

**Sample-shipping form for RNA and DNA samples**

Please ship samples in RNAse-free buffer on dry-ice in parafilm-wrapped and sealed tubes. Tubes should be firmly placed in an extra container within the dry ice-box. The concentration for the sample should be >200 ng/µl. Ideally, 5 µg of total RNA should be provided.

Quotation number or Project-Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Email address of responsible person:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Please state Billing address**

**Please state VAT-ID** (important for Exempt of VAT in accordance with no 9 of Art 6 of VAT)

**Sample description and preferred names**:

Please define biological replicates by “BR”.

|  |  |  |  |
| --- | --- | --- | --- |
| **Number** | **Sample description (optional)** | **Preferred abbreviation**  **(max 6 characters)** | **Quantity** |
| 1 |  |  |  |
| 2 |  |  |  |
| 3 |  |  |  |
| 4 |  |  |  |
| 5 |  |  |  |
| 6 |  |  |  |
| 7 |  |  |  |
| 8 |  |  |  |
| 9 |  |  |  |
| 10 |  |  |  |
| 11 |  |  |  |
| 12 |  |  |  |

**Alternatively and for more than 12 samples, please send an excel file to “customerservice@genxpro.de”**

**For nucleic acids only:**

**Quantification method:** (please define)\_\_\_\_\_\_\_\_\_\_­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Purification method:**

Column □ Ethanol precipitation □

Others □ (please define)\_\_\_\_\_\_\_\_\_\_­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

DNAse digested \*(for RNA) yes □ no □

RNAse digested (for DNA) yes □ no □

Pelleted yes □ no □

Buffer/liquid: (please define)\_\_\_\_\_\_\_\_\_\_­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\* DNAse treatment should be performed in solution and not on columns

**Gel picture or Agilent 2100 trace: please paste here or send via e-mail to** [**Customerservice@genxpro.de**](mailto:Customerservice@genxpro.de) **including the quotation number.**

**Concerning bioinformatics:**

**Annotation:**

Please define Database to which the sample shall be annotated. If no database is stated, NCBI-refseq, ENSEMBL databases or TIGR-gene indices will be used whenever possible.

Preferred database (URL):

**Data storage:** Data will be stored 6 Month after delivery. Please state if additional storage on an external hard-drive for an additional fee of 125 EUR is required: yes □ no □

**For gene expression analysis, pairwise comparisons:**

Please define the samples which should be compared in pairwise comparisons using the preferred abbreviations from the above tables. Please note that if not otherwise stated in the quotation, the amount of pairwise comparisons is limited to the amount of samples. Additional comparisons/Analyses can be ordered for 125 EUR each.

If “in silico” pools of samples shall be compared, please define the pools by parentheses.

Biological replicates (BR) will be treated using negative binomial statistics in pairwise comparisons for calculations of p-values for differential expression.

|  |  |  |
| --- | --- | --- |
| **Comparison** | **Samples 1** | **Samples 2** |
| 1 |  |  |
| 2 |  |  |
| 3 |  |  |
| 4 |  |  |
| 5 |  |  |
| 6 |  |  |
| 7 |  |  |
| 8 |  |  |
| 9 |  |  |
| 10 |  |  |
| 11 |  |  |
| 12 |  |  |

**Alternatively and for more than 12 comparisons, please send an excel file to** [**customerservice@genxpro.de**](mailto:customerservice@genxpro.de)