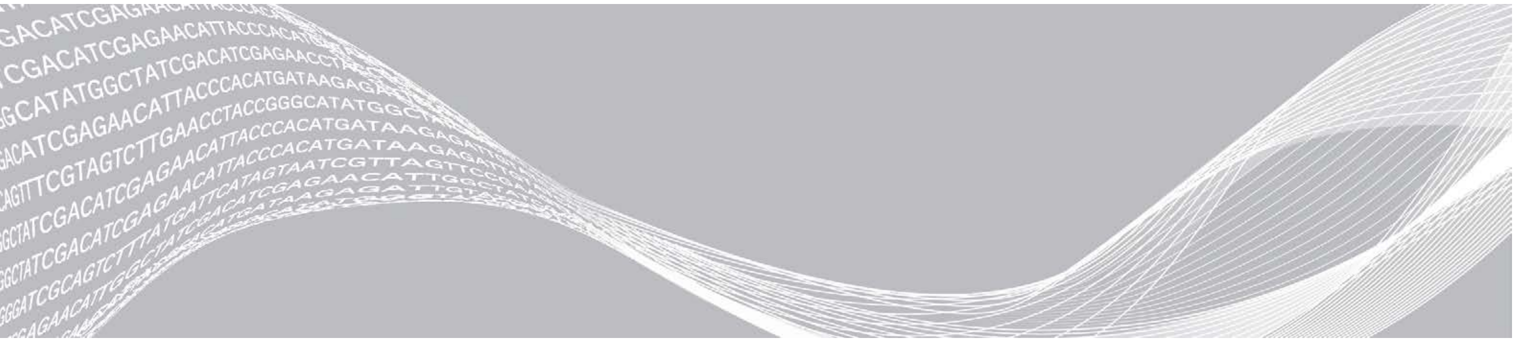
Illumina Adapter Sequences



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Introduction

This document lists the 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′ CAAGCAGAAGACGGCATACGAGAT[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

CAAGCAGAAGACGGCATACGAGAT[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	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

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	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
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

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
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

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	TAAGGCGA
[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 CD and UD 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

`CAAGCAGAAGACGGCATACGAGAT[i7]GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG`

i7 Index Name	i7 Bases for Sample Sheet
Q7005	GTGAATAT
Q7006	ACAGGCGC
Q7007	CATAGAGT
Q7008	TGCGAGAC
Q7015	TCTCTACT
Q7016	CTCTCGTC
Q7017	CCAAGTCT
Q7018	TTGGACTC

i7 Index Name	i7 Bases for Sample Sheet
Q7023	GCAGAATT
Q7024	ATGAGGCC
Q7025	ACTAAGAT
Q7026	GTCGGAGC
Q7027	AGCCTCAT
Q7028	GATTCTGC
Q7029	TCGTAGTG
Q7030	CTACGACA
Q7035	ATGGCATG
Q7036	GCAATGCA
Q7039	CTTATCGG
Q7040	TCCGCTAA
Q7041	GATCTATC
Q7042	AGCTCGCT
Q7047	ACACTAAG
Q7048	GTGTCGGA

Index 2 (i5) Adapters

`AATGATACGGCGACCACCGAGATCTACAC[i5]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
Q5003	CGCAGACG	CGTCTGCG
Q5004	TATGAGTA	TACTCATA
Q5007	ACATAGCG	CGCTATGT
Q5008	GTGCGATA	TATCGCAC
Q5009	CCAACAGA	TCTGTTGG
Q5010	TTGGTGAG	CTCACCAA
Q5013	AACCGCGG	CCGCGGTT
Q5014	GGTTATAA	TTATAACC
Q5017	CTAGCTTG	CAAGCTAG
Q5018	TCGATCCA	TGGATCGA
Q5025	ATACCAAG	CTTGGTAT
Q5026	GCGTTGGA	TCCAACGC
Q5027	CTTCACGG	CCGTGAAG
Q5028	TCCTGTAA	TTACAGGA
Q5029	CCTCGGTA	TACCGAGG
Q5030	TTCTAACG	CGTTAGAA

