**Technical Terms:**

1. Overview of Service

|  |  |
| --- | --- |
| Species Name | Microorganism |
| Sample Type | Purified genomic DNA Sample from fresh tissues |
| Sample Number | SAM\_NUM\_1 |
| Library Type | PCR-free Library |
| Data Output | 30,000 raw reads, 50,000 raw reads or 100,000 raw reads per sample |
| Bioinformatics | VAR\_ALY |
| Turnaround Time | VAR\_TAT working days upon next day after the library preparation confirmation from client |

1. Overview of Product

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Types | Region | Fragment Length | Primer | Primer sequences（5’- 3’） |
| **Bacterial 16S** | V4 | 300 bp | 515F | GTGCCAGCMGCCGCGGTAA |
| 806R | GGACTACHVGGGTWTCTAAT |
| V3-V4 | 470 bp | 341F | CCTAYGGGRBGCASCAG |
| 806R | GGACTACNNGGGTATCTAAT |
| V4-V5 | 450 bp | 515F | GTGCCAGCMGCCGCGGTAA |
| 907R | CCGTCAATTCCTTTGAGTTT |
| V5-V7  (for endophytic) | 300-400 bp | 799F | AACMGGATTAGATACCCKG |
| 1193R | ACGTCATCCCCACCTTCC |
| **Archaeal16S** | V4 -V5 | 400-500bp | Arch519F | CAGCCGCCGCGGTAA |
| Arch915R | GTGCTCCCCCGCCAATTCCT |
| **Archaeal 1106F** | V8 | 300bp | 1106F | TTWAGTCAGGCAACGAGC |
| 1378R | TGTGCAAGGAGCAGGGAC |
| **Fungal18S** | V4 | 350 bp | 528F | GCGGTAATTCCAGCTCCAA |
| 706R | AATCCRAGAATTTCACCTCT |
| V9 | 200 bp | 1380F | CCCTGCCHTTTGTACACAC |
| 1510R | CCTTCYGCAGGTTCACCTAC |
| **Fungal ITS** | ITS1 | 200-400 bp | ITS5-1737F | GGAAGTAAAAGTCGTAACAAGG |
| ITS2-2043R | GCTGCGTTCTTCATCGATGC |
| ITS2 | 380 bp | ITS3-2024F | GCATCGATGAAGAACGCAGC |
| ITS4-2409R | TCCTCCGCTTATTGATATGC |
|  | ITS1-1F  (for endophytic) | 200-400 bp | ITS1-1F-F | CTTGGTCATTTAGAGGAAGTAA |
| ITS1-1F-R | GCTGCGTTCTTCATCGATGC |

1. Sample Requirements

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample Type | Remarks | Amount | Fragment size | Concentration | Volume | Purity |
| Genomic DNA | - | ≥150ng | - | ≥5ng/μL | ≥30μL | 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 will be subjected to different QC standards as appeared on the final QC report sent by Novogene.