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# FPmatching, v76

Matches Fluidigm fingerprint report to reference set of CCLE SNP6.0 array data.\nTakes old Fluidigm software report or new PED style report (saved as .csv).\nAlso backwards compatible with Sequenom reports (Combine 100k and AffySNP6.0 reports together into one file first).

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**Algorithm Version:**

## Introduction

[Why use this module? What does it do? If this is one of a set of modules, how does this module fit in the set?]

## Algorithm

[if applicable: a short overview of the algorithm in normal prose, followed by any details; write overview as if you are explaining to a novice]

## References

[appropriate papers cited]

## Parameters

Name	Description
platereport *	Should be .csv format
platemapping	Should be .csv format
format *	New PED style report OR Old Fluidigm software format OR Sequenom style report (expects combined 100k and SNP6.0 file)
FPSet *	Name of the fingerprinting set, ex. Plate_27

Name	Description
refFile	Optional file of known CCLE matches for creating the KnownMatch.CCLE column

\* - required

## Input Files

1. [parameter name]  
[Description. For example: The segmentation file contains the segmented data for all the samples identified by GLAD, CBS, or some other segmentation algorithm. (See GLAD file format in the GenePattern file formats documentation.) It is a six column, tab-delimited file with an optional first line identifying the columns. Positions are in base pair units.]

## Output Files

1. [File name]  
[Description of the content, file format, and how to interpret the results.]

## Example Data

[provide example data, including input files and parameter settings]. (we'll put the input files on the ftp site and link to them from the doc)

## Requirements

[any software requirements for running this, e.g., version of R, licensing]

## Platform Dependencies

### Task Type:

RNAi

### CPU Type:

any

### Operating System:

any

### Language:

R

## Version Comments

Version	Release Date	Description
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Version	Release Date	Description
76		updates for Sequenom
15		Checks reference file, updated output file. Added cleaned names column



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