Nanodigmbio

NadPrep EZ DNA Library Preparation Kit v2 User Manual V2.3

NadPrep EZ DNA Library Preparation Module v2
NadPrep Universal Stubby UDI Adapter Module
NadPrep UDI Adapter Module (for Illumina®)

Thoroughly Read This Manual Before Operation.
For Research Use Only.
Version2.3

Statement

For research use only. Not for use in diagnostic procedures.

This instruction is intended for use with the NadPrep EZ DNA Library Preparation Kit v2.

Revision History

Version	Data Released	Change
2.3	Nov 2024	Add compatible index primers in NadPrep Universal Stubby Adapter (UDI) Module.
2.2	Nov 2023	Revise description of storage temperatures for kit and components.
2.1	Aug 2022	Add compatible index primers in NadPrep Universal Stubby Adapter (UDI) Modules; Upgrade the package form of NadPrep UDI Adapter Set D Module.
2.0	Jan 2022	Upgrade from the v1 of library preparation module to v2; Add support of NadPrep Universal Stubby Adapter (UDI) Module.
1.1	Aug 2021	Add method of Library construction of DNA fragments with a main distribution ranging from 300 bp to 350 bp; Add i5 index sequences oriented for NovaSeq® platforms.
1.0	Jan 2021	Original version

Content

Announcement

Environment

- Temperature: 20-25°C; Humidity: 40-60%.
- The personal protective equipment should be equipped during the experiment period.

Temperature Control

- Avoid repeated freezing and thawing.
- Unless otherwise specified, the preparation of enzymatic reaction should be carried out on ice/cold metal bath.
- The fragmentase should be added at the end of reaction mix preparation to prevent its activity at room temperature.
- Make sure the thermal cycler reaches the designated temperature before loading any reaction tube in.

Avoid Cross-contamination

- Briefly centrifuge all the tubes to collect the contents to the bottom before opening the lids.
- Physically separate the laboratory space, equipment and consumables among different steps.
- Clean the lab area using 0.5% sodium hypochlorite once finishing the experiment.

Others

- Make sure the regents are fully thawed and thoroughly mixed prior to use.
- Unless otherwise specified, all the centrifuge steps are conducted at room temperature (20-25°C).
- Unless otherwise specified, all mixing steps listed as "mix thoroughly" should be performed by either vortexing for 10 sec or pipetting up and down for 10 times, and then briefly centrifuge to collect the contents.

Introduction

NadPrep EZ DNA Library Preparation Kit v2 is designed for preparation of high-quality sequencing libraries from double-stranded DNA (dsDNA) on Illumina platforms. To simplify the experimental process, multiple processes were applied in one single step, including the fragmentation, end repair and adapter ligation. This A-T ligation-based kit applies to the whole genome sequencing with DNA input ranging from 5 to 500 ng, and is compatible with hybridization capture based targeted sequencing.

The kit contains magnetic beads for DNA purification, and is optimized on size selection with NadPrep Universal Stubby Adapter (UDI) Module and NadPrep UDI Adapter Module (for Illumina®). All the components have been verified by quality control with a stable and remarkable performance.

Kit Content

NadPrep EZ DNA Library Preparation Kit v2 consists of Library Preparation Module and Adapter Module, which can be used in multiple combinations as required.

NadPrep EZ DNA Library Preparation Module v2

Catalog#	Item	Package/Storage
1002601	NadPrep EZ DNA Library Preparation Module v2, 24 rxn	Box1 / -25 ~ -15°C Box2 / 2 ~ 8°C
1002602	NadPrep EZ DNA Library Preparation Module v2, 96 rxn	Box1 / -25 ~ -15°C Box2 / 2 ~ 8°C

Package#	Component	Volume 1002601 24 rxn	Volume 1002602 96 rxn	Storage
Box1	FERA Buffer	150 μL	575 μL	-25 ~ -15°C
	FERA Enzyme	150 μL	575 μL	-25 ~ -15°C
	Enhancer Buffer	250 μL	950 μL	-25 ~ -15°C
	Ligation Buffer	750 μL	2×1,500 μL	-25 ~ -15°C
	DNA Ligase	60 μL	230 μL	-25 ~ -15°C
	2X HiFi PCR Master Mix	720 μL	2×1,600 μL	-25 ~ -15°C
	Nuclease Free Water	2.5 mL	8 mL	-25 ~ -15°C*
	TE Solution	1 mL	4 mL	-25 ~ -15°C*
Box2	NadPrep SP Beads	4 mL	15 mL	2 ~ 8°C

***Store at 2 ~ 8°C after opening.**

NadPrep Universal Stubby Adapter (UDI) Module

Catalog#	Item	Universal Stubby Adapter Volume	Universal UDI-Index Primer Mix # & Volume	Amplification Primer Mix II Volume	Storage
1003240	NadPrep® Universal Stubby Adapter (UDI) Module Set A1, 24 rxn	60 µL	1-12 & 12×15 µL (Tube)	20 µL	-25 ~ -15°C
1003241	NadPrep® Universal Stubby Adapter (UDI) Module Set B1, 96 rxn	230 µL	1-24 & 24×25 µL (Tube)	75 µL	-25 ~ -15°C
1003242	NadPrep® Universal Stubby Adapter (UDI) Module Set B2, 96 rxn	230 µL	25-48 & 24×25 µL (Tube)	75 µL	-25 ~ -15°C
1003251	NadPrep® Universal Stubby Adapter (UDI) Module Set E1, 96 rxn	260 µL	1-96 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003252	NadPrep® Universal Stubby Adapter (UDI) Module Set E2, 96 rxn	260 µL	97-192 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003253	NadPrep® Universal Stubby Adapter (UDI) Module Set E3, 96 rxn	260 µL	193-288 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003254	NadPrep® Universal Stubby Adapter (UDI) Module Set E4, 96 rxn	260 µL	289-384 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003255	NadPrep® Universal Stubby Adapter (UDI) Module Set E5, 96 rxn	260 µL	385-480 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003256	NadPrep® Universal Stubby Adapter (UDI) Module Set E6, 96 rxn	260 µL	481-576 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003257	NadPrep® Universal Stubby Adapter (UDI) Module Set E7, 96 rxn	260 µL	577-672 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003258	NadPrep® Universal Stubby Adapter (UDI) Module Set E8, 96 rxn	260 µL	673-768 & 96×8 µL (Plate)	75 µL	-25 ~ -15°C
1003261	NadPrep® Universal Stubby Adapter (UDI) Module Set F1, 1152 rxn	2×1350 µL	1-96 & 96×72µL (Tube)	900 µL	-25 ~ -15°C
1003262	NadPrep® Universal Stubby Adapter (UDI) Module Set F2, 1152 rxn	2×1350 µL	97-192 & 96×72 µL (Tube)	900 µL	-25 ~ -15°C
1003263	NadPrep® Universal Stubby Adapter (UDI) Module Set F3, 1152 rxn	2×1350 µL	193-288 & 96×72µL (Tube)	900 µL	-25 ~ -15°C
1003264	NadPrep® Universal Stubby Adapter (UDI) Module Set F4, 1152 rxn	2×1350 µL	289-384 & 96×72 µL (Tube)	900 µL	-25 ~ -15°C

NadPrep UDI Adapter Module (for Illumina®)

Catalog#	Item	Scale	NadPrep UDI Adapter#	NadPrep UDI Adapter Volume	Storage
1003221	NadPrep UDI Adapter Kit Set C1 (for Illumina®)	24 rxn	1–12	12×10 µL (Tube)	-25 ~ -15°C
1003211	NadPrep UDI Adapter Kit Set A (for Illumina®)	96 rxn	1–12	12×22 µL (Tube)	-25 ~ -15°C
1003212	NadPrep UDI Adapter Kit Set B (for Illumina®)	96 rxn	13–24	12×22 µL (Tube)	-25 ~ -15°C
1003213	NadPrep UDI Adapter Kit Set A&B (for Illumina®)	192 rxn	1–24	24×22 µL (Tube)	-25 ~ -15°C
1003224	NadPrep UDI Adapter Kit Set D1 (for Illumina®)	480 rxn	1–96	96×3.5 µL (Plate)*	-25 ~ -15°C

*NadPrep UDI Adapter Kit Set D1 (for Illumina®), 480 rxn is packaged in 96 rxn/plate for 5 plates.

Equipment and Consumable

Equipment

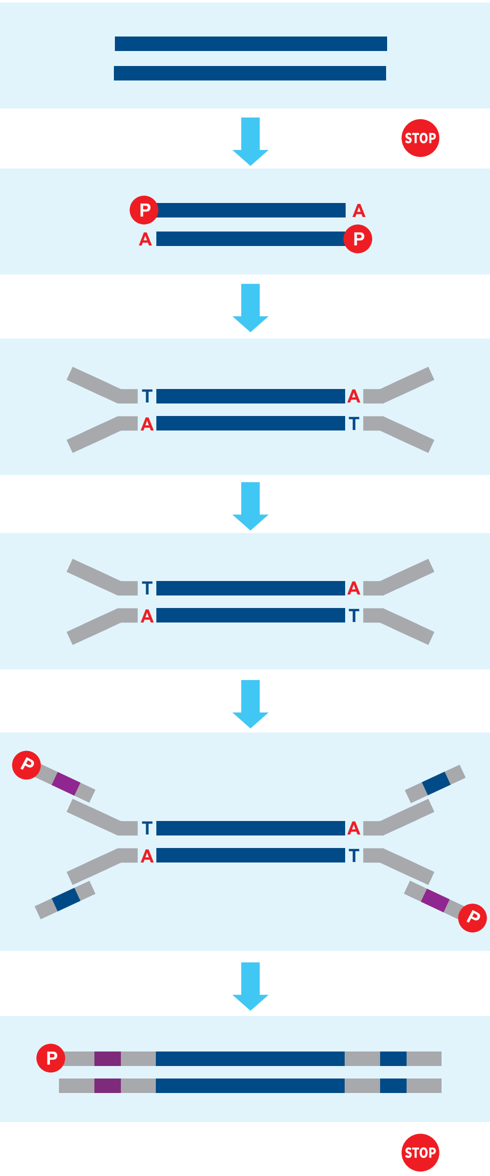
Item	Description
Digital electrophoresis	Agilent 2100 Electrophoresis Bioanalyzer® system (Cat # G2939AA) Agilent 2200 TapeStation system (Cat # G2965AA) Bioptic Qsep100 capillary gel electrophoresis system or equivalent
Pipettor	General laboratory supplier
Thermal cycler	General laboratory supplier
Benchtop centrifuge	General laboratory supplier
Microcentrifuge	General laboratory supplier
Vortex mixer	General laboratory supplier
Magnet stand	Thermo Fisher DynaMag™ -2 Magnet (Cat # 12321D) Thermo Fisher DynaMag™ -96 Side Magnet (Cat # 12331D) BORTHEE-96 Side Magnet (Cat # MAG-96-11) or equivalent
Qubit fluorometer	Thermo Fisher Qubit™ 3.0 Fluorometer (Cat # Q33216) or equivalent
Timer	General laboratory supplier

Consumable

Item	Description
Absolute Ethanol	General laboratory supplier, analytical grade
0.2 mL PCR Tube	Axygen MAXYMum Recovery™ PCR Tubes, 0.2 mL flat cap (Cat # PCR-02-L-C) or equivalent
Amplification Primer*	NadPrep Amplification Primer Mix (for Illumina®), 16 rxn (Cat # 1004101) NadPrep Amplification Primer Mix (for Illumina®), 96 rxn (Cat # 1004102) NadPrep Amplification Primer Mix II (for Illumina®), 24 rxn (Cat # 1004103) NadPrep Amplification Primer Mix II (for Illumina®), 96 rxn (Cat # 1004104)

* When NadPrep UDI Adapter Module (for Illumina®) is selected as adapter, it must be used together.

Workflow



Workflow	gDNA/FFPE DNA	Duration
	Fragmentation and End Repair & A-tailing Option Size Selection	40-60 min
	Adapter Ligation	15 min
	Post-ligation Cleanup or Option Size Selection	30 min or Option 60 min
	Library Amplification	20 min
	Post-Amplification Cleanup	30 min

NadPrep Universal Stubby Adapter

STOP Safe Stopping Point

Option Optional Step

*The schematic diagram takes the NadPrep Universal Stubby Adapter as an example.

Protocol

Sample Requirement

Sample Quality: gDNA without serious degradation (tested by gel electrophoresis analysis); FFPE DNA with one clear strip with about 15 kb in size (refer to **Appendix 1: Grading Standard of FFPE DNA**).

Input Amount: 5-500 ng, > 0.5 ng/μL (quantified by Qubit™ 3.0 Fluorometer).

Sample Purification: High quality DNA input, with OD_{260}/OD_{280}=1.8-2.0 and OD_{260}/OD_{230}=2.0-2.5.

Note: EDTA inhibits the activity of fragment enzyme. If the extracted DNA sample contains EDTA, the sample must be pretreated according to Step 1, otherwise the enzymatic digestion effect will be affected.

Step 1: Sample Pretreatment

Before the experiment, please confirm the sample solvent:

1. If the DNA sample contains EDTA, 1.8X NadPrep SP Beads is recommended to be used for purification of the sample, and library preparation shall be conducted after the sample is eluted with Nuclease Free Water. If purification is not carried out, the final concentration of EDTA in the system shall be calculated according to the following table, or the DNA system shall be configured by adding corresponding volumes of Enhancer Buffer and Nuclease Free Water according to the sample volume containing EDTA (1 mM);

2. Sample pretreatment is not required for gDNA or FFPE DNA samples with purity meeting the requirements and without EDTA; this step can be skipped.

Example: the sample solvent contains 1 mM EDTA, and the sample concentration is 100 ng/μL, and 250 ng input DNA is used for fragmentation, then the final concentration of EDTA in the fragmented DNA system is calculated as 250 ng/100 (ng/μL)*1 mM/50 μL = 0.05 mM; or the volume of sample containing EDTA (1 mM) is calculated as 250 ng/100 (ng/μL) = 2.5 μL.

For samples containing EDTA, the method of configuring DNA system with Enhancer Buffer is as follows:

Final Concentration of EDTA in the System	Volume of Sample Containing EDTA (1 mM)	Volume of Enhancer Buffer	Volume of Nuclease Free Water
0.015-0.05 mM	0.75-2.5 μL	0.5 μL	37-38.75 μL
0.1 mM	5 μL	1.5 μL	33.5 μL
0.2 mM	10 μL	4 μL	26 μL
0.3 mM	15 μL	5 μL	20 μL
0.4 mM	20 μL	6 μL	14 μL
0.5 mM	25 μL	7 μL	8 μL
0.6 mM	30 μL	8 μL	2 μL

Note: When the final concentration of EDTA in the system is greater than 0.6 mM, excessive volume of Enhancer Buffer needs to be added, which may lead to the decline in data quality.

Step 2: Fragmentation and End Repair & A-tailing

1. Thaw FERA Buffer at room temperature. Mix thoroughly and centrifuge to collect the contents. Keep the tube on ice.
2. Thaw FERA Enzyme on ice. Briefly vortex and centrifuge to collect the contents.
3. Set up each reaction in a 0.2 mL PCR tube on ice as follows:

DNA System ❗[1]	40 µL
FERA Buffer	5 µL
FERA Enzyme ❗[2]	5 µL
Total	**50 µL**

❗ **Note [1]: If the input DNA is less than 40 µL, add Nuclease Free Water to a total volume of 40 µL. When the sample Input is ≤ 10 ng, add 1 µL of Enhancer Buffer to obtain the expected fragment size. At this time, the input DNA should be ≤ 39 µL.**

❗ **Note [2]: When configuring FERA Enzyme and FERA as Mix for addition, pipette continuously for 3-5 times. Pipette slowly and carefully to ensure the expected volume.**

4. Mix thoroughly and centrifuge to collect the contents.
5. Incubate the tube in the thermal cycler programmed as follows. Make sure the thermal cycler is stabilized at 25°C before loading.

25°C	See the following table for enzymatic digestion time
65°C	30 min
10°C	Hold

❗ **Note: The heated lid should be set at 70°C.**

Expected Insert Size	Recommended enzymatic digestion time ❗
200 bp	30 min
250 bp	25 min
300 bp	20 min
350 bp	15 min

❗ **Note: The above enzymatic digestion time is applicable to blood gDNA samples without degradation. If the sample quality varies, the enzymatic digestion size may be different. It is suggested to adjust the fragmented enzymatic digestion time according to the reference time. The fragmented enzymatic digestion time shall not be less than 10 min, as insufficient enzymatic digestion time will affect the efficiency of library preparation.**

6. Store the unused reagents at -25 ~ -15°C.

Option **Optional steps: For gDNA or FFPE DNA samples, fragments size can be selected according to downstream analysis requirements. For specific methods, see Appendix 2 1.1.**

The following process applies to NadPrep Universal Stubby Adapter (UDI).

Step 3: Adapter Ligation

1. Thaw Ligation Buffer at room temperature, mix thoroughly and centrifuge to collect the contents. Keep the tube on ice.

Note: The Ligation Buffer is viscous. Please pipette slowly and carefully to ensure the expected volume.

2. Thaw DNA Ligase on ice. Briefly vortex and centrifuge to collect the contents.
3. Remove the tube in **Step 2** from the thermal cycler and set up each reaction on ice as follows:

Product of **Step 2**	50 μL
NadPrep Universal Stubby Adapter (as appropriate) [1]	2 μL
Ligation Buffer [2]	26 μL
DNA Ligase [2]	2 μL
Total	**80 μL**

Note [1]: Make sure to add NadPrep Universal Stubby Adapter before other reagents to avoid the adapter self-ligation.

Note [2]: If working on multiple samples, prepare Ligation Master Mix in advance with Ligation Buffer and DNA Ligase.

Important note:

- The dilution ratio of NadPrep Universal Stubby Adapter according to the amount of input DNA is recommended as follows:

Input DNA (Fragmented DNA/cfDNA)	Adapter Stock Concentration	Dilution Ratio	Adapter Insert Molar Ratio
500 ng	15 μM	*	10:1-6:1
250 ng	15 μM	*	20:1-12:1
100 ng	15 μM	*	50:1-30:1
50 ng	15 μM	*	100:1-60:1
25 ng	15 μM	*	200:1-100:1
10 ng	15 μM	2.5	200:1-100:1
5 ng	15 μM	5	200:1-100:1

Note: When the input DNA ≤ 10 ng, the adapter should be diluted prior to use. For other fragment distribution, please adjust dilution ratio according to recommended adapter and insert molar ratio.

4. Mix thoroughly and centrifuge to collect the contents.
5. Incubate the tube in the thermal cycler programmed as follows. Make sure the thermal cycler is stabilized at 20°C before loading.

20°C	15 min
4°C	Hold

Note: The heated lid should be left open.

Step 4: Post-ligation Cleanup

Option **For gDNA or FFPE DNA samples, fragments can be screened according to downstream analysis requirements. For specific methods, see Appendix 2 1.2.**

1. Equilibrate the NadPrep SP Beads to room temperature for a minimum of 30 min. Thoroughly vortex the beads prior to use.

2. Add 40 µL of NadPrep SP Beads to the same tube from **Step 3**. Mix thoroughly and then incubate the tube at 25°C for 5-10 min.

3. Briefly centrifuge and then place the tube on the magnet stand until the solution is clear (5 min). Carefully remove and discard the supernatant without disturbing the beads.

