Reproductive phenotype predicts adult bite-force performance in sex-reversed dragons (*Pogona vitticeps*)

- Supplementary Information

ADDITIONAL TABLES

Table S1 Sample composition.

	Juvenile	Adult	total
ZZf	9	17	26
ZWf	22	11	33
ZZm	21	11	32
total	52	39	91

Table S2 Results from analysis of variance (ANOVAs) testing for differences between adult males and females. ZWf, concordant females (n = 11), ZZm, males (n = 11). Mass, body mass (g); SVL, snout-vent length (mm); HLrr, head length directly from the tip of the rostrum to the posterior end of the retroarticular process (mm); HLrq, head length from the tip of the rostrum to the posteroventral corner of the tympanum (approximately the position of the quadrate-articular jaw joint) (mm); HWqu, head width measured at the posteroventral corner of the tympanum (mm); HWmt, head width measured at the midpoint of the temporal region (mm); HDmt, and head depth measured at the midpoint of the temporal region (mm); BF at tips, bite force at the tips corrected for out lever (N) (Lappin and Jones 2014); BF no lever, bite force without lever correction (N) Degrees of freedom 2, 20 for all tests. * Significant at p = 0.05. ** Significant at p = 0.01.

		ZWf		**ZWf and ZZm difference**			
response	**F**	**Mean**	**± SE**	**Mean**	**± SE**	**t**	**p**
log(Mass)	0.027	5.416	0.086	0.020	0.122	0.165	0.871
log(SVL)	0.235	5.213	0.029	0.020	0.041	0.484	0.633
log(Bite Force)	4.277	3.894	0.112	0.327	0.158	2.068	0.052
log(Bite Force nl)	3.864	4.109	0.120	0.334	0.170	1.966	0.063
log(HLroret)	3.748	3.949	0.029*	0.079	0.041	1.936	0.067
log(HLroqu)	6.440	3.738	0.027*	0.096	0.038	2.538	0.020*
log(HWqu)	4.519	3.628	0.031*	0.094	0.044	2.126	0.046*
log(HWmt)	1.400	3.592	0.034*	0.057	0.048	1.183	0.251
log(HDmt)	6.236	3.193	0.039*	0.138	0.055	2.497	0.021*

Table S3 Test for allometry of bite force no lever vs SVL, Mass, and head dimension in the full sample of *Pogona vitticeps* (n = 91). Adult and juvenile ZZf, sex-reversed females (n = 26), ZWf, concordant females (n = 33), ZZm, males (n = 32). Standard error (SE) was used to define upper and lower limits. Allometry is considered positive when the lower limit of the slope is greater than 0.667 for mass and 2.0 for linear measurements (the isometric predictions) and negative when the upper limit of the slope is lower than 0.667 for mass and 2.0 for linear measurements.

genotype	predictor	slope	SE	upper limit	lower limit	df	t	p	Predicted isometry	adj.r2	allometry
ZZf	log(SVL)	1.848	0.205	2.052	1.643	24	9.02	<0.001	2.000	0.76	-
ZWf	log(SVL)	1.883	0.143	2.026	1.740	31	13.15	<0.001	2.000	0.84	-
ZZm	log(SVL)	2.286	0.141	2.427	2.145	30	16.20	<0.001	2.000	0.89	positive
ZZf	log(Mass)	0.602	0.057	0.659	0.545	24	10.51	<0.001	0.667	0.81	negative
ZWf	log(Mass)	0.606	0.042	0.648	0.564	31	14.49	<0.001	0.667	0.87	negative
ZZm	log(Mass)	0.749	0.039	0.788	0.710	30	19.17	<0.001	0.667	0.92	positive
ZZf	log(HLroret)	2.102	0.205	2.307	1.897	24	10.24	<0.001	2.000	0.81	-
ZWf	log(HLroret)	2.018	0.154	2.172	1.863	31	13.06	<0.001	2.000	0.84	-
ZZm	log(HLroret)	2.319	0.134	2.453	2.186	30	17.36	<0.001	2.000	0.91	positive
ZZf	log(HLroqu)	2.207	0.214	2.421	1.992	24	10.29	<0.001	2.000	0.81	-
ZWf	log(HLroqu)	2.300	0.173	2.473	2.127	31	13.28	<0.001	2.000	0.85	positive
ZZm	log(HLroqu)	2.499	0.128	2.628	2.371	30	19.46	<0.001	2.000	0.92	positive
ZZf	log(HWqu)	2.004	0.162	2.166	1.843	24	12.40	<0.001	2.000	0.86	-
ZWf	log(HWqu)	1.971	0.158	2.129	1.812	31	12.45	<0.001	2.000	0.83	-
ZZm	log(HWqu)	2.300	0.106	2.406	2.194	30	21.69	<0.001	2.000	0.94	positive
ZZf	log(HWmt)	2.225	0.191	2.416	2.034	24	11.67	<0.001	2.000	0.84	positive
ZWf	log(HWmt)	2.201	0.167	2.368	2.033	31	13.14	<0.001	2.000	0.84	positive
ZZm	log(HWmt)	2.486	0.145	2.631	2.341	30	17.20	<0.001	2.000	0.90	positive
ZZf	log(HDmt)	2.129	0.202	2.331	1.927	24	10.53	<0.001	2.000	0.81	-
ZWf	log(HDmt)	2.008	0.156	2.164	1.852	31	12.87	<0.001	2.000	0.84	-
ZZm	log(HDmt)	2.263	0.114	2.377	2.149	30	19.84	<0.001	2.000	0.93	positive

Table S4 Bite force scaling comparison in the full sample of *Pogona vitticeps* (n = 91) for standardised bite force and non-standardised bite force. Adult and juvenile ZZf, sex-reversed females (n = 26), ZWf, concordant females (n = 33), ZZm, males (n = 32). Degrees of freedom 85, 1, 2, 2 for all tests. SE, standard error, * Significant at p = 0.05

