

Non-clinal sims analysis

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9/20/2021

Make sure to set the working directory in the above code chunk

Read in data

```
out.df <- read.table(file = "summary_20220428_20220726.txt", header=TRUE)
head(out.df)
```

```
##      seed n_samp_tot n_samp_per_pop sd_fitness_among_inds sd_fitness_among_pops
## 1 1231094      1000           10      0.05272602      0.01977273
## 2 1231095      1000           10      0.04519923      0.01541145
## 3 1231096      1000           10      0.05348903      0.02022721
## 4 1231097      1000           10      0.05446050      0.01731323
## 5 1231098      1000           10      0.05093029      0.01832588
## 6 1231099      1000           10      0.07552882      0.02341833
##  final_LA K  Bonf_alpha numCausalLowMAFsamples all_corr_phen_temp
## 1 0.500854 2 1.918428e-06           39      0.9545790
## 2 0.505075 9 1.730523e-06          104      0.9545764
## 3 0.499265 9 1.508614e-06           22      0.9723022
## 4 0.499365 9 1.531065e-06           24      0.9720233
## 5 0.501054 6 6.395498e-06           12      0.9708565
## 6 0.478131 3 2.022981e-06           34      0.9247450
##  subsamp_corr_phen_temp all_corr_phen_sal subsamp_corr_phen_sal
## 1           0.8893387           NA           NA
## 2           0.9006961           NA           NA
## 3           0.8873320           NA           NA
## 4           0.8895298           NA           NA
## 5           0.8921410           NA           NA
## 6           0.8525464           NA           NA
##  num_causal_prefilter num_causal_postfilter num_non_causal num_neut_prefilter
## 1           2628           310           25753           26587
## 2           3144           382           28511           30284
## 3           3149           482           32661           33031
## 4           3131           470           32187           32548
## 5           1823           257           7561           7753
## 6           2948           364           24352           25004
##  num_neut_postfilter num_neut_neutralgenome num_causal_temp num_causal_sal
## 1           26587           12867           310           0
## 2           30284           14060           382           0
## 3           33031           16379           480           0
```

## 4	32548	16243	469	0
## 5	7753	3749	257	0
## 6	25004	12197	364	0
##	num_multiallelic	meanFst	va_temp_total	va_sal_total
## 1	0	0.18039488	0.01185008	0
## 2	0	0.16985797	0.01343736	0
## 3	0	0.13396101	0.01405264	0
## 4	0	0.08714633	0.01337458	0
## 5	0	0.31813358	0.01605415	0
## 6	0	0.12616527	0.01930127	0
##	Va_sal_sample	nSNPs	median_causal_temp_cor	median_causal_sal_cor
## 1	0	26063	0.3580437	NA
## 2	0	28893	0.4138162	NA
## 3	0	33143	0.4157033	NA
## 4	0	32657	0.4112619	NA
## 5	0	7818	0.3925022	NA
## 6	0	24716	0.2974287	NA
##	median_neut_temp_cor	median_neut_sal_cor	cor_VA_temp_prop	cor_VA_sal_prop
## 1	0.3820531	0.04816897	0.8451605	0
## 2	0.4536498	0.04175877	0.7846421	0
## 3	0.4029319	0.03844065	0.7830061	0
## 4	0.3451512	0.04529330	0.7631297	0
## 5	0.4432208	0.05141380	0.8171677	0
## 6	0.2243095	0.19531471	0.6459740	0
##	cor_TPR_temp	cor_TPR_sal	cor_FDR_allSNPs_temp	cor_FDR_neutSNPs_temp
## 1	0.4612903	NA	0.9894449	0.9791241
## 2	0.5314136	NA	0.9886134	0.9769893
## 3	0.5416667	NA	0.9854586	0.9711015
## 4	0.5351812	NA	0.9833466	0.9669693
## 5	0.5408560	NA	0.9711199	0.9447316
## 6	0.3076923	NA	0.9813892	0.9575114
##	cor_FDR_allSNPs_sal	cor_FDR_neutSNPs_sal	num_causal_sig_temp_corr	
## 1	NA	NA	143	
## 2	NA	NA	203	
## 3	NA	NA	260	
## 4	1	NA	251	
## 5	NA	NA	139	
## 6	1	1	112	
##	num_causal_sig_sal_corr	num_notCausal_sig_temp_corr		
## 1	0	13405		
## 2	0	17625		
## 3	0	17620		
## 4	0	14821		
## 5	0	4674		
## 6	0	5906		
##	num_notCausal_sig_sal_corr	num_neut_sig_temp_corr	num_neut_sig_sal_corr	
## 1	0	6707	0	
## 2	0	8619	0	
## 3	0	8737	0	
## 4	1	7348	0	
## 5	0	2376	0	
## 6	4344	2524	2133	
##	cor_AUCPR_temp_allSNPs	cor_AUCPR_temp_neutSNPs	cor_AUCPR_sal_allSNPs	
## 1	0.01064045	0.02148047	NA	

## 2	0.01053868	0.02130552	NA
## 3	0.01286086	0.02546132	NA
## 4	0.01566591	0.03219810	NA
## 5	0.02696219	0.05312152	NA
## 6	0.02255358	0.06178401	NA
##	cor_AUCPR_sal_neutSNPs	cor_af_temp_noutliers	cor_af_sal_noutliers
## 1	NA	13548	0
## 2	NA	17828	0
## 3	NA	17880	0
## 4	NA	15072	1
## 5	NA	4813	0
## 6	NA	6018	4344
##	cor_FPR_temp_neutSNPs	cor_FPR_sal_neutSNPs	LEA3.2_lfmm2_Va_temp_prop
## 1	0.5212559	0.0000000	0.27826502
## 2	0.6130156	0.0000000	0.00000000
## 3	0.5334269	0.0000000	0.00000000
## 4	0.4523795	0.0000000	0.00000000
## 5	0.6337690	0.0000000	0.03610723
## 6	0.2069361	0.1748791	0.17163124
##	LEA3.2_lfmm2_Va_sal_prop	LEA3.2_lfmm2_TPR_temp	LEA3.2_lfmm2_TPR_sal
## 1	NA	0.022580645	NA
## 2	NA	0.000000000	NA
## 3	NA	0.000000000	NA
## 4	NA	0.000000000	NA
## 5	NA	0.003891051	NA
## 6	NA	0.005494505	NA
##	LEA3.2_lfmm2_FDR_allSNPs_temp	LEA3.2_lfmm2_FDR_allSNPs_sal	
## 1	0.9789790	NA	
## 2	NA	1	
## 3	NA	1	
## 4	1.0000000	NA	
## 5	0.9500000	NA	
## 6	0.8666667	NA	
##	LEA3.2_lfmm2_FDR_neutSNPs_temp	LEA3.2_lfmm2_FDR_neutSNPs_sal	
## 1	0.9263158	NA	
## 2	NA	NA	
## 3	NA	NA	
## 4	1.0000000	NA	
## 5	0.8750000	NA	
## 6	0.0000000	NA	
##	LEA3.2_lfmm2_AUCPR_temp_allSNPs	LEA3.2_lfmm2_AUCPR_temp_neutSNPs	
## 1	0.01339495	0.02655237	
## 2	0.01367013	0.02786249	
## 3	0.01426730	0.02851768	
## 4	0.01310529	0.02513767	
## 5	0.03463172	0.06672248	
## 6	0.01437720	0.02928224	
##	LEA3.2_lfmm2_AUCPR_sal_allSNPs	LEA3.2_lfmm2_AUCPR_sal_neutSNPs	
## 1	NA	NA	
## 2	NA	NA	
## 3	NA	NA	
## 4	NA	NA	
## 5	NA	NA	
## 6	NA	NA	

```

## LEA3.2_lfmm2_mlog10P_tempenv_noutliers LEA3.2_lfmm2_mlog10P_salenv_noutliers
## 1 333 0
## 2 0 1
## 3 0 1
## 4 6 0
## 5 20 0
## 6 15 0
## LEA3.2_lfmm2_num_causal_sig_temp LEA3.2_lfmm2_num_neut_sig_temp
## 1 7 88
## 2 0 0
## 3 0 0
## 4 0 2
## 5 1 7
## 6 2 0
## LEA3.2_lfmm2_num_causal_sig_sal LEA3.2_lfmm2_num_neut_sig_sal
## 1 0 0
## 2 0 0
## 3 0 0
## 4 0 0
## 5 0 0
## 6 0 0
## LEA3.2_lfmm2_FPR_neutSNPs_temp LEA3.2_lfmm2_FPR_neutSNPs_sal RDA1_propvar
## 1 0.006839201 0 0.985
## 2 0.000000000 0 0.989
## 3 0.000000000 0 0.988
## 4 0.000123130 0 0.980
## 5 0.001867165 0 0.991
## 6 0.000000000 0 0.596
## RDA2_propvar RDA1_propvar_corr RDA2_propvar_corr RDA1_temp_cor RDA1_sal_cor
## 1 0.015 0.765 0.235 0.9999982 0.001912722
## 2 0.011 0.835 0.165 0.9999971 0.002425692
## 3 0.012 0.842 0.158 0.9999982 0.001888450
## 4 0.020 0.841 0.159 0.9999700 -0.007739672
## 5 0.009 0.816 0.184 0.9999640 0.008484251
## 6 0.404 0.597 0.403 -0.9360957 0.351745296
## RDA2_temp_cor RDA2_sal_cor RDA_Va_temp_prop RDA_Va_temp_prop_corr
## 1 -0.001912722 0.9999982 0.1248244 0.000000000
## 2 -0.002425692 0.9999971 0.3566111 0.017427370
## 3 -0.001888450 0.9999982 0.1750594 0.000000000
## 4 0.007739672 0.9999700 0.1339135 0.000000000
## 5 -0.008484251 0.9999640 0.3123098 0.036329553
## 6 -0.351745296 -0.9360957 0.3414487 0.004385126
## RDA_Va_sal_prop RDA_Va_sal_prop_corr RDA_TPR RDA_TPR_corr RDA_FDR_allSNPs
## 1 0 0 0.006451613 0.000000000 0.9918699
## 2 0 0 0.041884817 0.015706806 0.9953502
## 3 0 0 0.010373444 0.000000000 0.9957519
## 4 0 0 0.014893617 0.000000000 0.9941812
## 5 0 0 0.073929961 0.015564202 0.9850039
## 6 0 0 0.027472527 0.002747253 0.9889258
## RDA_FDR_allSNPs_corr num_RDA_sig_causal num_RDA_sig_neutral
## 1 1.0000000 2 118
## 2 0.9966979 16 1545
## 3 1.0000000 5 526
## 4 1.0000000 7 557

```

## 5	0.9833333	19	583
## 6	0.9979550	10	271
##	num_RDA_sig_causal_corr	num_RDA_sig_neutral_corr	RDA_FDR_neutSNPs
## 1	0	200	0.9833333
## 2	6	867	0.9897502
## 3	0	458	0.9905838
## 4	0	577	0.9875887
## 5	4	122	0.9684385
## 6	1	213	0.9644128
##	RDA_FDR_neutSNPs_corr	RDA_AUCPR_allSNPs	RDA_AUCPR_neutSNPs
## 1	1.0000000	0.008249728	0.01647883
## 2	0.9931271	0.008916531	0.01857113
## 3	1.0000000	0.009025124	0.01784801
## 4	1.0000000	0.009215389	0.01812750
## 5	0.9682540	0.025358473	0.05094037
## 6	0.9953271	0.014302424	0.02930863
##	RDA_AUCPR_neutSNPs_corr	RDA_FPR_neutSNPs	RDA_FPR_neutSNPs_corr
## 1	0.01597697	0.009170747	0.01554364
## 2	0.01824752	0.109886202	0.06166430
## 3	0.01820267	0.032114293	0.02796264
## 4	0.01825734	0.034291695	0.03552299
## 5	0.05046366	0.155508136	0.03254201
## 6	0.01982718	0.022218578	0.01746331
##	RDA_RDAmutpred_cor_tempEffect	RDA_RDAmutpred_cor_salEffect	
## 1	0.2566239	NA	
## 2	0.2709340	NA	
## 3	0.3199777	NA	
## 4	0.3397117	NA	
## 5	0.2064143	NA	
## 6	0.2864279	NA	
##	RDA_absRDAmutpred_cor_tempVa	RDA_absRDAmutpred_cor_salVa	
## 1	-0.04251831	NA	
## 2	-0.06383708	NA	
## 3	-0.06156140	NA	
## 4	-0.04360391	NA	
## 5	-0.05007068	NA	
## 6	-0.02697188	NA	
##	RDA_RDAmutpred_cor_tempEffect_structcorr		
## 1	0.1711607		
## 2	0.1695575		
## 3	0.2590273		
## 4	0.1412525		
## 5	0.2089774		
## 6	0.1483359		
##	RDA_RDAmutpred_cor_salEffect_structcorr		
## 1	NA		
## 2	NA		
## 3	NA		
## 4	NA		
## 5	NA		
## 6	NA		
##	RDA_absRDAmutpred_cor_tempVa_structcorr		
## 1	0.002950593		
## 2	0.011548773		

```

## 3 -0.006744183
## 4 -0.006811228
## 5 0.018943112
## 6 0.011844784
## RDA_absRDAmutpred_cor_salVa_structcorr RDA_cor_RDA20000temppredict_tempPhen
## 1 NA 0.8530879
## 2 NA 0.8661742
## 3 NA 0.8458619
## 4 NA 0.8566006
## 5 NA 0.8297057
## 6 NA 0.8109670
## RDA_cor_RDA20000salpredict_salPhen
## 1 NA
## 2 NA
## 3 NA
## 4 NA
## 5 NA
## 6 NA
## RDA_cor_RDA20000temppredict_tempPhen_structcorr
## 1 -0.03541745
## 2 0.02470470
## 3 0.12927728
## 4 0.04149750
## 5 0.11539940
## 6 0.15610811
## RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal
## 1 NA -0.9938219 -0.002423473
## 2 NA -0.9763521 -0.002856465
## 3 NA -0.9806495 -0.001193085
## 4 NA -0.9894438 0.006933632
## 5 NA -0.9624753 -0.006417090
## 6 NA -0.9180515 0.333573860
## cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp
## 1 -0.02040717 -0.001688470 0.07027960 -0.001851458 -0.23741491
## 2 0.15699463 0.006663054 -0.64036018 -0.002311619 0.16118062
## 3 0.02289691 -0.002251339 -0.05164944 -0.001922661 -0.66955922
## 4 -0.03159957 -0.011695024 0.09041291 -0.007667182 -0.49064055
## 5 0.18621652 0.005399774 -0.64151191 -0.008355460 0.20361826
## 6 -0.33266762 -0.910485583 0.14489884 -0.108366523 -0.05450648
## cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp
## 1 -0.002823011 -0.09231664 0.9995526 0.9926958
## 2 -0.000199728 0.75497199 0.9963113 0.6504534
## 3 -0.002378429 0.07609171 0.9999081 0.9968609
## 4 0.011008515 -0.12306538 -0.9998272 0.9916547
## 5 -0.005102881 0.79034742 0.9976490 0.5947952
## 6 -0.018196703 -0.47679972 -0.9712646 0.8782899
## cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase
## 1 0.001339894 NA 0.2290323 NA
## 2 0.084015793 NA 0.3272251 NA
## 3 0.004567194 NA 0.3270833 NA
## 4 0.004580758 NA 0.2430704 NA
## 5 0.060281782 NA 0.4202335 NA
## 6 -0.236378957 NA 0.2252747 NA
## gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines

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```

## 1          0.9667914          NA
## 2          0.9696749          NA
## 3          0.9616699          NA
## 4          0.9497354          NA
## 5          0.9174312          NA
## 6          0.9382065          NA
## clinalparadigm_temp_proptop5GWASclines clinalparadigm_sal_propsigGWASclines
## 1          0.6554106          NA
## 2          0.5384083          NA
## 3          0.5530760          NA
## 4          0.5021433          NA
## 5          0.5882353          NA
## 6          0.3446602          NA
## clinalparadigm_temp_propsigGWASclines
## 1          0.6050302
## 2          0.5794083
## 3          0.5593769
## 4          0.4777563
## 5          0.6314615
## 6          0.3099063

```

```
tail(out.df)
```

```

##      seed n_samp_tot n_samp_per_pop sd_fitness_among_inds
## 2245 1233338      1000           10      0.06989773
## 2246 1233339      1000           10      0.10457515
## 2247 1233340      1000           10      0.10815036
## 2248 1233341      1000           10      0.09447908
## 2249 1233342      1000           10      0.10039771
## 2250 1233343      1000           10      0.11933530
##      sd_fitness_among_pops final_LA K   Bonf_alpha numCausalLowMAFsample
## 2245      0.03432623 0.390202 2 4.302186e-06      0
## 2246      0.05800045 0.378143 3 2.037324e-06      0
## 2247      0.05691502 0.386475 3 1.950687e-06      0
## 2248      0.04351184 0.406991 1 1.582930e-06      0
## 2249      0.04816428 0.411540 2 1.608648e-06      0
## 2250      0.06758560 0.361984 1 6.179706e-06      0
##      all_corr_phen_temp subsamp_corr_phen_temp all_corr_phen_sal
## 2245      0.8105442      0.6442488      0.9331842
## 2246      0.6134233      0.5623938      0.8856847
## 2247      0.6300670      0.5378167      0.9092372
## 2248      0.7915280      0.6228879      0.9145244
## 2249      0.8020544      0.6425425      0.9127410
## 2250      0.8163458      0.6347974      0.8849650
##      subsamp_corr_phen_sal num_causal_prefilter num_causal_postfilter
## 2245      0.8112850      8      5
## 2246      0.8061503      11      6
## 2247      0.8075816      8      6
## 2248      0.8166540      10      7
## 2249      0.8128461      14      9
## 2250      0.7608153      12      8
##      num_non_causal num_neut_prefilter num_neut_postfilter
## 2245      11617      11843      11843
## 2246      24536      25257      25257

```

##	2247	25626	26975	26975	
##	2248	31580	31942	31942	
##	2249	31073	31405	31405	
##	2250	8083	8197	8197	
##		num_neut_neutralgenome	num_causal_temp	num_causal_sal	num_multiallelic
##	2245	5810	5	5	0
##	2246	12346	6	6	0
##	2247	12834	6	6	0
##	2248	15946	7	7	0
##	2249	15689	9	9	0
##	2250	3947	8	8	0
##		meanFst	va_temp_total	va_sal_total	Va_temp_sample
##	2245	0.14301783	0.14320895	0.06757681	0.13713509
##	2246	0.13350458	0.05299476	0.07273692	0.08494197
##	2247	0.13740776	0.09929097	0.10670097	0.22910565
##	2248	0.08708807	0.13554966	0.10110684	0.13249490
##	2249	0.06704804	0.16714222	0.16315859	0.16734136
##	2250	0.17379409	0.08556485	0.10592398	0.08049695
##		median_causal_temp_cor	median_causal_sal_cor	median_neut_temp_cor	
##	2245	0.2754918	0.5180941	0.2414407	
##	2246	0.3026247	0.4175574	0.1850624	
##	2247	0.2000535	0.3990216	0.2321665	
##	2248	0.2967283	0.4868710	0.2257370	
##	2249	0.3428889	0.3406402	0.1621695	
##	2250	0.3033895	0.3424647	0.2488890	
##		median_neut_sal_cor	cor_VA_temp_prop	cor_VA_sal_prop	cor_TPR_temp
##	2245	0.22546761	0.8516887	0.9978557	0.4000000
##	2246	0.12090175	0.4727327	0.8630538	0.1666667
##	2247	0.10810696	0.7985926	0.7317329	0.1666667
##	2248	0.09267506	0.6560965	0.8820640	0.4285714
##	2249	0.10404740	0.1136390	0.4316080	0.3333333
##	2250	0.13587417	0.3901235	0.8777962	0.3750000
##		cor_TPR_sal	cor_FDR_allSNPs_temp	cor_FDR_neutSNPs_temp	cor_FDR_allSNPs_sal
##	2245	0.8000000	0.9993947	0.9987358	0.9985337
##	2246	0.6666667	0.9997394	0.9995287	0.9949749
##	2247	0.5000000	0.9998285	0.9996431	0.9933775
##	2248	0.8571429	0.9995787	0.9991545	0.9692308
##	2249	0.3333333	0.9989027	0.9976285	0.9916201
##	2250	0.5000000	0.9987903	0.9974958	0.9913043
##		cor_FDR_neutSNPs_sal	num_causal_sig_temp_corr	num_causal_sig_sal_corr	
##	2245	0.9968774	2	4	
##	2246	0.9840000	1	4	
##	2247	0.9732143	1	3	
##	2248	0.8378378	3	6	
##	2249	0.9700000	3	3	
##	2250	0.9743590	3	4	
##		num_notCausal_sig_temp_corr	num_notCausal_sig_sal_corr		
##	2245	3302	2724		
##	2246	3836	792		
##	2247	5830	450		
##	2248	7118	189		
##	2249	2731	355		
##	2250	2477	456		
##		num_neut_sig_temp_corr	num_neut_sig_sal_corr	cor_AUCPR_temp_allSNPs	

##	2245	1580	1277	0.0056220144
##	2246	2121	246	0.0007501130
##	2247	2801	109	0.0003226524
##	2248	3545	31	0.0003352525
##	2249	1262	97	0.0050843070
##	2250	1195	152	0.0013870159
##	cor_AUCPR_temp_neutSNPs cor_AUCPR_sal_allSNPs cor_AUCPR_sal_neutSNPs			
##	2245	0.0161350441	0.09787865	0.4036255
##	2246	0.0013167008	0.24012890	0.3423103
##	2247	0.0006630059	0.17086955	0.1834894
##	2248	0.0006712386	0.40553013	0.7821320
##	2249	0.0109923069	0.11638113	0.1367044
##	2250	0.0029380064	0.02439708	0.2860155
##	cor_af_temp_noutliers cor_af_sal_noutliers cor_FPR_temp_neutSNPs			
##	2245	3304	2728	0.27194492
##	2246	3837	796	0.17179653
##	2247	5831	453	0.21824840
##	2248	7121	195	0.22231281
##	2249	2734	358	0.08043852
##	2250	2480	460	0.30276159
##	cor_FPR_sal_neutSNPs LEA3.2_lfmm2_Va_temp_prop LEA3.2_lfmm2_Va_sal_prop			
##	2245	0.219793460	0.0000000	0.9578289
##	2246	0.019925482	0.4727327	0.9998981
##	2247	0.008493065	0.0000000	0.9412170
##	2248	0.001944061	0.0000000	0.8820640
##	2249	0.006182676	0.0000000	0.9171033
##	2250	0.038510261	0.0000000	0.8777962
##	LEA3.2_lfmm2_TPR_temp LEA3.2_lfmm2_TPR_sal LEA3.2_lfmm2_FDR_allSNPs_temp			
##	2245	0.0000000	0.6000000	NA
##	2246	0.1666667	0.8333333	0
##	2247	0.0000000	0.6666667	NA
##	2248	0.0000000	0.8571429	NA
##	2249	0.0000000	0.5555556	NA
##	2250	0.0000000	0.5000000	NA
##	LEA3.2_lfmm2_FDR_allSNPs_sal LEA3.2_lfmm2_FDR_neutSNPs_temp			
##	2245	0.9302326		NA
##	2246	0.9180328		0
##	2247	0.9680000		NA
##	2248	0.8888889		NA
##	2249	0.9253731		NA
##	2250	0.9090909		NA
##	LEA3.2_lfmm2_FDR_neutSNPs_sal LEA3.2_lfmm2_AUCPR_temp_allSNPs			
##	2245	0.0		0.2881630
##	2246	0.0		0.5981415
##	2247	0.2		0.2337020
##	2248	0.0		0.5925314
##	2249	0.0		0.2628556
##	2250	0.0		0.2117759
##	LEA3.2_lfmm2_AUCPR_temp_neutSNPs LEA3.2_lfmm2_AUCPR_sal_allSNPs			
##	2245	0.6313777		0.2881630
##	2246	0.8340475		0.5981415
##	2247	0.7153403		0.2337020
##	2248	1.0000000		0.5925314
##	2249	0.5658529		0.2628556

```

## 2250          0.5088647          0.2117759
##      LEA3.2_lfmm2_AUCPR_sal_neutSNPs LEA3.2_lfmm2_mlog10P_tempenv_noutliers
## 2245          0.6313777          0
## 2246          0.8340475          1
## 2247          0.7153403          0
## 2248          1.0000000          0
## 2249          0.5658529          0
## 2250          0.5088647          0
##      LEA3.2_lfmm2_mlog10P_salenv_noutliers LEA3.2_lfmm2_num_causal_sig_temp
## 2245          43          0
## 2246          61          1
## 2247         125          0
## 2248          54          0
## 2249          67          0
## 2250          44          0
##      LEA3.2_lfmm2_num_neut_sig_temp LEA3.2_lfmm2_num_causal_sig_sal
## 2245          0          3
## 2246          0          5
## 2247          0          4
## 2248          0          6
## 2249          0          5
## 2250          0          4
##      LEA3.2_lfmm2_num_neut_sig_sal LEA3.2_lfmm2_FPR_neutSNPs_temp
## 2245          0          0
## 2246          0          0
## 2247          1          0
## 2248          0          0
## 2249          0          0
## 2250          0          0
##      LEA3.2_lfmm2_FPR_neutSNPs_sal RDA1_propvar RDA2_propvar RDA1_propvar_corr
## 2245          0.000000e+00          0.550          0.450          0.665
## 2246          0.000000e+00          0.742          0.258          0.558
## 2247          7.791803e-05          0.716          0.284          0.772
## 2248          0.000000e+00          0.835          0.165          0.752
## 2249          0.000000e+00          0.684          0.316          0.624
## 2250          0.000000e+00          0.739          0.261          0.673
##      RDA2_propvar_corr RDA1_temp_cor RDA1_sal_cor RDA2_temp_cor RDA2_sal_cor
## 2245          0.335          0.5015364 -0.865136554 -0.865136554 -0.5015364
## 2246          0.442          0.9999502 -0.009981000  0.009981000  0.9999502
## 2247          0.228          0.9999683 -0.007965626  0.007965626  0.9999683
## 2248          0.248          0.9991421  0.041413317 -0.041413317  0.9991421
## 2249          0.376          0.9996593  0.026102226 -0.026102226  0.9996593
## 2250          0.327          0.9800515  0.198743495 -0.198743495  0.9800515
##      RDA_Va_temp_prop RDA_Va_temp_prop_corr RDA_Va_sal_prop
## 2245          0.4763587          0.8519800          0.9578289
## 2246          0.9996855          0.9996855          0.9998981
## 2247          0.9995510          0.2009584          0.9742365
## 2248          0.9677581          0.9677581          0.8820640
## 2249          0.9861608          0.9861608          0.9986455
## 2250          0.8073374          0.8955353          0.8777962
##      RDA_Va_sal_prop_corr RDA_TPR RDA_TPR_corr RDA_FDR_allSNPs
## 2245          0.7328738 0.6000000          0.6000000          0.9931193
## 2246          0.9998981 0.8333333          0.8333333          0.9929478
## 2247          0.9412170 0.8333333          0.6666667          0.9968133

```

##	2248	0.8820640	0.8571429	0.8571429	0.9963280
##	2249	0.9986455	0.8888889	0.8888889	0.9944328
##	2250	0.9096928	0.5000000	0.6250000	0.9838710
##		RDA_FDR_allSNPs_corr	num_RDA_sig_causal	num_RDA_sig_neutral	
##	2245	0.9934211	3		118
##	2246	0.9932249	5		230
##	2247	0.9972318	5		573
##	2248	0.9955720	6		597
##	2249	0.9951190	8		479
##	2250	0.9814815	4		62
##		num_RDA_sig_causal_corr	num_RDA_sig_neutral_corr	RDA_FDR_neutSNPs	
##	2245		3	152	0.9752066
##	2246		5	244	0.9787234
##	2247		4	523	0.9913495
##	2248		6	486	0.9900498
##	2249		8	498	0.9835729
##	2250		5	92	0.9393939
##		RDA_FDR_neutSNPs_corr	RDA_AUCPR_allSNPs	RDA_AUCPR_neutSNPs	
##	2245	0.9806452	0.1317274		0.6023902
##	2246	0.9799197	0.3896916		0.6725673
##	2247	0.9924099	0.1915153		0.5139129
##	2248	0.9878049	0.3830535		0.8575997
##	2249	0.9841897	0.1615562		0.6298882
##	2250	0.9484536	0.2032180		0.5029961
##		RDA_AUCPR_neutSNPs_corr	RDA_FPR_neutSNPs	RDA_FPR_neutSNPs_corr	
##	2245	0.2991643	0.02030981		0.02616179
##	2246	0.6819382	0.01862952		0.01976349
##	2247	0.5028327	0.04464703		0.04075113
##	2248	0.8575851	0.03743886		0.03047786
##	2249	0.6418724	0.03053095		0.03174198
##	2250	0.3320560	0.01570813		0.02330884
##		RDA_RDAmutpred_cor_tempEffect	RDA_RDAmutpred_cor_salEffect		
##	2245	0.6000000		0.6000000	
##	2246	0.8666667		0.6000000	
##	2247	0.6000000		0.6000000	
##	2248	0.5238095		0.3333333	
##	2249	0.5555556		0.7777778	
##	2250	0.5000000		0.2857143	
##		RDA_absRDAmutpred_cor_tempVa	RDA_absRDAmutpred_cor_salVa		
##	2245	0.020465239		0.01871735	
##	2246	0.011409116		0.01826038	
##	2247	0.002784945		0.01793393	
##	2248	0.017384447		0.02012018	
##	2249	0.017285637		0.01862984	
##	2250	0.020696744		0.02400657	
##		RDA_RDAmutpred_cor_tempEffect_structcorr			
##	2245		0.36606915		
##	2246		-0.07001212		
##	2247		-0.07228499		
##	2248		0.15434486		
##	2249		0.12235804		
##	2250		0.27521121		
##		RDA_RDAmutpred_cor_salEffect_structcorr			
##	2245		0.9208180		

##	2246	0.8150453			
##	2247	0.8026655			
##	2248	0.7288245			
##	2249	0.7696911			
##	2250	0.6602084			
##	RDA_absRDAmutpred_cor_tempVa_structcorr				
##	2245	0.04635961			
##	2246	0.01113341			
##	2247	0.02638952			
##	2248	0.06395474			
##	2249	0.07991070			
##	2250	0.08556552			
##	RDA_absRDAmutpred_cor_salVa_structcorr				
##	2245	0.07122715			
##	2246	0.10423641			
##	2247	0.09238268			
##	2248	0.11222190			
##	2249	0.08011436			
##	2250	0.11534351			
##	RDA_cor_RDA20000temppredict_tempPhen RDA_cor_RDA20000salpredict_salPhen				
##	2245	0.6025624	0.6970451		
##	2246	0.5688492	0.7562831		
##	2247	0.5073146	0.6932780		
##	2248	0.5917726	0.7525031		
##	2249	0.6272143	0.7680113		
##	2250	0.5661217	0.6653819		
##	RDA_cor_RDA20000temppredict_tempPhen_structcorr				
##	2245	0.02969630			
##	2246	0.08385813			
##	2247	0.18613306			
##	2248	0.05323003			
##	2249	0.12648538			
##	2250	0.23854195			
##	RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal				
##	2245	0.2459241	-0.49592948	0.707550286	
##	2246	0.7608327	-0.03745187	0.010848786	
##	2247	0.6778338	-0.42331353	-0.036871726	
##	2248	0.7661762	-0.96800660	-0.035807738	
##	2249	0.7672155	-0.04223546	0.005524909	
##	2250	0.6262283	0.78322231	0.099152034	
##	cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp				
##	2245	-0.79041718	-0.49531715	-0.11538104	-0.196778909
##	2246	-0.93219015	0.01444962	-0.02798592	0.012589562
##	2247	0.85072814	-0.05730822	-0.07053397	-0.038642435
##	2248	-0.01224008	0.01880353	-0.01140580	-0.033516495
##	2249	0.95953676	0.03045830	-0.01491703	0.005465646
##	2250	-0.41323121	-0.29453651	0.36840281	-0.066577901
##	cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp				
##	2245	-0.59810083	0.90723798	-0.7652270	-0.41739868
##	2246	-0.01327245	0.99957697	0.9980697	-0.01001944
##	2247	-0.04185963	0.92380303	0.9857150	0.37884682
##	2248	NA	0.02513634	0.9995552	-0.99878157
##	2249	-0.01555213	0.99870326	-0.9987481	0.02746745
##	2250	NA	0.80908546	-0.9986383	0.58076635

```
##      cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase
## 2245      -6.375626e-01      1.0000000      0.8000000      0.9982047
## 2246      5.599139e-02      1.0000000      0.6666667      0.9990089
## 2247      1.607696e-01      1.0000000      0.3333333      0.9990226
## 2248      -6.278494e-05      1.0000000      0.7142857      0.9987023
## 2249      2.751841e-02      0.8888889      1.0000000      0.9985967
## 2250      -2.590842e-02      0.7500000      0.8750000      0.9975440
##      gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines
## 2245      0.9944828      0.3144330
## 2246      0.9959225      0.4234528
## 2247      0.9990610      0.3182527
## 2248      0.9943439      0.1227848
## 2249      0.9601770      0.2232947
## 2250      0.9964340      0.5333333
##      clinalparadigm_temp_proptop5GWASclines
## 2245      0.2817869
## 2246      0.2060261
## 2247      0.1224649
## 2248      0.2430380
## 2249      0.1273312
## 2250      0.2074074
##      clinalparadigm_sal_propsigGWASclines clinalparadigm_temp_propsigGWASclines
## 2245      0.23302128      0.2378011
## 2246      0.06177726      0.1958369
## 2247      0.03441465      0.1351293
## 2248      0.01704694      0.2437673
## 2249      0.02904430      0.1463104
## 2250      0.09349593      0.2850657
```

```
load("src/Ob-final_params-20220428.RData")
sims.df <- final
head(sims.df)
```

```
##                                     level reps
## 1  highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 11      highly-polygenic_1-trait__Est-Clines_N-cline-N-to-S_m-constant      1
## 21      highly-polygenic_1-trait__Est-Clines_N-equal_m_breaks      1
## 31      highly-polygenic_1-trait__Est-Clines_N-equal_m-constant      1
## 41      highly-polygenic_1-trait__Est-Clines_N-variable_m-variable      1
## 51  highly-polygenic_1-trait__SS-Clines_N-cline-center-to-edge_m-constant      1
##      arch      demog_name
## 1  highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 11 highly-polygenic_1-trait      Est-Clines_N-cline-N-to-S_m-constant
## 21 highly-polygenic_1-trait      Est-Clines_N-equal_m_breaks
## 31 highly-polygenic_1-trait      Est-Clines_N-equal_m-constant
## 41 highly-polygenic_1-trait      Est-Clines_N-variable_m-variable
## 51 highly-polygenic_1-trait  SS-Clines_N-cline-center-to-edge_m-constant
##      demog_level_sub demog_level MIG_x MIG_y xcline ycline
## 1  N-cline-center-to-edge_m-constant Est-Clines 0.49 0.07 linear linear
## 11      N-cline-N-to-S_m-constant Est-Clines 0.49 0.07 linear linear
## 21      N-equal_m_breaks Est-Clines 0.49 0.07 linear linear
## 31      N-equal_m-constant Est-Clines 0.49 0.07 linear linear
## 41      N-variable_m-variable Est-Clines 0.49 0.07 linear linear
## 51 N-cline-center-to-edge_m-constant  SS-Clines 0.03 0.03 linear linear
```

```
##      demog METAPOP_SIDE_x METAPOP_SIDE_y Nequal isVariableM MIG_breaks
## 1  Estuary             10             10      4           0           0
## 11 Estuary             10             10      2           0           0
## 21 Estuary             10             10      0           0           1
## 31 Estuary             10             10      0           0           0
## 41 Estuary             10             10      3           1           0
## 51      SS             10             10      4           0           0
##      arch_level_sub      arch_level MU_base MU_QTL_proportion SIGMA_QTN_1
## 1      1-trait highly-polygenic 1e-07           0.25           0.002
## 11     1-trait highly-polygenic 1e-07           0.25           0.002
## 21     1-trait highly-polygenic 1e-07           0.25           0.002
## 31     1-trait highly-polygenic 1e-07           0.25           0.002
## 41     1-trait highly-polygenic 1e-07           0.25           0.002
## 51     1-trait highly-polygenic 1e-07           0.25           0.002
##      SIGMA_QTN_2 SIGMA_K_1 SIGMA_K_2 N_traits ispleiotropy      seed
## 1      0.002      0.5      0.5      1           0 1231094
## 11     0.002      0.5      0.5      1           0 1231095
## 21     0.002      0.5      0.5      1           0 1231096
## 31     0.002      0.5      0.5      1           0 1231097
## 41     0.002      0.5      0.5      1           0 1231098
## 51     0.002      0.5      0.5      1           0 1231099
```

```
final.df <- merge(sims.df, out.df, all.x=TRUE)
head(final.df)
```

```
##      seed
## 1 1231094
## 2 1231095
## 3 1231096
## 4 1231097
## 5 1231098
## 6 1231099
##
##                                     level reps
## 1 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 2      highly-polygenic_1-trait__Est-Clines_N-cline-N-to-S_m-constant      1
## 3              highly-polygenic_1-trait__Est-Clines_N-equal_m_breaks      1
## 4              highly-polygenic_1-trait__Est-Clines_N-equal_m-constant      1
## 5              highly-polygenic_1-trait__Est-Clines_N-variable_m-variable      1
## 6 highly-polygenic_1-trait__SS-Clines_N-cline-center-to-edge_m-constant      1
##      arch      demog_name
## 1 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 2 highly-polygenic_1-trait      Est-Clines_N-cline-N-to-S_m-constant
## 3 highly-polygenic_1-trait      Est-Clines_N-equal_m_breaks
## 4 highly-polygenic_1-trait      Est-Clines_N-equal_m-constant
## 5 highly-polygenic_1-trait      Est-Clines_N-variable_m-variable
## 6 highly-polygenic_1-trait  SS-Clines_N-cline-center-to-edge_m-constant
##      demog_level_sub demog_level MIG_x MIG_y xcline ycline
## 1 N-cline-center-to-edge_m-constant Est-Clines 0.49 0.07 linear linear
## 2      N-cline-N-to-S_m-constant Est-Clines 0.49 0.07 linear linear
## 3              N-equal_m_breaks Est-Clines 0.49 0.07 linear linear
## 4              N-equal_m-constant Est-Clines 0.49 0.07 linear linear
## 5              N-variable_m-variable Est-Clines 0.49 0.07 linear linear
## 6 N-cline-center-to-edge_m-constant  SS-Clines 0.03 0.03 linear linear
##      demog METAPOP_SIDE_x METAPOP_SIDE_y Nequal isVariableM MIG_breaks
```

## 1	Estuary	10	10	4	0	0		
## 2	Estuary	10	10	2	0	0		
## 3	Estuary	10	10	0	0	1		
## 4	Estuary	10	10	0	0	0		
## 5	Estuary	10	10	3	1	0		
## 6	SS	10	10	4	0	0		
##	arch_level_sub	arch_level	MU_base	MU_QTL_proportion	SIGMA_QTN_1			
## 1	1-trait	highly-polygenic	1e-07	0.25	0.002			
## 2	1-trait	highly-polygenic	1e-07	0.25	0.002			
## 3	1-trait	highly-polygenic	1e-07	0.25	0.002			
## 4	1-trait	highly-polygenic	1e-07	0.25	0.002			
## 5	1-trait	highly-polygenic	1e-07	0.25	0.002			
## 6	1-trait	highly-polygenic	1e-07	0.25	0.002			
##	SIGMA_QTN_2	SIGMA_K_1	SIGMA_K_2	N_traits	ispleiotropy	n_samp_tot		
## 1	0.002	0.5	0.5	1	0	1000		
## 2	0.002	0.5	0.5	1	0	1000		
## 3	0.002	0.5	0.5	1	0	1000		
## 4	0.002	0.5	0.5	1	0	1000		
## 5	0.002	0.5	0.5	1	0	1000		
## 6	0.002	0.5	0.5	1	0	1000		
##	n_samp_per_pop	sd_fitness_among_inds	sd_fitness_among_pops	final_LA	K			
## 1	10	0.05272602	0.01977273	0.500854	2			
## 2	10	0.04519923	0.01541145	0.505075	9			
## 3	10	0.05348903	0.02022721	0.499265	9			
## 4	10	0.05446050	0.01731323	0.499365	9			
## 5	10	0.05093029	0.01832588	0.501054	6			
## 6	10	0.07552882	0.02341833	0.478131	3			
##	Bonf_alpha	numCausalLowMAFsample	all_corr_phen_temp	subsamp_corr_phen_temp				
## 1	1.918428e-06	39	0.9545790	0.8893387				
## 2	1.730523e-06	104	0.9545764	0.9006961				
## 3	1.508614e-06	22	0.9723022	0.8873320				
## 4	1.531065e-06	24	0.9720233	0.8895298				
## 5	6.395498e-06	12	0.9708565	0.8921410				
## 6	2.022981e-06	34	0.9247450	0.8525464				
##	all_corr_phen_sal	subsamp_corr_phen_sal	num_causal_prefilter					
## 1	NA	NA	2628					
## 2	NA	NA	3144					
## 3	NA	NA	3149					
## 4	NA	NA	3131					
## 5	NA	NA	1823					
## 6	NA	NA	2948					
##	num_causal_postfilter	num_non_causal	num_neut_prefilter	num_neut_postfilter				
## 1	310	25753	26587	26587				
## 2	382	28511	30284	30284				
## 3	482	32661	33031	33031				
## 4	470	32187	32548	32548				
## 5	257	7561	7753	7753				
## 6	364	24352	25004	25004				
##	num_neut_neutralgenome	num_causal_temp	num_causal_sal	num_multiallelic				
## 1	12867	310	0	0				
## 2	14060	382	0	0				
## 3	16379	480	0	0				
## 4	16243	469	0	0				
## 5	3749	257	0	0				

## 6	12197	364	0	0
##	meanFst	va_temp_total	va_sal_total	Va_temp_sample
## 1	0.18039488	0.01185008	0	0.01356519
## 2	0.16985797	0.01343736	0	0.01276814
## 3	0.13396101	0.01405264	0	0.01370501
## 4	0.08714633	0.01337458	0	0.01305077
## 5	0.31813358	0.01605415	0	0.01622973
## 6	0.12616527	0.01930127	0	0.02072472
##	median_causal_temp_cor	median_causal_sal_cor	median_neut_temp_cor	
## 1	0.3580437	NA	0.3820531	
## 2	0.4138162	NA	0.4536498	
## 3	0.4157033	NA	0.4029319	
## 4	0.4112619	NA	0.3451512	
## 5	0.3925022	NA	0.4432208	
## 6	0.2974287	NA	0.2243095	
##	median_neut_sal_cor	cor_VA_temp_prop	cor_VA_sal_prop	cor_TPR_temp
## 1	0.04816897	0.8451605	0	0.4612903
## 2	0.04175877	0.7846421	0	0.5314136
## 3	0.03844065	0.7830061	0	0.5416667
## 4	0.04529330	0.7631297	0	0.5351812
## 5	0.05141380	0.8171677	0	0.5408560
## 6	0.19531471	0.6459740	0	0.3076923
##	cor_FDR_allSNPs_temp	cor_FDR_neutSNPs_temp	cor_FDR_allSNPs_sal	
## 1	0.9894449	0.9791241	NA	
## 2	0.9886134	0.9769893	NA	
## 3	0.9854586	0.9711015	NA	
## 4	0.9833466	0.9669693	1	
## 5	0.9711199	0.9447316	NA	
## 6	0.9813892	0.9575114	1	
##	cor_FDR_neutSNPs_sal	num_causal_sig_temp_corr	num_causal_sig_sal_corr	
## 1	NA	143	0	
## 2	NA	203	0	
## 3	NA	260	0	
## 4	NA	251	0	
## 5	NA	139	0	
## 6	1	112	0	
##	num_notCausal_sig_temp_corr	num_notCausal_sig_sal_corr	num_neut_sig_temp_corr	
## 1	13405	0	6707	
## 2	17625	0	8619	
## 3	17620	0	8737	
## 4	14821	1	7348	
## 5	4674	0	2376	
## 6	5906	4344	2524	
##	num_neut_sig_sal_corr	cor_AUCPR_temp_allSNPs	cor_AUCPR_temp_neutSNPs	
## 1	0	0.01064045	0.02148047	
## 2	0	0.01053868	0.02130552	
## 3	0	0.01286086	0.02546132	
## 4	0	0.01566591	0.03219810	
## 5	0	0.02696219	0.05312152	
## 6	2133	0.02255358	0.06178401	
##	cor_AUCPR_sal_allSNPs	cor_AUCPR_sal_neutSNPs	cor_af_temp_noutliers	
## 1	NA	NA	13548	
## 2	NA	NA	17828	
## 3	NA	NA	17880	

## 4	NA	NA	15072
## 5	NA	NA	4813
## 6	NA	NA	6018
##	cor_af_sal_noutliers	cor_FPR_temp_neutSNPs	cor_FPR_sal_neutSNPs
## 1	0	0.5212559	0.0000000
## 2	0	0.6130156	0.0000000
## 3	0	0.5334269	0.0000000
## 4	1	0.4523795	0.0000000
## 5	0	0.6337690	0.0000000
## 6	4344	0.2069361	0.1748791
##	LEA3.2_lfmm2_Va_temp_prop	LEA3.2_lfmm2_Va_sal_prop	LEA3.2_lfmm2_TPR_temp
## 1	0.27826502	NA	0.022580645
## 2	0.00000000	NA	0.000000000
## 3	0.00000000	NA	0.000000000
## 4	0.00000000	NA	0.000000000
## 5	0.03610723	NA	0.003891051
## 6	0.17163124	NA	0.005494505
##	LEA3.2_lfmm2_TPR_sal	LEA3.2_lfmm2_FDR_allSNPs_temp	
## 1	NA	0.9789790	
## 2	NA	NA	
## 3	NA	NA	
## 4	NA	1.0000000	
## 5	NA	0.9500000	
## 6	NA	0.8666667	
##	LEA3.2_lfmm2_FDR_allSNPs_sal	LEA3.2_lfmm2_FDR_neutSNPs_temp	
## 1	NA	0.9263158	
## 2	1	NA	
## 3	1	NA	
## 4	NA	1.0000000	
## 5	NA	0.8750000	
## 6	NA	0.0000000	
##	LEA3.2_lfmm2_FDR_neutSNPs_sal	LEA3.2_lfmm2_AUCPR_temp_allSNPs	
## 1	NA	0.01339495	
## 2	NA	0.01367013	
## 3	NA	0.01426730	
## 4	NA	0.01310529	
## 5	NA	0.03463172	
## 6	NA	0.01437720	
##	LEA3.2_lfmm2_AUCPR_temp_neutSNPs	LEA3.2_lfmm2_AUCPR_sal_allSNPs	
## 1	0.02655237	NA	
## 2	0.02786249	NA	
## 3	0.02851768	NA	
## 4	0.02513767	NA	
## 5	0.06672248	NA	
## 6	0.02928224	NA	
##	LEA3.2_lfmm2_AUCPR_sal_neutSNPs	LEA3.2_lfmm2_mlog10P_tempenv_noutliers	
## 1	NA	333	
## 2	NA	0	
## 3	NA	0	
## 4	NA	6	
## 5	NA	20	
## 6	NA	15	
##	LEA3.2_lfmm2_mlog10P_salenv_noutliers	LEA3.2_lfmm2_num_causal_sig_temp	
## 1	0	7	

## 2		1		0	
## 3		1		0	
## 4		0		0	
## 5		0		1	
## 6		0		2	
##	LEA3.2_lfmm2_num_neut_sig_temp	LEA3.2_lfmm2_num_causal_sig_sal			
## 1	88		0		
## 2	0		0		
## 3	0		0		
## 4	2		0		
## 5	7		0		
## 6	0		0		
##	LEA3.2_lfmm2_num_neut_sig_sal	LEA3.2_lfmm2_FPR_neutSNPs_temp			
## 1	0	0.006839201			
## 2	0	0.000000000			
## 3	0	0.000000000			
## 4	0	0.000123130			
## 5	0	0.001867165			
## 6	0	0.000000000			
##	LEA3.2_lfmm2_FPR_neutSNPs_sal	RDA1_propvar	RDA2_propvar	RDA1_propvar_corr	
## 1	0	0.985	0.015	0.765	
## 2	0	0.989	0.011	0.835	
## 3	0	0.988	0.012	0.842	
## 4	0	0.980	0.020	0.841	
## 5	0	0.991	0.009	0.816	
## 6	0	0.596	0.404	0.597	
##	RDA2_propvar_corr	RDA1_temp_cor	RDA1_sal_cor	RDA2_temp_cor	RDA2_sal_cor
## 1	0.235	0.9999982	0.001912722	-0.001912722	0.9999982
## 2	0.165	0.9999971	0.002425692	-0.002425692	0.9999971
## 3	0.158	0.9999982	0.001888450	-0.001888450	0.9999982
## 4	0.159	0.9999700	-0.007739672	0.007739672	0.9999700
## 5	0.184	0.9999640	0.008484251	-0.008484251	0.9999640
## 6	0.403	-0.9360957	0.351745296	-0.351745296	-0.9360957
##	RDA_Va_temp_prop	RDA_Va_temp_prop_corr	RDA_Va_sal_prop	RDA_Va_sal_prop_corr	
## 1	0.1248244	0.000000000	0	0	
## 2	0.3566111	0.017427370	0	0	
## 3	0.1750594	0.000000000	0	0	
## 4	0.1339135	0.000000000	0	0	
## 5	0.3123098	0.036329553	0	0	
## 6	0.3414487	0.004385126	0	0	
##	RDA_TPR	RDA_TPR_corr	RDA_FDR_allSNPs	RDA_FDR_allSNPs_corr	
## 1	0.006451613	0.000000000	0.9918699	1.0000000	
## 2	0.041884817	0.015706806	0.9953502	0.9966979	
## 3	0.010373444	0.000000000	0.9957519	1.0000000	
## 4	0.014893617	0.000000000	0.9941812	1.0000000	
## 5	0.073929961	0.015564202	0.9850039	0.9833333	
## 6	0.027472527	0.002747253	0.9889258	0.9979550	
##	num_RDA_sig_causal	num_RDA_sig_neutral	num_RDA_sig_causal_corr		
## 1	2	118	0		
## 2	16	1545	6		
## 3	5	526	0		
## 4	7	557	0		
## 5	19	583	4		
## 6	10	271	1		

##	num_RDA_sig_neutral_corr	RDA_FDR_neutSNPs	RDA_FDR_neutSNPs_corr	
## 1	200	0.9833333	1.0000000	
## 2	867	0.9897502	0.9931271	
## 3	458	0.9905838	1.0000000	
## 4	577	0.9875887	1.0000000	
## 5	122	0.9684385	0.9682540	
## 6	213	0.9644128	0.9953271	
##	RDA_AUCPR_allSNPs	RDA_AUCPR_neutSNPs	RDA_AUCPR_neutSNPs_corr	RDA_FPR_neutSNPs
## 1	0.008249728	0.01647883	0.01597697	0.009170747
## 2	0.008916531	0.01857113	0.01824752	0.109886202
## 3	0.009025124	0.01784801	0.01820267	0.032114293
## 4	0.009215389	0.01812750	0.01825734	0.034291695
## 5	0.025358473	0.05094037	0.05046366	0.155508136
## 6	0.014302424	0.02930863	0.01982718	0.022218578
##	RDA_FPR_neutSNPs_corr	RDA_RDAmutpred_cor_tempEffect		
## 1	0.01554364	0.2566239		
## 2	0.06166430	0.2709340		
## 3	0.02796264	0.3199777		
## 4	0.03552299	0.3397117		
## 5	0.03254201	0.2064143		
## 6	0.01746331	0.2864279		
##	RDA_RDAmutpred_cor_salEffect	RDA_absRDAmutpred_cor_tempVa		
## 1	NA	-0.04251831		
## 2	NA	-0.06383708		
## 3	NA	-0.06156140		
## 4	NA	-0.04360391		
## 5	NA	-0.05007068		
## 6	NA	-0.02697188		
##	RDA_absRDAmutpred_cor_salVa	RDA_RDAmutpred_cor_tempEffect_structcorr		
## 1	NA	0.1711607		
## 2	NA	0.1695575		
## 3	NA	0.2590273		
## 4	NA	0.1412525		
## 5	NA	0.2089774		
## 6	NA	0.1483359		
##	RDA_RDAmutpred_cor_salEffect_structcorr			
## 1	NA			
## 2	NA			
## 3	NA			
## 4	NA			
## 5	NA			
## 6	NA			
##	RDA_absRDAmutpred_cor_tempVa_structcorr			
## 1	0.002950593			
## 2	0.011548773			
## 3	-0.006744183			
## 4	-0.006811228			
## 5	0.018943112			
## 6	0.011844784			
##	RDA_absRDAmutpred_cor_salVa_structcorr	RDA_cor_RDA20000temppredict_tempPhen		
## 1	NA	0.8530879		
## 2	NA	0.8661742		
## 3	NA	0.8458619		
## 4	NA	0.8566006		

