Supplementary 1

Supplementary figures

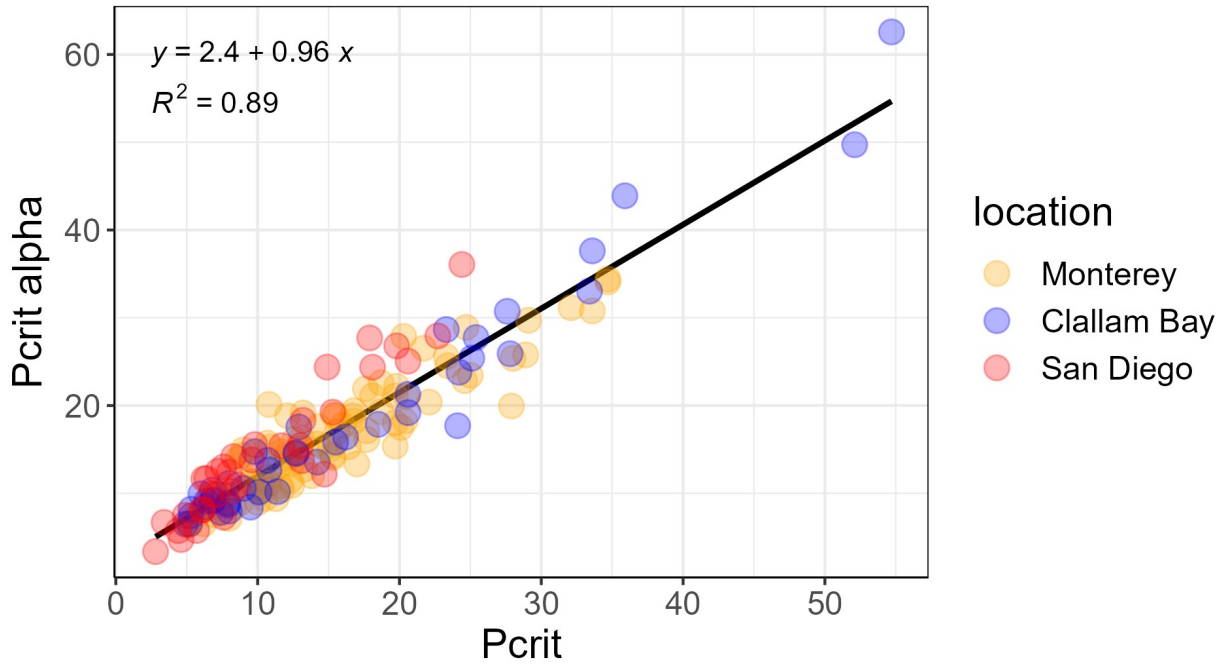

Fig. S1. Linear relationships between the critical oxygen partial pressure for *S. purpuratus* quantified using the limiting low oxygen level for SMR (p_{crit}) and the oxygen level where supply capacity (α) is maximized (p_{crit} alpha), units are oxygen in percent saturation.

