Deciphering the Genetic Architecture of Cooked Rice Texture

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Supplementary Figures

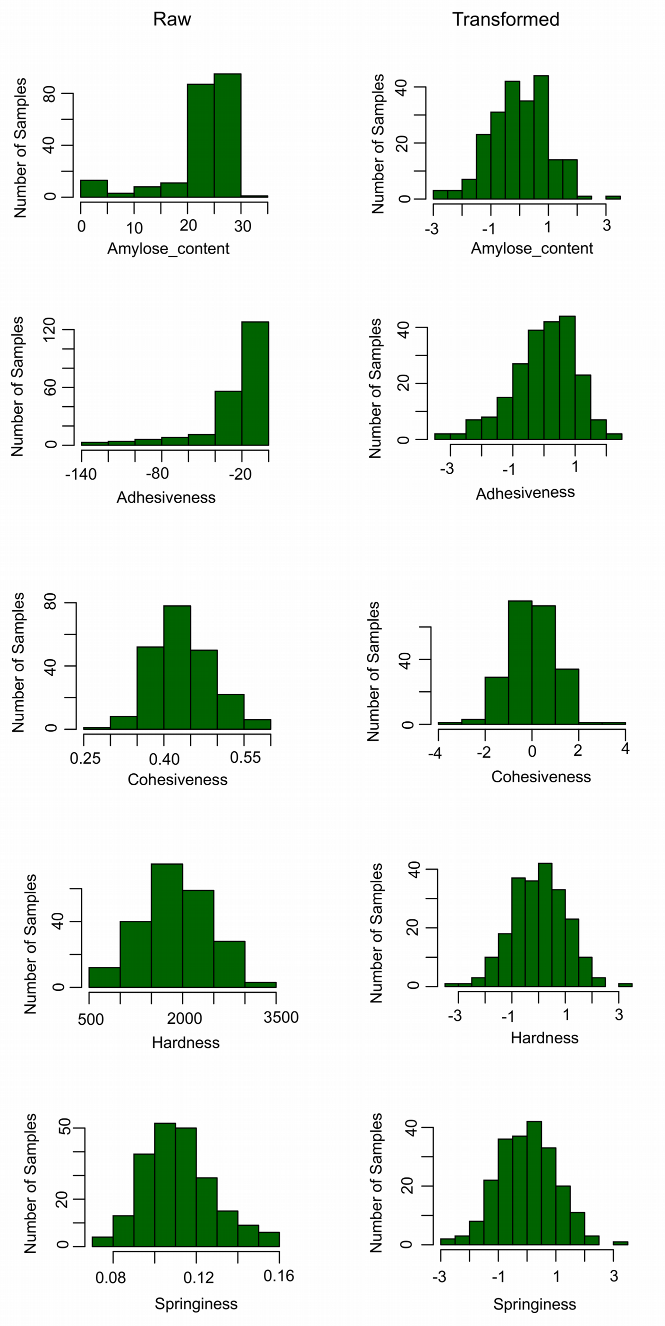


Figure S1: Raw and transformed phenotype distribution plotted as histogram. Left column represented raw phenotype distribution while right column showed as transformed phenotype distribution.

