Table S7

Materials and methods

Functional divergence and functional distance analyses

   Site-specific evolutionary rates after gene duplication (type I functional divergence)

may differ in the protein family, possibly due to altered functional constraints [1].

Maximum likelihood estimate for θ, the coefficient of type I functional divergence, was

measured with the program DIVERGE (version 2.0) [2]. A *de novo* neighbor-joining tree

was constructed with Poisson distance and re-rooted. Four clusters of the phylogenetic

tree, each corresponding to one of the four CatSper groups, were then selected for

likelihood ratio tests analysis.

   After the coefficient of type I functional divergence for each pair of clusters was

calculated, the functional branch length for each cluster, b_F, was estimated to indicate the

degree of altered functional constraints [2]. The value of b_F is related to the evolutionary

rates of duplicated genes compared with the ancestral gene. $b_F = 0$ suggests the site-

specific evolutionary rates of the duplicated gene nearly identical to those of the ancestral

gene.

Table S2. Functional divergence between CatSper protein subfamilies

*θ	CatS-2	CatS-3	CatS-4
CatS-1	0.525 ± 0.129	0.433 ± 0.116	0.483 ± 0.146
CatS-2	\	0.408 ± 0.076	0.536 ± 0.116
CatS-3	\	\	0.336 ± 0.092

*θ - Coefficients of type I functional divergence, all $p < 0.05$.

References:

[1]   X. Gu, Maximum-likelihood approach for gene family evolution under functional
       divergence, Mol. Biol. Evol. 18 (2001) 453-64.
[2]   X. Gu, K. Vander Velden, DIVERGE: phylogeny-based analysis for functional-
       structural divergence of a protein family, Bioinformatics 18 (2002) 500-1.