log(Bite Force)							ZZf				ZWf				ZZm				
	predicted		genotype		Intercept		slope				slope				slope				
predictor	F	p	F	p	F	p		SE	t	p	difference	SE	t	p	difference	SE	t	p	adj.r2
log(Mass)	740.470	0.0	1.755	0.179	5.128	0.008	0.567	0.047	12.152	0.0	-0.028	0.290	-0.095	0.924	-0.586	0.274	-2.137	0.035*	0.89
log(SVL)	548.895	0.0	1.295	0.279	3.392	0.038	1.747	0.169	10.350	0.0	-0.200	1.117	-0.179	0.858	-2.211	1.053	-2.100	0.039*	0.86
log(HLroret)	664.744	0.0	0.283	0.754	1.710	0.187	1.983	0.173	11.472	0.0	0.191	0.842	0.226	0.822	-1.007	0.782	-1.288	0.201	0.88
log(HLroqu)	737.186	0.0	0.596	0.553	1.444	0.242	2.094	0.173	12.095	0.0	-0.345	0.834	-0.413	0.681	-1.160	0.752	-1.542	0.127	0.89
log(HWqu)	798.455	0.0	0.373	0.690	2.738	0.070	1.895	0.147	12.885	0.0	0.076	0.674	0.113	0.910	-1.101	0.620	-1.776	0.079	0.90
log(HWmt)	692.954	0.0	0.721	0.489	1.713	0.187	2.095	0.176	11.930	0.0	0.013	0.796	0.016	0.987	-1.015	0.730	-1.390	0.168	0.89
log(HDmt)	671.280	0.0	0.391	0.677	1.101	0.337	2.003	0.173	11.543	0.0	0.232	0.670	0.347	0.730	-0.584	0.617	-0.947	0.346	0.88
log(Bite Force nl)							ZZf				ZWf				ZZm				
	predicted		genotype		Intercept		slope				slope				slope				
predictor	F	p	F	p	F	p		SE	t	p	difference	SE	t	p	difference	SE	t	p	adj.r2
log(Mass)	672.621	0.0	1.814	0.169	3.816	0.026	0.602	0.051	11.828	0.0	0.030	0.316	0.095	0.925	-0.510	0.299	-1.706	0.092	0.88
log(SVL)	510.221	0.0	1.420	0.247	2.569	0.083	1.848	0.182	10.158	0.0	-0.099	1.204	-0.082	0.935	-2.019	1.135	-1.780	0.079	0.85
log(HLroret)	585.343	0.0	0.356	0.702	1.110	0.334	2.102	0.191	11.016	0.0	0.353	0.930	0.380	0.705	-0.770	0.863	-0.892	0.375	0.87
log(HLroqu)	642.079	0.0	0.685	0.507	0.882	0.418	2.207	0.192	11.483	0.0	-0.259	0.926	-0.280	0.780	-0.987	0.835	-1.183	0.240	0.88
log(HWqu)	733.142	0.0	0.504	0.606	1.941	0.150	2.004	0.160	12.556	0.0	0.160	0.731	0.219	0.827	-0.951	0.672	-1.415	0.161	0.89
log(HWmt)	628.116	0.0	0.840	0.435	1.054	0.353	2.225	0.191	11.619	0.0	0.147	0.868	0.169	0.866	-0.783	0.796	-0.983	0.328	0.87
log(HDmt)	646.783	0.0	0.391	0.677	0.826	0.441	2.129	0.184	11.562	0.0	0.363	0.711	0.511	0.611	-0.422	0.655	-0.645	0.521	0.88

ADDITIONAL FIGURES

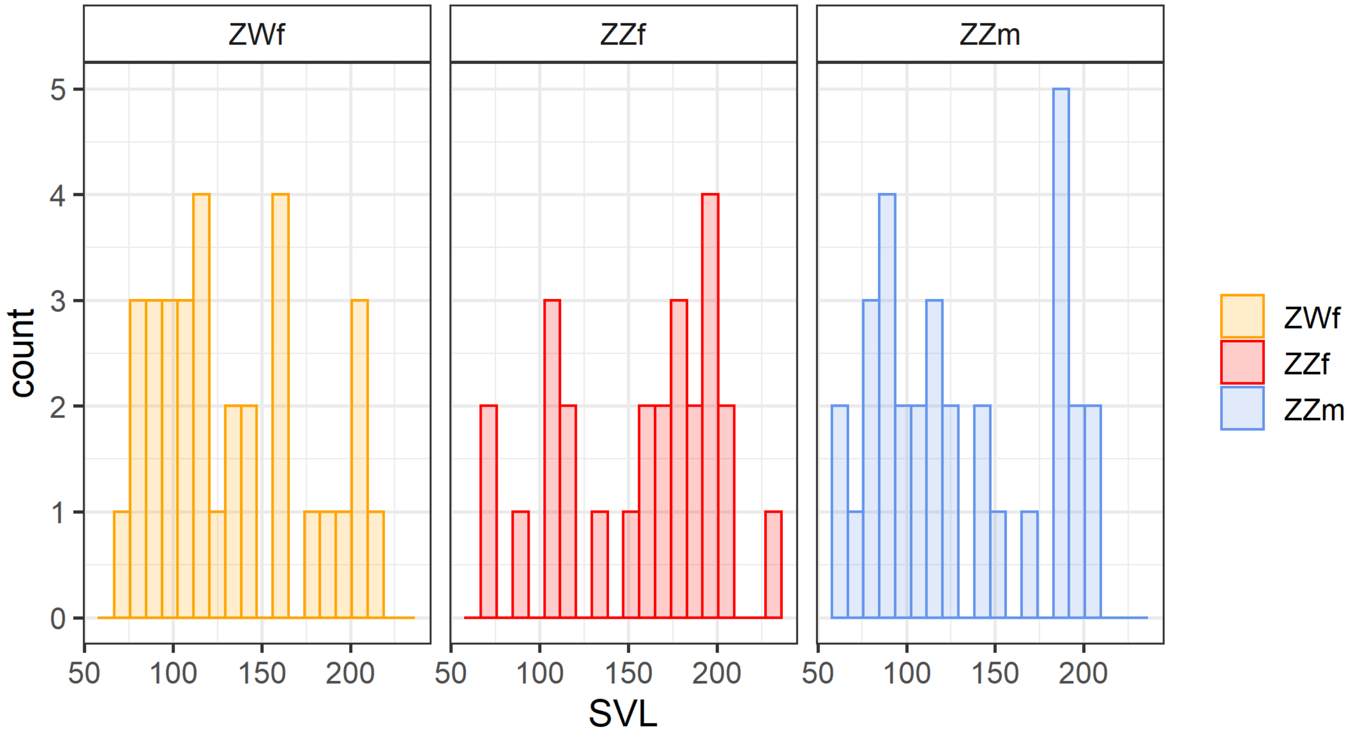

Figure S1 Full sample organised by genotype and 20 mm bins of snout-vent-length.

