Supporting Information

Liao and Zhang 10.1073/pnas.0800387105

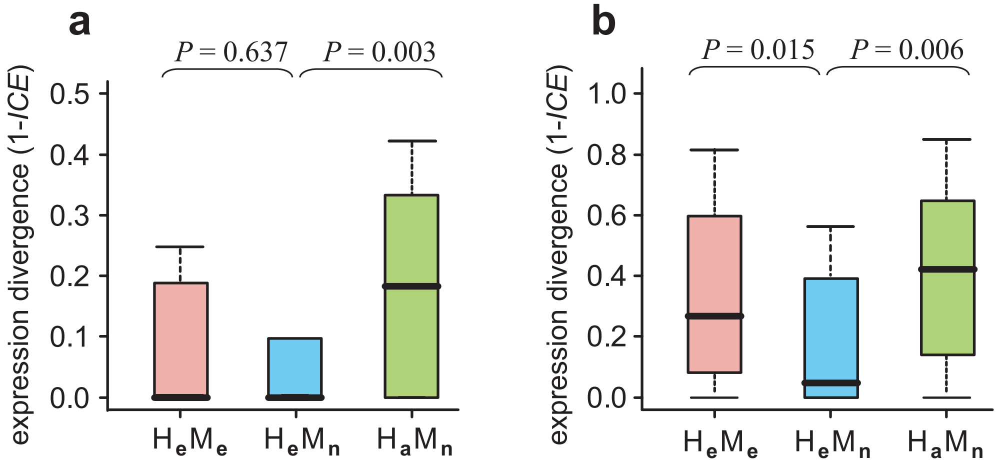

Fig. S1. Expression-profile divergence, measured by 1 − *ICE*, between human and mouse orthologous genes [ExonArray data (*a*) and GeneAtlas v2 data (*b*)]. *ICE* (index of coexpression) between two genes is defined as the number of tissues in which both genes are expressed divided by the geometric mean of the number of tissues where each gene is expressed (see *Methods*). Values of upper quartile, median, and lower quartile are indicated in each box. The bars indicate semiquartile ranges. H and M indicate human and mouse, respectively, and the subscripts e, n, and a indicate essential, nonessential, and any genes, respectively. The *P* values are determined by two-tailed Mann–Whitney *U* tests.

