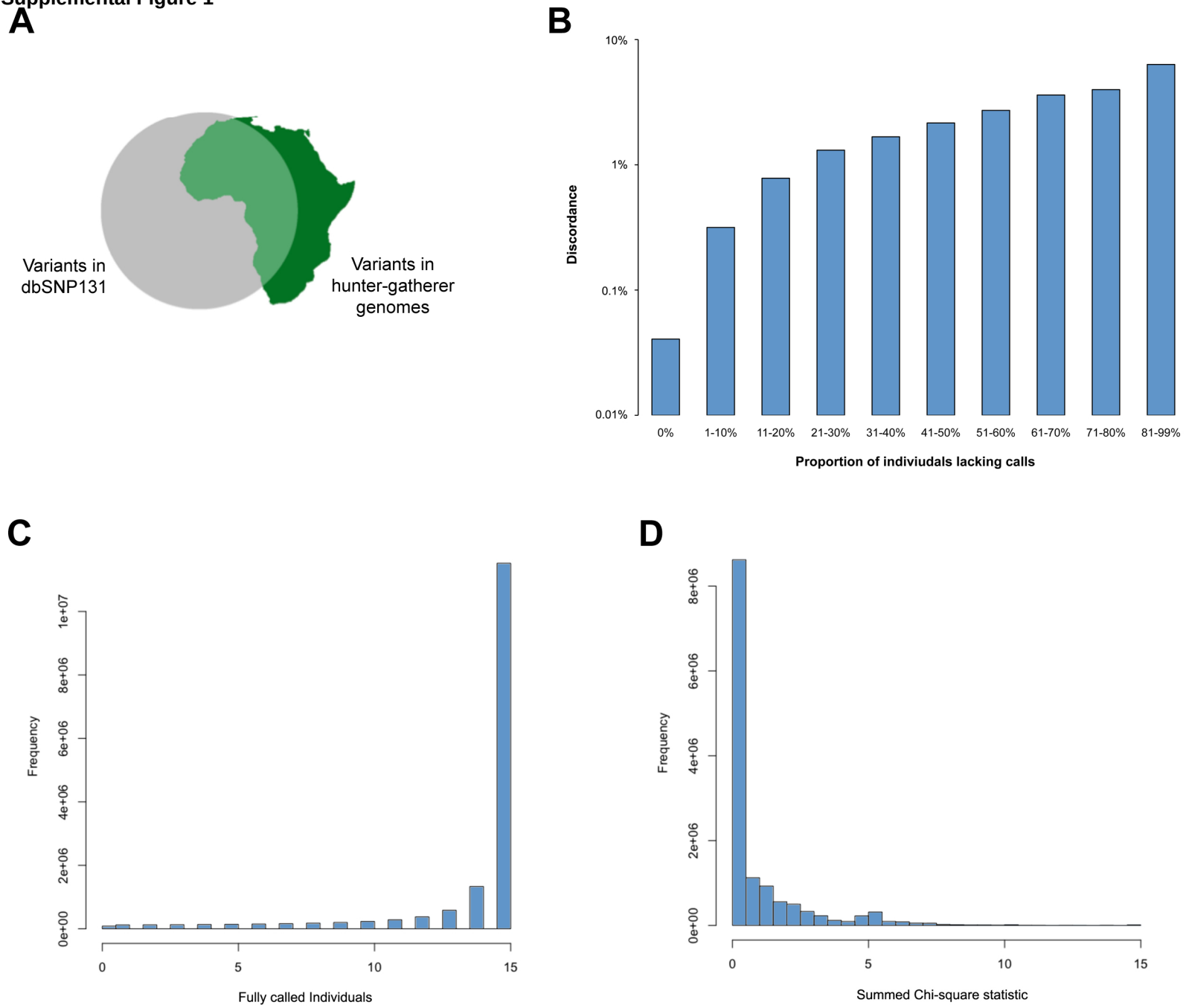
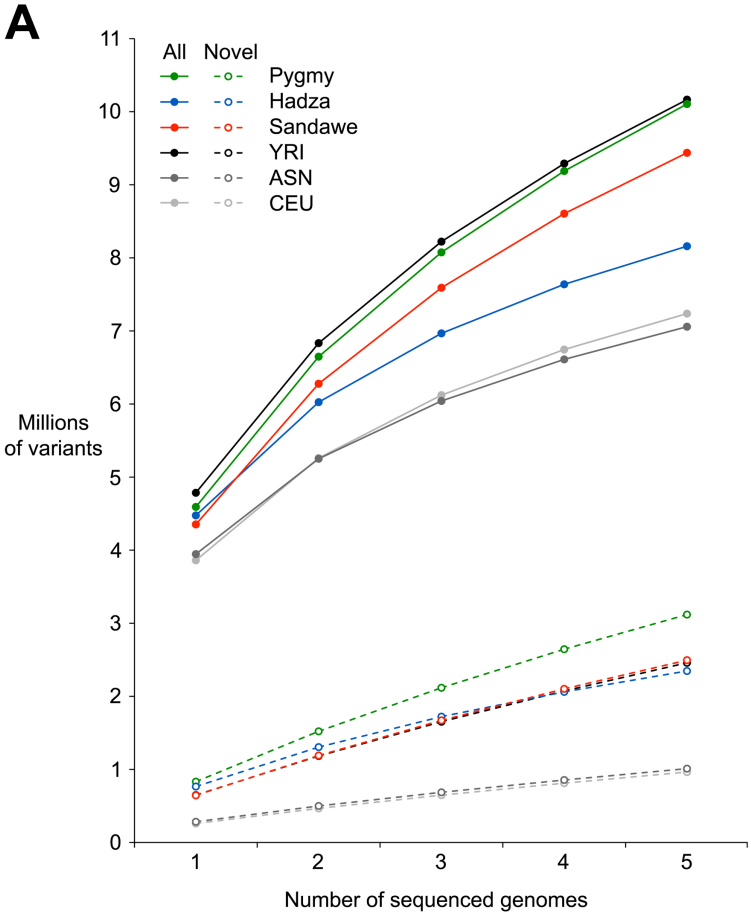
Supplemental Figure 1



