What is T1K?

Overview

T1K (The ONE genotyper for Kir and HLA) is a computational tool to infer the alleles for the polymorphic genes such as KIR and HLA. T1K calculates the allele abundances based on the RNA-seq/WES/WGS read alignments on the provided allele reference sequences. The abundances are used to pick the true alleles for each gene. T1K provides the post analysis steps, including novel SNP detection and single-cell representation. T1K supports both single-end and paired-end sequencing data with any read length.

t1k Outputs

Files

Output	Description
`*_hla_genotype.tsv`	File with HLA typing results
`*_kir_genotype.tsv`	File with KIR typing results

Note: KIR typing results are only available for whole genome and exome analyses

File Headers

The output files from t1k do not contain headers. Here are the appropriate headers for each column in both the HLA and KIR results files.

gene_name	num_diff_alleles	allele_1	abundance_1	quality_1	allele_2	abundance_2	quality_2	secondary_alleles

Gene Name: The name of the HLA or KIR gene being analyzed.

Num Diff Alleles: The number of different alleles detected for the gene specified in the 'gene_name' column.

Allele 1: The first allele detected for the gene.

Abundance 1: The estimated frequency or proportion of the specified allele within the analyzed sample, measured in fragments per thousand bases (FPK).

Quality 1: The quality score or confidence level associated with the detection of the first allele.

Allele 2: The second allele detected for the gene, if applicable (note: homozygous individuals will only have values in the columns related to allele 1).*

Abundance 2: The estimated frequency or proportion of the specified allele within the analyzed sample, measured in fragments per thousand bases (FPK), if applicable.*

Quality 2: The quality score or confidence level associated with the detection of the first allele, if applicable.*

Secondary Alleles: Secondary alleles or alternative variants detected for the gene, beyond the primary alleles specified in 'allele_1' and 'allele_2'. These secondary alleles may have lower abundance or confidence compared to the primary alleles.**

*Note: In the case of missing alleles or homozygous alleles, the triple (allele, abundance, quality) will be ". 0 -1" as place holders. It is recommended to ignore alleles with quality less or equal to 0.

**Note: The last column is the secondary alleles, that meet the abundance filtering criteria but filtered by tie breaking procedure. The secondary alleles contains "|" separated fields, and each field is separated to three subfields by ";" for allele, abundance and quality.