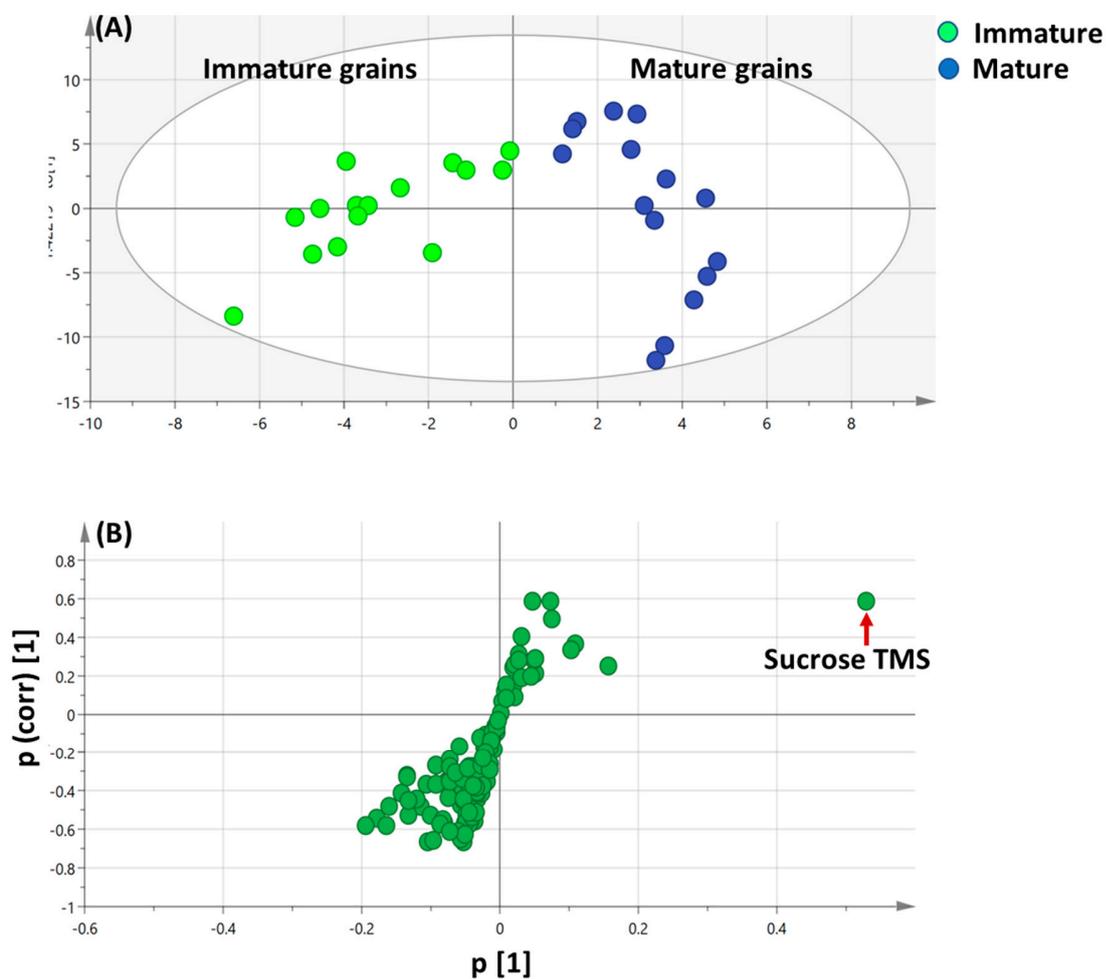
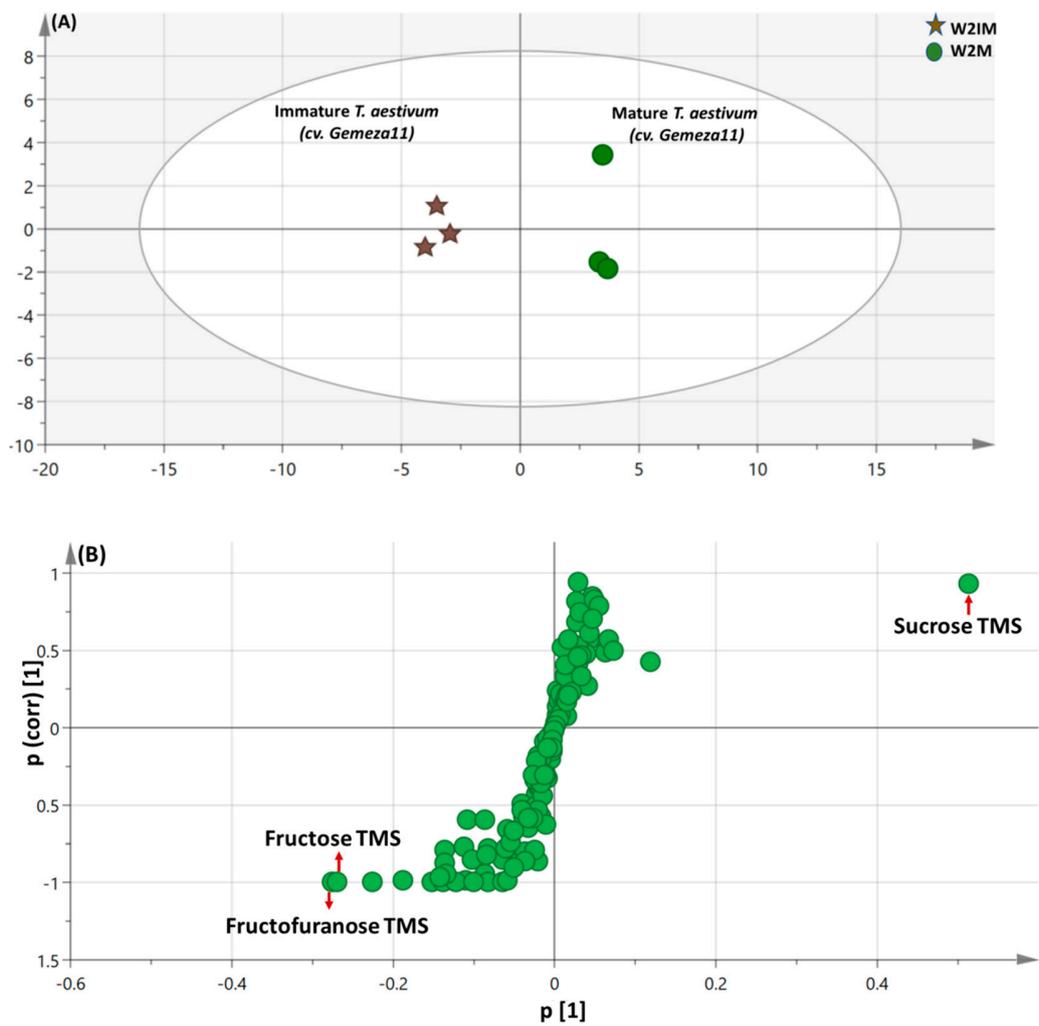


