

quantify\_genes  
sample: Sample1

quantify\_genes  
sample: Sample2

collate\_outputs

all

```
graph TD; A["quantify_genes<br/>sample: Sample1"] --> C["collate_outputs"]; B["quantify_genes<br/>sample: Sample2"] --> C; C --> D["all"];
```

The diagram illustrates a workflow for processing gene quantification data. It starts with two parallel steps at the top: 'quantify\_genes sample: Sample1' (enclosed in a green dashed box) and 'quantify\_genes sample: Sample2' (enclosed in a green dashed box). Arrows from both of these steps point down to a central step, 'collate\_outputs' (enclosed in a red dashed box). From 'collate\_outputs', an arrow points down to the final step, 'all' (enclosed in a green dashed box).