Illumina Adapter Sequences

This document provides the nucleotide sequences that comprise Illumina oligonucleotides used in Illumina sequencing technologies. These sequences are provided for the sole purpose of understanding and publishing the results of your sequencing experiments.

Proprietary to Illumina

The oligonucleotides are proprietary to Illumina. Their manufacture, use, and sequence information are protected by intellectual property, including issued or pending patents, copyright, and trade secrets. Illumina reserves all rights in the oligonucleotides and their sequence information, except for the strictly limited permissions as follows.

Most Illumina oligonucleotides are specially modified and purified in a proprietary manner to enable and optimize their performance with Illumina instruments. Illumina is the only authorized supplier of the oligos. Illumina has no control over the quality, composition, or compatibility of reagents from unauthorized suppliers. We cannot troubleshoot or provide other support for experiments performed with unauthorized reagents, and we cannot guarantee the performance of Illumina products when used with such reagents.

Limited Permissions

Your permission to copy or distribute sequence information is limited to within your institution for use only with Illumina instruments and associated equipment, consumables, and software. You may not copy or distribute this information outside your institution, except under the following circumstances.

You may distribute outside your institution and publish the sequence information in presentations, manuscripts, or publications authored by you, if the following copyright notice is included:

Oligonucleotide sequences © 2019 Illumina, Inc. All rights reserved.

If you modify or adapt any sequence information contained in this letter and distribute or publish the modified sequences, you must include the following copyright notice:

Oligonucleotide sequences © 2019 Illumina, Inc. All rights reserved. Derivative works created by Illumina customers are authorized for use with Illumina instruments and products only. All other uses are strictly prohibited.

For all other uses of the sequence information or for questions on custom oligonucleotides, please contact Illumina to discuss the permissions or licenses that might be required.

© 2019 Illumina, Inc. All rights reserved.

All trademarks are the property of Illumina, Inc. or their respective owners. For specific trademark information, see www.illumina.com/company/legal.html.

For Research Use Only. Not for use in diagnostic procedures.

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. The index adapters are 10 bases long, instead of the typical eight bases.

Index 1 (i7) Adapters

CAAGCAGAAGACGGCATACGAGAT[i7]GTCTCGTGGGCTCGG

Index 2 (i5) Adapters

AATGATACGGCGACCACCGAGATCTACAC[i5]TCGTCGGCAGCGTC

Plate A Index Adapters

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

For Research Use Only. Not for use in diagnostic procedures.

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
UDP0018	GGTTGCCTCT	AGAGGCAACC	CTAATGATGG	CCATCATTAG
UDP0019	CTAATGATGG	CCATCATTAG	GGTTGCCTCT	AGAGGCAACC
UDP0020	TCGGCCTATC	GATAGGCCGA	CGCACATGGC	GCCATGTGCG
UDP0021	AGTCAACCAT	ATGGTTGACT	GGCCTGTCCT	AGGACAGGCC
UDP0022	GAGCGCAATA	TATTGCGCTC	CTGTGTTAGG	CCTAACACAG
UDP0023	AACAAGGCGT	ACGCCTTGTT	TAAGGAACGT	ACGTTCCTTA
UDP0024	GTATGTAGAA	TTCTACATAC	CTAACTGTAA	TTACAGTTAG
UDP0025	TTCTATGGTT	AACCATAGAA	GGCGAGATGG	CCATCTCGCC
UDP0026	CCTCGCAACC	GGTTGCGAGG	AATAGAGCAA	TTGCTCTATT
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

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
UDP0056	CTCGTGCGTT	AACGCACGAG	GCCTCGGATA	TATCCGAGGC
UDP0057	TTAGGATAGA	TCTATCCTAA	CGTCGACTGG	CCAGTCGACG
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

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
UDP0094	CAATCTATGA	TCATAGATTG	GATTAAGGTG	CACCTTAATC
UDP0095	GGTGGAATAC	GTATTCCACC	ATGTAGACAA	TTGTCTACAT
UDP0096	TGGACGGAGG	CCTCCGTCCA	CACATCGGTG	CACCGATGTG

Plate B Index Adapters

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
UDP0097	CTGACCGGCA	TGCCGGTCAG	CCTGATACAA	TTGTATCAGG
UDP0098	GAATTGAGTG	CACTCAATTC	TTAAGTTGTG	CACAACTTAA
UDP0099	GCGTGTGAGA	TCTCACACGC	CGGACAGTGA	TCACTGTCCG
UDP0100	TCTCCATTGA	TCAATGGAGA	GCACTACAAC	GTTGTAGTGC
UDP0101	ACATGCATAT	ATATGCATGT	TGGTGCCTGG	CCAGGCACCA
UDP0102	CAGGCGCCAT	ATGGCGCCTG	TCCACGGCCT	AGGCCGTGGA
UDP0103	ACATAACGGA	TCCGTTATGT	TTGTAGTGTA	TACACTACAA
UDP0104	TTAATAGACC	GGTCTATTAA	CCACGACACG	CGTGTCGTGG
UDP0105	ACGATTGCTG	CAGCAATCGT	TGTGATGTAT	ATACATCACA
UDP0106	TTCTACAGAA	TTCTGTAGAA	GAGCGCAATA	TATTGCGCTC
UDP0107	TATTGCGTTC	GAACGCAATA	ATCTTACTGT	ACAGTAAGAT
UDP0108	CATGAGTACT	AGTACTCATG	ATGTCGTGGT	ACCACGACAT
UDP0109	TAATTCTACC	GGTAGAATTA	GTAGCCATCA	TGATGGCTAC
UDP0110	ACGCTAATTA	TAATTAGCGT	TGGTTAAGAA	TTCTTAACCA
UDP0111	CCTTGTTAAT	ATTAACAAGG	TGTTGTTCGT	ACGAACAACA
UDP0112	GTAGCCATCA	TGATGGCTAC	CCAACAACAT	ATGTTGTTGG
UDP0113	CTTGTAATTC	GAATTACAAG	ACCGGCTCAG	CTGAGCCGGT
UDP0114	TCCAATTCTA	TAGAATTGGA	GTTAATCTGA	TCAGATTAAC
UDP0115	AGAGCTGCCT	AGGCAGCTCT	CGGCTAACGT	ACGTTAGCCG
UDP0116	CTTCGCCGAT	ATCGGCGAAG	TCCAAGAATT	AATTCTTGGA
UDP0117	TCGGTCACGG	CCGTGACCGA	CCGAACGTTG	CAACGTTCGG
UDP0118	GAACAAGTAT	ATACTTGTTC	TAACCGCCGA	TCGGCGGTTA
UDP0119	AATTGGCGGA	TCCGCCAATT	CTCCGTGCTG	CAGCACGGAG
UDP0120	GGCCTGTCCT	AGGACAGGCC	CATTCCAGCT	AGCTGGAATG
UDP0121	TAGGTTCTCT	AGAGAACCTA	GGTTATGCTA	TAGCATAACC
UDP0122	ACACAATATC	GATATTGTGT	ACCACACGGT	ACCGTGTGGT
UDP0123	TTCCTGTACG	CGTACAGGAA	TAGGTTCTCT	AGAGAACCTA
UDP0124	GGTAACGCAG	CTGCGTTACC	TATGGCTCGA	TCGAGCCATA
UDP0125	TCCACGGCCT	AGGCCGTGGA	CTCGTGCGTT	AACGCACGAG
UDP0126	GATACCTCCT	AGGAGGTATC	CCAGTTGGCA	TGCCAACTGG

