MAYO CLINIC LABORATORIES

TEST CHANGE

Notification Date: April 23, 2024
Effective Date: April 30, 2024

MayoComplete Solid Tumor Panel, Next-Generation Sequencing, Tumor

Test ID: MCSTP

Explanation: On the effective date, MCSTP will be updated to expand the reportable range for copy number variants (CNVs) due to the incorporation of an in-house proprietary pipeline that offers high-resolution view and B allele frequency plot to assess loss of heterozygosity. This update will allow for the viewing of inactivated genes due to deletion and will assist in a higher sensitivity for calling CNVs. There are no test-build changes associated with this update.

Note: Genes Interrogated by MayoComplete Solid Tumor Panel will not be updated until April 30, 2024.

Current Genetics Information	New Genetics Information
This test uses targeted next-generation sequencing to estimate tumor mutational burden, determine microsatellite instability status, and identify somatic sequence variants, gene amplifications, fusions, and specific transcript variants in solid tumors. This panel includes a DNA subpanel for the detection of sequence alterations in 515 genes and amplification of 59 genes as well as an RNA subpanel for the detection of fusions involving 55 genes and specific splice variants involving *EGFR*, *AR*, and *MET*. See Genes Interrogated by MayoComplete Solid Tumor Panel for details regarding genes interrogated by this test. **Note:** This test is performed to evaluate for somatic (ie, tumor-specific) alterations within the genes listed. Although germline (ie, inherited) alterations may be detected, this test cannot distinguish between germline and somatic alterations with absolute certainty. Follow-up germline testing using whole blood can be performed for confirmation of suspected clinically relevant germline alterations. Germline testing should be performed along with genetic counselling.	This test uses targeted next-generation sequencing to estimate tumor mutational burden and detect microsatellite instability, sequence variants, gene amplifications, homozygous gene deletions, fusions, and specific transcript variants in solid tumors. This panel includes a DNA subpanel for the detection of sequence alterations in 515 genes, amplification of 96 genes, homozygous deletion of 133 genes, as well as an RNA subpanel for the detection of fusions involving 55 genes and specific splice variants involving *EGFR*, *AR*, and *MET*. Sequence variants and copy number changes are concomitantly interpreted to evaluate for complete inactivation of 31 tumor suppressor genes. See Genes Interrogated by MayoComplete Solid Tumor Panel for details regarding genes interrogated by this test. **Note:** This test is performed to evaluate for somatic (ie, tumor-specific) alterations within the genes listed. Although germline (ie, inherited) alterations may be detected, this test cannot distinguish between germline and somatic alterations with absolute certainty. Follow-up germline testing using whole blood can be performed for confirmation of suspected clinically relevant germline alterations. Germline testing should be performed along with genetic counselling.

Questions

Contact Michelle Raths, Laboratory Resource Coordinator at 800-533-1710.