

Supplementary information for:

## Model selection emphasises the importance of non-chromosomal information in genetic studies

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Table S2: Complexity of best statistical models chosen by LASSO for hierarchical interactions.

Gene deletion	Intercept	1 Predictor	2 Predictors	3 Predictors
<i>MCM22</i>	943	55	1	1
<i>PEP12</i>	0	0	0	1000
<i>PEP7</i>	0	0	0	1000
<i>PHO88</i>	357	20	156	467
<i>SKI8</i>	0	3	0	997
<i>VPS16</i>	0	126	4	870
<i>PHO88(killer)</i>	0	44	3	953
<i>PHO88(non-killer)</i>	992	6	1	1
<i>SKI8(killer)</i>	0	12	0	988
<i>SKI8(non-killer)</i>	2	3	0	995

LASSO for hierarchical interactions was applied in each of the 1000 modelling repeats for all gene deletion experiments. Except for the control *MCM22* and the *PHO88(non-killer)* experiment most cases required three predictors in order to describe the given data best.