

Supplementary materials to “GWASinlps: Nonlocal
prior based iterative SNP selection tool for
genome-wide association studies” by Nilotpall Sanyal,
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Supplementary Table 1: True positive rate (TPR) of variable selection for Simulation 1 datasets with number of real genotyped SNPs $p = (10000, 15000, 2000)$, sample size $n = (2000, 3000, 5000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$), GWASinlps piMOM method ($\tau = 0.008$, $k_0 = 1$, $r_{xx} = 0.2$), Zellner’s g-prior based method within our structured screen-and-select framework, LASSO ($\lambda = 1.1se$), Elastic Net ($\lambda = 1.1se$, $\alpha = 0.75, 0.5, 0.25$), and pi-MASS. For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins, whereas for pi-MASS 10,000 iterations were used after 1,000 burn-ins. For Zellner prior $g = n$ was used. All the figures are averaged over 100 replicates.

		$h^2=0.1$			$h^2=0.2$			$h^2=0.3$			$h^2=0.4$			$h^2=0.5$		
		n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K
p=10K	pi-MASS	0.05	0.05	0.05	0.15	0.15	0.1	0.2	0.2	0.175	0.25	0.25	0.2	0.3	0.3	0.25
	LASSO min	0.3	0.3	0.325	0.45	0.5	0.45	0.55	0.6	0.6	0.6	0.675	0.65	0.65	0.7	0.7
	LASSO 1se	0.2	0.15	0.15	0.35	0.35	0.35	0.45	0.5	0.5	0.55	0.6	0.6	0.6	0.675	0.65
	EN 0.075 min	0.3	0.3	0.325	0.45	0.5	0.5	0.55	0.6	0.6	0.6	0.7	0.65	0.65	0.7	0.7
	EN 0.075 1se	0.15	0.15	0.15	0.35	0.35	0.375	0.45	0.5	0.5	0.55	0.6	0.6	0.6	0.7	0.65
	EN 0.050 min	0.35	0.3	0.35	0.45	0.5	0.5	0.55	0.6	0.6	0.65	0.7	0.65	0.7	0.75	0.7
	EN 0.050 1se	0.15	0.15	0.15	0.35	0.35	0.4	0.5	0.5	0.5	0.55	0.6	0.6	0.65	0.7	0.65
	EN 0.025 min	0.35	0.3	0.35	0.5	0.5	0.5	0.575	0.65	0.6	0.65	0.7	0.65	0.7	0.75	0.7
	EN 0.025 1se	0.2	0.2	0.15	0.4	0.4	0.4	0.5	0.525	0.55	0.6	0.65	0.6	0.65	0.7	0.7
	zellner	0.2	0.2	0.2	0.3	0.3	0.35	0.4	0.45	0.45	0.5	0.6	0.55	0.55	0.65	0.6
	pMOM	0.2	0.2	0.25	0.3	0.35	0.35	0.4	0.5	0.45	0.5	0.6	0.55	0.55	0.65	0.6
piMOM	0.2	0.2	0.25	0.3	0.35	0.35	0.4	0.5	0.45	0.5	0.6	0.55	0.6	0.65	0.65	
p=15K	pi-MASS	0.1	0.1	0.05	0.15	0.2	0.15	0.2	0.3	0.15	0.25	0.3	0.2	0.25	0.35	0.25
	LASSO min	0.3	0.45	0.35	0.45	0.6	0.55	0.5	0.7	0.6	0.55	0.75	0.7	0.6	0.75	0.7
	LASSO 1se	0.25	0.3	0.25	0.35	0.45	0.45	0.45	0.6	0.55	0.5	0.65	0.65	0.55	0.75	0.7
	EN 0.075 min	0.3	0.45	0.35	0.45	0.6	0.55	0.5	0.7	0.6	0.6	0.75	0.7	0.65	0.75	0.7
	EN 0.075 1se	0.25	0.3	0.25	0.35	0.5	0.45	0.45	0.6	0.55	0.55	0.7	0.65	0.6	0.75	0.7
	EN 0.050 min	0.35	0.45	0.4	0.45	0.6	0.55	0.55	0.7	0.625	0.6	0.75	0.7	0.65	0.75	0.7
	EN 0.050 1se	0.25	0.3	0.25	0.4	0.5	0.475	0.5	0.6	0.6	0.55	0.7	0.65	0.65	0.75	0.7
	EN 0.025 min	0.35	0.45	0.4	0.5	0.6	0.55	0.6	0.7	0.65	0.65	0.75	0.7	0.7	0.75	0.75
	EN 0.025 1se	0.3	0.3	0.3	0.4	0.5	0.5	0.5	0.6	0.6	0.6	0.7	0.65	0.65	0.75	0.7
	zellner	0.2	0.3	0.25	0.3	0.4	0.4	0.4	0.55	0.5	0.45	0.65	0.6	0.5	0.7	0.65
	pMOM	0.2	0.3	0.25	0.3	0.45	0.4	0.4	0.55	0.5	0.45	0.65	0.6	0.5	0.7	0.65
piMOM	0.2	0.3	0.25	0.3	0.45	0.4	0.4	0.55	0.5	0.45	0.65	0.6	0.5	0.7	0.7	
p=20K	pi-MASS	0.15	0.15	0.1	0.2	0.25	0.2	0.25	0.3	0.2	0.3	0.35	0.25	0.35	0.4	0.275
	LASSO min	0.4	0.5	0.5	0.5	0.65	0.65	0.6	0.7	0.7	0.65	0.7	0.75	0.7	0.75	0.75
	LASSO 1se	0.35	0.4	0.35	0.45	0.6	0.55	0.55	0.65	0.65	0.6	0.7	0.7	0.65	0.75	0.75
	EN 0.075 min	0.425	0.5	0.5	0.55	0.65	0.65	0.6	0.7	0.7	0.65	0.7	0.75	0.7	0.75	0.75
	EN 0.075 1se	0.35	0.4	0.35	0.475	0.6	0.6	0.55	0.65	0.65	0.6	0.7	0.7	0.65	0.75	0.75
	EN 0.050 min	0.45	0.55	0.5	0.55	0.65	0.65	0.65	0.7	0.7	0.7	0.75	0.75	0.75	0.75	0.75
	EN 0.050 1se	0.35	0.4	0.35	0.5	0.6	0.6	0.6	0.65	0.65	0.65	0.7	0.7	0.7	0.75	0.75
	EN 0.025 min	0.45	0.55	0.5	0.6	0.65	0.65	0.65	0.7	0.7	0.7	0.75	0.75	0.75	0.75	0.75
	EN 0.025 1se	0.35	0.4	0.35	0.55	0.6	0.6	0.65	0.65	0.675	0.7	0.7	0.7	0.75	0.75	0.75
	zellner	0.3	0.4	0.35	0.4	0.6	0.55	0.5	0.65	0.65	0.55	0.7	0.7	0.55	0.75	0.75
	pMOM	0.3	0.4	0.35	0.4	0.55	0.55	0.475	0.65	0.65	0.55	0.7	0.7	0.55	0.7	0.75
piMOM	0.3	0.4	0.35	0.4	0.575	0.55	0.5	0.65	0.65	0.55	0.7	0.7	0.55	0.75	0.75	

