

scNMT-seq

Version 2

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Working

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ABSTRACT

Here we describe the full wetlab protocol for scNMT-seq (single-cell nucleosome position, methylome and transcriptome sequencing), a plate-based single-cell multi-omic method.

In scNMT-seq, a GpC methyltransferase is used to label non-nucleosome bound DNA thus encoding chromatin accessibility information within the genomic DNA. Bisulfite conversion is then used to discriminate the two chromatin states which can be read from GpC dinucleotide positions. Endogenous DNA methylation is read from the CpG positions of the same molecules and gene expression data is obtained by capturing poly-A RNA on magnetic beads and physically separating before the gDNA is bisulfite converted. This mRNA on beads is processed using Smart-seq2. The protocol is carried out in 96w plates and typically takes 3-4 days to complete.

GUIDELINES

scNMT-seq is essentially a combination of the following methods:

1. NOMe-seq:

[Genome-wide mapping of nucleosome positioning and DNA methylation within individual DNA molecules](#)

Kelly T., Liu Y. *et al*/2012

doi: 10.1101/gr.143008.112

2. G&T-seq:

[G&T-seq: parallel sequencing of single-cell genomes and transcriptomes](#)

Macauley I. *et al*/2015

doi: 10.1038/nmeth.3370

3. Smartseq2:

[Smart-seq2 for sensitive full-length transcriptome profiling in single cells](#)

Picelli S. *et al*/2013

doi: 10.1038/nmeth.2639

4. scBS-seq:

[Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity](#)

Smallwood S., Lee H. *et al*/2014

doi: 10.1038/nmeth.3035

Protocols for each of these individual methods have been published elsewhere, however the full step-by-step protocol for scNMT-seq had not previously been available as a single document.

General guidelines

As with other single-cell sequencing methods it is important to minimise sources of contamination. We perform all pre-PCR pipetting steps in a dedicated pre-PCR room. Prior to starting, all surfaces and pipettes are wiped down with a dilute bleach solution (e.g. RNase away or similar) to mitigate RNase and DNA contamination and all tubes and PCR plates are subjected to UV irradiation. We also recommend aliquoting reagents such as oligos and dNTPs so that each tube is used once then discarded.

We use an automated pipetting robot (Agilent Bravo Workstation) for each of the pre-PCR magnetic bead portions of the protocol. This reduces hands-on time and increases reproducibility of the method. However, it is also possible to perform the whole protocol by hand with an appropriate magnet and multichannel pipettes.

Sequencing of libraries should be possible on any Illumina instrument unless certain restrictions are programmed in such as with the X10. We routinely use HiSeq 2000/2500 v4 and NextSeq500. RNA-seq libraries should be sequenced on a separate lane or flowcell to the BS-

seq libraries. We have had success with read-depths of 0.5-2M per cell for the RNA-seq and 2-10M per cell for the BS-seq. We recommend paired-end with mid-long read lengths (75-125bp) for the BS-seq to maximise cytosine coverage. However, it is possible that much lower read-depths could yeild informative data, especially in studies with large numbers of cells.

Indexes are incorporated into the BS-seq libraries during the final amplification step. We use the iPCRTag indexing system, which means that a custom index read primer needs to be spiked-in with the other i7 index primers for sequencing. However, another indexing system (e.g. Truseq) could be used by re-designing the second strand synthesis oligo (SSO) appropriately.

MATERIALS

| NAME | CATALOG # | VENDOR |
|---|---------------------|----------------------------|
| GpC Methyltransferase (M.CviPI) - 1,000 units | M0227L | New England Biolabs |
| RLT Plus Buffer | | Qiagen |
| IGEPAL-CA630 | I3021 SIGMA-ALDRICH | Sigma Aldrich |
| Kapa HiFi Hotstart ReadyMix (2x) | KK2612 | Kapa Biosystems |
| Recombinant RNasin(R) RNase Inhibitor, 10,000u | N2515 | Promega |
| Agencourt AMPure XP SPRI beads | A63881 | Beckman Coulter |
| Nextera XT DNA Sample Preparation Kit, 96 samples | FC-131-1096 | illumina |
| Nextera XT Index Kit, 96 indices, 384 samples | FC-131-1002 | illumina |
| Dynabeads MyOne Streptavidin C1 | 65001 | Invitrogen - Thermo Fisher |
| Superscript II | 18064014 | Invitrogen - Thermo Fisher |
| EZ-96 DNA Methylation-Direct MagPrep | D5044 | Zymo Research |
| Klenow (3'→ 5' exo-) (High Concentration) | P7010-HC-L | Enzymatics |

