**ScatterFoldChanges**

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ScatterFoldChanges is a script to generate volcano plot (scatter plot of adjusted p value against fold change) and GeneExpression-FoldChange plot (scatter plot of gene expression level against fold change). The dataset is derived from DESeq2 analysis. The requirement and parameters are described below.

**Uploading file format:** An excel file (.xlsx format) containing the three columns of values: baseMean (baseMean), Fold change (log2FoldChange), adjusted p value (padj) is required. The

example file (TestExample.xlsx) for test is published alongside with the script.

**Parameters:**

limitedFC1: The limit of fold change for differentially expressed genes, and the default value is 0.75. The regulated genes should satisfy the following condition: log2(foldchange) ≥ 0.75 or log2(foldchange) ≤ -0.75.

limitedGeneExp: The limit of gene expression level for differentially expressed genes,and the default value is 2. The regulated genes should satisfy the following condition: log10(baseMean) ≥ 2.

**Output:**

The outputs include two scatter plot images volcano plot (Vplot.png) and GeneExpression-FoldChange plot (ExpFCplot.png). The up-regulated genes and down-regulated genes can be copied out from “up” and “down” matrix in the Workspace.