Supplementary Table 2: False discovery rate (FDR) of variable selection for Simulation 1 datasets with number of real genotyped SNPs $p = (10000, 15000, 2000)$, sample size $n = (2000, 3000, 5000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$), GWASinlps piMOM method ($\tau = 0.008$, $k_0 = 1$, $r_{xx} = 0.2$), Zellner’s g-prior based method within our structured screen-and-select framework, LASSO ($\lambda = 1.1se$), Elastic Net ($\lambda = 1.1se$, $\alpha = 0.75, 0.5, 0.25$), and pi-MASS. For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins, whereas for pi-MASS 10,000 iterations were used after 1,000 burn-ins. For Zellner prior $g = n$ was used. All the figures are averaged over 100 replicates.

		$h^2=0.1$			$h^2=0.2$			$h^2=0.3$			$h^2=0.4$			$h^2=0.5$		
		n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K
p=10K	pi-MASS	0.5	0.6	0.6	0.3333	0.4286	0.5	0.2222	0.25	0.3333	0.2	0.2361	0.25	0.1429	0.2222	0.2361
	LASSO min	0.8947	0.8978	0.8951	0.8854	0.8856	0.8804	0.883	0.8781	0.8796	0.8879	0.8756	0.8788	0.8815	0.8755	0.879
	LASSO 1se	0.5	0.3333	0.2	0.6132	0.5279	0.4118	0.6414	0.5455	0.4721	0.6609	0.56	0.4791	0.6667	0.5646	0.5086
	EN 0.075 min	0.9022	0.9039	0.888	0.8969	0.8896	0.8947	0.895	0.8802	0.8926	0.8957	0.8832	0.8829	0.8922	0.8865	0.8871
	EN 0.075 1se	0.5278	0.375	0.25	0.6396	0.5132	0.4167	0.691	0.5918	0.5228	0.7066	0.6066	0.5298	0.7078	0.6301	0.5437
	EN 0.050 min	0.9091	0.9079	0.9	0.9024	0.8991	0.9043	0.9084	0.8899	0.9039	0.9084	0.8923	0.9004	0.9056	0.8983	0.8983
	EN 0.050 1se	0.5714	0.4	0.3333	0.7019	0.5882	0.5	0.75	0.644	0.5918	0.7676	0.675	0.6268	0.7818	0.6967	0.6301
	EN 0.025 min	0.9231	0.92	0.9151	0.9285	0.9164	0.9179	0.9281	0.9172	0.9231	0.9286	0.9159	0.9267	0.9288	0.9233	0.9302
	EN 0.025 1se	0.7101	0.5	0.4143	0.8052	0.6927	0.633	0.83	0.7436	0.697	0.8466	0.7749	0.75	0.8556	0.7969	0.7819
	zellner	0.4	0.4286	0.375	0.3636	0.3	0.3205	0.3333	0.25	0.2697	0.3077	0.2	0.25	0.2583	0.1429	0.1875
	pMOM	0.5	0.5	0.4286	0.4	0.375	0.3636	0.3604	0.3077	0.3101	0.3333	0.2426	0.2941	0.2857	0.1875	0.2667
piMOM	0.5	0.5	0.4286	0.4167	0.4	0.4083	0.3571	0.3529	0.3604	0.3333	0.2667	0.3333	0.2941	0.2353	0.2941	
p=15K	pi-MASS	0.5	0.5	0.75	0.3333	0.2857	0.5714	0.2679	0.25	0.5	0.25	0.2	0.4286	0.2111	0.1818	0.375
	LASSO min	0.8993	0.8784	0.9038	0.8929	0.8667	0.8925	0.891	0.8673	0.8866	0.8856	0.8654	0.881	0.8797	0.8707	0.8893
	LASSO 1se	0.625	0.2857	0.4	0.6667	0.3923	0.5263	0.6667	0.4545	0.5652	0.6765	0.4564	0.5667	0.6667	0.4807	0.582
	EN 0.075 min	0.9028	0.8827	0.908	0.8994	0.8763	0.9026	0.8957	0.8796	0.8968	0.8925	0.879	0.8926	0.8923	0.877	0.8939
	EN 0.075 1se	0.6667	0.3333	0.4444	0.7048	0.4667	0.5612	0.7312	0.5209	0.6071	0.726	0.542	0.6192	0.7282	0.5588	0.64
	EN 0.050 min	0.9128	0.8929	0.9135	0.9035	0.8889	0.9068	0.9043	0.8861	0.9078	0.9	0.8919	0.9032	0.9043	0.8889	0.9067
	EN 0.050 1se	0.7222	0.3693	0.5	0.7568	0.5	0.6	0.77	0.603	0.685	0.78	0.625	0.6842	0.7818	0.6283	0.7111
	EN 0.025 min	0.9253	0.9082	0.9304	0.9212	0.9106	0.9251	0.9235	0.9135	0.9281	0.9226	0.9167	0.9308	0.9215	0.9229	0.9321
	EN 0.025 1se	0.7778	0.4641	0.6172	0.8248	0.6552	0.7179	0.8333	0.7222	0.7692	0.8378	0.7544	0.7951	0.8471	0.7786	0.8148
	zellner	0.4444	0.2857	0.3333	0.4	0.2	0.3038	0.3846	0.1667	0.2941	0.3798	0.1765	0.233	0.3529	0.1381	0.1875
	pMOM	0.4773	0.2929	0.3875	0.4444	0.2265	0.3333	0.4167	0.1938	0.3077	0.4	0.2	0.25	0.3571	0.1765	0.199
piMOM	0.5	0.3333	0.4444	0.4615	0.2727	0.3846	0.433	0.25	0.3431	0.4059	0.2426	0.2941	0.3889	0.199	0.2426	
p=20K	pi-MASS	0.4143	0.3333	0.5556	0.3333	0.25	0.4286	0.2857	0.2222	0.375	0.2792	0.2222	0.3636	0.25	0.1938	0.3333
	LASSO min	0.9018	0.8807	0.8799	0.8918	0.886	0.871	0.8906	0.8803	0.8721	0.8848	0.881	0.8766	0.8803	0.8828	0.8735
	LASSO 1se	0.5	0.3	0.4	0.5918	0.381	0.4444	0.6429	0.4091	0.48	0.625	0.4583	0.5	0.6286	0.4907	0.5081
	EN 0.075 min	0.899	0.8869	0.8894	0.8969	0.8841	0.8804	0.8938	0.8863	0.8876	0.8893	0.8905	0.8839	0.8885	0.8938	0.8881
	EN 0.075 1se	0.5625	0.3333	0.4365	0.6414	0.4286	0.5	0.6765	0.5	0.5333	0.6708	0.5333	0.5625	0.6744	0.5588	0.5632
	EN 0.050 min	0.9081	0.8921	0.9005	0.9014	0.8982	0.8969	0.8996	0.9048	0.8982	0.8975	0.9043	0.9016	0.8969	0.9047	0.9021
	EN 0.050 1se	0.622	0.3571	0.4868	0.7027	0.52	0.5769	0.7222	0.5667	0.6107	0.7358	0.6329	0.65	0.7411	0.647	0.6591
	EN 0.025 min	0.917	0.9103	0.9177	0.9184	0.9151	0.9164	0.9188	0.9214	0.927	0.92	0.9279	0.9276	0.9203	0.9312	0.9319
	EN 0.025 1se	0.7	0.5263	0.5882	0.7805	0.6325	0.6923	0.8	0.7071	0.7407	0.8182	0.7544	0.7699	0.8272	0.7852	0.8027
	zellner	0.3333	0.2222	0.2361	0.3333	0.1667	0.1938	0.3077	0.1765	0.1429	0.2857	0.1429	0.1765	0.2667	0.1667	0.2105
	pMOM	0.3333	0.2222	0.25	0.3333	0.1538	0.1875	0.3101	0.1429	0.1429	0.2857	0.1333	0.1765	0.2857	0.125	0.2105
piMOM	0.375	0.25	0.2727	0.3333	0.2	0.2143	0.3333	0.1875	0.1875	0.3125	0.1765	0.2105	0.3125	0.1875	0.2222	