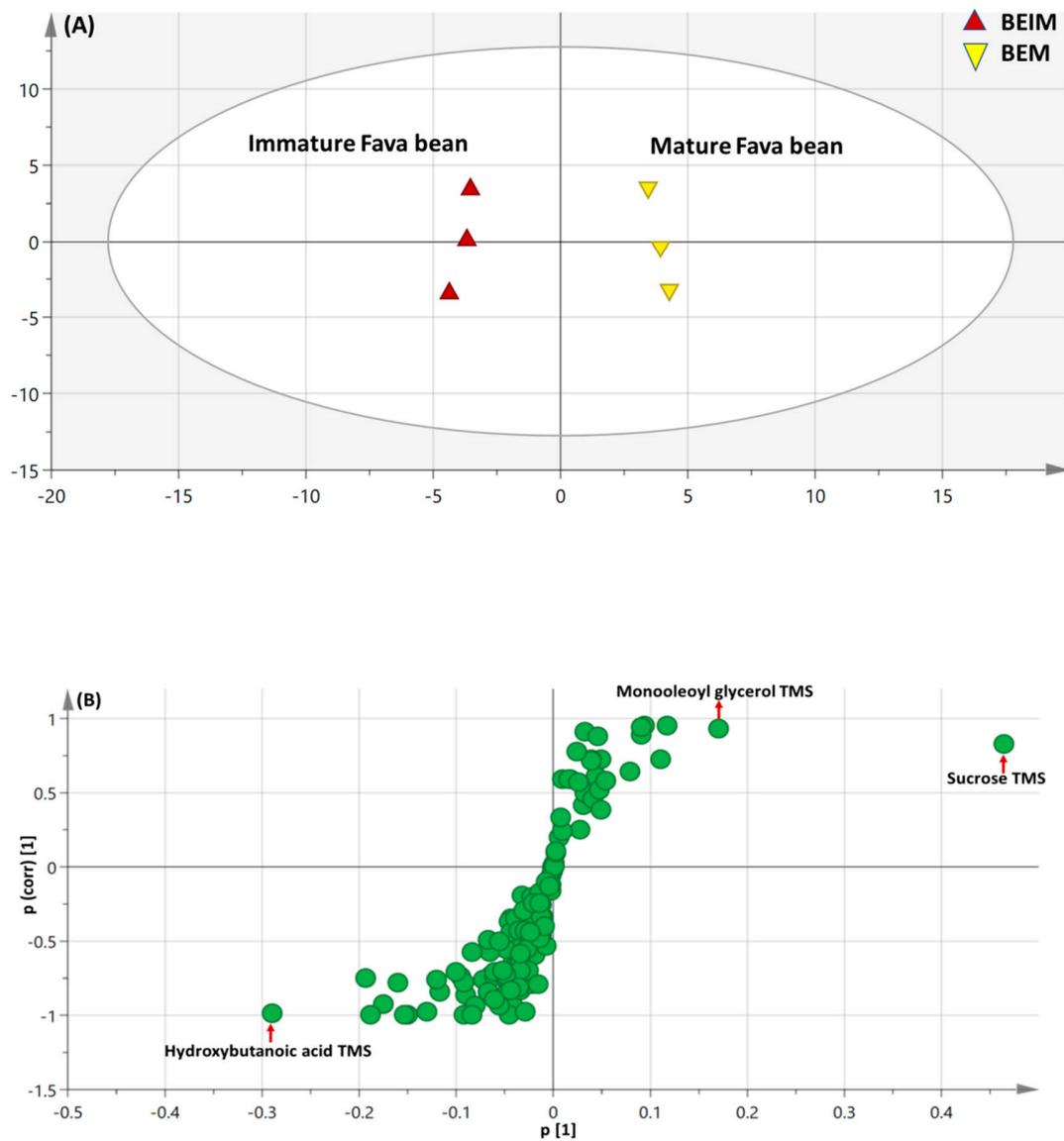
**Figure S1.** GC/MS chromatogram of the n-alkanes series (C20-C40) according to their retention indices (RI).



