Table S1: Western chimpanzee pedigree sequencing properties. Mapped coverage was calculated after removing PCR duplicates and against the panTro3 reference genome.

Individual	Total Sequence (Gb)	Mean coverage	Genome covered by > 15x	# Illumina lanes
A	185.00	63.81	97.80	6
B	166.90	57.54	97.00	5
C	74.20	25.59	87.60	2
D	103.60	35.73	94.70	3
E	66.10	22.78	82.60	2
F	90.20	31.11	94.00	3
G	70.80	24.42	86.00	2
H	72.10	24.85	86.80	2
I	84.90	29.28	90.60	2
Average	101.53	35.01	90.79	

Table S2: Properties of inferred cross-over breakpoints (excluding complex events). Start_bp and End_bp represent the panTro3 coordinates of the 95% credible interval. A 'best-guess' range was calculated as the two consecutive sites with the largest change in the posterior probability.

Chr	Cross-over breakpoint range (95% CI)		Number of sites in 95% CI	Change in posterior probability over cross-over breakpoint range		'Best guess' SNV interval for breakpoint	
	Start (bp)	End (bp)		5' transmission vector	3' transmission vector	Start (bp)	End (bp)
1	2,441,847	2,505,066	41	-0.978	0.976	2,441,847	2,445,577
1	2,995,244	3,006,208	2	-0.998	0.996	3,005,424	3,006,208
1	10,232,552	10,250,285	4	-0.999	0.999	10,240,430	10,250,285
1	13,545,724	13,546,685	1	-1.000	1.000	13,545,724	13,546,685
1	17,341,138	17,394,727	21	-0.999	1.000	17,341,138	17,343,545
1	19,698,531	19,717,500	18	-0.976	0.977	19,703,005	19,703,451
1	47,089,507	47,114,126	19	-1.000	1.000	47,101,077	47,101,905
1	56,125,791	56,169,855	95	-0.966	0.965	56,125,791	56,125,962
1	56,868,170	56,871,573	2	-0.998	0.998	56,868,170	56,871,221
1	73,311,236	73,315,328	4	-0.996	0.996	73,311,236	73,311,412
1	74,660,121	74,666,594	3	-1.000	1.000	74,660,121	74,663,007
1	78,222,576	78,227,450	2	-1.000	1.000	78,222,576	78,227,044
1	81,705,285	81,707,949	4	-1.000	1.000	81,705,285	81,706,090
1	100,068,136	100,075,910	6	-1.000	1.000	100,068,136	100,070,322
1	107,073,526	107,074,796	1	-1.000	1.000	107,073,526	107,074,796
1	140,252,972	140,256,204	4	-1.000	1.000	140,252,972	140,253,601
1	167,949,628	167,953,570	2	-0.999	0.999	167,949,628	167,953,221
1	170,675,861	170,680,617	2	-1.000	0.999	170,675,861	170,680,265
1	177,723,536	177,731,223	7	-1.000	1.000	177,723,536	177,725,185
1	180,727,670	180,755,380	6	-0.987	0.987	180,727,670	180,727,785
1	192,571,877	192,576,000	2	-1.000	1.000	192,573,891	192,576,000
1	193,187,751	193,202,550	9	-0.994	0.994	193,202,355	193,202,550
1	213,951,525	213,962,770	14	-1.000	1.000	213,951,525	213,951,646
1	214,206,657	214,483,663	50	-0.976	0.978	214,482,811	214,483,663
1	218,213,266	218,227,309	4	-1.000	1.000	218,213,266	218,222,220
1	219,495,928	219,504,113	7	-0.999	1.000	219,495,928	219,497,619
1	223,664,146	223,666,641	1	-0.995	0.995	223,664,146	223,666,641
2A	5,455,120	5,500,180	65	-0.970	0.970	5,455,120	5,455,194
2A	5,848,124	5,848,624	1	-0.994	0.994	5,848,124	5,848,624
2A	9,733,226	9,763,261	37	-1.000	1.000	9,733,226	9,734,908
2A	33,887,049	33,889,525	2	-0.999	1.000	33,887,049	33,887,354
2A	42,748,835	42,807,454	32	-0.989	0.998	42,806,619	42,807,454
