a.

TOOL	MDL	IF	SNP	CHR	POS	PVAL	SCR	THR	SGN
GWASpoly	additive	0.99	c2_25471	10	48808404	0.000	5.28	4.48	T
GWASpoly	additive	0.99	c2_45611	10	48203431	0.000	5.07	4.48	T
GWASpoly	additive	0.99	c1_8019	10	48863165	0.000	4.93	4.48	T
GWASpoly	additive	0.99	c2_45606	10	48218826	0.000	4.32	4.48	F
GWASpoly	additive	0.99	c2_549	9	16527499	0.001	3.25	4.48	F
GWASpoly	additive	0.99	c2_9925	1	81410256	0.002	2.77	4.48	F
GWASpoly	additive	0.99	c1_8021	10	48862950	0.002	2.66	4.48	F
GWASpoly	additive	0.99	c2_12125	1	71450400	0.002	2.64	4.48	F
PLINK	additive	1.28	c1_16001	10	47539878	0.000	3.94	4.52	F
PLINK	additive	1.28	c2_17192	1	70472766	0.001	2.86	4.52	F
PLINK	additive	1.28	c2_12125	1	71450400	0.002	2.75	4.52	F
PLINK	additive	1.28	c2_45606	10	48218826	0.002	2.72	4.52	F
PLINK	additive	1.28	c2_45611	10	48203431	0.002	2.64	4.52	F
PLINK	additive	1.28	c2_14903	1	87322718	0.003	2.50	4.52	F
PLINK	additive	1.28	c1_13530	10	48149399	0.003	2.50	4.52	F
PLINK	additive	1.28	c2_2201	1	77738822	0.003	2.49	4.52	F
SHEsis	general	3.56	c1_8019	10	48863165	0.000	10.99	4.52	T
SHEsis	general	3.56	c1_13526	10	48020996	0.000	10.05	4.52	T
SHEsis	general	3.56	c2_45603	10	48073593	0.000	9.89	4.52	T
SHEsis	general	3.56	c2_25471	10	48808404	0.000	9.65	4.52	T
SHEsis	general	3.56	c2_53380	1	70371898	0.000	8.97	4.52	T
SHEsis	general	3.56	c2_45606	10	48218826	0.000	8.17	4.52	T
SHEsis	general	3.56	c1_16351	10	48761642	0.000	8.00	4.52	T
SHEsis	general	3.56	c2_45611	10	48203431	0.000	7.73	4.52	T
TASSEL	general	1.00	c2_16999	8	54838024	0.001	2.96	4.52	F
TASSEL	general	1.00	c2_4342	7	14924207	0.001	2.92	4.52	F
TASSEL	general	1.00	c2_16998	8	54838005	0.001	2.86	4.52	F
TASSEL	general	1.00	c2_17191	1	70474651	0.002	2.67	4.52	F
TASSEL	general	1.00	c2_9925	1	81410256	0.002	2.65	4.52	F
TASSEL	general	1.00	c1_16001	10	47539878	0.002	2.63	4.52	F
TASSEL	general	1.00	c2_45606	10	48218826	0.005	2.34	4.52	F
TASSEL	general	1.00	c2_45611	10	48203431	0.005	2.31	4.52	F

Column headers: MDL: Model, **IF**: Inflation factor, **SNP**: marker name, **CHR**: Chromosome, **PVAL:** p-value, **SCR:** score as -log10 (p-value), **THR:** significance threshold as -log10 (α / m), where α is the significance level, and m is the number of tested markers, and **SGN:** significance threshold as true (T) or false (F) whether score > threshold or not.

b.

c.