Supplementary Material

Samples used in the Simulation

Inidividual	POPid	Country
HAP6977126	Agta	Philipines
HAP6977127	Agta	Philipines
HAP6977145	Agta	Philipines
HAP6977146	Agta	Philipines
HAP6977147	Agta	Philipines
HAP6977148	Agta	Philipines
HAP6977149	Agta	Philipines
HAP6977150	Agta	Philipines
DenisovaPinky	Altai	Denisova
AltaiNea	Altai	Neanderthal
HG00096	CEU	United Kingdom
ERR1025614	CEU	Bulgaria
NA12891	CEU	European
NA12892	CEU	European
HG00419	CHB	China
NA18525	CHB	Chinese
ERR1019060	CHB	China
ERR1347731	CHB	China
HAP6977162	Kosipe	PNG
HAP6977163	Kosipe	PNG
HAP6977164	Kosipe	PNG
HAP6977165	Kosipe	PNG
HAP6977166	Kosipe	PNG
HAP6977167	Kosipe	PNG
HAP6977168	Kosipe	PNG
HAP6977169	Kosipe	PNG
HAP6977170	Kosipe	PNG
HAP6977171	Kosipe	PNG
HAP6792314	Temiar	Malaysia
HAP6792315	Temiar	Malaysia
HAP6792316	Temiar	Malaysia
HAP6792317	Temiar	Malaysia
HAP6792318	Temiar	Malaysia
HAP6792319	Temiar	Malaysia
ERR1419171	Yoruba	Nigeria
ERR1419179	Yoruba	Nigeria
NA19238	Yoruba	Nigeria
NA19239	Yoruba	Nigeria

S.Table 1: Samples used in the ABC-DL experiment. Only 1 sample per population is used at a time. We used combinations of different samples for each population to capture more of the diversity of each population in the analysis

Prior Distribution of Parameters for the Demographic Model

Parameter	Min Value	Max Value
missclasification	0	0,0005
migrationEU_to_EA	0	1,00E-04
migrationEU_to_AFR	0	1,00E-04
migrationAFR_to_EU	0	1,00E-04
migrationEA_to_EU	0	1,00E-04
NeAFR	1000	800000
NeEU	1000	20000
NeEA	1000	20000
NeMAL	1000	20000
NePHIL	1000	20000
NePNG	1000	20000
NeN	1000	40000
NeD	1000	40000
NeEMH	1000	20000
NeEEA	1000	20000
NeXa	1000	40000
NeD2	1000	40000
NeD3	1000	40000
NeN2	1000	40000
DEMOGRAPHIC EVENTS IN NO EOOA INTROGRESSION MODELS		
tPNG_PHIL	1034,482759	2068,965517
NePNG_PHIL	500	20000
tMAL_PNG_PHIL	ScalePNG_PHIL	1827,586207
NeMAL_PNG_PHIL	500	20000
tEA_MAL_PNG_PHIL	ScaleEA_MAL_AND	2068,965517
NeEA_MAL_PNG_PHIL	1000	20000
tEU_EA_MAL_PNG_PHIL	ScaleEA_MAL_PNG_PHIL	2586,206897
NeEU_EA_MAL_PNG_PHIL	500	5000
tAFR_EU_EA_MAL_PNG_PHIL	ScaleEU_EA_MAL_PNG_PHIL	3448,275862
NeAFR_EU_EA_MAL_PNG_PHIL	1000	40000
tXa_AFR_EU_EA_MAL_PNG_PHIL	ScaleAFR_EU_EA_MAL_PNG_PHIL	15517,24138
NeXa_AFR_EU_EA_MAL_PNG_PHIL	1000	40000
tD_D2	1413,793103	9758,62069
NeD_D2	1000	20000
tD_D2_D3	ScaleD_D2	13103,44828
NeD_D2_D3	1000	20000
tN_N2	1724,137931	8620,689655
NeN_N2	1000	20000
tN_N2_D_D2_D3	ScaleD_D2_D3	15517,24138
NeN_N2_D_D2_D3	1000	80000

tANCESTRAL	ScaleXa_AFR_EU_EA_MAL_PNG_PHIL	22413,7931
NeANCESTRAL	1000	40000
DEMOGRAPHIC EVENTS IN EOOA INTROGRESSION MODELS		
tEMH_AFR_EU_EA_MAL_PNG_PHIL	ScaleAFR_EU_EA_MAL_PNG_PHIL	5172,413793
NeEMH_AFR_EU_EA_MAL_PNG_PHIL	1000	40000
tXa_EMH_AFR_EU_EA_MAL_PNG_PHIL	ScaleEMH_AFR_EU_EA_MAL_PNG_PHIL	15517,24138
NeXa_EMH_AFR_EU_EA_MAL_PNG_PHIL	1000	40000
DEMOGRAPHIC EVENTS MODEL E		
tEMH_EEA	4000	5000
NeEEA_EMH	1000	1000
INTROGRESSION EVENTS IN ALL MODELS		
tIntrogressionN_Eurasia	ScaleEU_EA_MAL_PNG_PHIL	ScaleAFR_EU_EA_MAL_PNG_PHIL
introgressionN_Eurasia	0,001	0,05
tIntrogressionD3_Asia	ScaleEA_MAL_PNG_PHIL	ScaleEU_EA_MAL_PNG_PHIL
introgressionD3_Asia	0,001	0,1
tIntrogressionD2_PNG	1379,310345	ScaleEA_MAL_PNG_PHIL
introgressionD2_PNG	0,001	0,1
tIntrogressionXa_AFR	517,2413793	ScaleAFR_EU_EA_MAL_PNG_PHIL
introgressionXa_AFR	0,001	0,1
INTROGRESSION EVENTS MODEL B		
tIntrogressionEMH_N	3448,275862	ScaleEMH_AFR_EU_EA_MAL_PNG_PHIL
introgressionEMH_N	0,001	0,1
tIntrogressionEMH_Asia	ScaleEA_MAL_PNG_PHIL	ScaleEU_EA_MAL_PNG_PHIL
introgressionEMH_Asia	0,001	0,1
INTROGRESSION EVENTS MODEL C		
tIntrogressionEMH_N	3448,275862	ScaleEMH_AFR_EU_EA_MAL_PNG_PHIL
introgressionEMH_N	0,001	0,1
tIntrogressionEMH_SA	ScaleMAL_PNG_PHIL	ScaleEA_MAL_PNG_PHIL
introgressionEMH_SA	0,001	0,1
tIntrogressionEMH_Asia	ScaleEA_MAL_PNG_PHIL	ScaleEU_EA_MAL_PNG_PHIL
introgressionEMH_Asia	0,001	0,1
INTROGRESSION EVENTS MODEL D		
tIntrogressionD3_EMH	3200	4000
introgressionD3_EMH	0,001	0,1
tIntrogressionEMH_N	4000	ScaleEMH_AFR_EU_EA_MAL_PNG_PHIL
introgressionEMH_N	0,001	0,1

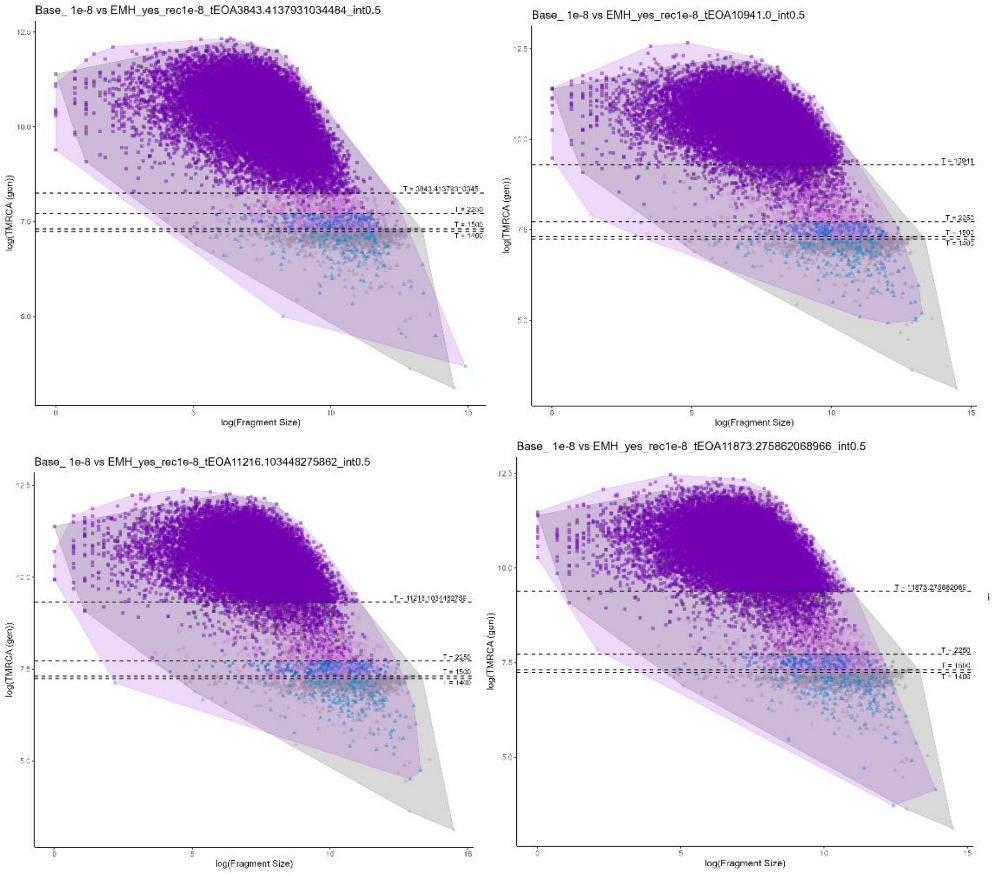
tIntrogressionEMH_Asia	ScaleEA_MAL_PNG_PHIL	ScaleEU_EA_MAL_PNG_PHIL
introgressionEMH_Asia	0,001	0,1
INTROGRESSION EVENTS MODEL E		
tIntrogressionEMH_N	4000	ScaleEMH_AFR_EU_EA_MAL_PNG_PHIL
introgressionEMH_N	0,001	0,1
tIntrogressionEEA_BEA	ScaleEU_EA_MAL_PNG_PHIL	ScaleAFR_EU_EA_MAL_PNG_PHIL
introgressionEEA_BEA	0,001	0,1