2A	46,441,412	46,446,273	2	-0.991	0.991	46,441,412	46,443,723
2A	67,765,118	68,011,933	342	-0.977	0.976	67,938,724	67,939,731
2A	80,499,309	80,501,001	3	-0.999	1.000	80,500,839	80,501,001
2A	81,141,703	81,142,893	2	-1.000	1.000	81,141,703	81,141,792
2A	81,843,955	81,845,318	3	-0.974	0.974	81,844,245	81,844,353
2A	99,846,475	99,847,026	2	-0.992	0.992	99,846,475	99,846,579
2A	106,121,023	106,124,492	1	-0.999	0.999	106,121,023	106,124,492
2A	106,593,968	106,604,691	4	-1.000	1.000	106,593,968	106,595,159
2A	109,566,577	109,891,969	315	-1.000	0.999	109,566,577	109,567,536
2A	111,367,877	111,378,240	11	-1.000	0.997	111,367,877	111,369,609
2A	111,830,564	111,911,311	103	-0.962	0.962	111,830,564	111,832,323
2B	117,375,213	117,491,991	113	-0.962	0.964	117,411,338	117,412,620
2B	120,155,683	120,200,849	14	-0.998	0.997	120,155,683	120,157,033
2B	121,323,648	121,339,621	8	-0.999	0.999	121,323,648	121,326,371
2B	122,057,259	122,187,750	75	-0.974	0.971	122,074,976	122,075,171
2B	122,885,204	122,887,334	5	-1.000	1.000	122,885,204	122,885,323
2B	149,506,879	149,508,834	2	-0.995	0.995	149,506,879	149,507,558
2B	154,892,774	154,975,977	93	-0.958	0.958	154,892,774	154,894,868
2B	184,240,584	184,244,092	4	-1.000	1.000	184,240,584	184,242,413
2B	218,229,569	218,233,445	3	-0.993	0.992	218,229,569	218,231,881

2B	228,166,348	228,170,841	4	-0.999	0.999	228,166,348	228,166,621
2B	239,288,386	239,292,244	5	-0.982	0.982	239,291,940	239,292,244
2B	241,849,147	242,015,635	295	-0.978	0.980	241,883,308	241,883,894
2B	242,679,190	242,693,766	13	-1.000	1.000	242,679,190	242,683,038
2B	245,576,136	245,669,053	139	-0.969	0.968	245,577,219	245,577,989
3	591,750	599,839	2	-1.000	0.999	591,750	594,013
3	3,664,956	3,674,874	9	-1.000	1.000	3,664,956	3,665,506
3	6,002,789	6,567,761	580	-0.966	0.978	6,060,086	6,061,550
3	7,574,910	7,577,089	5	-0.989	1.000	7,575,992	7,577,089
3	12,573,323	12,574,457	2	-0.995	0.997	12,574,342	12,574,457
3	16,592,674	18,556,475	1590	-0.976	0.975	18,354,301	18,356,435
3	19,185,789	20,556,385	1340	-0.967	0.967	19,185,789	19,186,542
3	24,267,410	24,488,634	210	-0.961	0.961	24,267,410	24,267,461
3	25,915,083	25,917,107	1	-0.977	0.977	25,915,083	25,917,107
3	32,179,221	32,259,319	77	-0.999	0.997	32,179,221	32,179,532
3	38,160,246	38,161,480	2	-0.998	0.998	38,160,246	38,161,008
3	61,570,730	61,575,636	8	-0.998	0.998	61,570,730	61,571,648
3	70,118,927	70,124,622	2	-0.987	0.988	70,118,927	70,120,798
3	74,244,857	74,252,179	22	-0.999	1.000	74,245,958	74,245,999
3	85,227,579	85,234,887	3	-0.997	0.997	85,227,579	85,234,065
3	86,148,266	86,564,337	347	-0.962	0.967	86,148,266	86,148,297
3	121,237,846	121,238,918	1	-0.988	0.988	121,237,846	121,238,918
3	132,703,955	132,985,912	159	-0.975	0.960	132,703,955	132,705,246
3	142,024,302	142,033,075	4	-0.998	0.998	142,031,085	142,033,075
3	177,291,534	177,292,847	4	-0.998	0.998	177,292,372	177,292,847
3	185,348,130	185,361,895	6	-0.994	0.993	185,348,130	185,349,449
3	197,508,910	197,520,026	8	-0.978	0.978	197,516,831	197,517,417
