

LIBRARY PREPARATION

NEBNext® Multiplex Oligos for Illumina® (96 Index Primers)

Instruction Manual

NEB #E6609S/L
96/384 reactions
Version 1.3 6/16





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The NEBNext Multiplex Oligos for Illumina (96 Index Primers) Includes:

The volumes provided are sufficient for preparation of up to 96 reactions (NEB #E6609S) and 384 reactions (NEB #E6609L). All reagents should be stored at –20°C.

NEBNext Adaptor for Illumina

USER Enzyme

NEBNext Index/Universal Primer Mix Plate

Each well contains the Universal PCR Primer plus one of the Index Primers

Required Materials Not Included:

Enzymes and buffers appropriate for DNA, ChIP or mRNA Library Preparation (NEB #E7645, E7595, E7420, E7530, E7370, E7445, E6040, E6110, E6240, E6056, E6000, E6200, E6100)

SPRIselect or AMPure® XP Beads (Beckman Coulter, Inc.)

DNA LoBind® Tubes (Eppendorf®)/PCR Plates

Magnetic Stand

Bioanalyzer® (Agilent Technologies, Inc.)

Freshly Prepared 80% Ethanol

Applications:

The NEBNext Multiplex Oligos for Illumina (96 Index Primers) contains adaptors and primers that are ideally suited for multiplex sample preparation for next-generation sequencing on the Illumina platform (Illumina, Inc.). Each of these components must pass rigorous quality control standards and is lot controlled, both individually and as a set of reagents.

Lot Control: The lots provided in the NEBNext Multiplex Oligos for Illumina (96 Index Primers) are managed separately and are qualified by additional functional validation. Individual reagents undergo standard enzyme activity and quality control assays, and also meet stringent criteria in the additional quality controls listed on each individual component page.

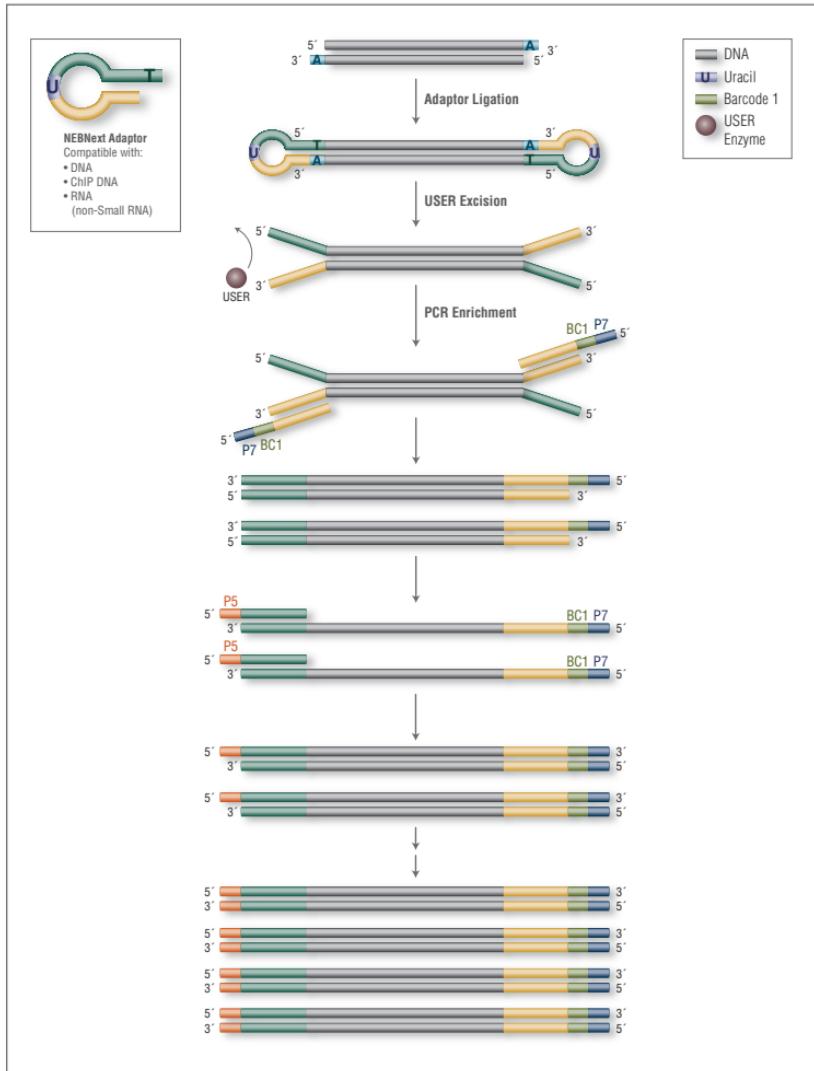
Functionally Validated: Each set of reagents is functionally validated together through construction and sequencing of genomic DNA libraries on the Illumina platform.

For larger volume requirements, customized and bulk packaging is available by purchasing through the OEM/Bulks department at NEB. Please contact OEM@neb.com for further information.

