



Figure S1: Distribution of identity by state (IBS) coefficients using different genotyping platforms. IBS coefficients for (1) trees genotyped using exome capture GBS (A), (2) trees genotyped using the Axiom NZPRAD02 genotyping array (B), and (3) trees genotyped using different platforms (C). The threshold separating unrelated trees from close relatives (IBS = 0.85) is shown as a red dashed line, while tri-modal distributions likely represent unrelated trees, second- and first-degree relatives, respectively.

Table S1. Description of field experiments used in single-step genomic evaluation.

Site	Trial series	Population	Number of genotypes tested	Longitude	Latitude	Experimental design
Kaingaroa	FR260 ^a	260	590	-38.2805	176.7255	sets-within-reps
Tarawera	FR260 ^a	260	656	-38.1703	176.5289	sets-within-reps
Woodhill	FR260 ^a	260	603	-36.5852	174.2644	sets-within-reps
Tarawera	FR305GF ^b	397	320	-38.1703	176.5289	sets-within-reps
Tarawera	FR305HD ^b	397	190	-38.1703	176.5289	sets-within-reps
Woodhill	FR305GF ^b	397	330	-36.5851	174.2644	sets-within-reps
Woodhill	FR305HD ^b	397	190	-36.5851	174.2644	sets-within-reps
Tarawera	FR353 ^c	399	535	-38.1734	176.527	incomplete blocks
Kinleith	FR353 ^c	399	524	-38.2585	176.0576	incomplete blocks
Woodhill	FR353 ^c	399	517	-36.7252	174.3876	incomplete blocks
Kaingaroa	Cloned Elites ^d	313/314	1282	-38.475	176.635	optimal design
Kinleith	Cloned Elites ^d	313	648	-38.3721	175.9282	optimal design
Rotu	Cloned Elites ^d	313	644	-35.8895	173.7782	optimal design
Mohaka	Cloned Elites ^d	313	539	-39.0737	176.9772	optimal design

^a Trial series “FR260” contains 1,849 non-genotyped individuals established through single-pair mating design using 47 parents and planted at three sites as a single tree plot, sets-within-reps design with six replicates.

^b Trial series “FR305” contains 520 clonally replicated individuals established through single-pair mating design using 64 parents and planted at two sites as a single tree plot, sets-within-reps design with six replicates. The series includes material from parent selected for different traits such as growth and form (“FR305GF”) and wood density (“FR305HD”).

^c Trial series “FR353” contains 542 clonally replicated individuals established through factorial mating design using 24 parents and planted at three sites as incomplete block design with 5 replicates and 9 incomplete blocks within replicate.

^d Trial series “Cloned Elites” contains 1,343 clonally replicated individuals planted at 4 sites using an optimal design [1].

Table S2. Simulation-based evaluation of parentage assignment using the *apparent* R package (see Materials and Methods).

Scenario	Family	Number of offspring tested	Statistically significant assignments (%)	Correct assignments based on genetic distance score (%)
1	QTL	93	92 (99%)	93 (100%)
	FWK	83	83 (100%)	83 (100%)
2	QTL	93	93 (100%)	93 (100%)
	FWK	83	83 (100%)	83 (100%)
3	QTL	93	92 (99%)	93 (100%)
	FWK	83	83 (100%)	83 (100%)
4	QTL	68	3 (4%)	68 (100%)
	FWK	58	56 (97%)	57 (98%)

Reference

- Butler, D. On the optimal design of experiments under the linear mixed model. PhD thesis, The University of Queensland, 2013. <http://espace.library.uq.edu.au/view/UQ:314932>, <http://espace.library.uq.edu.au/view/UQ:314932>.