3	200,569,370	200,578,128	3	-0.998	0.998	200,569,370	200,569,687
4	2,500,770	2,507,786	4	-0.998	0.998	2,500,770	2,501,514
4	3,089,615	3,103,452	4	-0.999	0.999	3,089,615	3,090,230
4	4,298,295	4,301,190	3	-1.000	1.000	4,298,295	4,299,514
4	10,354,453	10,367,367	4	-0.978	0.978	10,366,254	10,367,367
4	15,663,521	15,688,189	3	-0.978	0.978	15,663,521	15,677,192
4	20,229,292	20,247,432	9	-1.000	1.000	20,229,292	20,229,516
4	24,718,463	24,856,347	210	-0.976	0.975	24,775,244	24,776,150
4	39,665,542	40,467,976	449	-0.974	0.967	39,913,017	39,916,859
4	41,781,860	41,785,929	1	-1.000	1.000	41,781,860	41,785,929
4	48,773,524	48,817,372	52	-0.963	0.963	48,773,524	48,775,085
4	75,178,722	75,186,828	8	-0.979	0.979	75,178,722	75,179,195
4	141,008,512	141,014,993	15	-0.998	0.998	141,008,512	141,008,719
4	156,323,245	156,333,670	5	-0.998	0.999	156,331,080	156,333,670
4	158,337,336	158,341,381	1	-1.000	1.000	158,337,336	158,341,381
4	161,087,122	161,132,435	21	-0.998	1.000	161,118,934	161,120,248
4	162,865,294	162,943,956	30	-1.000	1.000	162,865,294	162,870,491
4	182,892,346	182,894,453	3	-1.000	1.000	182,892,346	182,892,709
4	184,610,507	184,613,308	2	-1.000	1.000	184,610,507	184,612,326
4	188,814,505	189,494,515	662	-0.999	0.975	188,814,505	188,814,869
4	188,828,730	189,982,900	1102	-0.993	0.977	188,828,730	188,831,679
5	1,207,806	1,227,381	24	-0.980	0.981	1,216,819	1,216,891
5	9,435,698	9,675,237	183	-0.996	1.000	9,435,698	9,441,227
5	11,484,840	11,492,310	7	-1.000	1.000	11,484,840	11,485,372
5	26,469,132	26,489,893	23	-0.999	0.991	26,472,906	26,473,860
5	30,983,042	30,984,782	1	-0.999	0.999	30,983,042	30,984,782
5	32,738,776	33,020,902	232	-0.964	0.964	32,744,478	32,746,008
5	37,697,810	37,698,911	2	-1.000	1.000	37,697,810	37,698,828
5	57,578,570	57,583,039	3	-0.994	0.994	57,580,750	57,583,039
5	57,991,361	57,993,707	2	-1.000	1.000	57,991,361	57,993,641
5	89,288,464	89,300,483	7	-1.000	1.000	89,288,464	89,288,953
5	91,723,109	91,725,227	1	-0.999	0.999	91,723,109	91,725,227
5	159,475,021	159,856,976	345	-0.978	0.970	159,475,021	159,477,274
5	162,106,063	162,108,625	4	-0.996	0.997	162,108,514	162,108,625
5	169,241,432	169,258,577	8	-0.994	0.992	169,241,432	169,245,488

5	179,608,944	179,612,841	7	-0.976	0.976	179,608,944	179,608,986
5	179,682,248	179,701,293	32	-1.000	1.000	179,682,248	179,682,378
5	182,141,565	182,144,226	1	-1.000	1.000	182,141,565	182,144,226
6	11,280,722	11,308,816	38	-0.997	0.999	11,307,354	11,308,816
6	24,171,606	24,188,963	11	-0.996	0.996	24,171,606	24,176,223
6	25,590,757	25,591,956	3	-1.000	1.000	25,590,757	25,591,148
6	49,982,712	49,985,257	5	-0.999	0.999	49,982,712	49,983,017
6	50,019,651	50,025,220	6	-1.000	1.000	50,019,651	50,021,033
6	87,013,116	87,015,061	4	-1.000	1.000	87,013,116	87,013,231
6	88,992,489	89,001,287	4	-0.997	0.996	88,992,489	88,993,665
6	95,469,655	95,485,337	7	-1.000	1.000	95,469,655	95,470,265
6	115,064,540	115,068,904	2	-1.000	1.000	115,064,540	115,067,571
6	137,998,852	138,016,767	9	-0.999	0.999	137,998,852	138,002,791