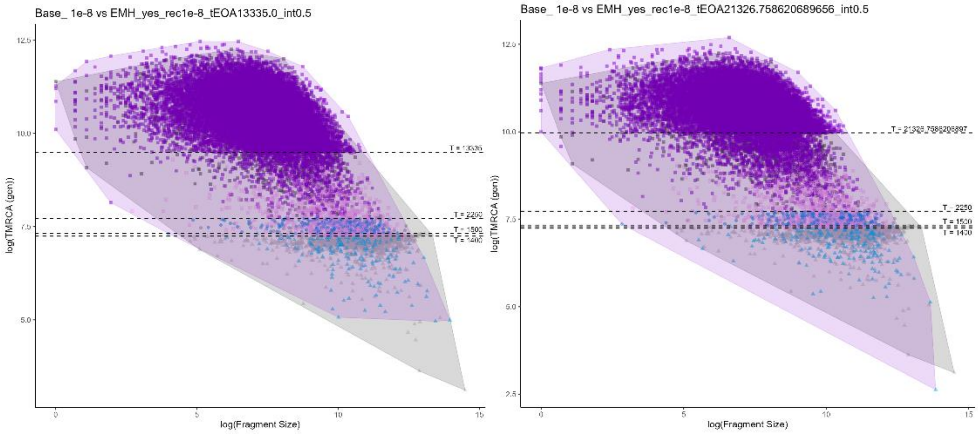
S.Table 2: Prior distribution of the parameters for the ABC-DL experiment. Time in generations where 1 gen = 29 years

Distribution of genomic fragments under different introgression scenarios

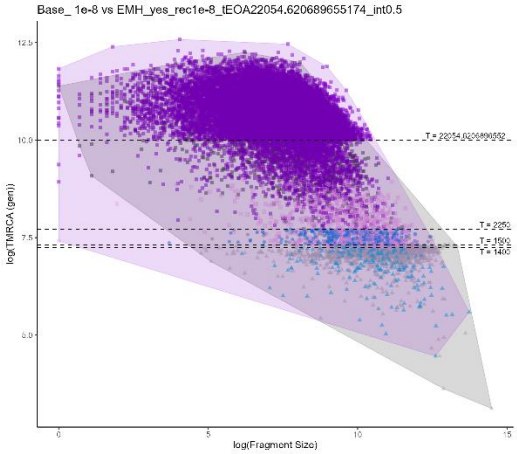
Supplementary Figures 1: Distribution of fragments under different recombination rates (1e-8 – A -, 2.35e-9 -B- & 5e-8 -C-) with the same introgression rate of 0.5 and a distribution of divergence time between source and sink populations of 3000 to 70000 generations

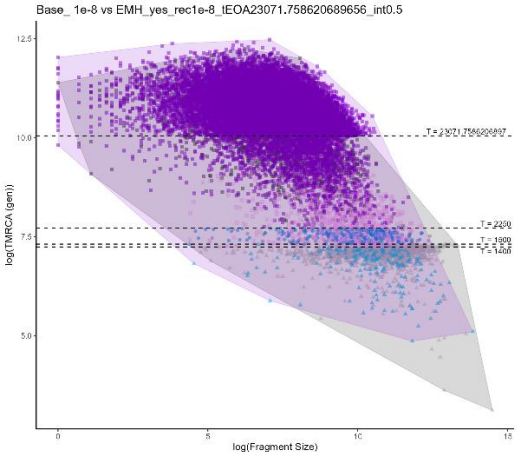
A_ Introgression rate of 0.5, recombination rate = 1e-8

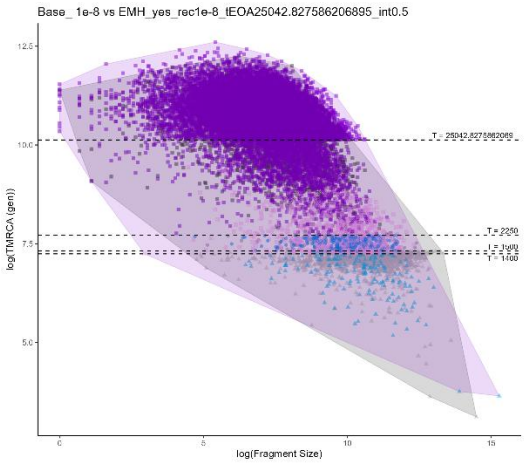


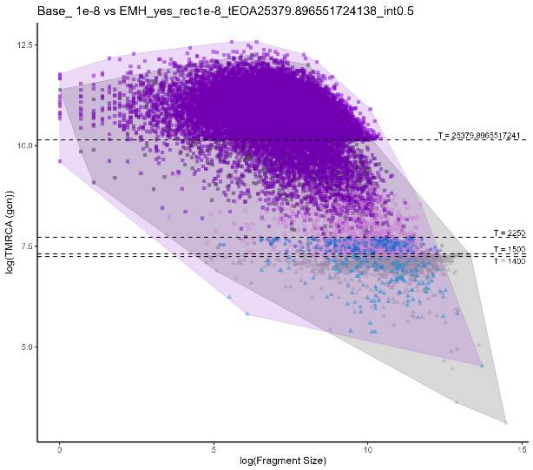

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA13335.0_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2252
T = 1500
T = 1400

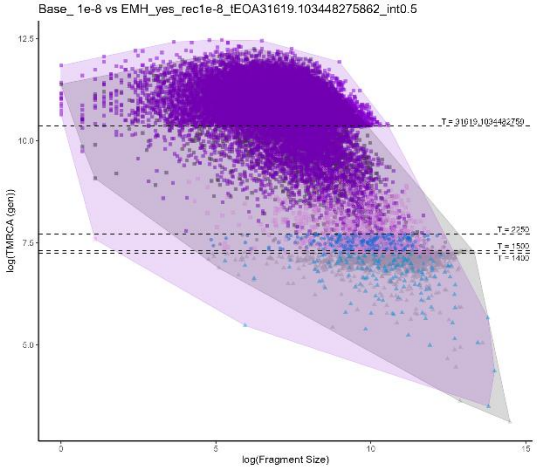
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA21326.758620689656_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

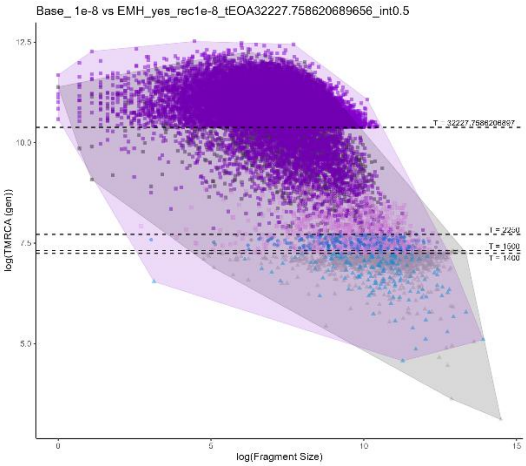

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA22054.620689655174_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2252
T = 1500
T = 1400

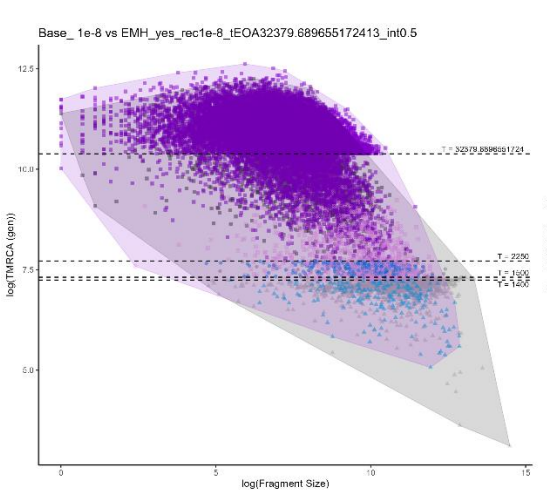

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA23071.758620689656_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

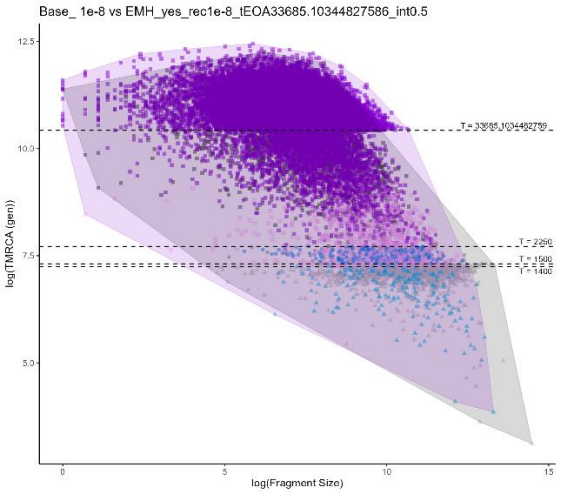

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA25042.827586206895_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1400

