

## REQUESTER'S INFORMATION

Name and Surname:	
Requesting Centre:	
Unit/Department:	
Telephone Number:	E-mail:

## QUOTATION NUMBER

## PROJECT NO.

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## SAMPLE TYPE

<input type="checkbox"/> DNA	<input type="checkbox"/> FFPE
<input type="checkbox"/> Total RNA	<input type="checkbox"/> Blood EDTA
<input type="checkbox"/> Library	<input type="checkbox"/> Frozen Tissue
<input type="checkbox"/> Others (specify): _____	

## PROJECT INFORMATION

Brief description of the project	
Type of study	<input type="checkbox"/> Germinal <input type="checkbox"/> Somatic (indicate tumour cellularity: _____ %)
Number of samples to be analysed	
Origin of the samples to be studied (organism)	<input type="checkbox"/> Human <input type="checkbox"/> Murine <input type="checkbox"/> Others (indicate species): _____

## SERVICE REQUESTED

### Sequencing:

Genome (WGS) 30X

Exome (WES) Sure Select

- |   |                                       |  |   |
|---|---------------------------------------|--|---|
| <input type="checkbox"/> All Exome V6 (60 Mb) | <input type="checkbox"/> 4-5Gb (~50X) | <input type="checkbox"/> 8-10Gb (~100X)  | <input type="checkbox"/> 18-20 Gb (~200X) |
| <input type="checkbox"/> V6 + COSMIC (66 Mb)  | <input type="checkbox"/> 5-6Gb (~50X) | <input type="checkbox"/> 9-10Gb (~100X)  | <input type="checkbox"/> 20-21 Gb (~200X) |
| <input type="checkbox"/> V6 + UTR (91 Mb)     | <input type="checkbox"/> 6-7Gb (~50X) | <input type="checkbox"/> 12-14Gb (~100X) | <input type="checkbox"/> 26-28Gb (~200X)  |

\*Depth (X) values are referential, as it is affected by several factors which are specific to the original sample

Transcriptome (RNA-seq)

- Type of RNA-seq  PolyA (mRNA)\*  Total\* (Ribo-Zero, mRNA and lncRNA)
- Millions of readings per sample  30M  50M  100M  Other: \_\_\_\_\_
- \*requires RIN>7 \*recommended for degraded RNA

Complete Flow Cell Libraries

- Library building kit: \_\_\_\_\_
- Medium size library: \_\_\_\_\_ Output per sample (Gb): \_\_\_\_\_
- Index kit: \_\_\_\_\_ Nucleotides \_\_\_\_\_  Single-Index  Dual-Index

NovaSeq 6000

- Flow Cell Type  SP<sub>(1,300-1,600M PE)</sub>  S1<sub>(2,600-3,200M PE)</sub>  S2<sub>(6,600-8,200M PE)</sub>  S4<sub>(16,000-20,000M PE)</sub>
- Length of readings  1x100bp  2x50 bp  2x100bp  2x150 bp  2x250 bp\*
- \*Only available for Flow Cell SP

MiniSeq

- MID-output<sub>(14-16 M PE)</sub>  2x150bp
- HIGH-output<sub>(44-50 M PE)</sub>  1x75bp  1x150bp  2x75 bp  2x150bp

Amplicons and Small genomes

- Size (Kb): \_\_\_\_\_ • Output per sample (Gb): \_\_\_\_\_

### CGH Array (Agilent)

- Stem Cells  180K  Leukaemia

## BIOINFORMATIC ANALYSIS

Reference genome  GRCh37/hg19  GRCh38/hg38  Other (please specify): \_\_\_\_\_

- Record table  Tabla de grupos  CNVs
- Bioinformatic advice  Tabla germinal vs somático

RNA-seq:  Bioinformatics (Alignment + Expression)  Differential Expression (fill in specific questionnaire)

## SAMPLE INFORMATION

Attached document with table to be filled in with the sample data, requiring at least the codes of the samples and their origin (blood, fresh tissue, tumour, paraffin, etc.)

## SAMPLE SHIPPING CONDITIONS

### DNAg or Total RNA:

The source material is genomic DNA or total RNA (treated with DNase) obtained from peripheral blood, fresh frozen tissue, tissues included in paraffin blocks (FFPE), saliva, cell lines, etc. The minimum amount of DNA or RNA required depends on the service requested, the research project and the type and quality of the samples (ask for details at [imasd@nimgenetics.com](mailto:imasd@nimgenetics.com)). The gDNA can be sent at room temperature (18-25 °C), while the total RNA must be sent in dry ice, in an insulated container, within a maximum of 18 hours.

### Bone marrow or peripheral blood:

3-5 ml in an EDTA tube. Shipment at room temperature within 48 hours after sample collection. **DO NOT FREEZE.**

### Tissues included in paraffin:

- Formaldehyde-fixed tissues in paraffin block. The tumour region needs to be marked on the block and it needs to include a report and/or plate of the anatomopathological study performed. In those cases where only blocks are available, consult the laboratory.
- Paraffin cuts of formaldehyde-fixed tissues. Contact the laboratory to define the number and thickness of the cuts recommended for each approach. It is recommended to include a report of the anatomopathological study performed or, in its absence, indicate the tumour type, the patient's gender, and the tumour tissue percentage on the sample sent.

Shipment at room temperature (18-25 °C). Avoid exposing blocks or cuts to high temperature situations by using refrigerated containers during the summer months. The study cannot be carried out in those cases with insufficient tumour sample in the submitted block/cut, or in those cases where the processing and/or fixation does not preserve the quality of the sample.

### Fresh frozen tissue:

25-50 mg (5-10 mm<sup>3</sup>) of frozen tissue in 2 ml Eppendorf type tubes with a round bottom and stored at -20 °C. Shipment is made on dry ice, in an insulated container, within a maximum of 18 hours.

## ADDRESS FOR SENDING SAMPLES

You can see the general conditions for the collection of samples on our website: [www.nimgenetics.com](http://www.nimgenetics.com)

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We are available at [imasd@nimgenetics.com](mailto:imasd@nimgenetics.com)

## BILLING INFORMATION

Entity:	Tax ID (NIF/CIF):
Address:	Authorized signature
Authorised person:	
E-mail:	

## BANK DETAILS NIMGenetics

Banco Santander  
CC-IBAN No.: ES53 0075 0436 7206 0013 4861  
Account holder: NIMGENETICS, S.L.