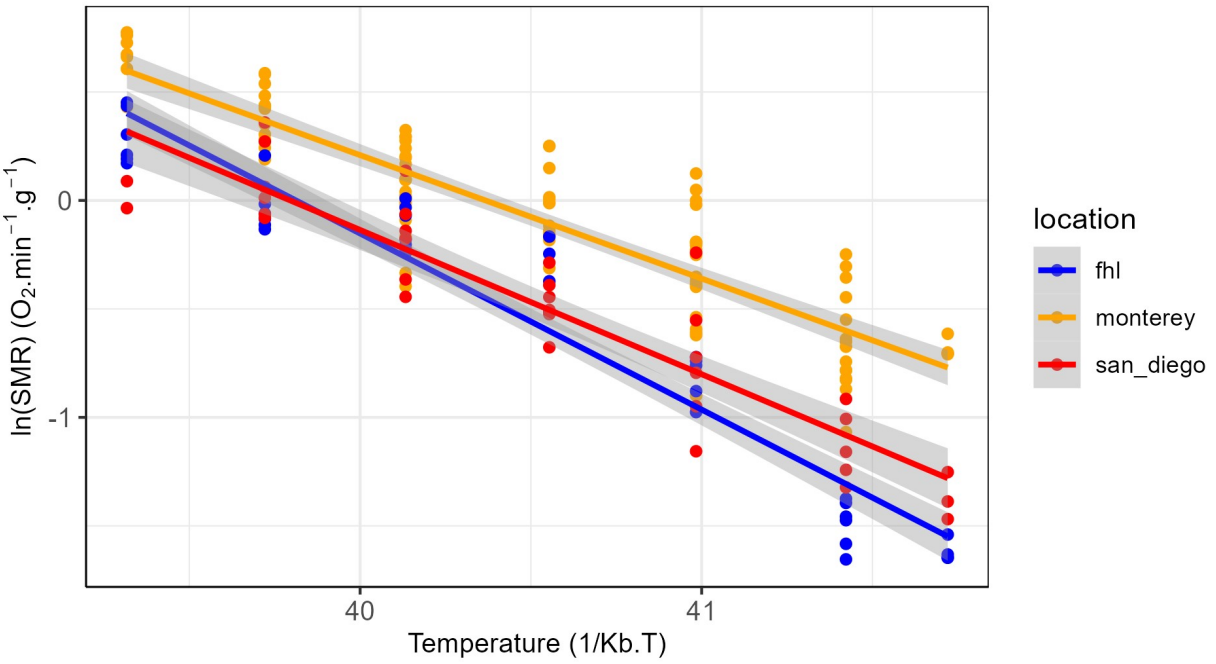

Fig. S2. Arrhenius plot per sampling location. Linear relationship between t standard metabolic rate (SMR) on a log scale and the inverse of temperature in Kelvin multiplied by the Boltzmann factor (inv_temp_arr). fhl = Clallam Bay, Monterey = Monterey, san_diego = San Diego.

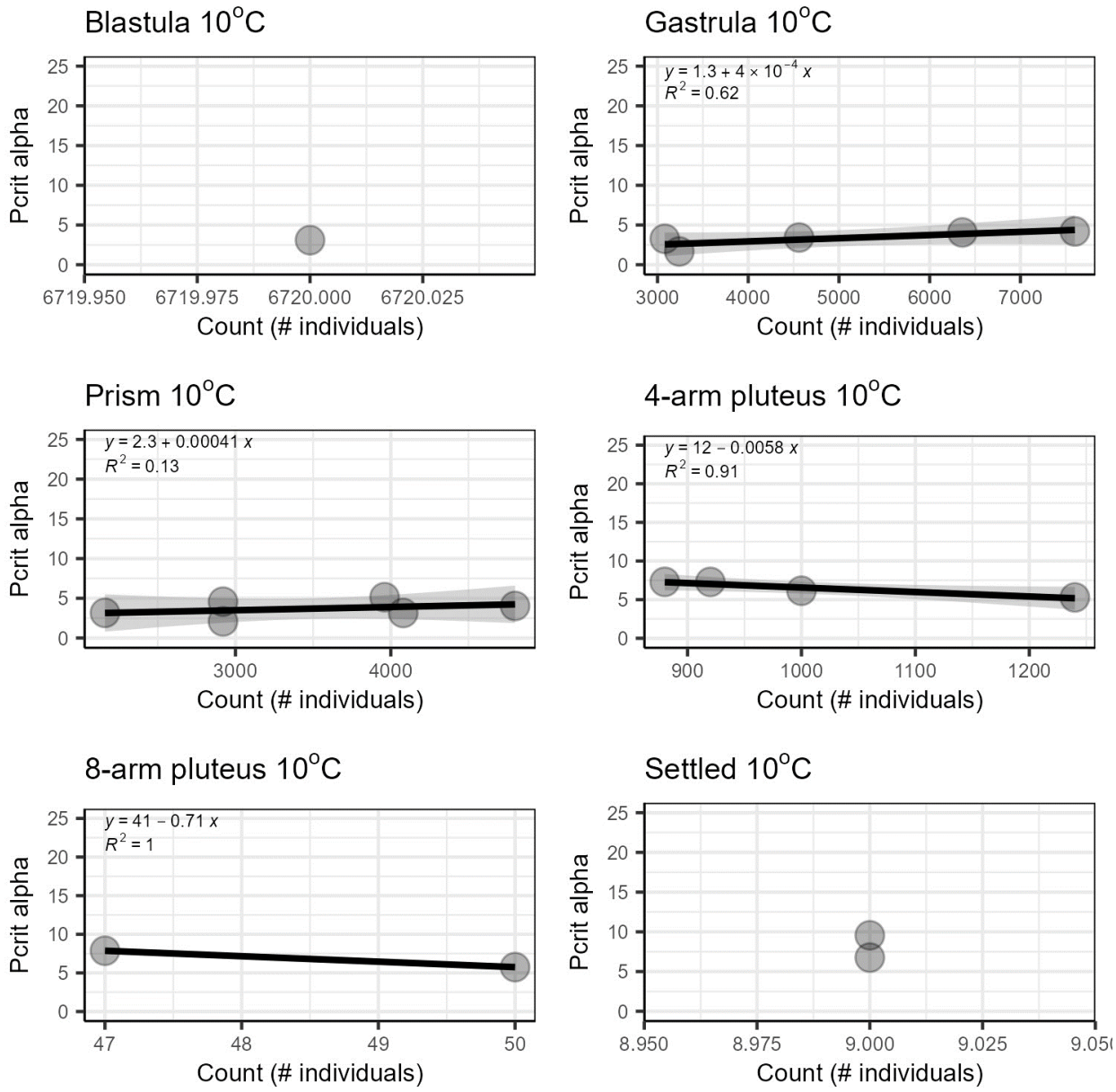

Fig. S3. Relationship between well density (number of individuals) and pO_{2crit} using the alpha method per developmental stage at 10°C. Data from successful trials are indicated by black points and solid line with shading is linear model and 95% confidence intervals.

