

runIGdetective_noCorr
species: mCanLor1

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graph TD; A[runIGdetective_noCorr<br/>species: mCanLor1] --> B[geneLociAutomate]; A --> C[dataPrepAutomate<br/>species: mCanLor1]; C --> D[convertPrimaryBam]; B --> E[mergeLoci]; D --> F[cigarProcessing]; E --> F; F --> G[all];
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The flowchart illustrates a bioinformatics pipeline for the mCanLor1 species. It begins with a red box labeled 'runIGdetective_noCorr species: mCanLor1'. This box has two outgoing arrows: one to a yellow box labeled 'geneLociAutomate' and another to a blue box labeled 'dataPrepAutomate species: mCanLor1'. From the blue box, an arrow points to a green box labeled 'convertPrimaryBam'. From the yellow box, an arrow points to an orange box labeled 'mergeLoci'. Both the green and orange boxes have arrows pointing to a teal box labeled 'cigarProcessing'. Finally, an arrow points from the teal box to a light green box labeled 'all'.

dataPrepAutomate
species: mCanLor1

geneLociAutomate

convertPrimaryBam

mergeLoci

cigarProcessing

all