Supplementary Table 3: True negative rate (TNR) of variable selection for Simulation 1 datasets with number of real genotyped SNPs $p = (10000, 15000, 2000)$, sample size $n = (2000, 3000, 5000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$), GWASinlps piMOM method ($\tau = 0.008$, $k_0 = 1$, $r_{xx} = 0.2$), Zellner’s g-prior based method within our structured screen-and-select framework, LASSO ($\lambda = 1.1se$), Elastic Net ($\lambda = 1.1se$, $\alpha = 0.75, 0.5, 0.25$), and pi-MASS. For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins, whereas for pi-MASS 10,000 iterations were used after 1,000 burn-ins. For Zellner prior $g = n$ was used. All the figures are averaged over 100 replicates.

		$h^2=0.1$			$h^2=0.2$			$h^2=0.3$			$h^2=0.4$			$h^2=0.5$		
		n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K
p=10K	pi-MASS	0.9998	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	0.9999	1	0.9999	0.9999	1
	LASSO min	0.995	0.9967	0.9975	0.9928	0.9953	0.9967	0.9919	0.9942	0.996	0.9907	0.9938	0.9956	0.9902	0.9936	0.9953
	LASSO 1se	0.9997	0.9999	1	0.999	0.9995	0.9998	0.9984	0.9992	0.9996	0.998	0.999	0.9995	0.9977	0.9988	0.9995
	EN 0.075 min	0.9944	0.9962	0.9975	0.9921	0.9947	0.9963	0.9907	0.9942	0.9955	0.9895	0.9933	0.9953	0.9892	0.9929	0.9951
	EN 0.075 1se	0.9996	0.9999	1	0.9988	0.9995	0.9998	0.998	0.999	0.9995	0.9973	0.9988	0.9994	0.997	0.9985	0.9993
	EN 0.050 min	0.9939	0.9959	0.9973	0.9914	0.994	0.996	0.9889	0.9936	0.995	0.9878	0.9927	0.9944	0.9867	0.9919	0.9944
	EN 0.050 1se	0.9995	0.9998	0.9999	0.9983	0.9994	0.9996	0.9972	0.9988	0.9993	0.9963	0.9984	0.9991	0.9956	0.998	0.999
	EN 0.025 min	0.992	0.995	0.9965	0.9873	0.9926	0.9945	0.9853	0.9906	0.9931	0.9831	0.9902	0.9924	0.982	0.9887	0.9913
	EN 0.025 1se	0.9991	0.9997	0.9999	0.9968	0.9988	0.9993	0.9952	0.9979	0.9989	0.9935	0.9972	0.9983	0.9921	0.9964	0.9978
	zellner	0.9997	0.9998	0.9999	0.9996	0.9998	0.9999	0.9996	0.9998	0.9999	0.9996	0.9998	0.9998	0.9996	0.9999	0.9999
	pMOM	0.9997	0.9998	0.9999	0.9996	0.9997	0.9998	0.9995	0.9997	0.9998	0.9995	0.9997	0.9998	0.9996	0.9998	0.9998
piMOM	0.9996	0.9997	0.9998	0.9996	0.9997	0.9998	0.9995	0.9997	0.9998	0.9995	0.9997	0.9997	0.9995	0.9997	0.9998	
p=15K	pi-MASS	0.9998	0.9999	0.9999	0.9999	0.9999	0.9998	0.9998	0.9999	0.9999	0.9998	0.9999	0.9999	0.9999	0.9999	0.9999
	LASSO min	0.9947	0.9961	0.9969	0.9928	0.9949	0.9958	0.9922	0.9943	0.9956	0.9915	0.9941	0.9954	0.9911	0.9935	0.9948
	LASSO 1se	0.9993	0.9999	0.9999	0.9986	0.9996	0.9995	0.9983	0.9994	0.9994	0.9979	0.9993	0.9993	0.9978	0.9992	0.9991
	EN 0.075 min	0.9941	0.9959	0.9967	0.992	0.9945	0.9956	0.9915	0.9937	0.9951	0.9909	0.9933	0.9947	0.9901	0.9931	0.9945
	EN 0.075 1se	0.9991	0.9998	0.9998	0.9983	0.9995	0.9995	0.9976	0.9992	0.9992	0.9972	0.999	0.999	0.997	0.9988	0.9989
