

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 Nextera, AmpliSeq for Illumina, TruSight, and TruSeq kits. Additional sections list TruSeq process controls and information on legacy kits.

For product compatibility information, visit the support pages for your library prep kit on the Illumina website (support.illumina.com).

Reverse Complements

Dual indexing on the following instruments requires the reverse complement of the Index 2 (i5) adapter sequence: iSeq 100, MiniSeq, NextSeq 550, NextSeq 500, HiSeq 4000, and HiSeq 3000 Systems.

- ▶ If you are manually creating a sample sheet for these systems, enter 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.

Adapter Trimming Sequences

Sections for kits that recommend adapter trimming include the adapter trimming sequences. The adapter sequence is the sequence of the adapter to be trimmed.

When read length exceeds DNA insert size, a run can sequence beyond the DNA insert and read bases from the sequencing adapter. To prevent these bases from appearing in FASTQ files, the adapter sequence is trimmed from the 3' ends of reads. Trimming the adapter sequence improves alignment accuracy and performance in Illumina FASTQ generation pipelines.

IEM, BaseSpace Sequence Hub Prep tab, and Local Run Manager record adapter trimming sequences for Illumina kits in the sample sheet. For specific settings, see the documentation for your software.

Sequences for Nextera Kits

Adapter Trimming

The following sequence is used for Read 1 and Read 2 adapter trimming.

```
CTGTCTCTTATACACATCT
```

Nextera Mate Pair Adapter Trimming

The following sequence includes two adapter sequences joined by a plus sign. When performing adapter trimming, the software independently assesses each adapter for trimming.

```
CTGTCTCTTATACACATCT+AGATGTGTATAAGAGACAG
```

Nextera Transposase Adapters

The transposase adapters are used for Nextera tagmentation.

Read 1

```
5' TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG
```

Read 2

5' GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG

PCR Primers

Index 1 Read

5' CAAGCAGAAGACGGCATAACGAGAT [i7] GTCTCGTGGGCTCGG

Index 2 Read

5' AATGATACGGCGACCACCGAGATCTACAC [i5] TCGTCGGCAGCGTC

IDT for Illumina Nextera DNA UD Indexes

These unique dual (UD) index adapters are arranged in the plate to enforce the recommended pairing strategy.

Index 1 (i7) Adapters

CAAGCAGAAGACGGCATAACGAGAT [i7] GTCTCGTGGGCTCGG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC [i5] TCGTCGGCAGCGTC

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	GAAC TGAGCG	TCGTGGAGCG	CGCTCCACGA
UDP0002	TATCTGACCT	AGGTCAGATA	CTACAAGATA	TATCTTGTAG
UDP0003	ATATGAGACG	CGTCTCATAT	TATAGTAGCT	AGCTACTATA
UDP0004	CTTATGGAAT	ATTCCATAAG	TGCTTGGTGG	CCACCAGGCA
UDP0005	TAATCTCGTC	GACGAGATTA	ACATTATCCT	AGGATAATGT
UDP0006	GCGCGATGTT	AACATCGCGC	GTCCACTGT	ACAAGTGGAC
UDP0007	AGAGCACTAG	CTAGTGCTCT	TGGAACAGTA	TACTGTTC
UDP0008	TGCCCTGATC	GATCAAGGCA	CCTTGTTAAT	ATTAACAAGG
UDP0009	CTACTCAGTC	GACTGAGTAG	GTTGATAGTG	CACTATCAAC
UDP0010	TCGTCTGACT	AGTCAGACGA	ACCAGCGACA	TGTCGCTGGT
UDP0011	GAACATACGG	CCGTATGTTT	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

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
UDP0020	TCGGCCTATC	GATAGGCCGA	CGCACATGGC	GCCATGTGCG
UDP0021	AGTCAACCAT	ATGGTTGACT	GGCCTGTCTT	AGGACAGGCC
UDP0022	GAGCGCAATA	TATTGCGCTC	CTGTGTTAGG	CCTAACACAG
UDP0023	AACAAGGCGT	ACGCCTTGTT	TAAGGAACGT	ACGTTCCCTTA
UDP0024	GTATGTAGAA	TTCTACATAC	CTAACTGTAA	TTACAGTTAG
UDP0025	TTCTATGGTT	AACCATAGAA	GGCGAGATGG	CCATCTCGCC
UDP0026	CCTCGCAACC	GGTTGCGAGG	AATAGAGCAA	TTGCTCTATT
UDP0027	TGGATGCTTA	TAAGCATCCA	TCAATCCATT	AATGGATTGA
UDP0028	ATGTCGTGGT	ACCACGACAT	TCGTATGCGG	CCGCATACGA
UDP0029	AGAGTGC GGC	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	GACAAC TGAA	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	GTCTGGATA	CGGTGGCGAA	TTGCCACCG
UDP0048	AGTGCCACTG	CAGTGGCACT	TAACAATAGG	CCTATTGTTA
UDP0049	GTGCAACACT	AGTGTTCGAC	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	TTCCGTGCA	TGCGACGGAA
UDP0055	TATTCCTCAG	CTGAGGAATA	CTTAACCACT	AGTGGTTAAG
UDP0056	CTCGTGCGTT	AACGCACGAG	GCCTCGGATA	TATCCGAGGC
UDP0057	TTAGGATAGA	TCTATCCTAA	CGTCGACTGG	CCAGTCGACG

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	ACAGTTCAG	CTGGAAGTGT
UDP0061	TGATTAGCCA	TGGCTAATCA	AGGCATGTAG	CTACATGCCT
UDP0062	TAACAGTGTT	AACACTGTTA	GCAAGTCTCA	TGAGACTTGC
UDP0063	ACCGCGCAAT	ATTGCGCGGT	TTGGCTCCGC	GCGGAGCCAA
UDP0064	GTTGCGCCA	TGGCGGAAC	AACTGATACT	AGTATCAGTT
UDP0065	AGACACATTA	TAATGTGTCT	GTAAGGCATA	TATGCCTTAC
UDP0066	GCGTTGGTAT	ATACCAACGC	AATTGCTGCG	CGCAGCAATT
UDP0067	AGCACATCCT	AGGATGTGCT	TTACAATTC	GGAATTGTAA
UDP0068	TTGTTCCGTG	CACGGAACAA	AACCTAGCAC	GTGCTAGGTT
UDP0069	AAGTACTCCA	TGGAGTACTT	TCTGTGTGGA	TCCACACAGA
UDP0070	ACGTCAATAC	GTATTGACGT	GGAATTCCAA	TTGGAATTCC
UDP0071	GGTGTAACAAG	CTTGTAACACC	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	CATTAGTGG	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
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	GGTGAATAC	GTATTCCACC	ATGTAGACAA	TTGTCTACAT
UDP0096	TGGACGGAGG	CCTCCGTCCA	CACATCGGTG	CACCGATGTG

Nextera DNA Indexes

Index 1 (i7) Adapters

The i7 index names vary by kit:

- ▶ H7xx—Nextera DNA CD Indexes (combinatorial dual)
- ▶ N7xx—Nextera XT Index Kit v2, Nextera Index Kit

i7 Index Name	Bases in Adapter	i7 Bases for Sample Sheet
[H/N]701	TCGCCTTA	TAAGGCCGA
[H/N]702	CTAGTACG	CGTACTAG
[H/N]703	TTCTGCCT	AGGCAGAA
[H/N]704	GCTCAGGA	TCCTGAGC
[H/N]705	AGGAGTCC	GGACTCCT
[H/N]706	CATGCCTA	TAGGCATG
[H/N]707	GTAGAGAG	CTCTCTAC
[H/N]708	CCTCTCTG	CAGAGAGG
[H/N]709	AGCGTAGC	GCTACGCT
[H/N]710	CAGCCTCG	CGAGGCTG
[H/N]711	TGCCTCTT	AAGAGGCA
[H/N]712	TCCTCTAC	GTAGAGGA
[H/N]714	TCATGAGC	GCTCATGA
[H/N]715	CCTGAGAT	ATCTCAGG
[H/N]716	TAGCGAGT	ACTCGCTA
[H/N]718	GTAGCTCC	GGAGCTAC
[H/N]719	TACTACGC	GCGTAGTA
[H/N]720	AGGCTCCG	CGGAGCCT
[H/N]721	GCAGCGTA	TACGCTGC
[H/N]722	CTGCGCAT	ATGCGCAG
[H/N]723	GAGCGCTA	TAGCGCTC
[H/N]724	CGCTCAGT	ACTGAGCG
[H/N]726	GTCTTAGG	CCTAAGAC
[H/N]727	ACTGATCG	CGATCAGT
[H/N]728	TAGCTGCA	TGCAGCTA
[H/N]729	GACGTCGA	TCGACGTC

Index 2 (i5) Adapters

The i5 index names vary by kit:

- ▶ E5xx—Nextera Rapid Capture Custom Enrichment Kit
- ▶ H5xx—Nextera DNA CD Indexes (combinatorial dual)
- ▶ N5xx—Nextera Index Kit
- ▶ S5xx—Nextera XT Index Kit v2

i5 Index Name	Bases in Adapter	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
[E/H/N/S]501	TAGATCGC	TAGATCGC	GCGATCTA
[E/H/N/S]502	CTCTCTAT	CTCTCTAT	ATAGAGAG
[E/H/N/S]503	TATCCTCT	TATCCTCT	AGAGGATA
[E/H/N/S]504	AGAGTAGA	AGAGTAGA	TCTACTCT
[E/H/N/S]505	GTAAGGAG	GTAAGGAG	CTCCTTAC
[E/H/N/S]506	ACTGCATA	ACTGCATA	TATGCAGT
[E/H/N/S]507	AAGGAGTA	AAGGAGTA	TACTCCTT
[E/H/N/S]508	CTAAGCCT	CTAAGCCT	AGGCTTAG
[E/H/N/S]510	CGTCTAAT	CGTCTAAT	ATTAGACG
[E/H/N/S]511	TCTCTCCG	TCTCTCCG	CGGAGAGA
[E/H/N/S]513	TCGACTAG	TCGACTAG	CTAGTCGA
[E/H/N/S]515	TTCTAGCT	TTCTAGCT	AGCTAGAA
[E/H/N/S]516	CCTAGAGT	CCTAGAGT	ACTCTAGG
[E/H/N/S]517	GCGTAAGA	GCGTAAGA	TCTTACGC
[E/H/N/S]518	CTATTAAG	CTATTAAG	CTTAATAG
[E/H/N/S]520	AAGGCTAT	AAGGCTAT	ATAGCCTT
[E/H/N/S]521	GAGCCTTA	GAGCCTTA	TAAGGCTC
[E/H/N/S]522	TTATGCGA	TTATGCGA	TCGCATAA

Sequences for AmpliSeq for Illumina Panels

These combinatorial dual (CD) index adapters are arranged in the plate to enforce the recommended pairing strategy.

Adapter Trimming

The following sequence is used for Read 1 and Read 2 adapter trimming.

CTGTCTCTTATACACATCT

Index 1 (i7) Adapters

CAAGCAGAAGACGGCATAACGAGAT [i 7] GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG

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) Adapters

AATGATACGGCGACCACCGAGATCTACAC [i 5] TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG

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	GGTATAAA	TTATAACC

Sequences for TruSight Kits

TruSight Amplicon Panels

TruSight amplicon panels include the 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
A706	AACCCCTC
A707	CCCAACCT
A708	CACCACAC
A709	GAAACCCA
A710	TGTGACCA
A711	AGGGTCAA
A712	AGGAGTGG

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
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 DNA Enrichment Kits

TruSight DNA enrichment kits include TruSeq Neurodegeneration, TruSight Cancer, TruSight Cardio, TruSight One, TruSight Inherited Disease, and TruSight Rapid Capture.

Index 1 (i7) Adapters

i7 Index Name	i7 Bases for Sample Sheet
N701	TAAGGCGA
N702	CGTACTAG
N703	AGGCAGAA
N704	TCCTGAGC
N705	GGA CTCT
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, MiniSeq, NextSeq, HiSeq 3000/4000
E501	TAGATCGC	GCGATCTA
E502	CTCTCTAT	ATAGAGAG
E503	TATCCTCT	AGAGGATA
E504	AGAGTAGA	TCTACTCT
E505	GTAAGGAG	CTCCTTAC

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
E506	ACTGCATA	TATGCAGT
E507	AAGGAGTA	TACTCCTT
E508	CTAAGCCT	AGGCTTAG
E517	GCGTAAGA	TCTTACGC

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RNA Index 1 (i7) Adapters

i7 Index Name	Index Primer	i7 Bases for Sample Sheet
D702	UP01	TCCGGAGA
D707	UP02	CTGAAGCT
D717	UP03	CGTAGCTC
D706	UP04	GAATTCGT
D712	UP05	AGCGATAG
D724	UP06	GCGATTAA
D705	UP07	ATTCAGAA
D715	UP09	TTAATCAG
D713	UP08	GAATAATC
D703	UP10	CGCTCATT
D710	UP11	TCCGCGAA
D701	UP12	ATTACTCG
D716	UP13	ACTGCTTA
D714	UP14	ATGCGGCT
D718	UP15	GCCTCTCT
D719	UP16	GCCGTAGG

RNA Index 2 (i5) Adapters

i5 Index Name	Index Primer	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
D503	UP01	CCTATCCT	AGGATAGG
D504	UP02	GGCTCTGA	TCAGAGCC
D509	UP03	TTCGGATG	CATCCGAA
D510	UP04	ACTCATAA	TTATGAGT
D513	UP05	TTATTCGT	ACGAATAA
D515	UP06	AGCAGATC	GATCTGCT
D501	UP07	TATAGCCT	AGGCTATA
D502	UP08	ATAGAGGC	GCCTCTAT

i5 Index Name	Index Primer	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
D505	UP09	AGGCGAAG	CTTCGCCT
D506	UP10	TAATCTTA	TAAGATTA
D517	UP11	TACTTACT	AGTAAGTA
D518	UP12	AGGAAGTC	GACTTCCT
D511	UP13	GCGCCTCT	AGAGGCGC
D512	UP14	CGCGGCTA	TAGCCGCG
D514	UP15	CCTACGAA	TTCGTAGG
D516	UP16	GCGGAGCG	CGCTCCGC

DNA Index 1 (i7) Adapters

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

DNA Index 2 (i5) Adapters

i5 Index Name	Index Primer	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
D507	CP01	CAGGACGT	ACGTCCTG
D508	CP02	GTACTGAC	GTCAGTAC
D519	CP03	GGCGACGG	CCGTCGCC
D520	CP04	CCTCGGAC	GTCCGAGG
D507	CP05	CAGGACGT	ACGTCCTG

i5 Index Name	Index Primer	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
D507	CP06	CAGGACGT	ACGTCCTG
D507	CP07	CAGGACGT	ACGTCCTG
D508	CP08	GTACTGAC	GTCAGTAC
D508	CP09	GTACTGAC	GTCAGTAC
D508	CP10	GTACTGAC	GTCAGTAC
D519	CP11	GGCGACGG	CCGTCGCC
D519	CP12	GGCGACGG	CCGTCGCC
D519	CP13	GGCGACGG	CCGTCGCC
D520	CP14	CCTCGGAC	GTCCGAGG
D520	CP15	CCTCGGAC	GTCCGAGG
D520	CP16	CCTCGGAC	GTCCGAGG

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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
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 RNA Pan-Cancer Panel

Universal Adapter

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Index Adapters

Index adapter sequences are six bases as underlined. Enter the six underlined bases in the sample sheet. The index numbering is not sequential, so indexes 17, 24, and 26 are skipped. Additionally, the bases preceding each index adapter sequence are the same, but the two bases following the index adapter sequence can vary.