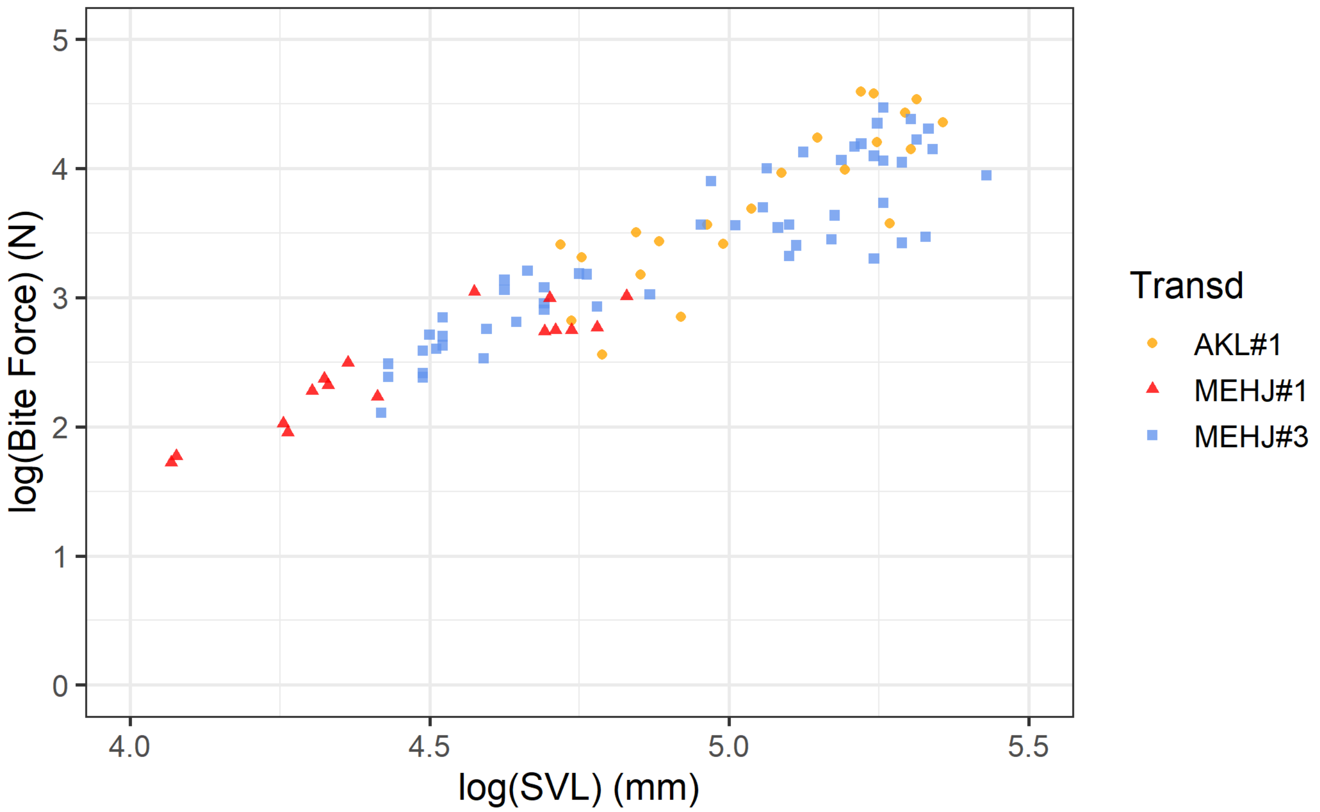

Figure S2 Relationships between log snout-vent length (SVL) and bite force (after out lever standardization) in *Pogona vitticeps* (n = 91) colour coded according to the transducer used (not genotype). The bite plates of MEHJ#1 are 20 mm wide whereas those of MEHJ#3 and AKL#1 are 25 mm wide.

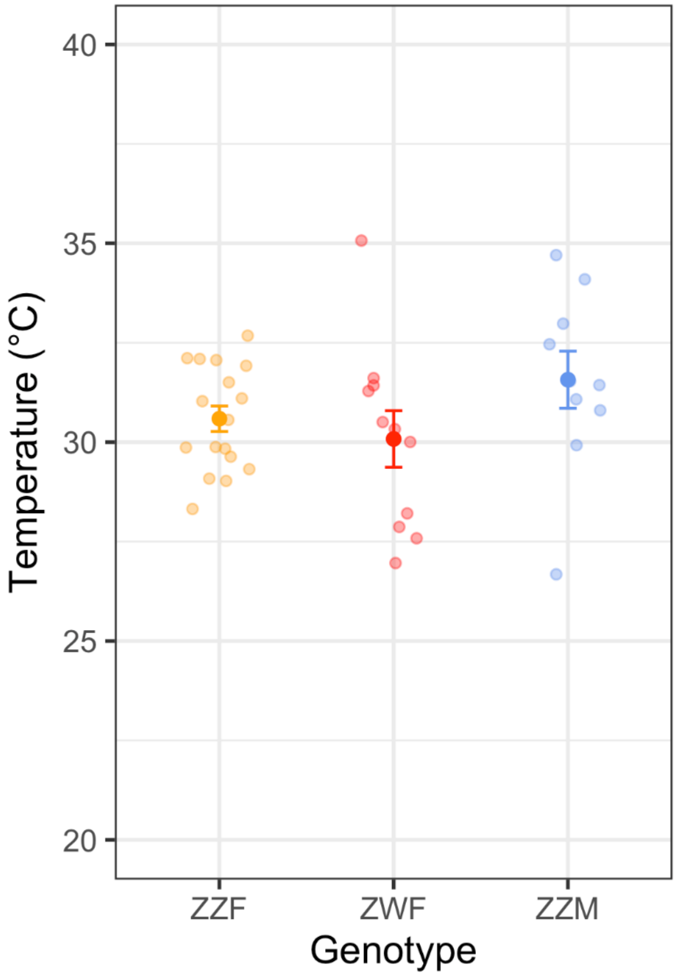

Figure S3 Surface temperature of adult *Pogona vitticeps* of known genotype (>150 SVL mm, n = 39). We measured body temperature using a Digitech QM-7221 digital temperature gun with dual laser targeting between the first and second trial.