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, HiSeq 3000/4000, MiniSeq, NextSeq
Q5031	CGCTCGTG	CACGAGCG
Q5032	TATCTACA	TGTAGATA
Q5035	CATTGTTG	CAACAATG
Q5036	TGCCACCA	TGGTGGCA
Q5039	ACGCCGCA	TGCGGCGT
Q5040	GTATTATG	CATAATAC

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	`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, 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`
E517	`GCGTAAGA`	`TCTTACGC`

TruSight Tumor 170

RNA Index 1 (i7) Adapters

i7 Index Name	Index Primer	i7 Bases for Sample Sheet
D702	UP01	`TCCGGAGA`
D707	UP02	`CTGAAGCT`
D717	UP03	`CGTAGCTC`

i7 Index Name	Index Primer	i7 Bases for Sample Sheet
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`
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`

i7 Index Name	Index Primer	i7 Bases for Sample Sheet
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
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

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
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′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACATCACGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 2

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 3

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAGGCATCTCGTATGCCGTCTTCTGCTTG

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′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 13

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTCAACAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 14

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 15

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTCAGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 16

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCCGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 18

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCCGCACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 19

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAAACGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 20

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGGCCTTATCTCGTATGCCGTCTTCTGCTTG

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

Sequences for TruSeq Kits

IDT for Illumina TruSeq DNA and RNA 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[i7]ATCTCGTATGCCGTCTTCTGCTTG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC[i5]ACACTCTTTCCCTACACGACGCTCTTCCGATCT

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

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
UDI0004	TTGGACTT	AAGTCCAA	TATGAGTA	TACTCATA
UDI0005	CAGTGGAT	ATCCACTG	AGGTGCGT	ACGCACCT
UDI0006	TGACAAGC	GCTTGTCA	GAACATAC	GTATGTTC
UDI0007	CTAGCTTG	CAAGCTAG	ACATAGCG	CGCTATGT
UDI0008	TCGATCCA	TGGATCGA	GTGCGATA	TATCGCAC
UDI0009	CCTGAACT	AGTTCAGG	CCAACAGA	TCTGTTGG
UDI0010	TTCAGGTC	GACCTGAA	TTGGTGAG	CTCACCAA
UDI0011	AGTAGAGA	TCTCTACT	CGCGGTTC	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	ACAGGCGC
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
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

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
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
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

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
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	CGCGGTTC	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 DNA and RNA 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

i7 Index Name	i7 Bases for Sample Sheet
D706	GAATTCGT
D707	CTGAAGCT
D708	TAATGCGC
D709	CGGCTATG
D710	TCCGCGAA
D711	TCTCGCGC
D712	AGCGATAG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC[i5]ACACTCTTTCCCTACACGACGCTCTTCCGATCT

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

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′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 3

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACTTAGGCATCTCGTATGCCGTCTTCTGCTTG

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′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCTTGTAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 13

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTCAACAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 14

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 15

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACATGTCAGAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 16

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACCCGTCCCGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 18

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTCCGCACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 19

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGAAACGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 20

5′ GATCGGAAGAGCACACGTCTGAACTCCAGTCACGTGGCCTTATCTCGTATGCCGTCTTCTGCTTG

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`	`GGAACTTA`
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′ GAAUUCCACCACGUUCCCGUGG`

RNA RT Primer (RTP)

`5′ GCCTTGGCACCCGAGAATTCCA`

RNA PCR Primer (RP1)

