

Table S1: Accuracies for purebred individuals for a trait with high heritability ($h^2 = 0.40$)

Correlation ¹	Training ²	Data/Region Size ³	HOL			RED			JER		
			1 SNP	100 SNPs	WG	1 SNP	100 SNPs	WG	1 SNP	100 SNPs	WG
1.00	Pure	HOL	_b 0.771 ^b	_b 0.780 ^a	_b 0.760 ^c	_d 0.128 ^a	_d 0.095 ^a	_d 0.080 ^b	_d 0.120 ^a	_c 0.059 ^b	_c 0.036 ^c
		RED	_c 0.170 ^a	_c 0.162 ^a	_c 0.127 ^b	_c 0.751 ^b	_c 0.757 ^a	_{bc} 0.741 ^c	_d 0.170 ^a	_c 0.123 ^b	_c 0.111 ^b
		JER	_c 0.042 ^a	_d 0.035 ^a	_d 0.040 ^a	_d 0.060 ^a	_d 0.057 ^a	_d 0.057 ^a	_c 0.643 ^b	_b 0.652 ^a	_b 0.638 ^c
	Combined	HOL+RED+JER	_b 0.777 ^a	_b 0.779 ^a	_b 0.757 ^b	_c 0.749 ^a	_c 0.752 ^a	_c 0.730 ^b	_{bc} 0.652 ^a	_b 0.646 ^a	_b 0.617 ^b
		HOL+RED+JER+MIX	_a 0.802 ^a	_a 0.803 ^a	_a 0.781 ^b	_b 0.774 ^a	_b 0.777 ^a	_{ab} 0.754 ^b	_a 0.732 ^a	_a 0.734 ^a	_a 0.701 ^b
	BOA	HOL+RED+JER+MIX uncor	_a 0.796 ^b	_a 0.804 ^a	_a 0.782 ^c	_{ab} 0.776 ^b	_{ab} 0.782 ^a	_a 0.763 ^c	_{ab} 0.723 ^b	_a 0.738 ^a	_a 0.713 ^c
0.50	Pure	HOL	_b 0.785 ^b	_b 0.790 ^a	_b 0.774 ^c	_d 0.101 ^a	_d 0.085 ^{ab}	_d 0.073 ^b	_d 0.102 ^a	_d 0.073 ^b	_e 0.067 ^b
		RED	_d 0.131 ^{ab}	_d 0.129 ^a	_d 0.116 ^b	_b 0.747 ^b	_b 0.754 ^a	_b 0.736 ^c	_d 0.079 ^a	_d 0.070 ^a	_e 0.043 ^b
		JER	_d 0.030 ^a	_d 0.039 ^a	_d 0.029 ^a	_d 0.023 ^a	_d 0.025 ^a	_d 0.024 ^a	_c 0.629 ^{ab}	_c 0.635 ^a	_{cd} 0.624 ^b
	Combined	HOL+RED+JER	_c 0.773 ^a	_c 0.774 ^a	_c 0.761 ^b	_c 0.729 ^a	_c 0.732 ^a	_c 0.716 ^b	_c 0.599 ^a	_c 0.587 ^b	_d 0.590 ^{ab}
		HOL+RED+JER+MIX	_{bc} 0.782 ^a	_{bc} 0.782 ^a	_{bc} 0.771 ^b	_{bc} 0.742 ^a	_{bc} 0.747 ^a	_{bc} 0.732 ^b	_b 0.695 ^a	_b 0.690 ^a	_{bc} 0.675 ^b