Supplemental Figure 2

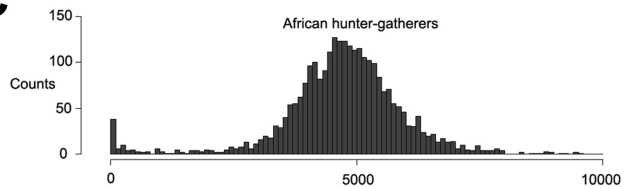
A



B

Population	Type of variant	α	β	Diploid genomes needed to reach 25 million variants
Pygmy	All	4.652×10^{6}	0.4912	30.67
	Novel	8.449×10^{5}	0.8227	61.40
Hadza	All	4.551×10^{6}	0.3742	94.87
	Novel	7.830×10^{5}	0.6982	142.68
Sandawe	All	4.415×10^{6}	0.4819	36.52
	Novel	6.524×10^{5}	0.8426	75.72
Yoruba (YRI)	All	4.852×10^{6}	0.4691	32.95
	Novel	6.565×10^{5}	0.8296	80.42
European (CEU)	All	3.926×10^{6}	0.3913	113.41
	Novel	2.862×10^{5}	0.7898	287.03
Asian (ASN)	All	4.007×10^{6}	0.3620	157.21
	Novel	2.623×10^{5}	0.8153	267.61

