Appendix S1: supplementary information on the acquisition and compilation of species distribution data

The original dataset was made up of 288 mammals, 13 species were removed from the database because they were absent of the phylogeny of Fritz *et al.*, 2009: *Capra cylindricornis*, *Capra aegagrus*, *Microtus dogramacii*, *Microtus nasarovi*, *Miniopterus fuliginosus*, *Mus cyprianus*, *Myotis aurascens*, *Myotis alcathoe*, *Ovis orientalis* (which is a sub-species of *Ovis avies* present in the dataset), *Plecotus macrobullaris*, *Spermophilus taurensis*, *Plecotus sardus*.

For amphibians, two species were excluded from the original data: *Pelophylax grafi* and *Pelophylax hispanicus* as they are considered as hybrid species (respectively hybrids of *P. perezi x P. ridibundus* and *P. bergeri x P. ridibundus*).

For birds, the original data set was made up of 509 species, 429 species have been considered, the remaining species were absent of the phylogenetic trees and have been excluded from the analysis.

Then, the final dataset included information on the spatial distribution of 275 mammals, 429 birds and 102 amphibians following a 10' resolution grid for Europe. For 47 endangered breeding birds we obtained the EOOs from Birdlife (courtesy of Ian May and Mark Balman). We collected species habitat relationships from expert opinion (M. Capula for amphibians; A. Montemaggiori for breeding birds; G. Amori, D. Russo, and L. Boitani for mammals) and published literature (see Maiorano *et al.*, 2013 for the full list of references); species with no information on habitat preference or with a too small EOO ($< 12km^2$) were excluded from the analyses. The data collected was used to assign to each of the 46 GlobCover land-use/land-cover classes (300m resolution, GlobCover, 2008) a suitability score with 3 possible values: 0, for unsuitable land-use/land-cover classes; 1, for land-use/land-cover classes that represent a secondary habitat (medium suitability); 2, for land-use/land-cover classes that represent the primary habitat (high suitability). For most of the species we also recorded the maximum and the minimum elevation at which species can be found, and for some species we recorded the maximum distance to water at which they can be found. We combined the elevation range with distance to water and habitat suitability scores to refine the available EOOs. When no reliable information on the elevation range, distance to water and habitat preferences was available, the entire EOO was considered.

Reference:

Maiorano L., Amori G., Capula M., Falcucci A., Masi M., Montemaggiori A., Pottier J., Psomas A., Rondinini C., Russo D., Zimmermann N.E., Boitani L., & Guisan A. (2013) Threats from Climate Change to Terrestrial Vertebrate Hotspots in Europe. *PLoS ONE*, **8**, e74989.

Appendix S2: Amphibian phylogenetic data acquisition, phylogenetic tree calibration and accession number for sequence retrieved in GenBank.

Data acquisition for amphibians

For amphibians, we selected all phylogenetic informative regions for which sequences were available in GenBank for at least 30% of the species. We downloaded 9 mitochondrial (12S, 16S, COI, cytb, ND1, ND2, ND4, tRNA-Leu, tRNA-Val) and 2 nuclear (RAG-1, rho) regions (see accession numbers below, p15-19). We found relevant molecular data for all species, but we excluded the two hybrid species *Pelophylax grafi* and *Pelophylax hispanicus* (AmphibiaWeb, 2012, http://amphibiaweb.org/). We included the snake *Xenopeltis unicolor* as an outgroup to root the tree. For each region, alignment was conducted with four programs (Clustal, Larkin *et al.*, 2007; Kalign, Lassmann & Sonnhammer, 2005; MAFFT, Katoh *et al.*, 2005; MUSCLE, Edgar, 2004), the best resulting alignment was selected based on Mumsa (Lassmann & Sonnhammer, 2005), and checked visually. Ambiguous regions of each alignment were removed with trimAl (Capella-Gutiérrez *et al.*, 2009). Phylogenetic analyses were conducted using a mixed supertree-supermatrix approach (Roquet *et al.*, 2013) by means of maximum-likelihood (ML) inference with RAxML (Stamatakis, 2006), constrained with a family-level tree extracted from Roelants *et al.*, 2007. Standard bootstrapping was conducted with 1000 replicates to assess clade support. We conducted 100 differents searches, but given that the topologies of the 100 trees were very similar and that the phylogenetic diversity matrices from all trees were highly correlated (Mantel test > 0.99), we finally run the following analysis with only the best tree (i.e. the one with the highest likelihood), which has been incorporated to TreeBASE (accession number: S13561).

Calibration of the amphibian phylogenetic tree

The best ML tree was dated with penalized-likelihood as implemented in r8s (Sanderson, 2003), using the following fossil data to constrain minimum ages for selected nodes: 155 mya for the crown-origin of salamanders (Evans *et al.*, 2005), 170 mya for Bombianura (Evans *et al.*, 1990), 250 mya for Batrachia (Rage & Roček, 1989), 110 mya for the split of Pelobatidae and Pelodytidae families (Evans & Milner, 1993), 145 mya for the split of Pelobatidae and Neobatrachia (Evans & Milner, 1993), and 61 mya for the split of Plethodidae and Proteidae (Gardner, 2003). Additionally, we set a minimum and maximum age (312-330 mya) for the split between diaspid (*Gallus gallus*, *Xenopeltis unicolor*) and synapsid amniotes (*Mus musculus)*, used here as outgroups, based on

Benton & Donoghue, 2007. The best smoothing value (here, 32) was determined by a cross-validation procedure, as indicated in Sanderson, 2003.

