Table S1. **Differentially expressed gene quantities compared across the two predominant eukaryotic compartments of the *Pocillopora damicornis* coral holobiont**. When the "More responsive compartment" has been left blank, this indicates that the differentially expressed gene (DEG) percentage (*i.e.*, "% DEGs;" #DEGs/total contig count x 100) from each compartment was similar. C=control temperature (27°C), H=high temperature (30°C), C2=controls sampled after 2 weeks, H2=high temperature corals sampled after 2 weeks, C36=control corals sampled after 36 weeks, H36=high temperature corals sampled after 36 weeks.

Comparison	α level	#contigs (%)	fold change or comparison	#contigs (%)	#coral contigs (% DEGs)	#*Symbiodinium* contigs (% DEGs)	Coral vs. *Symbiodinium* % DEGs two-sample proportion test *Z*-score	More responsive compartment
C vs. H	10^{0}	236,435 (100%)	10	1,564 (0.661%)	564 (1.17%)	66 (0.429%)	8.070***	host coral
	10^{-1}	35,773 (15.1%)	10	590 (0.250%)	157 (0.326%)	39 (0.254%)	1.40	
	10^{-2}	5,092 (2.15%)	10	133 (0.056%)	28 (0.058%)	9 (0.059%)	0.022	
	10^{-3}	897 (0.379%)	10	32 (0.014%)	4 (<0.01%)	3 (<0.01%)	1.15	
	10^{-4}	265 (0.112%)	2	49 (0.021%)	8 (0.017%)	6 (0.039%)	1.63	
	10^{-5}	109 (0.046%)	2	10 (<0.01%)	1 (<0.01%)	0	0.565	
	10^{-6}	80 (0.034%)	C=0, H>0	65 (0.028%)	1 (<0.01%)	6 (0.039%)	3.80*	*Symbiodinium*
			C>0, H=0	13 (<0.01%)	2 (<0.01%)	0	0.799	
	10^{-7}	58 (0.025%)	C=0, H>0	52 (0.022%)	1 (<0.01%)	6 (0.039%)	3.80**	*Symbiodinium*
			C>0, H=0	5 (<0.01%)	1 (<0.01%)	0	0.565	
	10^{-8}	43 (0.018%)	C=0, H>0	40 (0.017%)	1 (<0.01%)	6 (0.039%)	3.80**	*Symbiodinium*
			C>0, H=0	3 (<0.01%)	0	0	no annotated results	
	10^{-9}	28 (0.012%)	C=0, H>0	25 (0.011%)	0	3 (<0.01%)	3.068*	*Symbiodinium*
			C>0, H=0	3 (<0.01%)	0	0	no annotated results	
No annotated contigs were differentially expressed at an α level of 10^{-10}.								
C2 vs. H2	10^{0}	236,435 (100%)	10	1,260 (0.533%)	546 (1.13%)	63 (0.410%)	8.010***	host coral
	10^{-1}	16,788 (7.10%)	10	208 (0.088%)	57 (0.118%)	15 (0.098%)	0.662	
	10^{-2}	1,546 (0.654%)	10	49 (0.021%)	13 (0.027%)	2 (0.013%)	0.981	
	10^{-3}	232 (0.098%)	10	9 (<0.01%)	2 (<0.01%)	1 (<0.01%)	0.371	
			2	43 (0.018%)	9 (0.019%)	5 (0.032%)	1.01	

			C=0, H>0	118 (0.050%)	5 (0.010%)	12 (0.078%)	4.47**	*Symbiodinium*
			C>0, H=0	11 (<0.01%)	2 (<0.01%)	0	0.799	
	10^{-4}	15 (<0.01%)	C=0, H>0	1 (<0.01%)	0	0	no annotated results	
			C>0, H=0	2 (<0.01%)	1 (<0.01%)	0	0.565	
	10^{-5}	No annotated contigs were differentially expressed at an α level of 10^{-5}.						
C36 vs. H36	10^{0}	236,435 (100%)	10	1,656 (0.700%)	579 (1.20%)	109 (0.709%)	5.13***	host coral
	10^{-1}	9,708 (4.11%)	10	265 (0.112%)	81 (0.168%)	31 (0.202%)	0.868	
	10^{-2}	735 (0.311%)	10	56 (0.024%)	15 (0.031%)	9 (0.059%)	1.53	
	10^{-3}	54 (0.023%)	10	12 (<0.01%)	5 (0.010%)	3 (<0.01%)	0.881	
			2	36 (0.015%)	8 (0.017%)	7 (0.046%)	2.04	
			C=0, H>0	5 (<0.01%)	4 (<0.01%)	0	1.13	
			C>0, H=0	5 (<0.01%)	2 (<0.01%)	0	0.799	
	10^{-4}	6 (<0.01%)	2	1 (<0.01%)	0	0	no annotated results	
			C=0, H>0	2 (<0.01%)	2 (<0.01%)	0	0.799	
			C>0, H=0	0	0	0	no annotated results	
	10^{-5}	No annotated contigs were differentially expressed at an α level of 10^{-5}.						
2 vs. 36	10^{0}	236,435 (100%)	10	3,195 (1.35%)	911 (1.89%)	219 (1.42%)	3.80**	host coral
	10^{-1}	70,938 (30.0%)	10	2,008 (0.849%)	460 (0.954%)	169 (1.099%)	1.59	
	10^{-2}	30,884 (13.1%)	10	529 (0.224%)	99 (0.205%)	52 (0.338%)	2.95*	*Symbiodinium*
	10^{-3}	13,086 (5.53%)	10	139 (0.059%)	25 (0.052%)	13 (0.085%)	1.45	
	10^{-4}	3,202 (1.35%)	10	39 (0.017%)	9 (0.019%)	5 (0.032%)	1.01	
	10^{-5}	516 (0.218%)	10	8 (<0.01%)	2 (<0.01%)	2 (<0.01%)	1.21	
			2	360 (0.152%)	45 (0.093%)	108 (0.702%)	13.4***	*Symbiodinium*
	10^{-6}	126 (0.053%)	2	36 (0.015%)	2 (<0.01%)	7 (0.046%)	3.76**	*Symbiodinium*
	10^{-7}	60 (0.025%)	2	3 (<0.01%)	1 (<0.01%)	1 (<0.01%)	0.853	
			C=0, H>0	14 (<0.01%)	1 (<0.01%)	0	0.565	
			C>0, H=0	43 (0.018%)	1 (<0.01%)	6 (0.039%)	3.80**	*Symbiodinium*
	10^{-8}	42 (0.018%)	C=0, H>0	3 (<0.01%)	0	0	no annotated results	
			C>0, H=0	39 (0.017%)	1 (<0.01%)	6 (0.039%)	3.80**	*Symbiodinium*
	10^{-9}	28 (0.012%)	C=0, H>0	25	0	3 (0.02%)	3.10**	*Symbiodinium*
			C>0, H=0	3 (<0.01%)	0	0	no annotated results	
	No annotated contigs were differentially expressed at an α level of 10^{-10}.							

