


For PCPs: complete this table for each contractor that was awarded a PCP Phase 1, 2 or 3 contract

Contractor Details	Type/ size of legal entity	Place of performance of contract activities	Logo
<p><u>Main contractor</u></p> <p>Agilent Technologies R&D Marketing GmbH & Co KG</p> <p>Hewlett Packard Strasse 8 76337 Waldbronn Dr. Andreas Polten +49 (0) 151 14758851 andreas_polten@agilent.com</p>	<p>Large Company</p>	<p>% of contract value allocated to main contractor: 100 %</p> <p>% of activities for the contract performed by the main contractor in EU Member States or countries associated with Horizon 2020: 80 %</p>	
<p><u>Other consortium member(s) (if applicable)</u></p> <p>na</p>	<p>na</p>	<p>na</p>	<p>na</p>
<p><u>Subcontractors (if applicable)</u></p> <p>na</p>	<p>na</p>	<p>na</p>	<p>na</p>

General Statement:

Agilent is a leader in life sciences, diagnostics and applied chemical markets. The company provides laboratories worldwide with instruments, services, consumables, applications and expertise, enabling customers to gain the insights they seek. Agilent’s expertise and trusted collaboration give them the highest confidence in our solutions.

Agilent offers a broad variety of high-quality workflow solutions for applications within genomics. Find everything you need to create your genomics workflow, from lab sample to library preparation, enrichment or hybridization, and more!

- https://www.agilent.com/en/solutions/genomics-applications-solutions?utm_source=sales&utm_medium=web&utm_campaign=DGG_FY22_TENDER_EM&utm_content=webpage

Project abstract (+/- 1000 characters maximum)

The scope of the proposed project is to develop a universal tumor panel for the detailed analysis of solid tumor samples with NGS. The fully automated library prep solution can be applied to a broad range of input specimen from fresh frozen samples, over FFPE DNA to cfDNA with an input amount in the range of 10-200ng of DNA. The enrichment solution will enable the detection of a broad range of



genomic aberrations, from small variants over copy number changes to gene fusion/translocation events. Furthermore, the calculation of therapeutic scores like TMB, MSI, and HRD will be supported as well as the monitoring of drug metabolizing genes. To improve the overall quality of the workflow, a system will be designed that allows tracking of samples throughout the entire workflow and to detect intra- and inter-run sample cross contamination.

The DNA sequencing protocol will be complemented by an RNA sequencing solution for a more sensitive detection of gene fusion events.

Previous EU funding

Is the project based on / a continuation of R&D activities that were previously funded by the EU?: NO

