

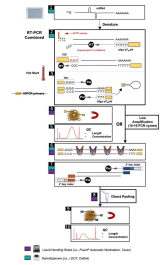
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Version 4

FLASH-seq protocol V.4

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Human Cell Atlas Metho...

The Single Cell Ninjas



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Protocol status: Working

We use this protocol and it's working

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Keywords: FLASH-Seq, single-cell, RNA-sequencing, full-length, tagmentation, single cell rna, cell rna, transcriptome of individual cell, rna, transcriptome, scrna, length scrna, seq protocol, terminal portion of the transcript, seq, transcript, handful of cell, gene, higher number of gene, individual cell, cell, seq method

Abstract

The single-cell RNA-sequencing (scRNA-seq) field has evolved tremendously since the first paper was published back in 2009. While the first methods analysed just a handful of cells, the throughput and performance rapidly increased over a very short timespan. However, it was not until the introduction of emulsion droplets methods, that the robust and reproducible analysis of thousands of cells became feasible. Despite generating data at a speed and a cost per cell that remains unmatched by full-length protocols like Smart-seq, scRNA-seq in droplets still comes with the drawback of addressing only the terminal portion of the transcripts, thus lacking the required sensitivity for comprehensively analyzing the transcriptome of individual cells. Building upon the existing Smart-seq2/3 workflows, we developed FLASH-seq (FS), a new full-length scRNA-seq method capable of detecting a significantly higher number of genes than both previous versions, requiring limited hands-on time and with a great potential for customization.



Materials

REAGENTS - CELL LYSIS MIX

- ☒ dNTP-Set 1 **Carl Roth Catalog #K039.2**
- ☒ Triton X-100 **Merck MilliporeSigma (Sigma-Aldrich) Catalog #X100-100ML**
- ☒ Recombinant RNase Inhibitor (40 U/uL) **Takara Bio Inc. Catalog #2313B**
- ☒ dCTP (100 mM solution) **Thermo Fisher Scientific Catalog #10217016**

REAGENTS - RT-PCR MIX

- ☒ KAPA HiFi HotStart ReadyMix (2x) **Roche Catalog #KK2602**
- ☒ SuperScript™ IV Reverse Transcriptase **Thermo Fisher Scientific Catalog #18090050**
- ☒ Magnesium Chloride (1M Solution) **Invitrogen - Thermo Fisher Catalog #AM9530G**

REAGENTS - MAGNETIC BEADS SOLUTION PREPARATION

- ☒ Polyethyleneglycol (MW=8000) **Merck MilliporeSigma (Sigma-Aldrich) Catalog #89510-1KG-F**
- ☒ Sodium chloride **Merck MilliporeSigma (Sigma-Aldrich) Catalog #59222C-1000ML**
- ☒ Sera-Mag SpeedBead Carboxylate-Modified Magnetic Particles (Hydrophobic), 15 mL **GE Healthcare Catalog #65152105050250**
- ☒ Sodium azide **Merck MilliporeSigma (Sigma-Aldrich) Catalog #S2002-25G**
- ☒ EDTA (0.5 M), pH 8.0 **Life Technologies Catalog #AM9260G**
- ☒ Tris-HCl pH 8.0 (1M solution) **Thermo Fisher Scientific Catalog #15568025**
- ☒ Tween-20 **Merck MilliporeSigma (Sigma-Aldrich) Catalog #P-7949**

If a commercial solution for sample cleanup is preferred, choose the following product:

- ☒ Agencourt AMPure XP **Beckman Coulter Catalog #A63880**

REAGENTS - SAMPLE & LIBRARY QC

- ☒ Quant-iT™ PicoGreen® dsDNA Assay Kit **Life Technologies Catalog #P11496**
- ☒ Nunc™ F96 MicroWell™ Polystyrene Plate black **Thermo Fisher Scientific Catalog #237105**
- ☒ Qubit™ 1X dsDNA HS Assay Kit **Invitrogen - Thermo Fisher Catalog #Q33231**
- ☒ Qubit™ Assay Tubes **Invitrogen - Thermo Fisher Catalog #Q32856**
- ☒ Agilent High Sensitivity DNA Kit **Agilent Technologies Catalog #5067-4626**

REAGENTS - TAGMENTATION WITH NEXTERA XT KIT

- ☒ Nextera XT DNA Library Preparation Kit **Illumina, Inc. Catalog #FC-131-1096**
- ☒ Nextera XT Index Kit v2 (set A B C D) **Illumina, Inc. Catalog #FC-131-2001; FC-131-2002; FC-131**

REAGENTS - TAGMENTATION WITH IN-HOUSE Tn5 TRANSPOSASE

⊗ KAPA HiFi plus dNTPs Roche Catalog #KK2102

⊗ NN-Dimethylformamide (DMF) solution Merck MilliporeSigma (Sigma-Aldrich) Catalog #D4551

⊗ SDS, 10% Solution Life Technologies Catalog #AM9822

⊗ TAPS Merck MilliporeSigma (Sigma-Aldrich) Catalog #T9659-100G

⊗ Sodium Hydroxide (pellet purity 98%) Merck MilliporeSigma (Sigma-Aldrich) Catalog #71690-1KG

GENERAL CONSUMABLES

⊗ RNase AWAY®; Spray Bottle, RNase in spray bottle; 475mL Thermo Fisher Catalog #7002

⊗ Adhesive PCR Plate Seals Thermo Fisher Scientific Catalog #AB0558

⊗ Aluminium foil seals for -80°C storage VWR International (Avantor) Catalog #391-1281

⊗ Twin.Tec® PCR plates 384 (LoBind colourless) Eppendorf Catalog #EP0030129547

⊗ UltraPure™ DNase/RNase-Free Distilled Water Thermo Fisher Scientific Catalog #10977023

⊗ DNA LoBind® 1.5 mL (PCR clean colourless) Eppendorf Catalog #30108051

⊗ Ethanol for molecular biology Merck MilliporeSigma (Sigma-Aldrich) Catalog #51976-500ML-F

OLIGONUCLEOTIDES - RT-PCR

	A	B	C
	Oligo ID	Sequence (5' → 3')	Purification / synthesis scale
	Smart dT30VN	/5Biosg/AAGCAGTGGTATCAACGCAGAGTACTT TTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN	desalted or HPLC
	FS TSO	/5Biosg/AAGCAGTGGTATCAACGCAGAGTACrGr GrG	desalted or HPLC

/5Biosg/ = C6-linker biotin

OLIGONUCLEOTIDES - IN-HOUSE Tn5 PROTOCOL ONLY

	A	B	C
	Oligo ID	Sequence (5' → 3')	Comments
	TN5MErev	/5Phos/ CTGTCTCTTATACACATCT	2 µM scale - desalted*

	A	B	C
	TN5ME-A	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG	1 μ M scale - desalted*
	TN5ME-B	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG	1 μ M scale - desalted*

* It is important to follow these recommendations. Ordering oligos at this scale but choosing “HPLC purification” will result in insufficient material for Tn5 loading. The scale indicated here is sufficient for producing 20-25 ml of loaded Tn5.