*p<0.01. **p<0.001. ***p<0.0001.

Table S2. Repeated-measures ANOVA results of host coral gene expression. Full gene names and the respective functional categories can be found in Table 1. Statistically significant differences ($p<0.05$) have been underlined for emphasis. R^2 values between data derived from the two gene expression quantification techniques can be found in Figs. S1 and S2. "HSD" = honestly significant difference.

Gene	**Illumina-derived data**			**Fig.**	**Real-time PCR-derived data**			**Fig.**
source of variation	Exact *F*	*p*	Tukey's HSD tests		Exact *F*	*p*	Tukey's HSD tests	
ca				S1a				S1b
treatment	4.0	0.12			3.8	0.15		
time	15	0.019	36>2		0.29	0.63		
treatment x time	8.4	0.044	H36(A)>all others(B)		1.8	0.27		
amylase				S1d				S1e
treatment	42	0.0029	high>control		0.96[a]	0.40		
time	79	<0.001	2>36		59	<0.01	2>36	
treatment x time	14	0.020	H2(A), C2(B), H36(BC), C36(C)		1.04	0.38		
iontrans				S1g				S1h
treatment	13	0.022	high>control		0.18[a]	0.72		
time	43	<0.01	36>2		0.078	0.81		
treatment x time	20.	0.011	H36(A), C36(B), C2(BC), H2(C)		10.3	0.084		
sftase				S1j				S1k
treatment	2.0[b]	0.23			0.01	0.93		
time	30.	<0.01	36>2		13	0.038		
treatment x time	4.5	0.102	C36(A), H36(AB), H2(BC), C2(C)		18	0.024		
mcp				S1m				S1n
treatment	1300	<0.001	high>control		0.27[a]	0.641		
time	42	<0.01	2>36		260	<0.001	2>36	
treatment x time	6.7	0.061	H2(A), C2(B), H36(BC), C36(C)		1.8	0.278		
lectin				S1p				S1q
treatment	150	<0.001	high>control		6.0[a]	0.071		
time	5.8	0.074	36>2		1.2	0.34		

treatment x time	6.1	0.069	H36(A)>all others(B)		1.4	0.31	
selectin				S1s			S1t
treatment	5.7	0.075			1.0[a]	0.38	
time	8.2	0.046	2>36		21	0.020	2>36
treatment x time	10.	0.034	H2(A)>all others (B)		0.90	0.41	H2(A), C2(AB), H36(AB), C36(B)
hsp70				S2a			S2b
treatment	1.2	0.34			0.36	0.58	
time	8.6	0.043	36>2		0.27	0.63	
treatment x time	0.90	0.40			0.015	0.91	
cu-zn-sod				S2d			S2e
treatment	5.0	0.090	control>high		9.1[b]	0.057	
time	24	<0.01	36>2		0.6	0.50	
treatment x time	0.039	0.85			1.4	0.33	
vwfα				S2g			S2h
treatment	17	0.015	high>control		0.12[b]	0.75	
time	0.28	0.63			0.39	0.58	
treatment x time	71	0.001	H36(A), C2(A), H2(B), C36(B)		0.20	0.69	
DNAp				S2j			S2k
treatment	102	<0.001	control>high		1.5[a]	0.29	
time	32	<0.01	36>2		8.3	0.045	36>2
treatment x time	<0.01	0.93	C36(A), C2(B), H36(B), H2(C)		0.42	0.55	
smc-csp				S2m			S2n
treatment	150	<0.001	control>high		0.25	0.65	
time	2.2	0.21			21	0.019	
treatment x time	0.65	0.47	C2(A), C36(A), H2(B), H36(B)		21	0.019	
gfp-like cp				S2p			S2q
treatment	6.6	0.062			3.2[a]	0.17	
time	7.1	0.056	36>2		0.046	0.84	
treatment x time	5.7	0.076	H36(A)>all others(B)		4.7	0.12	H36(A), C2(AB), H2(AB), C36(B)

[a]log-transformed data. [b]rank-transformed data.

