Quotation

Quotation no. : QN180620-046
Quote date : 20.06.2018
Valid until : 20.07.2018
Prepared by : ▮▮▮▮▮

Ordered by : ▮▮▮▮▮
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Service Description	Quantity	Unit	Unit Price	Amount
Ready to run libraries, HiSeq2500 2x100bp High Throughput Mode	4	Run	2000	8000
Total Project Price (EUR, VAT excluded)				8000

The Scope of Work

1. **Ready to run libraries** will be provided by the user (at least 10nM, >10µl). Detailed protocol of library preparation will be provided.
2. No custom sequencing primer required. Customer will check the library structure and its compatibility with Illumina platform on its own side.
3. Libraries will be pooled together for **4 HiSeq2500 High Throughput Mode in 2x100bp** configuration.
4. No total throughput nor throughput per sample and/or % of data with Q20/Q30 is guaranteed due to the library unknown nature.
5. By default, no spike-in control will be used, unless requested by the user.
6. Information regarding the library kit used to prepare the sample will be provided by the client along with the index and adapter sequences. Incorrect or insufficient information may leads sequencing run failure.
7. If the sample requires custom sequencing primer, the primer at 100pmol/µl is expected to be submitted along with the sample, or oligo synthesis service should be requested by the client.
8. Raw data in FASTQ file format will be delivered via FTP download links.
9. Macrogen offers free shipping of initial sample delivery through Macrogen-FedEx shipment system.
10. The final throughput and the % of results with Q_{20}/Q_{30} quality index is not guaranteed.
11. Standard turnaround time of 4-6 weeks after quality control step will be applied.
12. Samples that failed quality control can be replaced within three months from initial delivery. After this time experiment will be either processed "as it is" or cancelled and the ordering part will be charged the QC costs.
13. Macrogen INC. shall under **no** circumstances be **liable** for any loss, damage, expense or **delay** to the shipments for any reason whatsoever whensaid shipments are in custody, possession or control of third parties (courier companies).

*Note: this is a special (contract) price not applicable for other orders.

Service terms and conditions

- The above quote is prepared for price estimation of this specific order, and can be changed under various circumstances.
- Signed quote, completed order form, and PO# (or other payment method) must be present when placing an order.
- Terms of payment: NET 30 days
  IBAN: ▮▮▮▮▮
  BIC: ▮▮▮▮▮
  BANK: ▮▮▮▮▮
- Sequencing raw data and its analyzed result will be discarded 3 months after the data delivery. Long term storage is to be negotiated separately.
- Whilst we are willing to examine client queries surrounding the data, we dictate that any formal objections should be addressed within 3 months after the data delivery.
- Processed sample and any unused sample (back-up, QC failed one, etc.) will be discarded 3 months after the data delivery, unless otherwise special request is made. At request, the samples can be returned at recipient's cost. Request should be made no later than 1 month after the data delivery. For the project amount of total €15,000 or above, the shipping and handling charge can be waived.
- During data storage period, analysis result of your sample might be used for sample quality check process, data validation, internal education or other investigation for better service by Macrogen.

By signing this quotation, I acknowledge that I have read and agree to the terms and conditions, and all of its provisions.

Name: _____

Date & Signature: _____

Additional Benefits and Sole Source Specifications

Large capacity (300,000 exomes per year) to provide fast turnaround time – With our current instrumentation set up, we can produce over 300,000 exomes, or equivalent genomes/transcriptomes/methylomes per year. With this capacity, we can provide a 6- to 10-week turnaround even for large projects with a high degree of complexity.

Publication-Quality Data generated by sequencing specialists who generated data for Nature and Nature Genetics publications – We only use next-generation sequencing specialists with proven skills in producing publication-quality data in top-tiered journals. For example, our specialists produced high-quality data to support the following recent publications.

- Young Seok Ju, et. al., "Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals" Nature Genetics, 3 July 2011 (doi:10.1038/ng.872)
- Hansoo Park et. al. "Discovery of common Asian copy number variants using integrated high-resolution array CGH and massively parallel DNA sequencing" Nature Genetics (2010) 42(5):400-405
- Jong-Il Kim et. al. "A highly annotated whole-genome sequence of a Korean individual" Nature (2009) 460(7258):1011-1015

Follow-on validation – Macrogen has a variety of genotyping and array-based platforms. For example, we can easily implement follow-on projects to help you validate SNP and CNV candidates at an affordable cost level, without you worrying about sending your samples to yet another service provider.
- Macrogen provide validations using genotyping platforms including TaqMan assays, CGH arrays, and Illumina Beadchip arrays
- Macrogen provide validations using sequencing platforms including MiSeq, Ion Torrent systems and ABI 3730XL capillary sequencer.

ISO Certification & Clinical-Grade Sequencing data – Macrogen, Inc., is ISO 9001 and ISO13485 certified to provide high quality data in our entire sample preparation and DNA sequencing processes. Macrogen generates sequencing data at clinical-grade quality for discovery and validation of genetic variants. Our sequencing and data generation processes are for research use only, not for use in diagnostic procedures