Genome-wide association study and selection signatures detect genomic regions associated with seed yield and oil quality in flax

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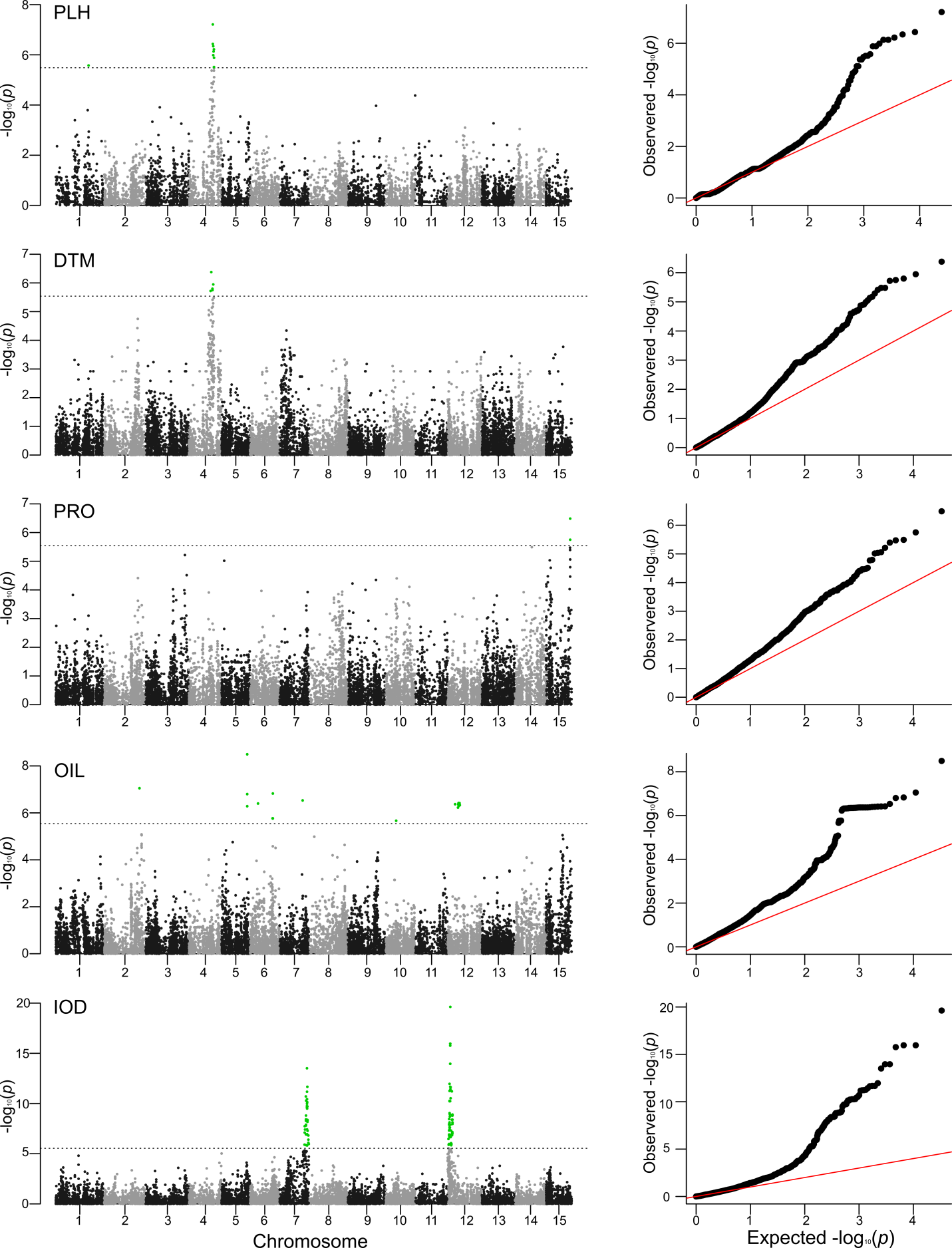
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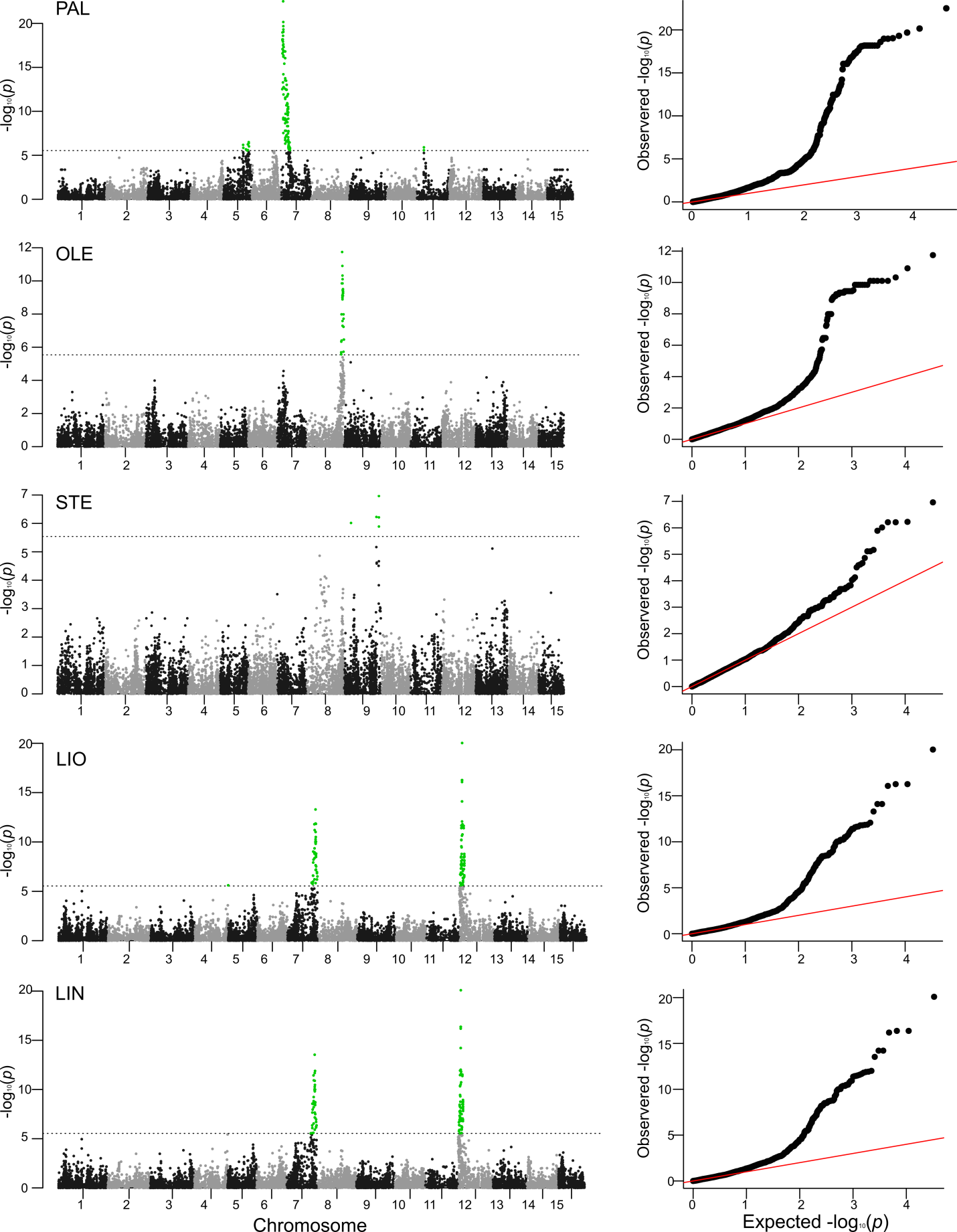
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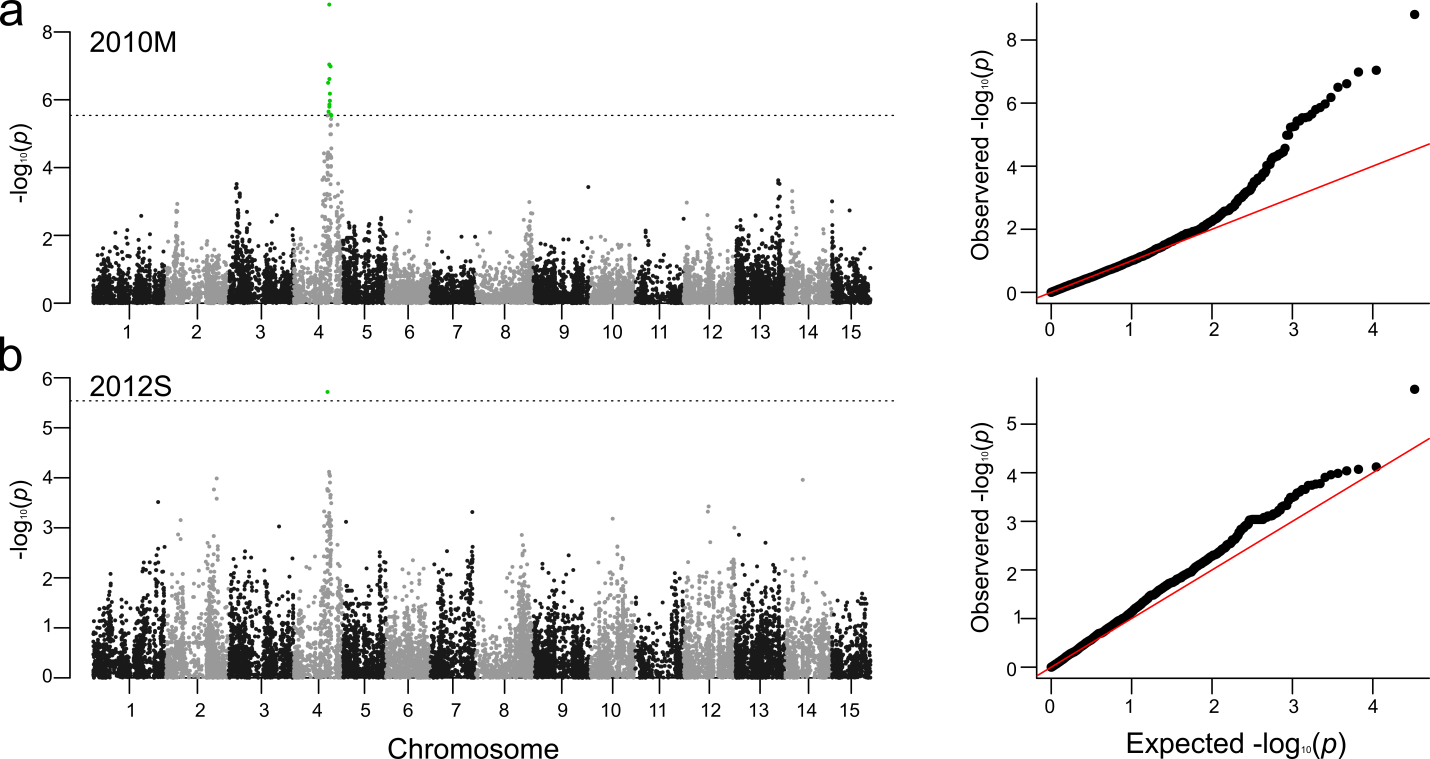
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**Figure S1.** Manhattan and quantile-quantile (Q-Q) plots of 10 traits using BLUP values of traits estimated from six or eight environments in the BM+EV+SU population using GLM. PLH: plant height; DTM: days to maturity; PRO: protein content (%); OIL: oil content (%); IOD: iodine value; PAL: palmitic acid content (%); STE: stearic acid content (%); OLE: oleic acid content (%); LIO: linoleic acid content (%); LIN: linolenic acid content (%).





**Figure S2.** Manhattan and quantile-quantile (Q-Q) plots of seed yield (YLD) using the BM+EV+SU combined population and GLM in two environments: (a) Morden 2010 and (b) Saskatoon 2012 showing the same QTL on chromosome 4.



**Figure S3.** Histograms of 11 seed yield related and seed quality traits. A normal curve is fitted for each histogram.

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