Index Adapter 1

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCACGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 2

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 3

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAGGCTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 4

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 5

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCACAGTGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 6

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCCAATTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 7

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCAGATCTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 8

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTGATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 9

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 10

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACTAGCTTTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 11

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 12

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 13

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTCAACATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 14

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 15

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTCAGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 16

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 18

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCCGCACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 19

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTAACGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 20

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCGGCCTTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 21

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTTTCGGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 22

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGTACGTAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 23

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGAGTGGATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 25

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTGATATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 27

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACATTCTTTATCTCGTATGCCGTCTTCTGCTTG

Sequences for TruSeq Kits

IDT for Illumina TruSeq DNA UD Indexes

These unique dual (UD) index adapters are arranged in the plate to enforce the recommended pairing strategy.

Adapter Trimming

The following sequences are used for adapter trimming.

Read 1

AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Read 2

AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

Index Adapters

Index 1 (i7) Adapters

GATCGGAAGAGCACACGTCTGAACTCCAGTCAC [i 7] ATCTCGTATGCCGTCTTCTGCTTG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC [i 5] AACTCTTTCCCTACACGACGCTCTTCCGATCT

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
UDI0001	AACCGCGG	CCGCGGTT	AGCGCTAG	CTAGCGCT
UDI0002	GGTTATAA	TTATAACC	GATATCGA	TCGATATC
UDI0003	CCAAGTCC	GGACTTGG	CGCAGACG	CGTCTGCG
UDI0004	TTGGACTT	AAGTCCAA	TATGAGTA	TACTCATA
UDI0005	CAGTGGAT	ATCCACTG	AGGTGCCGT	ACGCACCT
UDI0006	TGACAAGC	GCTTGTC A	GAACATAC	GTATGTTC
UDI0007	CTAGCTTG	CAAGCTAG	ACATAGCG	CGCTATGT
UDI0008	TCGATCCA	TGGATCGA	GTGCGATA	TATCGCAC
UDI0009	CCTGAACT	AGTTCAGG	CCAACAGA	TCTGTGTTG
UDI0010	TTCAGGTC	GACCTGAA	TTGGTGAG	CTCACCAA
UDI0011	AGTAGAGA	TCTCTACT	CGCGGTTTC	GAACCGCG
UDI0012	GACGAGAG	CTCTCGTC	TATAACCT	AGGTTATA
UDI0013	AGACTTGG	CCAAGTCT	AAGGATGA	TCATCCTT
UDI0014	GAGTCCAA	TTGGACTC	GGAAGCAG	CTGCTTCC
UDI0015	CTTAAGCC	GGCTTAAG	TCGTGACC	GGTCACGA
UDI0016	TCCGGATT	AATCCGGA	CTACAGTT	AACTGTAG
UDI0017	CTGTATTA	TAATACAG	ATATTCAC	GTGAATAT
UDI0018	TCACGCCG	CGGCGTGA	GCGCCTGT	ACAGGCCG
UDI0019	ACTTACAT	ATGTAAGT	ACTCTATG	CATAGAGT
UDI0020	GTCCGTGC	GCACGGAC	GTCTCGCA	TGCGAGAC
UDI0021	AAGGTACC	GGTACCTT	AAGACGTC	GACGTCTT
UDI0022	GGAACGTT	AACGTTCC	GGAGTACT	AGTACTCC
UDI0023	AATTCTGC	GCAGAATT	ACCGGCCA	TGGCCGGT
UDI0024	GGCCTCAT	ATGAGGCC	GTTAATTG	CAATTAAC
UDI0025	ATCTTAGT	ACTAAGAT	AACCGCGG	CCGCGGTT
UDI0026	GCTCCGAC	GTCGGAGC	GGTTATAA	TTATAACC
UDI0027	ATACCAAG	CTTGGTAT	CCAAGTCC	GGACTTGG
UDI0028	GCGTTGGA	TCCAACGC	TTGGACTT	AAGTCCAA
UDI0029	CTTCACGG	CCGTGAAG	CAGTGGAT	ATCCACTG

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
UDI0030	TCCTGTAA	TTACAGGA	TGACAAGC	GCTTGTCA
UDI0031	AGAATGCC	GGCATTCT	CTAGCTTG	CAAGCTAG
UDI0032	GAGGCATT	AATGCCTC	TCGATCCA	TGGATCGA
UDI0033	CCTCGGTA	TACCGAGG	CCTGAACT	AGTTCAGG
UDI0034	TTCTAACG	CGTTAGAA	TTCAGGTC	GACCTGAA
UDI0035	ATGAGGCT	AGCCTCAT	AGTAGAGA	TCTCTACT
UDI0036	GCAGAATC	GATTCTGC	GACGAGAG	CTCTCGTC
UDI0037	CACTACGA	TCGTAGTG	AGACTTGG	CCAAGTCT
UDI0038	TGTCGTAG	CTACGACA	GAGTCCAA	TTGGACTC
UDI0039	ACCACTTA	TAAGTGGT	CTTAAGCC	GGCTTAAG
UDI0040	GTTGTCCG	CGGACAAC	TCCGGATT	AATCCGGA
UDI0041	ATCCATAT	ATATGGAT	CTGTATTA	TAATACAG
UDI0042	GCTTGCGC	GCGCAAGC	TCACGCCG	CGGCGTGA
UDI0043	AGTATCTT	AAGATACT	ACTTACAT	ATGTAAGT
UDI0044	GACGCTCC	GGAGCGTC	GTCCGTGC	GCACGGAC
UDI0045	CATGCCAT	ATGGCATG	AAGGTACC	GGTACCTT
UDI0046	TGCATTGC	GCAATGCA	GGAACGTT	AACGTTCC
UDI0047	ATTGGAAC	GTTCCAAT	AATTCTGC	GCAGAATT
UDI0048	GCCAAGGT	ACCTTGGC	GGCCTCAT	ATGAGGCC
UDI0049	CGAGATAT	ATATCTCG	ATCTTAGT	ACTAAGAT
UDI0050	TAGAGCGC	GCGCTCTA	GCTCCGAC	GTCGGAGC
UDI0051	AACCTGTT	AACAGGTT	ATACCAAG	CTTGGTAT
UDI0052	GGTTCACC	GGTGAACC	GCGTTGGA	TCCAACGC
UDI0053	CATTGTTG	CAACAATG	CTTCACGG	CCGTGAAG
UDI0054	TGCCACCA	TGGTGGCA	TCCTGTAA	TTACAGGA
UDI0055	CTCTGCCT	AGGCAGAG	AGAATGCC	GGCATTCT
UDI0056	TCTCATTC	GAATGAGA	GAGGCATT	AATGCCTC
UDI0057	ACGCCGCA	TGCGGCGT	CCTCGGTA	TACCGAGG
UDI0058	GTATTATG	CATAATAC	TTCTAACG	CGTTAGAA
UDI0059	GATAGATC	GATCTATC	ATGAGGCT	AGCCTCAT
UDI0060	AGCGAGCT	AGCTCGCT	GCAGAATC	GATTCTGC
UDI0061	CAGTTCCG	CGGAACTG	CACTACGA	TCGTAGTG
UDI0062	TGACCTTA	TAAGGTCA	TGTCGTAG	CTACGACA
UDI0063	CTAGGCAA	TTGCCTAG	ACCACTTA	TAAGTGGT
UDI0064	TCGAATGG	CCATTCGA	GTTGTCCG	CGGACAAC
UDI0065	CTTAGTGT	ACACTAAG	ATCCATAT	ATATGGAT
UDI0066	TCCGACAC	GTGTCGGA	GCTTGCGC	GCGCAAGC
UDI0067	AACAGGAA	TTCCTGTT	AGTATCTT	AAGATACT