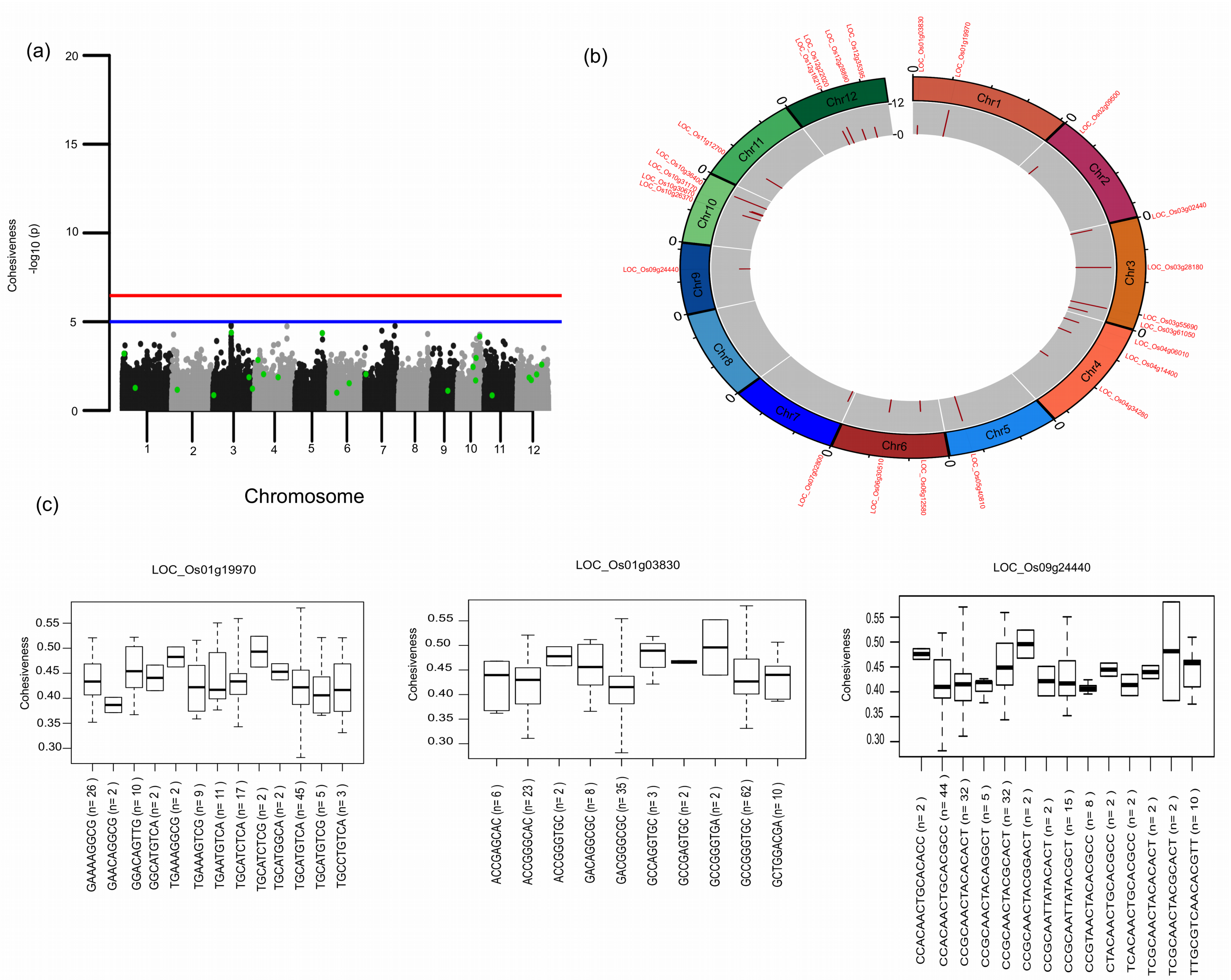


Figure S2: Genetic regions identified through ML-GWAS and SL-GWAS for cohesiveness (COH). **(a)** Single locus association overlaid with multi-locus associations (QTNs) shown as green dots with significant threshold of LOD ≥ 3 score. **(b)** Circos representing the physical positioning of 12 chromosomes with locus IDs of significant QTNs identified in ML-GWAS, followed by depiction of LOD score in the innermost circle. **(c)** Phenotypic distribution of haplotypes shown as boxplot for selected genes identified from ML-GWAS method.