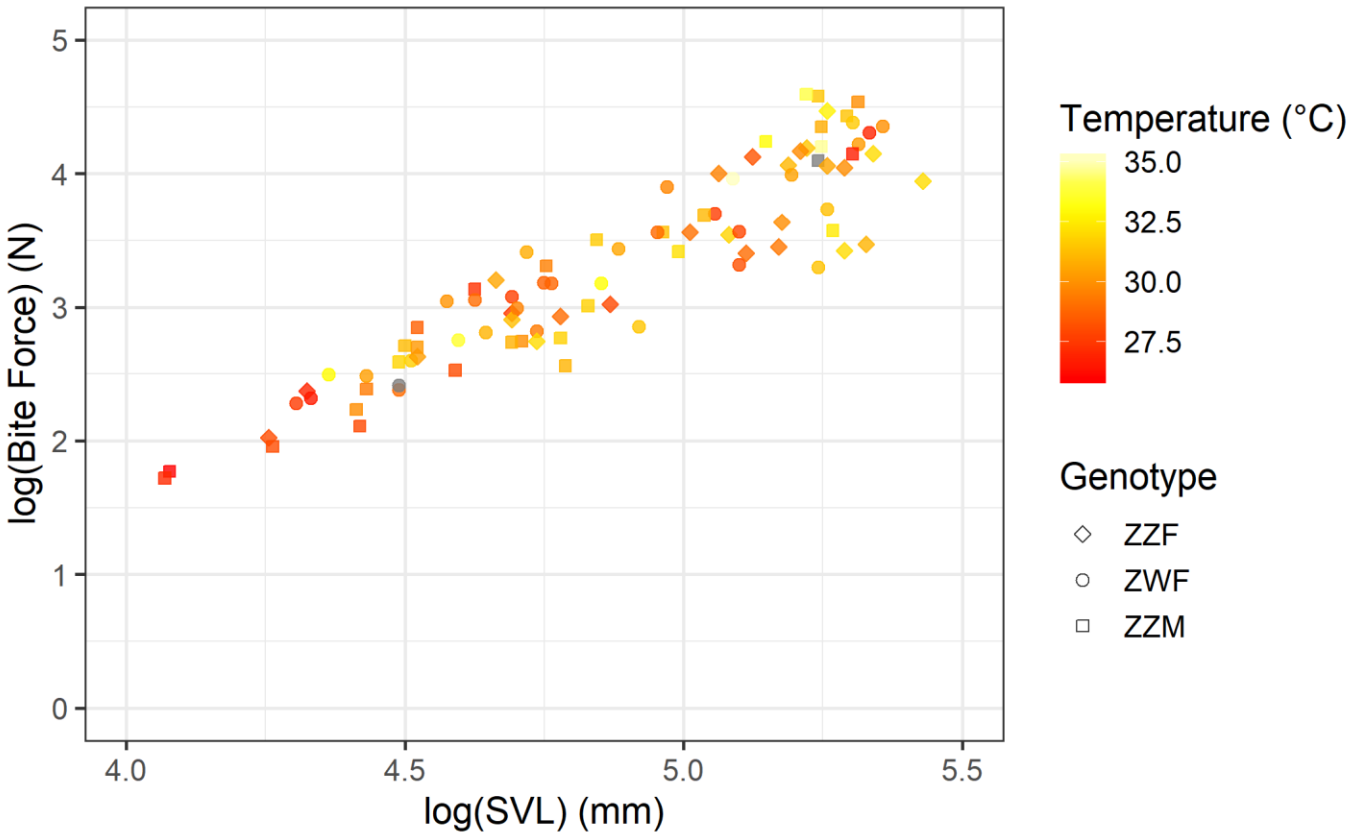

Figure S4 Relationships between log snout-vent length (SVL) and bite force in *Pogona vitticeps* (n = 91) of three different genotypes colour coded for surface body temperature. Grey points represent individuals with uncertain external temperature**.** There is no obvious relationship to body temperature. ZZf, sex-reversed females (n = 26), ZWf, concordant females (n = 33), ZZm, males (n = 32).

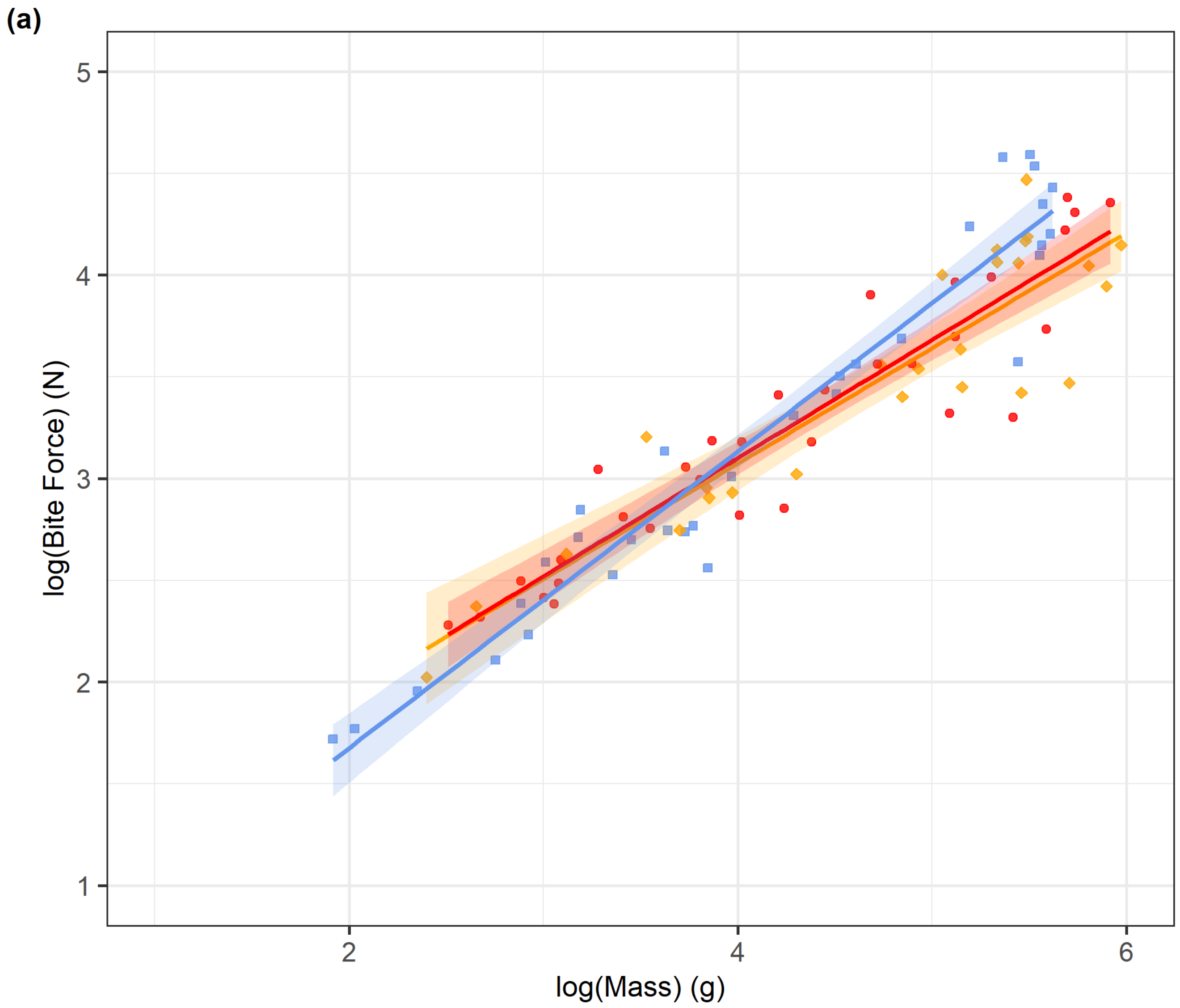

Figure S5 Relationships between log mass and bite force in *Pogona vitticeps* (n = 91) of three different genotypes. ZZf, sex-reversed females (n = 26), ZWf, concordant females (n = 33), ZZm, males (n = 32).