Table S3. **Repeated-measures ANOVA results of *Symbiodinium* gene expression.** Full gene names and the respective functional categories can be found in Table 1. Statistically significant differences ($p<0.05$) are underlined for emphasis. R^2 values between data derived from the two gene expression quantification techniques can be found in Figs. S3 and S4. Genes for which both techniques yielded significant temperature treatment effects (in the model as a whole or in the post-hoc tests) have been emphasized in bold font. "HSD" = honestly significant difference.

Gene	**Illumina-derived data**			**Fig.**	**Real-time PCR-derived data**			**Fig.**
source of variation	Exact *F*	*p*	Tukey's HSD tests		Exact *F*	*p*	Tukey's HSD tests	
transketolase				S3a				S3b
treatment	22[a]	0.043			1.0[a]	0.42		
time	13	0.071	2>36		32	0.030	2>36	
treatment x time	0.033	0.87	C2(A), H2(AB), H36(BC), C36(C)		5.2	0.15	C2(A), H2(AB), H36(B), C36(B)	
zifl1l				S3d				S3e
treatment	21	<0.01	control>high		15[a]	0.060	control>high	
time	32	<0.01	2>36		12	0.076	2>36	
treatment x time	11	0.029	C2(A)>all others(B)		2.0	0.29	C2(A)>all others (B)	
nrt2				S3g				S3h
treatment	0.031	0.87			0.18	0.69		
time	81	<0.001	2>36		22	<0.01		
treatment x time	0.015	0.91	C2(A), H2(A), C36 (B), H36(B)		0.21	0.67	C2(A), H2(AB), H36(BC), C36(C)	
vdic				S3j				S3k
treatment	25	<0.01	high>control		0.077	0.81		
time	78	<0.001	2>36		28	0.035	2>36	
treatment x time	9.4	0.038	H2(A), C2(B), H36(C), C36(C)		2.0	0.29	C2(AB), H2(A), H36(AB), C36(A)	
K^+ *channel*				S3m				S3n
treatment	2.9[b]	0.16			<0.01	0.98		
time	88	<0.001	2>36		27	0.036	2>36	
treatment x time	4.6	0.099	H2(A), C2(A), C36(B), H36(B)		0.81	0.46		
Ca^{2+} *channel*				S3p				S3q

treatment	9.5	0.037	control>high	0.10[b]	0.78	
time	34	<0.01	2>36	7.8	0.11	2>36
treatment x time	3.8	0.12	C2(A)>all others(B)	0.17	0.72	C2(A), H2(AB), H36(AB), C36(B)
rbcL			S3s			S3t
treatment	11[c]	0.030	high>control	0.32	0.60	
time	45	<0.01	2>36	24	<0.01	2>36
treatment x time	0.058	0.82	H2(A), C2(A), H36(B), C36(B)	0.019	0.90	H2(A), C2(AB), H36(BC), C36(C)
psI			S3v			S3w
treatment	12	0.027	high>control	6.7[a]	0.061	
time	49	0.002	2>36	26	<0.01	2>36
treatment x time	0.17	0.70	H2(A), C2(AB), H36(BC), C36(C)	1.9	0.24	H2(A), C2(A), H36(AB), C36(B)
pgpase			S3y			S3z
treatment	3.0	0.16		0.32	0.60	
time	16	0.016	2>36	15	0.018	2>36
treatment x time	0.29	0.62	H2(A), C2(A), H36(AB), C36(B)	0.034	0.86	H2(A), C2(AB), H36(AB), C36(B)
hsp40			S4a			S4b
treatment	0.068[c]	0.81		0.63[a]	0.49	
time	32	<0.01	36>2	5.2	0.11	
treatment x time	0.39	0.57		0.064	0.82	
hsp70			S4d			S4e
treatment	9.3	0.038	high>control	7.4	0.053	
time	34	<0.01	2>36	30	<0.01	2>36
treatment x time	<0.01	0.94	H2(A), C2(AB), H36(BC), C36(C)	2.8	0.17	C2(A), H2(A), H36(B), C36(B)
hsp90			S4g			S4h
treatment	13	0.023	high>control	0.66[a]	0.48	
time	32	<0.01	2>36	66	<0.01	
treatment x time	0.17	0.71	H2(A), C2(B), H36(B), C36(C)	2.7	0.20	C2(A), H2(A), H36(B), C36(B)
apx1			S4j			S4k
treatment	0.14	0.49		0.16[a]	0.71	
time	17	0.014	2>36	34	<0.01	2>36
treatment x time	0.17	0.70	C2(A), H2(A), H36(AB), C36(B)	0.901	0.40	C2(A), H2(A), H36(B), C36(B)
ubiqlig			S4m			S4n
treatment	32	<0.01	high>control	14	0.033	high>control

time	1900	<0.001	2>36	26	0.015	2>36
treatment x time	102	<0.001	H2(A), C2(B), H36(B), C36 (C)	0.31	0.62	H2(A), C2(AB), H36(BC), C36(C)
cildyn			S4p			S4q
treatment	8.7	0.042	high>control	1.1[a]	0.36	
time	48	<0.01	2>36	5.2	0.11	2>36
treatment x time	8.7	0.042	H2(A)>all others(B)	1.2	0.36	
RNA helicase			S4s			S4t
treatment	35	<0.01	high>control	0.23[a]	0.68	
time	73	<0.001	2>36	1300	<0.01	2>36
treatment x time	34	<0.01	H2(A), C2(B), H36(B), C36(C)	75	0.013	H2(A), C2(A), H36(AB), C36(B)