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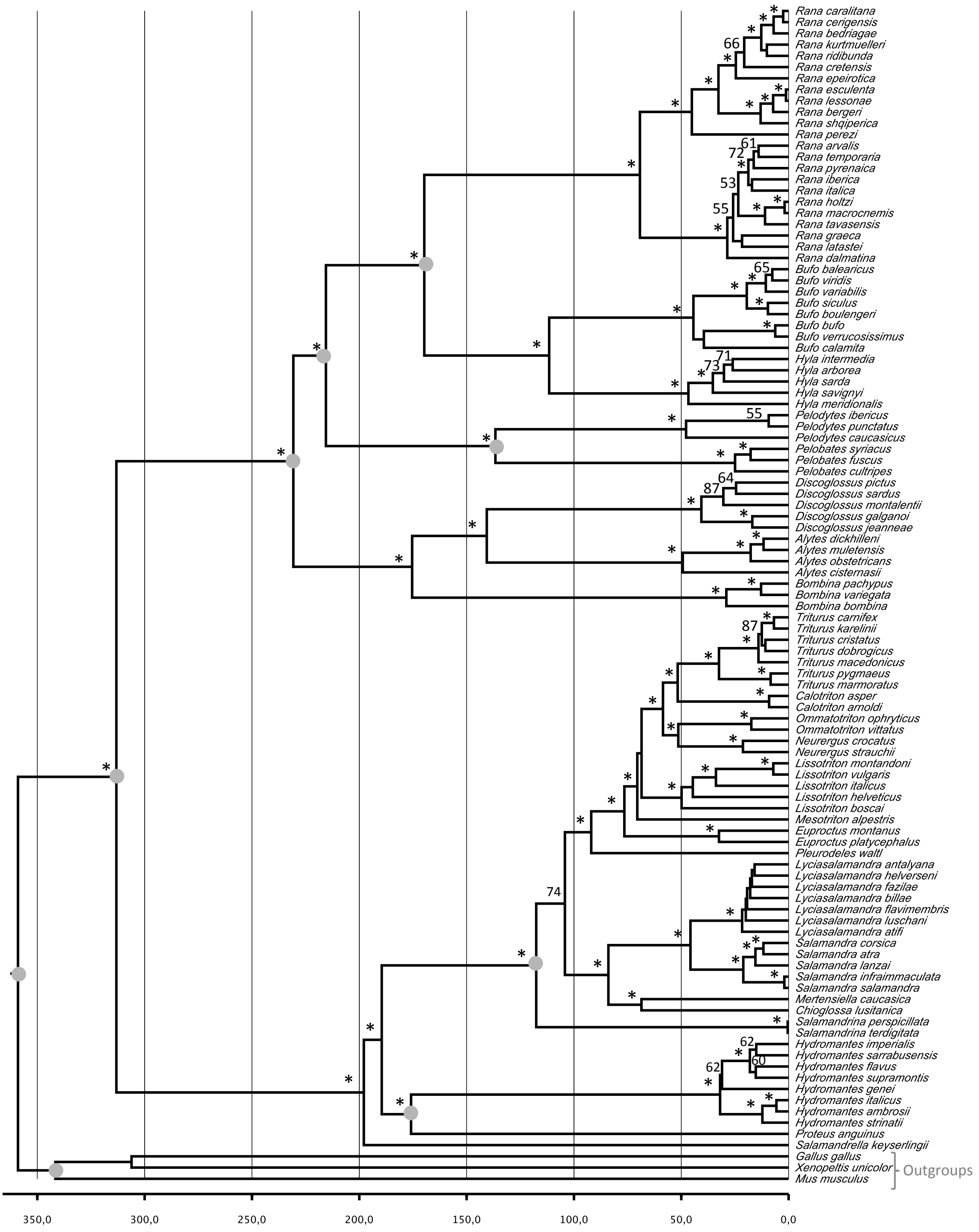
Figure S1 Maximum-likelihood tree with highest likelihood for the European amphibians. Clades with bootstrap support values (BS) ranging from 90 to 100% are indicated with the symbol *. Numbers above branches indicate BS ranging from 50 to 89%. BS values below 50% are not reported. Grey circles indicate nodes where an age constraint was applied based on fossil data.



Accession numbers for sequences retrieved from GenBank to infer a phylogenetic tree for European amphibian species. Species are ordered by alphabetical order.