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
UDP0127	CAACGTCAGC	GCTGACGTTG	TGTTCGCATT	AATGCGAACA
UDP0128	CGGTTATTAG	CTAATAACCG	AACCGCATCG	CGATGCGGTT
UDP0129	CGCGCCTAGA	TCTAGGCGCG	CGAAGGTTAA	TTAACCTTCG
UDP0130	TCTTGGCTAT	ATAGCCAAGA	AGTGCCACTG	CAGTGGCACT
UDP0131	TCACACCGAA	TTCGGTGTGA	GAACAAGTAT	ATACTTGTTC
UDP0132	AACGTTACAT	ATGTAACGTT	ACGATTGCTG	CAGCAATCGT
UDP0133	CGGCCTCGTT	AACGAGGCCG	ATACCTGGAT	ATCCAGGTAT
UDP0134	CATAACACCA	TGGTGTTATG	TCCAATTCTA	TAGAATTGGA
UDP0135	ACAGAGGCCA	TGGCCTCTGT	TGAGACAGCG	CGCTGTCTCA
UDP0136	TGGTGCCTGG	CCAGGCACCA	ACGCTAATTA	TAATTAGCGT
UDP0137	TAGGAACCGG	CCGGTTCCTA	TATATTCGAG	CTCGAATATA
UDP0138	AATATTGGCC	GGCCAATATT	CGGTCCGATA	TATCGGACCG
UDP0139	ATAGGTATTC	GAATACCTAT	ACAATAGAGT	ACTCTATTGT
UDP0140	CCTTCACGTA	TACGTGAAGG	CGGTTATTAG	CTAATAACCG
UDP0141	GGCCAATAAG	CTTATTGGCC	GATAACAAGT	ACTTGTTATC
UDP0142	CAGTAGTTGT	ACAACTACTG	AGTTATCACA	TGTGATAACT
UDP0143	TTCATCCAAC	GTTGGATGAA	TTCCAGGTAA	TTACCTGGAA
UDP0144	CAATTGGATT	AATCCAATTG	CATGTAGAGG	CCTCTACATG
UDP0145	GGCCATCATA	TATGATGGCC	GATTGTCATA	TATGACAATC
UDP0146	AATTGCTGCG	CGCAGCAATT	ATTCCGCTAT	ATAGCGGAAT
UDP0147	TAAGGAACGT	ACGTTCCTTA	GACCGCTGTG	CACAGCGGTC
UDP0148	CTATACGCGG	CCGCGTATAG	TAGGAACCGG	CCGGTTCCTA
UDP0149	ATTCAGAATC	GATTCTGAAT	AGCGGTGGAC	GTCCACCGCT
UDP0150	GTATTCTCTA	TAGAGAATAC	TATAGATTCG	CGAATCTATA
UDP0151	CCTGATACAA	TTGTATCAGG	ACAGAGGCCA	TGGCCTCTGT
UDP0152	GACCGCTGTG	CACAGCGGTC	ATTCCTATTG	CAATAGGAAT
UDP0153	TTCAGCGTGG	CCACGCTGAA	TATTCCTCAG	CTGAGGAATA
UDP0154	AACTCCGAAC	GTTCGGAGTT	CGCCTTCTGA	TCAGAAGGCG
UDP0155	ATTCCGCTAT	ATAGCGGAAT	GCGCAGAGTA	TACTCTGCGC
UDP0156	TGAATATTGC	GCAATATTCA	GGCGCCAATT	AATTGGCGCC
UDP0157	CGCAATCTAG	CTAGATTGCG	AGATATGGCG	CGCCATATCT
UDP0158	AACCGCATCG	CGATGCGGTT	CCTGCTTGGT	ACCAAGCAGG
UDP0159	CTAGTCCGGA	TCCGGACTAG	GACGAACAAT	ATTGTTCGTC
UDP0160	GCTCCGTCAC	GTGACGGAGC	TGGCGGTCCA	TGGACCGCCA
UDP0161	AGATGGAATT	AATTCCATCT	CTTCAGTTAC	GTAACTGAAG
UDP0162	ACACCGTTAA	TTAACGGTGT	TCCTGACCGT	ACGGTCAGGA
UDP0163	GATAACAAGT	ACTTGTTATC	CGCGCCTAGA	TCTAGGCGCG
UDP0164	CTGGTACACG	CGTGTACCAG	AGGATAAGTT	AACTTATCCT