OLIGONUCLEOTIDES - ALL TAGMENTATION PROTOCOLS (when not ordering the Nextera Index Kit)

One can order the 4 Nextera XT Index Kit v2 (set A, B, C, D) sets, as described above or, alternatively, get them manufactured by any oligonucleotide provider. Below is the list of 24 N7xx and 16 S5xx adaptors required to multiplex 384 samples.

Prepare working dilution plates containing unique combinations of N7xx + S5xx adaptors, each with a final concentration of 5 μ M.

	A	B
	Oligo ID	Sequence (5' → 3')
	Nextera_v2_N71 4	/5Biosg/CAAGCAGAAGACGGCATACGAGATTCATGAGCGTCTCGTGGGC TCG*G
	Nextera_v2_N71 5	/5Biosg/CAAGCAGAAGACGGCATACGAGATCCTGAGATGTCTCGTGGGC TCG*G
	Nextera_v2_N71 6	/5Biosg/CAAGCAGAAGACGGCATACGAGATTAGCGAGTGTCTCGTGGGC TCG*G
	Nextera_v2_N71 8	/5Biosg/CAAGCAGAAGACGGCATACGAGATGTAGCTCCGTCTCGTGGGC TCG*G
	Nextera_v2_N71 9	/5Biosg/CAAGCAGAAGACGGCATACGAGATTACTACGCGTCTCGTGGGC TCG*G
	Nextera_v2_N72 0	/5Biosg/CAAGCAGAAGACGGCATACGAGATAGGCTCCGGTCTCGTGGGC TCG*G
	Nextera_v2_N72 1	/5Biosg/CAAGCAGAAGACGGCATACGAGATGCAGCGTAGTCTCGTGGGC TCG*G
	Nextera_v2_N72 2	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTGCGCATGTCTCGTGGGC TCG*G
	Nextera_v2_N72 3	/5Biosg/CAAGCAGAAGACGGCATACGAGATGAGCGCTAGTCTCGTGGGC TCG*G
	Nextera_v2_N72 4	/5Biosg/CAAGCAGAAGACGGCATACGAGATCGCTCAGTGTCTCGTGGGC TCG*G



A	B
Nextera_v2_N72 6	/5Biosg/CAAGCAGAAGACGGCATAACGAGATGTCTTAGGGTCTCGTGGGC TCG*G
Nextera_v2_N72 7	/5Biosg/CAAGCAGAAGACGGCATAACGAGATACTGATCGGTCTCGTGGGC TCG*G
Nextera_v2_N72 8	/5Biosg/CAAGCAGAAGACGGCATAACGAGATTAGCTGCAGTCTCGTGGGC TCG*G
Nextera_v2_N72 9	/5Biosg/CAAGCAGAAGACGGCATAACGAGATGACGTGAGTCTCGTGGGC TCG*G
Nextera_v2_S50 2	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCTCTCTATTCGTTCGG CAGCGT*C
Nextera_v2_S51 3	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTCGACTAGTCGTTCGG CAGCGT*C
Nextera_v2_S50 3	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTATCCTCTTCGTTCGG CAGCGT*C
Nextera_v2_S51 5	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTTCTAGCTTCGTTCGG CAGCGT*C
Nextera_v2_S50 5	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGTAAGGAGTCGTTCGG CAGCGT*C
Nextera_v2_S51 6	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCCTAGAGTTCGTTCGG CAGCGT*C
Nextera_v2_S50 6	/5Biosg/AATGATACGGCGACCACCGAGATCTACACACTGCATATTCGTTCGG CAGCGT*C
Nextera_v2_S51 7	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGCGTAAGATTCGTTCGG CAGCGT*C
Nextera_v2_S50 7	/5Biosg/AATGATACGGCGACCACCGAGATCTACACAAGGAGTATTCGTTCGG CAGCGT*C
Nextera_v2_S51 8	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCTATTAAGTCGTTCGG CAGCGT*C
Nextera_v2_S50 8	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCTAAGCCTTCGTTCGG CAGCGT*C
Nextera_v2_S52 0	/5Biosg/AATGATACGGCGACCACCGAGATCTACACAAGGCTATTCGTTCGG CAGCGT*C
Nextera_v2_S51 0	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCGTCTAATTCGTTCGG CAGCGT*C
Nextera_v2_S52 1	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGAGCCTTATTCGTTCGG CAGCGT*C
Nextera_v2_S511	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTCTCTCCGTTCGTTCGG CAGCGT*C

A	B
Nextera_v2_S52 2	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTTATGCGATCGTCGG CAGCGT*C

All oligonucleotides carry a 5'-biotin (/5Biosg/) and a phosphorothioate bond (*) between the last and the second last nucleotide. For cost reasons, we ordered desalted oligos and not HPLC purified.

OLIGONUCLEOTIDES - ALL TAGMENTATION PROTOCOLS (when not ordering the Nextera Index Kit)

To increase the multiplex capabilities, we designed an additional set of 32 S5xx and 48 N7xx adaptors (non-UDI).

A	B
Oligo ID	Sequence
Nextera_extra_i7_1	/5Biosg/CAAGCAGAAGACGGCATACGAGATGCCTATCAGTCTCGTGGGC TCG*G
Nextera_extra_i7_2	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTTGGATGGTCTCGTGGGC TCG*G
Nextera_extra_i7_3	/5Biosg/CAAGCAGAAGACGGCATACGAGATAGTCTCACGTCTCGTGGGC TCG*G
Nextera_extra_i7_4	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTCATCAGGTCTCGTGGGC TCG*G
Nextera_extra_i7_5	/5Biosg/CAAGCAGAAGACGGCATACGAGATTGTACCGTGTCTCGTGGGC TCG*G
Nextera_extra_i7_6	/5Biosg/CAAGCAGAAGACGGCATACGAGATAAGTCGAGGTCTCGTGGGC TCG*G
Nextera_extra_i7_7	/5Biosg/CAAGCAGAAGACGGCATACGAGATCACGTTGTGTCTCGTGGGC TCG*G
Nextera_extra_i7_8	/5Biosg/CAAGCAGAAGACGGCATACGAGATTACAGCAGTCTCGTGGGC TCG*G
Nextera_extra_i7_9	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTACTTGGGTCTCGTGGGC TCG*G
Nextera_extra_i7_10	/5Biosg/CAAGCAGAAGACGGCATACGAGATCCTCAGTTGTCTCGTGGGC TCG*G
Nextera_extra_i7_11	/5Biosg/CAAGCAGAAGACGGCATACGAGATTCCTACCTGTCTCGTGGGC TCG*G
Nextera_extra_i7_12	/5Biosg/CAAGCAGAAGACGGCATACGAGATATGGCGAAGTCTCGTGGGC TCG*G
Nextera_extra_i7_13	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTTACCTGGTCTCGTGGGC TCG*G