## 5	NA	0.8297057
## 6	NA	0.8109670
## RDA_cor_RDA20000salpredict_salPhen		
## 1	NA	
## 2	NA	
## 3	NA	
## 4	NA	
## 5	NA	
## 6	NA	
## RDA_cor_RDA20000temppredict_tempPhen_structcorr		
## 1	-0.03541745	
## 2	0.02470470	
## 3	0.12927728	
## 4	0.04149750	
## 5	0.11539940	
## 6	0.15610811	
## RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal		
## 1	NA -0.9938219 -0.002423473	
## 2	NA -0.9763521 -0.002856465	
## 3	NA -0.9806495 -0.001193085	
## 4	NA -0.9894438 0.006933632	
## 5	NA -0.9624753 -0.006417090	
## 6	NA -0.9180515 0.333573860	
## cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp		
## 1	-0.02040717 -0.001688470 0.07027960 -0.001851458 -0.23741491	
## 2	0.15699463 0.006663054 -0.64036018 -0.002311619 0.16118062	
## 3	0.02289691 -0.002251339 -0.05164944 -0.001922661 -0.66955922	
## 4	-0.03159957 -0.011695024 0.09041291 -0.007667182 -0.49064055	
## 5	0.18621652 0.005399774 -0.64151191 -0.008355460 0.20361826	
## 6	-0.33266762 -0.910485583 0.14489884 -0.108366523 -0.05450648	
## cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp		
## 1	-0.002823011 -0.09231664 0.9995526 0.9926958	
## 2	-0.000199728 0.75497199 0.9963113 0.6504534	
## 3	-0.002378429 0.07609171 0.9999081 0.9968609	
## 4	0.011008515 -0.12306538 -0.9998272 0.9916547	
## 5	-0.005102881 0.79034742 0.9976490 0.5947952	
## 6	-0.018196703 -0.47679972 -0.9712646 0.8782899	
## cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase		
## 1	0.001339894 NA 0.2290323 NA	
## 2	0.084015793 NA 0.3272251 NA	
## 3	0.004567194 NA 0.3270833 NA	
## 4	0.004580758 NA 0.2430704 NA	
## 5	0.060281782 NA 0.4202335 NA	
## 6	-0.236378957 NA 0.2252747 NA	
## gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines		
## 1	0.9667914 NA	
## 2	0.9696749 NA	
## 3	0.9616699 NA	
## 4	0.9497354 NA	
## 5	0.9174312 NA	
## 6	0.9382065 NA	
## clinalparadigm_temp_proptop5GWASclines clinalparadigm_sal_propsigGWASclines		
## 1	0.6554106 NA	
## 2	0.5384083 NA	

## 3	0.5530760	NA
## 4	0.5021433	NA
## 5	0.5882353	NA
## 6	0.3446602	NA
## clinalparadigm_temp_propsigGWASclines		
## 1	0.6050302	
## 2	0.5794083	
## 3	0.5593769	
## 4	0.4777563	
## 5	0.6314615	
## 6	0.3099063	

```
(vars <- t(final.df[1,]))
```

##	1
## seed	"1231094"
## level	"highly-polygenic_1-trait__Est-Clines_N-cline-center"
## reps	"1"
## arch	"highly-polygenic_1-trait"
## demog_name	"Est-Clines_N-cline-center-to-edge_m-constant"
## demog_level_sub	"N-cline-center-to-edge_m-constant"
## demog_level	"Est-Clines"
## MIG_x	"0.49"
## MIG_y	"0.07"
## xcline	"linear"
## ycline	"linear"
## demog	"Estuary"
## METAPOP_SIDE_x	"10"
## METAPOP_SIDE_y	"10"
## Nequal	"4"
## isVariableM	"0"
## MIG_breaks	"0"
## arch_level_sub	"1-trait"
## arch_level	"highly-polygenic"
## MU_base	"1e-07"
## MU_QTL_proportion	"0.25"
## SIGMA_QTN_1	"0.002"
## SIGMA_QTN_2	"0.002"
## SIGMA_K_1	"0.5"
## SIGMA_K_2	"0.5"
## N_traits	"1"
## ispleiotropy	"0"
## n_samp_tot	"1000"
## n_samp_per_pop	"10"
## sd_fitness_among_inds	"0.05272602"
## sd_fitness_among_pops	"0.01977273"
## final_LA	"0.500854"
## K	"2"
## Bonf_alpha	"1.918428e-06"
## numCausalLowMAFsample	"39"
## all_corr_phen_temp	"0.954579"
## subsamp_corr_phen_temp	"0.8893387"
## all_corr_phen_sal	NA
## subsamp_corr_phen_sal	NA

## num_causal_prefilter	"2628"
## num_causal_postfilter	"310"
## num_non_causal	"25753"
## num_neut_prefilter	"26587"
## num_neut_postfilter	"26587"
## num_neut_neutralgenome	"12867"
## num_causal_temp	"310"
## num_causal_sal	"0"
## num_multiallelic	"0"
## meanFst	"0.1803949"
## va_temp_total	"0.01185008"
## va_sal_total	"0"
## Va_temp_sample	"0.01356519"
## Va_sal_sample	"0"
## nSNPs	"26063"
## median_causal_temp_cor	"0.3580437"
## median_causal_sal_cor	NA
## median_neut_temp_cor	"0.3820531"
## median_neut_sal_cor	"0.04816897"
## cor_VA_temp_prop	"0.8451605"
## cor_VA_sal_prop	"0"
## cor_TPR_temp	"0.4612903"
## cor_TPR_sal	NA
## cor_FDR_allSNPs_temp	"0.9894449"
## cor_FDR_neutSNPs_temp	"0.9791241"
## cor_FDR_allSNPs_sal	NA
## cor_FDR_neutSNPs_sal	NA
## num_causal_sig_temp_corr	"143"
## num_causal_sig_sal_corr	"0"
## num_notCausal_sig_temp_corr	"13405"
## num_notCausal_sig_sal_corr	"0"
## num_neut_sig_temp_corr	"6707"
## num_neut_sig_sal_corr	"0"
## cor_AUCPR_temp_allSNPs	"0.01064045"
## cor_AUCPR_temp_neutSNPs	"0.02148047"
## cor_AUCPR_sal_allSNPs	NA
## cor_AUCPR_sal_neutSNPs	NA
## cor_af_temp_noutliers	"13548"
## cor_af_sal_noutliers	"0"
## cor_FPR_temp_neutSNPs	"0.5212559"
## cor_FPR_sal_neutSNPs	"0"
## LEA3.2_lfmm2_Va_temp_prop	"0.278265"
## LEA3.2_lfmm2_Va_sal_prop	NA
## LEA3.2_lfmm2_TPR_temp	"0.02258065"
## LEA3.2_lfmm2_TPR_sal	NA
## LEA3.2_lfmm2_FDR_allSNPs_temp	"0.978979"
## LEA3.2_lfmm2_FDR_allSNPs_sal	NA
## LEA3.2_lfmm2_FDR_neutSNPs_temp	"0.9263158"
## LEA3.2_lfmm2_FDR_neutSNPs_sal	NA
## LEA3.2_lfmm2_AUCPR_temp_allSNPs	"0.01339495"
## LEA3.2_lfmm2_AUCPR_temp_neutSNPs	"0.02655237"
## LEA3.2_lfmm2_AUCPR_sal_allSNPs	NA
## LEA3.2_lfmm2_AUCPR_sal_neutSNPs	NA
## LEA3.2_lfmm2_mlog10P_tempenv_noutliers	"333"

## LEA3.2_lfmm2_mlog10P_salenv_noutliers	"0"
## LEA3.2_lfmm2_num_causal_sig_temp	"7"
## LEA3.2_lfmm2_num_neut_sig_temp	"88"
## LEA3.2_lfmm2_num_causal_sig_sal	"0"
## LEA3.2_lfmm2_num_neut_sig_sal	"0"
## LEA3.2_lfmm2_FPR_neutSNPs_temp	"0.006839201"
## LEA3.2_lfmm2_FPR_neutSNPs_sal	"0"
## RDA1_propvar	"0.985"
## RDA2_propvar	"0.015"
## RDA1_propvar_corr	"0.765"
## RDA2_propvar_corr	"0.235"
## RDA1_temp_cor	"0.9999982"
## RDA1_sal_cor	"0.001912722"
## RDA2_temp_cor	"-0.001912722"
## RDA2_sal_cor	"0.9999982"
## RDA_Va_temp_prop	"0.1248244"
## RDA_Va_temp_prop_corr	"0"
## RDA_Va_sal_prop	"0"
## RDA_Va_sal_prop_corr	"0"
## RDA_TPR	"0.006451613"
## RDA_TPR_corr	"0"
## RDA_FDR_allSNPs	"0.9918699"
## RDA_FDR_allSNPs_corr	"1"
## num_RDA_sig_causal	"2"
## num_RDA_sig_neutral	"118"
## num_RDA_sig_causal_corr	"0"
## num_RDA_sig_neutral_corr	"200"
## RDA_FDR_neutSNPs	"0.9833333"
## RDA_FDR_neutSNPs_corr	"1"
## RDA_AUCPR_allSNPs	"0.008249728"
## RDA_AUCPR_neutSNPs	"0.01647883"
## RDA_AUCPR_neutSNPs_corr	"0.01597697"
## RDA_FPR_neutSNPs	"0.009170747"
## RDA_FPR_neutSNPs_corr	"0.01554364"
## RDA_RDAmutpred_cor_tempEffect	"0.2566239"
## RDA_RDAmutpred_cor_saleEffect	NA
## RDA_absRDAmutpred_cor_tempVa	"-0.04251831"
## RDA_absRDAmutpred_cor_salVa	NA
## RDA_RDAmutpred_cor_tempEffect_structcorr	"0.1711607"
## RDA_RDAmutpred_cor_saleEffect_structcorr	NA
## RDA_absRDAmutpred_cor_tempVa_structcorr	"0.002950593"
## RDA_absRDAmutpred_cor_salVa_structcorr	NA
## RDA_cor_RDA20000temppredict_tempPhen	"0.8530879"
## RDA_cor_RDA20000salpredict_salPhen	NA
## RDA_cor_RDA20000temppredict_tempPhen_structcorr	"-0.03541745"
## RDA_cor_RDA20000salpredict_salPhen_structcorr	NA
## cor_PC1_temp	"-0.9938219"
## cor_PC1_sal	"-0.002423473"
## cor_PC2_temp	"-0.02040717"
## cor_PC2_sal	"-0.00168847"
## cor_LFMMU1_temp	"0.0702796"
## cor_LFMMU1_sal	"-0.001851458"
## cor_LFMMU2_temp	"-0.2374149"
## cor_LFMMU2_sal	"-0.002823011"

```
## cor_PC1_LFMMU1_temp          "-0.09231664"
## cor_PC1_LFMMU1_sal           "0.9995526"
## cor_PC2_LFMMU1_temp         "0.9926958"
## cor_PC2_LFMMU1_sal           "0.001339894"
## gwas_TPR_sal                 NA
## gwas_TPR_temp                "0.2290323"
## gwas_FDR_sal_neutbase        NA
## gwas_FDR_temp_neutbase       "0.9667914"
## clinalparadigm_sal_proptop5GWASclines NA
## clinalparadigm_temp_proptop5GWASclines "0.6554106"
## clinalparadigm_sal_propsigGWASclines NA
## clinalparadigm_temp_propsigGWASclines "0.6050302"
```

```
ref <- final.df[,c("seed", "level", "num_causal_postfilter")]
```

```
### Make sure 10 reps of each simulation
```

```
count <- data.frame(notNA=tapply(final.df$K, final.df$level,
  function(x){sum(!is.na(x))}
))
count
```

##	notNA
## highly-polygenic_1-trait__SS-Mtn_N-equal_m-constant	10
## highly-polygenic_1-trait__SS-Mtn_N-variable_m-variable	10
## highly-polygenic_1-trait__Est-Clines_N-equal_m_breaks	10
## highly-polygenic_1-trait__Est-Clines_N-equal_m-constant	10
## highly-polygenic_1-trait__SS-Clines_N-cline-center-to-edge_m-constant	10
## highly-polygenic_1-trait__SS-Clines_N-equal_m-constant	10
## highly-polygenic_1-trait__SS-Mtn_N-cline-center-to-edge_m-constant	10
## highly-polygenic_1-trait__SS-Clines_N-cline-N-to-S_m-constant	10
## highly-polygenic_1-trait__Est-Clines_N-variable_m-variable	10
## highly-polygenic_1-trait__SS-Clines_N-equal_m_breaks	10
## highly-polygenic_1-trait__SS-Clines_N-variable_m-variable	10
## highly-polygenic_1-trait__SS-Mtn_N-equal_m_breaks	10
## highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant	10
## highly-polygenic_1-trait__Est-Clines_N-cline-N-to-S_m-constant	10
## highly-polygenic_1-trait__SS-Mtn_N-cline-N-to-S_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-cline-N-to-S_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-cline-center-to-edge_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-equal_m_breaks	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-equal_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-variable_m-variable	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-variable_m-variable	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-cline-center-to-edge_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-equal_m_breaks	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-equal_m_breaks	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-equal_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-variable_m-variable	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-cline-N-to-S_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-equal_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-cline-N-to-S_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-cline-center-to-edge_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-unequal-S__SS-Mtn_N-cline-center-to-edge_m-constant	10
## highly-polygenic_2-trait-no-pleiotropy-unequal-S__SS-Clines_N-equal_m_breaks	10

[illegible]

[illegible]

```

## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-cline-N-to-S_m-constant 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-equal_m_breaks 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-cline-center-to-edge_m-constant 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-cline-N-to-S_m-constant 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-variable_m-variable 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-variable_m-variable 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-equal_m-constant 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-cline-N-to-S_m-constant 10
## mod-polygenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-equal_m-constant 10
## oliogenic_1-trait__SS-Clines_N-equal_m-constant 10
## oliogenic_1-trait__SS-Mtn_N-cline-N-to-S_m-constant 10
## oliogenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_1-trait__Est-Clines_N-variable_m-variable 10
## oliogenic_1-trait__Est-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_1-trait__SS-Mtn_N-cline-center-to-edge_m-constant 10
## oliogenic_1-trait__Est-Clines_N-equal_m_breaks 10
## oliogenic_1-trait__Est-Clines_N-equal_m-constant 10
## oliogenic_1-trait__SS-Clines_N-equal_m_breaks 10
## oliogenic_1-trait__SS-Mtn_N-variable_m-variable 10
## oliogenic_1-trait__SS-Mtn_N-equal_m_breaks 10
## oliogenic_1-trait__SS-Clines_N-variable_m-variable 10
## oliogenic_1-trait__SS-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_1-trait__SS-Mtn_N-equal_m-constant 10
## oliogenic_1-trait__SS-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-variable_m-variable 10
## oliogenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-equal_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-equal_m-constant 10
## oliogenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-equal_m_breaks 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Mtn_N-variable_m-variable 10
## oliogenic_2-trait-no-pleiotropy-equal-S__Est-Clines_N-variable_m-variable 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-no-pleiotropy-equal-S__SS-Clines_N-equal_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__Est-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__Est-Clines_N-equal_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Mtn_N-equal_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__Est-Clines_N-variable_m-variable 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__Est-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Mtn_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Clines_N-equal_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Clines_N-variable_m-variable 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Mtn_N-equal_m_breaks 10
## oliogenic_2-trait-no-pleiotropy-unequal-S__Est-Clines_N-equal_m_breaks 10

```

```

## oliogenic_2-trait-no-pleiotropy-unequal-S__SS-Mtn_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__Est-Clines_N-equal_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__Est-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Clines_N-equal_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Mtn_N-equal_m_breaks 10
## oliogenic_2-trait-pleiotropy-equal-S__Est-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Mtn_N-equal_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Mtn_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Mtn_N-variable_m-variable 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Clines_N-variable_m-variable 10
## oliogenic_2-trait-pleiotropy-equal-S__Est-Clines_N-variable_m-variable 10
## oliogenic_2-trait-pleiotropy-equal-S__Est-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-pleiotropy-equal-S__SS-Mtn_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-variable_m-variable 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-equal_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-equal_m_breaks 10
## oliogenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-equal_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-equal_m_breaks 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-cline-N-to-S_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-equal_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__Est-Clines_N-cline-center-to-edge_m-constant 10
## oliogenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-variable_m-variable 10

```

```

### Make sure no NAs in population structure
sum(is.na(final.df$K))

```

```
## [1] 0
```

```

# Check the levels
levels(final.df$demog_level_sub)

```

```

## [1] "N-equal_m-constant" "N-cline-N-to-S_m-constant"
## [3] "N-cline-center-to-edge_m-constant" "N-equal_m_breaks"
## [5] "N-variable_m-variable"

```

```
levels(final.df$arch_level_sub)
```

```

## [1] "1-trait" "2-trait-no-pleiotropy-equal-S"
## [3] "2-trait-no-pleiotropy-unequal-S" "2-trait-pleiotropy-equal-S"
## [5] "2-trait-pleiotropy-unequal-S"

```

Copy graphs

This optional code is for copying figures for one replicate of each of the 225 levels.

GGtheme for all figures

```
ggtheme <- theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), p
```

Color schemes

viridis For SS, SS-Mtn, Estuary mako for demography sub level (m and N) magma for arch_level_sub
rocket for arch_level scale_color_viridis(name="Genic level", discrete=TRUE, option="rocket", begin=0,
end=0.9)

Reorder levels

```
str(final.df$arch_level)
```

```
## Ord.factor w/ 3 levels "highly-polygenic"<...: 1 1 1 1 1 1 1 1 1 1 ...
```

```
levels(final.df$arch_level)
```

```
## [1] "highly-polygenic" "mod-polygenic"      "oligogenic"
```

```
final.df$arch_level <- factor(final.df$arch_level, levels=c( "oligogenic", "mod-polygenic", "highly-polygenic"))
```

```
levels(final.df$arch_level) <- c("oligogenic", "mod.\npolygenic", "highly\npolygenic")  
str(final.df$arch_level)
```

```
## Ord.factor w/ 3 levels "oligogenic"<"mod.\npolygenic"<...: 3 3 3 3 3 3 3 3 3 3 ...
```

```
levels(final.df$arch_level_sub)
```

```
## [1] "1-trait"                                "2-trait-no-pleiotropy-equal-S"  
## [3] "2-trait-no-pleiotropy-unequal-S"      "2-trait-pleiotropy-equal-S"  
## [5] "2-trait-pleiotropy-unequal-S"
```

```
final.df$ispleiotropy <- factor(final.df$ispleiotropy)  
levels(final.df$ispleiotropy) <- c("No pleiotropy", "Pleiotropy")  
head(final.df$ispleiotropy)
```

```
## [1] No pleiotropy No pleiotropy No pleiotropy No pleiotropy No pleiotropy  
## [6] No pleiotropy  
## Levels: No pleiotropy Pleiotropy
```

```
final.df$arch_level_sub <-  
  factor(final.df$arch_level_sub,  
    levels=c("1-trait", "2-trait-no-pleiotropy-equal-S",  
             "2-trait-pleiotropy-equal-S",
```

```

      "2-trait-no-pleiotropy-unequal-S",
      "2-trait-pleiotropy-unequal-S"), ordered=TRUE)

levels(final.df$arch_level_sub) <- c("1 trait", "2 traits, no pleiotropy, equal S",
      "2 traits, pleiotropy, equal S",
      "2 traits, no pleiotropy, unequal S",
      "2 traits, pleiotropy, unequal S")

levels(final.df$arch_level_sub) <- c("1 trait", "2 traits\nno pleiotropy\nequal S",
      "2 traits\npleiotropy\nequal S",
      "2 traits\nno pleiotropy\nunequal S",
      "2 traits\npleiotropy\nunequal S")

final.df$demog_level <- factor(final.df$demog_level, levels=c("SS-Clines", "SS-Mtn", "Est-Clines"), ordered=TRUE)

final.df$demog_level_sub<- factor(final.df$demog_level_sub, levels=c("N-equal_m-constant", "N-equal_m-breaks", "N-cline-N-to-S_m-constant", "N-cline-center-to-edge_m-constant", "N-variable_m-variable"), ordered=TRUE)

final.df$demog_level_sub <- as.factor(final.df$demog_level_sub)

levels(final.df$demog_level_sub)

```

```

## [1] "N-equal_m-constant"          "N-equal_m-breaks"
## [3] "N-cline-N-to-S_m-constant"    "N-cline-center-to-edge_m-constant"
## [5] "N-variable_m-variable"

```

```

levels(final.df$demog_level_sub) <- c("N equal\nm constant", "N equal\nm breaks", "N latitude cline\nm constant", "N central cline\nm constant", "N variable\nm variable")
levels(final.df$demog_level_sub)

```

```

## [1] "N equal\nm constant"          "N equal\nm breaks"
## [3] "N latitude cline\nm constant" "N central cline\nm constant"
## [5] "N variable\nm variable"

```

Plot mean FST

```

### Check for missing data
sum(is.na(final.df$meanFst))

```

```
## [1] 0
```

```
summary(final.df$meanFst)
```

```

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.05211 0.08755 0.13028 0.13349 0.15535 0.49555

```

```
sum(is.na(final.df$arch_level_sub))
```

```
## [1] 0
```

```
sum(is.na(final.df$demog_level))
```

```
## [1] 0
```

```
nrow(final.df)
```

```
## [1] 2250
```

```
### Table of mean FST for different levels - no evidence of missing data
```

```
tapply(final.df$meanFst, list(final.df$demog_level, final.df$demog_level_sub), mean)
```

```
##          N equal\nm constant N equal\nm breaks N latitude cline\nm constant
## SS-Clines      0.05787589      0.08295596      0.1248306
## SS-Mtn         0.06375824      0.08924858      0.1331580
## Est-Clines     0.08761539      0.13069710      0.1582141
##          N central cline\nm constant N variable\nm variable
## SS-Clines      0.1297529      0.1607639
## SS-Mtn         0.1388368      0.1676450
## Est-Clines     0.1872237      0.2897629
```

```
tapply(final.df$meanFst, list(final.df$demog_level, final.df$demog_level_sub), length)
```

```
##          N equal\nm constant N equal\nm breaks N latitude cline\nm constant
## SS-Clines      150      150      150
## SS-Mtn         150      150      150
## Est-Clines     150      150      150
##          N central cline\nm constant N variable\nm variable
## SS-Clines      150      150
## SS-Mtn         150      150
## Est-Clines     150      150
```

```
tapply(final.df$meanFst, list(final.df$demog_level, final.df$arch_level_sub), mean)
```

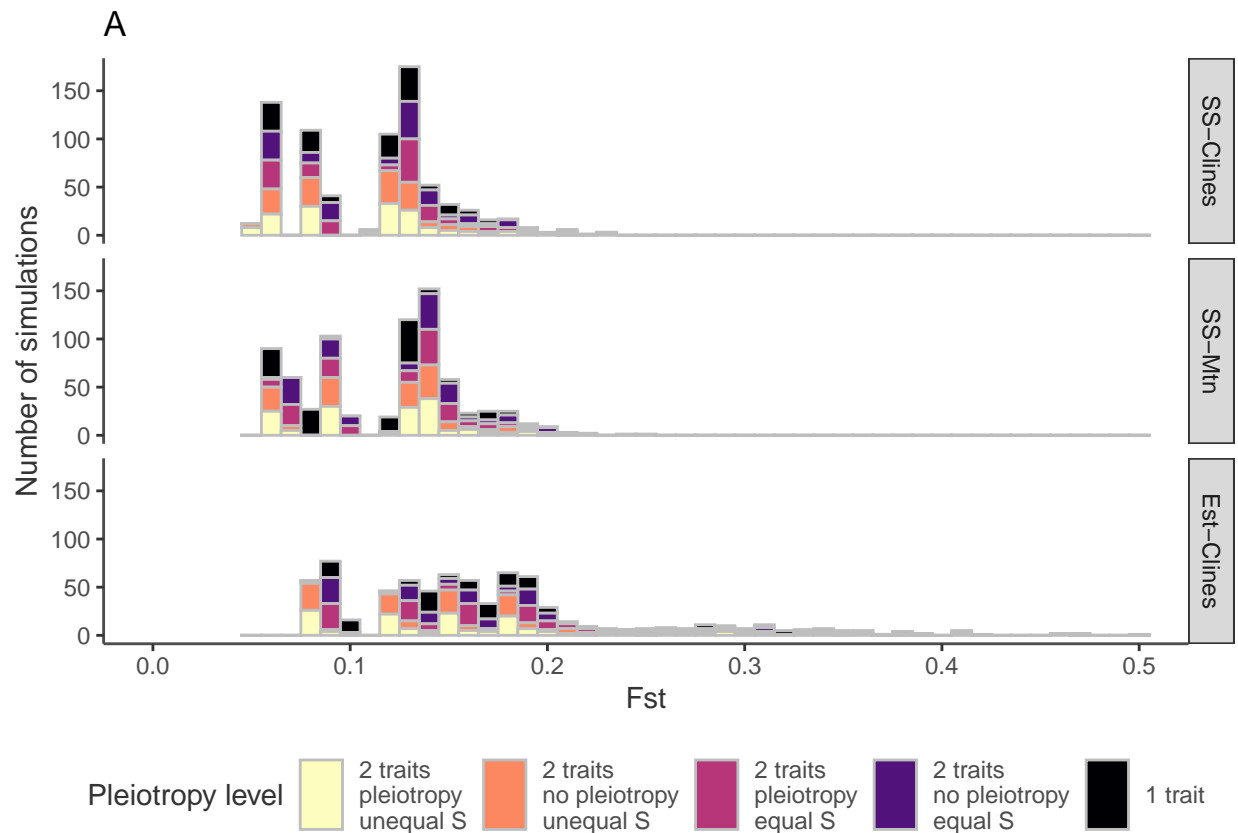
```
##          1 trait 2 traits\nno pleiotropy\nequal S
## SS-Clines 0.1096657      0.1146675
## SS-Mtn    0.1117598      0.1237163
## Est-Clines 0.1824936      0.1767900
##          2 traits\nnpleiotropy\nequal S 2 traits\nno pleiotropy\nunequal S
## SS-Clines      0.1135987      0.1086960
## SS-Mtn         0.1222853      0.1185259
## Est-Clines     0.1682394      0.1629417
##          2 traits\nnpleiotropy\nunequal S
## SS-Clines      0.1095514
## SS-Mtn         0.1163594
## Est-Clines     0.1630485
```

```
tapply(final.df$meanFst, list(final.df$demog_level, final.df$arch_level_sub), length)
```

```
##          1 trait 2 traits\nno pleiotropy\nequal S
## SS-Clines      150                      150
## SS-Mtn         150                      150
## Est-Clines     150                      150
##          2 traits\nnpleiotropy\nequal S 2 traits\nno pleiotropy\nunequal S
## SS-Clines              150                      150
## SS-Mtn                 150                      150
## Est-Clines             150                      150
##          2 traits\nnpleiotropy\nunequal S
## SS-Clines              150
## SS-Mtn                 150
## Est-Clines             150
```

Distribution of FST as a function of architecture

```
f <- ggplot(final.df) + geom_histogram(aes(x=meanFst, fill=arch_level_sub), binwidth=0.01, color="grey")
  coord_cartesian(xlim = c(0.0, 0.5)) + # does not give an error for bins with missing values
  #xlim(0,0.5) + #gives an error for bins with missing values
  facet_grid(demog_level~.) + scale_fill_viridis(option="magma", discrete=TRUE, name="Pleiotropy level")
f
```



```
pdf(paste0(outputs,"FST_Demog.pdf"), width=8, height=6)
```

Distribution of FST as a function of demography

```
ggplot(final.df) + geom_histogram(aes(x=meanFst, fill=demog_level_sub), binwidth=0.01, color="grey",
  dev.off()
```

```
## pdf
```

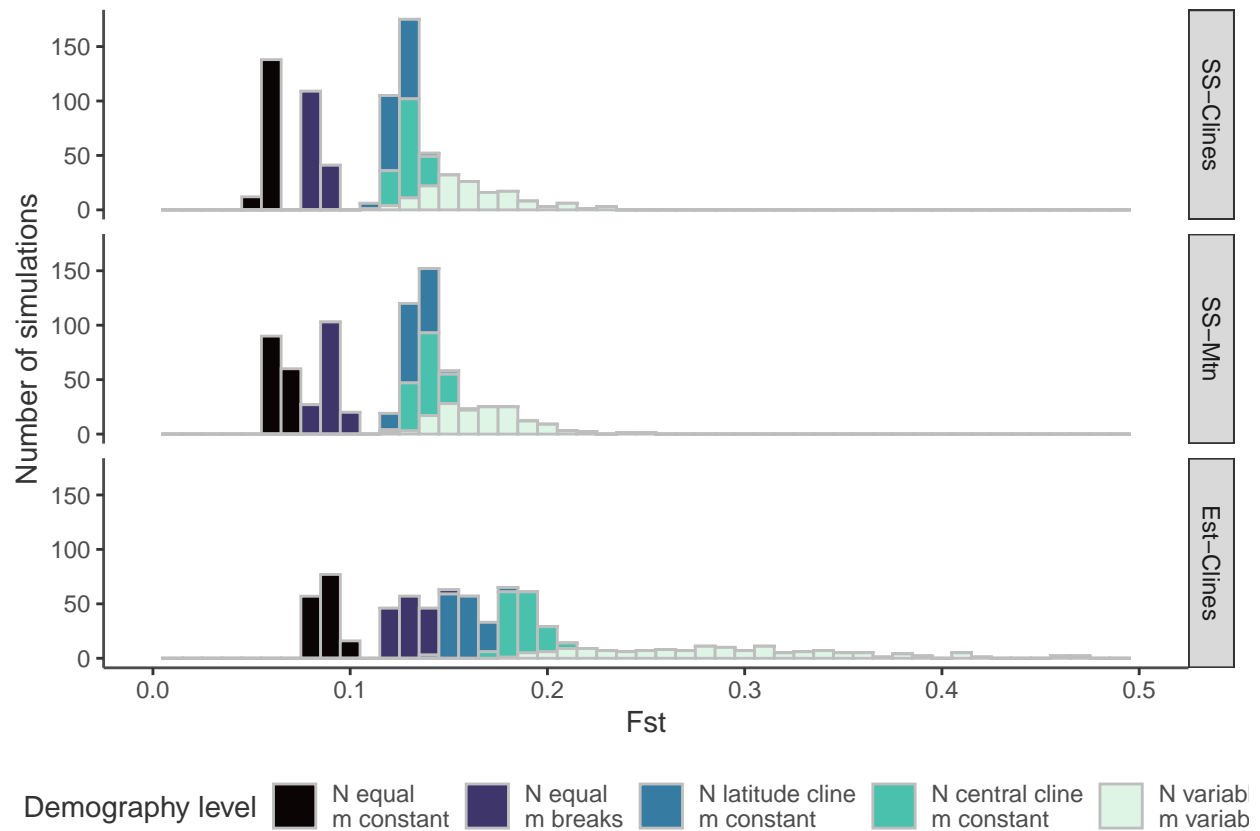


```
## 2
```

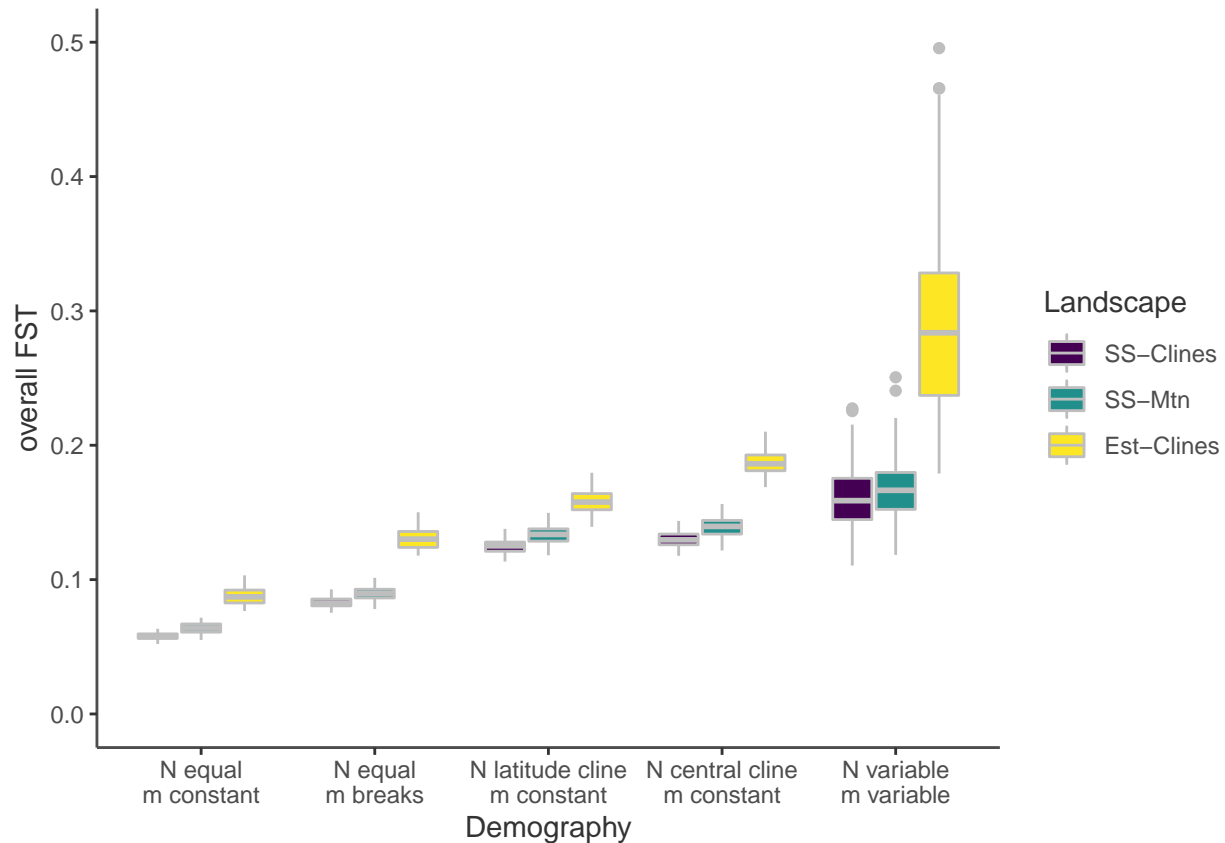
```
ggplot(final.df) + geom_histogram(aes(x=meanFst, fill=demog_level_sub, position="stack"), binwidth=0.
```

```
## Warning: Ignoring unknown aesthetics: position
```

```
## Warning: Removed 30 rows containing missing values (geom_bar).
```



```
ggplot(final.df, aes(x=as.factor(demog_level_sub), y=meanFst, fill=demog_level)) + geom_boxplot(color="
```

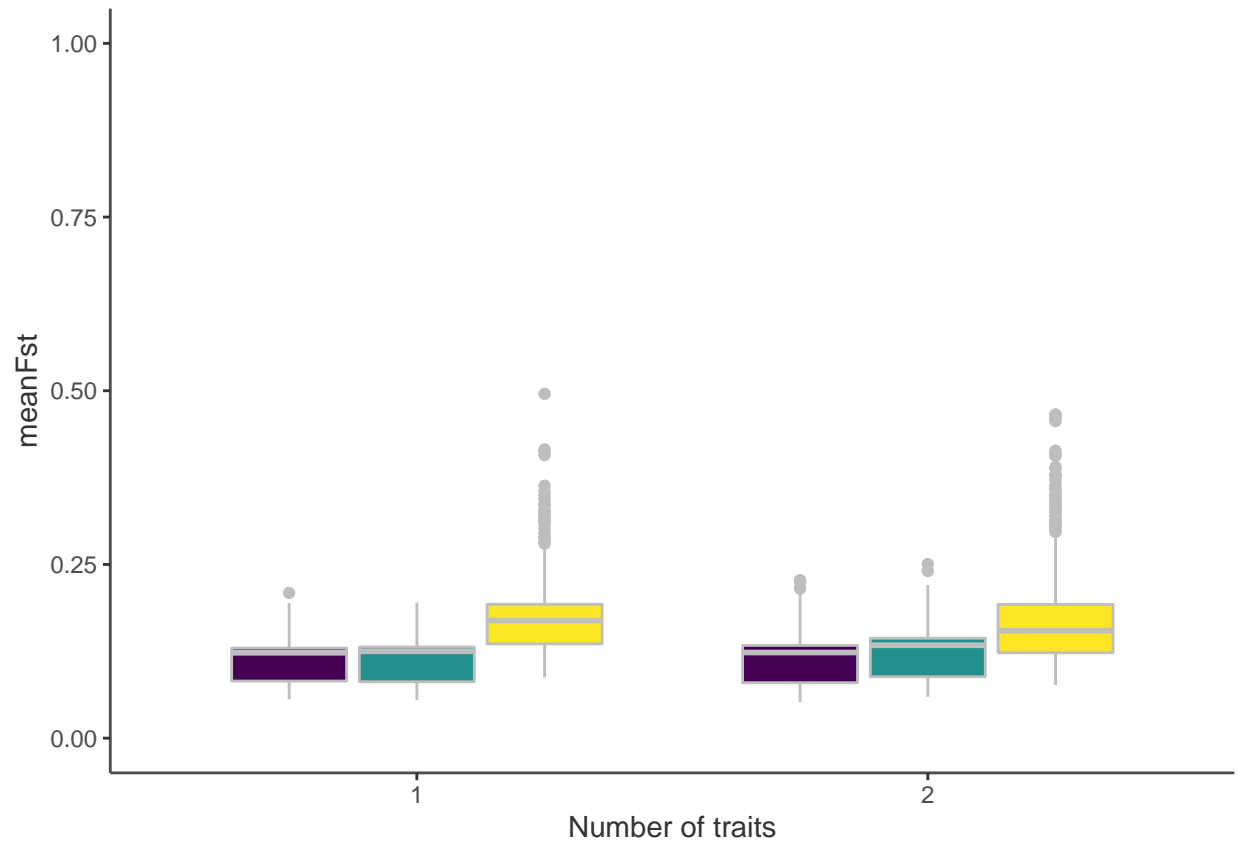


```
a<-tapply(final.df$meanFst,final.df$demog_name, mean, na.rm=TRUE)
b<- tapply(final.df$final_LA,final.df$demog_name, mean, na.rm=TRUE)

cbind(Fst=a,LA=b)
```

	Fst	LA
## SS-Clines_N-equal_m-constant	0.05787589	0.4829661
## SS-Mtn_N-equal_m-constant	0.06375824	0.4866809
## Est-Clines_N-equal_m-constant	0.08761539	0.4280998
## SS-Clines_N-cline-N-to-S_m-constant	0.12483060	0.4772134
## SS-Mtn_N-cline-N-to-S_m-constant	0.13315802	0.4776251
## Est-Clines_N-cline-N-to-S_m-constant	0.15821409	0.4212553
## SS-Clines_N-cline-center-to-edge_m-constant	0.12975290	0.4762261
## SS-Mtn_N-cline-center-to-edge_m-constant	0.13883682	0.4791905
## Est-Clines_N-cline-center-to-edge_m-constant	0.18722368	0.4203116
## SS-Clines_N-equal_m_breaks	0.08295596	0.4877002
## SS-Mtn_N-equal_m_breaks	0.08924858	0.4903118
## Est-Clines_N-equal_m_breaks	0.13069710	0.4295439
## SS-Clines_N-variable_m-variable	0.16076391	0.4713436
## SS-Mtn_N-variable_m-variable	0.16764502	0.4669084
## Est-Clines_N-variable_m-variable	0.28976287	0.4251321

```
ggplot(final.df, aes(x=as.factor(N_traits), y=meanFst, fill=demog_level)) + geom_boxplot(color="grey")
```



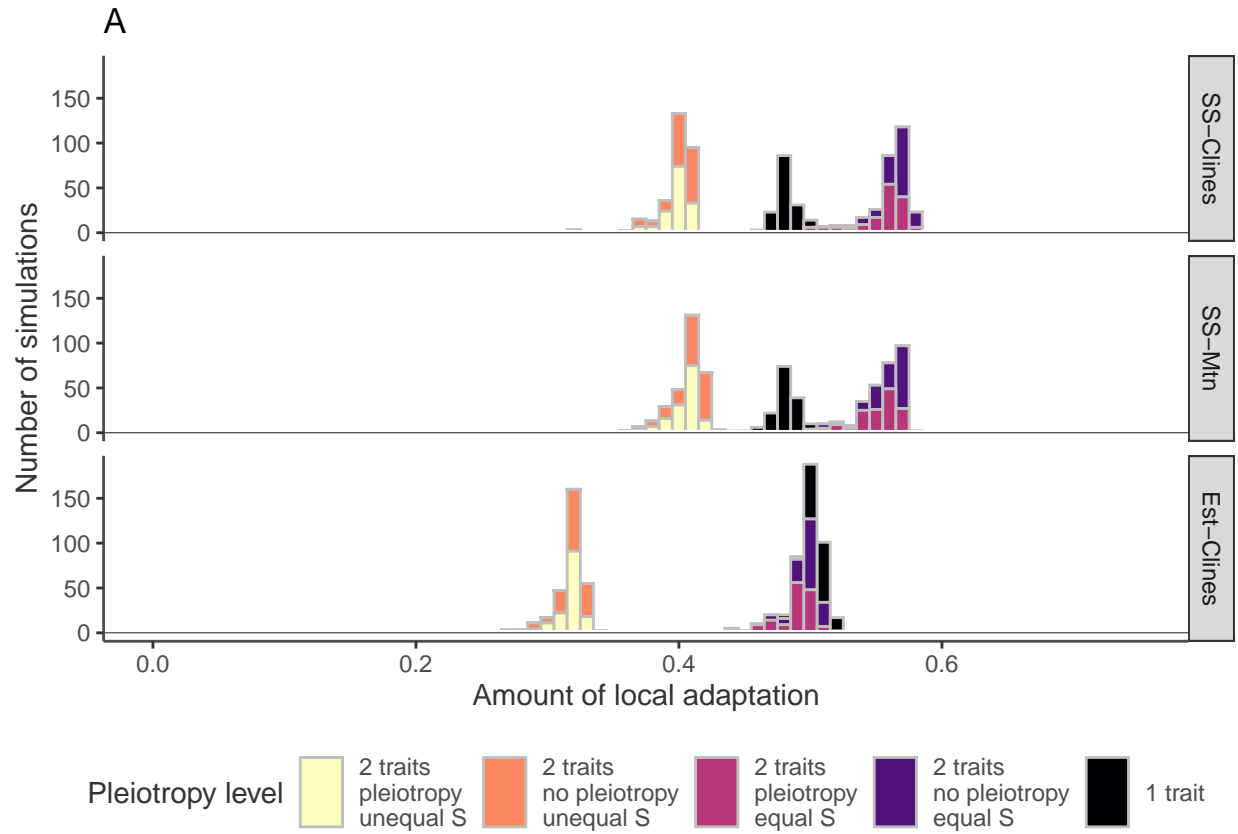
Degree local adaptation

Visualize the degree of local adaptation

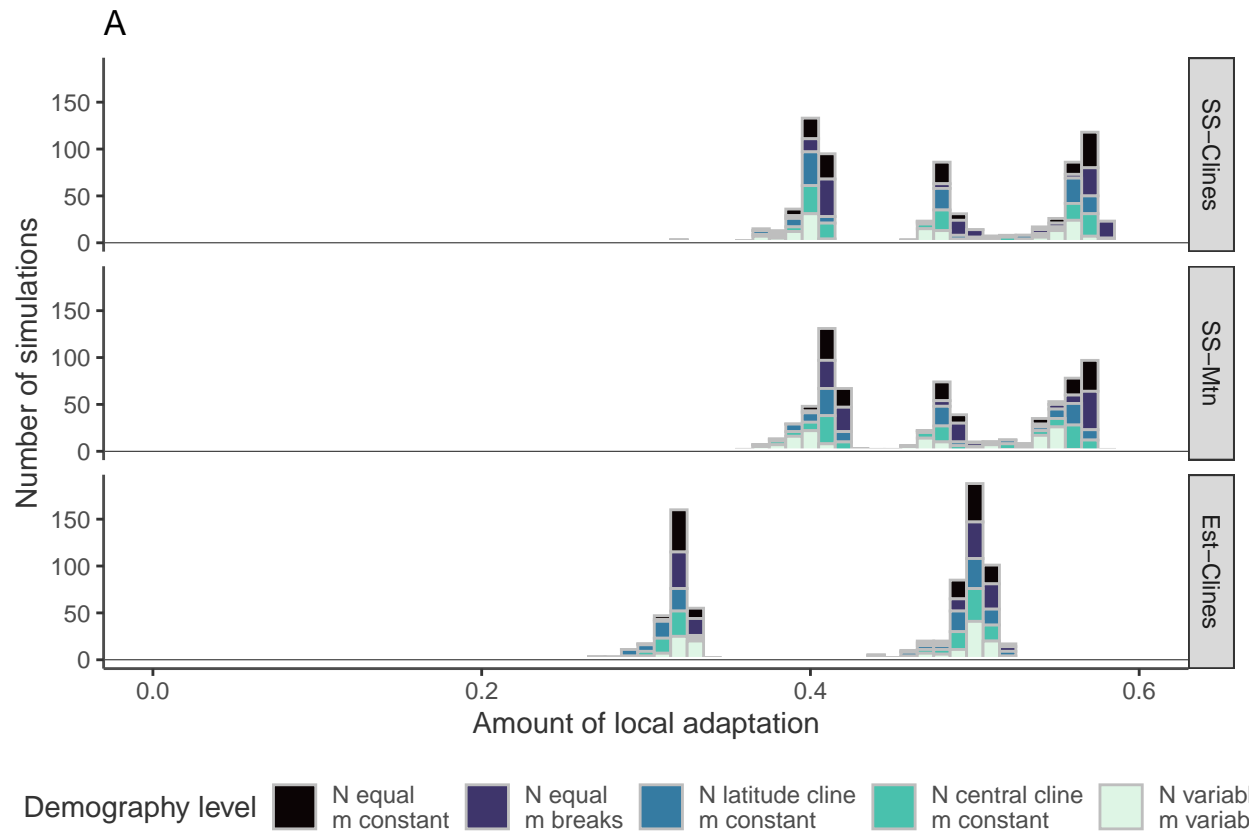
```
summary(final.df$final_LA)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.2509  0.4033  0.4821  0.4614  0.5201  0.5796
```

```
l1 <- ggplot(final.df) + geom_histogram(aes(x=final_LA, fill=arch_level_sub), binwidth=0.01, color="white",
guides(fill = guide_legend(reverse = TRUE))) + ggtitle("A") + geom_hline(yintercept=0, color="white",
l1
```



```
ggplot(final.df) + geom_histogram(aes(x=final_LA, fill=demog_level_sub), binwidth=0.01, color="grey") +
  guides(fill = guide_legend(reverse = FALSE)) + ggtitle("A") + geom_hline(yintercept=0, color="white")
```



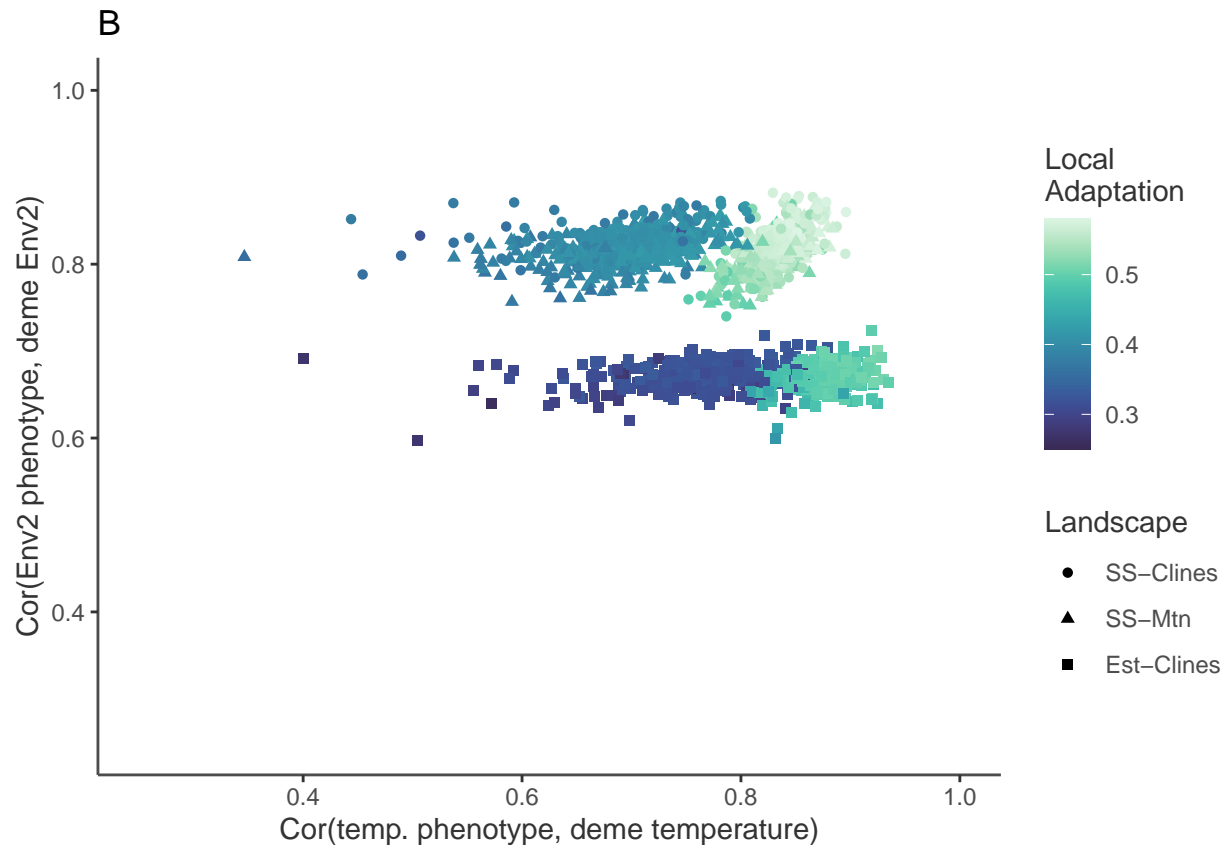
```
12<- ggplot(final.df) +
  geom_point(aes(x=subsamp_corr_phen_temp,
                 y=subsamp_corr_phen_sal,
                 color=final_LA,shape=demog_level)) +
  ggtheme +
  scale_color_viridis(option="mako", name="Local\nAdaptation", begin=0.2, end=1) + coord_cartesian(
12
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
## Warning: Removed 1 rows containing missing values (geom_hline).
```

```
## Warning: Removed 1 rows containing missing values (geom_hline).
```



in this case, the removed points have an NA because the "sal" trait was not adaptive in 450 simulations
ggplot(final.df, aes(x=as.factor(N_traits), y=meanFst, fill=demog_level)) + geom_boxplot(color="grey")

```
sum(is.na(final.df$subsamp_corr_phen_temp))
```

```
## [1] 0
```

```
sum(is.na(final.df$subsamp_corr_phen_sal))
```

```
## [1] 450
```

```
pdf(paste0(outputs, "AmountLA.pdf"), width=7, height=8)
grid.arrange(l1, l2, nrow=2)
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
## Warning: Removed 1 rows containing missing values (geom_hline).
```

```
## Warning: Removed 1 rows containing missing values (geom_hline).
```

```
dev.off()
```

```
## pdf  
## 2
```

