

Index sequences - 770210-96: Plate B (97-192)

When sequencing, assign 17 cycles for Index1 and 8 cycles for Index2.

Index1 (i7) Number	Index1 (i7) Sequence	Index1 (i7) Sequence + UMI	Index2 (i5) Number	Index2 (i5) Forward Sequence	Index2 (i5) Reverse Complement Sequence
97	GCCTATCA	GCCTATCANNNNNNNNNN	597	CGACCATT	AATGGTCG
98	CTTGATG	CTTGATGNNNNNNNNNN	598	GATAGCGA	TCGCTATC
99	AGTCTCAC	AGTCTCACNNNNNNNNNN	599	AATGGACG	CGTCCATT
100	CTCATCAG	CTCATCAGNNNNNNNNNN	600	CGCTAGTA	TACTAGCG
101	TGTACCGT	TGTACCGTNNNNNNNNNN	601	TCTCTAGG	CCTAGAGA
102	AAGTCGAG	AAGTCGAGNNNNNNNNNN	602	ACATTGCG	CGCAATGT
103	CACGTTGT	CACGTTGTNNNNNNNNNN	603	TGAGGTGT	ACACCTCA
104	TCACAGCA	TCACAGCANNNNNNNNNN	604	AATGCCTC	GAGGCATT
105	CTACTTGG	CTACTTGGNNNNNNNNNN	605	CTGGAGTA	TACTCCAG
106	CCTCAGTT	CCTCAGTTNNNNNNNNNN	606	GTATGCTG	CAGCATAC
107	TCCTACCT	TCCTACCTNNNNNNNNNN	607	TGGAGAGT	ACTCTCCA
108	ATGGCGAA	ATGGCGAANNNNNNNNNN	608	CGATAGAG	CTCTATCG
109	CTTACCTG	CTTACCTGNNNNNNNNNN	609	CTCATTGC	GCAATGAG
110	CTCGATAC	CTCGATACNNNNNNNNNN	610	ACCAGCTT	AAGCTGGT
111	TCCGTGAA	TCCGTGAANNNNNNNNNN	611	GAATCGTG	CACGATTC
112	TAGAGCTC	TAGAGCTCNNNNNNNNNN	612	AGGCTTCT	AGAAGCCT
113	TGACTGAC	TGACTGACNNNNNNNNNN	613	CAGTTCTG	CAGAACTG

114	TAGACGTG	TAGACGTGNNNNNNNNNN	614	TTGGTGAG	CTCACCAA
115	CCGGAATT	CCGGAATTNNNNNNNNNN	615	CATTCGGT	ACCGAATG
116	CTCCTAGA	CTCCTAGANNNNNNNNNN	616	TGTGAAGC	GCTTCACA
117	CAACGGAT	CAACGGATNNNNNNNNNN	617	TAAGTGGC	GCCACTTA
118	TGGCTATC	TGGCTATCNNNNNNNNNN	618	ACGTGATG	CATCACGT
119	CGGTCATA	CGGTCATANNNNNNNNNN	619	GTAGAGCA	TGCTCTAC
120	TCCAATCG	TCCAATCGNNNNNNNNNN	620	GTCAGTTG	CAACTGAC
121	GAGCTTGT	GAGCTTGTNNNNNNNNNN	621	ATTCGAGG	CCTCGAAT
122	GAAGGTTT	GAAGGTTTNNNNNNNNNN	622	GATACTGG	CCAGTATC
123	ATCTCGCT	ATCTCGCTNNNNNNNNNN	623	GCCTTGTT	AACAAGGC
124	AGTTACGG	AGTTACGGNNNNNNNNNN	624	TTGGTCTC	GAGACCAA
125	GTGTCTGA	GTGTCTGANNNNNNNNNN	625	CCGACTAT	ATAGTCGG
126	TGACTTCG	TGACTTCGNNNNNNNNNN	626	GTCCTAAG	CTTAGGAC
127	TGGATCAC	TGGATCACNNNNNNNNNN	627	ACCAATGC	GCATTGGT
128	ACACCAGT	ACACCAGTNNNNNNNNNN	628	GATGCACT	AGTGCATC
129	CAGGTTAG	CAGGTTAGNNNNNNNNNN	629	GCTGGATT	AATCCAGC
130	AGTTGGCT	AGTTGGCTNNNNNNNNNN	630	ATGGTTGC	GCAACCAT
131	TCAACTGG	TCAACTGGNNNNNNNNNN	631	CAGAATCG	CGATTCTG
132	CTGCACTT	CTGCACTTNNNNNNNNNN	632	GAACGCTT	AAGCGTTC
133	ACACGGTT	ACACGGTTNNNNNNNNNN	633	TCGAACCA	TGGTTCGA
134	AATACGCG	AATACGCGNNNNNNNNNN	634	CTATCGCA	TGCGATAG
135	TGCGAACT	TGCGAACTNNNNNNNNNN	635	TACGGTTG	CAACCGTA
136	GCTGACTA	GCTGACTANNNNNNNNNN	636	GAGATGTC	GACATCTC
137	GTGGTGTT	GTGGTGTTNNNNNNNNNN	637	CTTACAGC	GCTGTAAG
138	GTGCTTAC	GTGCTTACNNNNNNNNNN	638	AGGAGGAA	TTCTCCT