`5′ AATGATACGGCGACCACCGAGATCTACACGTTCAGAGTTCTACAGTCCGA`

RNA PCR Index Primers

`5′ CAAGCAGAAGACGGCATACGAGAT[6 bases]GTGACTGGAGTTCCTTGGCACCCGAGAATTCCA`

Index Adapters

Index Name	Six-Base Sequence in Adapter	Six-Base Sequence for Sample Sheet
Index 1 (RPI1)	`CGTGAT`	`ATCACG`
Index 2 (RPI2)	`ACATCG`	`CGATGT`
Index 3 (RPI3)	`GCCTAA`	`TTAGGC`
Index 4 (RPI4)	`TGGTCA`	`TGACCA`
Index 5 (RPI5)	`CACTGT`	`ACAGTG`
Index 6 (RPI6)	`ATTGGC`	`GCCAAT`
Index 7 (RPI7)	`GATCTG`	`CAGATC`
Index 8 (RPI8)	`TCAAGT`	`ACTTGA`
Index 9 (RPI9)	`CTGATC`	`GATCAG`
Index 10 (RPI10)	`AAGCTA`	`TAGCTT`
Index 11 (RPI11)	`GTAGCC`	`GGCTAC`
Index 12 (RPI12)	`TACAAG`	`CTTGTA`
Index 13 (RPI13)	`TTGACT`	`AGTCAA`
Index 14 (RPI14)	`GGAACT`	`AGTTCC`
Index 15 (RPI15)	`TGACAT`	`ATGTCA`
Index 16 (RPI16)	`GGACGG`	`CCGTCC`
Index 17 (RPI17)	`CTCTAC`	`GTAGAG`
Index 18 (RPI18)	`GCGGAC`	`GTCCGC`
Index 19 (RPI19)	`TTTCAC`	`GTGAAA`
Index 20 (RPI20)	`GGCCAC`	`GTGGCC`
Index 21 (RPI21)	`CGAAAC`	`GTTTCG`

Index Name	Six-Base Sequence in Adapter	Six-Base Sequence for Sample Sheet
Index 22 (RPI22)	CGTACG	CGTACG
Index 23 (RPI23)	CCACTC	GAGTGG
Index 24 (RPI24)	GCTACC	GGTAGC
Index 25 (RPI25)	ATCAGT	ACTGAT
Index 26 (RPI26)	GCTCAT	ATGAGC
Index 27 (RPI27)	AGGAAT	ATTCCT
Index 28 (RPI28)	CTTTTG	CAAAAG
Index 29 (RPI29)	TAGTTG	CAACTA
Index 30 (RPI30)	CCGGTG	CACCGG
Index 31 (RPI31)	ATCGTG	CACGAT
Index 32 (RPI32)	TGAGTG	CACTCA
Index 33 (RPI33)	CGCCTG	CAGGCG
Index 34 (RPI34)	GCCATG	CATGGC
Index 35 (RPI35)	AAAATG	CATTTT
Index 36 (RPI36)	TGTTGG	CCAACA
Index 37 (RPI37)	ATTCCG	CGGAAT
Index 38 (RPI38)	AGCTAG	CTAGCT
Index 39 (RPI39)	GTATAG	CTATAC
Index 40 (RPI40)	TCTGAG	CTCAGA
Index 41 (RPI41)	GTCGTC	GACGAC
Index 42 (RPI42)	CGATTA	TAATCG
Index 43 (RPI43)	GCTGTA	TACAGC

Index Name	Six-Base Sequence in Adapter	Six-Base Sequence for Sample Sheet
Index 44 (RPI44)	`ATTATA`	`TATAAT`
Index 45 (RPI45)	`GAATGA`	`TCATTC`
Index 46 (RPI46)	`TCGGGA`	`TCCCGA`
Index 47 (RPI47)	`CTTCGA`	`TCGAAG`
Index 48 (RPI48)	`TGCCGA`	`TCGGCA`

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`
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`

i7 Index Name	i7 Bases for Sample Sheet
R726	ATGAGC
R727	ATTCCT
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	GGAACTTA
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

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTT
AAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGAT
```

CTE2 - 250bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGAC
CGTCTGGAGAACACTTGCCCATCAGTGCTTTTGAACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGA
CCACACCTGCTAGAAGATGGAGGTATGCAGCCCGTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAG
GGCAGATGGCGGCCGCGAT
```

CTE2 - 350bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGG
TTCTGCACAACTTATGCACCTCTATTAGATCATTGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAAC
ATGAGAAGAGCGGAATAGATGGCCGGATGTTTGGTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTG
TCCGGTCAAATAACCCCCTCACAATAAGTGTAATGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAG
GCGTGAGGTCATGCTATCCCCCTCTGAAGACGCGGCCGCGAT
```

CTE2 - 450bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATA
CCACTTTGAGGCATGTAATATGGTACTGAGCTTCGGCACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGC
TATATGTCATGGATAAAGGCAGCCCCCTATATCTTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGT
CTTAATGACCTCCACAGCTCTAAACGTAATTCATCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTG
ATAATGCTCATAATGCTGCCCAGCAATTTCCTCCCTTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGG
CTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAACGCTAGCTTAGGTCTTCTGCGGCCGCGAT
```