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
UDP0165	CGAAGGTTAA	TTAACCTTCG	AGGCCAGACA	TGTCTGGCCT
UDP0166	ATCGCATATG	CATATGCGAT	CCTTGAACGG	CCGTTCAAGG
UDP0167	ATCATAGGCT	AGCCTATGAT	CACCACCTAC	GTAGGTGGTG
UDP0168	GATTGTCATA	TATGACAATC	TTGCTTGTAT	ATACAAGCAA
UDP0169	CCAACAACAT	ATGTTGTTGG	CAATCTATGA	TCATAGATTG
UDP0170	TTGGTGGTGC	GCACCACCAA	TGGTACTGAT	ATCAGTACCA
UDP0171	GCGAACGCCT	AGGCGTTCGC	TTCATCCAAC	GTTGGATGAA
UDP0172	CAACCGGAGG	CCTCCGGTTG	CATAACACCA	TGGTGTTATG
UDP0173	AGCGGTGGAC	GTCCACCGCT	TCCTATTAGC	GCTAATAGGA
UDP0174	GACGAACAAT	ATTGTTCGTC	TCTCTAGATT	AATCTAGAGA
UDP0175	CCACTGGTCC	GGACCAGTGG	CGCGAGCCTA	TAGGCTCGCG
UDP0176	TGTTAGAAGG	CCTTCTAACA	GATAAGCTCT	AGAGCTTATC
UDP0177	TATATTCGAG	CTCGAATATA	GAGATGTCGA	TCGACATCTC
UDP0178	CGCGACGATC	GATCGTCGCG	CTGGATATGT	ACATATCCAG
UDP0179	GCCTCGGATA	TATCCGAGGC	GGCCAATAAG	CTTATTGGCC
UDP0180	TGAGACAGCG	CGCTGTCTCA	ATTACTCACC	GGTGAGTAAT
UDP0181	TGTTCGCATT	AATGCGAACA	AATTGGCGGA	TCCGCCAATT
UDP0182	TCCAAGAATT	AATTCTTGGA	TTGTCAACTT	AAGTTGACAA
UDP0183	GCTGTAGGAA	TTCCTACAGC	GGCGAATTCT	AGAATTCGCC
UDP0184	ATACCTGGAT	ATCCAGGTAT	CAACGTCAGC	GCTGACGTTG
UDP0185	GTTGGACCGT	ACGGTCCAAC	TCTTACATCA	TGATGTAAGA
UDP0186	ACCAAGTTAC	GTAACTTGGT	CGCCATACCT	AGGTATGGCG
UDP0187	GTGTGGCGCT	AGCGCCACAC	CTAATGTCTT	AAGACATTAG
UDP0188	GGCAGTAGCA	TGCTACTGCC	CAACCGGAGG	CCTCCGGTTG
UDP0189	TGCGGTGTTG	CAACACCGCA	GGCAGTAGCA	TGCTACTGCC
UDP0190	GATTAAGGTG	CACCTTAATC	TTAGGATAGA	TCTATCCTAA
UDP0191	CAACATTCAA	TTGAATGTTG	CGCAATCTAG	CTAGATTGCG
UDP0192	GTGTTACCGG	CCGGTAACAC	GAGTTGTACT	AGTACAACTC

Plate C Index Adapters

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
UDP0193	TATCATGAGA	TCTCATGATA	AACACGTGGA	TCCACGTGTT
UDP0194	CTTGGCCTCG	CGAGGCCAAG	GTGTTACCGG	CCGGTAACAC
UDP0195	GTCTCGTGAA	TTCACGAGAC	AGATTGTTAC	GTAACAATCT
UDP0196	CCATCCACGC	GCGTGGATGG	TTGACCAATG	CATTGGTCAA
UDP0197	ACAACCAGGA	TCCTGGTTGT	CTGACCGGCA	TGCCGGTCAG

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
UDP0198	AGCAGAATTA	TAATTCTGCT	TCTCATCAAT	ATTGATGAGA
UDP0199	CAGTCGTGCG	CGCACGACTG	GGACCAACAG	CTGTTGGTCC
UDP0200	GTCTAACCTC	GAGGTTAGAC	AATGTATTGC	GCAATACATT
UDP0201	GAACTCGGTT	AACCGAGTTC	GATCTCTGGA	TCCAGAGATC
UDP0202	AGTTATCACA	TGTGATAACT	CAGGCGCCAT	ATGGCGCCTG
UDP0203	GTAGCATACT	AGTATGCTAC	TTAATAGACC	GGTCTATTAA
UDP0204	CTTCAGTTAC	GTAACTGAAG	GGAGTCGCGA	TCGCGACTCC
UDP0205	AGTCCGAGGA	TCCTCGGACT	AACGCCAGAG	CTCTGGCGTT
UDP0206	ACAGTTCCAG	CTGGAACTGT	CGTAATTAAC	GTTAATTACG
UDP0207	CCGCATATTC	GAATATGCGG	ACGAGACTGA	TCAGTCTCGT
UDP0208	TTATCCGATC	GATCGGATAA	GTATCGGCCG	CGGCCGATAC
UDP0209	ATAGTCTAGC	GCTAGACTAT	AATACGACAT	ATGTCGTATT
UDP0210	TATAGTAGCT	AGCTACTATA	GTTATATGGC	GCCATATAAC
UDP0211	ACTCCGGTGG	CCACCGGAGT	GCCTGCCATG	CATGGCAGGC
UDP0212	GTGCGGTAAG	CTTACCGCAC	TAAGACCTAT	ATAGGTCTTA
UDP0213	GATATCCTAA	TTAGGATATC	TATACCATGG	CCATGGTATA
UDP0214	TCGCGTATAA	TTATACGCGA	GCCGTCTGTT	AACAGACGGC
UDP0215	ATTCTAAGCG	CGCTTAGAAT	CAGAGTGATA	TATCACTCTG
UDP0216	AGCGCTTCGG	CCGAAGCGCT	TGCTAACTAT	ATAGTTAGCA
UDP0217	GTTGATAGTG	CACTATCAAC	TCAGTTAATG	CATTAACTGA
UDP0218	AATAGAGCAA	TTGCTCTATT	GTGACCTTGA	TCAAGGTCAC
UDP0219	CTAACTGTAA	TTACAGTTAG	ACATGCATAT	ATATGCATGT
UDP0220	GCGTACTTAG	CTAAGTACGC	AACATACCTA	TAGGTATGTT
UDP0221	TACCGAACTA	TAGTTCGGTA	CCATGTGTAG	CTACACATGG
UDP0222	GTAGTAATAG	CTATTACTAC	GAGTCTCTCC	GGAGAGACTC
UDP0223	GGTTATGCTA	TAGCATAACC	GCTATGCGCA	TGCGCATAGC
UDP0224	ACAATAGAGT	ACTCTATTGT	ATCGCATATG	CATATGCGAT
UDP0225	GCTTCCACTA	TAGTGGAAGC	AGTACCTATA	TATAGGTACT
UDP0226	AGATATGGCG	CGCCATATCT	GACCGGAGAT	ATCTCCGGTC
UDP0227	AATATGAAGC	GCTTCATATT	CGTTCAGCCT	AGGCTGAACG
UDP0228	TAGCGCTAGT	ACTAGCGCTA	TTACTTCCTC	GAGGAAGTAA
UDP0229	AGTTAAGAGC	GCTCTTAACT	CACGTCCACC	GGTGGACGTG
UDP0230	CAGATACCAC	GTGGTATCTG	GCTACTATCT	AGATAGTAGC
UDP0231	ACGGCCGTCA	TGACGGCCGT	AGTCAACCAT	ATGGTTGACT
UDP0232	GTAATTACTG	CAGTAATTAC	CGAGGCGGTA	TACCGCCTCG
UDP0233	AAGTCTTGTA	TACAAGACTT	CAGGTGTTCA	TGAACACCTG
UDP0234	GTCACCACAG	CTGTGGTGAC	GACAGACAGG	CCTGTCTGTC
UDP0235	ATTAGTGGAG	CTCCACTAAT	TGTACTTGTT	AACAAGTACA

