

```

import sys

##species specific SNPs filtered file
wildfile = open(sys.argv[1], "r")

##target genotype filtered file
targetfile = open(sys.argv[2], "r")

chr = ''
pos = ''
ref = ''
alt = ''

wild = {}

##put species-specific in a hash
for line in wildfile:

    line=line.strip()
    line=line.split()

    if line[0].startswith('#'):
        continue

    wild[line[0]+":"+line[1]+":"+line[3]+":"+line[4]] = 1

##select overlap as introgressed regions
for x in targetfile:

    x=x.strip()
    hold=x.split()

    chr=hold[0]
    pos=hold[1]
    ref=hold[3]
    alt=hold[4]

    if (chr+":"+pos+":"+ref+":"+alt) in wild:

        print(x)

wildfile.close()
targetfile.close()

```