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Service	Public and CERCA Institutions (€)	
Sample and Library Quality control (FGQC)	**Batch**	**Sample**
QC Consultancy (per hour)	89,47	0,00
Nanodrop quantification and purity	15,50	1,75
DNA quantitation with Qubit (batch max. size=40)	22,17	1,82
RNA quantitation with Qubit (batch max. size=40)	23,36	2,39
DNA quantitation with Qubit Flex (batch max. size=96)	59,32	2,04
RNA quantitation with Qubit Flex (batch max. size=96)	68,45	2,61
DNA fragment analysis with Bioanalyzer DNA 1000 Chip (batch max. size=12)	77,98	1,69
DNA Full Quality Control, normal input (quantitation + fragment analysis DNA 1000) (batch max. size=12)	100,14	3,51
DNA fragment analysis with Bioanalyzer DNA HS Chip (batch max. size=11)	107,36	1,64
DNA Full Quality Control, low input (quantitation + fragment analysis DNA HS) (batch max. size=11)	129,53	3,46
RNA fragment analysis with Bioanalyzer RNA Nano Chip (batch max. size=12)	78,83	2,19
RNA Full Quality Control, normal input (quantitation + fragment analysis RNA Nano) (batch max. size=12)	102,19	4,58
RNA fragment analysis with Bioanalyzer Pico Chip (batch max. size=11)	83,19	1,79
RNA Quality Control, low input (quantitation + fragment analysis RNA Pico) (batch max. size=11)	106,55	4,18
RNA fragment analysis with small RNA Chip (batch max. size=11)	97,77	1,79
smallRNA QC (quantitation + fragment analysis) (batch max. size=11)	121,13	4,18
Agarose gel electrophoresis (batch max. size=24)	58,39	3,39
Discount for 1/2 shared DNA1000 chip	-16,10	0,00
Discount for 1/3 shared DNA1000 chip	-21,47	0,00
Discount for 1/2 shared HS chip	-30,09	0,00
Discount for 1/3 shared HS chip	-40,12	0,00

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Service	Public and CERCA Institutions (€)	
Sample and Library Quality control (FGQC)	**Batch**	**Sample**
Discount for 1/2 shared Nano chip	-16,51	0,00
Discount for 1/3 shared Nano chip	-22,01	0,00
Discount for 1/2 shared Pico chip	-18,58	0,00
Discount for 1/3 shared Pico chip	-24,77	0,00
Tapestation with user's reagents	36,04	1,23
Tapestation D1000 Assay	36,14	3,53
Tapestation D1000-HS Assay	36,14	4,87
Tapestation D5000 Assay	36,14	3,88
Tapestation D5000-HS Assay	36,14	5,45
Tapestation gDNA Assay	36,14	4,91
Tapestation cfDNA Assay	36,14	4,87
Tapestation RNA Assay	36,14	4,02
Tapestation RNA-HS Assay	36,14	4,53
Nucleic Acids Extraction and Purification (FGEP)	**Batch**	**Sample**
DNA purification (batch max. size=40)	51,09	4,97
DNA purification + Qubit (batch max. size=40)	73,25	6,79
DNA extraction from cells processing (batch max. size=24)	45,43	2,25
DNA extraction from cells + purification + Qubit (batch max. size=24)	118,68	9,04
DNA extraction from FFPE processing (batch max. size=24)	299,60	24,68
DNA extraction from FFPE + Qubit + Bioanalyzer (11) (batch max. size=11)	429,12	28,14
RNA purification processing (batch max. size=40)	51,09	6,02
RNA purification + Qubit + Bioanalyzer Nano (batch max. size=11)	153,28	10,59
Small-RNA bead purification (batch max. size=40)	52,84	7,47
Small-RNA size selection (6% TBE PAGE) (batch max. size=8)	159,21	9,50