	EN 0.050 min	0.9933	0.9951	0.9963	0.9914	0.9937	0.9952	0.9897	0.993	0.9942	0.9892	0.9922	0.994	0.9879	0.9922	0.9935
	EN 0.050 1se	0.9988	0.9997	0.9997	0.9976	0.9994	0.9993	0.9968	0.9988	0.9989	0.996	0.9985	0.9987	0.9956	0.9984	0.9984
	EN 0.025 min	0.9913	0.9943	0.9953	0.9884	0.992	0.9938	0.9863	0.9905	0.9925	0.985	0.9897	0.9918	0.9839	0.9884	0.9907
	EN 0.025 1se	0.9981	0.9997	0.9996	0.9962	0.9988	0.9989	0.9948	0.9979	0.9982	0.9938	0.9973	0.9977	0.9929	0.9966	0.9972
	zellner	0.9997	0.9999	0.9999	0.9996	0.9999	0.9998	0.9995	0.9999	0.9998	0.9994	0.9998	0.9998	0.9995	0.9999	0.9999
	pMOM	0.9996	0.9998	0.9999	0.9996	0.9998	0.9998	0.9995	0.9998	0.9998	0.9994	0.9998	0.9998	0.9994	0.9998	0.9998
piMOM	0.9996	0.9998	0.9998	0.9995	0.9998	0.9998	0.9994	0.9997	0.9998	0.9994	0.9997	0.9998	0.9994	0.9998	0.9998	
p=20K	pi-MASS	0.9998	0.9999	0.9999	0.9998	0.9999	0.9999	0.9998	0.9999	0.9999	0.9998	0.9999	0.9999	0.9998	0.9999	0.9999
	LASSO min	0.9925	0.995	0.9965	0.9917	0.9936	0.996	0.9907	0.9933	0.9956	0.9907	0.9931	0.9951	0.9904	0.9927	0.9953
	LASSO 1se	0.9993	0.9998	0.9998	0.9986	0.9995	0.9996	0.9981	0.9994	0.9995	0.998	0.9993	0.9994	0.9979	0.9991	0.9993
	EN 0.075 min	0.992	0.9947	0.9961	0.991	0.9934	0.9956	0.99	0.9928	0.9949	0.9896	0.9924	0.9948	0.9893	0.992	0.9944
	EN 0.075 1se	0.9992	0.9997	0.9998	0.9983	0.9994	0.9995	0.9977	0.9992	0.9993	0.9974	0.999	0.9992	0.9972	0.9988	0.9991
	EN 0.050 min	0.9915	0.9941	0.9959	0.9898	0.9925	0.9946	0.989	0.9913	0.9944	0.9883	0.9911	0.9936	0.9876	0.9906	0.9935
	EN 0.050 1se	0.9988	0.9997	0.9997	0.9976	0.9992	0.9993	0.9969	0.9989	0.999	0.9965	0.9984	0.9988	0.996	0.9982	0.9987
	EN 0.025 min	0.9897	0.9932	0.9947	0.9865	0.9907	0.9935	0.9853	0.9891	0.9918	0.9838	0.9877	0.9911	0.9826	0.9866	0.9902
	EN 0.025 1se	0.9984	0.9994	0.9995	0.9964	0.9986	0.9988	0.9949	0.9979	0.9982	0.994	0.9972	0.9978	0.9933	0.9966	0.9972
	zellner	0.9997	0.9999	0.9999	0.9996	0.9999	0.9999	0.9996	0.9998	0.9999	0.9996	0.9999	0.9999	0.9996	0.9998	0.9998
	pMOM	0.9997	0.9999	0.9999	0.9996	0.9999	0.9999	0.9996	0.9999	0.9999	0.9996	0.9999	0.9999	0.9996	0.9999	0.9998
piMOM	0.9997	0.9998	0.9999	0.9996	0.9998	0.9999	0.9995	0.9998	0.9999	0.9995	0.9998	0.9998	0.9995	0.9998	0.9998	

Supplementary Table 4: Mean squared error (MSE) for Simulation 1 datasets with number of real genotyped SNPs $p = (10000, 15000, 2000)$, sample size $n = (2000, 3000, 5000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$), GWASinlps piMOM method ($\tau = 0.008$, $k_0 = 1$, $r_{xx} = 0.2$), Zellner’s g-prior based method within our structured screen-and-select framework, LASSO ($\lambda = 1.1se$), Elastic Net ($\lambda = 1.1se$, $\alpha = 0.75, 0.5, 0.25$), and pi-MASS. For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins, whereas for pi-MASS 10,000 iterations were used after 1,000 burn-ins. For Zellner prior $g = n$ was used. All the figures are averaged over 100 replicates.