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
UDI0068	GGTGAAGG	CCTTCACC	GACGCTCC	GGAGCGTC
UDI0069	CCTGTGGC	GCCACAGG	CATGCCAT	ATGGCATG
UDI0070	TTCACAAT	ATTGTGAA	TGCATTGC	GCAATGCA
UDI0071	ACACGAGT	ACTCGTGT	ATTGGAAC	GTTCCAAT
UDI0072	GTGTAGAC	GTCTACAC	GCCAAGGT	ACCTTGGC
UDI0073	GTTAATTG	CAATTAAC	CGAGATAT	ATATCTCG
UDI0074	ACCGGCCA	TGGCCGGT	TAGAGCGC	GCGCTCTA
UDI0075	GGAGTACT	AGTACTCC	AACCTGTT	AACAGGTT
UDI0076	AAGACGTC	GACGTCTT	GGTTCACC	GGTGAACC
UDI0077	GTCTCGCA	TGCGAGAC	CATTGTTG	CAACAATG
UDI0078	ACTCTATG	CATAGAGT	TGCCACCA	TGGTGGCA
UDI0079	GCGCCTGT	ACAGGCGC	CTCTGCCT	AGGCAGAG
UDI0080	ATATTCAC	GTGAATAT	TCTCATTC	GAATGAGA
UDI0081	CTACAGTT	AACTGTAG	ACGCCGCA	TGCGGCGT
UDI0082	TCGTGACC	GGTCACGA	GTATTATG	CATAATAC
UDI0083	GGAAGCAG	CTGCTTCC	GATAGATC	GATCTATC
UDI0084	AAGGATGA	TCATCCTT	AGCGAGCT	AGCTCGCT
UDI0085	TATAACCT	AGGTTATA	CAGTTCCG	CGGAACTG
UDI0086	CGCGGTTT	GAACCGCG	TGACCTTA	TAAGGTCA
UDI0087	TTGGTGAG	CTCACCAA	CTAGGCAA	TTGCCTAG
UDI0088	CCAACAGA	TCTGTTGG	TCGAATGG	CCATTCGA
UDI0089	GTGCGATA	TATCGCAC	CTTAGTGT	ACACTAAG
UDI0090	ACATAGCG	CGCTATGT	TCCGACAC	GTGTCGGA
UDI0091	GAACATAC	GTATGTTC	AACAGGAA	TTCCTGTT
UDI0092	AGGTGCGT	ACGCACCT	GGTGAAGG	CCTTCACC
UDI0093	TATGAGTA	TACTCATA	CCTGTGGC	GCCACAGG
UDI0094	CGCAGACG	CGTCTGCG	TTCACAAT	ATTGTGAA
UDI0095	GATATCGA	TCGATATC	ACACGAGT	ACTCGTGT
UDI0096	AGCGCTAG	CTAGCGCT	GTGTAGAC	GTCTACAC

TruSeq CD Indexes

Combinatorial dual (CD) index adapters (formerly TruSeq HT).

Adapter Trimming

The following sequences are used for adapter trimming.

Read 1

AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Read 2

AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

Index 1 (i7) Adapters

GATCGGAAGAGCACACGTCTGAACTCCAGTCAC [i7] ATCTCGTATGCCGTCTTCTGCTTG

i7 Index Name	i7 Bases for Sample Sheet
D701	ATTACTCG
D702	TCCGGAGA
D703	CGCTCATT
D704	GAGATTCC
D705	ATTCAGAA
D706	GAATTCGT
D707	CTGAAGCT
D708	TAATGCGC
D709	CGGCTATG
D710	TCCGCGAA
D711	TCTCGCGC
D712	AGCGATAG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC [i5] ACACTCTTCCCTACACGACGCTCTTCCGATCT

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	GTA CTGAC	GTCAGTAC

TruSeq Single Indexes

Adapter Trimming

The following sequences are used for adapter trimming.

Read 1

AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Read 2

AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT

TruSeq Universal Adapter

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

DNA and RNA Index Adapters

Index adapter sequences are six bases as underlined. Enter the six underlined bases in the sample sheet.

The index numbering is not sequential, so indexes 17, 24, and 26 are skipped. Additionally, the bases preceding each index adapter sequence are the same, but the two bases following the index adapter sequence can vary.

Index Adapter 1

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCACGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 2

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 3

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACTAGGCATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 4

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 5

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 6

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCCAATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 7

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCAGATCATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 8

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 9

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCAGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 10

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACTAGCTTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 11

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGGCTACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 12

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATTCTCGTATGCCGTCTTCTGCTTG

Index Adapter 13

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTCAACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 14

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 15

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTCAGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 16

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 18

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCGCACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 19

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTAACCGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 20

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCGCTTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 21

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTTTCGGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 22

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGTACGTAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 23

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACGAGTGGATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 25

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACACTGATATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 27

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCACATTCCTTTATCTCGTATGCCGTCTTCTGCTTG

TruSeq Amplicon Kits

Includes TruSeq Custom Amplicon v1.5, 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
A705	ACCCAGCA
A706	AACCCCTC
A707	CCCAACCT
A708	CACCACAC
A709	GAAACCCA
A710	TGTGACCA
A711	AGGGTCAA
A712	AGGAGTGG

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
A501	TGAACCTT	AAGGTTCA
A502	TGCTAAGT	ACTTAGCA
A503	TGTTCTCT	AGAGAACA
A504	TAAGACAC	GTGTCTTA
A505	CTAATCGA	TCGATTAG
A506	CTAGAACA	TGTTCTAG
A507	TAAGTTCC	GGAAGTTA
A508	TAGACCTA	TAGGTCTA

TruSeq Small RNA

Adapter Trimming

The following sequence is used for adapter trimming.

