

PTRG_03457 CGTCATGCAGTCCGTGCGCTGCTGCCTTTACTAGTGCAGAAATCGGGAAATGCCGTGCGCCAAACTTTCCAGCTACCTAACTCTTTCAGCCTACTACTT
 DW7_94 CGTCATGCAGTCCGTGCGCTGCTGCCTTTACTAGTGCAGAAATCGGGAAATGCCGTGCGCCAAACTTTCCAGCTACCTAACTCTTTCAGCCTACTACTT
 DW7_14025 CGTTATGCAGTCCGTGCGCTGCTGCCTTTACTAGTGCAGAAATCGGGAAATGCCGTGCGCCAAACTTTCCAGCTACCTAACTCTTTCAGCCTACTACTT
 PTRG_00559 AGCTACCTAACTCTTTCAGCCTACTACTT
 SD20_20175 CTTTCAGCCTACTACTT

DW7_94 TCTTAATTGTCGACCACATTTATCACAGTAATTAATCACATACGTGCGCTACGTTCAATCATCTACTCTACTACGCAATGGCAAGGACAAAACACGGCCT
 DW7_14025 TCTTAATTGTCGACCACATTTATCACAGTAATTAATCACATACGTGCGCTACGTTCAATCATCTACTCTACTACGCAATGGCAAGGACAAAACACGGCCT
 PTRG_00559 TCTTAATTGTCGACCACATTTATCACAGTAATTAATCACATACGTGCGCTACGTTCAATCATCTACTCTACTACGCAATGGCAAGGACAAAACACGGCCT
 SD20_20175 TCTTAATTGTCGACCACATTTATCACAGTAATTAATCACATACGTGCGCTACGTTCAATCATCTACTCTACTACGCAATGGCAAGGACAAAACACGGCCT
 PTRG_03457 TCTTAATTGTCGACCACATTTATCACAGTAATTAATCACATACGTGCGCTACGTTCAATCATCTACTCTACTACGCAATGGCAAGGACAAAACACGGCCT

DW_94 AAGGTCACCGGTAAGCCG
 DW_14025 AAGGTCACCGGTAAGCCG
 PTRG_00559 AAGGTCACCGGTAAGCCGCGGGTGGTCTGATGGCAAGACAGTTACTGGCGGCAAGCCGGCTCAGAAGGCCCTTGTAGTAAGGCTAGACGTCGAAG
 SD20_20175 AAGGTCACCGGTAAGCCGCGGGTGGTCTGATGGCAAGACAGTTACTGGCGGCAAGCCGGCTCAGAAGGCCCTTGTAGTAAGGCTAGACGTCGAAG
 PTRG_03457 AAGGTCACCGGTAAGCCGCGGGTGGTCTGATGGCAAGACAGTTACTGGCGGCAAGCCGGCTCAGAAGGCCCTTGTAGTAAGGCTAGACGTCGAAG

PTRG_00559 TAGCAGGAAAGTCTACGCGAAAGGCACCTGTAGCTGTTAAGAAGAAGCGCAAGTTAAGGCCGGCAgtaggttatacacagt~~g~~tttatacacagctat~~ttt~~
 SD20_20175 TAGCAGGAAAGTCTACGCGAAAGGCACCTGTAGCTGTTAAGAAGAAGCGCAAGTTAAGGCCGGCAgtaggttatacacagt~~g~~tttatacacagctat~~ttt~~
 DW7_11351 AAGAAGCGCAAGTTAAGGCCGGCAgtaggttatacacagt~~g~~tttatacacagctat~~ttt~~
 PTRG_03457 TAGCAGGAAAGTCTACGCGAAAGGCACCTGTAGCTGTTAAGAAGAAGCGCAAGTTAAGGCCGGCAgtaggttatacacagt~~g~~tttatacacagctat~~ttt~~

PTRG_00559 ctaatttagcttagCTGTGCGATTACGGGAAATCAAGAGATACCAGAGAGGTTTTGAACACTCTTGCAGAAACTCCCCCTTTCCCGGTAGTGCAGGAA
 SD20_20175 ctaatttagcttagCTGTGCGATTACGGGAAATCAAGAGATACCAGAGAGGTTTTGAACACTCTTGCAGAAACTCCCCCTTTCCCGGTAGTGCAGGAA
 DW7_11351 ctaatttagcttagCTGTGCGATTACTCAAAATTAAGAGATACCAGAGAGGTTTTGAACACTCTTGCAGAAACTCCCCCTTTCCCGGTAGTGCAGGAA
 PTRG_03457 ctaatttagcttagCTGTGCGATTACGGGAAATCAAGAGATACCAGAGAGGTTTTGAACACTCTTGCAGAAACTCCCCCTTTCCCGGTAGTGCAGGAA