❗ **Note: The incubation time should be adjusted according to the actual performance of various magnet stands to ensure that the solution is completely clarified.**

4. Keep the tube on the magnet stand, add 150 µL of 80% freshly prepared ethanol without disturbing the beads. Incubate the tube on the magnet stand at room temperature for 30 sec. Carefully remove and discard the ethanol.

5. Repeat step 4 once.

6. Briefly centrifuge and then place the tube on the magnet stand. Carefully remove all residual ethanol without disturbing the beads by using a 10-µL pipette tip.

7. Open the lid, dry the beads on the magnet stand at room temperature for 5 min.

❗ **Note: Over-dried beads may be more difficult to suspend.**

8. Remove the tube off the magnet stand. Add 20 µL of Nuclease Free Water into the tube with beads inside for **Step 5**.

Step 5: Library Amplification

1. Thaw 2X HiFi PCR Master Mix and NadPrep Universal UDI-Index Primer Mix on ice. Mix thoroughly and centrifuge to collect the contents.

2. Set up each library amplification reaction in a 0.2 mL PCR tube on ice as follows (add in order from top to bottom):

Purified post-ligation from **Step 4**	20 µL
NadPrep Universal UDI-Index Primer Mix	5 µL
2X HiFi PCR Master Mix	25 µL
Total	**50 µL**

3. Mix thoroughly and centrifuge to collect the contents.

4. Incubate the tube in the thermal cycler and run the Cycling Program IV set as follows, with the heated lid set at 105°C.

98°C	2 min	1 cycle
98°C 60°C 72°C	15 sec 30 sec 30 sec	Varies (refer to the following table)
72°C	2 min	1 cycle
4°C	Hold	-

Input DNA	Recommended PCR Cycles of NadPrep Universal Stubby Adapter	
	Library Yield ⩾ 500 ng	Library Yield ⩾ 1,000 ng
500 ng	3	3
250 ng	3	4
100 ng	4-5	5-6
50 ng	5-6	6-7
25 ng	6-7	7-8
10 ng	8-9	9-10
5 ng	9-10	10-11

Important note:

The selection of PCR cycles shall take into account the following:

- If double-sided size selection has been performed, one or two additional cycles are necessary.
- The recommended cycles of DNA samples from different grades of FFPE is shown in Appendix 1: Grading Standard of FFPE Samples.
- If the library is constructed for hybridization capture-based targeted sequencing, the library yield should be twice as much as the capture input by adjusting the PCR cycles;
- To obtain 500 ng of library yield, the DNA input should be less than 250 ng.

The following process applies to NadPrep UDI Adapter (for Illumina®).

Step 3: Adapter Ligation

1. Thaw Ligation Buffer at room temperature, mix thoroughly and centrifuge to collect the contents. Keep the tube on ice.

Note: The Ligation Buffer is viscous. Please pipette slowly and carefully to ensure the expected volume.

2. Thaw DNA Ligase on ice. Briefly vortex and centrifuge to collect the contents.
3. Remove the tube in **Step 2** from the thermal cycler and set up each reaction on ice as follows:

Product of **Step 2**	50 μL
NadPrep UDI Adapter (as appropriate) [1]	2 μL
Ligation Buffer [2]	26 μL
DNA Ligase [2]	2 μL
Total	**80 μL**

Note [1]: Make sure to add NadPrep UDI Adapter before other reagents to avoid the adapter self-ligation.

Note [2]: If working on multiple samples, prepare Ligation Master Mix in advance with Ligation Buffer and DNA Ligase.

Important note:

- The dilution ratio of NadPrep UDI Adapter according to the amount of input DNA is recommended as follows:

Input DNA (Fragmented DNA/cfDNA)	Adapter Stock Concentration	Dilution Ratio	Adapter Insert Molar Ratio
500 ng	15 μM	*	10:1-6:1
250 ng	15 μM	*	20:1-12:1
100 ng	15 μM	*	50:1-30:1
50 ng	15 μM	*	100:1-60:1
25 ng	15 μM	2	200:1-100:1
10 ng	15 μM	5	200:1-100:1
5 ng	15 μM	10	200:1-100:1

Note: When the input DNA ≤ 25 ng, the adapter should be diluted prior to use. For other fragment distribution, please adjust dilution ratio according to recommended adapter and insert molar ratio.

4. Mix thoroughly and centrifuge to collect the contents.
5. Incubate the tube in the thermal cycler programmed as follows. Make sure the thermal cycler is stabilized at 20°C before loading.

20°C	15 min
4°C	Hold

Note: The heated lid should be left open.

Step 4: Post-ligation Cleanup

Option **For gDNA or FFPE DNA samples, fragments can be screened according to downstream analysis requirements. For specific methods, see Appendix 2 1.2.**

1. Equilibrate the NadPrep SP Beads to room temperature for a minimum of 30 min. Thoroughly vortex the beads prior to use.

2. Add 30 µL of NadPrep SP Beads to the same tube from **Step 3**. Mix thoroughly and then incubate the tube at 25°C for 5-10 min.

3. Briefly centrifuge and then place the tube on the magnet stand until the solution is clear (5 min). Carefully remove and discard the supernatant without disturbing the beads.

Note: The incubation time should be adjusted according to the actual performance of various magnet stands to ensure that the solution is completely clarified.

4. Keep the tube on the magnet stand, add 150 µL of 80% freshly prepared ethanol without disturbing the beads. Incubate the tube on the magnet stand at room temperature for 30 sec. Carefully remove and discard the ethanol.

5. Repeat step 4 once.

6. Briefly centrifuge and then place the tube on the magnet stand. Carefully remove all residual ethanol without disturbing the beads by using a 10-µL pipette tip.

7. Open the lid, dry the beads on the magnet stand at room temperature for 5 min.

Note: Over-dried beads may be more difficult to suspend.

8. Remove the tube off the magnet stand. Add 20 µL of Nuclease Free Water into the tube with beads inside for **Step 5**.

Step 5: Library Amplification

1. Thaw 2X HiFi PCR Master Mix and Amplification Primer Mix/Amplification Primer Mix II on ice. Mix thoroughly and centrifuge to collect the contents.

2. Set up each library amplification reaction in a 0.2 mL PCR tube on ice as follows:

Purified post-ligation from **Step 4**	20 µL
2X HiFi PCR Master Mix	25 µL
Amplification Primer Mix/Amplification Primer Mix II	5 µL
Total	**50 µL**

3. Mix thoroughly and centrifuge to collect the contents.

4. Incubate the tube in the thermal cycler and run the Cycling Program IV set as follows, with the heated lid set at 105°C.

98°C	2 min	1 cycle
98°C 60°C 72°C	15 sec 30 sec 30 sec	Varies (refer to the following table)
72°C	2 min	1 cycle
4°C	Hold	-

Input DNA	Recommended PCR Cycles of NadPrep UDI Adapter	
	Library Yield ⩾ 500 ng	Library Yield ⩾ 1,000 ng
500 ng	4	4
250 ng	4	5
100 ng	5-6	6-7
50 ng	6-7	7-8
25 ng	7-8	8-9
10 ng	9-10	10-11
5 ng	10-11	11-12

Important note:

The selection of PCR cycles shall take into account the following:

- If double-sided size selection has been performed, one or two additional cycles are necessary.
- The recommended cycles of DNA samples from different grades of FFPE is shown in Appendix 1: Grading Standard of FFPE Samples.
- If the library is constructed for hybridization capture-based targeted sequencing, the library yield should be twice as much as the capture input by adjusting the PCR cycles;
- To obtain 500 ng of library yield, the DNA input should be less than 250 ng.

Step 6: Post-amplification Cleanup

Note: Equilibrate the NadPrep SP Beads to room temperature for a minimum of 30 min. Thoroughly vortex the beads for 45 sec at high-speed.

1. Add 50 µL of NadPrep SP Beads into the Library Amplification tube. Mix thoroughly and then incubate the tube at 25°C for 5-10 min.

2. Briefly centrifuge and then place the tube on a magnet stand until the solution is clear (~5 min). Carefully remove and discard the supernatant without disturbing the beads.

Note: The incubation time should be adjusted according to the actual performance of various magnet stands to ensure that the solution is completely clarified.

3. Keeping the tube on the magnet stand, add 150 µL of freshly prepared 80% ethanol without disturbing the beads. Incubate the tube on the magnet stand at room temperature for 30 sec. Carefully remove and discard the ethanol.

4. Repeat step 3 once.

5. Briefly centrifuge and then place the tube on the magnet stand. Carefully remove all residual ethanol without disturbing the beads by using a 10-µL pipette tip.

6. Dry the beads on the magnet stand at room temperature for 5 min.

Note: Over-dried beads may be more difficult to suspend.

7. Remove the tube off the magnet stand. Thoroughly resuspend the beads in 20 µL of TE solution. Incubate the tube at 25°C for 2 min.

8. Briefly centrifuge and place the tube on the magnet stand. Incubate for 2 min until the solution is clear. Transfer the clear supernatant to a new 0.2 mL PCR tube. Avoid transfer of NadPrep SP Beads.

STOP **Safe Stopping Point:** The DNA library can be stored at 2 ~ 8°C for one week or -25 ~ -15°C for longer.

Step 7: Library Evaluation

1. The Qubit™ fluorometer or qPCR is recommended for library quantification.
2. The Bioanalyzer® 2100 (Agilent) or Qsep 100 (Bioptic) is recommended for size distribution analysis.
3. The quality control standards include:
   a. No adapter dimers or free adapters.
   b. Relatively concentrated size distribution.
   c. Suitable for MGI platform in size.

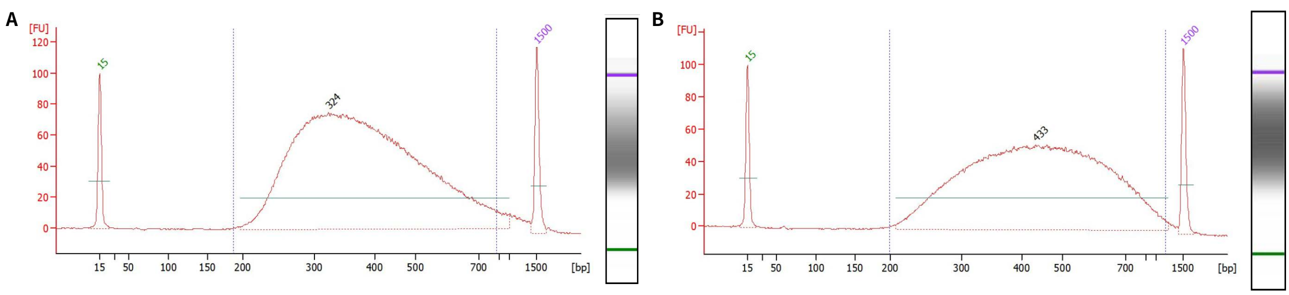


Fig 1. Example of size distribution of library. Use NadPrep EZ DNA Library Preparation Module V2 coupled with NadPrep Universal Stubby Adapter (UDI) Module for size distribution of library (Agilent 2100, DNA 1000 Kit) after the library preparation of **A.** gDNA samples (with average insert fragment of 250 bp) and **B.** gDNA samples (with average insert fragment of 300 bp) respectively.

Step 8: Sequencing

The library can be directly sequenced on Illumina platform or sequenced on MGI platform after circularized with NadPrep Universal Circularization Kit v2 (only for NadPrep EZ DNA Library Preparation Module v2 coupled with NadPrep Universal Stubby Adapter (UDI) Module).
For targeted sequencing, please refer to the hybridization capture protocol (for Illumina®) from Nanodigmbio (www.njnad.com).

Appendix 1: Grading Standard of FFPE DNA

FFPE DNA was classified into three grades. The corresponding experimental parameters were recommended as follows:

Grade	Grading Standard by Gel Electrophoresis	Recommended Input	Fragmentation Time (250 bp)	Recommended PCR Cycle (250 bp)
FFPE B+	One clear and slight trailing strip with about 15 kb in size	⩾ 100 ng	Consistent with gDNA	Consistent with gDNA
FFPE B	One indistinct strip with about 15 kb in size, with medium diffusion	⩾ 100 ng	Reduce five minutes or more than gDNA	One or two extra cycles more than gDNA
FFPE C	Multiple strips ranging from 200 bp to 2,500 bp, with severe diffusion	⩾ 100 ng	Reduce ten minutes or more than gDNA	Two or three extra cycles more than gDNA
FFPE D	Stripes mainly ranging from 250 bp to 1,000 bp, with severe diffusion	⩾ 100 ng	Reduce fifteen minutes or more than gDNA	Three or four extra cycles more than gDNA

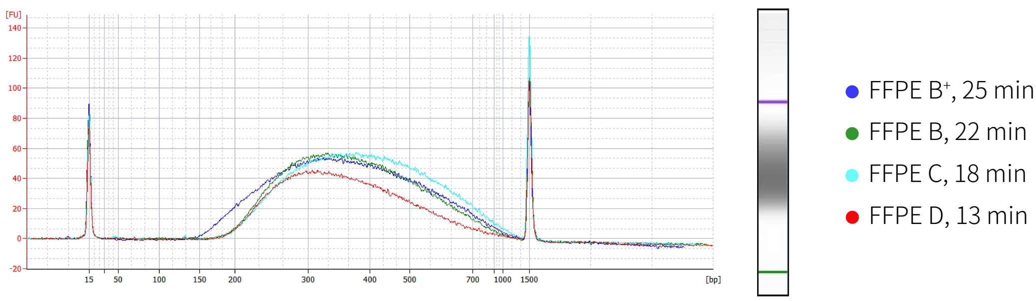


Fig 2. Example of size distribution of library. Use NadPrep EZ DNA Library Preparation Module v2 coupled with NadPrep Universal Stubby Adapter (UDI) Module for size distribution of library (Agilent 2100, DNA 1000 Kit) after the library preparation of FFPE samples (with average insert fragment of 250 bp).

Appendix 0: Size Selection

The NadPrep DNA Universal Library Preparation Kit v2 is compatible with a variety of size selection modes. Please choose the appropriate size selection modes according to the sample type, application direction, workflow and sequencing requirements.

Size Selection	Applicable Situation	Advantage	Disadvantage
Step 2 Option Double-sided size selection after fragmentation	Sufficient DNA input; Broad size distribution of DNA fragments after fragmentation	Narrow size distribution, high ligation efficiency and uniform sequencing data	Loss of sample
Step 4 Option Double-sided size selection after adapter ligation	Sufficient DNA input; Broad size distribution of libraries after adapter ligation	Narrow size distribution, Uniform sequencing data	Strict double-sized selection parameters based on library size

Note: Double-sided size selection during library construction can generate even size distribution and is therefore beneficial to data evenness after multiplexed capture and/or multiplexed sequencing. However, loss of sample is unavoidable due to extra handling steps. Please refer to the table to choose appropriate method.

1.1 Double-sided Size Selection after DNA Fragmentation (Optional Step after Step 2)

The volume of beads for double-sided size selection of fragmented product of **Step 2** are recommended as follows:

Important notes:

- The average size of the fragmented DNA should coincide the predicted size, to avoid the aggravation of sample loss.
- The DNA input should be over 200 ng if the double-sided size selection is performed with the PCR free library.

Expected DNA Size Distribution [1]	Sample Volume	Volume of NadPrep SP Beads(V1)	Volume of NadPrep SP Beads (V2)[2]
200 bp	50 µL	45 µL	50 µL
250 bp	50 µL	40 µL	50 µL
300 bp	50 µL	35 µL	50 µL
350 bp	50 µL	30 µL	50 µL

Note [1]: For WGS, it is recommended to select DNA fragments with a mean length of 300-350 bp. For targeted sequencing, it is recommended to select DNA fragments with a mean length of 250-300 bp.

Note [2]: The beads in V2 should be concentrated. Please refer to Appendix 1.1 step 3 as follows.

1. Equilibrate the NadPrep SP Beads to room temperature for a minimum of 30 min. Thoroughly vortex the beads for 45 sec at high-speed.

2. Transfer 50 µL of fragmented DNA in **Step 2 Fragmentation and End Repair & A-tailing** into a new 0.2 mL PCR tube. Add V1 volume of NadPrep SP Beads into the tube. Mix thoroughly and then incubate at 25°C for 5-10 min.

Note: If the fragmented DNA is less than 50 µL, add Nuclease Free Water to a total of 50 µL.

3. Prepare V2 volume of NadPrep SP Beads in a new 0.2 mL PCR tube. Briefly centrifuge and then place the tube on a magnet stand until the solution is clear (~5 min). Carefully remove and discard 40 µL of the supernatant without disturbing the beads. Remove the PCR tube off the magnet stand and mix the residues thoroughly.

Note: The incubation time should be adjusted according to the actual performance of various magnet stands to ensure that the solution is completely clarified.

4. Briefly centrifuge and then place the PCR tube in **Appendix 1.1** step 2. on the magnet stand until the solution is clear (~5 min). Transfer all the supernatant (50 µL+V1) into the PCR tube in **Appendix 1.1** step 3. Mix thoroughly and then incubate at 25°C for 5-10 min.

Note: Keep the supernatant (50 µL+V1) and discard the beads.

5. Briefly centrifuge and then place the tube on the magnet stand until the solution is clear (~5 min). Carefully remove and discard the supernatant without disturbing the beads.

6. Keeping the tube on the magnet stand, add 150 µL of freshly prepared 80% ethanol without disturbing the beads. Incubate the tube on the magnet stand at room temperature for 30 sec. Carefully remove and discard the ethanol solution.

7. Repeat step 6 once.

8. Briefly centrifuge and then place the tube on the magnet stand. Carefully remove all residual ethanol without disturbing the beads by using a 10-µL pipette tip.

9. Dry the beads on the magnet stand at room temperature for 5 min.

Note: Over-dried beads may be more difficult to suspend.

10. Remove the tube off the magnet stand. Thoroughly resuspend the beads in 43 µL of Nuclease Free Water. Incubate the tube at 25°C for 2 min.

11. Briefly centrifuge and then place the tube on the magnet stand. Incubate for 2 min until the supernatant is clear (collect 1 µL of supernatant for quantification). Transfer the supernatant (~40 µL) containing DNA to a new 0.2 mL PCR tube. Keep the tube on ice and directly perform **Step 3 Adapter Ligation**.

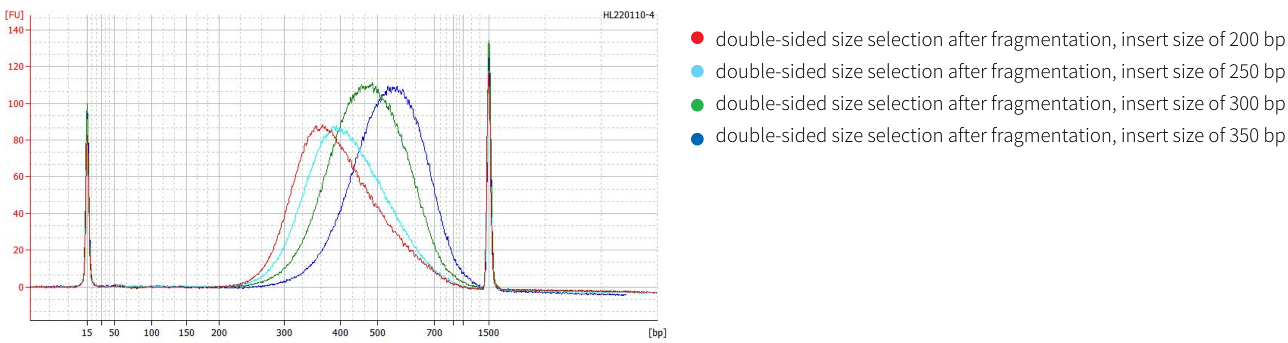


Fig 3. DNA size distribution with double-sided size selection after fragmentation (Covaris™) by using Agilent 2100 Analyzer.

