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Determining phenological patterns associated with the onset of senescence in a wheat MAGIC mapping population

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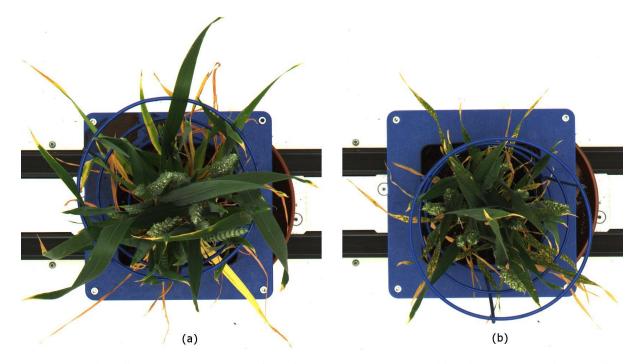
1 Supplementary material

2

3 Table S1 Infection type score table

score	description
0	No visible symptoms
1	Small lesion surrounded by necrotic tissue
2	Small lesion surrounded by necrotic tissue
3	Medium sized lesion surrounded only by chlorotic tissue
4	Large lesion surrounded by green tissue

- 4
- 5
- 6
- 7



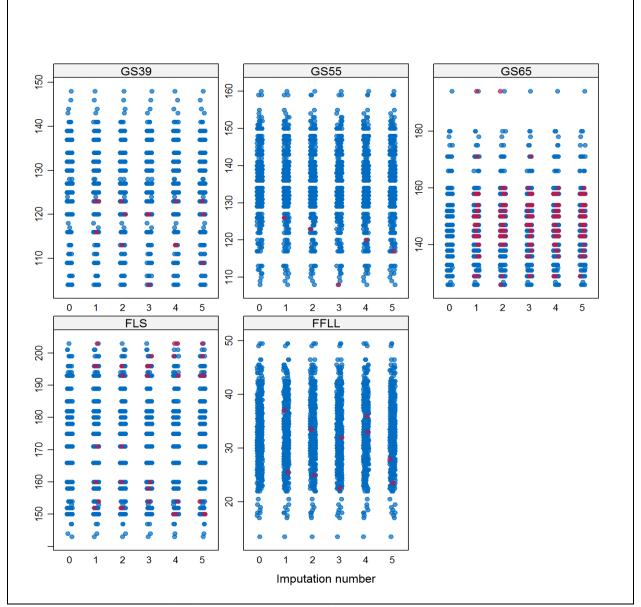


9 Figure S1 Plant disease symptoms on selected RILs. (a) Score 0. No chlorotic or necrotic lesions. (b)

10 Score 4. Clear signs of lesions on most leaves. Images were taken at 165 DAS.

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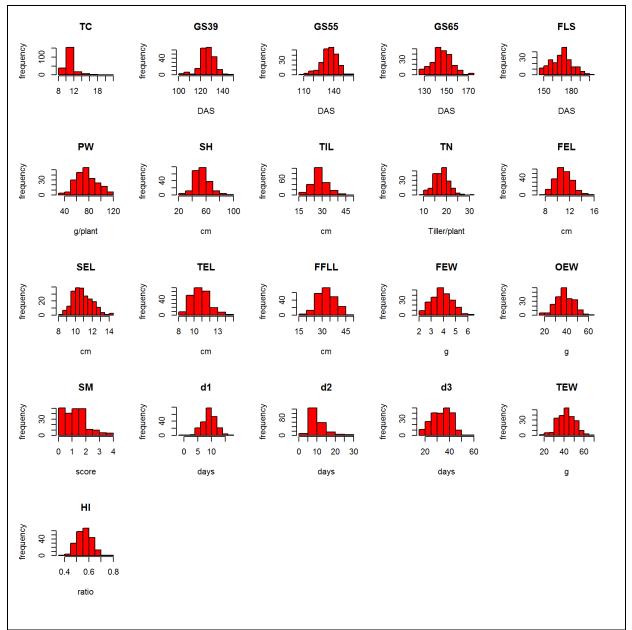