Workflow Overview:

Designed for use in library prep for DNA, ChIP DNA and RNA (but not Small RNA), the NEBNext Adaptors enable high-efficiency adaptor ligation and high library yields, with minimized adaptor-dimer formation. Incorporating a novel hairpin loop structure, the NEBNext Adaptor ligates with increased efficiency to end-repaired, dA-tailed DNA. The loop contains a U, which is removed by treatment with USER Enzyme (a combination of UDG and Endo VIII), to open up the loop and make it available as a substrate for PCR. During PCR, barcodes can be incorporated by use of the NEBNext index primers, thereby enabling multiplexing. The 96 8-base index primers included in this kit are pre-mixed with the universal primer and are packaged in a single-use 96-well plate with a pierceable foil seal. NEBNext Oligos can be used with NEBNext products, and with other standard Illumina-compatible library preparation protocols.

Figure 1: Workflow demonstrating the use of NEBNext Multiplex Oligos for Illumina (96 Index Primers)



Please Refer to the Kit Specific Protocol for using the NEBNext Multiplex Oligos for Illumina:

The following kits are designed for use with the NEBNext Multiplex Oligos for Illumina:

- #E7645, NEBNext Ultra II DNA Library Prep Kit for Illumina
- #E7595, NEBNext Ultra II Ligation Module
- #E7420, NEBNext Ultra Directional RNA Library Prep Kit for Illumina
- #E7530, NEBNext Ultra RNA Library Prep Kit for Illumina
- #E7370, NEBNext Ultra DNA Library Prep Kit for Illumina
- #E7445, NEBNext Ultra Ligation Module
- #E6040, NEBNext DNA Library Prep Master Mix Set for Illumina
- #E6110, NEBNext mRNA Library Prep Master Mix Set for Illumina
- #E6240, NEBNext ChIP-Seq Library Prep Master Mix Set for Illumina
- #E6056, NEBNext Quick Ligation Module
- #E6000, NEBNext DNA Library Prep Reagent Set for Illumina
- #E6200, NEBNext ChIP-Seq Library Prep Reagent Set for Illumina
- #E6100, NEBNext mRNA Library Prep Reagent Set for Illumina

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Setting up the PCR Reaction

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Symbols



This caution sign signifies a step in the protocol that has multiple paths leading to the same end point but is dependent on a user variable, like the amount of input DNA.

1.1. PCR Amplification



For < 96 samples, follow the protocol in Section 1.1A. For 96 samples, follow the protocol in Section 1.1B.

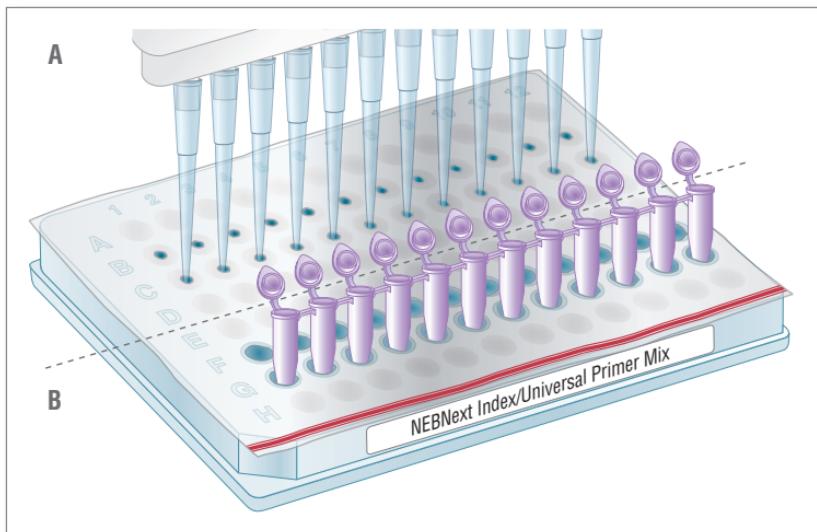
1.1A. Setting up the PCR reactions (< 96 samples)

- 1.1A.1. Determine the number of libraries that will be amplified and pooled for subsequent sequencing.
- 1.1A.2. Ensure that you choose a valid combination of barcode primers based on color balance guidelines in Chapter 2.
- 1.1A.3. Thaw the NEBNext Index/Universal Primer Mix plate for 10-15 minutes at room temperature.
- 1.1A.4. Remove the hard plastic plate cover. Briefly centrifuge the plate (280 ×g for ~1 min) to collect all of the primer at the bottom of each well.
- 1.1A.5. Orient the NEBNext Index/Universal Primer Mix Plate as indicated in Figure 1.1 (red stripe towards the user). With a pipette tip, pierce the desired well(s) (Figure 1.1A) and transfer the volume of primer mix required for the PCR reaction to the PCR plate/tubes (see specific library construction manual for protocol). It is important to change pipette tips before piercing a new well to avoid cross contamination of indexed primers. Alternatively, the wells can be pierced using the bottom of clean PCR strip tubes (see Figure 1.1B) prior to pipetting the primer mix. Use a new, clean strip tube for each new well to be pierced.

