Request For Information for Childhood Cancer Data Initiative Multi-omics Research Characterization

1. Please provide your contact information, including name, institution/organization, telephone numbers, e-mail address, and website URL.
2. What size is your organization with respect to NAICS code identified in this notice (i.e., "small" or "other than small")? If your organization is a small business under NAICS code, what type of small business (i.e., small, disadvantaged business, woman-owned small business, economically disadvantaged, woman-owned small business, veteran-owned small business, service-disabled veteran-owned small business, 8(a), or HUBZone small business)? Specify all that apply.
3. Based on the provided Statement of Work (SOW) DRAFT, do you possess more than one capability of molecular characterization based on the 3 Task Areas and/or a variety of platforms within each Task Area needed?

[ ]  Yes

[ ]  No

1. Do you have flexibility to switch in between different platforms within a task area (e.g., switching from WGS to RNA-seq)?
2. Describe your experience in working with pediatric or other rare cancers.
3. Describe your experience in generating and delivering primary data and derived data in relevant Task Areas (e.g., somatic mutation or gene fusion calls, structural variants such as CNV, INDEL, translocation; identification of unique proteins and posttranslational modification (PTM) sites and metabolites).
4. Check each of the validated platforms and analyses you are capable of performing according to the Task Areas for each source sample type. If you are not capable of performing an assay for a particular source, leave blank.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Analyses | Fresh frozen tissue  | FFPE  | Blood or bone marrow  | Purified analytes (e.g., DNA, proteins)  | Other input materials\*\* |
| WES |[ ] [ ] [ ] [ ] [ ]
| WGS  |[ ] [ ] [ ] [ ] [ ]
| Long read DNA/RNA seq  |[ ] [ ] [ ] [ ] [ ]
| Total RNA-seq |[ ] [ ] [ ] [ ] [ ]
| mRNA-seq |[ ] [ ] [ ] [ ] [ ]
| MicroRNA-seq  |[ ] [ ] [ ] [ ] [ ]
| Methylation arrays  |[ ] [ ] [ ] [ ] [ ]
| WG bisulfate seq  |[ ] [ ] [ ] [ ] [ ]
| ATAC-seq |[ ] [ ] [ ] [ ] [ ]
| sc/sn DNA/RNA/ Methylation-seq |[ ] [ ] [ ] [ ] [ ]
| Targeted DNA/RNA panels |[ ] [ ] [ ] [ ] [ ]
| Circulating tumor DNA analysis |[ ] [ ] [ ] [ ] [ ]
| Global proteomics |[ ] [ ] [ ] [ ] [ ]
| Phosphoproteomics  |[ ] [ ] [ ] [ ] [ ]
| sc proteomics  |[ ] [ ] [ ] [ ] [ ]
| Additional protein PTM profiling\*\*  |[ ] [ ] [ ] [ ] [ ]
| Metabolomic profiling  |[ ] [ ] [ ] [ ] [ ]

Specify “Other Input Materials” if applicable:

Specify “Additional PTM profiling” if applicable:

1. Describe the range of starting material amounts (from minimal to ideal) that correspond to the range of analytical outputs/coverage/depth (from minimal to ideal) in the table below. For example, you may enter an input material range of “100-300 ug of extracted proteins from fresh frozen tissue” in the middle column and an output range of “8,000-12,000 unique proteins" in the right column. Leave blank if you are unable to perform an analysis.

|  |  |  |
| --- | --- | --- |
| Analyses | Specify a range (amount/ volume) of starting materials (original specimens or analytes extracted) | Describe the corresponding range of coverage/depth/ analytical Output to the given range of starting materials |
| WES  |  |  |
| WGS  |  |  |
| Long read DNA/RNA seq |  |  |
| Total RNA-seq |  |  |
| mRNA-seq |  |  |
| MicroRNA-seq |  |  |
| Methylation arrays  |  |  |
| WG-bisulfate seq |  |  |
| ATAC-seq |  |  |
| sc/sn DNA/RNA/ Methylation-seq |  |  |
| Targeted DNA/RNA panels |  |  |
| Circulating tumor DNA analysis |  |  |
| Global proteomics |  |  |
| Phosphoproteomics |  |  |
| sc proteomics |  |  |
| Additional protein PTM profiling |  |  |
| Metabolomic profiling  |  |  |

1. The NCI seeks to understand whether it is feasible to assign fixed prices to the 3 Task Areas in the SOW DRAFT. The fixed unit prices should include all labor, materials, ODCs, indirect costs and fee to perform the activities in each Task Area including the submission of deliverables. It is envisioned that there would be multiple fixed unit process depending on the activity. It is not necessary for one vendor to meet all of the capabilities described in the Statement of Work (SOW); however, vendors should be in the business of providing services for either Task Areas 1, 2 or 3. Please review the SOW DRAFT for specific activities in each Task Area.

a) Based on the SOW DRAFT, can a fixed price or fixed unit price structure be established for the required activities under each Task Area?

[ ]  Yes

[ ]  No

b) If fixed prices are not feasible, what cost/pricing structure or combination of cost/pricing structures is feasible for the types of activities required?

1. Describe your QA/QC procedures to ensure the quality of analytes and molecular characterization outputs.
2. How long will it take for your site to be ready to receive and analyze samples/analytes upon NCI identifying a new sequencing or characterization need?
3. If you are required to extract, enrich and purify analytes from original specimens such as tumor tissues or blood prior to characterization, what is your throughput (e.g., you can extract 50 cases (tumors with matched normal) per week)?
4. Vendors are encouraged to comment on any aspect of the SOW DRAFT that they think will provide more clarity to the requirement whether technical or business related, and/or summarize their analytical capability in a short narrative.