MATERIALS TEXT

| Name | Sequence (5' to 3') |
|------------------------|--|
| bio-Smartseq2-dT | /5BiotinTEG/AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTT TTTTTTTTTTTTTVN |
| Smartseq2 TSO | AAGCAGTGGTATCAACGCAGAGTACATrGrG+G |
| ISPCR | AAGCAGTGGTATCAACGCAGAGT |
| First strand oligo | /5SpC3/CTACACGACGCTCTTCCGATCTNNNNNN |
| Second strand oligo | TGCTGAACCGCTCTTCCGATCTNNNNNN |
| PE1.0 | AATGATACGGCGACCAACGAGATCTACACTCTTCCCTACACGACGCTCTT CCGATC*T |
| iPCRTag | CAAGCAGAAGACGGCATACGAGATXXXXXXXXXGAGATCGGTCTCGGCATT CCTGCTGAACCGCTCTTCCGATC*T |
| iTag sequencing primer | AAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTC |

Oligo sequences. All oligos should be ordered with HPLC purification.

Single-cell collection and methylase reaction

- 1
- Prepare GpC methylase reaction buffer:

| Reagent | amount per sample | 96 well plate (x120) |
|------------------------------------|-------------------|----------------------|
| Nuclease free water | 1.425 | 171 |
| GpC methyltransferase buffer (10x) | 0.25 | 30 |
| SAM | 0.0125 | 1.5 |
| IGEPAL CA-630 (1%) | 0.25 | 30 |
| RNase-in (40U/ul) | 0.0625 | 7.5 |
| M.CviPI (4U/ul) | 0.5 | 60 |
| Total | 2.5 | 300 |

- 2 Collect single cells in  **2.5 µl** of freshly prepared GpC methylase reaction mix (keep chilled on ice)

Centrifuge at $\geq 1000g$ for $\geq 10s$.




We have successfully used both flow sorting and manual pipetting for single-cell collections.

- 3 Incubate on a thermocycler:

 **00:15:00**  **37 °C**

- 4 Add  **5 µl** RLT plus

Centrifuge at $\geq 1000g$ for $\geq 10s$.

- 5 Store at  **-80 °C**

Prepare oligo-dT on beads

- 6 Pipette  **55 µl** Dynabeads (MyOne Streptavidin C1) into a microcentrifuge tube. Place on a magnet and remove supernatant.

- 7 Resuspend beads in  **55 µl** solution A (0.1M NaOH, 0.05M NaCl) by pipetting. Place on a magnet and remove supernatant.

- 8  **go to step #7 : Repeat solution A wash one more time**

- 9 Resuspend beads in  **55 µl** solution B (0.1M NaCl). Place on magnet and remove supernatant.

- 10  **go to step #8 : Repeat solution B wash once.**

- 11 Resuspend beads in  **55 µl** 2x B&W (2 M NaCl, 10 mM Tris-HCl, 1 mM EDTA). Place on magnet and remove supernatant.

- 12  **go to step #11**

13 Resuspend beads in **55 µl 2x B&W** and **55 µl bio-Smartseq2-dT (100uM)**.



bio-Smartseq2-dT: 5'-Biotin-TEG-AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN-3' (IDT, purified with HPLC and resuspended in nuclease free water)

14 Rotate tube containing beads such that beads remain in solution for a minimum of **00:15:00**.



Beads can be prepared in advance and stored at **4 °C** for up to 1 month

Wash oligo dT beads and prepare for dispensing

15 Place on magnet and remove supernatant. Resuspend beads in **110 µl 1x B&W buffer (1M NaCl, 5mM Tris, 0.5mM EDTA)**. Place on magnet and remove supernatant.