TGGAATTCTCGGGTGCCAAGG

RNA 5' Adapter (RA5)

5' GUUCAGAGUUCUACAGUCCGACGAUC

RNA 3' Adapter (RA3)

5' TGGAATTCTCGGGTGCCAAGG

Stop Oligo (STP)

5' GAAUCCACCACGUUCCCGUGG

RNA RT Primer (RTP)

5' GCCTTGGCACCCGAGAATTCCA

RNA PCR Primer (RP1)

5' AATGATACGGCGACCACCGAGATCTACACGTTTCAGAGTTCTACAGTCCGA

RNA PCR Index Primers

5' CAAGCAGAAGACGGCATAACGAGAT[6 bases]GTGACTGGAGTTCCTTGGCACCCGAGAATTCCA

Index Adapters

Index Name	Six-Base Sequence for Sample Sheet
Index 1 (RPI1)	CGTGAT
Index 2 (RPI2)	ACATCG
Index 3 (RPI3)	GCCTAA
Index 4 (RPI4)	TGGTCA
Index 5 (RPI5)	CACTGT
Index 6 (RPI6)	ATTGGC
Index 7 (RPI7)	GATCTG
Index 8 (RPI8)	TCAAGT
Index 9 (RPI9)	CTGATC
Index 10 (RPI10)	AAGCTA
Index 11 (RPI11)	GTAGCC
Index 12 (RPI12)	TACAAG
Index 13 (RPI13)	TTGACT
Index 14 (RPI14)	GGAACT
Index 15 (RPI15)	TGACAT
Index 16 (RPI16)	GGACGG
Index 17 (RPI17)	CTCTAC
Index 18 (RPI18)	GCGGAC
Index 19 (RPI19)	TTTCAC
Index 20 (RPI20)	GGCCAC
Index 21 (RPI21)	CGAAAC
Index 22 (RPI22)	CGTACG
Index 23 (RPI23)	CCACTC
Index 24 (RPI24)	GCTACC
Index 25 (RPI25)	ATCAGT

Index Name	Six-Base Sequence for Sample Sheet
Index 26 (RPI26)	GCTCAT
Index 27 (RPI27)	AGGAAT
Index 28 (RPI28)	CTTTTG
Index 29 (RPI29)	TAGTTG
Index 30 (RPI30)	CCGGTG
Index 31 (RPI31)	ATCGTG
Index 32 (RPI32)	TGAGTG
Index 33 (RPI33)	CGCCTG
Index 34 (RPI34)	GCCATG
Index 35 (RPI35)	AAAATG
Index 36 (RPI36)	TGTTGG
Index 37 (RPI37)	ATCCCG
Index 38 (RPI38)	AGCTAG
Index 39 (RPI39)	GTATAG
Index 40 (RPI40)	TCTGAG
Index 41 (RPI41)	GTCGTC
Index 42 (RPI42)	CGATTA
Index 43 (RPI43)	GCTGTA
Index 44 (RPI44)	ATTATA
Index 45 (RPI45)	GAATGA
Index 46 (RPI46)	TCGGGA
Index 47 (RPI47)	CTTCGA
Index 48 (RPI48)	TGCCGA

TruSeq Targeted RNA Expression

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
R709	GATCAG
R710	TAGCTT
R711	GGCTAC

i7 Index Name	i7 Bases for Sample Sheet
R712	CTTGTA
R713	AGTCAA
R714	AGTTCC
R715	ATGTCA
R716	CCGTCC
R717	GTAGAG
R718	GTCCGC
R719	GTGAAA
R720	GTGGCC
R721	GTTTCG
R722	CGTACG
R723	GAGTGG
R724	GGTAGC
R725	ACTGAT
R726	ATGAGC
R727	ATTCTT
R728	CAAAAG
R729	CAACTA
R730	CACCGG
R731	CACGAT
R732	CACTCA
R733	CAGGCG
R734	CATGGC
R735	CATTTT
R736	CCAACA
R737	CGGAAT
R738	CTAGCT
R739	CTATAC
R740	CTCAGA
R741	GACGAC
R742	TAATCG
R743	TACAGC
R744	TATAAT
R745	TCATTC
R746	TCCCGA
R747	TCGAAG
R748	TCGGCA

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
A501	TGAACCTT	AAGGTTCA
A502	TGCTAAGT	ACTTAGCA
A503	TGTTCTCT	AGAGAACA
A504	TAAGACAC	GTGTCTTA
A505	CTAATCGA	TCGATTAG
A506	CTAGAACA	TGTTCTAG
A507	TAAGTTCC	GGAACCTA
A508	TAGACCTA	TAGGTCTA

Process Controls for TruSeq Kits

TruSeq DNA PCR-Free, TruSeq Nano DNA, TruSeq RNA (v2/LT/HT), and TruSeq Exome kits include the following process controls.

**NOTE**

Current versions of Sequencing Analysis Viewer (SAV) do not show metrics for control sequences.

CTE2 - 150bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTT
AAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGAT
```

CTE2 - 250bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGATCCTTATCTGTCAAAAACCGCTAATGTCCGTTCTAAGAC
CGTCTGGAGAACACTTGCCCATCAGTGCTTTTGAACCTTTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGA
CCACACCTGCTAGAAGATGGAGGTATGCAGCCCCTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAG
GGCAGATGGCGGCCGCGAT
```

CTE2 - 350bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGATCCTAGAGACCATTTCGCGATTCCATGAGACTCCAAGGG
TTCTGCACAACCTTATGCACCTCTATTAGATCATTGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAAC
ATGAGAAGAGCGGAATAGATGGCCGGATGTTTGGTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTG
TCCGGTCAAATAACCCCTCACAAATAAGTGTAAATGTCATGGGATAATCAAAGACTAAGGGAGGGCTTTTATAGAAG
GCGTGAGGTATGCTATCCCCCTCTGAAGACGCGGCCGCGAT
```

CTE2 - 450bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATA
CCACTTTGAGGCATGTAATATGGTACTGAGCTTCGGCACAGGGCTCAAATTCATCATTAAATGTCTCCGATGTGGC
TATATGTCATGGATAAAGGCAGCCCCCTATATCTTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGT
CTTAATGACCTCCACAGCTCTAAACGTAATTCATCTGGCTTTGCCTGTACTTACTTCTCCATGAAAAAAGTGTTG
ATAATGCTCATAATGCTGCCAGCAATTTCTCCCTTCTCAAGACTATTCTGGCTTCTGGGTACTTAAAAACAGGG
CTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAACGCTAGCTTAGGTCTTCTGCGGCCGCGAT
```

CTE2 - 550bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACA
CAGGACCCAGGCGTGCAAGTCAATTTTCAGCTGACTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTT
AGAGAAAAAAACCACACCTCTAATGTGTTGGGCACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCA
TTGGGAATAACATAACCCCCACTGTGATTAAGACTGGCACTGTCCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTG
TGATTCCCTCTGGCAAACCTTATAGAGGACAAGCAGAATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTG
CCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATGGTGGATATTCACAGCTGAAAGTGGTATTGGCATTFTTTTC
TGAGGACACAACGAGGAAATCTGATAAATACGGCCACCTGAAGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGA
GCGGCCGCGAT

CTE2 - 650bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTTCGCGCTCGT
CTAGTCTGTGCTGTTGCCTGGATAGTAAATTATCATGGTACAACTTTTAAAGAGCCAGTTAAATGGAGATGGATTTA
AAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGTCATTAATAATCCCAACAGATTGCCCTGGCCTGACCCCTAAATG
CAATTTTGGGATTCCCTTTTAGTTGCTTTTCAATAAATGTACCAGCGCAGTAAAAAAGCACAAAGTATATTGTTTA
TGTAACCTCACTATCTCATTTGCACTGGTTACATGGCAGCTTCAGACTGACTAAAACCTACTTTTCCACCATGGTT
CAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTA
CTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCACACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAA
AGGCTTCCGGACCAACCCTTGTCTTTATGGTGTCTGTGTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATT
TATCCGATCGTTTATATGGGCGTGCGGCCGCGAT

