

genome\_binning  
patient: F001

SNP\_calling\_and\_BAF  
patient: F001

combine\_bin\_and\_SNPs

global\_clustering

plot\_clustering\_results

final

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graph TD; A[genome_binning<br/>patient: F001] --> C[combine_bin_and_SNPs]; B[SNP_calling_and_BAF<br/>patient: F001] --> C; C --> D[global_clustering]; C --> F[final]; D --> E[plot_clustering_results]; E --> F; D --> F;
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The flowchart illustrates a genomic analysis pipeline for patient F001. It begins with two parallel input steps: 'genome\_binning' (green border) and 'SNP\_calling\_and\_BAF' (red border). Both lead to a central step 'combine\_bin\_and\_SNPs' (teal border). From here, the process branches into 'global\_clustering' (light green border) and 'final' (orange border). 'global\_clustering' further leads to 'plot\_clustering\_results' (blue border), which then leads to 'final'. Additionally, there is a direct path from 'global\_clustering' to 'final' and a curved path from 'combine\_bin\_and\_SNPs' to 'final'.