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Service	Public and CERCA Institutions (€)	
Nucleic Acids Extraction and Purification (FGEP)	**Batch**	**Sample**
DNase I digestion (batch max. size=40)	15,12	3,86
RNA extraction from cells (batch max. size=24)	60,55	3,31
RNA extraction from cells + DNase + purification + Qubit + Bioanalyzer Pico (batch max. size=11)	233,31	17,37
Affymetrix Microarrays (FGAM)	**Batch**	**Sample**
Microarray Consultancy (per hour)	89,47	0,00
Affymetrix Microarray Gene Expression - Processing (batch max. size=24)	583,47	128,06
Affymetrix Microarray Gene Expression Full Service (includes Bioanalyzer and Qubit) (batch max. size=11)	705,52	133,99
Labeling and Array Processing (for transcriptome-amplified samples) - Processing (batch max. size=24)	329,39	73,17
Processing of Affymetrix Human PrimeView	603,33	243,73
Affymetrix Human Primeview Full Service (batch max. size=11)	725,38	249,65
Processing of Affymetrix GeneChip Drosophila Genome	603,33	306,12
Affymetrix GeneChip Drosophila Genome Full Service (batch max. size=11)	725,38	312,05
Processing of Affymetrix Clariom S Mouse	603,33	253,46
Affymetrix Clariom S Mouse Full Service (batch max. size=11)	725,38	259,38
Processing of Affymetrix Clariom S Human	603,33	261,20
Affymetrix Clariom S Human Full Service (batch max. size=11)	725,38	267,13
Pico profiling (FGPP)	**Batch**	**Sample**
Extractions, Amplifications, and Picoprofiling Consultancy (per hour)	89,47	0,00
Transcriptome amplification (25 ng total RNA) (batch max. size=30)	383,60	62,54
PicoProfiling Full Service (Extraction + Purification + Transcriptome Amplification) (batch max. size=30)	525,87	77,48
Library amplification/reamplification	217,25	43,17

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Service	Public and CERCA Institutions (€)	
NGS Libraries (FGLP)	**Batch**	**Sample**
NGS Consultancy (per hour)	89,47	0,00
DNA sample fragmentation (batch max. size=24)	40,99	6,77
WGS and ChIP-seq [1ng - 1 µg] - Processing (batch max. size=40)	480,85	58,48
Library preparation for WGS - Full Service (batch max. size=11)	818,57	75,75
Library preparation for ChIP-seq [> 500 pg] - Full Service (batch max. size=11)	777,57	68,97
RNA-seq Library NEB - Processing (batch max. size=40)	302,58	77,60
RNA-seq Stranded Library NEB - Processing (batch max. size=40)	360,85	78,00
Poly-A Capture for high quality samples NEB [10 ng - 1 µg total RNA] - Processing (batch max. size=40)	81,30	10,97
Ribodepletion Ribo-Zero Illumina [1-5 µg total RNA] - Processing (batch max. size=16)	75,20	62,96
RNA-seq Stranded mRNA Library Illumina - Processing (batch max. size=40)	301,29	53,40
Non-stranded bulk mRNA-seq NEB (high-quality, polyA mRNA-seq) - Full Service (batch max. size=11)	653,27	100,18
RNAseq Stranded total RNA Library Illumina - Processing (batch max. size=40)	360,86	96,86
Stranded bulk mRNAseq NEB (high-quality sample; polyA mRNA-seq) - Full Service (batch max. size=11)	711,54	100,58
RNAseq Stranded mRNA Illumina - Full Service (batch max. size=11)	570,67	65,01
RNAseq Stranded total RNA Illumina (mRNA- and lncRNA-seq) - Full Service (batch max. size=11)	630,25	108,47
Low-input stranded mRNA- and lncRNA-seq Library [0.25-10 ng total RNA, or 10-1,000 cells; Smarter] - Processing (batch max. size=40)	761,57	121,29
Low-input stranded mRNA- and lncRNA-seq Library [0.01-10 ng total RNA, or 1-500 cells; Ovation] - Processing (batch max. size=32)	980,66	91,76
RIP-seq Library - Processing (batch max. size=40)	540,84	79,05

