Illumina Adapter Sequences

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Introduction

This document lists the index adapter sequences for Illumina library prep kits. The sequences are grouped into sections for AmpliSeq for Illumina, TruSight kits, Nextera kits, and TruSeq kits. An appendix lists TruSeq controls and information for legacy Illumina kits.

The dual-indexing workflow on the following systems requires the reverse complement of the Index 2 (i5) adapter sequence: iSeq 100, MiniSeq, NextSeq 550, NextSeq 500, HiSeq 4000, and HiSeq 3000.

- If you are manually creating a sample sheet for these systems, include the reverse complement of the sequence.
- If you are using Illumina Experiment Manager (IEM), BaseSpace Sequence Hub Prep tab, or Local Run Manager to record the adapter sequences, the software automatically creates the reverse complement.

AmpliSeq for Illumina Panels

AmpliSeq Comprehensive Cancer Panel for Illumina, AmpliSeq Cancer HotSpot Panel v2 for Illumina, AmpliSeq Focus Panel for Illumina, AmpliSeq Comprehensive Panel v3 for Illumina, AmpliSeq BRCA Panel for Illumina, AmpliSeq Immune Response Panel for Illumina, AmpliSeq Transcriptome Human Gene Expression Panel for Illumina, AmpliSeq Exome Panel for Illumina, AmpliSeq Custom DNA Panel for Illumina.

These combinatorial dual index adapters have been arranged in the plate to enforce the recommended pairing strategy.

Index 1 (i7) Adapters

`CAAGCAGAAGACGGCATACGAGAT[i7]GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG`

Index 2 (i5) Adapters

`AATGATACGGCGACCACCGAGATCTACAC[i5]TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG`

Adapter Trimming

The following sequence is needed for adapter trimming.

`CTGTCTCTTATACACATCT`

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
Q7005	GTGAATAT
Q7006	ACAGGCGC
Q7007	CATAGAGT
Q7008	TGCGAGAC
Q7015	TCTCTACT
Q7016	CTCTCGTC
Q7017	CCAAGTCT

i7 Index Name	i7 Bases for Sample Sheet
Q7018	TTGGACTC
Q7023	GCAGAATT
Q7024	ATGAGGCC
Q7025	ACTAAGAT
Q7026	GTCGGAGC

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, HiSeq 3000/4000, MiniSeq, NextSeq
Q5001	AGCGCTAG	CTAGCGCT
Q5002	GATATCGA	TCGATATC
Q5007	ACATAGCG	CGCTATGT
Q5008	GTGCGATA	TATCGCAC
Q5009	CCAACAGA	TCTGTTGG
Q5010	TTGGTGAG	CTCACCAA
Q5013	AACCGCGG	CCGCGGTT
Q5014	GGTTATAA	TTATAACC

TruSight Amplicon Panels

Includes TruSight Myeloid Sequencing Panel and TruSight Tumor 26.

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
A701	ATCACGAC
A702	ACAGTGGT
A703	CAGATCCA
A704	ACAAACGG
A705	ACCCAGCA

i7 Index Name	i7 Bases for Sample Sheet
A706	AACCCCTC
A707	CCCAACCT
A708	CACCACAC
A709	GAAACCCA
A710	TGTGACCA
A711	AGGGTCAA
A712	AGGAGTGG

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
A501	TGAACCTT	AAGGTTCA
A502	TGCTAAGT	ACTTAGCA
A503	TGTTCTCT	AGAGAACA
A504	TAAGACAC	GTGTCTTA
A505	CTAATCGA	TCGATTAG
A506	CTAGAACA	TGTTCTAG
A507	TAAGTTCC	GGAACTTA
A508	TAGACCTA	TAGGTCTA

TruSight Cardio

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
N701	TAAGGCGA
N702	CGTACTAG
N703	AGGCAGAA
N704	TCCTGAGC

i7 Index Name	i7 Bases for Sample Sheet
N705	GGACTCCT
N706	TAGGCATG
N707	CTCTCTAC
N708	CAGAGAGG
N709	GCTACGCT
N710	CGAGGCTG
N711	AAGAGGCA
N712	GTAGAGGA

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, NextSeq, HiSeq 3000/4000
E502	CTCTCTAT	ATAGAGAG
E503	TATCCTCT	AGAGGATA
E504	AGAGTAGA	TCTACTCT
E505	GTAAGGAG	CTCCTTAC

TruSight One

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
N701	TAAGGCGA
N702	CGTACTAG
N703	AGGCAGAA
N704	TCCTGAGC
N705	GGACTCCT
N706	TAGGCATG
N707	CTCTCTAC
N708	CAGAGAGG

i7 Index Name	i7 Bases for Sample Sheet
N709	GCTACGCT
N710	CGAGGCTG
N711	AAGAGGCA
N712	GTAGAGGA

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
E502	CTCTCTAT	ATAGAGAG
E503	TATCCTCT	AGAGGATA
E504	AGAGTAGA	TCTACTCT
E505	GTAAGGAG	CTCCTTAC

TruSight Rapid Capture

Includes TruSight Cancer and TruSight Inherited Disease.

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
N701	TAAGGCGA
N702	CGTACTAG
N703	AGGCAGAA
N704	TCCTGAGC
N705	GGACTCCT
N706	TAGGCATG
N707	CTCTCTAC
N708	CAGAGAGG
N709	GCTACGCT
N710	CGAGGCTG

i7 Index Name	i7 Bases for Sample Sheet
N711	AAGAGGCA
N712	GTAGAGGA

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
E501	TAGATCGC	GCGATCTA
E502	CTCTCTAT	ATAGAGAG
E503	TATCCTCT	AGAGGATA
E504	AGAGTAGA	TCTACTCT
E505	GTAAGGAG	CTCCTTAC
E506	ACTGCATA	TATGCAGT
E507	AAGGAGTA	TACTCCTT
E508	CTAAGCCT	AGGCTTAG

TruSight Tumor 15

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
R701	ATCACG
R702	CGATGT
R703	TTAGGC
R704	TGACCA
R705	ACAGTG
R706	GCCAAT
R707	CAGATC
R708	ACTTGA

i7 Index Name	i7 Bases for Sample Sheet
R709	GATCAG
R711	GGCTAC
R712	CTTGTA

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
A501	TGAACCTT	AAGGTTCA
A502	TGCTAAGT	ACTTAGCA

TruSight Tumor 170

Index 1 (i7) Adapters (RNA)

i7 Index Name	i7 Bases for Sample Sheet	Index Primer
D702	TCCGGAGA	UP01
D707	CTGAAGCT	UP02
D717	CGTAGCTC	UP03
D706	GAATTCGT	UP04
D712	AGCGATAG	UP05
D724	GCGATTAA	UP06
D705	ATTCAGAA	UP07
D715	TTAATCAG	UP09
D713	GAATAATC	UP08
D703	CGCTCATT	UP10
D710	TCCGCGAA	UP11
D701	ATTACTCG	UP12
D716	ACTGCTTA	UP13
D714	ATGCGGCT	UP14

i7 Index Name	i7 Bases for Sample Sheet	Index Primer
D718	GCCTCTCT	UP15
D719	GCCGTAGG	UP16

Index 2 (i5) Adapter (RNA)

i5 Index Name	i5 Bases for Sample Sheet	Index Primer
D503	AGGATAGG	UP01
D504	TCAGAGCC	UP02
D509	CATCCGAA	UP03
D510	TTATGAGT	UP04
D513	ACGAATAA	UP05
D515	GATCTGCT	UP06
D501	AGGCTATA	UP07
D502	GCCTCTAT	UP08
D505	CTTCGCCT	UP09
D506	TAAGATTA	UP10
D517	AGTAAGTA	UP11
D518	GACTTCCT	UP12
D511	AGAGGCGC	UP13
D512	TAGCCGCG	UP14
D514	TTCGTAGG	UP15
D516	CGCTCCGC	UP16

Index 1 (i7) Adapters (DNA)

i7 Index Name	i7 Bases for Sample Sheet	Index Primer
D721	CATCGAGG	CP01
D723	CTCGACTG	CP02
D709	CGGCTATG	CP03
D711	TCTCGCGC	CP04
D723	CTCGACTG	CP05
D709	CGGCTATG	CP06
D711	TCTCGCGC	CP07
D721	CATCGAGG	CP08
D709	CGGCTATG	CP09
D711	TCTCGCGC	CP10
D721	CATCGAGG	CP11
D723	CTCGACTG	CP12
D711	TCTCGCGC	CP13
D721	CATCGAGG	CP14
D723	CTCGACTG	CP15
D709	CGGCTATG	CP16