		$h^2=0.1$			$h^2=0.2$			$h^2=0.3$			$h^2=0.4$			$h^2=0.5$		
		n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K
p=10K	pi-MASS	94.715	101.752	98.529	48.884	53.175	51.306	34.054	37.439	36.103	27.147	29.742	28.577	23.381	26.195	24.043
	LASSO min	80.986	87.265	83.412	35.606	38.330	36.824	20.637	22.317	21.298	13.191	14.095	13.519	8.807	9.445	9.062
	LASSO 1se	87.941	95.591	91.973	39.392	42.519	40.926	22.869	24.927	23.894	14.664	15.967	15.322	9.746	10.627	10.274
	EN 0.075 min	80.963	86.966	84.204	35.538	38.007	36.649	20.604	22.020	21.206	13.187	14.146	13.587	8.777	9.388	9.039
	EN 0.075 1se	88.488	95.714	91.602	39.510	42.711	41.180	22.911	24.833	23.912	14.637	15.912	15.388	9.758	10.603	10.292
	EN 0.050 min	81.001	86.859	83.580	35.655	38.091	36.726	20.585	22.185	21.108	13.114	14.066	13.483	8.706	9.329	8.949
	EN 0.050 1se	88.554	95.729	92.000	39.432	42.565	40.988	22.929	24.988	23.997	14.749	15.928	15.490	9.757	10.618	10.276
	EN 0.025 min	80.426	87.208	83.728	35.377	38.076	36.693	20.484	21.897	20.931	12.997	13.943	13.400	8.672	9.264	8.796
	EN 0.025 1se	88.522	95.394	92.479	39.480	42.666	41.402	23.024	25.015	24.229	14.770	16.074	15.508	9.863	10.702	10.409
	zellner	88.378	104.353	100.418	38.684	43.561	41.476	22.209	24.232	23.249	14.214	15.540	14.719	9.488	10.240	9.710
pMOM	83.200	89.907	85.449	36.909	39.326	37.651	21.362	22.766	21.847	13.646	14.594	13.958	9.066	9.727	9.269	
piMOM	82.788	89.598	85.385	36.872	39.225	37.480	21.333	22.703	21.740	13.512	14.516	13.868	9.031	9.676	9.223	
p=15K	pi-MASS	103.041	101.511	96.673	52.577	52.975	49.734	36.297	37.453	34.577	28.366	30.484	27.396	24.199	26.207	23.421
	LASSO min	90.946	87.935	84.587	40.222	38.732	37.350	23.373	22.548	21.760	15.036	14.439	13.848	9.997	9.584	9.223
	LASSO 1se	96.218	94.226	90.663	42.862	41.943	40.310	25.065	24.448	23.579	16.088	15.767	15.177	10.760	10.470	10.105
	EN 0.075 min	91.170	87.928	84.195	40.245	38.895	37.299	23.309	22.465	21.611	14.962	14.403	13.812	9.971	9.569	9.225
	EN 0.075 1se	96.502	94.514	90.731	42.973	41.962	40.468	25.048	24.480	23.550	16.113	15.700	15.110	10.735	10.455	10.103
	EN 0.050 min	90.760	87.881	84.034	40.188	38.522	37.117	23.257	22.447	21.557	14.951	14.342	13.860	9.919	9.565	9.161
	EN 0.050 1se	96.814	94.159	90.763	42.978	42.114	40.573	25.117	24.498	23.653	16.129	15.737	15.158	10.769	10.452	10.145
	EN 0.025 min	90.590	87.518	83.940	40.122	38.546	37.066	23.179	22.392	21.396	14.959	14.309	13.684	9.945	9.442	9.033
	EN 0.025 1se	96.725	94.571	90.997	43.071	41.996	40.614	25.133	24.605	23.692	16.179	15.819	15.285	10.828	10.570	10.165
	zellner	96.218	99.701	92.057	42.356	41.724	39.232	24.356	23.783	22.865	15.667	15.432	14.634	10.385	10.192	9.718
pMOM	92.713	90.028	86.385	41.091	39.816	37.955	23.849	23.061	22.047	15.276	14.740	14.121	10.216	9.811	9.418	
piMOM	92.572	89.763	85.928	40.961	39.573	37.746	23.760	23.007	21.951	15.258	14.676	14.052	10.155	9.793	9.384	
p=20K	pi-MASS	95.432	91.162	90.292	49.810	47.339	46.551	36.005	32.688	32.457	29.056	25.919	25.875	26.580	22.080	22.163
	LASSO min	82.745	78.724	79.759	36.681	34.860	35.334	21.364	20.318	20.537	13.705	13.032	13.214	9.134	8.668	8.800
	LASSO 1se	86.737	82.970	84.137	38.608	36.990	37.443	22.424	21.581	21.811	14.405	13.854	14.025	9.625	9.216	9.340
	EN 0.075 min	82.679	78.606	79.631	36.560	34.843	35.391	21.330	20.297	20.536	13.728	13.021	13.194	9.126	8.658	8.774
	EN 0.075 1se	86.807	83.125	83.961	38.559	36.985	37.374	22.475	21.549	21.783	14.463	13.838	13.978	9.621	9.236	9.333
	EN 0.050 min	82.581	78.817	79.689	36.527	34.720	35.326	21.341	20.168	20.550	13.711	12.978	13.124	9.103	8.665	8.776
	EN 0.050 1se	86.876	83.145	84.206	38.639	37.010	37.392	22.547	21.597	21.831	14.467	13.850	14.042	9.636	9.252	9.359
	EN 0.025 min	82.465	78.729	79.541	36.489	34.704	35.192	21.285	20.195	20.396	13.674	12.923	13.090	9.094	8.615	8.686
	EN 0.025 1se	87.140	83.333	84.370	38.677	37.057	37.603	22.542	21.725	21.913	14.501	13.977	14.137	9.658	9.294	9.388
	zellner	86.646	82.735	83.123	37.772	36.133	36.457	21.926	21.027	21.147	14.046	13.561	13.585	9.394	8.976	9.004
pMOM	84.429	80.277	81.116	37.300	35.512	35.841	21.708	20.649	20.892	13.945	13.282	13.403	9.285	8.861	8.924	
piMOM	84.195	80.137	80.705	37.243	35.448	35.774	21.665	20.621	20.858	13.933	13.277	13.367	9.272	8.823	8.894	

Supplementary Table 5: l_1 estimation error in effect sizes (β -error) for Simulation 1 datasets with number of real genotyped SNPs $p = (10000, 15000, 2000)$, sample size $n = (2000, 3000, 5000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$), GWASinlps piMOM method ($\tau = 0.008$, $k_0 = 1$, $r_{xx} = 0.2$), Zellner’s g-prior based method within our structured screen-and-select framework, LASSO ($\lambda = 1.1se$), Elastic Net ($\lambda = 1.1se$, $\alpha = 0.75, 0.5, 0.25$), and pi-MASS. For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins, whereas for pi-MASS 10,000 iterations were used after 1,000 burn-ins. For Zellner prior $g = n$ was used. All the figures are averaged over 100 replicates.

