

Next-Generation sequencing Sample submission guidelines

| This is the lowest quantity needed. We highly recommend you provide at least 2× more! |  |      |                  | eded. We highly<br>east 2× more! | See the FAQ section of our NGS website for additional recommendations and useful tips! |  |
|---|--|------|------------------|----------------------------------|--|--|
|   | Sample type  |      | Lowest<br>amount | Concentration<br>by Qubit        | Shipping   | Remarks  |
| Illumina  | gDNA / Amplicons<br>Standard DNA library           |      | 350 / 250 ng     | >10 ng/µl                        | ≤ 10°C   |  |
|   | gDNA / Amplicons<br>PCR-free library               |      | 2 µg             | >20 ng/µl                        |  |  |
|   | gDNA<br>Whole-exome sequencing                     |      | 600 ng           |                                  |  | All samples – Lowest volume required is 20 μl!<br>DNA samples – Non-degraded DNA dissolved in EB or low TE buffer<br>(<0,1 mM EDTA), RNA-free and without traces of organic solutions<br>(OD260/280 = 1,8-2,0).<br>Amplicons and samples for Tailed Amplicon Library must have size<br>between 200-900 bp including tails and must be purified. See<br>additional instructions on our website! |
|   | gDNA<br>Amplicon metagenomics                      |      | - 40 ng          | approx. 5 ng/µl                  |  |  |
|   | Tailed amplicon library                            |      |                  |                                  |  |  |
|   | Customer-prepared library<br>ShareSeq Data Package |      | <b>30</b> μl     | >5 nM                            |  |  |
|   | Customer-prepared library<br>10B and S4 Lane       |      | 80 µl            |                                  |  |  |
|   | Customer-prepared library<br>25B Lane              |      | 140 μl           |                                  |  | <b>Customer-prepared libraries (Ready-to-Run)</b> for Illumina ShareSeq<br>Data Package / Lane Sequencing must be provided as a final pool with  |
|   | Total RNA  |      | 1,5 µg           | >50 ng/µl                        |  | max. 8 b dual indexes, primer and primer-dimer free.<br>Required fragment distribution is:<br>• 300-700 bp (PE150)   |
|   | dsRNA  |      | 200 ng           | >20 ng/µl                        |  |  |
| Pac Bio   | Please inquire                                     |      |                  |                                  |  | • 400-1000 bp (PE250)  |
| Oxford<br>Nanopore  | gDNA<br>Standard DNA library                       |      | 2 μg             | >40 ng/µl                        | ≤ -20°C  | <b>RNA samples</b> – Non-degraded RNA (RIN >7) dissolved in RNAse-free water, DNA-free and without traces of organic solutions.  |
|   | Amplicons<br>Standard DNA library                  |      | 300 fmol         | >30 fmol/µl                      |  |  |
|   | gDNA<br>Amplicon metagenoi                         | mics | 40 ng            | approx. 5 ng/µl                  |  |  |

It is recommended to measure concentration using fluorescence-based assays such as Qubit. We strongly advice **not to use Nanodrop** since UV-based measurements are in general inaccurate and **may result in significant overestimation, even by orders of magnitude**!

Deliver/mail your samples to: **SEQme, U Slovanky 2067, 26301 Dobris, Czech Republic.** We recommend low-bind 0,2 ml strips or 96-well plates.