Number of loci

```
# Create a dataframe for plotting  
numloc_df <- gather(final.df, key=filter, value=num_loci_causal, num_causal_prefilter, num_causal_postfilter)  
  
numloc_df$filter <- factor(numloc_df$filter, levels = c("num_causal_prefilter", "num_causal_postfilter"))  
  
levels(numloc_df$filter) <- c("Pre MAF filter", "Post filter MAF > 0 .01")  
str(numloc_df$filter)
```

```
## Ord.factor w/ 2 levels "Pre MAF filter"<..: 1 1 1 1 1 1 1 1 1 1 ...
```

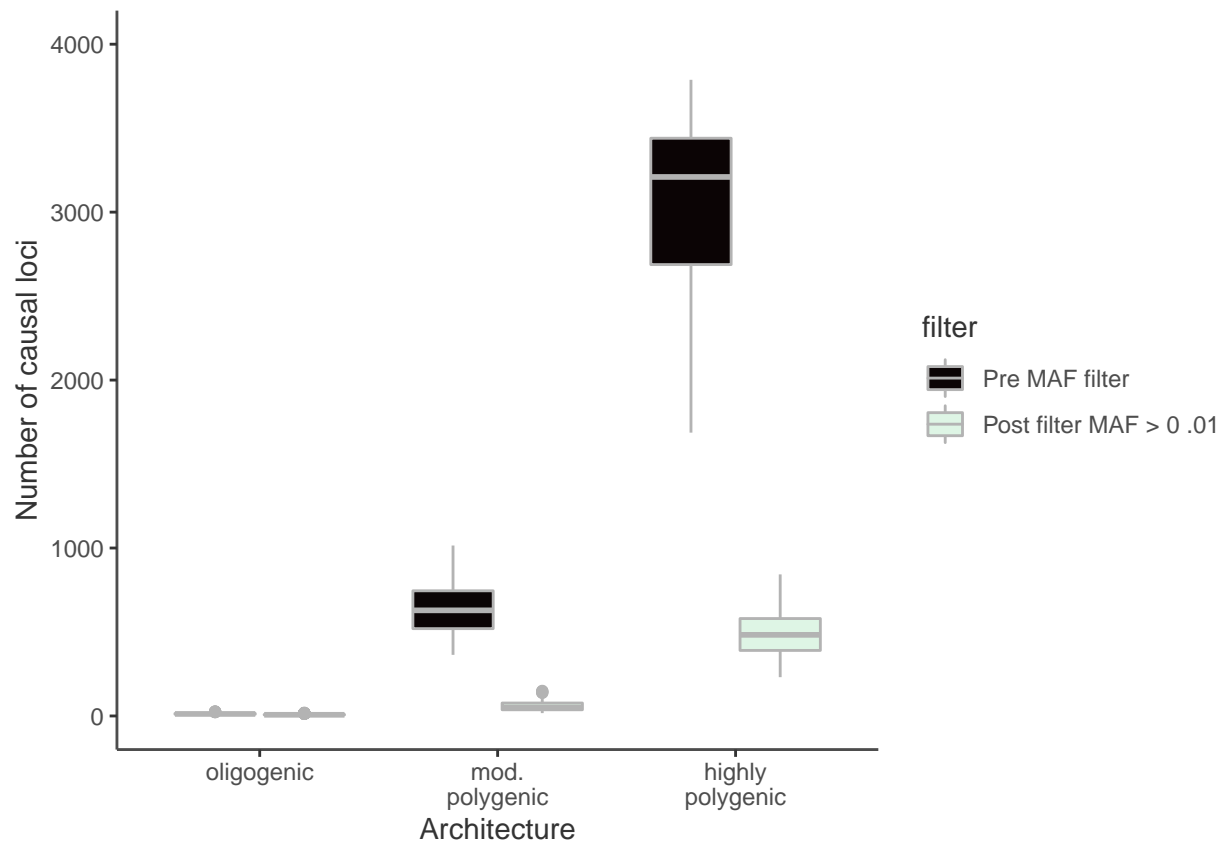
```
tapply( numloc_df$num_loci_causal, list(numloc_df$filter,numloc_df$arch_level), mean, na.rm=TRUE)
```

```
##               oligogenic mod.\npolygenic highly\npolygenic  
## Pre MAF filter      12.36267      646.8533      3042.847  
## Post filter MAF > 0 .01    7.83600      58.1440      498.948
```

```
str(numloc_df$arch_level)
```

```
## Ord.factor w/ 3 levels "oligogenic"<"mod.\npolygenic"<..: 3 3 3 3 3 3 3 3 3 3 ...
```

```
# Plot QTN loci  
m<- ggplot(numloc_df ) + geom_boxplot(aes(y=num_loci_causal,x = arch_level, fill=filter), color="grey70")  
m
```



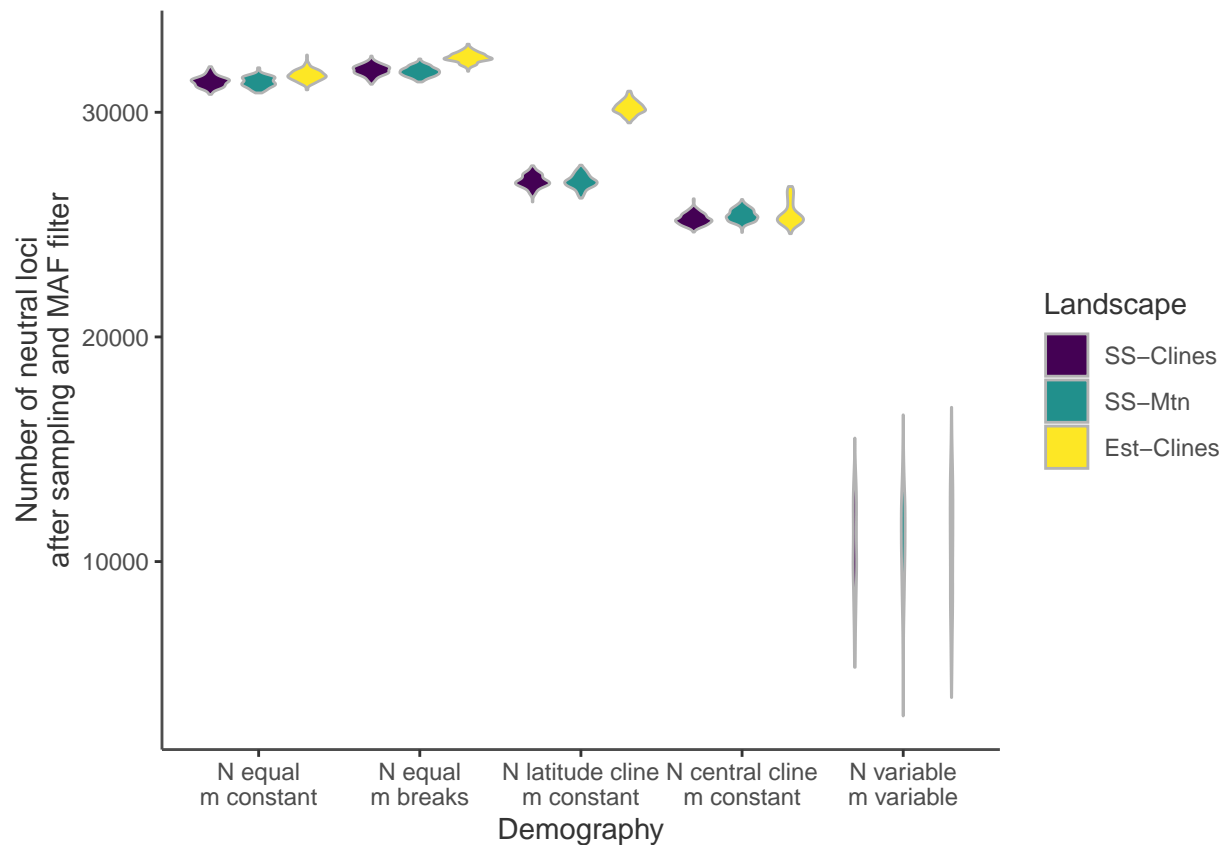
```
# Check no missing data
sum(is.na(final.df$num_neut_prefilter))
```

```
## [1] 0
```

```
sum(is.na(final.df$num_neut_postfilter))
```

```
## [1] 0
```

```
# Plot neutral loci
n <- ggplot(final.df) + geom_violin(aes(y=num_neut_postfilter, x=demog_level_sub, fill=demog_level), col=
n
```

```
tapply(final.df$num_neut_postfilter, list(final.df$demog_level_sub), median, na.rm=TRUE)
```

```
##          N equal\nm constant          N equal\nm breaks
##                31450.0                31997.0
## N latitude cline\nm constant N central cline\nm constant
##                27139.5                25316.0
##          N variable\nm variable
##                10753.5
```

```
tapply(final.df$num_neut_postfilter, list(final.df$demog_level_sub), mean, na.rm=TRUE)
```

```
##          N equal\nm constant          N equal\nm breaks
##                31450.10                32042.55
## N latitude cline\nm constant N central cline\nm constant
##                28013.50                25384.45
##          N variable\nm variable
##                10641.12
```

```
pdf(paste0(outputs,"NumLociPrePostfilter.pdf"), width=7, height=8)
  grid.arrange(m, n, nrow=2)
dev.off()
```

```
## pdf
##    2
```

K (Number of populations)

What determines K?

```
K_mod <- summary(aov(K~arch + demog_level_sub + demog_level + arch*demog_level_sub*demog_level, data=final.df))
K_mod
```

```
##              Df Sum Sq Mean Sq  F value    Pr(>F)
## arch          14    144      10      3.630 5.36e-06 ***
## demog_level_sub  4   1458     364    128.881 < 2e-16 ***
## demog_level      2   6885    3443   1217.544 < 2e-16 ***
## arch:demog_level_sub 56    262      5     1.654 0.00183 **
## arch:demog_level   28    199      7     2.513 2.10e-05 ***
## demog_level_sub:demog_level  8   1972     246    87.177 < 2e-16 ***
## arch:demog_level_sub:demog_level 112    633      6     1.998 8.25e-09 ***
## Residuals      2025   5726      3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Percent of variance (SS) explained by each

```
pervarK <- round(K_mod[[1]][,2]/sum(K_mod[[1]][,2]),2)
data.frame(name=rownames(K_mod[[1]]),pervarK)
```

```
##              name pervarK
## 1 arch          0.01
## 2 demog_level_sub 0.08
## 3 demog_level     0.40
## 4 arch:demog_level_sub 0.02
## 5 arch:demog_level 0.01
## 6 demog_level_sub:demog_level 0.11
## 7 arch:demog_level_sub:demog_level 0.04
## 8 Residuals      0.33
```

mostly determined by demography

```
summary(final.df$K)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.000   2.000   3.000   4.121   5.000   11.000
```

```
pdf(paste0(outputs,"K_by_demog.pdf"), width=6, height=6)
ggplot(final.df) + geom_histogram(aes(x=K, fill=demog_level), binwidth=1, color="grey") + ggtheme + c
guides(fill = guide_legend(reverse = FALSE)) + geom_hline(yintercept=0, color="white", size=1) + ge
dev.off()
```

```
## pdf
##    2
```

Statistical models

MODELS FOR DIVERGENCE (FST) AND FOR AMOUNT Local adaptation (LA)

```
levels(final.df$arch)
```

```
## [1] "highly-polygenic_1-trait"
## [2] "highly-polygenic_2-trait-no-pleiotropy-equal-S"
## [3] "highly-polygenic_2-trait-no-pleiotropy-unequal-S"
## [4] "highly-polygenic_2-trait-pleiotropy-equal-S"
## [5] "highly-polygenic_2-trait-pleiotropy-unequal-S"
## [6] "mod-polygenic_1-trait"
## [7] "mod-polygenic_2-trait-no-pleiotropy-equal-S"
## [8] "mod-polygenic_2-trait-no-pleiotropy-unequal-S"
## [9] "mod-polygenic_2-trait-pleiotropy-equal-S"
## [10] "mod-polygenic_2-trait-pleiotropy-unequal-S"
## [11] "oliogenic_1-trait"
## [12] "oliogenic_2-trait-no-pleiotropy-equal-S"
## [13] "oliogenic_2-trait-no-pleiotropy-unequal-S"
## [14] "oliogenic_2-trait-pleiotropy-equal-S"
## [15] "oliogenic_2-trait-pleiotropy-unequal-S"
```

```
levels(final.df$demog_level)
```

```
## [1] "SS-Clines" "SS-Mtn" "Est-Clines"
```

```
levels(final.df$demog_level_sub)
```

```
## [1] "N equal\nm constant" "N equal\nm breaks"
## [3] "N latitude cline\nm constant" "N central cline\nm constant"
## [5] "N variable\nm variable"
```

```
## ANOVA for degree LA
```

```
LA_mod <- summary(aov(final_LA~arch + demog_level_sub + demog_level + arch*demog_level_sub*demog_level,
LA_mod
```

```
##
## arch Df Sum Sq Mean Sq F value Pr(>F)
## demog_level_sub 4 0.065 0.0162 214.755 <2e-16 ***
## demog_level 2 1.499 0.7495 9907.658 <2e-16 ***
## arch:demog_level_sub 56 0.034 0.0006 7.943 <2e-16 ***
## arch:demog_level 28 0.862 0.0308 407.106 <2e-16 ***
## demog_level_sub:demog_level 8 0.018 0.0023 30.331 <2e-16 ***
## arch:demog_level_sub:demog_level 112 0.011 0.0001 1.283 0.0272 *
## Residuals 2025 0.153 0.0001
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Percent of SS for each explanatory variable
```

```
pervarLA <- round(LA_mod[[1]][,2]/sum(LA_mod[[1]][,2]),2)
```

```
## ANOVA for FST
```

```
FST_mod <- summary(aov(meanFst ~ arch + demog_level_sub + demog_level + arch*demog_level_sub*demog_level,
FST_mod
```

```
##               Df Sum Sq Mean Sq  F value    Pr(>F)
## arch          14  0.035  0.0025    6.982 3.09e-14 ***
## demog_level_sub  4  4.839  1.2099 3426.501 < 2e-16 ***
## demog_level      2  1.578  0.7889 2234.390 < 2e-16 ***
## arch:demog_level_sub  56  0.032  0.0006    1.597  0.00353 **
## arch:demog_level    28  0.046  0.0016    4.629 1.82e-14 ***
## demog_level_sub:demog_level  8  0.655  0.0819  231.995 < 2e-16 ***
## arch:demog_level_sub:demog_level 112  0.047  0.0004    1.187  0.09334 .
## Residuals      2025  0.715  0.0004
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Perent of SS for each explanatory variable
pervarFST <- round(FST_mod[[1]][,2]/sum(FST_mod[[1]][,2]),2)

data.frame(name=rownames(FST_mod[[1]]),pervarLA, pervarFST)
```

```
##               name pervarLA pervarFST
## 1 arch          0.82      0.00
## 2 demog_level_sub 0.00      0.61
## 3 demog_level      0.10      0.20
## 4 arch:demog_level_sub 0.00      0.00
## 5 arch:demog_level  0.06      0.01
## 6 demog_level_sub:demog_level 0.00      0.08
## 7 arch:demog_level_sub:demog_level 0.00      0.01
## 8 Residuals      0.01      0.09
```

MODELS FOR allele frequency (AF) clines

```
# Create a dataframe for analysis with both traits
stat_df <- gather(final.df, key=trait, value=cor_TPR, cor_TPR_temp, cor_TPR_sal)
tail(stat_df)
```

```
##          seed
## 4495 1233338
## 4496 1233339
## 4497 1233340
## 4498 1233341
## 4499 1233342
## 4500 1233343
##
##                                     level
## 4495      oliogenic_2-trait-pleiotropy-unequal-S__SS-Clines_N-variable_m-variable
## 4496 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-cline-center-to-edge_m-constant
## 4497      oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-cline-N-to-S_m-constant
## 4498      oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-equal_m_breaks
## 4499      oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-equal_m-constant
## 4500      oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable
##      reps          arch
## 4495   10 oliogenic_2-trait-pleiotropy-unequal-S
## 4496   10 oliogenic_2-trait-pleiotropy-unequal-S
## 4497   10 oliogenic_2-trait-pleiotropy-unequal-S
## 4498   10 oliogenic_2-trait-pleiotropy-unequal-S
```

```

## 4499 10 oliogenic_2-trait-pleiotropy-unequal-S
## 4500 10 oliogenic_2-trait-pleiotropy-unequal-S
##
##          demog_name          demog_level_sub
## 4495      SS-Clines_N-variable_m-variable      N variable\nm variable
## 4496 SS-Mtn_N-cline-center-to-edge_m-constant      N central cline\nm constant
## 4497      SS-Mtn_N-cline-N-to-S_m-constant      N latitude cline\nm constant
## 4498      SS-Mtn_N-equal_m_breaks          N equal\nm breaks
## 4499      SS-Mtn_N-equal_m-constant          N equal\nm constant
## 4500      SS-Mtn_N-variable_m-variable      N variable\nm variable
##
##      demog_level MIG_x MIG_y xcline ycline demog METAPOP_SIDE_x METAPOP_SIDE_y
## 4495      SS-Clines 0.03 0.03 linear linear      SS              10              10
## 4496      SS-Mtn 0.03 0.03      V linear      SS              10              10
## 4497      SS-Mtn 0.03 0.03      V linear      SS              10              10
## 4498      SS-Mtn 0.03 0.03      V linear      SS              10              10
## 4499      SS-Mtn 0.03 0.03      V linear      SS              10              10
## 4500      SS-Mtn 0.03 0.03      V linear      SS              10              10
##
##      Nequal isVariableM MIG_breaks          arch_level_sub arch_level
## 4495      3          1          0 2 traits\npleiotropy\nunequal S oligogenic
## 4496      4          0          0 2 traits\npleiotropy\nunequal S oligogenic
## 4497      2          0          0 2 traits\npleiotropy\nunequal S oligogenic
## 4498      0          0          1 2 traits\npleiotropy\nunequal S oligogenic
## 4499      0          0          0 2 traits\npleiotropy\nunequal S oligogenic
## 4500      3          1          0 2 traits\npleiotropy\nunequal S oligogenic
##
##      MU_base MU_QTL_proportion SIGMA_QTN_1 SIGMA_QTN_2 SIGMA_K_1 SIGMA_K_2
## 4495      1e-07          0.001          0.4          0.4          0.5          4
## 4496      1e-07          0.001          0.4          0.4          0.5          4
## 4497      1e-07          0.001          0.4          0.4          0.5          4
## 4498      1e-07          0.001          0.4          0.4          0.5          4
## 4499      1e-07          0.001          0.4          0.4          0.5          4
## 4500      1e-07          0.001          0.4          0.4          0.5          4
##
##      N_traits ispleiotropy n_samp_tot n_samp_per_pop sd_fitness_among_inds
## 4495      2      Pleiotropy      1000          10      0.06989773
## 4496      2      Pleiotropy      1000          10      0.10457515
## 4497      2      Pleiotropy      1000          10      0.10815036
## 4498      2      Pleiotropy      1000          10      0.09447908
## 4499      2      Pleiotropy      1000          10      0.10039771
## 4500      2      Pleiotropy      1000          10      0.11933530
##
##      sd_fitness_among_pops final_LA K      Bonf_alpha numCausalLowMAFs sample
## 4495      0.03432623 0.390202 2 4.302186e-06          0
## 4496      0.05800045 0.378143 3 2.037324e-06          0
## 4497      0.05691502 0.386475 3 1.950687e-06          0
## 4498      0.04351184 0.406991 1 1.582930e-06          0
## 4499      0.04816428 0.411540 2 1.608648e-06          0
## 4500      0.06758560 0.361984 1 6.179706e-06          0
##
##      all_corr_phen_temp subsamp_corr_phen_temp all_corr_phen_sal
## 4495      0.8105442          0.6442488          0.9331842
## 4496      0.6134233          0.5623938          0.8856847
## 4497      0.6300670          0.5378167          0.9092372
## 4498      0.7915280          0.6228879          0.9145244
## 4499      0.8020544          0.6425425          0.9127410
## 4500      0.8163458          0.6347974          0.8849650
##
##      subsamp_corr_phen_sal num_causal_prefilter num_causal_postfilter
## 4495      0.8112850          8          5
## 4496      0.8061503          11         6

```

##	4497	0.8075816	8	6			
##	4498	0.8166540	10	7			
##	4499	0.8128461	14	9			
##	4500	0.7608153	12	8			
##	num_non_causal num_neut_prefilter num_neut_postfilter						
##	4495	11617	11843	11843			
##	4496	24536	25257	25257			
##	4497	25626	26975	26975			
##	4498	31580	31942	31942			
##	4499	31073	31405	31405			
##	4500	8083	8197	8197			
##	num_neut_neutralgenome num_causal_temp num_causal_sal num_multiallelic						
##	4495	5810	5	0			
##	4496	12346	6	0			
##	4497	12834	6	0			
##	4498	15946	7	0			
##	4499	15689	9	0			
##	4500	3947	8	0			
##	meanFst va_temp_total va_sal_total Va_temp_sample Va_sal_sample nSNPs						
##	4495	0.14301783	0.14320895	0.06757681	0.13713509	0.06623635	11622
##	4496	0.13350458	0.05299476	0.07273692	0.08494197	0.09831001	24542
##	4497	0.13740776	0.09929097	0.10670097	0.22910565	0.10650756	25632
##	4498	0.08708807	0.13554966	0.10110684	0.13249490	0.10066003	31587
##	4499	0.06704804	0.16714222	0.16315859	0.16734136	0.16310813	31082
##	4500	0.17379409	0.08556485	0.10592398	0.08049695	0.09935857	8091
##	median_causal_temp_cor median_causal_sal_cor median_neut_temp_cor						
##	4495	0.2754918	0.5180941	0.2414407			
##	4496	0.3026247	0.4175574	0.1850624			
##	4497	0.2000535	0.3990216	0.2321665			
##	4498	0.2967283	0.4868710	0.2257370			
##	4499	0.3428889	0.3406402	0.1621695			
##	4500	0.3033895	0.3424647	0.2488890			
##	median_neut_sal_cor cor_VA_temp_prop cor_VA_sal_prop cor_FDR_allSNPs_temp						
##	4495	0.22546761	0.8516887	0.9978557	0.9993947		
##	4496	0.12090175	0.4727327	0.8630538	0.9997394		
##	4497	0.10810696	0.7985926	0.7317329	0.9998285		
##	4498	0.09267506	0.6560965	0.8820640	0.9995787		
##	4499	0.10404740	0.1136390	0.4316080	0.9989027		
##	4500	0.13587417	0.3901235	0.8777962	0.9987903		
##	cor_FDR_neutSNPs_temp cor_FDR_allSNPs_sal cor_FDR_neutSNPs_sal						
##	4495	0.9987358	0.9985337	0.9968774			
##	4496	0.9995287	0.9949749	0.9840000			
##	4497	0.9996431	0.9933775	0.9732143			
##	4498	0.9991545	0.9692308	0.8378378			
##	4499	0.9976285	0.9916201	0.9700000			
##	4500	0.9974958	0.9913043	0.9743590			
##	num_causal_sig_temp_corr num_causal_sig_sal_corr						
##	4495	2	4				
##	4496	1	4				
##	4497	1	3				
##	4498	3	6				
##	4499	3	3				
##	4500	3	4				
##	num_notCausal_sig_temp_corr num_notCausal_sig_sal_corr						

##	4495	3302	2724
##	4496	3836	792
##	4497	5830	450
##	4498	7118	189
##	4499	2731	355
##	4500	2477	456
##	num_neut_sig_temp_corr num_neut_sig_sal_corr cor_AUCPR_temp_allSNPs		
##	4495	1580	1277 0.0056220144
##	4496	2121	246 0.0007501130
##	4497	2801	109 0.0003226524
##	4498	3545	31 0.0003352525
##	4499	1262	97 0.0050843070
##	4500	1195	152 0.0013870159
##	cor_AUCPR_temp_neutSNPs cor_AUCPR_sal_allSNPs cor_AUCPR_sal_neutSNPs		
##	4495	0.0161350441	0.09787865 0.4036255
##	4496	0.0013167008	0.24012890 0.3423103
##	4497	0.0006630059	0.17086955 0.1834894
##	4498	0.0006712386	0.40553013 0.7821320
##	4499	0.0109923069	0.11638113 0.1367044
##	4500	0.0029380064	0.02439708 0.2860155
##	cor_af_temp_noutliers cor_af_sal_noutliers cor_FPR_temp_neutSNPs		
##	4495	3304	2728 0.27194492
##	4496	3837	796 0.17179653
##	4497	5831	453 0.21824840
##	4498	7121	195 0.22231281
##	4499	2734	358 0.08043852
##	4500	2480	460 0.30276159
##	cor_FPR_sal_neutSNPs LEA3.2_lfmm2_Va_temp_prop LEA3.2_lfmm2_Va_sal_prop		
##	4495	0.219793460	0.0000000 0.9578289
##	4496	0.019925482	0.4727327 0.9998981
##	4497	0.008493065	0.0000000 0.9412170
##	4498	0.001944061	0.0000000 0.8820640
##	4499	0.006182676	0.0000000 0.9171033
##	4500	0.038510261	0.0000000 0.8777962
##	LEA3.2_lfmm2_TPR_temp LEA3.2_lfmm2_TPR_sal LEA3.2_lfmm2_FDR_allSNPs_temp		
##	4495	0.0000000	0.6000000 NA
##	4496	0.1666667	0.8333333 0
##	4497	0.0000000	0.6666667 NA
##	4498	0.0000000	0.8571429 NA
##	4499	0.0000000	0.5555556 NA
##	4500	0.0000000	0.5000000 NA
##	LEA3.2_lfmm2_FDR_allSNPs_sal LEA3.2_lfmm2_FDR_neutSNPs_temp		
##	4495	0.9302326	NA
##	4496	0.9180328	0
##	4497	0.9680000	NA
##	4498	0.8888889	NA
##	4499	0.9253731	NA
##	4500	0.9090909	NA
##	LEA3.2_lfmm2_FDR_neutSNPs_sal LEA3.2_lfmm2_AUCPR_temp_allSNPs		
##	4495	0.0	0.2881630
##	4496	0.0	0.5981415
##	4497	0.2	0.2337020
##	4498	0.0	0.5925314
##	4499	0.0	0.2628556

```

## 4500          0.0          0.2117759
##      LEA3.2_lfmm2_AUCPR_temp_neutSNPs LEA3.2_lfmm2_AUCPR_sal_allSNPs
## 4495          0.6313777          0.2881630
## 4496          0.8340475          0.5981415
## 4497          0.7153403          0.2337020
## 4498          1.0000000          0.5925314
## 4499          0.5658529          0.2628556
## 4500          0.5088647          0.2117759
##      LEA3.2_lfmm2_AUCPR_sal_neutSNPs LEA3.2_lfmm2_mlog10P_tempenv_noutliers
## 4495          0.6313777          0
## 4496          0.8340475          1
## 4497          0.7153403          0
## 4498          1.0000000          0
## 4499          0.5658529          0
## 4500          0.5088647          0
##      LEA3.2_lfmm2_mlog10P_salenv_noutliers LEA3.2_lfmm2_num_causal_sig_temp
## 4495          43          0
## 4496          61          1
## 4497         125          0
## 4498          54          0
## 4499          67          0
## 4500          44          0
##      LEA3.2_lfmm2_num_neut_sig_temp LEA3.2_lfmm2_num_causal_sig_sal
## 4495          0          3
## 4496          0          5
## 4497          0          4
## 4498          0          6
## 4499          0          5
## 4500          0          4
##      LEA3.2_lfmm2_num_neut_sig_sal LEA3.2_lfmm2_FPR_neutSNPs_temp
## 4495          0          0
## 4496          0          0
## 4497          1          0
## 4498          0          0
## 4499          0          0
## 4500          0          0
##      LEA3.2_lfmm2_FPR_neutSNPs_sal RDA1_propvar RDA2_propvar RDA1_propvar_corr
## 4495          0.000000e+00          0.550          0.450          0.665
## 4496          0.000000e+00          0.742          0.258          0.558
## 4497          7.791803e-05          0.716          0.284          0.772
## 4498          0.000000e+00          0.835          0.165          0.752
## 4499          0.000000e+00          0.684          0.316          0.624
## 4500          0.000000e+00          0.739          0.261          0.673
##      RDA2_propvar_corr RDA1_temp_cor RDA1_sal_cor RDA2_temp_cor RDA2_sal_cor
## 4495          0.335          0.5015364 -0.865136554 -0.865136554 -0.5015364
## 4496          0.442          0.9999502 -0.009981000  0.009981000  0.9999502
## 4497          0.228          0.9999683 -0.007965626  0.007965626  0.9999683
## 4498          0.248          0.9991421  0.041413317 -0.041413317  0.9991421
## 4499          0.376          0.9996593  0.026102226 -0.026102226  0.9996593
## 4500          0.327          0.9800515  0.198743495 -0.198743495  0.9800515
##      RDA_Va_temp_prop RDA_Va_temp_prop_corr RDA_Va_sal_prop
## 4495          0.4763587          0.8519800          0.9578289
## 4496          0.9996855          0.9996855          0.9998981
## 4497          0.9995510          0.2009584          0.9742365

```


##	4498	0.9677581	0.9677581	0.8820640	
##	4499	0.9861608	0.9861608	0.9986455	
##	4500	0.8073374	0.8955353	0.8777962	
##		RDA_Va_sal_prop_corr	RDA_TPR	RDA_TPR_corr	RDA_FDR_allSNPs
##	4495	0.7328738	0.6000000	0.6000000	0.9931193
##	4496	0.9998981	0.8333333	0.8333333	0.9929478
##	4497	0.9412170	0.8333333	0.6666667	0.9968133
##	4498	0.8820640	0.8571429	0.8571429	0.9963280
##	4499	0.9986455	0.8888889	0.8888889	0.9944328
##	4500	0.9096928	0.5000000	0.6250000	0.9838710
##		RDA_FDR_allSNPs_corr	num_RDA_sig_causal	num_RDA_sig_neutral	
##	4495	0.9934211		3	118
##	4496	0.9932249		5	230
##	4497	0.9972318		5	573
##	4498	0.9955720		6	597
##	4499	0.9951190		8	479
##	4500	0.9814815		4	62
##		num_RDA_sig_causal_corr	num_RDA_sig_neutral_corr	RDA_FDR_neutSNPs	
##	4495		3	152	0.9752066
##	4496		5	244	0.9787234
##	4497		4	523	0.9913495
##	4498		6	486	0.9900498
##	4499		8	498	0.9835729
##	4500		5	92	0.9393939
##		RDA_FDR_neutSNPs_corr	RDA_AUCPR_allSNPs	RDA_AUCPR_neutSNPs	
##	4495	0.9806452	0.1317274	0.6023902	
##	4496	0.9799197	0.3896916	0.6725673	
##	4497	0.9924099	0.1915153	0.5139129	
##	4498	0.9878049	0.3830535	0.8575997	
##	4499	0.9841897	0.1615562	0.6298882	
##	4500	0.9484536	0.2032180	0.5029961	
##		RDA_AUCPR_neutSNPs_corr	RDA_FPR_neutSNPs	RDA_FPR_neutSNPs_corr	
##	4495	0.2991643	0.02030981	0.02616179	
##	4496	0.6819382	0.01862952	0.01976349	
##	4497	0.5028327	0.04464703	0.04075113	
##	4498	0.8575851	0.03743886	0.03047786	
##	4499	0.6418724	0.03053095	0.03174198	
##	4500	0.3320560	0.01570813	0.02330884	
##		RDA_RDAmutpred_cor_tempEffect	RDA_RDAmutpred_cor_salEffect		
##	4495	0.6000000	0.6000000		
##	4496	0.8666667	0.6000000		
##	4497	0.6000000	0.6000000		
##	4498	0.5238095	0.3333333		
##	4499	0.5555556	0.7777778		
##	4500	0.5000000	0.2857143		
##		RDA_absRDAmutpred_cor_tempVa	RDA_absRDAmutpred_cor_salVa		
##	4495	0.020465239	0.01871735		
##	4496	0.011409116	0.01826038		
##	4497	0.002784945	0.01793393		
##	4498	0.017384447	0.02012018		
##	4499	0.017285637	0.01862984		
##	4500	0.020696744	0.02400657		
##		RDA_RDAmutpred_cor_tempEffect_structcorr			
##	4495		0.36606915		

```

## 4496 -0.07001212
## 4497 -0.07228499
## 4498 0.15434486
## 4499 0.12235804
## 4500 0.27521121
## RDA_RDAmutpred_cor_salEffect_structcorr
## 4495 0.9208180
## 4496 0.8150453
## 4497 0.8026655
## 4498 0.7288245
## 4499 0.7696911
## 4500 0.6602084
## RDA_absRDAmutpred_cor_tempVa_structcorr
## 4495 0.04635961
## 4496 0.01113341
## 4497 0.02638952
## 4498 0.06395474
## 4499 0.07991070
## 4500 0.08556552
## RDA_absRDAmutpred_cor_salVa_structcorr
## 4495 0.07122715
## 4496 0.10423641
## 4497 0.09238268
## 4498 0.11222190
## 4499 0.08011436
## 4500 0.11534351
## RDA_cor_RDA20000temppredict_tempPhen RDA_cor_RDA20000salpredict_salPhen
## 4495 0.6025624 0.6970451
## 4496 0.5688492 0.7562831
## 4497 0.5073146 0.6932780
## 4498 0.5917726 0.7525031
## 4499 0.6272143 0.7680113
## 4500 0.5661217 0.6653819
## RDA_cor_RDA20000temppredict_tempPhen_structcorr
## 4495 0.02969630
## 4496 0.08385813
## 4497 0.18613306
## 4498 0.05323003
## 4499 0.12648538
## 4500 0.23854195
## RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal
## 4495 0.2459241 -0.49592948 0.707550286
## 4496 0.7608327 -0.03745187 0.010848786
## 4497 0.6778338 -0.42331353 -0.036871726
## 4498 0.7661762 -0.96800660 -0.035807738
## 4499 0.7672155 -0.04223546 0.005524909
## 4500 0.6262283 0.78322231 0.099152034
## cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp
## 4495 -0.79041718 -0.49531715 -0.11538104 -0.196778909 0.41792225
## 4496 -0.93219015 0.01444962 -0.02798592 0.012589562 -0.15180910
## 4497 0.85072814 -0.05730822 -0.07053397 -0.038642435 -0.08318736
## 4498 -0.01224008 0.01880353 -0.01140580 -0.033516495 NA
## 4499 0.95953676 0.03045830 -0.01491703 0.005465646 0.09588969
## 4500 -0.41323121 -0.29453651 0.36840281 -0.066577901 NA

```

```

##      cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp
## 4495    -0.59810083      0.90723798      -0.7652270      -0.41739868
## 4496    -0.01327245      0.99957697      0.9980697      -0.01001944
## 4497    -0.04185963      0.92380303      0.9857150      0.37884682
## 4498           NA      0.02513634      0.9995552      -0.99878157
## 4499    -0.01555213      0.99870326      -0.9987481      0.02746745
## 4500           NA      0.80908546      -0.9986383      0.58076635
##      cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase
## 4495    -6.375626e-01      1.0000000      0.8000000      0.9982047
## 4496     5.599139e-02      1.0000000      0.6666667      0.9990089
## 4497     1.607696e-01      1.0000000      0.3333333      0.9990226
## 4498    -6.278494e-05      1.0000000      0.7142857      0.9987023
## 4499     2.751841e-02      0.8888889      1.0000000      0.9985967
## 4500    -2.590842e-02      0.7500000      0.8750000      0.9975440
##      gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines
## 4495           0.9944828           0.3144330
## 4496           0.9959225           0.4234528
## 4497           0.9990610           0.3182527
## 4498           0.9943439           0.1227848
## 4499           0.9601770           0.2232947
## 4500           0.9964340           0.5333333
##      clinalparadigm_temp_proptop5GWASclines
## 4495           0.2817869
## 4496           0.2060261
## 4497           0.1224649
## 4498           0.2430380
## 4499           0.1273312
## 4500           0.2074074
##      clinalparadigm_sal_propsigGWASclines clinalparadigm_temp_propsigGWASclines
## 4495           0.23302128           0.2378011
## 4496           0.06177726           0.1958369
## 4497           0.03441465           0.1351293
## 4498           0.01704694           0.2437673
## 4499           0.02904430           0.1463104
## 4500           0.09349593           0.2850657
##      trait      cor_TPR
## 4495 cor_TPR_sal 0.8000000
## 4496 cor_TPR_sal 0.6666667
## 4497 cor_TPR_sal 0.5000000
## 4498 cor_TPR_sal 0.8571429
## 4499 cor_TPR_sal 0.3333333
## 4500 cor_TPR_sal 0.5000000

```

```
# Check the levels in the new dataframe
```

```
unique(stat_df$demog_level)
```

```
## [1] Est-Clines SS-Clines SS-Mtn
## Levels: SS-Clines < SS-Mtn < Est-Clines
```

```
unique(stat_df$demog_level_sub)
```

```
## [1] N central cline\nm constant N latitude cline\nm constant
## [3] N equal\nm breaks           N equal\nm constant
```

```
## [5] N variable\nm variable
## 5 Levels: N equal\nm constant < ... < N variable\nm variable
```

```
unique(stat_df$demog_name)
```

```
## [1] Est-Clines_N-cline-center-to-edge_m-constant
## [2] Est-Clines_N-cline-N-to-S_m-constant
## [3] Est-Clines_N-equal_m_breaks
## [4] Est-Clines_N-equal_m-constant
## [5] Est-Clines_N-variable_m-variable
## [6] SS-Clines_N-cline-center-to-edge_m-constant
## [7] SS-Clines_N-cline-N-to-S_m-constant
## [8] SS-Clines_N-equal_m_breaks
## [9] SS-Clines_N-equal_m-constant
## [10] SS-Clines_N-variable_m-variable
## [11] SS-Mtn_N-cline-center-to-edge_m-constant
## [12] SS-Mtn_N-cline-N-to-S_m-constant
## [13] SS-Mtn_N-equal_m_breaks
## [14] SS-Mtn_N-equal_m-constant
## [15] SS-Mtn_N-variable_m-variable
## 15 Levels: SS-Clines_N-equal_m-constant ... Est-Clines_N-variable_m-variable
```

```
unique(stat_df$arch_level_sub)
```

```
## [1] 1 trait 2 traits\nno pleiotropy\nequal S
## [3] 2 traits\nno pleiotropy\nunequal S 2 traits\npleiotropy\nequal S
## [5] 2 traits\npleiotropy\nunequal S
## 5 Levels: 1 trait < ... < 2 traits\npleiotropy\nunequal S
```

```
unique(stat_df$arch)
```

```
## [1] highly-polygenic_1-trait
## [2] highly-polygenic_2-trait-no-pleiotropy-equal-S
## [3] highly-polygenic_2-trait-no-pleiotropy-unequal-S
## [4] highly-polygenic_2-trait-pleiotropy-equal-S
## [5] highly-polygenic_2-trait-pleiotropy-unequal-S
## [6] mod-polygenic_1-trait
## [7] mod-polygenic_2-trait-no-pleiotropy-equal-S
## [8] mod-polygenic_2-trait-no-pleiotropy-unequal-S
## [9] mod-polygenic_2-trait-pleiotropy-equal-S
## [10] mod-polygenic_2-trait-pleiotropy-unequal-S
## [11] oliogenic_1-trait
## [12] oliogenic_2-trait-no-pleiotropy-equal-S
## [13] oliogenic_2-trait-no-pleiotropy-unequal-S
## [14] oliogenic_2-trait-pleiotropy-equal-S
## [15] oliogenic_2-trait-pleiotropy-unequal-S
## 15 Levels: highly-polygenic_1-trait ...
```

```
## Statistical model with both traits
stat_df$trait <- factor(stat_df$trait)
levels(stat_df$trait)
```

```
## [1] "cor_TPR_sal" "cor_TPR_temp"
```

```
levels(stat_df$N_traits)
```

```
## NULL
```

```
modelsum <- summary(aov(cor_TPR ~ trait + arch + demog + demog_level + final_LA + arch*trait*demog,
modelsum
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## trait          1  64.20   64.20 5513.30 <2e-16 ***
## arch          14 159.27   11.38  977.03 <2e-16 ***
## demog           1   4.39    4.39  377.02 <2e-16 ***
## demog_level     1  10.19   10.19  874.72 <2e-16 ***
## final_LA        1   1.06    1.06   91.11 <2e-16 ***
## trait:arch      11   9.11    0.83   71.15 <2e-16 ***
## arch:demog      14  15.03    1.07   92.22 <2e-16 ***
## trait:demog      1  38.34   38.34 3292.79 <2e-16 ***
## trait:arch:demog 11   1.76    0.16   13.77 <2e-16 ***
## Residuals     3994  46.50    0.01
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 450 observations deleted due to missingness
```

```
### Percent of variation (SS) explained by each explanatory variable
pervar <- data.frame(variable = rownames(modelsum[[1]]), SS = modelsum[[1]][,2])
pervar$pervar <- round(pervar$SS/sum(pervar$SS)*100, 1)
pervar
```

```
##      variable      SS pervar
## 1 trait      64.195195  18.3
## 2 arch     159.267513  45.5
## 3 demog       4.389962   1.3
## 4 demog_level 10.185003   2.9
## 5 final_LA     1.060798   0.3
## 6 trait:arch   9.112923   2.6
## 7 arch:demog  15.033251   4.3
## 8 trait:demog  38.340187  11.0
## 9 trait:arch:demog 1.763571   0.5
## 10 Residuals  46.504897  13.3
```

```
## Statistical model with only temperature trait
```

```
modelsum <- summary(aov(cor_TPR_temp ~ arch + demog + demog_level + final_LA + arch*demog*demog_level
pervar_temp <- data.frame(variable = rownames(modelsum[[1]]), SS = modelsum[[1]][,2])
pervar_temp$pervar <- round(pervar_temp$SS/sum(pervar_temp$SS)*100, 1)
pervar_temp
```

```
##      variable      SS pervar
## 1 arch     111.4892548  76.8
## 2 demog      7.5012931   5.2
## 3 demog_level 0.5870414   0.4
```

```
## 4 final_LA          0.1096110    0.1
## 5 arch:demog        4.6914989    3.2
## 6 arch:demog_level  0.4397451    0.3
## 7 Residuals        20.3182657   14.0
```

```
## Statistical model with only salinity trait
```

```
modelsum <- summary(aov(cor_TPR_sal ~ arch + demog + demog_level + final_LA + arch*demog*demog_level
pervar_sal <- data.frame(variable = rownames(modelsum[[1]]), SS = modelsum[[1]][,2])
pervar_sal$pervar <- round(pervar_sal$SS/sum(pervar_sal$SS)*100, 1)
pervar_sal
```

```
##          variable      SS pervar
## 1 arch          56.8911818   40.5
## 2 demog         38.5015498   27.4
## 3 demog_level   15.4485976   11.0
## 4 final_LA       0.2370578    0.2
## 5 arch:demog     9.6827706    6.9
## 6 arch:demog_level 1.0917684    0.8
## 7 Residuals     18.6684705   13.3
```

```
data.frame(variable = pervar_temp$variable, temp_AFcors = pervar_temp$pervar, sal_AFcors = pervar_sal$pervar)
```

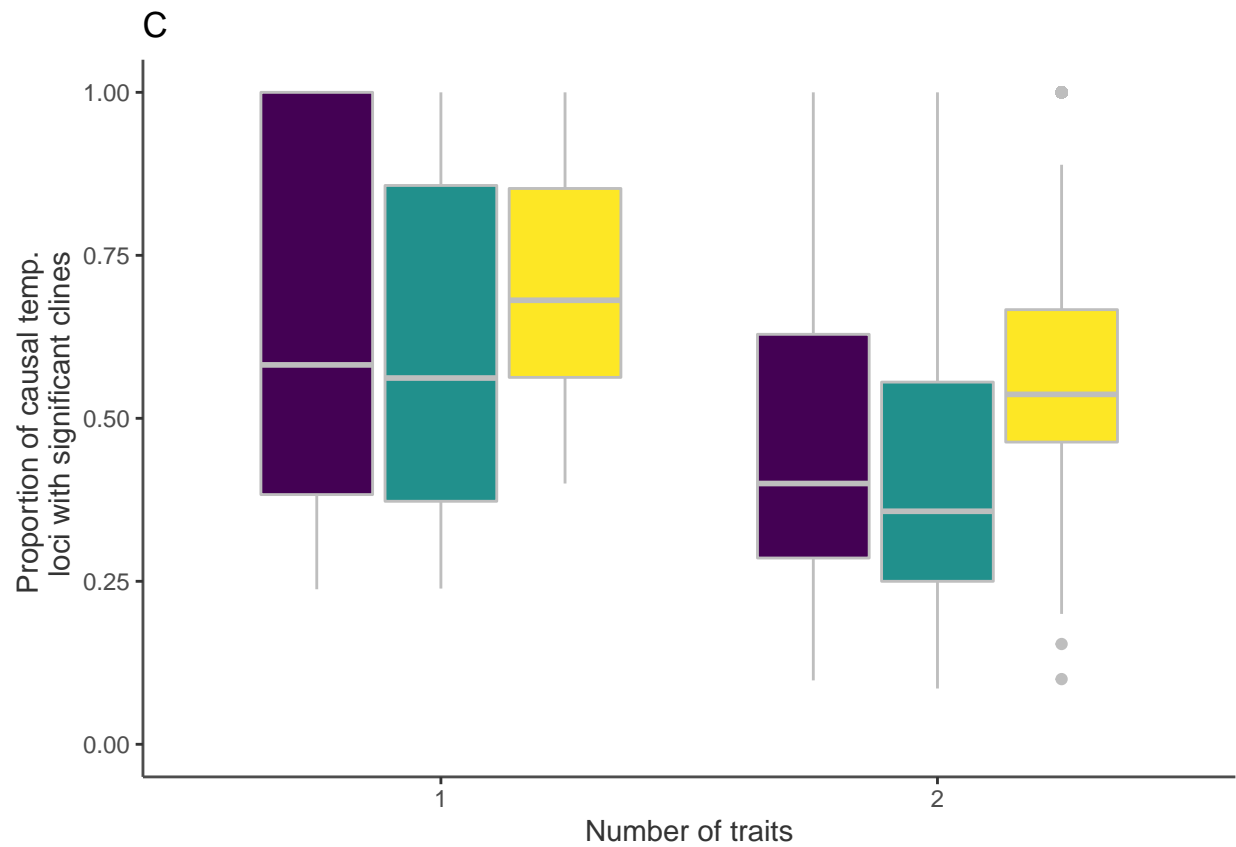
```
##          variable temp_AFcors sal_AFcors
## 1 arch          76.8         40.5
## 2 demog          5.2         27.4
## 3 demog_level     0.4         11.0
## 4 final_LA        0.1          0.2
## 5 arch:demog       3.2          6.9
## 6 arch:demog_level 0.3          0.8
## 7 Residuals       14.0         13.3
```

How does demography and genetic architecture contribute to the evolution of phenotypic clines without clines in causal allele frequencies?

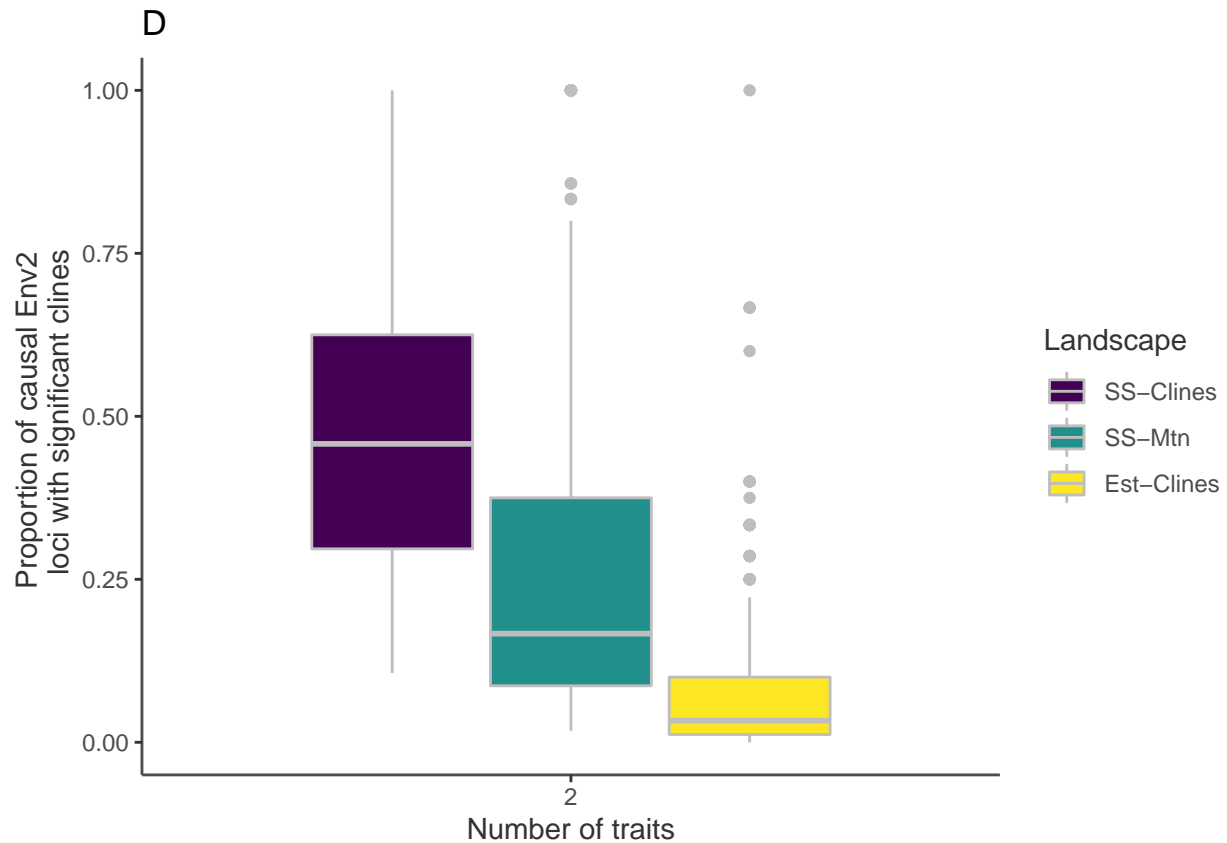
Number of loci with correlations - demog

```
# Plote temperatue clines as a function of number of traits and landscape
```

```
a<- ggplot(final.df, aes(x=as.factor(N_traits), y=cor_TPR_temp, fill=demog_level)) + geom_boxplot(color=
a
```



```
# Plot Env2 clines as a function of landscape (only 2 trait simulations)
forb <- final.df[final.df$N_traits==2,]
forb$N_traits <- factor(forb$N_traits)
b<- ggplot(forb, aes(x=N_traits, y=cor_TPR_sal, fill=demog_level)) + geom_boxplot(color="grey") + ggthemes::ggtheme("b")
```



```
### Pleiotropy vs no pleiotropy - only relevant for sims with 2 traits
subdf_arch <- final.df[final.df$N_traits==2,]
unique(final.df$SIGMA_K_1)
```