		$h^2=0.1$			$h^2=0.2$			$h^2=0.3$			$h^2=0.4$			$h^2=0.5$		
		n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K	n=2K	n=3K	n=5K
p=10K	pi-MASS	4.502	4.502	4.479	4.726	4.706	4.605	4.894	4.950	4.864	5.145	5.073	5.005	5.310	5.311	5.181
	LASSO min	3.407	3.354	3.207	2.734	2.614	2.516	2.303	2.161	2.107	2.009	1.830	1.823	1.758	1.539	1.542
	LASSO 1se	3.809	3.807	3.804	2.976	2.916	2.824	2.494	2.366	2.315	2.153	2.010	1.946	1.889	1.674	1.644
	EN 0.075 min	3.442	3.378	3.247	2.778	2.650	2.553	2.374	2.217	2.161	2.048	1.878	1.868	1.785	1.592	1.608
	EN 0.075 1se	3.841	3.844	3.772	3.008	2.944	2.866	2.528	2.433	2.375	2.229	2.040	2.009	1.942	1.730	1.725
	EN 0.050 min	3.481	3.416	3.291	2.863	2.739	2.661	2.468	2.336	2.287	2.174	2.018	2.007	1.943	1.751	1.754
	EN 0.050 1se	3.862	3.857	3.863	3.070	3.024	2.958	2.643	2.533	2.508	2.345	2.185	2.170	2.114	1.903	1.908
	EN 0.025 min	3.547	3.529	3.437	3.078	2.954	2.894	2.775	2.656	2.582	2.553	2.396	2.346	2.367	2.175	2.146
	EN 0.025 1se	3.943	3.931	3.933	3.310	3.217	3.182	2.993	2.858	2.806	2.749	2.568	2.520	2.564	2.350	2.308
	zellner	3.783	3.690	3.326	3.118	2.605	2.548	2.674	2.040	2.099	2.055	1.479	1.681	1.707	1.024	1.217
	pMOM	4.172	4.225	3.742	3.225	2.928	2.844	2.672	2.230	2.229	2.087	1.609	1.766	1.776	1.107	1.356
piMOM	4.100	4.095	3.740	3.109	2.828	2.798	2.519	2.158	2.183	2.007	1.563	1.737	1.636	1.107	1.313	
p=15K	pi-MASS	4.436	4.537	4.477	4.500	4.756	4.621	4.571	4.997	4.774	4.670	5.130	4.917	4.784	5.374	5.089
	LASSO min	3.331	2.793	2.990	2.766	2.112	2.317	2.463	1.690	1.933	2.240	1.401	1.629	1.983	1.160	1.376
	LASSO 1se	3.667	3.354	3.470	2.881	2.425	2.563	2.518	1.925	2.099	2.268	1.589	1.756	2.024	1.324	1.496
	EN 0.075 min	3.391	2.829	3.018	2.860	2.153	2.361	2.583	1.763	1.981	2.334	1.465	1.697	2.161	1.229	1.465
	EN 0.075 1se	3.664	3.368	3.471	3.029	2.434	2.582	2.697	1.964	2.134	2.453	1.637	1.825	2.259	1.386	1.574
	EN 0.050 min	3.482	2.897	3.074	3.033	2.252	2.455	2.800	1.884	2.099	2.613	1.612	1.844	2.456	1.386	1.617
	EN 0.050 1se	3.733	3.326	3.478	3.216	2.551	2.691	2.952	2.087	2.286	2.769	1.783	1.986	2.617	1.530	1.747
	EN 0.025 min	3.637	3.062	3.220	3.310	2.525	2.697	3.122	2.211	2.409	2.980	1.989	2.194	2.859	1.796	2.004
	EN 0.025 1se	3.838	3.497	3.587	3.461	2.782	2.962	3.273	2.424	2.609	3.120	2.179	2.365	3.004	1.983	2.156
	zellner	3.853	2.838	3.127	3.094	1.994	2.345	2.684	1.495	1.814	2.334	1.102	1.415	2.068	0.780	1.109
	pMOM	4.053	3.203	3.453	3.190	2.153	2.433	2.730	1.517	1.895	2.432	1.203	1.422	2.129	0.861	1.125
piMOM	3.937	3.180	3.417	3.116	2.101	2.371	2.586	1.542	1.855	2.407	1.196	1.467	2.103	0.834	1.135	
p=20K	pi-MASS	4.543	4.511	4.510	4.700	4.652	4.699	4.874	4.780	4.860	5.018	4.922	5.009	5.257	5.068	5.150
	LASSO min	2.813	2.406	2.511	2.263	1.773	1.846	1.997	1.429	1.462	1.788	1.176	1.197	1.606	0.981	0.989
	LASSO 1se	3.077	2.860	2.970	2.369	2.075	2.153	2.045	1.637	1.666	1.834	1.325	1.370	1.627	1.101	1.130
	EN 0.075 min	2.978	2.440	2.558	2.561	1.818	1.900	2.348	1.481	1.526	2.193	1.236	1.267	2.064	1.043	1.059
	EN 0.075 1se	3.223	2.868	3.018	2.685	2.094	2.196	2.435	1.656	1.741	2.262	1.377	1.435	2.142	1.140	1.205
	EN 0.050 min	3.089	2.494	2.649	2.694	1.923	2.013	2.500	1.596	1.666	2.362	1.361	1.418	2.245	1.171	1.218
	EN 0.050 1se	3.337	2.964	3.072	2.848	2.187	2.309	2.624	1.784	1.890	2.459	1.516	1.624	2.344	1.308	1.399
	EN 0.025 min	3.218	2.687	2.853	2.886	2.187	2.324	2.726	1.925	2.042	2.612	1.731	1.828	2.516	1.565	1.652
	EN 0.025 1se	3.480	3.096	3.215	3.071	2.477	2.605	2.892	2.160	2.279	2.754	1.928	2.042	2.655	1.745	1.843
	zellner	2.829	2.239	2.344	2.316	1.414	1.500	2.141	1.015	1.000	1.931	0.772	0.816	1.733	0.649	0.572
	pMOM	3.025	2.373	2.470	2.379	1.447	1.553	2.172	1.054	1.025	1.914	0.811	0.827	1.810	0.700	0.645
piMOM	2.996	2.392	2.464	2.338	1.433	1.516	2.120	1.051	1.009	1.964	0.823	0.798	1.793	0.665	0.612	