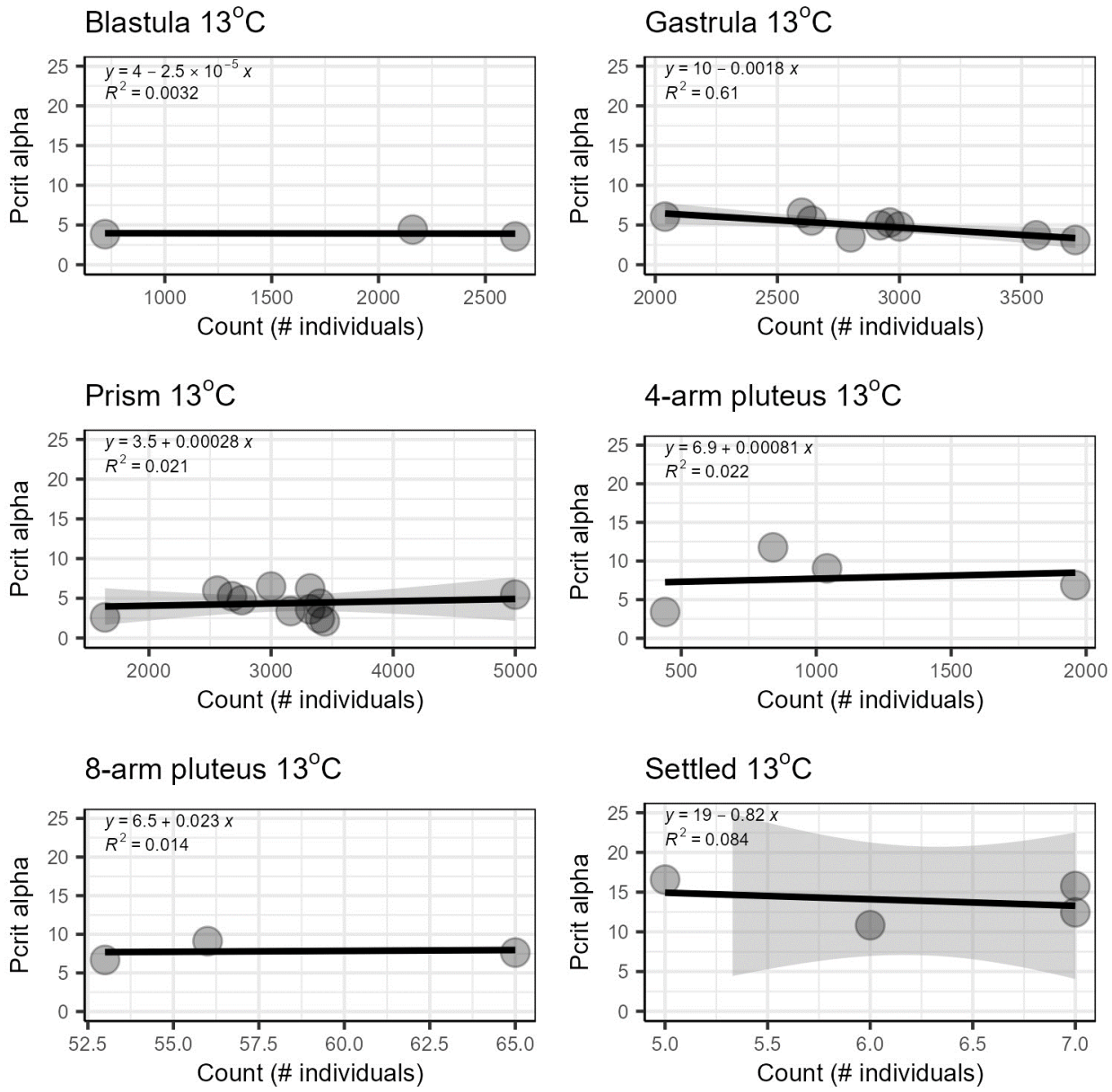

Fig. S4. Relationship between well density (number of individuals) and pO_{2crit} using the alpha method per developmental stage at 13°C. Data from successful trials are indicated by black points and solid line with shading is linear model and 95% confidence intervals.