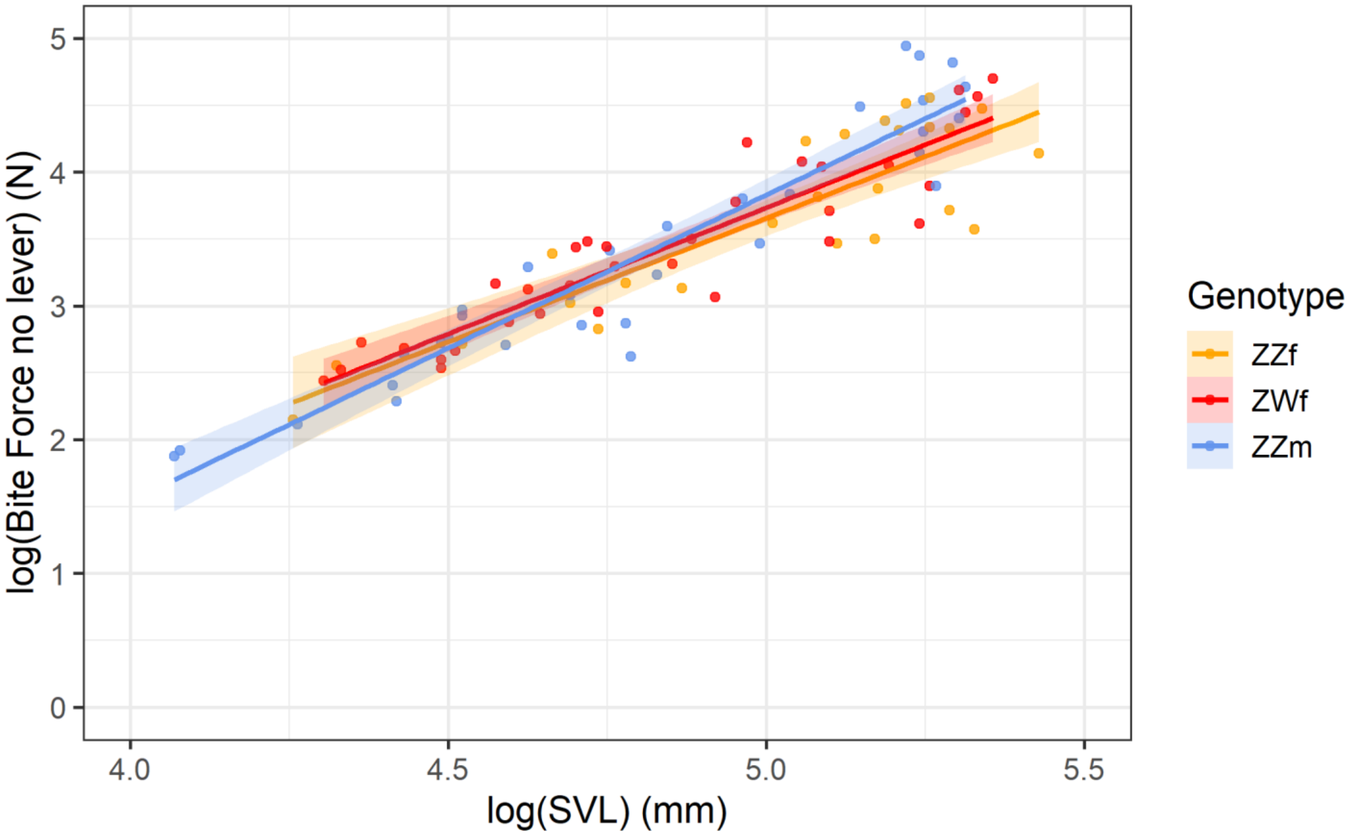

Figure S6 Relationships between log snout-vent length (SVL) and bite force (with no lever correction) in *Pogona vitticeps* (n = 91) of three different genotypes. ZZf, sex-reversed females (n = 26), ZWf, concordant females (n = 33), ZZm, males (n = 32).

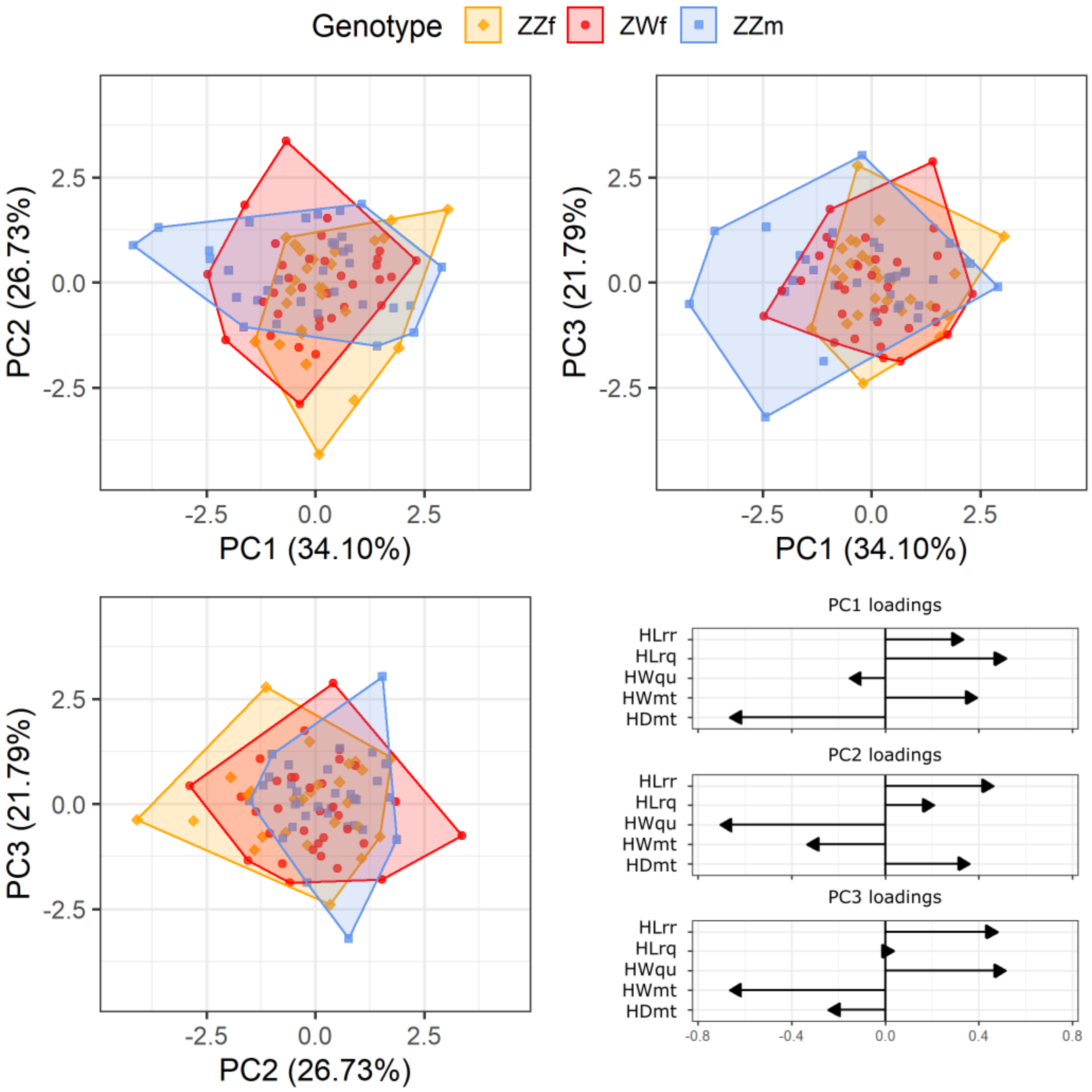

Figure S7 Head shape differences among *Pogona vitticeps* of known genotype (n = 91) according to a principal components analysis of log shape ratios of five head dimensions. PC1 (34.0%) mainly represents head length vs head depth, PC2 (26.7%) mainly represents head width vs all other dimensions, and PC3 (21.8%) represents head width at the mid temporal region vs head width at the jaw joints (quadrate bones). Arrows indicate the loading of each head dimension for each PC axis.

