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# Corrigendum: Genome-wide adaptive complexes to underground stresses in blind mole rats *Spalax*

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In Fig. 2 of this Article, the CLOCK protein sequence of the blind mole rat (*Spalax*) was inadvertently used to represent that of the naked mole rat (*Heterocephalus glaber*) in both the sequence alignment (Fig. 2a) and the resulting phylogenetic tree (Fig. 2b). On the basis of this analysis, it was proposed that the expanded glutamine-rich region of these proteins arose by convergent evolution. However, an alignment and phylogenetic tree using the correct sequences (new Fig. 2a,b) does not support this conclusion. We thank Frédéric Delsuc for identifying this error, which does not affect the main findings of the paper.

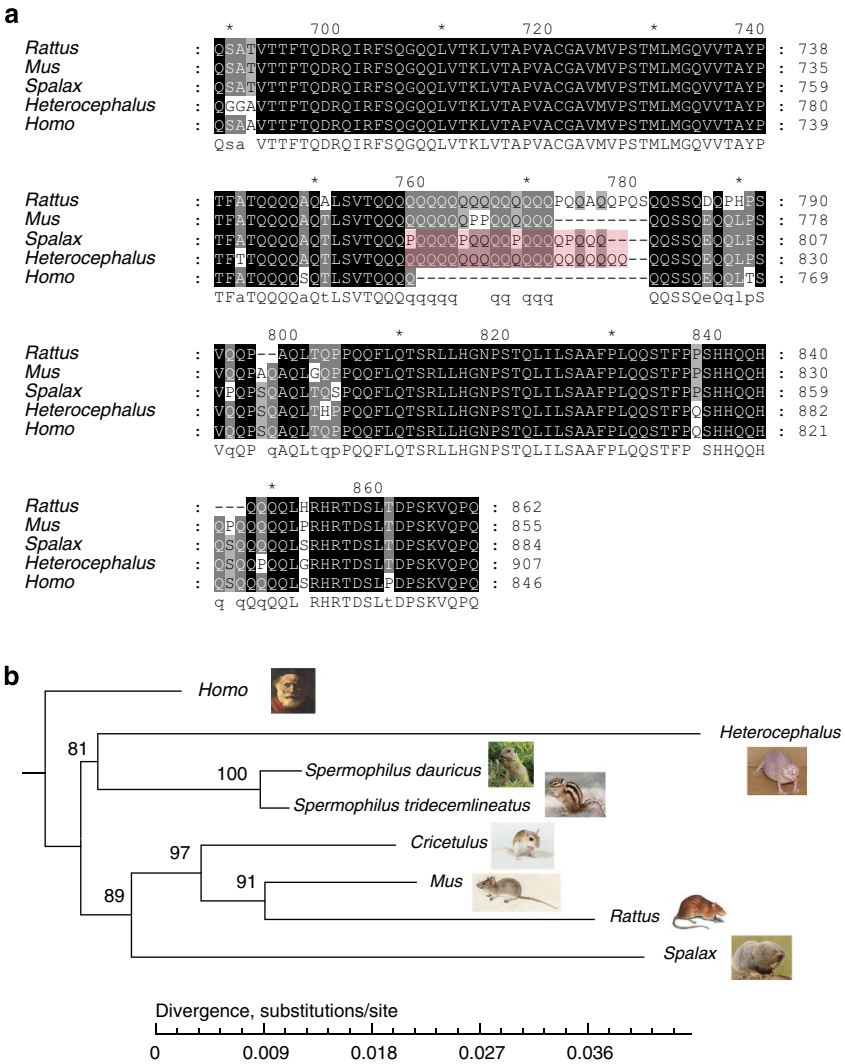


**Figure 2 | Evolution of BMR and NMR CLOCK proteins.** (**a**) The Q-rich domain of BMR (*Spalax*) CLOCK proteins compared with that of NMR (*Heterocephalus*), human (*Homo*), rat (*Rattus*) and mouse (*Mus*). Red box indicates the expanded glutamine-rich area in BMR with 4 P substitutions. (**b**) Phylogenetic tree of the CLOCK protein. The rooted tree describes the similarity relationships among the CLOCK proteins of BMR, NMR, mouse, rat, thirteen-lined ground squirrel (*Spermophilus tridecemlineatus*), Daurian ground squirrel (*S. dauricus*), Chinese hamster (*Cricetulus*) and human (*Homo*).