CTE2 - 550bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACA
CAGGACCCAGGCGTGCAAGTCAATTTCAGCTGACTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTT
AGAGAAAAAAAACCACACCTCTAATGTGTTGGGCACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCA
TTGGGAATAACATACCCCCCACTGTGATTAAGACTGGCACTGTCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTG
TGATTCCCTCTGGCAAACTTATAGAGGACAAGCAGAATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTG
CCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATGGTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTC
TGAGGACACAACGAGGAAATCTGATAAATACGGCCACCTGAAGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGA
GCGGCCGCGAT
```

CTE2 - 650bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGT
CTAGTCTGTGCTGTTGCCTGGATAGTAAATTATCATGGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTA
AAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGTCATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATG
CAATTTTGGGATTCCCTTTTAGTTGCTTTCATTAAAATGTACCAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTA
TGTAACTCACTATCTCATTTGCACTGGTTACATGGCAGCTTCAGACTGACTAAAACTACACTTTTCCCACCATGGTT
CAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTA
CTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCACACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAA
AGGCTTCCGGACCAACCCTTGTTTCTTTATGGTGCTTGTGTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATT
TATCCGATCGTTTATATGGGCGTGCGGCCGCGAT
```

CTE2 - 750bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTT
GTTGCCCCGCCTGATGTTGCCACTACTTGCTCATGACAGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTT
TCCAAGTACAGTTGTAGGGTACTCCTTATACTGATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTA
GGAGTTGAGCTTCACAAATTCACCAGGTAAGCCCAAATTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTG
TCTAATATATTAAAAGAGGGATTTTCTTTGCTGTATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTA
TTGCTGGCCTAGGGGCTTTTGCTCCTACACGAACACCACTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATT
CATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAGCATTCACTTGGTTGGTTTAAGTGGAGGCAACTCCATTATC
TTCTAGCATACCCTTCCCAGGCTACATGTAGAAAGAGATCTGTTGGGCCCCACTATTTTTTCACCCAGGGAAGCCTA
CTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTCATGTAGAAGTCATCCACTTTTAACACCAGGAGGTGGATGTGGG
GCCAGGAAATATGTCAATAACGATACGGGACTTCTAACAGTGACTCGCGGCCGCGAT
```

CTE2 - 850bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACG
ATGGATATTTTCTTTCTAAACTTTAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGA
GGAAGATCCAGACTACAATAGAATATGTGGCCAAAACTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATA
ACCTCCTCACAAAAAGTACACAAATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTT
TAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCA
CATACCCTCTCCCAGAGTCCATTCTCTAAAACTTGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGG
TCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGT
CTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACATTTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGG
TCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGG
TGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGA
GGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGC
GAT
```

CTE1 - 123bp

```
GATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAATCGA
AGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCA
```

CTE1 - 223bp

```
GATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTGAACC
TTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCCGTTA
GTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCA
```

CTE1 - 323bp

```
GATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCTATTAGATCATTGTG
TTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTGGTGG
CTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACAATAAGTGTAATGTC
ATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGCGGCC
GCGATATCCTGCAGATGCA
```

CTE1 - 423bp

```
GATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTACTGAGCTTCGGC
ACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTATATCTTTT
TTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTCATCTG
GCTTTGCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATAATGCTGCCCAGCAATTTCCTCCCTT
```

CTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAAC
GCTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 523bp

GATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTTCAGCTGACTAC
ACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAAACCACACCTCTAATGTGTTGGGCACT
AGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCCACTGTGATTAAGACTGG
CACTGTCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACTTATAGAGGACAAGCAGAA
TAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTTCATG
GTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGGCCAC
CTGAAGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGAGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 623bp

GATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGTAAATTATCATG
GTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGTCATT
AAATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGGGATTCCCTTTTAGTTGCTTTCATTAAAA
TGTACCAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTATCTCATTTGCACTGGTTACATGGCA
GCTTCAGACTGACTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCAACAAAAGCAATTTT
TTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCTCCAC
ACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGTGCTT
GTGTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGATATC
CTGCAGATGCA

CTE1 - 723bp

GATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCCTGATGTTGCCACTACTTGCTCATGAC
AGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACTCCTTATACTGATTC
TTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGCCCAAA
TTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATTTTCTTTGCTGTATT
GCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAACACC
ACTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTACCAACTATCGCTAAG
CATTCACTTGGTTGGTTTAAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGGCTACATGTAGAAAGAG
ATCTGTTGGGCCCCACTATTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGTCATG
TAGAAGTCATCCACTTTTAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTTCTAA
CAGTGACTCGCGGCCGCGATATCCTGCAGATGCA

CTE1 - 823bp

GATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAAACTTTAAACAAACAGTGG
AGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAATATGTGGCCAAAAC
TCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAAATGGCTAAATAACA
GAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTT
ATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAAACTTGAA
GCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAA
TAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACAT
TTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCC
AAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTG
GGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCT
GGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCA

CTA - 150bp

GGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAA
TCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 250bp

GGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTG
AACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCC
GTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCA
TCCAGTACTAGTATGGCCC

CTA - 350bp

GGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCTATTAGATCAT
TGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTG
GTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACAATAAGTGTAA
TGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGC
GGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 450bp

GGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGGTACTGAGCTT
CGGCACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGCCCCCTATATC
TTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAAACGTAATTCA
TCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATAATGCTGCCCAGCAATTTCCTC
CCTTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAAATTGCACTCT
AAACGCTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 550bp

GGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAATTTCAGCTGA
CTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAAACCACACCTCTAATGTGTTGGG
CACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCCACTGTGATTAAGA
CTGGCACTGTCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACTTATAGAGGACAAGC
AGAATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATGTCTTGCCCTT
CATGGTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTGATAAATACGG
CCACCTGAAGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGAGCGGCCGCGATATCCTGCAGATGCATCCAGTAC
TAGTATGGCCC

CTA - 650bp

GGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGATAGTAAATTAT
CATGGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCCCCAGGTGTGT
CATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGGGATTCCCTTTTAGTTGCTTTCATT
AAAATGTACCAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTATCTCATTTGCACTGGTTACAT
GGCAGCTTCAGACTGACTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCAACAAAAGCAA
TTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCAGTTTTTCCCT
CCACACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTTTCTTTATGGT
GCTTGTGTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGTGCGGCCGCGA
TATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 750bp

GGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCCTGATGTTGCCACTACTTGCTCA
TGACAGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACTCCTTATACTG
ATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCACCAGGTAAGCC
CAAATTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATTTTCTTTGCTG
TATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCTCCTACACGAA
CACCACTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTACCAACTATCGC
TAAGCATTCACTTGGTTGGTTTAAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGGCTACATGTAGAA
AGAGATCTGTTGGGCCCCACTATTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGATTTTCTGTGT
CATGTAGAAGTCATCCACTTTTAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGATACGGGACTT
CTAACAGTGACTCGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC

CTA - 850bp

GGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAAACTTTAAACAAACA
GTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAATATGTGGCCA
AAACTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAAATGGCTAAAT
AACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTCTTGATCCCAA
TGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAAACT
TGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGA
GTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAAGTG
ACATTTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTCATGGTT
CTCCAAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATG
TGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCC
CCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGG
CCC

CTL - 150bp

AGTATGGCCCGGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGT
AAGTTGCAAATCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 250bp

AGTATGGCCCGGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATC
AGTGCTTTTGAACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGG
TATGCAGCCCGTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCC
TGCAGATGCATCCAGTACA

CTL - 350bp

AGTATGGCCCGGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCT
ATTAGATCATTGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGC
CGGATGTTTGGTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACA
ATAAGTGTAATGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCT
CTGAAGACGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 450bp