Alytes cisternasii: GU086775 (12S), GU086783 (16S), AY442019 (cytb), GU086861 (ND4); *Alytes dickhilleni:* AY333672 (12S), AY333710 (16S), AY442020 (cytb), EF441309 (ND4), DQ019494 (RAG1), AY341817 (Rho); *Alytes muletensis*: AY341621 (12S), AY341680, AY333709 (16S), AY341728 (cytb), EF441310 (ND4), AY323755 (RAG1), AY323731 (Rho); *Alytes obstetricans*: AY585337 (12S), AY585337 (16S), AY585337 (COI), AY585337 (cytb), AY523757 (ND1), AY585337 (ND2), EF441308 (ND4), AY583334 (RAG1), DQ283825 (Rho), AY585337 (tRNA-Leu), DQ283112 (tRNA-Val); *Bombina bombina*: AY458591 (12S), EU115993 (16S), EU531208 (COI), DQ146949 (cytb), NC_006402 (ND1), NC_006402 (ND2), DQ138574 (ND4), DQ283920 (Rho), NC_006402 (tRNA-Leu), EU531340 (tRNA-Val); *Bombina pachypus*: EU531353 (12S), AY500228 (16S), EU531204 (COI), EU531283 (cytb), EU531378 (Rho), EU531353 (tRNA-Val); *Bombina variegata*: AJ440764 (12S), AY971143 (16S), NC_009258 (COI), EF212809 (cytb), AY523758 (ND1), NC_009258 (ND2), DQ138530 (ND4), AY523750 (RAG1), DQ283919 (Rho), NC_009258 (tRNA-Leu), DQ283249 (tRNA-Val); *Bufo balearicus*: EU497437 (16S), DQ629598 (ND1), DQ629598 (ND2), EU497608 (RAG1); *Bufo boulengeri*: EU497487 (16S), DQ629602 (ND1), DQ629602 (ND2), EU497607 (RAG1); *Bufo bufo*: AY325988 (12S), FJ882806 (16S), AB159262 (cytb), DQ629612 (ND1), DQ629612 (ND2), AY583336 (RAG1), BBU59921 (Rho), FJ882806 (tRNA-Leu), FJ882806 (tRNA-Val); *Bufo calamita*: BCU52726 (12S), BCU52759 (16S), L10963 (cytb), DQ629607 (ND1), DQ629607 (ND2), EU497610 (RAG1), EU938400 (tRNA-Val); *Bufo siculus*: EU497456 (16S), DQ629608 (ND1), DQ629608 (ND2), EU497609 (RAG1); *Bufo variabilis*: GQ489062 (12S), DQ629600 (ND1), DQ629600 (ND2); *Bufo verrucosissimus*: FJ882807 (12S), FJ882807 (16S), FJ882807 (ND1), FJ882807 (ND2), FJ882807 (tRNA-Leu), FJ882807 (tRNA-Val); *Bufo viridis*: BVU52727 (12S), AY680267 (16S), AB159263 (cytb), FJ882813 (ND1), DQ629606 (ND2), EU497603 (RAG1), DQ283940 (Rho), FJ882813 (tRNA-Leu), FJ882813 (tRNA-Val); *Calotriton arnoldi*: DQ092300 (12S), DQ092282 (16S), DQ092240 (cytb); *Calotriton asper*: EU880307 (12S), EU880307 (16S), EU880307 (COI), DQ821198 (cytb), DQ517766 (ND1), GU982452 (ND2), AM900489 (ND4), AY583348 (RAG1), DQ517766 (tRNA-Leu); *Chioglossa lusitanica*: EU880308 (12S), EU880308 (16S), NC_002333 (COI), DQ821196 (cytb), DQ517767 (ND1), EU880308 (ND2), EU880308 (ND4), AY583347 (RAG1), DQ517767 (tRNA-Leu), EU880308 (tRNA-Val); *Discoglossus galganoi*: AY585339 (12S), AY585339 (16S), NC_006690 (COI), NC_006690 (cytb), NC_006690 (ND1), NC_006690 (ND2), AY442114 (ND4), AY583338 (RAG1), DQ283915 (Rho), NC_006690 (tRNA-Leu), DQ283243 (tRNA-Val); *Discoglossus jeanneae*: AY347445 (12S), AY442036 (16S), DQ902149 (cytb), DQ902267 (ND2), AY442135 (ND4); *Discoglossus montalentii*: AY347465 (12S), DQ642116 (16S), AY347432 (cytb); *Discoglossus pictus*: AY347473 (12S), AY523761 (16S), GU799101 (cytb), AY523761 (ND1), AY442137 (ND4), AY364202 (RAG1), AY364387 (Rho), AY364342 (tRNA-Val); *Discoglossus sardus*: AY347466 (12S), AY333713 (16S), EU744911 (cytb), AY323757 (RAG1), AY323733 (Rho); *Euproctus montanus*: EU880316 (12S), EU880316 (16S), DQ821199 (cytb), DQ517776 (ND1), DQ517776 (ND2), EU880316 (ND4), DQ517776 (tRNA-Leu); *Euproctus platycephalus*: EU880317 (12S), EU880317 (16S), COI AP003580 (COI), DQ821201 (cytb), DQ517777 (ND1), DQ517777 (ND2), EU880317 (ND4); *Hydromantes ambrosii*: EU116985 (12S), EU116987 (16S), FJ602259 (cytb), FJ602322 (RAG1); *Hydromantes flavus*: FJ602090 (12S), EU116996 (16S), FJ602265 (cytb), FJ602327 (RAG1); *Hydromantes genei*: FJ602109 (12S), FJ602164 (16S), FJ602275 (cytb), FJ602343 (RAG1); *Hydromantes imperialis*: FJ602129 (12S), EU116993 (16S), FJ602297 (cytb), FJ602361 (RAG1); *Hydromantes italicus*: AY728215 (12S), AY728215 (16S), AY728215 (COI), FJ602304 (cytb), AY728215 (ND1), AY728215 (ND2), AY728215 (ND4), EU275792 (RAG1), AY728215 (tRNA-Leu), AY728215 (tRNA-Val); *Hydromantes sarrabusensis*: FJ602126 (12S), FJ602294 (cytb), FJ602359 (RAG1); *Hydromantes strinatii*: EU116972 (12S), EU116990 (16S), FJ602309 (cytb), FJ602369 (RAG1); *Hydromantes supramontis*: FJ602141 (12S), EU116998 (16S), FJ602318 (cytb), FJ602377 (RAG1); *Hyla arborea*: DQ055835 (12S), AY843601 (16S), FJ226837 (COI), FJ226920 (cytb), DQ055814 (ND1), FJ227066 (RAG1), AY844575 (Rho), AY843601 (tRNA-Val); *Hyla intermedia*: (16S), FJ226838 (COI), JF318125 (cytb), FJ227096 (RAG1); *Hyla meridionalis*: AY819370 (12S), GQ916810 (16S), FJ226807 (COI), FJ226897 (cytb), DQ902200 (ND1), DQ902278 (ND2), AY583339 (RAG1), GQ916820 (Rho), AY523763 (tRNA-Leu), EF566953 (tRNA-Val); *Hyla sarda*: (16S), FJ226843 (COI), FJ226927 (cytb), FJ227092 (RAG1); *Hyla savignyi*: DQ055843 (12S), AY843665 (16S), FJ226849 (COI), FJ226934 (cytb), DQ055829 (ND1), FJ227059 (RAG1), GQ916813 (Rho), DQ055829 (tRNA-Leu), AY843665 (tRNA-Val); *Gallus gallus*: AP003580 (12S), AP003580 (16S), AP003580 (COI), AP003580 (cytb), AP003580 (ND1), AP003580 (ND2), AP003580 (ND4), NM_001031188 (RAG1), NM_205490 (Rho), AP003580 (tRNA-Leu), AP003580 (tRNA-Val); *Lissotriton boscai*: DQ092287 (12S), DQ092268 (16S), EF525956 (COI), DQ821219 (cytb), DQ517831 (ND1), DQ517831 (ND2), DQ491754 (ND4), DQ517831 (tRNA-Leu); *Lissotriton helveticus*: DQ092286 (12S), DQ092267 (16S), EF525990 (COI), DQ821239 (cytb), AY951504 (ND2), AY951649 (ND4); *Lissotriton italicus*: DQ092288 (12S), DQ092269 (16S), DQ821243 (cytb), AY951502 (ND2), AY951653 (ND4); *Lissotriton montandoni*: (16S), EF526011 (COI), DQ821259 (cytb), DQ517842 (ND1), DQ517842 (ND2), AY951606 (ND4), DQ517842 (tRNA-Leu); *Lissotriton vulgaris*: EU880339 (12S),