	BOA	HOL+RED+JER+MIX uncor	_a 0.804 ^a	_a 0.807 ^a	_a 0.792 ^b	_a 0.774 ^b	_a 0.780 ^a	_a 0.762 ^c	_{ab} 0.730 ^a	_a 0.738 ^a	_{ab} 0.712 ^b
0.25	Pure	HOL	_b 0.782 ^b	_b 0.788 ^a	_b 0.772 ^c	_d 0.053 ^a	_d 0.041 ^{ab}	_d 0.034 ^b	_d 0.089 ^a	_d 0.066 ^{ab}	_d 0.058 ^b
		RED	_d 0.080 ^a	_d 0.081 ^a	_d 0.080 ^a	_b 0.742 ^b	_b 0.750 ^a	_b 0.730 ^c	_d 0.017 ^a	_d 0.012 ^a	_d 0.003 ^a
		JER	_d 0.026 ^a	_d 0.034 ^a	_d 0.025 ^a	_d 0.017 ^a	_d 0.014 ^a	_d 0.019 ^a	_{bc} 0.632 ^a	_b 0.639 ^a	_{bc} 0.627 ^b
	Combined	HOL+RED+JER	_c 0.764 ^a	_c 0.766 ^a	_c 0.755 ^b	_c 0.716 ^b	_c 0.721 ^a	_c 0.705 ^c	_c 0.587 ^a	_c 0.573 ^b	_c 0.581 ^{ab}
		HOL+RED+JER+MIX	_{bc} 0.769 ^a	_c 0.768 ^{ab}	_{bc} 0.761 ^b	_{bc} 0.725 ^a	_{bc} 0.731 ^a	_{bc} 0.718 ^b	_b 0.689 ^a	_b 0.680 ^b	_b 0.667 ^c
	BOA	HOL+RED+JER+MIX uncor	_a 0.803 ^a	_a 0.805 ^a	_a 0.790 ^b	_a 0.771 ^b	_a 0.777 ^a	_a 0.759 ^c	_a 0.735 ^a	_a 0.743 ^a	_a 0.716 ^b
0.25	Pure	HOL	_b 0.782 ^b	_b 0.788 ^a	_b 0.772 ^c	_d 0.053 ^a	_d 0.041 ^{ab}	_d 0.034 ^b	_d 0.089 ^a	_d 0.066 ^{ab}	_d 0.058 ^b
		RED	_d 0.080 ^a	_d 0.081 ^a	_d 0.080 ^a	_b 0.742 ^b	_b 0.750 ^a	_b 0.730 ^c	_d 0.017 ^a	_d 0.012 ^a	_d 0.003 ^a
		JER	_d 0.026 ^a	_d 0.034 ^a	_d 0.025 ^a	_d 0.017 ^a	_d 0.014 ^a	_d 0.019 ^a	_{bc} 0.632 ^a	_b 0.639 ^a	_{bc} 0.627 ^b
	Combined	HOL+RED+JER	_c 0.764 ^a	_c 0.766 ^a	_c 0.755 ^b	_c 0.716 ^b	_c 0.721 ^a	_c 0.705 ^c	_c 0.587 ^a	_c 0.573 ^b	_c 0.581 ^{ab}
		HOL+RED+JER+MIX	_{bc} 0.769 ^a	_c 0.768 ^{ab}	_{bc} 0.761 ^b	_{bc} 0.725 ^a	_{bc} 0.731 ^a	_{bc} 0.718 ^b	_b 0.689 ^a	_b 0.680 ^b	_b 0.667 ^c
	BOA	HOL+RED+JER+MIX cor	_a 0.805 ^a	_a 0.806 ^a	_a 0.790 ^b	_a 0.772 ^a	_a 0.775 ^a	_a 0.758 ^b	_a 0.740 ^a	_a 0.741 ^a	_a 0.715 ^b

