

run\_count\_rna

run\_count\_hto

demultiplex

summary

all

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graph TD; A[run_count_rna] --> C[demultiplex]; A --> D[summary]; B[run_count_hto] --> C; B --> D; C --> E[all]; D --> E;
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The diagram is a flowchart with five nodes, each in a rounded rectangle. The top row has two nodes: 'run\_count\_rna' (green border) and 'run\_count\_hto' (blue border). The middle row has two nodes: 'demultiplex' (yellow border) and 'summary' (red border). The bottom row has one node: 'all' (green border). Arrows point from 'run\_count\_rna' to both 'demultiplex' and 'summary'. Arrows point from 'run\_count\_hto' to both 'demultiplex' and 'summary'. Arrows point from both 'demultiplex' and 'summary' to 'all'.