[a]log-transformed data. [b]square root-transformed data. [c]rank-transformed data.

Supplemental figure captions

Fig. S1. Host coral metabolism, transport, and cell adhesion gene expression. mRNA expression levels of genes (see full names in Table 1.) involved in metabolism (a-f), transport (g-o), and cell adhesion (p-u) were determined with either Illumina RNA-Seq (fragments per kilobases mapped [fpkm]; a, d, g, j, m, p, and s) or real-time PCR (inverse-log threshold cycle [C_t] values normalized to recovery of the Solaris™ [Thermo-Scientific] RNA spike; b, e, h, k, n, q, and t) in both control (hollow diamonds of a, b, d, e, g, h, j, k, m, n, p, q, s, and t) and high temperature (black triangles of a, b, d, e, g, h, j, k, m, n, p, q, s, and t) samples. The correlation between these two techniques was also assessed for both the control (white and black diamonds at the 2 and 36-week sampling times, respectively) and high temperature (white and black triangles at the time 2 and 36-week sampling times, respectively) samples (c, f, i, l, o, r, and u), and linear regression *t*-tests were conducted to determine the significance of the correlations. In a, b, d, e, g, h, j, k, m, n, p, q, s, and t, error bars represent standard error of the mean. Letters adjacent to either control or high temperature icons in certain panels denote significance at $p<0.05$ by Tukey's honestly significant difference tests. One biological replicate from the control treatment group sampled after two weeks was considered to be an outlier and was neither analyzed nor plotted.

Fig. S2. Expression of host coral genes involved in the stress response and other processes. mRNA expression levels of genes (see full names in Table 1.) involved in the stress response (a-f) and other processes (g-r) were determined with either Illumina RNA-Seq (fragments per kilobases mapped [fpkm]; a, d, g, j, m, and p) or real-time PCR (inverse-log threshold cycle [C_t] values normalized to recovery of the Solaris™ [Thermo-Scientific] RNA spike; b, e, h, k, n, and q) in both control (hollow diamonds of a, b, d, e, g, h, j, k, m, n, p, and q) and high temperature (black triangles of a, b, d, e, g, h, j, k, m, n, p, and q) samples. The correlation between these two

techniques was also assessed for both the control (white and black diamonds at the 2 and 36-week sampling times, respectively) and high temperature (white and black triangles at the time 2 and 36-week sampling times, respectively) samples (c, f, i, l, o, and r), and linear regression *t*-tests were conducted to determine the significance of the correlations. In a, b, d, e, g, h, j, k, m, n, p, and q, error bars represent standard error of the mean. Letters adjacent to either control or high temperature icons in certain panels denote significance at $p<0.05$ by Tukey's honestly significant difference tests. One biological replicate from the control treatment group sampled after two weeks was considered to be an outlier and was neither analyzed nor plotted.

Fig. S3. *Symbiodinium* metabolism, ion transport, and photosynthesis gene expression. mRNA expression of genes (see full names in Table 1.) involved in metabolism (a-i), ion transport (j-r), and photosynthesis (s-aa) was determined with either Illumina RNA-Seq (fragments per kilobases mapped [fpkm]; a, d, g, j, m, p, s, v, and y) or real-time PCR (inverse-log threshold cycle [C_t] values normalized to recovery of the Solaris™ [Thermo-Scientific] RNA spike; b, e, h, k, n, q, t, w, and z) in both control (hollow diamonds of a, b, d, e, g, h, j, k, m, n, p, q, s, t, v, w, y, and z) and high temperature (black triangles of a, b, d, e, g, h, j, k, m, n, p, q, s, t, v, w, y, and z) samples. The correlation between these techniques was assessed for both control (white and black diamonds at the 2 and 36-week sampling times, respectively) and high temperature (white and black triangles at the time 2 and 36-week sampling times, respectively) samples (c, f, i, l, o, r, u, x, and aa), and linear regression *t*-tests were conducted to determine the significance of the correlations. In a, b, d, e, g, h, j, k, m, n, p, q, s, t, v, w, y, and z, error bars represent standard error of the mean. Letters adjacent to either control or high temperature icons in certain panels denote significance ($p<0.05$) by Tukey's honestly significant difference tests. One biological replicate from the control treatment group sampled after two weeks was considered to be an outlier and was neither analyzed nor plotted.

