

# Package ‘Neoantimon’

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**Type** Package

**Title** Neoantimon: An R package for automatic identification of tumor-specific neoantigens from sequencing data

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**Description** This Package is developed to calculate candidates neoantigens from Mutation Data (.vcf) requiring netMHCpan3.0, netMHCIIpan3.1, human refMrna, and, refFlat. If you do not have some of these files, see README.md.

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**VignetteBuilder** knitr

**Suggests** knitr,  
rmarkdown

**LazyData** TRUE

**Imports** utils

**RoxygenNote** 6.0.1

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MainINDELClass1

*Calculate Neoantigen Candidates on Indels for MHC Class1***Description**

Calculate Neoantigen Candidates on Indels for MHC Class1

**Usage**

```
MainINDELClass1(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIIpan-3.1/netMHCIIpan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(8,
  9, 10, 11, 12, 13))
```

**Arguments**

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR ( <a href="http://annovar.openbioinformatics.org/en">http://annovar.openbioinformatics.org/en</a> ) or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c2); sample_hla_table_c2;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT ( <a href="https://www.crick.ac.uk/peter-van-loo/software/ASCAT">https://www.crick.ac.uk/peter-van-loo/software/ASCAT</a> ) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

Purity	Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).
netMHCpan_dir	The file directory to netMHCpan (Default="lib/netMHCpan-3.0/netMHCpan").
refDNA	refDNA information to be used to calculate RNA VAF (Default="ib/GRCh37.fa").
refFlat_file	refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep=""))
refMrna_1	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep="")) This file is automaticalluy generated through the command in README, but includes NM_IDs.
refMrna_3	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep="")) This file is automaticalluy generated through the command in README, but includes the amino acid sequence.
samtools_dir	The file directory to samtools (Default="samtools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF .
bcftools_dir	The file directory to netMHCpan (Default="bcftools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.
Chr_Column	The column number describing Chromosome number in input_file (Default=1).
Mutation_Start_Column	The column number describing Mutation Start Position in input_file (Default=2)
Mutation_End_Column	The column number describing Mutation End Position in input_file (Default=3).
Mutation_Ref_Column	The column number describing Mutation Ref in input_file (Default=4).
Mutation_Alt_Column	The column number describing Mutation Alt in input_file (Default=5).
NM_ID_Column	The column number describing NM IDs in input_file (Default=10).
Depth_Normal_Column	The column number describing the read count from normal cells (Default = NA)
Depth_Tumor_Column	The column number describing the read count from tumor cells (Default = NA)
ambiguous_between_exon	The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).
ambiguous_codon	The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).
peptide_length	Peptide Length to be generated (Default=8,9,10,11,12,13).

## Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

## Description

Calculate Neoantigen Candidates on Indels for MHC Class2

## Usage

```
MainINDELClass2(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIPan-3.1/netMHCIPan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(15))
```

## Arguments

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR ( <a href="http://annovar.openbioinformatics.org/en">http://annovar.openbioinformatics.org/en</a> ) or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c2); sample_hla_table_c2;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT ( <a href="https://www.crick.ac.uk/peter-van-loo/software/ASCAT">https://www.crick.ac.uk/peter-van-loo/software/ASCAT</a> ) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

Purity	Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).
netMHCpan_dir	The file directory to netMHCpan (Default="lib/netMHCIIpan-3.1/netMHCpan").
refDNA	refDNA information to be used to calculate RNA VAF (Default="lib/GRCh37.fa").
refFlat_file	refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep=""))
refMrna_1	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep="")) This file is automaticalluy generated through the command in README, but includes NM_IDs.
refMrna_3	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep="")) This file is automaticalluy generated through the command in README, but includes the amino acid sequence.
samtools_dir	The file directory to samtools (Default="samtools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF .
bcftools_dir	The file directory to netMHCpan (Default="bcftools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.
Chr_Column	The column number describing Chromosome number in input_file (Default=1).
Mutation_Start_Column	The column number describing Mutation Start Position in input_file (Default=2)
Mutation_End_Column	The column number describing Mutation End Position in input_file (Default=3).
Mutation_Ref_Column	The column number describing Mutation Ref in input_file (Default=4).
Mutation_Alt_Column	The column number describing Mutation Alt in input_file (Default=5).
NM_ID_Column	The column number describing NM IDs in input_file (Default=10).
Depth_Normal_Column	The column number describing the read count from normal cells (Default = NA)
Depth_Tumor_Column	The column number describing the read count from tumor cells (Default = NA)
ambiguous_between_exon	The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).
ambiguous_codon	The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).
peptide_length	Peptide Length to be generated (Default=15 in HLA Class2).

## Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

---

MainMergeClass1	<i>Merge Results from MainSnvClass1.R</i>
-----------------	---

---

### Description

Merge Results from MainSnvClass1.R

### Usage

```
MainMergeClass1(hmdir = getwd(), input_dir, input_file_prefix,
  Tumor_RNA_BASED_ON_DNA = TRUE, INDEL = FALSE)
```

### Arguments

hmdir	Home directory for the analysis (Default=getwd()).
input_dir	Directory storing netMHCpan Results (Required).
input_file_prefix	File prefix of netMHCpan Results (Required). If you have "sample_annovar.txt.NO_JOB_ID.HLACL please set "sample_annovar", "sample_annovar.txt" or "sample_annovar.txt.NO_JOB_ID".
Tumor_RNA_BASED_ON_DNA	In calculating tumor specific RNA expression, TRUE uses variant allele frequency on DNA. Otherwise, use VAF on RNA (Default=TRUE).
INDEL	If the targeting results are generated from Indels, Please check TRUE.

### Value

void (Calculated Neoantigen Files will be generated as .tsv files.)

---

MainMergeClass2	<i>Merge Results from MainSnvClass2.R</i>
-----------------	---

---

### Description

Merge Results from MainSnvClass2.R

### Usage

```
MainMergeClass2(hmdir = getwd(), input_dir, input_file_prefix,
  Tumor_RNA_BASED_ON_DNA = TRUE, INDEL = FALSE)
```

### Arguments

hmdir	Home directory for the analysis (Default=getwd()).
input_dir	Directory storing netMHCpan Results (Required).
input_file_prefix	File prefix of netMHCpan Results (Required). If you have "sample_annovar.txt.NO_JOB_ID.HLACL please set "sample_annovar", "sample_annovar.txt" or "sample_annovar.txt.NO_JOB_ID".
Tumor_RNA_BASED_ON_DNA	In calculating tumor specific RNA expression, TRUE uses variant allele frequency on DNA. Otherwise, use VAF on RNA (Default=TRUE).
INDEL	If the targeting results are generated from Indels, Please check TRUE.

**Value**

void (Calculated Neoantigen Files will be generated as .tsv files.)

---

MainSNVClass1	<i>Calculate Neoantigen Candidates on SNVs for MHC ClassI</i>
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---

**Description**

Calculate Neoantigen Candidates on SNVs for MHC ClassI

**Usage**

```
MainSNVClass1(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIipan-3.1/netMHCIipan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(8,
  9, 10, 11, 12, 13))
```

**Arguments**

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR ( <a href="http://annovar.openbioinformatics.org/en/">http://annovar.openbioinformatics.org/en/</a> ) or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c1); sample_hla_table_c1;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT ( <a href="https://www.crick.ac.uk/peter-van-loo/software/ASCAT">https://www.crick.ac.uk/peter-van-loo/software/ASCAT</a> ) output files. The columns are "Chromosome Position

	Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").
Purity	Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).
netMHCpan_dir	The file directory to netMHCpan (Default="lib/netMHCpan-3.0/netMHCpan").
refDNA	refDNA information to be used to calculate RNA VAF (Default="lib/GRCh37.fa").
refFlat_file	refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep=""))
refMrna_1	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep="")) This file is automaticalluy generated through the command in README, but includes NM_IDs.
refMrna_3	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep="")) This file is automaticalluy generated through the command in README, but includes the amino acid sequence.
samtools_dir	The file directory to samtools (Default="samtools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF .
bcftools_dir	The file directory to netMHCpan (Default="bcftools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.
Chr_Column	The column number describing Chromosome number in input_file (Default=1).
Mutation_Start_Column	The column number describing Mutation Start Position in input_file (Default=2)
.	.
Mutation_End_Column	The column number describing Mutation End Position in input_file (Default=3).
Mutation_Ref_Column	The column number describing Mutation Ref in input_file (Default=4).
Mutation_Alt_Column	The column number describing Mutation Alt in input_file (Default=5).
NM_ID_Column	The column number describing NM IDs in input_file (Default=10).
Depth_Normal_Column	The column number describing the read count from normal cells (Default = NA)
Depth_Tumor_Column	The column number describing the read count from tumor cells (Default = NA)
ambiguous_between_exon	The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).
ambiguous_codon	The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).
peptide_length	Peptide Length to be generated (Default=8,9,10,11,12,13).

## Value

void (Calculated Neoantigen Files will be generated as .tsv files.)



## Description

Calculate Neoantigen Candidates on SNVs for MHC Class2

## Usage

```
MainSNVClass2(input_file, HLA_file, file_name_in_HLA_table = input_file,
  hmdir = getwd(), job_ID = "NO_JOB_ID", RNAseq_file = NA, RNA_bam = NA,
  CNV = NA, ccfp_dir = paste(hmdir, "lib/ccfp.jar", sep = ""),
  Purity = NA, netMHCpan_dir = paste(hmdir,
  "lib/netMHCIIpan-3.1/netMHCIIpan", sep = ""), refDNA = paste(hmdir,
  "lib/GRCh37.fa", sep = ""), refFlat_file = paste(hmdir, "/data/refFlat.txt",
  sep = ""), refMrna_1 = paste(hmdir, "/data/refMrna.cut1.fa", sep = ""),
  refMrna_3 = paste(hmdir, "/data/refMrna.cut3.fa", sep = ""),
  samtools_dir = "samtools", bcftools_dir = "bcftools", Chr_Column = 1,
  Mutation_Start_Column = 2, Mutation_End_Column = 3,
  Mutation_Ref_Column = 4, Mutation_Alt_Column = 5, NM_ID_Column = 10,
  Depth_Normal_Column = NA, Depth_Tumor_Column = NA,
  ambiguous_between_exon = 0, ambiguous_codon = 0, peptide_length = c(15))
```

## Arguments

input_file	(Required) An input vcf file annotated by, e.g., ANNOVAR ( <a href="http://annovar.openbioinformatics.org/en">http://annovar.openbioinformatics.org/en</a> ) or other softwares. See by data(sample_vcf); sample_vcf;
HLA_file	(Required) A tab separated file indicating HLA types . The 1st column is input_file name, and the following columns indicate HLA types. See by data(sample_hla_table_c2); sample_hla_table_c2;
file_name_in_HLA_table	If the name (1st column) in HLA table is not input_file, indicate the corresponding name (Default=input_file).
hmdir	Home directory for the analysis (Default=getwd()).
job_ID	Job-Id to be attached in output files (Default="NO_JOB_ID").
RNAseq_file	(Default=NA) A file including RNA expressions. The 1st, 2nd and 3rd columns are "GeneSymbol Chr:ExonStart-ExonEnd(locus) Expression Amount", respectively. The 1st row should be any header. See by data(sample_rna_exp); sample_rna_exp;
RNA_bam	RNA bam file to calculate variant allele frequency of RNA at each mutation (Default=NA).
CNV	A file including copy number variation to calculate cancer cell fraction probability (CCFP) (Default=NA). The format is according to ASCAT ( <a href="https://www.crick.ac.uk/peter-van-loo/software/ASCAT">https://www.crick.ac.uk/peter-van-loo/software/ASCAT</a> ) output files. The columns are "Chromosome Position Log R segmented LogR BAF segmented BAF Copy number Minor allele Raw copy number" The 1st row should be the above header. See data(sample_copynum); sample_copynum;
ccfp_dir	The file directory to CCFP.pl (Default="lib/ccfp.jar").