¹ Correlation of simulated QTL effects. Different alphabets mean significantly different values at a Type 1 error rate of 0.05 with Bonferroni correction. Subscripts (within region size) and superscripts (within data) stand for comparisons within column and row, respectively, for each correlation scenario.

² The methods classified based on the data and model used to estimate SNP effects

³ Data: Data included in reference population. Region Size: Number of SNPs assigned the same variance.

Table S2: Accuracies for purebred individuals for a trait with low heritability ($h^2 = 0.05$)

Correlation ¹	Training ²	Data/Region Size ³	HOL			RED			JER		
			1 SNP	100 SNPs	WG	1 SNP	100 SNPs	WG	1 SNP	100 SNPs	WG
1.00	Pure	HOL	c0.469 ^a	c0.470 ^{ab}	a0.466 ^b	e0.019 ^a	d0.010 ^b	d0.022 ^{ab}	c-0.023 ^a	c-0.023 ^a	b-0.021 ^a
		RED	d0.055 ^a	d0.047 ^a	b0.047 ^a	bd0.421 ^a	bc0.420 ^{ab}	bc0.417 ^b	c0.044 ^a	c0.043 ^a	b0.045 ^a
		JER	d-0.008 ^a	d-0.002 ^a	b0.002 ^a	e0.036 ^a	d0.035 ^a	d0.040 ^a	ab0.319 ^a	ab0.319 ^a	a0.321 ^a
	Combined	HOL+RED+JER	bc0.467 ^a	c0.472 ^a	a0.463 ^a	cd0.415 ^a	c0.411 ^a	c0.408 ^a	b0.291 ^a	b0.294 ^a	a0.289 ^a
		HOL+RED+JER+MIX	ab0.501 ^a	b0.503 ^{ab}	a0.494 ^b	ab0.453 ^a	ab0.450 ^{ab}	ab0.445 ^b	ab0.389 ^a	a0.385 ^a	a0.381 ^a
	BOA	HOL+RED+JER+MIX uncor	abc0.500 ^a	abc0.501 ^a	a0.497 ^a	ac0.451 ^a	a0.451 ^{ab}	a0.447 ^b	ab0.387 ^a	ab0.382 ^a	a0.383 ^a
		HOL+RED+JER+MIX cor	a0.503 ^a	a0.506 ^{ab}	a0.495 ^b	ab0.454 ^a	ab0.450 ^{ab}	ab0.444 ^b	a0.392 ^a	a0.389 ^a	a0.382 ^a
0.50	Pure	HOL	b0.476 ^a	a0.478 ^a	a0.474 ^a	d0.028 ^a	c0.024 ^a	c0.030 ^a	c0.007 ^a	c0.017 ^a	c0.010 ^a
		RED	c0.068 ^a	b0.080 ^a	b0.071 ^a	c0.410 ^a	b0.412 ^a	b0.410 ^a	c0.024 ^a	c0.030 ^a	c0.028 ^a
		JER	c0.018 ^a	b0.015 ^a	b0.012 ^a	d0.016 ^{ab}	c0.013 ^b	c0.026 ^a	b0.260 ^a	b0.260 ^a	b0.264 ^a
	Combined	HOL+RED+JER	b0.466 ^a	a0.467 ^a	a0.464 ^a	c0.399 ^a	b0.393 ^a	b0.397 ^a	b0.240 ^a	b0.238 ^a	b0.243 ^a
		HOL+RED+JER+MIX	b0.487 ^a	a0.483 ^a	a0.482 ^a	bc0.433 ^a	b0.432 ^a	ab0.432 ^a	a0.378 ^a	a0.374 ^a	a0.372 ^a
	BOA	HOL+RED+JER+MIX uncor	ab0.502 ^a	a0.498 ^a	a0.499 ^a	ab0.457 ^a	a0.459 ^a	a0.455 ^a	a0.383 ^a	a0.388 ^a	a0.384 ^a
		HOL+RED+JER+MIX cor	a0.504 ^a	a0.502 ^a	a0.499 ^a	a0.455 ^a	a0.457 ^a	a0.450 ^a	a0.390 ^a	a0.394 ^a	a0.382 ^a
0.25	Pure	HOL	ab0.473 ^a	a0.474 ^a	ab0.471 ^a	c0.012 ^a	d0.007 ^a	e0.014 ^a	c0.005 ^a	c0.016 ^a	c0.007 ^a
		RED	c0.050 ^a	b0.059 ^a	c0.054 ^a	b0.407 ^a	b0.409 ^a	c0.407 ^a	c-0.006 ^a	c-0.006 ^a	c0.000 ^a
		JER	c0.017 ^a	b0.014 ^a	c0.012 ^a	c0.024 ^b	d0.017 ^b	e0.032 ^a	b0.260 ^a	b0.260 ^a	b0.265 ^a
	Combined	HOL+RED+JER	b0.459 ^a	a0.458 ^a	b0.458 ^a	b0.392 ^a	c0.385 ^a	d0.391 ^a	b0.228 ^a	b0.226 ^a	b0.233 ^a
		HOL+RED+JER+MIX	b0.476 ^a	a0.472 ^a	b0.473 ^a	b0.423 ^a	bc0.417 ^a	bcd0.424 ^a	a0.372 ^a	a0.364 ^a	a0.368 ^a
	BOA	HOL+RED+JER+MIX uncor	a0.499 ^a	a0.494 ^a	a0.495 ^a	a0.454 ^b	a0.458 ^a	ab0.453 ^{ab}	a0.388 ^a	a0.392 ^a	a0.389 ^a
		HOL+RED+JER+MIX cor	a0.501 ^a	a0.497 ^a	ab0.495 ^a	a0.454 ^{ab}	a0.458 ^a	a0.451 ^b	a0.393 ^a	a0.397 ^a	a0.384 ^a

¹ Correlation of simulated QTL effects. Different alphabets mean significantly different values at a Type 1 error rate of 0.05 with Bonferroni correction. Subscripts (within region size) and superscripts (within data) stand for comparisons within column and row, respectively, for each correlation scenario.

