Supporting Information

Liao et al. 10.1073/pnas.0910339107

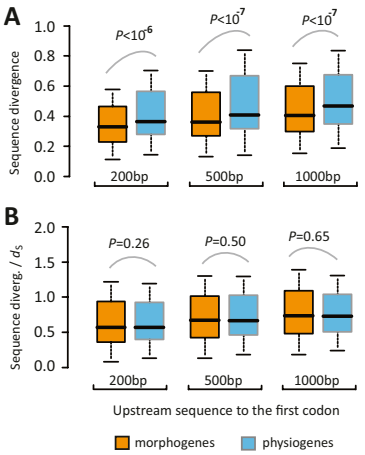

Fig. S1. Evolutionary divergences between mouse and human orthologous genes in noncoding regions upstream of the first codon. (*A*) Sequence divergence (1 – identity). (*B*) Sequence divergence, controlled for local mutation rates by d_S. The values of upper quartile, median, and lower quartile are indicated in each box, whereas the bars outside the box indicate semiquartile ranges. *P* values are from a Mann–Whitney *U* test.

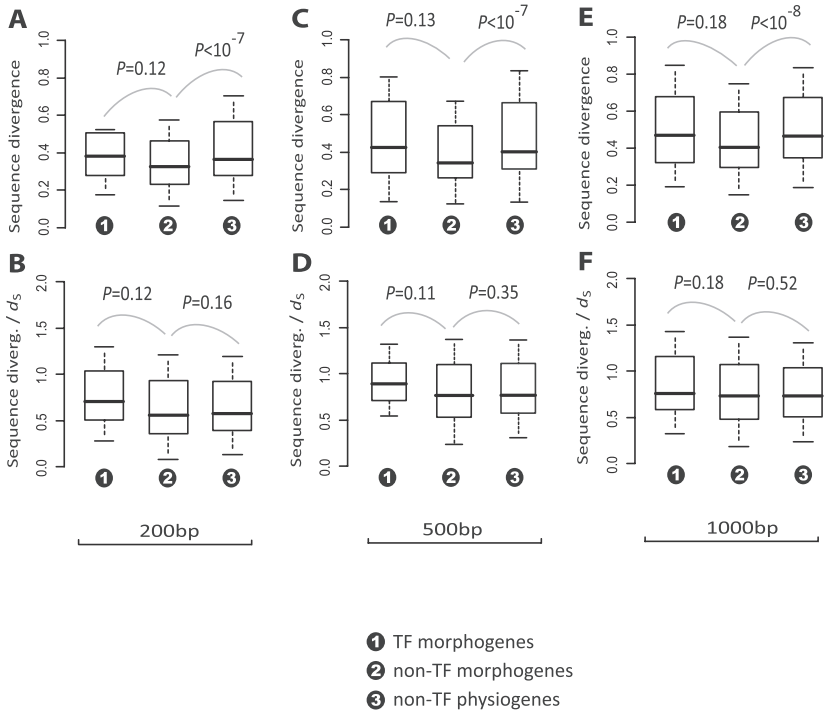

Fig. S2. Comparison of sequence divergences between mouse and human orthologous genes in noncoding regions upstream of the first codon among morphogenes encoding transcription factors (TFs), morphogenes encoding non-TFs, and physiogenes encoding non-TFs. Physiogenes encoding TFs are not examined due to the extremely small sample size. Sequence divergences within 200 bp, 500 bp, and 1000 bp are presented in *A*, *C*, and *E*, respectively, while the divergences controlled for local mutation rates are presented in *B*, *D*, and *F*, respectively. The values of upper quartile, median, and lower quartile are indicated in each box, whereas the bars outside the box indicate semiquartile ranges. *P* values are from a Mann–Whitney *U* test.

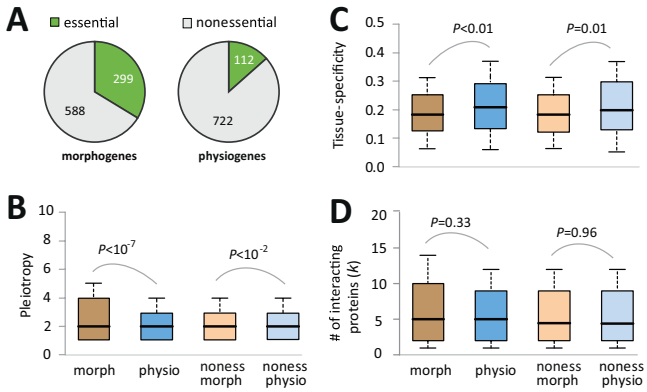

Fig. S3. Comparison of morphogenes and physiogenes in basic properties when 30% of traits are randomly removed. (*A*) Morphogenes are more likely to be essential than physiogenes ($P < E\text{-}22$, χ^2 test). (*B*) Morphogenes are more pleiotropic than physiogenes. (*C*) Morphogenes are less tissue specific than physiogenes. (*D*) Morphogenes and physiogenes have similar numbers of protein–protein interaction partners.