For Research Use Only. Not for use in diagnostic procedures.

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
UDP0236	TGCTAACTAT	ATAGTTAGCA	CTCTAAGTAG	CTACTTAGAG
UDP0237	TAAGACCTAT	ATAGGTCTTA	GTCACCACAG	CTGTGGTGAC
UDP0238	TGGTTAAGAA	TTCTTAACCA	TCTACATACC	GGTATGTAGA
UDP0239	ACTCTTCCTT	AAGGAAGAGT	CACGTTAGGC	GCCTAACGTG
UDP0240	GTCTCCTTCC	GGAAGGAGAC	TGGTGAGTCT	AGACTCACCA
UDP0241	TCCGCGTTCA	TGAACGCGGA	CTTCGAAGGA	TCCTTCGAAG
UDP0242	AGGTTGCAGG	CCTGCAACCT	GTAGAGTCAG	CTGACTCTAC
UDP0243	GAACCATGAA	TTCATGGTTC	GACATTGTCA	TGACAATGTC
UDP0244	TTGAGAGGAT	ATCCTCTCAA	TCCGCAAGGC	GCCTTGCGGA
UDP0245	TGGTCTAGTG	CACTAGACCA	ACTGCCTTAT	ATAAGGCAGT
UDP0246	AGTGGATAAT	ATTATCCACT	TACGCACGTA	TACGTGCGTA
UDP0247	GGCACGCCAT	ATGGCGTGCC	CGCTTGAAGT	ACTTCAAGCG
UDP0248	GATCTCTGGA	TCCAGAGATC	CTGCACTTCA	TGAAGTGCAG
UDP0249	TGCTGGACAT	ATGTCCAGCA	CAGCGGACAA	TTGTCCGCTG
UDP0250	CCGAACGTTG	CAACGTTCGG	GGATCCGCAT	ATGCGGATCC
UDP0251	ATTAATACGC	GCGTATTAAT	TGCGGTGTTG	CAACACCGCA
UDP0252	TAGTCACAAC	GTTGTGACTA	ACATAACGGA	TCCGTTATGT
UDP0253	GGTATTGAGA	TCTCAATACC	GACGTTCGCG	CGCGAACGTC
UDP0254	CAAGATGCTT	AAGCATCTTG	CATTCAACAA	TTGTTGAATG
UDP0255	ACGAGACTGA	TCAGTCTCGT	CACGGATTAT	ATAATCCGTG
UDP0256	TTATCTTGCA	TGCAAGATAA	TTGAGGACGG	CCGTCCTCAA
UDP0257	AGATTGTTAC	GTAACAATCT	CTCTGTATAC	GTATACAGAG
UDP0258	TCTACCGCTG	CAGCGGTAGA	GCAACAGGTG	CACCTGTTGC
UDP0259	AACGGTATGA	TCATACCGTT	GGTAACGCAG	CTGCGTTACC
UDP0260	CAATGGCGCC	GGCGCCATTG	ACCGCGCAAT	ATTGCGCGGT
UDP0261	CTAATTCGCT	AGCGAATTAG	AGCCGGAACA	TGTTCCGGCT
UDP0262	CATGGTCTAA	TTAGACCATG	TCCTAGGAAG	CTTCCTAGGA
UDP0263	ATACTGTGTG	CACACAGTAT	TTGAGCCTAA	TTAGGCTCAA
UDP0264	GCCGACAAGA	TCTTGTCGGC	CCACCTGTGT	ACACAGGTGG
UDP0265	CGAGGCGGTA	TACCGCCTCG	CCTCGCAACC	GGTTGCGAGG
UDP0266	GATATAACAG	CTGTTATATC	GTATAGCTGT	ACAGCTATAC
UDP0267	TCGCCGGTTA	TAACCGGCGA	GCTACATTAG	CTAATGTAGC
UDP0268	AGACTCTCTT	AAGAGAGTCT	TACGAATCTT	AAGATTCGTA
UDP0269	GCTCGCCTAC	GTAGGCGAGC	TAGGAGCGCA	TGCGCTCCTA
UDP0270	AGGATAAGTT	AACTTATCCT	GTACTGGCGT	ACGCCAGTAC
UDP0271	GAGACATAAT	ATTATGTCTC	AGTTAAGAGC	GCTCTTAACT
UDP0272	AGCTGTTATA	TATAACAGCT	TCGCGTATAA	TTATACGCGA
UDP0273	GTATCATTGG	CCAATGATAC	GAGTGTGCCG	CGGCACACTC

For Research Use Only. Not for use in diagnostic procedures.