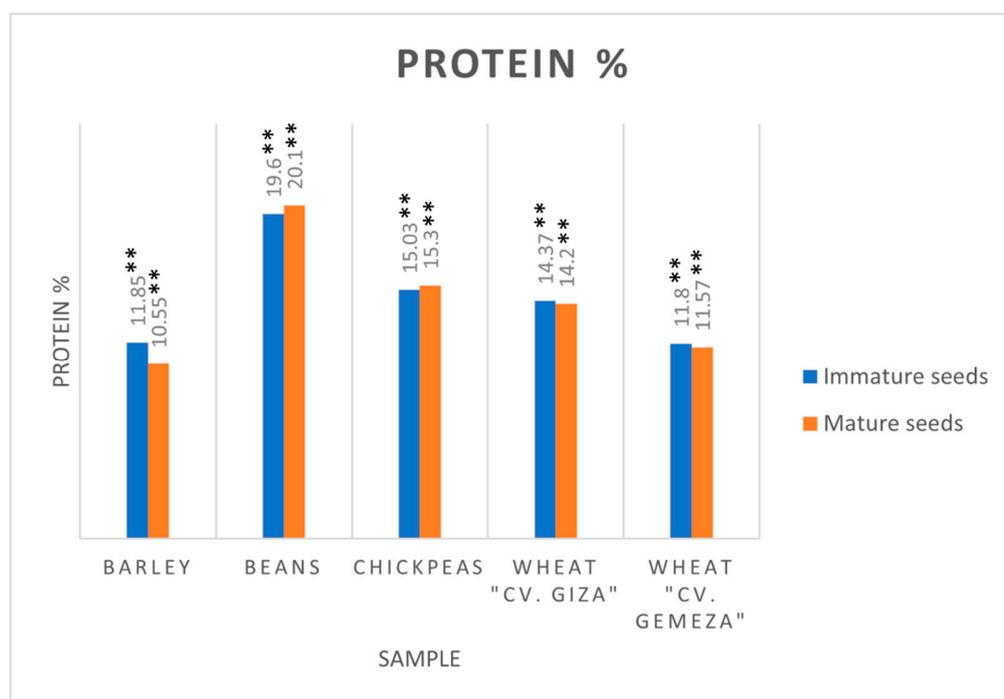
**Figure S2.** GC/MS dataset based OPLS-DA score plot (A) derived from modelling silylated primary metabolites of all mature samples against all immature ones ( $n = 3$ ). The respective loading S-plots (B) shows the covariance  $p[1]$  against the correlation  $p(\text{corr})[1]$  of the variables of the discriminating component of the OPLS-DA model. Cut-off values of  $p = 0.001$  was used. Designated variables are highlighted and identifications are discussed in the text.