Note: Each well contains the Universal Primer and the Index Primer. There is enough primer in each well for one PCR reaction. Do not reuse primer if the seal has been previously pierced to avoid contamination with other indexed primers.

- 1.1A.6. Proceed with the PCR reaction according to the specific library construction manual.

Figure 1.1: NEBNext Index/Universal Primer Mix plate.



1.1B. Setting up the PCR reactions (96 samples)

- 1.1B.1. Thaw the NEBNext Index/Universal Primer Mix plate for 10-15 minutes at room temperature.
- 1.1B.2. Remove the hard plastic plate cover. Briefly centrifuge the plate ($280 \times g$ for ~1 min) to collect all of the primer at the bottom of each well.
- 1.1B.3. Orient the NEBNext Index/Universal Primer Plate as indicated in Figure 1.1 (red stripe towards the user). With a pipette tip, pierce the wells (Figure 1.1A) and transfer the volume of primer mix required for the PCR reaction to the PCR plate (see specific library construction manual for protocol). It is important to change pipette tips before piercing a new well to avoid cross contamination of indexed primers. Alternatively, the wells can be pierced using the bottom of clean PCR strip tubes (see Figure 1.1B) prior to pipetting the primer mix. Use a new, clean strip tube for each new well to be pierced.

Note: Each well contains the Universal Primer and the Index Primer. There is enough primer in each well for one PCR reaction. Do not reuse primer if the seal has been previously pierced to avoid contamination with other indexed primers.

- 1.1B.4. Proceed with the PCR reaction according to the specific library construction manual.

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Index Pooling Guidelines

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For a link to download a sample sheet with the index sequences for use with the Illumina Experiment Manager (IEM) please go to our FAQ's tab on www.neb.com/E6609 – NEBNext Multiplex Oligos for Illumina (96 Index Primers) (NEB #E6609).

For the HiSeq®/MiSeq®, Illumina uses a red laser/LED to sequence bases A and C and a green laser/LED to sequence bases G and T. For each cycle, both the red and the green channel need to be read to ensure proper image registration (i.e. A or C must be in each cycle, and G or T must be in each cycle). If this color balance is not maintained, sequencing the index read could fail. Table 2.1 lists some valid combinations (up to 4-plex) that can be sequenced together. For combinations > 4 choose any 4-plex combination and add any other index as needed.

Table 2.1

PLEX	INDEX PRIMER
2	P18-B6 and P22-B10 P37-D1 and P42-D6 P52-E4 and P76-G4 P68-F8 and P95-H11
3	P4-A4, P11-A11, and P12-A12 P15-B3, P22-B10, and, P24-B12 P25-C1, P31-C7, and P33-C9 P37-D1, P42-D6, and, P48-D12 P49-E1, P54-E6, and, P55-E7 P64-F4, P69-F9, and P71-F11 P76-G4, P77-G5, and P83-G11 P87-H3, P93-H9, and P94-H10

Table 2.1 (continued)

PLEX	INDEX PRIMER
4	P1-A1, P2-A2, P3-A3, and P4-A4
	P5-A5, P6-A6, P8-A8, and P10-A10
	P13-B1, P14-B2, P15-B3, and P16-B4
	P17-B5, P18-B6, P19-B7, and P20-B8
	P25-C1, P26-C2, P27-C3, and P30-C6
	P28-C4, P29-C5, P32-C8, and P35-C11
	P37-D1, P38-D2, P39-D3, and P40-D4
	P45-D9, P46-D10, P47-D11, and P48-D12
	P49-E1, P50-E2, P51-E3, and P52-E4
	P56-E8, P58-E10, P59-E11, and P60-E12
	P61-F1, P62-F2, P63-F3, and P69-F9
	P64-F4, P65-F5, P66-F6, and P67-F7
	P73-G1, P74-G2, P75-G3, and P76-G4
	P80-G8, P82-G10, P83-G11, and P84-G12
	P85-H1, P86-H2, P87-H3, and P89-H5
	P91-H7, P94-H10, P95-H11, and P96-H12

Table 2.2 lists each index sequence color coded to correspond to the red/green channel. For combinations of valid indices, ensure that you will have signal in both the red and green channels in each cycle. See examples below:

GOOD									
PRIMER	INDEX SEQUENCE				PRIMER	INDEX SEQUENCE			
P1-A1	T	T	A	C	C	G	A	C	
P2-A2	A	G	T	G	A	C	C	T	
P3-A3	T	C	G	G	A	T	T	C	
P4-A4	C	A	A	G	G	T	A	C	
	✓	✓	✓	✓	✓	✓	✓	✓	

BAD									
PRIMER	INDEX SEQUENCE				PRIMER	INDEX SEQUENCE			
P9-A9	C	G	C	A	A	C	T	A	
P10-A10	C	G	T	A	T	C	T	C	
P11-A11	G	T	A	C	A	C	C	T	
P12-A12	C	G	G	C	A	T	T	A	
	✓	✗	✓	✗	✓	✓	✓	✓	