Index 2 (i5) Adapter (DNA)

i5 Index Name	i5 Bases for Sample Sheet	Index Primer
D507	ACGTCCTG	CP01
D508	GTCAGTAC	CP02
D519	CCGTCGCC	CP03
D520	GTCCGAGG	CP04
D507	ACGTCCTG	CP05
D507	ACGTCCTG	CP06
D507	ACGTCCTG	CP07

i5 Index Name	i5 Bases for Sample Sheet	Index Primer
D508	GTCAGTAC	CP08
D508	GTCAGTAC	CP09
D508	GTCAGTAC	CP10
D519	CCGTCGCC	CP11
D519	CCGTCGCC	CP12
D519	CCGTCGCC	CP13
D520	GTCCGAGG	CP14
D520	GTCCGAGG	CP15
D520	GTCCGAGG	CP16

TruSight RNA Pan-Cancer Panel

Universal Adapter

5′ AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Adapter, Index 1–12

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]ATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 13

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]CAATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 14

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]GTATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 15 and Index 21

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]GAATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 16 and Index 19

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]CGATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 18

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]ACATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 20 and Index 27

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]TTATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 22

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]TAATCTCGTATGCCGTCTTCTGCTTG

Adapter, Index 23 and Index 25

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[6 bases]ATATCTCGTATGCCGTCTTCTGCTTG

Index Adapters

In this set of adapters, index numbering does not include numbers 17, 24, or 26.

LT Set A/B	Index Name	6-Base Sequence for Sample Sheet
B	AR001	ATCACG
A	AR002	CGATGT
B	AR003	TTAGGC
A	AR004	TGACCA
A	AR005	ACAGTG
A	AR006	GCCAAT
A	AR007	CAGATC
B	AR008	ACTTGA
B	AR009	GATCAG
B	AR010	TAGCTT
B	AR011	GGCTAC
A	AR012	CTTGTA
A	AR013	AGTCAA
A	AR014	AGTTCC
A	AR015	ATGTCA
A	AR016	CCGTCC
A	AR018	GTCCGC
A	AR019	GTGAAA
B	AR020	GTGGCC
B	AR021	GTTTCG
B	AR022	CGTACG
B	AR023	GAGTGG
B	AR025	ACTGAT

LT Set A/B	Index Name	6-Base Sequence for Sample Sheet
B	AR027	ATTCCT

Illumina Nextera Adapters

Nextera Transposase Adapters

(Used for Nextera tagmentation)

Read 1

5′ TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG

Read 2

5′ GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG

Nextera Index Kit – PCR Primers

Index 1 Read

5′ CAAGCAGAAGACGGCATACGAGAT[i7]GTCTCGTGGGCTCGG

Index 2 Read

5′ AATGATACGGCGACCACCGAGATCTACAC[i5]TCGTCGGCAGCGTC

Nextera Index Kit - Index 1 (i7) Adapters

Bases in Adapter	i7 Index Name	i7 Bases for Sample Sheet
TCGCCTTA	N701	TAAGGCGA
CTAGTACG	N702	CGTACTAG
TTCTGCCT	N703	AGGCAGAA
GCTCAGGA	N704	TCCTGAGC
AGGAGTCC	N705	GGACTCCT
CATGCCTA	N706	TAGGCATG
GTAGAGAG	N707	CTCTCTAC
CCTCTCTG	N708	CAGAGAGG
AGCGTAGC	N709	GCTACGCT
CAGCCTCG	N710	CGAGGCTG
TGCCTCTT	N711	AAGAGGCA
TCCTCTAC	N712	GTAGAGGA

Nextera Index Kit - Index 2 (i5) Adapters

The i5 index names vary for different Nextera products.

- N50x—Nextera DNA
- S50x—Nextera XT
- E50x—Nextera Enrichment and Nextera Rapid Capture Enrichment

Bases in Adapter	i5 Index Name	i5 Bases for Sample Sheet iSeq, NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet MiniSeq, NextSeq, HiSeq 3000/4000
TAGATCGC	[N/S/E]501	TAGATCGC	GCGATCTA
CTCTCTAT	[N/S/E]502	CTCTCTAT	ATAGAGAG
TATCCTCT	[N/S/E]503	TATCCTCT	AGAGGATA
AGAGTAGA	[N/S/E]504	AGAGTAGA	TCTACTCT
GTAAGGAG	[N/S/E]505	GTAAGGAG	CTCCTTAC
ACTGCATA	[N/S/E]506	ACTGCATA	TATGCAGT
AAGGAGTA	[N/S/E]507	AAGGAGTA	TACTCCTT
CTAAGCCT	[N/S/E]508	CTAAGCCT	AGGCTTAG
GCGTAAGA	[N/S/E]517	GCGTAAGA	TCTTACGC

Nextera XT Index Kit v2 - Index 1 (i7) Adapters

Bases in Adapter	i7 Index Name	i7 Bases for Sample Sheet
TCGCCTTA	N701	TAAGGCGA
CTAGTACG	N702	CGTACTAG
TTCTGCCT	N703	AGGCAGAA
GCTCAGGA	N704	TCCTGAGC
AGGAGTCC	N705	GGACTCCT
CATGCCTA	N706	TAGGCATG
GTAGAGAG	N707	CTCTCTAC
CAGCCTCG	N710	CGAGGCTG
TGCCTCTT	N711	AAGAGGCA
TCCTCTAC	N712	GTAGAGGA
TCATGAGC	N714	GCTCATGA

Bases in Adapter	i7 Index Name	i7 Bases for Sample Sheet
CCTGAGAT	N715	ATCTCAGG
TAGCGAGT	N716	ACTCGCTA
GTAGCTCC	N718	GGAGCTAC
TACTACGC	N719	GCGTAGTA
AGGCTCCG	N720	CGGAGCCT
GCAGCGTA	N721	TACGCTGC
CTGCGCAT	N722	ATGCGCAG
GAGCGCTA	N723	TAGCGCTC
CGCTCAGT	N724	ACTGAGCG
GTCTTAGG	N726	CCTAAGAC
ACTGATCG	N727	CGATCAGT
TAGCTGCA	N728	TGCAGCTA
GACGTCGA	N729	TCGACGTC

Nextera XT Index Kit v2 - Index 2 (i5) Adapters

Bases in Adapter	i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
CTCTCTAT	S502	CTCTCTAT	ATAGAGAG
TATCCTCT	S503	TATCCTCT	AGAGGATA
GTAAGGAG	S505	GTAAGGAG	CTCCTTAC
ACTGCATA	S506	ACTGCATA	TATGCAGT
AAGGAGTA	S507	AAGGAGTA	TACTCCTT
CTAAGCCT	S508	CTAAGCCT	AGGCTTAG
CGTCTAAT	S510	CGTCTAAT	ATTAGACG
TCTCTCCG	S511	TCTCTCCG	CGGAGAGA
TCGACTAG	S513	TCGACTAG	CTAGTCGA
TTCTAGCT	S515	TTCTAGCT	AGCTAGAA

Bases in Adapter	i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
CCTAGAGT	S516	CCTAGAGT	ACTCTAGG
GCGTAAGA	S517	GCGTAAGA	TCTTACGC
CTATTAAG	S518	CTATTAAG	CTTAATAG
AAGGCTAT	S520	AAGGCTAT	ATAGCCTT
GAGCCTTA	S521	GAGCCTTA	TAAGGCTC
TTATGCGA	S522	TTATGCGA	TCGCATAA

Nextera DNA CD Indexes - Index 1 (i7) Adapters

Bases in Adapter	i7 Index Name	i7 Bases for Sample Sheet
TCGCCTTA	H701	TAAGGCGA
CTAGTACG	H702	CGTACTAG
TTCTGCCT	H703	AGGCAGAA
AGGAGTCC	H705	GGACTCCT
CATGCCTA	H706	TAGGCATG
GTAGAGAG	H707	CTCTCTAC
CAGCCTCG	H710	CGAGGCTG
TGCCTCTT	H711	AAGAGGCA
TCCTCTAC	H712	GTAGAGGA
TCATGAGC	H714	GCTCATGA
AGGCTCCG	H720	CGGAGCCT
GAGCGCTA	H723	TAGCGCTC

Nextera DNA CD Indexes - Index 2 (i5) Adapters

Bases in Adapter	i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
TATCCTCT	H503	TATCCTCT	AGAGGATA
GTAAGGAG	H505	GTAAGGAG	CTCCTTAC
ACTGCATA	H506	ACTGCATA	TATGCAGT
CGTCTAAT	H510	CGTCTAAT	ATTAGACG
TCGACTAG	H513	TCGACTAG	CTAGTCGA
CCTAGAGT	H516	CCTAGAGT	ACTCTAGG
GCGTAAGA	H517	GCGTAAGA	TCTTACGC
TTATGCGA	H522	TTATGCGA	TCGCATAA

IDT for Illumina UD Indexes

These unique dual (UD) index adapters have been duplexed in the plate to enforce the recommended pairing strategy.