A	B
Nextera_extra_i7_1 4	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTCGATACGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 5	/5Biosg/CAAGCAGAAGACGGCATACGAGATTCCGTGAAGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 6	/5Biosg/CAAGCAGAAGACGGCATACGAGATTAGAGCTCGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 7	/5Biosg/CAAGCAGAAGACGGCATACGAGATTGACTGACGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 8	/5Biosg/CAAGCAGAAGACGGCATACGAGATTAGACGTGGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 9	/5Biosg/CAAGCAGAAGACGGCATACGAGATCCGGAATTGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 20	/5Biosg/CAAGCAGAAGACGGCATACGAGATCTCCTAGAGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 21	/5Biosg/CAAGCAGAAGACGGCATACGAGATCAACGGATGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 22	/5Biosg/CAAGCAGAAGACGGCATACGAGATTGGCTATCGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 23	/5Biosg/CAAGCAGAAGACGGCATACGAGATCGGTCATAGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 24	/5Biosg/CAAGCAGAAGACGGCATACGAGATTCCAATCGGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 25	/5Biosg/CAAGCAGAAGACGGCATACGAGATGAGCTTGTGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 26	/5Biosg/CAAGCAGAAGACGGCATACGAGATGAAGGTTCTCGTGGG CTCG*G
Nextera_extra_i7_1 27	/5Biosg/CAAGCAGAAGACGGCATACGAGATATCTCGCTGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 28	/5Biosg/CAAGCAGAAGACGGCATACGAGATAGTTACGGGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 29	/5Biosg/CAAGCAGAAGACGGCATACGAGATGTGTCTGAGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 30	/5Biosg/CAAGCAGAAGACGGCATACGAGATTGACTTCGGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 31	/5Biosg/CAAGCAGAAGACGGCATACGAGATTGGATCACGTCTCGTGGGC TCG*G
Nextera_extra_i7_1 32	/5Biosg/CAAGCAGAAGACGGCATACGAGATACACCAAGTGTCTCGTGGGC TCG*G



A	B
Nextera_extra_i7_33	/5Biosg/CAAGCAGAAGACGGCATAACGAGATCAGGTTAGGTCTCGTGGGC TCG*G
Nextera_extra_i7_34	/5Biosg/CAAGCAGAAGACGGCATAACGAGATAGTTGGCTGTCTCGTGGGC TCG*G
Nextera_extra_i7_35	/5Biosg/CAAGCAGAAGACGGCATAACGAGATTCAACTGGGTCTCGTGGG CTCG*G
Nextera_extra_i7_36	/5Biosg/CAAGCAGAAGACGGCATAACGAGATCTGCACTTGTCTCGTGGGC TCG*G
Nextera_extra_i7_37	/5Biosg/CAAGCAGAAGACGGCATAACGAGATACACGGTTGTCTCGTGGGC TCG*G
Nextera_extra_i7_38	/5Biosg/CAAGCAGAAGACGGCATAACGAGATAATACGCGGTCTCGTGGGC TCG*G
Nextera_extra_i7_39	/5Biosg/CAAGCAGAAGACGGCATAACGAGATTGCGAACTGTCTCGTGGG CTCG*G
Nextera_extra_i7_40	/5Biosg/CAAGCAGAAGACGGCATAACGAGATGCTGACTAGTCTCGTGGGC TCG*G
Nextera_extra_i7_41	/5Biosg/CAAGCAGAAGACGGCATAACGAGATGTGGTGTCTCGTGGGC TCG*G
Nextera_extra_i7_42	/5Biosg/CAAGCAGAAGACGGCATAACGAGATGTGCTTACGTCTCGTGGGC TCG*G
Nextera_extra_i7_43	/5Biosg/CAAGCAGAAGACGGCATAACGAGATTCAAGGACGTCTCGTGGG CTCG*G
Nextera_extra_i7_44	/5Biosg/CAAGCAGAAGACGGCATAACGAGATTGAACCTGGTCTCGTGGG CTCG*G
Nextera_extra_i7_45	/5Biosg/CAAGCAGAAGACGGCATAACGAGATAGTTGGGTCTCGTGGGC TCG*G
Nextera_extra_i7_46	/5Biosg/CAAGCAGAAGACGGCATAACGAGATGTACTCTCGTCTCGTGGGC TCG*G
Nextera_extra_i7_47	/5Biosg/CAAGCAGAAGACGGCATAACGAGATCCGTATCTGTCTCGTGGGC TCG*G
Nextera_extra_i7_48	/5Biosg/CAAGCAGAAGACGGCATAACGAGATCGAAGAACGTCTCGTGGG CTCG*G

All oligonucleotides carry a 5'-biotin (/5Biosg/) and a phosphorothioate bond (*) between the last and the second last nucleotide. For cost reasons, we ordered desalted oligos and not HPLC purified.

Prepare working dilution plates containing unique combinations of N7xx + S5xx adaptors, each with a final concentration of 5 μ M.



A	B
Oligo ID	Sequence
Nextera_extra_i5_1	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCGACCATTTTCGTCGG CAGCGT*C
Nextera_extra_i5_2	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGATAGCGATCGTCGG CAGCGT*C
Nextera_extra_i5_3	/5Biosg/AATGATACGGCGACCACCGAGATCTACACAATGGACGTCGTCGG CAGCGT*C
Nextera_extra_i5_4	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCGCTAGTATCGTCGG CAGCGT*C
Nextera_extra_i5_5	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTCTCTAGGTCGTCGG CAGCGT*C
Nextera_extra_i5_6	/5Biosg/AATGATACGGCGACCACCGAGATCTACACACATTGCGTCGTCGG CAGCGT*C
Nextera_extra_i5_7	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTGAGGTGTTTCGTCGG CAGCGT*C
Nextera_extra_i5_8	/5Biosg/AATGATACGGCGACCACCGAGATCTACACAATGCCTCTCGTCGG CAGCGT*C
Nextera_extra_i5_9	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCTGGAGTATCGTCGG CAGCGT*C
Nextera_extra_i5_10	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGTATGCTGTCGTCGG CAGCGT*C
Nextera_extra_i5_11	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTGGAGAGTTTCGTCGG CAGCGT*C
Nextera_extra_i5_12	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCGATAGAGTCGTCGG CAGCGT*C
Nextera_extra_i5_13	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCTCATTGCTCGTCGG CAGCGT*C
Nextera_extra_i5_14	/5Biosg/AATGATACGGCGACCACCGAGATCTACACACCAGCTTTTCGTCGG CAGCGT*C
Nextera_extra_i5_15	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGAATCGTGTCGTCGG CAGCGT*C
Nextera_extra_i5_16	/5Biosg/AATGATACGGCGACCACCGAGATCTACACAGGCTTCTTCGTCGG CAGCGT*C
Nextera_extra_i5_17	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCAGTTCTGTCGTCGG CAGCGT*C
Nextera_extra_i5_18	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTTGGTGAGTCGTCGG CAGCGT*C