Fig. S4. Expression of *Symbiodinium* genes involved in the stress response and other processes. mRNA expression of genes (see full names in Table 1.) involved in the stress response (a-o) and other processes (p-u) was determined with either Illumina RNA-Seq (fragments per kilobases mapped [fpkm]; a, d, g, j, m, p, and s) or real-time PCR (inverse-log threshold cycle [C_t] values normalized to recovery of the Solaris™ [Thermo-Scientific, USA] RNA spike; b, e, h, k, n, q, and t) in both control (hollow diamonds of a, b, d, e, g, h, j, k, m, n, p, q, s, and t) and high temperature (black triangles of a, b, d, e, g, h, j, k, m, n, p, q, s, and t) samples. The correlation between these two techniques was assessed across the control (white and black diamonds at the 2 and 36-week sampling times, respectively) and high temperature (white and black triangles at the time 2 and 36-week sampling times, respectively) samples (c, f, i, l, o, and r), and linear regression *t*-tests were conducted to determine the significance of the correlations. In a, b, d, e, g, h, j, k, m, n, p, q, s, and t error bars represent standard error of the mean. Letters adjacent to either control or high temperature icons in certain panels denote significance at $p<0.05$ by Tukey's honestly significant difference tests. One biological replicate from the control treatment group sampled after two weeks was considered to be an outlier and was neither analyzed nor plotted.

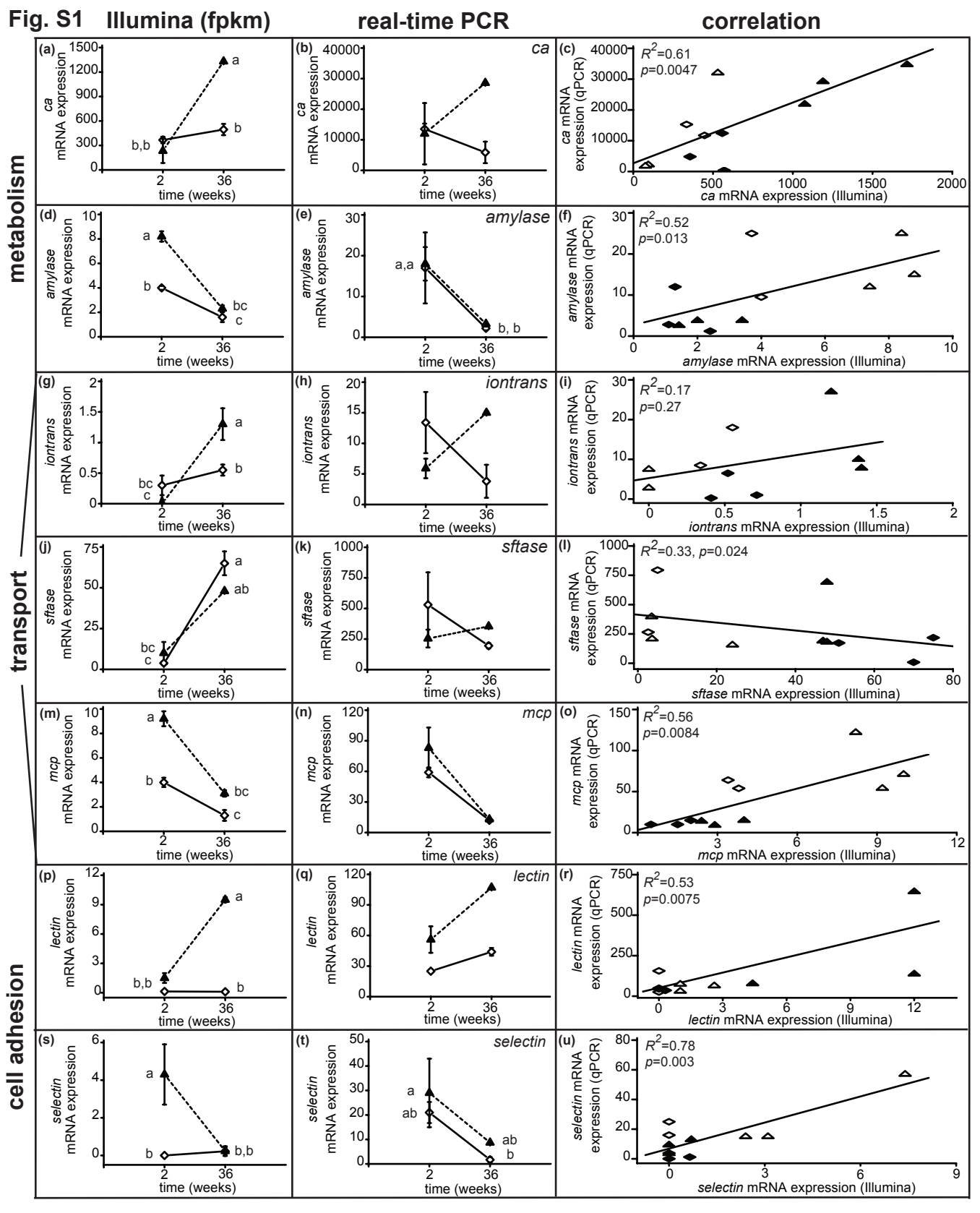
Fig. S1
Illumina (fpkm)
real-time PCR
correlation
metabolism
transport
cell adhesion
(a)
ca
mRNA expression
b,b
a
b
time (weeks)
(b)
ca
(c)
R2=0.61
p=0.0047
ca mRNA expression (qPCR)
ca mRNA expression (Illumina)
(d)
amylase
bc
c
(e)
amylase
a,a
b, b
(f)
R2=0.52
p=0.013
amylase mRNA expression (qPCR)
amylase mRNA expression (Illumina)
(g)
iontrans
bc
c
(h)
iontrans
(i)
R2=0.17
p=0.27
iontrans mRNA expression (qPCR)
iontrans mRNA expression (Illumina)
(j)
sftase
ab
(k)
sftase
(l)
R2=0.33, p=0.024
sftase mRNA expression (qPCR)
sftase mRNA expression (Illumina)
(m)
mcp
(n)
mcp
(o)
R2=0.56
p=0.0084
mcp mRNA expression (qPCR)
mcp mRNA expression (Illumina)
(p)
lectin
(q)
lectin
(r)
R2=0.53
p=0.0075
lectin mRNA expression (qPCR)
lectin mRNA expression (Illumina)
(s)
selectin
(t)
selectin
(u)
R2=0.78
p=0.003
selectin mRNA expression (qPCR)
selectin mRNA expression (Illumina)