139	TCAAGGAC	TCAAGGACNNNNNNNNNN	639	GACGAATG	CATTCGTC
140	TGAACCTG	TGAACCTGNNNNNNNNN	640	GAAGAGGT	ACCTCTTC
141	AGTGTTGG	AGTGTTGGNNNNNNNNN	641	CGTCAATG	CATTGACG
142	GTACTCTC	GTACTCTCNNNNNNNNN	642	TACCAGGA	TCCTGGTA
143	CCGTATCT	CCGTATCTNNNNNNNNN	643	CGTACGAA	TTCGTACG
144	CGAAGAAC	CGAAGAACNNNNNNNNN	644	GACTTAGG	CCTAAGTC
145	AGCGGAAT	AGCGGAATNNNNNNNNN	645	AGTGCAGT	ACTGCACT
146	GTGAGCTT	GTGAGCTTNNNNNNNNN	646	TTGATCCG	CGGATCAA
147	CGTGATCA	CGTGATCANNNNNNNNN	647	TGCCATTC	GAATGGCA
148	TCGCATTG	TCGCATTGNNNNNNNNN	648	CTTGCTGT	ACAGCAAG
149	TGACGCAT	TGACGCATNNNNNNNNN	649	CCTACTGA	TCAGTAGG
150	CCGATGTA	CCGATGTANNNNNNNNN	650	CCAAGTTG	CAACTTGG
151	TTCGCAGT	TTCGCAGTNNNNNNNNN	651	TGATCGGA	TCCGATCA
152	ACGACAGA	ACGACAGANNNNNNNNN	652	TAGTTGCG	CGCAACTA
153	AGCTTGAG	AGCTTGAGNNNNNNNNN	653	GTCTGATC	GATCAGAC
154	GAGTGGTT	GAGTGGTTNNNNNNNNN	654	CGTTATGC	GCATAACG
155	GCTGTAAG	GCTGTAAGNNNNNNNNN	655	GCTCTGTA	TACAGAGC
156	CCAAGACT	CCAAGACTNNNNNNNNN	656	TTACCGAG	CTCGGTAA
157	ATTGCGTG	ATTGCGTGNNNNNNNNN	657	GCCATAAC	GTTATGGC
158	CTGAAGCT	CTGAAGCTNNNNNNNNN	658	CTCAGAGT	ACTCTGAG
159	TAACGAGG	TAACGAGGNNNNNNNNN	659	CGAGACTA	TAGTCTCG
160	TCGTCTCA	TCGTCTCANNNNNNNNN	660	TGTGCGTT	AACGCACA
161	TTCCTGTG	TTCCTGTGNNNNNNNNN	661	TTCAGGAG	CTCCTGAA
162	CGTTGAGT	CGTTGAGTNNNNNNNNN	662	GACTATGC	GCATAGTC
163	AGTCGCTT	AGTCGCTTNNNNNNNNN	663	AGGTTCGA	TCGAACCT