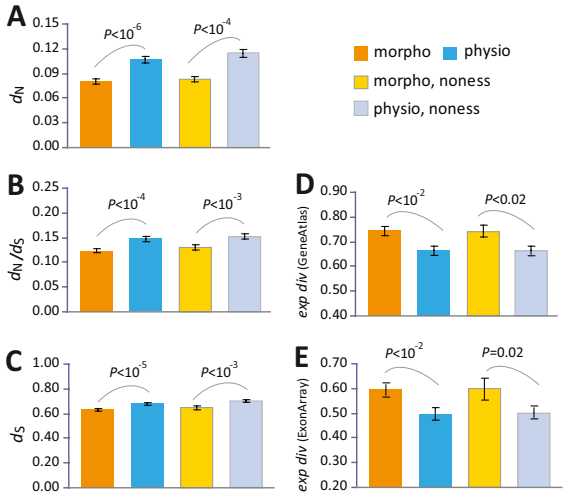

Fig. S4. Evolutionary divergences between mouse and human orthologous genes measured by (*A*) nonsynonymous distance (d_N), (*B*) d_N/d_s, (*C*) synonymous distance (d_s), (*D*) expression-profile distance from GeneAtlas data, and (*E*) expression-profile distance from ExonArrays data. Morphogenes and physiogenes are redefined after the random removal of 30% of traits associated with each gene. Error bars show one standard error of the mean. *P* values are from a Mann–Whitney *U* test. Morpho, morphogenes; noness, nonessential; physio, physiogenes.

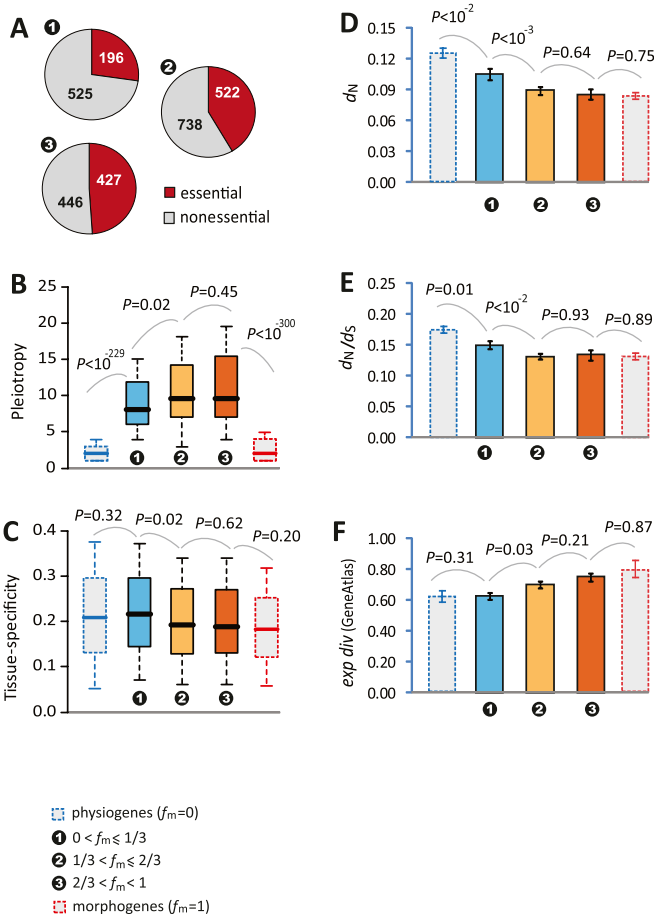

Fig. S5. Comparison among five groups of genes classified on the basis of the fraction (f_m) of mutant phenotypes that are morphological. (*A*) Numbers of essential and nonessential genes. (*B*) Degree of pleiotropy. (*C*) Tissue specificity in gene expression. (*D*) Nonsynonymous distances between human and mouse orthologs. (*E*) Ratio of nonsynonymous to synonymous distances. (*F*) Gene expression-profile divergences between human and mouse orthologs. Note that the higher pleiotropy of the three middle groups of genes than the two boundary groups in *B* is likely due to the ascertainment bias that the middle groups are examined for more traits per mutant mouse. *P* values are from a Mann-Whitney U test.

Other Supporting Information Files

Table S1 (DOC)
Table S2 (DOC)
Table S3 (DOC)
Table S4 (DOC)