16 [go to step #15](#)

17 Place on magnet and remove supernatant. Resuspend beads in:
830 µl Nuclease free water,
110 µl 5x first strand buffer (Invitrogen, Superscript II),
43 µl RNasin (Promega),
10 µl Diluted ERCC spike-in



This assumes 2.5ul GpC reaction plus 5ul RLtplus. If using bigger volumes, adjust upward in proportion.



ERCC spike-in is optional. The concentration used will depend on cell type (RNA content).

mRNA separation

18 Prepare G&T-seq wash buffer:

| Reagent | 96 well plate |
|--|---------------|
| Nuclease free water | 3430 |
| 5x First strand buffer (Invitrogen Superscript II) | 430 |
| DTT (100mM, Invitrogen Superscript II) | 430 |
| Tween-20 (100%) | 22 |
| Recombinant RNasin (40U/ul) | 43 |


| | |
|--------------|-------------|
| Total | 4355 |
|--------------|-------------|

19 Prepare RT mastermix:

| Reagent | amount per sample | 96 well plate (x110) |
|---|-------------------|----------------------|
| Nuclease free water | 3.715 | 408.65 |
| 5x First strand buffer (Superscript II) | 2 | 220 |
| Betaine (5M) | 2 | 220 |
| DTT (100mM, Superscript II) | 0.5 | 55 |
| dNTPs (10mM each) | 1 | 110 |
| MgCl ₂ (1M) | 0.06 | 6.6 |
| Smartseq2 TSO (100uM) | 0.1 | 11 |
| Recombinant RNasin (40U/ul) | 0.125 | 13.75 |
| Superscript II (200U/ul) | 0.5 | 55 |
| Total | 10 | 1100 |

20 Manually pipette 10 µl of prepared oligo-dT beads to each well of the sample plate using a multichannel pipette.


21 Mix at maximum speed for 00:10:00

 We perform mRNA separation steps on an Agilent Bravo liquid handling robot. If performing this step manually, intermittent vortexing for 10 minutes achieves the same result.

22 Place on magnet until beads pellet. Aspirate 17.5 µl and transfer to empty lobind plate for gDNA collection.


23 Add 15 µl of G&T-seq wash buffer off magnet.

24 Mix at maximum speed for 00:01:00

 If performing manually, a thorough vortexing here suffices.


25 Place on magnet until beads pellet. Aspirate 15 µl and transfer to empty lobind plate for gDNA collection.

26 go to step #22 Repeat steps 22-25 twice more.

 Lysate (17.5ul) combined with 3 washes (15ul each) should now have been collected into the gDNA plate

Pause point. gDNA can be frozen at -20°C for later processing.

27 Add  **10 µl RT mastermix** to beads.

28 Mix at maximum speed for  **00:01:00**

Reverse transcription

29 Incubate on a thermocycler as follows:

 **01:00:00**  **42 °C**


 **00:30:00**  **50 °C**

 **00:10:00**  **60 °C**



Vortex plate at 30 and 60 minute time points to resuspend beads.

cDNA amplification

30 Add  **12 µl PCR mastermix** by hand using a multichannel pipette.

| Reagent | amount per cell | 96 well plate |
|-----------------------|-----------------|---------------|
| KAPA HiFi 2x Readymix | 11 | 1210 |
| ISPCR primer (10uM) | 0.25 | 27.5 |
| Water | 0.75 | 82.5 |
| Total | 12 | 1320 |

31 Cycle as follows:

 **00:03:00**  **98 °C**

18 Cycles of:

 **00:00:20**  **98 °C**

 **00:00:15**  **67 °C**

 **00:06:00**  **72 °C**

Followed by:

 **00:05:00**  **72 °C**

 **00:00:00 pause - usually overnight**  **4 °C**



Cycle number depends on cell type. 18 is sufficient for mouse ES cells and embryo cells.



Pause point. cDNA can be frozen at -20°C for later processing.

cDNA purification using 1x AMPure XP

32



This section is performed outside of pre-PCR room.

Add **18 µl** AMPure XP beads. Mix thoroughly and incubate for 5 minutes.

33 Place on magnet until beads precipitate. Remove supernatant. Wash twice with 80% ethanol. Remove supernatant and air-dry beads for 5 minutes at room temperature.

