

Fig. S1. Distribution of number of measurements per bird

Number of birds with a count of their body mass measurements (A) and their metabolic rate measurements (B). Note the different scales on the X-axes.

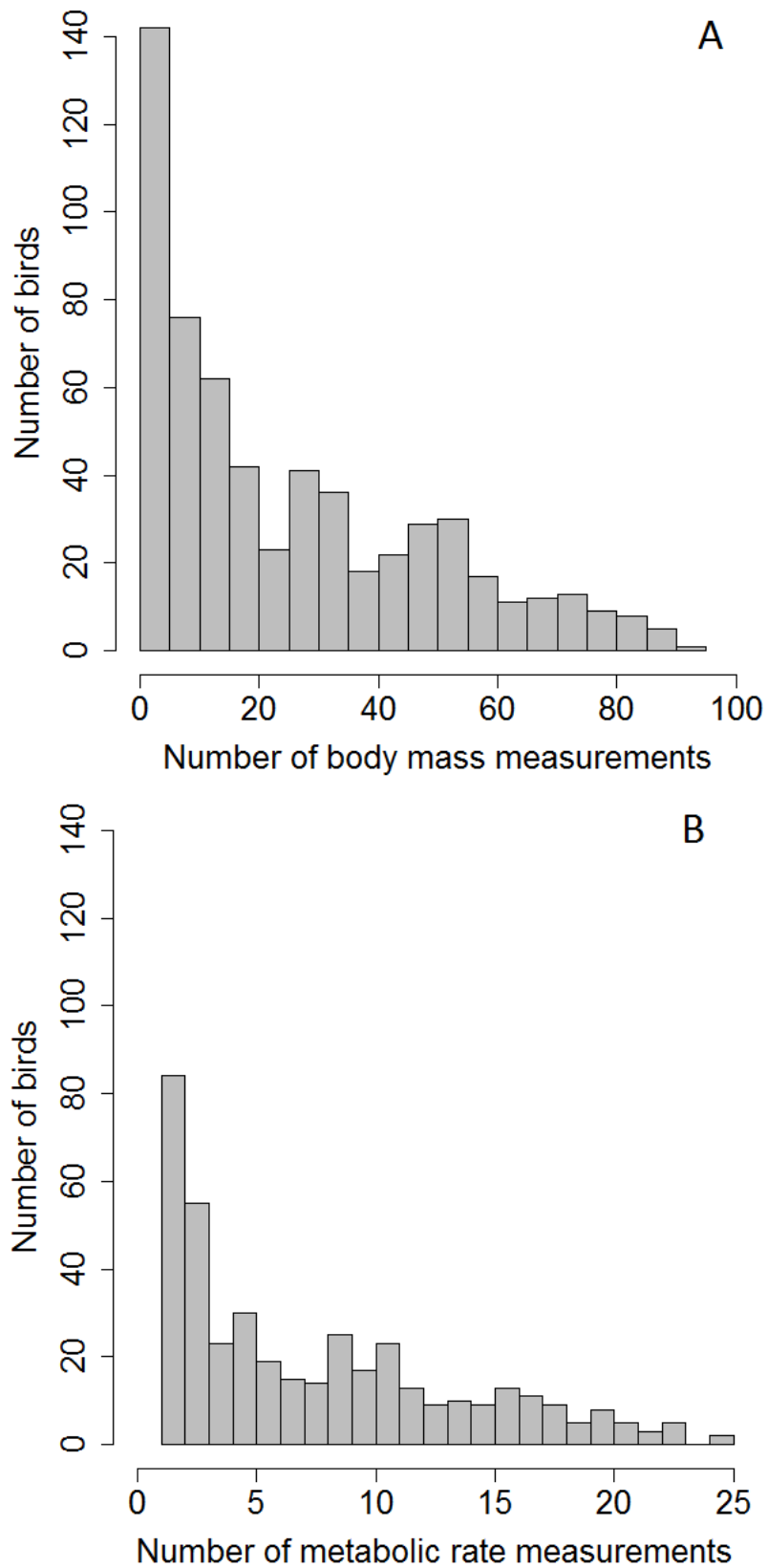


Table S1. Body mass variance components and repeatability

Variance components and repeatability estimates ($\pm 95\%$ CI) for the body mass traits shown in Fig. 3.