TruSeq UD Indexes

Index 1 (i7) Adapters

GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[i7]ATCTCGTATGCCGTCTTCTGCTTG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC[i5]ACACTCTTTCCCTACACGACGCTCTTCCGATCT

UD Index Name	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDI0001	CCGCGGTT	AGCGCTAG	CTAGCGCT
UDI0002	TTATAACC	GATATCGA	TCGATATC
UDI0003	GGACTTGG	CGCAGACG	CGTCTGCG
UDI0004	AAGTCCAA	TATGAGTA	TACTCATA
UDI0005	ATCCACTG	AGGTGCGT	ACGCACCT
UDI0006	GCTTGTCA	GAACATAC	GTATGTTC
UDI0007	CAAGCTAG	ACATAGCG	CGCTATGT
UDI0008	TGGATCGA	GTGCGATA	TATCGCAC

UD Index Name	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDI0009	AGTTCAGG	CCAACAGA	TCTGTTGG
UDI0010	GACCTGAA	TTGGTGAG	CTCACCAA
UDI0011	TCTCTACT	CGCGGTTC	GAACCGCG
UDI0012	CTCTCGTC	TATAACCT	AGGTTATA
UDI0013	CCAAGTCT	AAGGATGA	TCATCCTT
UDI0014	TTGGACTC	GGAAGCAG	CTGCTTCC
UDI0015	GGCTTAAG	TCGTGACC	GGTCACGA
UDI0016	AATCCGGA	CTACAGTT	AACTGTAG
UDI0017	TAATACAG	ATATTCAC	GTGAATAT
UDI0018	CGGCGTGA	GCGCCTGT	ACAGGCGC
UDI0019	ATGTAAGT	ACTCTATG	CATAGAGT
UDI0020	GCACGGAC	GTCTCGCA	TGCGAGAC
UDI0021	GGTACCTT	AAGACGTC	GACGTCTT
UDI0022	AACGTTCC	GGAGTACT	AGTACTCC
UDI0023	GCAGAATT	ACCGGCCA	TGGCCGGT
UDI0024	ATGAGGCC	GTTAATTG	CAATTAAC
UDI0025	ACTAAGAT	AACCGCGG	CCGCGGTT
UDI0026	GTCGGAGC	GGTTATAA	TTATAACC
UDI0027	CTTGGTAT	CCAAGTCC	GGACTTGG
UDI0028	TCCAACGC	TTGGACTT	AAGTCCAA
UDI0029	CCGTGAAG	CAGTGGAT	ATCCACTG
UDI0030	TTACAGGA	TGACAAGC	GCTTGTCA
UDI0031	GGCATTCT	CTAGCTTG	CAAGCTAG
UDI0032	AATGCCTC	TCGATCCA	TGGATCGA
UDI0033	TACCGAGG	CCTGAACT	AGTTCAGG
UDI0034	CGTTAGAA	TTCAGGTC	GACCTGAA
UDI0035	AGCCTCAT	AGTAGAGA	TCTCTACT
UDI0036	GATTCTGC	GACGAGAG	CTCTCGTC
UDI0037	TCGTAGTG	AGACTTGG	CCAAGTCT
UDI0038	CTACGACA	GAGTCCAA	TTGGACTC
UDI0039	TAAGTGGT	CTTAAGCC	GGCTTAAG
UDI0040	CGGACAAC	TCCGGATT	AATCCGGA
UDI0041	ATATGGAT	CTGTATTA	TAATACAG

UD Index Name	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDI0042	GCGCAAGC	TCACGCCG	CGGCGTGA
UDI0043	AAGATACT	ACTTACAT	ATGTAAGT
UDI0044	GGAGCGTC	GTCCGTGC	GCACGGAC
UDI0045	ATGGCATG	AAGGTACC	GGTACCTT
UDI0046	GCAATGCA	GGAACGTT	AACGTTCC
UDI0047	GTTCCAAT	AATTCTGC	GCAGAATT
UDI0048	ACCTTGGC	GGCCTCAT	ATGAGGCC
UDI0049	ATATCTCG	ATCTTAGT	ACTAAGAT
UDI0050	GCGCTCTA	GCTCCGAC	GTCGGAGC
UDI0051	AACAGGTT	ATACCAAG	CTTGGTAT
UDI0052	GGTGAACC	GCGTTGGA	TCCAACGC
UDI0053	CAACAATG	CTTCACGG	CCGTGAAG
UDI0054	TGGTGGCA	TCCTGTAA	TTACAGGA
UDI0055	AGGCAGAG	AGAATGCC	GGCATTCT
UDI0056	GAATGAGA	GAGGCATT	AATGCCTC
UDI0057	TGCGGCGT	CCTCGGTA	TACCGAGG
UDI0058	CATAATAC	TTCTAACG	CGTTAGAA
UDI0059	GATCTATC	ATGAGGCT	AGCCTCAT
UDI0060	AGCTCGCT	GCAGAATC	GATTCTGC
UDI0061	CGGAACTG	CACTACGA	TCGTAGTG
UDI0062	TAAGGTCA	TGTCGTAG	CTACGACA
UDI0063	TTGCCTAG	ACCACTTA	TAAGTGGT
UDI0064	CCATTCGA	GTTGTCCG	CGGACAAC
UDI0065	ACACTAAG	ATCCATAT	ATATGGAT
UDI0066	GTGTCGGA	GCTTGCGC	GCGCAAGC
UDI0067	TTCCTGTT	AGTATCTT	AAGATACT
UDI0068	CCTTCACC	GACGCTCC	GGAGCGTC
UDI0069	GCCACAGG	CATGCCAT	ATGGCATG
UDI0070	ATTGTGAA	TGCATTGC	GCAATGCA
UDI0071	ACTCGTGT	ATTGGAAC	GTTCCAAT
UDI0072	GTCTACAC	GCCAAGGT	ACCTTGGC
UDI0073	CAATTAAC	CGAGATAT	ATATCTCG
UDI0074	TGGCCGGT	TAGAGCGC	GCGCTCTA

UD Index Name	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDI0075	AGTACTCC	AACCTGTT	AACAGGTT
UDI0076	GACGTCTT	GGTTCACC	GGTGAACC
UDI0077	TGCGAGAC	CATTGTTG	CAACAATG
UDI0078	CATAGAGT	TGCCACCA	TGGTGGCA
UDI0079	ACAGGCGC	CTCTGCCT	AGGCAGAG
UDI0080	GTGAATAT	TCTCATTC	GAATGAGA
UDI0081	AACTGTAG	ACGCCGCA	TGCGGCGT
UDI0082	GGTCACGA	GTATTATG	CATAATAC
UDI0083	CTGCTTCC	GATAGATC	GATCTATC
UDI0084	TCATCCTT	AGCGAGCT	AGCTCGCT
UDI0085	AGGTTATA	CAGTTCCG	CGGAACTG
UDI0086	GAACCGCG	TGACCTTA	TAAGGTCA
UDI0087	CTCACCAA	CTAGGCAA	TTGCCTAG
UDI0088	TCTGTTGG	TCGAATGG	CCATTCGA
UDI0089	TATCGCAC	CTTAGTGT	ACACTAAG
UDI0090	CGCTATGT	TCCGACAC	GTGTCGGA
UDI0091	GTATGTTC	AACAGGAA	TTCCTGTT
UDI0092	ACGCACCT	GGTGAAGG	CCTTCACC
UDI0093	TACTCATA	CCTGTGGC	GCCACAGG
UDI0094	CGTCTGCG	TTCACAAT	ATTGTGAA
UDI0095	TCGATATC	ACACGAGT	ACTCGTGT
UDI0096	CTAGCGCT	GTGTAGAC	GTCTACAC