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
UDP0274	AATAGGCCTC	GAGGCCTATT	CTAGTCCGGA	TCCGGACTAG
UDP0275	CCGCTTAGCT	AGCTAAGCGG	ATTAATACGC	GCGTATTAAT
UDP0276	TCCTAGGAAG	CTTCCTAGGA	CCTAGAGTAT	ATACTCTAGG
UDP0277	TCACAGATCG	CGATCTGTGA	TAGGAAGACT	AGTCTTCCTA
UDP0278	ACTTGTCCAC	GTGGACAAGT	CCGTGGCCTT	AAGGCCACGG
UDP0279	TGTACTTGTT	AACAAGTACA	GGATATATCC	GGATATATCC
UDP0280	CACTTAATCT	AGATTAAGTG	CACCTCTTGG	CCAAGAGGTG
UDP0281	CAGAGTGATA	TATCACTCTG	AACGTTACAT	ATGTAACGTT
UDP0282	GGCGAATTCT	AGAATTCGCC	CGGCAAGCTC	GAGCTTGCCG
UDP0283	AGTGGTCAGG	CCTGACCACT	TCTTGGCTAT	ATAGCCAAGA
UDP0284	CATTCCAGCT	AGCTGGAATG	ACGGAATGCG	CGCATTCCGT
UDP0285	CTCGTTATCA	TGATAACGAG	GTTCCGCAGG	CCTGCGGAAC
UDP0286	CCTTACTATG	CATAGTAAGG	ACCAAGTTAC	GTAACTTGGT
UDP0287	AGAAGCCAAT	ATTGGCTTCT	TGGCTCGCAG	CTGCGAGCCA
UDP0288	TAATCGGTAC	GTACCGATTA	AACTAACGTT	AACGTTAGTT

Plate D Index Adapters

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
UDP0289	GGAATTGTTC	GAACAATTCC	TAGAGTTGGA	ATCTCAACCT
UDP0290	CCGGACCACA	TGTGGTCCGG	AGAGCACTAG	TCTCGTGATC
UDP0291	GACTTAGAAG	CTTCTAAGTC	ACTCTACAGG	TGAGATGTCC
UDP0292	TGGCAATATT	AATATTGCCA	CGGTGACACC	GCCACTGTGG
UDP0293	GAATGCACGA	TCGTGCATTC	GCGTTGGTAT	CGCAACCATA
UDP0294	CGTGTATCTT	AAGATACACG	TGTGCTAACA	ACACGATTGT
UDP0295	ATTCATTGCA	TGCAATGAAT	CCAGAAGTAA	GGTCTTCATT
UDP0296	TCCTTCATAG	CTATGAAGGA	CTTATACCTG	GAATATGGAC
UDP0297	TCTAGTCTTC	GAAGACTAGA	ACTAGAACTT	TGATCTTGAA
UDP0298	CTCGACTCCT	AGGAGTCGAG	TTAGGCTTAC	AATCCGAATG
UDP0299	AGTGAGTGAA	TTCACTCACT	TATCATGAGA	ATAGTACTCT
UDP0300	GAAGCGGACC	GGTCCGCTTC	CTCACACAAG	GAGTGTGTTC
UDP0301	GCTCTCGTTG	CAACGAGAGC	GAATTGAGTG	CTTAACTCAC
UDP0302	GGACCTCAAT	ATTGAGGTCC	CGGATTATAT	GCCTAATATA
UDP0303	GAGTCTCTCC	GGAGAGACTC	TTGAAGCAGA	AACTTCGTCT
UDP0304	AACGGAGCGG	CCGCTCCGTT	TACGGCGAAG	ATGCCGCTTC
UDP0305	TGTGATGTAT	ATACATCACA	TCTCCATTGA	AGAGGTAACT
UDP0306	AACATACCTA	TAGGTATGTT	CGAGACCAAG	GCTCTGGTTC

