**Table S8. Association analysis between the markers (GhGPAT16-1624 and GhGPAT26-172 from *GhGPAT16* and *GhGPAT26* genes) and cottonseed oil content in a BILa population.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Trait | SNP maarkers | 2015AYb | 2016AY | 2016XJc |
| Seed oil content (%) | *GhGPAT16-1624* | -0.262\*\* | -0.045 | -0.059 |
| *GhGPAT26-172* | 0.128 | 0.183\* | 0.11 |

a  BIL population was developed from a cross between Upland cotton CRI 36 and *G.barbadense* Hai 7124 through one generation of backcrossing using CRI 36 as the recurrent parent followed by seven generations of selfing.

b AY: Anyang

c XJ: Xinjiang

\* and \*\* indicate correlation at the 0.05 and 0.01 significant levels, respectively.