164	TAGGTAGG	TAGGTAGGNNNNNNNNNN	664	AGTCTGTG	CACAGACT
165	CAGGAGAT	CAGGAGATNNNNNNNNNN	665	ACCTAAGG	CCTTAGGT
166	CATCGTGA	CATCGTGANNNNNNNNNN	666	TGCAGGTA	TACCTGCA
167	TGTTGTGG	TGTTGTGGNNNNNNNNNN	667	AAGGACAC	GTGTCCTT
168	ACAGACCT	ACAGACCTNNNNNNNNNN	668	CAACCTAG	CTAGGTTG
169	GTCCTTCT	GTCCTTCTNNNNNNNNNN	669	CTGACACA	TGTGTCAG
170	TGATACGC	TGATACGCNNNNNNNNNN	670	ACTCGTTG	CAACGAGT
171	CTGTGTTG	CTGTGTTGNNNNNNNNNN	671	AGCTCCTA	TAGGAGCT
172	AACGTGGA	AACGTGGANNNNNNNNNN	672	TACATCGG	CCGATGTA
173	GTTGCGAT	GTTGCGATNNNNNNNNNN	673	CACAAGTC	GACTTGTG
174	AACGACGT	AACGACGTNNNNNNNNNN	674	CGGATTGA	TCAATCCG
175	CGTATTCG	CGTATTCGNNNNNNNNNN	675	AGTCGACA	TGTCGACT
176	AGCAAGCA	AGCAAGCANNNNNNNNNN	676	GTCTCCTT	AAGGAGAC
177	TGTTCGAG	TGTTCGAGNNNNNNNNNN	677	GAGATACG	CGTATCTC
178	CTCCATGT	CTCCATGTNNNNNNNNNN	678	ATCGGTGT	ACACCGAT
179	CGTCTTGT	CGTCTTGTNNNNNNNNNN	679	TCTCGCAA	TTGCGAGA
180	ATAAGGCG	ATAAGGCGNNNNNNNNNN	680	TCTAACGC	GCGTTAGA
181	TGTCTGCT	TGTCTGCTNNNNNNNNNN	681	CAATCGAC	GTCGATTG
182	CGCTTAAC	CGCTTAACNNNNNNNNNN	682	GAGGACTT	AAGTCCTC
183	GATCCATG	GATCCATGNNNNNNNNNN	683	TGGAGTTG	CAACTCCA
184	ACCTCTGT	ACCTCTGTNNNNNNNNNN	684	CTAGGCAT	ATGCCTAG
185	GCCACTTA	GCCACTTANNNNNNNNNN	685	CTCTACTC	GAGTAGAG
186	ACCTGACT	ACCTGACTNNNNNNNNNN	686	AGAAGCGT	ACGCTTCT
187	GTTAAGGC	GTTAAGGCNNNNNNNNNN	687	TCGAAGGT	ACCTTCGA
188	ATGCCAAC	ATGCCAACNNNNNNNNNN	688	GTCGGTAA	TTACCGAC

189	AGAGGTTG	AGAGGTTGNNNNNNNNN	689	ACGATGAC	GTCATCGT
190	ACCATCCA	ACCATCCANNNNNNNNN	690	TCCGTATG	CATACGGA
191	GTGGATAG	GTGGATAGNNNNNNNNN	691	CTAGGTGA	TCACCTAG
192	CTGAGATC	CTGAGATCNNNNNNNNN	692	CATTGCCT	AGGCAATG

SureSeq: For Research Use Only; Not for Use in Diagnostic Procedures