1.2 Double-sided Size Selection after Adapter Ligation (Optional Step for Step 4 Post-ligation Cleanup)

The volume of beads for double-sided size selection of ligated product of **Step 3** are recommended as follows:

Important notes:

- This step is not recommended for input DNA ⩽ 50 ng or DNA with low quality.

The conditions of double-sided size selection with NadPrep Universal Stubby Adapter as follows:

Expected DNA Size Distribution	Volume of NadPrep SP Beads (V1)	Volume of NadPrep SP Beads (V2)
200 bp	34 μL	32 μL
250 bp	26 μL	30 μL
300 bp	22 μL	28 μL
350 bp	20 μL	25 μL

The conditions of double-sided size selection with NadPrep UDI Adapter as follows:

Expected DNA Size Distribution	Volume of NadPrep SP Beads (V1)	Volume of NadPrep SP Beads (V2)
200 bp	26 μL	30 μL
250 bp	22 μL	28 μL
300 bp	20 μL	26 μL
350 bp	18 μL	25 μL

1. Equilibrate the NadPrep SP Beads to room temperature for a minimum of 30 min. Thoroughly vortex the beads for 45 sec at high-speed.
2. Add V1 volume of NadPrep SP beads into the PCR tube of **Step 3 Adapter Ligation**. Mix thoroughly and then incubate at 25°C for 5-10 min.
3. Briefly centrifuge and then place the tube on the magnet stand until the solution is clear (~5 min). Carefully remove and discard the supernatant without disturbing the beads.

Note: The incubation time should be adjusted according to the actual performance of various magnet stands to ensure that the solution is completely clarified.

4. Keeping the tube on the magnet stand, add 150 µL of freshly prepared 80% ethanol solution without disturbing the beads. Incubate the tube on the magnet stand at room temperature for 30 sec. Carefully remove and discard the ethanol solution.

5. Repeat step 4 once.

6. Briefly centrifuge and then place the tube on the magnet stand. Carefully remove all residual ethanol solution without disturbing the beads by using a 10-µL pipette tip.

7. Dry the beads on the magnet stand at room temperature for 5 min.

Note: Over-dried beads may be more difficult to suspend.

8. Remove the tube off the magnet stand. Thoroughly resuspend the beads in 50 µL of Nuclease Free Water. Incubate the tube at 25°C for 2 min.

9. Add V2 volume of beads and then mix thoroughly. Incubate at 25°C for 5-10 min.

10. Briefly centrifuge and then place the tube on the magnet stand until the solution is clear (~5 min). Transfer all the supernatant (50 µL+V2) to a new 0.2 mL PCR tube.

Note: Keep the supernatant (50 µL+V2) and discard the beads.

11. Add 30 µL of NadPrep SP Beads to the supernatant (from Step 10). Mix thoroughly and incubate at 25°C for 5-10 min.

12. Briefly centrifuge and then place the tube on the magnet stand until the solution is clear (~5 min). Carefully remove and discard the supernatant without disturbing the beads.

13. Keeping the tube on the magnet stand, add 150 µL of freshly prepared 80% ethanol solution without disturbing the beads. Incubate the tube on the magnet stand at room temperature for 30 sec. Carefully remove and discard the ethanol solution.

14. Repeat step 13 once.

15. Briefly centrifuge and then place the tube on the magnet stand. Carefully remove all residual ethanol without disturbing the beads by using a 10-µL pipette tip.

16. Dry the beads on the magnet stand at room temperature for 5 min.

Note: Over-dried beads may be more difficult to suspend.

17. Remove the tube off the magnet stand. Add 20 µL of Nuclease Free Water into the tube with beads inside. Keep the tube on ice and directly perform **Step 5 Library amplification**.

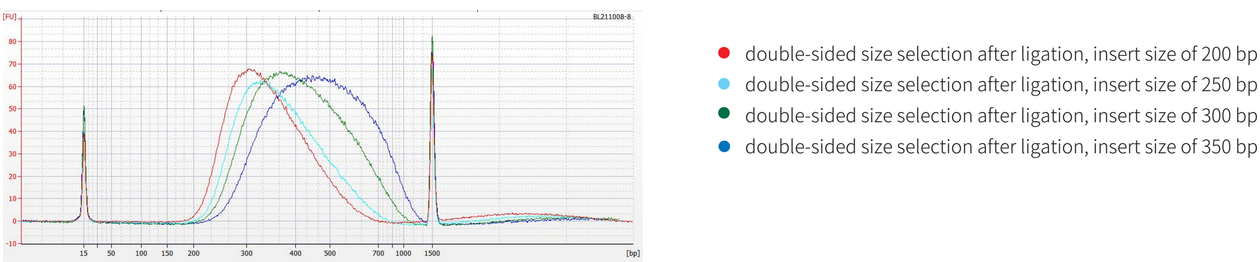


Fig 4. Library size distribution with double-sided size selection after ligation by using Agilent 2100 Analyzer.

Appendix 3: NadPrep Universal Stubby Adapter (UDI) Index Information

The index sequences of NadPrep Universal UDI-Index Primer Mix in NadPrep Universal Stubby Adapter (UDI) Module are listed as follows:

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X, NextSeq®, MiniSeq®, NovaSeq® v1.5 systems)	i7 index (all Illumina® systems)	i5 index	i7 index
1	GTGATAAGCA	TGCTTATCAC	TTGTGTCCTC	TGCTTATCAC	GAGGACACAA
2	TCCTATTAGG	CCTAATAGGA	CACCTCAGGA	CCTAATAGGA	TCCTGAGGTG
3	CATGGCGTAC	GTACGCCATG	GGTACGTACT	GTACGCCATG	AGTACGTACC
4	AGACCGCCTT	AAGGCGGTCT	ACAGAAGTAG	AAGGCGGTCT	CTACTTCTGT
5	CGTGCCGATT	AATCGGCACG	TAAGGAGTCA	AATCGGCACG	TGACTCCTTA
6	TTCAGGTGGC	GCCACCTGAA	ACTTCCAGAT	GCCACCTGAA	ATCTGGAAGT
7	AAGTTACTCG	CGAGTAACTT	GTCCATCAGG	CGAGTAACTT	CCTGATGGAC
8	GCACATACAA	TTGTATGTGC	CGGATGTCTC	TTGTATGTGC	GAGACATCCG
9	GGACTGTGGA	TCCACAGTCC	TGCAAGCCTA	TCCACAGTCC	TAGGCTTGCA
10	CCTAATAACG	CGTTATTAGG	AAGCTCGTGT	CGTTATTAGG	ACACGAGCTT
11	AAGGCACTAT	ATAGTGCCTT	GTATGTAGAG	ATAGTGCCTT	CTCTACATAC
12	TTCTGCGCTC	GAGCGCAGAA	CCTGCATACC	GAGCGCAGAA	GGTATGCAGG
13	GCTCTGCTTC	GAAGCAGAGC	ACCTGGTCAA	GAAGCAGAGC	TTGACCAGGT
14	TAGTCATACG	CGTATGACTA	TGGACCGATG	CGTATGACTA	CATCGGTCCA
15	CTAAGTACGA	TCGTACTTAG	GATCATCTGT	TCGTACTTAG	ACAGATGATC
16	AGCGACGGAT	ATCCGTCGCT	CTAGTAAGCC	ATCCGTCGCT	GGCTTACTAG
17	CGAGGCGAAT	ATTCGCCTCG	GGACCGTAAC	ATTCGCCTCG	GTTACGGTCC
18	TAGCCGCTTG	CAAGCGGCTA	CTGTACGCGA	CAAGCGGCTA	TCGCGTACAG
19	GTTAATAGCC	GGCTATTAAC	TCTGGAAGTT	GGCTATTAAC	AACTTCCAGA
20	ACCTTATCGA	TCGATAAGGT	AACATTCTCG	TCGATAAGGT	CGAGAATGTT
21	CCAGATTCGT	ACGAATCTGG	GTCTGGAGAC	ACGAATCTGG	GTCTCCAGAC
22	TTGATCCGCA	TGCGGATCAA	CGTGACCTTG	TGCGGATCAA	CAAGGTCACG
23	GACTGAATAG	CTATTCAGTC	AAGCTAGACA	CTATTCAGTC	TGTCTAGCTT
24	AGTCCGGATC	GATCCGGACT	TCAACTTCGT	GATCCGGACT	ACGAAGTTGA
25	GTCGGCTGTA	TACAGCCGAC	TCTAGCACCA	TACAGCCGAC	TGGTGCTAGA
26	TGATCAATGC	GCATTGATCA	GGCTAAGAAT	GCATTGATCA	ATTCTTAGCC
27	ACTAATGCCG	CGGCATTAGT	CTACCTCTTG	CGGCATTAGT	CAAGAGGTAG
28	CAGCTGCAAT	ATTGCAGCTG	AAGGTGTGGC	ATTGCAGCTG	GCCACACCTT
29	CGGCAAGGAT	ATCCTTGCCG	GGCAGAAGGA	ATCCTTGCCG	TCCTTCTGCC
30	AATATGTCGC	GCGACATATT	CATGAGTCTG	GCGACATATT	CAGACTCATG

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X, NextSeq®, MiniSeq®, NovaSeq® v1.5 systems)	i7 index (all Illumina® systems)	i5 index	i7 index
31	TTATGCCACA	TGTGGCATAA	ATATCTGTCC	TGTGGCATAA	GGACAGATAT
32	GCCGCTATTG	CAATAGCGGC	TCGCTCCAAT	CAATAGCGGC	ATTGGAGCGA
33	CGTACCTGTG	CACAGGTACG	GATGTCGGAG	CACAGGTACG	CTCCGACATC
34	GCATATAAGC	GCTTATATGC	AGAAGACATC	GCTTATATGC	GATGTCTTCT
35	AAGGTAGTCT	AGACTACCTT	CTGCAGTCGA	AGACTACCTT	TCGACTGCAG
36	TTCCGGCCAA	TTGGCCGGAA	TCCTCTATCT	TTGGCCGGAA	AGATAGAGGA
37	GGCATAGCGA	TCGCTATGCC	CTGTTCCGGT	TCGCTATGCC	ACCGGAACAG
38	TAGGCTAACT	AGTTAGCCTA	AACAGATCAG	AGTTAGCCTA	CTGATCTGTT
39	ACATAGTGAC	GTCACTATGT	TGTCCTATTC	GTCACTATGT	GAATAGGACA
40	CTTCGCCTTG	CAAGGCGAAG	GCAGAGGACA	CAAGGCGAAG	TGTCCTCTGC
41	GAGTGCACGA	TCGTGCACTC	GGTCGACCAA	TCGTGCACTC	TTGGTCGACC
42	TGCGAATTCT	AGAATTCGCA	CCATTGAATG	AGAATTCGCA	CATTCAATGG
43	CCAATGGAAG	CTTCCATTGG	TAGAACTTGC	CTTCCATTGG	GCAAGTTCTA
44	ATTCCTCGTC	GACGAGGAAT	ATCGCTGGCT	GACGAGGAAT	AGCCAGCGAT
45	GATGTGTGAA	TTCACACATC	ATCCGATTAC	TTCACACATC	GTAATCGGAT
46	ATGCACAATG	CATTGTGCAT	GAGGCTAGTT	CATTGTGCAT	AACTAGCCTC
47	TCAAGAGCGC	GCGCTCTTGA	CCATTGGCGA	GCGCTCTTGA	TCGCCAATGG
48	CGCTCTCTCT	AGAGAGAGCG	TGTAACCACG	AGAGAGAGCG	CGTGGTTACA
49	CGAATATACC	GGTATATTCG	ACCAGTAGCA	GGTATATTCG	TGCTACTGGT
50	TACGCCGGAA	TTCCGGCGTA	CTGTTGGTTG	TTCCGGCGTA	CAACCAACAG
51	GCTTATATGG	CCATATAAGC	TGAGCCTCGT	CCATATAAGC	ACGAGGCTCA
52	ATGCGGCCTT	AAGGCCGCAT	GATCAACAAC	AAGGCCGCAT	GTTGTTGATC
53	GGTTCGTCAC	GTGACGAACC	TACTGCTGAT	GTGACGAACC	ATCAGCAGTA
54	TAGAATGTGG	CCACATTCTA	GCGATTGTTG	CCACATTCTA	CAACAATCGC
55	CCAGTAAGTA	TACTTACTGG	CTTGAGCACC	TACTTACTGG	GGTGCTCAAG
56	ATCCGCCACT	AGTGGCGGAT	AGACCAACGA	AGTGGCGGAT	TCGTTGGTCT
57	AGATCACACC	GGTGTGATCT	AGTGTGAGAT	GGTGTGATCT	ATCTCACACT
58	GCCGTGATAA	TTATCACGGC	TAGCGTTCCG	TTATCACGGC	CGGAACGCTA
59	CATAATGCGT	ACGCATTATG	CCAACAGTTA	ACGCATTATG	TAACTGTTGG
60	TTGCGCTGTG	CACAGCGCAA	GTCTACCAGC	CACAGCGCAA	GCTGGTAGAC

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X, NextSeq®, MiniSeq®, NovaSeq® v1.5 systems)	i7 index (all Illumina® systems)	i5 index	i7 index
61	GTATAGTTGC	GCAACTATAC	CAGCCGTAAT	GCAACTATAC	ATTACGGCTG
62	TCCACTAGAT	ATCTAGTGGA	ACTAGCCTCC	ATCTAGTGGA	GGAGGCTAGT
63	CGTGTAGCTG	CAGCTACACG	TTCTTAGCGG	CAGCTACACG	CCGCTAAGAA
64	AAGCGCCACA	TGTGGCGCTT	GGAGATAGTA	TGTGGCGCTT	TACTATCTCC
65	AGAGGTGCGT	ACGCACCTCT	GGCATGGTAA	ACGCACCTCT	TTACCATGCC
66	TTGTCAAGAC	GTCTTGACAA	CCTCGTCGTT	GTCTTGACAA	AACGACGAGG
67	CCTAACCATA	TATGGTTAGG	AAGTCATCCG	TATGGTTAGG	CGGATGACTT
68	GACCTGTTCG	CGAACAGGTC	TTAGACAAGC	CGAACAGGTC	GCTTGTCTAA
69	CCTCTAGCAC	GTGCTAGAGG	CAGGCTGTGA	GTGCTAGAGG	TCACAGCCTG
70	GAATATCTGG	CCAGATATTC	GCTCAATGTT	CCAGATATTC	AACATTGAGC
71	TGCAGGAATA	TATTCCTGCA	ATCTTCACAC	TATTCCTGCA	GTGTGAAGAT
72	ATGGCCTGCT	AGCAGGCCAT	TGAAGGCACG	AGCAGGCCAT	CGTGCCTTCA
73	ATGCAGCGGA	TCCGCTGCAT	AACGCCACCT	TCCGCTGCAT	AGGTGGCGTT
74	TATAGATCCG	CGGATCTATA	GCGTGATAAG	CGGATCTATA	CTTATCACGC
75	GGCTTCAATT	AATTGAAGCC	TTACTTGTGC	AATTGAAGCC	GCACAAGTAA
76	CCAGCTGTAC	GTACAGCTGG	CGTAAGCGTA	GTACAGCTGG	TACGCTTACG
77	CCACGGTGTT	AACACCGTGG	CGTAGTGGTG	AACACCGTGG	CACCACTACG
78	GAGAATAAGG	CCTTATTCTC	GTGTCGTTGC	CCTTATTCTC	GCAACGACAC
79	TGTGCCGCAA	TTGCGGCACA	TCAGTAACCA	TTGCGGCACA	TGGTTACTGA
80	ATCTTACTCC	GGAGTAAGAT	AACCACCAAT	GGAGTAAGAT	ATTGGTGGTT
81	GCTGCAGCAT	ATGCTGCAGC	TCATCCGCTT	ATGCTGCAGC	AAGCGGATGA
82	CAATATTGCC	GGCAATATTG	CATGTAATGG	GGCAATATTG	CCATTACATG
83	ATGATGATGG	CCATCATCAT	GGCCATTGCA	CCATCATCAT	TGCAATGGCC
84	TGCCGCCATA	TATGGCGGCA	ATGAGGCAAC	TATGGCGGCA	GTTGCCTCAT
85	TCTCTGTGTG	CACACAGAGA	AGCATCGGCT	CACACAGAGA	AGCCGATGCT
86	CGGTGAACAA	TTGTTCACCG	TTGTCTTCAG	TTGTTCACCG	CTGAAGACAA
87	GAAGATCAGT	ACTGATCTTC	CCAGGACATA	ACTGATCTTC	TATGTCCTGG
88	ATCACCGTCC	GGACGGTGAT	GATCAGATGC	GGACGGTGAT	GCATCTGATC
89	TGCTAGAGGC	GCCTCTAGCA	TATAGGCCAG	GCCTCTAGCA	CTGGCCTATA
90	CATGTTGTCA	TGACAACATG	GTAGCCTGCT	TGACAACATG	AGCAGGCTAC

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
91	ATAAGCCAAG	CTTGGCTTAT	CCGTTAATTC	CTTGGCTTAT	GAATTAACGG
92	GCGCCATCTT	AAGATGGCGC	AGCCATGAGA	AAGATGGCGC	TCTCATGGCT
93	TTCCGAACGC	GCGTTCGGAA	TAATGCGCGG	GCGTTCGGAA	CCGCGCATTA
94	GGAACTTAAG	CTTAAGTTCC	CTTCTTAACC	CTTAAGTTCC	GGTTAAGAAG
95	CATTAGCTCT	AGAGCTAATG	GCCGAATTAA	AGAGCTAATG	TTAATTCGGC
96	ACGGTCGGTA	TACCGACCGT	AGGACGCGTT	TACCGACCGT	AACGCGTCCT
97	CTTGTGGCCA	TGGCCACAAG	GGATGGAGGA	TGGCCACAAG	TCCTCCATCC
98	AAGAACATGC	GCATGTTCTT	CCTATTCTTC	GCATGTTCTT	GAAGAATAGG
99	GGCTGATATT	AATATCAGCC	TTCCAATACG	AATATCAGCC	CGTATTGGAA
100	TCACCTCGAG	CTCGAGGTGA	AAGGCCGCAT	CTCGAGGTGA	ATGCGGCCTT
101	CCATTCATAG	CTATGAATGG	GGAAGGTGTT	CTATGAATGG	AACACCTTCC
102	AAGGAGGCGA	TCGCCTCCTT	CCGCTTATAA	TCGCCTCCTT	TTATAAGCGG
103	TTCACACATC	GATGTGTGAA	ATTGCCGACG	GATGTGTGAA	CGTCGGCAAT
104	GGTCGTTGCT	AGCAACGACC	TACTAACCGC	AGCAACGACC	GCGGTTAGTA
105	CCACGCAGAA	TTCTGCGTGG	ACTGCATGTC	TTCTGCGTGG	GACATGCAGT
106	AAGTCATCCT	AGGATGACTT	TTATTCGCCG	AGGATGACTT	CGGCGAATAA
107	TTCATGCATG	CATGCATGAA	CGCCATATAT	CATGCATGAA	ATATATGGCG
108	GGTGATGTGC	GCACATCACC	GAGAGGCAGA	GCACATCACC	TCTGCCTCTC
109	CCTATCCGTG	CACGGATAGG	TCCGGTCACT	CACGGATAGG	AGTGACCGGA
110	AAGTGTGACC	GGTCACACTT	CTATTATCGC	GGTCACACTT	GCGATAATAG
111	TTAGCGATGA	TCATCGCTAA	GGTAACAGAA	TCATCGCTAA	TTCTGTTACC
112	GGCCAATCAT	ATGATTGGCC	AAGCCGGTTG	ATGATTGGCC	CAACCGGCTT
113	CGCTAAGACC	GGTCTTAGCG	CCGAATGGAC	GGTCTTAGCG	GTCCATTCGG
114	AATCCGTCTT	AAGACGGATT	GGATTATTCG	AAGACGGATT	CGAATAATCC
115	TTAGTCCTGG	CCAGGACTAA	TTCGCCAATT	CCAGGACTAA	AATTGGCGAA
116	GCGAGTAGAA	TTCTACTCGC	AATCGGCCGA	TTCTACTCGC	TCGGCCGATT
117	TGAGGATTCG	CGAATCCTCA	ATGCGGCTCT	CGAATCCTCA	AGAGCCGCAT
118	AATCCTGGAA	TTCCAGGATT	CAATTCAGAG	TTCCAGGATT	CTCTGAATTG
119	CCGAAGCATT	AATGCTTCGG	GGTAATTAGC	AATGCTTCGG	GCTAATTACC
120	GTCTTCACGC	GCGTGAAGAC	TCCGCAGCTA	GCGTGAAGAC	TAGCTGCGGA

