**Supplementary Figure Legends**

**Figure S1: Hierarchical clustering of highly predicted SVM score of HEV-human protein pairs**. Hierarchical clustering analysis was done using TIBCO Spotfire software with complete linkage clustering method, cosine correlation distance measure, average value ordering weight, scale between 0 and 1 normalization and empty value replace by 0 for both (row and column) dendrogram. The high, average and low SVM predicted scores are marked in red, white and blue, respectively.

**Figure S2: A network of HBC-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HBC protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node, whereas other human proteins are representing by slate grey node.

**Figure S3: A network of HBP-human protein interactions predicted by our proposed method.** The network visualized by Cytoscape 3.0.2. The HBP protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node, whereas other human proteins are representing by slate grey node.

**Figure S4: A network of HEORF1 (Genotype 1)-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HEORF1 (Genotype 1) protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node whereas other human proteins are representing by slate grey node.

**Figure S5: A network of HEORF2 (Genotype 1)-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HEORF2 (Genotype 1) protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node whereas other human proteins are representing by slate grey node.

**Figure S6: A network of HEORF3 (Genotype 1)-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HEORF3 (Genotype 1) protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node whereas other human proteins are representing by slate grey node.

**Figure S7: A network of HEORF1 (Genotype 4)-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HEORF1 (Genotype 4) protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node whereas other human proteins are representing by slate grey node.

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**Figure S8: A network of HEORF2 (Genotype 4)-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HEORF2 (Genotype 4) protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node whereas other human proteins are representing by slate grey node.

**Figure S9: A network of HEORF2 (Genotype 4)-human protein interactions predicted by our proposed method**. The network visualized by Cytoscape 3.0.2. The HEORF2 (Genotype 4) protein is representing by cyan node. The significant gene ontology enriched human proteins are representing by salmon node whereas other human proteins are representing by slate grey node.

**Figure S10:** The ROC curves showing performance on balance and imbalance datasets of *E. coli*, using optimal subset of features (DDA, degree and AAC).

**Figure S11:** Frequency plot of *Salmonella* Typhi protein pairs predicted scores.

**Figure S12-15:** Frequency plot of *Vibrio cholerae* protein pairs predicted scores.

**Figure S16-21:** Frequency plot of *Shigella flexneri* protein pairs predicted scores.

**Figure S22:** Frequency plot of *Yersinia entrocolitica* protein pairs predicted scores.

**Figure S23:** Frequency plot of average GO semantic similarity of HPS and Random S. Typhi PPIs.

**Figure S24:** Venn-diagram of positive and negative sRNAs datasets (1 to 10). All sequences are unique.

**Figure S25:** Venn diagram of All reviewed and DisGeNET human proteins.

**Figure S26:** Venn diagram of positive curated and Befree text mining disease-associated proteins (DisGeNET confident score > greater than 0.002738764 ).

**Figure S27:** Venn diagram of highly predicted infectious disease-associated proteins and virus and bacteria targeted interaction of human proteins by PHISTO.

**Figure S28:** Venn diagram of disease ontology terms.

**Figure S29:** Venn diagram of bacterial and viral targeted human proteins GO terms.