CTE2 - 750bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTT
GTTGCCCGCCTGATGTTGCCACTACTTGCTCATGACAGTTTTTTTTAGGCAATGCAAACCTACTATTTGATATTTTTT
TCCAAGTACAGTTGTAGGGTACTCCTTATACTGATTCTTCTGAGCCTGTACGGGGAGCATTAGGTAAGTACTGATGTAGTA
GGAGTTGAGCTTCACAAATTCACCAGGTAAGCCAAATTTATTTTTCTGCTTGGACAGGTCACCTCACATGGGTCTG
TCTAATATATTTAAAAGAGGGATTTTCTTTGCTGTATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTA
TTGCTGGCCTAGGGGCTTTTGTCTTACACGAACACCCTCTGTAATAATTTGAGGTCGTCCTTAGAGTCAAACCATT
CATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAGCATTCACTTGGTTGGTTTAAAGTGGAGGCAACTCCATTATC
TTCTAGCATAACCCTTCCAGGCTACATGTAGAAAGAGATCTGTTGGGCCCACTATTTTTTACCAGGGAAGCCTA
CTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTATGTAGAAAGTCACTTTTAAACACCAGGAGGTGGATGTGGG
GCCAGGAAATATGTCAATAACGATACGGGACTTCTAACAGTACTCGCGGCCGCGAT

CTE2 - 850bp

ATCCTGCAGATGCATCCAGTACTAGTATGGCCCCGGGGGATCCTTAAAGTCGTGTCTTCTCCTACGATCTTGTGAACG
ATGGATATTTTTCTTTCTAAACTTTAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGA
GGAAGATCCAGACTACAATAGAATATGTGGCCAAAACCTCCTCGCAACTTCAGCAGCAAAAAGGATATTATTGACATA
ACCTCCTCACAAAAGTACACAAAATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTT
TAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTTATTTCCATGTGAGGGACATTAATTTGAGTAACCTTTGCCA
CATAACCCTCTCCAGAGTCCATTCTCTAAAACCTGAAAGCTCCGCCCTTTTTACGCACATTAGGCTTCCAATTACGG
TCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAATAAGAACCATCACAAAAGGAACCCAGAAGCCGGGAGTGT
CTACCAAAAAAATTCAGGGTTAAAAAAGTGACATTTTCTCCTGTTTTTACACATGATTTTGAATGCTGATGGG
TCCACGTCCAGCTCTAAAGGTAGGTTTATGGTTCTCCAAAGTTGCTTTCTTGTGTCAGAAATGAGCCACATCAGGTAGG
TGGGGAAGTAGATCAGTGAGGATGCTTACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGA
GGGCCCGCTATGAAAAAAGATTCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCG
GAT

CTE1 - 123bp

GATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCGA
AGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 223bp

GATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTGAACC
TTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCCCGTTA
GTAGGAGTAATACTACCCAGCTTATAACCCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 323bp

GATCCTAGAGACCATTTCGCGATTCCATGAGACTCCAAGGGTCTGCACAACCTTATGCACCTCTATTAGATCATTGTG
TTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTGGTGG
CTTTGATATATTGTGAGGAGCATTGCGAACCTAGAGCTGTCCGGTCAAATAACCCCTCACAATAAGTGTAATGTC
ATGGGATAATCAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGCGGCC
GCGATATCCTGCAGATGCA

CTE1 - 423bp

GATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTACTGAGCTTCGGC
ACAGGGCTCAAATTCATCATTAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTATATCTTTT
TTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTCATCTG
GCTTTGCCTGTACTTACTTCCCTCCATGAAAAAAGTGTGATAATGCTCATAATGCTGCCAGCAATTTCTCCCTT
CTCAAGACTATTCTGGCTTCCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACCTCTAAC
GCTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 523bp

GATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTTTCAGCTGACTAC
ACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAACCACACCTCTAATGTGTTGGGCACT
AGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATAACCCCCACTGTGATTAAGACTGG
CACTGTCCATAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACCTATAGAGGACAAGCAGAA
TAAACCAATTCAGGTTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATG
GTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGGCCAC
CTGAAGTCTAGCTCGGAGTTAAACAATTTACCACGTTTLAGAGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 623bp

GATCCGCTCGCACTTAGCCTGTTAAGGGGTTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGTAAATTATCATG
GTACAACTTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGTCATT
AAATATCCCAACAGATTGCCCTGGCCTGACCCCTAAATGCAATTTGGGATTCCCTTTTAGTTGCTTTTCAATAAAA
TGTACCAGCGCAGTAAAAAAGCACAAAGTATATTGTTTATGTAACCTACTATCTCATTTGCACTGGTTACATGGCA
GCTTCAGACTGACTAAAACCTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTT
TTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCAC
ACCTCCCAGAGATACTTTCAGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGTGCTT
GTGTCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGATATC
CTGCAGATGCA

CTE1 - 723bp

GATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCGCCTGATGTTGCCACTACTTGCTCATGAC
AGTTTTTTTTAGGCAATGCAAACACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACTCCTTATACTGATTC
TTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGCCCAA
TTTATTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATTTTCTTTGCTGTATT
GCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAACACC
ACTCTGTAAAATTTGAGGTGCTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAG
CATTCACTTGGTTGGTTTAAAGTGGAGGCAACTCCATTATCTTCTAGCATAACCCTTCCCAGGCTACATGTAGAAAAGAG
ATCTGTTGGGCCCCACTATTTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTCTATG
TAGAAGTCATCCACTTTTAAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTTCTAA
CAGTGACTCGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 823bp

GATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTTCTTTCTAAACTTTAAACAAACAGTGG
AGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAATATGTGGCCAAAAC
TCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAAATGGCTAAATAACA
GAGCCCCCTTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTT
ATTTCCATGTGAGGGACATTAATTTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAAACCTGAA
GCTCCGCCCTTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAA
TAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATCAAGGGTTAAAAAAAAGTGACAT
TTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTTCATGGTTCTCC
AAAGTTGCTTTTCTGTGAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTG
GGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCT
GGCGCCTCCGCACTTAAAGAATTGATGACCGTGCAGGCGCGATATCCTGCAGATGCA

CTA - 150bp

GGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAA
TCGAAGTTTTAGATTGAGTTCTACGTGCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 250bp

GGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTG
AACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCC
GTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCA
TCCAGTACTAGTATGGCCC

CTA - 350bp

GGGGATCCTAGAGACCATTTCGCGATTCCATGAGACTCCAAGGGTCTGCACAACCTTATGCACCTCTATTAGATCAT
TGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTG
GTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCCTAGAGCTGTCCGGTCAAATAACCCCTCACATAAGTGATA
TGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGCGTGAGGTTCATGCTATCCCCCTCTGAAGACGC
GGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 450bp

GGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTACTGAGCTT
CGGCACAGGGCTCAAATTTGCATCATTTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTATATC
TTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTCA
TCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAGTGTGATAATGCTCATAATGCTGCCAGCAATTTCTC
CCTTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACTCT
AAACGCTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 550bp

GGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTTTCAGCTGA
CTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTLAGAGAAAAAACCACACCTCTAATGTGTTGGG
CACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCACTGTGATTAAGA
CTGGCACTGTCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACCTTATAGAGGACAAGC
AGAATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTT
CATGGTGGATATTCACAGCTGAAAAGTGGTATTGGCATTTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGG
CCACCTGAAGTCTAGCTCGGAGTTACAATTTACCACGTTTLAGAGCGGCCGCGATATCCTGCAGATGCATCCAGTAC
TAGTATGGCCC