Purity	Tumor purity or tumor contents ratio required to calculate CCFP (Default=NA).
netMHCpan_dir	The file directory to netMHCpan (Default="lib/netMHCIIpan-3.1/netMHCpan").
refDNA	refDNA information to be used to calculate RNA VAF (Default="lib/GRCh37.fa").
refFlat_file	refFlat file to be used in constructing peptide. (Default=paste(hmdir,"lib/refFlat.txt",sep=""))
refMrna_1	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut1.fa",sep="")) This file is automatically generated through the command in README, but includes NM_IDs.
refMrna_3	refMrna file to be used in constructing peptide (Default=paste(hmdir,"lib/refMrna.merge.cut3.fa",sep="")) This file is automatically generated through the command in README, but includes the amino acid sequence.
samtools_dir	The file directory to samtools (Default="samtools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF .
bcftools_dir	The file directory to netMHCpan (Default="bcftools"). It should be indicated when you indicate RNA-bam and try to calculate RNA VAF . samtools 0_x_x includes bcftools in the directory.
Chr_Column	The column number describing Chromosome number in input_file (Default=1).
Mutation_Start_Column	The column number describing Mutation Start Position in input_file (Default=2)
Mutation_End_Column	The column number describing Mutation End Position in input_file (Default=3).
Mutation_Ref_Column	The column number describing Mutation Ref in input_file (Default=4).
Mutation_Alt_Column	The column number describing Mutation Alt in input_file (Default=5).
NM_ID_Column	The column number describing NM IDs in input_file (Default=10).
Depth_Normal_Column	The column number describing the read count from normal cells (Default = NA)
Depth_Tumor_Column	The column number describing the read count from tumor cells (Default = NA)
ambiguous_between_exon	The maximum number to permit the differences between Exon-Lengths from refFlat and refMrna (Default=0).
ambiguous_codon	The maximum number to permit the differences between inputfile- and refMrna-oriented translation START/END position (Default=0).
peptide_length	Peptide Length to be generated (Default=15 in HLA Class2).

**Value**

void (Calculated Neoantigen Files will be generated as .tsv files.)

---

Neoantimon

*Neoantimon*

---

**Description**

Calculate Lists of Candidate Neoantigens on SNVs and Indels to MHC Class1 and Class2. First use MainSNVClass1, MainSNVClass2, MainINDELClass1, and MainINDELClass2.

---

sample_copynum	<i>A Format / Sample file for Copy Number Information</i>
----------------	---

---

**Description**

A dataset containing the copy number information obtained by, e.g., ASCAT.

**Usage**

```
data(sample_copynum)
```

**Format**

A data frame with 7 rows and 9 variables

---

sample_hla_table_c1	<i>A Format / Sample file for HLA CLASS1 Table</i>
---------------------	--

---

**Description**

A dataset containing the HLA types of patients in each row.

**Usage**

```
data(sample_hla_table_c1)
```

**Format**

A data frame with 3 rows and at most 7 variables

---

sample_hla_table_c2	<i>A Format / Sample file for HLA CLASS2 Table</i>
---------------------	--

---

**Description**

A dataset containing the HLA types of patients in each row.

**Usage**

```
data(sample_hla_table_c2)
```

**Format**

A data frame with at least 3 row and at most 10 variables

---

sample_rna_exp	<i>A Format / Sample file for RNA Expression Information</i>
----------------	--

---

**Description**

A dataset containing the RNA expression amount of patient for each gene.

**Usage**

```
data(sample_rna_exp)
```

**Format**

A data frame with 22 rows and 3 variables

---

sample_vcf	<i>A Format / Sample file for Analyzed vcf file.</i>
------------	--

---

**Description**

A dataset containing the variant information of a patient.

**Usage**

```
data(sample_vcf)
```

**Format**

A data frame with 9 rows and 38 variables

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