C



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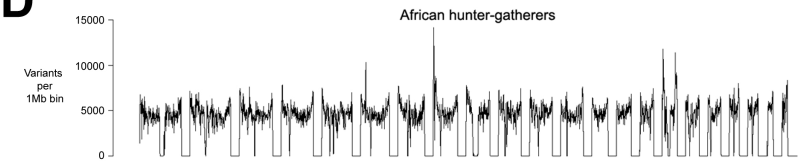
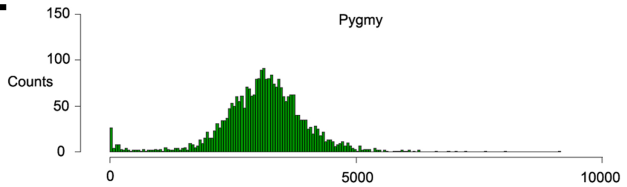


E



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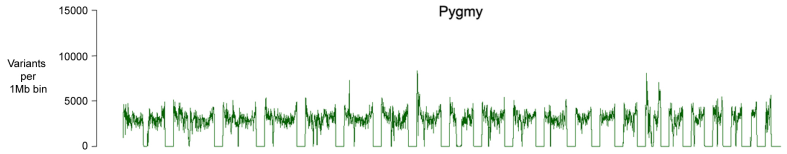
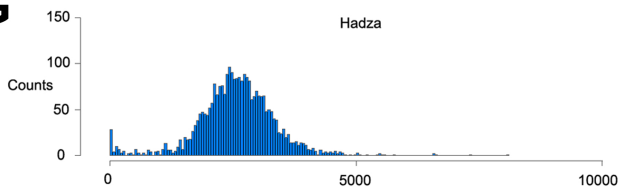
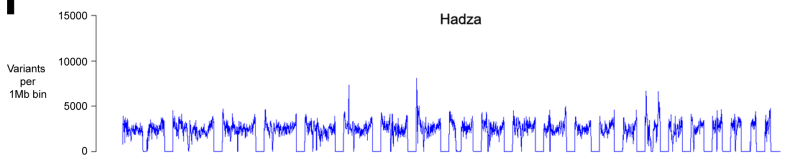