Dataset	Variance		Repeatability
	Between-individual	Within-individual	
Whole population			
Body mass	1.75 (1.54-1.96)	0.70 (0.68-0.71)	0.72 (0.69-0.74)
Size-adjusted	1.06 (0.91-1.19)	0.69 (0.68-0.71)	0.60 (0.57-0.64)
Benign environment			
Body mass	2.07 (1.76-2.46)	0.83 (0.80-0.86)	0.72 (0.68-0.84)
Size-adjusted	1.10 (0.93-1.36)	0.83 (0.81-0.87)	0.57 (0.52-0.62)
Harsh environment			
Body mass	1.22 (1.00-1.43)	0.55 (0.54-0.57)	0.69 (0.65-0.72)
Size-adjusted	0.77 (0.65-0.94)	0.54 (0.53-0.57)	0.58 (0.54-0.64)

Fig. S2. Association between ambient temperature and basal metabolic rate in the thermoneutral zone

The thermoneutral zone of the zebra finch was previously identified as ranging from 29.5°C till 40°C and the minimum oxygen consumption was measured at 34.9°C (Calder, 1964). Yet, these estimates were based on 72 measurements and larger datasets may find a different thermoneutral zone. In our data, using T_a ranges as identified in Calder (1964) we found a quadratic association between MR and T_a with the minimum BMR occurring at 34.8°C (T_a : $F=4.2$ $p<10^{-4}$; T_a^2 : $F=5.6$ $p<10^{-7}$; $N=1233$ measurements on 386 birds). This minimum is consistent with the earlier results of Calder et al. (1964). However, within this T_a range the distribution of BMR around the minimum would be asymmetric (Fig. S2) with a difference between maximum and minimum BMR of 0.027W (or 1 SD BMR, Table 1). Here, we chose a narrower and more symmetric distribution of BMR around the minimum of 34.8°C and, given the distribution of our data, determined the thermoneutral zone between 32°C and 39°C (Fig. S2). Hence, although we used a dataset that was over ten times as large as what was used previously, we identified a thermoneutral zone that is overall very consistent with that of earlier studies.

Dashed line shows model results.

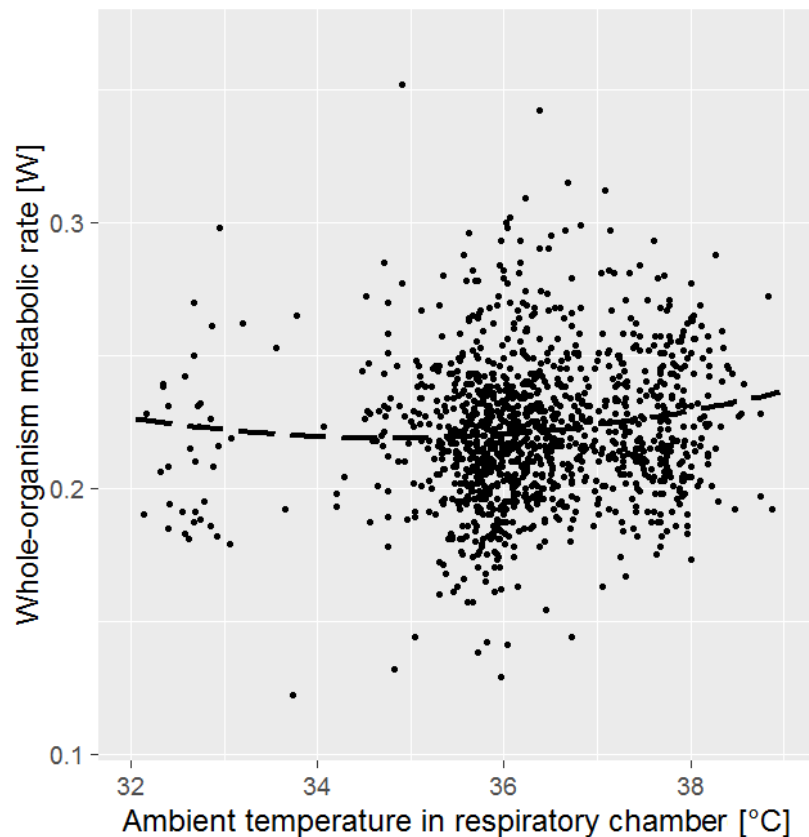


Table S2. Metabolic rate variance components and repeatabilityVariance components and repeatability estimates (\pm 95% CI) for the metabolic rate traits in Fig. 4.