A	B
Nextera_extra_i5_19	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCATTTCGGTTCGTCGG CAGCGT*C
Nextera_extra_i5_20	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTGTGAAGCTCGTCGG CAGCGT*C
Nextera_extra_i5_21	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTAAGTGGCTCGTCGG CAGCGT*C
Nextera_extra_i5_22	/5Biosg/AATGATACGGCGACCACCGAGATCTACACACGTGATGTCGTCGG CAGCGT*C
Nextera_extra_i5_23	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGTAGAGCATCGTCGG CAGCGT*C
Nextera_extra_i5_24	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGTCAGTTGTCGTCGG CAGCGT*C
Nextera_extra_i5_25	/5Biosg/AATGATACGGCGACCACCGAGATCTACACATTTCGAGGTCGTCGG CAGCGT*C
Nextera_extra_i5_26	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGATACTGGTCGTCGG CAGCGT*C
Nextera_extra_i5_27	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGCCTTGTTTCGTCGG CAGCGT*C
Nextera_extra_i5_28	/5Biosg/AATGATACGGCGACCACCGAGATCTACACTTGGTCTCTCGTCGG CAGCGT*C
Nextera_extra_i5_29	/5Biosg/AATGATACGGCGACCACCGAGATCTACACCCGACTATTCGTCGG CAGCGT*C
Nextera_extra_i5_30	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGTCCTAAGTCGTCGG CAGCGT*C
Nextera_extra_i5_31	/5Biosg/AATGATACGGCGACCACCGAGATCTACACACCAATGCTCGTCGG CAGCGT*C
Nextera_extra_i5_32	/5Biosg/AATGATACGGCGACCACCGAGATCTACACGATGCACTTCGTCGG CAGCGT*C

All oligonucleotides carry a 5'-biotin (/5Biosg/) and a phosphorothioate bond (*) between the last and the second last nucleotide. For cost reasons, we ordered desalted oligos and not HPLC purified.

Prepare working dilution plates containing unique combinations of N7xx + S5xx adaptors, each with a final concentration of 5 µM.



Before start

The protocol should be carried out in a clean environment, ideally on a dedicated PCR workstation or on a separate bench used only for this purpose. Before starting, clean the bench and wipe any piece of equipment with RNaseZAP or 0.5% sodium hypochlorite. Rinse with nuclease-free water to avoid corrosion of delicate equipment.

Work quickly and preferably on ice.

Reagent mixes should be prepared shortly before use.

Mix thoroughly each mix before dispensing. For higher accuracy use liquid handling robots and/or nanodispensers whenever possible. In FLASH-Seq we use the I.DOT (Dispendix) for all the dispensing steps and the Fluent 780 liquid handling robot (Tecan) for sample cleanup, reagent transfers and pooling.

The protocol described below is meant to be carried out in 384-well plates. When using 96-well plates, we recommend using 5 times larger volume to guarantee successful cell sorting and prevent evaporation issues.

Always use LoBind plates and tubes (especially for long-term storage) to prevent the cDNA/DNA from sticking to plastic.

Prepare lysis mix

15m

1

Prepare the following lysis mix:

	A	B	C	D
	Reagent	Reaction concentration	Volume (μl)	384-well plate
	Triton-X100 (10% v/v)	0.2%	0.020	8.448
	dNTP mix (25 mM each)	6 mM	0.240	101.376
	SMART dT30VN (100 μM)	1.8 μM	0.018	7.603
	RNAse inhibitor (40 U/μL)	1.2 U/μl	0.030	12.672
	DTT (100 mM)	1.2 mM	0.012	5.069
	FS TSO (100 μM)	9.2 μM	0.092	38.861
	dCTP (100 mM)	9 mM	0.090	38.016
	Betaine (5 M)	1 M	0.200	84.480
	Nuclease-free water	-	0.298	125.875
	Total volume (μl)		1.000	422.400

Add  1 μL lysis mix to each well of a 384-well plate

Seal the plate with a PCR seal and quickly spin it down to collect the lysis mix to the bottom.

Proceed immediately to the next step or store the plate at  -20 °C long-term. Plates that are going to be used on the same day can be stored in the fridge or kept on ice.

Note

SAFE STOPPING POINT - Plates containing lysis buffer can be stored for >6 months at

 -20 °C

Sample collection

10m

- 2 Sort single cells into 384-well plates containing  1 µL lysis mix.

Seal the plate with an aluminium seal. If processing multiple plates at once, keep each plate on dry ice until ready to transfer them all at  -80 °C for long-term storage.

Plates containing single cells should ideally be processed within 6 months.

Cell lysis

3m

- 3 Remove the plates from the  -80 °C freezer and check that the aluminium seal is still intact. If damaged or not sticking to the plate anymore, wait a few minutes for the plate to partially thaw, remove the damaged foil and replace it with a new one.

Place the plate in a thermocycler with a heated lid and incubate for  00:03:00 at  72 °C , followed by a  4 °C hold step.

Spin down any condensation droplets that may have formed during the incubation and return the plate to a cool rack. Proceed quickly to the next step. If not ready with the RT-PCR mix, keep the plate on the cool rack at all times.

RT-PCR reaction

15m

- 4 While the plate is in the thermocycler, prepare the following RT-PCR mix:

	A	B	C	D
	Reagent	Reaction concentration	Volume (µl)	384-well plate
	DTT (0.1 M)	4.8 mM	0.238	100.531
	MgCl ₂ (1 M)	9.2 mM	0.046	19.430
	Betaine (5 M)	800 mM	0.800	337.920
	RNAse inhibitor (40 U/µl)	0.8 U/µl	0.096	40.550
	SuperScript IV (200 U/µl)	2.00 U/µl	0.050	21.120
	KAPA HiFi HotStart ReadyMix (2 x)	1 x	2.500	1056.000
	Nuclease-free water	-	0.270	114.048

A	B	C	D
Total volume (μl)		4.000	1689.600

Add  4 μL RT-PCR mix into each well of the 384-well plate.

Seal the plate with a PCR seal, gently vortex and spin down to collect the liquid at the bottom.