Nextera UD Indexes

Index 1 (i7) Adapters

CAAGCAGAAGACGGCATACGAGAT[i7]GTCTCGTGGGCTCGG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC[i5]TCGTCGGCAGCGTC

UD Index Name	i7 Bases in Adapter	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500*	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDP0001	CGCTCAGTTC	GAACTGAGCG	TCGTGGAGCG	CGCTCCACGA
UDP0002	TATCTGACCT	AGGTCAGATA	CTACAAGATA	TATCTTGTAG
UDP0003	ATATGAGACG	CGTCTCATAT	TATAGTAGCT	AGCTACTATA
UDP0004	CTTATGGAAT	ATTCCATAAG	TGCCTGGTGG	CCACCAGGCA
UDP0005	TAATCTCGTC	GACGAGATTA	ACATTATCCT	AGGATAATGT
UDP0006	GCGCGATGTT	AACATCGCGC	GTCCACTTGT	ACAAGTGGAC
UDP0007	AGAGCACTAG	CTAGTGCTCT	TGGAACAGTA	TACTGTTCCA
UDP0008	TGCCTTGATC	GATCAAGGCA	CCTTGTTAAT	ATTAACAAGG
UDP0009	CTACTCAGTC	GACTGAGTAG	GTTGATAGTG	CACTATCAAC
UDP0010	TCGTCTGACT	AGTCAGACGA	ACCAGCGACA	TGTCGCTGGT
UDP0011	GAACATACGG	CCGTATGTTC	CATACACTGT	ACAGTGTATG
UDP0012	CCTATGACTC	GAGTCATAGG	GTGTGGCGCT	AGCGCCACAC
UDP0013	TAATGGCAAG	CTTGCCATTA	ATCACGAAGG	CCTTCGTGAT
UDP0014	GTGCCGCTTC	GAAGCGGCAC	CGGCTCTACT	AGTAGAGCCG
UDP0015	CGGCAATGGA	TCCATTGCCG	GAATGCACGA	TCGTGCATTC
UDP0016	GCCGTAACCG	CGGTTACGGC	AAGACTATAG	CTATAGTCTT
UDP0017	AACCATTCTC	GAGAATGGTT	TCGGCAGCAA	TTGCTGCCGA
UDP0018	GGTTGCCTCT	AGAGGCAACC	CTAATGATGG	CCATCATTAG
UDP0019	CTAATGATGG	CCATCATTAG	GGTTGCCTCT	AGAGGCAACC
UDP0020	TCGGCCTATC	GATAGGCCGA	CGCACATGGC	GCCATGTGCG
UDP0021	AGTCAACCAT	ATGGTTGACT	GGCCTGTCCT	AGGACAGGCC
UDP0022	GAGCGCAATA	TATTGCGCTC	CTGTGTTAGG	CCTAACACAG
UDP0023	AACAAGGCGT	ACGCCTTGTT	TAAGGAACGT	ACGTTCCTTA
UDP0024	GTATGTAGAA	TTCTACATAC	CTAACTGTAA	TTACAGTTAG
UDP0025	TTCTATGGTT	AACCATAGAA	GGCGAGATGG	CCATCTCGCC
UDP0026	CCTCGCAACC	GGTTGCGAGG	AATAGAGCAA	TTGCTCTATT

UD Index Name	i7 Bases in Adapter	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500*	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDP0027	TGGATGCTTA	TAAGCATCCA	TCAATCCATT	AATGGATTGA
UDP0028	ATGTCGTGGT	ACCACGACAT	TCGTATGCGG	CCGCATACGA
UDP0029	AGAGTGCGGC	GCCGCACTCT	TCCGACCTCG	CGAGGTCGGA
UDP0030	TGCCTGGTGG	CCACCAGGCA	CTTATGGAAT	ATTCCATAAG
UDP0031	TGCGTGTCAC	GTGACACGCA	GCTTACGGAC	GTCCGTAAGC
UDP0032	CATACACTGT	ACAGTGTATG	GAACATACGG	CCGTATGTTC
UDP0033	CGTATAATCA	TGATTATACG	GTCGATTACA	TGTAATCGAC
UDP0034	TACGCGGCTG	CAGCCGCGTA	ACTAGCCGTG	CACGGCTAGT
UDP0035	GCGAGTTACC	GGTAACTCGC	AAGTTGGTGA	TCACCAACTT
UDP0036	TACGGCCGGT	ACCGGCCGTA	TGGCAATATT	AATATTGCCA
UDP0037	GTCGATTACA	TGTAATCGAC	GATCACCGCG	CGCGGTGATC
UDP0038	CTGTCTGCAC	GTGCAGACAG	TACCATCCGT	ACGGATGGTA
UDP0039	CAGCCGATTG	CAATCGGCTG	GCTGTAGGAA	TTCCTACAGC
UDP0040	TGACTACATA	TATGTAGTCA	CGCACTAATG	CATTAGTGCG
UDP0041	ATTGCCGAGT	ACTCGGCAAT	GACAACTGAA	TTCAGTTGTC
UDP0042	GCCATTAGAC	GTCTAATGGC	AGTGGTCAGG	CCTGACCACT
UDP0043	GGCGAGATGG	CCATCTCGCC	TTCTATGGTT	AACCATAGAA
UDP0044	TGGCTCGCAG	CTGCGAGCCA	AATCCGGCCA	TGGCCGGATT
UDP0045	TAGAATAACG	CGTTATTCTA	CCATAAGGTT	AACCTTATGG
UDP0046	TAATGGATCT	AGATCCATTA	ATCTCTACCA	TGGTAGAGAT
UDP0047	TATCCAGGAC	GTCCTGGATA	CGGTGGCGAA	TTCGCCACCG
UDP0048	AGTGCCACTG	CAGTGGCACT	TAACAATAGG	CCTATTGTTA
UDP0049	GTGCAACACT	AGTGTTGCAC	CTGGTACACG	CGTGTACCAG
UDP0050	ACATGGTGTC	GACACCATGT	TCAACGTGTA	TACACGTTGA
UDP0051	GACAGACAGG	CCTGTCTGTC	ACTGTTGTGA	TCACAACAGT
UDP0052	TCTTACATCA	TGATGTAAGA	GTGCGTCCTT	AAGGACGCAC
UDP0053	TTACAATTCC	GGAATTGTAA	AGCACATCCT	AGGATGTGCT
UDP0054	AAGCTTATGC	GCATAAGCTT	TTCCGTCGCA	TGCGACGGAA
UDP0055	TATTCCTCAG	CTGAGGAATA	CTTAACCACT	AGTGGTTAAG
UDP0056	CTCGTGCGTT	AACGCACGAG	GCCTCGGATA	TATCCGAGGC
UDP0057	TTAGGATAGA	TCTATCCTAA	CGTCGACTGG	CCAGTCGACG

