

add_spikeins_genome



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graph TD; A[add_spikeins_genome] --> B[generate_genome]; B --> D[align]; C[trim] --> D; E[demultiplexing_and_trim] --> D; D --> F[overview_STAR_results]
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A flowchart illustrating a STAR alignment pipeline. The process starts with 'add_spikeins_genome' (green border), which leads to 'generate_genome' (cyan border). 'generate_genome' then leads to 'align' (orange border). 'trim' (green border) also leads to 'align'. 'demultiplexing_and_trim' (red border) also leads to 'align'. Finally, 'align' leads to 'overview_STAR_results' (blue border).

generate_genome

trim

demultiplexing_and_trim

align

overview_STAR_results