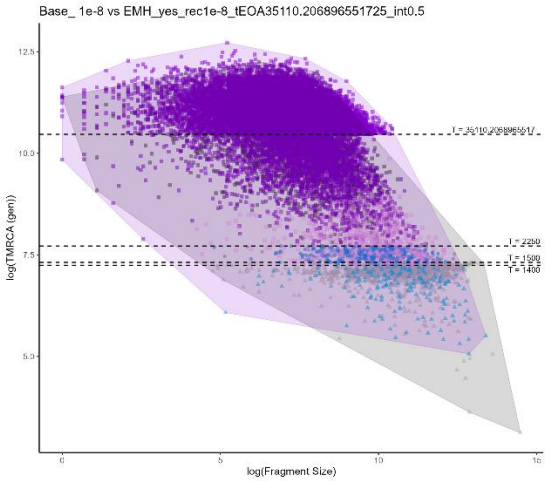

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA25379.896551724138_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2252
T = 1500
T = 1400

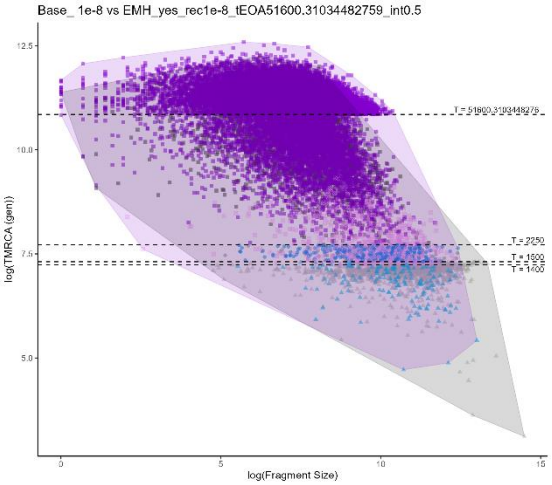

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA31619.103448275862_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

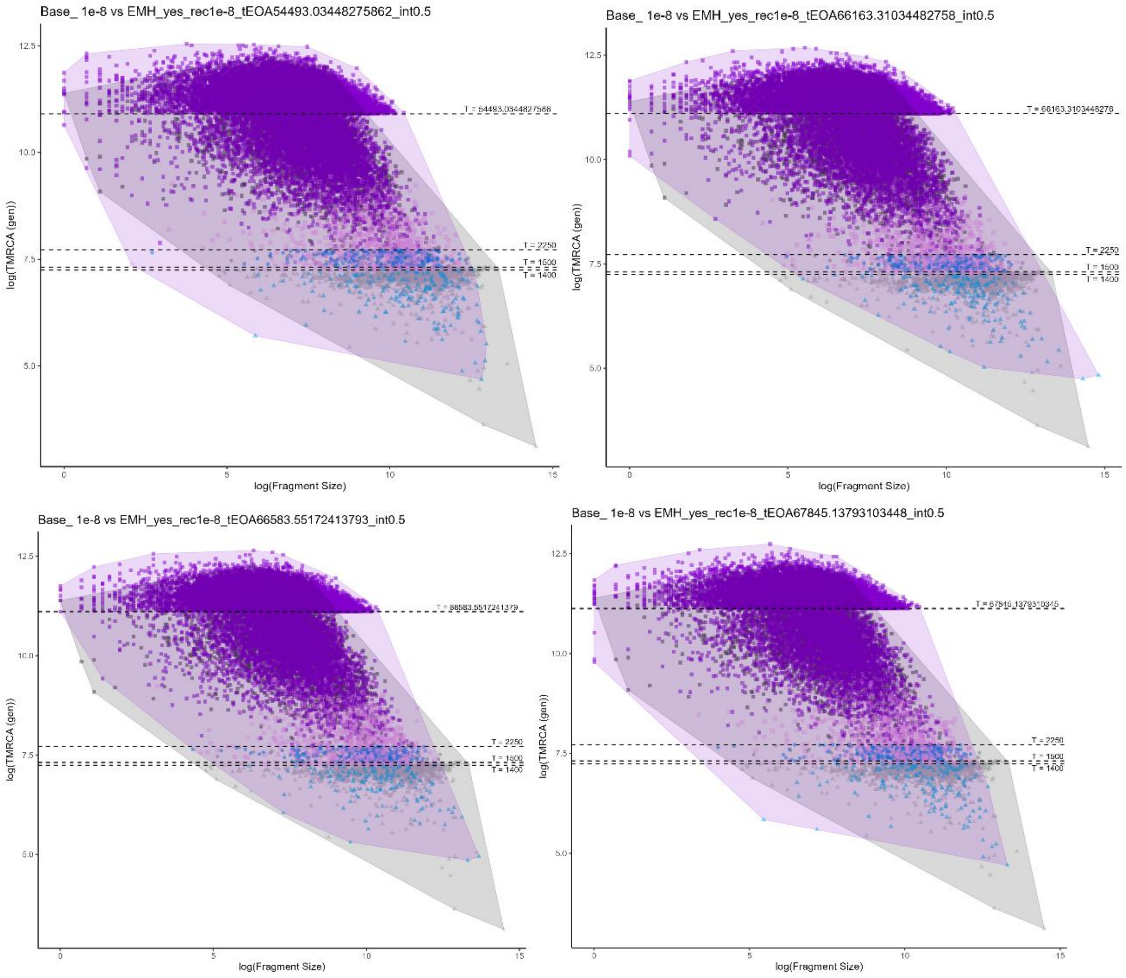

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA32227.758620689656_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400


Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA32379.689655172413_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

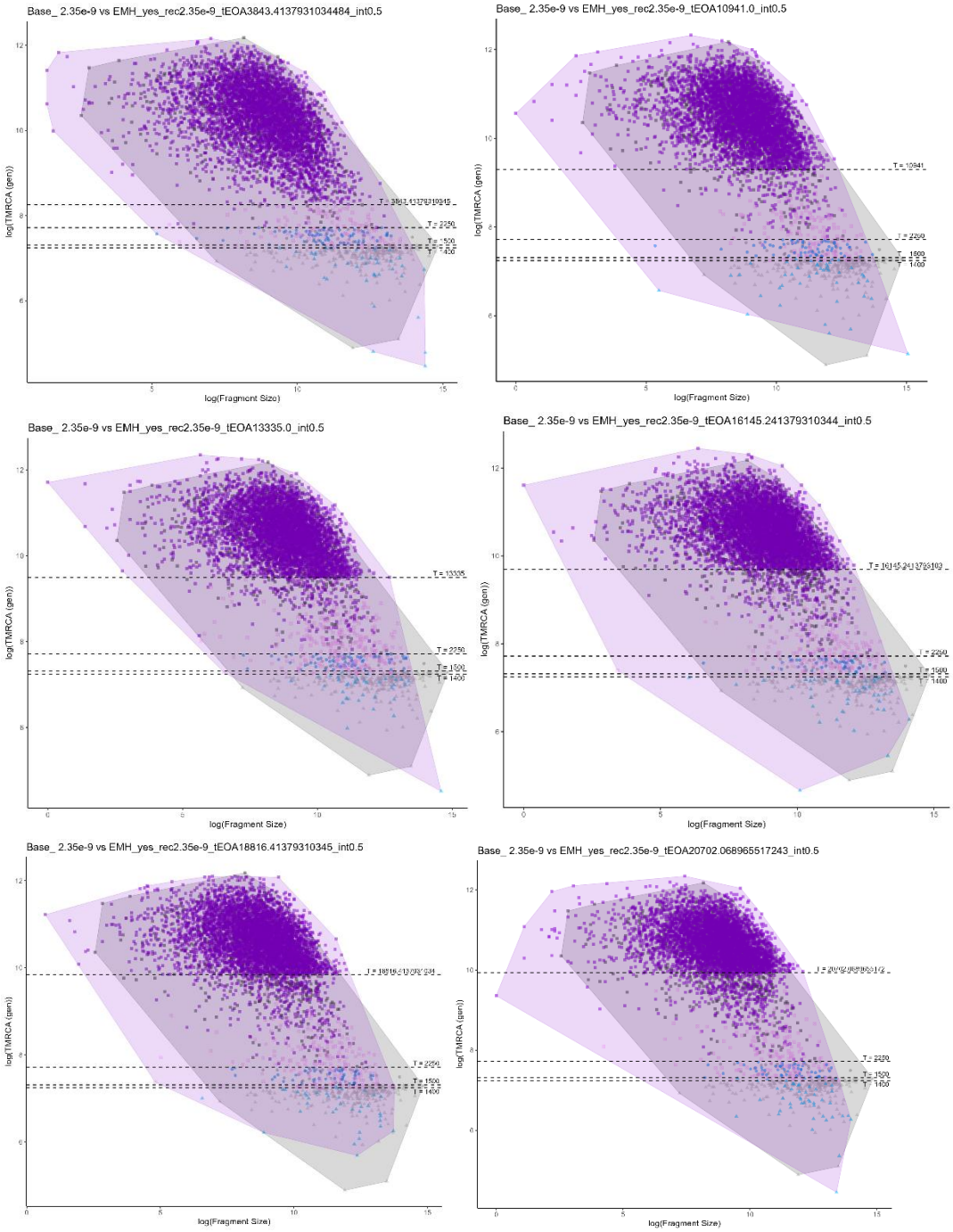

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA33685.10344827586_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

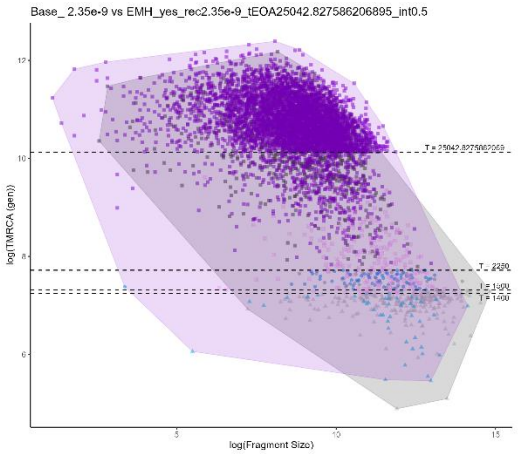

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA35110.206896551725_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