UD Index Name	i7 Bases in Adapter	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500*	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDP0058	CCGAAGCGAG	CTCGCTTCGG	TACTAGTCAA	TTGACTAGTA
UDP0059	GGACCAACAG	CTGTTGGTCC	ATAGACCGTT	AACGGTCTAT
UDP0060	TTCCAGGTAA	TTACCTGGAA	ACAGTTCCAG	CTGGAACTGT
UDP0061	TGATTAGCCA	TGGCTAATCA	AGGCATGTAG	CTACATGCCT
UDP0062	TAACAGTGTT	AACACTGTTA	GCAAGTCTCA	TGAGACTTGC
UDP0063	ACCGCGCAAT	ATTGCGCGGT	TTGGCTCCGC	GCGGAGCCAA
UDP0064	GTTCGCGCCA	TGGCGCGAAC	AACTGATACT	AGTATCAGTT
UDP0065	AGACACATTA	TAATGTGTCT	GTAAGGCATA	TATGCCTTAC
UDP0066	GCGTTGGTAT	ATACCAACGC	AATTGCTGCG	CGCAGCAATT
UDP0067	AGCACATCCT	AGGATGTGCT	TTACAATTCC	GGAATTGTAA
UDP0068	TTGTTCCGTG	CACGGAACAA	AACCTAGCAC	GTGCTAGGTT
UDP0069	AAGTACTCCA	TGGAGTACTT	TCTGTGTGGA	TCCACACAGA
UDP0070	ACGTCAATAC	GTATTGACGT	GGAATTCCAA	TTGGAATTCC
UDP0071	GGTGTACAAG	CTTGTACACC	AAGCGCGCTT	AAGCGCGCTT
UDP0072	CCACCTGTGT	ACACAGGTGG	TGAGCGTTGT	ACAACGCTCA
UDP0073	GTTCCGCAGG	CCTGCGGAAC	ATCATAGGCT	AGCCTATGAT
UDP0074	ACCTTATGAA	TTCATAAGGT	TGTTAGAAGG	CCTTCTAACA
UDP0075	CGCTGCAGAG	CTCTGCAGCG	GATGGATGTA	TACATCCATC
UDP0076	GTAGAGTCAG	CTGACTCTAC	ACGGCCGTCA	TGACGGCCGT
UDP0077	GGATACCAGA	TCTGGTATCC	CGTTGCTTAC	GTAAGCAACG
UDP0078	CGCACTAATG	CATTAGTGCG	TGACTACATA	TATGTAGTCA
UDP0079	TCCTGACCGT	ACGGTCAGGA	CGGCCTCGTT	AACGAGGCCG
UDP0080	CTGGCTTGCC	GGCAAGCCAG	CAAGCATCCG	CGGATGCTTG
UDP0081	ACCAGCGACA	TGTCGCTGGT	TCGTCTGACT	AGTCAGACGA
UDP0082	TTGTAACGGT	ACCGTTACAA	CTCATAGCGA	TCGCTATGAG
UDP0083	GTAAGGCATA	TATGCCTTAC	AGACACATTA	TAATGTGTCT
UDP0084	GTCCACTTGT	ACAAGTGGAC	GCGCGATGTT	AACATCGCGC
UDP0085	TTAGGTACCA	TGGTACCTAA	CATGAGTACT	AGTACTCATG
UDP0086	GGAATTCCAA	TTGGAATTCC	ACGTCAATAC	GTATTGACGT
UDP0087	CATGTAGAGG	CCTCTACATG	GATACCTCCT	AGGAGGTATC
UDP0088	TACACGCTCC	GGAGCGTGTA	ATCCGTAAGT	ACTTACGGAT

UD Index Name	i7 Bases in Adapter	i7 Bases for Sample Sheet	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500*	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
UDP0089	GCTTACGGAC	GTCCGTAAGC	CGTGTATCTT	AAGATACACG
UDP0090	CGCTTGAAGT	ACTTCAAGCG	GAACCATGAA	TTCATGGTTC
UDP0091	CGCCTTCTGA	TCAGAAGGCG	GGCCATCATA	TATGATGGCC
UDP0092	ATACCAACGC	GCGTTGGTAT	ACATACTTCC	GGAAGTATGT
UDP0093	CTGGATATGT	ACATATCCAG	TATGTGCAAT	ATTGCACATA
UDP0094	CAATCTATGA	TCATAGATTG	GATTAAGGTG	CACCTTAATC
UDP0095	GGTGGAATAC	GTATTCCACC	ATGTAGACAA	TTGTCTACAT
UDP0096	TGGACGGAGG	CCTCCGTCCA	CACATCGGTG	CACCGATGTG

* i5 bases in adapter are the same sequences as the i5 Bases for Sample Sheet NovaSeq, etc.

TruSeq CD Indexes

Combinatorial dual (CD) index adapters for use with TruSeq (formerly known as TruSeq HT).

D501–D508 Adapters

AATGATACGGCGACCACCGAGATCTACAC[**i5**]ACACTCTTTCCCTACACGACGCTCTTCCGATCT

D701–D712 Adapters

GATCGGAAGAGCACACGTCTGAACTCCAGTCAC[**i7**]ATCTCGTATGCCGTCTTCTGCTTG

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
D701	ATTACTCG
D702	TCCGGAGA
D703	CGCTCATT
D704	GAGATTCC
D705	ATTCAGAA
D706	GAATTCGT
D707	CTGAAGCT
D708	TAATGCGC

i7 Index Name	i7 Bases for Sample Sheet
D709	CGGCTATG
D710	TCCGCGAA
D711	TCTCGCGC
D712	AGCGATAG

Index 2 (i5) Adapters

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
D501	TATAGCCT	AGGCTATA
D502	ATAGAGGC	GCCTCTAT
D503	CCTATCCT	AGGATAGG
D504	GGCTCTGA	TCAGAGCC
D505	AGGCGAAG	CTTCGCCT
D506	TAATCTTA	TAAGATTA
D507	CAGGACGT	ACGTCCTG
D508	GTACTGAC	GTCAGTAC

TruSeq Single Indexes

Index sequences are 6 bases as underlined. Enter the underlined 6 bases on the sample sheet.

TruSeq Universal Adapter

5′ AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

TruSeq Index Adapters (Index 1–27)

Index numbers 17, 24, and 26 are reserved.

TruSeq Adapter, Index 1

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCACGATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 2

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 3

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAGGCATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 4

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 5

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 6

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCCAATATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 7

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCAGATCATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 8

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTGAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 9

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 10

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACTAGCTTATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 11

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 12

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 13

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTCAACAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 14

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 15

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTCAGAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 16

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCCGATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 18

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCCGCACATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 19

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAAACGATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 20

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGGCCTTATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 21

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTTTCGGAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 22

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGTACGTAATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 23

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGAGTGGATATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 25

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTGATATATCTCGTATGCCGTCTTCTGCTTG

TruSeq Adapter, Index 27

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACATTCCTTTATCTCGTATGCCGTCTTCTGCTTG

TruSeq Amplicon Kits

Includes TruSeq Custom Amplicon 1.5, TruSeq Amplicon Cancer Panel, and TruSeq Custom Amplicon Low Input.

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
A701	ATCACGAC
A702	ACAGTGGT
A703	CAGATCCA
A704	ACAAACGG

i7 Index Name	i7 Bases for Sample Sheet
A705	ACCCAGCA
A706	AACCCCTC
A707	CCCAACCT
A708	CACCACAC
A709	GAAACCCA
A710	TGTGACCA
A711	AGGGTCAA
A712	AGGAGTGG

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
A501	TGAACCTT	AAGGTTCA
A502	TGCTAAGT	ACTTAGCA
A503	TGTTCTCT	AGAGAACA
A504	TAAGACAC	GTGTCTTA
A505	CTAATCGA	TCGATTAG
A506	CTAGAACA	TGTTCTAG
A507	TAAGTTCC	GGAACTTA
A508	TAGACCTA	TAGGTCTA

TruSeq DNA Methylation

Index PCR Primers

5′ CAAGCAGAAGACGGCATACGAGAT[6 bases]GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Index Adapters

Index Name	6-Base Sequence for Sample Sheet
Index 1	ATCACG

Index Name	6-Base Sequence for Sample Sheet
Index 2	CGATGT
Index 3	TTAGGC
Index 4	TGACCA
Index 5	ACAGTG
Index 6	GCCAAT
Index 7	CAGATC
Index 8	ACTTGA
Index 9	GATCAG
Index 10	TAGCTT
Index 11	GGCTAC
Index 12	CTTGTA

TruSeq Ribo Profile

3’ Adapter

5′ AGATCGGAAGAGCACACGTCT

Forward PCR Primer

5′ ATGATACGGCGACCACCGAGATCTACACGTTCAGAGTTCTACAGTCCGACG

Index PCR Primers

5′ CAAGCAGAAGACGGCATACGAGAT[6 bases]GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Index Adapters

Index Name	Six-Base Sequence for Sample Sheet
A001	ATCACG
A002	CGATGT
A003	TTAGGC
A004	TGACCA
A005	ACAGTG

Index Name	Six-Base Sequence for Sample Sheet
A006	GCCAAT
A007	CAGATC
A008	ACTTGA
A009	GATCAG
A010	TAGCTT
A011	GGCTAC
A012	CTTGTA

TruSeq Synthetic Long-Read DNA

Double-stranded DNA adapter containing long-range PCR primer binding site, sequencing primer binding site, and end marker sequence.