² The methods classified based on the data and model used to estimate SNP effects

³ Data: Data included in reference population. Region Size: Number of SNPs assigned the same variance.

Table S3: Accuracies for admixed individuals (MIX) for a trait with high heritability ($h^2 = 0.40$)

Correlation ¹	Training ²	Data/Region Size ³	MIX		
			1 SNP	100 SNPs	WG
1.00	Pure	HOL	_e 0.578 ^a	_e 0.576 ^a	_e 0.562 ^b
		RED	_f 0.395 ^a	_f 0.395 ^a	_f 0.372 ^b
		JER	_g 0.178 ^a	_g 0.179 ^a	_g 0.175 ^a
		HOL/RED/JER	_d 0.687 ^b	_d 0.704 ^a	_d 0.685 ^b
	Combined	HOL+RED+JER	_c 0.732 ^a	_c 0.732 ^a	_c 0.710 ^b
		HOL+RED+JER+MIX	_a 0.794 ^a	_a 0.798 ^a	_a 0.775 ^b
	BOA	HOL+RED+JER+MIX uncor	_b 0.772 ^b	_b 0.782 ^a	_b 0.762 ^c
		HOL+RED+JER+MIX cor	_a 0.794 ^b	_a 0.799 ^a	_a 0.776 ^c
0.50	Pure	HOL	_d 0.411 ^a	_d 0.415 ^a	_d 0.410 ^a
		RED	_e 0.275 ^a	_e 0.274 ^a	_e 0.268 ^a
		JER	_f 0.114 ^a	_f 0.117 ^a	_f 0.114 ^a
		HOL/RED/JER	_c 0.531 ^a	_c 0.533 ^{ab}	_c 0.521 ^b
	Combined	HOL+RED+JER	_c 0.560 ^a	_c 0.556 ^{ab}	_c 0.554 ^b
		HOL+RED+JER+MIX	_b 0.827 ^a	_b 0.824 ^a	_b 0.817 ^b
	BOA	HOL+RED+JER+MIX uncor	_a 0.876 ^a	_a 0.877 ^a	_a 0.870 ^b
		HOL+RED+JER+MIX cor	_a 0.877 ^a	_a 0.877 ^a	_a 0.870 ^b
0.25	Pure	HOL	_d 0.358 ^a	_d 0.363 ^a	_d 0.360 ^a
		RED	_e 0.231 ^a	_e 0.231 ^a	_e 0.231 ^a
		JER	_e 0.106 ^a	_e 0.109 ^a	_e 0.106 ^a
		HOL/RED/JER	_c 0.482 ^a	_c 0.482 ^{ab}	_c 0.469 ^b
	Combined	HOL+RED+JER	_c 0.513 ^a	_c 0.509 ^{ab}	_c 0.509 ^b
		HOL+RED+JER+MIX	_b 0.840 ^a	_b 0.837 ^a	_b 0.829 ^b
	BOA	HOL+RED+JER+MIX uncor	_a 0.897 ^a	_a 0.898 ^a	_a 0.892 ^b
		HOL+RED+JER+MIX cor	_a 0.897 ^a	_a 0.897 ^a	_a 0.892 ^b

¹ Correlation of simulated QTL effects. Different alphabets mean significantly different values at a Type 1 error rate of 0.05 with Bonferroni correction. Subscripts (within region size) and superscripts (within data) stand for comparisons within column and row, respectively, for each correlation scenario.

² The methods classified based on the data and model used to estimate SNP effects

³ Data: Data included in reference population. Region Size: Number of SNPs assigned the same variance.