```
## [1] 0.5
```

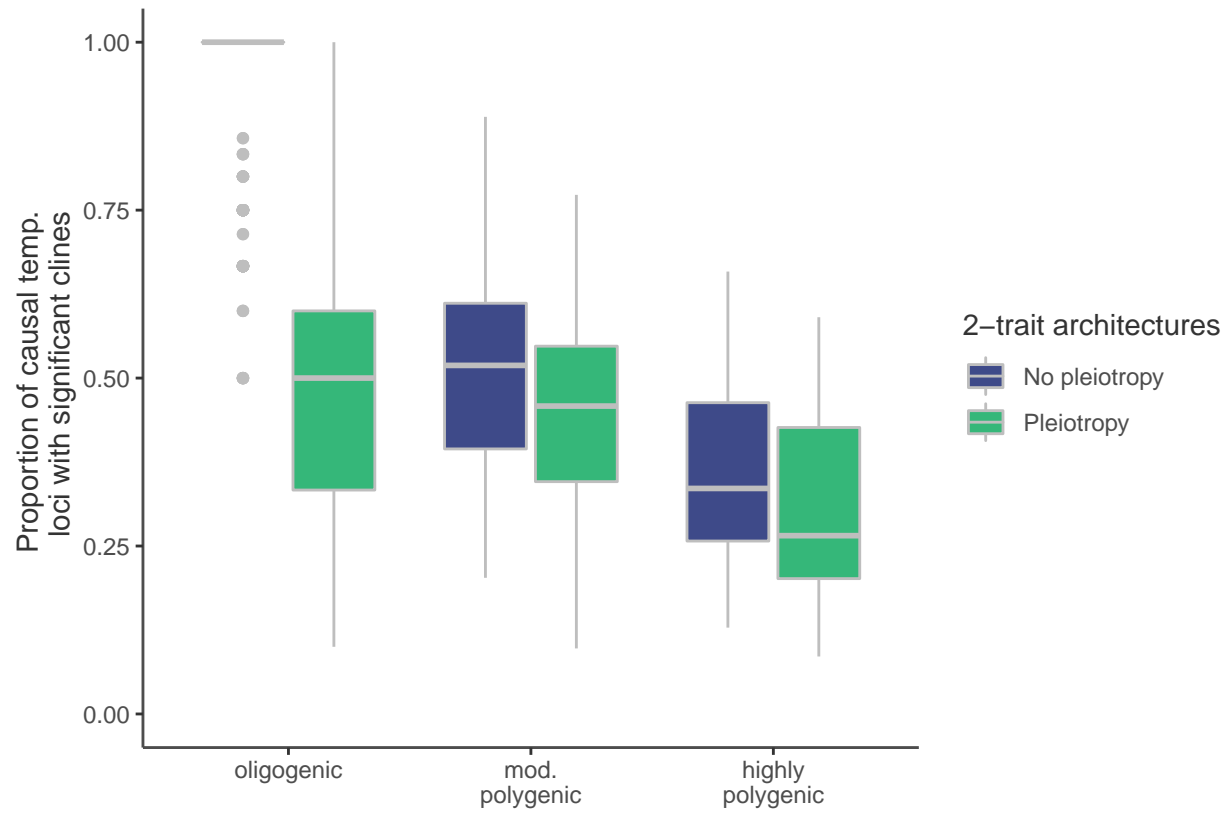
```
unique(subdf_arch$SIGMA_K_2)
```

```
## [1] 0.5 4.0
```

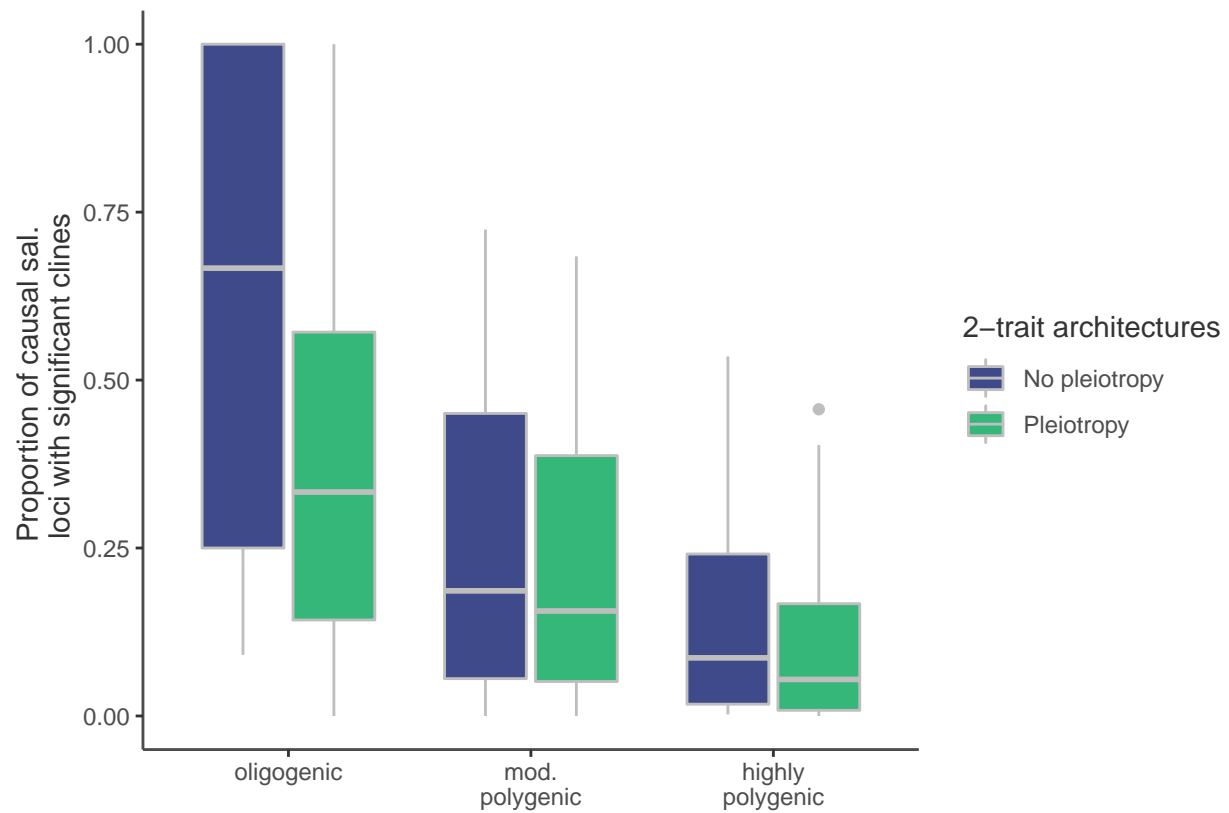
```
subdf_arch$SIGMA_K_2 <- as.factor(subdf_arch$SIGMA_K_2)
my_col_arch <- c(viridis(10)[3], viridis(10)[7])
```

```
# temp only
```

```
f1 <- ggplot(subdf_arch, aes(x=arch_level, y=cor_TPR_temp, fill=as.factor(ispleiotropy))) + geom_boxplot()
f1
```

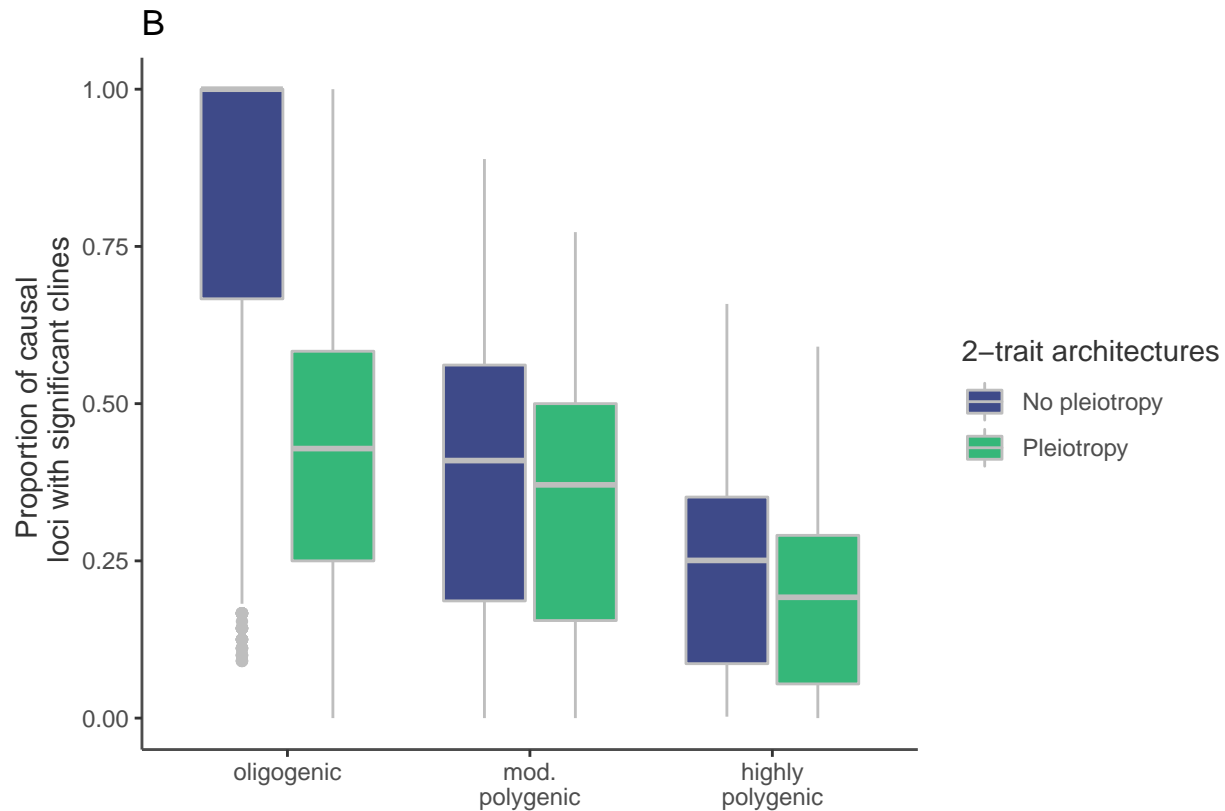



```
# env2 only
f2 <- ggplot(subdf_arch, aes(x=arch_level, y=cor_TPR_sal, fill=as.factor(ispleiotropy))) + geom_boxplot()
f2
```



```
# Combine data together from f1 and f2 for a single plot
# because they both show the same pattern
pleiotropy.df <- gather(subdf_arch, key=trait, value=cor_TPR, cor_TPR_temp, cor_TPR_sal)

fboth <- ggplot(pleiotropy.df, aes(x=arch_level, y=cor_TPR, fill=as.factor(ispleiotropy))) + geom_boxplot()
fboth
```



```
## Phenotypic clines vs. af clines
```

```
### For each trait, I want to plot the (correlation between the trait and environment) vs. (correlation
```

```
final.df$N_traits2 <- final.df$N_traits
final.df$N_traits2[final.df$N_traits==1] <- "1 Trait"
final.df$N_traits2[final.df$N_traits==2] <- "2 Traits"
final.df$ispleiotropy <- factor(final.df$ispleiotropy)
head(final.df$ispleiotropy)
```

```
## [1] No pleiotropy No pleiotropy No pleiotropy No pleiotropy No pleiotropy
```

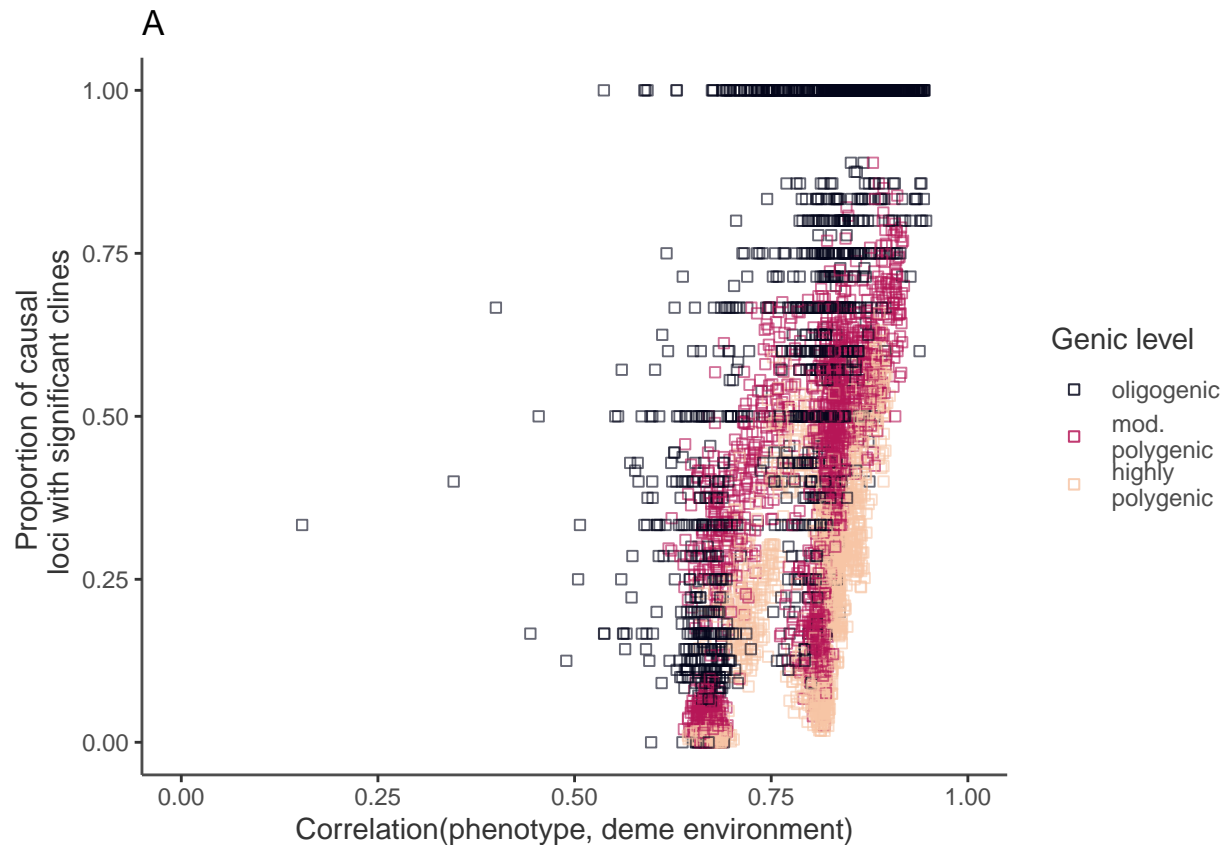
```
## [6] No pleiotropy
```

```
## Levels: No pleiotropy Pleiotropy
```

```
f3 <- ggplot(final.df) +
  geom_point(aes(x=subsamp_corr_phen_temp, y=cor_TPR_temp, color=arch_level#, shape=ispleiotropy
    ), alpha=0.6, fill="grey", shape=0) +
  geom_point(aes(x=subsamp_corr_phen_sal, y=cor_TPR_sal, color=arch_level#, shape=ispleiotropy
    ), alpha=0.6, fill="grey", shape=0) +
  ggtheme + ylim(0,1) + xlim(0,1) +
  xlab("Correlation(phenotype, deme environment)") +
  ylab("Proportion of causal \n loci with significant clines") + scale_color_viridis(name="Genic level")
  ggtitle("A") ## ## facet_grid(~N_traits2)
  # facet_grid(~arch_level_sub)
```

```
f3
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```



```
# 450 missing values expected (simulations without the Env2 trait)
```

```
pdf(paste0(outputs, "WhatDrivesNonClines.pdf"), width=6, height=8)
grid.arrange(f3, fboth, a, b, nrow=3, ncol=2, layout_matrix=matrix(c(1,1,2,2,3,4), nrow=3, byrow=TRUE))
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
# 450 missing values expected (simulations without the Env2 trait)
dev.off()
```

```
## pdf
## 2
```

Percent of GWAS hits with clines

```
head(final.df$clinalparadigm_temp_propsigGWASclines)
```

```
## [1] 0.6050302 0.5794083 0.5593769 0.4777563 0.6314615 0.3099063
```

```
sum(is.na(final.df$clinalparadigm_temp_propsigGWASclines))
```

```
## [1] 1
```

```
plotdf <- data.frame(propsigGWASclines=c(final.df$clinalparadigm_sal_propsigGWASclines,final.df$clinalp
propClines=c(final.df$cor_TPR_sal,final.df$cor_TPR_temp),
arch_level=factor(rep("a",nrow(final.df)*2)))
plotdf$arch_level <- c(as.character(final.df$arch_level, final.df$arch_level))
str(plotdf)
```

```
## 'data.frame': 4500 obs. of 3 variables:
## $ propsigGWASclines: num NA NA NA NA NA NA NA NA NA NA NA ...
## $ propClines : num NA NA NA NA NA NA NA NA NA NA NA ...
## $ arch_level : chr "highly\npolygenic" "highly\npolygenic" "highly\npolygenic" "highly\npoly"
```

```
summary(lm(propsigGWASclines~propClines*arch_level, data=plotdf))
```

```
##
## Call:
## lm(formula = propsigGWASclines ~ propClines * arch_level, data = plotdf)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.37677 -0.07902 -0.01619  0.05425  0.76866
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.001683   0.006292   0.268   0.7891
## propClines        1.051200   0.021509  48.872 < 2e-16 ***
## arch_levelmod.\npolygenic -0.020949   0.009667  -2.167   0.0303 *
## arch_leveloligogenic    0.050248   0.010200   4.927 8.71e-07 ***
## propClines:arch_levelmod.\npolygenic -0.291569   0.027169 -10.732 < 2e-16 ***
## propClines:arch_leveloligogenic    -0.747232   0.024263 -30.797 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1321 on 4043 degrees of freedom
## (451 observations deleted due to missingness)
## Multiple R-squared:  0.5648, Adjusted R-squared:  0.5642
## F-statistic: 1049 on 5 and 4043 DF, p-value: < 2.2e-16
```

```
pdf(paste0(outputs,"PropGWASClinal.pdf"), width=6, height=5)
ggplot(plotdf, aes(y=propsigGWASclines,
x=propClines, color=arch_level)) +
  geom_point( alpha=0.5) +xlim(0,1) + ylim(0,1) + ggtheme +
  geom_smooth(method="glm", level=0.95) + xlab("Proportion of QTNs that are clinal (ground truth)") + y
  geom_abline(intercept=0, slope=1, color="grey")
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 451 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 451 rows containing missing values (geom_point).
```

```
## Warning: Removed 3 rows containing missing values (geom_smooth).
```

```
dev.off()
```

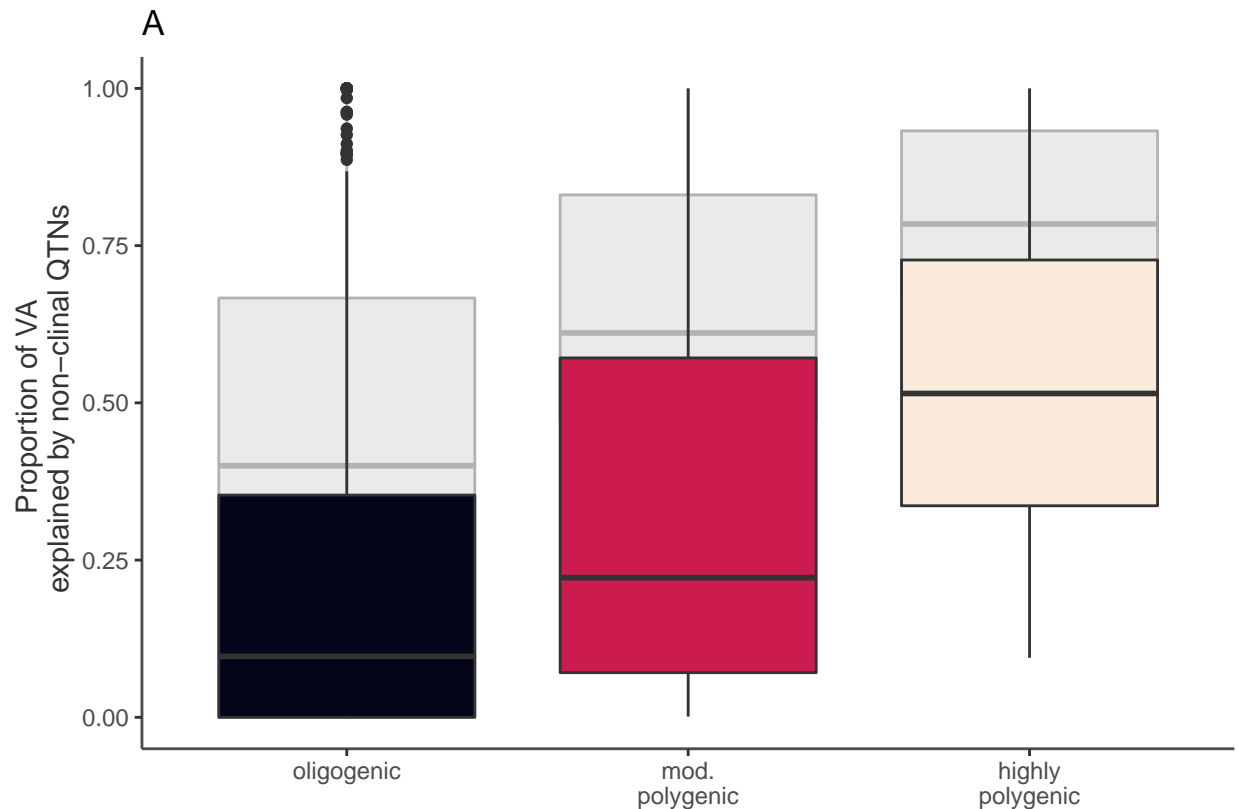
```
## pdf
## 2
```

Percent of Va explained by clinal loci

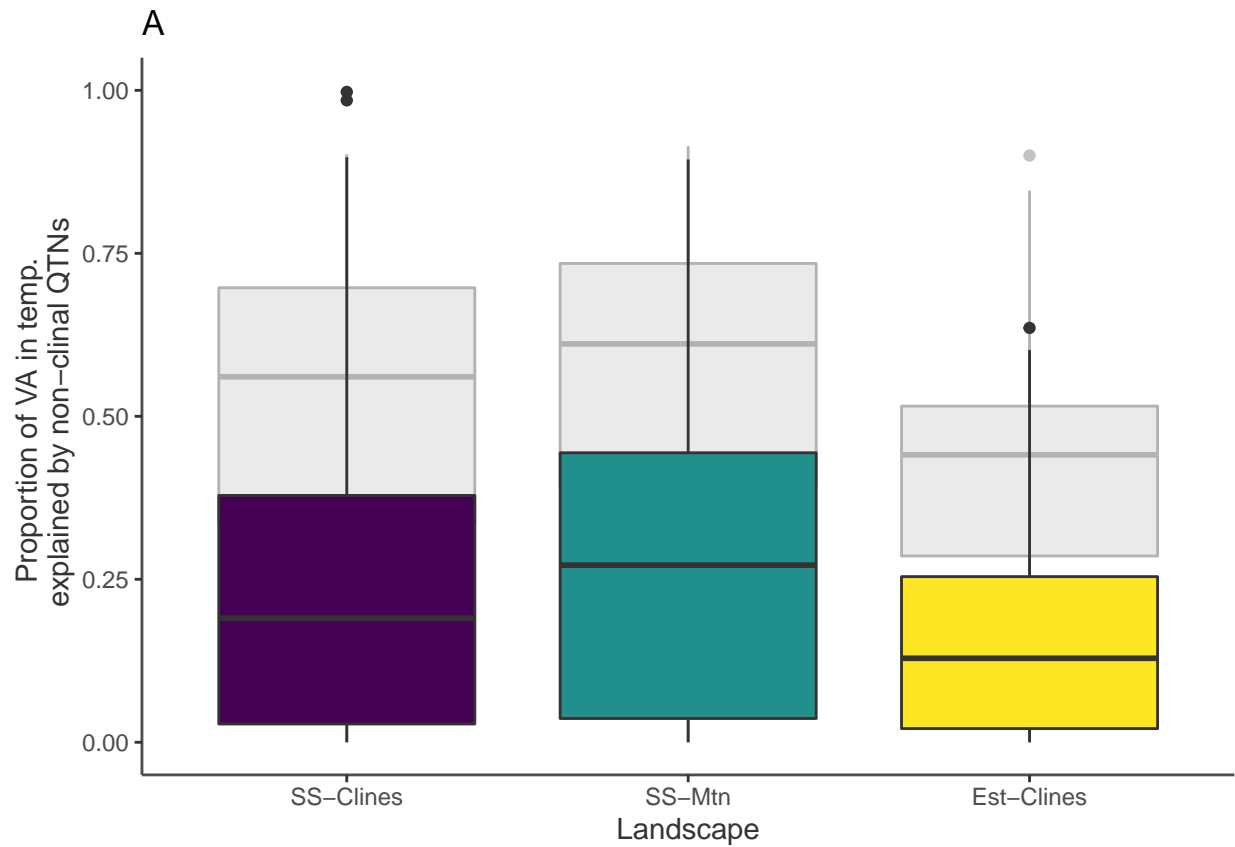
Same plots as above, but for the percent of the additive genetic variance (Va). If clinal loci explain a major proportion of Va, then it could be argued that QTN loci that do not have clinal patterns are not as “important” to discover.

```
# Reorganize data for plotting
pleiotropy.df2 <- gather(subdf_arch, key=trait, value=cor_VA_prop, cor_VA_temp_prop, cor_VA_sal_prop)
pleiotropy.df3 <- gather(subdf_arch, key=trait, value=cor_TPR, cor_TPR_temp, cor_TPR_sal)

fboth2 <- ggplot() +
  geom_boxplot(aes(x=arch_level, y=1-cor_TPR), data=pleiotropy.df3, color="grey70", alpha=0.8, fill="grey70") +
  geom_boxplot(aes(x=arch_level, y=1-cor_VA_prop, fill=arch_level), data=pleiotropy.df2, color="grey20")
fboth2
```

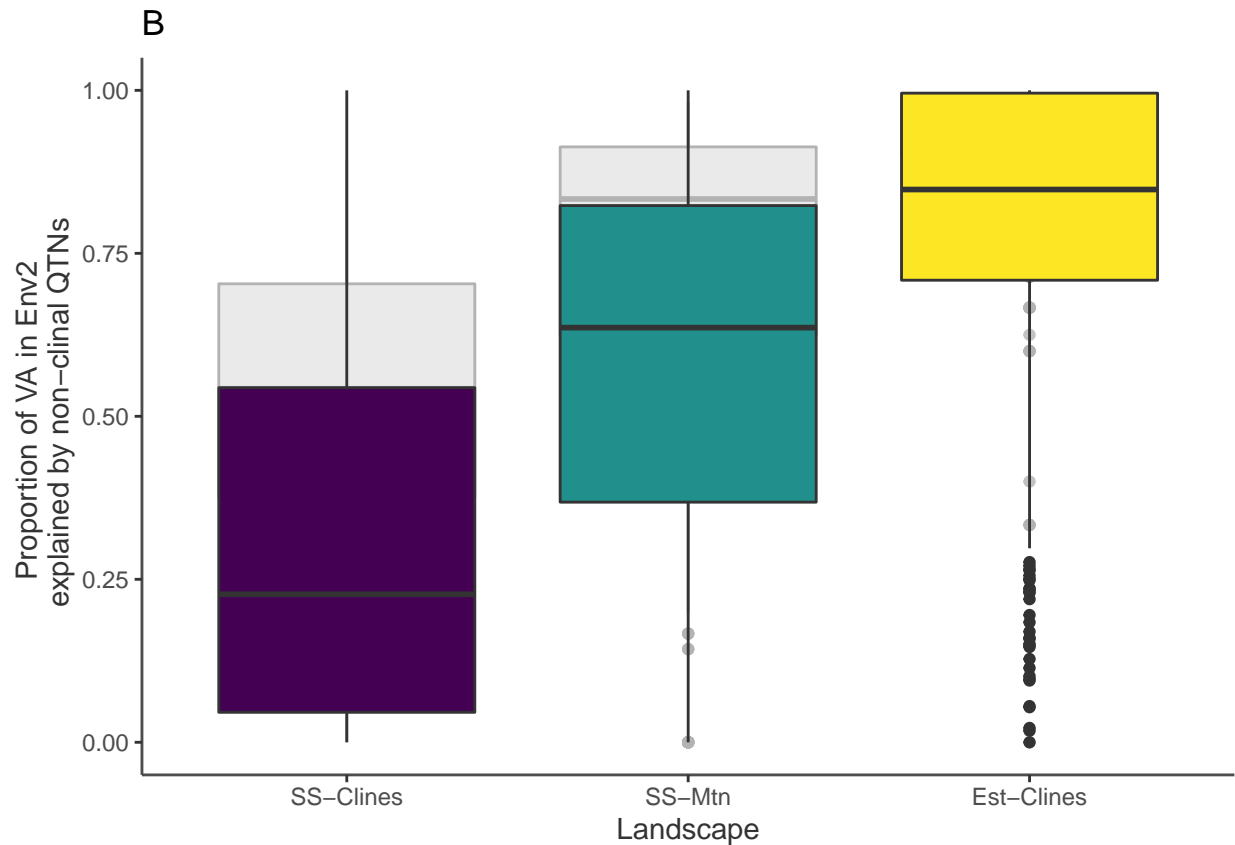


```
a1<- ggplot() +
  geom_boxplot(aes(x=demog_level, y=1-cor_TPR_temp), data=final.df, color="grey70", alpha=0.8, fill="grey70") +
  geom_boxplot(data=final.df, aes(x=demog_level, y=1-cor_VA_temp_prop, fill=demog_level),color="grey20")
a1
```



```
b1<- ggplot()+
  geom_boxplot(aes(x=demog_level, y=1-cor_TPR_sal), data=final.df, color="grey70", alpha=0.8, fill="grey70")+
  geom_boxplot(data=final.df, aes(x=demog_level, y=1-cor_VA_sal_prop, fill=demog_level),color="grey20")
b1
```

Warning: Removed 450 rows containing non-finite values (stat_boxplot).



```
pdf(paste0(outputs, "WhatDrivesNonClines_VA.pdf"), width=7, height=3)
# grid.arrange(fboth2, a1,b1, nrow=2, ncol=2, layout_matrix=matrix(c(1,1,2,3), nrow=2, byrow=TRUE))
grid.arrange(a1,b1, ncol=2)
```

```
## Warning: Removed 450 rows containing non-finite values (stat_boxplot).
```

```
dev.off()
```

```
## pdf
## 2
```

Demography sub level

```
unique(final.df$demog)
```

```
## [1] Estuary SS
## Levels: Estuary SS
```

```
unique(final.df$demog_level)
```

```
## [1] Est-Clines SS-Clines SS-Mtn
## Levels: SS-Clines < SS-Mtn < Est-Clines
```



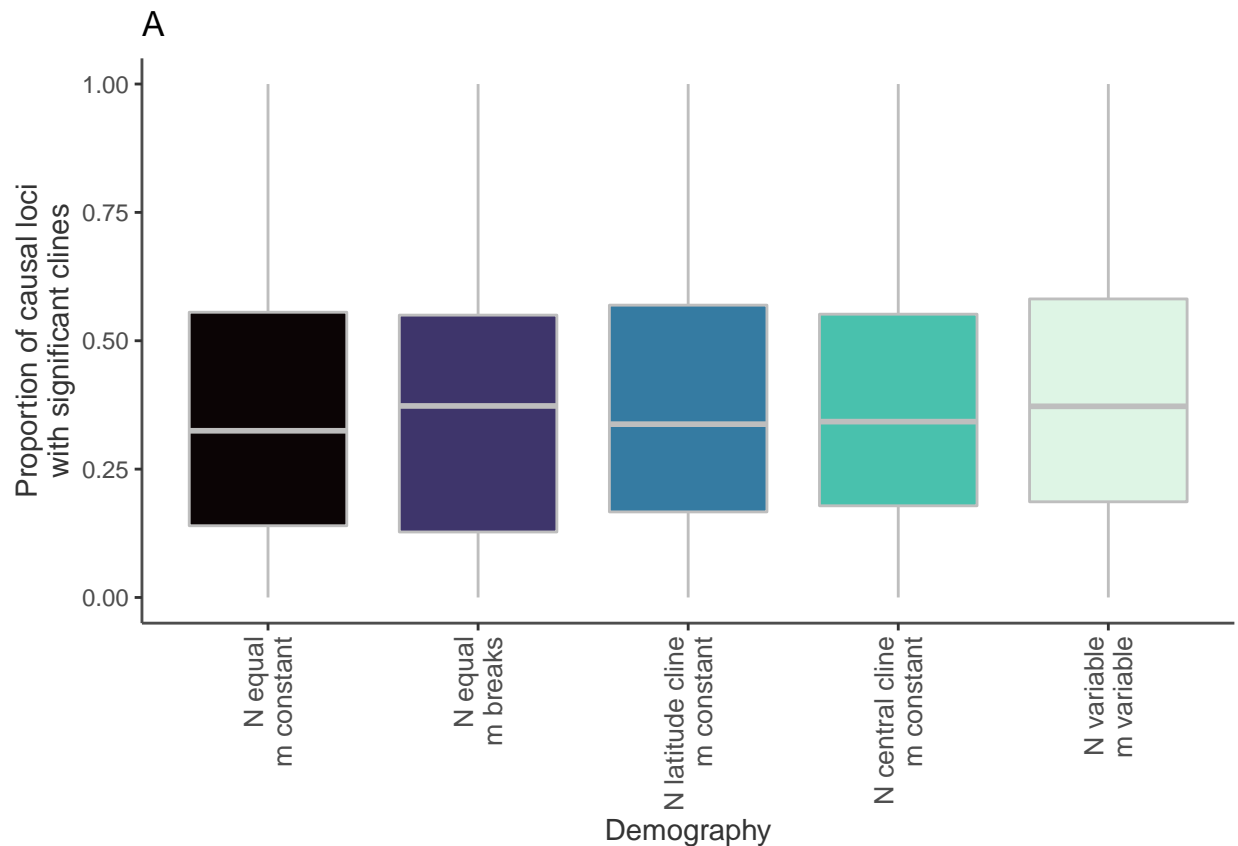
```
unique(final.df$demog_level_sub)
```

```
## [1] N central cline\nm constant  N latitude cline\nm constant
## [3] N equal\nm breaks             N equal\nm constant
## [5] N variable\nm variable
## 5 Levels: N equal\nm constant < ... < N variable\nm variable
```

```
pleiotropy.df$demog_level_sub <- as.factor(pleiotropy.df$demog_level_sub)
levels(pleiotropy.df$demog_level_sub) <- c("N equal\nm constant", "N equal\nm breaks", "N latitude cline\nm constant", "N central cline\nm constant", "N variable\nm variable")
```

```
## Sub demograph - mako color
```

```
d1 <- ggplot(pleiotropy.df, aes(x=as.factor(demog_level_sub), y=cor_TPR, fill=as.factor(demog_level_sub)))
d1
```

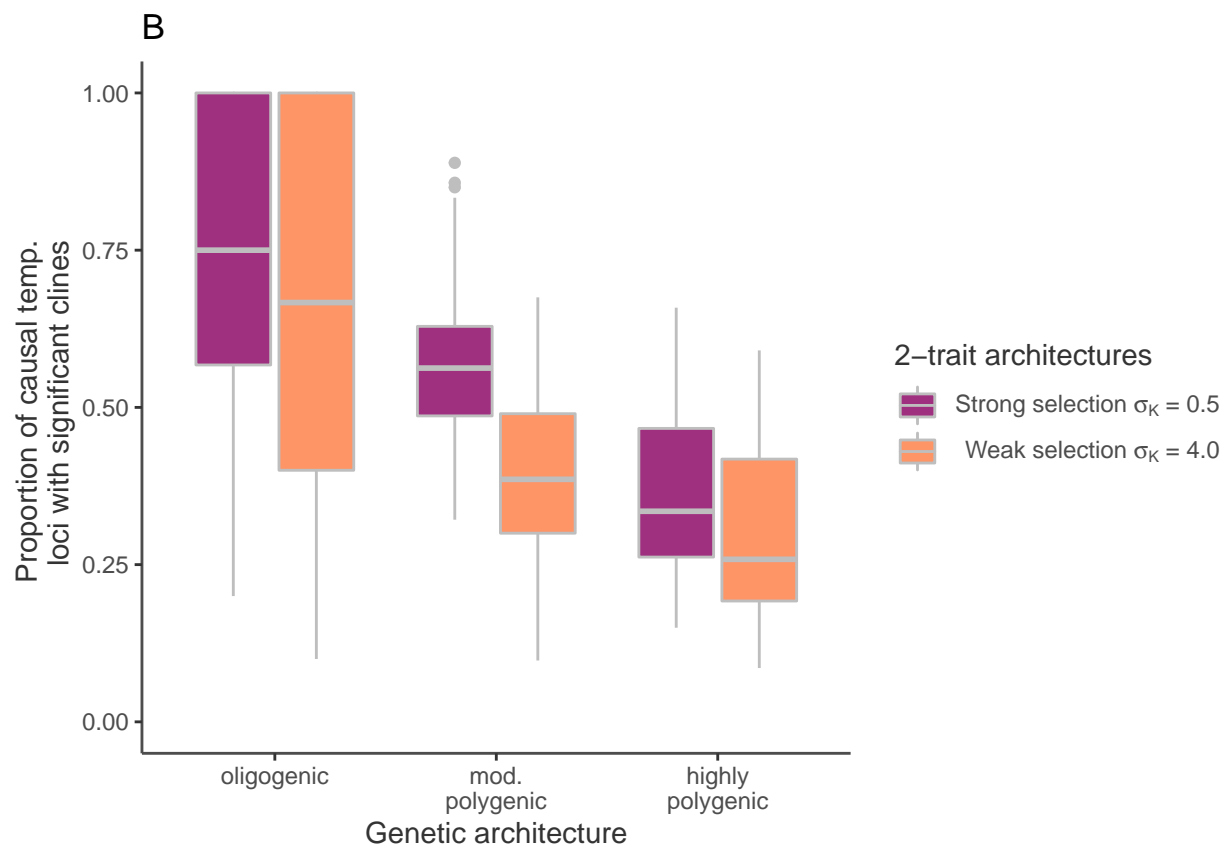


```
## Strength of selection - magma color
```

```
my_col_S <- c(magma(10)[5], magma(10)[8])
```

```
s1<- ggplot(subdf_arch, aes(x=arch_level, y=cor_TPR_temp, fill=as.factor(SIGMA_K_2))) + geom_boxplot(col=
  expression(paste("Strong selection ", sigma[K], " = 0.5")),
  expression(paste("Weak selection ", sigma[K], " = 4.0"))
```

```
), name="2-trait architectures") + ylim(0,1) + xlab("Genetic architecture") + ggtitle("B")
s1
```



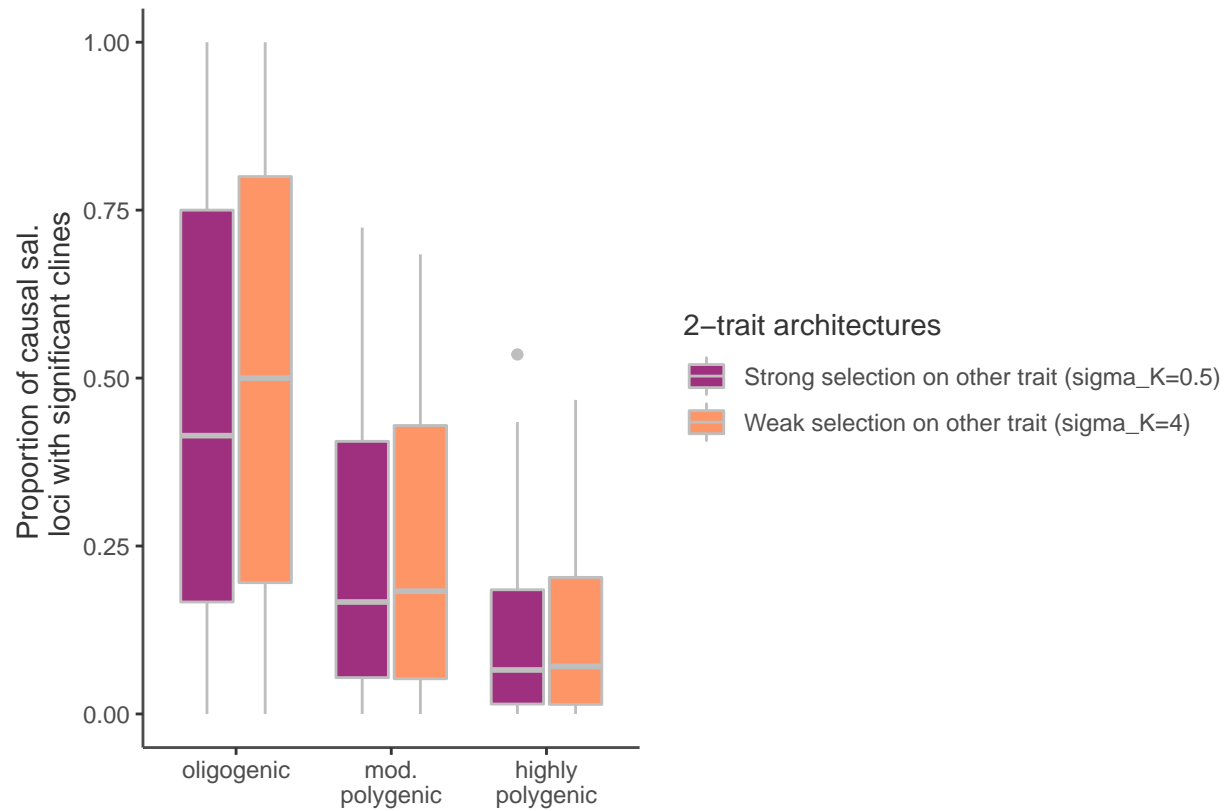
```
pdf(paste0(outputs, "WhatDrivesNonClines-subdemog-selection.pdf"), width=6, height=8)
  grid.arrange(d1, s1, nrow=2)
dev.off()
```

```
## pdf
## 2
```

Does hanging strength of selection on trait 1 (temp) affect the number of allele frequency clines that evolve in trait 2 (env2)? Graph suggests no.

```
#+ theme(legend.title=element_text("2-trait\narchitectures"))

ggplot(subdf_arch, aes(x=arch_level, y=cor_TPR_sal, fill=as.factor(SIGMA_K_2))) + geom_boxplot(color="g
```



Distribution of the correlation between structure and deme environment

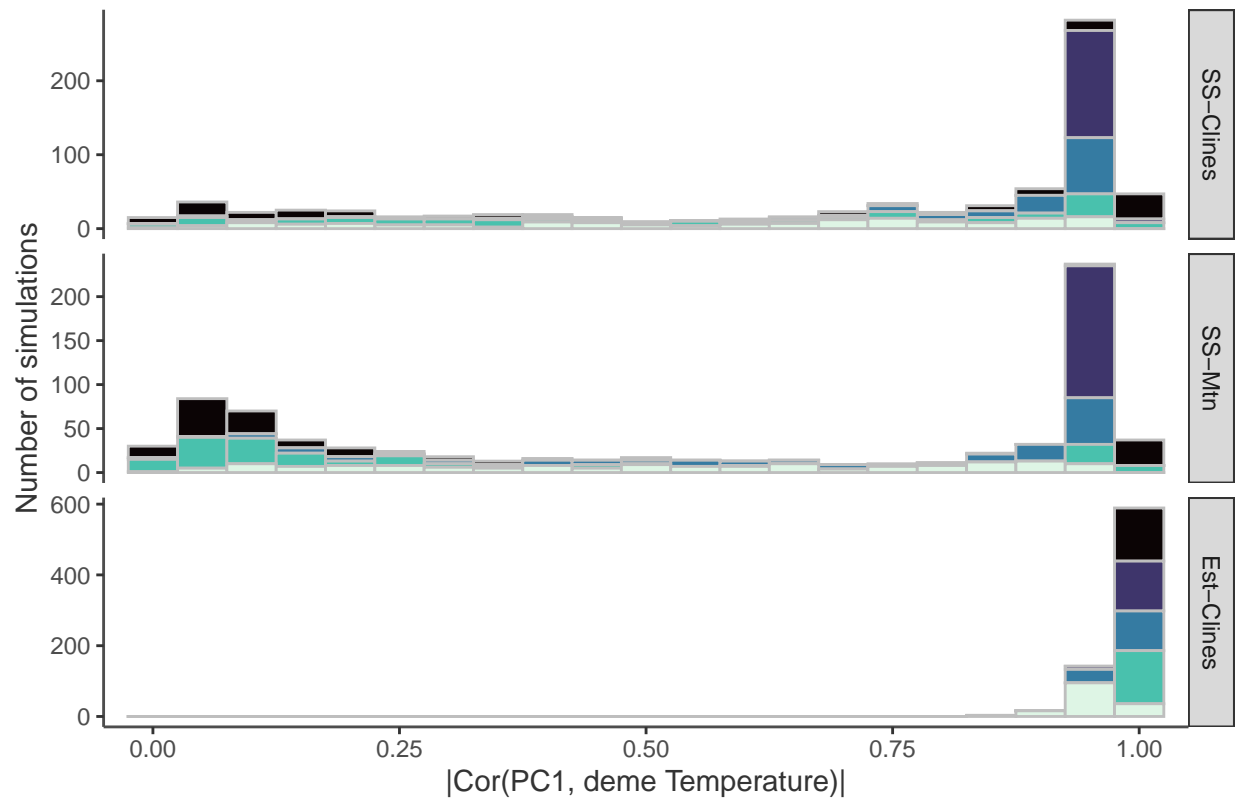
```
sum(is.na(final.df$cor_PC1_temp))
```

```
## [1] 0
```

```
# First PC axis with temp
```

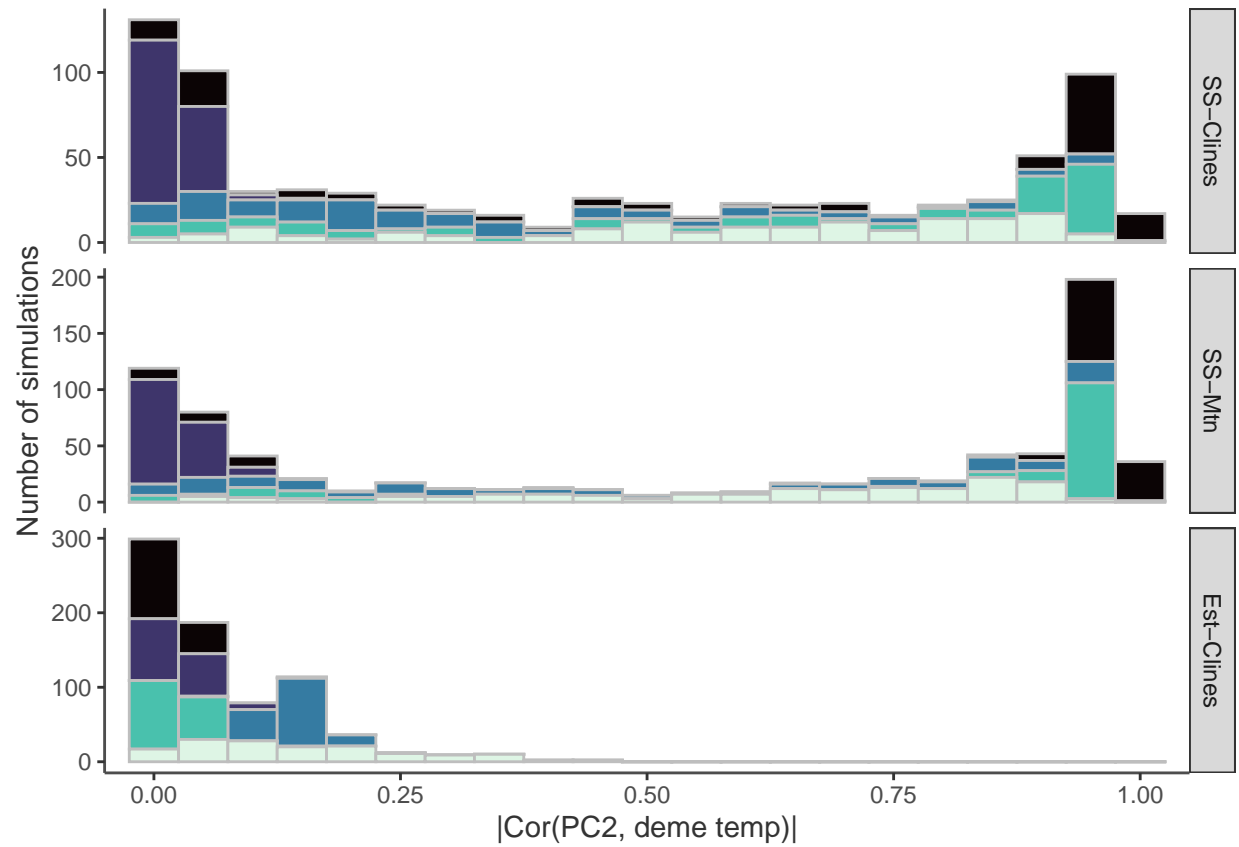
```
sc1<- ggplot(final.df) + geom_histogram(aes(x=abs(cor_PC1_temp), fill=demog_level_sub), binwidth=0.05,
sc1
```

A) Temperature



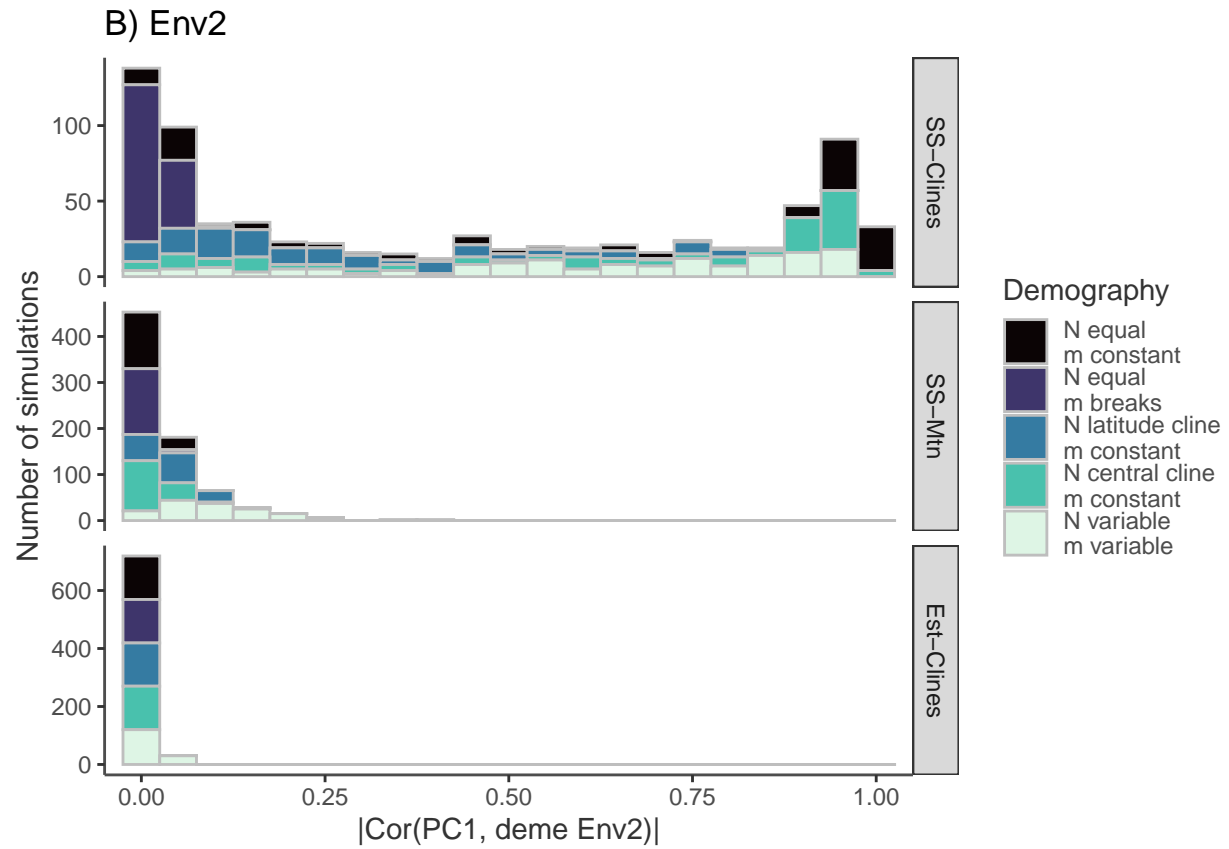
2nd PC axis with temp

```
sc2<-ggplot(final.df) + geom_histogram(aes(x=abs(cor_PC2_temp), fill=demog_level_sub), binwidth=0.05, c
sc2
```



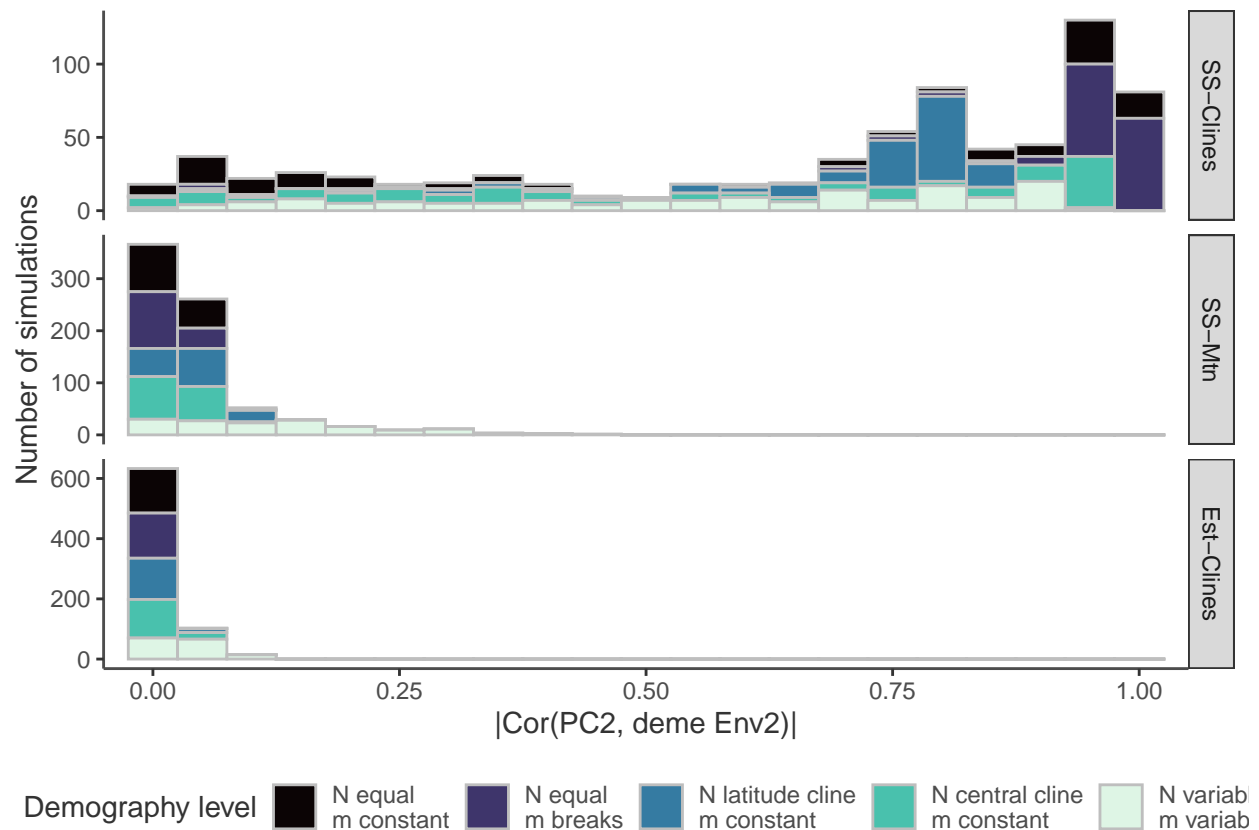
1st PC axis with Env2

```
sc3<-ggplot(final.df) + geom_histogram(aes(x=abs(cor_PC1_sal), fill=demog_level_sub), binwidth=0.05, col="black")
sc3
```



2nd PC axis with Env2

```
sc4<-ggplot(final.df) + geom_histogram(aes(x=abs(cor_PC2_sal), fill=demog_level_sub), binwidth=0.05, c
sc4
```



```
pdf(paste0(outputs, "StructureEnvCor_facetDemog.pdf"), width=12, height=9)
  grid.arrange(sc1, sc3, layout_matrix=matrix(c(1,1,1,2,2,2,2),
                                              nrow=1), nrow=1)
dev.off()
```

```
## pdf
## 2
```

Under what conditions can we reliably identify the alleles with effects on adaptive phenotypes using genetic-environment associations (latent factor mixed models, uncorrected correlations, and redundancy analysis)?