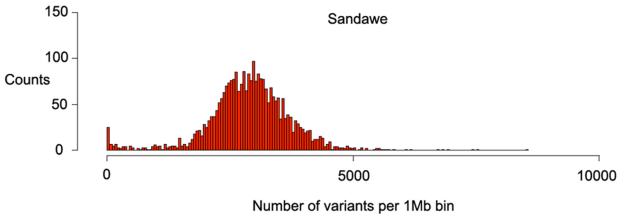
G



H



I



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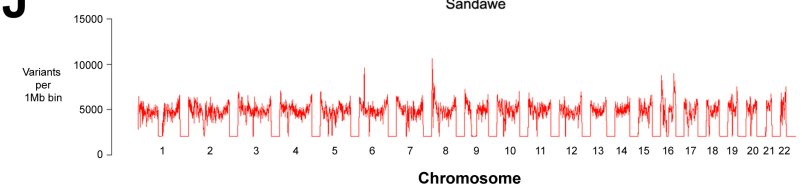
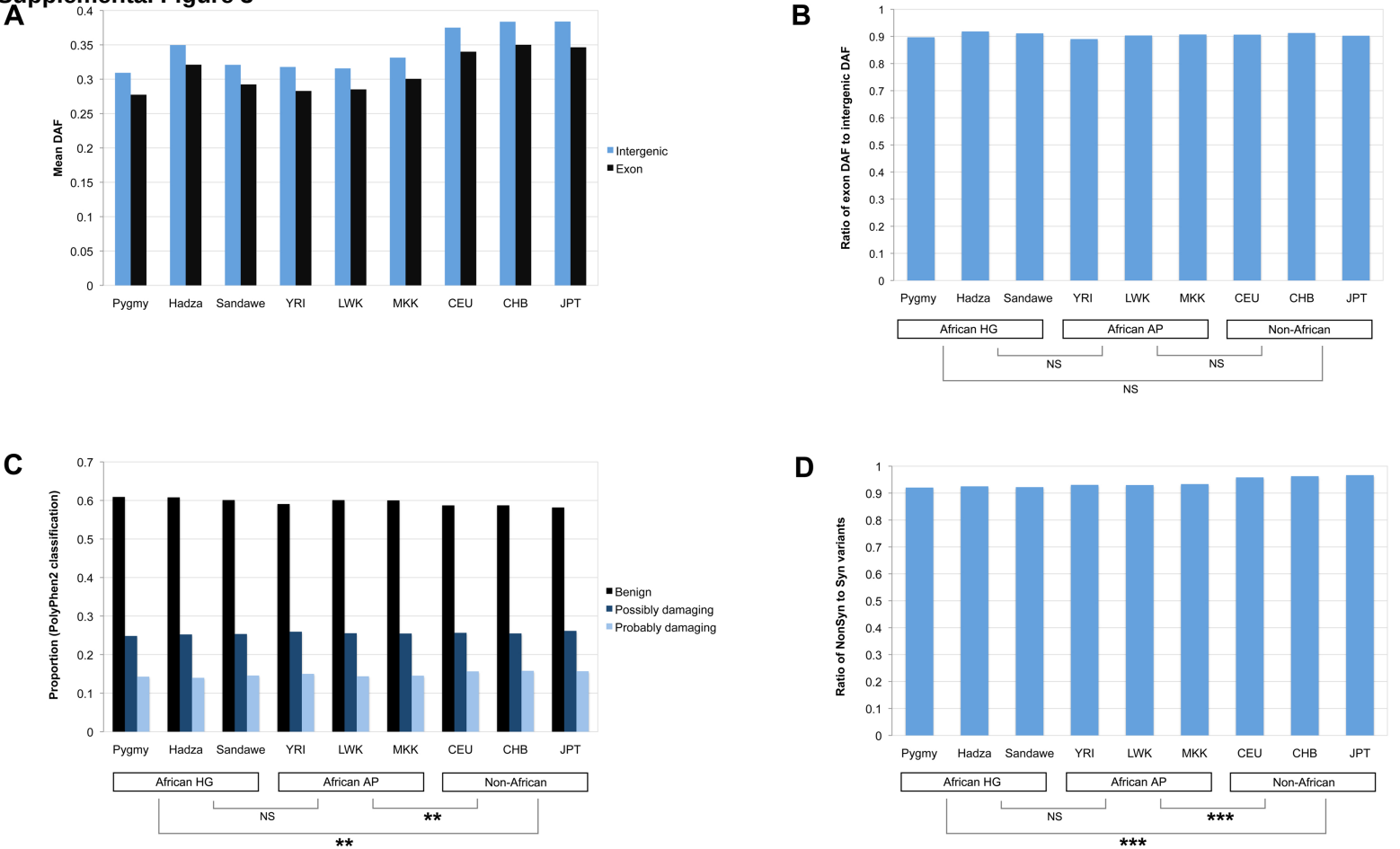


