

Sample	SAMPLE1
Barcode	i388
Run, R1, R2	i388_run1, 103, 151
Run, R1, R2	i388_run2, 103, 151
Run, R1, R2	i388_run3, 103, 151
Beacon RT oligo	ggtgtcctaaacttacgcNNNNNNNWSNNNWWWNNNSWWNNNNNNNTCAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Beacon RT oligo	ggtgtcctaaacttacgcNNNNNNNWSNNNWWWNNNSWWNNNNNNNTCAGAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Beacon RT oligo	ggtgtcctaaacttacgcNNNNNNNWSNNNWWWNNNSWWNNNNNNNTCAGTCAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Target RT oligo	TGTGCTCTCCGATCTTNNNNNNNWSNNNWWWNNNSWWNNNNNNNTCTTACTCCTGGAGGCCATGT
Target RT oligo	TGTGCTCTCCGATCTGANNNNNNNWSNNNWWWNNNSWWNNNNNNNTCTTGAAGTTCACCTTGATGC
Target RT oligo	TGTGCTCTCCGATCTACTNNNNNNNWSNNNWWWNNNSWWNNNNNNCCATGGTCTTCTTCTGCATT
Sample	SAMPLE2
Barcode	i786, 103, 151
Run, R1, R2	i786_run1, 103, 151
Run, R1, R2	i786_run2, 103, 151
Run, R1, R2	i786_run3, 103, 151
Beacon RT oligo	ggtgtcctaaacttacgcTNNNNNNNWSNNNWWWNNNSWWNNNNNNNAAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Beacon RT oligo	ggtgtcctaaacttacgcNNNNNNNWSNNNWWWNNNSWWNNNNNNNAGTAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Beacon RT oligo	ggtgtcctaaacttacgcNNNNNNNWSNNNWWWNNNSWWNNNNNNNAGTCAAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Target RT oligo	TGTGCTCTCCGATCTTNNNNNNNWSNNNWWWNNNSWWNNNNNNNTCTTACTCCTGGAGGCCATGT
Target RT oligo	TGTGCTCTCCGATCTGANNNNNNNWSNNNWWWNNNSWWNNNNNNNATCTTGAAGTTCACCTTGATGC
Target RT oligo	TGTGCTCTCCGATCTACTNNNNNNNWSNNNWWWNNNSWWNNNNNNCCATGGTCTTCTTCTGCATT
Sample	SAMPLE3
Barcode	i289
Run, R1, R2	i289, 103, 151
Beacon RT oligo	GAGGTGTCCTAAACTTACGCTNNNNNNNWSNNNWWWNNNSWWNNNNNNNACAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Beacon RT oligo	GAGGTGTCCTAAACTTACGCNNNNNNNWSNNNWWWNNNSWWNNNNNNNACTGAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Beacon RT oligo	GAGGTGTCCTAAACTTACGCNNNNNNNWSNNNWWWNNNSWWNNNNNNNACTGACAGATCGGAAGAGCGTCGAGAGAAGTGGGGTGGCTTN
Target RT oligo	CGTGTGCTCTCCGATCTACTNNNNNNNWSNNNWWWNNNSWWNNNNNNNTACTCCTGGAGGCCATGT
Target RT oligo	CGTGTGCTCTCCGATCTTNNNNNNNWSNNNWWWNNNSWWNNNNNNNTCTTGAAGTTCACCTTGATGC
Target RT oligo	CGTGTGCTCTCCGATCTGANNNNNNNWSNNNWWWNNNSWWNNNNNNNACCATGGTCTTCTTCTGCATT

TABLE S1: Oligonucleotides used for each sample during 4-plex (ACTB, GAPDH, GFP, RFP) reverse transcription, related to Figures 2, 4-6, and 5. Lower case nucleotides indicate sequence areas during read parsing for which a 6% error rate is accepted, whereas upper case nucleotides afford zero error tolerance. Read-lengths labeled R1 (beginning at the 3' end of the beacon UMI) and R2 (beginning at the 5' end of the target UMI) are shown. All reverse transcription oligonucleotides were obtained as ultramers from IDT Inc.