AY147255 (16S), EF526059 (COI), DQ821272 (cytb), DQ517847 (ND1), FJ588972 (ND2), AY951596 (ND4), DQ517847 (tRNA-Leu); *Lyciasalamandra antalyana*: EU430956 (16S), DQ517778 (ND1), DQ517778 (ND2), DQ517778 (tRNA-Leu); *Lyciasalamandra atifi*: AF154053 (12S), AF154053 (16S), AF154053 (COI), AF154053 (cytb), DQ517779 (ND1), DQ517779 (ND2), NC_002756 - ND4 gene (ND4), AY456261 (RAG1), DQ517779 (tRNA-Leu); *Lyciasalamandra billae*: EU430969 (16S), DQ517781 (ND1), DQ517781 (ND2), DQ517781 (tRNA-Leu); *Lyciasalamandra fazilae*: EU430976 (16S), DQ473604 (cytb), DQ517782 (ND1), DQ517782 (ND2), DQ517782 (tRNA-Leu); *Lyciasalamandra flavimembris*: EU880318 (12S), EU880318 (16S), EU880318 (COI), EU880318 (cytb), EU880318 (ND1), EU880318 (ND2), EU880318 (ND4), EU880318 (tRNA-Leu), EU880318 (tRNA-Val); *Lyciasalamandra helverseni*: EU880319 (12S), EU430970 (16S), DQ473603 (cytb), DQ517785 (ND1), DQ517785 (ND2), DQ517785 (tRNA-Leu); *Lyciasalamandra luschani*: EU880335 (12S), EU430978 (16S), AY196286 (cytb), DQ517783 (ND1), DQ517783 (ND2), AY323753 (RAG1), DQ517783 (tRNA-Leu); *Mertensiella caucasica*: EF029949 (12S), EU880319 (16S), EU880319 (COI), EU880319 (cytb), EU880319 (ND1), EU880319 (ND2), EU880319 (ND4), EU880319 (tRNA-Leu), EU880319 (tRNA-Val); *Mesotriton alpestris*: EU880321 (12S), EU880335 (16S), EU880335 (COI), EU880335 (cytb), EU880335 (ND1), EU880335 (ND2), EU880335 (ND4), EU880335 (tRNA-Leu), EU880335 (tRNA-Val); *Mus musculus*: FJ374651 (12S), FJ374651 (16S), FJ374651 (COI), FJ374651 (cytb), FJ374651 (ND1), FJ374651 (ND2), FJ374651 (ND4), MUSRAG1A (RAG1), BC013125 (Rho), FJ374651 (tRNA-Leu), FJ374651 (tRNA-Val); *Neurergus crocatus*: EU880338 (12S), EU430953 (16S), AY336661 (cytb), DQ517788 (ND1), DQ517788 (ND2), DQ517788 (tRNA-Leu); *Neurergus strauchii*: NC_008144 (12S), EU880321 (16S), EU880321 (COI), EU880321 (cytb), EU880321 (ND1), EU880321 (ND2), EU880321 (ND4), EU880321 (tRNA-Leu), EU880321 (tRNA-Val); *Ommatotriton ophryticus*: EU483499 (16S), EF526035 (COI), DQ821267 (cytb), DQ517844 (ND1), DQ517844 (ND2), DQ517844 (tRNA-Leu); *Ommatotriton vittatus*: AJ440773 (12S), EU880338 (16S), EU880338 (COI), EU880338 (cytb), EU880338 (ND1), EU880338 (ND2), EU880338 (ND4), EU880338 (tRNA-Leu), EU880338 (tRNA-Val); *Pelobates cultripes*: DQ642131 (12S), NC_008144 (16S), AJ871086 (COI), DQ333373 (cytb), AY523760 (ND1), NC_008144 (ND2), NC_008144 (ND4), AY323758 (RAG1), AY364386 (Rho), AY523760 (tRNA-Leu), AY364341 (tRNA-Val); *Pelobates fuscus*: AJ440771 (12S), DQ283113 (16S), EF133852 (cytb), DQ283826 (Rho), DQ283113 (tRNA-Val); *Pelobates syriacus*: DQ642137 (12S), DQ642108 (16S), DQ333372 (cytb); *Pelodytes caucasicus*: AB530454 (12S), AY236811 (16S), AY236777 (cytb); *Pelodytes ibericus*: EU880330 (12S), AY236813 (16S), AY236779 (cytb); *Pelodytes punctatus*: GQ368659 (12S), AB530454 (16S), AY236783 (cytb), AY523762 (ND1), DQ283824 (Rho), AY523762 (tRNA-Leu), DQ283111 (tRNA-Val);

Pleurodeles waltl: AB058865 (12S), EU880330 (16S), EU880330 (COI), EU880330 (cytb), EU880330 (ND1), EU880330 (ND2), EU880330 (ND4), AY523736 (RAG1), EU880330 (tRNA-Leu), EU880330 (tRNA-Val); *Proteus anguinus*: AJ318086 (12S), GQ368659 (16S), GQ368659 (cytb), GQ368659 (ND1), GQ368659 (ND2), GQ368659 (ND4), AY650138 (RAG1), GQ368659 (tRNA-Leu), GQ368659 (tRNA-Val); *Rana arvalis*: AJ222712 (12S), AY147938 (16S), AY522426 (cytb), AY147989 (Rho); *Rana bedriagae*: AJ318087 (12S), AY147937 (16S), DQ474141 (cytb), EU835642 (ND1), GU812077 (ND2), AY148008 (Rho); *Rana bergeri*: AY043038 (12S), EU835640 (ND1), GU812135 (ND2); *Rana caralitana*: (16S), EU835650 (ND1); *Rana cerigensis*: AY147979 (16S), DQ474144 (cytb), EU835643 (ND1), AY148009 (Rho); *Rana cretensis*: AJ002595 (12S), AY147980 (16S), DQ474152 (cytb), EU835581 (ND1), GU812138 (ND2), AY148010 (Rho); *Rana dalmatina*: AB023396 (12S), AY147941 (16S), AY147962 (cytb), AY147992 (Rho); *Rana epeirotica*: AY043040 (12S), AY147981 (16S), DQ474155 (cytb), EU835649 (ND1), GU812141 (ND2), AY148011 (Rho); *Rana esculenta*: AY043047 (12S), AB029944 (cytb), AM887973 (ND2); *Rana graeca*: AY043043 (12S), AY147942 (16S), AY147963 (cytb), AY147993 (Rho); *Rana holtzi*: AY043044 (12S), AY147943 (16S), AY147964 (cytb), AY147994 (Rho); *Rana iberica*: AJ222654 (12S), AY147944 (16S), AY147965 (cytb), AY147995 (Rho); *Rana italica*: AY043039 (12S), AY147945 (16S), EU595505 (cytb), AY147996 (Rho); *Rana kurtmuelleri*: AY322321 (12S), DQ474227 (16S), DQ474176 (cytb); *Rana latastei*: AY043046 (12S), AY147946 (16S), AY147967 (cytb), AY147997 (Rho); *Rana lessonae*: AF161041 (12S), AY147982 (16S), EU047797 (cytb), EU835584 (ND1), AM887976 (ND2), AY148012 (Rho), AY322321 (tRNA-Val); *Rana macrocnemis*: EU746401 (12S), AY147947 (16S), AF373160 (cytb), AY607311 (ND1), AY607311 (ND2), AY147998 (Rho); *Rana perezi*: AB023397 (12S), AY147985 (16S), DQ902145 (cytb), DQ902201 (ND1), GU812144 (ND2), AY148015 (Rho); *Rana pyrenaica*: AJ222651 (12S), AY147950 (16S), EU746402 (COI), AY147971 (cytb), AY148001 (Rho); *Rana ridibunda*: AY326063 (12S), AY147983 (16S), AB029945 (cytb), EU835652 (ND1), AM900638 (ND2), AY148013 (Rho); *Rana shqiperica*: AY928616 (12S), EU835582 (ND1), GU812149 (ND2); *Rana tavasensis*: AY147949 (16S), AY147970 (cytb), AY148000 (Rho); *Rana temporaria*: AY928618 (12S), AY326063 (16S), FN813812 (COI), AY522428 (cytb), AF314018 (ND1), AF314018 (ND2), AY323776 (RAG1), RTU59920 (Rho), AY326063 (tRNA-Val); *Salamandra atra*: DQ221222 (12S), AY042786 (cytb), DQ517816 (ND1), DQ517816 (ND2), DQ517816 (tRNA-Leu); *Salamandra corsica*: AY928617 (12S), AY928614 (cytb), DQ517818 (ND1), DQ517818 (ND2), DQ517818 (tRNA-Leu); *Salamandra infraimmaculata*: EU880331 (12S), EU430954 (16S), DQ221242 (cytb), DQ517822 (ND1), DQ517822 (ND2), DQ517822 (tRNA-Leu); *Salamandra lanzai*: DQ333814 (12S), EF191040 (16S), AF356699 (cytb), DQ517820 (ND1), DQ517820 (ND2), DQ517820 (tRNA-Leu);

