



A Eurofins Genomics Company

GATC Biotech AG  
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Germany

### Customer Details

Name:  
Institute/Company name:  
Offer/Project No.:  
Email:  
Phone:

### Please fill out the form and include with your sample shipment

#### 1. Basic information

Kit:  Storage buffer used:   
Method used:

#### 2. Application

<input type="checkbox"/> RNA	<input type="checkbox"/> Genome	<input type="checkbox"/> Amplicons*	<input type="checkbox"/> Enrichment
<input type="checkbox"/> Small/miRNA	<input type="checkbox"/> Bisulfite treated*	<input type="checkbox"/> Other: <input type="text"/>	

\*To increase the library nucleotide balance, a spike-in of 20% PhiX will be used for samples with low diversity or unbalanced base composition (e.g., amplicons, bisulfite converted samples)

#### 3. For Nextera XT libraries, please complete the following fields

Libraries are prepared according to manufacturer's „Nextera® XT DNA Library Prep Reference Guide“. Normalised Nextera XT „Pooled Amplicon Library“ (PAL) will be provided as starting material.

Bead-based normalisation

Manual / Standard normalisation

Nextera XT „ready-to-load“ libraries can only be accepted for data packages of 280 Mio, 22 Mio and 12 Mio reads as these libraries are less stable and more susceptible to degradation.

Please do not fill in if only Nextera XT indices have been used without the normalisation step of the Nextera XT library preparation protocol.

#### 4. Compatibility

Libraries are compatible with Illumina primers (sequencing and index).

Libraries require use of custom sequencing primers that will be provided together with the samples.  
Concentration of custom primer sent: 100 µM in at least 15 µl

#### 5. Indexing system

Libraries are prepared using the Illumina indexing system:

Index sequences are included in the adapter and will be sequenced in an additional read.

Raw data sorting according to Illumina index read(s) will be performed by default according to the information provided in the additional Excel file „K-1466-NGSelect RTL index sequences used“.

Single index

Dual index

Libraries are prepared using a custom „in-line“ system:

Tags/barcodes are adjacent to the sample DNA and read as part of the sequence read.

Raw data sorting according to customer specific tags at read start can be offered at additional costs. Sorting will be performed according to the information provided in the additional Excel file „K-1466-NGSelect RTL index sequences used“.

We highly recommend to avoid the “in-line” barcoding strategy and use the Illumina index system instead (i.e. the barcodes are read in a separate read and do not interfere with cluster registration). It is important to ensure that the base composition of the indices is balanced to optimize the ability of the image analysis software to distinguish signals.