**Table S1:** Phenotypic correlation between the seeds minerals content.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Correlation between the two experimental sites | | | | |  | Correlation between different minerals | | | |
|  | Ca | K | S | P |  | **Traits** | **Ca** | **K** | **S** |
| Ca | 0.92\*\*\* |  |  |  |  | **K** | 0.20\* |  |  |
| K |  | 0.80\*\*\* |  |  |  | **S** | 0.21\* | 0.67\*\*\* |  |
| S |  |  | 0.98\*\*\* |  |  | **P** | 0.18\* | 0.65\*\*\* | 0.47\*\*\* |
| P |  |  |  | 0.75\*\*\* |  |  |  |  |  |

\* Significant at the 0.05 probability level.

\*\*\* Significant at the 0.001 probability level.

**Table S2:** The 32 reported QTLs associated with Ca, K, P and S content in seeds. The models that detected a significant marker-trait association are abbreviated as follows: C for CMLM, M for MLMM and F for FarmCPU.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Traits** | **Gm** | **Peak SNP** | **QTL N°** | **P** | **R2** | **FDR** | **Effect** | **MODELS** |
| Ca | 1 | 37,012,421 | Ca\_#1 | 6.02E-11 | NA | 2.5E-06 | 0.05 | F |
| Ca | 4 | 41,894,618 | Ca\_#2 | 2.12E-11 | NA | 1.0E-06 | -0.05 | F |
| Ca | 6 | 3,354,869 | Ca\_#3 | 2.94E-08 | 0.20 | 4.5E-03 | -0.06 | C/M |
| Ca | 9 | 6,092,970 | Ca\_#4 | 3.70E-08 | 0.21 | 4.5E-03 | -0.07 | C/M/F |
| Ca | 9 | 21,562,118 | Ca\_#5 | 1.05E-11 | NA | 6.4E-07 | 0.01 | F |
| Ca | 18 | 4,907,739 | Ca\_#6 | 4.11E-12 | NA | 3.3E-07 | -0.03 | F |
| Ca | 20 | 3,830,121 | Ca\_#7 | 1.35E-06 | NA | 4.7E-02 | -0.02 | F |
|  |  |  |  |  |  |  |  |  |
| K | 4 | 49,071,552 | K\_#1 | 1.75E-06 | 0.17 | 6.1E-03 | -0,30 | C/F |
| K | 8 | 47,147,391 | K\_#2 | 4.22E-07 | 0.19 | 2.0E-03 | -0,41 | C |
| K | 10 | 1,925,709 | K\_#3 | 4.31E-10 | 0.31 | 4.9E-05 | -0,57 | C/M/F |
| K | 14 | 1,771,702 | K\_#4 | 4.37E-08 | 0.23 | 3.8E-04 | -0,52 | C |
| K | 14 | 42,498 | K\_#5 | 3.21E-06 | 0.16 | 9.3E-03 | -0,27 | C |
| K | 15 | 6,097,078 | K\_#6 | 1.78E-08 | NA | 8.7E-04 | 0,17 | F |
| K | 17 | 39,070,739 | K\_#7 | 3.54E-09 | NA | 2.2E-04 | 0,20 | F |
| K | 19 | 49,929,548 | K\_#8 | 7.20E-09 | 0.26 | 1.2E-04 | -0,48 | C |
| K | 20 | 31,865,721 | K\_#9 | 1.54E-08 | 0.24 | 2.1E-04 | -0,48 | C |
| K | 20 | 39,090,716 | K\_#10 | 9.01E-08 | NA | 3.7E-03 | 0,13 | F |
|  |  |  |  |  |  |  |  |  |
| P | 4 | 49071286 | P\_#1 | 6.12E-08 | 0.22 | 1.5E-02 | -0.30 | C/M/F |
| P | 15 | 48783732 | P\_#2 | 2.16E-08 | NA | 1.3E-03 | 0.13 | F |
| P | 20 | 31872237 | P\_#3 | 3.61E-12 | NA | 8.8E-07 | -0.09 | F |
| P | 20 | 33742119 | P\_#4 | 3.58E-08 | NA | 1.7E-03 | -0.06 | F |
| P | 20 | 42478388 | P\_#5 | 1.35E-08 | NA | 1.1E-03 | 0.09 | F |
|  |  |  |  |  |  |  |  |  |
| S | 3 | 22,917,408 | S\_#1 | 7.81E-11 | NA | 9.5E-06 | 0.10 | F |
| S | 5 | 1,095,389 | S\_#2 | 1.17E-05 | 0.14 | 4.0E-02 | 0.26 | C |
| S | 8 | 12,150,272 | S\_#3 | 4.93E-06 | 0.15 | 2.1E-02 | 0.30 | C |
| S | 10 | 1,602,998 | S\_#4 | 2.84E-08 | 0.23 | 4.0E-03 | 0.46 | C/M |
| S | 14 | 58,133 | S\_#5 | 2.69E-07 | 0.19 | 6.6E-03 | 0.26 | C |
| S | 14 | 1,755,083 | S\_#6 | 5.32E-07 | 0.18 | 8.1E-03 | 0.43 | C |
| S | 15 | 3,986,243 | S\_#7 | 2.80E-07 | 0.19 | 2.3E-02 | 0.15 | M/F |
| S | 19 | 49,914,498 | S\_#8 | 7.28E-07 | 0.18 | 8.6E-03 | 0.34 | C |
| S | 20 | 2,246,105 | S\_#9 | 4.07E-06 | 0.15 | 1.9E-02 | 0.17 | C |
| S | 20 | 39,076,484 | S\_#10 | 9.13E-07 | 0.18 | 9.7E-03 | 0.20 | C/M/F |