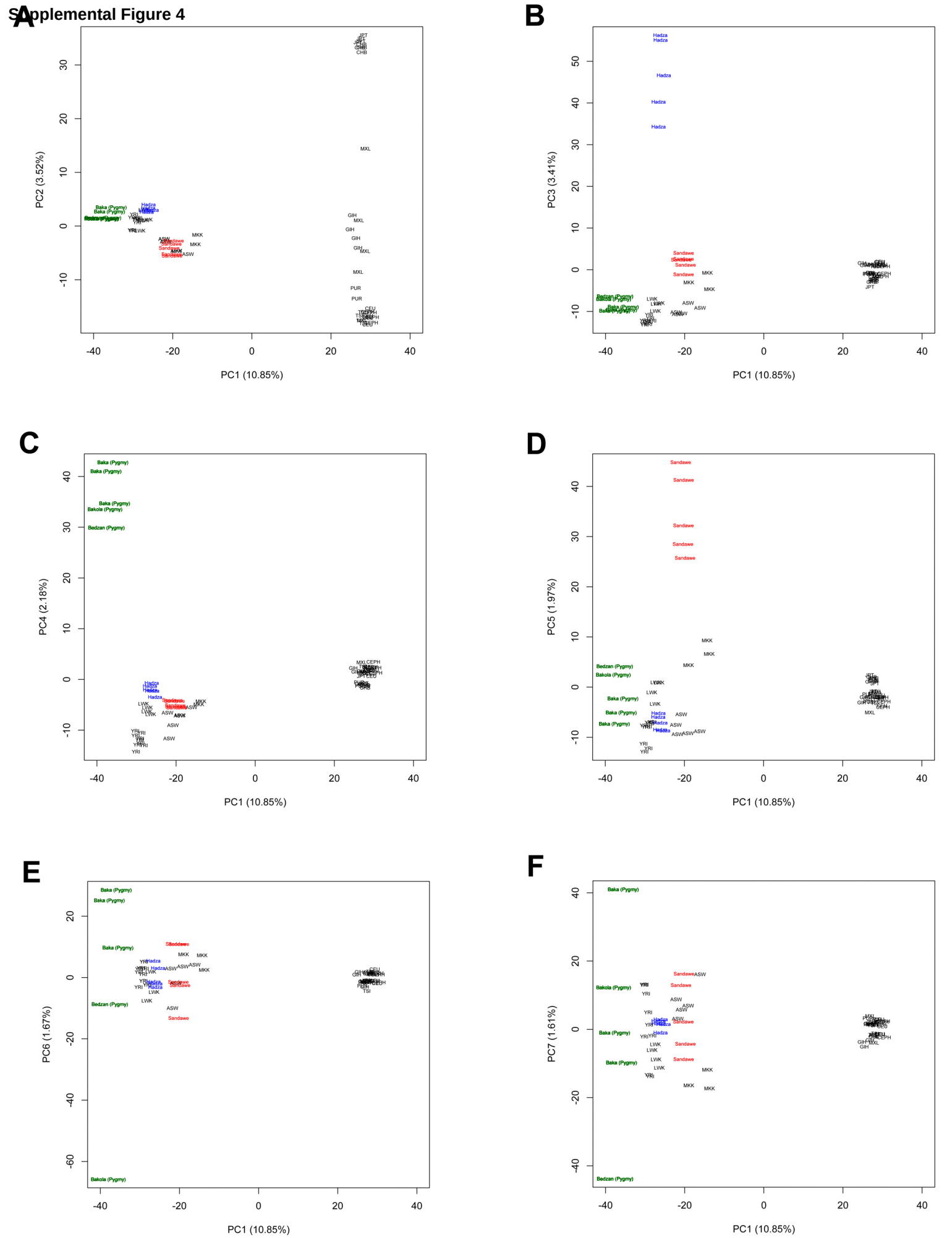
Supplemental Figure 3



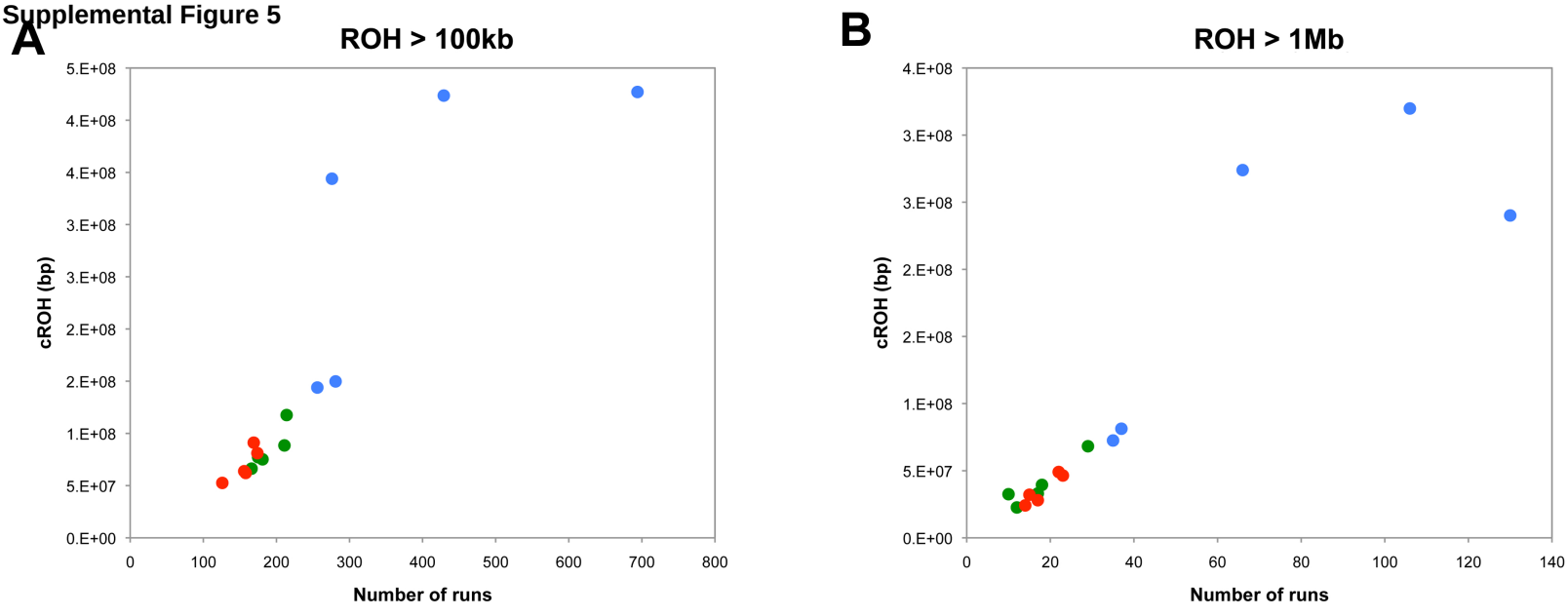
E

Comparison	Selective signature	Test	p-value
Means differ among all three groups	DAF ratio (intergenic/exon)	One-way ANOVA ($F_{(2,6)}$=0.842)	4.76×10^{-1}
	PolyPhen-2 "probably damaging" proportion	One-way ANOVA ($F_{(2,6)}$=25.0)	1.22×10^{-3} **
	Nonsynonymous/synonymous ratio	One-way ANOVA ($F_{(2,6)}$=107)	2.03×10^{-5} ***
African HG vs. African AP	DAF ratio (intergenic/exon)	Tukey HSD	4.88×10^{-1}
	PolyPhen-2 "probably damaging" proportion	Tukey HSD	2.70×10^{-1}
	Nonsynonymous/synonymous ratio	Tukey HSD	6.35×10^{-2}
African HG vs. Non-African	DAF ratio (intergenic/exon)	Tukey HSD	6.01×10^{-1}
	PolyPhen-2 "probably damaging" proportion	Tukey HSD	5.45×10^{-3} **
	Nonsynonymous/synonymous ratio	Tukey HSD	8.34×10^{-5} ***
African AP vs. Non-African	DAF ratio (intergenic/exon)	Tukey HSD	9.76×10^{-1}
	PolyPhen-2 "probably damaging" proportion	Tukey HSD	1.20×10^{-3} **
	Nonsynonymous/synonymous ratio	Tukey HSD	2.14×10^{-5} ***

