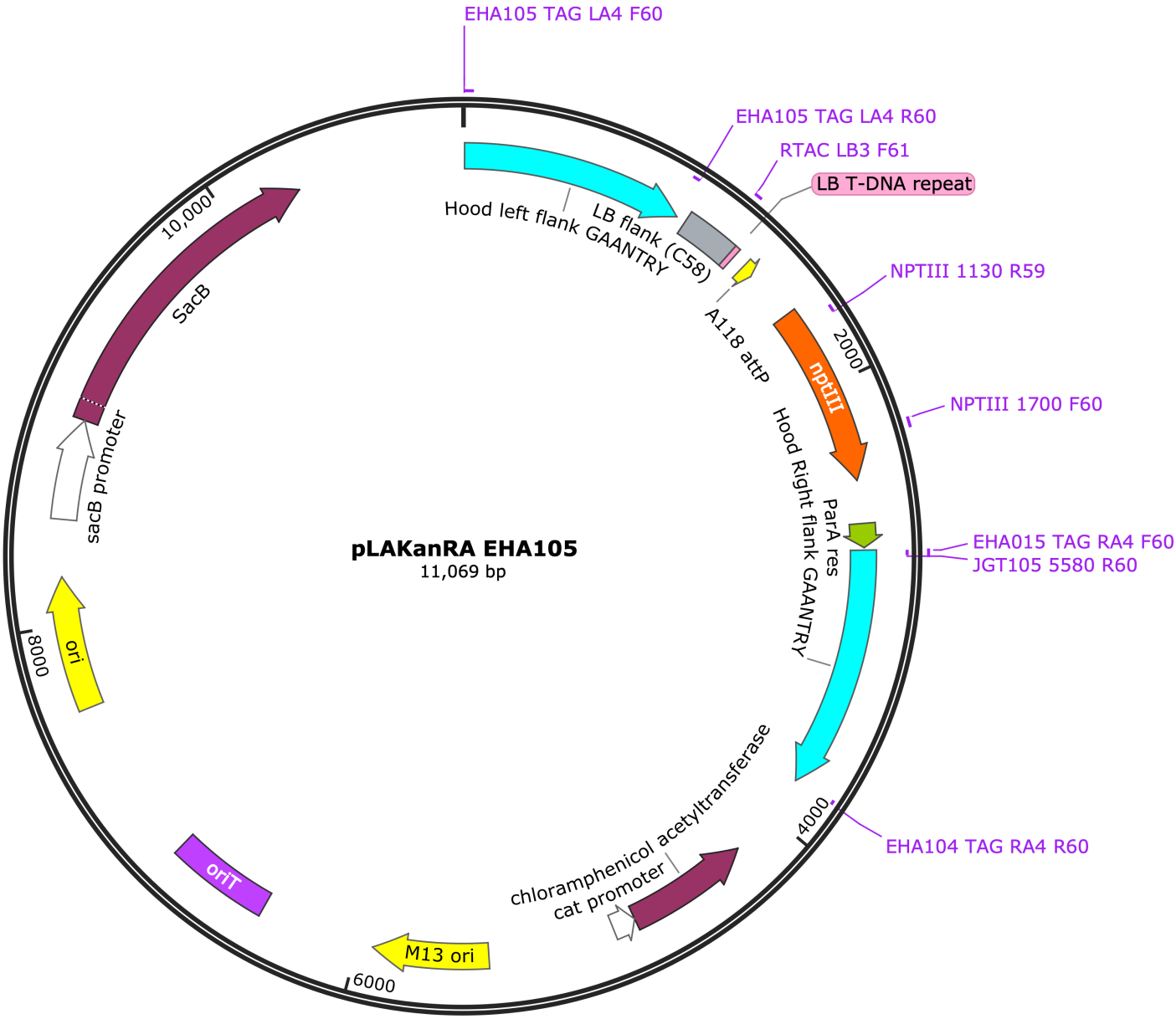
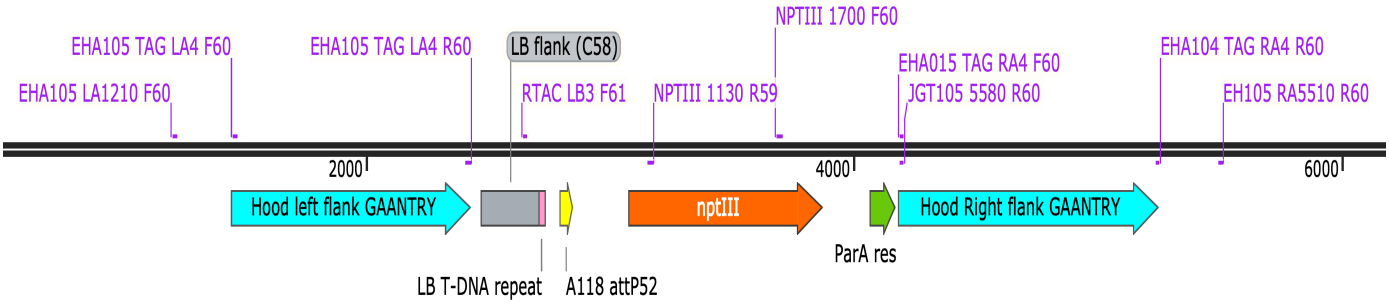


Supplementary Figure S1. Schematic representation of the pLAKanRA EHA105 T-DNA targeting plasmid. Electro-competent EHA105 cells were transformed with pLAKanRA EHA105 and selected on kanamycin plates. Homologous recombination facilitates correct placement of the GA*A*NTRY technology within the EHA105 pTi virulence plasmid. Counter selection on 5% sucrose/kanamycin plates ensures removal of the vector backbone due to presence of the *sacB* gene. PCR and sequencing was used to verify integrity and correct placement of genetic elements.