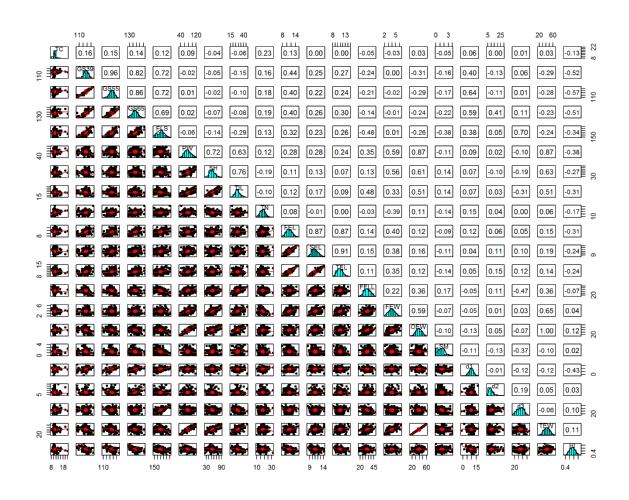
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Figure S2 Comparing the distributions of original and imputed data for those traits with missing data. Original data are shown in red, imputed data in blue. The output shows the imputed data for each

14 Original data are shown in red, imputed data in blue. The output shows the imput 15 observation (first column left) within each imputed dataset (remaining five columns).



16 Figure S3 Frequency distribution of all traits for all RILs



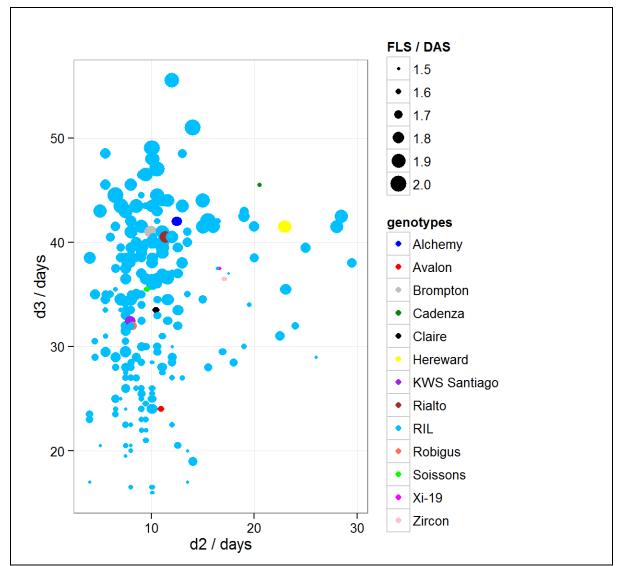
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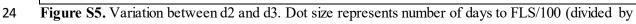
Figure S4 Pair-wise correlation analysis of all traits analysed in this study. Lower panels (below the diagonal) provide a pairwise scatter plot of the traits (provided on the diagonal). For example, first

20 scatter plot corresponds to TC on the vertical axis and to GS39 on the vertical axis. The upper panels

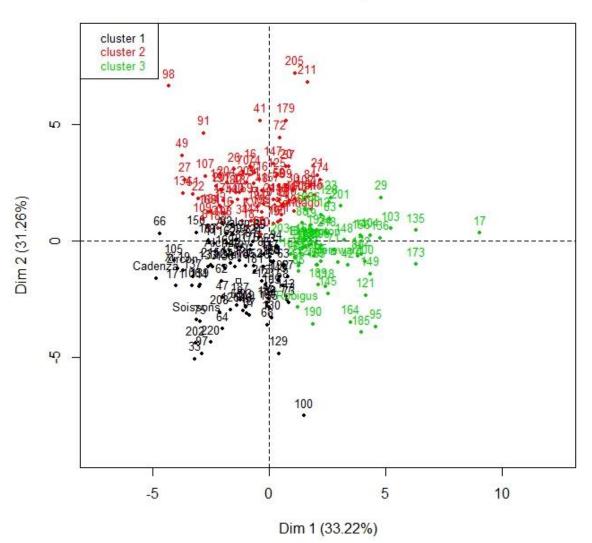
21 indicate the correlation coefficients. Diagonal panel also provides the frequency distribution for each

22 trait value over the population.





100 to be able to show the dots in the plot). Blue dots correspond to RILs. Colour dots correspond toMAGIC parents.



Factor map

- 29 Figure S6. Hierarchical Clustering on Principal Components. Biplot shows a projection plot of the
- 30 magic lines onto the first two PCs to see if there is any clustering of individuals's phenotypes. MAGIC
- 31 parents and elite lines are labelled only to facilitate interpretation.