Table 2.2 Index Sequences

INDEX PRIMER	INDEX SEQUENCE READ							
P1-A1	T	T	A	C	C	G	A	C
P2-A2	A	G	T	G	A	C	C	T
P3-A3	T	C	G	G	A	T	T	C
P4-A4	C	A	A	G	G	T	A	C
P5-A5	T	C	C	T	C	A	T	G
P6-A6	G	T	C	A	G	T	C	A
P7-A7	C	G	A	A	T	A	C	G
P8-A8	T	C	T	A	G	G	A	G
P9-A9	C	G	C	A	A	C	T	A
P10-A10	C	G	T	A	T	C	T	C
P11-A11	G	T	A	C	A	C	C	T
P12-A12	C	G	G	C	A	T	T	A
P13-B1	T	C	G	T	C	T	G	A
P14-B2	A	G	C	C	T	A	T	C
P15-B3	C	T	G	T	A	C	C	A
P16-B4	A	G	A	C	C	T	T	G
P17-B5	A	G	G	A	T	A	G	C
P18-B6	C	C	T	T	C	C	A	T
P19-B7	G	T	C	C	T	T	G	A
P20-B8	T	G	C	G	T	A	A	C
P21-B9	C	A	C	A	G	A	C	T
P22-B10	T	T	A	C	G	T	G	C
P23-B11	C	C	A	A	G	G	T	T
P24-B12	C	A	C	G	C	A	A	T
P25-C1	T	T	C	C	A	G	G	T
P26-C2	T	C	A	T	C	T	C	C
P27-C3	G	A	G	A	G	T	A	C
P28-C4	G	T	C	G	T	T	A	C
P29-C5	G	G	A	G	G	A	A	T
P30-C6	A	G	G	A	A	C	A	C
P31-C7	C	A	G	T	G	C	T	T
P32-C8	C	T	T	G	C	T	A	G

INDEX PRIMER	INDEX SEQUENCE READ							
P33-C9	T	G	G	A	A	G	C	A
P34-C10	A	G	C	T	A	A	G	C
P35-C11	G	A	A	C	G	G	T	T
P36-C12	G	G	A	A	T	G	T	C
P37-D1	T	A	C	G	G	T	C	T
P38-D2	C	C	A	G	T	A	T	C
P39-D3	T	C	T	A	C	G	C	A
P40-D4	G	T	A	A	C	C	G	A
P41-D5	G	A	C	G	T	C	A	T
P42-D6	C	T	T	A	C	A	G	C
P43-D7	T	C	C	A	T	T	G	C
P44-D8	A	G	C	G	A	G	A	T
P45-D9	C	A	A	T	A	G	C	C
P46-D10	A	A	G	A	C	A	C	C
P47-D11	C	C	A	G	T	T	G	A
P48-D12	T	G	G	T	G	A	A	G
P49-E1	A	A	G	A	C	C	G	T
P50-E2	T	T	G	C	G	A	G	A
P51-E3	G	C	A	A	T	T	C	C
P52-E4	G	A	A	T	C	C	G	T
P53-E5	C	C	G	C	T	T	A	A
P54-E6	T	A	C	C	T	G	C	A
P55-E7	G	T	C	G	A	T	T	G
P56-E8	T	A	T	G	G	C	A	C
P57-E9	C	T	C	G	A	A	C	A
P58-E10	C	A	A	C	T	C	C	A
P59-E11	G	T	C	A	T	C	G	T
P60-E12	G	G	A	C	A	T	C	A
P61-F1	C	A	G	G	T	T	C	A
P62-F2	G	A	A	C	G	A	A	G
P63-F3	C	T	C	A	G	A	A	G
P64-F4	C	A	T	G	A	G	C	A

INDEX PRIMER	INDEX SEQUENCE READ								
P65-F5	G	A	C	G	A	A	C	T	
P66-F6	A	G	A	C	G	C	T	A	
P67-F7	A	T	A	A	C	G	C	C	
P68-F8	G	A	A	T	C	A	C	C	
P69-F9	G	G	C	A	A	G	T	T	
P70-F10	G	A	T	C	T	T	G	C	
P71-F11	C	A	A	T	G	C	G	A	
P72-F12	G	G	T	G	T	A	C	A	
P73-G1	T	A	G	G	A	G	C	T	
P74-G2	C	G	A	A	T	T	G	C	
P75-G3	G	T	C	C	T	A	A	G	
P76-G4	C	T	T	A	G	G	A	C	
P77-G5	T	C	C	A	C	G	T	T	
P78-G6	C	A	A	C	A	C	A	G	
P79-G7	G	C	C	T	T	A	A	C	
P80-G8	G	T	A	A	G	G	T	G	
P81-G9	A	G	C	T	A	C	C	A	
P82-G10	C	T	T	C	A	C	T	G	
P83-G11	G	G	T	T	G	A	A	C	
P84-G12	G	A	T	A	G	C	C	A	
P85-H1	T	A	C	T	C	C	A	G	
P86-H2	G	G	A	A	G	A	G	A	
P87-H3	G	C	G	T	T	A	G	A	
P88-H4	A	T	C	T	G	A	C	C	
P89-H5	A	A	C	C	A	G	A	G	
P90-H6	G	T	A	C	C	A	C	A	
P91-H7	G	G	T	A	T	A	G	G	
P92-H8	C	G	A	G	A	G	A	A	
P93-H9	C	A	G	C	A	T	A	C	
P94-H10	C	T	C	G	A	C	T	T	
P95-H11	C	T	T	C	G	G	T	T	
P96-H12	C	C	A	C	A	A	C	A	

