Table S1. Number and length of inferred TSM events, as well as proportion of homozygous loci and resolved and ancestral (of the former) allelic state in different samples. Only unmasked loci are included.

				Length (bp)		Allele (%)		Polarization (%)	
ID	Population	Region	n	average	maxim.	homozyg.	singleton	resolved	ancestral
HG02011	ACB	AFR	1046	10.67	171	30.50	7.58	89.50	49.68
NA19983	ASW	AFR	1077	10.77	171	27.48	8.41	88.03	53.74
HG03125	ESN	AFR	1073	10.43	171	29.45	7.12	88.01	51.32
HG03371	ESN	AFR	1070	10.44	171	31.40	8.43	89.09	52.57
HG02587	GWD	AFR	1097	10.81	180	26.71	9.59	89.44	51.73
HG02818	GWD	AFR	1038	10.64	100	29.38	8.07	88.07	53.01
HG03065	MSL	AFR	1060	10.48	171	30.94	8.81	89.84	53.09
HG03486	MSL	AFR	1064	10.90	180	28.85	8.39	88.17	52.08
NA19238	YRI	AFR	1121	10.44	97	28.37	8.60	90.29	51.28
NA19239	YRI	AFR	1092	10.47	171	29.30	8.91	89.03	52.46
NA12329	CEU	EUR	922	10.70	180	35.03	3.07	88.84	52.32
NA12878	CEU	EUR	921	10.49	171	36.48	2.61	89.48	54.42
HG00171	FIN	EUR	883	10.28	171	34.65	3.63	90.05	54.27
HG00096	GBR	EUR	937	10.67	171	36.07	3.11	89.23	53.17
HG01505	IBS	EUR	920	10.79	180	32.83	4.03	89.46	52.61
NA20509	TSI	EUR	882	10.47	180	35.49	4.52	89.12	55.34
NA24385	AZK	EUR	872	10.48	171	36.24	2.71	89.58	54.86
HG00864	CDX	EAS	942	10.61	171	39.17	4.33	88.67	50.42
NA18534	CHB	EAS	923	10.59	171	39.98	4.34	87.99	52.15
HG00512	CHS	EAS	917	10.52	171	39.91	2.82	89.12	50.67
HG00513	CHS	EAS	929	10.69	180	41.87	3.57	88.41	50.24
NA18939	JPT	EAS	927	10.50	171	42.29	3.16	89.76	50.30
HG01596	KHV	EAS	910	10.78	171	39.01	4.12	88.50	50.00
HG03009	BEB	SAS	878	10.45	171	35.76	3.85	88.52	52.76
NA20847	GIH	SAS	938	10.55	171	35.82	4.59	89.15	53.46
HG03732	ITU	SAS	920	10.37	171	35.87	3.57	88.15	52.77
HG02492	PJL	SAS	879	10.80	180	39.59	3.14	87.94	52.39
HG03683	STU	SAS	939	10.22	97	33.97	4.06	89.80	50.89
HG01114	CLM	AMR	923	10.64	171	33.69	3.86	87.66	53.83
NA19650	MXL	AMR	906	10.58	171	35.76	3.43	88.41	52.93
HG00731	PUR	AMR	949	10.63	171	34.56	3.09	88.55	52.91
HG00732	PUR	AMR	955	10.60	171	34.87	3.23	88.20	51.36