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
121	CAGTCGGCAT	ATGCCGACTG	GGAGTCCATC	ATGCCGACTG	GATGGACTCC
122	ACCAGACATA	TATGTCTGGT	CCTTATGGAA	TATGTCTGGT	TTCCATAAGG
123	TTAGACTGCC	GGCAGTCTAA	TTCACATTCG	GGCAGTCTAA	CGAATGTGAA
124	GGTCTTATGG	CCATAAGACC	AAGCGGACGT	CCATAAGACC	ACGTCCGCTT
125	GACGGTGATC	GATCACCGTC	TGGCGGCATA	GATCACCGTC	TATGCCGCCA
126	ACGTTCCTAA	TTAGGAACGT	CCTGTTACAT	TTAGGAACGT	ATGTAACAGG
127	CTAACAAGCT	AGCTTGTTAG	ATATAAGGCG	AGCTTGTTAG	CGCCTTATAT
128	TGTCAGTCGG	CCGACTGACA	GACACCTTGC	CCGACTGACA	GCAAGGTGTC
129	TAGCGACCTC	GAGGTCGCTA	TCGCGCTTGT	GAGGTCGCTA	ACAAGCGCGA
130	ACTGAGAACA	TGTTCTCAGT	ATATTGGACC	TGTTCTCAGT	GGTCCAATAT
131	GTATCTTGGT	ACCAAGATAC	CATAATCCAG	ACCAAGATAC	CTGGATTATG
132	CGCATCGTAG	CTACGATGCG	GGCGCAAGTA	CTACGATGCG	TACTTGCGCC
133	CATCCTTACG	CGTAAGGATG	TGGCCAACTC	CGTAAGGATG	GAGTTGGCCA
134	AGGTAGAGAC	GTCTCTACCT	ATTGTGCAAG	GTCTCTACCT	CTTGCACAAT
135	TTCGTAGCGT	ACGCTACGAA	CCATATTGGT	ACGCTACGAA	ACCAATATGG
136	GCAAGCCTTA	TAAGGCTTGC	GACAGCGTCA	TAAGGCTTGC	TGACGCTGTC
137	CTGAGTGTGA	TCACACTCAG	GTCACACCTC	TCACACTCAG	GAGGTGTGAC
138	AGTCACCAAC	GTTGGTGACT	ACGTTGAAGA	GTTGGTGACT	TCTTCAACGT
139	TACTCAAGCG	CGCTTGAGTA	CGACACTTAT	CGCTTGAGTA	ATAAGTGTCG
140	GCAGTGTCTT	AAGACACTGC	TATGGTGGCG	AAGACACTGC	CGCCACCATA
141	CATGGTGCGA	TCGCACCATG	AGTAAGTACC	TCGCACCATG	GGTACTTACT
142	ATAACGCACT	AGTGCGTTAT	CTCCTTACTA	AGTGCGTTAT	TAGTAAGGAG
143	GGCTACATAG	CTATGTAGCC	GAGTGCCTGT	CTATGTAGCC	ACAGGCACTC
144	TCGCTATGTC	GACATAGCGA	TCAGCAGGAG	GACATAGCGA	CTCCTGCTGA
145	CAGTCATGTT	AACATGACTG	CCACTAGAAG	AACATGACTG	CTTCTAGTGG
146	ATCAGTATGG	CCATACTGAT	GGTGATTCTT	CCATACTGAT	AAGAATCACC
147	GGACAGGCAA	TTGCCTGTCC	TTCTCCAGGA	TTGCCTGTCC	TCCTGGAGAA
148	TCTGTCCACC	GGTGGACAGA	AAGAGGCTCC	GGTGGACAGA	GGAGCCTCTT
149	AGATTCCGCG	CGCGGAATCT	ATCCTATGCA	CGCGGAATCT	TGCATAGGAT
150	CACCGAATAA	TTATTCGGTG	CCTTATACGT	TTATTCGGTG	ACGTATAAGG

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X， NextSeq®, MiniSeq®， NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
151	TTGAAGTCTC	GAGACTTCAA	GGAAGCCTTG	GAGACTTCAA	CAAGGCTTCC
152	GCTGCTGAGT	ACTCAGCAGC	TAGGCGGAAC	ACTCAGCAGC	GTTCCGCCTA
153	GACGCTAACG	CGTTAGCGTC	CTCTCGGACA	CGTTAGCGTC	TGTCCGAGAG
154	CCACAATTAC	GTAATTGTGG	GCACGTCCTT	GTAATTGTGG	AAGGACGTGC
155	ATTAGCCGTT	AACGGCTAAT	TGGATATGAG	AACGGCTAAT	CTCATATCCA
156	TGGTTGGCGA	TCGCCAACCA	AATGACATGC	TCGCCAACCA	GCATGTCATT
157	GATGGCGCTT	AAGCGCCATC	ATGCGATAGA	AAGCGCCATC	TCTATCGCAT
158	CTACAACAAG	CTTGTTGTAG	TAATTCGGTC	CTTGTTGTAG	GACCGAATTA
159	AGGATTAGGA	TCCTAATCCT	CCTAAGCTCG	TCCTAATCCT	CGAGCTTAGG
160	TCCTCGTTCC	GGAACGAGGA	GGCGCTACAT	GGAACGAGGA	ATGTAGCGCC
161	ACTCGGACTG	CAGTCCGAGT	GGTCAGCGAA	CAGTCCGAGT	TTCGCTGACC
162	GAGAATCTCA	TGAGATTCTC	TTAGCTACTC	TGAGATTCTC	GAGTAGCTAA
163	TTCTTCTGAC	GTCAGAAGAA	CACTTAGTGT	GTCAGAAGAA	ACACTAAGTG
164	CGAGCAGAGT	ACTCTGCTCG	ACGAGCTACG	ACTCTGCTCG	CGTAGCTCGT
165	CAGACAAGGT	ACCTTGTCTG	GGCTGTAGTT	ACCTTGTCTG	AACTACAGCC
166	GCTCACGAAG	CTTCGTGAGC	CCAATAGCGG	CTTCGTGAGC	CCGCTATTGG
167	ATAGGTTCTC	GAGAACCTAT	TTGGCCTTAA	GAGAACCTAT	TTAAGGCCAA
168	TGCTTGCTCA	TGAGCAAGCA	AATCAGCACC	TGAGCAAGCA	GGTGCTGATT
169	TTATCTCTCC	GGAGAGATAA	GAACGAACCG	GGAGAGATAA	CGGTTCGTTC
170	GCTGGCAAGA	TCTTGCCAGC	TCGGTCGAGT	TCTTGCCAGC	ACTCGACCGA
171	CAGAAGTGAT	ATCACTTCTG	CGTTCTCTTA	ATCACTTCTG	TAAGAGAACG
172	AGCCTAGCTG	CAGCTAGGCT	ATCAAGTGAC	CAGCTAGGCT	GTCACTTGAT
173	ACGGACCGAT	ATCGGTCCGT	CGACGGTCTT	ATCGGTCCGT	AAGACCGTCG
174	GGCTTGGTTA	TAACCAAGCC	TCCGTTAGGC	TAACCAAGCC	GCCTAACGGA
175	TAACGAACGG	CCGTTCGTTA	GTGTCACTAA	CCGTTCGTTA	TTAGTGACAC
176	CTTACTTACC	GGTAAGTAAG	AATAACGACG	GGTAAGTAAG	CGTCGTTATT
177	GGCCAAGGTA	TACCTTGGCC	TCTGGCGTCA	TACCTTGGCC	TGACGCCAGA
178	TAAGCGTCAG	CTGACGCTTA	AGCTATTAGG	CTGACGCTTA	CCTAATAGCT
179	ACTATTCAGC	GCTGAATAGT	CTGATAACTC	GCTGAATAGT	GAGTTATCAG
180	CTGTGCATCT	AGATGCACAG	GAACCGCGAT	AGATGCACAG	ATCGCGGTTC

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181	ACGGTATAGC	GCTATACCGT	AGCGCAGGTT	GCTATACCGT	AACCTGCGCT
182	TAATGCGCCT	AGGCGCATTA	CATATGACCG	AGGCGCATTA	CGGTCATATG
183	CGTCCTATAA	TTATAGGACG	GCGTACTTAA	TTATAGGACG	TTAAGTACGC
184	GTCAAGCGTG	CACGCTTGAC	TTACGTCAGC	CACGCTTGAC	GCTGACGTAA
185	CCAACTGCCT	AGGCAGTTGG	CCATGCAGTG	AGGCAGTTGG	CACTGCATGG
186	TATTGACGGC	GCCGTCAATA	GGTCTGTTAT	GCCGTCAATA	ATAACAGACC
187	GTGGAGATTA	TAATCTCCAC	TTCGATCACA	TAATCTCCAC	TGTGATCGAA
188	AGCCTCTAAG	CTTAGAGGCT	AAGACAGCGC	CTTAGAGGCT	GCGCTGTCTT
189	CTGCCATGCA	TGCATGGCAG	GGCGAATCCT	TGCATGGCAG	AGGATTCGCC
190	AACAAGGCAC	GTGCCTTGTT	CCACTCATTA	GTGCCTTGTT	TAATGAGTGG
191	GGATTCATGT	ACATGAATCC	AATTCGCAGC	ACATGAATCC	GCTGCGAATT
192	TCTGGTCATG	CATGACCAGA	TTGAGTGGAG	CATGACCAGA	CTCCACTCAA
193	CCACAGTCGA	TCGACTGTGG	CTGGTAGGCA	TCGACTGTGG	TGCCTACCAG
194	AACAGCGACC	GGTCGCTGTT	AATTACTCGG	GGTCGCTGTT	CCGAGTAATT
195	TTGTCACTTG	CAAGTGACAA	GCAACTCAAT	CAAGTGACAA	ATTGAGTTGC
196	GGTGTTAGAT	ATCTAACACC	TGCCGGATTC	ATCTAACACC	GAATCCGGCA
197	CTGGTAACGC	GCGTTACCAG	GCAGTCAGTC	GCGTTACCAG	GACTGACTGC
198	AACAGTTGCG	CGCAACTGTT	ATGTAGCACT	CGCAACTGTT	AGTGCTACAT
199	TGATCGGAAT	ATTCCGATCA	CATACATTGG	ATTCCGATCA	CCAATGTATG
200	GCTCACCTTA	TAAGGTGAGC	TGCCGTGCAA	TAAGGTGAGC	TTGCACGGCA
201	CCGCACTGAA	TTCAGTGCGG	AGACTGGCCT	TTCAGTGCGG	AGGCCAGTCT
202	AACATGATCC	GGATCATGTT	CTTGAATTGG	GGATCATGTT	CCAATTCAAG
203	GTATGAGCTT	AAGCTCATAC	GACTCTAATC	AAGCTCATAC	GATTAGAGTC
204	TGTGCTCAGG	CCTGAGCACA	TCGAGCCGAA	CCTGAGCACA	TTCGGCTCGA
205	CTAGGTAGCC	GGCTACCTAG	ACTTAAGCCT	GGCTACCTAG	AGGCTTAAGT
206	AACCACTCGG	CCGAGTGGTT	CGGAGCATTA	CCGAGTGGTT	TAATGCTCCG
207	TGTACGGATA	TATCCGTACA	TTACCTCGAC	TATCCGTACA	GTCGAGGTAA
208	GCGTTACTAT	ATAGTAACGC	GACGTGTAGG	ATAGTAACGC	CCTACACGTC
209	CCATTGTTGT	ACAACAATGG	TCGGTGGTCA	ACAACAATGG	TGACCACCGA
210	AACCGAGGAC	GTCCTCGGTT	GATCCTTATC	GTCCTCGGTT	GATAAGGATC

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211	GGTACTACCA	TGGTAGTACC	CTATGAACAG	TGGTAGTACC	CTGTTCATAG
212	TTGGACCATG	CATGGTCCAA	AGCAACCGGT	CATGGTCCAA	ACCGGTTGCT
213	CCGCCACAAT	ATTGTGGCGG	TAGTCCTGAG	ATTGTGGCGG	CTCAGGACTA
214	AACAACACGA	TCGTGTTGTT	GGCGTGAATT	TCGTGTTGTT	AATTCACGCC
215	GTATTGTGTC	GACACAATAC	CTTAATCTCC	GACACAATAC	GGAGATTAAG
216	TGTGGTGTCG	CGACACCACA	ACACGAGCGA	CGACACCACA	TCGCTCGTGT
217	CTTCCTCCGA	TCGGAGGAAG	TGCGGACCTT	TCGGAGGAAG	AAGGTCCGCA
218	AAGAGGAACG	CGTTCCTCTT	ACGTATTGAC	CGTTCCTCTT	GTCAATACGT
219	TCCTAAGGTT	AACCTTAGGA	GATATCATCG	AACCTTAGGA	CGATGATATC
220	GGAGTCTTAC	GTAAGACTCC	CTACCGGAGA	GTAAGACTCC	TCTCCGGTAG
221	GGAGGTATGA	TCATACCTCC	GTGCACGCAT	TCATACCTCC	ATGCGTGCAC
222	AAGCCGTAAT	ATTACGGCTT	CACACGCATA	ATTACGGCTT	TATGCGTGTG
223	TCTAACGGCC	GGCCGTTAGA	TCTTGTTGGC	GGCCGTTAGA	GCCAACAAGA
224	CTCTTACCTG	CAGGTAAGAG	AGAGTAATCG	CAGGTAAGAG	CGATTACTCT
225	CTTGCTAACA	TGTTAGCAAG	TGTGGCCGAA	TGTTAGCAAG	TTCGGCCACA
226	AAGCGGTTAC	GTAACCGCTT	CACCAGATTC	GTAACCGCTT	GAATCTGGTG
227	GGATACGGTT	AACCGTATCC	GTATCTTACG	AACCGTATCC	CGTAAGATAC
228	TCCATACCGG	CCGGTATGGA	ACGATAGCGT	CCGGTATGGA	ACGCTATCGT
229	CGCATACTTC	GAAGTATGCG	GGAACGGATC	GAAGTATGCG	GATCCGTTCC
230	AATCGCAGCA	TGCTGCGATT	TTCTGAAGAG	TGCTGCGATT	CTCTTCAGAA
231	TTAGAGTCGG	CCGACTCTAA	CATCTCTTCT	CCGACTCTAA	AGAAGAGATG
232	GCGTCTGAAT	ATTCAGACGC	ACGGATCCGA	ATTCAGACGC	TCGGATCCGT
233	CTCCTCATGT	ACATGAGGAG	CGCAAGGCAA	ACATGAGGAG	TTGCCTTGCG
234	AATTGGCCAC	GTGGCCAATT	TCGGTACTTC	GTGGCCAATT	GAAGTACCGA
235	TGAACATGTG	CACATGTTCA	GATTCCAAGG	CACATGTTCA	CCTTGGAATC
236	GCGGATGACA	TGTCATCCGC	ATACGTTGCT	TGTCATCCGC	AGCAACGTAT
237	TGGTGTAGGC	GCCTACACCA	CTCGACAGTC	GCCTACACCA	GACTGTCGAG
238	ACAACAGTCT	AGACTGTTGT	GCACTGTTAG	AGACTGTTGT	CTAACAGTGC
239	CTCGAGTCTA	TAGACTCGAG	TGTTCTCCGA	TAGACTCGAG	TCGGAGAACA
240	GATCTCCAAG	CTTGGAGATC	AAGAGAGACT	CTTGGAGATC	AGTCTCTCTT

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241	TGCCGATACC	GGTATCGGCA	GTCCGTCCAT	GGTATCGGCA	ATGGACGGAC
242	ACAATGGTTG	CAACCATTGT	TAGATGATGG	CAACCATTGT	CCATCATCTA
243	CATTACAGGT	ACCTGTAATG	CGTGAAGATA	ACCTGTAATG	TATCTTCACG
244	GTGGCTCCAA	TTGGAGCCAC	ACATCCTGCC	TTGGAGCCAC	GGCAGGATGT
245	GTCGAGGTTC	GAACCTCGAC	TAGTGCACAT	GAACCTCGAC	ATGTGCACTA
246	ACACGCAAGT	ACTTGCGTGT	GGTGCGCTTA	ACTTGCGTGT	TAAGCGCACC
247	CGTTCTTGCA	TGCAAGAACG	ATCATTGAGG	TGCAAGAACG	CCTCAATGAT
248	TAGATACCAG	CTGGTATCTA	CCACAATGCC	CTGGTATCTA	GGCATTGTGG
249	GAGCTCAGAC	GTCTGAGCTC	TTGTGGCTGC	GTCTGAGCTC	GCAGCCACAA
250	ACCAATTCTG	CAGAATTGGT	AGAATTGGTG	CAGAATTGGT	CACCAATTCT
251	TGTTGAGAGA	TCTCTCAACA	CATCCATCAT	TCTCTCAACA	ATGATGGATG
252	CTAGCGCTCT	AGAGCGCTAG	GCCGACAACA	AGAGCGCTAG	TGTTGTCGGC
253	CCATCTGGTT	AACCAGATGG	TAGCTCAGAG	AACCAGATGG	CTCTGAGCTA
254	AAGCTGAAGA	TCTTCAGCTT	ACAGGATTCC	TCTTCAGCTT	GGAATCCTGT
255	TTCAACTCCG	CGGAGTTGAA	CGTTCGGATT	CGGAGTTGAA	AATCCGAACG
256	GGTGGACTAC	GTAGTCCACC	GTCAATCCGA	GTAGTCCACC	TCGGATTGAC
257	TGTCGATCAT	ATGATCGACA	GTTATCGGTA	ATGATCGACA	TACCGATAAC
258	ACGAAGCTCG	CGAGCTTCGT	TAATAGACGC	CGAGCTTCGT	GCGTCTATTA
259	CACTTCGATA	TATCGAAGTG	ACGCCTCTAG	TATCGAAGTG	CTAGAGGCGT
260	GTAGCTAGGC	GCCTAGCTAC	CGCGGATACT	GCCTAGCTAC	AGTATCCGCG
261	CAGTTCCGTA	TACGGAACTG	TATGGCAATG	TACGGAACTG	CATTGCCATA
262	AGCGCATTGT	ACAATGCGCT	AGCCAAGTCC	ACAATGCGCT	GGACTTGGCT
263	TTACAGAACC	GGTTCTGTAA	GTATCGTCAA	GGTTCTGTAA	TTGACGATAC
264	GCTAGTGCAG	CTGCACTAGC	CCGATTCGGT	CTGCACTAGC	ACCGAATCGG
265	GGCACTCCTA	TAGGAGTGCC	CTAGTGCCTA	TAGGAGTGCC	TAGGCACTAG
266	CAACAGAAGT	ACTTCTGTTG	TACAGAGACC	ACTTCTGTTG	GGTCTCTGTA
267	ATTGTCTTCG	CGAAGACAAT	GCTTACATAG	CGAAGACAAT	CTATGTAAGC
268	TCGTGAGGAC	GTCCTCACGA	AGGCCTTGGT	GTCCTCACGA	ACCAAGGCCT
269	GTTAGTCGAT	ATCGACTAAC	TAGTATCGTG	ATCGACTAAC	CACGATACTA
270	CAATTCGCGG	CCGCGAATTG	GGTATAGTGT	CCGCGAATTG	ACACTATACC