Supplemental Figure 4



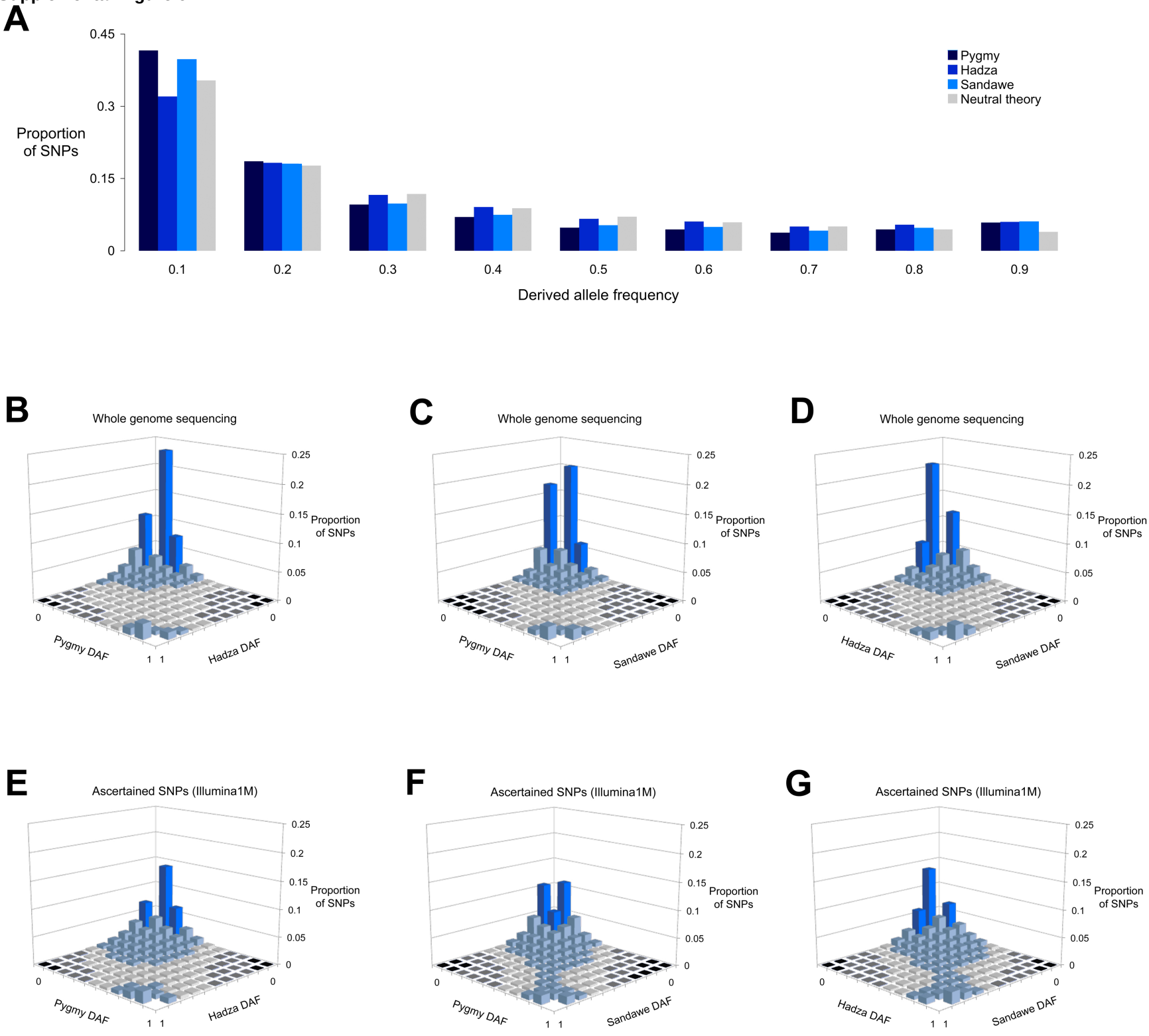
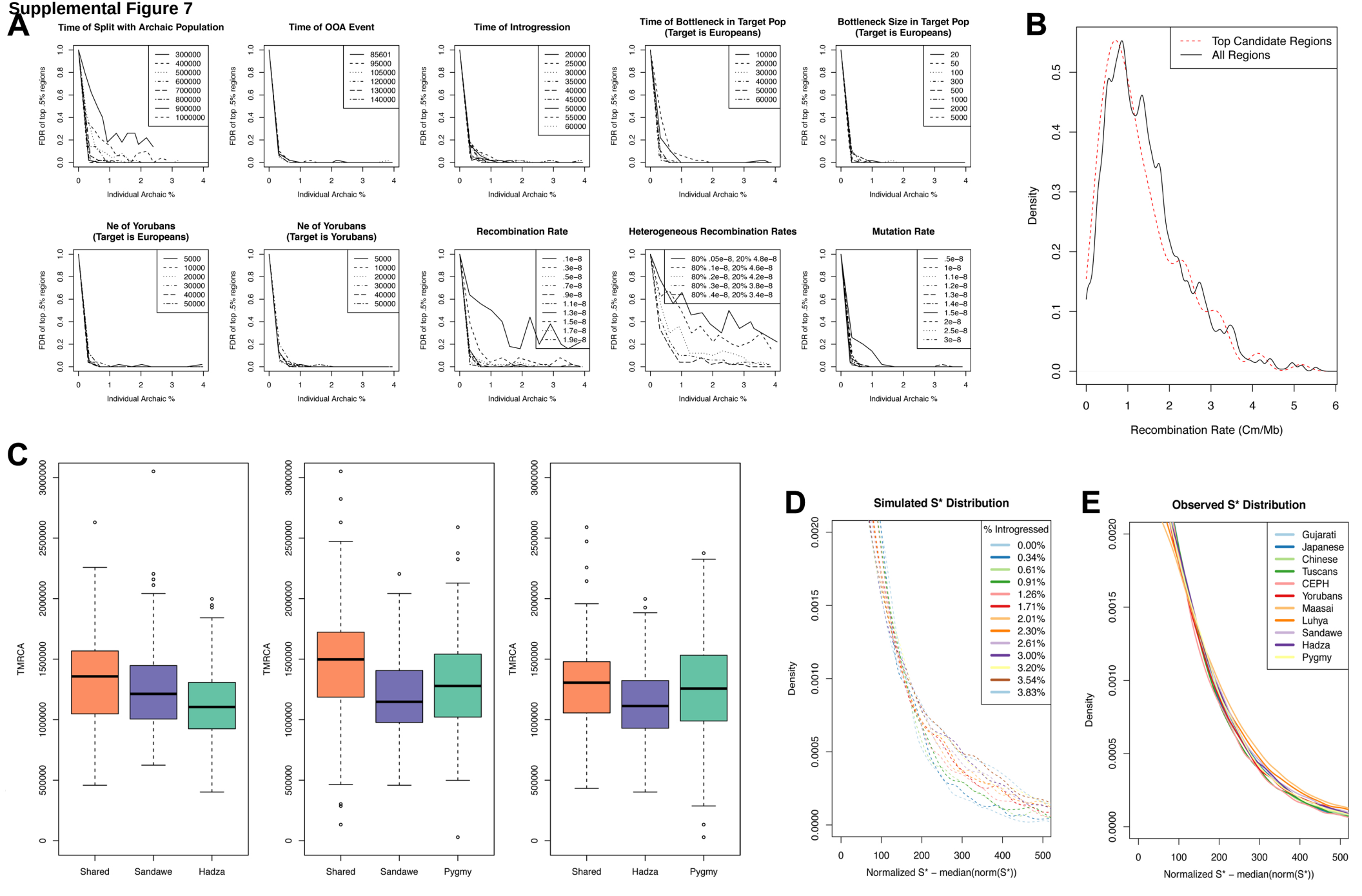
Supplemental Figure 5



C

Statistics	Pygmy	Hadza	Sandawe
ROH >100kb			
Number of ROH	189 ± 22	387 ± 285	157 ± 19
cROH	84.9 ± 19.9 Mb	297.6 ± 141.6 Mb	70.1 ± 15.6 Mb
CV (of cROH)	0.234	0.476	0.222
ROH >1Mb			
Number of ROH	17.2 ± 7.4	74.8 ± 42.2	18.2 ± 4.1
cROH	39.2 ± 17.3 Mb	197.5 ± 113.7Mb	35.9 ± 11.2 Mb
CV (of cROH)	0.442	0.576	0.311

Supplemental Figure 6



Supplemental Figure 7