

## Index sequences - 770200-96: Plate A (1-96)

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 |
|--------------------|----------------------|----------------------------|--------------------|------------------------------|-----------------------------------------|
| 1                  | CTGATCGT             | CTGATCGTNNNNNNNNNN         | 501                | ATATGCGC                     | GCGCATAT                                |
| 2                  | ACTCTCGA             | ACTCTCGANNNNNNNNNN         | 502                | TGGTACAG                     | CTGTACCA                                |
| 3                  | TGAGCTAG             | TGAGCTAGNNNNNNNNNN         | 503                | AACCGTTC                     | GAACGGTT                                |
| 4                  | GAGACGAT             | GAGACGATNNNNNNNNNN         | 504                | TAACCGGT                     | ACCGGTTA                                |
| 5                  | CTTGTCGA             | CTTGTCGANNNNNNNNNN         | 505                | GAACATCG                     | CGATGTTC                                |
| 6                  | TTCCAAGG             | TTCCAAGGNNNNNNNNNN         | 506                | CCTTGTAG                     | CTACAAGG                                |
| 7                  | CGCATGAT             | CGCATGATNNNNNNNNNN         | 507                | TCAGGCTT                     | AAGCCTGA                                |
| 8                  | ACGGAACA             | ACGGAACANNNNNNNNNN         | 508                | GTTCTCGT                     | ACGAGAAC                                |
| 9                  | CGGCTAAT             | CGGCTAATNNNNNNNNNN         | 509                | AGAACGAG                     | CTCGTTCT                                |
| 10                 | ATCGATCG             | ATCGATCGNNNNNNNNNN         | 510                | TGCTTCCA                     | TGGAAGCA                                |
| 11                 | GCAAGATC             | GCAAGATCNNNNNNNNNN         | 511                | CTTCGACT                     | AGTCGAAG                                |
| 12                 | GCTATCCT             | GCTATCCTNNNNNNNNNN         | 512                | CACCTGTT                     | AACAGGTG                                |
| 13                 | TACGCTAC             | TACGCTACNNNNNNNNNN         | 513                | ATCACACG                     | CGTGTGAT                                |
| 14                 | TGGACTCT             | TGGACTCTNNNNNNNNNN         | 514                | CCGTAAGA                     | TCTTACGG                                |
| 15                 | AGAGTAGC             | AGAGTAGCNNNNNNNNNN         | 515                | TACGCCTT                     | AAGGCGTA                                |
| 16                 | ATCCAGAG             | ATCCAGAGNNNNNNNNNN         | 516                | CGACGTTA                     | TAACGTCTG                               |
| 17                 | GACGATCT             | GACGATCTNNNNNNNNNN         | 517                | ATGCACGA                     | TCGTGCAT                                |

|    |           |                     |     |           |           |
|----|-----------|---------------------|-----|-----------|-----------|
| 18 | AACTGAGC  | AACTGAGCNNNNNNNNNN  | 518 | CCTGATTG  | CAATCAGG  |
| 19 | CTTAGGAC  | CTTAGGACNNNNNNNNNN  | 519 | GTAGGAGT  | ACTCCTAC  |
| 20 | GTGCCATA  | GTGCCATANNNNNNNNNNN | 520 | ACTAGGAG  | CTCCTAGT  |
| 21 | GAATCCGA  | GAATCCGANNNNNNNNNNN | 521 | CACTAGCT  | AGCTAGTG  |
| 22 | TCGCTGTT  | TCGCTGTTNNNNNNNNNN  | 522 | ACGACTTG  | CAAGTCGT  |
| 23 | TTCGTTGG  | TTCGTTGGNNNNNNNNNN  | 523 | CGTGTGTA  | TACACACG  |
| 24 | AAGCACTG  | AAGCACTGNNNNNNNNNNN | 524 | GTTGACCT  | AGGTCAAC  |
| 25 | CCTTGATC  | CCTTGATCNNNNNNNNNN  | 525 | ACTCCATC  | GATGGAGT  |
| 26 | GTCGAAGA  | GTCGAAGANNNNNNNNNNN | 526 | CAATGTGG  | CCACATTG  |
| 27 | ACCACGAT  | ACCACGATNNNNNNNNNN  | 527 | TTGCAGAC  | GTCTGCAA  |
| 28 | GATTACCG  | GATTACCGNNNNNNNNNN  | 528 | CAGTCCAA  | TTGGACTG  |
| 29 | GCACAACT  | GCACAACTNNNNNNNNNN  | 529 | ACG TTCAG | CTGAACGT  |
| 30 | GCGTCATT  | GCGTCATTNNNNNNNNNN  | 530 | AACGTCTG  | CAGACGTT  |
| 31 | ATCCGGTA  | ATCCGGTANNNNNNNNNNN | 531 | TATCGGTC  | GACCGATA  |
| 32 | CGTTGCAA  | CGTTGCAANNNNNNNNNNN | 532 | CGCTCTAT  | ATAGAGCG  |
| 33 | GTGAAGTG  | GTGAAGTGNNNNNNNNNN  | 533 | GATTGCTC  | GAGCAATC  |
| 34 | CATGGCTA  | CATGGCTANNNNNNNNNNN | 534 | GATGTGTG  | CACACATC  |
| 35 | ATGCCTGT  | ATGCCTGTNNNNNNNNNN  | 535 | CGCAATCT  | AGATTGCG  |
| 36 | CAACACCT  | CAACACCTNNNNNNNNNN  | 536 | TGGTAGCT  | AGCTACCA  |
| 37 | TGTGACTG  | TGTGACTGNNNNNNNNNNN | 537 | GATAGGCT  | AGCCTATC  |
| 38 | GTCATCGA  | GTCATCGANNNNNNNNNNN | 538 | AGTGGATC  | GATCCACT  |
| 39 | AGCACTTC  | AGCACTTCNNNNNNNNNN  | 539 | TTGGACGT  | ACGTCCAA  |
| 40 | GAAGGAAG  | GAAGGAAGNNNNNNNNNN  | 540 | ATGACGTC  | GACGTCAT  |
| 41 | GTTGTTTCG | GTTGTTTCGNNNNNNNNNN | 541 | GAAGTTGG  | CCAAC TTC |
| 42 | CGGTTGTT  | CGGTTGTTNNNNNNNNNN  | 542 | CATACCAC  | GTGGTATG  |