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Service	Public and CERCA Institutions (€)	
NGS Libraries (FGLP)	**Batch**	**Sample**
Library preparation for RIP-seq (low-quality sample) - Full Service (batch max. size=11)	885,43	153,62
Library preparation for RIP-seq (high-quality sample) - Full Service (batch max. size=11)	891,52	101,63
Hi-C-seq library - Processing (batch max. size=40)	421,47	80,24
Library preparation for HiC-seq - Full Service	810,05	90,62
smallRNA library [0.1-1 µg total RNA] - Processing (max batch size: 24)	481,58	63,57
Library preparation for smallRNA-seq - Full Service (max. Batch size 11)	1.068,62	91,28
Library pooling for sequencing - Processing	109,67	6,58
Library pooling for sequencing - Full Workflow	261,36	11,87
T4 PNK dephosphorylation (max batch size: 24)	62,78	6,55
ATAC-seq - Processing (no Tn5)	367,20	57,52
ATAC-seq - Processing (no Tn5) + QCs (cells, libraries)	447,76	71,41
ATAC-seq - Processing (Tn5 50k-2x/25k-4x/10k-10x)	367,20	184,39
ATAC-seq - Processing (Tn5 50k-2x/25k-4x/10k-10x) + QCs (cells, libraries)	447,76	198,28
qPCR (FGQP)	**Batch**	**Sample**
qPCR Consultancy (per hour)	89,47	0,00
Analysis per plate (absolute/relative quantification; Variant detection by High Resolution Melting)	297,92	0,00
QuantStudio 6 Pro self-service (per hour)	17,06	0,00
Illumina library quantification using SYBR qPCR (1-12 libraries per 96-well plate)	138,97	10,64
RT reaction (first strand)	73,44	10,90
Primer design and optimization (unit: transcript of interest)	250,63	6,40
PCR Concentrations and Annealing Optimization (unit: pair of primers)	140,21	28,37
96-well qPCR set up and run (unit: pair of primers; batch max size=96)	140,10	13,63

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Service	Public and CERCA Institutions (€)	
Single-cell (FGSC)	**Batch**	**Sample**
Single Cell Consultancy (per hour)	89,47	0,00
Cell Counting & Viability Quality Control (batch max. size=8)	28,93	6,70
10x GEMs and cDNA with user's reagents (batch max. size=8 w/o multiplex)	269,58	11,26
10x GEX Library with user's reagents (batch max. size=8, w/o multiplex)	368,22	15,28
10x GEMs+GEX+QCs(Cells,Qubit,BA) with user's reagents (batch max. size=11, w/o multiplex)	947,94	41,98
10x 3'GEMs and cDNA with FG reagents (batch max. size=8, w/o multiplex)	698,18	2.076,14
10x GEX Library with FG reagents	398,01	28,59
10x 3'GEMs+GEX+QCs(Cells,Qubit,BA) with FG reagents (batch max. size=8, w/o multiplex)	1.406,33	2.120,17
10x FB Library with user's reagents (batch max. size=8)	143,04	15,34
10x 3'FB Library with FG reagents (batch max. size=8)	172,83	84,44
10x 3'GEMs+GEX+FB+QCs(Cells,Qubit,BA) with FG reagents (batch max. size=8)	1.708,68	2.208,08
10x 5'GEMs and cDNA with FG reagents (batch max. size=8, w/o multiplex)	712,83	2.409,50
10x BCR/TCR Amplification with user's reagents	124,47	9,07
10x BCR/TCR Amplification with FG reagents	154,11	143,82
10x Chromium 5'-Gene Expression v2 BCR/TCR - Full Workflow (batch max. size=8, w/o multiplex)	1.973,09	2.625,94
10x ATAC Transposition (batch max. size=8, w/o multiplex)	73,23	2,91
10x ATAC GEMs + cleanup with user's reagents (batch max. size=8, w/o multiplex)	266,50	11,23
10x ATAC GEMs + cleanup with FG reagents	694,85	2.296,25
10x ATAC Library v2 with user's reagents (batch max. size=8, w/o multiplex)	363,49	10,97
10x ATAC Library v2 with FG reagents	378,39	24,28