Long Reads Adapter

5′ CCGGTTCTTCCCTGCCGAACCCTATCTTCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTACGCTTGCAT

TruSeq Small RNA

RNA 5’ Adapter (RA5)

5′ GUUCAGAGUUCUACAGUCCGACGAUC

RNA 3’ Adapter (RA3)

5′ TGGAATTCTCGGGTGCCAAGG

Stop Oligo (STP)

5′ GAAUUCCACCACGUUCCCGUGG

RNA RT Primer (RTP)

5′ GCCTTGGCACCCGAGAATTCCA

RNA PCR Primer (RP1)

5′ AATGATACGGCGACCACCGAGATCTACACGTTCAGAGTTCTACAGTCCGA

RNA PCR Index Primers (RPI1–RPI48)

Index sequence is 6 bases as underlined. Enter the underlined 6 bases on the sample sheet. Index sequences are read in the reverse complement in TruSeq small RNA libraries.

RNA PCR Primer, Index 1 (RPI1)

5′ CAAGCAGAAGACGGCATACGAGATCGTGATGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 2 (RPI2)

5′ CAAGCAGAAGACGGCATACGAGATACATCGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 3 (RPI3)

5′ CAAGCAGAAGACGGCATACGAGATGCCTAAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 4 (RPI4)

5′ CAAGCAGAAGACGGCATACGAGATTGGTCAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 5 (RPI5)

5′ CAAGCAGAAGACGGCATACGAGATCACTGTGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 6 (RPI6)

5′ CAAGCAGAAGACGGCATACGAGATATTGGCGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 7 (RPI7)

5′ CAAGCAGAAGACGGCATACGAGATGATCTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 8 (RPI8)

5′ CAAGCAGAAGACGGCATACGAGATTCAAGTGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 9 (RPI9)

5′ CAAGCAGAAGACGGCATACGAGATCTGATCGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 10 (RPI10)

5′ CAAGCAGAAGACGGCATACGAGATAAGCTAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 11 (RPI11)

5′ CAAGCAGAAGACGGCATACGAGATGTAGCCGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 12 (RPI12)

5′ CAAGCAGAAGACGGCATACGAGATTACAAGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 13 (RPI13)

5′ CAAGCAGAAGACGGCATACGAGATTTGACTGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 14 (RPI14)

5′ CAAGCAGAAGACGGCATACGAGATGGAACTGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 15 (RPI15)

5′ CAAGCAGAAGACGGCATACGAGATTGACATGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 16 (RPI16)

5′ CAAGCAGAAGACGGCATACGAGATGGACGGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 17 (RPI17)

5′ CAAGCAGAAGACGGCATACGAGATCTCTACGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 18 (RPI18)

5′ CAAGCAGAAGACGGCATACGAGATGCGGACGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 19 (RPI19)

5′ CAAGCAGAAGACGGCATACGAGATTTTCACGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 20 (RPI20)

5′ CAAGCAGAAGACGGCATACGAGATGGCCACGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 21 (RPI21)

5′ CAAGCAGAAGACGGCATACGAGATCGAAACGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 22 (RPI22)

5′ CAAGCAGAAGACGGCATACGAGATCGTACGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 23 (RPI23)

5′ CAAGCAGAAGACGGCATACGAGATCCACTCGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 24 (RPI24)

5′ CAAGCAGAAGACGGCATACGAGATGCTACCGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 25 (RPI25)

5′ CAAGCAGAAGACGGCATACGAGATATCAGTGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 26 (RPI26)

5′ CAAGCAGAAGACGGCATACGAGATGCTCATGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 27 (RPI27)

5′ CAAGCAGAAGACGGCATACGAGATAGGAATGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 28 (RPI28)

5′ CAAGCAGAAGACGGCATACGAGATCTTTTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 29 (RPI29)

5′ CAAGCAGAAGACGGCATACGAGATTAGTTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 30 (RPI30)

5′ CAAGCAGAAGACGGCATACGAGATCCGGTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 31 (RPI31)

5′ CAAGCAGAAGACGGCATACGAGATATCGTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 32 (RPI32)

5′ CAAGCAGAAGACGGCATACGAGATTGAGTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 33 (RPI33)

5′ CAAGCAGAAGACGGCATACGAGATCGCCTGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 34 (RPI34)

5′ CAAGCAGAAGACGGCATACGAGATGCCATGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 35 (RPI35)

5′ CAAGCAGAAGACGGCATACGAGATAAAATGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 36 (RPI36)

5′ CAAGCAGAAGACGGCATACGAGATTGTTGGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 37 (RPI37)

5′ CAAGCAGAAGACGGCATACGAGATATTCCGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 38 (RPI38)

5′ CAAGCAGAAGACGGCATACGAGATAGCTAGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 39 (RPI39)

5′ CAAGCAGAAGACGGCATACGAGATGTATAGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 40 (RPI40)

5′ CAAGCAGAAGACGGCATACGAGATTCTGAGGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 41 (RPI41)

5′ CAAGCAGAAGACGGCATACGAGATGTCGTCGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 42 (RPI42)

5′ CAAGCAGAAGACGGCATACGAGATCGATTAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 43 (RPI43)

5′ CAAGCAGAAGACGGCATACGAGATGCTGTAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 44 (RPI44)

5′ CAAGCAGAAGACGGCATACGAGATATTATAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 45 (RPI45)

5′ CAAGCAGAAGACGGCATACGAGATGAATGAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 46 (RPI46)

5′ CAAGCAGAAGACGGCATACGAGATTCGGGAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 47 (RPI47)

5′ CAAGCAGAAGACGGCATACGAGATCTTCGAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

RNA PCR Primer, Index 48 (RPI48)

5′ CAAGCAGAAGACGGCATACGAGATTGCCGAGTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

TruSeq Targeted RNA Expression

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet	i7 Index Name	i7 Bases for Sample Sheet
R701	ATCACG	R725	ACTGAT
R702	CGATGT	R726	ATGAGC
R703	TTAGGC	R727	ATTCCT
R704	TGACCA	R728	CAAAAG
R705	ACAGTG	R729	CAACTA
R706	GCCAAT	R730	CACCGG
R707	CAGATC	R731	CACGAT
R708	ACTTGA	R732	CACTCA
R709	GATCAG	R733	CAGGCG
R710	TAGCTT	R734	CATGGC
R711	GGCTAC	R735	CATTTT
R712	CTTGTA	R736	CCAACA
R713	AGTCAA	R737	CGGAAT
R714	AGTTCC	R738	CTAGCT
R715	ATGTCA	R739	CTATAC
R716	CCGTCC	R740	CTCAGA
R717	GTAGAG	R741	GACGAC
R718	GTCCGC	R742	TAATCG
R719	GTGAAA	R743	TACAGC
R720	GTGGCC	R744	TATAAT
R721	GTTTCG	R745	TCATTC
R722	CGTACG	R746	TCCCGA
R723	GAGTGG	R747	TCGAAG
R724	GGTAGC	R748	TCGGCA

Index 2 (i5) Adapter

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
A501	TGAACCTT	AAGGTTCA
A502	TGCTAAGT	ACTTAGCA
A503	TGTTCTCT	AGAGAACA
A504	TAAGACAC	GTGTCTTA
A505	CTAATCGA	TCGATTAG
A506	CTAGAACA	TGTTCTAG
A507	TAAGTTCC	GGAACTTA
A508	TAGACCTA	TAGGTCTA

Appendix

Process Controls for TruSeq Kits

Included in TruSeq DNA PCR-Free, TruSeq Nano DNA, TruSeq RNA (v1/v2/LT/HT), and TruSeq Exome Kits.

