

The ONE™ 16S 96 x indexes – Set A

Introduction

YouSeq's dual index adapters are designed for YouSeq specific library preparation kits to construct libraries for multiplexed sequencing on Illumina® Sequencers. Set A offers a total of 96 unique sequences. For increased throughput, additional Set B, Set C and Set D each provide a further 96 unique indexes.

These sequences were chosen together as they are statistically optimized sequences to help reduce risk of patient to patient contamination.

Best Practices

- Limit the number of freeze/thaw cycles, YouSeq recommend a maximum of 5 in total
- Ensure operators use strict Good Laboratory Practices in order to prevent adapter contamination

Layout of the plate

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	2	3	4	5	6	7	8	9	10	11	12
B	13	14	15	16	17	18	19	20	21	22	23	24
C	25	26	27	28	29	30	31	32	33	34	35	36
D	37	38	39	40	41	42	43	44	45	46	47	48
E	49	50	51	52	53	54	55	56	57	58	59	60
F	61	62	63	64	65	66	67	68	69	70	71	72
G	73	74	75	76	77	78	79	80	81	82	83	84
H	85	86	87	88	89	90	91	92	93	94	95	96

Notes. The line item describes a selection of adapters suitable for analysis of 96 samples

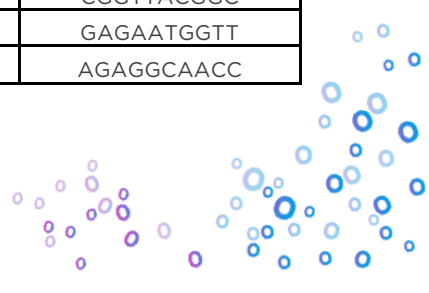
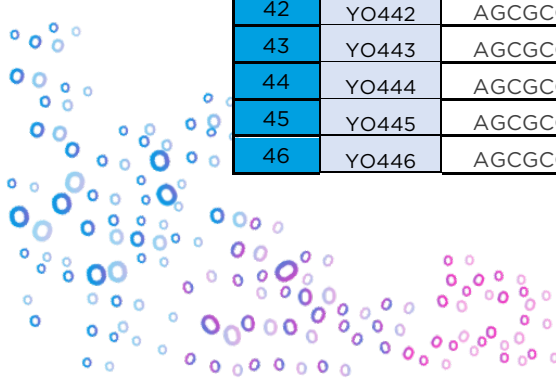
The digital download is available via the website, to help input the sequences (www.youseq.com). If having issues downloading or locating the sequences, please contact us via hello@youseq.com . .



Index sequences

Index no	Index Code	iSeq 100, Miniseq, NextSeq, HiSeq 3000/4000	
		17 Bases for sample sheet	15 Bases for sample sheet
1	YO401	CACTATCAAC	CTACTCAGTC
2	YO402	CACTATCAAC	TCGTCTGACT
3	YO403	CACTATCAAC	GAACATACGG
4	YO404	CACTATCAAC	CCTATGACTC
5	YO405	CACTATCAAC	TAATGGCAAG
6	YO406	CACTATCAAC	GTGCCGCTTC
7	YO407	CACTATCAAC	CGGCAATGGA
8	YO408	CACTATCAAC	GCCGTAACCG
9	YO409	CACTATCAAC	AACCATTCTC
10	YO410	CACTATCAAC	GGTTGCCTCT
11	YO411	CACTATCAAC	CTAATGATGG
12	YO412	CACTATCAAC	TCGGCCTATC
13	YO413	TGTCGCTGGT	CTACTCAGTC
14	YO414	TGTCGCTGGT	TCGTCTGACT
15	YO415	TGTCGCTGGT	GAACATACGG
16	YO416	TGTCGCTGGT	CCTATGACTC
17	YO417	TGTCGCTGGT	TAATGGCAAG
18	YO418	TGTCGCTGGT	GTGCCGCTTC
19	YO419	TGTCGCTGGT	CGGCAATGGA
20	YO420	TGTCGCTGGT	GCCGTAACCG
21	YO421	TGTCGCTGGT	AACCATTCTC
22	YO422	TGTCGCTGGT	GGTTGCCTCT
23	YO423	TGTCGCTGGT	CTAATGATGG
24	YO424	TGTCGCTGGT	TCGGCCTATC
25	YO425	ACAGTGTATG	CTACTCAGTC
26	YO426	ACAGTGTATG	TCGTCTGACT
27	YO427	ACAGTGTATG	GAACATACGG
28	YO428	ACAGTGTATG	CCTATGACTC
29	YO429	ACAGTGTATG	TAATGGCAAG
30	YO430	ACAGTGTATG	GTGCCGCTTC
31	YO431	ACAGTGTATG	CGGCAATGGA
32	YO432	ACAGTGTATG	GCCGTAACCG
33	YO433	ACAGTGTATG	AACCATTCTC
34	YO434	ACAGTGTATG	GGTTGCCTCT
35	YO435	ACAGTGTATG	CTAATGATGG
36	YO436	ACAGTGTATG	TCGGCCTATC
37	YO437	AGCGCCACAC	CTACTCAGTC
38	YO438	AGCGCCACAC	TCGTCTGACT
39	YO439	AGCGCCACAC	GAACATACGG
40	YO440	AGCGCCACAC	CCTATGACTC
41	YO441	AGCGCCACAC	TAATGGCAAG
42	YO442	AGCGCCACAC	GTGCCGCTTC
43	YO443	AGCGCCACAC	CGGCAATGGA
44	YO444	AGCGCCACAC	GCCGTAACCG
45	YO445	AGCGCCACAC	AACCATTCTC
46	YO446	AGCGCCACAC	GGTTGCCTCT