Salamandra salamandra: AY928620 (12S), EU880331 (16S), EU880331 (COI), EU880331 (cytb), EU880331 (ND1), EU880331 (ND2), EU880331 (ND4), AY650135 (RAG1), DQ284037 (Rho), EU880331 (tRNA-Leu), EU880331 (tRNA-Val); *Salamandrella keyserlingii*: EU880332 (12S), DQ333814 (16S), DQ333814 (COI), DQ333814 (cytb), AY593155 (ND1), AY916031 (ND2), DQ333814 (ND4), AY650145 (RAG1), DQ333814 (tRNA-Leu), DQ333814 (tRNA-Val); *Salamandrina perspicillata*: HQ697272 (12S), DQ821208 (cytb), EU880332 (ND4); *Salamandrina terdigitata*: EU880336 (12S), EU880332 (16S), EU880332 (COI), EU880332 (cytb), DQ517823 (ND1), DQ517823 (ND2), DQ517823 (tRNA-Leu), EU880332 (tRNA-Val); *Triturus carnifex*: HQ697277 (12S), HQ697272 (16S), EF525960 (COI), DQ821225 (cytb), DQ517832 (ND1), DQ517832 (ND2), GU982386 (ND4), DQ517832 (tRNA-Leu); *Triturus cristatus*: EU880337 (12S), EU880336 (16S), EU880336 (COI), EU880336 (cytb), DQ517834 (ND1), DQ517834 (ND2), EU880336 (ND4), DQ284038 (Rho), DQ517834 (tRNA-Leu), EU880336 (tRNA-Val); *Triturus dobrogicus*: NC_015791 (12S), HQ697274 (16S), EF525985 (COI), DQ821237 (cytb), DQ517836 (ND1), DQ517836 (ND2), GU982390 (ND4), DQ517836 (tRNA-Leu); *Triturus karelinii*: HQ697277 (16S), EF526007 (COI), DQ821250 (cytb), DQ517837 (ND1), DQ517837 (ND2), GU982451 (ND4), DQ517837 (tRNA-Leu); *Triturus macedonicus*: NC_015794 (12S), HQ697278 (16S), DQ821229 (cytb), DQ517833 (ND1), GQ258962 (ND2), GU982388 (ND4), DQ517833 (tRNA-Leu); *Triturus marmoratus*: EU880337 (16S), EU880337 (COI), EU880337 (cytb), DQ517839 (ND1), DQ517839 (ND2), EU880337 (ND4), AY583354 (RAG1), DQ517839 (tRNA-Leu), EU880337 (tRNA-Val); *Triturus pygmaeus*: HQ697280 (16S), EF526024 (COI), DQ821261 (cytb), DQ517843 (ND1), DQ517843 (ND2), GU982382 (ND4), DQ517843 (tRNA-Leu); *Xenopeltis unicolor*: AB179620 (12S), AB179620 (COI), AB179620 (cytb), AB179620 (ND1), AB179620 (ND2), AB179620 (ND4), EU402870 (RAG1), FJ497233 (Rho), AB179620 (tRNA-Leu), AB179620 (tRNA-Val);

Appendix S3. Parameter estimates for the quadratic (Tab. S1) and the linear (Tab. S2) relationship between SD and QE_{PD} for the three taxonomic groups.

Table S1: Parameter estimates for the quadratic relationship between the species diversity (SD) and the phylogenetic diversity (QE_{PD}) for a) Mammals, b) birds and c) amphibians. Estimates were calculated with a trend surface analysis, i.e. using a generalized additive model with latitude and longitude of each grid cell used as a smooth factor to account for large-scale autocorrelation structure.

a)

	QE_{PD}*: $R^2 = 0.93$		
	Estimate ± s.e.	*t*	*p*
Intercept	1.91 ± 9.54E-03	200.0	< 0.001
SD	1.76E-01 ± 5.93E-04	297.1	< 0.001
SD^2	-2.05E-03 ± 9.32E-06	-219.9	< 0.001

*Smooth term QE_{PD}: estimated degrees of freedom = 48.89, $F = 1149$, $p < 0.001$

b)

	QE_{PD}*: $R^2 = 0.59$		
	Estimate ± s.e.	*t*	*p*
Intercept	3.43 ± 1.45E-02	235.75	< 0.001
SD	9.85E-03 ± 3.80E-04	25.94	< 0.001
SD^2	-2.41-05 ± 2.4E-06	-10.02	< 0.001

*Smooth term QE_{PD}: estimated degrees of freedom = 48.95, $F = 1469$, $p < 0.001$

c)

	QE_{PD}*: $R^2 = 0.83$		
	Estimate ± s.e.	*t*	*p*
Intercep	1.08 ± 6.00E-03	178.9	< 0.001
SD	0.24 ± 2.00E-03	129.2	< 0.001
SD^2	-0.009 ± 1.25E-04	-70.3	< 0.001

*Smooth term QE_{PD}: estimated degrees of freedom = 48.99, $F = 1501$, $p < 0.001$

Table S2: Parameter estimates for the linear relationship between the species diversity (SD) and the phylogenetic diversity (QE_{PD}) for a) Mammals, b) birds and c) amphibians.

a)

	QE_{PD}*: $R^2 = 0.87$		
	Estimate ± s.e.	*t*	*p*
Intercept	3.27 ± 9.63E-03	340.3	< 0.001
SD	5.52E-02 ± 2.96E-04	186.4	< 0.001

b)

	QE_{PD}*: $R^2 = 0.59$		
	Estimate ± s.e.	*t*	*p*
Intercept	3.54 ± 9.58E-03	369.8	< 0.001
SD	6.21E-03 ± 1.13E-04	54.86	< 0.001

c)

	QE_{PD}*: $R^2 = 0.82$		
	Estimate ± s.e.	*t*	*p*
Intercept	1.41 ± 3.8E-03	364.9	< 0.001
SD	1.18E-02 ± 6.53E-04	180.7	< 0.001

Appendix S4. Relationships between QE_{PD} and SD for the three taxonomic groups (Fig. S2). Co-variation of SD (Fig. S3), QE_{PD} (Fig. S4) and QE_{RES} (Fig. S5) among taxonomic groups.

Figure S2: Relationship between phylogenetic diversity (QE_{PD}) and species diversity (SD) for the 3 groups of vertebrate.

