StringTie Gene Abudance Report Element

The element summarizes gene abundance output of StringTie and saves the result into a common tab-delimited text file. The first two columns of the file are "Gene ID" and "Gene name". Each other column contains "FPKM" values for the genes from an input gene abundance file.

Parameters in GUI

Parameter	Description	Default value
Output file	Specify the name of the output tab-delimited text file.	

Parameters in Workflow File

Type: stringtie-gene-abundance-report

Parameter	Parameter in the GUI	Type
output-url	**Output file**	*string*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Input StringTie gene abundance file(s) url

Name in Workflow File: in

Slots:

Slot in GUI	Slot in Workflow File	Type
Input URL	url	*string*