

# Galaxy Workflow ' wgcna-analysis'

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Step	Annotation
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Step 1: Input dataset	
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<b>input</b> <i>select at runtime</i>	
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Step 2: Input dataset	
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<b>input</b> <i>select at runtime</i>	
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Step 3: WGCNA: preprocessing	
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<b>Gene expression data</b> Output dataset 'output' from step 1  <b>Display analysis code in report?</b> False	
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Step 4: WGCNA: construct network	
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<b>R workspace from WGCNA: preprocessing</b> Output dataset 'preprocessing_workspace' from step 3  <b>Height</b> 15.0  <b>Trait data</b> Output dataset 'output' from step 2  <b>Display analysis code in report?</b> False	
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Step 5: WGCNA: eigengene visualization	
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<b>R workspace from WGCNA: construct network</b> Output dataset 'construct_network_workspace' from step 4  <b>Soft threshold power</b> 6  <b>Number of genes</b> 400  <b>Display analysis code in report?</b> False	
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