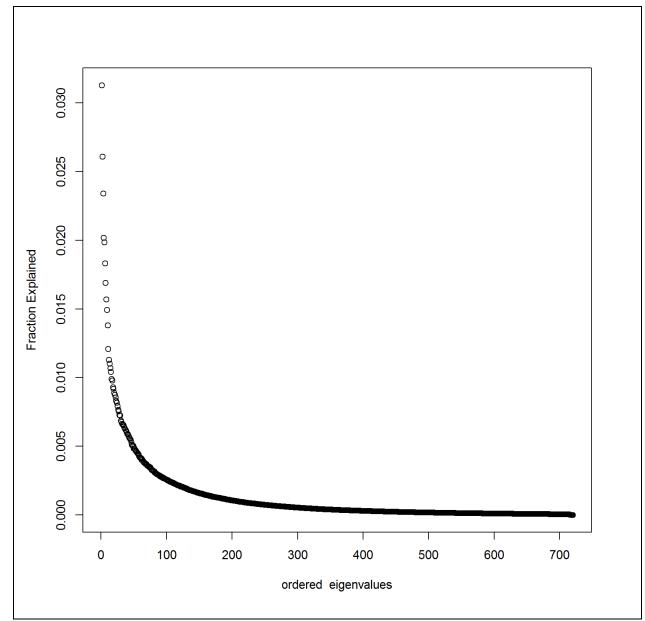


Figure S7. Biplot of a PCA analysis by eigenvalue decomposition of the marker based relationship
matrix (A). First PC accounts for less than 4% of the total spectrum.

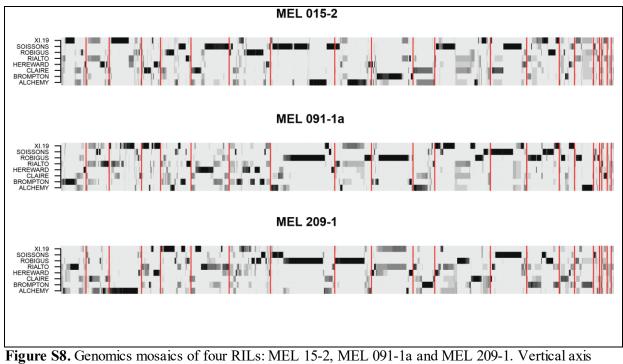
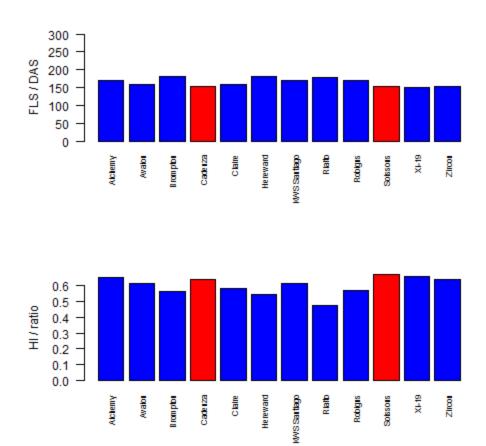
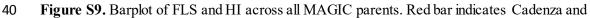
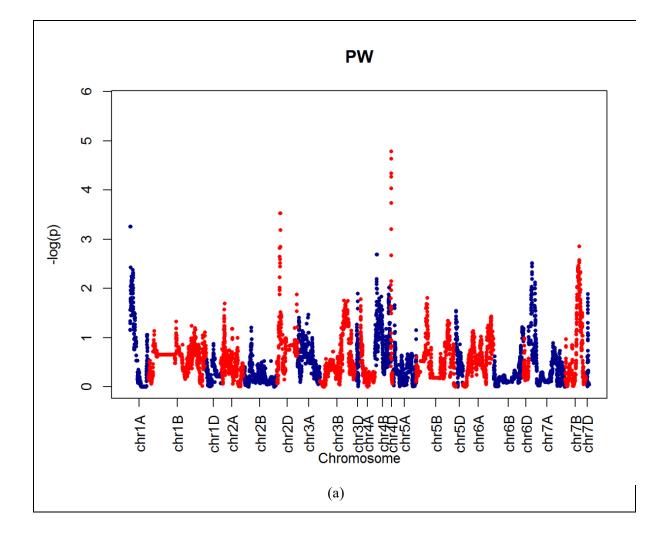


Figure S8. Genomics mosaics of four RILs: MEL 15-2, MEL 091-1a a
represents the MAGIC parents and horizontal represent chromosomes.