6	150,889,020	150,892,950	4	-0.996	0.996	150,889,020	150,891,772
6	154,338,020	154,358,157	4	-0.996	0.996	154,352,405	154,358,157
6	166,338,755	166,343,442	3	-0.997	0.997	166,338,755	166,342,194
6	168,070,094	168,082,178	7	-1.000	1.000	168,070,094	168,071,497
6	169,556,636	169,556,711	1	-0.999	0.999	169,556,636	169,556,711
6	170,073,085	170,078,301	1	-0.994	0.994	170,073,085	170,078,301
6	170,724,621	171,543,928	741	-0.977	0.976	170,941,291	170,942,186
7	6,348,527	6,352,997	9	-1.000	1.000	6,349,119	6,350,365
7	10,518,784	10,525,782	22	-1.000	1.000	10,518,784	10,518,838
7	11,118,540	11,124,248	4	-0.999	0.999	11,123,929	11,124,248
7	17,610,007	17,620,761	6	-1.000	1.000	17,610,007	17,610,755
7	18,024,956	18,187,484	286	-0.966	0.967	18,048,551	18,049,586
7	27,898,891	27,904,612	2	-0.994	0.994	27,898,891	27,900,811
7	29,814,810	29,857,164	27	-1.000	1.000	29,814,810	29,816,242
7	48,381,636	48,385,193	2	-1.000	1.000	48,382,039	48,385,193
7	83,908,479	83,913,525	4	-1.000	1.000	83,908,479	83,911,625
7	95,211,027	95,217,794	12	-0.995	0.995	95,211,027	95,211,094
7	116,110,106	116,133,811	10	-1.000	1.000	116,110,106	116,110,387
7	122,192,431	122,194,741	4	-0.999	0.999	122,192,431	122,192,646
7	125,330,999	126,607,072	1277	-0.975	0.978	125,452,698	125,455,673
7	126,632,267	128,599,126	1953	-0.976	0.977	128,023,685	128,024,122
7	147,977,909	147,978,614	1	-1.000	1.000	147,977,909	147,978,614
7	148,707,594	148,709,325	1	-0.997	0.997	148,707,594	148,709,325
7	151,615,969	151,618,325	3	-1.000	1.000	151,615,969	151,617,049
7	152,625,222	154,462,036	1796	-1.000	1.000	152,625,222	152,625,531
7	155,141,874	155,225,328	5	-0.999	1.000	155,141,874	155,143,159
7	156,128,902	156,141,973	44	-1.000	0.994	156,128,902	156,129,105
7	158,724,978	159,504,421	346	-0.997	0.999	158,724,978	158,725,451
8	986,839	1,030,283	52	-0.977	0.979	1,029,306	1,030,283
8	4,919,749	4,923,013	3	-0.999	0.999	4,919,749	4,920,055
8	6,967,967	7,471,114	57	-0.994	0.994	7,065,104	7,071,705
8	15,499,679	15,501,791	3	-1.000	1.000	15,499,679	15,500,504
8	15,510,115	15,878,897	441	-1.000	0.999	15,510,115	15,510,176
8	19,222,264	19,337,976	101	-0.960	0.960	19,222,264	19,222,412
8	32,422,762	32,433,044	8	-0.982	0.983	32,432,277	32,432,595
8	63,141,750	63,145,920	1	-1.000	1.000	63,141,750	63,145,920
8	63,290,289	63,291,205	1	-0.995	0.995	63,290,289	63,291,205
8	72,975,276	73,013,850	6	-1.000	1.000	72,975,276	72,977,861
8	120,149,417	120,187,411	28	-0.998	0.998	120,186,150	120,187,411
8	121,409,215	121,410,736	2	-0.984	0.983	121,409,215	121,409,801
8	124,290,396	124,294,306	4	-1.000	1.000	124,290,396	124,292,755
8	126,193,232	126,197,187	3	-1.000	1.000	126,193,232	126,194,835
8	131,206,217	131,209,574	4	-1.000	1.000	131,206,217	131,206,365
8	139,474,158	139,500,818	3	-0.996	0.997	139,474,158	139,500,458
8	139,879,142	139,900,186	14	-1.000	1.000	139,879,142	139,885,625
8	140,298,573	140,305,002	5	-1.000	1.000	140,298,573	140,301,933
8	141,347,153	141,354,119	2	-0.986	0.986	141,347,153	141,353,714