AGTATGGCCCGGGGGATCCGTATACGTTTCTAATTTGTAGTTAACGGTTGGATACCACTTTGAGGCATGTAATATGG
TACTGAGCTTCGGCACAGGGCTCAAATTGCATCATTAAATGTCTCCGATGTGGCTATATGTCATGGATAAAGGCAGC
CCCCTATATCTTTTTTTGTGGCAGCATGGGTCCATCAAAGCAATTATTCAGGGTCTTAATGACCTCCACAGCTCTAA

ACGTAATTCATCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAAGTGTTGATAATGCTCATAATGCTGCCCAG
CAATTTCCTCCCTTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGGCTTAGAGTATGGCTGCTGACAAA
ATTGCACTCTAAACGCTAGCTTAGGTCTTCTGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 550bp

AGTATGGCCCGGGGGATCCGTTAGCTATCGTTCGCGAGAAAGTTAGTAGACACACAGGACCCAGGCGTGCAAGTCAA
TTTCAGCTGACTACACCGATTCTGGTTAAAAGAGCCTATGGCCACCCTTATTTTAGAGAAAAAAAACCACACCTCTA
ATGTGTTGGGCACTAGAAAAAGCTAACTACCTAGTCCGTTTCTGGACGACTTCATTGGGAATAACATACCCCCCACT
GTGATTAAGACTGGCACTGTCCTAATGCTTTCTTCAATAGGTTTGGCTCATGTGTGATTCCCTCTGGCAAACTTATA
GAGGACAAGCAGAATAAACCAATTCAAGGTCGTTGTAGCTGAAGGCCTGGCCTGCCTGACAGTTAATTATGAGCATG
TCTTGCCCTTCATGGTGGATATTCACAGCTGAAAGTGGTATTGGCATTTTTTTCTGAGGACACAACGAGGAAATCTG
ATAAATACGGCCACCTGAAGTCTAGCTCGGAGTTAACAATTTACCACGTTTAGAGCGGCCGCGATATCCTGCAGATG
CATCCAGTACA

CTL - 650bp

AGTATGGCCCGGGGGATCCGCTCGCACTTAGCCTGTTAAGGGGTTCGCGCTCGTCTAGTCTGTGCTGTTGCCTGGAT
AGTAAATTATCATGGTACAAACTTTTAAGAGCCAGTTAAATGGAGATGGATTTAAAAAGAGTTATTGTAAAGTCTCC
CCAGGTGTGTCATTAAATATCCCAACAGATTGCCCTGGCCTGACCCCCTAAATGCAATTTTGGGATTCCCTTTTAGT
TGCTTTCATTAAAATGTACCAGCGCAGTAAAAAAAGCACAAAGTATATTGTTTATGTAACTCACTATCTCATTTGCA
CTGGTTACATGGCAGCTTCAGACTGACTAAAACTACACTTTTCCCACCATGGTTCAAAGATCAACAGAACTGGGCCA
ACAAAAGCAATTTTTTCATGTGGTCTAACTACCAACTTATTATGAGTTAAGTTACTTTTAGGTTTAAAATCACAGCA
GTTTTTCCCTCCACACCTCCCAGAGATACTTTCAGGGTGGCTAAACTTGGCTAAAGGCTTCCGGACCAACCCTTGTT
TCTTTATGGTGCTTGTGTCCTGACAACCGCGTAAGGCATGGAAATTCAGCTATTTATCCGATCGTTTATATGGGCGT
GCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 750bp