Place it in a thermocycler with heated lid and start the following RT-PCR program:

A	B	C	D	E
Step		Temperature	Time	Cycles
RT		50°C	60 min	1 x
PCR	initial denaturation	98°C	3 min	1 x
	denaturation	98°C	20 sec	18-21 x*
	annealing	67°C	20 sec	
	elongation	72°C	6 min	
		15°C	Hold	

*Adjust the number of cycles according to the cell type used. We recommend 18-19 cycles for HEK 293T cells and 21 cycles for hPBMC. As a rule of thumb, we typically start with 1-2 less PCR cycles compared to the Smart-seq2 protocol.

Note

SAFE STOPPING POINT - Amplified cDNA before purification can be stored for several months at  -20 °C

Magnetic beads working solution preparation

1h



- 5 You can either use AMPure XP beads, SPRI beads or prepare your own solution of SeraMag beads containing 18% w/v PEG to reduce costs. A detailed protocol for making your own magnetic bead solution is described in:

Citation

Picelli S (2019). Full-Length Single-Cell RNA Sequencing with Smart-seq2. Methods in molecular biology (Clifton, N.J.).

https://doi.org/10.1007/978-1-4939-9240-9_3

LINK

Below is a short description of how to prepare 50 ml of working solution:

A	B	C
Reagent	Amount to add	Final concentration
Sodium chloride	2.92 gr	1 M
Tris-HCl, pH = 8.0 (1 M)	500 µl	10 mM
EDTA (500 mM)	100 µl	1 mM
PEG (MW=8000)	9.5 gr	18% w/v
Nuclease-free solution	to a final volume of 50 ml	-

Add all components to a 50-ml Falcon tube but do not add the total amount of nuclease-free water yet.

Solubilise the PEG by stirring and heating the solution at  37 °C .

While the PEG is dissolving, prepare the Sera-Mag SpeedBeads™. Vortex thoroughly to ensure complete resuspension and then withdraw  1 mL Sera-Mag SpeedBeads™ stock solution. Transfer it into a new 1.5-ml tube.

Pellet the beads by placing the tube on a magnetic stand. Wait until the solution clears and then discard the supernatant.



Add  1 mL 10 mM Tris-HCl pH 8.0 + 1 mM EDTA (TE buffer) and resuspend the beads off the magnet.

Pellet the beads again, wait until the solution is clear, discard the supernatant and resuspend off the magnet with  0.9 mL TE buffer.

Once the PEG solution is clear, add the resuspended beads prepared in the previous step.

Add  50 μ L Tween-20 (10% v/v) and  250 μ L sodium azide (NaN_3 , 10% w/v) and adjust the volume to  50 mL with nuclease-free water.

Store at  4 °C . Do not freeze.

Note

Confirm that the beads have been properly prepared by cleaning-up a control sample (i.e., amplified cDNA from total RNA) and running a High Sensitivity DNA chip on the Agilent Bioanalyzer. Batch-to-batch variations in PEG concentration will influence size-cutoffs.

Note

Add Tween-20 at the end, to prevent foaming during PEG resuspension.

Safety information

Sodium azide is extremely toxic and should be handled under a fume hood.

cDNA purification

25m

- 6 Remove the Sera-Mag SpeedBeads™ working solution (or AMPure XP beads or SPRI beads when using a commercial solution) from the  4 °C storage and equilibrate it at room temperature for  00:15:00 .

29m

**Note**

We recommend adding extra nuclease-free water to each sample, to increase the volume, simplify the handling and improve recovery rate. We generally add  10 μL nuclease-free water to  5 μL amplified cDNA.

Add a 0.8 x volume ratio Sera-Mag SpeedBeads™ working solution to each well. Mix thoroughly by pipetting or vortexing.

Incubate the plate off the magnetic stand for  00:05:00 at  Room temperature .

Place the plate on the magnetic stand and leave it for  00:05:00 or until the solution appears clear.

Remove the supernatant without disturbing the beads.

Remove the plate from the magnetic stand, add  15 μL nuclease-free water and mix well by pipetting or vortexing to resuspend the beads. Do not let the bead pellet to dry completely, as it can decrease the final cDNA yield!

Incubate  00:02:00 off the magnetic stand.

Place the plate back on the magnetic stand and incubate for  00:02:00 or until the solution appears clear.

Remove  14 μL of the supernatant and transfer it to a new plate.

Note

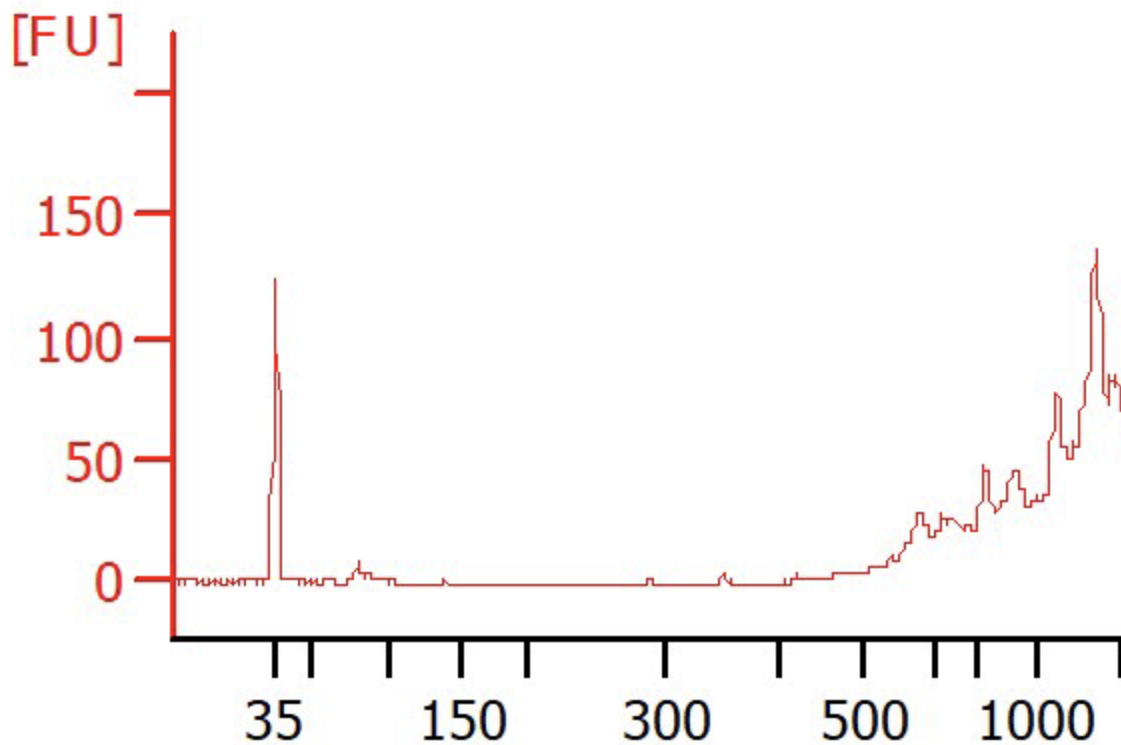
SAFE STOPPING POINT - Amplified and purified cDNA can be stored for several months at  -20 °C . We recommend using LoBind plates to avoid material losses upon long-term storage.