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271	AGGCAATACC	GGTATTGCCT	CTCGCCTCAA	GGTATTGCCT	TTGAGGCGAG
272	TCCGCGATTA	TAATCGCGGA	ACACGGAACC	TAATCGCGGA	GGTTCCGTGT
273	GTCACTGGTA	TACCAGTGAC	GTTCTAGCTC	TACCAGTGAC	GAGCTAGAAC
274	CATGTCACAT	ATGTGACATG	ACCAACTAGT	ATGTGACATG	ACTAGTTGGT
275	AGATGGTACC	GGTACCATCT	CAAGCGCTAA	GGTACCATCT	TTAGCGCTTG
276	TCGCAACTGG	CCAGTTGCGA	TGGTGTAGCG	CCAGTTGCGA	CGCTACACCA
277	TCAACCTTGG	CCAAGGTTGA	GGTGTCGACA	CCAAGGTTGA	TGTCGACACC
278	CATTGAGACC	GGTCTCAATG	CTAAGATTGC	GGTCTCAATG	GCAATCTTAG
279	AGGCATCGAA	TTCGATGCCT	TACCATACTG	TTCGATGCCT	CAGTATGGTA
280	GTCGTGACTT	AAGTCACGAC	ACGTCGCGAT	AAGTCACGAC	ATCGCGACGT
281	GGCTCCTCAA	TTGAGGAGCC	GTTGATGCAT	TTGAGGAGCC	ATGCATCAAC
282	CCGAATAGTT	AACTATTCGG	AGACTACGTA	AACTATTCGG	TACGTAGTCT
283	AATGTAGAGG	CCTCTACATT	TCGACCTACC	CCTCTACATT	GGTAGGTCGA
284	TTACGGCTCC	GGAGCCGTAA	CACTGGATGG	GGAGCCGTAA	CCATCCAGTG
285	TACCTCACAG	CTGTGAGGTA	GATCGTGGTC	CTGTGAGGTA	GACCACGATC
286	CCTAGTTGGT	ACCAACTAGG	CTCGTATTAG	ACCAACTAGG	CTAATACGAG
287	GGAGAAGATA	TATCTTCTCC	TCGTACAACT	TATCTTCTCC	AGTTGTACGA
288	ATGTCGCTCC	GGAGCGACAT	AGAACGCCGA	GGAGCGACAT	TCGGCGTTCT
289	AGACTCAGGA	TCCTGAGTCT	TTGCTCACCG	TCCTGAGTCT	CGGTGAGCAA
290	CCTGCATATC	GATATGCAGG	CGTGGTTATT	GATATGCAGG	AATAACCACG
291	TAGAAGGCCT	AGGCCTTCTA	GCATAACGAA	AGGCCTTCTA	TTCGTTATGC
292	GTCTGTCTAG	CTAGACAGAC	AACACGGTGC	CTAGACAGAC	GCACCGTGTT
293	AGGAGTGCAC	GTGCACTCCT	CAGTCGTTGG	GTGCACTCCT	CCAACGACTG
294	CCTTCAAGTA	TACTTGAAGG	GTTAGAAGCT	TACTTGAAGG	AGCTTCTAAC
295	TACGAGTAGT	ACTACTCGTA	TGCCTTCATA	ACTACTCGTA	TATGAAGGCA
296	GTACTCCTCG	CGAGGAGTAC	ACAGACGCAC	CGAGGAGTAC	GTGCGTCTGT
297	GACCACAAGG	CCTTGTGGTC	GTGTTCCACC	CCTTGTGGTC	GGTGGAACAC
298	CGTTGATTCC	GGAATCAACG	CACGATACAA	GGAATCAACG	TTGTATCGTG
299	ATAGTGGCAA	TTGCCACTAT	TCTACAGTTG	TTGCCACTAT	CAACTGTAGA
300	TCGACTCGTT	AACGAGTCGA	AGACGGTGGT	AACGAGTCGA	ACCACCGTCT

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301	TAGCAGCCAG	CTGGCTGCTA	GAACAGCCTG	CTGGCTGCTA	CAGGCTGTTC
302	CTAGGAATTC	GAATTCCTAG	TCTTCCTGCA	GAATTCCTAG	TGCAGGAAGA
303	AGTATTGGCT	AGCCAATACT	AGCGTTATAC	AGCCAATACT	GTATAACGCT
304	GCCTCCTAGA	TCTAGGAGGC	CTGAGAGAGT	TCTAGGAGGC	ACTCTCTCAG
305	AGACGACTGC	GCAGTCGTCT	AGGTTCACCG	GCAGTCGTCT	CGGTGAACCT
306	CTCAATGACT	AGTCATTGAG	CTCCAATTGT	AGTCATTGAG	ACAATTGGAG
307	TCTTCGAGAA	TTCTCGAAGA	TATACGCATC	TTCTCGAAGA	GATGCGTATA
308	GAGGTCTCTG	CAGAGACCTC	GCAGGTGGAA	CAGAGACCTC	TTCCACCTGC
309	ATGCTTGGAG	CTCCAAGCAT	TCCTGTGGAC	CTCCAAGCAT	GTCCACAGGA
310	GGATACCTCC	GGAGGTATCC	GAGGTATTCA	GGAGGTATCC	TGAATACCTC
311	CATGCAACTA	TAGTTGCATG	CGTAACAATG	TAGTTGCATG	CATTGTTACG
312	TCCAGGTAGT	ACTACCTGGA	ATACCGCCGT	ACTACCTGGA	ACGGCGGTAT
313	GGTTGCAGTA	TACTGCAACC	CTAGCGCAGT	TACTGCAACC	ACTGCGCTAG
314	TCAGAAGCAC	GTGCTTCTGA	TCGAGAATTG	GTGCTTCTGA	CAATTCTCGA
315	ATGCTTCTGT	ACAGAAGCAT	GGCTTCTCAA	ACAGAAGCAT	TTGAGAAGCC
316	CACACGTACG	CGTACGTGTG	AATCATGGCC	CGTACGTGTG	GGCCATGATT
317	CTCTAGGCCA	TGGCCTAGAG	AACAGTGCCT	TGGCCTAGAG	AGGCACTGTT
318	ACAATCCTAG	CTAGGATTGT	CTGTTATGAC	CTAGGATTGT	GTCATAACAG
319	GGTGGAAGTT	AACTTCCACC	GCTCACCTTA	AACTTCCACC	TAAGGTGAGC
320	TAGCCTTAGC	GCTAAGGCTA	TGAGCGAAGG	GCTAAGGCTA	CCTTCGCTCA
321	TGGACTCACA	TGTGAGTCCA	CCTACACGAG	TGTGAGTCCA	CTCGTGTAGG
322	ACCTAAGTGC	GCACTTAGGT	AGGTTCTTCT	GCACTTAGGT	AGAAGAACCT
323	GAACTGAGTG	CACTCAGTTC	GACCAGAATA	CACTCAGTTC	TATTCTGGTC
324	CTTGGCTCAT	ATGAGCCAAG	TTAGGTGCGC	ATGAGCCAAG	GCGCACCTAA
325	GTTCGAACCT	AGGTTCGAAC	GGTCCACGTA	AGGTTCGAAC	TACGTGGACC
326	ACGACTTAAC	GTTAAGTCGT	TTCATCTTGG	GTTAAGTCGT	CCAAGATGAA
327	TGAGACGGTA	TACCGTCTCA	CAAGATGAAC	TACCGTCTCA	GTTCATCTTG
328	CACTTGCTGG	CCAGCAAGTG	ACGTGGACCT	CCAGCAAGTG	AGGTCCACGT
329	CATGCCTAGT	ACTAGGCATG	GAGACACACG	ACTAGGCATG	CGTGTGTCTC
330	ATACATGGCC	GGCCATGTAT	ATTCACGTGT	GGCCATGTAT	ACACGTGAAT

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331	TGGATACTTG	CAAGTATCCA	CCATGTTCTA	CAAGTATCCA	TAGAACATGG
332	GCCTGGACAA	TTGTCCAGGC	TGCGTGAGAC	TTGTCCAGGC	GTCTCACGCA
333	CATCTAGTGG	CCACTAGATG	TTCCGCATGG	CCACTAGATG	CCATGCGGAA
334	ATAGAGCGAT	ATCGCTCTAT	GAGTCGTATA	ATCGCTCTAT	TATACGACTC
335	GGCAGCAACA	TGTTGCTGCC	AGAATTCCAC	TGTTGCTGCC	GTGGAATTCT
336	TCGTCTTCTC	GAGAAGACGA	CCTGAAGGCT	GAGAAGACGA	AGCCTTCAGG
337	GAACGGCCAT	ATGGCCGTTC	CTGAACACAG	ATGGCCGTTC	CTGTGTTCAG
338	ATTAACGGTG	CACCGTTAAT	AGCGCGCATT	CACCGTTAAT	AATGCGCGCT
339	CGGTTAATGA	TCATTAACCG	GATCTTGTGA	TCATTAACCG	TCACAAGATC
340	TCCGCTTACC	GGTAAGCGGA	TCATGATGCC	GGTAAGCGGA	GGCATCATGA
341	GCTGTACGAG	CTCGTACAGC	CCGTACTCCA	CTCGTACAGC	TGGAGTACGG
342	CAGAGTAACC	GGTTACTCTG	AATGCAGTTC	GGTTACTCTG	GAACTGCATT
343	TTACCGTCTA	TAGACGGTAA	GGAAGTCAAG	TAGACGGTAA	CTTGACTTCC
344	AGCTACGTGT	ACACGTAGCT	TTCCTGAGGT	ACACGTAGCT	ACCTCAGGAA
345	TCTCGCATCG	CGATGCGAGA	TGTGCGTGAA	CGATGCGAGA	TTCACGCACA
346	CAATCACCAT	ATGGTGATTG	ACCTACGTTC	ATGGTGATTG	GAACGTAGGT
347	GTGAATGAGA	TCTCATTCAC	CAGCTTAACG	TCTCATTCAC	CGTTAAGCTG
348	AGCGTGTGTC	GACACACGCT	GTAAGACCGT	GACACACGCT	ACGGTCTTAC
349	GCACCTTCAT	ATGAAGGTGC	AGTCACAAGA	ATGAAGGTGC	TCTTGTGACT
350	CGCTTACAGA	TCTGTAAGCG	CCATCGGTTC	TCTGTAAGCG	GAACCGATGG
351	TATAGGAGTC	GACTCCTATA	GTCGGTTCAG	GACTCCTATA	CTGAACCGAC
352	ATGGACGTCG	CGACGTCCAT	TAGATACGCT	CGACGTCCAT	AGCGTATCTA
353	TCTGTGCGTA	TACGCACAGA	GAGTGAGGTA	TACGCACAGA	TACCTCACTC
354	GAACATTCCT	AGGAATGTTC	ACCGATCTCT	AGGAATGTTC	AGAGATCGGT
355	CTGAGAGAAG	CTTCTCTCAG	CTAACCTAAC	CTTCTCTCAG	GTTAGGTTAG
356	AGCTCCATGC	GCATGGAGCT	TGTCTGACGG	GCATGGAGCT	CCGTCAGACA
357	ATACCTGCGA	TCGCAGGTAT	GACTTAGCAC	TCGCAGGTAT	GTGCTAAGTC
358	GCCGAATTAG	CTAATTCGGC	TGAACGTAGA	CTAATTCGGC	TCTACGTTCA
359	TATAGCCATC	GATGGCTATA	ACGCACAGTT	GATGGCTATA	AACTGTGCGT
360	CGGTTGAGCT	AGCTCAACCG	CTTGGTCTCG	AGCTCAACCG	CGAGACCAAG

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361	CTACATCCAC	GTGGATGTAG	AAGAACCGTG	GTGGATGTAG	CACGGTTCTT
362	GGTATAAGTG	CACTTATACC	CCTCCTGTAT	CACTTATACC	ATACAGGAGG
363	TCGTCGTAGT	ACTACGACGA	GTCGTATCGC	ACTACGACGA	GCGATACGAC
364	AACGGCGTCA	TGACGCCGTT	TGATGGAACA	TGACGCCGTT	TGTTCCATCA
365	TAGTCTGCTA	TAGCAGACTA	GCTGAGATCT	TAGCAGACTA	AGATCTCAGC
366	GTAAGACACG	CGTGTCTTAC	AACTCATAGG	CGTGTCTTAC	CCTATGAGTT
367	CGCGAGATAT	ATATCTCGCG	TTAAGCCGAC	ATATCTCGCG	GTCGGCTTAA
368	ACTCTCTGGC	GCCAGAGAGT	CGGCTTGCTA	GCCAGAGAGT	TAGCAAGCCG
369	GCCATCTCAA	TTGAGATGGC	TCCTAGACTG	TTGAGATGGC	CAGTCTAGGA
370	TAACCACGCC	GGCGTGGTTA	GTTGGCGAAT	GGCGTGGTTA	ATTCGCCAAC
371	CTTGAGGAGT	ACTCCTCAAG	AAGACTCTCA	ACTCCTCAAG	TGAGAGTCTT
372	AGGTGTATTG	CAATACACCT	CGACTATGGC	CAATACACCT	GCCATAGTCG
373	ATGCCAGGCT	AGCCTGGCAT	TTGCACTGGT	AGCCTGGCAT	ACCAGTGCAA
374	TCCTTGAATC	GATTCAAGGA	AATGGTCTCA	GATTCAAGGA	TGAGACCATT
375	CGAAGTTCAA	TTGAACTTCG	GGCATAGATC	TTGAACTTCG	GATCTATGCC
376	GATGACCTGG	CCAGGTCATC	CCATCGACAG	CCAGGTCATC	CTGTCGATGG
377	AGTGAGTTCT	AGAACTCACT	TTCGGCGATA	AGAACTCACT	TATCGCCGAA
378	TCGATAGAGC	GCTCTATCGA	GAGCAATTAC	GCTCTATCGA	GTAATTGCTC
379	GAACGTCGAA	TTCGACGTTC	ACTTCGACGT	TTCGACGTTC	ACGTCGAAGT
380	CTCTCCACTG	CAGTGGAGAG	CGAATTCGCG	CAGTGGAGAG	CGCGAATTCG
381	CGAACCGTAC	GTACGGTTCG	CCGCACTGAA	GTACGGTTCG	TTCAGTGCGG
382	TTCCTGAGCA	TGCTCAGGAA	GAATTGCTCT	TGCTCAGGAA	AGAGCAATTC
383	AAGGAACCTT	AAGGTTCCTT	TGTACTAAGG	AAGGTTCCTT	CCTTAGTACA
384	GCTTGTTAGG	CCTAACAAGC	ATCGGAGCTC	CCTAACAAGC	GAGCTCCGAT
385	ACCTTGTGTT	AACACAAGGT	GACCTCGGTT	AACACAAGGT	AACCGAGGTC
386	GGAAGTGACC	GGTCACTTCC	CGGAAGCTGA	GGTCACTTCC	TCAGCTTCCG
387	TATCCTCTGG	CCAGAGGATA	ACGCGTTCAA	CCAGAGGATA	TTGAACGCGT
388	CTAGACCAAT	ATTGGTCTAG	GTTGCAAGTC	ATTGGTCTAG	GACTTGCAAC
389	AGCAGTACTA	TAGTACTGCT	TTCTGGATCG	TAGTACTGCT	CGATCCAGAA
390	AAGCCATGAG	CTCATGGCTT	GCAGAACATT	CTCATGGCTT	AATGTTCTGC

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391	TCTTAGCCGA	TCGGCTAAGA	AATTCCTACC	TCGGCTAAGA	GGTAGGAATT
392	GCGATAATAC	GTATTATCGC	TGAAGACCAA	GTATTATCGC	TTGGTCTTCA
393	AGAGGCATGG	CCATGCCTCT	CTTCTGAGTA	CCATGCCTCT	TACTCAGAAG
394	TTCTATCCTC	GAGGATAGAA	AAGTGCCAGG	GAGGATAGAA	CCTGGCACTT
395	TGTCTGGACT	AGTCCAGACA	GCAAGTATAC	AGTCCAGACA	GTATACTTGC
396	CAGCGGTGAA	TTCACCGCTG	TGGCAATGGC	TTCACCGCTG	GCCATTGCCA
397	ACAACTACAG	CTGTAGTTGT	TTCGTTACCT	CTGTAGTTGT	AGGTAACGAA
398	GAGGAAGTAA	TTACTTCCTC	CTTGCGGTAA	TTACTTCCTC	TTACCGCAAG
399	ATTGTCAGCT	AGCTGACAAT	GGAACACATT	AGCTGACAAT	AATGTGTTCC
400	TCGCCAGATC	GATCTGGCGA	ACATAGTCCT	GATCTGGCGA	AGGACTATGT
401	TCGACACAGA	TCTGTGTCGA	GAGATCTTGT	TCTGTGTCGA	ACAAGATCTC
402	GAATCCACAG	CTGTGGATTC	CGTGCTAACC	CTGTGGATTC	GGTTAGCACG
403	CCTCTTGATT	AATCAAGAGG	ATAAGGCCTC	AATCAAGAGG	GAGGCCTTAT
404	ATCTGGAGGT	ACCTCCAGAT	TCGTACGGAA	ACCTCCAGAT	TTCCGTACGA
405	GGTGAGCTCA	TGAGCTCACC	ATTCCACCGA	TGAGCTCACC	TCGGTGGAAT
406	CTCCAATTCC	GGAATTGGAG	TACGTACTCT	GGAATTGGAG	AGAGTACGTA
407	TGACGTCAAT	ATTGACGTCA	GGCCTTAGAG	ATTGACGTCA	CTCTAAGGCC
408	AAGAATGGAC	GTCCATTCTT	CCAAGTGAGA	GTCCATTCTT	TCTCACTTGG
409	ATTCCACACA	TGTGTGGAAT	GGTTGTAACT	TGTGTGGAAT	AGTTACAACC
410	TGGTTCTGAA	TTCAGAACCA	CTCCTCGCAA	TTCAGAACCA	TTGCGAGGAG
411	TACAATGCTC	GAGCATTGTA	TATGACTGTG	GAGCATTGTA	CACAGTCATA
412	GTAGTGGTGC	GCACCACTAC	AGAACAGTCC	GCACCACTAC	GGACTGTTCT
413	CGATCCATTG	CAATGGATCG	ATGCTGCGGA	CAATGGATCG	TCCGCAGCAT
414	ACAAGACTGT	ACAGTCTTGT	GACTCACAGC	ACAGTCTTGT	GCTGTGAGTC
415	CGCGGTTCAT	ATGAACCGCG	TCTCGGTTAT	ATGAACCGCG	ATAACCGAGA
416	ATTCGGAACA	TGTTCCGAAT	GGATATACCA	TGTTCCGAAT	TGGTATATCC
417	ACACAAGAAC	GTTCTTGTGT	CGCAGATCCA	GTTCTTGTGT	TGGATCTGCG
418	GTTACCAGCG	CGCTGGTAAC	TAGCCTATGG	CGCTGGTAAC	CCATAGGCTA
419	GAGTTGGCTC	GAGCCAACTC	ACTGACCATA	GAGCCAACTC	TATGGTCAGT
420	TTCGGTTAGT	ACTAACCGAA	GGCTACTGCT	ACTAACCGAA	AGCAGTAGCC