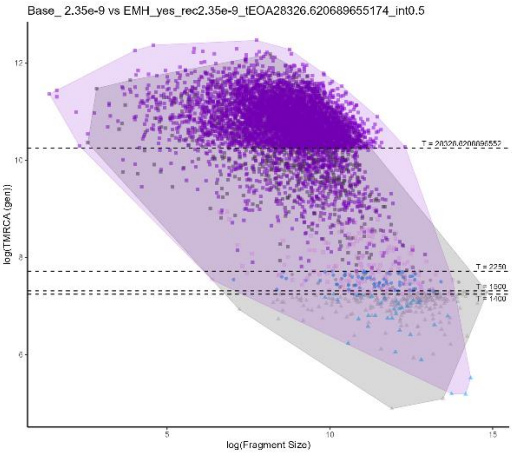

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA51600.31034482759_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

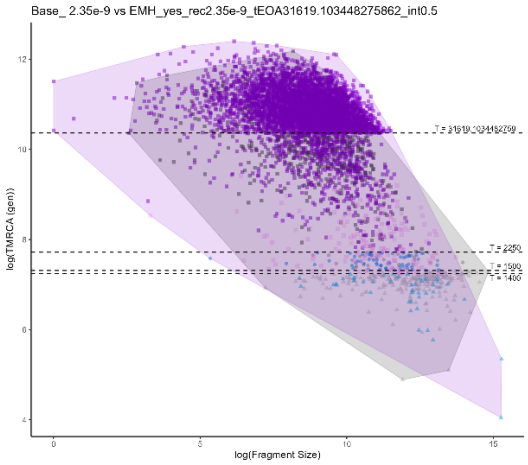

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA54493.03448275862_int0.5
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA66163.31034482758_int0.5
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA66583.55172413793_int0.5
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13793103448_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

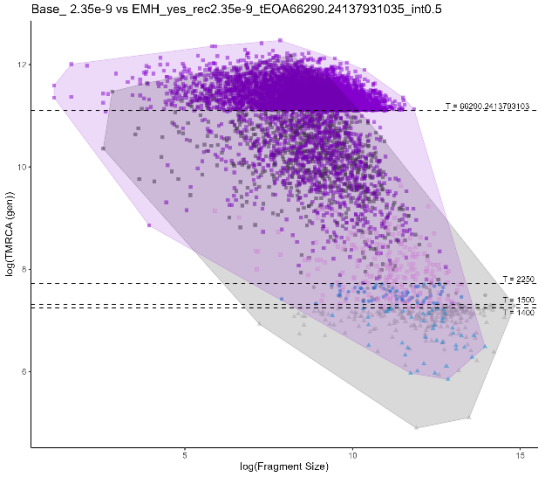
B_Introgression rate of 0.5, recombination rate = 2.35e-9



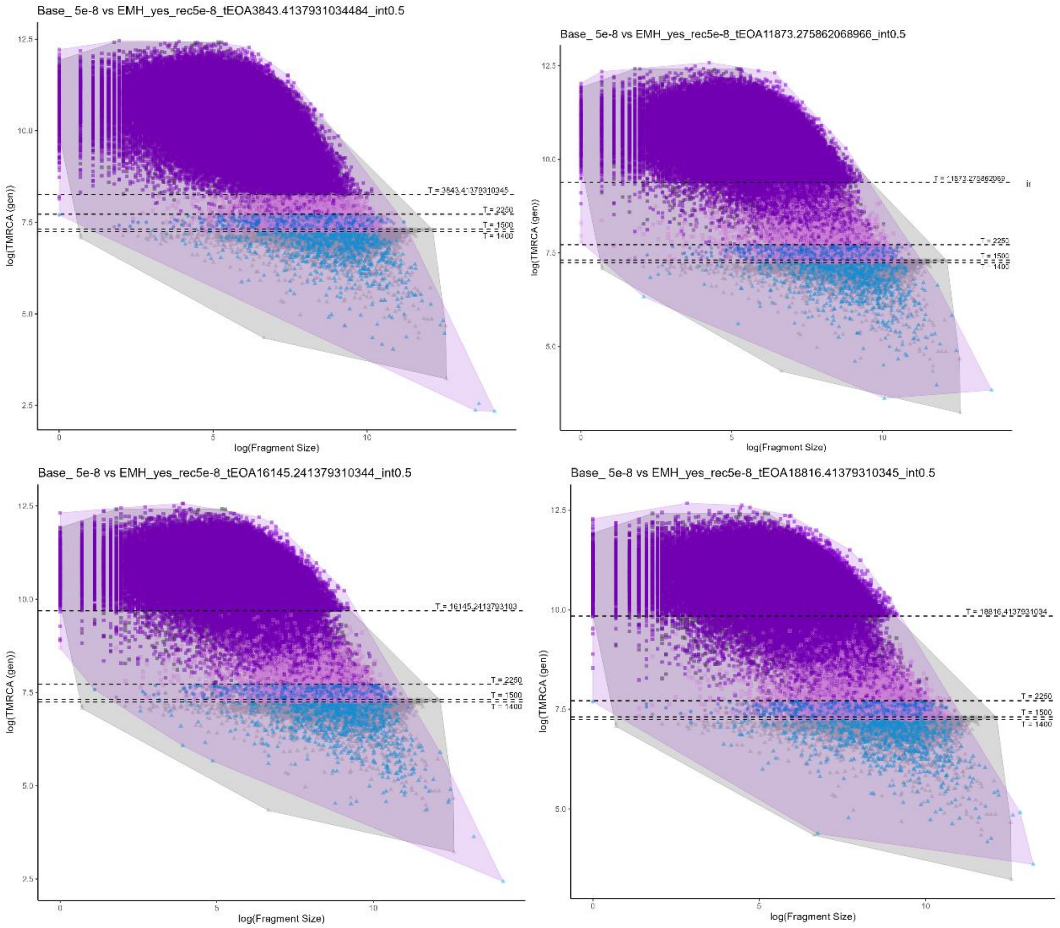

Base_ 2.35e-9 vs EMH_yes_rec2.35e-9_tEOA25042.827586206895_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1600
T = 1400

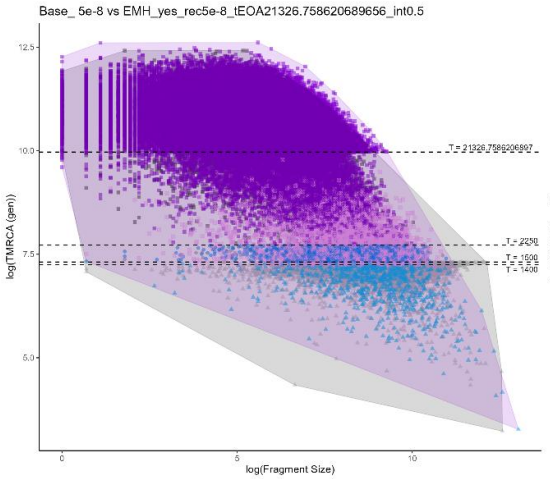

Base_ 2.35e-9 vs EMH_yes_rec2.35e-9_tEOA28326.620689655174_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1600
T = 1400

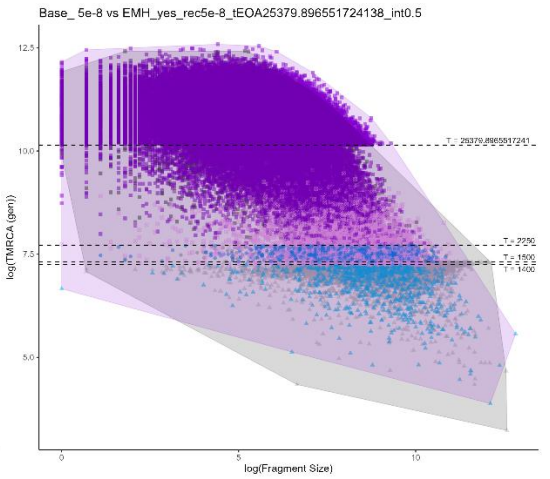

Base_ 2.35e-9 vs EMH_yes_rec2.35e-9_tEOA31619.103448275862_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1600
T = 1400

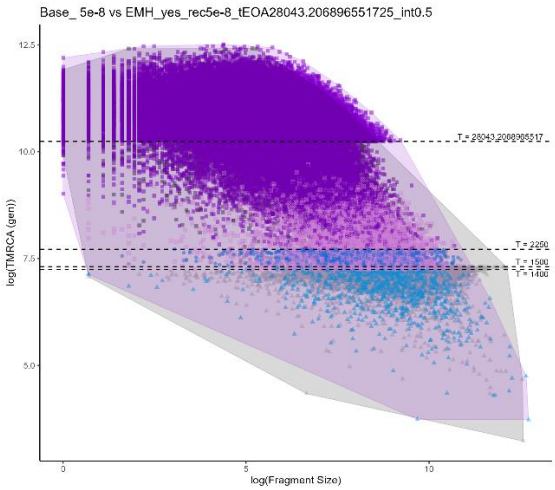

Base_ 2.35e-9 vs EMH_yes_rec2.35e-9_tEOA66290.24137931035_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1600
T = 1400

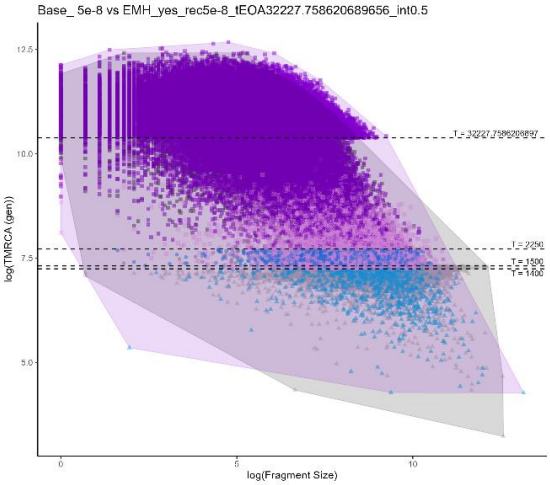
C_Introgression rate of 0.5, recombination rate 5 e-8