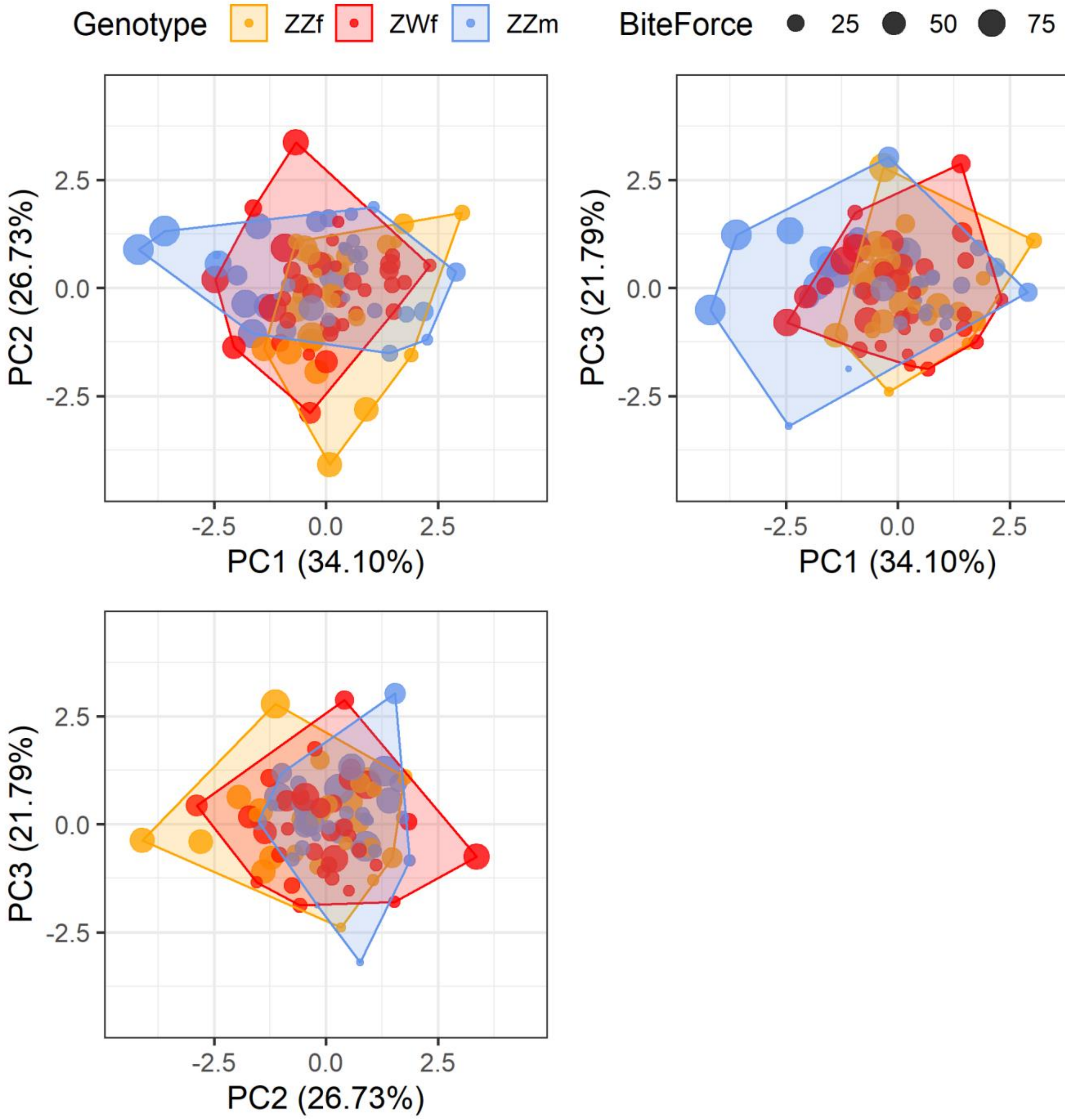

Figure S8 Head shape differences among *Pogona vitticeps* of known genotype (n = 91) according to a principal components analysis of log shape ratios of five head dimensions. Same plot as Figure S6 but with points scaled to bite force.