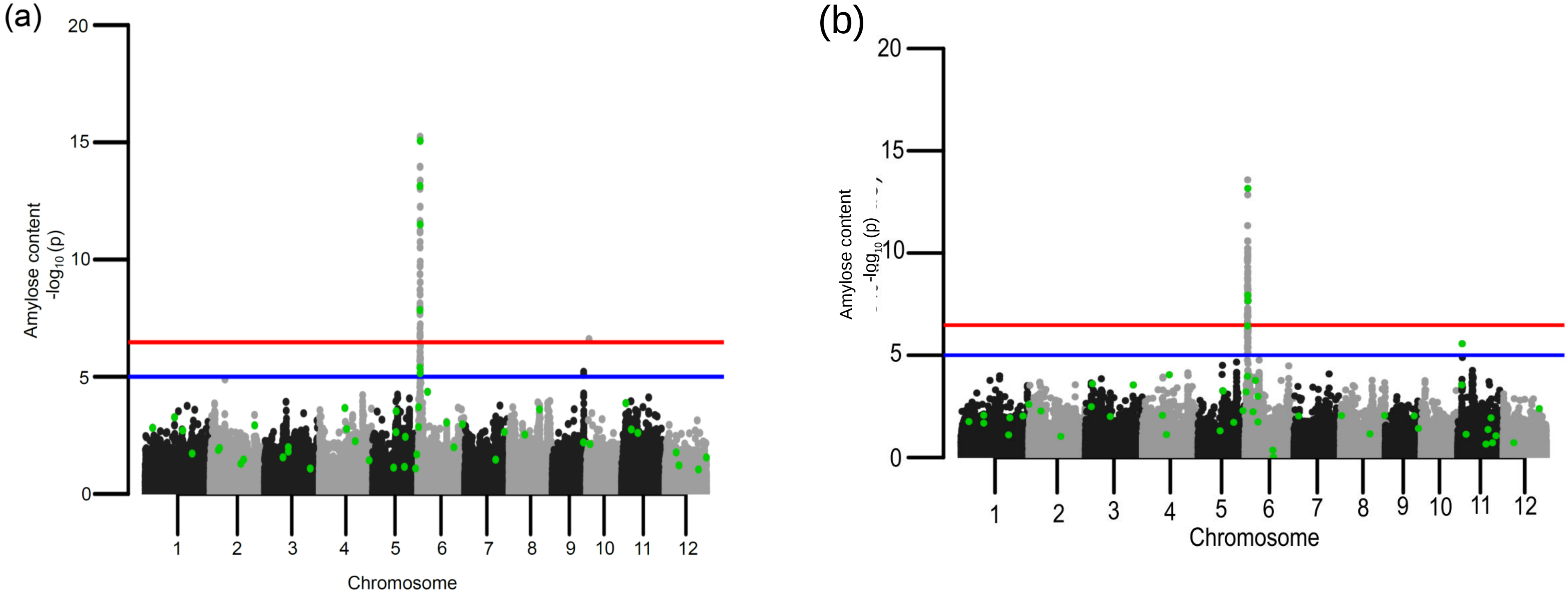


Figure S3 : GWAS conducted for AC under two different seasons 2014ds **(a)** and 2014ws **(b)**. Genome-wide significant threshold line [$-\log_{10}(P) = 6.47$] is drawn as red, whereas suggestive line is represented by blue line at $-\log_{10}(P)$ of 5. The heritability values were observed consistent across both of the seasons ($h^2 = 0.86$ in 2014ds, and $h^2 = 0.85$ in 2014ws).