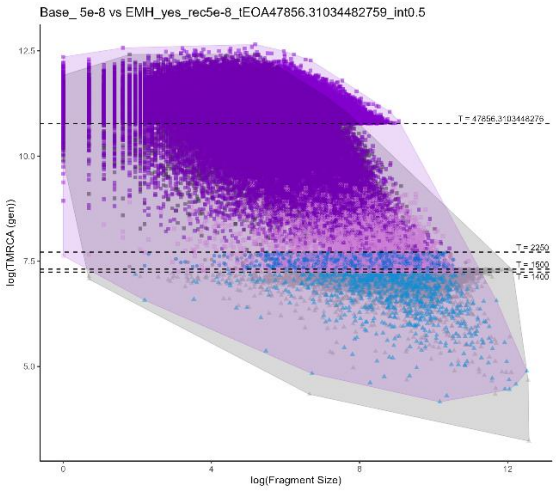


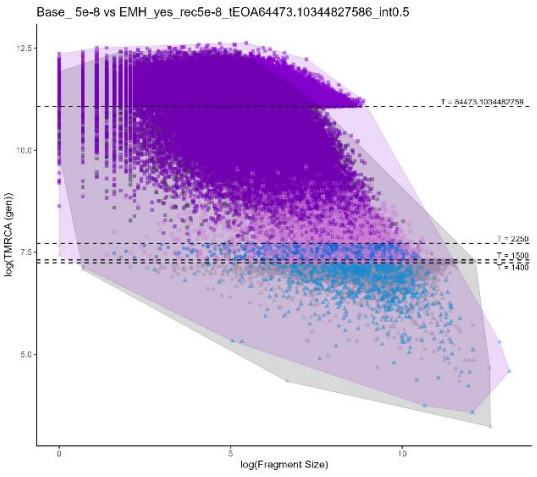

Base_ 5e-8 vs EMH_yes_rec5e-8_tEOA21326.758620689656_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400


Base_ 5e-8 vs EMH_yes_rec5e-8_tEOA25379.896551724138_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400


Base_ 5e-8 vs EMH_yes_rec5e-8_tEOA28043.206896551725_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

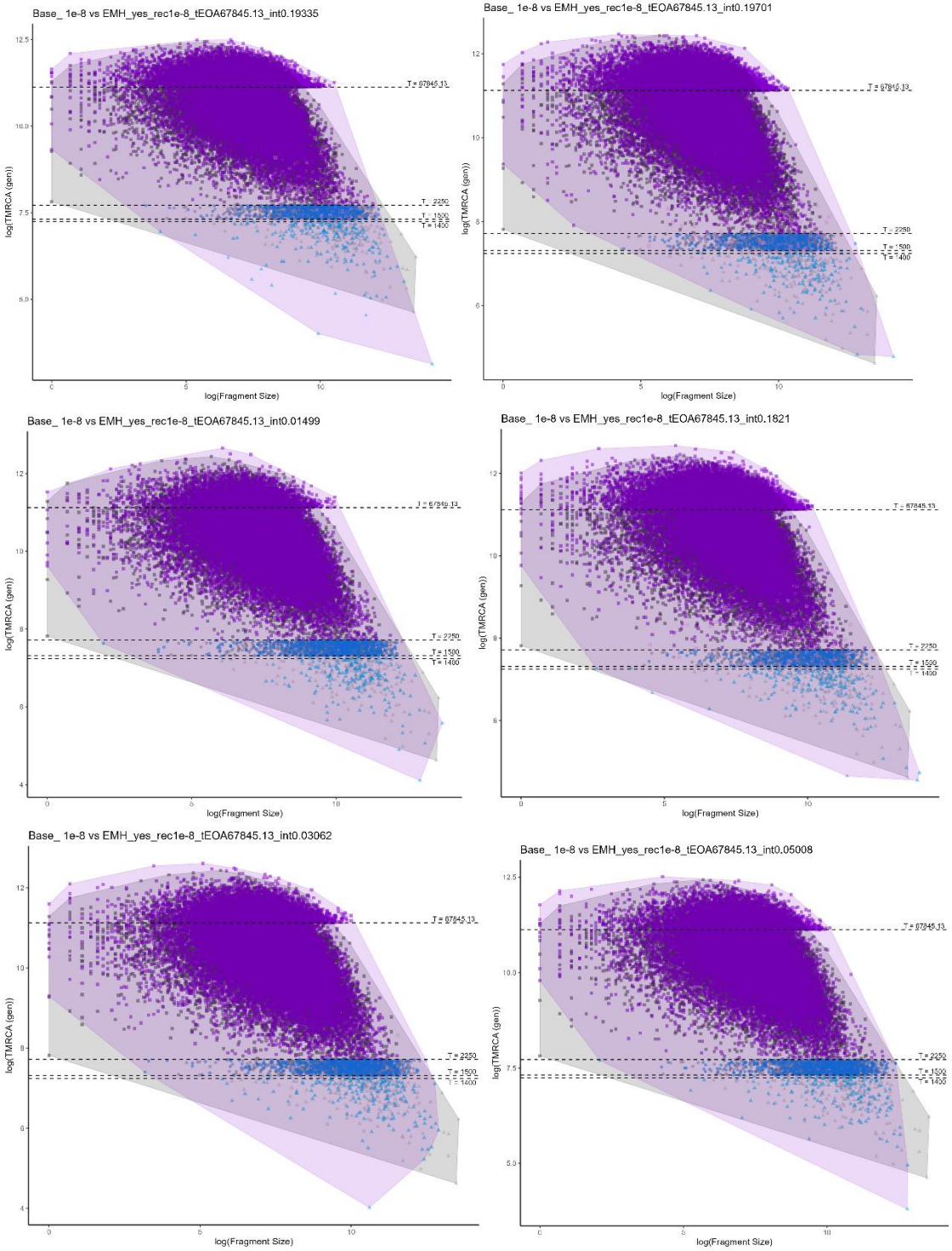

Base_ 5e-8 vs EMH_yes_rec5e-8_tEOA32227.758620689656_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

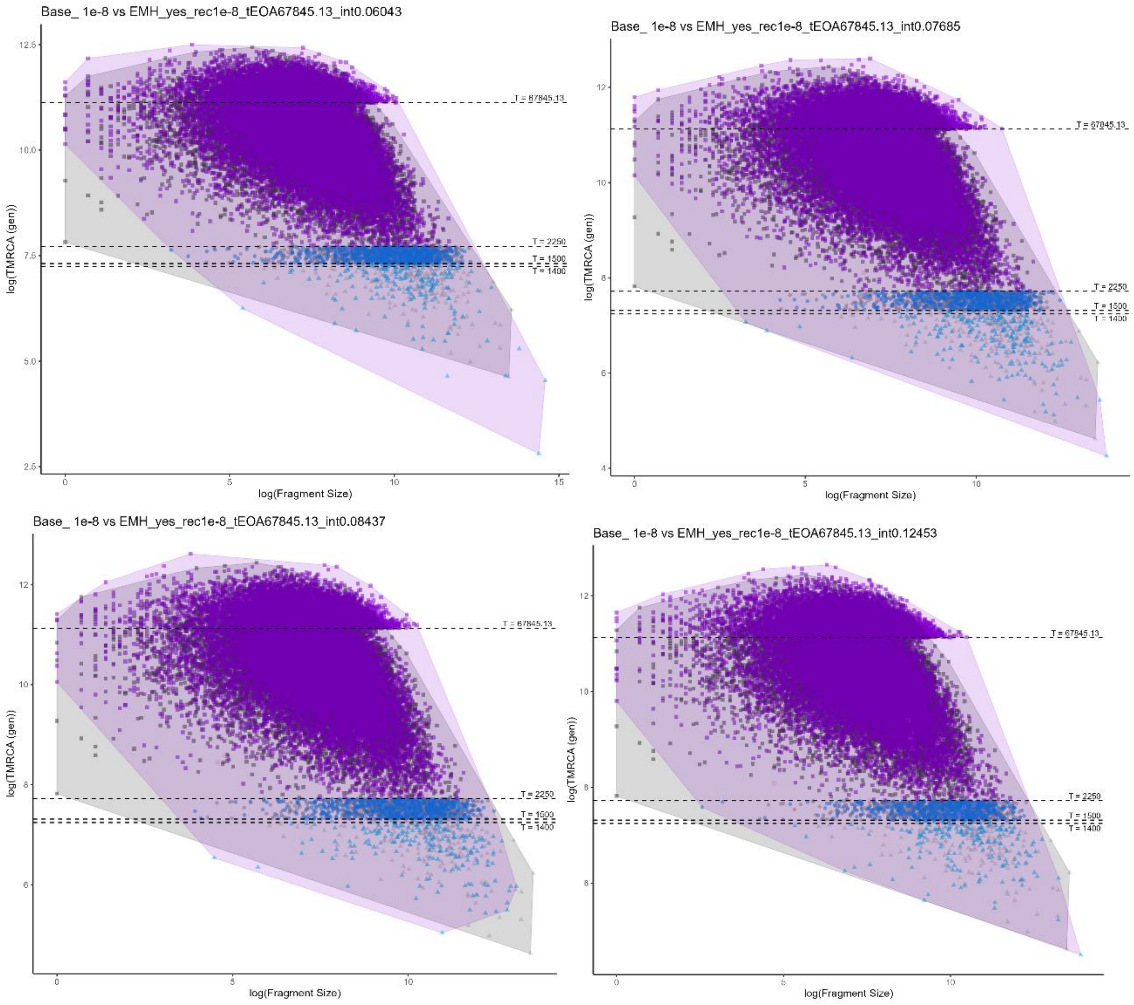

Base_ 5e-8 vs EMH_yes_rec5e-8_tEOA47856.31034482759_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

