Table S8 Single nucleotide polymorphisms (SNPs) contained in a single forward regression genome wide association analysis (GWAS) model for 20-kernel seed weight in the maize nested association mapping (NAM) population. Effect is relative to B73.

Marker	chr	AGPv2 Position	cM	Effect	P value
PZE0123124739	1	23,099,268	39.91	-0.07	1.11E-16
PZE01201470169	1	201,639,860	115.12	-0.11	1.24E-09
PZE01237261221	1	237,965,327	140.05	-0.11	3.95E-15
PZE0207620470	2	7,663,333	22.98	-0.06	5.77E-17
PZE0219925121	2	20,005,607	50.23	0.15	1.15E-10
PZE0228682197	2	28,761,283	60.29	0.06	2.21E-17
PZE02207653607	2	210,665,344	116.70	0.11	2.08E-09
PZE0305630836	3	5,850,072	21.63	0.09	1.39E-08
PZE03182929802	3	184,677,342	94.84	0.13	1.35E-15
PZE03209569396	3	211,128,687	120.01	-0.16	5.34E-13
PZE04207608568	4	201,957,506	108.82	0.08	2.04E-20
PZE0545748962	5	46,424,011	59.89	-0.11	1.89E-15
PZE05209672404	5	210,474,175	129.99	0.25	1.87E-13
PZE0692901122	6	64,157,406	19.51	0.08	2.05E-09
PZE06159136863	6	159,014,181	80.65	-0.08	1.20E-10
PZE07148539524	7	154,191,204	86.44	0.09	1.15E-08
PZE07156647853	7	162,259,418	99.46	0.06	4.55E-14
PZE08103597003	8	104,822,548	58.93	-0.05	3.20E-13
PZE0961486830	9	NA	45.68	0.19	4.67E-24
PZE09131782056	9	136,179,349	66.59	0.06	2.23E-12
PZE1025657301	10	25,657,714	35.72	-0.09	7.26E-10