

• HLAscan v1.0

1. Contents

(1) hla-ref (DB) contents

Name	Description
exn	Collection of exon boundary
IMGT_HLA	FASTA files for each genes (reference)
Gene_list	HLA gene lists files

(2) tool

Name	Description
allele_count_cpu	BAM filter
bwa	Alignment
ghaplo_scan	Covert BAM files into FASTQ format
haplo_scan_v4.0	Determine gene types
haplo_scan_v4.0-hla.py	Action script
samtools	Calculate a depth

2. Installation environment

- python 2.7

3. Usage

(1) Download the files

(2) Set the configuration

```
cd hla-paper
vi haplo_scan_v4.0-hla.py

#PROGRAMS
PROG_BAMTOFASTQ = "./ghaplo_scan"
```

```
PROG_BWA = "/bwa"
PROG_FILTEREDBAM = "/allele_count_cpu"
PROG_SAMTOOLS = "/samtools"
PROG_HLASCAN = "/haplo_scan_v4.0"

#DATABASE
FA_FILE = "/hla-ref-5gene/IMGT_HLA/"      #fixed
SGENE = ""                                #fixed
GENE_634 = ""                             #fixed
EXON_7255 = ""                            #fixed
GENE_BOUND = "/hla-ref-5gene/exn/"

python  ./haplo_scan_v4.0-hla.py [bam] [gene list] [output path]
ex) python  ./haplo_scan_v4.0-hla.py ../NA12878.5gene.bam ../hla-ref/gene_list  ../test-out
```

(3) Use script

```
python  ./haplo_scan_v4.0-hla.py [bam] [gene list] [output path]
ex) python  ./haplo_scan_v4.0-hla.py ../NA12878.5gene.bam ../hla-ref/gene_list  ../test-out
```