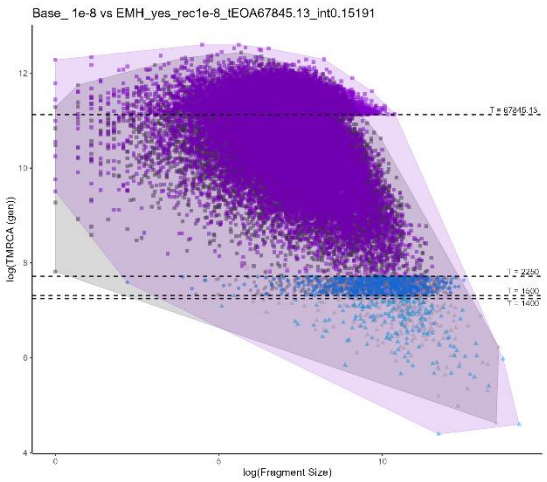

Base_ 5e-8 vs EMH_yes_rec5e-8_tEOA64473.10344827586_int0.5
log(TMRCA (gen))
log(Fragment Size)
T = 2250
T = 1500
T = 1400

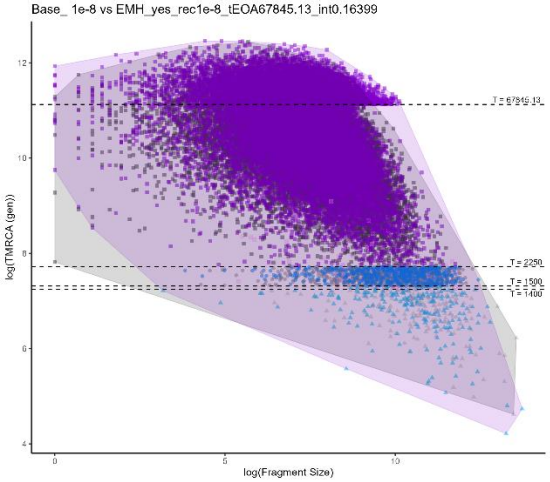
Supplementary Figures 2: Distribution of fragments under recombination rate of 1e-8 with the same divergence time between source and sink populations of 67845 generations ago (~1.9Mya) and a distribution of introgression rates of 0.01 to 0.2

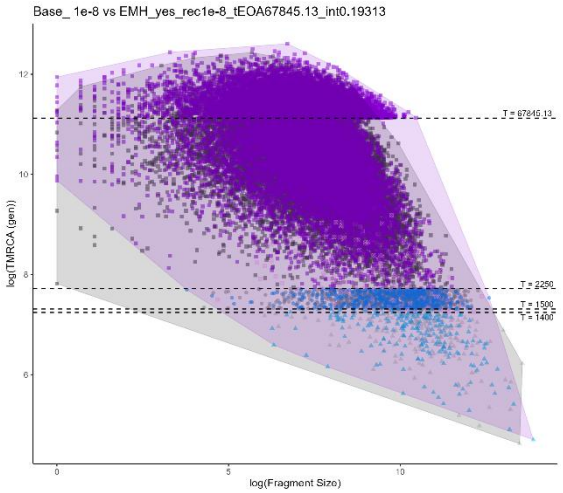
TMRCA of 67845 generations ago & recombination rate 1e-8




Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.06043
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.07685
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.08437
Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.12453
log(TMRCA (gen))
log(Fragment Size)
T = 67845.13
T = 2250
T = 1500
T = 1400

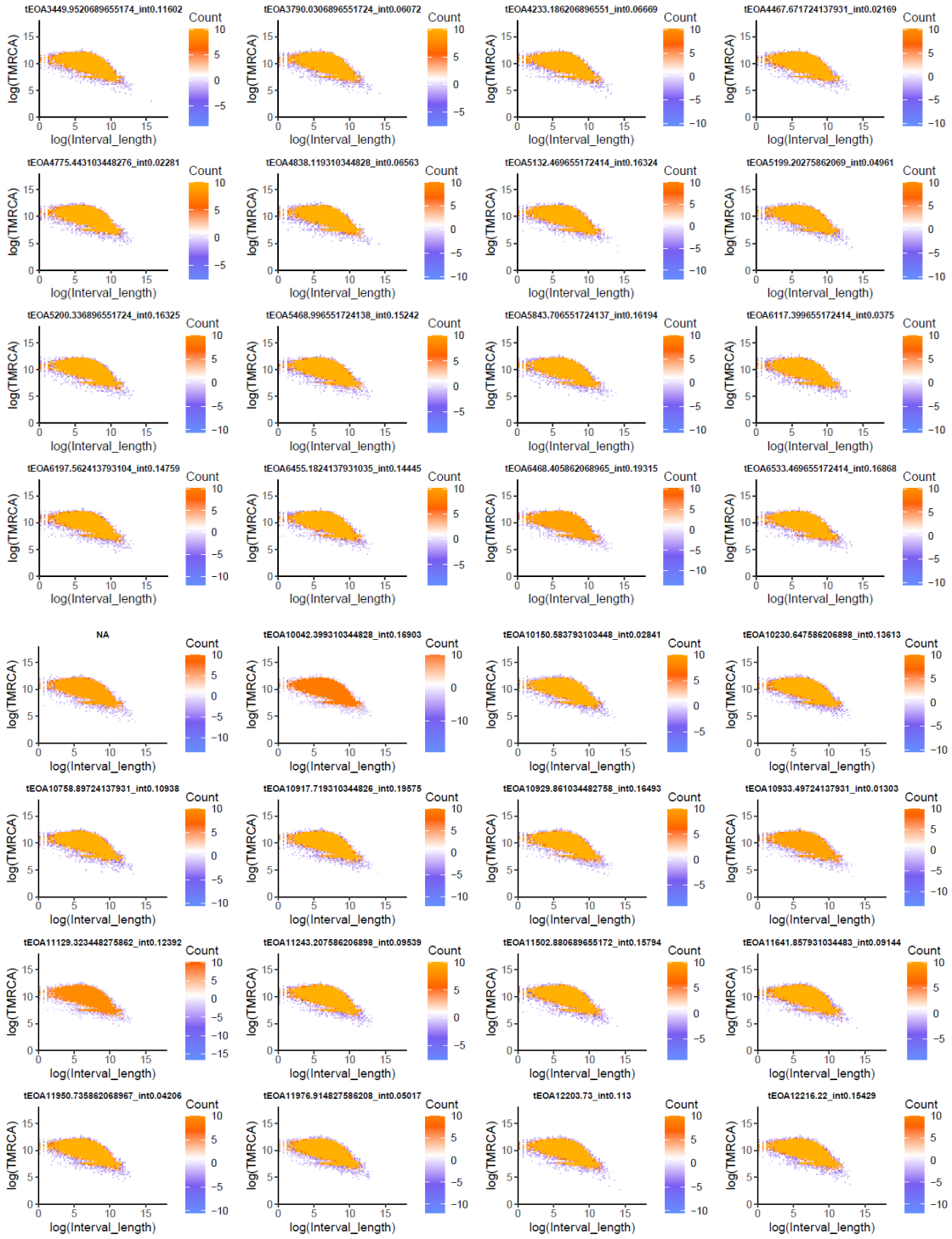

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.15191
log(TMRCA (gen))
log(Fragment Size)
T = 67845.13
T = 2250
T = 1500
T = 1400