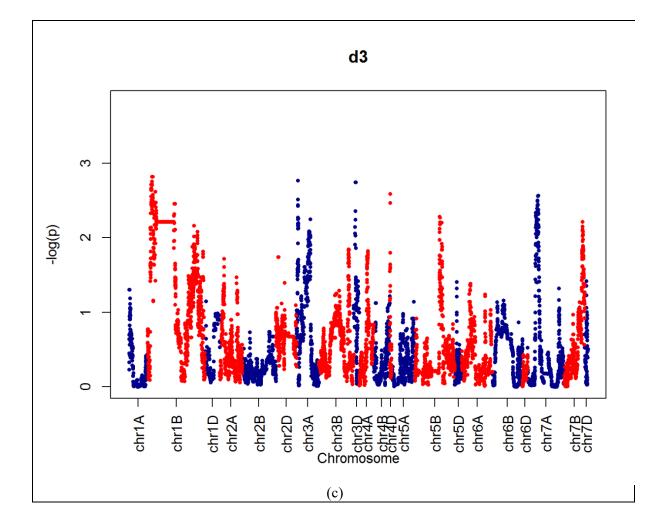


41 Soissons. DAS (Days after sowing)

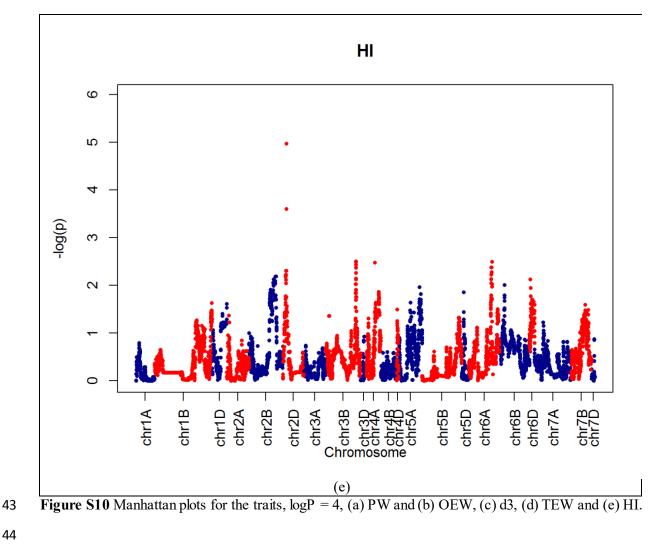


OEW S 4 c -log(p) 2 0 Т chr1A chr1D chr2A chr2B Chromosome chr3D chr4A chr4A chr4A chr5A Chr2A C chr5B chr5D chr6A chr6B chr6D chr7A chr7B chr7D chr1B chr2D chr3A (b)

mapping population

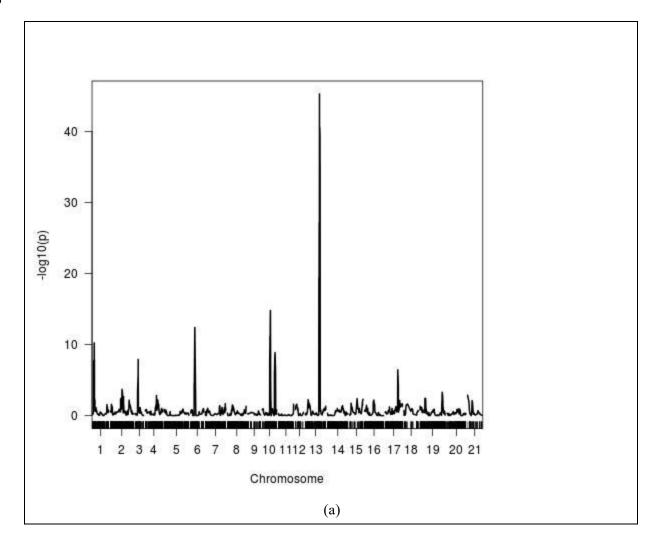


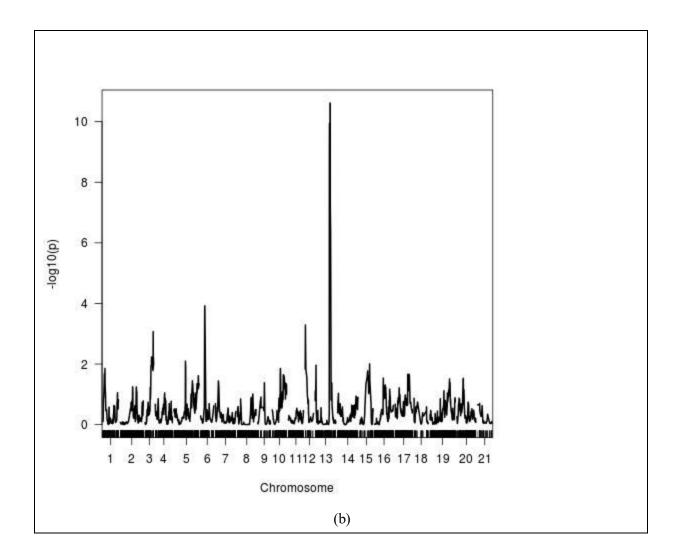
TEW S 4 ო -log(p) 2 0 Τ chr1A chr1D chr2A chr2B Chromosome chr3D chr4A chr4A chr4A chr5A Chr2A C chr5B chr5D chr6A chr6B chr6D chr7A chr7B chr7D chr1B chr2D chr3A (d)