|    |          |                    |     |           |          |
|----|----------|--------------------|-----|-----------|----------|
| 43 | ACTGAGGT | ACTGAGGTNNNNNNNNNN | 543 | CTGTTGAC  | GTCAACAG |
| 44 | TGAAGACG | TGAAGACGNNNNNNNNNN | 544 | TGGCATGT  | ACATGCCA |
| 45 | GTTACGCA | GTTACGCANNNNNNNNNN | 545 | ATCGCCAT  | ATGGCGAT |
| 46 | AGCGTGTT | AGCGTGTTNNNNNNNNNN | 546 | TTGCGAAG  | CTTCGCAA |
| 47 | GATCGAGT | GATCGAGTNNNNNNNNNN | 547 | AGTTCGTC  | GACGAACT |
| 48 | ACAGCTCA | ACAGCTCANNNNNNNNNN | 548 | GAGCAGTA  | TACTGCTC |
| 49 | GAGCAGTA | GAGCAGTANNNNNNNNNN | 549 | ACAGCTCA  | TGAGCTGT |
| 50 | AGTTCGTC | AGTTCGTCNNNNNNNNNN | 550 | GATCGAGT  | ACTCGATC |
| 51 | TTGCGAAG | TTGCGAAGNNNNNNNNNN | 551 | AGCGTGTT  | AACACGCT |
| 52 | ATCGCCAT | ATCGCCATNNNNNNNNNN | 552 | GTTACGCA  | TGCGTAAC |
| 53 | TGGCATGT | TGGCATGTNNNNNNNNNN | 553 | TGAAGACG  | CGTCTTCA |
| 54 | CTGTTGAC | CTGTTGACNNNNNNNNNN | 554 | ACTGAGGT  | ACCTCAGT |
| 55 | CATACCAC | CATACCACNNNNNNNNNN | 555 | CGGTTGTT  | AACAACCG |
| 56 | GAAGTTGG | GAAGTTGGNNNNNNNNNN | 556 | GTTGTTTCG | CGAACAAC |
| 57 | ATGACGTC | ATGACGTCNNNNNNNNNN | 557 | GAAGGAAG  | CTTCCTTC |
| 58 | TTGGACGT | TTGGACGTNNNNNNNNNN | 558 | AGCACTTC  | GAAGTGCT |
| 59 | AGTGGATC | AGTGGATCNNNNNNNNNN | 559 | GTCATCGA  | TCGATGAC |
| 60 | GATAGGCT | GATAGGCTNNNNNNNNNN | 560 | TGTGACTG  | CAGTCACA |
| 61 | TGGTAGCT | TGGTAGCTNNNNNNNNNN | 561 | CAACACCT  | AGGTGTTG |
| 62 | CGCAATCT | CGCAATCTNNNNNNNNNN | 562 | ATGCCTGT  | ACAGGCAT |
| 63 | GATGTGTG | GATGTGTGNNNNNNNNNN | 563 | CATGGCTA  | TAGCCATG |
| 64 | GATTGCTC | GATTGCTCNNNNNNNNNN | 564 | GTGAAGTG  | CACTTCAC |
| 65 | CGCTCTAT | CGCTCTATNNNNNNNNNN | 565 | CGTTGCAA  | TTGCAACG |
| 66 | TATCGGTC | TATCGGTCNNNNNNNNNN | 566 | ATCCGGTA  | TACCGGAT |
| 67 | AACGTCTG | AACGTCTGNNNNNNNNNN | 567 | GCGTCATT  | AATGACGC |