NEBNext Adaptor for Illumina

#E6612A: 0.96 ml

Concentration: 15 μ M

Note: Large kit contains 4 x 0.96 ml

5'-/5'Phos/GAT CGG AAG AGC ACA CGT CTG AAC TCC AGT C/ideoxyU/A CAC TCT TTC CCT ACA CGA CGC TCT TCC GAT C-s-T-3'

Where -s- indicates phosphorothioate bond.

Store at -20°C

Quality Control Assays

16-Hour Incubation: 50 μ l reactions containing this adaptor and 1 μ g of HindIII digested Lambda DNA incubated for 16 hours at 37°C results in no detectable non-specific nuclease degradation as determined by agarose gel electrophoresis. 50 μ l reactions containing this reaction buffer at 1X concentration and 1 μ g T3 DNA incubated for 16 hours at 37°C also results in no detectable non-specific nuclease degradation as determined by agarose gel electrophoresis.

Endonuclease Activity: Incubation of a minimum of 5 μ l of this adaptor with 1 μ g of ϕ X174 RF 1 DNA in assay buffer for 4 hours at 37°C in 50 μ l reactions results in < 10% conversion to RF II as determined by agarose gel electrophoresis.

Phosphatase Activity: Incubation of a minimum of 10 μ l of this adaptor in protein phosphatase assay buffer (1 M diethanolamine @ pH 9.8 and 0.5 mM MgCl₂) containing 2.5 mM *p*-nitrophenyl phosphate at 37°C for 4 hours yields no detectable *p*-nitrophenylene anion as determined by spectrophotometric analysis at 405 nm.

RNase Activity: Incubation of this adaptor with 40 ng of a FAM-labeled RNA transcript for 16 hours at 37°C results in no detectable RNase activity as determined by polyacrylamide gel electrophoresis.

Lot Controlled

USER Enzyme

#E6610A: 0.288 ml

#E6610AA: 0.576 ml

(2 vials)

Store at -20°C

Supplied in: 50 mM KCl, 5 mM NaCl, 10 mM Tris-HCl (pH 7.4 @ 25°C), 0.1 mM EDTA, 1 mM DTT, 175 µg/ml BSA and 50% Glycerol

Quality Control Assays

Non-Specific DNase Activity (16 Hour): A 50 µl reaction in NEBuffer 1 containing 1 µg of Lambda DNA and a minimum of 50 units of Uracil DNA Glycosylase incubated for 16 hours at 37°C results in a DNA pattern free of detectable nuclease degradation as determined by agarose gel electrophoresis. A 50 µl reaction in Endonuclease VIII Reaction Buffer containing 1 µg of Lambda-HindIII DNA and a minimum of 25 units of Endonuclease VIII incubated for 16 hours at 37°C results in a DNA pattern free of detectable nuclease degradation as determined by agarose gel electrophoresis.

Exonuclease Activity (Radioactivity Release): A 50 µl reaction in NEBuffer 1 containing 1 µg of a mixture of single and double-stranded [³H] *E. coli* DNA and a minimum of 50 units of Uracil DNA Glycosylase incubated for 4 hours at 37°C releases < 0.1% of the total radioactivity. A 50 µl reaction in Endonuclease VIII Reaction Buffer containing 1 µg of a mixture of single and double-stranded [³H] *E. coli* DNA and a minimum of 10 units of Endonuclease VIII incubated for 4 hours at 37°C releases < 0.5% of the total radioactivity.

Endonuclease Activity (Nicking): A 50 µl reaction in UDG Reaction Buffer containing 1 µg of supercoiled φX174 DNA and a minimum of 50 units of Uracil DNA Glycosylase incubated for 4 hours at 37°C results in < 10% conversion to the nicked form as determined by agarose gel electrophoresis.

Phosphatase Activity: Incubation of a minimum of 10 µl of USER at a 1X concentration in protein phosphatase assay buffer (1 M diethanolamine @ pH 9.8 and 0.5 mM MgCl₂) containing 2.5 mM *p*-nitrophenyl phosphate at 37°C for 4 hours yields no detectable *p*-nitrophenylene anion as determined by spectrophotometric analysis at 405 nm.