Compare methods AUC

AUC stands for area under the curve, here I use the Precision-Recall curve

```
# Check for missing data
sum(is.na(final.df$cor_AUCPR_temp_neutSNPs))
```

```
## [1] 0
```

```
sum(is.na(final.df$cor_AUCPR_sal_neutSNPs)) #expected 450 missing
```

```
## [1] 450
```

```
sum(is.na(final.df$LEA3.2_lfmm2_AUCPR_temp_neutSNPs))
```

```
## [1] 0
```

```
sum(is.na(final.df$LEA3.2_lfmm2_AUCPR_sal_neutSNPs)) #expected 450 missing
```

```
## [1] 450
```

```
sum(is.na(final.df$RDA_AUCPR_neutSNPs))
```

```
## [1] 0
```

```
sum(is.na(final.df$RDA_AUCPR_neutSNPs_corr))
```

```
## [1] 0
```

```
# Reorganize data for plotting
```

```
comparemethods.AUC <- gather(final.df, key=method, value=AUCPR, cor_AUCPR_temp_neutSNPs, LEA3.2_lfmm2_AUCPR_sal_neutSNPs)
```

```
levels(factor(comparemethods.AUC$method))
```

```
## [1] "cor_AUCPR_sal_neutSNPs" "cor_AUCPR_temp_neutSNPs"
```

```
## [3] "LEA3.2_lfmm2_AUCPR_sal_neutSNPs" "LEA3.2_lfmm2_AUCPR_temp_neutSNPs"
```

```
## [5] "RDA_AUCPR_neutSNPs" "RDA_AUCPR_neutSNPs_corr"
```

```
comparemethods.AUC$methodtype <- factor(comparemethods.AUC$method)
```

```
comparemethods.AUC$methodtype <-  
  revalue(comparemethods.AUC$methodtype,  
    c(  
      "cor_AUCPR_temp_neutSNPs"= "Cor(p, Temp.)",  
      "LEA3.2_lfmm2_AUCPR_temp_neutSNPs" = "LFMM - Temp\n(structure correction)",  
      "cor_AUCPR_sal_neutSNPs"="Cor(p, Env2)",  
      "LEA3.2_lfmm2_AUCPR_sal_neutSNPs" = "LFMM - Env2\n(structure correction)",  
      "RDA_AUCPR_neutSNPs" = "RDA",  
      "RDA_AUCPR_neutSNPs_corr" = "pRDA\n(structure correction)" ))
```

```
comparemethods.AUC$methodtype <- factor(comparemethods.AUC$methodtype,  
  levels = c("Cor(p, Temp.)",  
    "LFMM - Temp\n(structure correction)",  
    "Cor(p, Env2)",  
    "LFMM - Env2\n(structure correction)",  
    "RDA",  
    "pRDA\n(structure correction)"),  
  ordered=TRUE)
```

```
# Sanity checks
```

```
levels(comparemethods.AUC$methodtype)
```



```
## [1] "Cor(p, Temp.)"          "LFMM - Temp\n(structure correction)"
## [3] "Cor(p, Env2)"           "LFMM - Env2\n(structure correction)"
## [5] "RDA"                    "pRDA\n(structure correction)"
```

```
table(comparemethods.AUC$methodtype)
```

```
##
##               Cor(p, Temp.) LFMM - Temp\n(structure correction)
##                   2250                                2250
##               Cor(p, Env2) LFMM - Env2\n(structure correction)
##                   2250                                2250
##                   RDA          pRDA\n(structure correction)
##                   2250                                2250
```

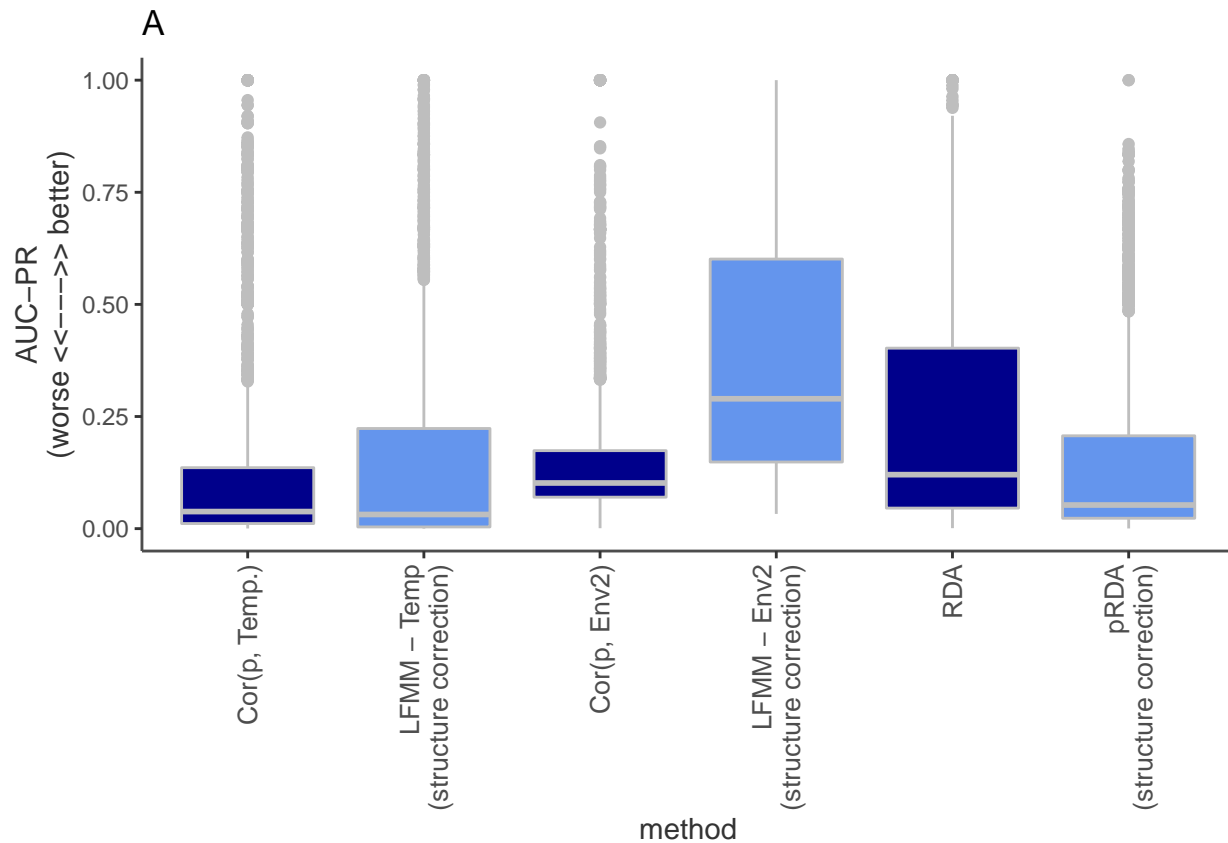
```
summary(comparemethods.AUC$AUCPR)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NA's
## 0.0000 0.0314 0.0890 0.2013 0.2791 1.0000     900
```

```
# Across all simulations, AUCPR
```

```
g <- ggplot(comparemethods.AUC, aes(x=as.factor(methodtype), y=AUCPR)) + geom_boxplot(color="grey", fill="darkblue")
g
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```



```
# tried a violin plot, but the boxplot is better
# 450 NAs are expected for the Env2 models
tapply(comparemethods.AUC$AUCPR,comparemethods.AUC$methodtype, function(x){sum(is.na(x))})
```

```
##                Cor(p, Temp.) LFMM - Temp\n(structure correction)
##                0
##                Cor(p, Env2) LFMM - Env2\n(structure correction)
##                450
##                RDA          pRDA\n(structure correction)
##                0
```

Compare methods FDR

False discovery rate (FDR) is the proportion of positive tests that are true positives. If there are no positive tests, then the statistic is undefined (NA).

```
#Check for NAs in temperature models
sum(is.na(final.df$cor_FDR_neutSNPs_temp))
```

```
## [1] 0
```

```
sum(is.na(final.df$LEA3.2_lfmm2_FDR_neutSNPs_temp))
```

```
## [1] 697
```

```
# A lot of NAs here
```

```
# Check NAs in FDR or temp/salinity model come from cases with 0 outliers
table(isFDR_NA=is.na(final.df$LEA3.2_lfmm2_FDR_neutSNPs_temp),
      is_0_outliers=(final.df$LEA3.2_lfmm2_num_causal_sig_temp==0 &
                      final.df$LEA3.2_lfmm2_num_neut_sig_temp==0))
```

```
##          is_0_outliers
## isFDR_NA FALSE TRUE
##   FALSE  1553    0
##   TRUE     0  697
```

```
table(isFDR_NA=is.na(final.df$LEA3.2_lfmm2_FDR_neutSNPs_sal),
      is_0_outliers=(final.df$LEA3.2_lfmm2_num_causal_sig_sal==0 &
                      final.df$LEA3.2_lfmm2_num_neut_sig_sal==0))
```

```
##          is_0_outliers
## isFDR_NA FALSE TRUE
##   FALSE  1689    0
##   TRUE     0  561
```

```
tapply(is.na(final.df$LEA3.2_lfmm2_FDR_neutSNPs_temp),
      list(final.df$demog_level, final.df$demog_level_sub), sum)
```

```
##          N equal\nm constant N equal\nm breaks N latitude cline\nm constant
## SS-Clines          40          41          62
## SS-Mtn             45          63          55
## Est-Clines         31          34          54
##          N central cline\nm constant N variable\nm variable
## SS-Clines          50          53
## SS-Mtn             56          58
## Est-Clines         9          46
```

NAs are evenly spread across the demographies, but slightly higher in the SS scenarios

#Check for NAs in RDA model

```
sum(is.na(final.df$RDA_FDR_neutSNPs))
```

```
## [1] 2
```

```
sum(is.na(final.df$RDA_FDR_neutSNPs_corr))
```

```
## [1] 0
```

reorganize data for plotting

```
comparemethods.FDR <- gather(final.df, key=method, value=FDR, cor_FDR_neutSNPs_temp, LEA3.2_lfmm2_FDR_n
```

```
comparemethods.FDR <- comparemethods.FDR[order(comparemethods.FDR$seed),]
tail(comparemethods.FDR)
```

```
##          seed
## 2250 1233343
## 4500 1233343
## 6750 1233343
## 9000 1233343
## 11250 1233343
## 13500 1233343
##
##                                     level reps
## 2250 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 4500 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 6750 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 9000 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 11250 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 13500 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
##
##                                     arch          demog_name
## 2250 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 4500 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 6750 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 9000 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 11250 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 13500 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
##
##          demog_level_sub demog_level MIG_x MIG_y xcline ycline demog
## 2250 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 4500 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 6750 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 9000 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
```

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## 11250 N variable\nm variable      SS-Mtn 0.03 0.03      V linear      SS
## 13500 N variable\nm variable      SS-Mtn 0.03 0.03      V linear      SS
##      METAPOPOP_SIDE_x METAPOPOP_SIDE_y Nequal isVariableM MIG_breaks
## 2250      10      10      3      1      0
## 4500      10      10      3      1      0
## 6750      10      10      3      1      0
## 9000      10      10      3      1      0
## 11250     10      10      3      1      0
## 13500     10      10      3      1      0
##      arch_level_sub arch_level MU_base MU_QTL_proportion
## 2250 2 traits\npleiotropy\nunequal S oligogenic 1e-07      0.001
## 4500 2 traits\npleiotropy\nunequal S oligogenic 1e-07      0.001
## 6750 2 traits\npleiotropy\nunequal S oligogenic 1e-07      0.001
## 9000 2 traits\npleiotropy\nunequal S oligogenic 1e-07      0.001
## 11250 2 traits\npleiotropy\nunequal S oligogenic 1e-07      0.001
## 13500 2 traits\npleiotropy\nunequal S oligogenic 1e-07      0.001
##      SIGMA_QTN_1 SIGMA_QTN_2 SIGMA_K_1 SIGMA_K_2 N_traits ispleiotropy
## 2250      0.4      0.4      0.5      4      2      Pleiotropy
## 4500      0.4      0.4      0.5      4      2      Pleiotropy
## 6750      0.4      0.4      0.5      4      2      Pleiotropy
## 9000      0.4      0.4      0.5      4      2      Pleiotropy
## 11250     0.4      0.4      0.5      4      2      Pleiotropy
## 13500     0.4      0.4      0.5      4      2      Pleiotropy
##      n_samp_tot n_samp_per_pop sd_fitness_among_inds sd_fitness_among_pops
## 2250      1000      10      0.1193353      0.0675856
## 4500      1000      10      0.1193353      0.0675856
## 6750      1000      10      0.1193353      0.0675856
## 9000      1000      10      0.1193353      0.0675856
## 11250     1000      10      0.1193353      0.0675856
## 13500     1000      10      0.1193353      0.0675856
##      final_LA K Bonf_alpha numCausalLowMAFsampl all_corr_phen_temp
## 2250 0.361984 1 6.179706e-06      0      0.8163458
## 4500 0.361984 1 6.179706e-06      0      0.8163458
## 6750 0.361984 1 6.179706e-06      0      0.8163458
## 9000 0.361984 1 6.179706e-06      0      0.8163458
## 11250 0.361984 1 6.179706e-06      0      0.8163458
## 13500 0.361984 1 6.179706e-06      0      0.8163458
##      subsamp_corr_phen_temp all_corr_phen_sal subsamp_corr_phen_sal
## 2250      0.6347974      0.884965      0.7608153
## 4500      0.6347974      0.884965      0.7608153
## 6750      0.6347974      0.884965      0.7608153
## 9000      0.6347974      0.884965      0.7608153
## 11250     0.6347974      0.884965      0.7608153
## 13500     0.6347974      0.884965      0.7608153
##      num_causal_prefilter num_causal_postfilter num_non_causal
## 2250      12      8      8083
## 4500      12      8      8083
## 6750      12      8      8083
## 9000      12      8      8083
## 11250     12      8      8083
## 13500     12      8      8083
##      num_neut_prefilter num_neut_postfilter num_neut_neutralgenome
## 2250      8197      8197      3947
## 4500      8197      8197      3947

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##	6750	8197	8197	3947
##	9000	8197	8197	3947
##	11250	8197	8197	3947
##	13500	8197	8197	3947
##	num_causal_temp	num_causal_sal	num_multiallelic	meanFst va_temp_total
##	2250	8	8	0 0.1737941 0.08556485
##	4500	8	8	0 0.1737941 0.08556485
##	6750	8	8	0 0.1737941 0.08556485
##	9000	8	8	0 0.1737941 0.08556485
##	11250	8	8	0 0.1737941 0.08556485
##	13500	8	8	0 0.1737941 0.08556485
##	va_sal_total	Va_temp_sample	Va_sal_sample	nSNPs median_causal_temp_cor
##	2250	0.105924	0.08049695	0.09935857 8091 0.3033895
##	4500	0.105924	0.08049695	0.09935857 8091 0.3033895
##	6750	0.105924	0.08049695	0.09935857 8091 0.3033895
##	9000	0.105924	0.08049695	0.09935857 8091 0.3033895
##	11250	0.105924	0.08049695	0.09935857 8091 0.3033895
##	13500	0.105924	0.08049695	0.09935857 8091 0.3033895
##	median_causal_sal_cor	median_neut_temp_cor	median_neut_sal_cor	
##	2250	0.3424647	0.248889	0.1358742
##	4500	0.3424647	0.248889	0.1358742
##	6750	0.3424647	0.248889	0.1358742
##	9000	0.3424647	0.248889	0.1358742
##	11250	0.3424647	0.248889	0.1358742
##	13500	0.3424647	0.248889	0.1358742
##	cor_VA_temp_prop	cor_VA_sal_prop	cor_TPR_temp	cor_TPR_sal
##	2250	0.3901235	0.8777962	0.375 0.5
##	4500	0.3901235	0.8777962	0.375 0.5
##	6750	0.3901235	0.8777962	0.375 0.5
##	9000	0.3901235	0.8777962	0.375 0.5
##	11250	0.3901235	0.8777962	0.375 0.5
##	13500	0.3901235	0.8777962	0.375 0.5
##	cor_FDR_allSNPs_temp	cor_FDR_allSNPs_sal	num_causal_sig_temp_corr	
##	2250	0.9987903	0.9913043	3
##	4500	0.9987903	0.9913043	3
##	6750	0.9987903	0.9913043	3
##	9000	0.9987903	0.9913043	3
##	11250	0.9987903	0.9913043	3
##	13500	0.9987903	0.9913043	3
##	num_causal_sig_sal_corr	num_notCausal_sig_temp_corr		
##	2250	4	2477	
##	4500	4	2477	
##	6750	4	2477	
##	9000	4	2477	
##	11250	4	2477	
##	13500	4	2477	
##	num_notCausal_sig_sal_corr	num_neut_sig_temp_corr	num_neut_sig_sal_corr	
##	2250	456	1195	152
##	4500	456	1195	152
##	6750	456	1195	152
##	9000	456	1195	152
##	11250	456	1195	152
##	13500	456	1195	152
##	cor_AUCPR_temp_allSNPs	cor_AUCPR_temp_neutSNPs	cor_AUCPR_sal_allSNPs	

##	2250	0.001387016	0.002938006	0.02439708
##	4500	0.001387016	0.002938006	0.02439708
##	6750	0.001387016	0.002938006	0.02439708
##	9000	0.001387016	0.002938006	0.02439708
##	11250	0.001387016	0.002938006	0.02439708
##	13500	0.001387016	0.002938006	0.02439708
##	cor_AUCPR_sal_neutSNPs cor_af_temp_noutliers cor_af_sal_noutliers			
##	2250	0.2860155	2480	460
##	4500	0.2860155	2480	460
##	6750	0.2860155	2480	460
##	9000	0.2860155	2480	460
##	11250	0.2860155	2480	460
##	13500	0.2860155	2480	460
##	cor_FPR_temp_neutSNPs cor_FPR_sal_neutSNPs LEA3.2_lfmm2_Va_temp_prop			
##	2250	0.3027616	0.03851026	0
##	4500	0.3027616	0.03851026	0
##	6750	0.3027616	0.03851026	0
##	9000	0.3027616	0.03851026	0
##	11250	0.3027616	0.03851026	0
##	13500	0.3027616	0.03851026	0
##	LEA3.2_lfmm2_Va_sal_prop LEA3.2_lfmm2_TPR_temp LEA3.2_lfmm2_TPR_sal			
##	2250	0.8777962	0	0.5
##	4500	0.8777962	0	0.5
##	6750	0.8777962	0	0.5
##	9000	0.8777962	0	0.5
##	11250	0.8777962	0	0.5
##	13500	0.8777962	0	0.5
##	LEA3.2_lfmm2_FDR_allSNPs_temp LEA3.2_lfmm2_FDR_allSNPs_sal			
##	2250	NA	0.9090909	
##	4500	NA	0.9090909	
##	6750	NA	0.9090909	
##	9000	NA	0.9090909	
##	11250	NA	0.9090909	
##	13500	NA	0.9090909	
##	LEA3.2_lfmm2_AUCPR_temp_allSNPs LEA3.2_lfmm2_AUCPR_temp_neutSNPs			
##	2250	0.2117759		0.5088647
##	4500	0.2117759		0.5088647
##	6750	0.2117759		0.5088647
##	9000	0.2117759		0.5088647
##	11250	0.2117759		0.5088647
##	13500	0.2117759		0.5088647
##	LEA3.2_lfmm2_AUCPR_sal_allSNPs LEA3.2_lfmm2_AUCPR_sal_neutSNPs			
##	2250	0.2117759		0.5088647
##	4500	0.2117759		0.5088647
##	6750	0.2117759		0.5088647
##	9000	0.2117759		0.5088647
##	11250	0.2117759		0.5088647
##	13500	0.2117759		0.5088647
##	LEA3.2_lfmm2_mlog10P_tempenv_noutliers			
##	2250		0	
##	4500		0	
##	6750		0	
##	9000		0	
##	11250		0	

##	13500		0		
##		LEA3.2_lfmm2_mlog10P_salenv_noutliers	LEA3.2_lfmm2_num_causal_sig_temp		
##	2250		44		0
##	4500		44		0
##	6750		44		0
##	9000		44		0
##	11250		44		0
##	13500		44		0
##		LEA3.2_lfmm2_num_neut_sig_temp	LEA3.2_lfmm2_num_causal_sig_sal		
##	2250		0		4
##	4500		0		4
##	6750		0		4
##	9000		0		4
##	11250		0		4
##	13500		0		4
##		LEA3.2_lfmm2_num_neut_sig_sal	LEA3.2_lfmm2_FPR_neutSNPs_temp		
##	2250		0		0
##	4500		0		0
##	6750		0		0
##	9000		0		0
##	11250		0		0
##	13500		0		0
##		LEA3.2_lfmm2_FPR_neutSNPs_sal	RDA1_propvar	RDA2_propvar	RDA1_propvar_corr
##	2250		0	0.739	0.261
##	4500		0	0.739	0.261
##	6750		0	0.739	0.261
##	9000		0	0.739	0.261
##	11250		0	0.739	0.261
##	13500		0	0.739	0.261
##		RDA2_propvar_corr	RDA1_temp_cor	RDA1_sal_cor	RDA2_temp_cor
##	2250		0.327	0.9800515	0.1987435
##	4500		0.327	0.9800515	0.1987435
##	6750		0.327	0.9800515	0.1987435
##	9000		0.327	0.9800515	0.1987435
##	11250		0.327	0.9800515	0.1987435
##	13500		0.327	0.9800515	0.1987435
##		RDA2_sal_cor			
##	2250		0.9800515		
##	4500		0.9800515		
##	6750		0.9800515		
##	9000		0.9800515		
##	11250		0.9800515		
##	13500		0.9800515		
##		RDA_Va_temp_prop	RDA_Va_temp_prop_corr	RDA_Va_sal_prop	
##	2250		0.8073374	0.8955353	0.8777962
##	4500		0.8073374	0.8955353	0.8777962
##	6750		0.8073374	0.8955353	0.8777962
##	9000		0.8073374	0.8955353	0.8777962
##	11250		0.8073374	0.8955353	0.8777962
##	13500		0.8073374	0.8955353	0.8777962
##		RDA_Va_sal_prop_corr	RDA_TPR	RDA_TPR_corr	RDA_FDR_allSNPs
##	2250		0.9096928	0.5	0.625
##	4500		0.9096928	0.5	0.625
##	6750		0.9096928	0.5	0.625
##	9000		0.9096928	0.5	0.625
##	11250		0.9096928	0.5	0.625
##	13500		0.9096928	0.5	0.625
##		RDA_FDR_allSNPs_corr	num_RDA_sig_causal	num_RDA_sig_neutral	
##	2250		0.9814815	4	62
##	4500		0.9814815	4	62
##	6750		0.9814815	4	62

##	9000	0.9814815	4	62
##	11250	0.9814815	4	62
##	13500	0.9814815	4	62
##	num_RDA_sig_causal_corr num_RDA_sig_neutral_corr RDA_AUCPR_allSNPs			
##	2250	5	92	0.203218
##	4500	5	92	0.203218
##	6750	5	92	0.203218
##	9000	5	92	0.203218
##	11250	5	92	0.203218
##	13500	5	92	0.203218
##	RDA_AUCPR_neutSNPs RDA_AUCPR_neutSNPs_corr RDA_FPR_neutSNPs			
##	2250	0.5029961	0.332056	0.01570813
##	4500	0.5029961	0.332056	0.01570813
##	6750	0.5029961	0.332056	0.01570813
##	9000	0.5029961	0.332056	0.01570813
##	11250	0.5029961	0.332056	0.01570813
##	13500	0.5029961	0.332056	0.01570813
##	RDA_FPR_neutSNPs_corr RDA_RDAmutpred_cor_tempEffect			
##	2250	0.02330884	0.5	
##	4500	0.02330884	0.5	
##	6750	0.02330884	0.5	
##	9000	0.02330884	0.5	
##	11250	0.02330884	0.5	
##	13500	0.02330884	0.5	
##	RDA_RDAmutpred_cor_salEffect RDA_absRDAmutpred_cor_tempVa			
##	2250	0.2857143	0.02069674	
##	4500	0.2857143	0.02069674	
##	6750	0.2857143	0.02069674	
##	9000	0.2857143	0.02069674	
##	11250	0.2857143	0.02069674	
##	13500	0.2857143	0.02069674	
##	RDA_absRDAmutpred_cor_salVa RDA_RDAmutpred_cor_tempEffect_structcorr			
##	2250	0.02400657	0.2752112	
##	4500	0.02400657	0.2752112	
##	6750	0.02400657	0.2752112	
##	9000	0.02400657	0.2752112	
##	11250	0.02400657	0.2752112	
##	13500	0.02400657	0.2752112	
##	RDA_RDAmutpred_cor_salEffect_structcorr			
##	2250	0.6602084		
##	4500	0.6602084		
##	6750	0.6602084		
##	9000	0.6602084		
##	11250	0.6602084		
##	13500	0.6602084		
##	RDA_absRDAmutpred_cor_tempVa_structcorr			
##	2250	0.08556552		
##	4500	0.08556552		
##	6750	0.08556552		
##	9000	0.08556552		
##	11250	0.08556552		
##	13500	0.08556552		
##	RDA_absRDAmutpred_cor_salVa_structcorr			
##	2250	0.1153435		


```

## 4500 0.1153435
## 6750 0.1153435
## 9000 0.1153435
## 11250 0.1153435
## 13500 0.1153435
## RDA_cor_RDA20000temppredict_tempPhen RDA_cor_RDA20000salpredict_salPhen
## 2250 0.5661217 0.6653819
## 4500 0.5661217 0.6653819
## 6750 0.5661217 0.6653819
## 9000 0.5661217 0.6653819
## 11250 0.5661217 0.6653819
## 13500 0.5661217 0.6653819
## RDA_cor_RDA20000temppredict_tempPhen_structcorr
## 2250 0.238542
## 4500 0.238542
## 6750 0.238542
## 9000 0.238542
## 11250 0.238542
## 13500 0.238542
## RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal
## 2250 0.6262283 0.7832223 0.09915203
## 4500 0.6262283 0.7832223 0.09915203
## 6750 0.6262283 0.7832223 0.09915203
## 9000 0.6262283 0.7832223 0.09915203
## 11250 0.6262283 0.7832223 0.09915203
## 13500 0.6262283 0.7832223 0.09915203
## cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp
## 2250 -0.4132312 -0.2945365 0.3684028 -0.0665779 NA
## 4500 -0.4132312 -0.2945365 0.3684028 -0.0665779 NA
## 6750 -0.4132312 -0.2945365 0.3684028 -0.0665779 NA
## 9000 -0.4132312 -0.2945365 0.3684028 -0.0665779 NA
## 11250 -0.4132312 -0.2945365 0.3684028 -0.0665779 NA
## 13500 -0.4132312 -0.2945365 0.3684028 -0.0665779 NA
## cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp
## 2250 NA 0.8090855 -0.9986383 0.5807664
## 4500 NA 0.8090855 -0.9986383 0.5807664
## 6750 NA 0.8090855 -0.9986383 0.5807664
## 9000 NA 0.8090855 -0.9986383 0.5807664
## 11250 NA 0.8090855 -0.9986383 0.5807664
## 13500 NA 0.8090855 -0.9986383 0.5807664
## cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase
## 2250 -0.02590842 0.75 0.875 0.997544
## 4500 -0.02590842 0.75 0.875 0.997544
## 6750 -0.02590842 0.75 0.875 0.997544
## 9000 -0.02590842 0.75 0.875 0.997544
## 11250 -0.02590842 0.75 0.875 0.997544
## 13500 -0.02590842 0.75 0.875 0.997544
## gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines
## 2250 0.996434 0.5333333
## 4500 0.996434 0.5333333
## 6750 0.996434 0.5333333
## 9000 0.996434 0.5333333
## 11250 0.996434 0.5333333
## 13500 0.996434 0.5333333

```

```
##          clinalparadigm_temp_proptop5GWASclines
## 2250          0.2074074
## 4500          0.2074074
## 6750          0.2074074
## 9000          0.2074074
## 11250         0.2074074
## 13500         0.2074074
##          clinalparadigm_sal_propsigGWASclines
## 2250          0.09349593
## 4500          0.09349593
## 6750          0.09349593
## 9000          0.09349593
## 11250         0.09349593
## 13500         0.09349593
##          clinalparadigm_temp_propsigGWASclines N_traits2
## 2250          0.2850657  2 Traits
## 4500          0.2850657  2 Traits
## 6750          0.2850657  2 Traits
## 9000          0.2850657  2 Traits
## 11250         0.2850657  2 Traits
## 13500         0.2850657  2 Traits
##          method          FDR
## 2250          cor_FDR_neutSNPs_temp 0.9974958
## 4500  LEA3.2_lfmm2_FDR_neutSNPs_temp      NA
## 6750          RDA_FDR_neutSNPs 0.9393939
## 9000          RDA_FDR_neutSNPs_corr 0.9484536
## 11250         cor_FDR_neutSNPs_sal 0.9743590
## 13500  LEA3.2_lfmm2_FDR_neutSNPs_sal 0.0000000
```

```
comparemethods.FDR$methodtype <- factor(comparemethods.FDR$method)

levels(comparemethods.FDR$methodtype)
```

```
## [1] "cor_FDR_neutSNPs_sal"          "cor_FDR_neutSNPs_temp"
## [3] "LEA3.2_lfmm2_FDR_neutSNPs_sal" "LEA3.2_lfmm2_FDR_neutSNPs_temp"
## [5] "RDA_FDR_neutSNPs"             "RDA_FDR_neutSNPs_corr"
```

```
comparemethods.FDR$methodtype <- revalue(comparemethods.FDR$methodtype,
                                           c("cor_FDR_neutSNPs_sal"="Cor(p, Env2)",
                                             "cor_FDR_neutSNPs_temp"= "Cor(p, Temp.)",
                                             "LEA3.2_lfmm2_FDR_neutSNPs_sal" = "LFMM - Temp.\n(structure correction)",
                                             "LEA3.2_lfmm2_FDR_neutSNPs_temp" = "LFMM - Env2\n(structure correction)",
                                             "RDA_FDR_neutSNPs" = "RDA",
                                             "RDA_FDR_neutSNPs_corr" = "pRDA\n(structure correction)" ))

comparemethods.FDR$methodtype <- factor(comparemethods.FDR$methodtype,
                                           levels = c("Cor(p, Temp.)",
                                                         "LFMM - Temp.\n(structure correction)",
                                                         "Cor(p, Env2)",
                                                         "LFMM - Env2\n(structure correction)",
                                                         "RDA",
                                                         "pRDA\n(structure correction)"),
                                           ordered=TRUE)
```

```
table(comparemethods.FDR$methodtype)
```

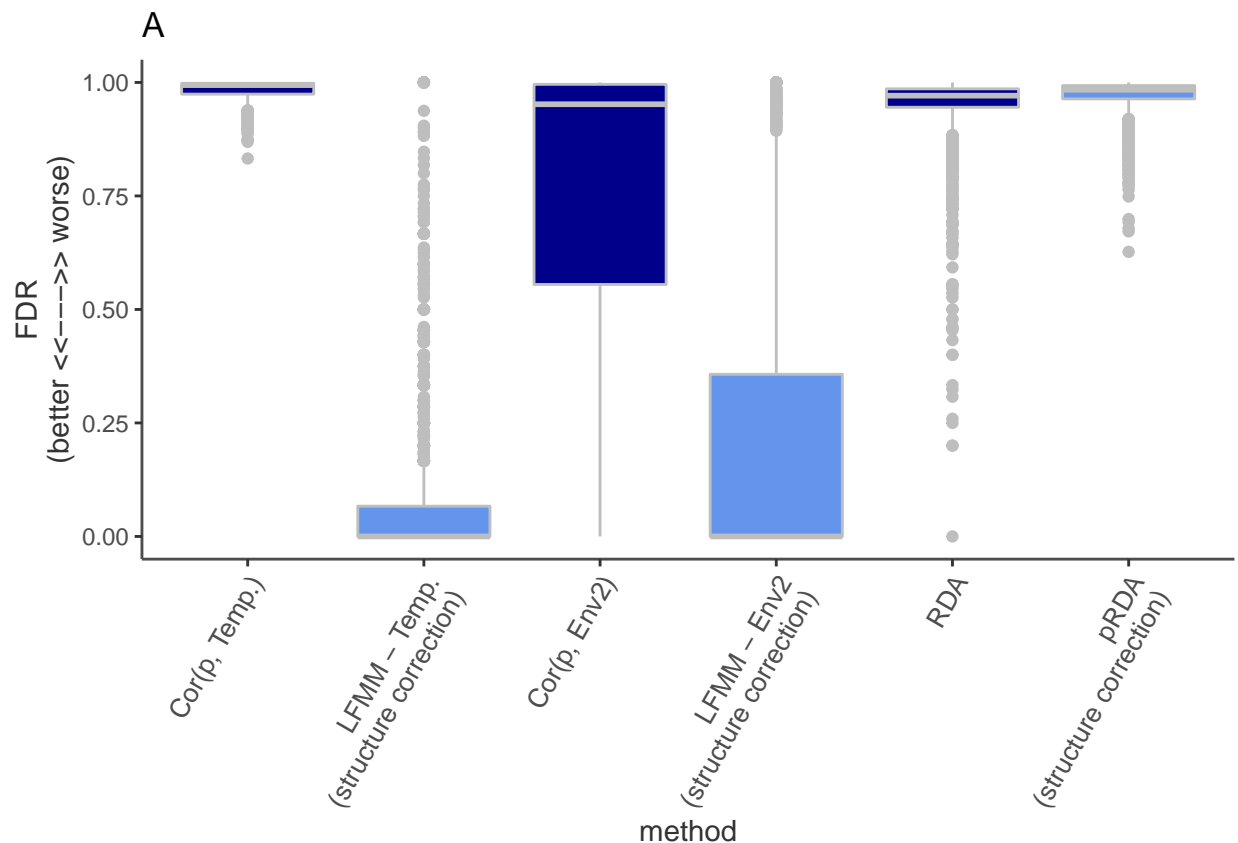
```
##
##               Cor(p, Temp.) LFMM - Temp.\n(structure correction)
##               2250                                           2250
##               Cor(p, Env2)  LFMM - Env2\n(structure correction)
##               2250                                           2250
##               RDA          pRDA\n(structure correction)
##               2250                                           2250
```

```
tapply(comparemethods.FDR$FDR,comparemethods.AUC$methodtype, function(x){sum(is.na(x))})
```

```
##               Cor(p, Temp.) LFMM - Temp.\n(structure correction)
##               266                                           248
##               Cor(p, Env2)  LFMM - Env2\n(structure correction)
##               248                                           210
##               RDA          pRDA\n(structure correction)
##               204                                           246
```

```
g2<- ggplot(comparemethods.FDR, aes(x=as.factor(methodtype), y=FDR)) + geom_boxplot(color="grey", fill="grey")
g2
```

```
## Warning: Removed 1422 rows containing non-finite values (stat_boxplot).
```



```
# There are more NAs because FDR has NAs for cases with no true positives (no power)
```

Compare methods POWER

Ideally, we would like power to be the same after correcting for pop structure as before we correct.

```
#Check for NAs in temperature models  
sum(is.na(final.df$cor_TPR_temp))
```

```
## [1] 0
```

```
sum(is.na(final.df$LEA3.2_lfmm2_TPR_temp))
```

```
## [1] 0
```

```
# Check for NAs in salinity model  
sum(is.na(final.df$cor_TPR_sal)) #450 expected
```

```
## [1] 450
```

```
sum(is.na(final.df$LEA3.2_lfmm2_TPR_sal))
```

```
## [1] 450
```

```
#Check for NAs in RDA model  
sum(is.na(final.df$RDA_TPR))
```

```
## [1] 0
```

```
sum(is.na(final.df$RDA_TPR))
```

```
## [1] 0
```

```
# reorganize data for plotting  
comparemethods.TPR <- gather(final.df, key=method, value=TPR, cor_TPR_temp, LEA3.2_lfmm2_TPR_temp, RDA_TPR)  
  
comparemethods.TPR <- comparemethods.TPR[order(comparemethods.TPR$seed),]  
tail(comparemethods.TPR)
```

```
##           seed  
## 2250 1233343  
## 4500 1233343  
## 6750 1233343  
## 9000 1233343  
## 11250 1233343  
## 13500 1233343  
##
```

level reps

```

## 2250 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 4500 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 6750 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 9000 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 11250 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
## 13500 oliogenic_2-trait-pleiotropy-unequal-S__SS-Mtn_N-variable_m-variable 10
##
##                                arch                                demog_name
## 2250 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 4500 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 6750 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 9000 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 11250 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
## 13500 oliogenic_2-trait-pleiotropy-unequal-S SS-Mtn_N-variable_m-variable
##
##      demog_level_sub demog_level MIG_x MIG_y xcline ycline demog
## 2250 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 4500 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 6750 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 9000 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 11250 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
## 13500 N variable\nm variable      SS-Mtn 0.03 0.03      V linear  SS
##
##      METAPOPOP_SIDE_x METAPOPOP_SIDE_y Nequal isVariableM MIG_breaks
## 2250              10              10      3              1              0
## 4500              10              10      3              1              0
## 6750              10              10      3              1              0
## 9000              10              10      3              1              0
## 11250             10              10      3              1              0
## 13500             10              10      3              1              0
##
##                                arch_level_sub arch_level MU_base MU_QTL_proportion
## 2250 2 traits\nnpleiotropy\nnunequal S oligogenic 1e-07              0.001
## 4500 2 traits\nnpleiotropy\nnunequal S oligogenic 1e-07              0.001
## 6750 2 traits\nnpleiotropy\nnunequal S oligogenic 1e-07              0.001
## 9000 2 traits\nnpleiotropy\nnunequal S oligogenic 1e-07              0.001
## 11250 2 traits\nnpleiotropy\nnunequal S oligogenic 1e-07              0.001
## 13500 2 traits\nnpleiotropy\nnunequal S oligogenic 1e-07              0.001
##
##      SIGMA_QTN_1 SIGMA_QTN_2 SIGMA_K_1 SIGMA_K_2 N_traits ispleiotropy
## 2250          0.4          0.4          0.5          4          2  Pleiotropy
## 4500          0.4          0.4          0.5          4          2  Pleiotropy
## 6750          0.4          0.4          0.5          4          2  Pleiotropy
## 9000          0.4          0.4          0.5          4          2  Pleiotropy
## 11250         0.4          0.4          0.5          4          2  Pleiotropy
## 13500         0.4          0.4          0.5          4          2  Pleiotropy
##
##      n_samp_tot n_samp_per_pop sd_fitness_among_inds sd_fitness_among_pops
## 2250          1000              10              0.1193353              0.0675856
## 4500          1000              10              0.1193353              0.0675856
## 6750          1000              10              0.1193353              0.0675856
## 9000          1000              10              0.1193353              0.0675856
## 11250         1000              10              0.1193353              0.0675856
## 13500         1000              10              0.1193353              0.0675856
##
##      final_LA K Bonf_alpha numCausalLowMAFsampl all_corr_phen_temp
## 2250 0.361984 1 6.179706e-06              0              0.8163458
## 4500 0.361984 1 6.179706e-06              0              0.8163458
## 6750 0.361984 1 6.179706e-06              0              0.8163458
## 9000 0.361984 1 6.179706e-06              0              0.8163458
## 11250 0.361984 1 6.179706e-06              0              0.8163458

```

```

## 13500 0.361984 1 6.179706e-06 0 0.8163458
## subsamp_corr_phen_temp all_corr_phen_sal subsamp_corr_phen_sal
## 2250 0.6347974 0.884965 0.7608153
## 4500 0.6347974 0.884965 0.7608153
## 6750 0.6347974 0.884965 0.7608153
## 9000 0.6347974 0.884965 0.7608153
## 11250 0.6347974 0.884965 0.7608153
## 13500 0.6347974 0.884965 0.7608153
## num_causal_prefilter num_causal_postfilter num_non_causal
## 2250 12 8 8083
## 4500 12 8 8083
## 6750 12 8 8083
## 9000 12 8 8083
## 11250 12 8 8083
## 13500 12 8 8083
## num_neut_prefilter num_neut_postfilter num_neut_neutralgenome
## 2250 8197 8197 3947
## 4500 8197 8197 3947
## 6750 8197 8197 3947
## 9000 8197 8197 3947
## 11250 8197 8197 3947
## 13500 8197 8197 3947
## num_causal_temp num_causal_sal num_multiallelic meanFst va_temp_total
## 2250 8 8 0 0.1737941 0.08556485
## 4500 8 8 0 0.1737941 0.08556485
## 6750 8 8 0 0.1737941 0.08556485
## 9000 8 8 0 0.1737941 0.08556485
## 11250 8 8 0 0.1737941 0.08556485
## 13500 8 8 0 0.1737941 0.08556485
## va_sal_total Va_temp_sample Va_sal_sample nSNPs median_causal_temp_cor
## 2250 0.105924 0.08049695 0.09935857 8091 0.3033895
## 4500 0.105924 0.08049695 0.09935857 8091 0.3033895
## 6750 0.105924 0.08049695 0.09935857 8091 0.3033895
## 9000 0.105924 0.08049695 0.09935857 8091 0.3033895
## 11250 0.105924 0.08049695 0.09935857 8091 0.3033895
## 13500 0.105924 0.08049695 0.09935857 8091 0.3033895
## median_causal_sal_cor median_neut_temp_cor median_neut_sal_cor
## 2250 0.3424647 0.248889 0.1358742
## 4500 0.3424647 0.248889 0.1358742
## 6750 0.3424647 0.248889 0.1358742
## 9000 0.3424647 0.248889 0.1358742
## 11250 0.3424647 0.248889 0.1358742
## 13500 0.3424647 0.248889 0.1358742
## cor_VA_temp_prop cor_VA_sal_prop cor_FDR_allSNPs_temp
## 2250 0.3901235 0.8777962 0.9987903
## 4500 0.3901235 0.8777962 0.9987903
## 6750 0.3901235 0.8777962 0.9987903
## 9000 0.3901235 0.8777962 0.9987903
## 11250 0.3901235 0.8777962 0.9987903
## 13500 0.3901235 0.8777962 0.9987903
## cor_FDR_neutSNPs_temp cor_FDR_allSNPs_sal cor_FDR_neutSNPs_sal
## 2250 0.9974958 0.9913043 0.974359
## 4500 0.9974958 0.9913043 0.974359
## 6750 0.9974958 0.9913043 0.974359

```

##	9000	0.9974958	0.9913043	0.974359
##	11250	0.9974958	0.9913043	0.974359
##	13500	0.9974958	0.9913043	0.974359
##	num_causal_sig_temp_corr num_causal_sig_sal_corr			
##	2250	3	4	
##	4500	3	4	
##	6750	3	4	
##	9000	3	4	
##	11250	3	4	
##	13500	3	4	
##	num_notCausal_sig_temp_corr num_notCausal_sig_sal_corr			
##	2250	2477	456	
##	4500	2477	456	
##	6750	2477	456	
##	9000	2477	456	
##	11250	2477	456	
##	13500	2477	456	
##	num_neut_sig_temp_corr num_neut_sig_sal_corr cor_AUCPR_temp_allSNPs			
##	2250	1195	152	0.001387016
##	4500	1195	152	0.001387016
##	6750	1195	152	0.001387016
##	9000	1195	152	0.001387016
##	11250	1195	152	0.001387016
##	13500	1195	152	0.001387016
##	cor_AUCPR_temp_neutSNPs cor_AUCPR_sal_allSNPs cor_AUCPR_sal_neutSNPs			
##	2250	0.002938006	0.02439708	0.2860155
##	4500	0.002938006	0.02439708	0.2860155
##	6750	0.002938006	0.02439708	0.2860155
##	9000	0.002938006	0.02439708	0.2860155
##	11250	0.002938006	0.02439708	0.2860155
##	13500	0.002938006	0.02439708	0.2860155
##	cor_af_temp_noutliers cor_af_sal_noutliers cor_FPR_temp_neutSNPs			
##	2250	2480	460	0.3027616
##	4500	2480	460	0.3027616
##	6750	2480	460	0.3027616
##	9000	2480	460	0.3027616
##	11250	2480	460	0.3027616
##	13500	2480	460	0.3027616
##	cor_FPR_sal_neutSNPs LEA3.2_lfmm2_Va_temp_prop LEA3.2_lfmm2_Va_sal_prop			
##	2250	0.03851026	0	0.8777962
##	4500	0.03851026	0	0.8777962
##	6750	0.03851026	0	0.8777962
##	9000	0.03851026	0	0.8777962
##	11250	0.03851026	0	0.8777962
##	13500	0.03851026	0	0.8777962
##	LEA3.2_lfmm2_FDR_allSNPs_temp LEA3.2_lfmm2_FDR_allSNPs_sal			
##	2250	NA	0.9090909	
##	4500	NA	0.9090909	
##	6750	NA	0.9090909	
##	9000	NA	0.9090909	
##	11250	NA	0.9090909	
##	13500	NA	0.9090909	
##	LEA3.2_lfmm2_FDR_neutSNPs_temp LEA3.2_lfmm2_FDR_neutSNPs_sal			
##	2250	NA	0	

##	4500	NA	0		
##	6750	NA	0		
##	9000	NA	0		
##	11250	NA	0		
##	13500	NA	0		
##	LEA3.2_lfmm2_AUCPR_temp_allSNPs LEA3.2_lfmm2_AUCPR_temp_neutSNPs				
##	2250	0.2117759	0.5088647		
##	4500	0.2117759	0.5088647		
##	6750	0.2117759	0.5088647		
##	9000	0.2117759	0.5088647		
##	11250	0.2117759	0.5088647		
##	13500	0.2117759	0.5088647		
##	LEA3.2_lfmm2_AUCPR_sal_allSNPs LEA3.2_lfmm2_AUCPR_sal_neutSNPs				
##	2250	0.2117759	0.5088647		
##	4500	0.2117759	0.5088647		
##	6750	0.2117759	0.5088647		
##	9000	0.2117759	0.5088647		
##	11250	0.2117759	0.5088647		
##	13500	0.2117759	0.5088647		
##	LEA3.2_lfmm2_mlog10P_tempenv_noutliers				
##	2250	0			
##	4500	0			
##	6750	0			
##	9000	0			
##	11250	0			
##	13500	0			
##	LEA3.2_lfmm2_mlog10P_salenv_noutliers LEA3.2_lfmm2_num_causal_sig_temp				
##	2250	44	0		
##	4500	44	0		
##	6750	44	0		
##	9000	44	0		
##	11250	44	0		
##	13500	44	0		
##	LEA3.2_lfmm2_num_neut_sig_temp LEA3.2_lfmm2_num_causal_sig_sal				
##	2250	0	4		
##	4500	0	4		
##	6750	0	4		
##	9000	0	4		
##	11250	0	4		
##	13500	0	4		
##	LEA3.2_lfmm2_num_neut_sig_sal LEA3.2_lfmm2_FPR_neutSNPs_temp				
##	2250	0	0		
##	4500	0	0		
##	6750	0	0		
##	9000	0	0		
##	11250	0	0		
##	13500	0	0		
##	LEA3.2_lfmm2_FPR_neutSNPs_sal RDA1_propvar RDA2_propvar RDA1_propvar_corr				
##	2250	0	0.739	0.261	0.673
##	4500	0	0.739	0.261	0.673
##	6750	0	0.739	0.261	0.673
##	9000	0	0.739	0.261	0.673
##	11250	0	0.739	0.261	0.673
##	13500	0	0.739	0.261	0.673

##	RDA2_propvar_corr	RDA1_temp_cor	RDA1_sal_cor	RDA2_temp_cor	RDA2_sal_cor
## 2250	0.327	0.9800515	0.1987435	-0.1987435	0.9800515
## 4500	0.327	0.9800515	0.1987435	-0.1987435	0.9800515
## 6750	0.327	0.9800515	0.1987435	-0.1987435	0.9800515
## 9000	0.327	0.9800515	0.1987435	-0.1987435	0.9800515
## 11250	0.327	0.9800515	0.1987435	-0.1987435	0.9800515
## 13500	0.327	0.9800515	0.1987435	-0.1987435	0.9800515
##	RDA_Va_temp_prop	RDA_Va_temp_prop_corr	RDA_Va_sal_prop		
## 2250	0.8073374	0.8955353	0.8777962		
## 4500	0.8073374	0.8955353	0.8777962		
## 6750	0.8073374	0.8955353	0.8777962		
## 9000	0.8073374	0.8955353	0.8777962		
## 11250	0.8073374	0.8955353	0.8777962		
## 13500	0.8073374	0.8955353	0.8777962		
##	RDA_Va_sal_prop_corr	RDA_FDR_allSNPs	RDA_FDR_allSNPs_corr		
## 2250	0.9096928	0.983871	0.9814815		
## 4500	0.9096928	0.983871	0.9814815		
## 6750	0.9096928	0.983871	0.9814815		
## 9000	0.9096928	0.983871	0.9814815		
## 11250	0.9096928	0.983871	0.9814815		
## 13500	0.9096928	0.983871	0.9814815		
##	num_RDA_sig_causal	num_RDA_sig_neutral	num_RDA_sig_causal_corr		
## 2250	4	62	5		
## 4500	4	62	5		
## 6750	4	62	5		
## 9000	4	62	5		
## 11250	4	62	5		
## 13500	4	62	5		
##	num_RDA_sig_neutral_corr	RDA_FDR_neutSNPs	RDA_FDR_neutSNPs_corr		
## 2250	92	0.9393939	0.9484536		
## 4500	92	0.9393939	0.9484536		
## 6750	92	0.9393939	0.9484536		
## 9000	92	0.9393939	0.9484536		
## 11250	92	0.9393939	0.9484536		
## 13500	92	0.9393939	0.9484536		
##	RDA_AUCPR_allSNPs	RDA_AUCPR_neutSNPs	RDA_AUCPR_neutSNPs_corr		
## 2250	0.203218	0.5029961	0.332056		
## 4500	0.203218	0.5029961	0.332056		
## 6750	0.203218	0.5029961	0.332056		
## 9000	0.203218	0.5029961	0.332056		
## 11250	0.203218	0.5029961	0.332056		
## 13500	0.203218	0.5029961	0.332056		
##	RDA_FPR_neutSNPs	RDA_FPR_neutSNPs_corr	RDA_RDAmutpred_cor_tempEffect		
## 2250	0.01570813	0.02330884	0.5		
## 4500	0.01570813	0.02330884	0.5		
## 6750	0.01570813	0.02330884	0.5		
## 9000	0.01570813	0.02330884	0.5		
## 11250	0.01570813	0.02330884	0.5		
## 13500	0.01570813	0.02330884	0.5		
##	RDA_RDAmutpred_cor_salEffect	RDA_absRDAmutpred_cor_tempVa			
## 2250	0.2857143	0.02069674			
## 4500	0.2857143	0.02069674			
## 6750	0.2857143	0.02069674			
## 9000	0.2857143	0.02069674			

##	11250	0.2857143	0.02069674
##	13500	0.2857143	0.02069674
##	RDA_absRDAmutpred_cor_salVa RDA_RDAmutpred_cor_tempEffect_structcorr		
##	2250	0.02400657	0.2752112
##	4500	0.02400657	0.2752112
##	6750	0.02400657	0.2752112
##	9000	0.02400657	0.2752112
##	11250	0.02400657	0.2752112
##	13500	0.02400657	0.2752112
##	RDA_RDAmutpred_cor_salEffect_structcorr		
##	2250	0.6602084	
##	4500	0.6602084	
##	6750	0.6602084	
##	9000	0.6602084	
##	11250	0.6602084	
##	13500	0.6602084	
##	RDA_absRDAmutpred_cor_tempVa_structcorr		
##	2250	0.08556552	
##	4500	0.08556552	
##	6750	0.08556552	
##	9000	0.08556552	
##	11250	0.08556552	
##	13500	0.08556552	
##	RDA_absRDAmutpred_cor_salVa_structcorr		
##	2250	0.1153435	
##	4500	0.1153435	
##	6750	0.1153435	
##	9000	0.1153435	
##	11250	0.1153435	
##	13500	0.1153435	
##	RDA_cor_RDA20000temppredict_tempPhen RDA_cor_RDA20000salpredict_salPhen		
##	2250	0.5661217	0.6653819
##	4500	0.5661217	0.6653819
##	6750	0.5661217	0.6653819
##	9000	0.5661217	0.6653819
##	11250	0.5661217	0.6653819
##	13500	0.5661217	0.6653819
##	RDA_cor_RDA20000temppredict_tempPhen_structcorr		
##	2250	0.238542	
##	4500	0.238542	
##	6750	0.238542	
##	9000	0.238542	
##	11250	0.238542	
##	13500	0.238542	
##	RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal		
##	2250	0.6262283	0.7832223 0.09915203
##	4500	0.6262283	0.7832223 0.09915203
##	6750	0.6262283	0.7832223 0.09915203
##	9000	0.6262283	0.7832223 0.09915203
##	11250	0.6262283	0.7832223 0.09915203
##	13500	0.6262283	0.7832223 0.09915203
##	cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp		
##	2250	-0.4132312 -0.2945365 0.3684028 -0.0665779	NA
##	4500	-0.4132312 -0.2945365 0.3684028 -0.0665779	NA