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421	CGAGCCTCAA	TTGAGGCTCG	CTAGTGTACC	TTGAGGCTCG	GGTACACTAG
422	AGCAGGCTCA	TGAGCCTGCT	TCTTCGGAGG	TGAGCCTGCT	CCTCCGAAGA
423	CAGTATAGAG	CTCTATACTG	TTGACCAGAC	CTCTATACTG	GTCTGGTCAA
424	GGTTCACCGT	ACGGTGAACC	CAACTTGCAA	ACGGTGAACC	TTGCAAGTTG
425	TGTTCGTTCG	CGAACGAACA	GGTTGATCGA	CGAACGAACA	TCGATCAACC
426	ACAGTCCATT	AATGGACTGT	ATAATGGTCG	AATGGACTGT	CGACCATTAT
427	CTGTGAAGAT	ATCTTCACAG	GACAACCATT	ATCTTCACAG	AATGGTTGTC
428	GCTATTCTGA	TCAGAATAGC	ACGGTCACAC	TCAGAATAGC	GTGTGACCGT
429	GACGAGGAAT	ATTCCTCGTC	CGGCCAATGT	ATTCCTCGTC	ACATTGGCCG
430	TTGACAGCGC	GCGCTGTCAA	TGGAATTGTC	GCGCTGTCAA	GACAATTCCA
431	AGCCGATGTC	GACATCGGCT	CAACGAGTCG	GACATCGGCT	CGACTCGTTG
432	TAACACAGTG	CACTGTGTTA	ACCTCCACAA	CACTGTGTTA	TTGTGGAGGT
433	ACTAGCGGAC	GTCCGCTAGT	GGAATCTCCT	GTCCGCTAGT	AGGAGATTCC
434	TTAGCAACGT	ACGTTGCTAA	AAGCGAGGAA	ACGTTGCTAA	TTCCTCGCTT
435	CACAATATCG	CGATATTGTG	CATTAGATCG	CGATATTGTG	CGATCTAATG
436	ACCTGGTATA	TATACCAGGT	TTCTTCTAGC	TATACCAGGT	GCTAGAAGAA
437	ACACTTCTTC	GAAGAAGTGT	ATTGCTCCTA	GAAGAAGTGT	TAGGAGCAAT
438	TGGTCAGCAG	CTGCTGACCA	GCGATAATCT	CTGCTGACCA	AGATTATCGC
439	GTATTCCAGA	TCTGGAATAC	TGTCGTAGTG	TCTGGAATAC	CACTACGACA
440	CGTGACTGCT	AGCAGTCACG	AAGTCCGAAC	AGCAGTCACG	GTTCGGACTT
441	AAGCCTCCAT	ATGGAGGCTT	CAAGTCACAA	ATGGAGGCTT	TTGTGACTTG
442	ATCTGAATGC	GCATTCAGAT	GCCTCATGGT	GCATTCAGAT	ACCATGAGGC
443	GGTAACAGAG	CTCTGTTACC	TGGCGTCTGT	CTCTGTTACC	ACAGACGCCA
444	CCGACTTCCA	TGGAAGTCGG	ACTCAGGACG	TGGAAGTCGG	CGTCCTGAGT
445	TCAGTGGAAC	GTTCCACTGA	TAGAGAGGTC	GTTCCACTGA	GACCTCTCTA
446	TGTCTCTGTT	AACAGAGACA	GTCTCGCTTC	AACAGAGACA	GAAGCGAGAC
447	AATTACCGGA	TCCGGTAATT	CTTAGCTCAA	TCCGGTAATT	TTGAGCTAAG
448	GTCATAATCG	CGATTATGAC	GCACAGAACT	CGATTATGAC	AGTTCTGTGC
449	TTAAGCTGGA	TCCAGCTTAA	CGTTGCATCT	TCCAGCTTAA	AGATGCAACG
450	TATGCTGCAC	GTGCAGCATA	ATGAATGCGA	GTGCAGCATA	TCGCATTCAT

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451	CCGATAACTG	CAGTTATCGG	ACACTATGTG	CAGTTATCGG	CACATAGTGT
452	GGCCTGCATT	AATGCAGGCC	TGCTAGAGCC	AATGCAGGCC	GGCTCTAGCA
453	AAGTACGTAC	GTACGTACTT	CAGCTACCAC	GTACGTACTT	GTGGTAGCTG
454	TCCTTATGCC	GGCATAAGGA	GTAGCCAATA	GGCATAAGGA	TATTGGCTAC
455	CTACGGCCTA	TAGGCCGTAG	GATGGATTGT	TAGGCCGTAG	ACAATCCATC
456	ACCTATGAGA	TCTCATAGGT	TCCATGGAGC	TCTCATAGGT	GCTCCATGGA
457	ATATCAGTCC	GGACTGATAT	CGTGGTGCTA	GGACTGATAT	TAGCACCACG
458	TCCGACAGGA	TCCTGTCGGA	ACGACAAGAC	TCCTGTCGGA	GTCTTGTCGT
459	AAGATTGCTG	CAGCAATCTT	GAATACCTCG	CAGCAATCTT	CGAGGTATTC
460	TATCGGTACG	CGTACCGATA	TGGCTGGTGT	CGTACCGATA	ACACCAGCCA
461	CGAGAACTAT	ATAGTTCTCG	CTTCAACGAC	ATAGTTCTCG	GTCGTTGAAG
462	GACAGAAGCG	CGCTTCTGTC	TCCACGTAGG	CGCTTCTGTC	CCTACGTGGA
463	GCATTGCCTC	GAGGCAATGC	GTCAGGCACA	GAGGCAATGC	TGTGCCTGAC
464	AGTACTGAAG	CTTCAGTACT	GGATTCACTT	CTTCAGTACT	AAGTGAATCC
465	ACATCGCCTA	TAGGCGATGT	AAGCTCCATA	TAGGCGATGT	TATGGAGCTT
466	TTCCAAGTCG	CGACTTGGAA	GTCAATATCC	CGACTTGGAA	GGATATTGAC
467	AGGACTAATC	GATTAGTCCT	CTATCGGCCT	GATTAGTCCT	AGGCCGATAG
468	CCTGGATGGA	TCCATCCAGG	GGTCAAGGTG	TCCATCCAGG	CACCTTGACC
469	GATAGCTGAT	ATCAGCTATC	CAGGTGCAGT	ATCAGCTATC	ACTGCACCTG
470	CGCGTTAGGT	ACCTAACGCG	TCACGACTAA	ACCTAACGCG	TTAGTCGTGA
471	TACCAGCTAT	ATAGCTGGTA	ATCGGTTGAA	ATAGCTGGTA	TTCAACCGAT
472	CTCTACGTCG	CGACGTAGAG	ACTTCATTGC	CGACGTAGAG	GCAATGAAGT
473	TTATGAGGCC	GGCCTCATAA	GGCGAGACAA	GGCCTCATAA	TTGTCTCGCC
474	ACCAAGCAGG	CCTGCTTGGT	CTGCCTTGTG	CCTGCTTGGT	CACAAGGCAG
475	GTGGACAGAA	TTCTGTCCAC	ACCTTCAAGT	TTCTGTCCAC	ACTTGAAGGT
476	CGACCTTCTG	CAGAAGGTCG	ATAACGCGCA	CAGAAGGTCG	TGCGCGTTAT
477	TTACACTCGT	ACGAGTGTAA	TGTGGAGTCC	ACGAGTGTAA	GGACTCCACA
478	TACGTTGTTC	GAACAACGTA	GAACTTCGGA	GAACAACGTA	TCCGAAGTTC
479	AATTCAGGCA	TGCCTGAATT	CATAACTTCG	TGCCTGAATT	CGAAGTTATG
480	TCGATGCTAA	TTAGCATCGA	TCCTGGCATT	TTAGCATCGA	AATGCCAGGA

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481	AATTCTCACG	CGTGAGAATT	CGATGCACGA	CGTGAGAATT	TCGTGCATCG
482	TCGCAGTGAC	GTCACTGCGA	ACTATACACC	GTCACTGCGA	GGTGTATAGT
483	GGCAGAGTTA	TAACTCTGCC	CGACCTGTGT	TAACTCTGCC	ACACAGGTCG
484	TTCTTAACGG	CCGTTAAGAA	GACAGTTGTA	CCGTTAAGAA	TACAACTGTC
485	CAATGCCAAT	ATTGGCATTG	TTGGCTGCCT	ATTGGCATTG	AGGCAGCCAA
486	ACAGGAGCCA	TGGCTCCTGT	CACAACCGAG	TGGCTCCTGT	CTCGGTTGTG
487	CGTTCTACTT	AAGTAGAACG	ACTGAGTAAC	AAGTAGAACG	GTTACTCAGT
488	ATGCAGATTC	GAATCTGCAT	GTCCTAGTAA	GAATCTGCAT	TTACTAGGAC
489	TCCATGGCTG	CAGCCATGGA	GATCTCGATA	CAGCCATGGA	TATCGAGATC
490	GTACCAAGAA	TTCTTGGTAC	TGATCTTCGC	TTCTTGGTAC	GCGAAGATCA
491	AGTGGTCAAT	ATTGACCACT	TCTCAGCGCT	ATTGACCACT	AGCGCTGAGA
492	CGTTACGTGG	CCACGTAACG	ACGAGAGTGG	CCACGTAACG	CCACTCTCGT
493	TACTTACGCA	TGCGTAAGTA	CGCGTCAGAA	TGCGTAAGTA	TTCTGACGCG
494	TGGCGTTAAC	GTTAACGCCA	GTCTCTGGAT	GTTAACGCCA	ATCCAGAGAC
495	GAAGAGTACA	TGTACTCTTC	CAGTGGAATC	TGTACTCTTC	GATTCCACTG
496	ATGACCATTC	GAATGGTCAT	ACTTGTCTGT	GAATGGTCAT	ACAGACAAGT
497	TGGTAGGAAG	CTTCCTACCA	AGCTGTACAA	CTTCCTACCA	TTGTACAGCT
498	GTAGTTCGGA	TCCGAACTAC	CTAGCATGAT	TCCGAACTAC	ATCATGCTAG
499	CCTAGTACAT	ATGTACTAGG	TAGATTCTCC	ATGTACTAGG	GGAGAATCTA
500	CACTGCGTCT	AGACGCAGTG	ACATACGATG	AGACGCAGTG	CATCGTATGT
501	TAACACCTTC	GAAGGTGTTA	TGTCGGTGGA	GAAGGTGTTA	TCCACCGACA
502	ACGGCATTCT	AGAATGCCGT	CTGGATGCCA	AGAATGCCGT	TGGCATCCAG
503	CTACTGTCTC	GAGACAGTAG	GCTAGACAGG	GAGACAGTAG	CCTGTCTAGC
504	AGGCGTAAGA	TCTTACGCCT	AGCATGTTCC	TCTTACGCCT	GGAACATGCT
505	TCATCCAGGA	TCCTGGATGA	TACGGAAGAA	TCCTGGATGA	TTCTTCCGTA
506	AGCATTCTCG	CGAGAATGCT	CGACTGACTC	CGAGAATGCT	GAGTCAGTCG
507	CAACGTCCTC	GAGGACGTTG	GCTTGCTTAT	GAGGACGTTG	ATAAGCAAGC
508	AGTGTGGAAT	ATTCCACACT	AGGCCACAGA	ATTCCACACT	TCTGTGGCCT
509	GCGCAAGTCA	TGACTTGCGC	GACAATGAGT	TGACTTGCGC	ACTCATTGTC
510	CTCAGCTCCA	TGGAGCTGAG	ATCTCCGGTG	TGGAGCTGAG	CACCGGAGAT

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511	AACACATGGT	ACCATGTGTT	TCTACTCGCG	ACCATGTGTT	CGCGAGTAGA
512	GATGCGAGAC	GTCTCGCATC	AGAGTCTCTT	GTCTCGCATC	AAGAGACTCT
513	AATCGACCGA	TCGGTCGATT	CACTGCAATT	TCGGTCGATT	AATTGCAGTG
514	TCGGAGTTCC	GGAACTCCGA	ACTGACTTGA	GGAACTCCGA	TCAAGTCAGT
515	CGATGGAGTG	CACTCCATCG	TAACCGGACC	CACTCCATCG	GGTCCGGTTA
516	GTCTCAGTAG	CTACTGAGAC	TCCATTCCAA	CTACTGAGAC	TTGGAATGGA
517	TACACTTGCA	TGCAAGTGTA	TTGTGAGGCG	TGCAAGTGTA	CGCCTCACAA
518	GTAATCGACG	CGTCGATTAC	GGAGAGTTAT	CGTCGATTAC	ATAACTCTCC
519	AGTGAGACGT	ACGTCTCACT	AAGGATAGCC	ACGTCTCACT	GGCTATCCTT
520	CACCTCCTAC	GTAGGAGGTG	TGTCCGGCTA	GTAGGAGGTG	TAGCCGGACA
521	ACTTCCGTCC	GGACGGAAGT	CTGCTCGTCT	GGACGGAAGT	AGACGAGCAG
522	AGCCAGTGGA	TCCACTGGCT	GCTAGTCGAA	TCCACTGGCT	TTCGACTAGC
523	CAGTGATCGG	CCGATCACTG	TGAGAGTCGC	CCGATCACTG	GCGACTCTCA
524	GTAACTAACC	GGTTAGTTAC	AGATAACCTG	GGTTAGTTAC	CAGGTTATCT
525	TGTGCCTTAT	ATAAGGCACA	TTCGCGGAGT	ATAAGGCACA	ACTCCGCGAA
526	TGAATACGTC	GACGTATTCA	CAGTATAGGA	GACGTATTCA	TCCTATACTG
527	GTCGGTAAGG	CCTTACCGAC	TAGAGCATTC	CCTTACCGAC	GAATGCTCTA
528	CAAGTGAGTT	AACTCACTTG	ATCCTAACCT	AACTCACTTG	AGGTTAGGAT
529	AAGTCGAGAG	CTCTCGACTT	AACGTAAGCA	CTCTCGACTT	TGCTTACGTT
530	TCCGGACTCA	TGAGTCCGGA	CCACAGCTGT	TGAGTCCGGA	ACAGCTGTGG
531	CTTAACACCT	AGGTGTTAAG	TATAGCGAAC	AGGTGTTAAG	GTTCGCTATA
532	GGTTATCTTC	GAAGATAACC	GGTCCTTCAC	GAAGATAACC	GTGAAGGACC
533	TGAGTAGATC	GATCTACTCA	TTGCGAGATA	GATCTACTCA	TATCTCGCAA
534	ATGCGGTGGT	ACCACCGCAT	GAATCCGACT	ACCACCGCAT	AGTCGGATTC
535	TAAGTTGCCT	AGGCAACTTA	CTGATTCTAG	AGGCAACTTA	CTAGAATCAG
536	ACACACCATG	CATGGTGTGT	ACGGCGATTG	CATGGTGTGT	CAATCGCCGT
537	AAGTGGTAGG	CCTACCACTT	TGACGGAGTA	CCTACCACTT	TACTCCGTCA
538	TTGGACGGAC	GTCCGTCCAA	ATTGATGAGC	GTCCGTCCAA	GCTCATCAAT
539	GGACTTCGCT	AGCGAAGTCC	GGCTAGCCAT	AGCGAAGTCC	ATGGCTAGCC
540	GATACAGCTA	TAGCTGTATC	TATGCCTTCG	TAGCTGTATC	CGAAGGCATA

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541	CACACCGCAT	ATGCGGTGTG	CCGATCCATT	ATGCGGTGTG	AATGGATCGG
542	CCTCCGATCT	AGATCGGAGG	GGTGTATAGA	AGATCGGAGG	TCTATACACC
543	AGTTGTCCTA	TAGGACAACT	CTGTCTGCAC	TAGGACAACT	GTGCAGACAG
544	GTAGGCAATG	CATTGCCTAC	TCACCAATCA	CATTGCCTAC	TGATTGGTGA
545	TGACAACTCT	AGAGTTGTCA	TGAGAACGGT	AGAGTTGTCA	ACCGTTCTCA
546	ACGTGCAAGC	GCTTGCACGT	GTCCTGAACA	GCTTGCACGT	TGTTCAGGAC
547	TATATCGGAG	CTCCGATATA	ACGAGTTGCC	CTCCGATATA	GGCAACTCGT
548	AATACTTCCG	CGGAAGTATT	CATTAAGCTG	CGGAAGTATT	CAGCTTAATG
549	GTGGTATCAA	TTGATACCAC	CTGCACCTAC	TTGATACCAC	GTAGGTGCAG
550	CTCACAGATA	TATCTGTGAG	CGCTCTGATG	TATCTGTGAG	CATCAGAGCG
551	CGACTGATGT	ACATCAGTCG	GCTGACTATT	ACATCAGTCG	AATAGTCAGC
552	GGCTCTTGTC	GACAAGAGCC	TACTTGGCTA	GACAAGAGCC	TAGCCAAGTA
553	TGTATCAGAC	GTCTGATACA	AAGCTTGGAT	GTCTGATACA	ATCCAAGCTT
554	CTGCCTTCCT	AGGAAGGCAG	TCCTGGTTCC	AGGAAGGCAG	GGAACCAGGA
555	ACCTTCCAGG	CCTGGAAGGT	GCTATCAAGA	CCTGGAAGGT	TCTTGATAGC
556	GAAGGATTGA	TCAATCCTTC	GTCGGACTGT	TCAATCCTTC	ACAGTCCGAC
557	ATAAGGCTTG	CAAGCCTTAT	CCATAACCTT	CAAGCCTTAT	AAGGTTATGG
558	GATCAGGCCT	AGGCCTGATC	AGTACTCCGC	AGGCCTGATC	GCGGAGTACT
559	GAATGAAGAC	GTCTTCATTC	TTGGCGGTTG	GTCTTCATTC	CAACCGCCAA
560	ACGCTTGATG	CATCAAGCGT	AGTTATAGCG	CATCAAGCGT	CGCTATAACT
561	ATCATCACGT	ACGTGATGAT	TGACGCGGAT	ACGTGATGAT	ATCCGCGTCA
562	CCAGGTTGAC	GTCAACCTGG	CAGAATAACC	GTCAACCTGG	GGTTATTCTG
563	GATCAGTTCA	TGAACTGATC	ATGGCACGGA	TGAACTGATC	TCCGTGCCAT
564	AGGTGACATC	GATGTCACCT	GGCAGCTTAA	GATGTCACCT	TTAAGCTGCC
565	TTCTCGGAAG	CTTCCGAGAA	CCTGTTGTGT	CTTCCGAGAA	ACACAACAGG
566	GCACCACCAA	TTGGTGGTGC	CACTCGACCA	TTGGTGGTGC	TGGTCGAGTG
567	TTGATGGCGG	CCGCCATCAA	ACACGTCGTG	CCGCCATCAA	CACGACGTGT
568	GGACATTGTT	AACAATGTCC	GGTATGCACC	AACAATGTCC	GGTGCATACC
569	ACAGCAGATG	CATCTGCTGT	TTGAACCGCT	CATCTGCTGT	AGCGGTTCAA
570	GGCCTTAGAA	TTCTAAGGCC	CGAACTAAGC	TTCTAAGGCC	GCTTAGTTCG