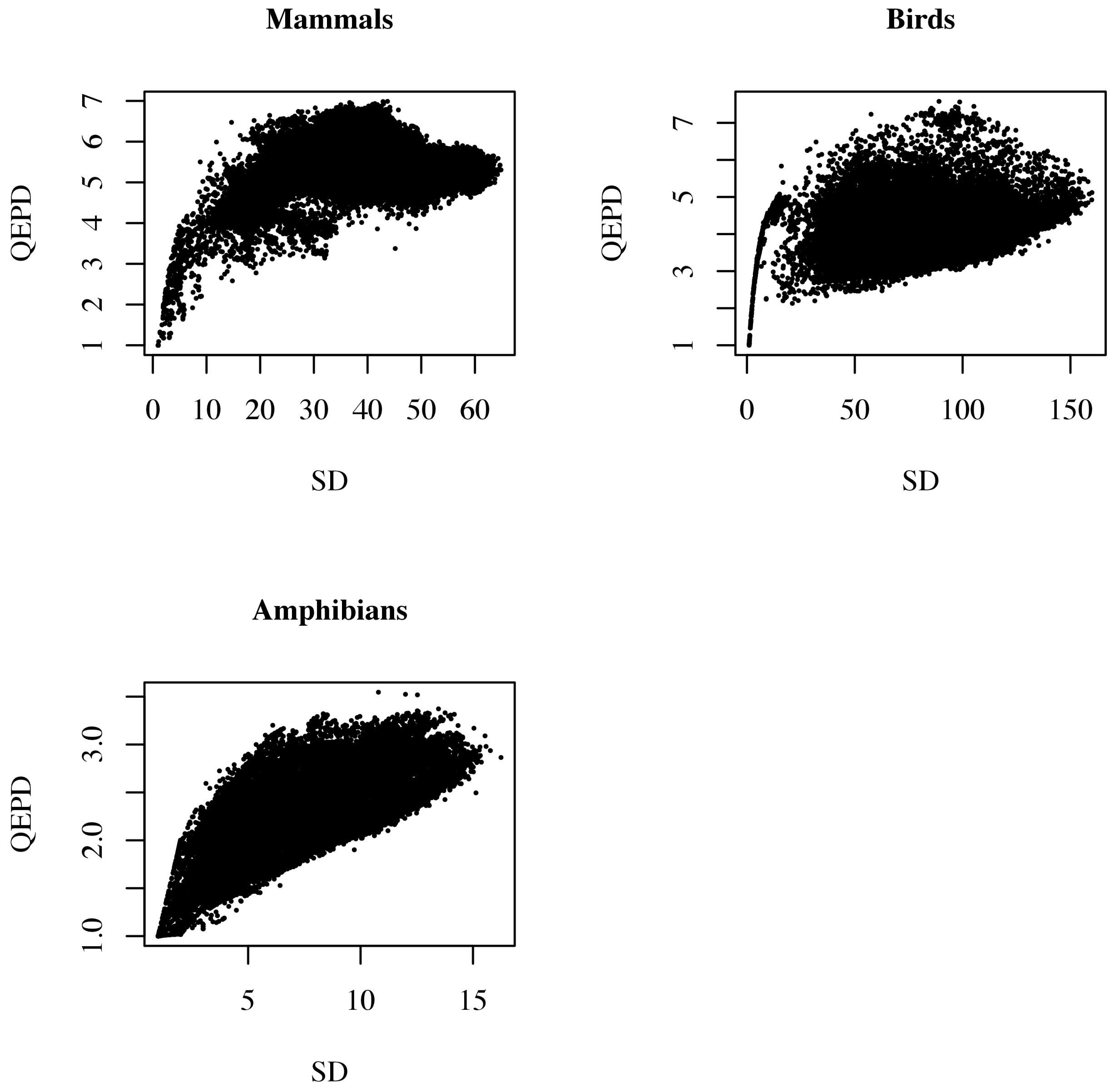


Figure S3: Co-variation of the species diversity (SD) among mammals, birds and amphibians (upper right panels) and their associated correlation factors estimated with the Pearson's product moment (lower left panels). The diagonal panels show the distribution of SD values for each group of species.

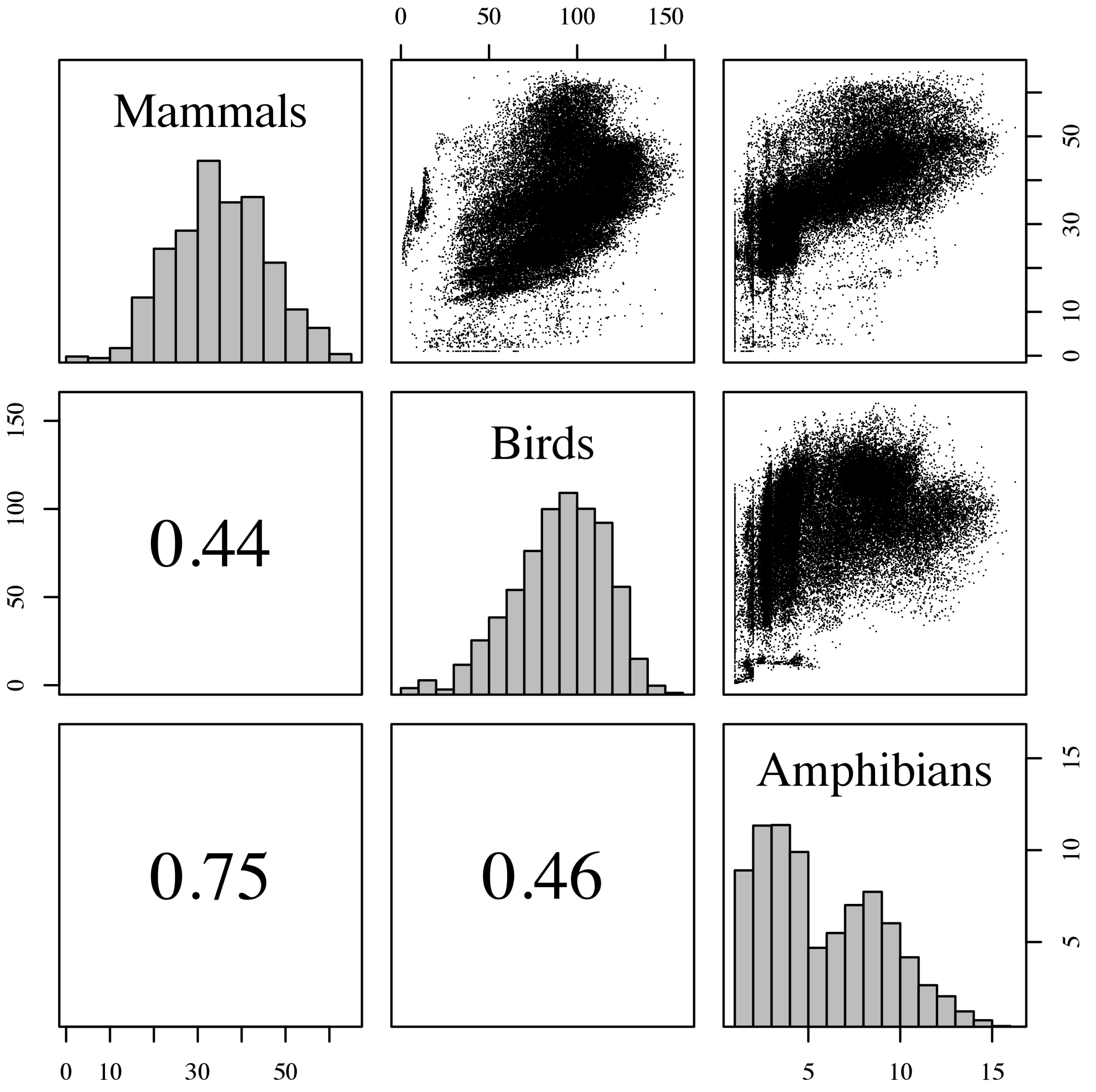


Figure S4: Co-variation of phylogenetic diversity (QE_{PD}) among mammals, birds and amphibians (upper right panels) and their associated correlation factors estimated with the Pearson's product moment correlation (lower left panels). The diagonal panels show the distribution of QE_{PD} values for each group of species (mammals, up left, birds, middle, amphibians, down right).