Lot Controlled

NEBNext Index/Universal Primer Mix

#E6611A: 1 plate (10 µl/well)

Concentration: 5 µM each primer

Note: Large kit contains 4 plates (10 µl/well).

Description: 96 Index Primers & the Universal Primer are included for producing barcoded libraries.

NEBNext Universal PCR Primer for Illumina:

5'-AAT GAT ACG GCG ACC ACC GAG ATC TAC ACT CTT TCC CTA CAC GAC GCT CTT CCG ATC-s-T-3'

Store at -20°C

Where -s- indicates phosphorothioate bond.

INDEX PRIMER	INDEX PRIMER SEQUENCE	EXPECTED INDEX SEQUENCE READ
P1-A1	5'-CAAGCAGAACGGCATACGAGAT <u>TCGGTAA</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TTACCGAC
P2-A2	5'-CAAGCAGAACGGCATACGAGAT <u>AGGTCACT</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	AGTGACCT
P3-A3	5'-CAAGCAGAACGGCATACGAGAT <u>GAATCCGA</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TCGGATT
P4-A4	5'-CAAGCAGAACGGCATACGAGAT <u>TACCTTG</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAAGGTAC
P5-A5	5'-CAAGCAGAACGGCATACGAGAT <u>CATGAGGA</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TCCTCATG
P6-A6	5'-CAAGCAGAACGGCATACGAGAT <u>TACTGAC</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	GTCAGTCA
P7-A7	5'-CAAGCAGAACGGCATACGAGAT <u>CGTATTG</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CGAATACG
P8-A8	5'-CAAGCAGAACGGCATACGAGAT <u>TCCTAGA</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TCTAGGAG
P9-A9	5'-CAAGCAGAACGGCATACGAGAT <u>TAGTTGCC</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CGCAACTA
P10-A10	5'-CAAGCAGAACGGCATACGAGAT <u>GAGATACG</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CGTATCTC
P11-A11	5'-CAAGCAGAACGGCATACGAGAT <u>AGGTGTAC</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	GTACACCT
P12-A12	5'-CAAGCAGAACGGCATACGAGAT <u>TAATGCC</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CGGCATTA
P13-B1	5'-CAAGCAGAACGGCATACGAGAT <u>TCAGACGAG</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TCGTCTGA
P14-B2	5'-CAAGCAGAACGGCATACGAGAT <u>GATAAGGCT</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGCCTATC
P15-B3	5'-CAAGCAGAACGGCATACGAGAT <u>GGTACAGG</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CTGTACCA
P16-B4	5'-CAAGCAGAACGGCATACGAGAT <u>CAAGGTCT</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	AGACCTTG
P17-B5	5'-CAAGCAGAACGGCATACGAGAT <u>GCTATCCT</u> GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGGATAGC
P18-B6	5'-CAAGCAGAACGGCATACGAGAT <u>ATGGAAGGGT</u> GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CCTTCCAT

NEBNext Index/Universal Primer Mix (Cont.)

INDEX PRIMER	INDEX PRIMER SEQUENCE	EXPECTED INDEX SEQUENCE READ
P19-B7	5'-CAAGCAGAAGACGGCATACGAGAT TCAAGGAC GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	GTCCTTGA
P20-B8	5'-CAAGCAGAAGACGGCATACGAGAT TTTACGCA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TGCGTAAC
P21-B9	5'-CAAGCAGAAGACGGCATACGAGAT AGTCTGTG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CACAGACT
P22-B10	5'-CAAGCAGAAGACGGCATACGAGAT GCACGTAA GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TTACGTGC
P23-B11	5'-CAAGCAGAAGACGGCATACGAGAT ACCTTGG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CCAAGGTT
P24-B12	5'-CAAGCAGAAGACGGCATACGAGAT ATTGCGTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CACGCAAT
P25-C1	5'-CAAGCAGAAGACGGCATACGAGAT ACCTGGAA GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TTCCAGGT
P26-C2	5'-CAAGCAGAAGACGGCATACGAGAT GGAGATGAG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TCATCTCC
P27-C3	5'-CAAGCAGAAGACGGCATACGAGAT GTACTCTC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GAGAGTAC
P28-C4	5'-CAAGCAGAAGACGGCATACGAGAT GTAAACGAC GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	GTCGTTAC
P29-C5	5'-CAAGCAGAAGACGGCATACGAGAT ATTCCTCC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGAGGAAT
P30-C6	5'-CAAGCAGAAGACGGCATACGAGAT GTGTT CCT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGGAACAC
P31-C7	5'-CAAGCAGAAGACGGCATACGAGAT AAGCACTG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CAGTGCTT
P32-C8	5'-CAAGCAGAAGACGGCATACGAGAT CTAGCAAG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CTTGCTAG
P33-C9	5'-CAAGCAGAAGACGGCATACGAGAT TGCTTCCA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TGGAAGCA
P34-C10	5'-CAAGCAGAAGACGGCATACGAGAT GCTTAGCT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGCTAACG
P35-C11	5'-CAAGCAGAAGACGGCATACGAGAT AACC GTTC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GAACGGTT
P36-C12	5'-CAAGCAGAAGACGGCATACGAGAT GACATTCC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGAATGTC
P37-D1	5'-CAAGCAGAAGACGGCATACGAGAT AGACCGTAGT GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TACGGTCT
P38-D2	5'-CAAGCAGAAGACGGCATACGAGAT GATACTGG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CCAGTATC