```

## 6750      -0.4132312  -0.2945365      0.3684028      -0.0665779      NA
## 9000      -0.4132312  -0.2945365      0.3684028      -0.0665779      NA
## 11250     -0.4132312  -0.2945365      0.3684028      -0.0665779      NA
## 13500     -0.4132312  -0.2945365      0.3684028      -0.0665779      NA
##          cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp
## 2250              NA      0.8090855      -0.9986383      0.5807664
## 4500              NA      0.8090855      -0.9986383      0.5807664
## 6750              NA      0.8090855      -0.9986383      0.5807664
## 9000              NA      0.8090855      -0.9986383      0.5807664
## 11250             NA      0.8090855      -0.9986383      0.5807664
## 13500             NA      0.8090855      -0.9986383      0.5807664
##          cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase
## 2250      -0.02590842      0.75      0.875      0.997544
## 4500      -0.02590842      0.75      0.875      0.997544
## 6750      -0.02590842      0.75      0.875      0.997544
## 9000      -0.02590842      0.75      0.875      0.997544
## 11250     -0.02590842      0.75      0.875      0.997544
## 13500     -0.02590842      0.75      0.875      0.997544
##          gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines
## 2250              0.996434              0.5333333
## 4500              0.996434              0.5333333
## 6750              0.996434              0.5333333
## 9000              0.996434              0.5333333
## 11250             0.996434              0.5333333
## 13500             0.996434              0.5333333
##          clinalparadigm_temp_proptop5GWASclines
## 2250              0.2074074
## 4500              0.2074074
## 6750              0.2074074
## 9000              0.2074074
## 11250             0.2074074
## 13500             0.2074074
##          clinalparadigm_sal_propsigGWASclines
## 2250              0.09349593
## 4500              0.09349593
## 6750              0.09349593
## 9000              0.09349593
## 11250             0.09349593
## 13500             0.09349593
##          clinalparadigm_temp_propsigGWASclines N_traits2      method
## 2250              0.2850657  2 Traits      cor_TPR_temp
## 4500              0.2850657  2 Traits LEA3.2_lfmm2_TPR_temp
## 6750              0.2850657  2 Traits      RDA_TPR
## 9000              0.2850657  2 Traits      RDA_TPR_corr
## 11250             0.2850657  2 Traits      cor_TPR_sal
## 13500             0.2850657  2 Traits LEA3.2_lfmm2_TPR_sal
##          TPR
## 2250  0.375
## 4500  0.000
## 6750  0.500
## 9000  0.625
## 11250 0.500
## 13500 0.500

```

```
comparemethods.TPR$methodtype <- factor(comparemethods.TPR$method)
```

```
levels(comparemethods.TPR$methodtype)
```

```
## [1] "cor_TPR_sal"          "cor_TPR_temp"          "LEA3.2_lfmm2_TPR_sal"
## [4] "LEA3.2_lfmm2_TPR_temp" "RDA_TPR"               "RDA_TPR_corr"
```

```
comparemethods.TPR$methodtype <- revalue(comparemethods.TPR$methodtype,
                                           c("cor_TPR_sal"="Cor(p, Env2)",
                                             "cor_TPR_temp"= "Cor(p, Temp.)",
                                             "LEA3.2_lfmm2_TPR_sal" = "LFMM - Env2\n(structure correction)",
                                             "LEA3.2_lfmm2_TPR_temp" = "LFMM - Temp.\n(structure correction)",
                                             "RDA_TPR" = "RDA",
                                             "RDA_TPR_corr" = "pRDA\n(structure correction)" ))
```

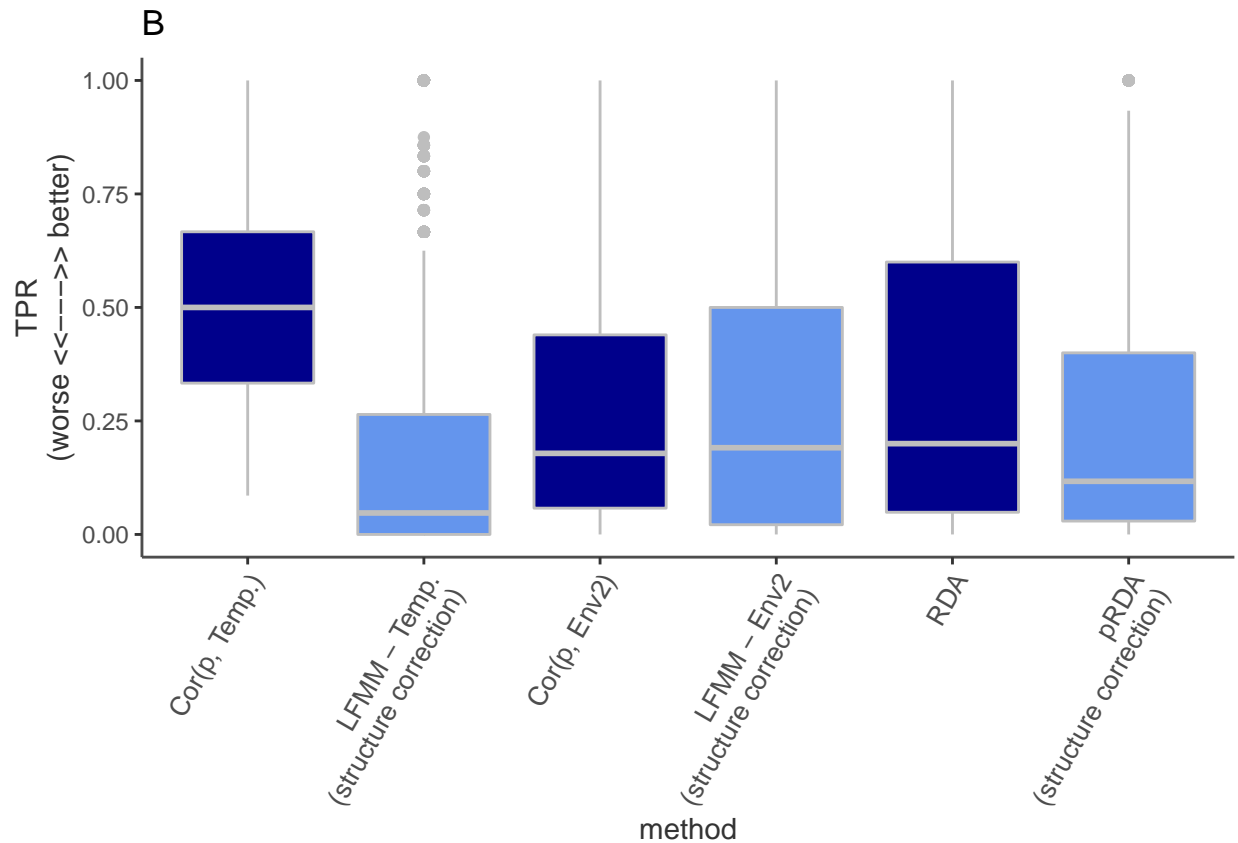
```
comparemethods.TPR$methodtype <- factor(comparemethods.TPR$methodtype,
                                         levels = c("Cor(p, Temp.)",
                                                       "LFMM - Temp.\n(structure correction)",
                                                       "Cor(p, Env2)",
                                                       "LFMM - Env2\n(structure correction)",
                                                       "RDA",
                                                       "pRDA\n(structure correction)" ),
                                         ordered=TRUE)
```

```
table(comparemethods.TPR$methodtype)
```

```
##
##          Cor(p, Temp.) LFMM - Temp.\n(structure correction)
##          2250          2250
##          Cor(p, Env2)  LFMM - Env2\n(structure correction)
##          2250          2250
##          RDA          pRDA\n(structure correction)
##          2250          2250
```

```
g3<- ggplot(comparemethods.TPR, aes(x=as.factor(methodtype), y=TPR)) + geom_boxplot(color="grey", fill="grey")
g3
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```



```
#pdf(paste0(outputs,"AUC-PR_FDR_TPR.pdf"), width=5, height=9)
#grid.arrange(g+ theme( axis.text.x = element_blank(), axis.title.x=element_blank()),
#             g2+ theme( axis.text.x = element_blank(), axis.title.x=element_blank()),
#             g3,
#             layout_matrix=matrix(c(1,1,1,2,2,2,3,3,3,3,3), nrow=11))
#dev.off()

pdf(paste0(outputs,"GEAs-AUC.pdf"), width=5, height=4)
g
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```

```
dev.off()
```

```
## pdf
## 2
```

LFMM - TPR vs STRUCTURE

- If overcorrected, then expect power to decrease as the correlation between the latent factor and env

```

### THIS IS THE GRAPH
# Fix colors for arch_level_sub,
# rename legend and make it taller,
# reorder the legend levels
# For the 2nd legend, there is no "1 trait sims"

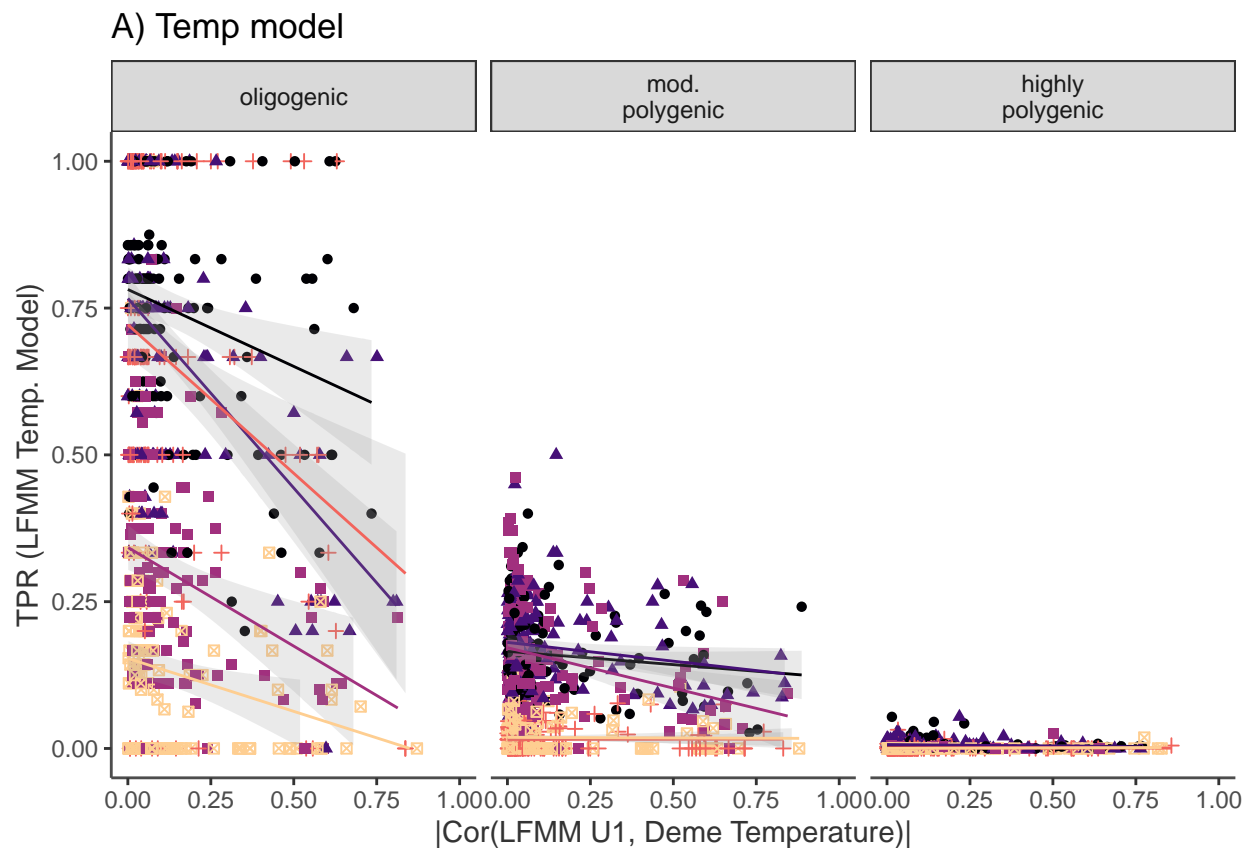
k1p <- ggplot(final.df) + geom_point(aes(x=abs(cor_LFMMU1_temp),y=LEA3.2_lfmm2_TPR_temp, color=arch_level_sub,
  xlab("|Cor(LFMM U1, Deme Temperature)|") +
  ylab("TPR (LFMM Temp. Model)" +
  scale_fill_viridis(option="magma", discrete=TRUE) +
  scale_color_viridis(option="magma", discrete=TRUE, begin=0, end=0.9) +
  geom_smooth(aes(x=abs(cor_LFMMU1_temp),y=LEA3.2_lfmm2_TPR_temp, color=arch_level_sub), alpha=0.2, met
  ylim(0,1) +xlim(0,1) + facet_wrap(~arch_level) + theme(legend.position = "none")
k1p # was not easy to change the color scheme here + scale_fill_viridis(option="mako", discrete=TRUE)

```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing missing values (geom_smooth).
```



```

k2p <- ggplot(final.df) +
  geom_point(aes(x=abs(cor_LFMMU1_sal),y=LEA3.2_lfmm2_TPR_sal, color=arch_level_sub, shape=arch_level_s
  xlab("|Cor(LFMM U1, Deme Env2)|") + ylab("TPR (LFMM Env2 Model)" +

```

```

geom_smooth(aes(x=abs(cor_LFMMU1_sal),y=LEA3.2_lfmm2_TPR_sal, color=arch_level_sub), alpha=0.2, method=
ylim(0,1) +xlim(0,1) + ggtitle("B) Env2 model") +
scale_fill_viridis(option="magma", discrete=TRUE) +
scale_color_viridis(option="magma", discrete=TRUE, begin=0, end=0.9) +
facet_wrap(~arch_level) + theme(legend.position = "bottom")
k2p

```

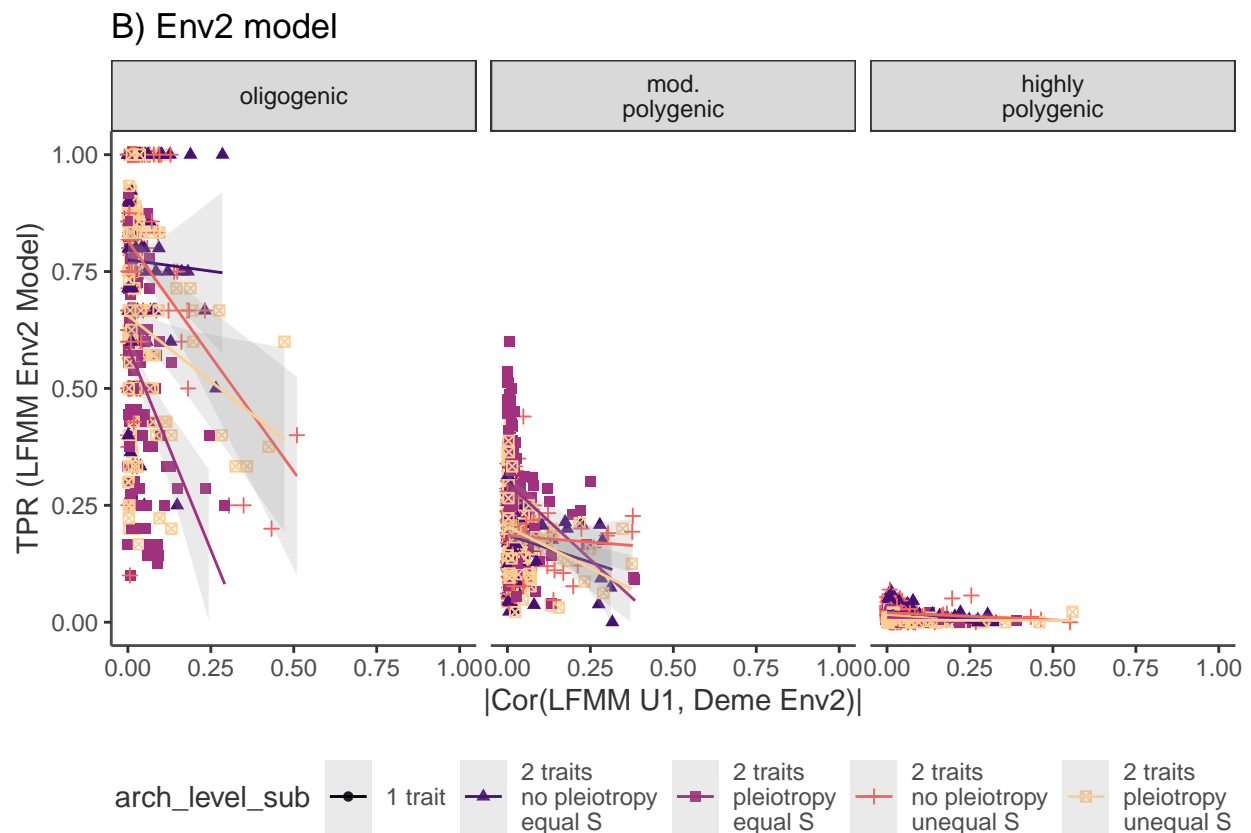
Warning: Using shapes for an ordinal variable is not advised

'geom_smooth()' using formula 'y ~ x'

Warning: Removed 450 rows containing non-finite values (stat_smooth).

Warning: Removed 450 rows containing missing values (geom_point).

Warning: Removed 32 rows containing missing values (geom_smooth).



```

lm_plot <- summary(lm(c(final.df$LEA3.2_lfmm2_TPR_temp,final.df$LEA3.2_lfmm2_TPR_sal) ~
c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal))
))
lm_plot

```

```
##
## Call:
## lm(formula = c(final.df$LEA3.2_lfmm2_TPR_temp, final.df$LEA3.2_lfmm2_TPR_sal) ~
##      c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal)))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.2668 -0.2453 -0.1162  0.1416  0.8827
##
## Coefficients:
##                                     Estimate
## (Intercept)                        0.266811
## c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal)) -0.237447
##                                     Std. Error
## (Intercept)                        0.005533
## c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal))  0.032261
##                                     t value Pr(>|t|)
## (Intercept)                        48.22  < 2e-16
## c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal)) -7.36 2.21e-13
##
## (Intercept)                        ***
## c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal)) ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3058 on 4048 degrees of freedom
## (450 observations deleted due to missingness)
## Multiple R-squared:  0.01321,    Adjusted R-squared:  0.01296
## F-statistic: 54.17 on 1 and 4048 DF,  p-value: 2.212e-13
```

```
(slope=lm_plot$coefficients[2,1])
```

```
## [1] -0.2374471
```

```
(int <- lm_plot$coefficients[1,1])
```

```
## [1] 0.266811
```

```
### Create a plot showing overall pattern
mydf <- data.frame(y=c(final.df$LEA3.2_lfmm2_TPR_temp,final.df$LEA3.2_lfmm2_TPR_sal) ,
                   x = c(abs(final.df$cor_LFMMU1_temp), abs(final.df$cor_LFMMU1_sal)))

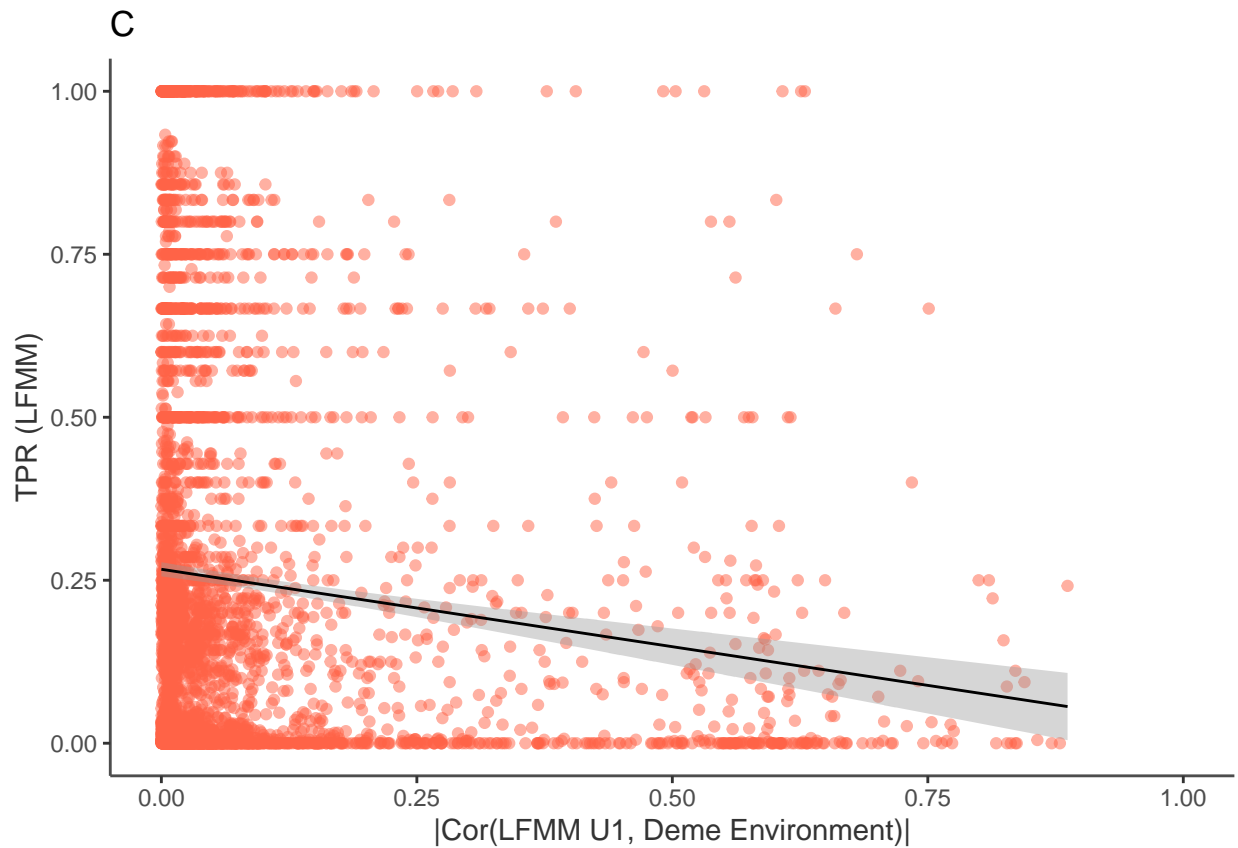
k3p <- ggplot(mydf) + geom_point(aes(x,y), alpha=0.5, color="tomato1") +
  ggtheme +
  xlab("|Cor(LFMM U1, Deme Environment)|") +
  ylab("TPR (LFMM)") +
  geom_smooth(aes(x,y), method="lm", size=0.5, color="black") +
  ggtitle("C") +
  ylim(0,1) +xlim(0,1) + theme(legend.position = "none")
k3p
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```



```
pdf(paste0(outputs,"LFMM-TPRvsStructure.pdf"), width=8, height=8)  
grid.arrange(k1p,k2p, nrow=2)
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing missing values (geom_smooth).
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
## Warning: Removed 32 rows containing missing values (geom_smooth).
```

```
# 450 missing values expected here
dev.off()
```

```
## pdf
## 2
```

```
pdf(paste0(outputs,"GEA_results.pdf"), width=5, height=9)
  grid.arrange(
    g2+ theme( axis.text.x = element_blank(), axis.title.x=element_blank()),
    g3,
    k3p,
    layout_matrix=matrix(c(1,1,1,2,2,2,2,3,3,3,3), nrow=12)
  )
```

```
## Warning: Removed 1422 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
dev.off()
```

```
## pdf
## 2
```

RDA checks

```
par(mfrow=c(2,2))
sum(is.na(final.df$RDA_RDAmutpred_cor_tempEffect))
```

```
## [1] 0
```

```
sum(is.na(final.df$RDA_RDAmutpred_cor_salEffect)) #450 expected
```

```
## [1] 450
```

```
sum(is.na(final.df$RDA_cor_RDA20000temppredict_tempPhen))
```

```
## [1] 0
```

```
sum(is.na(final.df$RDA_cor_RDA20000salpredict_salPhen)) #450 expected
```

```
## [1] 450
```

```
# Seeds with really bad performance (no structure correction)  
final.df$seed[which(final.df$RDA_RDAmutpred_cor_tempEffect < 0)]
```

```
## [1] 1231305
```

```
final.df$seed[which(final.df$RDA_RDAmutpred_cor_salEffect < 0)]
```

```
## [1] 1231259 1231713 1231725 1232658 1233108 1233333
```

```
final.df$seed[which(final.df$RDA_cor_RDA20000temppredict_tempPhen < 0)]
```

```
## integer(0)
```

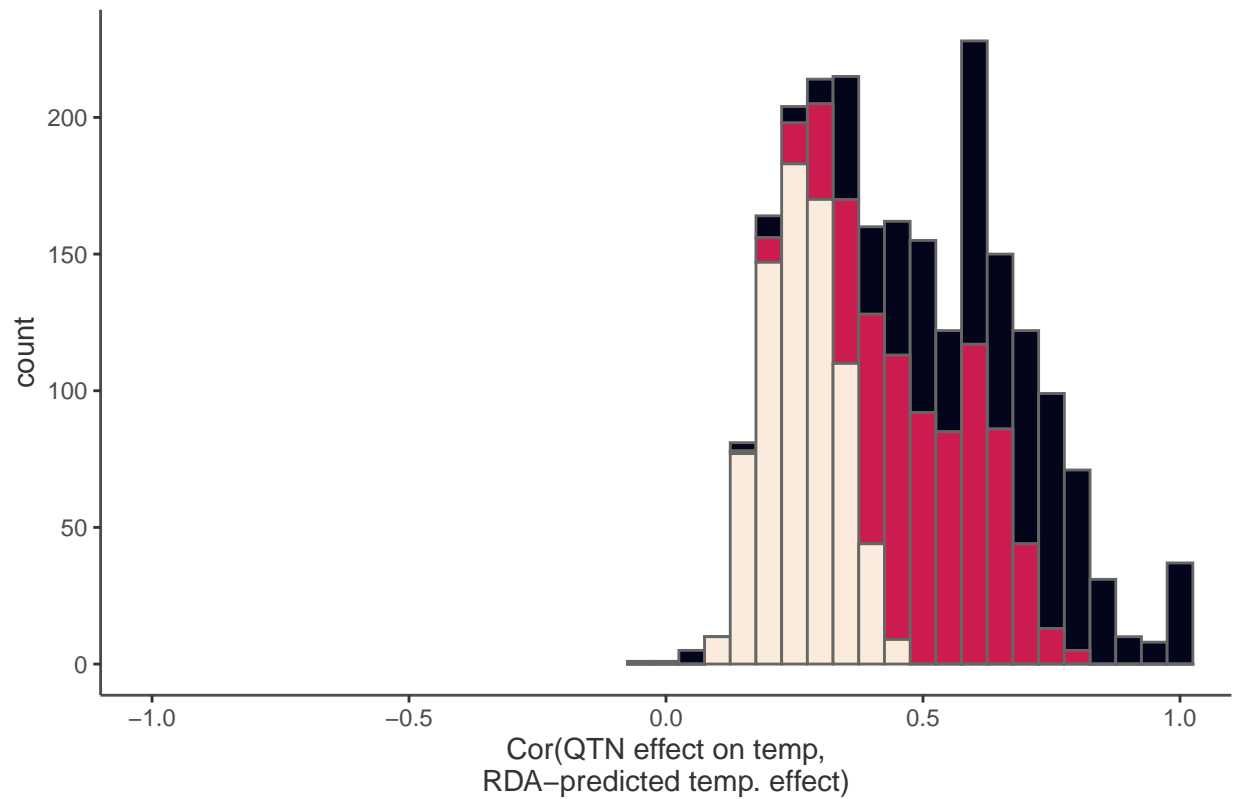
```
final.df$seed[which(final.df$RDA_cor_RDA20000salppredict_salPhen < 0)]
```

```
## integer(0)
```

Can redundancy analysis identify mutations with pleiotropic effects?

```
g1<- ggplot(final.df, aes(x=RDA_RDAmutpred_cor_tempEffect, fill=arch_level)) + geom_histogram(color="green")  
g1
```

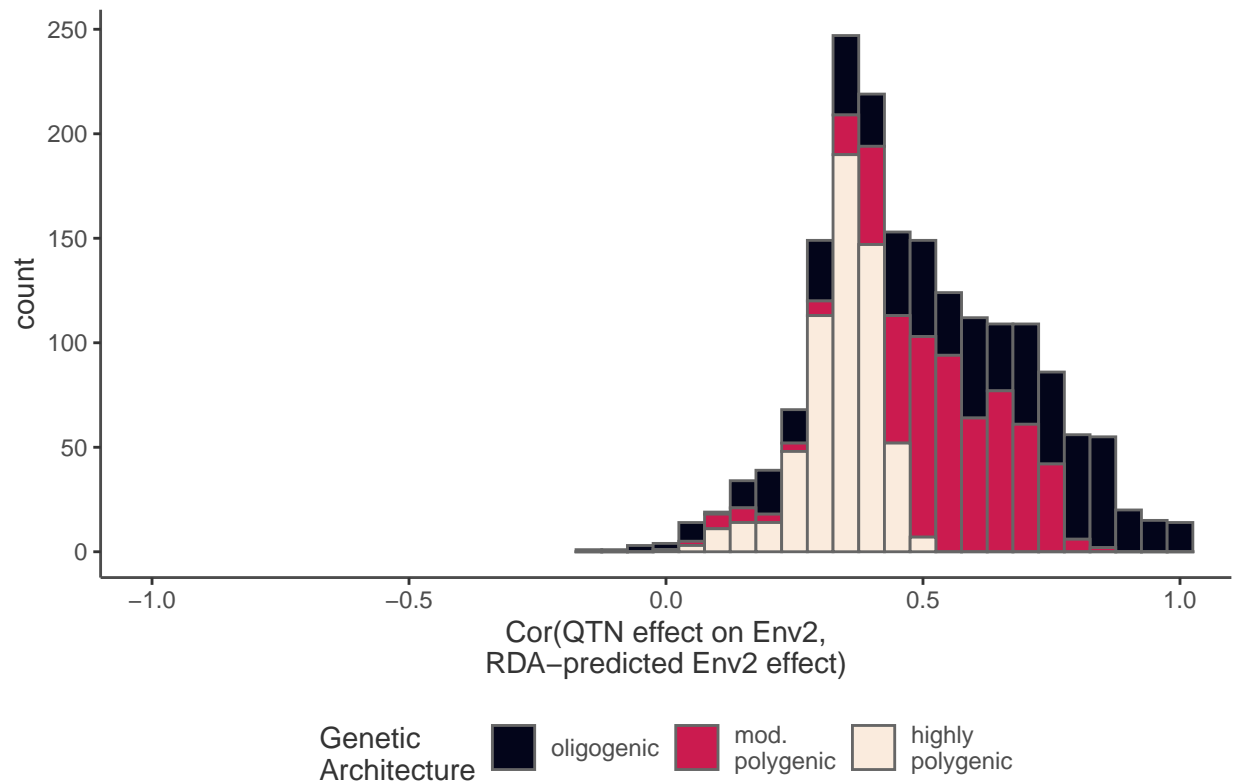
A) Temperature mutation effect



```
g2 <- ggplot(final.df, aes(x=RDA_RDAmutpred_cor_salEffect, fill=arch_level)) + geom_histogram(color="green", fill="white")
g2
```

```
## Warning: Removed 450 rows containing non-finite values (stat_bin).
```

B) Env2 mutation effect

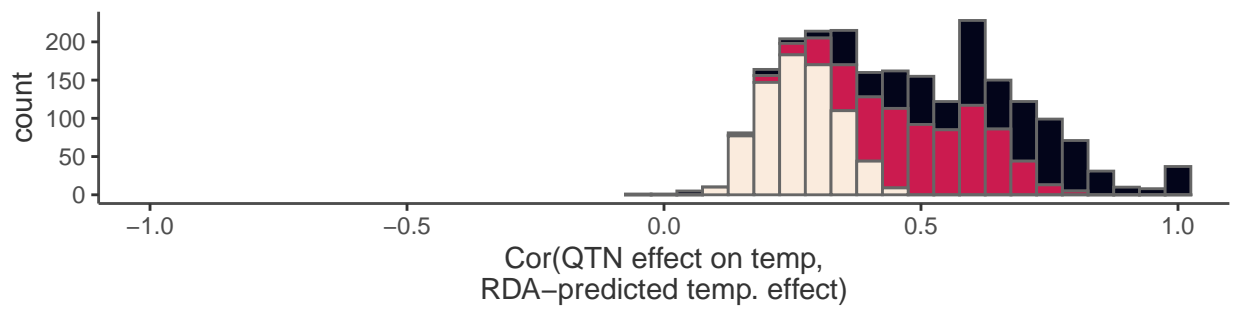


removing 450 expected

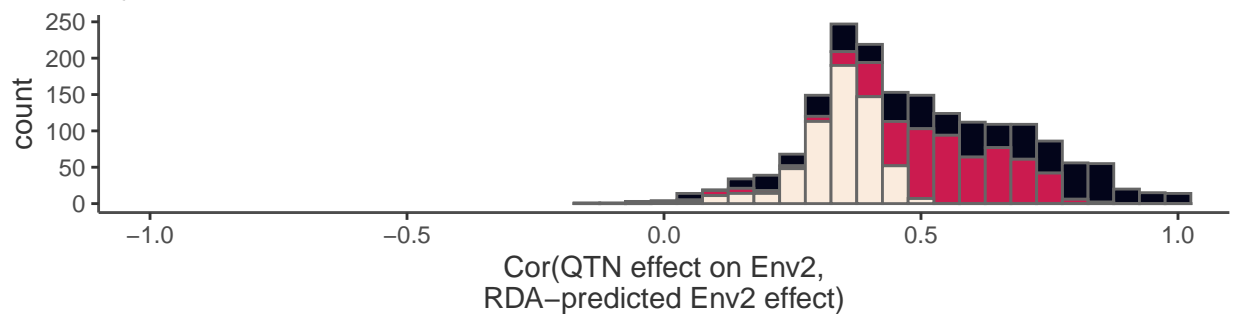
```
grid.arrange(g1, g2,
  layout_matrix = matrix(c(1,1,1,2,2,2,2), nrow=7))
```

Warning: Removed 450 rows containing non-finite values (stat_bin).

A) Temperature mutation effect



B) Env2 mutation effect



Genetic Architecture

- oligogenic
- mod. polygenic
- highly polygenic

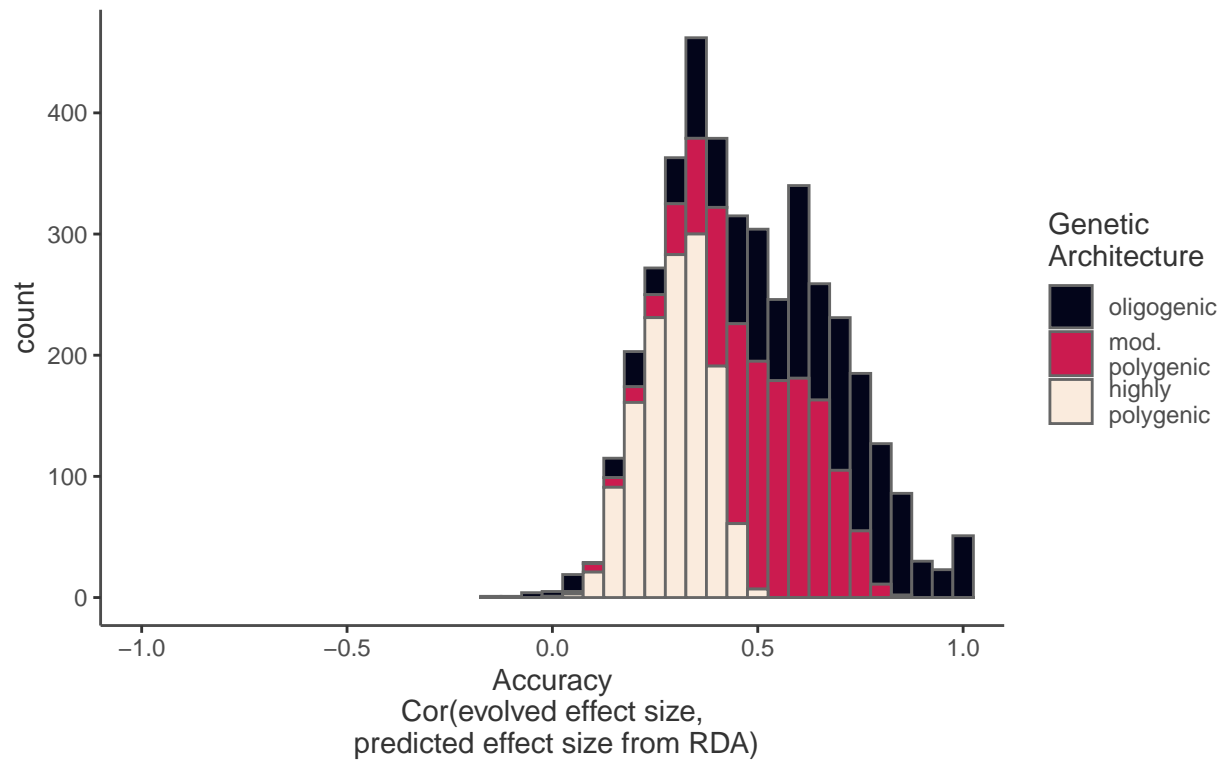
They show the same pattern, so combine for analysis:

```
forhist <- gather(final.df, key=env, value=Accuracy, RDA_RDAmutpred_cor_tempEffect, RDA_RDAmutpred_cor_Env2)

g3 <- ggplot(forhist, aes(x=Accuracy, fill=arch_level)) + geom_histogram(color="grey40", binwidth=0.05)
g3
```

Warning: Removed 450 rows containing non-finite values (stat_bin).

D) Accuracy of RDA prediction
(QTN effect size, no structure correction)

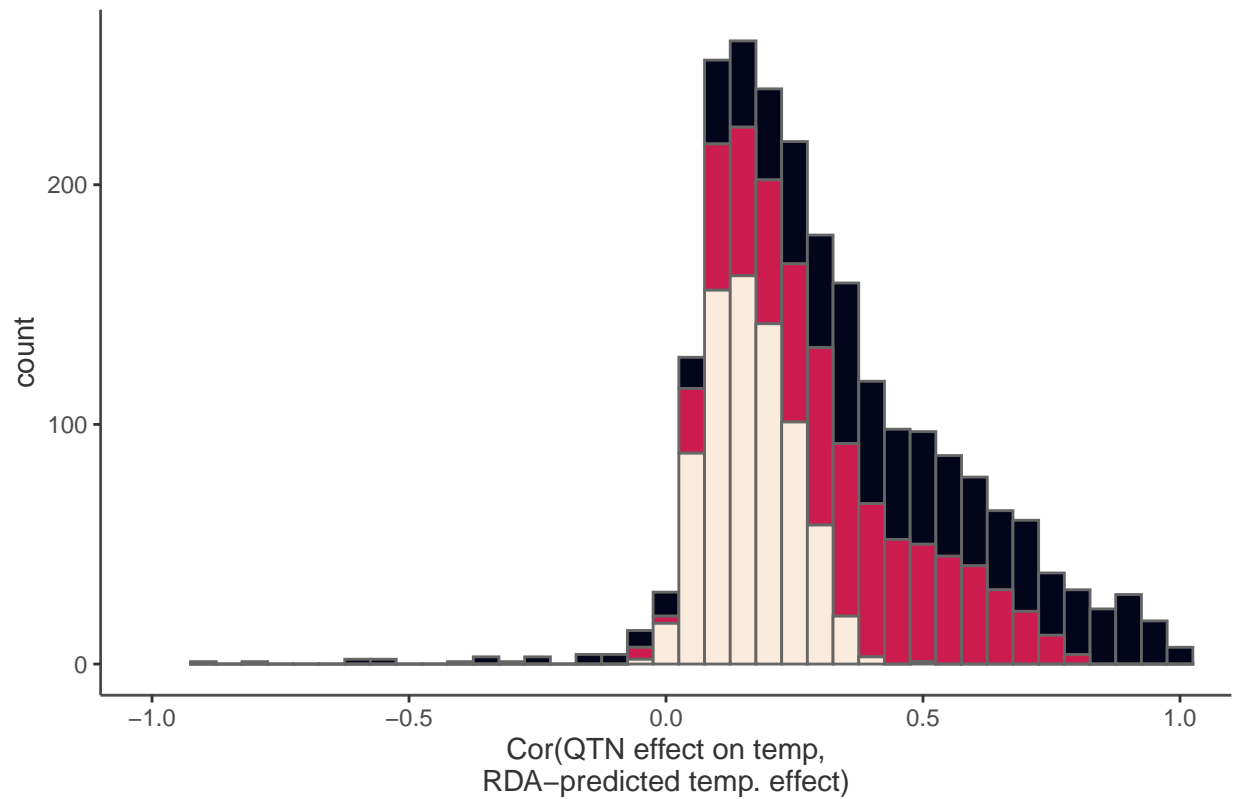


450 missing values expected

Same analysis as above, but with structure correction

```
g1sc<- ggplot(final.df, aes(x=RDA_RDAmutpred_cor_tempEffect_structcorr, fill=arch_level)) + geom_histogram()
g1sc
```

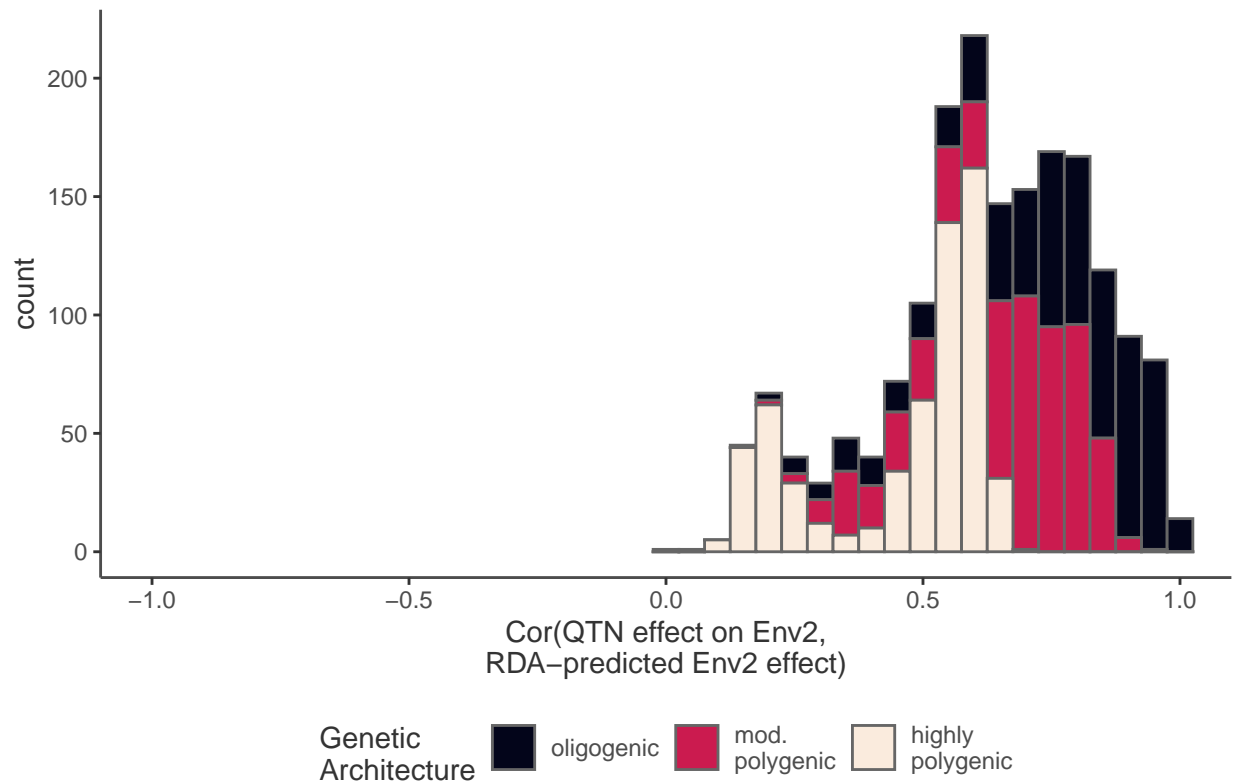
A) Temperature mutation effect with structure correction



```
g2sc <- ggplot(final.df, aes(x=RDA_RDAmutpred_cor_salEffect_structcorr, fill=arch_level)) + geom_histogram()
g2sc
```