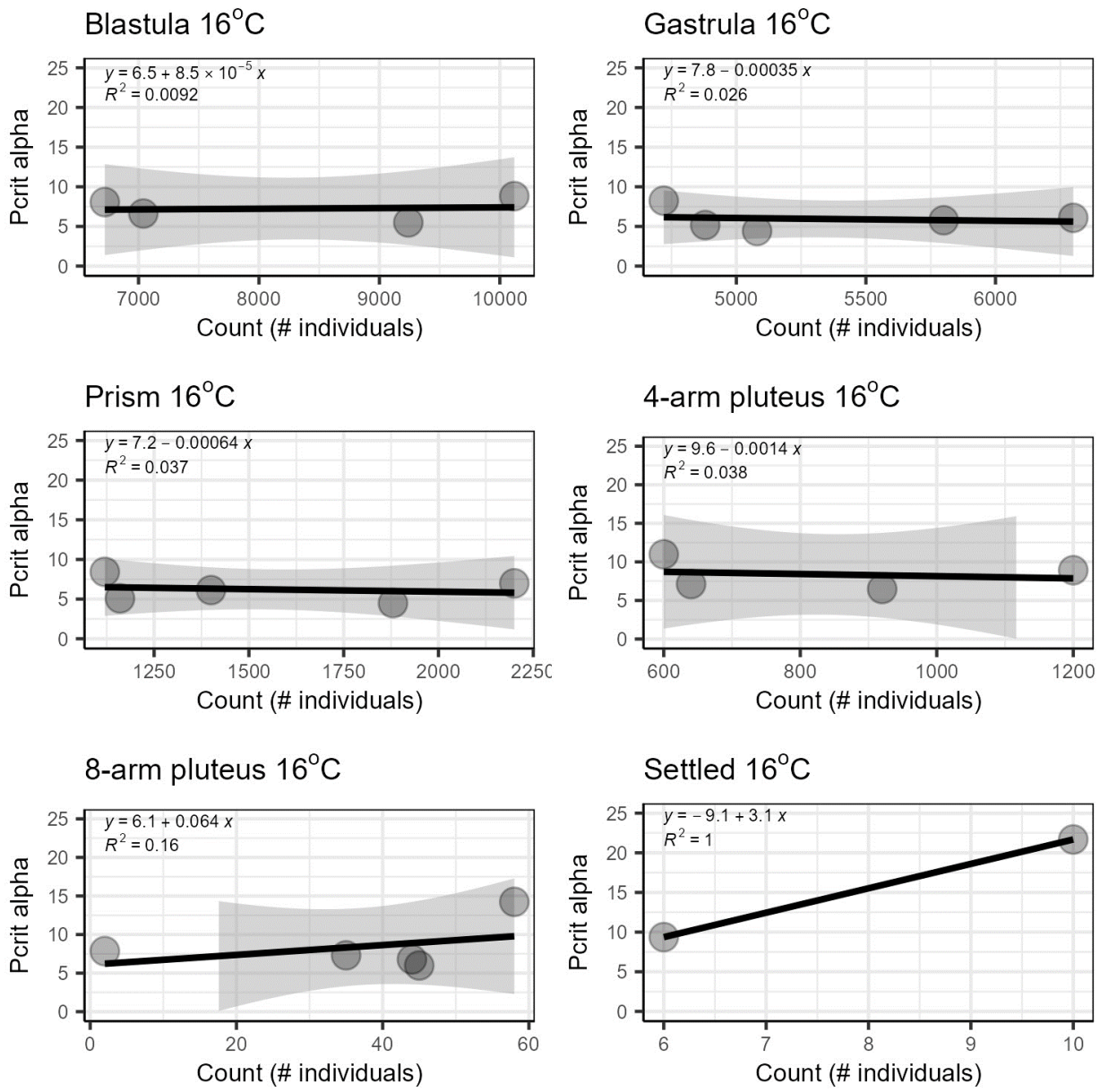

Fig. S5. Relationship between well density (number of individuals) and pO_{2crit} using the alpha method per developmental stage at 16°C. Data from successful trials are indicated by black points and solid line with shading is linear model and 95% confidence intervals.

