

	Work instruction	Code	Revision	Date	Owner
	Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit Page: 1 of 7



Quick Agendo Sample Submission Guide

Genomics Unit

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Work instruction	Code	Revision	Date	Owner
Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit
				Page: 2 of 7

Quick Agendo Sample Submission Guide

NGS complementary services: Automated electrophoresis	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Plate Number	It allows only numbers. Starting from 1 to indicate plate 1 up to 3 plates
Well Position	A01 to H12 by columns. Positions D12 and H12 must remain empty.
Sample Name (same as in tube)	Between 1 and 4 alphanumeric characters, underscore included (e.g. TE_1)
Sample Type	Choose 1 of the following (spelling must match exactly): gDNA, fragmented DNA, cDNA, PCR amplicons, Total RNA, polyA RNA, rRNA-depleted RNA, smallRNA, WG Library, Exome-Capture Library, Amplicon Library, mRNA Library, rRNA-Ribodepleted Library, smallRNA Library, ChIP Library, ATAC Library, Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Concentration (ng/ul)	Integer or decimal with . as separator
Volume (ul)	Integer or decimal with . as separator
Expected size (bp) for libraries	Integer
Observations	Any desired comment about the sample

NGS complementary services: Covaris	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Sample Name (same as in tube)	Between 1 and 4 alphanumeric characters, underscore included (e.g. TE_1)
Desired fragment size (bp)	Base Pairs (bp)
Volume (ul)	Integer or decimal with . as separator
Duty Factor (%)	Completed by the Genomics Unit
Peak Power (W)	Completed by the Genomics Unit
Cycles / burst	Completed by the Genomics Unit
Time (s)	Completed by the Genomics Unit
Observations	Any desired comment about the sample

Work instruction	Code	Revision	Date	Owner
Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit
				Page: 3 of 7

NGS Library Prep and Sequencing: Whole and Targeted Genome

Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Sample Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Sample Type	Choose 1 of the following (spelling must match exactly): cDNA,cfDNA,Cloned DNA,ctDNA,gDNA,WGA-DNA,PCR amplicons,Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Volume (ul)	Integer or decimal with . as separator
Concentration (ng/ul)	Integer or decimal with . as separator
Nanodrop 260/280	Integer or decimal with . as separator
Nanodrop 260/230	Integer or decimal with . as separator
Sample Replacement	Is it a replacement of a previous sample? yes or no
Observations	Any desired comment about the sample

NGS Library Prep and Sequencing: Transcriptome

Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Sample Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Sample Type	Choose 1 of the following (spelling must match exactly): cfRNA,nuclearRNA,polyA RNA,rRNA-depleted RNA,smallRNA,Total RNA,Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Volume (ul)	Integer or decimal with . as separator
Concentration (ng/ul)	Integer or decimal with . as separator
Nanodrop 260/280	Integer or decimal with . as separator
Nanodrop 260/230	Integer or decimal with . as separator
Sample Replacement	Is it a replacement of a previous sample? yes or no
Observations	Any desired comment about the sample

Work instruction	Code	Revision	Date	Owner
Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit
				Page: 4 of 7

NGS Library Prep and Sequencing: Epigenome	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Sample Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Sample Type	Choose 1 of the following (spelling must match exactly): CHIP DNA, Cloned DNA, ctDNA, CUT&RUN DNA, gDNA, HiC DNA, WGA-DNA, PCR amplicons, Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Volume (ul)	Integer or decimal with . as separator
Concentration (ng/ul)	Integer or decimal with . as separator
Nanodrop 260/280	Integer or decimal with . as separator
Nanodrop 260/230	Integer or decimal with . as separator
Sample Replacement	Is it a replacement of a previous sample? yes or no
Observations	Any desired comment about the sample

NGS Libraries Ready for Sequencing	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Library Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Sequence index i7	i7 index sequence, at least 6bp long, must only contain A,C,G,T; in case the library only has an i5 index the i7 sequence must be XXXXXX
Sequence index i5	i5 index sequence, at least 6bp long, must only contain A,C,G,T
Pool name (mandatory for each library belonging to a pool)	Between 2 and 6 alphanumeric characters (i.e. letters, numbers and underscore)
Library or Pool Volume (ul)	Integer or decimal with . as separator
Library or Pool Molarity (nM)	Integer or decimal with . as separator
Library or Pool Concentration (ng/ul)	Integer or decimal with . as separator
Library or Pool Average Size (bp)	Integer
Library Replacement	Is it a replacement of a previous library? yes or no
Observations	Any desired comment about the library

Work instruction	Code	Revision	Date	Owner
Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit
				Page: 5 of 7

NGS Library Prep and Sequencing: Single Cell genomics and transcriptomics	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Sample Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Sample Type	Choose 1 of the following (spelling must match exactly): Cell pellet, Cell suspension, Cells in lysis buffer, Frozen tissue, Isolated nuclei, cDNA, Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Volume (ul)	Integer or decimal with . as separator
Cell or Nuclei Concentration (cells/ul or nuclei/ul)	Integer or decimal with . as separator
Target Recovery	Integer or decimal with . as separator. For SMART-seq put 1.
Low RNA Content (only for scGE)	Yes or No
Sample Replacement	Is it a replacement of a previous sample? yes or no
Observations	Any desired comment about the sample

Work instruction	Code	Revision	Date	Owner
Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit
				Page: 6 of 7

NGS Library Prep and Sequencing: Plates - DNA	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Plate Number	It allows only numbers. Starting from 1 to indicate plate 1 up to 3 plates
Plate Name	Between 2 and 50 alphanumeric characters, underscore included (e.g. PL_123)
Well Position	A01 to H12 by columns. Positions D12 and H12 must remain empty.
Sample Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Sample Type	Choose 1 of the following (spelling must match exactly): cDNA,cfDNA,ChIP DNA,Cloned DNA,ctDNA,CUT&RUN DNA,gDNA,HiC DNA,WGA-DNA,PCR amplicons,Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Volume (ul)	Integer or decimal with . as separator
Concentration (ng/ul)	Integer or decimal with . as separator
Nanodrop 260/280	Integer or decimal with . as separator
Nanodrop 260/230	Integer or decimal with . as separator
Sample Replacement	Is it a replacement of a previous sample? yes or no
Observations	Any desired comment about the sample

Work instruction	Code	Revision	Date	Owner
Quick Agendo Sample Submission Guide	GEN-MG-006	1	12/02/2025	Genomics Unit
				Page: 7 of 7

NGS Library Prep and Sequencing: Plates - RNA	
Sample field	Description
Sample No.	Automatically generated by Agendo
Code	Automatically generated by Agendo
Plate Number	It allows only numbers. Starting from 1 to indicate plate 1 up to 3 plates
Plate Name	Between 2 and 50 alphanumeric characters, underscore included (e.g. PL_123)
Well Position	A01 to H12 by columns. Positions D12 and H12 must remain empty.
Sample Name	Between 2 and 15 alphanumeric characters, underscore included (e.g. TE_123)
Sample Type	Choose 1 of the following (spelling must match exactly): Total RNA,Other
Sample Species Name (Use NCBI taxonomy)	Must start with a capital letter word, might be followed by more words, separated by spaces from each other (e.g. Homo sapiens, Mus musculus, Microbiota)
Volume (ul)	Integer or decimal with . as separator
Concentration (ng/ul)	Integer or decimal with . as separator
Nanodrop 260/280	Integer or decimal with . as separator
Nanodrop 260/230	Integer or decimal with . as separator
Sample Replacement	Is it a replacement of a previous sample? yes or no
Observations	Any desired comment about the sample