

Index sequences - 770230-96: Plate D (289-384)

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
289	CATTGCCT	CATTGCCTNNNNNNNNNN	789	CTGAGATC	GATCTCAG
290	CTAGGTGA	CTAGGTGANNNNNNNNN	790	GTGGATAG	CTATCCAC
291	TCCGTATG	TCCGTATGNNNNNNNNNN	791	ACCATCCA	TGGATGGT
292	ACGATGAC	ACGATGACNNNNNNNNNN	792	AGAGGTTG	CAACCTCT
293	GTCGGTAA	GTCGGTAANNNNNNNNN	793	ATGCCAAC	GTTGGCAT
294	TCGAAGGT	TCGAAGGTNNNNNNNNNN	794	GTTAAGGC	GCCTTAAC
295	AGAAGCGT	AGAAGCGTNNNNNNNNNN	795	ACCTGACT	AGTCAGGT
296	CTCTACTC	CTCTACTCNNNNNNNNNN	796	GCCACTTA	TAAGTGGC
297	CTAGGCAT	CTAGGCATNNNNNNNNNN	797	ACCTCTGT	ACAGAGGT
298	TGGAGTTG	TGGAGTTGNNNNNNNNNN	798	GATCCATG	CATGGATC
299	GAGGACTT	GAGGACTTNNNNNNNNNN	799	CGCTTAAC	GTTAAGCG
300	CAATCGAC	CAATCGACNNNNNNNNNN	800	TGTCTGCT	AGCAGACA
301	TCTAACGC	TCTAACGCNNNNNNNNNN	801	ATAAGGCG	CGCCTTAT
302	TCTCGCAA	TCTCGCAANNNNNNNNN	802	CGTCTTGT	ACAAGACG
303	ATCGGTGT	ATCGGTGTNNNNNNNNNN	803	CTCCATGT	ACATGGAG
304	GAGATACG	GAGATACGNNNNNNNNNN	804	TGTTTCGAG	CTCGAACA
305	GTCTCCTT	GTCTCCTTNNNNNNNNNN	805	AGCAAGCA	TGCTTGCT

306	AGTCGACA	AGTCGACANNNNNNNNNN	806	CGTATTCTG	CGAATACG
307	CGGATTGA	CGGATTGANNNNNNNNNN	807	AACGACGT	ACGTCGTT
308	CACAAGTC	CACAAGTCNNNNNNNNNN	808	GTTGCGAT	ATCGCAAC
309	TACATCGG	TACATCGGNNNNNNNNNN	809	AACGTGGA	TCCACGTT
310	AGCTCCTA	AGCTCCTANNNNNNNNNN	810	CTGTGTTG	CAACACAG
311	ACTCGTTG	ACTCGTTGNNNNNNNNNN	811	TGATACGC	GCGTATCA
312	CTGACACA	CTGACACANNNNNNNNNN	812	GTCCTTCT	AGAAGGAC
313	CAACCTAG	CAACCTAGNNNNNNNNNN	813	ACAGACCT	AGGTCTGT
314	AAGGACAC	AAGGACACNNNNNNNNNN	814	TGTTGTGG	CCACAACA
315	TGCAGGTA	TGCAGGTANNNNNNNNNN	815	CATCGTGA	TCACGATG
316	ACCTAAGG	ACCTAAGGNNNNNNNNNN	816	CAGGAGAT	ATCTCCTG
317	AGTCTGTG	AGTCTGTGNNNNNNNNNN	817	TAGGTAGG	CCTACCTA
318	AGGTTCGA	AGGTTCGANNNNNNNNNN	818	AGTCGCTT	AAGCGACT
319	GACTATGC	GACTATGCNNNNNNNNNN	819	CGTTGAGT	ACTCAACG
320	TTCAGGAG	TTCAGGAGNNNNNNNNNN	820	TTCCTGTG	CACAGGAA
321	TGTGCGTT	TGTGCGTTNNNNNNNNNN	821	TCGTCTCA	TGAGACGA
322	CGAGACTA	CGAGACTANNNNNNNNNN	822	TAACGAGG	CCTCGTTA
323	CTCAGAGT	CTCAGAGTNNNNNNNNNN	823	CTGAAGCT	AGCTTCAG
324	GCCATAAC	GCCATAACNNNNNNNNNN	824	ATTGCGTG	CACGCAAT
325	TTACCGAG	TTACCGAGNNNNNNNNNN	825	CCAAGACT	AGTCTTGG
326	GCTCTGTA	GCTCTGTANNNNNNNNNN	826	GCTGTAAG	CTTACAGC
327	CGTTATGC	CGTTATGCNNNNNNNNNN	827	GAGTGGTT	AACCACTC
328	GTCTGATC	GTCTGATCNNNNNNNNNN	828	AGCTTGAG	CTCAAGCT
329	TAGTTGCG	TAGTTGCGNNNNNNNNNN	829	ACGACAGA	TCTGTCGT
330	TGATCGGA	TGATCGGANNNNNNNNNN	830	TTCGCAGT	ACTGCGAA

