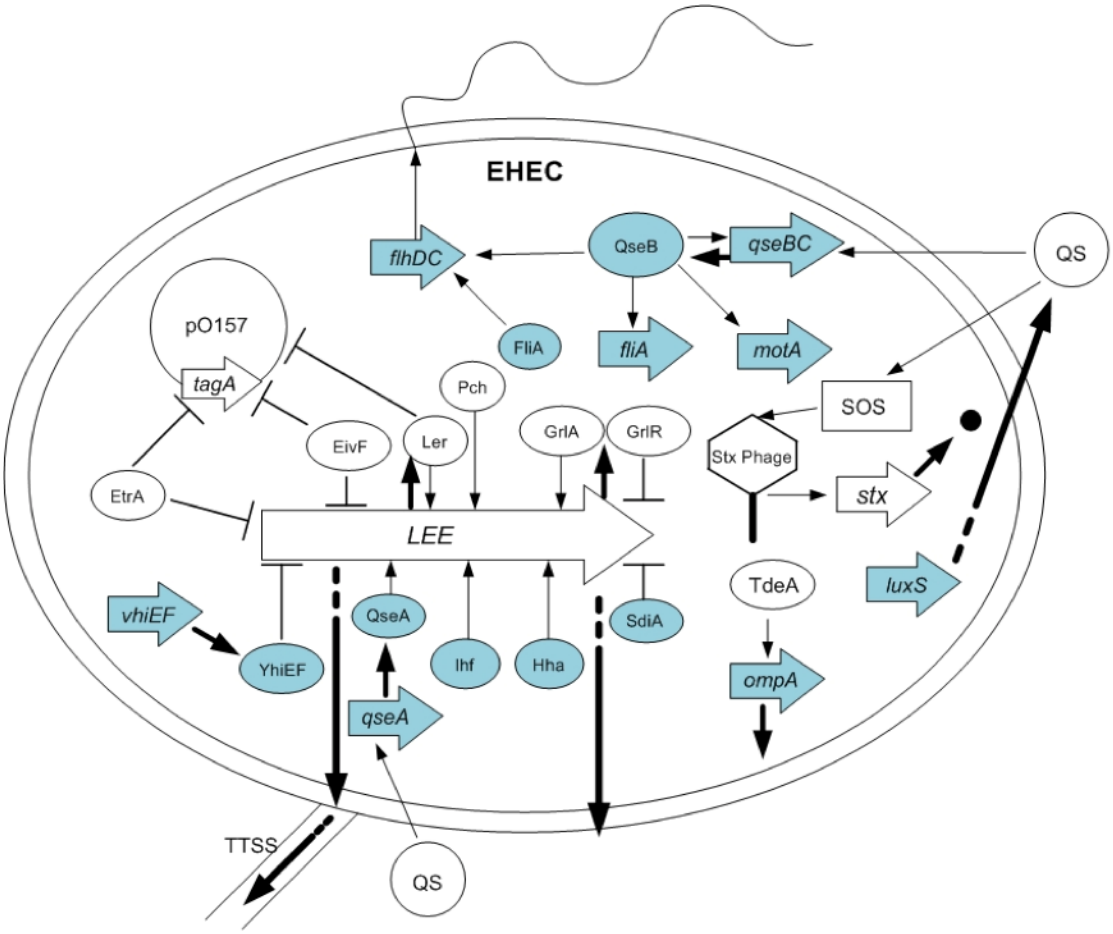
Supplementary information

Supplementary Figure 1 | The molecular genetic program of EHEC's pathogenicity and toxicity. Illustrated is the interplay of those genes and proteins that are associated with EHEC's pathogenicity or toxicity capabilities (see text). Elements colored in blue are conserved in *E. coli* K-12. Abbreviations and symbols: Arrows = genes, circles = proteins, QS = quorum sensing, TTSS = type III secretion system

Supplementary Table 1 | Transferred regulatory interactions from E. coli K-12 to E. coli pathogens for nine conserved genes associated with pathogenicity or toxicity. The table lists the inter-species transferred transcriptional gene regulatory interactions for nine evolutionarily conserved genes associated with *E. coli* pathogenicity or toxicity: *qseB*, *flhD*, *flhB*, *fliA*, *motA*, *ompA*, *ompR*, *yhiF* (*dctR* in *E. coli* K-12), and *yhiE* (*gadE* in *E. coli* K-12). For each of the genes and for each of the pathogenic *E. coli* species, we present cases where the transcription factor is conserved, the target gene is conserved, and the binding site is conserved as well. Finally, we summarize the results for each target gene over all pathogens.

Supplementary Table 2 | Transcription factor binding sites for eight EHEC-specific genes associated with EHEC's pathogenicity or toxicity in *E. coli* O157:H7 str. EDL933. By utilizing the TFBScan feature of EhecRegNet we found potential binding sites (BSs) for eight genes in the EDL933 strain that are not conserved in *E. coli* K-12: *ler*, *stx1A*, *stx1B*, *stx2A*, *stx2B*, *eivF*, *grlA* and *grlR*. We used a p-value cut-off of 10^{-5}. Note that for *grlR* we did not identify BSs for this rather conservative cut-off. Here, we present BSs for a less restrictive p-value cut-off of 10^{-4}. Genes marked with * have not been annotated with a name in *E. coli* O157:H7 EDL933. We give the name of the homologous gene in *E. coli* O157:H7 str. TW14359.



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