Quality control check (highly recommended!)

45m

- 7 Check the cDNA quality on Agilent Bioanalyzer High Sensitivity DNA chip. A good sample is characterised by a low proportion of fragments <400 bp, absence of residual primers (ca. 100 bp) and an average cDNA size of 1.8–2.2 Kb.

Expected result



Example of amplified cDNA from a single hPBMC (21 cycles)

cDNA quantification (optional but recommended)

15m

- 8 Allow the Quant-iT PicoGreen reagent to warm to Room temperature before opening the vial. PicoGreen is light sensitive; while thawing, wrap in aluminium foil.

2m

Prepare a 1 x working solution TE using 20 x TE (supplied) and nuclease-free water.

Prepare a 1:400 dilution PicoGreen solution and always use a plastic vessel.

Prepare the standard curve using Lambda DNA standard (supplied at a concentration of **100 ng/μl**, with the PicoGreen kit) and 1 x TE in 8 tubes, as below. The stock tubes can be used multiple times, keep any leftover in the fridge at **4 °C** between experiments.

Vortex well and spin down the DNA standards before every use. Not vortexing thoroughly the standards is going to negatively affect the standard curve and your readings! Serial dilutions should be prepared as shown in the table below.

A	B	C	D
Tube no.	Contents	Concentration	Final volume
1	90 μl TE + 10 μl Lambda DNA stock	10 ng/μl	100 μl
2	50 μl from Tube 1 + 50 μl TE	5 ng/μl	100 μl
3	50 μl from Tube 2 + 50 μl TE	2.5 ng/μl	100 μl
4	50 μl from Tube 3 + 50 μl TE	1.25 ng/μl	100 μl
5	50 μl from Tube 4 + 50 μl TE	0.625 ng/μl	100 μl
6	50 μl from Tube 5 + 50 μl TE	0.3125 ng/μl	100 μl
7	50 μl from Tube 6 + 50 μl TE	0.15625 ng/μl	100 μl
8	TE only	blank	-

Prepare the PicoGreen solution by pipetting **0.5 μL** PicoGreen dye + **99.5 μL** 1 X TE for each sample. Vortex to mix.

Pipette **1 μL** each of the 7 standards + 1 Blank into a black, flat-bottom Nunc™ F96 MicroWell™ plate. Place the standards on one column.

Pipet **1 μL** of your samples into the center of each well of the Nunc™ F96 MicroWell™ polystyrene plate.

Add **99 μL** PicoGreen + TE mix into every well. There is no need to mix.

Cover the plate with the provided plastic (transparent) lid to prevent possible contaminations.

Allow  00:02:00 for the dye to bind the DNA. Protect from light but keep at room temperature. For optimal results, the plate should be read within the next hour.

Use a plate reader to measure fluorescence (excitation: 485 nm; emission: 530 nm; read from top; endpoint reading).

Plate normalisation

10m

- 9 Prepare a normalisation plate by adding  1 μL purified cDNA and nuclease-free water to a final concentration of  150 $\text{pg}/\mu\text{L}$.

Tagmentation and enrichment PCR

1h

- 10 This step can be carried out either by using the commercially available **Nextera XT kit** or a **in-house Tn5 transposase**, as described below. Indexing primers can be purchased from Illumina (Nextera XT index kit v2) or ordered from your local oligo manufacturer. In the "Materials" section we have added additional sequences for higher multiplexing.

10.1 Tagmentation with the Nextera XT kit

13m

Note

Please note that the volumes described here are a mere suggestion. For example, decreasing the final volume by a factor 2 (while still using the same amount of cDNA and ATM) would give comparable results but significantly reduce costs.

Prepare the tagmentation mix as described below:

	A	B
	Reagent	Volume (μL)
	ATM (Amplification Tagment Mix)	0.250
	TD (Tagmentation DNA buffer)	2.000
	Nuclease-free water	0.500
	Total volume (μL)	3.000

Dispense  3 μL tagmentation mix in a new 96-well or 384-well plate.

Add  1 μL normalized cDNA ($150 \text{ pg}/\mu\text{l}$) to each well containing the tagmentation mix.

Seal the plate, vortex, spin down, and carry out the tagmentation reaction:  55 °C for  00:08:00 ,  4 °C hold. Upon completion proceed immediately to the next step.

Add  1 μL NT buffer to each well. Seal the plate, vortex, spin down and incubate  00:05:00 at room temperature. Do not put the plate back on ice.

Add  2 μL N7xx + S5xx index adaptors ($5 \text{ micromolar } (\mu\text{M})$ each).

Add  3 μL NPM solution to each well.

Seal the plate, vortex, spin down, and place it in a thermocycler and carry out the enrichment PCR reaction. Adjust the number of PCR cycles according to the number of processed cells.

	A	B	C	D	E
	Step		Temperatur e	Time	Cycles
	gap filling		72°C	3 min	1 x
	enrichment PCR	initial denaturatio n	95°C	30 sec	1 x
		denaturatio n	95°C	10 sec	12-14 x
		annealing	55°C	30 sec	
		elongation	72°C	30 sec	
			15°C	hold	

Note

SAFE STOPPING POINT - The final unpurified sequencing library can be stored for several months at  -20 °C

10.2 Tagmentation with in-house Tn5 transposase

8m

Note

Please note that the Tn5 transposase amount indicated below is a suggested starting point for tagmenting  150 pg/μl cDNA. Optimisation might be necessary, depending on the specific activity of each batch of Tn5.

Prepare the tagmentation mix as described below:

	A	B	C
	Reagent	Volume (μl)	Final concentration
	TAPS-Mg buffer, pH=7.3 (5 x)	0.800	10 mM TAPS, 5 mM MgCl ₂
	Dimethylformamide (DMF) (100%)	0.800	20%
	Tn5 transposase (2 μM working dil.)	0.125	62.5 nmol
	Nuclease-free water	1.275	
	Total volume (μl)	3.000	

Safety information

Dimethylformamide (DMF) is toxic and should be handled under the hood according to local safety regulations.

Dispense  3 μL tagmentation mix in a new 384-well plate.

Add  1 μL normalized cDNA ( 150 pg/μl) to each well containing the tagmentation mix.

Seal the plate, vortex, spin down, and carry out the tagmentation reaction:  55 °C for  00:08:00 ,  4 °C hold. Upon completion proceed immediately to the next step.

