

Bor 4	1	GTTTTTTTTTTTTTTTAACTACTACTACAAGTTTATTAGATTGTATAAGGTTGAT	57
Lp2-2	1	GTTTTTTTTTTTTTTTAACTACTACTACAAGTTTATTAGATTGTATAAGGTTGAT	57
Bs 1	1	GTTTTTTTTTTTTTTTAACTACTACTACAAGTTTATTAGATTGTATAAGGTTGAT	57
Kort 0	1	GTTTTTTTTTTTTTTTAACTACTACTACAAGTTTATTAGATTGTATAAGGTTGAT	57
Bor 4	58	ACAAATAAGAGAGTAAGAAACGAGGAAGAACAATAAAGGACTGATACAGAGTAGTAG	114
Lp2-2	58	ACAAATAAGAGAGTAAGAAACGAGGAAGAACAATAAAGGACTGATACAGAGTAGTAG	114
Bs 1	58	ACAAATAAGAGAGTAAGAAACGAGGAAGAACAATAAAGGACTGATACAGAGTAGTAG	114
Kort 0	58	ACAAATAAGAGAGTAAGAAACGAGGAAGAACAATAAAGGACTGATACAGAGTAGTAG	114
Bor 4	115	TAGACAAAACATATTGAGCCATCTTATCTGCAGCAC	171
Lp2-2	115	TAGACAAAACATATTGAGCCATCTTATCTGCAGCAC	171
Bs 1	115	TAGACAAAACATATTGAGCCATCTTATCTGCAGCAC	171
Kort 0	115	TAGACAAAACATATTGAGCCATCTTATCTGCAGCAC	171
Bor 4	172	CGAGAAGAGTGACGTTGGATAGTTTTGCCATCCAATGACGAATATCGAACAGGAGAG	228
Lp2-2	172	CGAGAAGAGTGACGTTGGATAGTTTTGCCATCCAATGACGAATATCGAACAGGAGAG	228
Bs 1	172	CGAGAAGAGTGACGTTGGATAGTTTTGCCATCCAATGACGAATATCGAACAGGAGAG	228
Kort 0	172	CGAGAAGAGTGACGTTGGATAGTTTTGCCATCCAATGACGAATATCGAACAGGAGAG	228
Bor 4	1369	CTAAACGAACTCGTAATCCTTGACAAAGTAACTCTTTT	1425
Lp2-2	1369	CTAAACGAACTCGTAATCCTTGACAAAGTAACTCTTTT	1425
Bs 1	1369	CTAAACGAACTCGTAATCCTTGACAAAGTAACTCTTTT	1425
Kort 0	1369	CTAAACGAACTCGTAATCCTTGACAAAGTAACTCTTTT	1425
Bor 4	1426	ATCCAAAAGATGTATAGGTTCTGTCAACGCTTCCAAATAAGAGGTTTGAGGATGAT	1482
Lp2-2	1426	ATCCAAAAGATGTATAGGTTCTGTCAACGCTTCCAAATAAGAGGTTTGAGGATGAT	1482
Bs 1	1426	ATCCAAAAGATGTATAGGTTCTGTCAACGCTTCCAAATAAGAGGTTTGAGGATGAT	1482
Kort 0	1426	ATCCAAAAGATGTATAGGTTCTGTCAACGCTTCCAAATAAGAGGTTTGAGGATGAT	1482
Bor 4	1483	ACATACCTTTATAAAGACGGGCCAAAAGACTCTGAGGATTTCTCAAAATTCTCCAAG	1539
Lp2-2	1483	ACATACCTTTATAAAGACGGGCCAAAAGACTCTGAGGATTTCTCAAAATTCTCCAAG	1539
Bs 1	1483	ACATACCTTTATAAAGACGGGCCAAAAGACTCTGAGGATTTCTCAAAATTCTCCAAG	1539
Kort 0	1483	ACATACCTTTATAAAGACGGGCCAAAAGACTCTGAGGATTTCTCAAAATTCTCCAAG	1539
Bor 4	2395	CTACCCGATCATAGGCCTTGCTTATATCAGTTTTAATCGCCAAATACCCATTCTGGC	2451
Lp2-2	2395	CTACCCGATCATAGGCCTTGCTTATATCAGTTTTAATCGCCAAATACCCATTCTGGC	2451
Bs 1	2395	CTACCCGATCATAGGCCTTGCTTATATCAGTTTTAATCGCCAAATACCCATTCTGGC	2451
Kort 0	2395	CTACCCGATCATAGGCCTTGCTTATATCAGTTTTAATCGCCAAATACCCATTCTGGC	2451
Bor 4	2452	ACTCCCTCTTCGACTTGAGTGAATGTAGAAGTTTCATGAGCCACTAGTACAT	2508
Lp2-2	2452	ACTCCCTCTTCGACTTGAGTGAATGTAGAAGTTTCATGAGCCACTAGTACAT	2508
Bs 1	2452	ACTCCCTCTTCGACTTGAGTGAATGTAGAAGTTTCATGAGCCACTAGTACAT	2508
Kort 0	2452	ACTCCCTCTTCGACTTGAGTGAATGTAGAAGTTTCATGAGCCACTAGTACAT	2508
Bor 4	2509	ATATATTACGACCA	2565
Lp2-2	2509	ATATATTACGACCA	2565
Bs 1	2509	ATATATTACGACCA	2565
Kort 0	2509	ATATATTACGACCA	2565
Bor 4	2566	AATCTGAGA	2574
Lp2-2	2566	AATCTGAGA	2574
Bs 1	2566	AATCTGAGA	2574
Kort 0	2566	AATCTGAGA	2574

Figure S1 Result of NMR19-4 sequence alignment and information of sgRNA sequence, position and PAM sequence in Bor 4, Lp2-2, Bs 1 and Krot 0. Yellow represents sgRNA and pink represents PAM sequence.