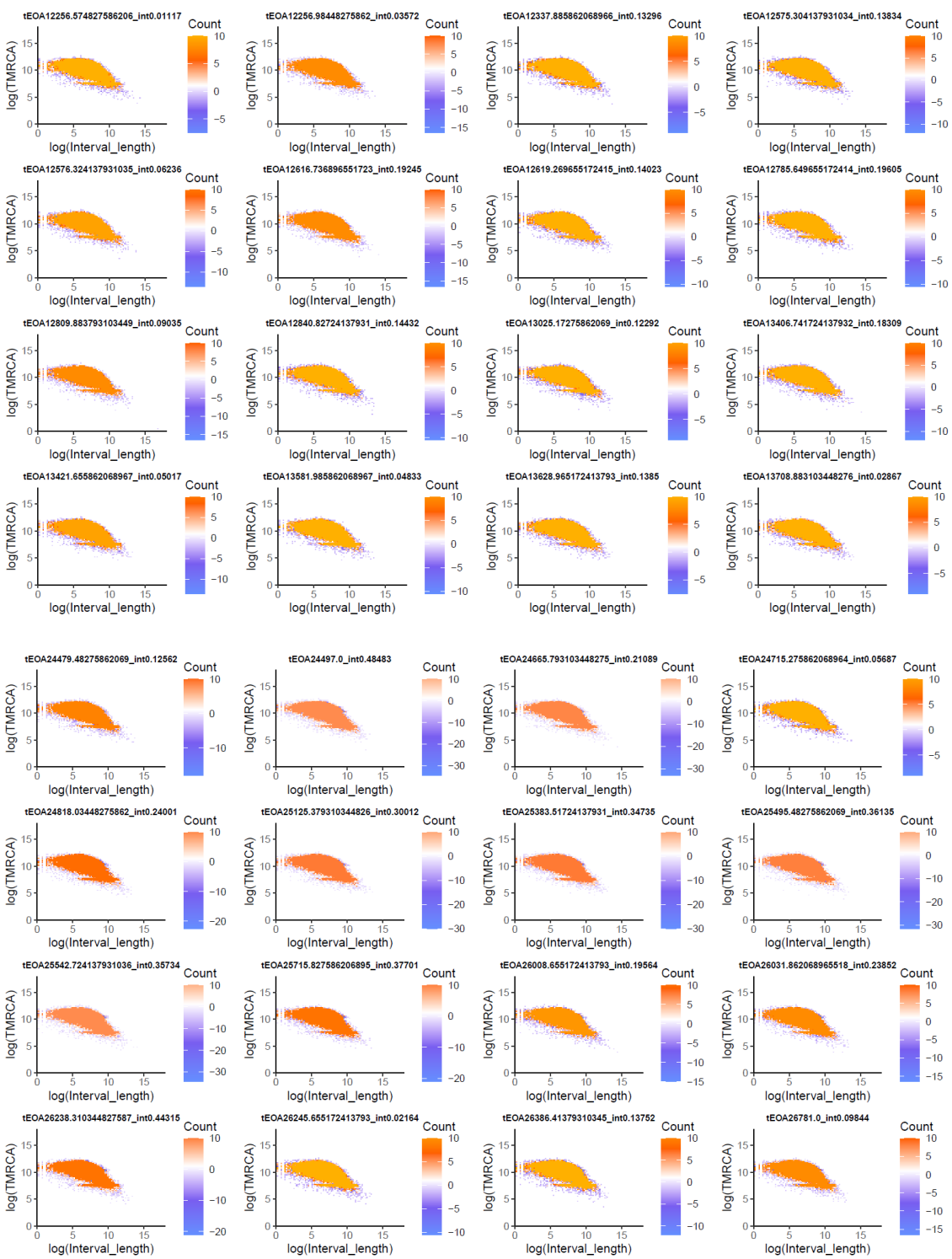

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.16399
log(TMRCA (gen))
log(Fragment Size)
T = 67845.13
T = 2250
T = 1500
T = 1400

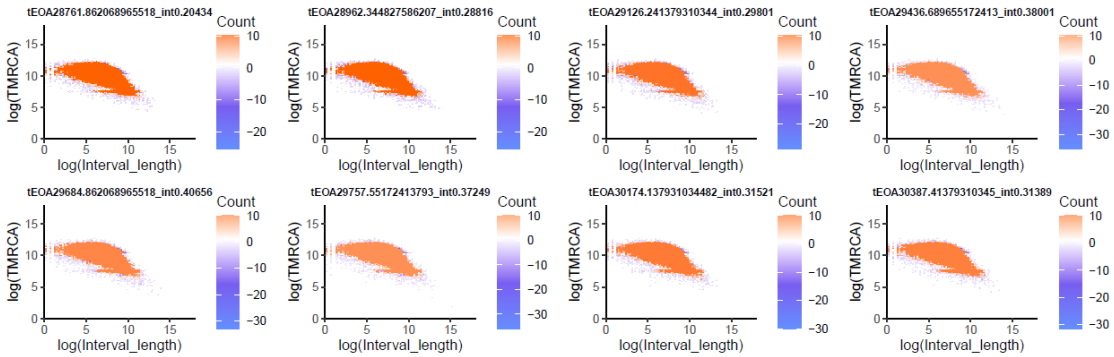

Base_ 1e-8 vs EMH_yes_rec1e-8_tEOA67845.13_int0.19313
log(TMRCA (gen))
log(Fragment Size)
T = 67845.13
T = 2250
T = 1500
T = 1400

Supplementary Figures 3: Cold plot figures with recombination rate of 1e-8 and distribution of combination of divergence time between. A: Cold plot under a multiplication between matrices scheme. Blue regions indicate regions where we there is an excess of fragments in either non-introgressed OR introgressed distributions respect to the mean number of fragments in a bin. B: Cold plot under a subtraction between matrices scheme. Red regions indicate regions where we there is an excess of fragments in introgressed model distributions against non-introgressed.

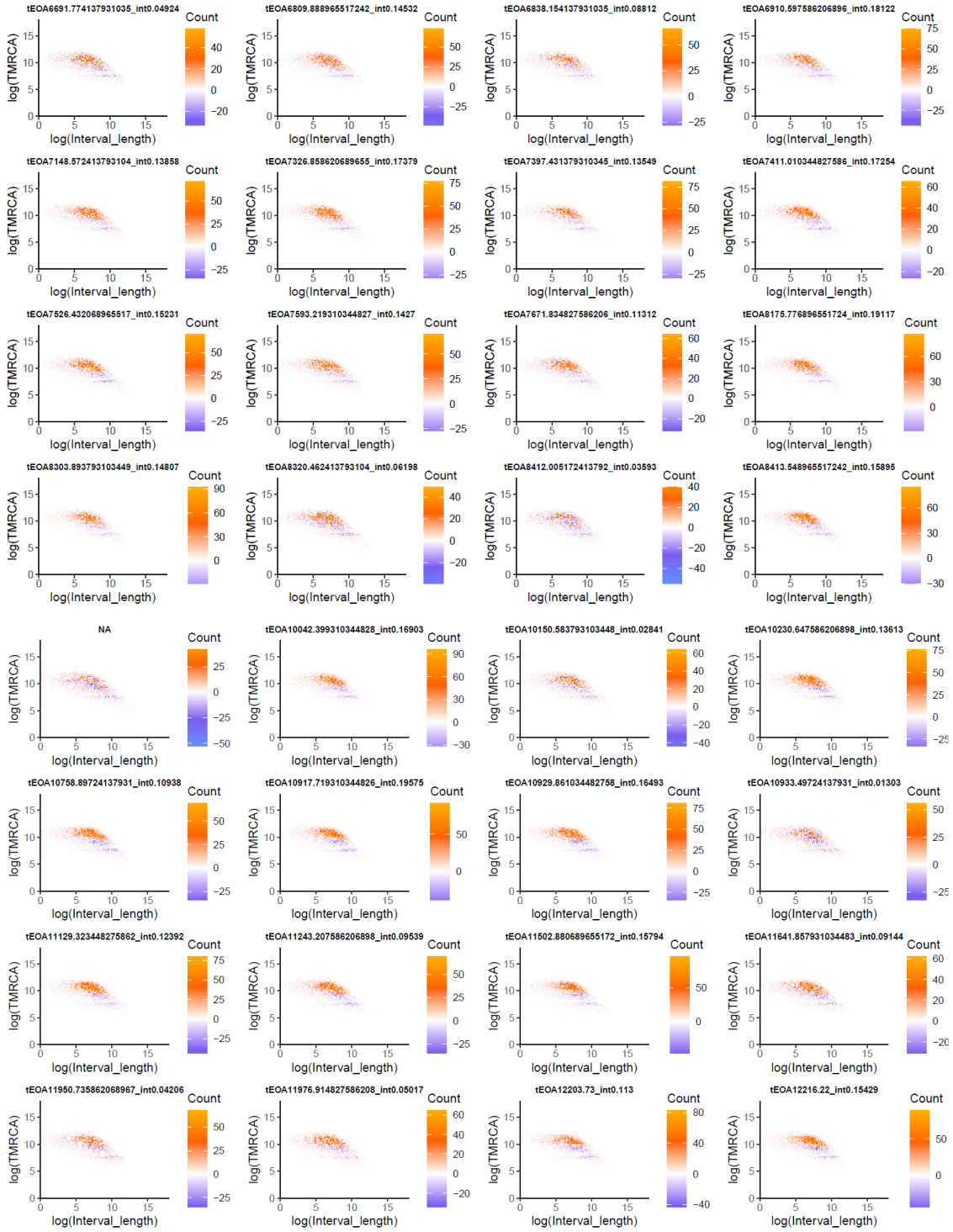
A_Cold plot figures from the multiplication cold plot

