**Genomic Regions Associated with Important Seed Quality Traits in Food-grade Soybeans**

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**Supplementary Table S1** Mean, standard error (α = 0.05), range, and parental means for soybean seed protein concentration (%, dry weight basis) in two RIL populations, ‘AC X790P’ x ‘S18-R6’ and ‘AC X790P’ x ‘S23-T5’, in five environments: Chatham 2015, Chatham 2016, Merlin 2015, Merlin 2016 and Palmyra 2016

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| **POPn\_1** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S16-R6** |
|  | Chatham 2015 | 43.13 (0.058) | 39.42 – 46.51 | 48.16 | 39.89 |
|  | Chatham 2016 | 42.86 (0.051) | 40.44 – 45.62 | 48.01 | 41.58 |
|  | Merlin 2015 | 42.84 (0.052) | 40.46 – 45.72 | 48.33 | 40.66 |
|  | Merlin 2016 | 43.62 (0.051) | 40.77 – 45.95 | 47.84 | 41.31 |
|  | Palmyra 2016 | 44.08 (0.056) | 41.73 – 47.26 | 48.04 | 41.24 |
|  | **Combined** | **43.31 (0.026)** | **41.53 – 45.27** | **48.08** | **40.93** |
|  |  |  |  |  |  |
| **POPn\_2** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S23-T5** |
|  | Chatham 2015 | 44.63 (0.073) | 40.39 – 48.58 | 49.31 | 42.74 |
|  | Chatham 2016 | 43.59 (0.061) | 40.62 – 47.49 | 47.56 | 41.15 |
|  | Merlin 2015 | 44.55 (0.065) | 41.24 – 48.01 | 48.48 | 42.16 |
|  | Merlin 2016 | 44.88 (0.062) | 41.69 – 48.74 | 47.94 | 43.51 |
|  | Palmyra 2016 | 45.35 (0.063) | 41.48 – 48.74 | 47.92 | 43.44 |
|  | **Combined** | **44.60 (0.032)** | **41.93 – 47.46** | **48.24** | **42.60** |
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**Supplementary Table S2** Mean, standard error (α = 0.05), range, and parental means for soybean seed yield (tonnes ha-1) in two RIL populations, ‘AC X790P’ x ‘S18-R6’ and ‘AC X790P’ x ‘S23-T5’, in five environments: Chatham 2015, Chatham 2016, Merlin 2015, Merlin 2016 and Palmyra 2016

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| **POPn\_1** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S16-R6** |
|  | Chatham 2015 | 3.19 (0.067) | 0.45 – 5.73 | 2.92 | 2.16 |
|  | Chatham 2016 | 4.90 (0.026) | 3.64 – 6.45 | 4.42 | 5.42 |
|  | Merlin 2015 | 3.68 (0.049) | 0.80 – 5.09 | 3.36 | 3.05 |
|  | Merlin 2016 | 2.90 (0.029) | 1.78 – 5.09 | 2.17 | 3.14 |
|  | Palmyra 2016 | 3.18 (0.025) | 2.20 – 3.94 | 2.45 | 4.11 |
|  | **Combined** | **3.57 (0.025)** | **2.55 – 4.49** | **3.06** | **3.57** |
|  |  |  |  |  |  |
| **POPn\_2** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S23-T5** |
|  | Chatham 2015 | 3.43 (0.081) | 0.76 – 5.83 | 3.03 | 3.99 |
|  | Chatham 2016 | 4.32 (0.033) | 2.55 – 5.50 | 4.07 | 5.35 |
|  | Merlin 2015 | 2.74 (0.039) | 0.98 – 4.00 | 2.95 | 3.27 |
|  | Merlin 2016 | 2.94 (0.025) | 1.91 – 3.84 | 2.91 | 3.38 |
|  | Palmyra 2016 | 3.21 (0.026) | 1.82 – 4.14 | 3.37 | 3.89 |
|  | **Combined** | **3.34 (0.024)** | **2.52 – 4.40** | **3.27** | **3.98** |
|  |  |  |  |  |  |

**Supplementary Table S3** Mean, standard error (α = 0.05), range, and parental means for soybean seed weight (100 seed weight in grams) in two RIL populations, ‘AC X790P’ x ‘S18-R6’ and ‘AC X790P’ x ‘S23-T5’, in five environments: Chatham 2015, Chatham 2016, Merlin 2015, Merlin 2016 and Palmyra 2016

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| **POPn\_1** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S16-R6** |
|  | Chatham 2015 | 20.37 (0.235) | 15.59 – 24.05 | 22.95 | 16.90 |
|  | Chatham 2016 | 23.57 (0.235) | 13.80 – 27.40 | 26.30 | 21.85 |
|  | Merlin 2015 | 18.99 (0.235) | 15.25 – 21.90 | 20.30 | 17.15 |
|  | Merlin 2016 | 22.56 (0.235) | 18.73 – 27.76 | 25.51 | 20.59 |
|  | Palmyra 2016 | 20.38 (0.235) | 13.80 – 23.45 | 21.00 | 19.65 |
|  | **Combined** | **21.18 (0.055)** | **18.08 – 23.88** | **23.21** | **19.23** |
|  |  |  |  |  |  |
| **POPn\_2** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S23-T5** |
|  | Chatham 2015 | 19.66 (0.211) | 16.95 – 24.15 | 22.40 | 17.10 |
|  | Chatham 2016 | 22.85 (0.210) | 13.45 – 26.95 | 28.93 | 19.83 |
|  | Merlin 2015 | 17.75 (0.212) | 14.23 – 22.05 | 21.65 | 14.50 |
|  | Merlin 2016 | 21.59 (0.210) | 17.97 – 25.26 | 25.42 | 19.23 |
|  | Palmyra 2016 | 19.57 (0.210) | 14.15 – 23.15 | 22.70 | 17.05 |
|  | **Combined** | **20.34 (0.057)** | **17.67 – 22.95** | **24.22** | **17.54** |
|  |  |  |  |  |  |

**Supplementary Table S4** Mean, standard error (α = 0.05), range, and parental means for soybean seed sucrose concentration (%, dry basis) in two RIL populations, ‘AC X790P’ x ‘S18-R6’ and ‘AC X790P’ x ‘S23-T5’, in five environments: Chatham 2015, Chatham 2016, Merlin 2015, Merlin 2016 and Palmyra 2016

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| **POPn\_1** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S16-R6** |
|  | Chatham 2015 | 6.25 (0.097) | 5.23 – 7.34 | 5.53 | 6.24 |
|  | Chatham 2016 | 6.15 (0.097) | 4.69 – 7.47 | 5.53 | 6.58 |
|  | Merlin 2015 | 6.16 (0.097) | 5.14 – 7.50 | 5.18 | 6.14 |
|  | Merlin 2016 | 5.12 (0.097) | 4.32 – 6.03 | 4.76 | 5.38 |
|  | Palmyra 2016 | 6.61 (0.097) | 5.75 – 7.68 | 6.29 | 6.77 |
|  | **Combined** | **6.06 (0.016)** | **5.44 – 6.82** | **5.46** | **6.22** |
|  |  |  |  |  |  |
| **POPn\_2** | **Environment** | **Mean (Std. Error)** | **Range**  | **AC X790P** | **S23-T5** |
|  | Chatham 2015 | 6.27 (0.114) | 5.22 – 7.45 | 5.89 | 6.29 |
|  | Chatham 2016 | 5.71 (0.113) | 4.04 – 6.71 | 5.06 | 6.07 |
|  | Merlin 2015 | 5.61 (0.114) | 3.97 – 7.09 | 5.05 | 5.42 |
|  | Merlin 2016 | 5.52 (0.113) | 4.37 – 6.74 | 5.63 | 5.68 |
|  | Palmyra 2016 | 6.09 (0.113) | 4.18 – 7.59 | 5.79 | 5.84 |
|  | **Combined** | **5.84 (0.014)** | **4.95 – 6.75** | **5.48** | **5.86** |
|  |  |  |  |  |  |

**Supplementary Table S5** Broad-sense heritability of protein concentration, sucrose concentration, seed weight and seed yield in two RIL populations evaluated in five environments (CHA15, CHA16, MER15, MER16 and PAL16)

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| --- | --- | --- | --- | --- |
|  | **Protein** | **Yield** | **Seed Weight** | **Sucrose** |
| **POPn\_1** | 0.9275 | 0.3603 | 0.8648 | 0.7035 |
| **POPn\_2** | 0.9501 | 0.2180 | 0.8924 | 0.8132 |