Supplementary Table 6: True positive rate (TPR), true negative rate (TNR), and false discovery rate (FDR) for Simulation 2 datasets with number of real genotyped SNPs $p \sim 8000$, sample size $n=(1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$). For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins. All the figures are averaged over 100 replicates.

	TPR			TNR			FDR		
	$h^2=0.05$	$h^2=0.1$	$h^2=0.15$	$h^2=0.05$	$h^2=0.1$	$h^2=0.15$	$h^2=0.05$	$h^2=0.1$	$h^2=0.15$
$n=1K$	0.0288	0.0864	0.1392	0.9321	0.8367	0.7494	0.9987	0.9985	0.9986
$n=1.5K$	0.0444	0.1292	0.2068	0.8653	0.693	0.6092	0.9991	0.999	0.999
$n=2K$	0.0676	0.1824	0.2748	0.7548	0.5665	0.4799	0.9993	0.9992	0.9992
$n=2.5K$	0.0904	0.218	0.3212	0.6263	0.4256	0.3702	0.9995	0.9994	0.9994
$n=3K$	0.1084	0.2352	0.3452	0.5537	0.4197	0.3065	0.9995	0.9994	0.9995
$n=3.5K$	0.1324	0.2576	0.3672	0.453	0.359	0.271	0.9996	0.9995	0.9996
$n=4K$	0.158	0.2976	0.4116	0.4049	0.2816	0.2349	0.9996	0.9996	0.9996
$n=4.5K$	0.1712	0.336	0.4324	0.3793	0.2648	0.2213	0.9996	0.9996	0.9996
$n=5K$	0.2012	0.3756	0.4612	0.3229	0.2004	0.1586	0.9997	0.9997	0.9997
$n=5.5K$	0.1992	0.3696	0.4636	0.3257	0.212	0.1544	0.9997	0.9997	0.9997
$n=6K$	0.2164	0.3916	0.4768	0.3171	0.1998	0.171	0.9997	0.9997	0.9997
$n=6.5K$	0.2412	0.3948	0.4852	0.2401	0.1725	0.1236	0.9997	0.9997	0.9998
$n=7K$	0.2416	0.4032	0.4952	0.2434	0.1592	0.1235	0.9997	0.9997	0.9998
$n=7.5K$	0.2812	0.4348	0.4972	0.1996	0.1565	0.1233	0.9998	0.9997	0.9998
$n=8K$	0.272	0.4396	0.5108	0.2371	0.1412	0.1037	0.9997	0.9998	0.9998
$n=8.5K$	0.306	0.4596	0.53	0.1952	0.1133	0.0949	0.9997	0.9998	0.9998
$n=9K$	0.3136	0.4656	0.5376	0.1807	0.139	0.1027	0.9998	0.9998	0.9998
$n=9.5K$	0.2876	0.4624	0.5412	0.2191	0.1231	0.1084	0.9997	0.9998	0.9998
$n=10K$	0.324	0.474	0.5532	0.1727	0.1057	0.083	0.9998	0.9998	0.9998

Supplementary Table 7: Relative prediction gain (RPG) in train data (three-quarter of samples) and test data for Simulation 2 datasets with number of real genotyped SNPs $p \sim 8000$, sample size $n=(1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500, 10000)$, and heritability $h^2 = (0.1, 0.2, 0.3, 0.4, 0.5)$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1$, $r_{xx} = 0.2$). For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins. All the figures are averaged over 100 replicates.

	RPG train			RPG test		
	$h^2=0.05$	$h^2=0.1$	$h^2=0.15$	$h^2=0.05$	$h^2=0.1$	$h^2=0.15$
$n=1K$	2.8594	1.9193	1.5057	1.2865	0.7461	0.7958
$n=1.5K$	1.661	1.2654	1.1547	0.8773	0.6071	0.7029
$n=2K$	1.0441	1.0572	1.0292	0.3713	0.5826	0.7551
$n=2.5K$	0.5375	0.9128	0.9752	-0.1814	0.6235	0.7842
$n=3K$	0.7171	0.9197	0.9436	0.3283	0.6543	0.7964
$n=3.5K$	0.5808	0.8826	0.9421	0.3432	0.6881	0.8248
$n=4K$	0.7196	0.853	0.9622	0.4367	0.7103	0.8949
$n=4.5K$	0.6775	0.8795	0.9514	0.44	0.7547	0.894
$n=5K$	0.7139	0.9144	0.9523	0.488	0.818	0.9035
$n=5.5K$	0.7227	0.9001	0.9501	0.553	0.8295	0.9163
$n=6K$	0.6915	0.9123	0.9496	0.549	0.8447	0.9169
$n=6.5K$	0.6493	0.8941	0.9446	0.4992	0.8332	0.9232
$n=7K$	0.6061	0.864	0.9463	0.4654	0.8261	0.9174
$n=7.5K$	0.7413	0.9114	0.93	0.6226	0.8674	0.916
$n=8K$	0.7364	0.9153	0.9483	0.6071	0.8849	0.9272
$n=8.5K$	0.7911	0.9203	0.9429	0.6642	0.9002	0.9375
$n=9K$	0.792	0.9387	0.9596	0.6999	0.9026	0.9457
$n=9.5K$	0.719	0.916	0.9574	0.6319	0.8989	0.942
$n=10K$	0.7777	0.914	0.9443	0.6929	0.9026	0.9501

Supplementary Table 8: Mean squared error (MSE) from the sensitivity analysis of GWASinlps tuning parameters k_0 , r_{xx} , and n_{skip} using the first 30 replicates of the Simulation 1 dataset with number of real genotyped SNPs $p = 10000$, sample size $n = 2000$, and heritability $h^2 = 0.5$, analyzed using GWASinlps pMOM method ($\tau = 0.022$, $k_0 = 1, 2, 3, 4, 5$, $r_{xx} = 0.2, 0.35, 0.5, 0.75, 0.9$, $n_{skip} = 1, 2, 3, 4, 5$). For GWASinlps SNP selection, 1,800 MCMC iterations were used after 200 burn-ins. All the figures are averaged over the 30 replicates.