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
UDP0307	GTGCTAGGTG	CACCTAGCAC	TGCTGGACAT	ACGACCTGTA
UDP0308	CATACTTGAA	TTCAAGTATG	GATGGTATCG	CTACCATAGC
UDP0309	CTTGTCTTAA	TTAAGACAAG	GGCTTAATTG	CCGAATTAAC
UDP0310	AAGAGAGGTG	CACCTCTCTT	CTCGACTCCT	GAGCTGAGGA
UDP0311	TGCACGAGAA	TTCTCGTGCA	ATACACAGAG	TATGTGTCTC
UDP0312	ACTTCCTAGC	GCTAGGAAGT	TCTCGGACGA	AGAGCCTGCT
UDP0313	GTGCTATTAA	TTAATAGCAC	ACCACGTCTG	TGGTGCAGAC
UDP0314	AGCGTGAATG	CATTCACGCT	GTTGTACTCA	CAACATGAGT
UDP0315	CCTTAGTGCC	GGCACTAAGG	TCAGGTCAAC	AGTCCAGTTG
UDP0316	TGTACCGAAT	ATTCGGTACA	AGTCCGAGGA	TCAGGCTCCT
UDP0317	GGAGATTAGT	ACTAATCTCC	CACTTAATCT	GTGAATTAGA
UDP0318	TACTAACACA	TGTGTTAGTA	TACTCTGTTA	ATGAGACAAT
UDP0319	TAGGTCGTTG	CAACGACCTA	GCGACTCGAT	CGCTGAGCTA
UDP0320	ATGCCGACCG	CGGTCGGCAT	CTAGGCAAGG	GATCCGTTCC
UDP0321	CTAGCGTCGA	TCGACGCTAG	CCTCTTCGAA	GGAGAAGCTT
UDP0322	TGCCTACGAG	CTCGTAGGCA	TCATCCTCTT	AGTAGGAGAA
UDP0323	ACTAGAACTT	AAGTTCTAGT	GGTAAGATAA	CCATTCTATT
UDP0324	CACCTCTTGG	CCAAGAGGTG	AACGAGCCAG	TTGCTCGGTC
UDP0325	AAGCAGATAT	ATATCTGCTT	TAGACAATCT	ATCTGTTAGA
UDP0326	GCCAGATCCA	TGGATCTGGC	CAATGCTGAA	GTTACGACTT
UDP0327	TTGGATTCAA	TTGAATCCAA	GTCACGGTGT	CAGTGCCACA
UDP0328	ACTAGCCGTG	CACGGCTAGT	GGTGTACAAG	CCACATGTTC
UDP0329	CGGCAAGCTC	GAGCTTGCCG	AGGTTGCAGG	TCCAACGTCC
UDP0330	GAAGCTAGCT	AGCTAGCTTC	TAATACGGAG	ATTATGCCTC
UDP0331	ACAAGGATTG	CAATCCTTGT	CGAAGACGCA	GCTTCTGCGT
UDP0332	GCAACAGGTG	CACCTGTTGC	ATTGACACAT	TAACTGTGTA
UDP0333	CAAGGTGACG	CGTCACCTTG	CAGCCGATTG	GTCGGCTAAC
UDP0334	ACCAGTCATT	AATGACTGGT	TCTCACGCGT	AGAGTGCGCA
UDP0335	CCGGAATCAT	ATGATTCCGG	CTCTGACGTG	GAGACTGCAC
UDP0336	TTGAGCCTAA	TTAGGCTCAA	TCGAATGGAA	AGCTTACCTT
UDP0337	CCACCTTACA	TGTAAGGTGG	AAGGCCTTGG	TTCCGGAACC
UDP0338	GTTGCAGTTG	CAACTGCAAC	TGAACGCAAC	ACTTGCGTTG
UDP0339	TCACTCATGT	ACATGAGTGA	CCGCTTAGCT	GGCGAATCGA
UDP0340	GACTGGTTGC	GCAACCAGTC	CACCGAGGAA	GTGGCTCCTT
UDP0341	ATCGTCGCTC	GAGCGACGAT	CGTATAATCA	GCATATTAGT
UDP0342	GGTGCGTTCG	CGAACGCACC	ATGACAGAAC	TACTGTCTTG
UDP0343	CGGCGTAAGA	TCTTACGCCG	ATTCATTGCA	TAAGTAACGT
UDP0344	GACATCAGCT	AGCTGATGTC	TCATGTCCTG	AGTACAGGAC

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
UDP0345	ACTAATTCAG	CTGAATTAGT	AATTCGATCG	TTAAGCTAGC
UDP0346	TTCCTCCTTA	TAAGGAGGAA	TTCCGACATT	AAGGCTGTAA
UDP0347	TGTGTAAGCT	AGCTTACACA	TGGCACGACC	ACCGTGCTGG
UDP0348	GTGGCTGGTT	AACCAGCCAC	GCCACAGCAC	CGGTGTCGTG
UDP0349	TCGACTTAAG	CTTAAGTCGA	CAGTAGTTGT	GTCATCAACA
UDP0350	CACGTTAGGC	GCCTAACGTG	AGCTCTCAAG	TCGAGAGTTC
UDP0351	TGAAGTAAGT	ACTTACTTCA	TCTGGAATTA	AGACCTTAAT
UDP0352	ACGGAATGCG	CGCATTCCGT	ATTAGTGGAG	TAATCACCTC
UDP0353	GTGTGATATC	GATATCACAC	GACTATATGT	CTGATATACA
UDP0354	ACACAGCGCT	AGCGCTGTGT	CGTTCGGAAC	GCAAGCCTTG
UDP0355	AGCGCGGTGA	TCACCGCGCT	TCGATACTAG	AGCTATGATC
UDP0356	CAAGGCTATC	GATAGCCTTG	TACCACAATG	ATGGTGTTAC
UDP0357	TGCGTCCAGG	CCTGGACGCA	TGGTATACCA	ACCATATGGT
UDP0358	AGGTGCGTAA	TTACGCACCT	GCTCTCGTTG	CGAGAGCAAC
UDP0359	GCAGCAACGA	TCGTTGCTGC	GTCTCGTGAA	CAGAGCACTT
UDP0360	ATCCTTGTCG	CGACAAGGAT	AAGGCCACCT	TTCCGGTGGA
UDP0361	GAAGGTACAC	GTGTACCTTC	CTGTGAGCTA	GACACTCGAT
UDP0362	TTGGCCAGGT	ACCTGGCCAA	TCACAGATCG	AGTGTCTAGC
UDP0363	AGGCCAGACA	TGTCTGGCCT	AGAAGCCAAT	TCTTCGGTTA
UDP0364	AGCATTAACT	AGTTAATGCT	ACTGCAGCCG	TGACGTCGGC
UDP0365	ATTACTCACC	GGTGAGTAAT	AACATCTAGT	TTGTAGATCA
UDP0366	GCGCAGAGTA	TACTCTGCGC	CCTTACTATG	GGAATGATAC
UDP0367	CGCCATACCT	AGGTATGGCG	GTGGCGAGAC	CACCGCTCTG
UDP0368	GCAGGCTGGA	TCCAGCCTGC	GCCAGATCCA	CGGTCTAGGT
UDP0369	GTTATATGGC	GCCATATAAC	ACACAATATC	TGTGTTATAG
UDP0370	CACTCGCACT	AGTGCGAGTG	TGGAGGTAAT	ACCTCCATTA
UDP0371	ACCGGCTCAG	CTGAGCCGGT	CCTTCACGTA	GGAAGTGCAT
UDP0372	ATAGACCGTT	AACGGTCTAT	CTATACGCGG	GATATGCGCC
UDP0373	TGAACGCAAC	GTTGCGTTCA	GTTGCAGTTG	CAACGTCAAC
UDP0374	GTGGTTGAAG	CTTCAACCAC	TTATGCGCCT	AATACGCGGA
UDP0375	ACTGAATAGA	TCTATTCAGT	TCTCAGTACA	AGAGTCATGT
UDP0376	GGACGTCTTG	CAAGACGTCC	AGTATACGGA	TCATATGCCT
UDP0377	GTTGTACTCA	TGAGTACAAC	ACGCTTGGAC	TGCGAACCTG
UDP0378	AGAACCGCGG	CCGCGGTTCT	GGAGTAGATT	CCTCATCTAA
UDP0379	CAGTATCAAT	ATTGATACTG	TACACGCTCC	ATGTGCGAGG
UDP0380	TCCATAATCC	GGATTATGGA	TCCGATAGAG	AGGCTATCTC
UDP0381	ATGAGAACCA	TGGTTCTCAT	CTCAAGGCCG	GAGTTCCGGC
UDP0382	TCGTGGTTGA	TCAACCACGA	CAAGTTCATA	GTTCAAGTAT