NA = Proportion de la variance phénotypique non déterminée (NA).

**Table S3:** The t-test results. Degree of significance (p-value) of the phenotypic contrast (difference between means) for Ca, K, P and S content between lines contrasting for the allele carried at each QTL (of the eight co-identified) in three environments. The three trials were conducted in Ottawa (ON) in 2017 (17) and 2018 (18), with (I) or without (N) supplemental irrigation. Phenotypic contrasts were declared significant using a Bonferroni correction ( α = 0.05/n, where n is the total number of the QTLs for a trait) significant differences are indicated using an asterisk.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Traits** | **Gm** | QTLs | Environments | | |
| I17 | I18 | N18 |
| Ca | 06 | Ca\_#3 | 1.3E-02\* | 3.6E-03\*\* | 2.3E-02\* |
| 09 | Ca\_#4 | 7.3E-01ns | 7.9E-01ns | 3.6E-01ns |
| K | 04 | K\_#1 | 2.4E-04\*\*\* | 6.5E-03\*\* | 2.3E-05\*\*\* |
| 10 | K\_#3 | 1.7E-02\* | 1.4E-01ns | 1.7E-04\*\*\* |
| P | 04 | P\_#1 | 3.2E-04\*\*\* | 3.5E-03\*\* | 2.6E-04\*\*\* |
| S | 10 | S\_#4 | 3.4E-04\*\*\* | 8.5E-03\*\* | 5.6E-04\*\*\* |
| 15 | S\_#7 | 1.3E-04\*\*\* | 7.0E-02ns | 4.2E-05\*\*\* |
| 20 | S\_#10 | 4.6E-03\*\* | 7.5E-03\*\* | 4.2E-04\*\*\* |

ns: not significant, *p*-value > 0.025, \*\* and \*\*\* Significant, *p*-value ≤ 0.001 and ≤ 0.0001, respectively.

**Table S4:** Summary of localized GWAS results showing the new peak SNPs (in bold) and old peak SNP associated with seeds Ca, K, P and S content.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **Gm** | **QTL N°** | **Peak SNP** | **P** | **R2** | **FDR** | **Effect** | **MODELS** |
| Ca | 06 | Ca\_#3 | **3,487,809** | **1.11E-08** | **0.23** | **2.4E-03** | **-0.07** | C/M |
| 3,354,869 | 2.94E-08 | 0.20 | 4.5E-03 | -0.06 |
| K | 04 | K\_#1 | **49,072,328** | **1.64E-06** | **0.18** | **3.7E-03** | **-0.30** | C/F |
| 49,071,552 | 1.75E-06 | 0.17 | 6.1E-03 | -0,30 |
| 10 | K\_#3 | **1,614,105** | **1,59E-10** | **0.32** | **3.3E-05** | **-0.57** | C/M/F |
| 1,925,709 | 4.31E-10 | 0.31 | 4.9E-05 | -0,57 |
| P | 04 | P\_#1 | **49,072,328** | **3.51E-08** | **0.22** | **7.4E-03** | **0.30** | C/M/F |
| 49,071,286 | 6.12E-08 | 0.22 | 1.5E-02 | -0.30 |
| S | 10 | S\_#4 | **1,609,531** | **1.24E-08** | **0.23** | **1.2E-04** | **-0.46** | C/M |
| 1,602,998 | 2.84E-08 | 0.23 | 4.0E-03 | -0.46 |
| 20 | S\_#10 | **39,064,722** | **1.44E-07** | **0.18** | **1.9E-02** | **0.23** | C/M/F |
| 39,076,484 | 9.13E-07 | 0.18 | 9.7E-03 | 0.20 |