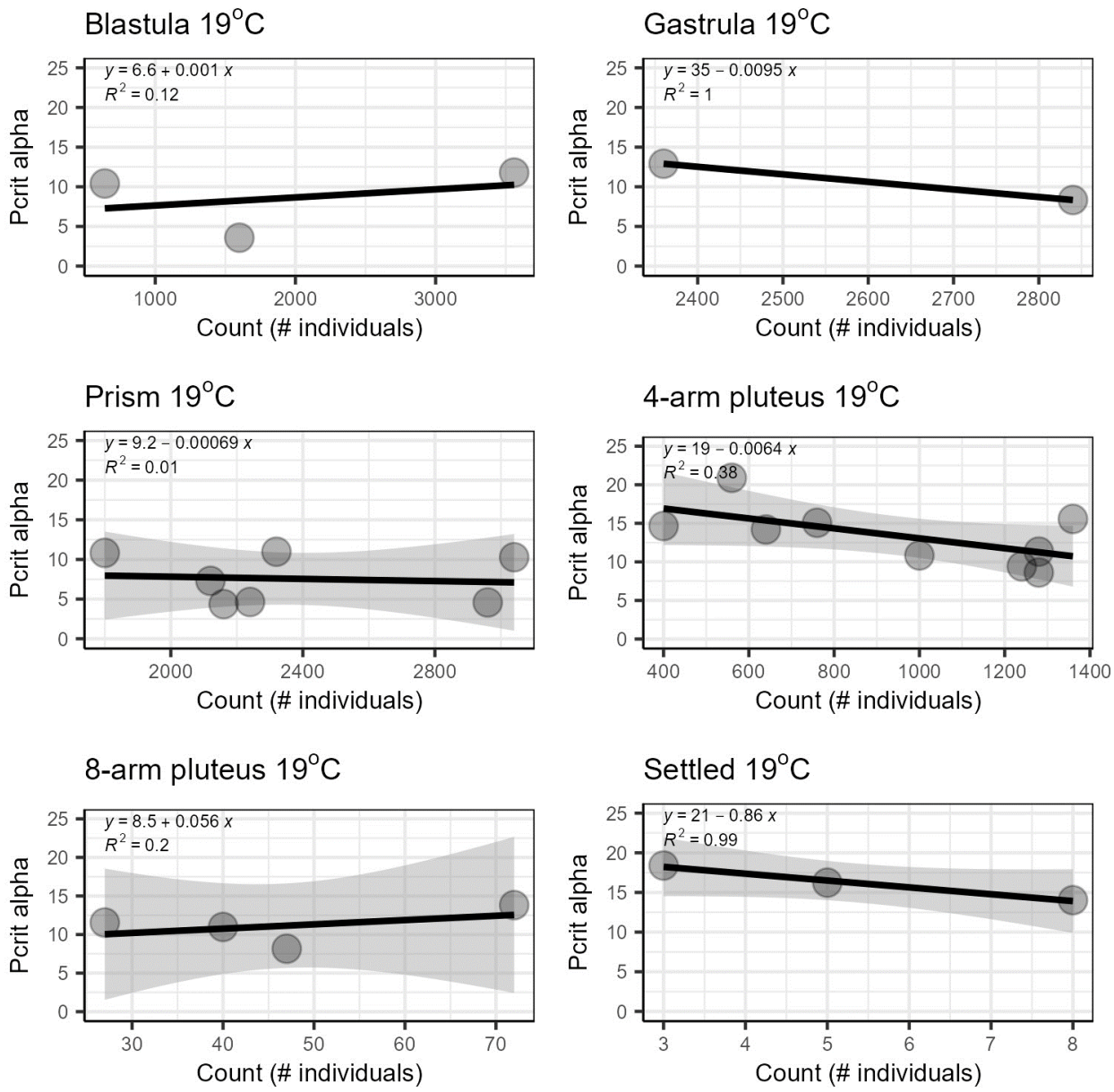

Fig. S6. Relationship between well density (number of individuals) and pO_{2crit} using the alpha method per developmental stage at 19°C. Data from successful trials are indicated by black points and solid line with shading is linear model and 95% confidence intervals.