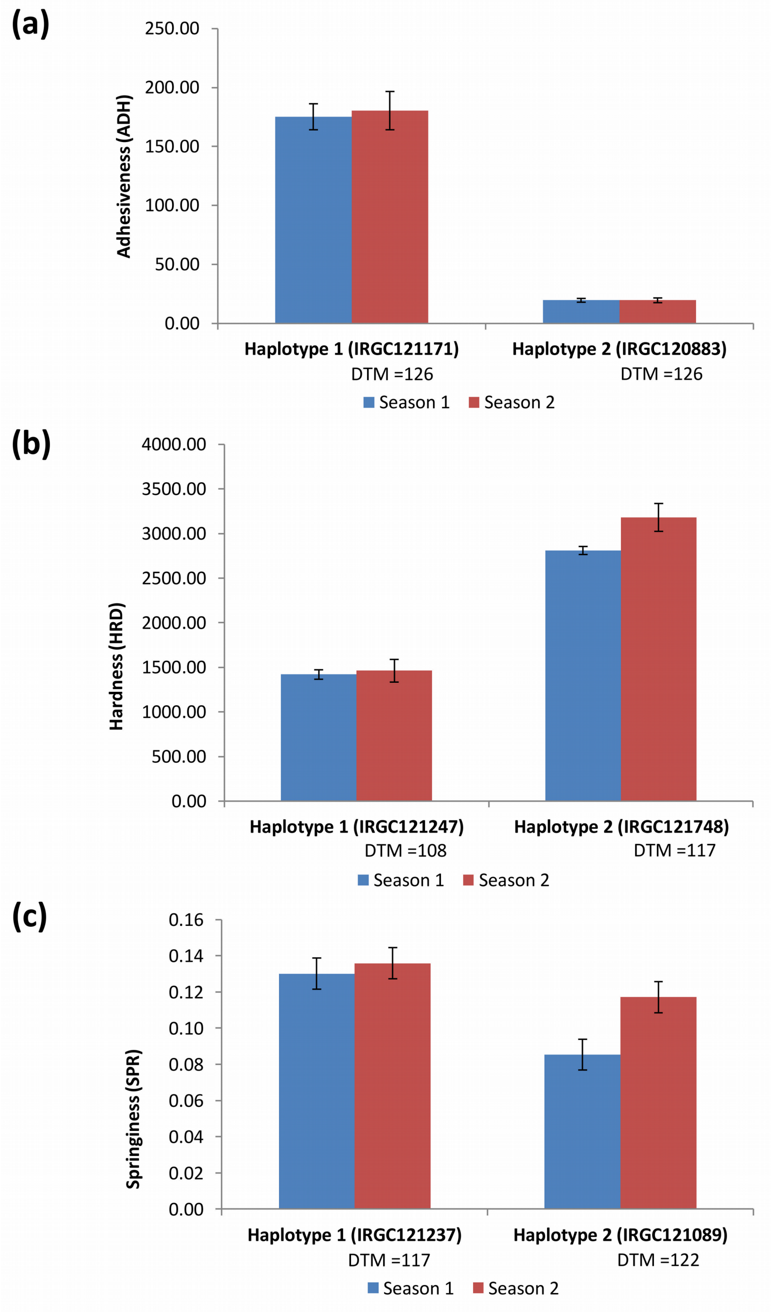


Figure S4: The behavior of key textural traits in two different seasons generated from lines with contrasting haplotype exhibiting the respective extreme phenotypic value. **(a)** Adhesiveness (ADH) trait was assessed in season 1 (2014 dry season) and season 2 (2015 dry season/2014 wet season) in lines harboring haplotype 1 (CCT) and haplotype 2 (CTT). Likewise, **(b)** Hardness (HRD) was measured between two independent seasons from contrasting lines possessing the haplotype 1 (CTAC) and haplotype 2 (CTAC), whereas **(c)** springiness was identified in lines with haplotype 1 (TCCAGGAGG) and haplotype 2 (TCCGAGGGG). Standard error is represented as the error bars.

