Features: 20 total Read 1 Sequencing primer ACACTCTTTCCCTACACGAC TruSeq Read 2 Sequencing primer GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT PE2 (P7Rd2-UDI0001) CAAGCAGAAGACGGCATACGAGATNNNNNNNGTGACTGGAGTTCAGACGTGT 100 om strand is the Sense Strand P7 adapter sequence i7 and read 2 sequencing primer binding site Normal inDrop library Structure part of PE2-N6 primer that binds PE2 primer PE2-N6 (Rd2rc-N6) primer s hexamer binding site CACTGACCTCAAGTCTGCACACGAGAAGGCTAGA i7 index read sequencing primer 200 Normal inDrop library Structure full cell barcode barcode 1 i5 index read Sequencing primer A G A T C G G A A G A G C G T C G T G T A G G G A A A G A G T G T NNNAAGGCGTCACAAGCAATCACTCNNNNNNNAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTNNNNNNNGTGTAGATCTCGGTGGTCGCCGTATC ***** 300 NNNTTCCGCAGTGTTCGTTAGTGAGNNNNNNNTCTAGCCTTCTCGCAGCACATCCCTTTCTCACANNNNNNCACATCTAGAGCCACCAGCGGCATAG Normal inDrop library Structure barcode 1 TCTAGCCTTCTCG TGTGCAGACTTGAGGTCAGTG TruSeq Read 2 Sequencing primer TCTAGCCTTCTCGCAGCACATCCCTTTCTCACA Read 1 Sequencing primer AGCACATCCCTTTCTCACANNNNNNNNCACATCTAGAGCCACCAGCGGCATAG PE1 (P5Rd1-UDI0001) 3 ' 303 P5 adapter length TAA PE1 (P5Rd..

Sequence: Supplementary file 3.dna (Linear / 303 bp)

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