

dataPrepAutomate
species: mCanLor1

runIGdetective_Corr
species: mCanLor1

convertPrimaryBam

geneLociAutomate

cigarProcessing

all

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graph TD; A["dataPrepAutomate<br/>species: mCanLor1"] --> B(convertPrimaryBam); C["runIGdetective_Corr<br/>species: mCanLor1"] --> D(geneLociAutomate); B --> E(cigarProcessing); D --> E; E --> F(all);
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The diagram is a flowchart with six nodes, each in a rounded rectangle with a colored border. The nodes are arranged in a top-down sequence. The top row has two nodes: 'dataPrepAutomate species: mCanLor1' (orange border) on the left and 'runIGdetective_Corr species: mCanLor1' (red border) on the right. Arrows point from each to the second row: 'convertPrimaryBam' (cyan border) from the left and 'geneLociAutomate' (yellow border) from the right. Arrows from both of these point to the third row: 'cigarProcessing' (blue border). An arrow from 'cigarProcessing' points to the final node in the bottom row: 'all' (green border).