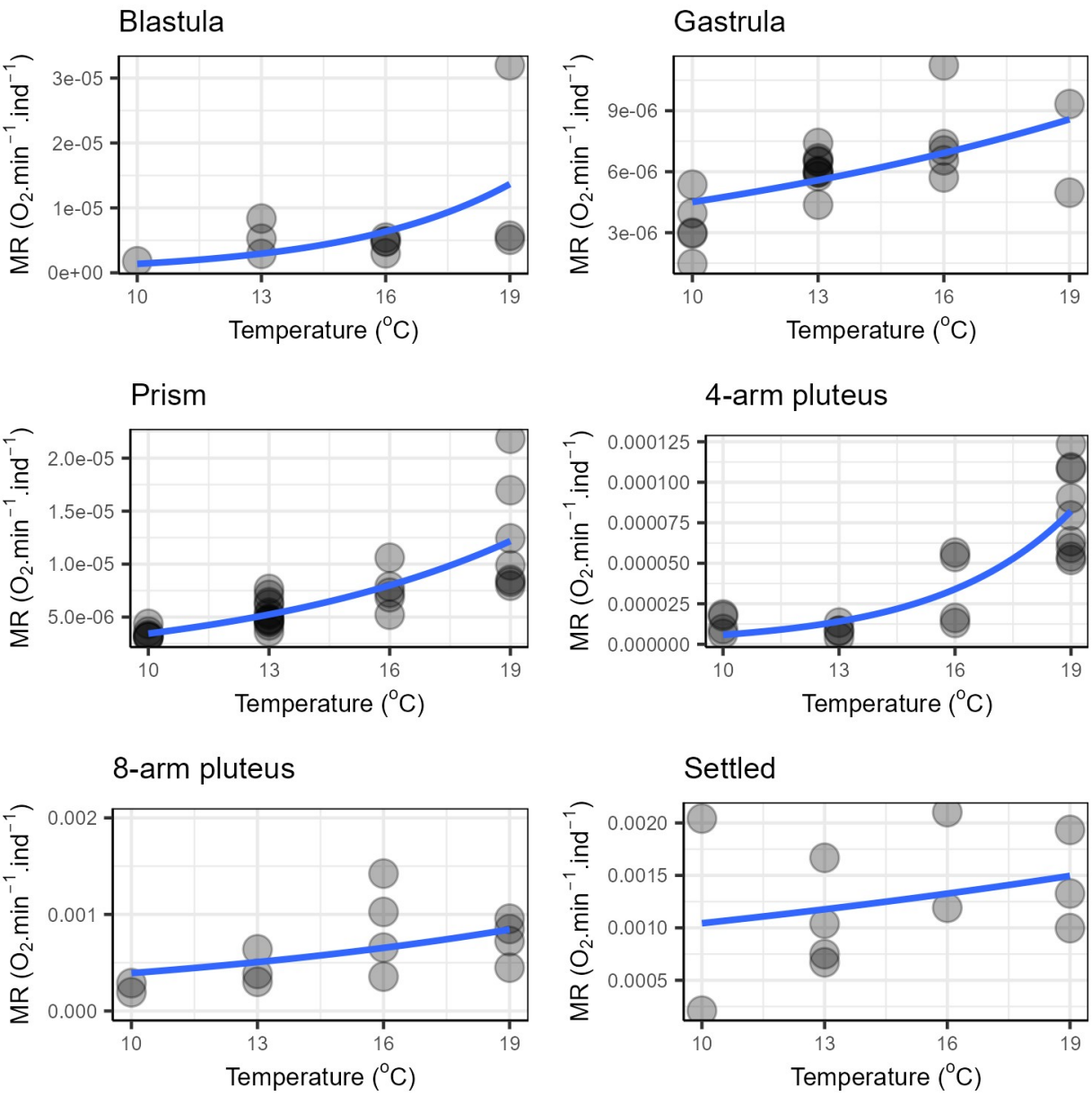

Fig. S7. Relationship between temperature and metabolic rate per individual per minute in each well for each developmental stage. Data from successful trials are indicated by black points and solid blue line is best fit exponential model.

Supplementary tables

Table S1. Checklist of information required to replicate respirometry studies on adult *S. purpuratus* following Killen et al. 2021.

#	Category	Response
Equipment, materials, and set-up		
1	body mass at time of respirometry	Following a respirometry trial organisms were immediately frozen and later thawed to measure their wet mass, dried in an oven at 50°C for ~ 24 hours to measure dry mass and then ashed to measure metabolic mass.
2	empty respirometer volume	two sized respirometers were used depending on the size of organism. The Large respirometer had a volume of 473.2 ml (16 oz) and the small respirometer had a volume of 177.4 ml (6 oz).
3	mixing device	water was continuously mixed via an in-line pump and circulation loop
4	respirometer volume to body mass ratio	respirometer volume:mass ratio ranged from 3.8 to 20.8 (information for each trial run is reported in Supplement 2).
5	material of tubing	clear thick wall vinyl tubing.
6	volume of tubing	volume of tubing in beg respirometers was 106.8 ml and volume of tubing for small respirometers was 97.6 ml.
7	volume of tubing included in analysis	confirmed
8	respirometer materials	polyethylene terephthalate plastic
9	oxygen probe type	Pyroscience OXSP5 sensor spots
10	sampling frequency of oxygen	Oxygen sampled every second throughout trial
11	oxygen probe placement	Oxygen probe placed in the circulation loop
12	flow rate/return to normoxia	Flushing flow rate was controlled via a one-way valve on the flush line. Flush flow rate was not directly measured but it was ensured chambers returned to 100% saturation following measurement periods
13	timing of flush/closed cycles	10 minute flush–5 minute measure or 5 minute flush–10 minute measure or 10 minute flush–10 minute measure depending on temp, organism size. Info in Supplement 2
14	measurement exclusion start and end	one minute was excluded from the start and end of each measurement cycle resulting in a 3 min measurement period for metabolic rate calculation
15	frequency and calibration of probe	Oxygen probes was calibrated in 100% saturated water only before each trial. We didn't calibrate at anoxia before each trial due to logistical reasons but ensured that oxygen in chambers leveled off at zero when it was entirely consumed by the organism.
16	software temperature compensation	Software temperature compensation was not used. In cases when the chiller turned on to maintain water during a measurement period the data were excluded

