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IDT
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Project abstract

We are proposing a comprehensive workflow that advances the existing technology and addresses current patient and clinical needs. It covers all steps of Lot 1 prior to sequencing: from flexible solutions for nucleic acid (NA) extraction from various input sample types, followed by QC of NA, continued with innovative NGS library preparation that allows efficient processing of low input or damaged patient samples into functional NGS libraries containing unique molecular identifiers (UMI) and unique dual indices (UDI). Libraries are subjected to targeted enrichment with high quality hybridization capture panels to detect novel and known variants, followed by QC of NGS libraries. The whole workflow is tightly controlled by usage of reference materials, samples stabilization, as well as innovative solution for connectivity, sample tracking and information transfer. Our approach goes beyond current state of the art, by being fully automated, scalable, cost-effective, with improved performance and consideration of regulatory requirements.
Altogether, our approach aims to improve cancer patient's needs by implementing fully standardized and secure methods into routine diagnostics.