Add  1 µL 0.2% SDS to each well. Seal the plate, vortex, spin down and incubate 5 min at room temperature. Do not put the plate back on ice.

Add  2 µL N7xx + S5xx index adaptors ( 5 micromolar (µM) each).

Add  3 µL enrichment PCR mix to each well:

	A	B	C
	Reagent	Volume (µl)	Final concentration
	KAPA HiFi enzyme (1 U/µl)	0.200	0.02 U/µl
	KAPA HiFi buffer (5 x)	2.000	1 x
	dNTPs (10 mM)	0.300	300 nM
	Nuclease-free water	0.500	
	Total volume (µl)	3.000	

Seal the plate, vortex, spin down, and place it in a thermocycler and carry out the enrichment PCR reaction. Adjust the number of PCR cycles according to the number of processed cells.

	A	B	C	D	E
	Step		Temperature	Time	Cycles
	gap filling		72°C	3 min	1 x
	enrichment PCR	initial denaturation	98°C	30 sec	1 x
		denaturation	98°C	10 sec	12-14 x
		annealing	55°C	30 sec	
		elongation	72°C	30 sec	



	A	B	C	D	E
			15°C	hold	

Library cleanup and quantification

30m

- 11 Take an aliquot from each sample for the final library cleanup (i.e. 5 µl). and transfer it to a 1.5-ml Eppendorf tube. The rest of the library can be stored long-term at -20 °C .

31m 30s

Remove the Sera-Mag SpeedBeads™ working solution from the 4 °C storage and equilibrate it at room temperature for 00:15:00 .

Add Sera-Mag SpeedBeads™ working solution to a final ratio of 0.8 x and mix well to homogenisation.

Incubate the tube off the magnetic stand for 00:05:00 at Room temperature .

Place the tube on the magnetic stand and leave it for 00:05:00 or until the solution appears clear.

Remove the supernatant without disturbing the beads.

Recommended: wash the pellet with 1 mL 80% v/v ethanol. Incubate 00:00:30 without removing the tube from the magnetic stand.

Remove any trace of ethanol and let the bead pellet dry for 00:02:00 or until small cracks appear. Do not cap the tube or remove it from the magnetic stand during this time. Do not completely air-dry the beads.

Remove the tube from the magnetic stand, add 50 µL nuclease-free water and mix well by pipetting or vortexing to resuspend the beads.

Incubate 00:02:00 off the magnetic stand.

Place the tube back on the magnetic stand and incubate for 00:02:00 or until the solution appears clear.

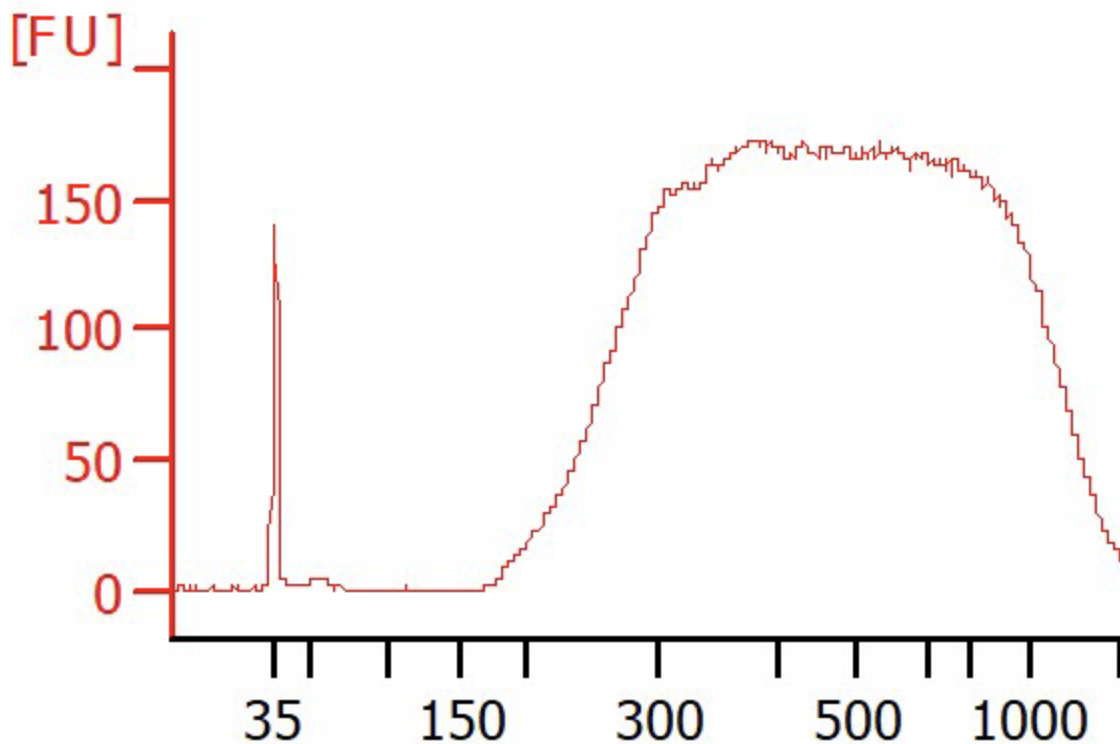
Remove 49 μL of the supernatant and transfer it to a new 1.5-ml LoBind tube. Store the cDNA at $-20\text{ }^{\circ}\text{C}$ long-term or until ready for sequencing.

Use Qubit fluorometer to quantify the library. Library yield can vary depending on the number of cells being pooled.

Check the final library size on the Agilent Bioanalyzer.

Use the average size indicated on the Bioanalyzer and the concentration reported after Qubit measurement to determine the exact molarity required for sequencing.

Expected result



Example of sequencing-ready library (pool of 384 HEK 293T cells).

Note

SAFE STOPPING POINT - The final purified sequencing library can be stored for several months at  -20 °C .

Pooling and sequencing

- 12 The purified library can be sequenced on any Illumina sequencer. Follow the specifications reported for each instrument. Single-End 75 bp is generally sufficient but longer read modes or Paired-End sequencing can be an option, depending on the question at hand.

Data processing

- 13 These instructions briefly describe the data processing of the sequencing results. The final pipeline will likely have to be adapted to the question at hand. The following lines assume that all the programs and their dependencies are installed on your machine and that the data are single-end reads (75 bp). Some values, such as the number of threads and RAM usage may have to be adapted to your machine settings.

It should be noted that there are many other ways to analyse full-length single-cell RNA-sequencing data. Pseudo-alignment tools (e.g., Salmon or Kallisto) or automatic pipelines (zUMIs) could be used as well.

