Saving VIPER ?

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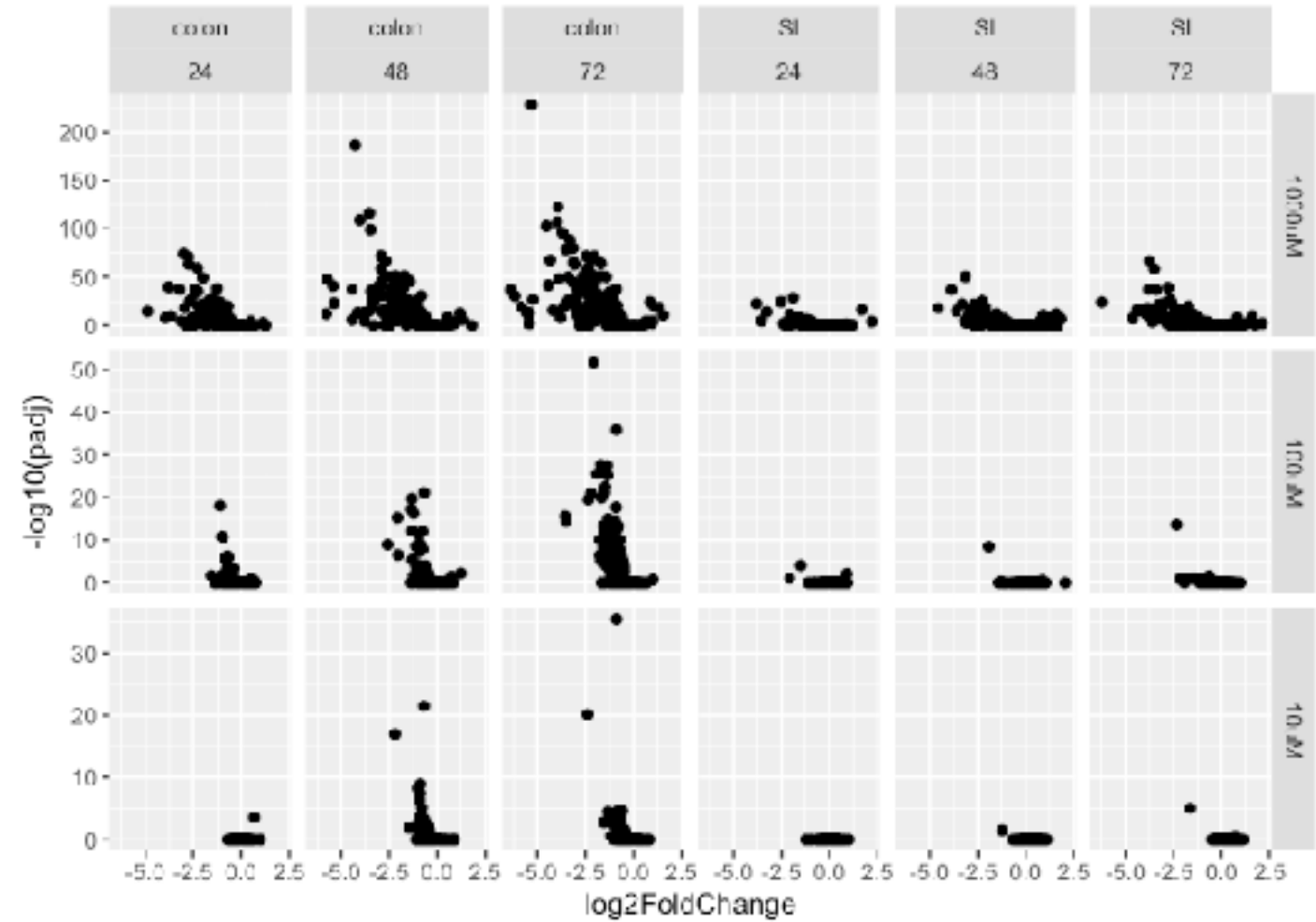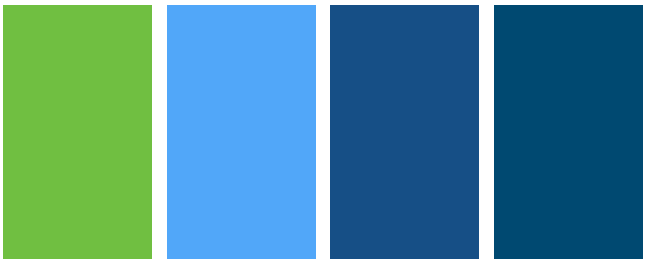JRC Computational Biomedicine RWTH Aachen, Faculty of Medicine