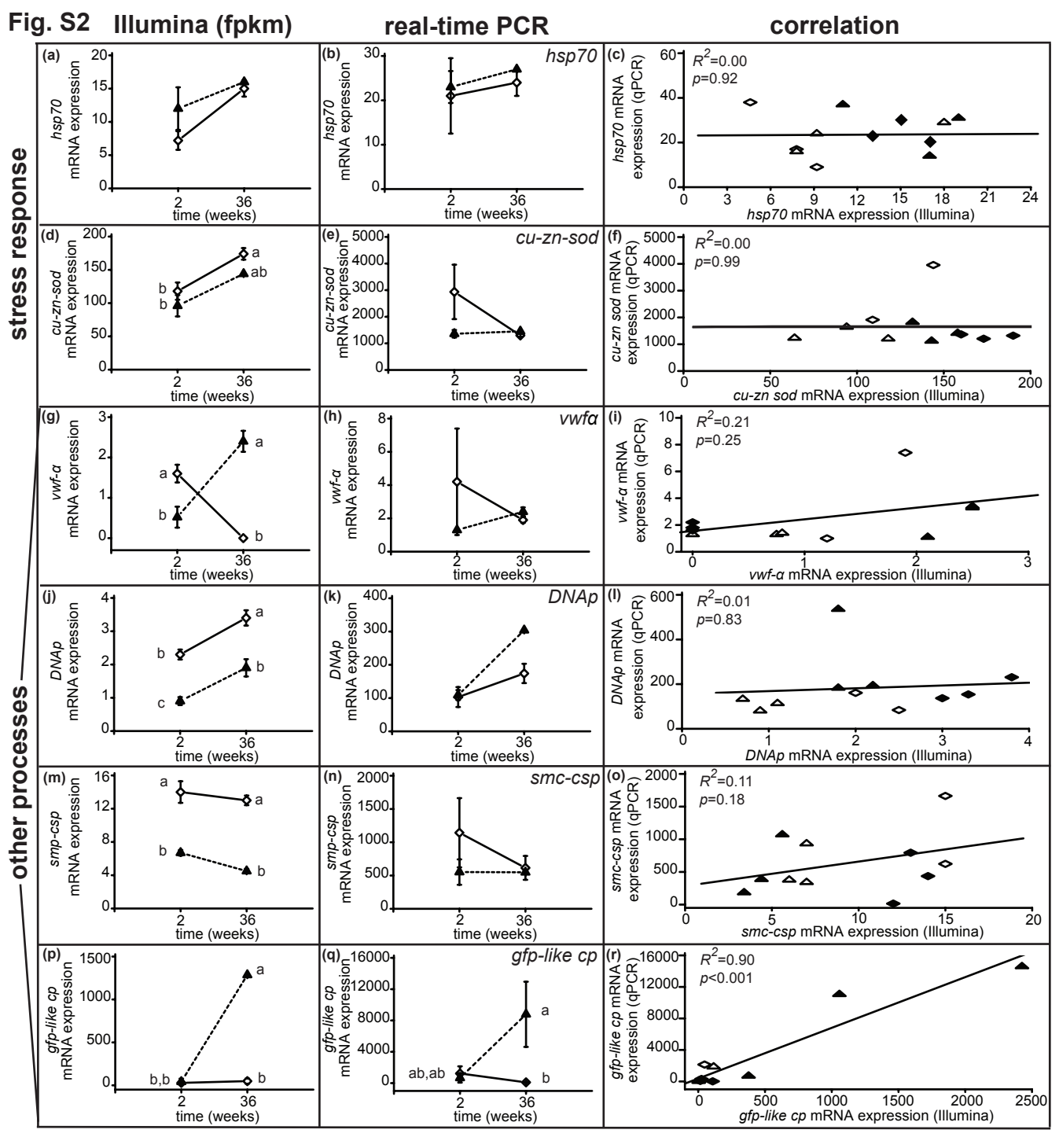
Fig. S2
Illumina (fpkm)
real-time PCR
correlation
stress response
other processes
(a)
hsp70 mRNA expression
time (weeks)
(b)
hsp70
(c)
R^2=0.00
p=0.92
hsp70 mRNA expression (qPCR)
hsp70 mRNA expression (Illumina)
(d)
cu-zn-sod mRNA expression
(e)
cu-zn-sod
(f)
R^2=0.00
p=0.99
cu-zn sod mRNA expression (qPCR)
cu-zn sod mRNA expression (Illumina)
(g)
vwf-α mRNA expression
(h)
vwfα
(i)
R^2=0.21
p=0.25
vwf-α mRNA expression (qPCR)
vwf-α mRNA expression (Illumina)
(j)
DNAp mRNA expression
(k)
DNAp
(l)
R^2=0.01
p=0.83
DNAp mRNA expression (qPCR)
DNAp mRNA expression (Illumina)
(m)
smp-csp mRNA expression
(n)
smc-csp
(o)
R^2=0.11
p=0.18
smc-csp mRNA expression (qPCR)
smc-csp mRNA expression (Illumina)
(p)
gfp-like cp mRNA expression
(q)
gfp-like cp
(r)
R^2=0.90
p<0.001
gfp-like cp mRNA expression (qPCR)
gfp-like cp mRNA expression (Illumina)