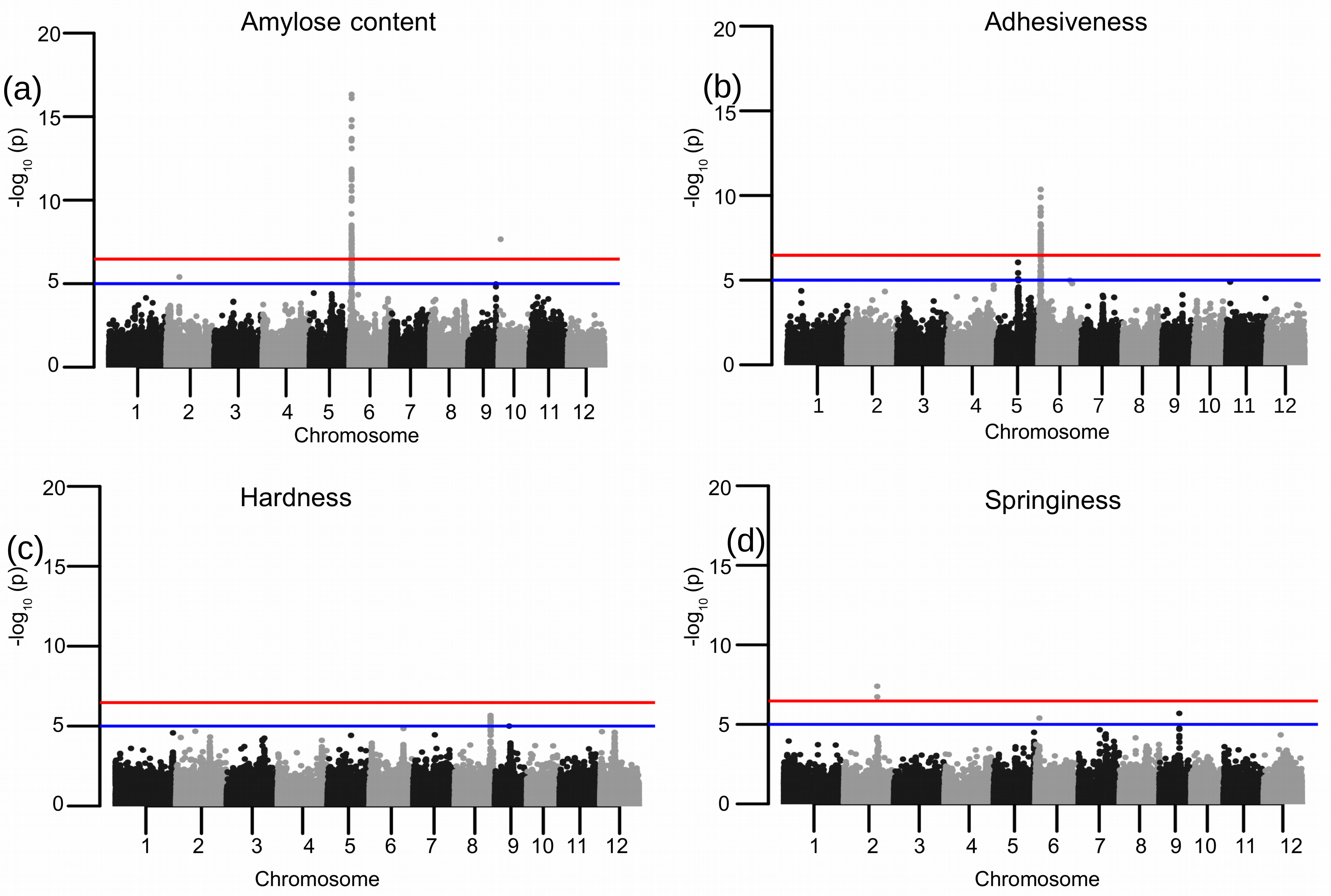


Figure S5: GWAS conducted for textural traits including AC, ADH, HDR, and SPR, while running days to maturity (DTM) as covariate. All of the prominent peaks for different textural traits-including amylose content **(a)**, adhesiveness **(b)**, hardness **(c)** and springiness **(d)**, were mapped in similar genomic regions as identified through earlier GWAS ran without covariate. This further suggests no influence of DTM on texture in the current core collection panel. Genome-wide significant threshold line [–log 10 (P) = 6.47] is drawn as red, whereas suggestive line is represented by blue line at –log 10 (P) of 5.