34 Elute cDNA in **25 µl water**

35 Check quality of a subset (e.g. 11 samples) of cDNA samples using a Bioanalyzer high sensitivity DNA chip.



Fragment size range of 1kb to 5kb. Concentration of 100 to 500 pg/ul. If concentration is higher then dilute samples with water prior to Nextera XT library prep.

Nextera XT library preparation

36



This section is performed outside of pre-PCR room.

In a 96 well or a 384 well plate, add 2.25ul Tagmentation mastermix to each well:

| Reagent | amount per sample | 96 well plate (x120) | 384 well plate |
|----------------------|-------------------|----------------------|----------------|
| Tagment DNA buffer | 1.5 | 180 | 650 |
| Amplicon tagment mix | 0.75 | 90 | 325 |
| Total | 2.25 | 270 | 975 |

37 Using a multi-channel pipette, add 0.75ul of cDNA sample (100-500pg/ul) to the mastermix. Vortex the plate and spin down.

38 In a thermocycler incubate as follows:

55 °C 00:05:00,

4 °C pause

39 Add **0.75 µl NT buffer** using multichannel pipette. Centrifuge then vortex to mix and centrifuge again.

40 Add **2.25 µl NPM (from Nextera XT kit)**

Add **1.5 µl pre-mixed and diluted i7 and i5 primers**

Using a multichannel pipette. Centrifuge and vortex to mix.



We prepare pre-mixed indexing primers in 96w plates for this step. Using multichannel pipettes, transfer each of 8 i5 primers to 12 columns and each of 12 i7 primers to 8 rows, then dilute 5-fold with water.

41 Cycle as follows:

🔥 72 °C ⌚ 00:05:00

🔥 95 °C ⌚ 00:02:00

10 cycles of:

🔥 95 °C


🔥 65 °C

🔥 72 °C

Followed by:

🔥 72 °C ⌚ 00:05:00


🔥 4 °C hold.



42 Pool  1 µl of each indexed cDNA library. Purify using 0.7x AMPure XP beads with 2x 80% ethanol washes.

43 QC using Bioanalyzer.

Genomic DNA purification

44

Add  50 µl AMPure XP beads to gDNA samples. Vortex thoroughly and incubate for ⌚ 00:30:00




45 Place on a magnet until beads pellet. Remove supernatant, wash twice with  100 µl 80% ethanol. Remove supernatant. Immediately resuspend in  10 µl of nuclease free water.



We use an Agilent Bravo for these wash steps.

Prepare bisulfite conversion reagent

46 Bisulfite reagent is prepared according to manufacturers instructions (Zymo EZ-methylation direct):

Add  7.9 ml **M-Solubilization Buffer** and  3 ml **M-Dilution Buffer** to a bottle of CT Conversion Reagent. Mix at room temperature with frequent vortexing or shaking for at least 10 minutes. Add  1.6 ml **M-Reaction Buffer** and vortex thoroughly.

Bisulfite conversion

47 Place gDNA sample plate on magnet to pellet beads.

48 Add  65 µl of prepared CT Conversion Reagent solution to each sample on the magnet.



Do not mix sample and beads with CT reagent – beads should remain pelleted during conversion to avoid excessive dissolving of magnetic beads.

- 49 Incubate on a thermocycler as follows:
- 🔥 98 °C ⌚ 00:08:00
 - 🔥 64 °C ⌚ 03:00:00
 - 🔥 4 °C pause until purification (maximum duration of overnight)

Desulphonation and purification

- 50 Add 🧴 533 µl Zymo Magbinding beads to 🧴 32 ml M-Binding buffer, mix and dispense 🧴 305 µl per well of deepwell plate using multichannel and reservoir.
- 51 Add sample to deepwell plate containing beads and binding buffer. Mix thoroughly then transfer 🧴 100 µl back to sample plate, mix thoroughly and transfer back to deepwell plate to maximise recovery of bisulfite converted DNA. Mix for ⌚ 00:05:00
- 52 Place on magnet until beads pellet. Remove supernatant.
- 53 Add 🧴 180 µl freshly prepared 80% ethanol. Mix thoroughly.
- 54 Place on magnet until beads pellet. Remove supernatant.
- 55 Add 🧴 100 µl M-Desulphonation buffer (Zymo). Mix thoroughly.
- 56 Incubate ⌚ 00:15:00