Table S4: Accuracies for admixed individuals (MIX) for a trait with low heritability ($h^2 = 0.05$)

Correlation ¹	Training ²	Data/Region Size ³	MIX		
			1 SNP	100 SNPs	WG
1.00	Pure	HOL	_d 0.363 ^a	_c 0.364 ^a	_c 0.362 ^a
		RED	_e 0.229 ^a	_d 0.225 ^{ab}	_d 0.221 ^b
		JER	_f 0.075 ^a	_e 0.077 ^a	_e 0.078 ^a
		HOL/RED/JER	_c 0.433 ^a	_b 0.436 ^a	_b 0.429 ^a
	Combined	HOL+RED+JER	_b 0.449 ^a	_b 0.449 ^a	_b 0.443 ^a
		HOL+RED+JER+MIX	_a 0.503 ^a	_a 0.501 ^{ab}	_a 0.496 ^b
	BOA	HOL+RED+JER+MIX uncor	_{bcd} 0.430 ^{ab}	_{bc} 0.434 ^a	_{bc} 0.424 ^b
		HOL+RED+JER+MIX cor	_a 0.500 ^a	_a 0.499 ^a	_a 0.493 ^a
0.50	Pure	HOL	_d 0.256 ^a	_d 0.256 ^a	_d 0.255 ^a
		RED	_e 0.157 ^a	_e 0.162 ^a	_e 0.155 ^a
		JER	_f 0.043 ^a	_f 0.043 ^a	_e 0.043 ^a
		HOL/RED/JER	_{cd} 0.303 ^{ab}	_{cd} 0.308 ^a	_{cd} 0.299 ^b
	Combined	HOL+RED+JER	_c 0.356 ^a	_c 0.356 ^a	_c 0.353 ^a
		HOL+RED+JER+MIX	_b 0.557 ^a	_b 0.546 ^a	_b 0.550 ^a
	BOA	HOL+RED+JER+MIX uncor	_a 0.674 ^{ab}	_a 0.676 ^a	_a 0.672 ^b
		HOL+RED+JER+MIX cor	_a 0.672 ^a	_a 0.673 ^a	_a 0.669 ^a
0.25	Pure	HOL	_{de} 0.226 ^a	_{de} 0.227 ^a	_{de} 0.226 ^a
		RED	_{ef} 0.136 ^a	_{ef} 0.138 ^a	_{ef} 0.134 ^a
		JER	_f 0.040 ^a	_f 0.041 ^a	_f 0.041 ^a
		HOL/RED/JER	_{cd} 0.271 ^{ab}	_{cd} 0.277 ^a	_{cd} 0.266 ^b
	Combined	HOL+RED+JER	_c 0.339 ^a	_c 0.338 ^a	_c 0.336 ^a
		HOL+RED+JER+MIX	_b 0.587 ^a	_b 0.573 ^b	_b 0.575 ^{ab}
	BOA	HOL+RED+JER+MIX uncor	_a 0.729 ^a	_a 0.730 ^{ab}	_a 0.727 ^b
		HOL+RED+JER+MIX cor	_a 0.728 ^a	_a 0.728 ^a	_a 0.725 ^a

¹ Correlation of simulated QTL effects. Different alphabets mean significantly different values at a Type 1 error rate of 0.05 with Bonferroni correction. Subscripts (within region size) and superscripts (within data) stand for comparisons within column and row, respectively, for each correlation scenario.

² The methods classified based on the data and model used to estimate SNP effects

³ Data: Data included in reference population. Region Size: Number of SNPs assigned the same variance.

Table S5: Accuracy for the low heritability ($h^2 = 0.05$) trait, using only 250 QTL and region size of 1 SNP

Correlation ¹	Training ²	Data ³ Validation population	HOL	RED	JER	MIX
0.50	Pure	HOL	_c 0.735	_d 0.302	_{de} 0.289	_e 0.401
		RED	_d 0.291	_c 0.686	_e 0.214	_f 0.291
		JER	_d 0.173	_d 0.126	_{cd} 0.412	_g 0.137
		HOL/RED/JER				_{cd} 0.525
	Combined	HOL+RED+JER	_c 0.712	_c 0.668	_c 0.462	_d 0.506
		HOL+RED+JER+MIX	_c 0.732	_{bc} 0.699	_b 0.579	_c 0.580
	BOA	HOL+RED+JER+MIX uncor	_b 0.781	_b 0.735	_{ab} 0.639	_b 0.804
		HOL+RED+JER+MIX cor	_a 0.795	_a 0.758	_a 0.683	_a 0.818

¹ Correlation of simulated QTL effects. Different alphabets mean significantly different values at a Type 1 error rate of 0.05 with Bonferroni correction. Subscripts (region size of 1 SNP) and superscripts (within data) stand for comparisons within column and row, respectively, for each correlation scenario.

² The methods classified based on the data and model used to estimate QTL effects

³ Data: Data included in reference population.