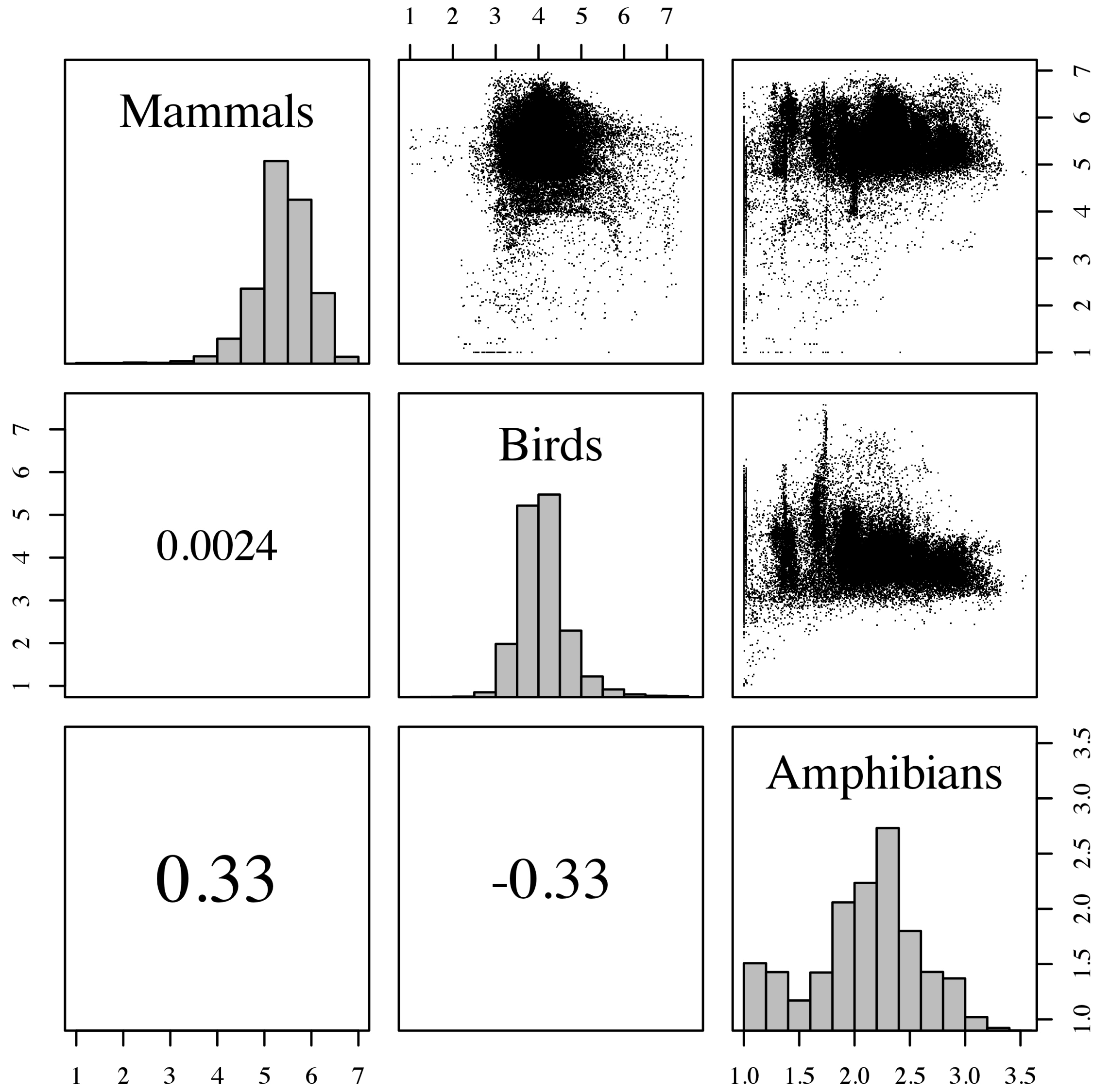
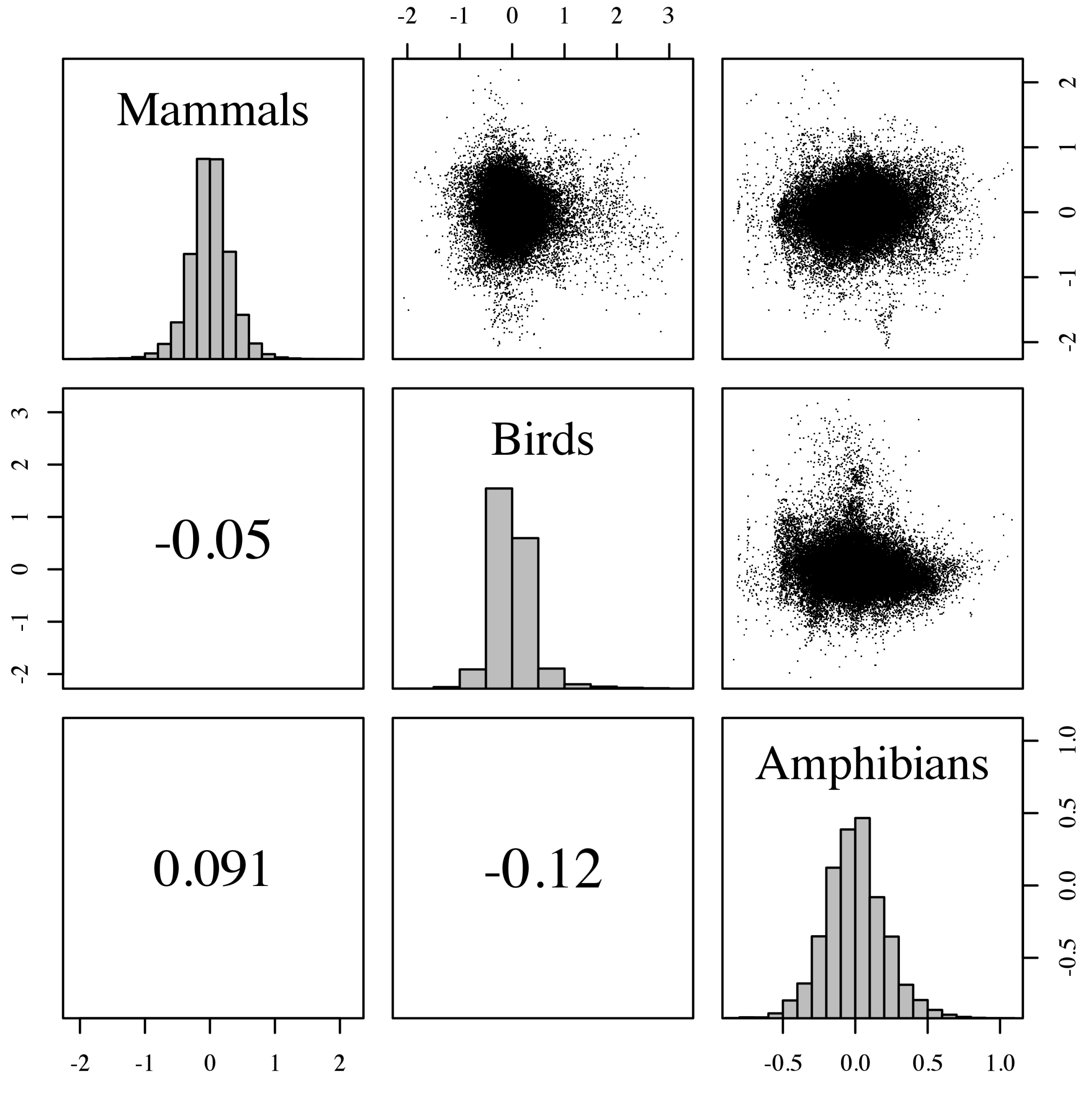