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
UDP0383	CAAGTTCATA	TATGAACTTG	AATCCTTAGG	TTAGGAATCC
UDP0384	CTTAACCACT	AGTGGTTAAG	GGTGGAATAC	CCACCTTATG

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
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

For Research Use Only. Not for use in diagnostic procedures.

i5 Index Name	i5 Bases for Sample Sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 Bases for Sample Sheet iSeq, HiSeq 3000/4000, MiniSeq, NextSeq
Q5017	CTAGCTTG	CAAGCTAG
Q5018	TCGATCCA	TGGATCGA
Q5025	ATACCAAG	CTTGGTAT
Q5026	GCGTTGGA	TCCAACGC
Q5027	CTTCACGG	CCGTGAAG
Q5028	TCCTGTAA	TTACAGGA
Q5029	CCTCGGTA	TACCGAGG
Q5030	TTCTAACG	CGTTAGAA
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

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

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
D706	UP04	GAATTCGT
D712	UP05	AGCGATAG
D724	UP06	GCGATTAA
D705	UP07	ATTCAGAA
D715	UP08	TTAATCAG
D713	UP09	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

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' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ATCACG</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 2

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CGATGT</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 3

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>TTAGGC</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 4

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>TGACCA</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 5

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ACAGTG</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 6

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GCCAAT</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 7

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CAGATC</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 8

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ACTTGA</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 9

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GATCAG</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 10

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>TAGCTT</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 11

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GGCTAC</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 12

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CTTGTA</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 13

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>AGTCAA</u>CAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 14

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>AGTTCC</u>GTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 15

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ATGTCA</u>GAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 16

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CCGTCC</u>CGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 18

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTCCGC</u>ACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 19

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTGAAA</u>CGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 20

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTGGCC</u>TTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 21

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTTTCG</u>GAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 22

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CGTACG</u>TAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 23

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GAGTGG</u>ATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 25

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ACTGAT</u>ATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 27

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ATTCCT</u>TTATCTCGTATGCCGTCTTCTGCTTG

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
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

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	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
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' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>ATCACG</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 2

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>CGATGT</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 3

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>TTAGGC</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 4

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>TGACCA</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 5

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>ACAGTG</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 6

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>GCCAAT</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 7

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>CAGATC</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 8

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>ACTTGA</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 9

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>GATCAG</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 10

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>TAGCTT</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 11

`5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC`<u>GGCTAC</u>`ATCTCGTATGCCGTCTTCTGCTTG`

Index Adapter 12

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CTTGTA</u>ATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 13

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>AGTCAA</u>CAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 14

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>AGTTCC</u>GTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 15

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ATGTCA</u>GAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 16

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CCGTCC</u>CGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 18

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTCCGC</u>ACATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 19

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTGAAA</u>CGATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 20

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTGGCC</u>TTATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 21

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GTTTCG</u>GAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 22

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>CGTACG</u>TAATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 23

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>GAGTGG</u>ATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 25

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ACTGAT</u>ATATCTCGTATGCCGTCTTCTGCTTG

Index Adapter 27

5' GATCGGAAGAGCACACGTCTGAACTCCAGTCAC<u>ATTCCT</u>TTATCTCGTATGCCGTCTTCTGCTTG

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 Name	Six-Base Sequence in Adapter	Six-Base Sequence for Sample Sheet
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 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 Name	Six-Base Sequence in Adapter	Six-Base Sequence for Sample Sheet
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 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

i7 Index Name	i7 Bases for Sample Sheet
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	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
CTTAATGACCTCCACAGCTCTAAACGTAATTCATCTGGCTTTGCCTGTACTTACTTCCTCCATGAAAAAAGTGTTG
ATAATGCTCATAATGCTGCCCAGCAATTTCCTCCCTTCTCAAGACTATTCTGGCTTCCTGGGTACTTAAAAACAGGG
CTTAGAGTATGGCTGCTGACAAAATTGCACTCTAAACGCTAGCTTAGGTCTTCTGCGGCCGCGAT
```

Document # 1000000002694 v11

For Research Use Only. Not for use in diagnostic procedures.

36

CTE2 - 550bp

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

CTE2 - 650bp

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

CTE2 - 750bp

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

CTE2 - 850bp

```
ATCCTGCAGATGCATCCAGTACTAGTATGGCCCGGGGGATCCTTAAGTCGTGTCCTTCTCCTACGATCTTGTGAACG
ATGGATATTTTCTTTCTAAACTTTAAACAAACAGTGGAGAGATGTTGTTGTGTGTGGAACGACGCTTAGCCTACCGA
GGAAGATCCAGACTACAATAGAATATGTGGCCAAAACTCTCCGCAACTTCAGCAGCAAAAGGATATTATTGACATA
ACCTCCTCACAAAAGTACACAAATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTT
TAGAATTTAAGATAATAAAGCTCTTGATCCCAATGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCA
CATACCCTCTCCCAGAGTCCATTCTCTAAAACTTGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGG
TCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGT
CTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACATTTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGG
TCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGG
TGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGA
GGGCCCGCTATGAAAAAAAGATTCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGC
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
ATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATTCTCTAAACTTGAA
GCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAGCTTTTGAAGAGTAA
TAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAAGTGACAT
TTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAGGTTCATGGTTCTCC
AAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGATGCTTCACATGTGTG
GGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAAGATTCTCTGTGCCCCCT
GGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCA
```

CTA - 150bp