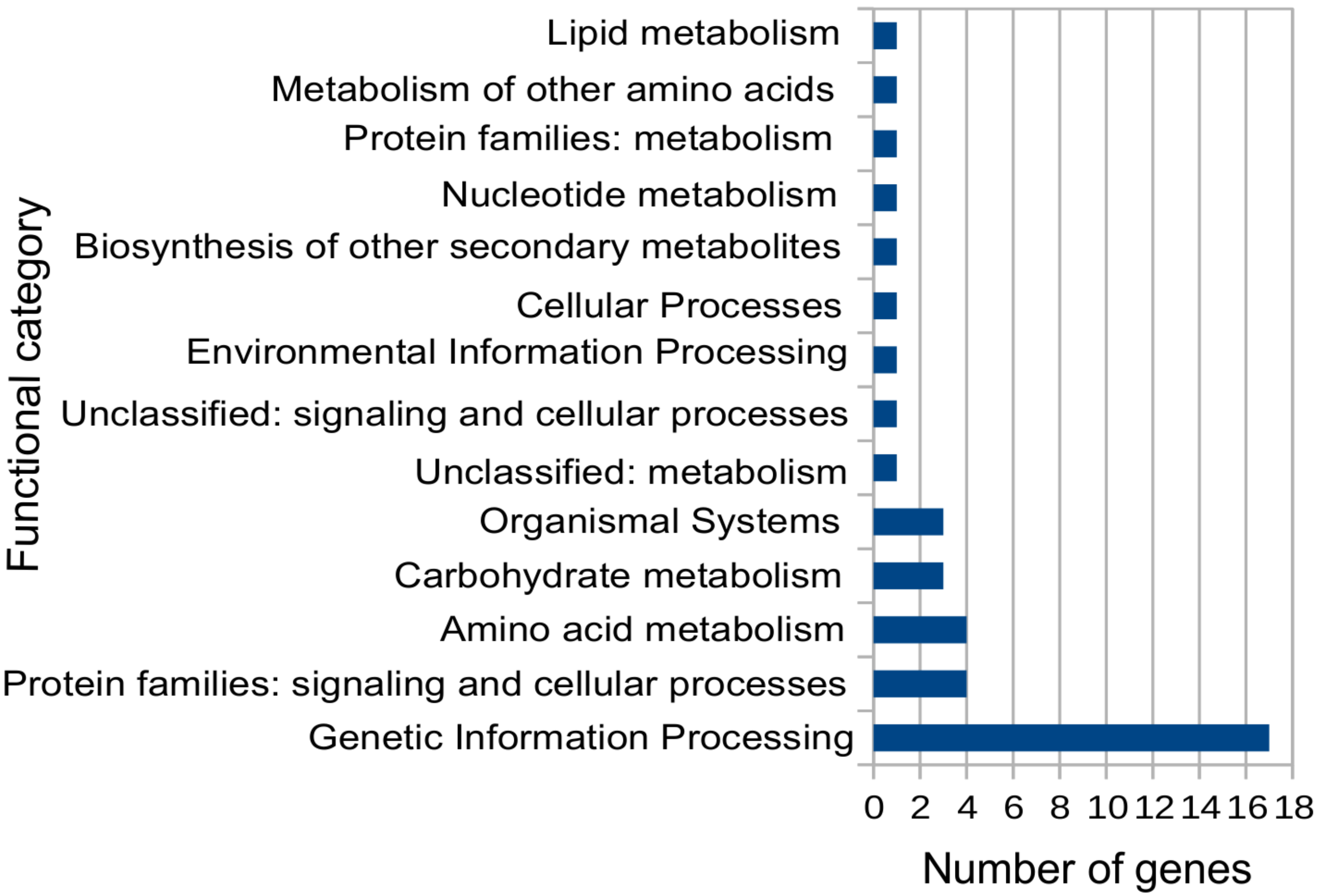
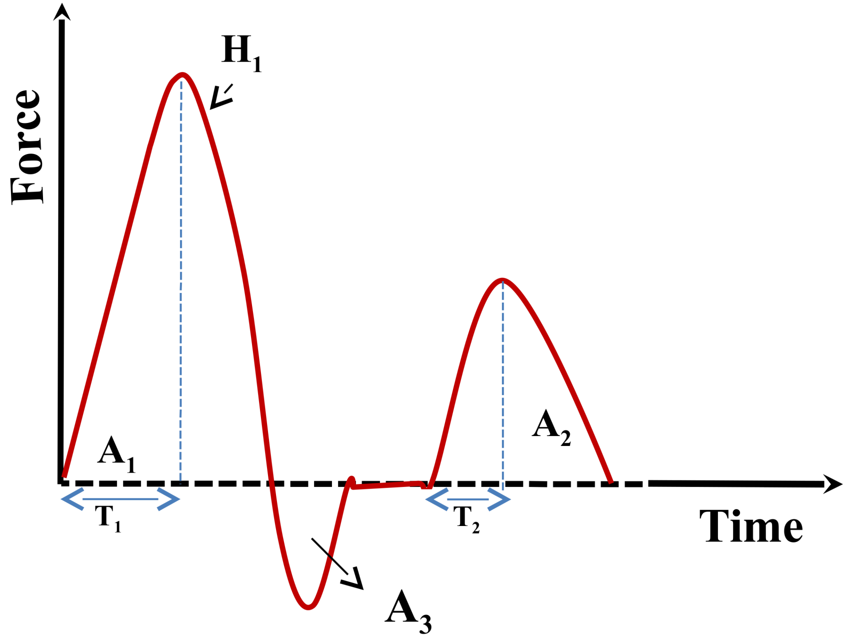


Figure S6 : KEGG analysis for the candidate genes identified in multi-locus GWAS for textural attributes and AC. A total of 40 candidate genes identified as significant QTNs were classified for the functional categories using the KEGG pathway chart.



Adhesiveness (ADH) = Negative force area under the first bite (A3).

Hardness (HRD) = Maximum force required (showed as H_1) for first compression cycle, simulating the force required to press the food using molars. Signifies the peak force of the first compression by the height of first curve.

Cohesiveness (COH) = Ratio of the positive force areas under second compression to that of first one (A_2/A_1).

Springiness (SPR) = Springiness (represented as T_2/T_1) is the height that the food recovers during the time that elapses from the upstroke to the peak in the second curve (T_2) to the time elapsed from starting point to the peak of the first curve (T_1), representing degree of sample height recovery.after partial compression.

Supplementary Note: Representation and definition of different textural attributes as detected in TPA (Texture profile analyzer)