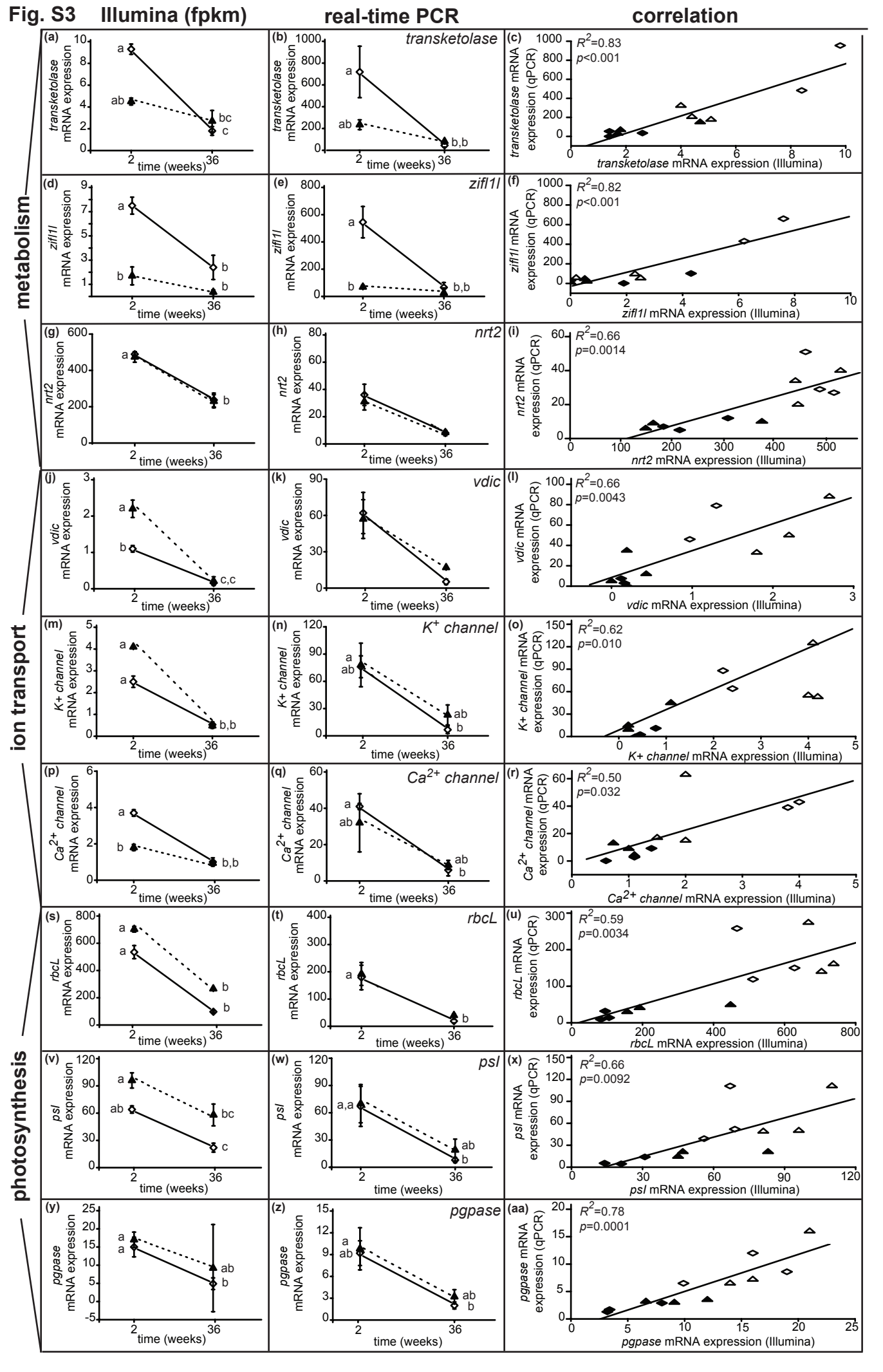
Fig. S3
Illumina (fpkm)
real-time PCR
correlation
metabolism
ion transport
photosynthesis
transketolase
zifl1l
nrt2
vdic
K+ channel
Ca2+ channel
rbcL
psl
pgpase
time (weeks)
R2=0.83
p<0.001
R2=0.82
p<0.001
R2=0.66
p=0.0014
R2=0.66
p=0.0043
R2=0.62
p=0.010
R2=0.50
p=0.032
R2=0.59
p=0.0034
R2=0.66
p=0.0092
R2=0.78
p=0.0001