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571	TTGAGGTAAC	GTTACCTCAA	GGTTAAGCTT	GTTACCTCAA	AAGCTTAACC
572	AGATAACGCT	AGCGTTATCT	GGCGGATGAA	AGCGTTATCT	TTCATCCGCC
573	TGTTGCATGC	GCATGCAACA	TTGCTGATTG	GCATGCAACA	CAATCAGCAA
574	CAGCACACCT	AGGTGTGCTG	CCTCATTAGA	AGGTGTGCTG	TCTAATGAGG
575	GAGAGGTCCA	TGGACCTCTC	AAGGCGACCA	TGGACCTCTC	TGGTCGCCTT
576	ATGGTTGTGG	CCACAACCAT	ATCTGTCCGC	CCACAACCAT	GCGGACAGAT
577	TTCACCTGCT	AGCAGGTGAA	CGGTAATGAT	AGCAGGTGAA	ATCATTACCG
578	AGATGTCAGA	TCTGACATCT	CTCGTTGCGA	TCTGACATCT	TCGCAACGAG
579	TAGGTGGCTG	CAGCCACCTA	GCACACATGA	CAGCCACCTA	TCATGTGTGC
580	GCTAAGTTAC	GTAACTTAGC	TACAATCCTC	GTAACTTAGC	GAGGATTGTA
581	CGCTCGAGTT	AACTCGAGCG	TCTCCGTACC	AACTCGAGCG	GGTACGGAGA
582	CCTCGAATGA	TCATTCGAGG	AACGTCTAAG	TCATTCGAGG	CTTAGACGTT
583	ATAATCTCGG	CCGAGATTAT	AGTGGCGTCT	CCGAGATTAT	AGACGCCACT
584	TAGAACGAAC	GTTCGTTCTA	GTCTTAGGTT	GTTCGTTCTA	AACCTAAGAC
585	TCACTAACGA	TCGTTAGTGA	AATAGCTGCA	TCGTTAGTGA	TGCAGCTATT
586	ATCACTTGAC	GTCAAGTGAT	GTCTCAGAAG	GTCAAGTGAT	CTTCTGAGAC
587	GGTGACCAGT	ACTGGTCACC	TCAGTGCTCC	ACTGGTCACC	GGAGCACTGA
588	GATCGTATTC	GAATACGATC	CGTCATACTT	GAATACGATC	AAGTATGACG
589	TTGTCTGATG	CATCAGACAA	TCGGATTGGC	CATCAGACAA	GCCAATCCGA
590	CATACGGACC	GGTCCGTATG	AATGGAGCAA	GGTCCGTATG	TTGCTCCATT
591	GCCGGTCTAT	ATAGACCGGC	CGGTTCATGT	ATAGACCGGC	ACATGAACCG
592	AGAATACCGA	TCGGTATTCT	GCCAGTTATT	TCGGTATTCT	AATAACTGGC
593	AGTAAGATGG	CCATCTTACT	CTGCGTTACA	CCATCTTACT	TGTAACGCAG
594	TGAGGACCAA	TTGGTCCTCA	TGAGTAGCAT	TTGGTCCTCA	ATGCTACTCA
595	CTGTAATGTC	GACATTACAG	GACTCGTTGA	GACATTACAG	TCAACGAGTC
596	GACCTTGACT	AGTCAAGGTC	CTACATCCGG	AGTCAAGGTC	CCGGATGTAG
597	ACCTACTCTA	TAGAGTAGGT	GATACCGGTC	TAGAGTAGGT	GACCGGTATC
598	CCAACGTATA	TATACGTTGG	ACACCTAATG	TATACGTTGG	CATTAGGTGT
599	TTAGTTCACG	CGTGAACTAA	ACCTTGTGCT	CGTGAACTAA	AGCACAAGGT
600	TGTTCCGAGC	GCTCGGAACA	TAGGTAGTAC	GCTCGGAACA	GTACTACCTA

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601	ATGTTGACGT	ACGTCAACAT	CACCGTCGAA	ACGTCAACAT	TTCGACGGTG
602	GCAAGATAAC	GTTATCTTGC	TTGAAGGTTC	GTTATCTTGC	GAACCTTCAA
603	TAGGCAGGAG	CTCCTGCCTA	GCCTTAACCA	CTCCTGCCTA	TGGTTAAGGC
604	CCTCATTCTT	AAGAATGAGG	TAAGCGTATC	AAGAATGAGG	GATACGCTTA
605	AGCAACCGCA	TGCGGTTGCT	GATATGAAGG	TGCGGTTGCT	CCTTCATATC
606	GATGTCTATC	GATAGACATC	AGTGTCCATT	GATAGACATC	AATGGACACT
607	TGAACGCTTA	TAAGCGTTCA	CCTGAACTGT	TAAGCGTTCA	ACAGTTCAGG
608	TAGCGCGAAG	CTTCGCGCTA	CGATGTGCAA	CTTCGCGCTA	TTGCACATCG
609	AGTCGAAGCC	GGCTTCGACT	CGAGACCAGT	GGCTTCGACT	ACTGGTCTCG
610	TCGTCGCCAA	TTGGCGACGA	ATTAGAGGAC	TTGGCGACGA	GTCCTCTAAT
611	ATCGCTGTCT	AGACAGCGAT	TACCTGACGC	AGACAGCGAT	GCGTCAGGTA
612	TGCAACCATT	AATGGTTGCA	CCGTCATCAA	AATGGTTGCA	TTGATGACGG
613	CAGGAGTTGG	CCAACTCCTG	GGACTCATAT	CCAACTCCTG	ATATGAGTCC
614	TGAGTCTCGC	GCGAGACTCA	ATTCTTGGTG	GCGAGACTCA	CACCAAGAAT
615	GTTACAACAC	GTGTTGTAAC	AACAACTCCA	GTGTTGTAAC	TGGAGTTGTT
616	GCAATAGATG	CATCTATTGC	CTTGCACATT	CATCTATTGC	AATGTGCAAG
617	AAGAGCCTGA	TCAGGCTCTT	TGCTTGGTCA	TCAGGCTCTT	TGACCAAGCA
618	GAACAAGCCG	CGGCTTGTTC	GCTCATTCAT	CGGCTTGTTC	ATGAATGAGC
619	CGCACTTATT	AATAAGTGCG	CTCACAACTT	AATAAGTGCG	AAGTTGTGAG
620	TGCATGACGC	GCGTCATGCA	TCAGGCCATG	GCGTCATGCA	CATGGCCTGA
621	GCTGAAGGAA	TTCCTTCAGC	TACCATTGGA	TTCCTTCAGC	TCCAATGGTA
622	GTTGACGTTA	TAACGTCAAC	AAGTTAGCTC	TAACGTCAAC	GAGCTAACTT
623	CTCTATTGAG	CTCAATAGAG	GTTAGGATAC	CTCAATAGAG	GTATCCTAAC
624	AAGTGCCGTC	GACGGCACTT	AGGAGCCACA	GACGGCACTT	TGTGGCTCCT
625	ACGACAACCA	TGGTTGTCGT	TGACGCACAA	TGGTTGTCGT	TTGTGCGTCA
626	CTATTGCTAC	GTAGCAATAG	CCTTACGATT	GTAGCAATAG	AATCGTAAGG
627	TCGTTCTCGG	CCGAGAACGA	ATTGTACTCC	CCGAGAACGA	GGAGTACAAT
628	GATGATAGGT	ACCTATCATC	TAGGACTCGA	ACCTATCATC	TCGAGTCCTA
629	TACAAGGAGA	TCTCCTTGTA	TCCAGTTGCG	TCTCCTTGTA	CGCAACTGGA
630	GTCCGCAGTT	AACTGCGGAC	GGAATGAACT	AACTGCGGAC	AGTTCATTCC

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
631	AGAGTATGCT	AGCATACTCT	GAACCAAGAA	AGCATACTCT	TTCTTGGTTC
632	CGACCGGTTA	TAACCGGTCG	CTCTTCCATT	TAACCGGTCG	AATGGAAGAG
633	ATATGGACGA	TCGTCCATAT	GGATACGCAA	TCGTCCATAT	TTGCGTATCC
634	AGAATTGTCC	GGACAATTCT	AACCGTCATT	GGACAATTCT	AATGACGGTT
635	TATGTTCCAG	CTGGAACATA	TCGTCTTGCC	CTGGAACATA	GGCAAGACGA
636	TGCCAATGTT	AACATTGGCA	AGAGTGCGCA	AACATTGGCA	TGCGCACTCT
637	ATGTCCGTGA	TCACGGACAT	GTCTTAATGG	TCACGGACAT	CCATTAAGAC
638	CCGGTCACTA	TAGTGACCGG	CTTACCTTCT	TAGTGACCGG	AGAAGGTAAG
639	GCCAGTTAAT	ATTAACTGGC	GAGTTAGAAG	ATTAACTGGC	CTTCTAACTC
640	AATACAGACG	CGTCTGTATT	CAACGACCTA	CGTCTGTATT	TAGGTCGTTG
641	AGCAATCAAC	GTTGATTGCT	GGTATTGGAA	GTTGATTGCT	TTCCAATACC
642	TATCGCGCGT	ACGCGCGATA	CAAGCGAATT	ACGCGCGATA	AATTCGCTTG
643	CCTTAATTCG	CGAATTAAGG	TGGTGCCACT	CGAATTAAGG	AGTGGCACCA
644	GAAGTTAGCA	TGCTAACTTC	CTTGTGTTGA	TGCTAACTTC	TCAACACAAG
645	TTGGCCTAGG	CCTAGGCCAA	ATGCAACGTT	CCTAGGCCAA	AACGTTGCAT
646	TGTTAGGTAC	GTACCTAACA	TCGCATGCAC	GTACCTAACA	GTGCATGCGA
647	TTCCTTGTTG	CAACAAGGAA	TTCAGTGTGG	CAACAAGGAA	CCACACTGAA
648	ACTCCACGTA	TACGTGGAGT	GAATGATCAC	TACGTGGAGT	GTGATCATTC
649	ATTCAGAGTG	CACTCTGAAT	TTGAGACTGA	CACTCTGAAT	TCAGTCTCAA
650	TCGACATTGC	GCAATGTCGA	GCTTATGTCT	GCAATGTCGA	AGACATAAGC
651	GGATGCTCGT	ACGAGCATCC	GAAGCCAGGT	ACGAGCATCC	ACCTGGCTTC
652	CAACTAGGAA	TTCCTAGTTG	TACCAGCCAC	TTCCTAGTTG	GTGGCTGGTA
653	CCTGTTCAGT	ACTGAACAGG	CGAATCTGTT	ACTGAACAGG	AACAGATTCG
654	AACGTCTACC	GGTAGACGTT	ATAGCACACT	GGTAGACGTT	AGTGTGCTAT
655	TTGAGCATAC	GTATGCTCAA	TTGCTAGCAG	GTATGCTCAA	CTGCTAGCAA
656	AACTGTGCTT	AAGCACAGTT	CGGTCTTATT	AAGCACAGTT	AATAAGACCG
657	ATTGGCTGAA	TTCAGCCAAT	ATGTTCGCAA	TTCAGCCAAT	TTGCGAACAT
658	GAACCTATCT	AGATAGGTTC	CATGACAACC	AGATAGGTTC	GGTTGTCATG
659	TCGGCGCATA	TATGCGCCGA	AGACTTCTGG	TATGCGCCGA	CCAGAAGTCT
660	GTCACTACTG	CAGTAGTGAC	TCCATCTGTA	CAGTAGTGAC	TACAGATGGA

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
661	CGGTGTGCAT	ATGCACACCG	GAACGGTTAT	ATGCACACCG	ATAACCGTTC
662	AGACAATTGG	CCAATTGTCT	TGTCAAGTTC	CCAATTGTCT	GAACTTGACA
663	TGACTGCGAA	TTCGCAGTCA	CCGTCAAGGA	TTCGCAGTCA	TCCTTGACGG
664	TCAAGCCACC	GGTGGCTTGA	TGGAGGTCCT	GGTGGCTTGA	AGGACCTCCA
665	TAATCAGCTG	CAGCTGATTA	TTCCAAGCAA	CAGCTGATTA	TTGCTTGGAA
666	GCAGATTGCA	TGCAATCTGC	CAGAGGTATT	TGCAATCTGC	AATACCTCTG
667	ATGGAACTGT	ACAGTTCCAT	AGATCTAGCA	ACAGTTCCAT	TGCTAGATCT
668	CGTACGACGA	TCGTCGTACG	AAGGTACTGT	TCGTCGTACG	ACAGTACCTT
669	ATTATCGAGG	CCTCGATAAT	GCACTTGGTC	CCTCGATAAT	GACCAAGTGC
670	TAATTCCTGC	GCAGGAATTA	CGTATCCTGG	GCAGGAATTA	CCAGGATACG
671	AGCCAACGAC	GTCGTTGGCT	GTAGAATCAC	GTCGTTGGCT	GTGATTCTAC
672	CTAGGCGGTT	AACCGCCTAG	CCTAGGAACT	AACCGCCTAG	AGTTCCTAGG
673	TCCAGACGAG	CTCGTCTGGA	TTACAGCGTT	CTCGTCTGGA	AACGCTGTAA
674	CGTCTCAACC	GGTTGAGACG	CGCTGTAAGC	GGTTGAGACG	GCTTACAGCG
675	GTATGTACGT	ACGTACATAC	GAGGCCATAT	ACGTACATAC	ATATGGCCTC
676	AACACGCTAA	TTAGCGTGTT	ATTGGAACCG	TTAGCGTGTT	CGGTTCCAAT
677	GGCGATGAAG	CTTCATCGCC	GCTATAGCTA	CTTCATCGCC	TAGCTATAGC
678	CGGATATGTA	TACATATCCG	AGAGGTTCGT	TACATATCCG	ACGAACCTCT
679	AAGGTTATGC	GCATAACCTT	AACCTCTTCA	GCATAACCTT	TGAAGAGGTT
680	ACATCGGTGC	GCACCGATGT	CCATAAGAGT	GCACCGATGT	ACTCTTATGG
681	TTCAGACCGT	ACGGTCTGAA	AGGTGTTGAT	ACGGTCTGAA	ATCAACACCT
682	ACAGATCTCC	GGAGATCTGT	TCCGAGGATC	GGAGATCTGT	GATCCTCGGA
683	TAACTCTGAG	CTCAGAGTTA	GAAGCACTAT	CTCAGAGTTA	ATAGTGCTTC
684	GGTACGAATT	AATTCGTACC	ATTGCAGCCA	AATTCGTACC	TGGCTGCAAT
685	ATGAGCTAGA	TCTAGCTCAT	CGGATTAAGA	TCTAGCTCAT	TCTTAATCCG
686	CGTTAAGCAT	ATGCTTAACG	CTACTACAGA	ATGCTTAACG	TCTGTAGTAG
687	TTGTGTTCCT	AGGAACACAA	GGTCACATGG	AGGAACACAA	CCATGTGACC
688	ACTGTGAGCG	CGCTCACAGT	GCGATCTCAC	CGCTCACAGT	GTGAGATCGC
689	ATATGTGTGG	CCACACATAT	GTCATGTCGT	CCACACATAT	ACGACATGAC
690	GACATGTCAT	ATGACATGTC	TGGCTTATCC	ATGACATGTC	GGATAAGCCA

Index #	Illumina i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	Illumina i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	Illumina i7 index all Illumina® systems	MGI i5 index	MGI i7 index
691	TAGCCACATA	TATGTGGCTA	TATTGAGCGT	TATGTGGCTA	ACGCTCAATA
692	CGAGGATCAC	GTGATCCTCG	ATCGCCAGAA	GTGATCCTCG	TTCTGGCGAT
693	ACGCAGTTAG	CTAACTGCGT	CCTCAACATT	CTAACTGCGT	AATGTTGAGG
694	TCACGGAGCT	AGCTCCGTGA	TAAGTCAGTG	AGCTCCGTGA	CACTGACTTA
695	CTTCACAACG	CGTTGTGAAG	CGCTAGGTAT	CGTTGTGAAG	ATACCTAGCG
696	CGTTATGAGT	ACTCATAACG	CCATGCCTCA	ACTCATAACG	TGAGGCATGG
697	AGAACAGCGT	ACGCTGTTCT	CAGGAATTGA	ACGCTGTTCT	TCAATTCCTG
698	TCCTGCAAGG	CCTTGCAGGA	TCAATGCAAC	CCTTGCAGGA	GTTGCATTGA
699	CTTCAGTCAA	TTGACTGAAG	AGACCTATCT	TTGACTGAAG	AGATAGGTCT
700	AATAAGCTCC	GGAGCTTATT	TATTCCGATC	GGAGCTTATT	GATCGGAATA
701	GAAGGCGGAA	TTCCGCCTTC	GTCCGTAAGA	TTCCGCCTTC	TCTTACGGAC
702	ACGATTCGAA	TTCGAATCGT	TCTTGTCCAA	TTCGAATCGT	TTGGACAAGA
703	TCCTGCTCTT	AAGAGCAGGA	GTAACGAGCT	AAGAGCAGGA	AGCTCGTTAC
704	CTCGAACACG	CGTGTTCGAG	TGGTGCTTGG	CGTGTTCGAG	CCAAGCACCA
705	ACTGTTACAC	GTGTAACAGT	TGCCACAATT	GTGTAACAGT	AATTGTGGCA
706	TGACACCACA	TGTGGTGTCA	GCTTCTATGA	TGTGGTGTCA	TCATAGAAGC
707	GGTAAGGTCG	CGACCTTACC	CAATTGTTCC	CGACCTTACC	GGAACAATTG
708	CTGTCGAGGT	ACCTCGACAG	GTTGCCTAGA	ACCTCGACAG	TCTAGGCAAC
709	AAGAGATAGC	GCTATCTCTT	TATCAAGCGG	GCTATCTCTT	CCGCTTGATA
710	CCATTACCAA	TTGGTAATGG	ATTAGTCGTC	TTGGTAATGG	GACGACTAAT
711	CACGGACTTC	GAAGTCCGTG	GGTCTAACAT	GAAGTCCGTG	ATGTTAGACC
712	GTACATTACG	CGTAATGTAC	TGGCAGTAAT	CGTAATGTAC	ATTACTGCCA
713	TAGGAGACAA	TTGTCTCCTA	CTCTAGTGAT	TTGTCTCCTA	ATCACTAGAG
714	AGATCTATCG	CGATAGATCT	TAGCTTGACC	CGATAGATCT	GGTCAAGCTA
715	TTACTGTGCG	CGCACAGTAA	GGAGCAACTG	CGCACAGTAA	CAGTTGCTCC
716	CCGAATCCTC	GAGGATTCGG	TATCACCTCA	GAGGATTCGG	TGAGGTGATA
717	GCTGGATTAA	TTAATCCAGC	ACGGAACAGG	TTAATCCAGC	CCTGTTCCGT
718	ACCGTCTCGT	ACGAGACGGT	GCTCGAGGTA	ACGAGACGGT	TACCTCGAGC
719	AGAGCGGAGA	TCTCCGCTCT	CTGATTAGCC	TCTCCGCTCT	GGCTAATCAG
720	GAACACGGAG	CTCCGTGTTC	CACTGCGCAA	CTCCGTGTTC	TTGCGCAGTG

