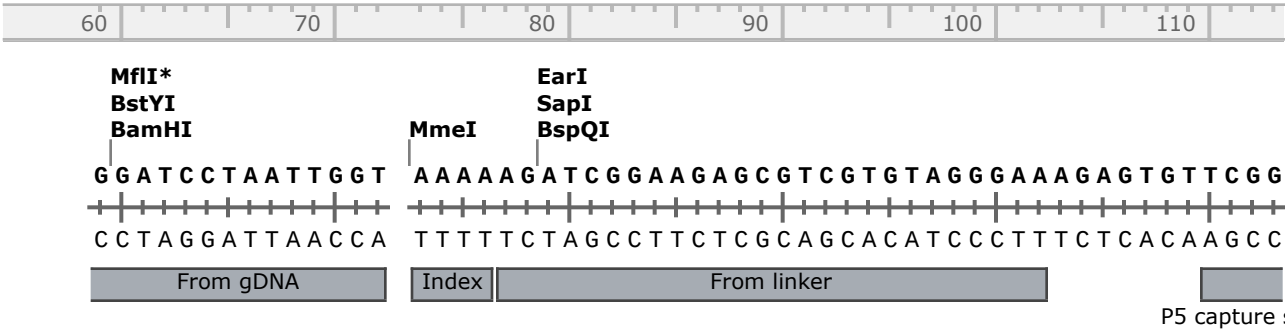




	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
1 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
2 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA TA
3 ←	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
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5 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
6 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGG- ACTTATCATCCAACCTGTTA AA
7 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTA NNNNN CAACCTGTTA C
8 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
9 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
10 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA
11 →	CAAGCAGAAGACGGGCATACGAGATTACGAAGACCGGGGACTTATCATCCAACCTGTTA C



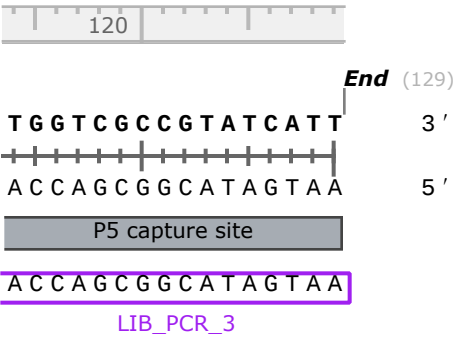
gDNA sequence

KROL517 Tn_InSeqA_F
CC ATGGTATA

Illumina Multiplexing Read 1 Sequencing Primer
TCTAGCCTTCTCGCAGCACATCCCTTTCTCACA

LIB_PCR_3
TCTAGCCTTCTCGCAGCACATCCCTTTCTCACAAGCC

	GGATCCTAATTGGT	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
1 →	AGATATCTTTANACN	AAAAAGATCGGAAGAGCGTCNTGTAGGGAAAGANGGTTCCG
2 →	TAAAGACC-AACCAA-	-AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
3 ←	GG-----TACC-----	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
4 →	AGGGC-TAAT--GC	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
5 →	C-ATTCAA-AAAA-----	--AAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
6 →	TAAA-----	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
7 →	AGCTATGACTTTCT	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
8 →	G-----TTATCG--	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
9 →	-----C-AA----GT	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG
10 →	--AT---AAT--GT	AAAAAGATCGGAAGAGCGTCGAAGTAGGGAAAGAGTGTTCGG
11 →	-----ATTGTG	AAAAAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTTCGG



	TGGTCGCCGTATCATT
1 ➡	TGGTCGCCGTAGCATT
2 ➡	TGGTCGCCGTATCATT
3 ⬅	TGGTCGCCGTATCATT
4 ➡	TGGTCGC- GTATCATT
5 ➡	TGGTCGCCGTATCATT
6 ➡	TGGTCGCCGTATCATT
7 ➡	TGGTCGCCGTATCATT
8 ➡	TGGTCGCCGTATCATT
9 ➡	TG
10 ➡	TGGTCGCCG- ATCATT
11 ➡	TGGTCGCCGTATCATT

Original Sequence: InSeqLibraryExample.dna

- 1: AM01_230207 ➡
1206 bases / Feb 7, 2023
45 .. 174 (14 mismatches, 1 gap)
- 2: AM02_230207 ➡
1143 bases / Feb 7, 2023
45 .. 174 (5 mismatches, 4 gaps)
- 3: AM03_230207 ⬅
1138 bases / Feb 7, 2023
43 .. 163 (2 mismatches, 2 gaps)
- 4: AM04_230207 ➡
1157 bases / Feb 7, 2023
44 .. 171 (3 mismatches, 4 gaps)
- 5: AM05_230207 ➡
1144 bases / Feb 7, 2023
43 .. 163 (3 mismatches, 2 gaps)
- 6: AM06_230207 ➡
1156 bases / Feb 7, 2023
45 .. 164 (2 gaps)
- 7: AM07_230207 ➡
1156 bases / Feb 7, 2023
45 .. 174 (13 mismatches, 1 gap)
- 8: AM09_230207 ➡
1140 bases / Feb 7, 2023
46 .. 167 (2 mismatches, 2 gaps)
- 9: AM10_230207 ➡
1122 bases / Feb 7, 2023
46 .. 151 (3 gaps)
- 10: AM11_230207 ➡
1176 bases / Feb 7, 2023
42 .. 162 (1 mismatch, 4 gaps)
- 11: AM12_230207 ➡
1166 bases / Feb 7, 2023
41 .. 162 (2 mismatches, 1 gap)