**Technical Terms:**

1. Overview of Service

|  |  |
| --- | --- |
| Species Name | *VAR\_SPECIES* |
| Sample Type | Purified genomic DNA sample |
| Sample Number | SAM\_NUM\_1 |
| Library Type | 350 bp insert DNA library or 10Kb/20Kb SMRTbell library |
| Data Output | DATA\_OUTPUT G raw data/library/sample |
| Bioinformatics | VAR\_ALY |
| Turnaround Time | VAR\_TAT business days starting after we receive the library preparation confirmation from client |

1. Sample Requirements

Illumina platform（350bp insert DNA Library）

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | Concentration | Purity |
| Genomic DNA | Required | ≥1 μg | ≥20 μL | ≥20 ng/μL | OD260/280=1.8-2.0, No degradation or RNA contamination |

PacBio platform（SMRTbell DNA Library）

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Volume | Concentration | Purity |
| HMW DNA | Required | ≥10 μg | ≥50 μL | ≥100 ng/μL | OD260/280=1.8-2.0, No degradation or RNA contamination |

Note:

1. Detailed requirements can be referred to the Sample Information Form (SIF).
2. Samples not meeting Novogene’s specifications can be designated by the customers as to be processed “at risk” and will be subjected to billing regardless of data quality. The turnaround time could be extend depending on circumstance.
3. The above-mentioned sample requirement is for post-QC samples. Please send us excess samples to account for nucleic acid used for QC experiments.
4. If the customer chooses to opt out certain procedures in Novogene standard QC pipeline, the samples will be graded as “Hold” or “Fail”.
5. Special samples such as FFPE DNA, MDA product will be subjected to different QC standards as appeared on the final QC report sent by Novogene.