



Figure S6. Phenotypic evaluation of *GN2.2* over-expressing lines.. A comparison of the relative expression levels, grain numbers of main panicles, panicle lengths, mean lengths of primary branches, numbers of secondary branches, plant heights and heading dates, between *GN2.2* over-expressing lines and their controls. CLb2 represents the ‘Teqing’ control line with an empty plasmid used for analysis. pOEB1 and pOEB3 represents *GN2.2* over-expressing transgenic lines used for analysis. All of the data above are presented as mean \pm SE (n = 20). The double asterisks represent significance differences determined by the Student’s *t*-test at the level of P < 0.01.