Package 'CloneFinder'

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Title Finding Subclones in SNP and Sequencing Data

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Description The ClonmeFinder package defines the classes used to identify
outliers (threshing) and compute the number of significant principal
components and number of clusters (reaping) in a joint application
of PCA and hierarchical clustering.

Depends R (>= 3.0)

Imports methods, graphics, mc2d, combinat

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URL <http://oompa.r-forge.r-project.org/>

NeedsCompilation no

R topics documented: