**Table S4**Results form nine coalescent simulation models representing various demographic scenarios.

Model	<b>Description</b> <sup>a</sup>	Mean Parallel Divergent SNPs (95% CI) <sup>b</sup>	Mean Skew (95% CI) <sup>c</sup>	Divergence Comparison with Highest Parallel Divergence (DCHPD) <sup>d</sup>	Parallel Divergent SNPs of DCHPD (95% CI) <sup>e</sup>	Most Skewed Divergence Comparison (MSDC) <sup>f</sup>	Skew of MSDC (95% CI) <sup>g</sup>
standard	cosi-based parameters. WA and PY follow Africa; EU follows Europe; EA, OC, SA follow Asia. Bottlenecks but N > 500 at all times	67.2 (62.2,71.3)	0.54 (0.52,0.56)	PY-WA vs. EU-EA	68.6 (56.7,82.7)	PY-WA vs. OC-EA	0.55 (0.51,0.64)
3nobottle	standard but no bottlenecks for out-of-Africa or for PY, OC, or SA	67.6 (62.8,71.2)	0.54 (0.53,0.57)	WA-OC vs. EA-SA	68.5 (56.8,79.8)	PY-WA vs. EU-SA	0.55 (0.50,0.62)
OC-EAmig1	standard but gene flow from EA to OC, 4Nm = 1	67.2 (63.1,72.3)	0.54 (0.53,0.57)	PY-WA vs. EU-OC	69.0 (56.1,82.9)	PY-OC vs. EA-SA	0.55 (0.50,0.65)
OC-EAmig10	standard but gene flow from EA to OC, 4Nm = 10	67.0 (62.6,72.4)	0.55 (0.53,0.57)	PY-WA vs. EU-EA	69.1 (55.7,80.3)	WA-OC vs. EA-SA	0.56 (0.50,0.63)
OC-EAmig100	standard but gene flow from EA to OC, 4Nm = 100	77.7 (74.1,81.7)	0.60 (0.59,0.62)	EU-OC vs. EA-SA	91.7 (77.3,104.3)	EU-OC vs. EA-SA	0.83 (0.77,0.90)
constantlow	standard but no bottlenecks or population growth, constant $N = 10,000$	74.1 (69.9,78.1)	0.53 (0.52,0.55)	PY-WA vs. OC-SA	78.0 (66.1,88.2)	EU-OC vs. EA-SA	0.55 (0.50,0.64)
nobottle 3tighterbottle	standard but no bottlenecks standard but tighter bottlenecks for PY, OC, and SA (N = 350 for 50 generations)	67.6 (63.8,71.2) 70.6 (66.7,73.6)	0.53 (0.52,0.55) 0.54 (0.52,0.56)	PY-EU vs. SA-EA PY-EU vs. OC-SA	68.4 (58.6,79.4) 72.9 (64.4,84.3)	PY-EU vs. SA-OC PY-EU vs. EA-SA	0.54 (0.50,0.60) 0.55 (0.50,0.63)
3tightestbottle	standard but even tighter bottlenecks for PY, OC, and SA (N = 150 for 50 generations)	77.5 (72.5,81.5)	0.57 (0.55,0.59)	PY-EU vs. OC-SA	90.4 (79.3,101.5)	PY-EU vs. EA-SA	0.64 (0.58,0.72)

<sup>&</sup>lt;sup>a</sup>Brief description of each model. All models join populations in the same order, SA-EA-OC-EU-WA-PY, at the same time points. Parameters follow the cosi model calibrated with HapMap data unless otherwise indicated. All bottlenecks last for 50 generations.

<sup>&</sup>lt;sup>b</sup>Mean number of parallel divergent SNPs across all divergence comparisons, with 95% confidence intervals.

Mean proportion of parallel divergent SNPs showing the major orientation across all divergence comparisons, with 95% confidence intervals.

<sup>&</sup>lt;sup>d</sup>Divergence comparison (out of 15) showing the highest number of parallel divergent SNPs

<sup>&</sup>lt;sup>e</sup>Mean number of parallel divergent SNPs for the divergence comparison identified in the previous column, with 95% confidence intervals.

<sup>&</sup>lt;sup>f</sup>Divergence comparison (out of 15) showing the highest major orientation frequency.

<sup>&</sup>lt;sup>g</sup>The proportion of parallel divergent SNPs showing the major orientation for the divergence comparison identified in the previous column, with 95% confidence intervals.