DATA SHEET – SAMPLE SUBMISSION

NGS – Integrative Genomics Core Unit (NIG, UMG)

DNA / RNA Sequencing Submission Form

📅 **Date:**

🧪 **Project Number (assigned by NIG):**

📌 **Project Title (one sentence):**

📝 **Short Project Description:**

CONTACT INFORMATION

Contact Person	Group Leader / Principal Investigator
Name:	**Name:**
Email:	**Email:**
Address:	**Address:**
Phone:	**Phone:**

PROJECT INFORMATION

Sequencing Mode and Instrument:

Instrument:

☐ NovaSeq6000 Illumina ☐ Oxford Nanopore ☐ Single-cell Shasta/iCELL8
☐ Single-cell PIP-Seq

Read Length (NovaSeq6000):

☐ 2×50 bp ☐ 2×100 bp ☐ 2×150 bp ☐ 2×200 bp ☐ 2×250 bp

Flow Cell Type (NovaSeq6000): For projects required only sequencing

☐ SP ☐ S1 ☐ S2 ☐ S4

Estimated million reads per sample: 📌 _____

Sample Pooling (XP reagents required): For projects required only sequencing

☐ Yes ☐ No

If **yes**, how many samples will be pooled? 📌 _____

Estimated million reads per pool: 📌 _____

APPLICATION TYPE

☐ Total RNA-Seq
☐ Stranded mRNA-Seq
☐ Non-stranded mRNA-Seq
☐ ATAC-Seq
☐ miRNA-Seq
☐ Small RNA-Seq
☐ Amplicon-Seq
☐ ChIP-Seq
☐ RRBS
☐ Bisulfite Sequencing
☐ Targeted DNA-Seq
☐ *De novo* Genome Sequencing
☐ Genome Resequencing
☐ Single-cell/nuclei RNA-Seq
☐ Single-cell/nuclei ATAC-Seq
☐ Single-cell/nuclei DNA-Seq
☐ Micro-Scale Bulk RNA-Seq
☐ Drug Screening RNA-Seq

SAMPLE INFORMATION

- Total number of samples (incl. biological replicates):
- Organism:
- Sample type:
- Extraction method (DNA/RNA):
- DNase treatment: ☐ Yes ☐ No ☐ Not applicable

Sample Name	conc.	µl	Sample Name	conc.	µl	Sample Name	conc.	µl
1.			10.			19.		
2.			11.			20.		
3.			12.			21.		
4.			13.			22.		
5.			14.			23.		
6.			15.			24.		
7.			16.			25.		
8.			17.			26.		
9.			18.			27.		

DATA ANALYSIS

Please select the desired level of analysis:

☐ **Basic:** Quality control, data conversion, FASTQ files only

☐ **Advanced:** Mapping, statistics, counting, normalization, DEG & GO analysis, data visualization
☐ **Individual/Custom:** _____

Sample Group Descriptions

Please describe your experimental groups below:

Sample Group	# of Biological Replicates	Description

Changes to Original Sample Setup

If the sample setup has changed compared to your original consultation with our bioinformatics team, please contact us at **nig@gwdg.de** before proceeding. This is especially important for projects requesting bioinformatics analysis.

Comparison with Previous Results

Are these samples intended for comparison with previous data generated by NIG?
☐ Yes ☐ No
If yes, **please specify the project number:** _____

Comparison with Future Results

Do you plan to compare these results with a future dataset?
☐ Yes ☐ No
If yes, please indicate the **expected timeline** and note that future protocol changes might limit direct comparability.

Leftover Material Disposal

By default, leftover samples are discarded after 1 year.

☐ I would like the material to be returned (additional shipping costs to be covered by the user).
☐ I agree to disposal after 1 year.

Data Storage

By default, result data is stored by NIG for **six months** after project completion. Long-term storage is available upon request:

☐ I request extended data storage at NIG (💶 €300/year/TB will be charged).
☐ No extended storage required.

Declaration of Agreement

☐ I have read and accepted the NIG policy (“Nutzerordnung”):
Download Policy (PDF)

📅 Date: _____

✍️ Signature (PI or responsible cost center): _____