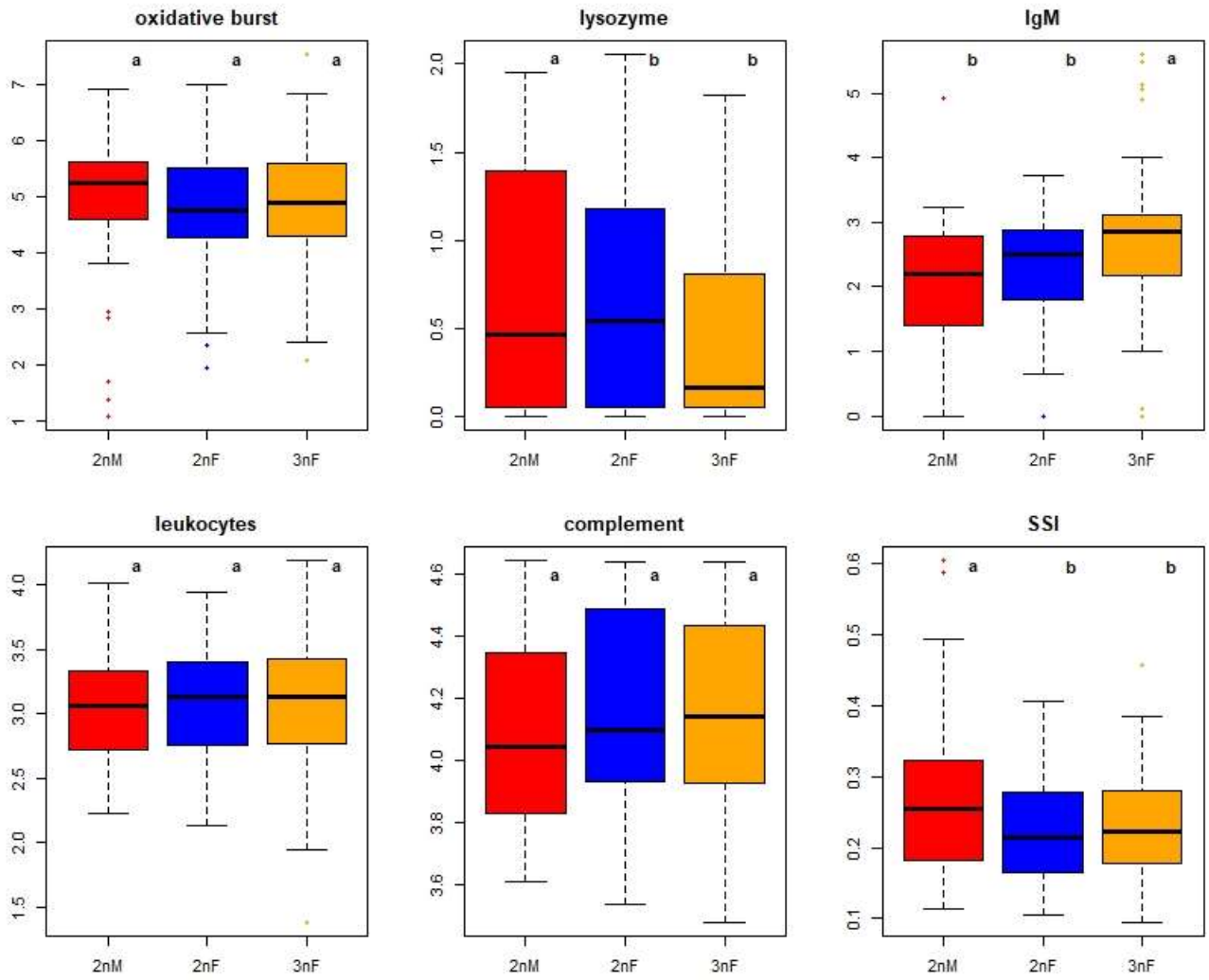**Fig. S1.** Physiological parameters (all log-transformed) in three fish groups. Horizontal line – median, box – interquartile range, whiskers – non-outlier range (i.e. 1.5*IQR), points – outliers. Fish groups that share the same letter do not significantly differ from each other according to *post-hoc* tests (Tukey HSD equivalents for LMM).
