Table S6. *rh5*:*rh5+6* qPCR results: statistics of LMM analyses

OreR excluded				OreR included			
REML criterion at convergence: 591.3				REML criterion at convergence: 685.4			
Number of obs: 112, groups: strain, 7; biorep, 2				Number of obs: 124, groups: strain, 8; biorep, 2			

Random effects:				Random effects:			
Groups	SD			Groups	SD		
strain	4.81			strain	7.95		
biorep	0.40			biorep	0.49		
Residual	3.27			Residual	3.61		

Fixed effects:				Fixed effects:			
	Est.	SE	t-value		Est.	SE	t-value
(Intercept)	67.21	3.47	19.36	(Intercept)	66.72	5.68	11.75
melanogaster	-20.36	4.87	-4.18	melanogaster	-26.49	7.31	-3.62
simulans	-10.98	4.45	-2.47	simulans	-10.95	7.31	-1.50
gender: male	-8.62	0.62	-13.95	gender: male	-7.64	0.65	-11.73

Linear mixed model fit by REML ['lmerMod']

Formula: **Rh5Percentage ~ species + (1 | strain) + (1 | biorep) + gender**