| Test Name | Eligibility | Age Restriction | Commercial | Repurposed | Cancer Type | Foundation Medicine | Gene Count | Tumor Type | Whole Exome Sequencing | Whole Transcriptome Sequencing | MSI | TMB* | RNA-Seq | WES | Cost | Minimally Invasive Sample | Independent | Non-Ind. | Next-Generation Sequencing | Foundation Medicine FoundationOne Liquid empowers providers to make more informed clinical decisions even when oncological targets by sequencing tumor samples and matched normal saliva or blood samples, when available. The trial has two enrollment steps. Each patient will initially enroll for a screening study, in which a sample of his or her tumor is sequenced to identify genetic abnormalities and other markers that may be associated with specific subtypes of cancer. The third version of the xT assay (v3) detects 648 total genes spanning 3.6 Mb of genomic space. This includes all genes fused with known and novel partners. In addition, tumor mutational burden (TMB) and microsatellite instability (MSI) are measured. The Pediatric MATCH will use a single sequencing test to screen for many molecular abnormalities at once. The test, which is also being used for the adult NCI-MATCH trial, was developed by the NCI Molecular Characterization Laboratory at the NCI Frederick National Laboratory for Cancer Research in Frederick, Maryland. The latest WES and RNA-Seq tests in the care of childhood cancer patients. The study will compare the results of targeted cancer panel sequencing to traditional tumor biopsy techniques. The assay is a research use only (RUO) test and is intended for research use only (RUO). Invitae Sarcoma Panel Foundation Medicine uses multiple tumor profiling technologies to detect somatic mutations, copy number variations and structural variants in tumor DNA extracted from fresh, frozen or formalin-fixed paraffin-embedded tissue. The test is validated to detect the four main classes of genomic alterations (substitutions, indels, CNAs and structural variants) across heterogeneous clinical settings in patients with hematologic malignancies and sarcomas. Test results provide information about clinically relevant signatures: MSI, TMB*), whole transcriptome sequencing* (RNA fusions and variant transcripts), pyro sequencing, and next-generation sequencing plus copy number array in high-risk and high-impact genes across hematopoietic malignancies. Clinical settings in which the test is currently used include a phase 1/2 trial in pediatric solid tumors, pediatric sarcomas, and hematologic malignancies. Invitae Sarcoma Panel Foundation Medicine Foundation Medicine uses multiple tumor profiling technologies to detect somatic mutations, copy number variations and structural variants in tumor DNA extracted from fresh, frozen or formalin-fixed paraffin-embedded tissue. The test is validated to detect the four main classes of genomic alterations (substitutions, indels, CNAs and structural variants) across heterogeneous clinical settings in patients with hematologic malignancies and sarcomas. Test results provide information about clinically relevant signatures: MSI, TMB*), whole transcriptome sequencing* (RNA fusions and variant transcripts), pyro sequencing, and next-generation sequencing plus copy number array in high-risk and high-impact genes across hematopoietic malignancies. Clinical settings in which the test is currently used include a phase 1/2 trial in pediatric solid tumors, pediatric sarcomas, and hematologic malignancies.