```
## Warning: Removed 450 rows containing non-finite values (stat_bin).
```

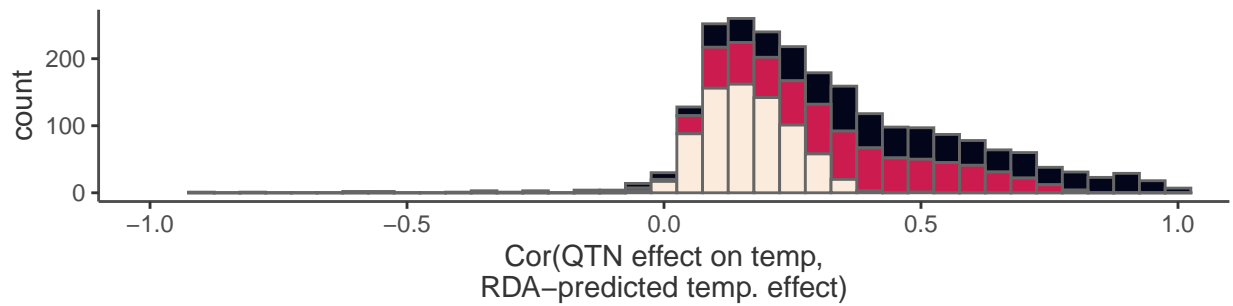

B) Env2 mutation effect with structure correction



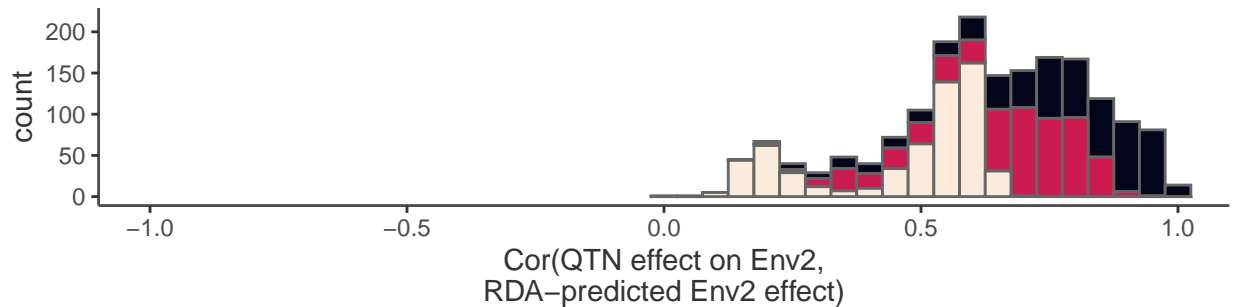
```
grid.arrange(g1sc, g2sc,
              layout_matrix = matrix(c(1,1,1,2,2,2,2), nrow=7))
```

```
## Warning: Removed 450 rows containing non-finite values (stat_bin).
```

A) Temperature mutation effect with structure correction



B) Env2 mutation effect with structure correction



Genetic Architecture

- oligogenic
- mod. polygenic
- highly polygenic

Another way to view the structure correction - boxplot

```
library(plyr)
```

```
### Temp
```

```
#### Check for missing data
```

```
sum(is.na(final.df$RDA_RDAmutpred_cor_tempEffect))
```

```
## [1] 0
```

```
sum(is.na(final.df$RDA_RDAmutpred_cor_tempEffect_structcorr))
```

```
## [1] 0
```

```
#### organize data
```

```
RDA_mutpredict <- gather(final.df, key=structcorr, value=Accuracy, RDA_RDAmutpred_cor_tempEffect, RDA_RDAmutpred_cor_tempEffect_structcorr)
```

```
RDA_mutpredict$demog_level <- factor(RDA_mutpredict$demog_level)
```

```
RDA_mutpredict$structcorr <- factor(RDA_mutpredict$structcorr)
```

```
RDA_mutpredict$structcorr <- revalue(RDA_mutpredict$structcorr, c( "RDA_RDAmutpred_cor_tempEffect" = "No (RDA)",
```

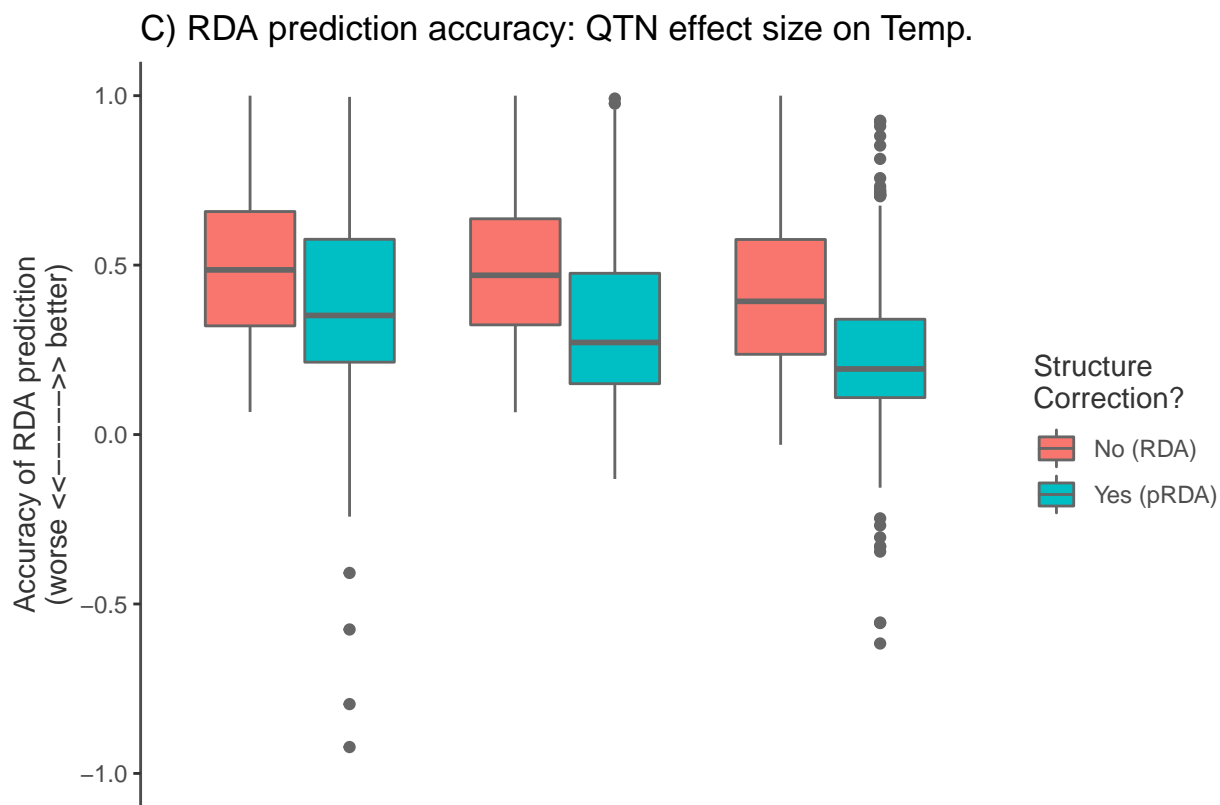
```
levels(RDA_mutpredict$structcorr)
```

```
## [1] "No (RDA)" "Yes (pRDA)"
```

```
# check again for missing data
sum(is.na(RDA_mutpredict$Accuracy))
```

```
## [1] 0
```

```
n <- ggplot(RDA_mutpredict, aes(y=Accuracy, x=demog_level, fill=structcorr)) + geom_boxplot(color="green")
theme(axis.text.x=element_blank()) + xlab("")
# Cor(Mutation effect on Temp., \nRDA-predicted Temp. effect)
n
```



```
# 450 rows
```

```
### Sal
```

```
RDA_mutpredict_sal <- gather(final.df, key=structcorr, value=Accuracy, RDA_RDAmutpred_cor_salEffect, 1)

RDA_mutpredict_sal$demog_level <- factor(RDA_mutpredict_sal$demog_level)
RDA_mutpredict_sal$structcorr <- factor(RDA_mutpredict_sal$structcorr)
RDA_mutpredict_sal$structcorr <- revalue(RDA_mutpredict_sal$structcorr, c( "RDA_RDAmutpred_cor_salEffect", "RDA_RDAmutpred_cor_salEffect"))
levels(RDA_mutpredict_sal$structcorr)
```

```
## [1] "No (RDA)" "Yes (pRDA)"
```

```

# check for NA values
sum(is.na(RDA_mutpredict_sal$Accuracy))

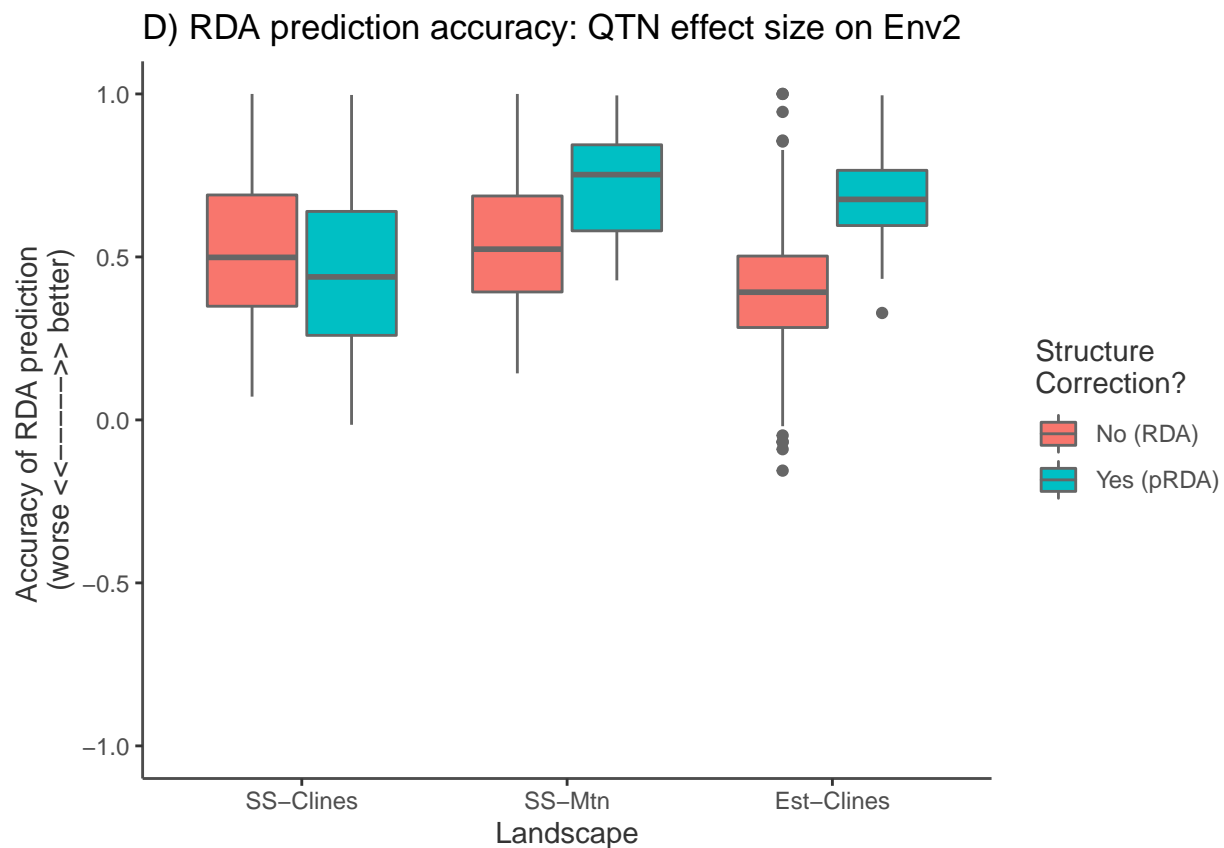
## [1] 900

# 900 expected (450 from each set combined to one data frame)

o <- ggplot(RDA_mutpredict_sal, aes(y=Accuracy,x=demog_level, fill=structcorr)) + geom_boxplot(color=
# "Cor(Mutation effect on Env2,\nRDA-predicted Env2 effect)"
o

## Warning: Removed 900 rows containing non-finite values (stat_boxplot).

```



```

pdf(paste0(outputs, "RDA-Predict-Muts.pdf"), width=5.5, height=7)
grid.arrange(g3, n,o)

```

```

## Warning: Removed 450 rows containing non-finite values (stat_bin).

## Warning: Removed 900 rows containing non-finite values (stat_boxplot).

dev.off()

```

```

## pdf
## 2

```

```
pdf(paste0(outputs, "RDA-Predict-Muts-nohist.pdf"), width=4, height=5.5)
grid.arrange(n,o)
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```

```
dev.off()
```

```
## pdf
## 2
```

What drives the population correction effect?

```
#####
## Temp
#####
## What drives the change in performance with structure correction?
final.df$change_temp_mut <- final.df$RDA_RDAmutpred_cor_tempEffect_structcorr - final.df$RDA_RDAmutpred_cor_temp
summary(aov(final.df$change_temp_mut~final.df$cor_PC1_temp + final.df$cor_PC2_temp +
            final.df$demog_level + final.df$demog_level_sub + final.df$arch_level))
```

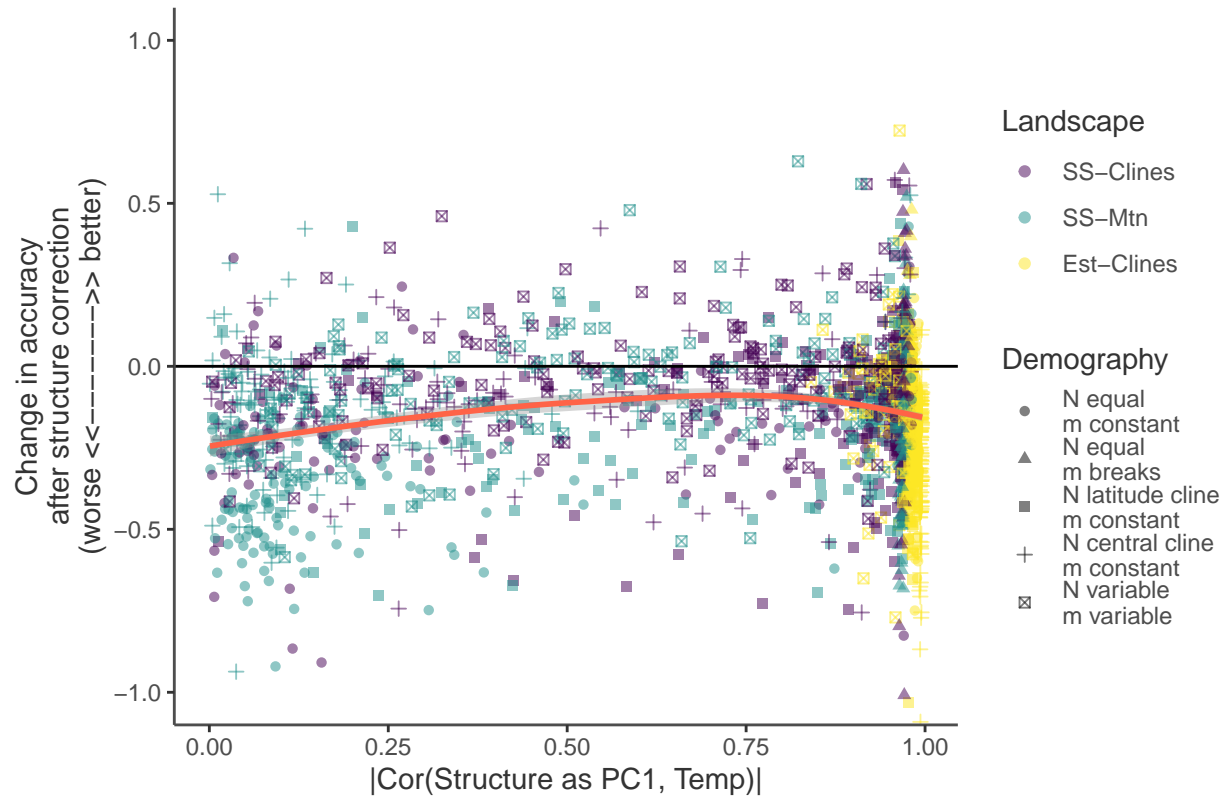
```
##               Df Sum Sq Mean Sq F value    Pr(>F)
## final.df$cor_PC1_temp      1    0.00  0.0002    0.005 0.942064
## final.df$cor_PC2_temp      1    0.43  0.4332   11.385 0.000753 ***
## final.df$demog_level       2    2.39  1.1972   31.465 3.34e-14 ***
## final.df$demog_level_sub    4    8.81  2.2021   57.878 < 2e-16 ***
## final.df$arch_level        2    3.20  1.5995   42.040 < 2e-16 ***
## Residuals                2239   85.19  0.0380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
p1 <- ggplot(final.df) +
  geom_point(aes(x=abs(cor_PC1_temp), y=change_temp_mut, color=demog_level, shape=demog_level_sub), alpha=0.5) +
  ylab("Change in accuracy\nafter structure correction\n(worse <-----> better)") + xlab("|Cor(Structure)|") +
  guides(color=guide_legend(title="Landscape"), shape=guide_legend("Demography")) + ggtitle("A) Mutation")
  geom_smooth(aes(x=abs(cor_PC1_temp), y=change_temp_mut, color="tomato", method="loess", span=1)) + scale_x_continuous(breaks=0:1)
p1
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

A) Mutation effect on Temperature



```
#####
## Env 2 trait
#####

## What drives the change in performance with structure correction?
final.df$change_sal_mut <- final.df$RDA_RDAmutpred_cor_salEffect_structcorr - final.df$RDA_RDAmutpred_cor_sal
summary(aov(final.df$change_sal_mut~final.df$cor_PC1_sal+ final.df$cor_PC2_sal +
  final.df$demog_level + final.df$demog_level_sub + final.df$arch_level))

##               Df Sum Sq Mean Sq F value    Pr(>F)
## final.df$cor_PC1_sal      1   3.80    3.802 173.383 < 2e-16 ***
## final.df$cor_PC2_sal      1   0.00    0.002   0.111   0.739
## final.df$demog_level       2  36.25   18.126 826.617 < 2e-16 ***
## final.df$demog_level_sub   4   4.43    1.107  50.473 < 2e-16 ***
## final.df$arch_level        2   1.16    0.582  26.540 4.38e-12 ***
## Residuals              1789   39.23    0.022
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 450 observations deleted due to missingness

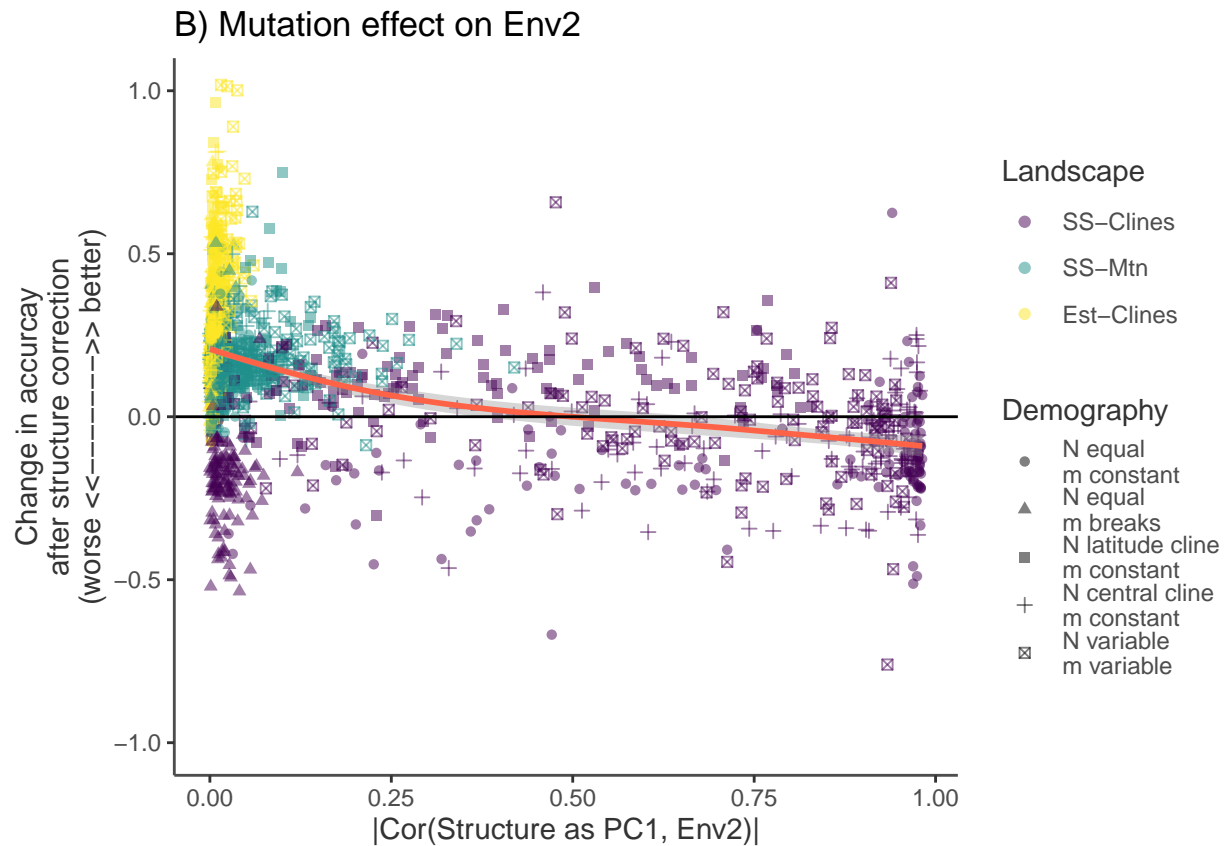
p2 <- ggplot(final.df) + geom_point(aes(x=abs(cor_PC1_sal), y=change_sal_mut, color=demog_level, shape=demog_level_sub)) +
  geom_smooth(aes(x=abs(cor_PC1_sal), y=change_sal_mut), method="loess", span=1, color="tomato") + scale_x_continuous(limits=c(0, 1))
p2
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```



```
pdf(paste0(outputs, "RDA-Predict-Muts-CovariateStructure.pdf"), width=6, height=7)
grid.arrange(p1, p2)
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
## pdf
## 2
```

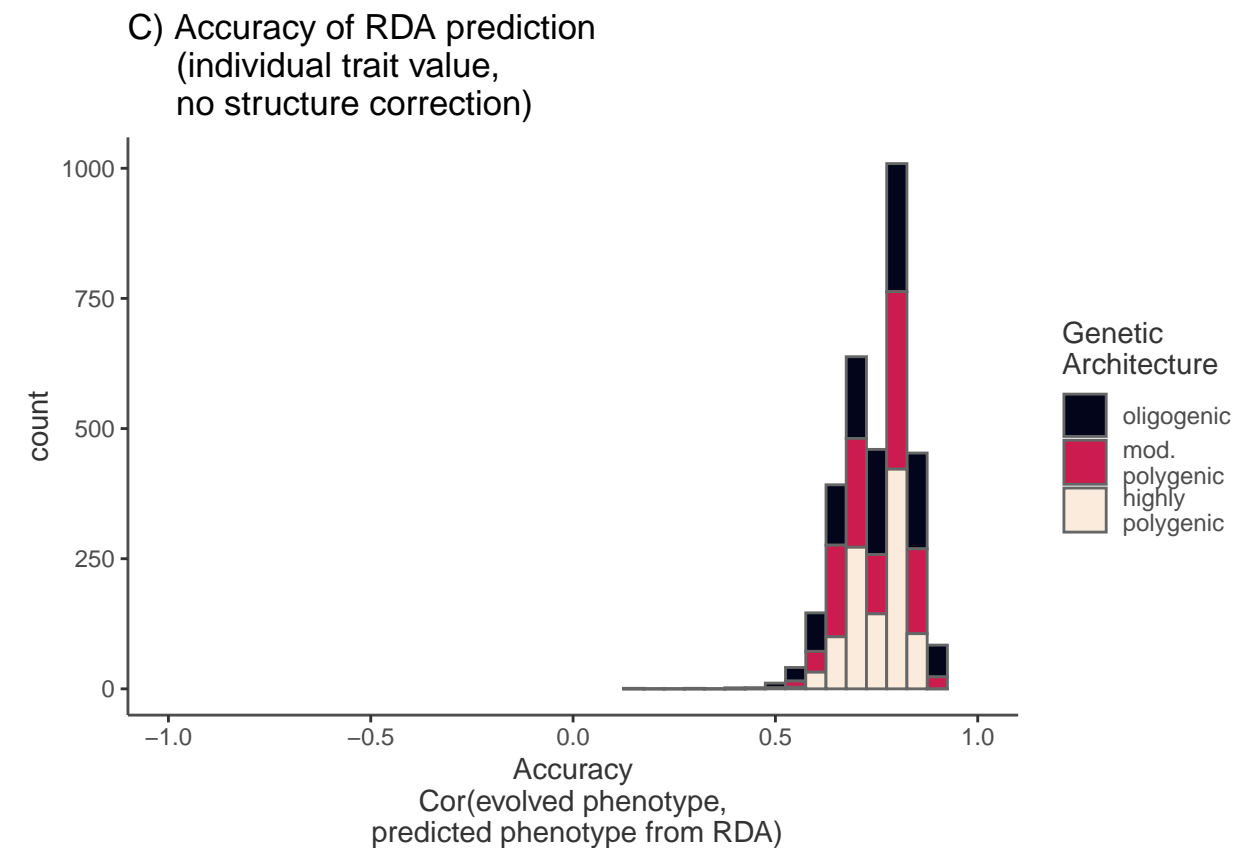
Under what conditions can redundancy analysis predict an individual's optimal environment, without knowledge of the genetic architecture of adaptation?

Visualize the effect of genetic architecture on phenotype prediction

```
forhist <- gather(final.df, key=env, value=Accuracy, RDA_cor_RDA20000temppredict_tempPhen, RDA_cor_RDA20000temppredict_tempPhen)

g4 <- ggplot(forhist, aes(x=Accuracy, fill=arch_level)) + geom_histogram(color="grey40", binwidth=0.05)
g4
```

```
## Warning: Removed 360 rows containing non-finite values (stat_bin).
```



Accuracy of RDA prediction maxed out by cor (phenotype, Env)

```
#Scatterplot
levels(final.df$demog_level_sub)
```



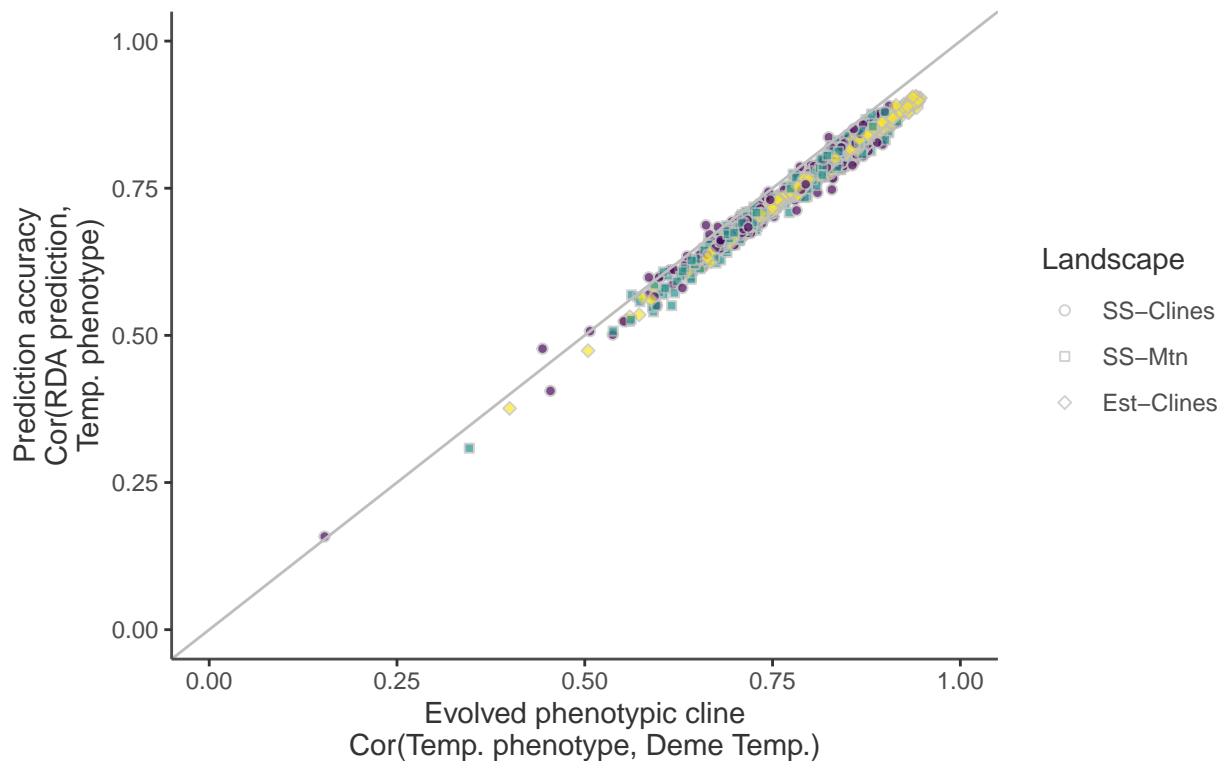
```
## [1] "N equal\nm constant"          "N equal\nm breaks"
## [3] "N latitude cline\nm constant" "N central cline\nm constant"
## [5] "N variable\nm variable"

forscatter <- filter(final.df, num_neut_postfilter>20000) %>% arrange(desc(demog_level_sub))

n1 <- ggplot(forscatter) + geom_point(aes(x=subsamp_corr_phen_temp,
      y=RDA_cor_RDA20000temppredict_tempPhen, bg=demog_level,
      shape=demog_level), color="grey",alpha=0.7) + ylim(0,1) + xlim(0,1) +
  ggtheme + geom_abline(slope=1, color="grey") +
  scale_shape_manual(values = c(21, 22, 23), name="Landscape") + guides(bg = "none") +
  xlab("Evolved phenotypic cline\nCor(Temp. phenotype, Deme Temp.)") +
  ylab("Prediction accuracy\nCor(RDA prediction,\nTemp. phenotype)") + ggtitle("A) Accuracy of RDA predi

n1
```

A) Accuracy of RDA prediction
(Temp. trait, no structure correction)

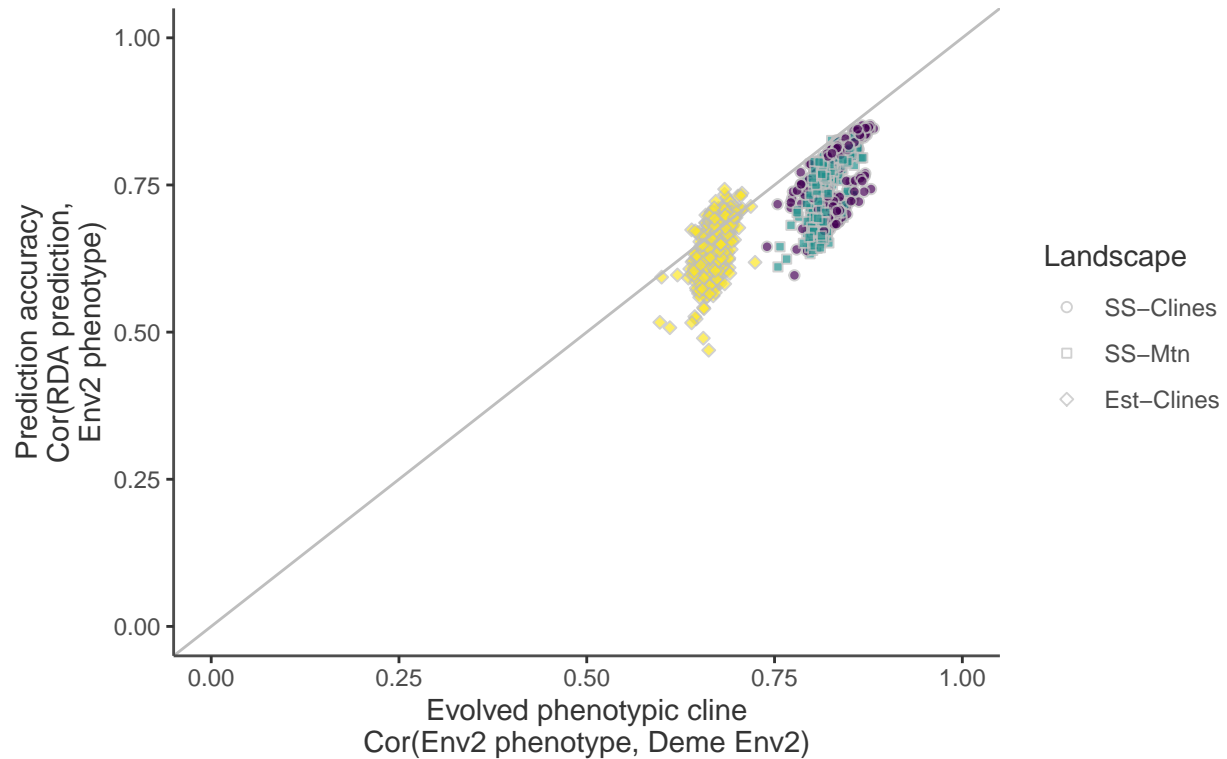


```
n2<- ggplot(forscatter) + geom_point(aes(x=subsamp_corr_phen_sal,
      y=RDA_cor_RDA20000salpredict_salPhen, bg=demog_level,
      shape=demog_level), alpha=0.7, color="grey") + ylim(0,1) + xlim(0,1) +
  ggtheme + geom_abline(slope=1, color="grey") +
  scale_shape_manual(values = c(21, 22, 23), name="Landscape") + guides(bg = "none") +
  xlab("Evolved phenotypic cline\nCor(Env2 phenotype, Deme Env2)") +
  ylab("Prediction accuracy\nCor(RDA prediction,\nEnv2 phenotype)") +
  ggtitle("B) Accuracy of RDA prediction\n      (Env2 trait, no structure correction)")

n2
```

```
## Warning: Removed 360 rows containing missing values (geom_point).
```

B) Accuracy of RDA prediction (Env2 trait, no structure correction)



```
# missing values expected due to filtering
```

```
pdf(paste0(outputs, "RDA-Demog-scatter.pdf"), width=6, height=10)  
grid.arrange(g4, n1, n2, ncol=1)
```

```
## Warning: Removed 360 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 360 rows containing missing values (geom_point).
```

```
dev.off()
```

```
## pdf  
## 2
```

```
pdf(paste0(outputs, "RDA-Demog-scatter-noHist.pdf"), width=4.5, height=7)  
grid.arrange(n1, n2)
```

```
## Warning: Removed 360 rows containing missing values (geom_point).
```

```
dev.off()
```

```
## pdf  
## 2
```

```
pdf(paste0(outputs,"RDA-Hists-PopMut.pdf"), width=5, height=7)  
grid.arrange(g4, g3)
```

```
## Warning: Removed 360 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 450 rows containing non-finite values (stat_bin).
```

```
dev.off()
```

```
## pdf  
## 2
```

Effect of structure correction

```
# Reorganize data
```

```
RDA_indpredict <- gather(final.df, key=structcorr, value=Accuracy, RDA_cor_RDA20000temppredict_tempPhen
```

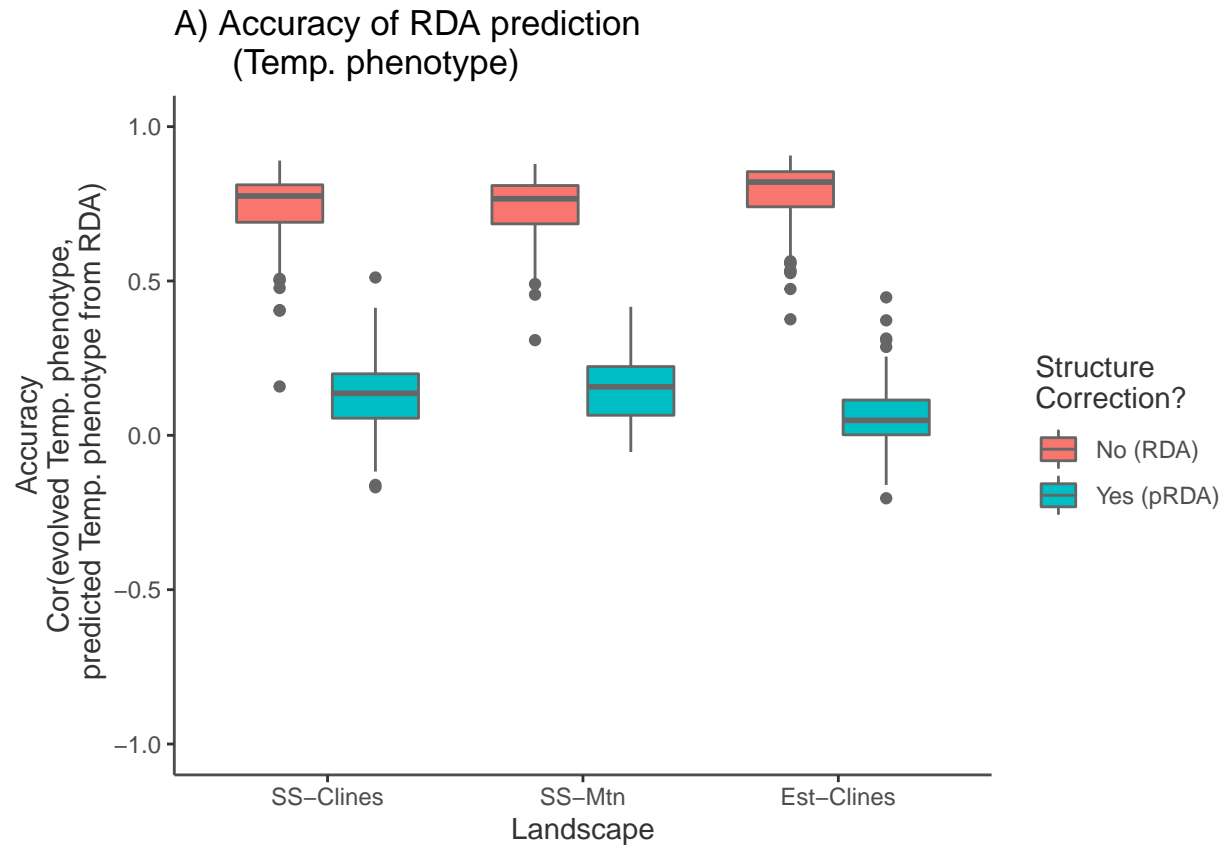
```
RDA_indpredict$demog_level <- factor(RDA_indpredict$demog_level)
```

```
RDA_indpredict$structcorr <- factor(RDA_indpredict$structcorr)
```

```
RDA_indpredict$structcorr <- revalue(RDA_indpredict$structcorr,c( "RDA_cor_RDA20000temppredict_tempPhen  
levels(RDA_indpredict$structcorr)
```

```
## [1] "No (RDA)" "Yes (pRDA)"
```

```
n <- ggplot(RDA_indpredict, aes(y=Accuracy,x=demog_level, fill=structcorr)) + geom_boxplot(color="grey4  
n
```



```
## Same as above for Env2 trait
```

```
RDA_indpredict_sal <- gather(final.df, key=structcorr, value=Accuracy, RDA_cor_RDA20000salpredict_salPh
```

```
RDA_indpredict_sal$demog_level <- factor(RDA_indpredict_sal$demog_level)
```

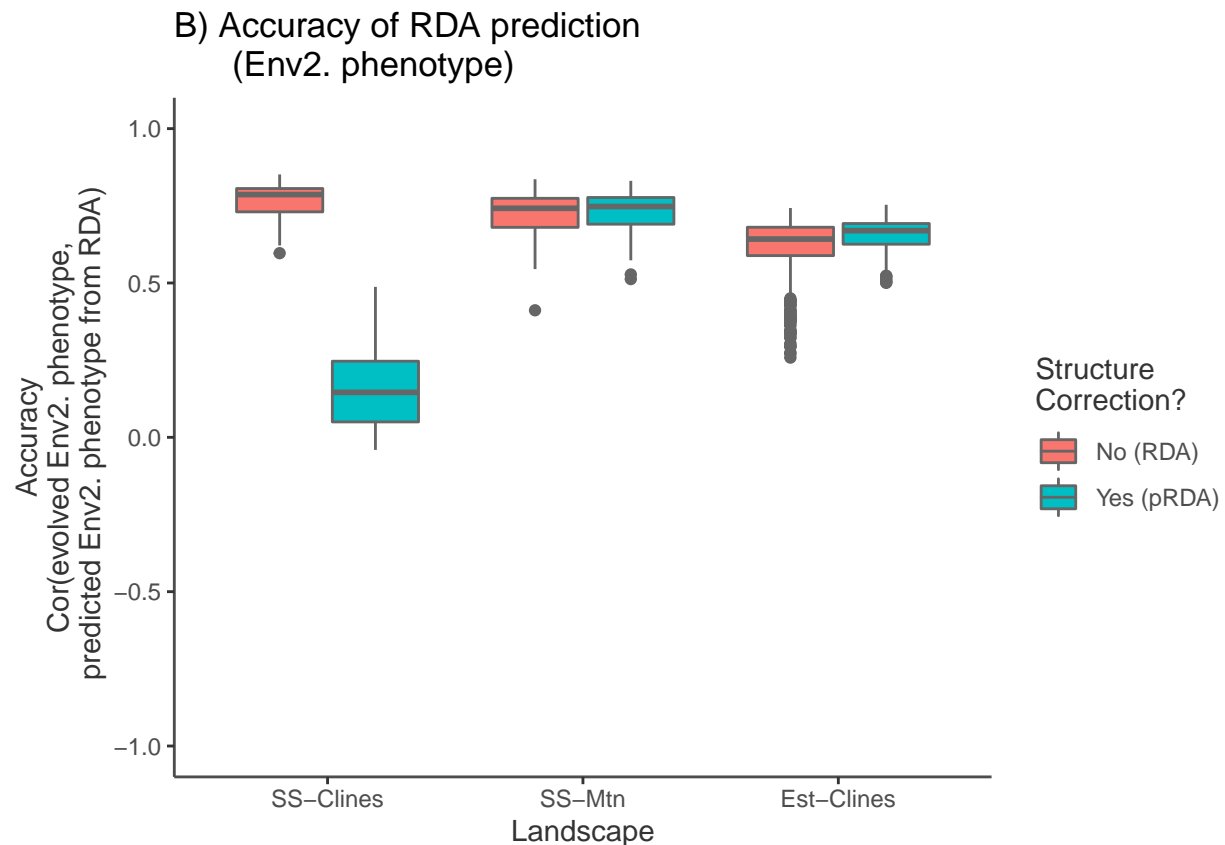
```
RDA_indpredict_sal$structcorr <- factor(RDA_indpredict_sal$structcorr)
```

```
RDA_indpredict_sal$structcorr <- revalue(RDA_indpredict_sal$structcorr, c( "RDA_cor_RDA20000salpredict_s  
levels(RDA_indpredict_sal$structcorr)
```

```
## [1] "No (RDA)" "Yes (pRDA)"
```

```
o <- ggplot(RDA_indpredict_sal, aes(y=Accuracy, x=demog_level, fill=structcorr)) + geom_boxplot(color="g  
o
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```



```
# 900 missing values expected
```

```
pdf(paste0(outputs,"RDA-Predict-Phen-struct.pdf"), width=5, height=7)
grid.arrange(n, o)
```

```
## Warning: Removed 900 rows containing non-finite values (stat_boxplot).
```

```
dev.off()
```

```
## pdf
## 2
```

Understand how correlation with PC affects structure correction

```
## Temp
## What drives the change in performance with structure correction?
final.df$change_temp <- final.df$RDA_cor_RDA20000temppredict_tempPhen_structcorr - final.df$RDA_cor_RDA20000temp
summary(aov(final.df$change_temp~final.df$cor_PC1_temp + final.df$cor_PC2_temp +
  final.df$demog_level + final.df$demog_level_sub + final.df$arch_level))
```

```
##
## final.df$cor_PC1_temp      Df Sum Sq Mean Sq F value    Pr(>F)
##                          1  4.453    4.453 413.204 < 2e-16 ***
```

```
## final.df$cor_PC2_temp      1  0.195    0.195  18.070 2.22e-05 ***
## final.df$demog_level      2  6.013    3.007 278.989 < 2e-16 ***
## final.df$demog_level_sub  4  9.961    2.490 231.062 < 2e-16 ***
## final.df$arch_level       2  0.032    0.016   1.489   0.226
## Residuals                 2239 24.129    0.011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
p1 <- ggplot(final.df) +
  geom_point(aes(x=abs(cor_PC1_temp), y=change_temp, color=demog_level, shape=demog_level_sub), alpha=0.2) +
  ylab("Change in accuracy\nafter structure correction\n(worse <<----->> better)") + xlab("|Cor(Structure as PC1, Temp)|") +
  guides(color=guide_legend(title="Landscape"), shape=guide_legend("Demography")) + ggtitle("A) Temperature Phenotype")
p1
```

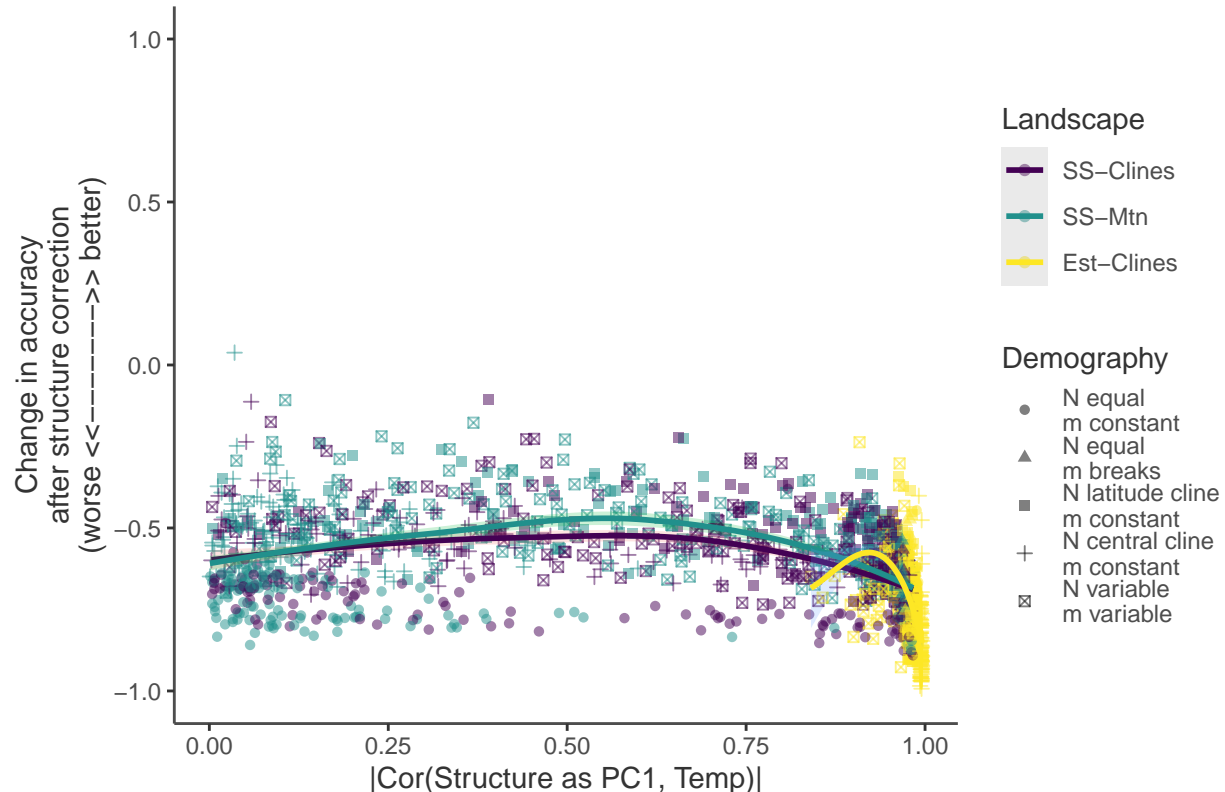
```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```

A) Temperature Phenotype



```
#####
## Env 2 trait
#####

## What drives the change in performance with structure correction?
final.df$change_sal <- final.df$RDA_cor_RDA2000salpredict_salPhen_structcorr - final.df$RDA_cor_RDA2000salpredict_salPhen_structcorr
summary(aov(final.df$change_sal~final.df$cor_PC1_sal+ final.df$cor_PC2_sal +
            final.df$demog_level + final.df$demog_level_sub + final.df$sarch_level))
```

```
##               Df Sum Sq Mean Sq  F value    Pr(>F)
## final.df$cor_PC1_sal      1  20.55    20.55 2509.144 < 2e-16 ***
## final.df$cor_PC2_sal      1   0.10     0.10  11.756 0.00062 ***
## final.df$demog_level      2 133.70    66.85 8160.706 < 2e-16 ***
## final.df$demog_level_sub   4   6.21     1.55  189.427 < 2e-16 ***
## final.df$sarch_level      2   0.01     0.00   0.562 0.57034
## Residuals                1789  14.66     0.01
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 450 observations deleted due to missingness
```

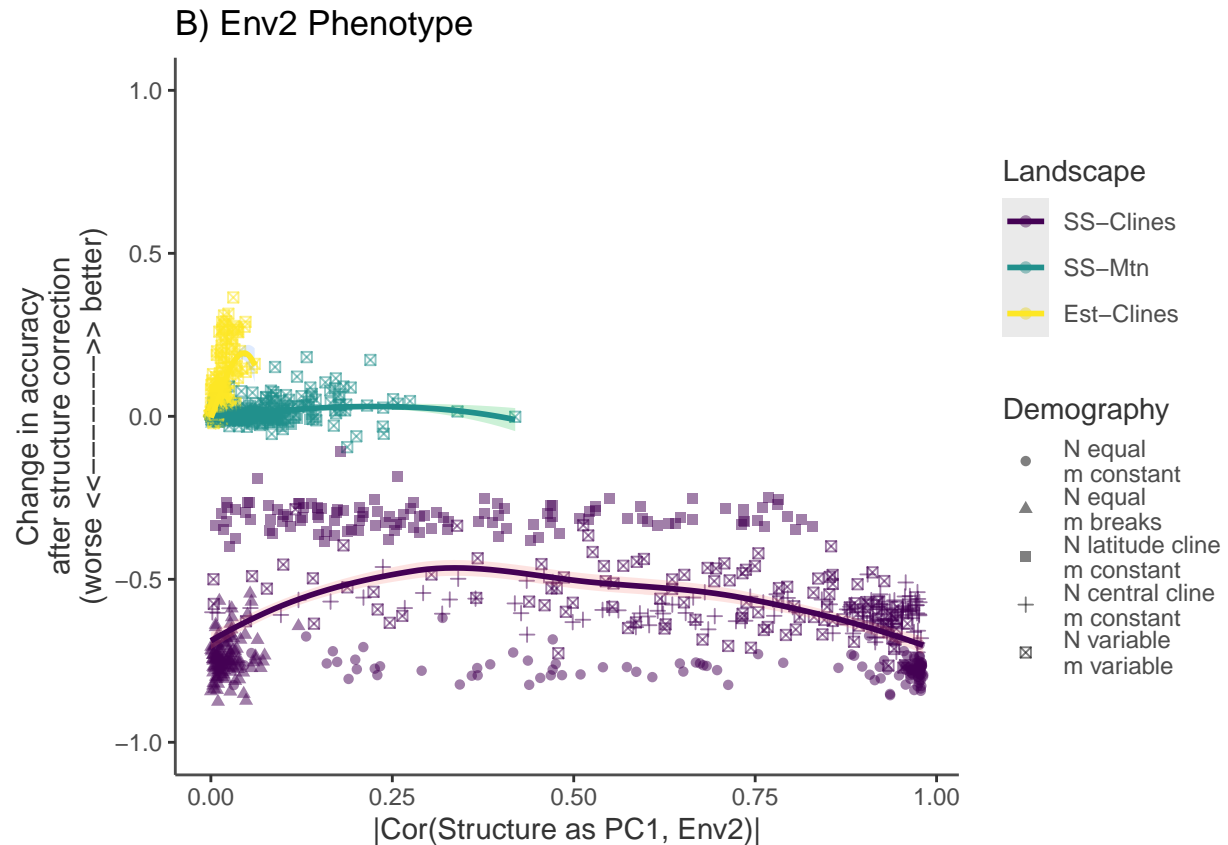
```
p2 <- ggplot(final.df) + geom_point(aes(x=abs(cor_PC1_sal), y=change_sal, color=demog_level, shape=demog_level),
  geom_smooth(aes(x=abs(cor_PC1_sal),y=change_sal, color=demog_level, fill=demog_level), alpha=0.2, method="lm"))
p2
```

```
## Warning: Using shapes for an ordinal variable is not advised
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 450 rows containing missing values (geom_point).
```



```
pdf(paste0(outputs, "RDA-Predict-Traits-CovariateStructure.pdf"), width=6, height=7)
grid.arrange(p1, p2)
```

```
## Warning: Using shapes for an ordinal variable is not advised
## 'geom_smooth()' using formula 'y ~ x'
## Warning: Removed 2 rows containing non-finite values (stat_smooth).
## Warning: Removed 2 rows containing missing values (geom_point).
## Warning: Using shapes for an ordinal variable is not advised
## 'geom_smooth()' using formula 'y ~ x'
## Warning: Removed 450 rows containing non-finite values (stat_smooth).
## Warning: Removed 450 rows containing missing values (geom_point).
```

```
dev.off()
```

```
## pdf
## 2
```



```
#hist(final.df$cor_RDA20000_RDloadings_tempPhen, xlim=c(0,1), breaks=seq(0,1,0.05))
#hist(final.df$cor_RDA20000_RDloadings_salPhen, xlim=c(0,1), breaks=seq(0,1,0.05))
```

Statistical models

```
length(levels(final.df$arch))
```

```
## [1] 15
```

```
# Stat models for temperature effect prediction
```

```
tm_me <- summary(aov(RDA_RDAmutpred_cor_tempEffect~ subsamp_corr_phen_temp + demog_level + demog_level:arch, data=final.df))
tm_me
```

```
##
## Df Sum Sq Mean Sq F value Pr(>F)
## subsamp_corr_phen_temp      1    2.42    2.423 228.140 < 2e-16 ***
## demog_level                 2    5.79    2.893 272.483 < 2e-16 ***
## demog_level_sub            4    0.48    0.119  11.199 5.48e-09 ***
## arch                       14   58.93    4.209 396.406 < 2e-16 ***
## demog_level:demog_level_sub  8    0.14    0.017   1.631  0.1109
## demog_level:arch           28    1.29    0.046   4.343 3.68e-13 ***
## demog_level_sub:arch       56    1.59    0.028   2.667 5.82e-10 ***
## demog_level:demog_level_sub:arch 112    1.47    0.013   1.236  0.0515 .
## Residuals                 2024   21.49    0.011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sm_me <- summary(aov(RDA_RDAmutpred_cor_salEffect~ subsamp_corr_phen_temp + demog_level + demog_level:arch, data=final.df))
sm_me
```

```
##
## Df Sum Sq Mean Sq F value Pr(>F)
## subsamp_corr_phen_temp      1  0.867    0.867  60.947 1.05e-14 ***
## demog_level                 2  7.493    3.746 263.414 < 2e-16 ***
## demog_level_sub            4  3.031    0.758  53.283 < 2e-16 ***
## arch                       11 23.549    2.141 150.526 < 2e-16 ***
## demog_level:demog_level_sub  8  1.386    0.173  12.177 < 2e-16 ***
## demog_level:arch           22  6.739    0.306  21.536 < 2e-16 ***
## demog_level_sub:arch       44  1.603    0.036   2.561 1.28e-07 ***
## demog_level:demog_level_sub:arch 88  1.769    0.020   1.413  0.00822 **
## Residuals                 1619 23.026    0.014
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 450 observations deleted due to missingness
```

```
# Stat models for phenotype prediction
```

```
tm_pp <- summary(aov(RDA_cor_RDA20000temppredict_tempPhen~ subsamp_corr_phen_temp + demog_level + demog_level:arch, data=final.df))
tm_pp
```

```
##
## Df Sum Sq Mean Sq F value Pr(>F)
## subsamp_corr_phen_temp      1 14.407   14.407 59565.024 < 2e-16 ***
```

```
## demog_level                2 0.009 0.005 19.303 4.96e-09 ***
## demog_level_sub            4 0.384 0.096 396.873 < 2e-16 ***
## arch                       14 0.027 0.002 8.071 < 2e-16 ***
## demog_level:demog_level_sub 8 0.039 0.005 20.105 < 2e-16 ***
## demog_level:arch           28 0.016 0.001 2.363 7.67e-05 ***
## demog_level_sub:arch        56 0.060 0.001 4.444 < 2e-16 ***
## demog_level:demog_level_sub:arch 112 0.034 0.000 1.248 0.0438 *
## Residuals                  2024 0.490 0.000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sm_pp <- summary(aov(RDA_cor_RDA20000salpredict_salPhen~ subsamp_corr_phen_sal + demog_level + demog_level_sub))
sm_pp
```

```
##                Df Sum Sq Mean Sq F value    Pr(>F)
## subsamp_corr_phen_sal      1  8.583   8.583 8167.415 < 2e-16 ***
## demog_level                2  0.499   0.249  237.396 < 2e-16 ***
## demog_level_sub            4  3.550   0.887  844.434 < 2e-16 ***
## arch                       11  0.076   0.007   6.591 7.49e-11 ***
## demog_level:demog_level_sub 8  1.187   0.148  141.149 < 2e-16 ***
## demog_level:arch           22  0.071   0.003   3.057 2.49e-06 ***
## demog_level_sub:arch       44  0.085   0.002   1.830 0.000815 ***
## demog_level:demog_level_sub:arch 88 0.176   0.002   1.900 1.93e-06 ***
## Residuals                 1619  1.701   0.001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 450 observations deleted due to missingness
```

```
# Calculate proportion of variance explained in SS
z<- data.frame(
  PropVarTempMutPred = round(tm_me[[1]][,2]/sum(tm_me[[1]][,2]), 2),
  PropVarTempPhenPred = round(tm_pp[[1]][,2]/sum(tm_pp[[1]][,2]), 2),
  PropVarEnv2MutPred = round(sm_me[[1]][,2]/sum(sm_me[[1]][,2]), 2),
  PropVarEnv2PhenPred = round(sm_pp[[1]][,2]/sum(sm_pp[[1]][,2]), 2))
# note the the 1st row is specific for each trait, I just took a shortcut for labeling the rowname
rownames(z) <- rownames(tm_me[[1]])

z
```

```
##                PropVarTempMutPred PropVarTempPhenPred
## subsamp_corr_phen_temp            0.03            0.93
## demog_level                      0.06            0.00
## demog_level_sub                   0.01            0.02
## arch                             0.63            0.00
## demog_level:demog_level_sub       0.00            0.00
## demog_level:arch                  0.01            0.00
## demog_level_sub:arch              0.02            0.00
## demog_level:demog_level_sub:arch  0.02            0.00
## Residuals                        0.23            0.03
##                PropVarEnv2MutPred PropVarEnv2PhenPred
## subsamp_corr_phen_temp            0.01            0.54
## demog_level                      0.11            0.03
## demog_level_sub                   0.04            0.22
```

## arch	0.34	0.00
## demog_level:demog_level_sub	0.02	0.07
## demog_level:arch	0.10	0.00
## demog_level_sub:arch	0.02	0.01
## demog_level:demog_level_sub:arch	0.03	0.01
## Residuals	0.33	0.11

The models clarify how the architecture determines the proportion of clines - architecture also largely determines how accurate the mutation prediction is - yet the RDA phenotype prediction is not sensitive to the architecture and it is driven more by how correlated the phenotype is with the environment.