331	CCAAGTTG	CCAAGTTGNNNNNNNNNN	831	CCGATGTA	TACATCGG
332	CCTACTGA	CCTACTGANNNNNNNNNN	832	TGACGCAT	ATGCGTCA
333	CTTGCTGT	CTTGCTGTNNNNNNNNNN	833	TCGCATTG	CAATGCGA
334	TGCCATTG	TGCCATTGNNNNNNNNNN	834	CGTGATCA	TGATCACG
335	TTGATCCG	TTGATCCGNNNNNNNNNN	835	GTGAGCTT	AAGCTCAC
336	AGTGCAGT	AGTGCAGTNNNNNNNNNN	836	AGCGGAAT	ATTCCGCT
337	GACTTAGG	GACTTAGGNNNNNNNNNN	837	CGAAGAAC	GTTCTTCG
338	CGTACGAA	CGTACGAANNNNNNNNNN	838	CCGTATCT	AGATACGG
339	TACCAGGA	TACCAGGANNNNNNNNNN	839	GTACTCTC	GAGAGTAC
340	CGTCAATG	CGTCAATGNNNNNNNNNN	840	AGTGTTGG	CCAACACT
341	GAAGAGGT	GAAGAGGTNNNNNNNNNN	841	TGAACCTG	CAGGTTCA
342	GACGAATG	GACGAATGNNNNNNNNNN	842	TCAAGGAC	GTCCTTGA
343	AGGAGGAA	AGGAGGAANNNNNNNNNN	843	GTGCTTAC	GTAAGCAC
344	CTTACAGC	CTTACAGCNNNNNNNNNN	844	GTGGTGTT	AACACCAC
345	GAGATGTC	GAGATGTCNNNNNNNNNN	845	GCTGACTA	TAGTCAGC
346	TACGTTTG	TACGTTTGNNNNNNNNNN	846	TGCGAACT	AGTTCGCA
347	CTATCGCA	CTATCGCANNNNNNNNNN	847	AATACGCG	CGCGTATT
348	TCGAACCA	TCGAACCANNNNNNNNNN	848	ACACGGTT	AACCGTGT
349	GAACGCTT	GAACGCTTNNNNNNNNNN	849	CTGCACTT	AAGTGCAG
350	CAGAATCG	CAGAATCGNNNNNNNNNN	850	TCAACTGG	CCAGTTGA
351	ATGGTTGC	ATGGTTGCNNNNNNNNNN	851	AGTTGGCT	AGCCAACT
352	GCTGGATT	GCTGGATTNNNNNNNNNN	852	CAGGTTAG	CTAACCTG
353	GATGCACT	GATGCACTNNNNNNNNNN	853	ACACCAGT	ACTGGTGT
354	ACCAATGC	ACCAATGCNNNNNNNNNN	854	TGGATCAC	GTGATCCA
355	GTCTAAG	GTCTAAGNNNNNNNNNN	855	TGACTTCG	CGAAGTCA

356	CCGACTAT	CCGACTATNNNNNNNNNN	856	GTGTCTGA	TCAGACAC
357	TTGGTCTC	TTGGTCTCNNNNNNNNNN	857	AGTTACGG	CCGTAACT
358	GCCTTGTT	GCCTTGTTNNNNNNNNNN	858	ATCTCGCT	AGCGAGAT
359	GATACTGG	GATACTGGNNNNNNNNNN	859	GAAGGTTC	GAACCTTC
360	ATTCGAGG	ATTCGAGGNNNNNNNNNN	860	GAGCTTGT	ACAAGCTC
361	GTCAGTTG	GTCAGTTGNNNNNNNNNN	861	TCCAATCG	CGATTGGA
362	GTAGAGCA	GTAGAGCANNNNNNNNNNN	862	CGGTCATA	TATGACCG
363	ACGTGATG	ACGTGATGNNNNNNNNNN	863	TGGCTATC	GATAGCCA
364	TAAGTGGC	TAAGTGGCNNNNNNNNNN	864	CAACGGAT	ATCCGTTG
365	TGTGAAGC	TGTGAAGCNNNNNNNNNN	865	CTCCTAGA	TCTAGGAG
366	CATTCGGT	CATTCGGTNNNNNNNNNN	866	CCGGAATT	AATTCCGG
367	TTGGTGAG	TTGGTGAGNNNNNNNNNN	867	TAGACGTG	CACGTCTA
368	CAGTTCTG	CAGTTCTGNNNNNNNNNN	868	TGACTGAC	GTCAGTCA
369	AGGCTTCT	AGGCTTCTNNNNNNNNNN	869	TAGAGCTC	GAGCTCTA
370	GAATCGTG	GAATCGTGNNNNNNNNNN	870	TCCGTGAA	TTCACGGA
371	ACCAGCTT	ACCAGCTTNNNNNNNNNN	871	CTCGATAC	GTATCGAG
372	CTCATTGC	CTCATTGCNNNNNNNNNN	872	CTTACCTG	CAGGTAAG
373	CGATAGAG	CGATAGAGNNNNNNNNNN	873	ATGGCGAA	TTCGCCAT
374	TGGAGAGT	TGGAGAGTNNNNNNNNNN	874	TCCTACCT	AGGTAGGA
375	GTATGCTG	GTATGCTGNNNNNNNNNN	875	CCTCAGTT	AACTGAGG
376	CTGGAGTA	CTGGAGTANNNNNNNNNNN	876	CTACTTGG	CCAAGTAG
377	AATGCCTC	AATGCCTCNNNNNNNNNN	877	TCACAGCA	TGCTGTGA
378	TGAGGTGT	TGAGGTGTNNNNNNNNNN	878	CACGTTGT	ACAACGTG
379	ACATTGCG	ACATTGCGNNNNNNNNNN	879	AAGTCGAG	CTCGACTT
380	TCTCTAGG	TCTCTAGGNNNNNNNNNN	880	TGTACCGT	ACGGTACA

381	CGCTAGTA	CGCTAGTANNNNNNNNN	881	CTCATCAG	CTGATGAG
382	AATGGACG	AATGGACGNNNNNNNNN	882	AGTCTCAC	GTGAGACT
383	GATAGCGA	GATAGCGANNNNNNNNN	883	CTTGGATG	CATCCAAG
384	CGACCATT	CGACCATTNNNNNNNNN	884	GCCTATCA	TGATAGGC

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