Requirements (tested version):

- bcl2fastq (v2.20)
- STAR (v2.7.3)
- FeatureCounts (v1.6.5)
- BBMAP (v38.86)
- samtools (v1.9)
- IGV

13.1 Sample demultiplexing

Sequencing results will be delivered as demultiplexed FASTQ or raw bcl2 files. To convert bcl2 files to FASTQ, bcl2fastq program (Illumina) can be used.

Command**new command name****# 0. Variables**

```
BASECALL_DIR="/path/to/flowcell/Data/Intensities/BaseCalls/"
```

```
OUTPUT_DIR="/path/to/output_folder/"
```

```
SAMPLESHEET="/path/to/Demultiplexing_SampleSheet.csv"
```

Command**new command name****# 1. Bcl2fastq**

```
ulimit -n 10000
```

```
cd /path/to/flowcell/
```

```
bcl2fastq --input-dir $BASECALL_DIR --output-dir $OUTPUT_DIR --sample-sheet $SAMPLESHEET --create-fastq-for-index-reads --no-lane-splitting
```

When sequencing on a NextSeq550 instrument, the sample sheet should contain the following information in a csv file:



```
[Header]
IEMFileVersion      5
Investigator Name   Your Name
Experiment Name      Experiment Title
Date                11/12/2021
Workflow            GenerateFASTQ
Application          NextSeq FASTQ Only
Instrument Type      NextSeq/MiniSeq
Assay               Nextera XT
Index Adapters      Nextera XT Index Kit (24 Indexes 96 Samples)
Chemistry            Amplicon

[Reads]
75

[Settings]
Adapter            CTGTCTCTTATACACATCT

[Data]
Sample_ID  Sample_Name  Sample_Plate  Sample_Well  I7_Index_ID  index  I5_Index_ID  index2  Sample_Project
Sample1_A1 Sample1_A1 001      A1          Nextera_extra_i7_25  ACAAGCTC  Nextera_extra_i5_17  CAGAACTG
```

Illumina Experiment Manager can be used to assist you in creating the sample sheet.

We recommend exploring the barcode combinations left in the undetermined reads looking to confirm that all the cells have been properly demultiplexed.

Command

new command name

```
zcat Undetermined_S0_I1_001.fastq.gz | awk -F' 1:N:0:' 'NR%4==1{print $2}' | sort | uniq -c > left_index.txt
sort -k1,1 left_index.txt
```

as well as the read distribution between samples:

Command

new command name

```
for file in ./out/*R1*
do
zcat $file | wc -l
done
```

13.2 Index the genome

The reference genome needs to be indexed prior to any mapping. The FASTA and GTF references can be obtained from ENSEMBL, Gencode, UCSC, ...

Command

new command name

```
# 0. Variables
OUTPUTREF="/path/to/STAR_indexed_genome/"
FASTA="GRCh38.primary_assembly.genome.fa"
GTF="gencode.v34.primary_assembly.annotation.gtf"
```

Command**new command name**

```
# 1. Genome indexing
# sjdbOverhang should be adapted based on the read length
(read_length - 1)
mkdir $OUTPUTREF
```

Command**new command name**

```
STAR --runThreadN 15 --runMode genomeGenerate --genomeDir $OUTPUTREF -
-genomeFastaFiles $FASTA --sjdbGTFfile $GTF --sjdbOverhang 74
```

13.3 **FASTQ trimming (optional)**

If you observe sequencing primer left-overs the FASTQ files can be trimmed using BBDOUK or Trimmomatic.

Command**new command name**

```
bbduk.sh -Xmx48g in=sample.fastq.gz out=cleaned.left.fastq t=32  
ktrim=l ref=adapters.fa k=23 mink=7 hdist=1 hdist2=0 tbo  
bbduk.sh -Xmx48g in=cleaned.left.fastq out=cleaned.fastq t=32 ktrim=r  
ref=adapters.fa k=23 mink=7 hdist=1 hdist2=0 tbo
```

Command**new command name**

```
mv FASTQ/cleaned.fastq FASTQ/sample.R1.fastq.gz
```

13.4 Mapping

The FASTQ file can then be mapped onto the reference genome. Example for one sample, use a loop or parallelise this task to process all the cells:

Command**new command name**

```
# 0. Variables
GENOME="/path/to/STAR_indexed_genome/"
FASTQ="/path/to/sample.R1.fastq.gz"
ID="sample_id"
```

Command**new command name**

```
# 1. Mapping
STAR --runThreadN 30 --limitBAMsortRAM 20000000000 --genomeLoad
LoadAndKeep --genomeDir "$GENOME" --readFilesIn "$FASTQ" --
readFilesCommand zcat --limitSjdbInsertNsj 2000000 --
outFilterIntronMotifs RemoveNoncanonicalUnannotated --outSAMtype BAM
SortedByCoordinate --outFileNamePrefix "$ID"_
```

Command

new command name

```
# 2. SAM to sorted BAM
# -F 260 filters out unmapped and secondary alignments
samtools view -@ 30 -Sb -F 260 "$ID"_Aligned.sortedByCoord.out.bam >
"$ID"_Aligned.sortedByCoord.filtered.bam
samtools index "$ID"_Aligned.sortedByCoord.filtered.bam
```

13.5 **Data visualization (optional)**

Once the reads have been mapped we highly recommend using the Integrated Genome Viewer (IGV) to visualise the mapping results and ensure that the results make sense. As a quick check-up visualise a few housekeeping genes (i.e., ACTB, GAPDH, ...) and cell specific markers to look for reads mapping to exon, intron, exon-intron junctions. Look for abnormalities such as read piles falling in intergenic or centromeric regions. No single-cell RNA sequencing protocol is perfect and non-specific priming, genomic DNA contaminations, ... can happen but should represent rare events. Recurrent soft-clipping could also indicate the presence of sequencing adaptor left-overs that could affect the mapping rate.

13.6 **Count matrix**

Finally, the number of reads associated with each gene can be obtained as follows:



Command

new command name

```
featureCounts -T 1 -t exon -g gene_name --fracOverlap 0.25 -a "$GTF" -  
o "$ID"_ReadCount.featureCounts.gencode.txt  
"$ID"_Aligned.sortedByCoord.filtered.bam
```

13.7 Post-processing

The post-processing steps will vary depending on the question at hand. The online book “Orchestrating Single-Cell Analysis with Bioconductor”

(<https://bioconductor.org/books/release/OSCA/>) is a gold mine of information that can be used to help you design your own pipeline. Alternatively, Seurat (R,

<https://satijalab.org/seurat/>) or scanpy (python,

<https://scanpy.readthedocs.io/en/stable/>) provide tools compatible with FLASH-seq

data. Given their similarities, we currently recommend using Smart-seq2 guidelines when processing FLASH-seq data.

Citations

Step 5

Picelli S. Full-Length Single-Cell RNA Sequencing with Smart-seq2.

https://doi.org/10.1007/978-1-4939-9240-9_3