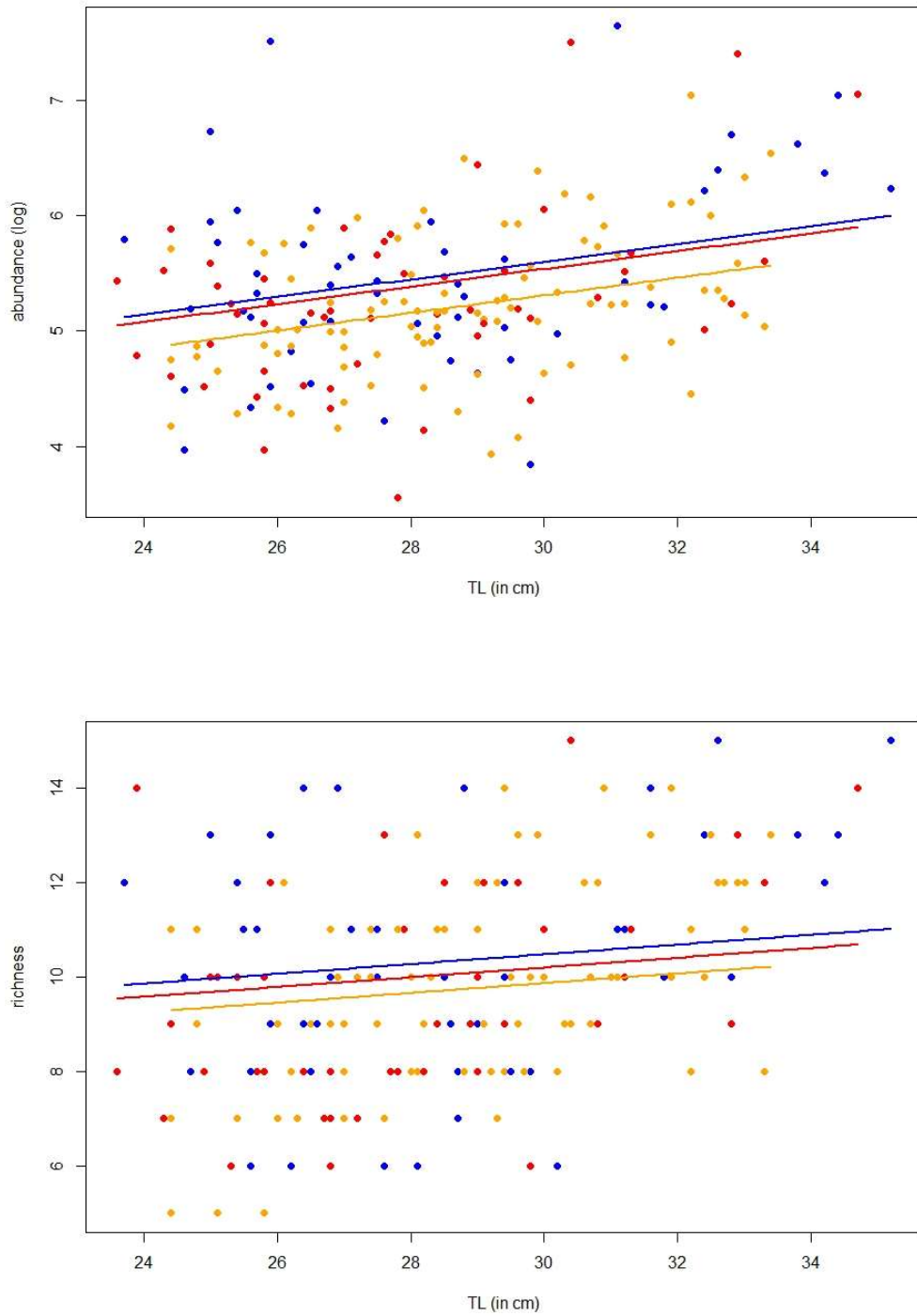
Fig. S2. Immunological parameters (all log-transformed) in three fish groups. Horizontal line – median, box – interquartile range, whiskers – non-outlier range (i.e. 1.5*IQR), points – outliers. Fish groups that share the same letter do not significantly differ from each other according to *post-hoc* tests (Tukey HSD equivalents for LMM).

