Table 1. Average expression levels (log$_{10}$ of the number of molecules) for each species, treatment, and species-treatment combinations for 20 genes of the phototransduction cascade

Gene	Species effect				Environmental effect				Species × environment					
	D. mel.	*D. sim.*	F	*P*	Light	Dark	F	*P*	*D. mel.* light	*D. sim.* light	*D. mel.* dark	*D. sim.* dark	F	*P*
ninaA	4.31	4.17	2.61	0.1224	4.20	4.28	2.47	0.1236	4.28	4.12	4.33	4.23	0.35	0.5585
Rh2	4.40	3.82	5.80	**0.0257**	4.10	4.12	0.02	0.8764	4.35	3.85	4.46	3.79	0.44	0.5090
Rh3	4.62	4.70	1.60	0.2200	4.63	4.70	2.77	0.1032	4.58	4.67	4.67	4.73	0.19	0.6662
Rh4	4.57	4.65	0.04	0.8388	4.60	4.62	0.07	0.7944	4.55	4.66	4.60	4.63	0.68	0.4145
Rh5	4.44	4.63	4.47	**0.0472**	4.52	4.55	0.33	0.5703	4.44	4.61	4.45	4.66	0.13	0.7180
Ggamma30A	4.43	4.23	1.39	0.2514	4.28	4.38	10.48	**0.0023**	4.38	4.18	4.48	4.29	0.01	0.9061
GBeta76C	4.97	4.95	0.12	0.7309	4.92	5.01	5.17	**0.0281**	4.94	4.89	5.00	5.01	0.56	0.4568
Galpha49B	5.68	5.55	2.27	0.1479	5.61	5.62	0.03	0.8689	5.67	5.55	5.69	5.54	0.10	0.7487
norpA	5.47	5.42	0.97	0.3376	5.41	5.48	2.61	0.1131	5.45	5.38	5.50	5.46	0.10	0.7531
inaC	5.05	5.15	0.54	0.4706	5.06	5.15	3.88	0.0553	5.02	5.10	5.08	5.21	0.31	0.5777
inaD	4.90	4.91	0.02	0.8892	4.88	4.93	1.51	0.2251	4.86	4.90	4.94	4.92	0.67	0.4164
ninaC	4.65	4.49	2.36	0.1444	4.53	4.62	2.69	0.1095	4.62	4.43	4.56	3.38	0.30	0.5871
trp	5.06	5.15	2.75	0.1132	5.05	5.16	5.11	**0.0291**	5.01	5.09	5.10	5.21	0.09	0.7630
trpl	4.98	5.65	45.12	**<.0001**	5.28	5.36	4.78	**0.0342**	4.94	5.61	5.02	5.70	0.02	0.8849
rdgC	3.91	3.75	8.39	**0.0089**	3.80	3.86	3.21	0.0804	3.89	3.70	3.92	3.81	1.41	0.2415
CdsA	4.65	4.56	1.66	0.2134	4.58	4.63	1.36	0.2507	4.64	4.52	4.67	4.59	0.25	0.6222
rdgB	5.79	5.83	0.27	0.6105	5.80	5.82	0.33	0.5677	5.75	5.84	5.83	5.81	1.42	0.2399
inaF	5.09	4.89	8.12	**0.0099**	4.98	5.00	0.19	0.6682	5.08	4.87	5.09	4.90	0.13	0.7163
Arr1	5.95	5.95	0.00	0.9956	5.91	6.00	4.97	**0.0309**	5.92	5.90	5.98	6.01	0.45	0.5071
Arr2	6.02	6.18	0.64	0.4339	6.06	6.13	3.09	0.0857	5.99	6.14	6.05	6.22	0.14	0.7130

Each effect and its significance were estimated using a Mixed Model ANOVA (using the SAS program PROC MIXED). Bold-faced type indicates *P* values < 0.05. *D. mel.*, *D. melanogaster*; *D. sim.*, *D. simulans*.