9	1,630,657	1,632,255	4	-0.991	0.992	1,630,657	1,630,996
9	3,185,761	3,192,754	2	-1.000	1.000	3,185,761	3,190,995

9	8,547,633	8,552,723	4	-1.000	1.000	8,547,633	8,550,262
9	13,650,075	13,665,508	16	-0.981	0.981	13,650,075	13,652,525
9	15,412,781	15,421,385	6	-0.990	0.991	15,412,781	15,414,318
9	24,968,658	24,973,175	2	-0.999	0.999	24,968,658	24,973,001
9	38,037,339	38,047,730	6	-1.000	1.000	38,037,339	38,038,446
9	39,233,243	39,251,670	19	-1.000	1.000	39,233,243	39,245,318
9	72,105,270	72,119,751	8	-0.978	0.977	72,105,270	72,105,818
9	72,880,818	72,881,965	1	-0.997	0.997	72,880,818	72,881,965
9	84,405,173	84,553,033	42	-0.954	0.954	84,405,173	84,405,780
9	84,485,350	85,071,626	257	-0.976	0.978	85,069,351	85,071,626
9	87,478,946	87,485,326	5	-0.993	0.993	87,478,946	87,482,721
9	100,004,771	100,005,957	1	-1.000	1.000	100,004,771	100,005,957
9	102,514,218	102,518,009	2	-1.000	1.000	102,514,218	102,515,853
9	106,248,206	106,254,268	4	-1.000	1.000	106,248,206	106,248,801
9	111,564,592	113,535,279	1769	-0.977	0.976	112,601,613	112,606,051
9	112,561,842	114,326,330	1553	-1.000	0.978	112,561,842	112,562,684
9	118,179,365	118,180,446	1	-1.000	1.000	118,179,365	118,180,446
9	119,054,671	119,055,135	1	-0.998	0.998	119,054,671	119,055,135
9	135,425,172	135,431,122	9	-0.979	0.979	135,425,172	135,426,412
9	136,358,512	136,398,419	17	-0.996	0.996	136,358,512	136,366,092
10	1,550,828	1,570,130	10	-1.000	1.000	1,550,828	1,556,164
10	2,095,159	2,142,015	75	-0.963	0.962	2,142,006	2,142,015
10	6,080,764	6,082,588	2	-0.997	0.997	6,080,764	6,082,529
10	14,568,985	14,569,761	2	-1.000	1.000	14,569,750	14,569,761
10	24,570,527	24,573,942	2	-1.000	1.000	24,573,321	24,573,942
10	25,196,003	25,199,949	7	-1.000	1.000	25,196,003	25,197,292
10	32,567,348	32,575,395	5	-1.000	1.000	32,567,348	32,568,159
10	50,544,017	50,544,339	1	-0.997	0.997	50,544,017	50,544,339
10	51,866,159	51,867,113	2	-0.999	0.999	51,866,159	51,866,958
10	60,290,608	60,302,988	10	-1.000	1.000	60,293,054	60,294,194
10	69,633,400	70,566,132	890	-0.969	0.969	69,633,697	69,638,220
10	70,918,199	71,533,704	326	-0.966	0.966	71,260,580	71,271,582
10	71,596,405	73,473,633	761	-0.978	0.975	73,421,810	73,422,586
10	77,188,862	77,190,553	3	-0.985	0.985	77,188,862	77,189,761
10	80,374,734	80,377,416	1	-0.999	0.999	80,374,734	80,377,416
10	87,574,089	87,574,122	1	-0.989	0.989	87,574,089	87,574,122
10	107,082,724	107,085,601	3	-1.000	1.000	107,082,724	107,082,969
10	121,019,435	121,035,196	21	-1.000	1.000	121,019,435	121,021,259
10	124,841,359	124,849,049	10	-1.000	1.000	124,841,359	124,841,676
10	128,110,535	128,121,899	8	-0.998	1.000	128,112,828	128,114,799
10	131,844,159	131,847,627	2	-1.000	1.000	131,844,159	131,847,244
11	1,628,694	1,640,720	2	-0.996	0.996	1,628,694	1,637,294
11	5,327,400	5,332,510	4	-0.982	0.982	5,327,400	5,327,766
11	11,850,457	11,851,616	2	-0.997	0.997	11,850,782	11,851,616
11	16,946,887	16,953,966	5	-0.997	0.997	16,948,707	16,948,997
11	19,630,509	19,639,213	6	-0.995	0.995	19,630,509	19,630,788
