

Table 4 Chromosome location of QTLs for grain size related traits in F₂ population

Traits	Chromosomes	QTLs	Intervals	LOD	PVE(%) ^a	Add ^b
GL	1	<i>qGL-1</i>	M008-RM11258	2.64	17.64	0.1713
	3	<i>qGL-3</i>	03M36.3-03M33.1	7.77	27.60	0.422
	4	<i>qGL-4</i>	RM16943-M09496	3.11	8.36	0.2493
	9	<i>qGL-9</i>	RM566-9M10.51	2.59	5.57	0.1167
GW	2	<i>qGW-2</i>	M018-RM1211	2.50	4.81	0.0809
	3	<i>qGW-3</i>	RM14391-M023	3.35	8.16	-0.0908
	5	<i>qGW-5a</i>	M06502-M040	9.40	21.33	0.1634
	5	<i>qGW-5b</i>	M13153-05M26.62	3.84	8.65	0.0917
LWR	2	<i>qLWR-2</i>	M018-RM1211	5.08	11.06	-0.1602
	3	<i>qLWR-3a</i>	03M24.29-RM5488	4.43	8.60	-0.1524
	3	<i>qLWR-3b</i>	RM14391-M023	3.91	10.91	0.1673
	5	<i>qLWR-5</i>	M06502-M040	7.51	16.86	-0.2005
TGW	12	<i>qLWR-12</i>	M110-12M27.47	3.14	14.34	-0.1995
	5	<i>qTGW-5</i>	M040-M09668	4.04	13.26	2.042
	6	<i>qTGW-6</i>	06M17.5-6M13.5	3.57	9.04	1.4532

Note: ^a The percentage of phenotypic variation of QTL explained; ^b The additive effects of QTL. Positive **Add** indicates the alleles derived from NYZ increasing the effect on that trait, and, whereas, negative **Add** indicates the alleles derived from NYZ decreasing the effect on that trait.