

Figure S7.
A Functional Classification of H-Inv Protein Families That Have Homologs in Each Taxonomic Group

H-Inv protein families were identified by clustering H-Inv proteins using the single-linkage clustering method. Then, the number of homologs for each H-Inv protein family was calculated. Mammalian species are excluded from the “animal” group. “eukaryote” represents eukaryotic species other than animals, fungi, and plants.

Single-linkage clustering. All of the H-Inv proteins were compared with themselves by BLASTP and clustered with the thresholds of E-values of 10^{-30} and 10^{-50} . The numbers of singleton families detected were 11,890 and 13,938 at the E-value of 10^{-30} and 10^{-50} , respectively.