Figure S5: Co-variation of the residuals (QE_{RES}) of the quadratic relationship between the species diversity (SD) and the phylogenetic diversity (QE_{PD}) among mammals birds and amphibians (upper right panels) and their associated correlation factors estimated with the Pearson's product moment correlation (lower left panels). The diagonal panels show the distribution of QE_{PD} values for each group of species.



Appendix S5. Supplementary analyses and details on the PAs assessment.

Table S3: Mean observed and expected percentage of representation of each convergence category (PC, positive convergence, NC, negative convergence, NeC, neutral convergence, D, divergence) within the 3 different protected area network. Standard deviation is indicated in the brackets.

		PC	NC	NeC	D	Others
WDPA	Observed	8.54	6.16	10.41	11.3	10.29
	Expected	10.43 (±0.94)	10.40 (±0.75)	10.42 (±0.25)	10.41 (±0.21)	10.40 (±0.07)
WDPA I, II	Observed	1.63	0.87	1.91	3.03	2.20
	Expected	2.26 (±0.51)	2.29 (±0.41)	2.28 (±0.13)	2.28 (±0.11)	2.28 (±0.04)
Natura 2000	Observed	16.41	17.73	13.64	20.08	18.16
	Expected	17.70 (±1.68)	17.74 (±1.35)	17.75 (±0.38)	17.75 (±0.37)	17.74 (±0.12)

Additional analyses:

To complete the protected areas (PAs) assessment, we conducted an additional analysis. First, we calculated the mean observed QE_{PD} value within PAs for each taxa and compare it to a null distribution where PAs were randomly distributed (1000 randomisations), results are shown in **table S4**. Second, we looked at the representation (R) of residuals within the protected areas (where $R = Ncat_{PROT} / Ncat_{TOT}$, see main text) for each taxa (mammals, birds and amphibians) separately and compare it to a null distribution were PAs were randomly distributed (1000 randomisations). The residual classes are decided as follow: 1 and -1 represent respectively the upper and lower 25% of the residuals distribution (normal distribution) and 0 for all values falling in between (see main text, materials and methods section), results are shown in **table S5**.

Table S4: Mean observed value of QE_{PD} (phylogenetic diversity) within and outside PAs compared to mean expected value of QE_{PD} when PAs are randomly distributed (1000 randomisations). Values written in blue represent a mean observed value of QE_{PD} significantly lower than expected and red written values represent mean observed QE_{PD} higher than expected.

	WDPA		WDPA I, IV		Natura 2000	
	Observed	Expected (±sd)	Observed	Expected (±sd)	Observed	Expected (±sd)
Mammals	5.35 (0.58) ***	5.38 (0.003)	5.31 (0.58)***	5.38 (0.004)	5.17 (0.60)***	5.18 (0.002)
Birds	4.04 (0.51)***	4.10 (0.002)	4.03 (0.52)***	4.10 (0.003)	3.86 (0.46)**	3.86 (0.001)
Amphibians	2.20 (0.46)***	2.08 (0.002)	2.20 (0.45) ***	2.08 (0.003)	2.22 (0.50)***	2.21 (0.001)

Table S5: Observed mean percent of representation of each residuals category for mammals, birds and amphibians within a) WDPA, b) WDPA I, II and c) Natura 2000 compared to a random distribution of protected area (Expected ± standard deviation). Red denotes mean observed values that are significantly larger than the mean expectation, while significantly smaller observed value are noted in blue. *** p≤0.001, **p≤0.01, *p≤0.05.

a)

	Mammals		Birds		Amphibians	
Residuals classes	Observed	Expected (±sd)	Observed	Expected (±sd)	Observed	Expected (±sd)
1	10.98	10.40 (0.62)	11.57*	10.40 (0.62)	11.57***	10.42 (0.59)
-1	7.83***	10.39 (0.61)	4.32***	10.40 (0.62)	4.32***	10.40 (0.59)
0	10.45***	10.41 (0.02)	10.54***	10.40 (0.02)	10.55*	10.41 (0.02)

b)

	Mammals		Birds		Amphibians	
Residuals classes	Observed	Expected (±sd)	Observed	Expected (±sd)	Observed	Expected (±sd)
1	5.05	4.66 (0.40)	6.32***	4.64 (0.39)	6.26***	4.64 (0.40)
-1	4.02	4.67 (0.42)	3.14***	4.68 (0.41)	1.89***	4.66 (0.39)
0	4.67	4.66 (0.014)	6.66***	4.67 (0.014)	4.70*	4.67 (0.015)

c)

	Mammals		Birds		Amphibians	
Residuals classes	Observed	Expected (±sd)	Observed	Expected (±sd)	Observed	Expected (±sd)
1	26.80 ***	17.71 (1.02)	34.60***	17.73 (1.05)	33.24***	17.73 (1.00)
-1	23.29 ***	17.77 (1.01)	17.77	17.76 (1.01)	19.63**	17.67 (1.03)
0	17.35 ***	17.74 (0.04)	17.30***	17.74 (0.03)	17.28***	17.74 (0.04)

Figure S6. Area of convergence and divergence across the 3 groups of vertebrates (mammals, birds and amphibians) in the Western Palearctic. See the methods section for more details on the classification scheme. “Mid negative convergence” and “mid positive convergence” are refined class from the category called “other” where "mid negative convergence" correspond to all declinations of the codes 00-1, 0-1-1 and 1-1-1 (9 codes in total) and "mid positive convergence correspond" to all declination of the codes 001, -111 and 011 (9 codes in total).