Measurement conditions		
17	trial temperature	Trial temperatures were either 5, 7, 10, 13, 16, 19 or 22°C and included in Supplement 2
18	how temperature was controlled	Temperature was controlled with an Inkbird temperature controller connected to an aquarium heater and chiller
19	photoperiod during respirometry	All respirometry was carried out in the dark (water bath coolers lids closed)
20	water cleaning	Ambient water bath was constantly aerated with an aquarium air pump. Water was replaced after each trial
21	volume of ambient water bath	Ambient water bath volume was approximately 150 liters
22	minimum oxygen level reached	oxygen levels during intermittent flow metabolic rate measurements never fell below 80% saturation
23	chambers visually shielded	Yes, chambers were placed inside closed cooler box's and thus visually shielded from all disturbance
24	how many animals per trial	3,4,5, 6 or 7 animals were run per trial
25	animals shielded from each other	Animals were not shielded from each other during trials however trials were carried out in the dark and the study species naturally occur in groups
26	fasting period	Specimens were placed directly into respirometers where they were given ~24 hours to adjust to the novel environment which is considered part of the fasting period = minimum 24 hours
27	duration of all trials	Indicated in text
28	acclimation time since capture	each specimen was given ~24 hours post transfer from wild to respirometry setup to acclimatize
Background respiration		
29	background respiration	Background respiration rates were measured in parallel in an empty container (alternated) throughout the duration of each trial.
30	how many background respiration slopes	Same as number of measurement slopes which is included in Supplement 2 for each trial.
31	how were changes in background respiration modelled	They were not modelled, rather matched to corresponding measurement periods.
32	level of background respiration as a percentage	Background respiration as a percentage of organismal respiration is reported in Supplement 2.
33	method and frequency of system cleaning	Respirometers were cleaned with bleach twice throughout the experiment period when respirometer sizes were swapped. Water was replaced after every trial.
Standard metabolic rate		
34	time to metabolic rate measurements	Animals were inside respirometers for ~ 24 hours before metabolic rate measurements were considered
35	hours of metabolic rate measurements	Metabolic rate measurements were recorded for ~ 24 hours for each trial

36	state metabolic rate determination technique	Metabolic rate was taken as 0.1 quantile following Chabot et al (2016).
37	total number of slopes used to estimate SMR	Number of slopes used to estimate SMR ranged from 7 - 92, the majority trials had more than 60 slopes. The number of slopes per trial is included in Supplement 2
38	state whether any time periods were removed	Following an ~ 24 hour acclimation period intermittent flow respirometry was run for ~ 24 hours = 80 - 96 potential measurements, We excluded measurements below an R2 threshold of 0.95 (unless stated otherwise in Supplement 2) and also measurements associated with blanks in the upper 0.95 or lower 0.05 quantiles (chilling or heating device kicked on).
39	R2 thresholds	0.95 (unless stated otherwise to include more slopes at cold temps). Included in Supplement 2
40	proportion of outlier data removed	Most trial runs excluded less than 20% of oxygen consumption rates as outliers. Information for each trial is reported in Supplement 2.
Data handling and statistics		
50	sample size	N = 174 metabolic rates and 168 p_{crit}
51	state how oxygen uptake rates were calculated	Oxygen uptake rates were calculated following equation outlined by Svendson et al 2016 and stipulated as equation 1 in the manuscript
52	confirm that volume (or mass) of animal was subtracted from resp volume	confirmed
53	specify whether body mass was accounted for	Oxygen uptake rates were converted to mass specific by dividing each rate by body mass and species specific allometric scaling exponents.

Table S2. Breakdown of Adult *SMR* replication per temperature treatment and per sampling location. Numbers present the total number of sample (n).

	Temperature (°C)							
Location	5	7	10	13	16	19	22	Total
Monterey	5	16	18	14	22	14	8	97
Clallam Bay	4	6	5	4	7	7	6	39
San Diego	3	5	6	6	6	6	2	34

Table S3. Modelling results of natural logarithm of standard metabolic rate as a linear function of Arrhenius temperature (inverse of temperature in Kelvin multiplied by Boltzmann constant) with sampling location as full interaction term (San Diego is reference population). Significant p-values are highlighted in bold. R^2 = 0.8871, degrees of freedom = 5, 164, *F*-statistic = 157.6

Effect	Estimate	SE	*t*	p
Intercept	-0.871	0.074	-11.836	**<2e-16**
Clallam Bay	0.045	0.094	0.479	0.633
Monterey	0.443	0.851	5.199	**5.9e-16**
Arrhenius temp	-0.675	0.051	-13.172	**<2e-16**
Arrhenius temp: Clallam Bay	-1.663	0.066	-2.512	**0.013**
Arrhenius temp: Monterey	0.045	0.060	0.753	0.453

Table S4. Standard metabolic rate Arrhenius model parameters (α_d and *E*) per each sampling location for temperatures between 5 and 22°C and temperature coefficient (Q_{10}) values.