Incubate for ≥ 15 minutes and ≤ 25 minutes

- 57 Place on magnet and remove supernatant.
- 58 Add 🧴 180 µl freshly prepared 80% ethanol. Mix thoroughly.
- 59 Place on magnet until beads pellet. Remove supernatant.
- 60 [🔄 go to step #58 : Repeat once more.](#)
- 61 Dry beads 🔥 60 °C ⌚ 00:10:00

62 Prepare first strand master mix for elution:

| Reagent | amount per sample | 96 well plate (x120) |
|------------------------------|-------------------|----------------------|
| Nuclease free water | 31.8 | 3816 |
| 10x Blue buffer (Enzymatics) | 4 | 480 |
| dNTP mix (10mM each) | 1.6 | 192 |
| First strand oligo (10uM) | 1.6 | 192 |
| Total | 39 | 4680 |



First strand oligo: /5SpC3/CTACACGACGCTCTCCGATCTNNNNNN (IDT, HPLC purified).
This primer contains the Illumina PE read 1 sequence.

63 Resuspend beads in 20 µl first strand synthesis mix. incubate at 60 °C 00:05:00

64 Place on magnet until beads pellet. Transfer 20 µl supernatant to fresh lobind PCR plate.

65 go to step #63 : Repeat elution once more.

First strand synthesis

66 Place sample plate on thermocycler at 65 °C 00:03:00 then immediately cool on ice.

67 Add 1 µl Klenow exo- (50 U/ul, Enzymatics) using multichannel and PCR strip.

68 Incubate on a thermocycler as follows:

4 °C 00:05:00

Slow ramp from 4 °C to 37 °C at 30s per 1C

37 °C 00:30:00

4 °C hold.

69 95 °C 00:00:45 95 °C for 45 seconds then immediately cool 4 °C using two ice blocks.

70 Add 2.5 µl first-strand extra cycles mix

| Reagent | amount per sample | 96 well plate (x110) |
|---------------------------|-------------------|----------------------|
| Nuclease free water | 0.65 | 71.5 |
| 10x Blue buffer | 0.25 | 27.5 |
| dNTP mix (10mM each) | 0.1 | 11 |
| First strand oligo (10uM) | 1 | 110 |

| | | |
|----------------------|------------|------------|
| Klenow exo- (50U/ul) | 0.5 | 55 |
| Total | 2.5 | 275 |



First strand oligo: /5SpC3/CTACACGACGCTCTCCGATCTNNNNNN (IDT, HPLC purified).
This primer contains the Illumina PE read 1 sequence.

71 Incubate on a thermocycler as follows:

4 °C **00:05:00**

Slow ramp from **4 °C** to **37 °C** at 30s per 1C

37 °C **00:30:00**

4 °C hold.

72 **go to step #69 Repeat first strand synthesis an additional 3 times**

73 Incubate the 5th and final round of first strand synthesis as follows:

4 °C **00:05:00**

Slow ramp from **4 °C** to **37 °C** at 30s per 1C

37 °C **01:30:00**

4 °C hold.

Exonuclease treatment

74 **50 µl Exonuclease mix**

| Reagent | amount per sample | 96 well plate(x120) |
|---------------------|-------------------|---------------------|
| Nuclease free water | 48 | 5760 |
| Exonuclease I (NEB) | 2 | 240 |
| Total | 50 | 600 |

75 37 °C for 1 hour. **37 °C** **01:00:00**

1st Strand Purification



76 Add **70 µl AMPureXP beads** per well of a deepwell plate. Transfer **100 µl** sample to deepwell plate. Mix thoroughly and incubate at room temperature for 10 minutes.