CTA - 650bp

GGGGGATCCGCTCGCACTTAGCCTGTAAAGGGGTTGCGGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGTAAATAT
CATGGTACAACTTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGT
CATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCCCTAAATGCAATTTTGGGATTCCTTTTTAGTTGCTTTTCATT
AAAATGTACCAGCGCAGTAAAAAAGCACAAAGTATATTGTTTATGTAACCTACTATCTCATTTGCACTGGTTACAT
GGCAGCTTCAGACTGACTAAAACCTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACCTGGGCCAACAAAAGCAA
TTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCT
CCACACCTCCCAGAGATACTTTCAAGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGT
GCTTGTGCTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGA
TATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 750bp

GGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCGCCTGATGTTGCCACTACTTGCTCA
TGACAGTTTTTTTTAGGCAATGCAAACCTACTATTTGATATTTTTTCCAAGTACAGTTGTAGGGTACTCCTTATACTG
ATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGCC
CAAATTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTTAAAAGAGGGATTTTTCTTTGCTG
TATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAA
CACCACCTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTTCATGGAGCGCTCTGTGCATCTACCAACTATCGC
TAAGCATTCACTTGGTTGGTTTAAAGTGGAGGCAACTCCATTATCTTCTAGCATAACCCTTCCCAGGCTACATGTAGAA
AGAGATCTGTTGGGCCCCACTATTTTTTACCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGT
CATGTAGAAGTCATCCACTTTTAAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTT
CTAACAGTGACTCGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 850bp

GGGGGATCCTTAAGTCGTGTCTCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAAACTTTAAACAAACA
GTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAATATGTGGCCA
AAACTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAAATGGCTAAAT
AACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTCTTGATCCCAA
TGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAAAC
TGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGA
GTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATCAAGGGTTAAAAAAAAGTG
ACATTTTTCTCCTGTTTTTTACACATGATTTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTTCATGGTT
CTCCAAAGTTGCTTTCTTGTGAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATG
TGTGGGCACCTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCC
CCCTGGCGCCTCCGCACCTTAAAGAATTGATGACCGTGC GGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGG
CCC

CTL - 150bp

AGTATGGCCCGGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGT
AAGTTGCAAATCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 250bp

AGTATGGCCCGGGGGATCCTTATCTGTCAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACAACCTTGCCCATC
AGTGCTTTTGAACCTTTTTTTTACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGG
TATGCAGCCCGTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCC
TGCAGATGCATCCAGTACA

CTL - 350bp

AGTATGGCCCGGGGGATCCTAGAGACCATTTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACCTTATGCACCTCT
ATTAGATCATTGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGC
CGGATGTTTGGTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCCTCACA
ATAAGTGTAATGTCATGGGATAATCAAAGACTAAGGGAGGGCTTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCT
CTGAAGACGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 450bp

AGTATGGCCCGGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGG
TACTGAGCTTCGGCACAGGGCTCAAATTGCATCATTAAATGTCCTCCGATGTGGCTATATGTCATGGATAAAGGCAGC
CCCCTATATCTTTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTTCAGGGTCTTAATGACCTCCACAGCTCTAA
ACGTAATTCATCTGGCTTTGCCTGTACTTACTTCCCTCCATGAAAAAAGTGTTGATAATGCTCATAATGCTGCCAG
CAATTTCCCTCCCTTCTCAAGACTATTCTGGCTTCCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAA
ATTGCACTCTAAACGCTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 550bp

AGTATGGCCCGGGGGATCCGTTAGCTATCGTTTCGCGAGAAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAA
TTTTAGCTGACTACACCGATTCTGGTTAAAGAGCCTATGGCCACCCTTATTTTATAGAGAAAAAAAACACACCTCTA
ATGTGTTGGGCACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATAACCCCCACT
GTGATTAAGACTGGCACTGTCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCTCTGGCAAACCTTATA
GAGGACAAGCAGAATAAACCAATTC AAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATG
TCTTGCCCTTCATGGTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTTCTGAGGACACAACGAGGAAAATCTG
ATAAATACGGCCACCTGAAGTCTAGCTCGGAGTTAAACAATTTACCACGTTTATAGAGCGGCCGCGATATCCTGCAGATG
CATCCAGTACA

CTL - 650bp

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AGTATGGCCCGGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGAT
AGTAAATTATCATGGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCC
CCAGGTGTGTCATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCTAAATGCAATTTTGGGATTCCCTTTTAGT
TGCTTTCATTAAAATGTACCAGCGCAGTAAAAAAGCACAAAGTATATTGTTTATGTAAC TACTATCTCATTTGCA
CTGGTTACATGGCAGCTTCAGACTGACTAAA TACTACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCA
ACAAAAGCAATTTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCA
GTTTTTCCCTCCACACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTT
TCTTTATGGTGCTTGTGTCTCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTTATATGGGCGT
GCGGCCGCGATATCCTGCAGATGCATCCAGTACA
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CTL - 750bp

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AGTATGGCCCGGGGGATCCTTGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCTGATGTTGCCAC
TACTTGCTCATGACAGTTTTTTTTTAGGCAATGCAACTACTATTTGATATTTTTTTTCCAAGTACAGTTGTAGGGTACT
CCTTATACTGATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAAATTCAC
CAGGTAAGCCCAAATTTATTTTTCTGCTTGACAGGTCCACCTCACATGGGTCTGTCTAATATATTTAAAAGAGGGATT
TTCTTTGCTGTATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCT
CCTACACGAACACCCTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTTCATGGAGCGCTCTGTGCATCTAC
CAACTATCGCTAAGCATTCACTTGGTTGGTTTAAAGTGGAGGCAACTCCATTATCTTCTAGCATAACCCTTCCCAGGCT
ACATGTAGAAAGAGATCTGTTGGGCCCCACTATTTTTTACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGA
TTTTCTGTGTCATGTAGAAGTCATCCACTTTTAAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGA
TACGGGACTTCTAACAGTGACTCGCGGCCGCGATATCCTGCAGATGCATCCAGTACA
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CTL - 850bp

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AGTATGGCCCGGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTTCTTTCTAAACTT
TAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAA
TATGTGGCCAAAACCTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAGTACACAA
ATGGCTAAATAACAGAGCCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTC
TTGATCCCAATGTTATTTCCATGTGAGGGACATTAATTTAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATT
CTCTAAAACCTGAAGCTCCGCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAG
CTTTTGAAGAGTAATAAGAACCATCACAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTC AAGGTTA
AAAAAAGTGACATTTTCTCCTGTTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAG
GTTTCATGGTTCTCCAAAGTTGCTTCTTGTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGAT
GCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGAT
TCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCATCCAGT
ACA
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Legacy Kits

This section lists legacy kits that are no longer sold.

Nextera DNA Sample Prep Kit (Epicentre Biotechnologies)

(Obsolete)

Transposon Sequences

5' -GCCTCCCTCGCGCCATCAGAGATGTGTATAAGAGACAG

5' -GCCTTGCCAGCCCCTCAGAGATGTGTATAAGAGACAG

Adapters (Showing Optional Bar Code)

5' -AATGATACGGCGACCACCGAGATCTACACGCTCCCTCGCGCCATCAG

5' -CAAGCAGAAGACGGCATAACGAGAT [barcode] CGGTCTGCCTTGCCAGCCCGCTCAG-3'

PCR Primers

5' -AATGATACGGCGACCACCGA

5' -CAAGCAGAAGACGGCATAACGA

TruSeq Synthetic Long-Read DNA

(Obsolete)

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

Long Reads Adapter

5' CCGGTTCTTCCCTGCCGAACCCTATCTTCGTGGCAGCGTCAGATGTGTATAAGAGACAGTACGCTTGCAT

TruSeq DNA Methylation

Adapter Trimming

The following sequence is used for adapter trimming.