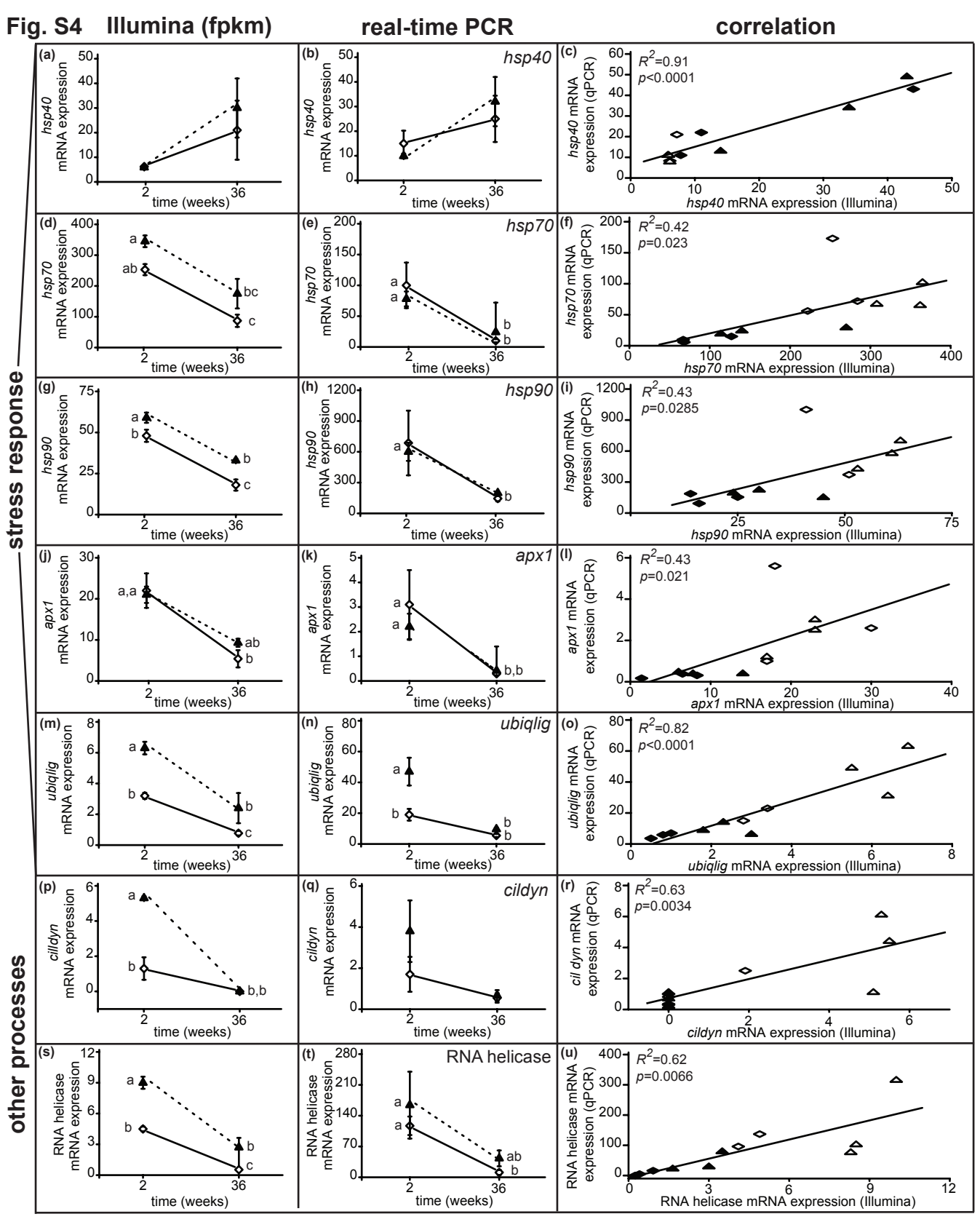
Fig. S4 Illumina (fpkm)
real-time PCR
correlation
stress response
other processes
(a)
hsp40
mRNA expression
time (weeks)
(b)
hsp40
(c)
R2=0.91
p<0.0001
hsp40 mRNA expression (qPCR)
hsp40 mRNA expression (Illumina)
(d)
hsp70
(e)
hsp70
(f)
R2=0.42
p=0.023
hsp70 mRNA expression (Illumina)
(g)
hsp90
(h)
hsp90
(i)
R2=0.43
p=0.0285
hsp90 mRNA expression (Illumina)
(j)
apx1
(k)
apx1
(l)
R2=0.43
p=0.021
apx1 mRNA expression (Illumina)
(m)
ubiqlig
(n)
ubiqlig
(o)
R2=0.82
p<0.0001
ubiqlig mRNA expression (Illumina)
(p)
cildyn
(q)
cildyn
(r)
R2=0.63
p=0.0034
cildyn mRNA expression (Illumina)
(s)
RNA helicase
(t)
RNA helicase
(u)
R2=0.62
p=0.0066
RNA helicase mRNA expression (Illumina)