2_get-somatic mission_control Overview of Biomarkers Pipeline Inputs (treasure_map.py and .R) get_somatic-Hartwig input directory features tmp_dir (Output directory) 3_get-isofox ref_dir (extra files) tmp_dir fps_dir (File paths directory) ref_dir code_dir (Code directory) 0_get-isofox 1_get-isofox Helper files - Contains helper files for all scripts get-cibersot get-neoeptiopes _dir after_burn o_dir 4_get-cnv _create-file-index 0_get-clinical fps_dir ref_dir Directory combine get_cnv-geneget_cnv-features features 0_get-clinical contains output 1_create-file-index from individual Clean pipelines 5_get-HLA 1_get-clinical ref_dir get_hla-features get_lilac-features launch_pad 6_get-svs prepare_the_engines.py - Turns all notebooks into scripts get_sv-features Scripts organised into 4 folders shown below 7_get-sigs - Need to be run run sequentially sig_dir space_flight 1_get-sigs 0_get-sigs engine 1 - contains quality controls checks * Python conda env example usage of the biomarkers dataset 8_get-summary engine_2 get-summary engine_3 9_get-drivers * R conda env after_burn 1_get-drivers 0_get-drivers