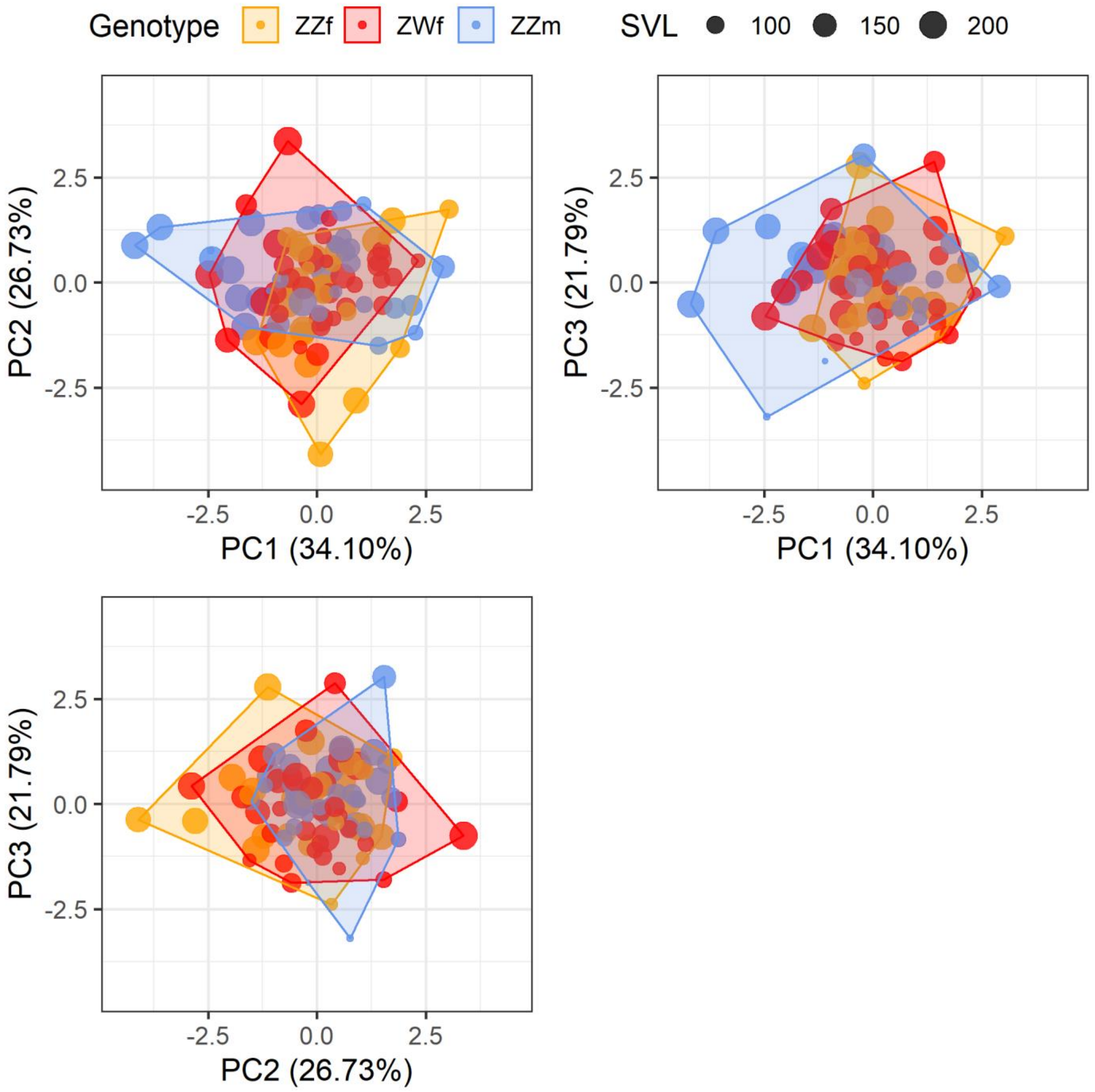

Figure S9 Head shape differences among *Pogona vitticeps* of known genotype (n = 91) according to a principal components analysis of log shape ratios of five head dimensions. Same plot as Figure S6 but with points scaled to SVL.

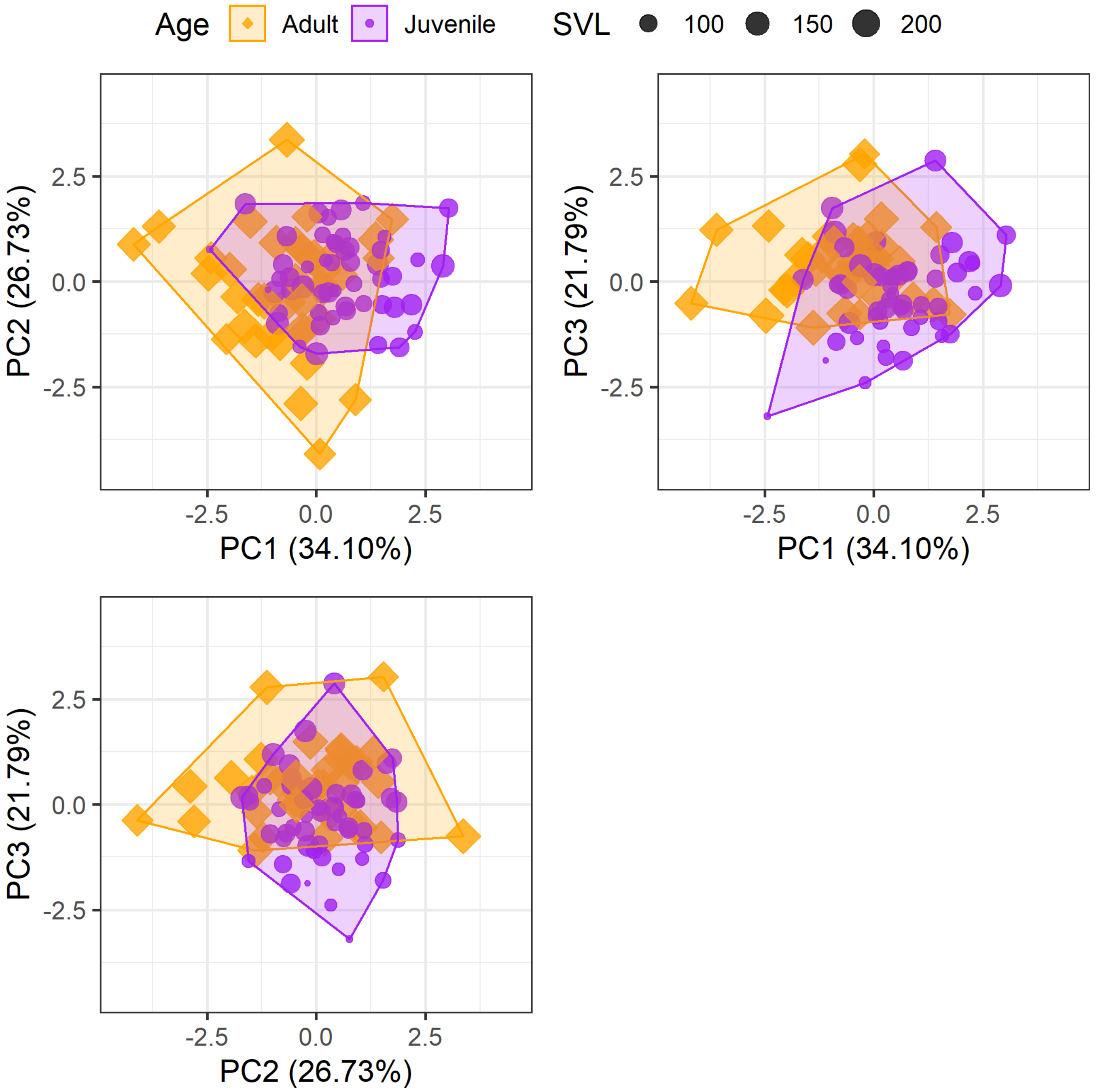

Figure S10 Head shape differences among *Pogona vitticeps* of known genotype (n = 91) according to a principal components analysis of log shape ratios of five head dimensions. Same plot as Figure S7 but with juveniles and adults indicated.