**Figure S3.** GC/MS based OPLS-DA score plot (A) derived from modelling silylated primary metabolites of mature vs. immature *T. aestivum* (cv. Gemeza 11) specimens (n = 3). The respective loading S-plots (B) shows the covariance  $p[1]$  against the correlation  $p(\text{corr})[1]$  of the variables of the discriminating component of the OPLS-DA model. Cut-off values of  $p = 0.09$  was used. Designated variables are highlighted and identifications are discussed in the text.



**Figure S4.** GC/MS based OPLS-DA score plot (A) derived from modelling silylated primary metabolites of mature vs. immature *V. faba* (cv. *Sakha 3*) specimens ( $n = 3$ ). The respective loading S-plots (B) shows the covariance  $p[1]$  against the correlation  $p(\text{corr})[1]$  of the variables of the discriminating component of the OPLS-DA model. Cut-off values of  $p = 0.06$  was used. Designated variables are highlighted and identifications are discussed in the text.



**Figure S5.** A bar graph showing diagrammatic values of the protein % (w/w) of both immature and mature seeds side by side. Each bar represents mean (n=3). \*\*Statistically non-significant ( $P$  value > 0.05, one-way ANOVA).

**Supplementary Table S1.** A summary of the total protein assay results, showing the nitrogen (%w/w) of each sample, as well as the protein (w/w) after factor conversion. All results are expressed as mean  $\pm$  SD, (n=3).

Samples	N% (w/w)	Protein% (w/w)
BIM	2.04 $\pm$ 0.32	11.85 $\pm$ 1.83 **
BM	1.82 $\pm$ 0.16	10.55 $\pm$ 0.93 **
BEIM	3.38 $\pm$ 0.66	19.6 $\pm$ 0.35 **
BEM	3.47 $\pm$ 0.42	20.1 $\pm$ 2.43 **
CIM	2.60 $\pm$ 0.13	15.03 $\pm$ 0.76 **
CM	2.63 $\pm$ 0.04	15.3 $\pm$ 0.2 **
W1IM	2.48 $\pm$ 0.09	14.37 $\pm$ 0.51 **
W1M	2.45 $\pm$ 0.08	14.2 $\pm$ 0.5 **
W2IM	2.04 $\pm$ 0.02	11.8 $\pm$ 0.1 **
W2M	1.99 $\pm$ 0.03	11.57 $\pm$ 0.21 **

\*\*Statistically non-significant ( $P$  value > 0.05, one-way ANOVA).