NovaSeq, MiSeq, HiSeq 2000/2500	
17 Bases for sample sheet	15 Bases for sample sheet
CACTATCAAC	GACTGAGTAG
CACTATCAAC	AGTCAGACGA
CACTATCAAC	CCGTATGTTC
CACTATCAAC	GAGTCATAGG
CACTATCAAC	CTTGCCATTA
CACTATCAAC	GAAGCGGCAC
CACTATCAAC	TCCATTGCCG
CACTATCAAC	CGGTTACGGC
CACTATCAAC	GAGAATGGTT
CACTATCAAC	AGAGGCAACC
CACTATCAAC	CCATCATTAG
CACTATCAAC	GATAGGCCGA
TGTCGCTGGT	GACTGAGTAG
TGTCGCTGGT	AGTCAGACGA
TGTCGCTGGT	CCGTATGTTC
TGTCGCTGGT	GAGTCATAGG
TGTCGCTGGT	CTTGCCATTA
TGTCGCTGGT	GAAGCGGCAC
TGTCGCTGGT	TCCATTGCCG
TGTCGCTGGT	CGGTTACGGC
TGTCGCTGGT	GAGAATGGTT
TGTCGCTGGT	AGAGGCAACC
TGTCGCTGGT	CCATCATTAG
TGTCGCTGGT	GATAGGCCGA
ACAGTGTATG	GACTGAGTAG
ACAGTGTATG	AGTCAGACGA
ACAGTGTATG	CCGTATGTTC
ACAGTGTATG	GAGTCATAGG
ACAGTGTATG	CTTGCCATTA
ACAGTGTATG	GAAGCGGCAC
ACAGTGTATG	TCCATTGCCG
ACAGTGTATG	CGGTTACGGC
ACAGTGTATG	GAGAATGGTT
ACAGTGTATG	AGAGGCAACC
ACAGTGTATG	CCATCATTAG
ACAGTGTATG	GATAGGCCGA
AGCGCCACAC	GACTGAGTAG
AGCGCCACAC	AGTCAGACGA
AGCGCCACAC	CCGTATGTTC
AGCGCCACAC	GAGTCATAGG
AGCGCCACAC	CTTGCCATTA
AGCGCCACAC	GAAGCGGCAC
AGCGCCACAC	TCCATTGCCG
AGCGCCACAC	CGGTTACGGC
AGCGCCACAC	GAGAATGGTT
AGCGCCACAC	AGAGGCAACC



47	YO447	AGCGCCACAC	CTAATGATGG
48	YO448	AGCGCCACAC	TCGGCCTATC
49	YO449	CCTTCGTGAT	CTACTCAGTC
50	YO450	CCTTCGTGAT	TCGTCTGACT
51	YO451	CCTTCGTGAT	GAACATACGG
52	YO452	CCTTCGTGAT	CCTATGACTC
53	YO453	CCTTCGTGAT	TAATGGCAAG
54	YO454	CCTTCGTGAT	GTGCCGCTTC
55	YO455	CCTTCGTGAT	CGGCAATGGA
56	YO456	CCTTCGTGAT	GCCGTAACCG
57	YO457	CCTTCGTGAT	AACCATTCTC
58	YO458	CCTTCGTGAT	GGTTGCCTCT
59	YO459	CCTTCGTGAT	CTAATGATGG
60	YO460	CCTTCGTGAT	TCGGCCTATC
61	YO461	AGTAGAGCCG	CTACTCAGTC
62	YO462	AGTAGAGCCG	TCGTCTGACT
63	YO463	AGTAGAGCCG	GAACATACGG
64	YO464	AGTAGAGCCG	CCTATGACTC
65	YO465	AGTAGAGCCG	TAATGGCAAG
66	YO466	AGTAGAGCCG	GTGCCGCTTC
67	YO467	AGTAGAGCCG	CGGCAATGGA
68	YO468	AGTAGAGCCG	GCCGTAACCG
69	YO469	AGTAGAGCCG	AACCATTCTC
70	YO470	AGTAGAGCCG	GGTTGCCTCT
71	YO471	AGTAGAGCCG	CTAATGATGG
72	YO472	AGTAGAGCCG	TCGGCCTATC
73	YO473	TCGTGCATTC	CTACTCAGTC
74	YO474	TCGTGCATTC	TCGTCTGACT
75	YO475	TCGTGCATTC	GAACATACGG
76	YO476	TCGTGCATTC	CCTATGACTC
77	YO477	TCGTGCATTC	TAATGGCAAG
78	YO478	TCGTGCATTC	GTGCCGCTTC
79	YO479	TCGTGCATTC	CGGCAATGGA
80	YO480	TCGTGCATTC	GCCGTAACCG
81	YO481	TCGTGCATTC	AACCATTCTC
82	YO482	TCGTGCATTC	GGTTGCCTCT
83	YO483	TCGTGCATTC	CTAATGATGG
84	YO484	TCGTGCATTC	TCGGCCTATC
85	YO485	CTATAGTCTT	CTACTCAGTC
86	YO486	CTATAGTCTT	TCGTCTGACT
87	YO487	CTATAGTCTT	GAACATACGG
88	YO488	CTATAGTCTT	CCTATGACTC
89	YO489	CTATAGTCTT	TAATGGCAAG
90	YO490	CTATAGTCTT	GTGCCGCTTC
91	YO491	CTATAGTCTT	CGGCAATGGA
92	YO492	CTATAGTCTT	GCCGTAACCG
93	YO493	CTATAGTCTT	AACCATTCTC
94	YO494	CTATAGTCTT	GGTTGCCTCT
95	YO495	CTATAGTCTT	CTAATGATGG
96	YO496	CTATAGTCTT	TCGGCCTATC

AGCGCCACAC	CCATCATTAG
AGCGCCACAC	GATAGGCCGA
CCTTCGTGAT	GACTGAGTAG
CCTTCGTGAT	AGTCAGACGA
CCTTCGTGAT	CCGTATGTTC
CCTTCGTGAT	GAGTCATAGG
CCTTCGTGAT	CTTGCCATTA
CCTTCGTGAT	GAAGCGGCAC
CCTTCGTGAT	TCCATTGCCG
CCTTCGTGAT	CGGTTACGGC
CCTTCGTGAT	GAGAATGGTT
CCTTCGTGAT	AGAGGCAACC
CCTTCGTGAT	CCATCATTAG
CCTTCGTGAT	GATAGGCCGA
AGTAGAGCCG	GACTGAGTAG
AGTAGAGCCG	AGTCAGACGA
AGTAGAGCCG	CCGTATGTTC
AGTAGAGCCG	GAGTCATAGG
AGTAGAGCCG	CTTGCCATTA
AGTAGAGCCG	GAAGCGGCAC
AGTAGAGCCG	TCCATTGCCG
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AGTAGAGCCG	GAGAATGGTT
AGTAGAGCCG	AGAGGCAACC
AGTAGAGCCG	CCATCATTAG
AGTAGAGCCG	GATAGGCCGA
TCGTGCATTC	GACTGAGTAG
TCGTGCATTC	AGTCAGACGA
TCGTGCATTC	CCGTATGTTC
TCGTGCATTC	GAGTCATAGG
TCGTGCATTC	CTTGCCATTA
TCGTGCATTC	GAAGCGGCAC
TCGTGCATTC	TCCATTGCCG
TCGTGCATTC	CGGTTACGGC
TCGTGCATTC	GAGAATGGTT
TCGTGCATTC	AGAGGCAACC
TCGTGCATTC	CCATCATTAG
TCGTGCATTC	GATAGGCCGA
CTATAGTCTT	GACTGAGTAG
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CTATAGTCTT	CCGTATGTTC
CTATAGTCTT	GAGTCATAGG
CTATAGTCTT	CTTGCCATTA
CTATAGTCTT	GAAGCGGCAC
CTATAGTCTT	TCCATTGCCG
CTATAGTCTT	CGGTTACGGC
CTATAGTCTT	GAGAATGGTT
CTATAGTCTT	AGAGGCAACC
CTATAGTCTT	CCATCATTAG
CTATAGTCTT	GATAGGCCGA

