Supplementary information

Data screening

Any measurements made under known stressors, such as unnatural salinities, extreme temperatures or hypoxic conditions were excluded. At extreme temperatures, cephalopods are unable to increase their oxygen consumption to match oxygen demands. However, none of the studies included here reported instances where animals encountered hypoxic stress caused by limitations in meeting oxygen demands due to high temperatures [1]. Additionally, we only included those results from experiments performed on animals which had been fasted beforehand for periods of between 6 - 24 h to minimise the effect of feeding on oxygen consumption, as respiration is typically elevated post-feeding due to specific dynamic action [2]. Experiments in which animals were fed during the measurement period were thus excluded (see Table S2). Stress effects from handling were minimised by only accepting data for animals that were allowed an acclimation period 0.25 - 168h in the respiratory chamber. The lower acclimation time limit was sufficient for *Octopus vulgaris* to settle on the experimental chamber floor and achieve a constant rate of oxygen consumption [3]. The upper time limit allowed acclimation of field-captured octopus to their new environment in substrate-containing (i.e. natural den-simulating) holding tanks where respiration measurements were subsequently carried out [4]. In one species (Illex illecebrosus), the b_R values were obtained from the equation relating oxygen consumption rates to body mass and activity by extrapolating to a zero activity [5,6]. When mass-specific respiration rate-body mass relationships were reported, rates were converted to respiration rates per individual. If multiple studies on a single species combined data together for calculating b_R , only b_R calculated from the most recent study was included in the data set, only b_R calculated from the most recent study was included in the data set. This occurred when new measurements for a species were integrated with previously published data to update the regression for the most

recent study. However, we avoided aggregating data from multiple studies for single species into new regressions ourselves to avoid combining data from different conditions. When necessary, raw data for the regressions were extracted from published figures using a webbased plot digitiser, WebPlotDigitizer [7].

The mass range for b_R

The body-mass range influences the accuracy of scaling regressions and therefore scaling exponents (b_R); generally the variability of b_R decreases as the mass range increases [8–10]. As most of the reduction in the standard deviation of b_R occurs when the mass range exceeds 1 order of magnitude [9], b_R values were omitted when mass ranges covered less than one order of magnitude or were not reported (following [11]). This additional screening step removed two species, and representation of one family. The relationship between ln *L* and b_R [$r^2 = 0.218$, p = 0.033, n = 21, $b_R = 0.621$ (95% CI: 0.526, 0.716) + 0.049 (95% CI: 0.028, 0.069) x ln L_R)], or between b_R and $1/b_L$ [$r^2 = 0.542$, p = 0.015, $b_R = 0.215$ (95% CI: -0.123, 0.552) + 1.650 (95% CI: 0.740, 2.561) x 1/b_L] are not materially affected, suggesting that the patterns found were robust. In general, the additional screening step improved the r^2 values of the relationships.

Lifestyle categorisation

Following [12], cephalopod species were categorised into pelagic, benthopelagic, benthic or bathypelagic lifestyles. Pelagic species live in the water column and often feed near the surface. Benthopelagic species occupy shelf waters, feeding, living near the bottom, but rarely rest on the bottom. Depending on depth, they are also associated with mid- and surface waters. Benthic species live on the bottom and are in direct contact with substrates. Bathypelagic species are deep-living species at depths of approximately 1000-5000 m. Data and species description used to classify the lifestyle of each species were obtained from relevant literature (Table A2).

Phylogenetic tree construction

The phylogenetic tree (fig. S1) was compiled following published phylogenies [13–17] based on molecular data. Branch length was calculated following [18].

Calculation of mass ranges for Figure 5

As the mass range of metabolic rate-body mass relationships differ between studies for species with more than one b_R value, the minimum and maximum mass plotted in Fig. 5 was based on the average minimum and maximum masses of multiple mass ranges. For instance, minimum mass of *Sepia officinalis* based on six metabolic rate-body mass relationships ranged from 0.1 - 15.00 g. The arithmetic mean of the six minimum mass values was then used as the minimum mass for the metabolic rate-body mass relationship for *Sepia officinalis* in Fig. 5.

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Figure legends

Figure S1 Phylogenetic tree of cephalopod species in our data set.

Figure S2 The range of logged wet masses for each mass-length and respiration-mass regression from which b_L and b_R values were derived. The correlation coefficients (*r*) of each regression are shown on the right-hand axis. In cases where multiple regressions were available and regression exponents were derived as arithmetic means, the mass range reflected is based on the mean minimum and maximum mass of all the regressions. The different lifestyles are represented by black (pelagic), red (benthopelagic), green (benthic) and blue (bathypelagic) symbols. The mass range for the respiration-mass relationship of *Onychoteuthis banksii* was not reported.

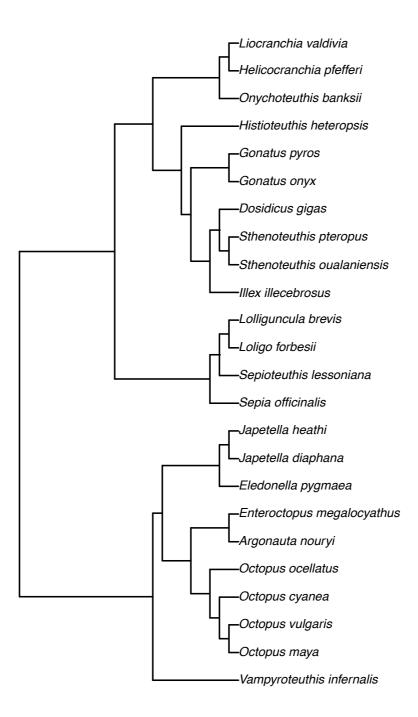


Figure S1

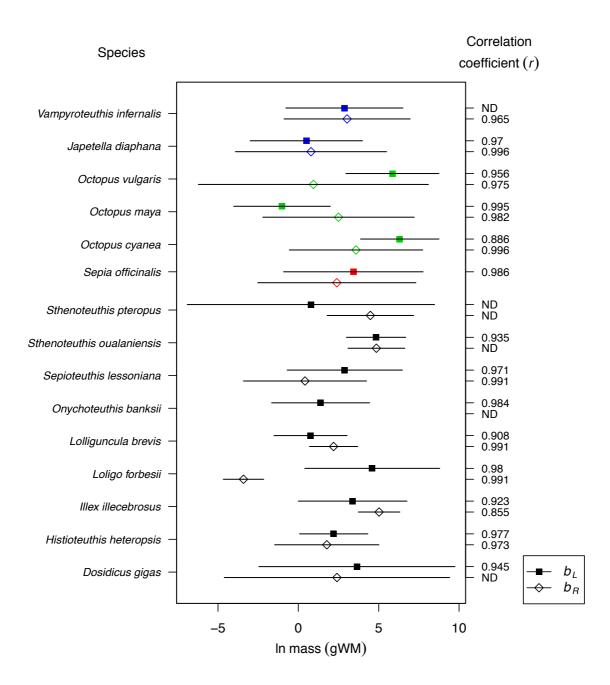


Figure S2