**Supplementary Table S6** Pearson correlation coefficients for seed protein and sucrose concentrations, 100-seed weight, and seed yield in five environments (Chatham 2015, Chatham 2016, Merlin 2015, Merlin 2016, and Palmyra 2016) as well as the combined environment for the recombinant inbred line populations.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **POPn\_1** | **CHA15** | Protein | Sucrose | Weight |  | **CHA16** | Protein | Sucrose | Weight |
|  | Yield | 0.33920\*\* | 0.07712ns | 0.45242\*\* |  | Yield | -0.14197\*\* | -0.19206\*\* | 0.07585ns |
|  | Weight | 0.47783\*\* | -0.05822ns |  |  | Weight | 0.24567\*\* | -0.23595\*\* |  |
|  | Sucrose | -0.34429\*\* |  |  |  | Sucrose | -0.34774\*\* |  |  |
|  |  |  |  |  |  |  |  |  |  |
|  | **MER15** | Protein | Sucrose | Weight |  | **MER16** | Protein | Sucrose | Weight |
|  | Yield | 0.28641\*\* | 0.14804\*\* | 0.33662\*\* |  | Yield | -0.22836\*\* | 0.16207\*\* | 0.17084\*\* |
|  | Weight | 0.45384\*\* | -0.13800\*\* |  |  | Weight | 0.41221\*\* | -0.16303\*\* |  |
|  | Sucrose | -0.23468\*\* |  |  |  | Sucrose | -0.35883\*\* |  |  |
|  |  |  |  |  |  |  |  |  |  |
|  | **PAL16** | Protein | Sucrose | Weight |  | **GMET** | Protein | Sucrose | Weight |
|  | Yield | -0.38017\*\* | 0.09885\* | 0.29201\*\* |  | Yield | 0.09280ns | 0.15572\*\* | 0.36310\*\* |
|  | Weight | 0.23137\*\* | -0.16674\*\* |  |  | Weight | 0.52630\*\* | -0.30735\*\* |  |
|  | Sucrose | -0.29171\*\* |  |  |  | Sucrose | -0.47392\*\* |  |  |
|  |  |  |  |  |  |  |  |  |  |
| **POPn\_2** | **CHA15** | Protein | Sucrose | Weight |  | **CHA16** | Protein | Sucrose | Weight |
|  | Yield | 0.32387\*\* | 0.15818\*\* | 0.45408\*\* |  | Yield | -0.15656\*\* | 0.11900ns | 0.15314\*\* |
|  | Weight | 0.35170\*\* | -0.08805ns |  |  | Weight | 0.26598\*\* | 0.03275ns |  |
|  | Sucrose | -0.50189\*\* |  |  |  | Sucrose | -0.50145\*\* |  |  |
|  |  |  |  |  |  |  |  |  |  |
|  | **MER15** | Protein | Sucrose | Weight |  | **MER16** | Protein | Sucrose | Weight |
|  | Yield | 0.03432ns | 0.00028ns | 0.21973\*\* |  | Yield | -0.16361\*\* | 0.14708\*\* | 0.20717\*\* |
|  | Weight | 0.19175\*\* | -0.20483\*\* |  |  | Weight | 0.08484ns | 0.07635ns |  |
|  | Sucrose | -0.37639\*\* |  |  |  | Sucrose | -0.57133\*\* |  |  |
|  |  |  |  |  |  |  |  |  |  |
|  | **PAL16** | Protein | Sucrose | Weight |  | **GMET** | Protein | Sucrose | Weight |
|  | Yield | -0.21593\*\* | 0.14572\*\* | 0.26574\*\* |  | Yield | -0.06051ns | 0.12515\*\* | 0.43606\*\* |
|  | Weight | 0.06262ns | 0.09917\*\* |  |  | Weight | 0.10500ns | -0.09426\*\* |  |
|  | Sucrose | -0.34754\*\* |  |  |  | Sucrose | -0.69523\*\* |  |  |
|  |  |  |  |  |  |  |  |  |  |
| ns Non-significant\*\*Significant at α = 0.05\*Significant at α = 0.01 |

**Supplementary Table S7** Summary ofmajor putative QTL (R2 > 10.0%) associated with soybean seed protein concentration, sucrose concentration and seed weight with potential use in marker-assisted selection, candidate genes, and co-localized QTL in the previous studies