PTRG_00559 TTTGCACAGGTGCACAAGGCCGATATCCGCTTTCAACGATCTGCAATCGAAGCTCTTCAGGAAGCTACAGAAGCTTTCTTAGTTGGTTATTTTgagggta
 SD20_20175 TTTGCACAGGTGCACAAGGCCGATATCCGCTTTCAACGATCTGCAATCGAAGCTCTTCAGGAAGCTACAGAAGCTTTCTTAGTTACTTATTTTgagggta
 DW7_11351 TTTGCACAGGTGCACAAGGCCGATATCCGCTTTCAACGATCTGCAATCGAAGCTCTTCAGGAAGCTACAGAAGCTTTCTTAGTTACTTATTTTgagggta
 PTRG_03457 TT-GCACAGGTGCACAAGGCCGATATCCGCTTTCAACGATCTGCAATCGAAGCTCTTCAGGAAGCTACAGAAGCTTTCTTAGTTGGTTATTTTgagggta

PTRG_00559 tagtctatctaccctatactat~~ttt~~ttcatttaataaactttttagACTGCAACATCAATGCTATTTCAGCAGAAAGGGTTACTATTCAAGAGAAGGATT
 SD20_20175 taatctatctaccctatactat~~ttt~~ttcatttaataaactttttagACTGCAACATCAATGCTATTTCAGCAGAAAGGGTTACTATTCAAGAGAAGGATT
 DW7_11351 tagtctatctatccctatactat~~ttt~~ttcatttaataaactttttagACTGCAACATCAATGCTATTTCAGCAGAAAGGGTTACTATTCAAGAGAAGGATT
 PTRG_03457 tagtctatctaccctatactat~~ttt~~ttcatttaataaactttttagACTGCAACATCAATGCTATTTCAGCAGAAAGGGTTACTATTCAAGAGAAGGATT

PTRG_00559 TCAATTGGCTAGGCGCTACTTTGGCGCGGAGTTACTAGCTTTTCTCTAGATTATAAGATATATCTAGATACACGTGCTTAAATGCTAGCTGGCGAAGCCT
 SD20_20175 TCAATTGGCTAGGCGCTACTTTGGCGCGGAGTTACTAGCTTTTCTCTAGATTATAAGATATATCTAGATACACGTGCTTAAATGCTAGCTGGCGAAGCCT
 DW7_11351 TCAATTAGCTAGGCGCTACTTTGGCGCGGAGTTACTAGCTTTTCTCTAGATTATAAGATATATCTAGATACACGTGCTTAAATGCTAGCTGGCGAAGCCT
 PTRG_03457 TCAATTGGCTAGGCGCTACTTTGGCGCGGAGTTACTAGCTTTTCTCTAGATTATAAGATATATCTAGATACACGTGCTTAAATGCTAGCTGGCGAAGCCT

PTRG_00559 CTGTATATTATAAATGAAACTAGTTAATGCTACACTG
 SD20_20175 CTGTATATTATAAATGAAACTAGTTAATGCTACACTGTTAATGCTACTG
 DW7_11351 CTGTATAGTATAAATGAAACTAGTTAATGCTACACTGTAATAATCTACTGTGATACTATATAAACTTTTCTTTTATTGAAATCTATATTATATCTTGC
 PTRG_03457 CTGTATATTATAAATGAAACTAGTTAATGCTACACTG

Figure S3 Alignment of novel H3-like (H3L) genes identified in three different *Ptr* isolates (PTRG numbers refer to genes identified in the reference genome of BFP-ToxAC, while DW7 and SD20 refer to the pathogenic DW7-ToxB and non-pathogenic SD20-NP strains, respectively). In all cases, contigs assembled *de novo* from Illumina reads suggest that copies of H3L genes in both DW7-ToxB and SD20-NP are inactive (note the many point mutations when compared to the PTRG sequences). DW7_14025 and SD20_20175 in particular lack a proper start codon (ATG to ATA change, underlined), while DW7_11351 contains several in-frame nonsense codons in addition to the conserved stop codon (underlined).