```
GGGGGATCCTACGTTCCAAATGCAGCGAGCTCGTATAACCCTTTAAGAGTTGCTCTTTTTGTTTGGTAAGTTGCAAA
TCGAAGTTTTAGATTGAGTTCTACGTCGAGCGGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC
```

CTA - 250bp

```
GGGGGATCCTTATCTGTCAAAACCGCTAATGTCCGTTCTAAGACCGTCTGGAGAACACTTGCCCATCAGTGCTTTTG
AACCTTTTTTTCACAGGTCCCTTCCGATTACACTGAGAAGCTGACCACACCTGCTAGAAGATGGAGGTATGCAGCCC
GTTAGTAGGAGTAATACTACCCAGCTTATAACCCTCAAACGTAGGGCAGATGGCGGCCGCGATATCCTGCAGATGCA
TCCAGTACTAGTATGGCCC
```

CTA - 350bp

```
GGGGGATCCTAGAGACCATTCGCGATTCCATGAGACTCCAAGGGTTCTGCACAACTTATGCACCTCTATTAGATCAT
TGTGTTCTACGAAGCCTGGACTGCATTACATATTCACAACCAACATGAGAAGAGCGGAATAGATGGCCGGATGTTTG
GTGGCTTTGATATATTGTGAGGAGCATTGCGAACCCTAGAGCTGTCCGGTCAAATAACCCCCTCACAATAAGTGTAA
TGTCATGGGATAATCAAAAGACTAAGGGAGGGCTTTTATAGAAGGCGTGAGGTCATGCTATCCCCCTCTGAAGACGC
GGCCGCGATATCCTGCAGATGCATCCAGTACTAGTATGGCCC
```

For Research Use Only. Not for use in diagnostic procedures.

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
GTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTAAAAAAAGTG
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
TATGTGGCCAAAACTCTCCGCAACTTCAGCAGCAAAAGGATATTATTGACATAACCTCCTCACAAAAAGTACACAA
ATGGCTAAATAACAGAGCCCCTCTTTTTACTAGGGAAATGGTGGATGTGGACTTTAGAATTTAAGATAATAAAGCTC
TTGATCCCAATGTTATTTCCATGTGAGGGACATTAAATTGAGTAACCTTTGCCACATACCCTCTCCCAGAGTCCATT
CTCTAAAACTTGAAGCTCCGCCCCTTTTTACGCACATTAGGCTTCCAATTACGGTCAATGGTCTTGAAGATTGGGAG
CTTTTGAAGAGTAATAAGAACCATCACAAAAAGGAACCCAGAAGCCGGGAGTGTCTACCAAAAAAATTCAAGGGTTA
AAAAAAAGTGACATTTTCTCCTGTTTTTTACACATGATTTTGAATGCTGATGGGTCCACGTCCAGCTCTAAAGGTAG
GTTCATGGTTCTCCAAAGTTGCTTTCTTGTCAGAATTGAGCCACATCAGGTAGGTGGGGAAGTAGATCAGTGAGGAT
GCTTCACATGTGTGGGCACTGGGAACAGAATGCTTCAATAACACGAGCTGACGAGGGCCCGCTATGAAAAAAAGAT
TCTCTGTGCCCCCTGGCGCCTCCGCACTTAAAGAATTGATGACCGTGCGGCCGCGATATCCTGCAGATGCATCCAGT
ACA
```

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 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′ 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
A005	ACAGTG
A006	GCCAAT
A007	CAGATC
A008	ACTTGA
A009	GATCAG
A010	TAGCTT
A011	GGCTAC
A012	CTTGTA

Oligonucleotide Sequences for Genomic DNA

(Obsolete)

For Research Use Only. Not for use in diagnostic procedures.

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

```
5' CGACAGGTTCAGAGTTCTACAGTCCGACGATC
```

Revision History

Document	Date	Description of Change
Document # 1000000002694 v11	April 2019	Added adapter sequences for IDT for Illumina Nextera DNA UD Indexes Sets B, C, and D.
Document # 1000000002694 v10	February 2019	Added sequences for AmpliSeq UD Indexes for Illumina and AmpliSeq CD Indexes. Renamed the following sections to include RNA: • *IDT for Illumina TruSeq DNA and RNA UD Indexes* • *TruSeq DNA and RNA CD Indexes* Corrected 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.

For Research Use Only. Not for use in diagnostic procedures.

Technical Assistance

For technical assistance, contact Illumina Technical Support.

Website:	www.illumina.com
Email:	techsupport@illumina.com

Illumina Customer Support Telephone Numbers

Region	Toll Free	Regional
North America	+1.800.809.4566	
Australia	+1.800.775.688	
Austria	+43 800006249	+43 19286540
Belgium	+32 80077160	+32 34002973
China	400.066.5835	
Denmark	+45 80820183	+45 89871156
Finland	+358 800918363	+358 974790110
France	+33 805102193	+33 170770446
Germany	+49 8001014940	+49 8938035677
Hong Kong	800960230	
Ireland	+353 1800936608	+353 016950506
Italy	+39 800985513	+39 236003759
Japan	0800.111.5011	
Netherlands	+31 8000222493	+31 207132960
New Zealand	0800.451.650	
Norway	+47 800 16836	+47 21939693
Singapore	+1.800.579.2745	
South Korea	+82 80 234 5300	
Spain	+34 911899417	+34 800300143
Sweden	+46 850619671	+46 200883979
Switzerland	+41 565800000	+41 800200442
Taiwan	00806651752	
United Kingdom	+44 8000126019	+44 2073057197
Other countries	+44.1799.534000	

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.

For Research Use Only. Not for use in diagnostic procedures.

illumina®