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Service	Public and CERCA Institutions (€)	
Single-cell (FGSC)	**Batch**	**Sample**
10x ATAC v2 GEMs+Library+QCs with FG reagents (batch max. size=8, w/o multiplex)	1.507,67	2.339,98
10x Multiome pre-split amplification (batch max. size=8, w/o multiplex)	154,48	10,99
10x Multiome GEMS+GEX+ATAC+QCs(BA) with user's reagents (batch max. size=8, w/o multiplex)	1.780,68	70,55
Singleron MATRIX+cDNA (user supplied reagents)	287,23	157,98
Singleron MATRIX+cDNA (user supplied reagents) + QCs (Cells,Qubit,BA)	467,85	169,96
Singleron GEXSCOPE (user supplied reagents)	188,88	7,82
Singleron GEXSCOPE (user supplied reagents) + QCs (Qubit,BA)	470,10	16,57
Singleron MATRIX+cDNA+GEXSCOPE (user supplied reagents) +QCs (Cells,Qubit,BA)	937,96	186,53
Singleron FOCUSCOPE (user supplied reagents)	149,72	12,67
Singleron FOCUSCOPE (user supplied reagents) + QCs (Qubit,BA)	301,41	17,95
Singleron SCIRCLE (user supplied reagents)	517,95	31,57
Singleron SCIRCLE (user supplied reagents) + QCs (Qubit,BA)	928,69	43,78
Singleron Reamplification (user supplied reagents)	144,02	19,17
Singleron Reamplification (user supplied reagents) + QCs (Qubit,BA)	273,55	22,63
Split-pool Processing (user supplied reagents)	2.067,25	0,80
Split-pool Processing + QCs (user supplied reagents)	2.341,87	30,05
Concentration of cell suspensions	20,41	2,24
Discount for 1/2 shared chromium controller chips	-189,84	0,00
Illumina NextSeq Sequencing (FGIL)	**Batch**	**Sample**
NextSeq550 denature and dilute libraries - Processing	97,04	3,06
NextSeq550 set up, load, and run (with user supplied reagents)	183,69	1,59
NS550 300 cycles Hi-output	6.165,54	1,59
NS550 300 cycles Mid-output	2.520,99	1,59

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Service	Public and CERCA Institutions (€)	
Illumina NextSeq Sequencing (FGIL)	**Batch**	**Sample**
NS550 150 cycles Hi-output	3.990,99	1,59
NS550 150 cycles Mid-output	1.634,79	1,59
NS550 75 cycles Hi-output	2.132,49	1,59
NextSeq2000 set up, load, and run	264,73	1,59
NS2k 600 cycles P1 (XLEAP)	1.935,28	1,59
NS2k 600 cycles P2 (XLEAP)	3.543,88	1,59
NS2k 300 cycles P1 (XLEAP)	1.363,03	1,59
NS2k 300 cycles P2 (XLEAP)	3.278,23	1,59
NS2k 300 cycles P3 (XLEAP)	5.069,53	1,59
NS2k 200 cycles P2 (XLEAP)	2.535,88	1,59
NS2k 200 cycles P3 (XLEAP)	3.868,33	1,59
NS2k 200 cycles P4 (XLEAP)	5.236,48	1,59
NS2k 100 cycles P1 (XLEAP)	1.055,16	1,59
NS2k 100 cycles P2 (XLEAP)	1.474,11	1,59
NS2k 100 cycles P3 (XLEAP)	2.867,46	1,59
NS2k 100 cycles P4 (XLEAP)	3.926,91	1,59
NS2k 50 cycles P3	2.416,27	1,59
NS2k 50 cycles P4 (XLEAP)	2.902,11	1,59
Xenium*	**Batch**	**Sample**
Xenium v1 (per run)	1.078,52	0,00
Xenium Prime (per run)**	1.147,38	0,00
Xenium extra day of use	393,52	0,00

**Histopathology Core Facility (CF) costs for sample preparation are not included in the fee.*

**10x Genomics panels and specific reagents will be charged separately.*

***For Xenium 5k, 1-2 extra days of run will be charged*

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Service	Public and CERCA Institutions (€)	
Courier (FGSH)	**Batch**	**Sample**
Submission and follow-up of libraries prepared by users - Processing	62,35	5,07
Externalized sequencing - Preparation, Registration, Data retrieval	111,45	3,05
R&D and Academic Support (FGRD)		
Custom R&D Services (per hour)	63,69	0,00
Scientific Training of Personnel (per hour)	62,72	0,00
New Products and Applications Seminar (per event)	-	-
E. coli ORF and shRNA clone collection (FGCL)		
Clone inoculation in LB tubes provided by user	20,44	1,29

Please be advised that any future increases in consumable prices (e.g. due to customs duties on imported consumables or new tenders) may result in fee adjustments. Should these external costs rise, our pricing might be updated accordingly.

New services prices will be approved retroactively at the subsequent Board Meeting