$n_{skip}=1$						$n_{skip}=2$					
	$r_{xx}=0.2$	$r_{xx}=0.35$	$r_{xx}=0.5$	$r_{xx}=0.75$	$r_{xx}=0.9$		$r_{xx}=0.2$	$r_{xx}=0.35$	$r_{xx}=0.5$	$r_{xx}=0.75$	$r_{xx}=0.9$
$k_0=1$	9.151	9.1	9.04	8.952	8.64	$k_0=1$	9.126	9.058	8.981	8.838	8.555
$k_0=2$	9.101	9.029	8.928	8.711	8.485	$k_0=2$	9.084	8.973	8.87	8.615	8.351
$k_0=3$	9.076	8.936	8.801	8.55	8.36	$k_0=3$	9.044	8.91	8.769	8.485	8.306
$k_0=4$	9.059	8.92	8.823	8.541	8.307	$k_0=4$	9.035	8.876	8.775	8.501	8.294
$k_0=5$	8.989	8.864	8.784	8.489	8.242	$k_0=5$	8.969	8.83	8.729	8.441	8.237

$n_{skip}=3$						$n_{skip}=4$					
	$r_{xx}=0.2$	$r_{xx}=0.35$	$r_{xx}=0.5$	$r_{xx}=0.75$	$r_{xx}=0.9$		$r_{xx}=0.2$	$r_{xx}=0.35$	$r_{xx}=0.5$	$r_{xx}=0.75$	$r_{xx}=0.9$
$k_0=1$	9.104	9.015	8.942	8.74	8.483	$k_0=1$	9.092	8.992	8.904	8.686	8.432
$k_0=2$	9.07	8.947	8.816	8.565	8.327	$k_0=2$	9.063	8.93	8.796	8.522	8.316
$k_0=3$	9.032	8.884	8.753	8.462	8.3	$k_0=3$	9.029	8.879	8.74	8.445	8.3
$k_0=4$	9.025	8.865	8.759	8.498	8.289	$k_0=4$	9.025	8.86	8.748	8.494	8.288
$k_0=5$	8.965	8.819	8.717	8.439	8.233	$k_0=5$	8.965	8.817	8.712	8.435	8.233

$n_{skip}=5$					
	$r_{xx}=0.2$	$r_{xx}=0.35$	$r_{xx}=0.5$	$r_{xx}=0.75$	$r_{xx}=0.9$
$k_0=1$	9.089	8.976	8.883	8.648	8.381
$k_0=2$	9.063	8.918	8.781	8.503	8.313
$k_0=3$	9.025	8.873	8.733	8.446	8.295
$k_0=4$	9.022	8.853	8.746	8.486	8.288
$k_0=5$	8.965	8.817	8.711	8.433	8.231

Supplementary Table 9: Chromosome numbers and base pair ids (Chrom:pos), frequency of appearance in the 20 SNP sets (freq), reference SNP ids (rs ID), and gene symbols (Gene) for the 14 GWASinlps pMOM selected SNPs from the TOP data.

Chrom:pos	freq	rs ID	gene
16:24018670	17	<i>rs4788421</i>	<i>PRKCB</i>
1:58331857	16	<i>rs12078749</i>	<i>DAB1</i>
1:94509224	15	<i>rs4847272</i>	<i>ABCA4</i>
3:114393973	15	<i>rs9850975</i>	<i>ZBTB20</i>
8:129030687	15	<i>rs17199763</i>	<i>MYC</i>
1:58609441	14	<i>rs17491825</i>	<i>DAB1</i>
1:217022081	12	<i>rs12083048</i>	<i>ESRRG</i>
11:83194086	9	<i>rs1975119</i>	<i>DLG2</i>
5:64247018	9	<i>rs1433599</i>	<i>CWC27</i>
7:43836596	9	<i>rs2158952</i>	<i>BLVRA</i>
8:133225904	9	<i>rs10092161</i>	<i>KCNQ3</i>
11:84626915	7	<i>rs11828539</i>	<i>DLG2</i>
14:30147686	7	<i>rs6571318</i>	<i>PRKD1</i>
3:105464766	7	<i>rs9657906</i>	<i>CBLB</i>
1:10591104	6	<i>rs12090079</i>	<i>PEX14</i>
4:114472389	6	<i>rs17446851</i>	<i>CAMK2D</i>
4:144353246	6	<i>rs7695623</i>	<i>GAB1</i>
8:27181903	6	<i>rs17057011</i>	<i>PTK2B</i>
10:21471450	5	<i>rs11012563</i>	<i>NEBL</i>
11:70901471	5	<i>rs3934692</i>	<i>SHANK2</i>
1:236886531	5	<i>rs2914919</i>	<i>ACTN2</i>
1:68378001	5	<i>rs12730964</i>	<i>GNG12</i>
3:60271645	5	<i>rs2201649</i>	<i>FHIT</i>
6:161154955	5	<i>rs1317026</i>	<i>PLG</i>
8:27389167	5	<i>rs17057312</i>	<i>EPHX2</i>
8:3964918	5	<i>rs17332636</i>	<i>CSMD1</i>

Supplementary Web Resources

HapMap 3: https://mathgen.stats.ox.ac.uk/impute/impute_v1.html#Using_IMPUTE_with_the_HapMap_Data

EIGENSOFT: <https://www.hsph.harvard.edu/alkes-price/software/>

TOP: <http://www.med.uio.no/klinmed/english/about/organization/divisions/mental-health-addiction/psychosis-research-centre-top/>