AGTATGGCCCGGGGGATCCTTGGACCGTTAATTCATATATCGAAGTAGCAGGTTGTTGCCCCGCCTGATGTTGCCAC
TACTTGCTCATGACAGTTTTTTTAGGCAATGCAAACTACTATTTGATATTTTTTTCCAAGTACAGTTGTAGGGTACT
CCTTATACTGATTCTTCTGAGCCTGTACGGGGAGCATTAGGTACTGATGTAGTAGGAGTTGAGCTTCACAAATTCAC
CAGGTAAGCCCAAATTTATTTTCTGCTTGGACAGGTCCACCTCACATGGGTCTGTCTAATATATTAAAAGAGGGATT
TTCTTTGCTGTATTGCAGCCCAGTATATCTGTTACTTACAGTAGTAGTCCATTATTGCTGGCCTAGGGGCTTTTGCT
CCTACACGAACACCACTCTGTAAAATTTGAGGTCGTCCTTAGAGTCAAACCATTCATGGAGCGCTCTGTGCATCTAC
CAACTATCGCTAAGCATTCACTTGGTTGGTTTAAGTGGAGGCAACTCCATTATCTTCTAGCATACCCTTCCCAGGCT
ACATGTAGAAAGAGATCTGTTGGGCCCCACTATTTTTTCACCCAGGGAAGCCTACTTTAGTTATAGCTTGCCAGAGA
TTTTCTGTGTCATGTAGAAGTCATCCACTTTTAACACCAGGAGGTGGATGTGGGGCCAGGAAATATGTCAATAACGA
TACGGGACTTCTAACAGTGACTCGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

CTL - 850bp

AGTATGGCCCGGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACGATGGATATTTTCTTTCTAAACTT
TAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGAGGAAGATCCAGACTACAATAGAA
TATGTGGCCAAAACTCTCCGCAACTTCAGCAGCAAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAA
ATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTC
TTGATCCCAATGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATT
CTCTAAAACTTGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAG
CTTTTGAAGAGTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTA
AAAAAAAGTGACATTTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAG
GTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGAT
GCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGAT

TCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCATCCAGTACA

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′-GCCTTGCCAGCCCGCTCAGAGATGTGTATAAGAGACAG

Adapters (Showing Optional Bar Code)

5′-AATGATACGGCGACCACCGAGATCTACACGCCTCCCTCGCGCCATCAG

5′-CAAGCAGAAGACGGCATACGAGAT[barcode]CGGTCTGCCTTGCCAGCCCGCTCAG-3'

PCR Primers

5′-AATGATACGGCGACCACCGA

5′-CAAGCAGAAGACGGCATACGA

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′ CCGGTTCTTCCCTGCCGAACCCTATCTTCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTACGCTTGCAT

TruSeq DNA Methylation

Adapter Trimming

The following sequence is used for adapter trimming.

Read 1

AGATCGGAAGAGCACACGTCTGAAC

Read 2

AGATCGGAAGAGCGTCGTGTAGGGA

TruSeq Universal Adapter

5′ AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT

Index PCR Primers

`5′ CAAGCAGAAGACGGCATACGAGAT[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 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′ ATGATACGGCGACCACCGAGATCTACACGTTCAGAGTTCTACAGTCCGACG`

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

i7 Index Name	Six-Base Sequence for Sample Sheet
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′ CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT`

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′ 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 Small RNA v1 and v1.5 Kits

(Obsolete)

RT Primer

5' CAAGCAGAAGACGGCATACGA

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' CAAGCAGAAGACGGCATACGA

Small RNA PCR Primer 2

5' AATGATACGGCGACCACCGACAGGTTCAGAGTTCTACAGTCCGA

Small RNA Sequencing Primer

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5' CGACAGGTTCAGAGTTCTACAGTCCGACGATC
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Revision History

Document	Date	Description of Change
Document # 1000000002694 v10	February 2019	Added UD index adapters and additional CD index adapters to the *Sequences for AmpliSeq for Illumina Panels* section. Fixed *IDT for Illumina TruSeq DNA UD Indexes* section to *IDT for Illumina TruSeq DNA and RNA UD Indexes*. Changed *TruSeq CD Indexes* section to *TruSeq DNA and RNA CD Indexes*. Clarified correct TruSeq Small RNA sequences needed for sample sheet.
Document # 1000000002694 v09	November 2018	Updated the document structure: • Consolidated sections by kit. • Consolidated index adapter tables for TruSight DNA Enrichment and Nextera DNA indexes. • Divided the *IDT for Illumina UD Indexes* 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 *Legacy Kits*. Added the following sequences and bases: • 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. Added the following miscellaneous information: • 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	Date	Description of Change
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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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**.

Document # 1000000002694 v10

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