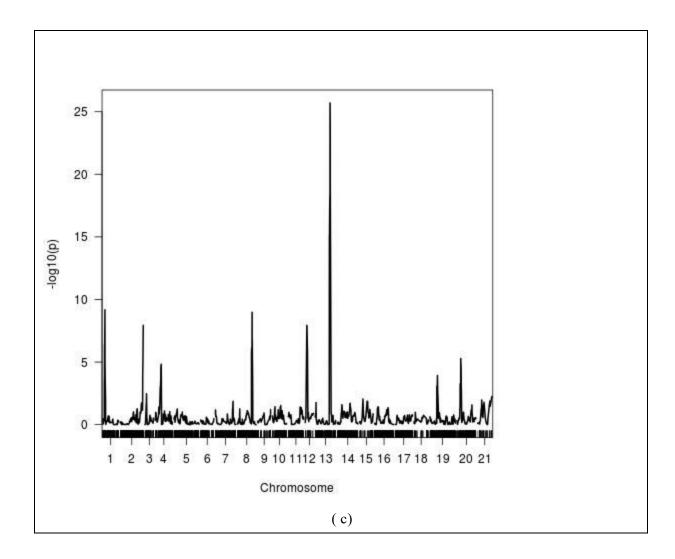


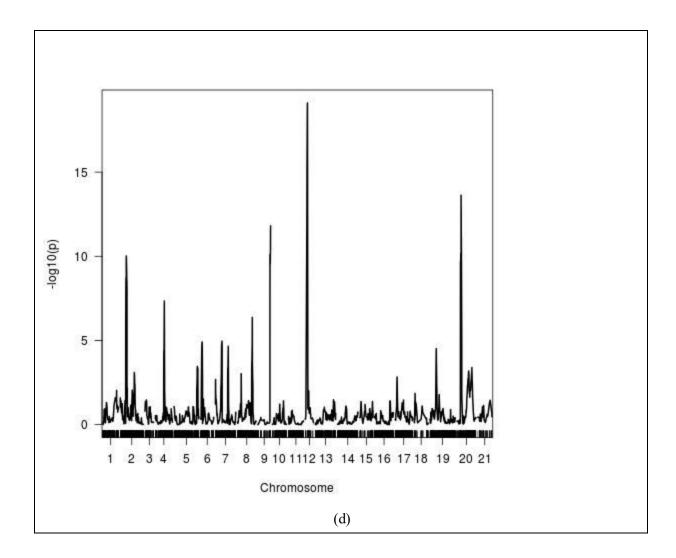
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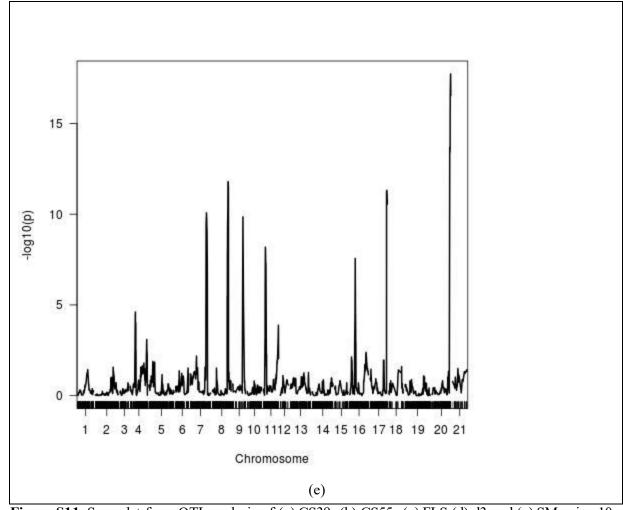


Figure S11. Scan plot from QTL analysis of (a) GS39, (b) GS55, (c) FLS (d) d3 and (e) SM using 10 covariates, where 1-21 = 1A,1B, 1D, 2A, 2B, 2D, 3A, 3B, 3D7D. Plots are produced by the R

49 package mpMap.