

dataPrepAutomate
species: mPumCon1

convertPrimaryBam

lociLocation
species: mPumCon1

cigarProcessing

coverageAnalysis

all

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graph TD; A["dataPrepAutomate<br/>species: mPumCon1"] --> B[convertPrimaryBam]; B --> C[cigarProcessing]; B --> D[coverageAnalysis]; E["lociLocation<br/>species: mPumCon1"] --> C; E --> D; C --> F[all]; D --> F;
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The diagram illustrates a data processing pipeline. It begins with a red-bordered box labeled 'dataPrepAutomate' with the subtext 'species: mPumCon1'. An arrow points down to an orange-bordered box labeled 'convertPrimaryBam'. From 'convertPrimaryBam', two arrows branch out: one to a light green-bordered box labeled 'cigarProcessing' and another to a teal-bordered box labeled 'coverageAnalysis'. A second input, a green-bordered box labeled 'lociLocation' with the subtext 'species: mPumCon1', has two arrows pointing to 'cigarProcessing' and 'coverageAnalysis'. Finally, arrows from both 'cigarProcessing' and 'coverageAnalysis' point to a blue-bordered box at the bottom labeled 'all'.