	Between-individual variance		Within-individual variance		Repeatability		Difference BMR-SMR
	BMR	SMR	BMR	SMR	BMR	SMR	
Whole population							
Whole-organism	0.00036 (0.00031-0.00047)	0.0012 (0.0010-0.0016)	0.00035 (0.00031-0.00038)	0.0021 (0.0020-0.0023)	0.54 (0.47-0.58)	0.39 (0.33-0.43)	0.15
Mass-adjusted	0.00013 (8.8 10 ⁻⁵ -0.00016)	0.00073 (0.00057-0.00093)	0.00032 (0.00029-0.00036)	0.0018 (0.0017-0.0019)	0.27 (0.22-0.35)	0.28 (0.24-0.35)	-0.01
Spring data							
Whole-organism	0.00036 (0.00026-0.00046)	0.0016 (0.0013-0.0020)	0.00030 (0.00025-0.00034)	0.00014 (0.0012-0.0015)	0.57 (0.47-0.63)	0.55 (0.48-0.61)	0.02
Mass-adjusted	0.00076 (0.00053-0.00094)	0.00073 (0.00056-0.00099)	0.00027 (0.00022-0.00030)	0.0011 (0.00096-0.0012)	0.26 (0.15-0.37)	0.40 (0.33-0.48)	-0.16
Autumn data							
Whole-organism	0.00038 (0.00028-0.00052)	0.0011 (0.00082-0.0014)	0.00035 (0.00030-0.00042)	0.0021 (0.0020-0.0024)	0.51 (0.42-0.61)	0.32 (0.27-0.40)	0.19
Mass-adjusted	0.000090 (1.0 10 ⁻¹² -0.00030)	0.00058 (0.00043-0.00084)	0.00037 (0.00012-0.00044)	0.0019 (0.0018-0.0022)	0.18 (0.08-0.29)	0.24 (0.17-0.30)	-0.06
Benign environment							
Whole-organism	0.00040 (0.00031-0.00058)	0.00093 (0.00065-0.0013)	0.00038 (0.00033-0.00044)	0.0028 (0.0026-0.0031)	0.53 (0.45-0.62)	0.24 (0.18-0.32)	0.25
Mass-adjusted	0.00013 (0.000084-0.00020)	0.00076 (0.00050-0.0011)	0.00033 (0.00029-0.00038)	0.0022 (0.0020-0.0024)	0.28 (0.19-0.39)	0.31 (0.21-0.49)	-0.03
Harsh environment							
Whole-organism	0.00018 (0.00013-0.00026)	0.00049 (0.00036-0.00072)	0.00032 (0.00028-0.00036)	0.0014 (0.0013-0.0015)	0.38 (0.28-0.47)	0.27 (0.21-0.35)	0.11
Mass-adjusted	0.000078 (0.000044-0.00013)	0.00026 (0.00012-0.00036)	0.00031 (0.00027-0.00036)	0.0013 (0.0012-0.0015)	0.24 (0.12-0.31)	0.15 (0.09-0.27)	0.08
All data							
Whole-organism	0.0016 (0.0012-0.0020)	0.00087 (0.00068-0.0011)	0.0023 (0.0021-0.0026)	0.0011 (0.0010-0.0013)	0.38 (0.32-0.47)	0.45 (0.37-0.52)	-0.07
Mass-adjusted	0.00088 (0.00058-0.0011)	0.000051 (0.00036-0.00068)	0.0019 (0.0016-0.0020)	0.00088 (0.00078-0.00099)	0.30 (0.24-0.40)	0.40 (0.29-0.45)	-0.10

Fig. S3. Phenotypic correlations between metabolic traits

Schematic (A, B) and data representations (C) of phenotypic correlations between metabolic traits. (A) Metabolic reaction norms of three individuals (1, 2 and 3) differ little in response to ambient temperature (T_a), generating a high between individual correlation between BMR and SMR. (B) Represents the alternative scenario, in which individuals differ in their metabolic response to a decrease in T_a : individuals with high BMR can have either high or low SMR, generating a low between individual correlation between BMR and SMR. (C) Data show that SMRs at various T_a 's correlate well with each other (C1 & C2) but that correlations between BMR and any of the SMR's are weak (C3-C6), hence consistent with the scenario shown in (B) and not in (A).

