

Fig. S1. Phenotypic distributions of the SK1/S288c six basic generations: a-c) phenotypic distributions of the non-segregating P₁ (SK1), P₂ (S288c) and F₁ generations, respectively; d-f) the distributions of the segregating F₂, Bc_{1,1} and Bc_{1,2} generations, respectively. The phenotypic ranges of the segregating generations are much wider than those of the non-segregating generations indicating a heterogeneous composition of phenotypes present in these generations. Also, the phenotypic spread and the multimodality of the segregating generations indicate that a considerable amount of small effect quantitative trait loci are responsible for the difference between sporulation efficiencies in the SK1 and S288c strains

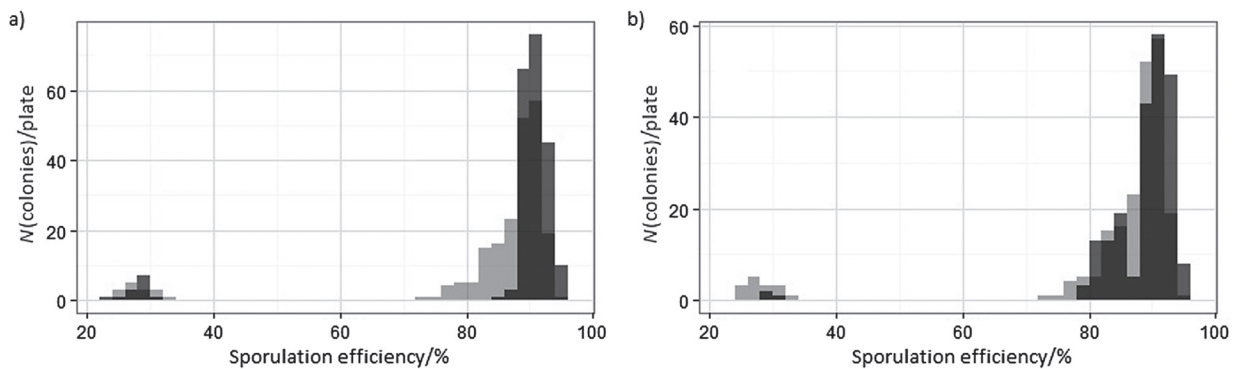


Fig. S2. Comparison of the experimental F₂ with the theoretical duplicate dominant (DD) epistasis phenotypic distributions: a) and b) the overlapping of the experimental F₂ distribution with the two- and three-locus DD-F₂ theoretical distributions, respectively. The theoretical distributions were simulated using the phenotype modelling method. The light grey areas represent the experimental F₂ distribution, the dark grey areas represent the theoretical DD-F₂ distributions and the black areas represent the overlapping of these distributions

Table S1. The mean values and variances of sporulation efficiencies of the SK1/S288c six basic generations

Generation	Cross	N	Mean value/%	Variance
P ₁ (SK1)	–	50	90.70	1.22
P ₂ (S288c)	–	50	8.60	0.93
F ₁	P ₁ ×P ₂	50	88.80	1.36
F ₂	F ₁ ×F ₁	136	67.46	588.08
Bc _{1,1}	P ₁ ×F ₁	66	84.65	69.89
Bc _{1,2}	P ₂ ×F ₁	78	53.86	501.67

N=number of observations

Table S2. Additive-dominance three-parameter inheritance model (9) of the SK1/S288c crosses

Parameter	Estimated value*/%	Degree of freedom	t-test	p-value
m	49.39±0.35	76	477.47	<0.001
[a]	40.64±0.35	98	392.88	<0.001
[d]	39.29±0.65	424	202.09	<0.001

*Values are presented as mean±standard deviation
 m=midparent value, [a]=additive genetic effect, [d]=dominance genetic effect

Note: although the scaling tests (9) predicted the presence of epistatic relationships between quantitative trait loci affecting the trait (data not shown), after the expansion of the basic three-parameter model to the six-parameter model, the newly added digenic interaction parameters proved to be insignificant. The inheritance model thus regressed back to the basic AD model of inheritance. This is probably because of the fact that the additive effects of the loci governing the trait are more prominent than the epistatic effects, which is in accordance with previous results (6)