Fig. S3. Parasite abundance (log-transformed) and parasite species richness as a function of fish host total length (TL) in three fish groups. Lines represent patterns predicted by LMM. Blue – 2nM, red – 2nF, orange – 3nF.

Table S1. Parameters of backward-stepwise selection of models predicting parasite abundance, richness and assemblage composition in three fish groups of gibel carp. Final models are marked with F and their parameters are in bold. Individual models are marked as m1-m11. TL = fish standard length, IM1, IM2, PH1, PH2 refer to PCA axis coordinates of physiological and immunological parameters, G – fish group, interactions are marked with ":" symbol, df – degrees of freedom, k – number of parameters in a PERMANOVA model, ΔAIC – AIC difference from the nearest nested model, P – P-value of likelihood ratio test between the model and the nearest nested model (not possible for PERMANOVA, P-values of the terms removed in the null model are provided instead), removed – term removed from the model in comparison with the nearest nested model. Terms that were removed from the model in expense of AIC increase of ≥ 2 (and removal of which resulted in significant likelihood ratio test) are in bold, terms with AIC increase between 0 and 2 (and with likelihood ratio test near to significance) are in italics.

a) abundance (log)

F		Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	df	AIC	ΔAIC	P	remove
	m1	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	18	373.3			
	m2	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G		16	370.0	–3.3	0.703	PH2:G
	m3	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G			14	366.9	–3.1	0.652	PH1:G
	m4	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G				12	364.3	–2.6	0.494	IM2:G
	m5	Int.	TL	IM1	IM2	PH1		G	IM1:G				11	362.3	–2.0	0.967	PH2
	m6	Int.	TL	IM1	IM2			G	IM1:G				10	361.6	–0.7	0.246	PH1:G
F	**m7**	**Int.**	**T**	**IM1**				**G**	**IM1:G**				**9**	**361.2**	–0.4	0.205	IM2
	m8	Int.	TL	IM1				G					8	374.5	**13.3**	**< 0.001**	**IM1:G**
	m9	Int.		IM1				G	IM1:G				7	374.5	**13.2**	**< 0.001**	**TL**

b) richness

F		Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	df	AIC	ΔAIC	P	remove
	m1	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	18	790.7			
	m2	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G		16	787.2	–3.5	0.772	PH2:G
	m3	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G			14	783.3	–3.9	0.949	PH1:G
	m4	Int.	TL	IM1	IM2	PH1	PH2	G	IM1:G				12	781.1	–2.2	0.404	IM2:G
	m5	Int.	TL	IM1	IM2	PH1	PH2	G					10	778.2	–2.9	0.583	IM1:G
	m6	Int.	TL	IM1	IM2	PH1		G					9	777.3	–0.9	0.301	PH2
	m7	Int.	TL	IM1	IM2			G					8	775.3	–2.0	0.963	PH1
	m8	Int.	TL	IM1				G					7	773.7	–1.5	0.486	IM2
	m9	Int.	TL					G					6	772.5	–1.3	0.391	IM1
	m10	Int.	TL										4	773.1	*0.6*	*0.099*	*G*
F	**m11**	**Int.**											**3**	**774.0**	*0.9*	*0.088*	*TL*

c) NMDS Axis 1 coordinates

F		Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	df	AIC	ΔAIC	P	remove
	m1	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	17	109.8			
	m2	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G		15	107.6	–2.3	0.420	PH2:G
	m3	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G			13	103.8	–3.7	0.881	PH1:G
	m4	Int.	IM1	IM2	PH1	PH2	G	IM1:G				11	105.3	*1.5*	*0.063*	*IM2:G*
	m5	Int.	IM1	IM2	PH1		G	IM1:G				10	103.6	–1.7	0.616	PH2
	m6	Int.	IM1	IM2			G	IM1:G				9	101.7	–1.9	0.716	PH1
F	**m7**	**Int.**	**IM1**				**G**	**IM1:G**				**8**	**99.7**	–2.0	0.852	IM2
	m8	Int.	IM1				G					6	108.3	**8.6**	**0.002**	**IM1:G**