CTE2 - 150bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAG
AGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGAT

CTE2 - 250bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGT
CTGGAGAACACTTGCCCATCAGTGCTTTTGAACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACAC
CTGCTAGAAGATGGAGGTATGCAGCCCGTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGG
CGGCCGCGAT

CTE2 - 350bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTC
TGCACAACTTATGCACCTCTATTAGATCATTGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGA
AGAGCGGAATAGATGGCCGGATGTTTGGTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAA
ATAACCCCCTCACAATAAGTGTAATGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCAT
GCTATCCCCCTCTGAAGACGCGGCCGCGAT

CTE2 - 450bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCA
CTTTGAGGCATGTAATATGGTACTGAGCTTCGGCACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATG
TCATGGATAAAGGCAGCCCCCTATATCTTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGAC
CTCCACAGCTCTAAACGTAATTCATCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATA
ATGCTGCCCAGCAATTTCCTCCCTTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTG
CTGACAAAATTGCACTCTAAACGCTAGCTTAGGTCTTCTGCGGCCGCGAT

CTE2 - 550bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAG
GACCCAGGCGTGCAAGTCAATTTCAGCTGACTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAA
AAAAAACCACACCTCTAATGTGTTGGGCACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATA
ACATACCCCCCACTGTGATTAAGACTGGCACTGTCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTG
GCAAACTTATAGAGGACAAGCAGAATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTA
TGAGCATGTCTTGCCCTTCATGGTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAA
ATCTGATAAATACGGCCACCTGAAGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGAGCGGCCGCGAT

CTE2 - 650bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTA
GTCTGTGCTGTTGCCTGGATAGTAAATTATCATGGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGA
GTTATTGTAAAGTCTCCCCAGGTGTGTCATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGG
GATTCCCTTTTAGTTGCTTTCATTAAAATGTACCAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTA
TCTCATTTGCACTGGTTACATGGCAGCTTCAGACTGACTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAA
CTGGGCCAACAAAAGCAATTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCA
CAGCAGTTTTTCCCTCCACACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTG
TTTCTTTATGGTGCTTGTGTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTG
CGGCCGCGAT

CTE2 - 750bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTT
GCCCCGCCTGATGTTGCCACTACTTGCTCATGACAGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAG
TACAGTTGTAGGGTACTCCTTATACTGATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAG
CTTCACAAATTCACCAGGTAAGCCCAAATTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTA
AAAGAGGGATTTTCTTTGCTGTATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGG
CTTTTGCTCCTACACGAACACCACTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCA
TCTACCAACTATCGCTAAGCATTCACTTGGTTGGTTTAAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGG
CTACATGTAGAAAGAGATCTGTTGGGCCCCACTATTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGAT
TTTCTGTGTCATGTAGAAGTCATCCACTTTTAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACG
GGACTTCTAACAGTGACTCGCGGCCGCGAT

CTE2 - 850bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATG
GATATTTTCTTTCTAAACTTTAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGA
TCCAGACTACAATAGAATATGTGGCCAAAACTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCA
CAAAAAGTACACAAATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGA
TAATAAAGCTCTTGATCCCAATGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAG
AGTCCATTCTCTAAAACTTGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATT
GGGAGCTTTTGAAGAGTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGT
TAAAAAAAAGTGACATTTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGG
TTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTT
CACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGT
GCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGAT

CTE1 - 123bp

GATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCGAAGT
TTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 223bp

GATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTGAACCTTT
TTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCCGTTAGTAGGA
GTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 323bp

GATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCTATTAGATCATTGTGTTC
TACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTGGTGGCTTTGA
TATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACAATAAGTGTAATGTCATGGGATAA
TCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGCGGCCGCGATATCCTGC
AGATGCA

CTE1 - 423bp

GATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTACTGAGCTTCGGCACA
GGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTATATCTTTTTTTGTG
GCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTCATCTGGCTTTGCCT
GTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATAATGCTGCCCAGCAATTTCCTCCCTTCTCAAGACTATT
CTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAACGCTAGCTTAGGTCTT
CTGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 523bp

GATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTTCAGCTGACTACACC
GATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAAACCACACCTCTAATGTGTTGGGCACTAGAAAA
AGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCCACTGTGATTAAGACTGGCACTGTCCT

AATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACTTATAGAGGACAAGCAGAATAAACCAATTCA
AGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATGGTGGATATTCACAGC
TGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGGCCACCTGAAGTCTAGCTCGGAG
TTAACAATTTACCACGTTTAGAGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 623bp

GATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGTAAATTATCATGGTA
CAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGTCATTAAATAT
CCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGGGATTCCCTTTTAGTTGCTTTCATTAAAATGTACCAGC
GCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTATCTCATTTGCACTGGTTACATGGCAGCTTCAGACTGA
CTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTTTTCATGTGGTCTAAC
TACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCACACCTCCCAGAGATACTTT
CAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGTGCTTGTGTCCTGACAACCGCGTAAG
GCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 723bp

GATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCCTGATGTTGCCACTACTTGCTCATGACAGT
TTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACTCCTTATACTGATTCTTCTGA
GCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGCCCAAATTTATTTTC
TGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATTTTCTTTGCTGTATTGCAGCCCAGTAT
ATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAACACCACTCTGTAAAATTTG
AGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAGCATTCACTTGGTTGGTTT
AAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGGCTACATGTAGAAAGAGATCTGTTGGGCCCCACTATTT
TTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTCATGTAGAAGTCATCCACTTTTAACACC
AGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTTCTAACAGTGACTCGCGGCCGCGATATCCTGC
AGATGCA

CTE1 - 823bp

GATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAAACTTTAAACAAACAGTGGAGA
GATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAATATGTGGCCAAAACTCTCCG
CAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAAATGGCTAAATAACAGAGCCCCTC
TTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTTATTTCCATGTGA
GGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAAACTTGAAGCTCCGCCCCTTTTT
ACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAATAAGAACCATCACAAAAA
GGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACATTTTCTCCTGTTTTTTACACAT
GATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTG
AGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCAATAA
CACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACC
GTGCGGCCGCGATATCCTGCAGATGCA

CTA - 150bp

GGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCG
AAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 250bp

GGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTGAAC
CTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCCGTTAGT
AGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCATCCAGTACT
AGTATGGCCC

CTA - 350bp

GGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCTATTAGATCATTGT
GTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTGGTGGCT

TTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACAATAAGTGTAATGTCATGGG
ATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGCGGCCGCGATATC
CTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 450bp

GGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTACTGAGCTTCGG
CACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTATATCTTTTTT
TGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTCATCTGGCTTT
GCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATAATGCTGCCCAGCAATTTCCTCCCTTCTCAAGAC
TATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAACGCTAGCTTAGG
TCTTCTGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 550bp

GGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTTCAGCTGACTA
CACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAAACCACACCTCTAATGTGTTGGGCACTAG
AAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCCACTGTGATTAAGACTGGCACTG
TCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACTTATAGAGGACAAGCAGAATAAACCAA
TTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATGGTGGATATTCA
CAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGGCCACCTGAAGTCTAGCTC
GGAGTTAACAATTTACCACGTTTAGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 650bp

GGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGTAAATTATCAT
GGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGTCATTAA
ATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGGGATTCCCTTTTAGTTGCTTTCATTAAAATGTAC
CAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTATCTCATTTGCACTGGTTACATGGCAGCTTCAGA
CTGACTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTTTTCATGTGGTC
TAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCACACCTCCCAGAGATA
CTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGTGCTTGTGTCCTGACAACCGCG
TAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGATATCCTGCAGATGCATCCAGTACT
AGTATGGCCC

CTA - 750bp

GGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCCTGATGTTGCCACTACTTGCTCATGA
CAGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACTCCTTATACTGATTCTT
CTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGCCCAAATTTAT
TTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATTTTCTTTGCTGTATTGCAGCCCA
GTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAACACCACTCTGTAAAA
TTTGAGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAGCATTCACTTGGTTG
GTTTAAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGGCTACATGTAGAAAGAGATCTGTTGGGCCCCACT
ATTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTCATGTAGAAGTCATCCACTTTTAA
CACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTTCTAACAGTGACTCGCGGCCGCGATATC
CTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 850bp

GGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAAACTTTAAACAAACAGTG
GAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAATATGTGGCCAAAACTC
TCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAAATGGCTAAATAACAGAGCC
CCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTTATTTCCAT
GTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAAACTTGAAGCTCCGCCCCT
TTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAATAAGAACCATCACA
AAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACATTTTCTCCTGTTTTTTAC
ACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGA

ATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCA
ATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGAT
GACCGTGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTL - 150bp

AGTATGGCCCGGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAG
TTGCAAATCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 250bp

AGTATGGCCCGGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGT
GCTTTTGAACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCA
GCCCGTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGC
ATCCAGTACA

CTL - 350bp

AGTATGGCCCGGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCTATT
AGATCATTGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATG
TTTGGTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACAATAAGTGTA
ATGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGCGG
CCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 450bp

AGTATGGCCCGGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTAC
TGAGCTTCGGCACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTA
TATCTTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTC
ATCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATAATGCTGCCCAGCAATTTCCTCCC
TTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAACG
CTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 550bp

AGTATGGCCCGGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTT
CAGCTGACTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAAACCACACCTCTAATGTGT
TGGGCACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCCACTGTGATTAAG
ACTGGCACTGTCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACTTATAGAGGACAAGCAG
AATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATGG
TGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGGCCACCTGA
AGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 650bp

AGTATGGCCCGGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGT
AAATTATCATGGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCCCCAGGT
GTGTCATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGGGATTCCCTTTTAGTTGCTTTCAT
TAAAATGTACCAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTATCTCATTTGCACTGGTTACATGG
CAGCTTCAGACTGACTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTTT
TCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCACACCT
CCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGTGCTTGTGTCCT
GACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGATATCCTGCAGATGC
ATCCAGTACA

CTL - 750bp

AGTATGGCCCGGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCCTGATGTTGCCACTAC
TTGCTCATGACAGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACTCCTTAT
ACTGATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGC

CCAAATTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATTTTCTTTGCTGTA
TTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAACACCA
CTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAGCATT
CACTTGGTTGGTTTAAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGGCTACATGTAGAAAGAGATCTGTT
GGGCCCCACTATTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTCATGTAGAAGTCAT
CCACTTTTAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTTCTAACAGTGACTCGCGG
CCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 850bp

AGTATGGCCCGGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAA
ACTTTAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTA
CAATAGAATATGTGGCCAAAACTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACA
AAAAGTACACAAATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATT
TAAGATAATAAAGCTCTTGATCCCAATGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACAT
ACCCTCTCCCAGAGTCCATTCTCTAAAACTTGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACG
GTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGG
AGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACATTTTCTCCTGTTTTTTACACATGATTTTGAAT
GCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTGAGC
CACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCA
ATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAG
AATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCATCCAGTACALegacy Kits

The kits listed in this section are no longer sold.

Nextera DNA Sample Prep Kit (Epicentre Biotechnologies)

(Obsolete)

As a replacement, use catalog # FC-121-1030 or catalog # FC-121-1031.

Transposon Sequences

5′-GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAG

5′-GCCTTGCCAGCCCGCTCAGAGATGTGTATAAGAGACAG

Adapters (showing optional bar code)

5′-AATGATACGGCGACCACCGAGATCTACACGCCTCCCTCGCGCCATCAG

5′-CAAGCAGAAGACGGCATACGAGAT[**barcode**]CGGTCTGCCTTGCCAGCCCGCTCAG-3'

PCR Primers

5′-AATGATACGGCGACCACCGA

5′-CAAGCAGAAGACGGCATACGA

Oligonucleotide Sequences for Genomic DNA

(Obsolete)

Adapters

5′ P-GATCGGAAGAGCTCGTATGCCGTCTTCTGCTTG

5′ ACACTCTTTCCCTACACGACGCTCTTCCGATCT

PCR Primers

5′ AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

5′ CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT

Genomic DNA Sequencing Primer

5′ ACACTCTTTCCCTACACGACGCTCTTCCGATCT

Oligonucleotide Sequences for Paired End DNA

(Obsolete)

PE Adapters

5′ P-GATCGGAAGAGCGGTTCAGCAGGAATGCCGAG

5′ ACACTCTTTCCCTACACGACGCTCTTCCGATCT

PE PCR Primer 1.0

5′ AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

PE PCR Primer 2.0

5′ CAAGCAGAAGACGGCATACGAGATCGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATCT

PE Read 1 Sequencing Primer

5′ ACACTCTTTCCCTACACGACGCTCTTCCGATCT

PE Read 2 Sequencing Primer

5′ CGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATCT

Oligonucleotide Sequences for the Multiplexing Sample Prep Oligo Only Kit

(Obsolete)

Multiplexing Adapters

5′ P-GATCGGAAGAGCACACGTCT

5′ ACACTCTTTCCCTACACGACGCTCTTCCGATCT

Multiplexing PCR Primer 1.0

5′ AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Multiplexing PCR Primer 2.0

5′ GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Multiplexing Read 1 Sequencing Primer

5′ ACACTCTTTCCCTACACGACGCTCTTCCGATCT

Multiplexing Index Read Sequencing Primer

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCAC

Multiplexing Read 2 Sequencing Primer

5′ GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

PCR Primer Index Sequences 1–12

PCR Primer, Index 1

5′ CAAGCAGAAGACGGCATACGAGATCGTGATGTGACTGGAGTTC

PCR Primer, Index 2

5′ CAAGCAGAAGACGGCATACGAGATACATCGGTGACTGGAGTTC

PCR Primer, Index 3

5′ CAAGCAGAAGACGGCATACGAGATGCCTAAGTGACTGGAGTTC

PCR Primer, Index 4

5′ CAAGCAGAAGACGGCATACGAGATTGGTCAGTGACTGGAGTTC

PCR Primer, Index 5

5′ CAAGCAGAAGACGGCATACGAGATCACTGTGTGACTGGAGTTC

PCR Primer, Index 6

5′ CAAGCAGAAGACGGCATACGAGATATTGGCGTGACTGGAGTTC

PCR Primer, Index 7

5′ CAAGCAGAAGACGGCATACGAGATGATCTGGTGACTGGAGTTC

PCR Primer, Index 8

5′ CAAGCAGAAGACGGCATACGAGATTCAAGTGTGACTGGAGTTC

PCR Primer, Index 9

5′ CAAGCAGAAGACGGCATACGAGATCTGATCGTGACTGGAGTTC

PCR Primer, Index 10

5′ CAAGCAGAAGACGGCATACGAGATAAGCTAGTGACTGGAGTTC

PCR Primer, Index 11

```
5′ CAAGCAGAAGACGGCATACGAGATGTAGCCGTGACTGGAGTTC
```

PCR Primer, Index 12

```
5′ CAAGCAGAAGACGGCATACGAGATTACAAGGTGACTGGAGTTC
```

Oligonucleotide Sequences for the v1 and v1.5 Small RNA Kits

(Obsolete)

RT Primer

```
5' CAAGCAGAAGACGGCATACGA
```

5' RNA Adapter

```
5' GUUCAGAGUUCUACAGUCCGACGAUC
```

3' RNA Adapter

```
5' P-UCGUAUGCCGUCUUCUGCUUGUidT
```

v1.5 Small RNA 3' Adapter

```
5' /5rApp/ATCTCGTATGCCGTCTTCTGCTTG/3ddC/
```

Small RNA PCR Primer 1

```
5' CAAGCAGAAGACGGCATACGA
```

Small RNA PCR Primer 2

```
5' AATGATACGGCGACCACCGACAGGTTCAGAGTTCTACAGTCCGA
```

Small RNA Sequencing Primer

```
5' CGACAGGTTCAGAGTTCTACAGTCCGACGATC
```

Revision History

Document	Date	Description of Change
Document # 1000000002694 v08	October 2018	Added IDT for Illumina UD indexes for Nextera.
Document # 1000000002694 v07	June 2018	Added the iSeq 100 Sequencing System, which requires a reverse complement.
Document # 1000000002694 v06	February 2018	Added TruSight Tumor 170 indexes.
Document # 1000000002694 v05	February 2018	Updated IDT for Illumina to include 96 indexes.
Document # 1000000002694 v04	January 2018	Added AmpliSeq for Illumina Panels.
Document # 1000000002694 v03	October 2017	Corrected i5 bases for Nextera DNA Flex kits for use with MiSeq and HiSeq sequencers. Reorganized TruSeq sections.
Document # 1000000002694 v02	September 2017	Added adapters for Nextera DNA Flex kits.
Document # 1000000002694 v01	February 2016	Added explanation of reverse complements in the sample sheet. Corrected i5 adapter names for TruSight One to E502–E505. Added adapters for TruSight RNA Pan-Cancer, TruSeq DNA Methylation, and TruSeq Ribo Profile. Added MiniSeq, which requires a reverse complement.
Document # 1000000002694 v00	October 2015	Added information for the following TruSight kits: • TruSight Cardio • TruSight Myeloid Sequencing Panel • TruSight One • TruSight Rapid Capture • TruSight Tumor 15 • TruSight Tumor 26 Created a TruSeq Amplicon section with information for the following kits: • TruSeq Custom Amplicon 1.5 • TruSeq Amplicon Cancer Panel • TruSeq Custom Amplicon Low Input Marked obsolete kits as **obsolete**. Grouped legacy kit information in new section titled Legacy Kits. Reformatted and reorganized the contents. Assigned document # 1000000002694.

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