77 Place plate on magnet and wait until beads pellet. Remove supernatant.

78 Add **180 µl 80% ethanol** off the magnet and mix thoroughly with pipetting.

79 Place plate on magnet and wait until beads pellet. Remove supernatant.

80 Add  **180 µl 80% ethanol** on the magnet.

81 Remove supernatant and air dry at  **50 °C**  **00:05:00**

82 Resuspend beads in  **49 µl second strand master mix**



| Reagent | amount per sample | 96 well plate (x120) |
|----------------------------|-------------------|----------------------|
| Nuclease free water | 40 | 4800 |
| 10x Blue buffer | 5 | 600 |
| dNTP mix (10mM each) | 2 | 240 |
| Second strand oligo (10uM) | 2 | 240 |
| Total | 49 | 5880 |











Second strand oligo: TGCTGAACCGCTCTCCGATCTNNNNNN (HPLC purified from IDT).
This primer contains the Illumina PE read 2 sequence. Users wishing to use Truseq indexing primers (instead of iPCRTag) should redesign this so that it matches the Truseq read 2 sequence (TCAGACGTGTGCTCTCCGATC).

83 Transfer second strand mix containing beads to a fresh 96w PCR plate.

Second strand synthesis


84 Incubate on a thermocycler:
 **98 °C**  **00:02:00**, then immediatly cool on ice.

85 Add  **0.5 µl Klenow exo- (50U/ul, Enzymatics)** and incubate:
 **4 °C**  **00:05:00**
Slow ramp from  **4 °C** to  **37 °C** at 30s per 1C
 **37 °C**  **01:30:00**
 **4 °C** hold.

2nd Strand Purification

86 Prepare an aliquot of AMPure buffer by pelleting AMPure XP beads using a magnet or centrifuge and taking the supernatant.

87 Add  **70 µl AMPure buffer** and  **50 µl water** per well of a deepwell plate.

88 Transfer sample, containing beads, to the deepwell plate containing AMPure buffer and water. Mix thoroughly then incubate at room temperature  **00:10:00**

89 Place plate on magnet and wait until beads pellet.

- 90 Remove supernatant.
- 91 Wash twice with 80% ethanol.
- 92 Remove supernatant. Air dry 🔥 50 °C ⌚ 00:05:00

- 93 Resuspend beads in 📄 48 µl PCR master mix:

| Reagent | amount per sample | 96 well plate(x120) |
|-------------------------|-------------------|---------------------|
| Water | 22 | 2640 |
| KAPA Hifi readymix (2x) | 25 | 3000 |
| PE1.0 (10uM) | 1 | 120 |
| Total | 48 | 5760 |



PE1.0: AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC*T (IDT, HPLC)
This primer contains the full Illumina P5 and PE read 1 sequences.

- 94 Add 📄 2 µl iTAG indexing primer (5uM)



We prepare iTAG primers in 96w plates for this step.
iPCRTag: CAAGCAGAAGACGGCATACGAGATXXXXXXXXXGAGATCGGTCTCGGCATT CCTGCTGAACCGCTCTTCCGATC*T
(IDT, HPLC, XXXXXXXX = 8nt index)
This primer contains the full Illumina P7 sequence, followed by an index, followed by the Illumina PE read 2 sequence.

- 95 Transfer samples to fresh 96w PCR plate.

Library amplification

- 96 Cycle as follows:
🔥 95 °C ⌚ 00:02:00
14 cycles of:
🔥 94 °C ⌚ 00:01:20
🔥 65 °C ⌚ 00:00:30
🔥 72 °C ⌚ 00:00:30
Followed by:
🔥 72 °C ⌚ 00:05:00
🔥 4 °C hold.

Library purification

- 97 All subsequent steps are performed outside of pre-PCR room.

98 Make 2 pools of 48 libraries (5ul each) in 1.5ml tubes.



The number of samples per pool depends on the number of indexes used. e.g. we typically use only 48 indexes and so make two pools of 48 samples each.

99 Purify each pool with **168 µl AMPure XP beads** (i.e. 0.7x ratio), 2x 80% ethanol washes and elute in **100 µl water**.

100 Purify each pool a second time **70 µl AMPure XP beads** (i.e. 0.7x ratio), 2x 80% ethanol washes and elute in **100 µl water**.

101 QC using a Bioanalyser high sensitivity chip.



Pooled and purified scBS libraries should have a fragment length of 300-1000bp (average 450-500). Pools containing smaller fragments (especially <200bp) will result in poor alignment rates due to the presence of adapter concatemers. These should be subjected to an additional 0.7x AMPure XP purification.



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