

Identification of unique homozygous SNPs in mutant

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Community rating: ?????

Takes SNP input from; SNP calling illumina seq data Part2. If divergent reference used input WT & mutant parent SNPs into this workflow. Then use Mutant Identification 1. If reference non-divergent use App:Filter homozygous SNP for mutant parent SNPs

Quick Start

- To use **Identification of unique homozygous SNPs in mutant**, import your data in SNP file VarScan format.

Test Data



Test data for this app appears directly in the link: File 1 <http://de.iplantcollaborative.org/dl/d/B624115B-A994-4C89-AE04-F1AD32DF330D/RIL25.snp>

File 2 <http://de.iplantcollaborative.org/dl/d/148A2528-21C7-4D3E-9C3C-BBF48D2E1A85/RIL71.snp>

Input File(s)

Use the files above as test input.

Parameters Used in App

When the app is run in the Discovery Environment, use the following parameters with the above input file(s) to get the output provided in the next section below.

- Default parameters only, no further configuration needed.

Output File(s)

Expect a text file named Final_mutant_specific_homozygotes.txt as output i.e. this will identify homozygous SNPs that are specific to the mutant parental line (SNPs from Workflow: SNP calling illumina seq data Part2).