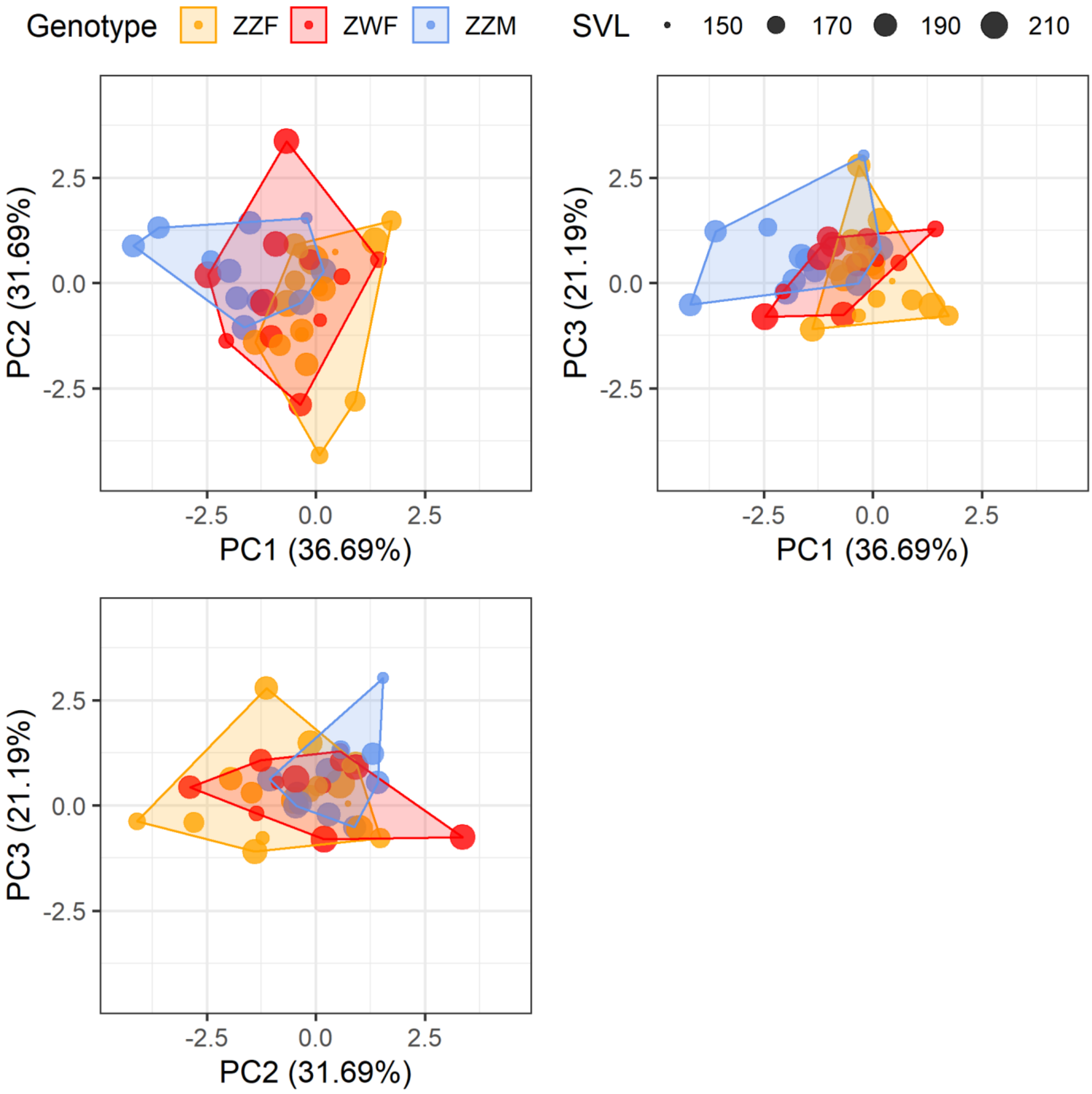

Figure S11 Head shape differences among adult *Pogona vitticeps* of known genotype (>150 SVL mm, n = 39) according to a principal components analysis of log shape ratios of five head dimensions. Same as previous plot but with points scaled to snout vent length.

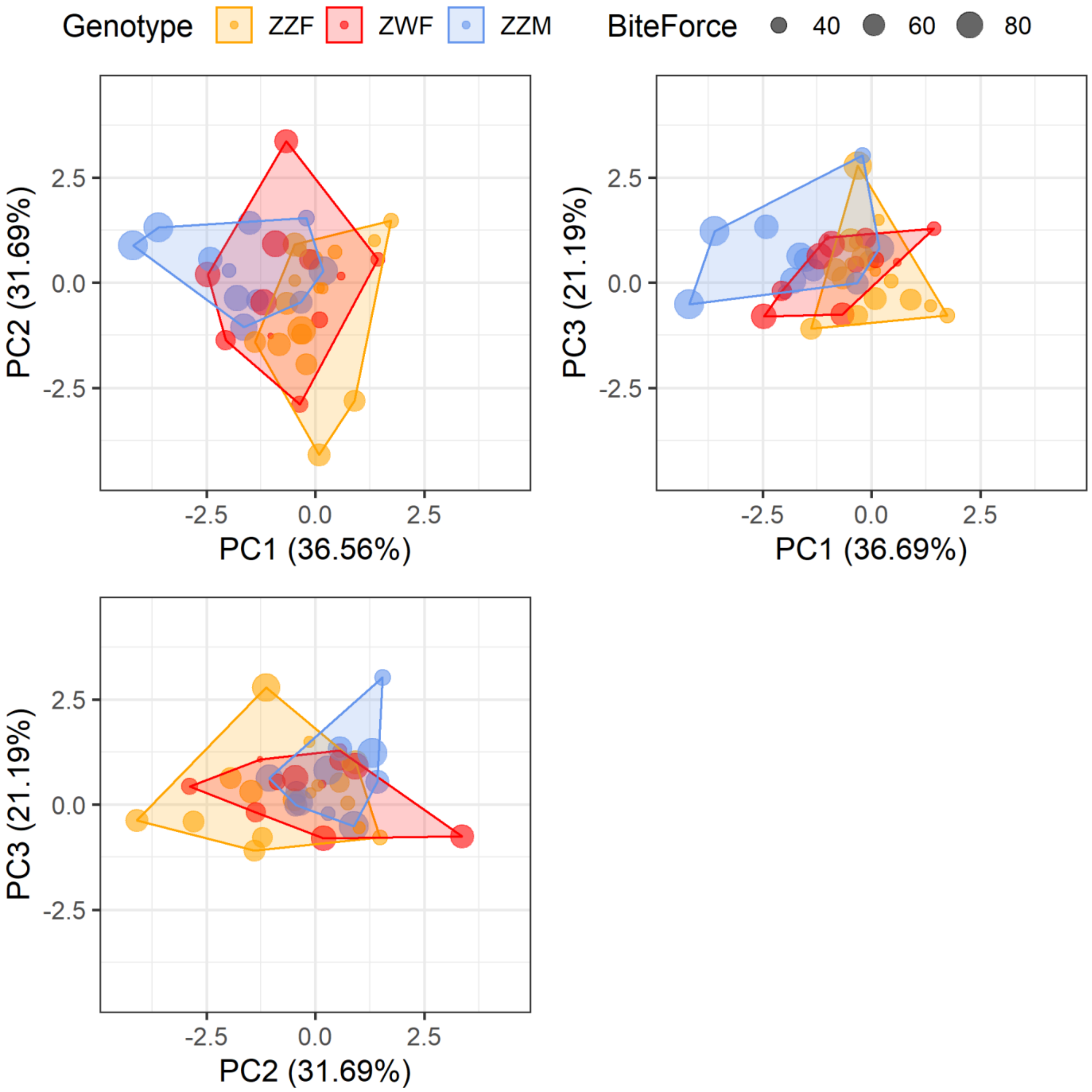

Figure S12 Head shape differences among adult *Pogona vitticeps* of known genotype (>150 SVL mm, n = 39) according to a principal components analysis of log shape ratios of five head dimensions. Same as previous plot but with points scaled to bite force.