Read 1

AGATCGGAAGAGCACACGTCTGAAC

Read 2

AGATCGGAAGAGCGTCGTGTAGGGA

TruSeq Universal Adapter

5' AATGATACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTTCCGATCT

Index PCR Primers

5' CAAGCAGAAGACGGCATAACGAGAT [6 bases] GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Index Adapters

Index Name	Six-Base Sequence for Sample Sheet
Index 1	ATCACG
Index 2	CGATGT
Index 3	TTAGGC
Index 4	TGACCA
Index 5	ACAGTG

Index Name	Six-Base Sequence for Sample Sheet
Index 6	GCCAAT
Index 7	CAGATC
Index 8	ACTTGA
Index 9	GATCAG
Index 10	TAGCTT
Index 11	GGCTAC
Index 12	CTTGTA

TruSeq Ribo Profile

Adapter Trimming

The following sequence is used for adapter trimming.

AGATCGGAAGAGCACACGTCT

3' Adapter

5' AGATCGGAAGAGCACACGTCT

Forward PCR Primer

5' ATGATACGGCGACCACCGAGATCTACACGTTTCAGAGTTCTACAGTCCGACG

Index PCR Primers

5' CAAGCAGAAGACGGCATACGAGAT [6 bases] GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Index Adapters

i7 Index Name	Six-Base Sequence for Sample Sheet
A001	ATCACG
A002	CGATGT
A003	TTAGGC
A004	TGACCA
A005	ACAGTG
A006	GCCAAT
A007	CAGATC
A008	ACTTGA
A009	GATCAG
A010	TAGCTT
A011	GGCTAC
A012	CTTGTA

Oligonucleotide Sequences for Genomic DNA

(Obsolete)

Adapters

5' P-GATCGGAAGAGCTCGTATGCCGTCTTCTGCTTG

5' ACACTCTTTCCCTACACGACGCTCTTCCGATCT

PCR Primers

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

5' CAAGCAGAAGACGGCATAACGAGCTCTTCCGATCT

Genomic DNA Sequencing Primer

5' ACACTCTTTCCCTACACGACGCTCTTCCGATCT

Oligonucleotide Sequences for Paired End (PE) DNA

(Obsolete)

PE Adapters

5' P-GATCGGAAGAGCGGTTCAGCAGGAATGCCGAG

5' ACACTCTTTCCCTACACGACGCTCTTCCGATCT

PE PCR Primer 1.0

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

PE PCR Primer 2.0

5' CAAGCAGAAGACGGCATAACGAGATCGGTCTCGGCATTCCTGCTGAACCGCTCTTCCGATCT

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' CAAGCAGAAGACGGCATAACGAGATCGTGATGTGACTGGAGTTC

PCR Primer, Index 2

5' CAAGCAGAAGACGGCATAACGAGATACATCGGTGACTGGAGTTC

PCR Primer, Index 3

5' CAAGCAGAAGACGGCATAACGAGATGCCTAAGTGACTGGAGTTC

PCR Primer, Index 4

5' CAAGCAGAAGACGGCATAACGAGATTGGTCAGTGACTGGAGTTC

PCR Primer, Index 5

5' CAAGCAGAAGACGGCATAACGAGATCACTGTGTGACTGGAGTTC

PCR Primer, Index 6

5' CAAGCAGAAGACGGCATAACGAGATATTGGCGTGACTGGAGTTC

PCR Primer, Index 7

5' CAAGCAGAAGACGGCATAACGAGATGATCTGGTGACTGGAGTTC

PCR Primer, Index 8

5' CAAGCAGAAGACGGCATAACGAGATTCAAGTGTGACTGGAGTTC

PCR Primer, Index 9

5' CAAGCAGAAGACGGCATAACGAGATCTGATCGTGACTGGAGTTC

PCR Primer, Index 10

5' CAAGCAGAAGACGGCATAACGAGATAAGCTAGTGACTGGAGTTC

PCR Primer, Index 11

5' CAAGCAGAAGACGGCATAACGAGATGTAGCCGTGACTGGAGTTC

PCR Primer, Index 12

5' CAAGCAGAAGACGGCATAACGAGATTACAAGGTGACTGGAGTTC

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

(Obsolete)

RT Primer

5' CAAGCAGAAGACGGCATAACGA

5' RNA Adapter

5' GUUCAGAGUUCUACAGUCCGACGAUC

3' RNA Adapter

5' P-UCGUAUGCCGUCUUCUGCUUGUIdT

Small RNA v1.5 3' Adapter

5' /5rApp/ATCTCGTATGCCGTCTTCTGCTTG/3ddC/

Small RNA PCR Primer 1

5' CAAGCAGAAGACGGCATAACGA

Small RNA PCR Primer 2

5' AATGATACGGCGACCACCGACAGGTTTCAGAGTTCTACAGTCCGA

Small RNA Sequencing Primer

5' CGACAGGTTTCAGAGTTCTACAGTCCGACGATC

Revision History

Document	Date	Description of Change
Document # 1000000002694 v09	November 2018	<p>Updated the document structure:</p> <ul style="list-style-type: none"> • Consolidated sections by kit. • Consolidated index adapter tables for TruSight DNA Enrichment and Nextera DNA indexes. • Divided the <i>IDT for Illumina UD Indexes</i> section between the Nextera and TruSeq sections. • Reorganized TruSight RNA Pan-Cancer Panel information for clarity and consistency. • Reorganized TruSeq Small RNA index adapters into a table. • Moved TruSeq Synthetic Long-Read DNA, TruSeq DNA Methylation, and TruSeq Ribo Profile sequences to <i>Legacy Kits</i>. <p>Added the following sequences and bases:</p> <ul style="list-style-type: none"> • Adapter trimming sequences where applicable. • Bases for [E/H/N/S]517, a Nextera DNA i5 adapter. • The i7 bases in adapter for TruSeq UD Indexes. • The universal adapter sequence for TruSeq DNA Methylation. • For TruSight Tumor 170, the i5 sample sheet bases for systems that do not require an i5 reverse complement. <p>Added the following miscellaneous information:</p> <ul style="list-style-type: none"> • The adapter sequences for TruSight RNA Pan-Cancer Panel and TruSeq Single Indexes can vary. • Current versions of Sequencing Analysis Viewer do not show metrics for control sequences
Document # 1000000002694 v08	October 2018	Added IDT for Illumina Nextera DNA UD Indexes.
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 CD Indexes for use with MiSeq and HiSeq systems. Reorganized TruSeq sections.
Document # 1000000002694 v02	September 2017	Added adapters for Nextera DNA CD Indexes.
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	Date	Description of Change
Document # 1000000002694 v00	October 2015	<p>Added information for the following TruSight kits:</p> <ul style="list-style-type: none">• TruSight Cardio• TruSight Myeloid Sequencing Panel• TruSight One• TruSight Rapid Capture• TruSight Tumor 15• TruSight Tumor 26 <p>Created a TruSeq Amplicon section with information for the following kits:</p> <ul style="list-style-type: none">• TruSeq Custom Amplicon 1.5• TruSeq Amplicon Cancer Panel• TruSeq Custom Amplicon Low Input <p>Marked obsolete kits as obsolete.</p> <p>Grouped legacy kit information in new section titled Legacy Kits.</p> <p>Reformatted and reorganized the contents.</p> <p>Assigned document # 1000000002694.</p>

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Safety data sheets (SDSs)—Available on the Illumina website at support.illumina.com/sds.html.

Product documentation—Available for download in PDF from the Illumina website. Go to support.illumina.com, select a product, then select **Documentation & Literature**.



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