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| --- | --- | --- | --- | --- |
| **Protein QTL** | **Chr.** | **Flanking Markers** | **Candidate Genes** | **Co-localized QTL in the Previous Studies** |
| **Protein** | **Seed Weight** | **Oil** | **Yield** | **References** |
| *qPro\_Gm01-2* | 1 | S01\_42371693 | - | S01\_42555910 |  |  |  |  |  |  |
| *qPro\_Gm02-3* | 2 | S02\_40793724 | - | S02\_41072417 | Glyma.02g220000Glyma.02g221500 | Seed protein 40-5 |  |  |  | Qi et al. 2014 |
| *qPro\_Gm04-3* | 4 | S04\_44592458 | - | S04\_45008840 |  | Seed protein 36-9Seed protein 19-1Seed protein 37-9 | Seed weight 47-3Seed weight 36-15 |  |  | Mao et al.,2013Stombaugh et al., 2004Wang et al., 2014Li et al., 2009Han et al., 2012 |
| *qPro\_Gm04-4* | 4 | S04\_48435528 | - | S04\_49024162 | Glyma.04g212500Glyma.04g214500 |  |  |  |  |  |
| *qPro\_Gm05-2* | 5 | S05\_38330071 | - | S05\_38993543 |  |  | Seed weight 34-9 |  |  | Han et al., 2012 |
| *qPro\_Gm06-1* | 6 | S06\_19074 | - | S06\_699413 | Glyma.06g004500Glyma.06g001800 |  |  |  |  |  |
| *qPro\_Gm06-3* | 6 | S06\_9128442 | - | S06\_11029737 | Glyma.06g113700Glyma.06g116400Glyma.06g119700 |  |  |  |  |  |
| *qPro\_Gm06-6* | 6 | S06\_30639643 | - | S06\_33589987 | Glyma.06g225600Glyma.06g225700 | Seed protein 28-1Seed protein 29-1Seed protein 35-2Seed protein 36-7Seed protein 36-8 | Seed weight 19-1 |  |  | Liang et al.,2010Palomeque et al.,2009Rossie et al., 2013Mao et al., 2013Funatsuki et al., 2005 |
| *qPro\_Gm08-2* | 8 | S08\_43864875 | - | S08\_43896183 |  |  |  |  |  |  |
| *qPro\_Gm12-3* | 12 | S12\_924424 | - | S12\_1147989 |  |  | Seed weight 16-3Seed weight 43-3 | Seed oil 44-2 |  | Funatsuki et al., 2005Kuroda et al., 2013Leit et al., 2016 |
| *qPro\_Gm12-4* | 12 | S12\_3518939 | - | S12\_3666689 |  |  | Seed weight 43-3 | Seed oil 44-2 |  | Kuroda et al., 2013 |
| *qPro\_Gm13-4* | 13 | S13\_282277833 | - | S13\_2825468 | Glyma.13g167800Glyma.13g167900 |  |  |  |  |  |
| *qPro\_Gm15-3* | 15 | S15\_10218629 | - | S15\_10877491 | Glyma.15g129800Glyma.15g130000Glyma.15g134800 | Seed protein 39-2Seed protein 3-6cqSeed protein-001Seed protein 5-1 |  | Seed oil 24-24mqSeed oil-013Seed oil 27-2 |  | Warrington et al., 2015Brummer et al., 1997Fasoula et al., 2004Lee et al., 2004Qi et al., 2011Reinprecht et al., 2006 |
| *qPro\_Gm18-4* | 18 | S18\_52660341 | - | S18\_53019901 |  | Seed protein 36-25 | Seed weight 6-6Seed weight 6-8 |  | Seed yield 27-3Seed yield 30-3 | Mao et al.,2013Yao et al., 2015Kim et al., 2012 |

**Supplementary Table S8** Major putative QTL (R2 > 10.0%) associated with soybean seed sucrose concentration, yield and seed weight with potential use in marker-assisted selection, identified by multiple QTL mapping (MQM) in RIL populations examined under combined Ontario environments in 2015 and 2016