11	20,776,287	20,777,212	1	-0.976	0.976	20,776,287	20,777,212
11	50,342,265	50,362,743	4	-1.000	1.000	50,350,914	50,362,743
11	68,637,033	68,641,770	1	-0.983	0.983	68,637,033	68,641,770
11	78,104,016	78,105,320	1	-0.999	0.999	78,104,016	78,105,320
11	85,074,016	85,074,353	1	-1.000	1.000	85,074,016	85,074,353
11	97,336,887	97,338,397	1	-0.995	0.995	97,336,887	97,338,397
11	112,109,174	112,114,033	4	-1.000	1.000	112,109,174	112,111,226
11	123,752,898	123,753,678	1	-0.997	0.997	123,752,898	123,753,678
11	125,355,248	125,372,269	14	-1.000	0.996	125,355,248	125,355,448
11	127,644,015	127,647,225	6	-1.000	1.000	127,644,015	127,644,977
11	131,324,185	131,334,934	14	-0.998	0.999	131,334,632	131,334,934
12	4,180,102	4,182,105	1	-0.985	0.985	4,180,102	4,182,105
12	15,774,545	15,777,073	2	-0.996	0.996	15,774,545	15,776,103
12	18,094,718	18,097,239	2	-0.999	0.999	18,094,718	18,095,370
12	25,910,632	25,924,647	1	-0.996	0.996	25,910,632	25,924,647
12	28,370,026	28,372,830	2	-0.987	0.986	28,370,026	28,371,507

12	47,957,583	47,961,545	2	-1.000	1.000	47,957,583	47,958,784
12	66,947,512	66,953,217	2	-1.000	1.000	66,947,512	66,952,973
12	95,614,649	95,616,866	1	-0.999	0.999	95,614,649	95,616,866
12	114,699,794	114,836,494	146	-0.967	0.962	114,699,794	114,701,048
12	116,185,494	116,188,813	1	-0.992	0.992	116,185,494	116,188,813
12	118,279,231	118,290,508	3	-0.968	0.968	118,289,910	118,290,508
12	122,493,091	122,529,899	12	-0.983	0.983	122,493,091	122,493,701
12	128,913,891	128,928,060	5	-0.999	0.999	128,926,781	128,928,060
12	130,360,229	130,374,202	12	-1.000	1.000	130,360,229	130,363,001
12	131,161,351	131,166,882	4	-0.998	0.998	131,161,351	131,162,265
12	131,929,345	131,935,511	5	-0.988	0.988	131,929,345	131,929,484
12	132,126,689	132,250,526	48	-0.958	0.958	132,126,689	132,127,813
13	21,303,955	21,306,162	2	-0.991	0.991	21,303,955	21,304,218
13	22,262,931	22,280,126	13	-1.000	1.000	22,262,931	22,263,066
13	22,395,101	22,426,767	11	-1.000	1.000	22,395,101	22,396,003
13	22,583,790	22,716,640	168	-0.999	0.999	22,583,790	22,585,337
13	30,283,145	30,305,683	14	-1.000	1.000	30,283,145	30,287,102
13	33,796,020	34,073,185	261	-0.976	0.975	33,952,204	33,955,121
13	36,248,915	36,249,663	2	-0.999	0.999	36,248,915	36,249,219
13	36,872,783	36,880,639	3	-0.996	0.996	36,872,783	36,875,145
13	70,421,599	70,422,544	2	-1.000	1.000	70,421,599	70,422,096
13	71,439,829	71,448,385	4	-0.996	0.996	71,439,829	71,444,213
13	83,670,502	83,683,804	6	-0.992	0.990	83,670,502	83,674,431
13	103,542,652	103,543,465	1	-1.000	1.000	103,542,652	103,543,465
13	103,974,684	103,978,881	6	-0.999	0.998	103,974,684	103,975,047
13	106,713,059	106,716,421	4	-0.998	0.998	106,715,494	106,716,421
13	107,410,781	107,421,913	7	-0.990	0.990	107,410,781	107,411,080
14	21,417,432	21,419,074	2	-0.994	0.994	21,417,432	21,418,964
14	24,110,324	24,119,076	5	-1.000	1.000	24,118,025	24,119,076
14	37,436,483	37,450,131	3	-0.995	0.995	37,437,723	37,450,131
14	49,000,662	49,010,576	10	-0.998	0.998	49,000,662	49,001,752