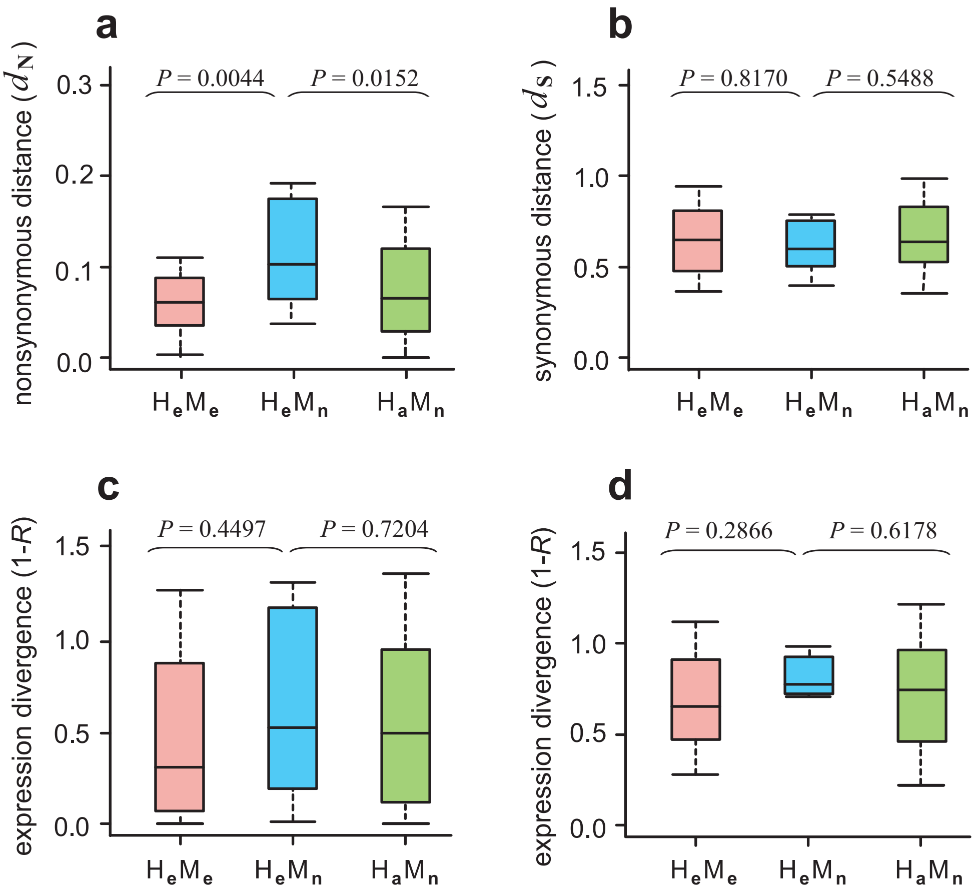

Fig. S2. The quartile plots of sequence divergence [*d*N (*a*) and *d*S (*b*)] and expression-profile divergence [ExonArray data (*c*) and GeneAtlas v2 data (*d*)] between human and mouse orthologous genes, after the removal of vacuole proteins. Values of upper quartile, median, and lower quartile are indicated in each box. The bars indicate semiquartile ranges. H and M indicate human and mouse, respectively, and the subscripts 1, 0, and a indicate essential, nonessential, and any genes, respectively. The *P* values are determined by Mann–Whitney *U* tests.

Table S1. Comparison between the mouse genes from the H_eM_n group and those from the H_eM_e group

Minimal protein sequence identity in defining paralogs	60%	70%	80%	Not required
Proportion of mouse genes that have paralogs (H_eM_n, H_eM_e; *P* value from Fisher's exact test*)	29.6% (8 of 27), 29.0% (27 of 93); *P* = 1.000	11.1% (3 of 27), 16.1% (15 of 93); *P* = 0.568	3.7% (1 of 27), 5.4% (5 of 93); *P* = 1.000	66.7% (18 of 27), 59.1% (55 of 93); *P* = 0.512
Average number of paralogs[†] (H_eM_n, H_eM_e; *P* value from the *U* test*)	2.13, 1.48; *P* = 0.787	2.66, 1.26; *P* = 0.097	1.00, 1.00; *P* = 1.000	4.33, 3.78; *P* = 0.415
Average protein sequence identity to the closest paralog[†] (H_eM_n, H_eM_e; *P* value from *U* test*)	66.8%, 72.9%; *P* = 0.098	73.7%, 78.2%; *P* = 0.190	80.0%, 85.4%; *P* = 0.333	56.2%, 58.3%; *P* = 0.568

*The null hypothesis is equal values between the H_eM_n and H_eM_e groups. Two-tailed tests were conducted.

[†] Only mouse genes that have paralog(s) are counted.

Table S2. Basal metabolic rates (*BMR*) and reproductive ages (*T*) of primates and several other mammals

Species name (common name)	Mean *BMR** (cal per gram of body mass per day)	Reproductive age $T^{\dagger}$ (year)	$BMR \times T$
Homo sapiens (human)	23.6	20.0[‡]	472.0
Pan troglodytes (chimpanzee)	27.9	13.5[§]	376.7
Gorilla gorilla (gorilla)	19.7	15.0[§]	295.5
Pongo pygmaeus (orangutan)	35.1	12.0[¶]	421.2
Papio anubis (olive baboon)	43.2	8.5[‖]	267.2
Macaca mulatta (Rhesus monkey)	37.0	4.5[§]	166.5
Chlorocebus aethiops (green monkey)	43.4	5.0[§]	216.5
Saguinus mystax (mustached tamarin)	88.4	1.5[§]	132.6
Otolemur crassicaudatus (greater galago)	68.4	2.0[§]	136.8
Eulemur fulvus (brown lemur)	57.6	1.5[§]	86.4
Tupaia glis (common tree shrew)	100.0	0.25[§]	25.0
Peromyscus maniculatus (deer mouse)	151.0	0.13[§]	19.6
Mus musculus (house mouse)	189.0	0.14[§]	26.5

$BMR \times T$ refers to the relative amount of metabolic waste generated per gram of body mass until reproduction.

[*] BMR of young adult males under resting/fasting condition [Tolmasoff *et al.* (1980) *Proc Natl Acad Sci USA* 77:2777–2781].

[†] Age at onset of male reproduction.

[‡] Fenner (2005) *Am J Phys Anthropol* 128:415–423.

[§] Animal Diversity Web (http://animaldiversity.ummz.umich.edu/).

[¶] Macdonald (2001) *The Encyclopedia of Mammals* (Andromeda Oxford, Abingdon, UK).

[‖] Strum and Western (1982) *Am J Primatol* 3:61–76.

Other Supporting Information Files

Dataset S1