INDEX PRIMER	INDEX PRIMER SEQUENCE	EXPECTED INDEX SEQUENCE READ
P39-D3	5'-CAAGCAGAAGACGGCATACGAGAT TGCGTAGA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TCTACGCA
P40-D4	5'-CAAGCAGAAGACGGCATACGAGAT TGGTTAC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GTAACCGA
P41-D5	5'-CAAGCAGAAGACGGCATACGAGAT ATGACGTC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GACGTCAT
P42-D6	5'-CAAGCAGAAGACGGCATACGAGAT GCTGTAAG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CTTACAGC
P43-D7	5'-CAAGCAGAAGACGGCATACGAGAT GCAATGGA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TCCATTGC
P44-D8	5'-CAAGCAGAAGACGGCATACGAGAT ATCTCGCT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGCGAGAT
P45-D9	5'-CAAGCAGAAGACGGCATACGAGAT GGCTATTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAATAGCC
P46-D10	5'-CAAGCAGAAGACGGCATACGAGAT GGTGTCTT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AAGACACC
P47-D11	5'-CAAGCAGAAGACGGCATACGAGAT TCAACTGG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CCAGTTGA
P48-D12	5'-CAAGCAGAAGACGGCATACGAGAT CTTCACCA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TGGTGAAG
P49-E1	5'-CAAGCAGAAGACGGCATACGAGAT ACGGTCTT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AAGACCGT
P50-E2	5'-CAAGCAGAAGACGGCATACGAGAT TCTCGCAA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TTGCGAGA
P51-E3	5'-CAAGCAGAAGACGGCATACGAGAT GGAATTGC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GCAATTCC
P52-E4	5'-CAAGCAGAAGACGGCATACGAGAT ACGGATTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GAATCCGT
P53-E5	5'-CAAGCAGAAGACGGCATACGAGAT TTAACCGG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CCGCTTAA
P54-E6	5'-CAAGCAGAAGACGGCATACGAGAT TGCAGGTA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TACCTGCA
P55-E7	5'-CAAGCAGAAGACGGCATACGAGAT CAATCGAC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GTCGATTG
P56-E8	5'-CAAGCAGAAGACGGCATACGAGAT TGCCATA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TATGGCAC
P57-E9	5'-CAAGCAGAAGACGGCATACGAGAT TGTTCGAG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CTCGAACAA
P58-E10	5'-CAAGCAGAAGACGGCATACGAGAT TGGAGTTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAACTCCA

NEBNext Index/Universal Primer Mix (Cont.)

INDEX PRIMER	INDEX PRIMER SEQUENCE	EXPECTED INDEX SEQUENCE READ
P59-E11	5'-CAAGCAGAAGACGGCATACGAGAT ACGATGAC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GTCATCGT
P60-E12	5'-CAAGCAGAAGACGGCATACGAGAT TGATGTCC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGACATCA
P61-F1	5'-CAAGCAGAAGACGGCATACGAGAT TGAACCTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAGGTTCA
P62-F2	5'-CAAGCAGAAGACGGCATACGAGAT CTTCGTTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GAACGAAG
P63-F3	5'-CAAGCAGAAGACGGCATACGAGAT CTTCTGAGG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CTCAGAAG
P64-F4	5'-CAAGCAGAAGACGGCATACGAGAT TGCTCATG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CATGAGCA
P65-F5	5'-CAAGCAGAAGACGGCATACGAGAT AGTCGTC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GACGAACT
P66-F6	5'-CAAGCAGAAGACGGCATACGAGAT TAGCGTCT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGACGCTA
P67-F7	5'-CAAGCAGAAGACGGCATACGAGAT GCGCTTAT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	ATAACGCC
P68-F8	5'-CAAGCAGAAGACGGCATACGAGAT GGTGATTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GAATCACC
P69-F9	5'-CAAGCAGAAGACGGCATACGAGAT AACTTGCC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGCAAGTT
P70-F10	5'-CAAGCAGAAGACGGCATACGAGAT GCAAGATC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GATCTTC
P71-F11	5'-CAAGCAGAAGACGGCATACGAGAT ICCGATTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAATCGCA
P72-F12	5'-CAAGCAGAAGACGGCATACGAGAT TGTACACCC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGTGTACA
P73-G1	5'-CAAGCAGAAGACGGCATACGAGAT ACCTCCTA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TAGGAGCT
P74-G2	5'-CAAGCAGAAGACGGCATACGAGAT GCAATTCG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CGAATTGC
P75-G3	5'-CAAGCAGAAGACGGCATACGAGAT CTTAGGAC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GTCCTAAG
P76-G4	5'-CAAGCAGAAGACGGCATACGAGAT GTCCTAAGG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CTTAGGAC
P77-G5	5'-CAAGCAGAAGACGGCATACGAGAT AACGTGGA GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	TCCACGTT
P78-G6	5'-CAAGCAGAAGACGGCATACGAGAT CTGTGTTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAACACAG

INDEX PRIMER	INDEX PRIMER SEQUENCE	EXPECTED INDEX SEQUENCE READ
P79-G7	5'-CAAGCAGAAGACGGCATACGAGAT TTAAGGC GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	GCCTAAC
P80-G8	5'-CAAGCAGAAGACGGCATACGAGAT CACCTAC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GTAAGGTG
P81-G9	5'-CAAGCAGAAGACGGCATACGAGAT TGGTAGCT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AGCTACCA
P82-G10	5'-CAAGCAGAAGACGGCATACGAGAT CACTGAAG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CTTCACTG
P83-G11	5'-CAAGCAGAAGACGGCATACGAGAT TTCAACCG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGTTGAAC
P84-G12	5'-CAAGCAGAAGACGGCATACGAGAT TGGCTATC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GATAGCCA
P85-H1	5'-CAAGCAGAAGACGGCATACGAGAT CTGGAGTA GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	TACTCCAG
P86-H2	5'-CAAGCAGAAGACGGCATACGAGAT TCTCTCC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGAAGAGA
P87-H3	5'-CAAGCAGAAGACGGCATACGAGAT TCTAACCG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GCGTTAGA
P88-H4	5'-CAAGCAGAAGACGGCATACGAGAT GTCAGAT GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	ATCTGACC
P89-H5	5'-CAAGCAGAAGACGGCATACGAGAT CTCTGGT GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	AACCAGAG
P90-H6	5'-CAAGCAGAAGACGGCATACGAGAT TGTGGTAC GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GTACCACA
P91-H7	5'-CAAGCAGAAGACGGCATACGAGAT CTATAACCG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	GGTATAGG
P92-H8	5'-CAAGCAGAAGACGGCATACGAGAT TTCTCTCG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CGAGAGAA
P93-H9	5'-CAAGCAGAAGACGGCATACGAGAT GTATGCTG GTGACTGGAGTTCA ACGTGTGCTTCCGATC-s-T-3'	CAGCATAAC
P94-H10	5'-CAAGCAGAAGACGGCATACGAGAT AAGTCGAGGT GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CTCGACTT
P95-H11	5'-CAAGCAGAAGACGGCATACGAGAT AACCGAAG GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CTTCGGTT
P96-H12	5'-CAAGCAGAAGACGGCATACGAGAT TGTTGTGGT GTGACTGGAGTTCA GACGTGTGCTTCCGATC-s-T-3'	CCACAACA

Quality Control Assays

16-Hour Incubation: 50 µl reactions containing 1 µl NEBNext Index/Universal Primer Mix and 1 µg of HindIII digested Lambda DNA incubated for 16 hours at 37°C results in no detectable non-specific nuclease degradation as determined by agarose gel electrophoresis. 50 µl reactions containing NEBNext Index/Universal Primer Mix for Illumina and 1 µg of T3 DNA incubated for 16 hours at 37°C results in no detectable non-specific nuclease degradation as determined by agarose gel electrophoresis.

Endonuclease Activity: Incubation of a 50 µl reaction containing 1 µl NEBNext Index/Universal Primer Mix with 1 µg of φX174 RF I supercoiled DNA for 4 hours at 37°C results in less than 10% conversion to RF II (nicked molecules) as determined by agarose gel electrophoresis.

RNase Activity: Incubation of a 10 µl reaction containing 1 µl NEBNext Index/Universal Primer Mix with 40 ng of RNA transcript for 16 hours at 37°C resulted in no detectable degradation of RNA as determined by gel electrophoresis.

Phosphatase Activity: Incubation of NEBNext Index/Universal Primer Mix in protein phosphatase assay buffer (1 M diethanolamine @ pH 9.8 and 0.5 mM MgCl₂) containing 2.5 mM *p*-nitrophenyl phosphate at 37°C for 4 hours yields no detectable *p*-nitrophenylene anion as determined by spectrophotometric analysis at 405 nm.

Lot Controlled

Revision History:

REVISION #	DESCRIPTION	DATE
1.0	N/A	3/16
1.1	Corrected note on page 6 and 7 from "Do not use reuse primer if the seal has been previously pierced to avoid contamination with other indexed primers." to "Do not reuse primer if the seal has been previously pierced to avoid contamination with other indexed primers."	4/16
1.2	Updated Figure 1.1 page 7.	5/16
1.3	Clarified primer concentration. Corrected primer sequences 5' end.	6/16

DNA CLONING
DNA AMPLIFICATION & PCR
EPIGENETICS
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LIBRARY PREP FOR NEXT GEN SEQUENCING
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