinal2SNP <- pblapply(transcriptID, newConsequencesFor2SNP)

print("End ...")

## Remove Null element

listFinal2SNP <- listFinal2SNP[lengths(listFinal2SNP) != 0]

## MNV recalcul

print("Recalcul ...")

recalculMNV2 <- data.frame(matrix(unlist(listFinal2SNP), nrow=length(listFinal2SNP), byrow=T))

colnames(recalculMNV2) <- c("chrom", "pos", "MNVid", "nbOfSnp", "gene",

"transcript","strand", "nbOfSamples", "idIndividuals", "codonInitial", "codonFinal",

"AAinitial", "AAfinal", "oldCons", "NewCons" )

## Suppression of SNP phase but not in a same sample

recalculMNV2 <- recalculMNV2[recalculMNV2$nbOfSamples != 0, ]

## Match genes transcript

recalculMNV2$gene <- geneTranscript[match(recalculMNV2$transcript, geneTranscript$tpId), "gnId"]

write.table(recalculMNV2, "recalculMNV2.tsv", quote = F, sep= "\t", row.names = F)

**#EOF**