	Model parameters		
Locations	α_d	*E*	Q_{10}
Monterey	9481147679	-0.569092	2.23
Clallam Bay	1.082042e+14	-0.811686	3.13
San Diego	314017929461	-0.665216	2.56

Table S5. Breakdown of Adult pO_{2crit} replication per temperature treatment and per sampling location. Numbers present the total number of sample (n).

	Temperature (°C)							
Location	5	7	10	13	16	19	22	Total
Monterey	5	16	17	14	21	10	8	91
Clallam Bay	4	6	5	4	7	7	6	39
San Diego	3	5	6	6	6	6	2	34

Table S6. Modelling results of critical oxygen level as a quadratic function of temperature with sampling location as full interaction term (San Diego is reference population). Significant p-values are highlighted in bold. R^2 = 0.691, degrees of freedom = 8, 155, *F*-statistic = 43.44

Effect	Estimate	SE	*t*	p
Intercept	7.418	1.863	3.982	**0.000**
temp	0.040	0.524	0.076	0.940
$temp^2$	0.075	0.031	2.398	**0.018**
Clallam Bay	3.600	2.480	1.450	0.149
Monterey	3.751	2.225	1.686	0.094
temp: Clallam Bay	-1.426	0.697	-2.045	**0.043**
temp: Monterey	-0.043	0.618	-0.069	0.945
$Temp^2$: Clallam Bay	0.078	0.041	1.915	0.058
$Temp^2$: Monterey	-0.017	0.036	-0.462	0.645

Table S7. Quadratic model parameters for the temperature-dependence (5 – 22°C) of critical oxygen partial pressure for each sampling location.

	Model parameters		
Location	*x*	*x2*	*c*
Monterey	-0.582	0.057	12.634
Clallam Bay	-2.909	0.152	21.751
San Diego	-0.707	0.075	9.087

Table S8. Breakdown of larval pO_{2crit} replication per temperature treatment and per developmental stage. Numbers present the total number of sample (n).

	Temperature (°C)				
Stage	10	13	16	19	Total
blastula	1	3	4	3	11
gastrula	5	5	9	2	21
prism	6	13	5	7	31
4-arm pluteus	4	4	4	9	21
8-arm pluteus	2	3	5	4	14
settled	2	4	2	4	12

Table S9. Critical oxygen partial pressure Arrhenius model parameters (α_d and E) for each developmental stage (blastula – adult) for temperatures between 10 and 19°C.

	Model parameters	
Stage	α_d	*E*
blastula	4.715384e+14	-0.798
gastrula	2.276318e+15	-0.834
prism	68118663974	-0.578
early-pluteus	127123436204	-0.580
late-pluteus	21219495	-0.366
settled	709986653	-0.441
adult	603258733	-0.548

Table S10. Linear model parameters for the relationship between well density (number of individuals) and pO_{2crit} using the alpha method for each developmental stage at (1) 10°C, (2) 13°C, (3) 16°C and (4) 19°C. df: degrees of freedom; Est.: coefficient of the slope; significant p values are highlighted in bold. NA indicates too few data to fit the model.

1) 10°C				
Stage	**df**	**est.**	***t***	**p**
blastula	NA	NA	NA	NA
gastrula	3	0.0004	2.205	0.12
prism	4	0.0004	0.768	0.49
4-arm pluteus	2	-0.0058	-4.502	0.05
8-arm pluteus	NA	NA	NA	NA
settled	NA	NA	NA	NA

2) 13°C				
Stage	**df**	**est.**	***t***	**p**
blastula	1	-0.00002	-0.057	0.964
gastrula	7	-0.0018	-3.287	**0.013**
prism	10	0.0003	0.461	0.655
4-arm pluteus	2	0.0008	0.21	0.853
8-arm pluteus	1	0.0229	0.117	0.926
settled	2	-0.8234	-0.429	0.71

3) 16°C				
Stage	**df**	**est.**	***t***	**p**
blastula	2	0.00009	0.136	0.904
gastrula	3	-0.0003	-0.283	0.796
prism	3	-0.0006	-0.341	0.755
4-arm pluteus	2	-0.0014	-0.281	0.805
8-arm pluteus	3	0.0636	0.766	0.499
settled	NA	NA	NA	NA

4) 19°C				
Stage	**df**	**est.**	***t***	**p**
blastula	1	0.001	0.367	0.776
gastrula	NA	NA	NA	NA
prism	5	-0.0007	-0.228	0.829
4-arm pluteus	7	-0.0064	-2.077	0.076
8-arm pluteus	2	0.0556	0.716	0.548
settled	1	-0.8633	-9.204	0.069