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **QTL Namez** | **Chr.** | **POPn** | **Flanking Markers** | **Size (cM)** | **LODy** | **ax** | **R2 (%)** | **Source** |
| *Sucrose* | *qSuc\_Gm01-1* | 1 | 1 | S01\_150451 | - | S01\_293924 | 2.30 | 5.70 | 0.1022 | 13.0 | S18-R6 |
|  | *qSuc\_Gm01-2* | 1 | 2 | S01\_42371693 | - | S01\_42555910 | 2.19 | 6.67 | 0.1472 | 14.5 | AC X790P |
|  | *qSuc\_Gm02-3* | 2 | 2 | S02\_40716331 | - | S02\_42411031 | 11.17 | 5.46 | 0.1993 | 10.7 | S23-T5 |
|  | *qSuc\_Gm03-2* | 3 | 2 | S03\_44917381 | - | S03\_45395338 | 8.73 | 5.20 | 0.1255 | 11.7 | S23-T5 |
|  | *qSuc\_Gm09-2* | 9 | 1 | S09\_49279854 | - | S09\_49546888 | 10.70 | 5.16 | 0.1700 | 11.9 | AC X790P |
|  | *qSuc\_Gm12-1* | 12 | 1 | S12\_3518939 | - | S12\_3666689 | 7.64 | 5.49 | 0.1495 | 12.4 | AC X790P |
|  | *qSuc\_Gm13-6* | 13 | 2 | S13\_31531708 | - | S13\_31639456 | 4.73 | 6.36 | 0.6121 | 11.2 | S23-T5 |
|  | *qSuc\_Gm14-2* | 14 | 2 | S14\_1086390 | - | S14\_1282950 | 6.75 | 4.95 | 0.3898 | 10.2 | AC X790P |
|  | *qSuc\_Gm16-1* | 16 | 2 | S16\_37420716 | - | S16\_37753573 | 1.64 | 6.69 | 0.1398 | 14.8 | S23-T5 |
|  | *qSuc\_Gm18-1* | 18 | 1 | S18\_49993979 | - | S18\_50225033 | 9.60 | 4.59 | 0.1866 | 10.2 | S18-R6 |
|  |  |  |  |  |  |  |  |  |  |  |  |
| *Seed Yield* | *qYld\_Gm15-4* | 15 | 2 | S15\_24465408 | - | S15\_25479719 | 2.22 | 5.98 | 1.6936 | 10.7 | S23-T5 |
|  | *qYld\_Gm20-4* | 20 | 2 | S20\_44438965 | - | S20\_44771176 | 1.94 | 6.45 | 0.9447 | 12.5 | AC X790P |
|  |  |  |  |  |  |  |  |  |  |  |  |
| *Seed Weight* | *qWt\_Gm02-1* | 2 | 2 | S02\_1883298 | - | S02\_2417746 | 14.93 | 4.85 | 0.9392 | 10.6 | S23-T5 |
|  | *qWt\_Gm03-1* | 3 | 2 | S03\_5818458 | - | S03\_19256703 | 10.58 | 6.05 | 0.4838 | 13.5 | S23-T5 |
|  | *qWt\_Gm04-1* | 4 | 1 | S04\_9555350 | - | S04\_9936875 | 2.54 | 5.04 | 0.4104 | 11.6 | S18-R6 |
|  | *qWt\_Gm04-2* | 4 | 1 | S04\_15438084 | - | S04\_15954764 | 2.83 | 4.89 | 0.4088 | 11.3 | AC X790P |
|  | *qWt\_Gm05-1* | 5 | 1 | S05\_4293377 | - | S05\_4392756 | 2.34 | 5.88 | 0.4526 | 13.4 | S18-R6 |
|  | *qWt\_Gm06-1* | 6 | 1 | S06\_19074 | - | S06\_798961 | 2.24 | 4.46 | 0.3927 | 10.3 | S18-R6 |
|  | *qWt\_Gm06-2* | 6 | **1** | S06\_7995062 | - | S06\_9128442 | 5.38 | 5.98 | 0.4536 | 13.1 | S18-R6 |
|  | *qWt\_Gm07-2* | 7 | 2 | S07\_2438965 | - | S07\_2788084 | 3.96 | 4.89 | 0.5651 | 10.1 | AC X790P |
|  | *qWt\_Gm08-1* | 8 | 1 | S08\_42089038 | - | S08\_43325761 | 5.83 | 5.59 | 0.5780 | 12.7 | S18-R6 |
|  | *qWt\_Gm11-1* | 11 | **1** | S11\_30385803 | - | S11\_30425212 | 1.12 | 5.59 | 0.4344 | 12.8 | AC X790P |
|  | *qWt\_Gm12-2* | 12 | 1 | S12\_3358348 | - | S12\_3518939 | 2.94 | 8.09 | 0.7896 | 15.8 | AC X790P |
|  | *qWt\_Gm13-1* | 13 | 1 | S13\_26716128 | - | S13\_27766926 | 10.80 | 5.71 | 0.6586 | 12.9 | S18-R6 |
|  | *qWt\_Gm14-4* | 14 | 2 | S14\_3738849 | - | S14\_4112800 | 10.60 | 5.03 | 1.1426 | 10.6 | AC X790P |
|  | *qWt\_Gm14-6* | 14 | 1 | S14\_6573275 | - | S14\_6976251 | 10.34 | 7.90 | 0.6402 | 15.8 | S18-R6 |
|  | *qWt\_Gm15-1* | 15 | 2 | S15\_1248951 | - | S15\_1528828 | 1.09 | 6.31 | 0.4874 | 14.0 | S23-T5 |
|  | *qWt\_Gm15-2* | 15 | 1 | S15\_6427154 | - | S15\_6747765 | 4.75 | 4.55 | 0.5919 | 10.3 | S18-R6 |
|  | *qWt\_Gm15-3* | 15 | 1 | S15\_7552589 | - | S15\_7756662 | 2.25 | 4.85 | 0.6126 | 11.1 | AC X790P |
|  | *qWt\_Gm15-6* | 15 | **1** | S15\_36957405 | - | S15\_37104746 | 1.68 | 5.37 | 0.4245 | 12.3 | AC X790P |
|  | *qWt\_Gm16-2* | 16 | 2 | S16\_36255272 | - | S16\_36735586 | 4.03 | 5.07 | 1.1719 | 11.3 | S23-T5 |
|  | *qWt\_Gm18-1* | 18 | 1 | S18\_2129860 | - | S18\_2460283 | 6.39 | 5.11 | 0.4214 | 11.8 | S18-R6 |
|  | *qWt\_Gm18-2* | 18 | 2 | S18\_5212723 | - | S18\_5214289 | 0.55 | 6.92 | 0.6039 | 15.3 | S23-T5 |
|  | *qWt\_Gm19-1* | 19 | 1 | S19\_49218060 | - | S19\_49654021 | 13.70 | 5.42 | 0.7695 | 12.4 | AC X790P |
|  |  |  |  |  |  |  |  |  |  |  |  |
| zQTL for the same trait detected in all individual environments (CHA15, CHA16, MER15, MER16 and PAL16) and the combined environment (GMET) with the same or overlapping marker interval was designated as one QTL. QTL highlighted in bold are novel QTL and were validated in the other RIL population.yLOD thresholds were calculated through a permutation test with 1,000 iterations and a Type I error rate of 0.001.xAdditive effects calculated as the absolute value of half the subtraction of the mean of genotypes with the ‘S18-R6’ (‘POPn\_1’) or ‘S23-T5’ (POPn\_2) allele (negative effect) from the mean of genotypes with the ‘AC X790P’ allele (positive allele). |