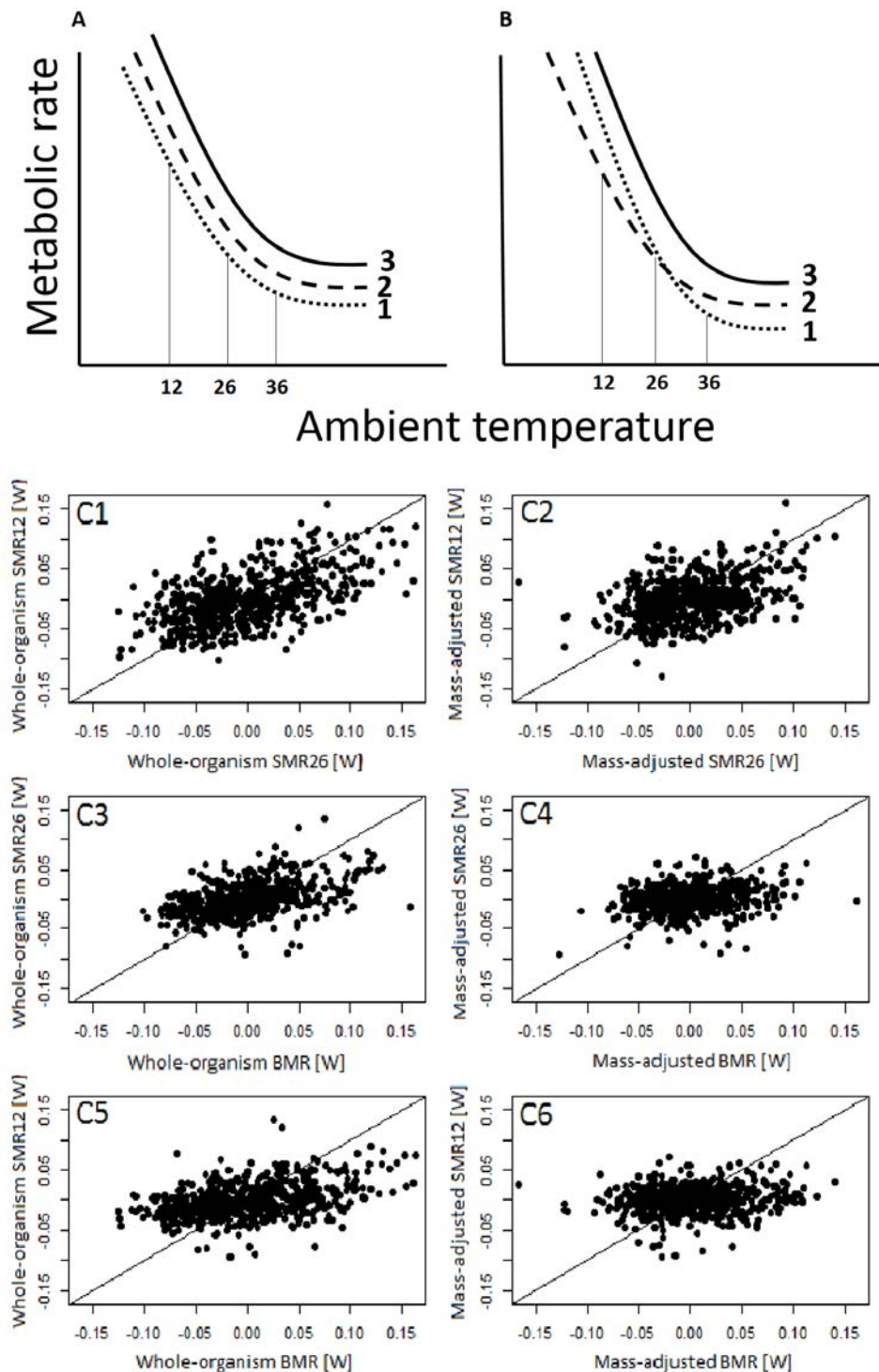


Fig. S4. Body temperature

Associations between (A) mass-adjusted metabolic rate and body temperature and (B) between *change* in mass-adjusted metabolic rate and body temperature at various ambient temperatures (T_a). (A) Mass-adjusted metabolic rate and body temperature correlate positively at $T_a=12^\circ\text{C}$, but this association decreases with increasing T_a . Dots show data, lines are results of model fits. (B) Within-individual differences in metabolic rate are not significantly correlated with differences in body temperatures when T_a declines from (A) 26°C to 12°C or (B) the thermoneutral zone to 26°C . Grey dots and dashed lines show raw data and model fit for benign environment, black triangles and full lines show raw data and model fit for harsh environment. For statistics see results section.