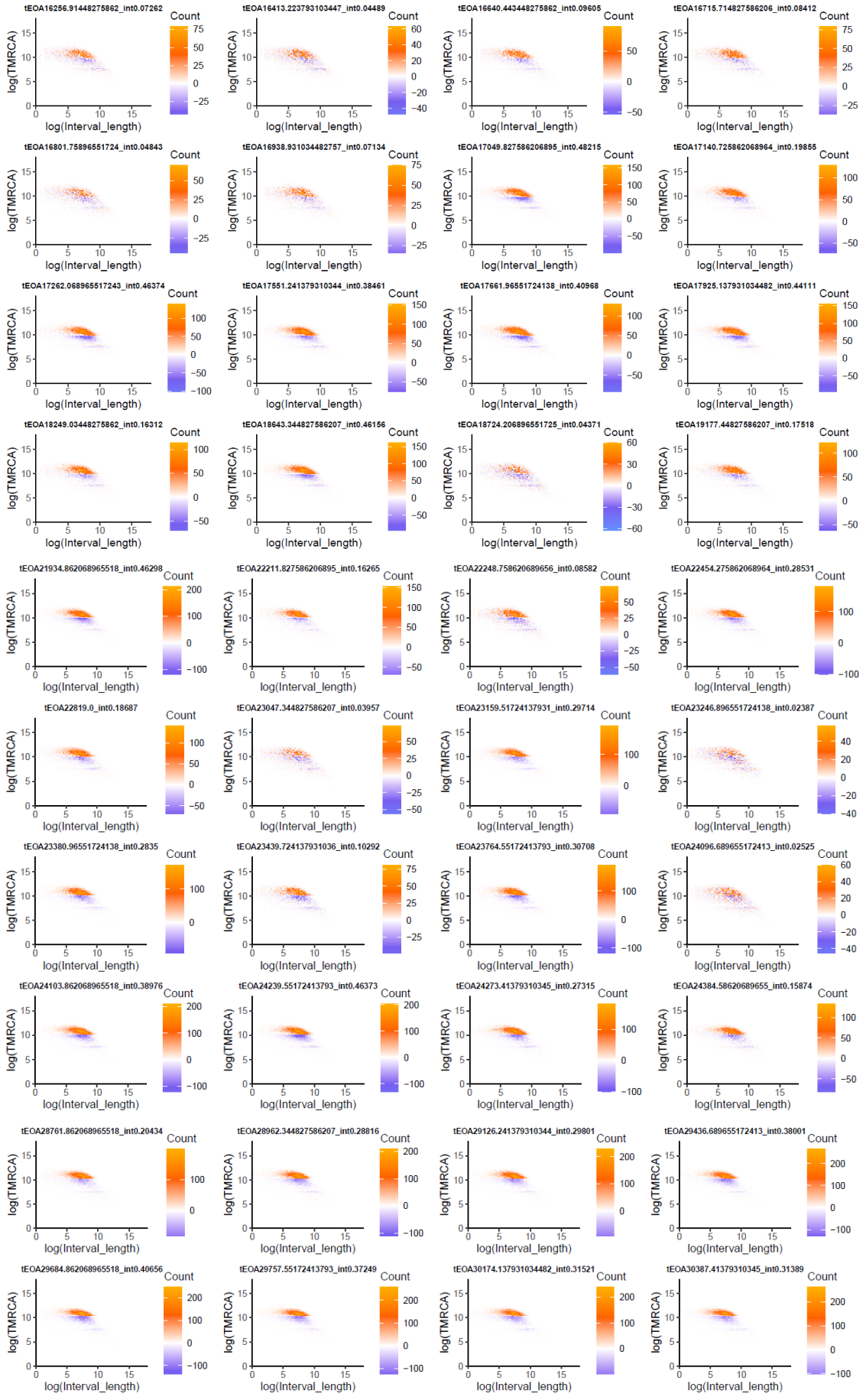


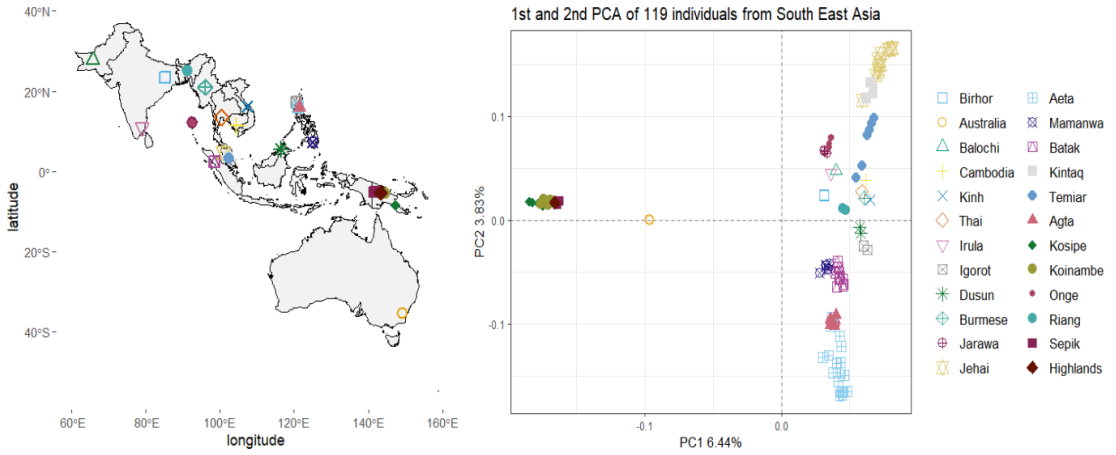

tEOA12256.574827586206_int0.01117
tEOA12256.98448275862_int0.03572
tEOA12337.885862068966_int0.13296
tEOA12575.304137931034_int0.13834
tEOA12576.324137931035_int0.06236
tEOA12616.736896551723_int0.19245
tEOA12619.269655172415_int0.14023
tEOA12785.649655172414_int0.19605
tEOA12809.883793103449_int0.09035
tEOA12840.82724137931_int0.14432
tEOA13025.17275862069_int0.12292
tEOA13406.741724137932_int0.18309
tEOA13421.655862068967_int0.05017
tEOA13581.985862068967_int0.04833
tEOA13628.965172413793_int0.1385
tEOA13708.883103448276_int0.02867
tEOA24479.48275862069_int0.12562
tEOA24497.0_int0.48483
tEOA24665.793103448275_int0.21089
tEOA24715.275862068964_int0.05687
tEOA24818.03448275862_int0.24001
tEOA25125.379310344826_int0.30012
tEOA25383.51724137931_int0.34735
tEOA25495.48275862069_int0.36135
tEOA25542.724137931036_int0.35734
tEOA25715.827586206895_int0.37701
tEOA26008.655172413793_int0.19564
tEOA26031.862068965518_int0.23852
tEOA26238.310344827587_int0.44315
tEOA26245.655172413793_int0.02164
tEOA26386.41379310345_int0.13752
tEOA26781.0_int0.09844
log(TMRCA)
log(Interval_length)
Count


tEOA28761.862068965518_int0.20434
tEOA28962.344827586207_int0.28816
tEOA29126.241379310344_int0.29801
tEOA29436.689655172413_int0.38001
tEOA29684.862068965518_int0.40656
tEOA29757.55172413793_int0.37249
tEOA30174.137931034482_int0.31521
tEOA30387.41379310345_int0.31389
log(TMRCA)
log(Interval_length)
Count

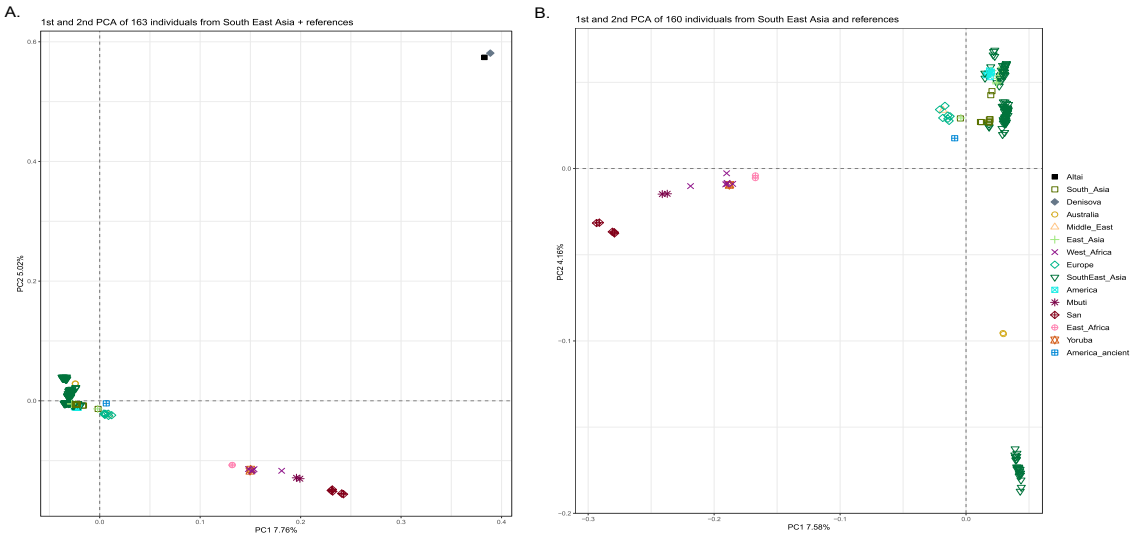
B_Cold plot figures from the substratction cold plot




tEOA16256.91448275862_int0.07262
tEOA16413.223793103447_int0.04489
tEOA16640.443448275862_int0.09605
tEOA16715.714827586206_int0.08412
tEOA16801.75896551724_int0.04843
tEOA16938.931034482757_int0.07134
tEOA17049.827586206895_int0.48215
tEOA17140.725862068964_int0.19855
tEOA17262.068965517243_int0.46374
tEOA17551.241379310344_int0.38461
tEOA17661.96551724138_int0.40968
tEOA17925.137931034482_int0.44111
tEOA18249.03448275862_int0.16312
tEOA18643.344827586207_int0.46156
tEOA18724.206896551725_int0.04371
tEOA19177.44827586207_int0.17518
tEOA21934.862068965518_int0.46298
tEOA22211.827586206895_int0.16265
tEOA22248.758620689656_int0.08582
tEOA22454.275862068964_int0.28531
tEOA22819.0_int0.18687
tEOA23047.344827586207_int0.03957
tEOA23159.51724137931_int0.29714
tEOA23246.896551724138_int0.02387
tEOA23380.96551724138_int0.2835
tEOA23439.724137931036_int0.10292
tEOA23764.55172413793_int0.30708
tEOA24096.689655172413_int0.02525
tEOA24103.862068965518_int0.38976
tEOA24239.55172413793_int0.46373
tEOA24273.41379310345_int0.27315
tEOA24384.58620689655_int0.15874
tEOA28761.862068965518_int0.20434
tEOA28962.344827586207_int0.28816
tEOA29126.241379310344_int0.29801
tEOA29436.689655172413_int0.38001
tEOA29684.862068965518_int0.40656
tEOA29757.55172413793_int0.37249
tEOA30174.137931034482_int0.31521
tEOA30387.41379310345_int0.31389
Count
log(TMRCA)
log(Interval_length)



Supplementary Figure 4: Distribution of samples from PCA of South, South East Asian and Oceanian populations (left). PCA of only South East Asian and Oceanian samples (right). We can observe a cluster of the Papuan populations (Koinambe, Kosipe, Sepik) separated from the rest of the SEA groups



Supplementary Figure 5: A. Principal Component Analysis (PCA) of all populations in the dataset including Neanderthal and Denisova populations. B. PCA removing non-Homo Sapiens populations, where we can obtain the structure of South East Asian groups as two different clusters, one including only South East Asians and a second one with more populations.