**Table S4.** Phenotypic segregation of $BC_3S_{2:4}$ populations derived from three introgression lines containing overlapping recombination events of QTL-*Pal9*.

| Population | Traits | *Pal9* –/– | *Pal9* +/– | *Pal9* +/+ | A | D | $R^2$ | *P* value |
|---|---|---|---|---|---|---|---|---|
| 08BL245-6 | C16:0 (mg/g) | 5.55 ± 0.34 | 6.34 ± 0.42 | 6.52 ± 0.46 | 0.33 | 0.16 | 45.0 | 3.25E–07 |
| | C16:0/ALL (%) | 12.99 ± 0.40 | 14.32 ± 0.69 | 15.6 ± 0.55 | 1.29 | 0.01 | 70.0 | 8.51E–14 |
| | SFA/ALL (%) | 15.04 ± 0.50 | 16.31 ± 0.67 | 17.59 ± 0.60 | 1.28 | 0.00 | 67.8 | 4.86E–13 |
| | UFA/ALL (%) | 83.47 ± 1.06 | 82.33 ± 0.69 | 80.83 ± 0.98 | –1.41 | 0.09 | 53.5 | 4.73E–09 |
| | SFA/UFA (%) | 18. 02± 1.05 | 19.81 ± 1.03 | 21.76± 1.21 | 2.12 | –0.04 | 66.7 | 1.13E–12 |
| 08BL248-2 | C16:0 (mg/g) | 5.69 ± 0.38 | 5.97 ± 0.44 | 6.42 ± 0.47 | 0.41 | –0.05 | 23.4 | 1.65E–03 |
| | C16:0/ALL (%) | 13.43 ± 0.27 | 14.46 ± 0.53 | 15.06 ± 0.53 | 0.70 | 0.11 | 53.0 | 6.35E–09 |
| | SFA/ALL (%) | 15.49 ± 0.27 | 16.23 ± 0.51 | 16.84 ± 0.35 | 0.64 | 0.03 | 48.8 | 5.41E–08 |
| | UFA/ALL (%) | 83.16 ± 0.31 | 82.45 ± 0.56 | 81.81 ± 0.36 | –0.66 | –0.02 | 45.7 | 2.32E–07 |
| | SFA/UFA (%) | 18.62 ± 0.27 | 19.68 ± 0.45 | 20.58 ± 0.33 | 1.01 | 0.04 | 48.2 | 7.16E–08 |
| 08BL168-7 | C16:0 (mg/g) | 4.06 ± 0.59 | 4.80 ± 0.73 | 5.16 ± 0.98 | 0.46 | 0.10 | 26.4 | 6.31E–03 |
| | C16:0/ALL (%) | 13.51 ± 0.42 | 14.68 ± 0.91 | 16.35 ± 0.79 | 1.55 | –0.13 | 64.2 | 4.39E–08 |
| | SFA/ALL (%) | 15.53 ± 0.53 | 16.80 ± 0.89 | 18.03 ± 0.82 | 1.24 | 0.01 | 54.0 | 1.83E–06 |
| | UFA/ALL (%) | 83.22 ± 0.54 | 81.81 ± 0.89 | 80.66 ± 0.79 | –1.22 | –0.06 | 56.3 | 7.83E–07 |
| | SFA/UFA (%) | 18.66 ± 1.03 | 20.53 ± 0.92 | 22.35 ± 0.87 | 2.23 | 0.02 | 54.0 | 1.83E–06 |

Two hundred and eighty six individuals of a $BC_3S_{:2:4}$ population derived from 08BL245-6, covering the downstream introgression from By804; 253 individuals from a $BC_3S_{:2:4}$ population derived from 08BL248-2, covering the upstream introgression; and 178 progenies containing only the 90-kb target genome region from By804, were genotyped and phenotyped for target traits. The kernels from at least 3 mature ears in the $BC_3S_{:2:4}$ family with the same genotype were pooled and measured for the target traits. ANOVA test in Excel was used to detect significance for the phenotypic segregations and gene effects of the homologous alleles of B73, By804 and the heterozygous alleles of QTL-*Pal9*. "A" represents the additive effect of By804 allele and "D" is the dominant effect. –/–, +/– and +/+ is the homozygous allele of B73, allele that are heterozygous for B73 and By804 and homozygous allele of By804 based on target genomic markers, respectively. The abbreviations of traits can be found in Table S2.