

Supplemental Table S1: Mini-casposon integration sites in pUC19

For mini-casposon with LE30/RE30:	Integration site
GAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC	589 (+)
ATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCAC	44 (+)
CATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCG	67 (+)
ACTATGCGGCATCAGAGCAGATTGTAAGTGCAGAGTGCACCATATGCG	173 (+)
ACGAAACGCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTAT	2669 (-)
TTAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTTACACTT	550 (-)
TTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGC	513 (-)
CGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTA	2560 (-)
ACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGA	510 (-)
TTGCTGGCCTTTTGTCTCACATGTTCTTTCCTGCGTTATCCCCTGAT	798 (-)
TCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGCGGGCTGGCTTAAC	129 (+)
GATGAGCACTTTTAAAGTTTGTGCTATGTGGCGCGGTATTATCCCCT	2259 (-)
TGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCGCGAGAC	12 (-)
ATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAAC	135 (-)
GGGAGCTGCATGTGTCAGAGGTTTTCACCGTCATCACCGAAACGCG	19 (-)
TACCGCCTTTGAGTGAGCTGATACCGCTCGCCGAGCCGAACGACCG	734 (-)
CTTACGCATCTGTGCGGTATTTACACCGCATATGGTGCCTCTCAG	186 (-)
GTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCC	1743 (-)
TAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCC	743 (-)
AAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAAC	2634 (+)
GTTTTCCAGTCACGACGTTGTAAACGACGGCCAGTGAATTCGAG	387 (+)
For mini-casposon with LE15/RE15:	
CTCTAGAGGATCCCCGGTACCGAGCTCGAATTCCTGCGCGTCGTT	398 (-)
TAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTC	2618 (-)
ACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAA	507 (-)
CCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCC	289 (-)
CTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCG	2482 (-)
TGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGT	1495 (+)
TTCATTAATGCAGCTGGCAGCAGGTTTCCCGACTGGAAAGCGGGC	612 (-)
ATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGT	50 (-)
TATTACGCCAGCTGGCGAA-GGGGGATGTGCTGCAAGGCGATTAAGT	327 (+)
AGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCT	2465 (-)
CGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATG	2660 (-)
TGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAA	1557 (+)
TGCGGTATTTACACCCGCATATGGTGCCTCTCAGTACAATCTGCT	175 (-)
TCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGCGGGCTGGCTTAAC	129 (+)
CTCCCCGCGGTTGGCCGATTCAATTAATGCAGCTGGCACGACAGGTT	631 (-)
TTCAACATTTCCGTGTGCGCCCTTATCCCTTTTTTGGCGCATTTTGC	2448 (-)
CTGTTGAGATCCAGTTTCGATGTAACCCACTCGTGCACCCAACCTGATC	2364 (+)
TTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCAC	1509 (-)
CGCGCGGGGAGAGGCGGTTTGGCGTATTGGGCGCTCTTCCGCTTCCT	680 (+)
GTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCAACAGTTGCG	273 (-)

Integration site is defined as the bp in pUC19 to which the casposon LE 5'-G (i.e., top strand in Fig. 1B) is joined. The bases in red indicate imperfect integration events: in the first case, the TSD sequence flanking the LE and the RE differed at the indicated bp, and in the second, both TSDs are missing a single bp of pUC19 sequence.