d) NMDS Axis 2 coordinates

F		Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	df	AIC	ΔAIC	P	remove
	m1	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	17	–115.7			
	m2	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G		15	–114.6	*1.1*	*0.077*	*PH2:G*
	m3	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G			13	–115.2	–0.7	0.192	PH1:G
	m4	Int.	IM1	IM2	PH1	PH2	G	IM1:G				11	–118.8	–3.6	0.816	IM2:G
	m5	Int.	IM1	IM2	PH1	PH2	G					9	–122.3	–3.5	0.775	IM1:G
	m6	Int.	IM1	IM2	PH1	PH2						7	–123.1	–0.8	0.198	G
	m7	Int.	IM1	IM2	PH1							6	–124.7	–1.6	0.536	PH2
	m8	Int.	IM1	IM2								5	–126.6	–1.9	0.712	PH1
F	**m9**	**Int.**	**IM1**									**4**	**–128.3**	–1.8	0.638	IM2

			IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	k	AIC	ΔAIC	P	remove
	m10	Int.										3	−124.0	**4.4**	**0.012**	**IM1**
		e) assemblage composition via PERMANOVA										k	AIC	ΔAIC	P	remove
	m1	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G	PH2:G	15	−554.8			
	m2	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G	PH1:G		13	−557.4	*−2.7*	0.772	PH2:G
	m3	Int.	IM1	IM2	PH1	PH2	G	IM1:G	IM2:G			11	−559.1	*−1.6*	0.308	PH1:G
F	**m4**	**Int.**	**IM1**	**IM2**	**PH1**	**PH2**	**G**	**IM1:G**				9	**−559.1**	*0.0*	*0.053*	*IM2:G*
	m5	Int.	IM1	IM2	PH1	PH2	G					7	−557.1	**2.0**	**0.006**	**IM1:G**
	m6	Int.	IM1	IM2	PH1		G	IM1:G				8	−555.9	**3.2**	**0.002**	**PH2**
	m7	Int.	IM1	IM2		PH2	G	IM1:G				8	−554.7	**4.3**	**0.001**	**PH1**
	m8	Int.	IM1		PH1	PH2	G	IM1:G				8	−556.4	**2.7**	**0.001**	**IM2**

Table S2. Extension of Table 3, presenting relationship between coordinates of the first two axes of immunology and physiology PCA (IM1, IM2, PH1, PH2) and four parasite load measures: parasite abundance (log-transformed), parasite species richness, and coordinates of the first two NMDS axes determining the percentage composition of the parasite assemblage. For each combination of response and predictor, marginal R^2 (explaining the variability of the fixed effect, in %) and AIC are presented. AIC and R^2 of the significant predictors (see Table 3) are in bold.

Response	Group	marginal R^2				AIC			
		IM1	IM2	PH1	PH2	IM1	IM2	PH1	PH2
Abundance	2nM	**18.9**	13.4	9.7	9.1	**110.4**	114.6	115.2	115.2
	2nF	**19.2**	5.6	7.8	6.1	**127.4**	131.4	130.6	130.6
	3nF	9.6	**22.5**	8.5	13.7	172.7	**169.0**	172.2	172.1
Richness	2nM	1.2	1.0	0.5	0.5	212.1	211.8	212.6	212.7
	2nF	0.7	1.9	0.8	1.6	236.2	236.3	236.3	236.1
	3nF	4.3	4.0	4.2	12.0	359.6	359.4	359.6	356.3
NMDS1	2nM	3.5	**8.1**	0.7	0.0	27.9	**27.7**	29.1	29.3
	2nF	**10.2**	2.2	2.3	0.5	**68.8**	70.5	70.2	71.0
	3nF	0.0	0.0	0.1	0.3	14.5	14.4	14.2	14.2
NMDS2	2nM	6.7	0.0	**13.4**	3.3	−21.6	−18.4	**−25.5**	−22.3
	2nF	6.2	2.0	0.1	**8.9**	−30.4	−29.3	−28.4	**−33.2**
	3nF	3.9	0.5	1.4	0.2	−22.2	−19.9	−21.2	−19.6