**Supplementary Table S9** Whole-seed (dry basis) calibration values for oil, protein, Moisture and fatty acid components, as provided by Perten Instruments. The coefficient of determination for cross-validation (R2CV) explains the proportion of variance that can be predicted between reference chemistry and predicted values. The minimum and maximum values are the limits of the prediction range. The SECV is the standard error of cross validation, where samples are removed from the validation set and predicted, and the total error for the dataset is calculated. Factors shows the number of factors included in the calibration equation for a given trait. Samples shows the total number of samples used in the calibration. Calibration file dates for each trait are listed.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait (%)** | **R2CV** | **Minimum** | **Maximum** | **SECV** | **Factors** | **Samples** | **Calibration File** |
| **Oil** | 0.83 | 13.6 | 26.5 | 0.8 | 19 | 3381 | 20170608 |
| **Protein** | 0.89 | 33.4 | 53.6 | 0.8 | 18 | 3607 | 20170608 |
| **Moisture** | 0.27 | 4.0 | 15.7 | 2.9 | 19 | 3531 | 20160609 |
| **Palmitic Acid** | 0.04 | 4.4 | 18.9 | 5.0 | 19 | 3490 | 20160609 |
| **Stearic Acid** | 0.60 | 2.4 | 6.9 | 0.5 | 19 | 3524 | 20160609 |
| **Oleic Acid** | 0.88 | 13.8 | 89.6 | 4.3 | 19 | 3423 | 20160609 |
| **Linoleic Acid** | 0.77 | 3.6 | 66.7 | 5.3 | 19 | 3434 | 20160609 |
| **Linolenic Acid** | 0.50 | 0.8 | 14.1 | 1.8 | 19 | 3514 | 20160609 |
| **Sucrose** | 0.33 | 1.2 | 10.3 | 1.2 | 20 | 1333 | 20160609 |