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
721	AGTCTTGTGA	TCACAAGACT	GGCATCTATT	TCACAAGACT	AATAGATGCC
722	TTAAGGCGAG	CTCGCCTTAA	CTATGAGGAA	CTCGCCTTAA	TTCCTCATAG
723	TCGTCAATTC	GAATTGACGA	ATGTCTACCA	GAATTGACGA	TGGTAGACAT
724	CACCACTTGT	ACAAGTGGTG	TGTTAGGTGA	ACAAGTGGTG	TCACCTAACA
725	TTCGCAGACT	AGTCTGCGAA	CCTGATCGCA	AGTCTGCGAA	TGCGATCAGG
726	GAGACTCCGT	ACGGAGTCTC	AACAAGAACG	ACGGAGTCTC	CGTTCTTGTT
727	TGCGGAGAAC	GTTCTCCGCA	TACCGAACAC	GTTCTCCGCA	GTGTTCGGTA
728	ACATATCGCG	CGCGATATGT	CATTGCTTGC	CGCGATATGT	GCAAGCAATG
729	ATCAGGACAG	CTGTCCTGAT	CGATTGAGTT	CTGTCCTGAT	AACTCAATCG
730	GAATTGCGTT	AACGCAATTC	GAGCATGCAA	AACGCAATTC	TTGCATGCTC
731	TGTGGAGCCT	AGGCTCCACA	TCAGGTTAGC	AGGCTCCACA	GCTAACCTGA
732	AGGAACAAGA	TCTTGTTCCT	GGTTCAATCA	TCTTGTTCCT	TGATTGAACC
733	CCAAGCTTCT	AGAAGCTTGG	AGCAAGCTGC	AGAAGCTTGG	GCAGCTTGCT
734	TGGCATTGGC	GCCAATGCCA	GAACGCTGTC	GCCAATGCCA	GACAGCGTTC
735	ACAACGCGGT	ACCGCGTTGT	ATTCGTCATG	ACCGCGTTGT	CATGACGAAT
736	GAGCTACCAC	GTGGTAGCTC	CAGATCCTAA	GTGGTAGCTC	TTAGGATCTG
737	TTGTAACCAG	CTGGTTACAA	TGCATCCTGA	CTGGTTACAA	TCAGGATGCA
738	GCACTATTCT	AGAATAGTGC	GAGGAGAATT	AGAATAGTGC	AATTCTCCTC
739	ATGGCCAACA	TGTTGGCCAT	TCTCGATGAA	TGTTGGCCAT	TTCATCGAGA
740	CATACTACTC	GAGTAGTATG	AGCGCATAAC	GAGTAGTATG	GTTATGCGCT
741	AGCCTGTCCA	TGGACAGGCT	CCAATTACCA	TGGACAGGCT	TGGTAATTGG
742	TCATGTCGGT	ACCGACATGA	AGTTCCGGAA	ACCGACATGA	TTCCGGAACT
743	ACAGGTGGAG	CTCCACCTGT	TTAAGGAAGC	CTCCACCTGT	GCTTCCTTAA
744	CAACTCAACT	AGTTGAGTTG	CGCAATGTGG	AGTTGAGTTG	CCACATTGCG
745	ACTTAGTAGC	GCTACTAAGT	TAAGAAGGCC	GCTACTAAGT	GGCCTTCTTA
746	AGGATATCCA	TGGATATCCT	ATGTGTTCGT	TGGATATCCT	ACGAACACAT
747	GCATCAAGAT	ATCTTGATGC	GTTCACCACT	ATCTTGATGC	AGTGGTGAAC
748	AGGAATGTTC	GAACATTCCT	CCGACGATGA	GAACATTCCT	TCATCGTCGG
749	TTCTACTAGC	GCTAGTAGAA	AGAATAGAGG	GCTAGTAGAA	CCTCTATTCT
750	CAGAGGCTAT	ATAGCCTCTG	CTCATTGTCA	ATAGCCTCTG	TGACAATGAG

Index #	Illumina			MGI	
	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index all Illumina® systems	i5 index	i7 index
751	ATTGTGAAGG	CCTTCACAAT	GCATTCGCTA	CCTTCACAAT	TAGCGAATGC
752	GTCCTTAACA	TGTTAAGGAC	TGTGAGCTAT	TGTTAAGGAC	ATAGCTCACA
753	AGGCGAGCTT	AAGCTCGCCT	GAACATAGGT	AAGCTCGCCT	ACCTATGTTC
754	TGCTCTCGAT	ATCGAGAGCA	TGGTTGGATA	ATCGAGAGCA	TATCCAACCA
755	GAATGGTTCA	TGAACCATTC	AACACCTGGT	TGAACCATTC	ACCAGGTGTT
756	ATCGAGAATC	GATTCTCGAT	TATCGATTCG	GATTCTCGAT	CGAATCGATA
757	CCAACATTGA	TCAATGTTGG	TCATTACAGC	TCAATGTTGG	GCTGTAATGA
758	ATTCTCCAGT	ACTGGAGAAT	TTAGAGCTCA	ACTGGAGAAT	TGAGCTCTAA
759	GGCATTATCA	TGATAATGCC	TTGGTGACAA	TGATAATGCC	TTGTCACCAA
760	ATCGTACATG	CATGTACGAT	CTGTGATATC	CATGTACGAT	GATATCACAG
761	TGTCTACGGC	GCCGTAGACA	CAAGTGGTCT	GCCGTAGACA	AGACCACTTG
762	AGAACCAATG	CATTGGTTCT	ATGACTAGGA	CATTGGTTCT	TCCTAGTCAT
763	GTCGACGACA	TGTCGTCGAC	TACTGTCGTA	TGTCGTCGAC	TACGACAGTA
764	CTTGGTATGT	ACATACCAAG	ACACACAAGG	ACATACCAAG	CCTTGTGTGT
765	GACTTATCCT	AGGATAAGTC	TGCCTAGCGT	AGGATAAGTC	ACGCTAGGCA
766	GCGTGAATCA	TGATTCACGC	GCTATCCTCT	TGATTCACGC	AGAGGATAGC
767	CTCCTGTTAT	ATAACAGGAG	TGCTAGTTGT	ATAACAGGAG	ACAACTAGCA
768	ATATTAGCGC	GCGCTAATAT	GTACACGGAC	GCGCTAATAT	GTCCGTGTAC

Note: The dual Index sequence are designed to be balanced within each group, with indexes 1-384 grouped every 4 and indexes 385-768 grouped every 8 (different color blocks in the table above). To achieve the best sequencing quality, it is recommended to use continuous indexes as indicated within one block in the table and involve at least 8 indexes for multiplexed sequencing. As the reading mode of the dual index differs in various Illumina® platforms, please select the corresponding sequence information according to the Illumina systems (select the first 8 or 10 bases).

Appendix 4: NadPrep UDI Adapter (for Illumina®) Information

The adapters in NadPrep UDI Adapter Kit (for Illumina®) are Y-shaped with 8 nt unique dual indexes. The index sequences in the Kit are listed as follows:

NadPrep UDI Adapter (Set D#，96-well Plate Position)	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index (all Illumina® systems)
NadPrep UDI Adapter 1 (Set D1， A1)	ATATGCGC	GCGCATAT	CTGATCGT
NadPrep UDI Adapter 2 (Set D1， B1)	TGGTACAG	CTGTACCA	ACTCTCGA
NadPrep UDI Adapter 3 (Set D1， C1)	AACCGTTC	GAACGGTT	TGAGCTAG
NadPrep UDI Adapter 4 (Set D1， D1)	TAACCGGT	ACCGGTTA	GAGACGAT
NadPrep UDI Adapter 5 (Set D1， E1)	GAACATCG	CGATGTTC	CTTGTCGA
NadPrep UDI Adapter 6 (Set D1， F1)	CCTTGTAG	CTACAAGG	TTCCAAGG
NadPrep UDI Adapter 7 (Set D1， G1)	TCAGGCTT	AAGCCTGA	CGCATGAT
NadPrep UDI Adapter 8 (Set D1， H1)	GTTCTCGT	ACGAGAAC	ACGGAACA
NadPrep UDI Adapter 9 (Set D1， A2)	AGAACGAG	CTCGTTCT	CGGCTAAT
NadPrep UDI Adapter 10 (Set D1， B2)	TGCTTCCA	TGGAAGCA	ATCGATCG
NadPrep UDI Adapter 11 (Set D1， C2)	CTTCGACT	AGTCGAAG	GCAAGATC
NadPrep UDI Adapter 12 (Set D1， D2)	CACCTGTT	AACAGGTG	GCTATCCT
NadPrep UDI Adapter 13 (Set D1， E2)	ATCACACG	CGTGTGAT	TACGCTAC
NadPrep UDI Adapter 14 (Set D1， F2)	CCGTAAGA	TCTTACGG	TGGACTCT
NadPrep UDI Adapter 15 (Set D1， G2)	TACGCCTT	AAGGCGTA	AGAGTAGC
NadPrep UDI Adapter 16 (Set D1， H2)	CGACGTTA	TAACGTCG	ATCCAGAG
NadPrep UDI Adapter 17 (Set D1， A3)	ATGCACGA	TCGTGCAT	GACGATCT
NadPrep UDI Adapter 18 (Set D1， B3)	CCTGATTG	CAATCAGG	AACTGAGC
NadPrep UDI Adapter 19 (Set D1， C3)	GTAGGAGT	ACTCCTAC	CTTAGGAC
NadPrep UDI Adapter 20 (Set D1， D3)	ACTAGGAG	CTCCTAGT	GTGCCATA
NadPrep UDI Adapter 21 (Set D1， E3)	CACTAGCT	AGCTAGTG	GAATCCGA
NadPrep UDI Adapter 22 (Set D1， F3)	ACGACTTG	CAAGTCGT	TCGCTGTT
NadPrep UDI Adapter 23 (Set D1， G3)	CGTGTGTA	TACACACG	TTCGTTGG
NadPrep UDI Adapter 24 (Set D1， H3)	GTTGACCT	AGGTCAAC	AAGCACTG
NadPrep UDI Adapter 25 (Set D1， A4)	ACTCCATC	GATGGAGT	CCTTGATC
NadPrep UDI Adapter 26 (Set D1， B4)	CAATGTGG	CCACATTG	GTCGAAGA
NadPrep UDI Adapter 27 (Set D1， C4)	TTGCAGAC	GTCTGCAA	ACCACGAT
NadPrep UDI Adapter 28 (Set D1， D4)	CAGTCCAA	TTGGACTG	GATTACCG
NadPrep UDI Adapter 29 (Set D1， E4)	ACGTTCAG	CTGAACGT	GCACAACT
NadPrep UDI Adapter 30 (Set D1， F4)	AACGTCTG	CAGACGTT	GCGTCATT

NadPrep UDI Adapter (Set D#，96-well Plate Position)	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®，NovaSeq® v1.5 systems)	i7 index (all Illumina® systems)
NadPrep UDI Adapter 31 (Set D1, G4)	TATCGGTC	GACCGATA	ATCCGGTA
NadPrep UDI Adapter 32 (Set D1, H4)	CGCTCTAT	ATAGAGCG	CGTTGCAA
NadPrep UDI Adapter 33 (Set D1, A5)	GATTGCTC	GAGCAATC	GTGAAGTG
NadPrep UDI Adapter 34 (Set D1, B5)	GATGTGTG	CACACATC	CATGGCTA
NadPrep UDI Adapter 35 (Set D1, C5)	CGCAATCT	AGATTGCG	ATGCCTGT
NadPrep UDI Adapter 36 (Set D1, D5)	TGGTAGCT	AGCTACCA	CAACACCT
NadPrep UDI Adapter 37 (Set D1, E5)	GATAGGCT	AGCCTATC	TGTGACTG
NadPrep UDI Adapter 38 (Set D1, F5)	AGTGGATC	GATCCACT	GTCATCGA
NadPrep UDI Adapter 39 (Set D1, G5)	TTGGACGT	ACGTCCAA	AGCACTTC
NadPrep UDI Adapter 40 (Set D1, H5)	ATGACGTC	GACGTCAT	GAAGGAAG
NadPrep UDI Adapter 41 (Set D1, A6)	GAAGTTGG	CCAACTTC	GTTGTTCG
NadPrep UDI Adapter 42 (Set D1, B6)	CATACCAC	GTGGTATG	CGGTTGTT
NadPrep UDI Adapter 43 (Set D1, C6)	CTGTTGAC	GTCAACAG	ACTGAGGT
NadPrep UDI Adapter 44 (Set D1, D6)	TGGCATGT	ACATGCCA	TGAAGACG
NadPrep UDI Adapter 45 (Set D1, E6)	ATCGCCAT	ATGGCGAT	GTTACGCA
NadPrep UDI Adapter 46 (Set D1, F6)	TTGCGAAG	CTTCGCAA	AGCGTGTT
NadPrep UDI Adapter 47 (Set D1, G6)	AGTTCGTC	GACGAACT	GATCGAGT
NadPrep UDI Adapter 48 (Set D1, H6)	GAGCAGTA	TACTGCTC	ACAGCTCA
NadPrep UDI Adapter 49 (Set D1, A7)	ACAGCTCA	TGAGCTGT	GAGCAGTA
NadPrep UDI Adapter 50 (Set D1, B7)	GATCGAGT	ACTCGATC	AGTTCGTC
NadPrep UDI Adapter 51 (Set D1, C7)	AGCGTGTT	AACACGCT	TTGCGAAG
NadPrep UDI Adapter 52 (Set D1, D7)	GTTACGCA	TGCGTAAC	ATCGCCAT
NadPrep UDI Adapter 53 (Set D1, E7)	TGAAGACG	CGTCTTCA	TGGCATGT
NadPrep UDI Adapter 54 (Set D1, F7)	ACTGAGGT	ACCTCAGT	CTGTTGAC
NadPrep UDI Adapter 55 (Set D1, G7)	CGGTTGTT	AACAACCG	CATACCAC
NadPrep UDI Adapter 56 (Set D1, H7)	GTTGTTCG	CGAACAAC	GAAGTTGG
NadPrep UDI Adapter 57 (Set D1, A8)	GAAGGAAG	CTTCCTTC	ATGACGTC
NadPrep UDI Adapter 58 (Set D1, B8)	AGCACTTC	GAAGTGCT	TTGGACGT
NadPrep UDI Adapter 59 (Set D1, C8)	GTCATCGA	TCGATGAC	AGTGGATC
NadPrep UDI Adapter 60 (Set D1, D8)	TGTGACTG	CAGTCACA	GATAGGCT
NadPrep UDI Adapter 61 (Set D1, E8)	CAACACCT	AGGTGTTG	TGGTAGCT
NadPrep UDI Adapter 62 (Set D1, F8)	ATGCCTGT	ACAGGCAT	CGCAATCT
NadPrep UDI Adapter 63 (Set D1, G8)	CATGGCTA	TAGCCATG	GATGTGTG
NadPrep UDI Adapter 64 (Set D1, H8)	GTGAAGTG	CACTTCAC	GATTGCTC

NadPrep UDI Adapter (Set D#，96-well Plate Position)	i5 index (HiSeq® 2000/2500, MiSeq®, NovaSeq® v1.0 systems)	i5 index (HiSeq® 3000, 4000, HiSeq® X，NextSeq®, MiniSeq®， NovaSeq® v1.5 systems)	i7 index (all Illumina® systems)
NadPrep UDI Adapter 65 (Set D1, A9)	CGTTGCAA	TTGCAACG	CGCTCTAT
NadPrep UDI Adapter 66 (Set D1, B9)	ATCCGGTA	TACCGGAT	TATCGGTC
NadPrep UDI Adapter 67 (Set D1, C9)	GCGTCATT	AATGACGC	AACGTCTG
NadPrep UDI Adapter 68 (Set D1, D9)	GCACAACT	AGTTGTGC	ACGTTCAG
NadPrep UDI Adapter 69 (Set D1, E9)	GATTACCG	CGGTAATC	CAGTCCAA
NadPrep UDI Adapter 70 (Set D1, F9)	ACCACGAT	ATCGTGGT	TTGCAGAC
NadPrep UDI Adapter 71 (Set D1, G9)	GTCGAAGA	TCTTCGAC	CAATGTGG
NadPrep UDI Adapter 72 (Set D1, H9)	CCTTGATC	GATCAAGG	ACTCCATC
NadPrep UDI Adapter 73 (Set D1, A10)	AAGCACTG	CAGTGCTT	GTTGACCT
NadPrep UDI Adapter 74 (Set D1, B10)	TTCGTTGG	CCAACGAA	CGTGTGTA
NadPrep UDI Adapter 75 (Set D1, C10)	TCGCTGTT	AACAGCGA	ACGACTTG
NadPrep UDI Adapter 76 (Set D1, D10)	GAATCCGA	TCGGATTC	CACTAGCT
NadPrep UDI Adapter 77 (Set D1, E10)	GTGCCATA	TATGGCAC	ACTAGGAG
NadPrep UDI Adapter 78 (Set D1, F10)	CTTAGGAC	GTCCTAAG	GTAGGAGT
NadPrep UDI Adapter 79 (Set D1, G10)	AACTGAGC	GCTCAGTT	CCTGATTG
NadPrep UDI Adapter 80 (Set D1, H10)	GACGATCT	AGATCGTC	ATGCACGA
NadPrep UDI Adapter 81 (Set D1, A11)	ATCCAGAG	CTCTGGAT	CGACGTTA
NadPrep UDI Adapter 82 (Set D1, B11)	AGAGTAGC	GCTACTCT	TACGCCTT
NadPrep UDI Adapter 83 (Set D1, C11)	TGGACTCT	AGAGTCCA	CCGTAAGA
NadPrep UDI Adapter 84 (Set D1, D11)	TACGCTAC	GTAGCGTA	ATCACACG
NadPrep UDI Adapter 85 (Set D1, E11)	GCTATCCT	AGGATAGC	CACCTGTT
NadPrep UDI Adapter 86 (Set D1, F11)	GCAAGATC	GATCTTGC	CTTCGACT
NadPrep UDI Adapter 87 (Set D1, G11)	ATCGATCG	CGATCGAT	TGCTTCCA
NadPrep UDI Adapter 88 (Set D1, H11)	CGGCTAAT	ATTAGCCG	AGAACGAG
NadPrep UDI Adapter 89 (Set D1, A12)	ACGGAACA	TGTTCCGT	GTTCTCGT
NadPrep UDI Adapter 90 (Set D1, B12)	CGCATGAT	ATCATGCG	TCAGGCTT
NadPrep UDI Adapter 91 (Set D1, C12)	TTCCAAGG	CCTTGGAA	CCTTGTAG
NadPrep UDI Adapter 92 (Set D1, D12)	CTTGTCGA	TCGACAAG	GAACATCG
NadPrep UDI Adapter 93 (Set D1, E12)	GAGACGAT	ATCGTCTC	TAACCGGT
NadPrep UDI Adapter 94 (Set D1, F12)	TGAGCTAG	CTAGCTCA	AACCGTTC
NadPrep UDI Adapter 95 (Set D1, G12)	ACTCTCGA	TCGAGAGT	TGGTACAG
NadPrep UDI Adapter 96 (Set D1, H12)	CTGATCGT	ACGATCAG	ATATGCGC

Note: As the reading mode of the dual index differs in various Illumina® platforms, please select the corresponding sequence information according to the Illumina systems.

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