*gcatcgaagaacttcaaagcctacttgc*cgacatcaggacgtgggacggcggtatccgcgagctcctcatcgacacgcagtgcgatcctgaaatgatcgaccgcgtcatggccgatgaaatgaaacgcggctcatagcttccatctct
cgatacccgaaaacgctttcgccggacgctcacgtctttatcaccgcgctttgccatgctgcatctcagttgaagggaatttgctagacacgaggacggaa*CCAGACGAACGTGAAGAATAACACAGC*GAATG
GCTTGGTTCCATCCTCGACGGGCAGATTGAGGTCCACGGTGACAAGCGCCTGACAAATAAACTGGCAATCGCCAAATTGTTTCCCAGCGTTC
ACTGAAATCGACTTACCGCACCTCTGCAGCAGCGGCAGGATATATGGCAGTGTAAACTCCATTTTCGAACGCGGTTCAGGGCACCTACGATT
ATCGAAAAAGGATAACGGCTGCAGGAATATATATGATTATGAAAAGTGCGGGCGTTGTGGCCTTACTGGGTGTGAAATCGCCGTCAGTTTTT
GAACTTACTGAACACGTGTTTGTGGCATTTAGTATAGCCGTATGCGGGATTTCTGCCTTCCGTTTTGTCAGCGGGAAGCCGCGAGACAGTGGA
ATGACCCGTACTGCAATCTGAGCCTATGAAAGAAACACAAAATCAATCAGCGAGAGAGAAACTTTTGTTTCTCTGAATCAAAAGCGGACCGA
GGCAATCATGCCATTTTATCGACTTTGAGCCTGAATTGAAGTTTATTCGCATCAACGAGTAAATACTTTAATGGTGATTGTAAGACGAAATAG
CTTAGGACCGTCATGAATACCTAACAGGTCCCACTAGAAGGCATCTTGATTTAATAAAATTGCTCATAACTCAGTTAAGAGCGCGACGATGT
ATTATGTGCCGATAGGACCGTAAATTATTCTGGGCAATTGTCGAATGAAATTATTTCGAATTTTATTTGCTGAAATAATTTCGCAATACATTAT
AATATAAGATAAATGTCTGAAAACAATACATAGTCCCATGTCAAATTACAAAGCAAGTGAACGGTGCATACGGCCGAATATGTCCGATCTTA
TTTGATATTTGAATTTAAAGTACTCAGTATTCAGAAATATTTCAATAACTGTGCGCATTCGTCAACAAAAAATTACGAAGCCTACTC*CTCTTCA*
*GAATCGTAGATGTCAAGGTGAGGTG*GCGGCCGCTGAATTCCTGCAGCCCGACGGTATCGATAAGCTTTGATCACAGGCAGCAACGCTCTGTCAT
CGTTACAATCAACATGCTACCCTCCGCGAGATCATCCGTGTTTCAAACCCGGCAGCTTAGTTGCCGTTCTTCCGAATAGCATCGGTAACATGA
GCAAAGTCTGCCGCCTTACAACGGCTCTCCCGCTGACGCCGTCCC*GGACTGATGGGCTGCCTGTATCG*AGTGGTGATTTTGTGCCGAGCTGCCG
GTCGGGGAGCTGTTGGCTGGCTGG*TGGCAGGATATATTGTGGTGTAAAC*AAATTGACGCTTAGACAACTTAATAACACATTGCGGACGTTTTT
AATGTACTGAATTAAA*TGTTTAGTTCCTCGTTTTCTCTCGTTGGAAGAAGAAGAAACGAGAAACTAAAATTA*GGGAGTACTCGTACGCTCGCG
TTGGCAGCATCACCCATAATTGTGGTTTCAAAATCGGCTCCGTCGATACTATGTTATACGCCAACTTTGAAAACAACTTTGAAAAAGCTGTTT
TCTGGTATTTAAGGTTTTAGAATGCAAGGAACAGTGAATTGGAGTTCGTCTTGTTATAATTAGCTTCTTGGGGTATCTTTAAATACTGTAGAA
AAGAGGAAGGAAATAATAA*ATGGCTAAAATGAGAATATCACCGGAATTGAAAAAACTGATCGAAAAATACCGCTGCGTAAAAGATAC**GGAA*
*GGAATGTCTCCTGCTAAGGTATATAAGC*TGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGGACAGCCGGTATAAAGGGACCACCTAT
GATGTGGAACGGGAAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGGTCCTGCACTTTGAACGGCATGATGGCTGGA
GCAATCTGCTCATGAGTGAGGCCGATGGCGTCCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCG
GAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTATACGAATAGCTTAGACAGCCGCTTAGCCGAATTGGATTACTTACTG
AATAACGATCTGGCCGATGTGGATTGCGAAAACTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTATGATTTTTTAAAGACGGA
AAAGCCCGAAGAGGAACTTGTCTTTTCCCACGGCGACCTGGGAGACAGCAACATCTTTGTGAAA*GATGGCAAAGTAAGTGGCTTTATTGATCTT*
*GG*GAGAAGCGGCAGGGCGGACAAGTGGTATGACATTGCCTTCTGCGTCCGGTCGATCAGGGAGGATATTGGGGAAGAACAGTATGTCGAGC
TATTTTTTGACTTACTGGGGATCAAGCCTGATTGGGAGAAAATAAAATATTATATTTTACTGGATGAATTGTTTTAGTACCTAGATGTGGCGC
AACGATGCCGGCGACAAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGGCCGAGGCCCACGGCAAGTATTTGGGCAA
GGGGTCGCTGGTATTCGTGCAGGGCAAGATTCGGAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACGTACGAAA*GGTCAAAT*
TGGGTATACCCATTTGGGCCTAGTCTAGCCGGCATGGCGCATTACAGCAATACGCAATTTAAATGCGCCTAGCGCATTTTCCCGACCTTAATG
*CGCCT*AAAGCGTCGAC*CACAGACACAGCAAGGTGTCCAC*CGCGCCGCCTTGTCCTGCGGCAACCTCGCTCATGGCTTTGCCGCCTGCTCGTCAT
CCGAGAAAGCAATGCTGTCAGGCTCGACAGCTCTGAATCTGGGCATTGTCACTTCTTACAATGACATGCTGAGTGCTCATCAGCCCTACGGC
AACTATCCAGACATCATCAAATCCGCGGCGCGCTCGGTTGGCGCCACCGCACAGGTTGCCGGCGGCGTGCCAGCTATGTGCGATGGTGTAAC
CCAGGGCCAGCCGGGGATGGATCTGTCGCTGTTCAGCCGAGATGTGATCGCGATGTCTACTGCGATTGCACTCAGCCACAACATGTTCGACG
CCGCCGTCTACCTTGGTGTCTGCGACAAGATCGTTCCTGGCCTTTTGATCGGAGCCCTTTCCTTCGGTCATCTTCCCGCGGTTTTTGTGCCAGC
GGGCCCGATGGTATCGGGTCTTTCGAACGATGAAAAGGCGCGCATCCGCCAACTGTCATCGGAAGGGAAGATTGATCGTCCGCAATTACTCG
ACGCCGAGGCAAAATCTTATCACTCTCCAGGTACATGCACCTTCTACGGCACAGCGAACTCAAACCAGATGCTCATGGAAATCATGGGCCTC
CACATTCCTGGTTCAAGCTTCGTAAACGCCAATACACCCCTTCGCGACGCACTCACTCGGGAGGCGACGCGCCGGGCGCTTTCGCTCACCGC
GGGAGGCAACAATTTCACCCCTATCGGTCACATCATTGATGAAAAGGCCATTGTAAACGGTATGGTCGGACTGCTAGCAACTGGCGGCTCGA
CAAATCATACACTGCATATCGTCGCCATTGCGCAGGCAGCCGGGCTGAACGTTACGTGGGAAGACATGAGCGACCTCAGCGATGTCGTGCCG
CTGCTGACTCGCGTCTATCCGAATGGCTCTGCAGACGTGAACCATTTTCACGCCGCAGGAGGAATTGGCTTTCTCATCCGCGAGCTGATCGAT
GGCGGCTTCTTGCATGAAGACGTCCAAACGATCTGGGGAACCGGCCTTGA*GAGCTACGCAGTCGAGGCAAG*attggctggcgacaagttggtctttgaacccacacc
ggcgggctcgcgcaatcccaaagtgcttgcacctgttagccgagccttctcgccgaatggaggtctgaagttgctatcaggcaacatcggcaaatcggtcattaaagtctctgccgtcaaaccggaaaaccgagtcgtggaggctccag
cacgtgtctttcatgcccaggaggagctccagaaggcgtttaaggatgg*cgagcttgagcgtgacatgattgc*

Supplementary Figure S2. JGT105: GA*A*NTRY *Agrobacterium tumefaciens* recipient strain target sequence that allows site specific recombination in place of the native T-DNA. A) Schematic representation. B) Sequence of JGT105 recipient strain. Color of text matches the diagram shown above. A 4312 bp portion of the JGT105 strain is shown. Primers (italic and purple) used for PCR and sequencing to verify integrity and correct placement of genetic elements for GA*A*NTRY within the virulence plasmid.