Interesting sims to look at

This code just copies some of the figures into a new folder that I can download from the cluster.

RDA predictions as a function of the number of loci and structure correction

```
rdapred <- read.table("summary_20220428_20220726_RDAPredictions.txt", header=TRUE)
head(rdapred)
```

```
##   i nloci Random_cor_RDAtempredict_tempphen Random_cor_RDAsalpredict_salphen
## 1 1     10                0.4739758                      NA
## 2 2     50                0.7151539                      NA
## 3 3    100                0.7974522                      NA
## 4 4    500                0.8329278                      NA
## 5 5   5000                0.8513302                      NA
## 6 6 20000                0.8530879                      NA
##   Random_cor_RDAtempredict_tempphen_structcorr
## 1                0.042232275
## 2                0.019313333
## 3               -0.001635637
## 4               -0.039277317
## 5               -0.033347381
## 6               -0.035417453
##   Random_cor_RDAsalpredict_salphen_structcorr   seed
## 1                      NA 1231094
## 2                      NA 1231094
## 3                      NA 1231094
## 4                      NA 1231094
## 5                      NA 1231094
## 6                      NA 1231094
```

```
rdapred_df <- merge(rdapred, final.df, by="seed", all.x=TRUE)
head(rdapred_df)
```

```
##           seed i nloci Random_cor_RDAtempredict_tempphen
## 1 1231094 1     10                0.4739758
```

```

## 2 1231094 2      50      0.7151539
## 3 1231094 3     100      0.7974522
## 4 1231094 4     500      0.8329278
## 5 1231094 5    5000      0.8513302
## 6 1231094 6   20000      0.8530879
## Random_cor_RDAasalpredict_salphen
## 1      NA
## 2      NA
## 3      NA
## 4      NA
## 5      NA
## 6      NA
## Random_cor_RDatempmpredict_tempphen_structcorr
## 1      0.042232275
## 2      0.019313333
## 3     -0.001635637
## 4     -0.039277317
## 5     -0.033347381
## 6     -0.035417453
## Random_cor_RDAasalpredict_salphen_structcorr
## 1      NA
## 2      NA
## 3      NA
## 4      NA
## 5      NA
## 6      NA
##
##                                     level reps
## 1 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 2 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 3 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 4 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 5 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
## 6 highly-polygenic_1-trait__Est-Clines_N-cline-center-to-edge_m-constant      1
##
##               arch               demog_name
## 1 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 2 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 3 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 4 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 5 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
## 6 highly-polygenic_1-trait Est-Clines_N-cline-center-to-edge_m-constant
##
##               demog_level_sub demog_level MIG_x MIG_y xcline ycline  demog
## 1 N central cline\nm constant Est-Clines  0.49  0.07 linear linear Estuary
## 2 N central cline\nm constant Est-Clines  0.49  0.07 linear linear Estuary
## 3 N central cline\nm constant Est-Clines  0.49  0.07 linear linear Estuary
## 4 N central cline\nm constant Est-Clines  0.49  0.07 linear linear Estuary
## 5 N central cline\nm constant Est-Clines  0.49  0.07 linear linear Estuary
## 6 N central cline\nm constant Est-Clines  0.49  0.07 linear linear Estuary
## METAPOPOP_SIDE_x METAPOPOP_SIDE_y Nequal isVariableM MIG_breaks arch_level_sub
## 1      10      10      4      0      0      1 trait
## 2      10      10      4      0      0      1 trait
## 3      10      10      4      0      0      1 trait
## 4      10      10      4      0      0      1 trait
## 5      10      10      4      0      0      1 trait
## 6      10      10      4      0      0      1 trait

```

```

##          arch_level MU_base MU_QTL_proportion SIGMA_QTN_1 SIGMA_QTN_2 SIGMA_K_1
## 1 highly\npolygenic 1e-07      0.25      0.002      0.002      0.5
## 2 highly\npolygenic 1e-07      0.25      0.002      0.002      0.5
## 3 highly\npolygenic 1e-07      0.25      0.002      0.002      0.5
## 4 highly\npolygenic 1e-07      0.25      0.002      0.002      0.5
## 5 highly\npolygenic 1e-07      0.25      0.002      0.002      0.5
## 6 highly\npolygenic 1e-07      0.25      0.002      0.002      0.5
## SIGMA_K_2 N_traits ispleiotropy n_samp_tot n_samp_per_pop
## 1      0.5      1 No pleiotropy      1000      10
## 2      0.5      1 No pleiotropy      1000      10
## 3      0.5      1 No pleiotropy      1000      10
## 4      0.5      1 No pleiotropy      1000      10
## 5      0.5      1 No pleiotropy      1000      10
## 6      0.5      1 No pleiotropy      1000      10
## sd_fitness_among_inds sd_fitness_among_pops final_LA K Bonf_alpha
## 1      0.05272602      0.01977273 0.500854 2 1.918428e-06
## 2      0.05272602      0.01977273 0.500854 2 1.918428e-06
## 3      0.05272602      0.01977273 0.500854 2 1.918428e-06
## 4      0.05272602      0.01977273 0.500854 2 1.918428e-06
## 5      0.05272602      0.01977273 0.500854 2 1.918428e-06
## 6      0.05272602      0.01977273 0.500854 2 1.918428e-06
## numCausalLowMAFsample all_corr_phen_temp subsamp_corr_phen_temp
## 1      39      0.954579      0.8893387
## 2      39      0.954579      0.8893387
## 3      39      0.954579      0.8893387
## 4      39      0.954579      0.8893387
## 5      39      0.954579      0.8893387
## 6      39      0.954579      0.8893387
## all_corr_phen_sal subsamp_corr_phen_sal num_causal_prefilter
## 1      NA      NA      2628
## 2      NA      NA      2628
## 3      NA      NA      2628
## 4      NA      NA      2628
## 5      NA      NA      2628
## 6      NA      NA      2628
## num_causal_postfilter num_non_causal num_neut_prefilter num_neut_postfilter
## 1      310      25753      26587      26587
## 2      310      25753      26587      26587
## 3      310      25753      26587      26587
## 4      310      25753      26587      26587
## 5      310      25753      26587      26587
## 6      310      25753      26587      26587
## num_neut_neutralgenome num_causal_temp num_causal_sal num_multiallelic
## 1      12867      310      0      0
## 2      12867      310      0      0
## 3      12867      310      0      0
## 4      12867      310      0      0
## 5      12867      310      0      0
## 6      12867      310      0      0
## meanFst va_temp_total va_sal_total Va_temp_sample Va_sal_sample nSNPs
## 1 0.1803949 0.01185008 0 0.01356519 0 26063
## 2 0.1803949 0.01185008 0 0.01356519 0 26063
## 3 0.1803949 0.01185008 0 0.01356519 0 26063
## 4 0.1803949 0.01185008 0 0.01356519 0 26063

```

## 5	0.1803949	0.01185008	0	0.01356519	0	26063
## 6	0.1803949	0.01185008	0	0.01356519	0	26063
##	median_causal_temp_cor	median_causal_sal_cor	median_neut_temp_cor			
## 1	0.3580437	NA	0.3820531			
## 2	0.3580437	NA	0.3820531			
## 3	0.3580437	NA	0.3820531			
## 4	0.3580437	NA	0.3820531			
## 5	0.3580437	NA	0.3820531			
## 6	0.3580437	NA	0.3820531			
##	median_neut_sal_cor	cor_VA_temp_prop	cor_VA_sal_prop	cor_TPR_temp	cor_TPR_sal	
## 1	0.04816897	0.8451605	0	0.4612903	NA	
## 2	0.04816897	0.8451605	0	0.4612903	NA	
## 3	0.04816897	0.8451605	0	0.4612903	NA	
## 4	0.04816897	0.8451605	0	0.4612903	NA	
## 5	0.04816897	0.8451605	0	0.4612903	NA	
## 6	0.04816897	0.8451605	0	0.4612903	NA	
##	cor_FDR_allSNPs_temp	cor_FDR_neutSNPs_temp	cor_FDR_allSNPs_sal			
## 1	0.9894449	0.9791241	NA			
## 2	0.9894449	0.9791241	NA			
## 3	0.9894449	0.9791241	NA			
## 4	0.9894449	0.9791241	NA			
## 5	0.9894449	0.9791241	NA			
## 6	0.9894449	0.9791241	NA			
##	cor_FDR_neutSNPs_sal	num_causal_sig_temp_corr	num_causal_sig_sal_corr			
## 1	NA	143	0			
## 2	NA	143	0			
## 3	NA	143	0			
## 4	NA	143	0			
## 5	NA	143	0			
## 6	NA	143	0			
##	num_notCausal_sig_temp_corr	num_notCausal_sig_sal_corr	num_neut_sig_temp_corr			
## 1	13405	0	6707			
## 2	13405	0	6707			
## 3	13405	0	6707			
## 4	13405	0	6707			
## 5	13405	0	6707			
## 6	13405	0	6707			
##	num_neut_sig_sal_corr	cor_AUCPR_temp_allSNPs	cor_AUCPR_temp_neutSNPs			
## 1	0	0.01064045	0.02148047			
## 2	0	0.01064045	0.02148047			
## 3	0	0.01064045	0.02148047			
## 4	0	0.01064045	0.02148047			
## 5	0	0.01064045	0.02148047			
## 6	0	0.01064045	0.02148047			
##	cor_AUCPR_sal_allSNPs	cor_AUCPR_sal_neutSNPs	cor_af_temp_noutliers			
## 1	NA	NA	13548			
## 2	NA	NA	13548			
## 3	NA	NA	13548			
## 4	NA	NA	13548			
## 5	NA	NA	13548			
## 6	NA	NA	13548			
##	cor_af_sal_noutliers	cor_FPR_temp_neutSNPs	cor_FPR_sal_neutSNPs			
## 1	0	0.5212559	0			
## 2	0	0.5212559	0			

## 3	0	0.5212559	0
## 4	0	0.5212559	0
## 5	0	0.5212559	0
## 6	0	0.5212559	0
##	LEA3.2_lfmm2_Va_temp_prop	LEA3.2_lfmm2_Va_sal_prop	LEA3.2_lfmm2_TPR_temp
## 1	0.278265	NA	0.02258065
## 2	0.278265	NA	0.02258065
## 3	0.278265	NA	0.02258065
## 4	0.278265	NA	0.02258065
## 5	0.278265	NA	0.02258065
## 6	0.278265	NA	0.02258065
##	LEA3.2_lfmm2_TPR_sal	LEA3.2_lfmm2_FDR_allSNPs_temp	
## 1	NA	0.978979	
## 2	NA	0.978979	
## 3	NA	0.978979	
## 4	NA	0.978979	
## 5	NA	0.978979	
## 6	NA	0.978979	
##	LEA3.2_lfmm2_FDR_allSNPs_sal	LEA3.2_lfmm2_FDR_neutSNPs_temp	
## 1	NA	0.9263158	
## 2	NA	0.9263158	
## 3	NA	0.9263158	
## 4	NA	0.9263158	
## 5	NA	0.9263158	
## 6	NA	0.9263158	
##	LEA3.2_lfmm2_FDR_neutSNPs_sal	LEA3.2_lfmm2_AUCPR_temp_allSNPs	
## 1	NA	0.01339495	
## 2	NA	0.01339495	
## 3	NA	0.01339495	
## 4	NA	0.01339495	
## 5	NA	0.01339495	
## 6	NA	0.01339495	
##	LEA3.2_lfmm2_AUCPR_temp_neutSNPs	LEA3.2_lfmm2_AUCPR_sal_allSNPs	
## 1	0.02655237	NA	
## 2	0.02655237	NA	
## 3	0.02655237	NA	
## 4	0.02655237	NA	
## 5	0.02655237	NA	
## 6	0.02655237	NA	
##	LEA3.2_lfmm2_AUCPR_sal_neutSNPs	LEA3.2_lfmm2_mlog10P_tempenv_noutliers	
## 1	NA	333	
## 2	NA	333	
## 3	NA	333	
## 4	NA	333	
## 5	NA	333	
## 6	NA	333	
##	LEA3.2_lfmm2_mlog10P_salenv_noutliers	LEA3.2_lfmm2_num_causal_sig_temp	
## 1	0	7	
## 2	0	7	
## 3	0	7	
## 4	0	7	
## 5	0	7	
## 6	0	7	
##	LEA3.2_lfmm2_num_neut_sig_temp	LEA3.2_lfmm2_num_causal_sig_sal	

##	1		88		0		
##	2		88		0		
##	3		88		0		
##	4		88		0		
##	5		88		0		
##	6		88		0		
##	LEA3.2_lfmm2_num_neut_sig_sal LEA3.2_lfmm2_FPR_neutSNPs_temp						
##	1		0		0.006839201		
##	2		0		0.006839201		
##	3		0		0.006839201		
##	4		0		0.006839201		
##	5		0		0.006839201		
##	6		0		0.006839201		
##	LEA3.2_lfmm2_FPR_neutSNPs_sal RDA1_propvar RDA2_propvar RDA1_propvar_corr						
##	1		0	0.985	0.015	0.765	
##	2		0	0.985	0.015	0.765	
##	3		0	0.985	0.015	0.765	
##	4		0	0.985	0.015	0.765	
##	5		0	0.985	0.015	0.765	
##	6		0	0.985	0.015	0.765	
##	RDA2_propvar_corr RDA1_temp_cor RDA1_sal_cor RDA2_temp_cor RDA2_sal_cor						
##	1		0.235	0.9999982	0.001912722	-0.001912722	0.9999982
##	2		0.235	0.9999982	0.001912722	-0.001912722	0.9999982
##	3		0.235	0.9999982	0.001912722	-0.001912722	0.9999982
##	4		0.235	0.9999982	0.001912722	-0.001912722	0.9999982
##	5		0.235	0.9999982	0.001912722	-0.001912722	0.9999982
##	6		0.235	0.9999982	0.001912722	-0.001912722	0.9999982
##	RDA_Va_temp_prop RDA_Va_temp_prop_corr RDA_Va_sal_prop RDA_Va_sal_prop_corr						
##	1		0.1248244		0		0
##	2		0.1248244		0		0
##	3		0.1248244		0		0
##	4		0.1248244		0		0
##	5		0.1248244		0		0
##	6		0.1248244		0		0
##	RDA_TPR RDA_TPR_corr RDA_FDR_allSNPs RDA_FDR_allSNPs_corr						
##	1	0.006451613		0	0.9918699		1
##	2	0.006451613		0	0.9918699		1
##	3	0.006451613		0	0.9918699		1
##	4	0.006451613		0	0.9918699		1
##	5	0.006451613		0	0.9918699		1
##	6	0.006451613		0	0.9918699		1
##	num_RDA_sig_causal num_RDA_sig_neutral num_RDA_sig_causal_corr						
##	1		2		118		0
##	2		2		118		0
##	3		2		118		0
##	4		2		118		0
##	5		2		118		0
##	6		2		118		0
##	num_RDA_sig_neutral_corr RDA_FDR_neutSNPs RDA_FDR_neutSNPs_corr						
##	1		200		0.9833333		1
##	2		200		0.9833333		1
##	3		200		0.9833333		1
##	4		200		0.9833333		1
##	5		200		0.9833333		1


```

## 6          200          0.983333          1
## RDA_AUCPR_allSNPs RDA_AUCPR_neutSNPs RDA_AUCPR_neutSNPs_corr RDA_FPR_neutSNPs
## 1          0.008249728          0.01647883          0.01597697          0.009170747
## 2          0.008249728          0.01647883          0.01597697          0.009170747
## 3          0.008249728          0.01647883          0.01597697          0.009170747
## 4          0.008249728          0.01647883          0.01597697          0.009170747
## 5          0.008249728          0.01647883          0.01597697          0.009170747
## 6          0.008249728          0.01647883          0.01597697          0.009170747
## RDA_FPR_neutSNPs_corr RDA_RDAmutpred_cor_tempEffect
## 1          0.01554364          0.2566239
## 2          0.01554364          0.2566239
## 3          0.01554364          0.2566239
## 4          0.01554364          0.2566239
## 5          0.01554364          0.2566239
## 6          0.01554364          0.2566239
## RDA_RDAmutpred_cor_salEffect RDA_absRDAmutpred_cor_tempVa
## 1          NA          -0.04251831
## 2          NA          -0.04251831
## 3          NA          -0.04251831
## 4          NA          -0.04251831
## 5          NA          -0.04251831
## 6          NA          -0.04251831
## RDA_absRDAmutpred_cor_salVa RDA_RDAmutpred_cor_tempEffect_structcorr
## 1          NA          0.1711607
## 2          NA          0.1711607
## 3          NA          0.1711607
## 4          NA          0.1711607
## 5          NA          0.1711607
## 6          NA          0.1711607
## RDA_RDAmutpred_cor_salEffect_structcorr
## 1          NA
## 2          NA
## 3          NA
## 4          NA
## 5          NA
## 6          NA
## RDA_absRDAmutpred_cor_tempVa_structcorr
## 1          0.002950593
## 2          0.002950593
## 3          0.002950593
## 4          0.002950593
## 5          0.002950593
## 6          0.002950593
## RDA_absRDAmutpred_cor_salVa_structcorr RDA_cor_RDA20000temppredict_tempPhen
## 1          NA          0.8530879
## 2          NA          0.8530879
## 3          NA          0.8530879
## 4          NA          0.8530879
## 5          NA          0.8530879
## 6          NA          0.8530879
## RDA_cor_RDA20000salpredict_salPhen
## 1          NA
## 2          NA
## 3          NA

```

```

## 4 NA
## 5 NA
## 6 NA
## RDA_cor_RDA20000temppredict_tempPhen_structcorr
## 1 -0.03541745
## 2 -0.03541745
## 3 -0.03541745
## 4 -0.03541745
## 5 -0.03541745
## 6 -0.03541745
## RDA_cor_RDA20000salpredict_salPhen_structcorr cor_PC1_temp cor_PC1_sal
## 1 NA -0.9938219 -0.002423473
## 2 NA -0.9938219 -0.002423473
## 3 NA -0.9938219 -0.002423473
## 4 NA -0.9938219 -0.002423473
## 5 NA -0.9938219 -0.002423473
## 6 NA -0.9938219 -0.002423473
## cor_PC2_temp cor_PC2_sal cor_LFMMU1_temp cor_LFMMU1_sal cor_LFMMU2_temp
## 1 -0.02040717 -0.00168847 0.0702796 -0.001851458 -0.2374149
## 2 -0.02040717 -0.00168847 0.0702796 -0.001851458 -0.2374149
## 3 -0.02040717 -0.00168847 0.0702796 -0.001851458 -0.2374149
## 4 -0.02040717 -0.00168847 0.0702796 -0.001851458 -0.2374149
## 5 -0.02040717 -0.00168847 0.0702796 -0.001851458 -0.2374149
## 6 -0.02040717 -0.00168847 0.0702796 -0.001851458 -0.2374149
## cor_LFMMU2_sal cor_PC1_LFMMU1_temp cor_PC1_LFMMU1_sal cor_PC2_LFMMU1_temp
## 1 -0.002823011 -0.09231664 0.9995526 0.9926958
## 2 -0.002823011 -0.09231664 0.9995526 0.9926958
## 3 -0.002823011 -0.09231664 0.9995526 0.9926958
## 4 -0.002823011 -0.09231664 0.9995526 0.9926958
## 5 -0.002823011 -0.09231664 0.9995526 0.9926958
## 6 -0.002823011 -0.09231664 0.9995526 0.9926958
## cor_PC2_LFMMU1_sal gwas_TPR_sal gwas_TPR_temp gwas_FDR_sal_neutbase
## 1 0.001339894 NA 0.2290323 NA
## 2 0.001339894 NA 0.2290323 NA
## 3 0.001339894 NA 0.2290323 NA
## 4 0.001339894 NA 0.2290323 NA
## 5 0.001339894 NA 0.2290323 NA
## 6 0.001339894 NA 0.2290323 NA
## gwas_FDR_temp_neutbase clinalparadigm_sal_proptop5GWASclines
## 1 0.9667914 NA
## 2 0.9667914 NA
## 3 0.9667914 NA
## 4 0.9667914 NA
## 5 0.9667914 NA
## 6 0.9667914 NA
## clinalparadigm_temp_proptop5GWASclines clinalparadigm_sal_propsigGWASclines
## 1 0.6554106 NA
## 2 0.6554106 NA
## 3 0.6554106 NA
## 4 0.6554106 NA
## 5 0.6554106 NA
## 6 0.6554106 NA
## clinalparadigm_temp_propsigGWASclines N_traits2 change_temp_mut
## 1 0.6050302 1 Trait -0.08546318

```

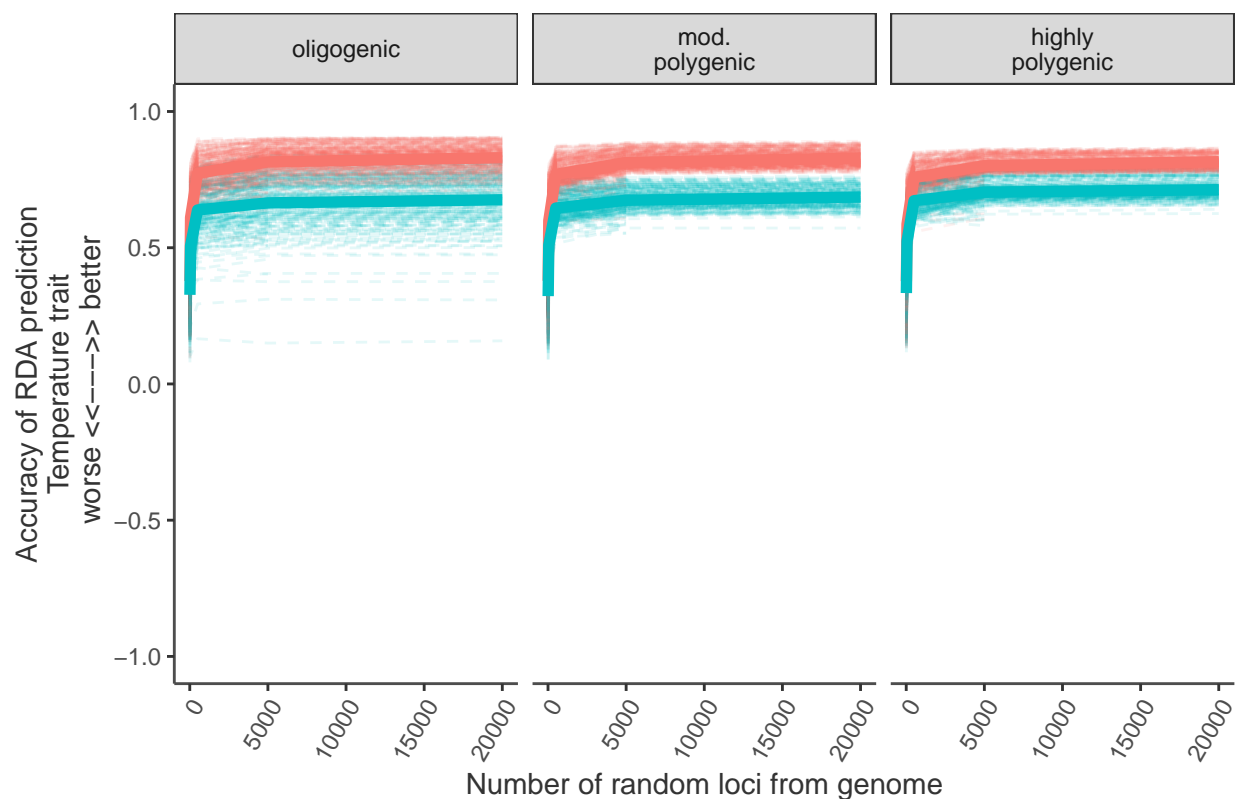
```
## 2          0.6050302  1 Trait    -0.08546318
## 3          0.6050302  1 Trait    -0.08546318
## 4          0.6050302  1 Trait    -0.08546318
## 5          0.6050302  1 Trait    -0.08546318
## 6          0.6050302  1 Trait    -0.08546318
## change_sal_mut change_temp change_sal
## 1          NA    -0.8885054         NA
## 2          NA    -0.8885054         NA
## 3          NA    -0.8885054         NA
## 4          NA    -0.8885054         NA
## 5          NA    -0.8885054         NA
## 6          NA    -0.8885054         NA
```

```
rdapred_df$SIGMA_K_2 <- as.factor(as.character(rdapred_df$SIGMA_K_2))

rdapred_df1 <- filter(rdapred_df, nloci %in% c(10,50,500,5000,20000))

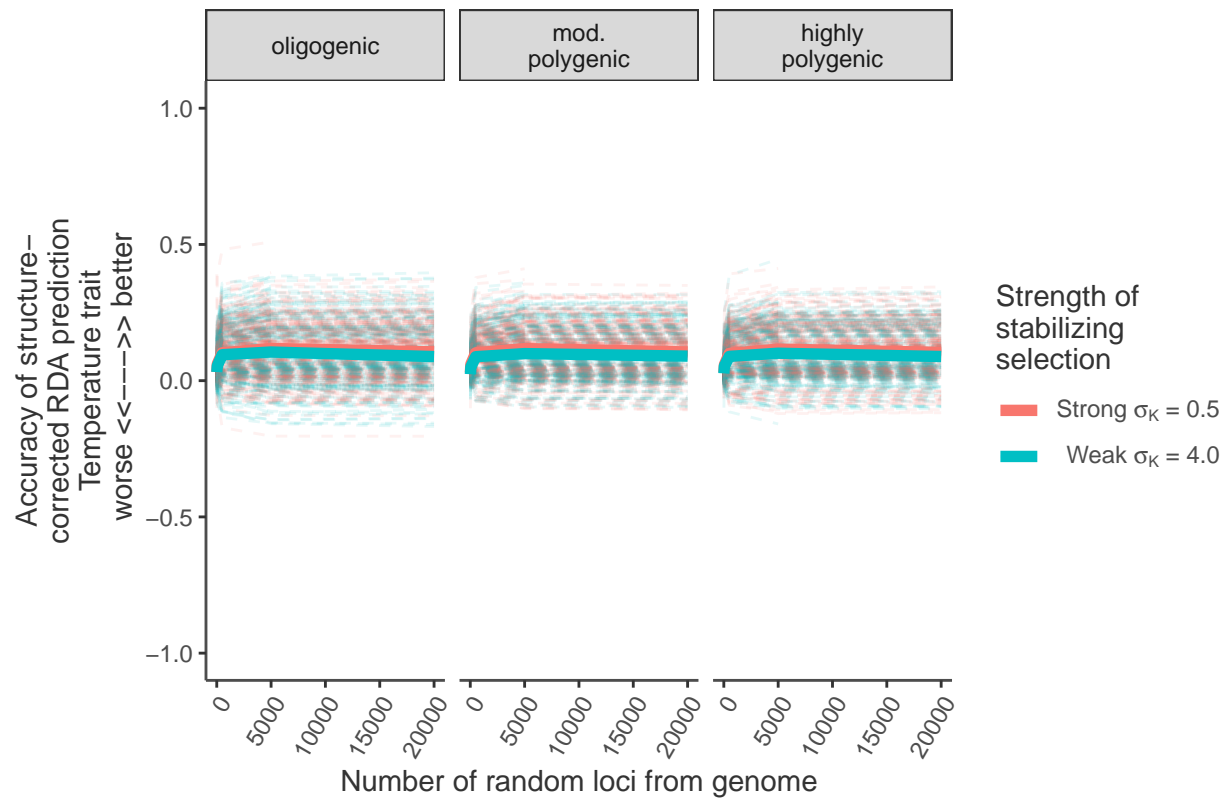
r1<- ggplot(rdapred_df1 ) +
  geom_line( aes(x=nloci, y=Random_cor_RDAtemppredict_tempphen, group=seed, color=SIGMA_K_2), alpha=0.1)
r1
```

A) Temperature trait



```
r2 <- ggplot(rdapred_df1) +
  geom_line(aes(x=nloci, y=Random_cor_RDAtemppredict_tempphen_structcorr, group=seed, color=SIGMA_K_2),
  expression(paste("Weak ", sigma[K], " = 4.0"))))
r2
```

B) Temperature trait with structure correction

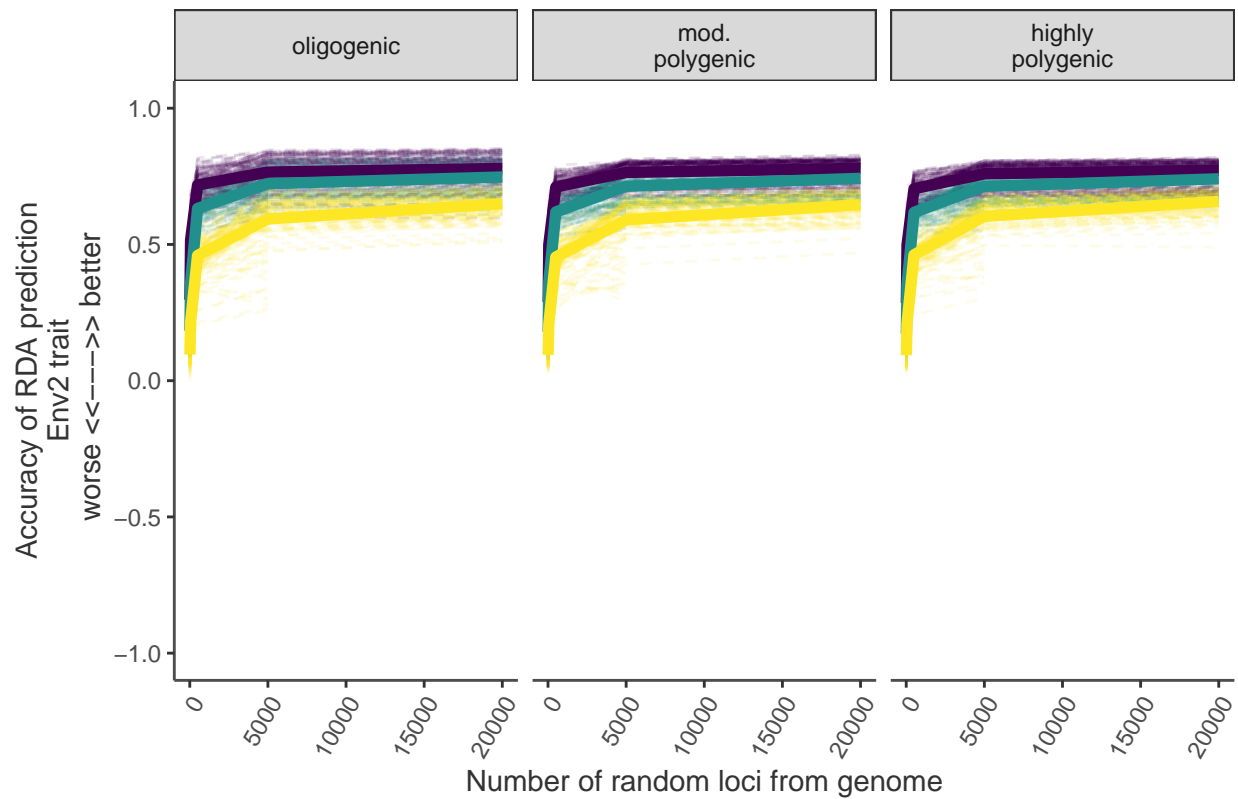


```
r3 <- ggplot(rdapred_df1) +  
  geom_line(aes(x=nloci, y=Random_cor_RDAsalpredict_salphen, group=seed, color=as.factor(demog_level)),  
  r3
```

```
## Warning: Removed 2160 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 2160 row(s) containing missing values (geom_path).
```

C) Env2 trait

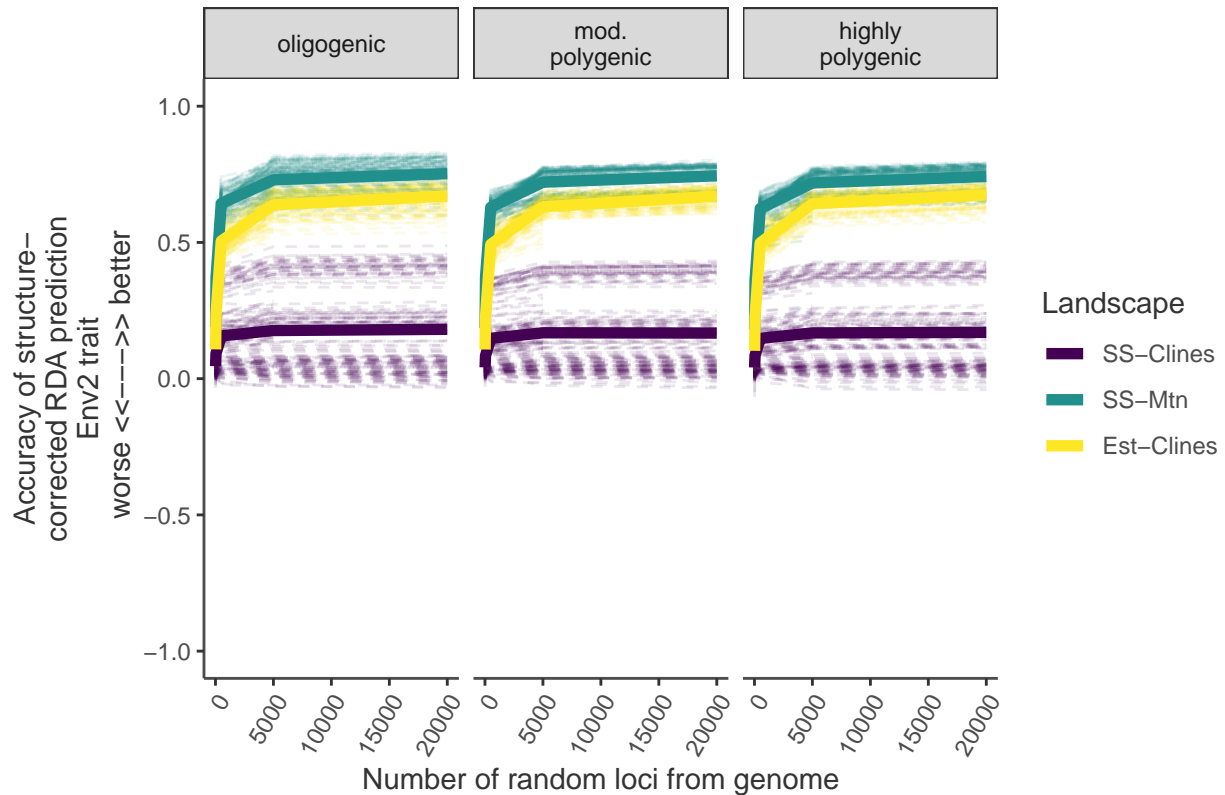


```
r4 <- ggplot(rdapred_df1) +  
  geom_line(aes(x=nloci, y=Random_cor_RDAsalpredict_salphen_structcorr, group=seed, color=as.factor(demo  
r4
```

```
## Warning: Removed 2160 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 2160 row(s) containing missing values (geom_path).
```

D) Env2 trait with structure correction



```
pdf(paste0(outputs,"RDAPredictionFunctionOfnLoci.pdf"), width=12, height=8)
grid.arrange(r1,r2, r3, r4, nrow=2, layout_matrix=matrix(c(1,1,1,1,2,2,2,2,2
,3,3,3,3,4,4,4,4,4),
nrow=2, byrow=TRUE)
)
```

```
## Warning: Removed 2160 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 2160 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 2160 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 2160 row(s) containing missing values (geom_path).
```

```
#missing values from simulations with low diversity that were filtered out
dev.off()
```

```
## pdf
## 2
```

```
# removed rows expected based on single-trait simulations
```

Accuracy of RDA trait prediction as a function of the number of QTN loci in the simulation and strength of selection on the trait. The strength of selection on the trait also determines the strength of selection on the

QTN loci in the architecture, how strongly they respond to selection, and the amount of LD around them when they sweep to high frequency in a deme or set of demes.

```
head(rdapred_df1[,40:50])
```

```
##      Bonf_alpha numCausalLowMAFsample all_corr_phen_temp subsamp_corr_phen_temp
## 1 1.918428e-06          39          0.9545790          0.8893387
## 2 1.918428e-06          39          0.9545790          0.8893387
## 3 1.918428e-06          39          0.9545790          0.8893387
## 4 1.918428e-06          39          0.9545790          0.8893387
## 5 1.918428e-06          39          0.9545790          0.8893387
## 6 1.730523e-06         104          0.9545764          0.9006961
##      all_corr_phen_sal subsamp_corr_phen_sal num_causal_prefilter
## 1              NA              NA              2628
## 2              NA              NA              2628
## 3              NA              NA              2628
## 4              NA              NA              2628
## 5              NA              NA              2628
## 6              NA              NA              3144
##      num_causal_postfilter num_non_causal num_neut_prefilter num_neut_postfilter
## 1              310          25753          26587          26587
## 2              310          25753          26587          26587
## 3              310          25753          26587          26587
## 4              310          25753          26587          26587
## 5              310          25753          26587          26587
## 6              382          28511          30284          30284
```

```
final.df$SIGMA_K_2 <- as.factor(final.df$SIGMA_K_2)
levels(final.df$demog_level_sub)
```

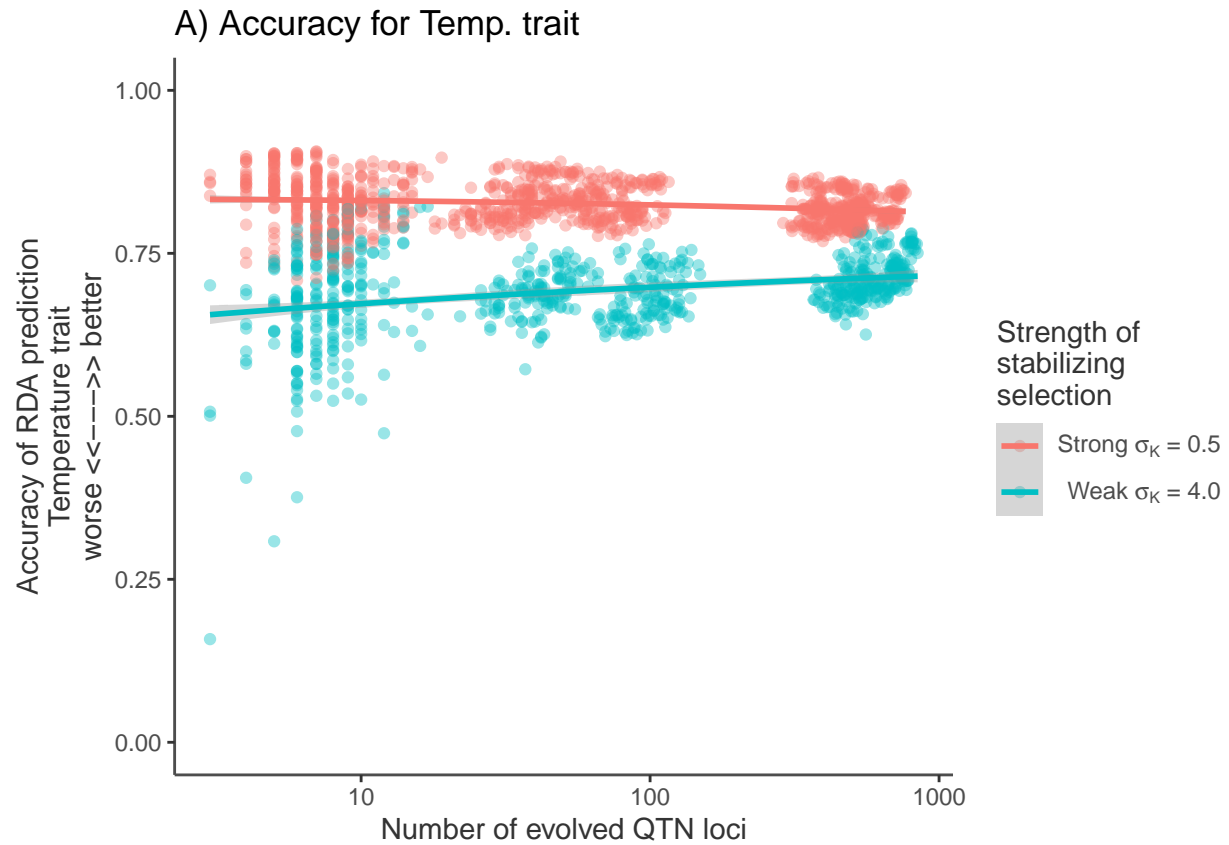
```
## [1] "N equal\nm constant"          "N equal\nm breaks"
## [3] "N latitude cline\nm constant"  "N central cline\nm constant"
## [5] "N variable\nm variable"
```

```
# Remove the demography that had the worse performance in Env2
# so as not to bias the loess smoother
```

```
final.df1 <- final.df %>% filter(demog_level_sub != "N variable\nm variable")
```

```
rr1 <- ggplot(final.df1) + geom_point(aes(x=num_causal_postfilter, y=RDA_cor_RDA20000temppredict_tempPhen),
  geom_smooth(aes(x=num_causal_postfilter, y=RDA_cor_RDA20000temppredict_tempPhen, color=SIGMA_K_2), method="loess",
  expression(paste("Weak ", sigma[K], " = 4.0"))))
rr1
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



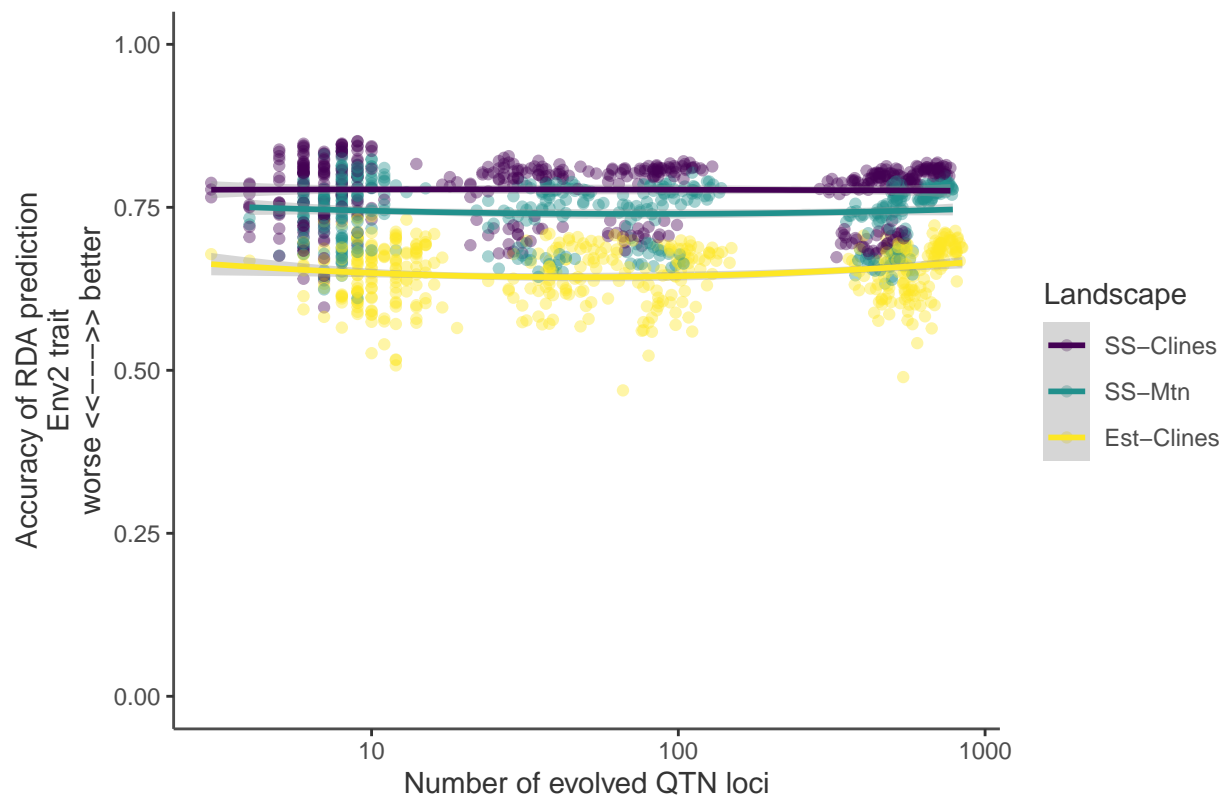
```
rr2 <- ggplot(final.df1) + geom_point(aes(x=num_causal_postfilter, y=RDA_cor_RDA20000salpredict_salPhen)) +
  geom_smooth(aes(x=num_causal_postfilter, y=RDA_cor_RDA20000salpredict_salPhen, color=demog_level), method="lm")
rr2
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 360 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 360 rows containing missing values (geom_point).
```


B) Accuracy for Env2 trait (always strong selection)



```
pdf(paste0(outputs,"RDAtraitpred_vs_nQTN.pdf"), width=10, height=5)
grid.arrange(rr1, rr2, nrow=1)
```

```
## 'geom_smooth()' using formula 'y ~ x'
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 360 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 360 rows containing missing values (geom_point).
```

```
dev.off()
```

```
## pdf
## 2
```