EMBL - University Hospital Heidelberg Molecular Medicine Partnership Unit
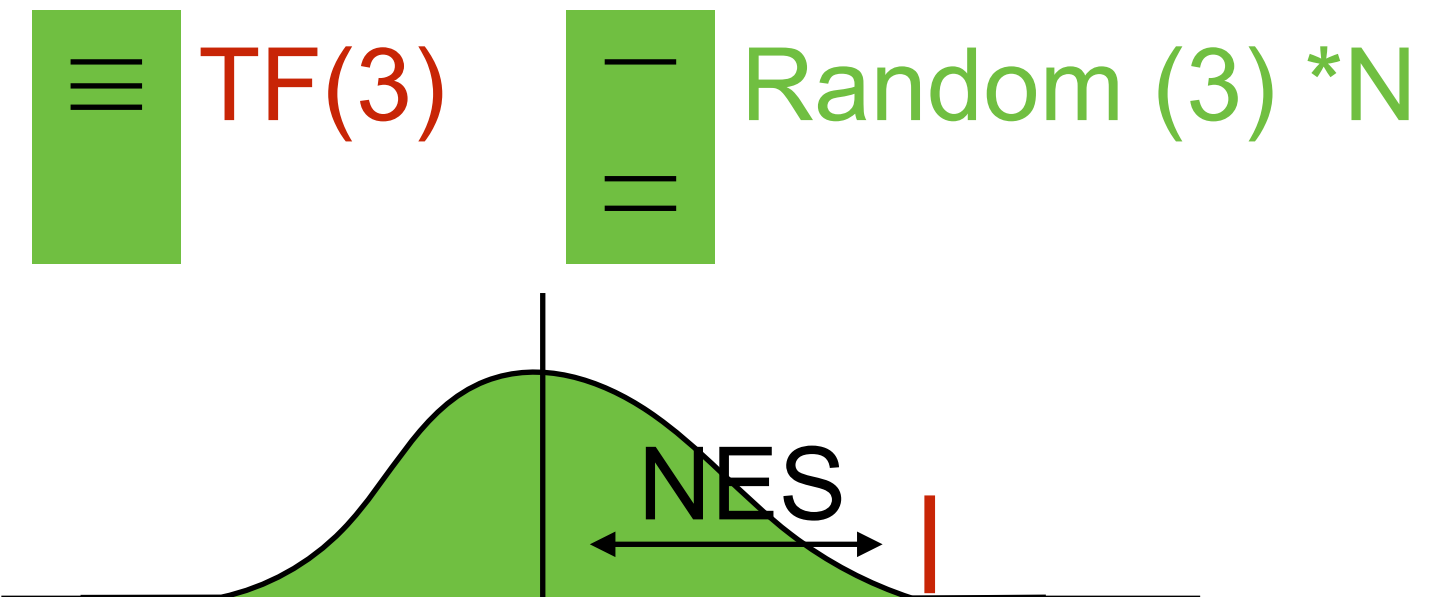
Input:

Samples

Genes

Input:

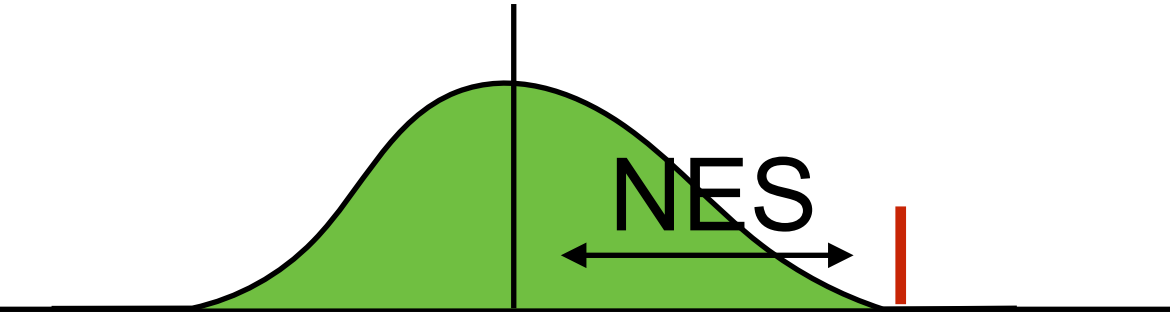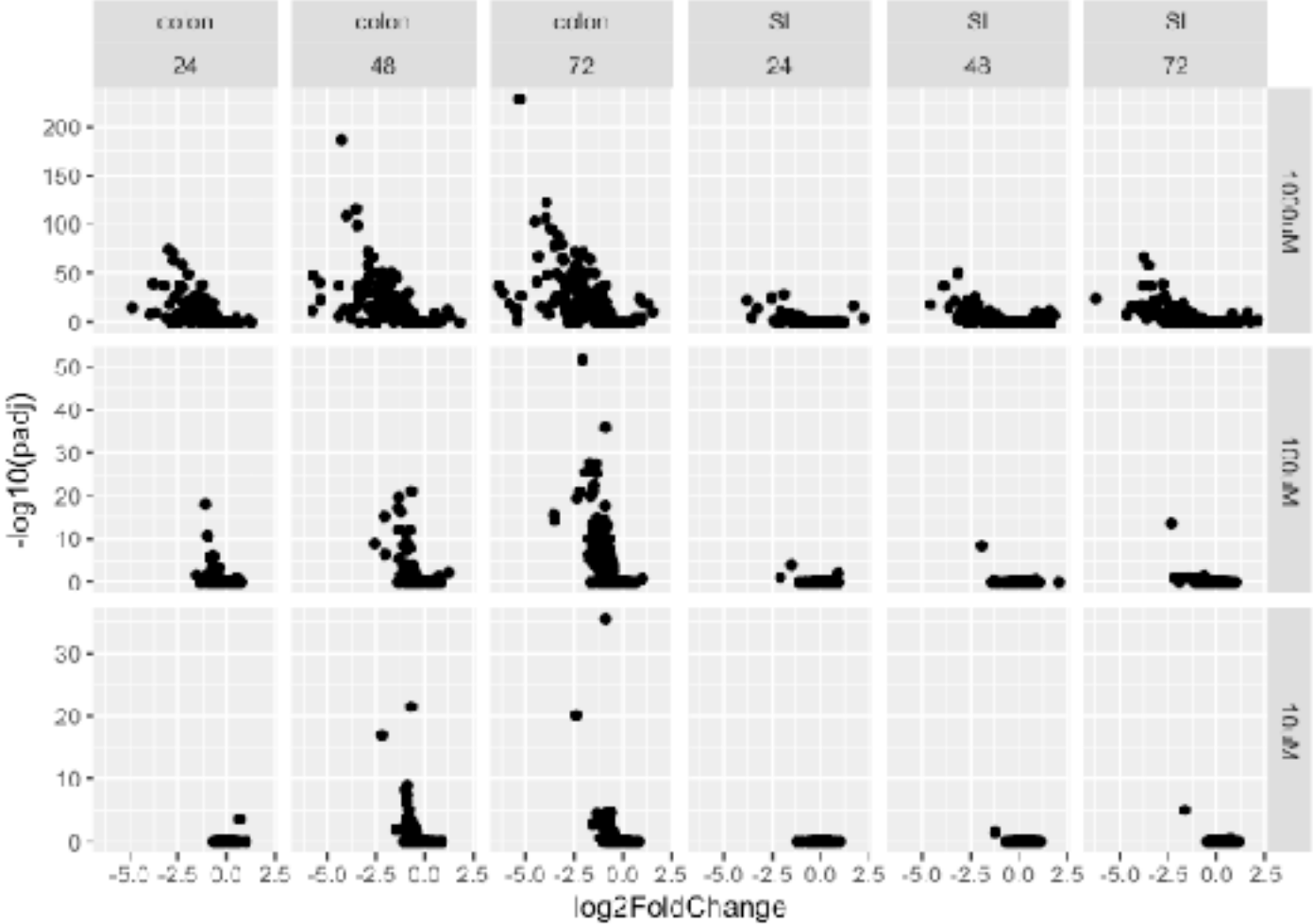Samples

Genes

Viper: (simplified)

Sample 1

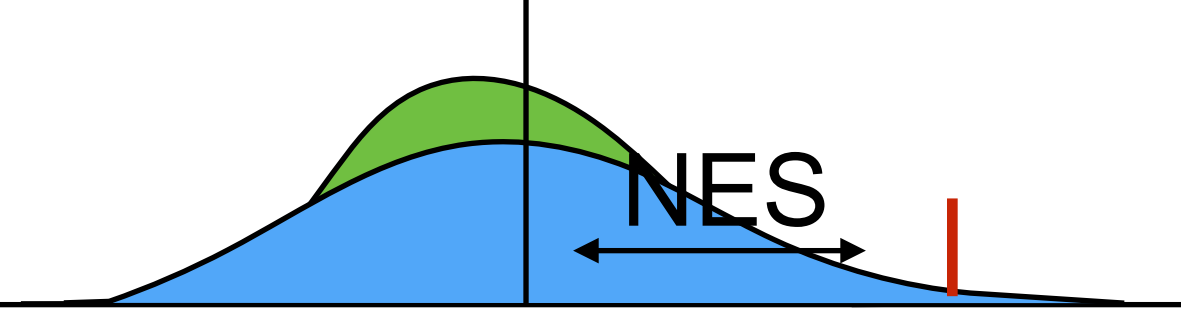≡ TF(3)   − Random (3) *N
         =

NES

Input:

Samples

Genes

Viper: (simplified)

Sample 1

TF(3)   Random (3) *N

NES

Sample 2

TF(3)   Random (3) *N

NES

Null distribution is based on the sample
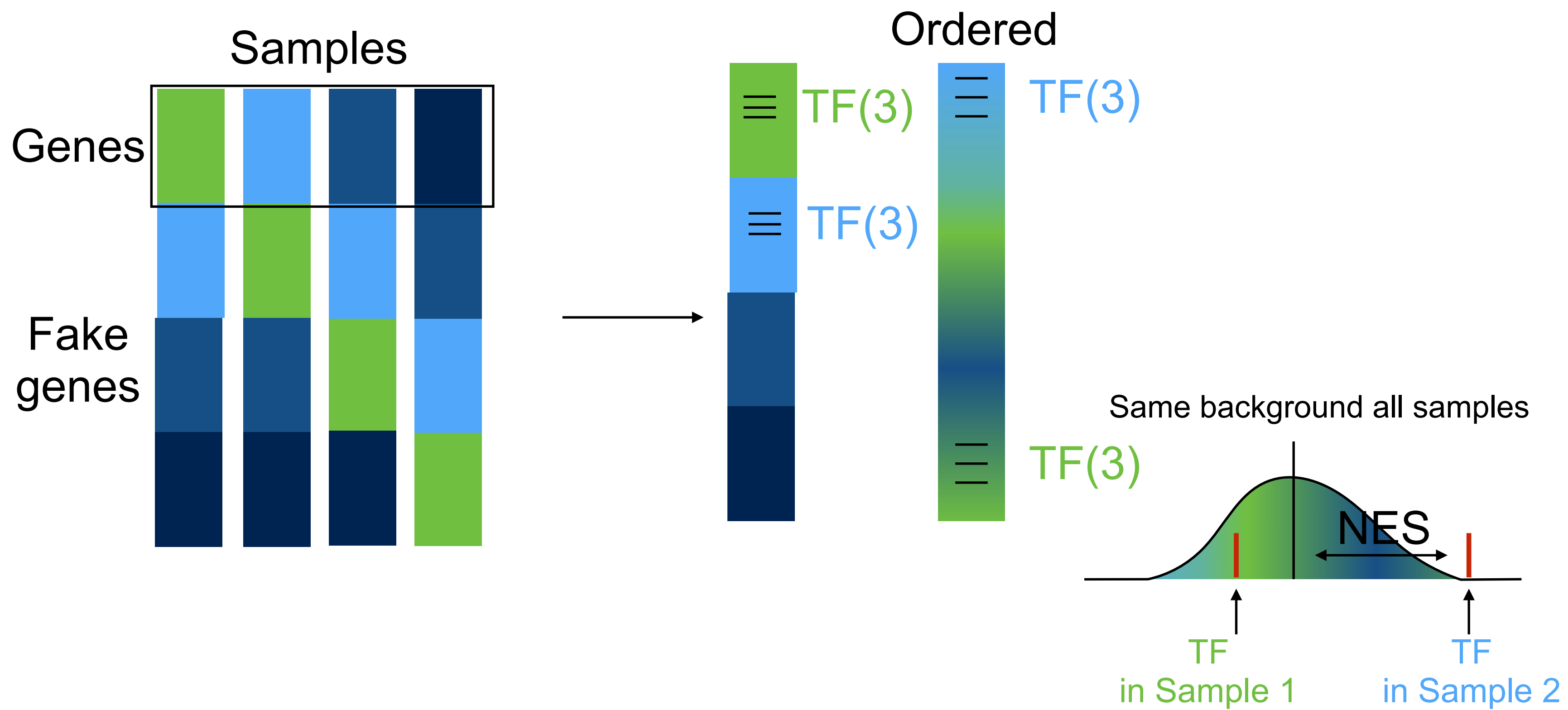
NES can be compared because the null distribution is identical.