|    |           |                     |     |           |           |
|----|-----------|---------------------|-----|-----------|-----------|
| 68 | ACG TTCAG | ACG TTCAGNNNNNNNNNN | 568 | GCACA ACT | AGTTGTGC  |
| 69 | CAG TCCAA | CAG TCCAANNNNNNNNNN | 569 | GATTACCG  | CGGTAATC  |
| 70 | TTG CAGAC | TTG CAGACNNNNNNNNNN | 570 | ACCACGAT  | ATCGTGGT  |
| 71 | CAATGTGG  | CAATGTGGNNNNNNNNNN  | 571 | GTCGAAGA  | TCTTCGAC  |
| 72 | ACTCCATC  | ACTCCATCNNNNNNNNNN  | 572 | CCTTGATC  | GATCAAGG  |
| 73 | GTTGACCT  | GTTGACCTNNNNNNNNNN  | 573 | AAGCACTG  | CAGTGCTT  |
| 74 | CGTGTGTA  | CGTGTGTANNNNNNNNNN  | 574 | TTCGTTGG  | CCAACGAA  |
| 75 | ACGACTTG  | ACGACTTGNNNNNNNNNN  | 575 | TCGCTGTT  | AACAGCGA  |
| 76 | CACTAGCT  | CACTAGCTNNNNNNNNNN  | 576 | GAATCCGA  | TCGGATTC  |
| 77 | ACTAGGAG  | ACTAGGAGNNNNNNNNNN  | 577 | GTGCCATA  | TATGGCAC  |
| 78 | GTAGGAGT  | GTAGGAGTNNNNNNNNNN  | 578 | CTTAGGAC  | GTCCTAAG  |
| 79 | CCTGATTG  | CCTGATTGNNNNNNNNNN  | 579 | AACTGAGC  | GCTCAGTT  |
| 80 | ATGCACGA  | ATGCACGANNNNNNNNNN  | 580 | GACGATCT  | AGATCGTC  |
| 81 | CGACGTTA  | CGACGTTANNNNNNNNNN  | 581 | ATCCAGAG  | CTCTGGAT  |
| 82 | TACGCCTT  | TACGCCTTNNNNNNNNNN  | 582 | AGAGTAGC  | GCTACTCT  |
| 83 | CCGTAAGA  | CCGTAAGANNNNNNNNNN  | 583 | TGGACTCT  | AGAGTCCA  |
| 84 | ATCACACG  | ATCACACGNNNNNNNNNN  | 584 | TACGCTAC  | GTAGCGTA  |
| 85 | CACCTGTT  | CACCTGTTNNNNNNNNNN  | 585 | GCTATCCT  | AGGATAGC  |
| 86 | CTTCGACT  | CTTCGACTNNNNNNNNNN  | 586 | GCAAGATC  | GATCTTGC  |
| 87 | TGCTTCCA  | TGCTTCCANNNNNNNNNN  | 587 | ATCGATCG  | CGATCGAT  |
| 88 | AGAACGAG  | AGAACGAGNNNNNNNNNN  | 588 | CGGCTAAT  | ATTAGCCG  |
| 89 | GTTCTCGT  | GTTCTCGTNNNNNNNNNN  | 589 | ACGGAACA  | TGTTCCGT  |
| 90 | TCAGGCTT  | TCAGGCTTNNNNNNNNNN  | 590 | CGCATGAT  | ATCATGCG  |
| 91 | CCTTG TAG | CCTTG TAGNNNNNNNNNN | 591 | TTCCAAGG  | CCTTG GAA |
| 92 | GAACATCG  | GAACATCGNNNNNNNNNN  | 592 | CTTGTCGA  | TCGACAAG  |

|    |          |                    |     |          |          |
|----|----------|--------------------|-----|----------|----------|
| 93 | TAACCGGT | TAACCGGTNNNNNNNNNN | 593 | GAGACGAT | ATCGTCTC |
| 94 | AACCGTTC | AACCGTTCNNNNNNNNNN | 594 | TGAGCTAG | CTAGCTCA |
| 95 | TGGTACAG | TGGTACAGNNNNNNNNNN | 595 | ACTCTCGA | TCGAGAGT |
| 96 | ATATGCGC | ATATGCGCNNNNNNNNNN | 596 | CTGATCGT | ACGATCAG |

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