14	57,997,106	57,998,548	1	-1.000	1.000	57,997,106	57,998,548
14	79,296,411	79,334,909	30	-0.999	0.999	79,296,411	79,296,491
14	85,259,381	85,312,417	66	-0.970	0.970	85,259,381	85,259,546
14	86,114,011	86,131,903	11	-0.983	0.983	86,114,011	86,115,268
14	95,043,537	95,057,965	14	-0.998	0.998	95,043,537	95,050,747
14	98,975,276	98,982,594	3	-1.000	1.000	98,975,276	98,975,956
14	99,319,164	99,324,279	8	-1.000	1.000	99,319,164	99,319,497
14	103,562,145	103,565,978	2	-1.000	1.000	103,562,145	103,563,824
14	104,878,950	104,908,741	14	-0.997	0.973	104,879,756	104,883,375
14	105,696,342	106,073,865	8	-0.989	0.988	105,696,342	105,696,442
15	21,711,253	21,823,866	5	-0.999	0.999	21,711,253	21,711,308
15	23,594,695	23,596,739	3	-0.998	0.999	23,596,163	23,596,739
15	24,264,401	24,265,361	2	-0.995	0.995	24,264,401	24,264,433
15	24,562,663	25,760,679	1255	-1.000	1.000	24,567,412	24,569,016
15	26,768,065	28,268,032	657	-1.000	1.000	26,768,065	26,768,543
15	50,694,698	50,699,905	5	-1.000	1.000	50,694,698	50,695,125
15	51,302,142	51,302,235	1	-0.997	0.997	51,302,142	51,302,235
15	55,513,899	55,518,680	1	-1.000	1.000	55,513,899	55,518,680
15	79,724,888	79,736,648	1	-1.000	1.000	79,724,888	79,736,648
15	85,564,910	85,571,575	2	-1.000	1.000	85,564,910	85,570,701
15	85,966,499	85,980,375	17	-0.998	0.998	85,966,499	85,968,201
15	86,858,229	86,866,038	1	-0.964	0.964	86,858,229	86,866,038
15	93,564,445	93,573,691	4	-1.000	1.000	93,570,581	93,572,961
15	98,818,827	98,822,189	2	-0.994	0.994	98,818,827	98,821,952
16	5,504,705	5,516,929	9	-1.000	1.000	5,515,494	5,516,929
16	5,963,271	6,079,635	218	-0.979	0.975	5,963,271	5,963,583
16	15,870,897	15,883,685	6	-0.991	0.994	15,878,790	15,883,685
16	19,851,052	19,857,413	8	-0.986	0.985	19,851,052	19,851,464
16	21,219,984	21,292,281	6	-0.998	0.999	21,219,984	21,220,717
16	24,101,033	24,102,096	1	-1.000	1.000	24,101,033	24,102,096
16	61,521,752	61,522,839	2	-1.000	0.999	61,521,752	61,521,759

16	75,816,898	75,826,704	14	-0.999	0.999	75,821,970	75,823,276
16	86,506,963	86,519,459	16	-1.000	1.000	86,506,963	86,507,557
16	86,517,647	86,977,729	574	-1.000	0.999	86,517,647	86,517,785
16	87,864,576	87,982,384	2	-1.000	1.000	87,864,576	87,864,652
16	88,778,616	88,803,628	16	-0.964	0.964	88,798,124	88,798,185
17	1,069,486	1,132,504	24	-0.977	0.976	1,069,486	1,069,815
17	5,131,101	5,141,770	3	-1.000	1.000	5,131,101	5,134,242
17	5,653,386	5,656,808	2	-1.000	1.000	5,653,760	5,656,808
17	10,959,640	10,960,625	1	-0.998	0.998	10,959,640	10,960,625
17	11,705,627	12,013,909	56	-0.966	0.966	11,901,554	11,905,051
17	21,669,817	21,888,620	200	-0.983	0.977	21,851,196	21,859,777
17	24,061,686	24,080,243	6	-1.000	1.000	24,061,686	24,063,441
17	25,958,292	26,026,148	5	-0.977	0.977	25,980,835	25,982,718
17	53,542,771	53,872,457	324	-0.999	1.000	53,547,612	53,549,162
17	56,137,142	56,138,067	1	-1.000	1.000	56,137,142	56,138,067
17	65,298,000	65,311,245	3	-0.999	0.998	65,298,000	65,308,827
17	66,410,587	66,421,225	2	-0.998	0.998	66,410,587	66,411,932
17	67,719,145	67,722,916	4	-0.997	0.997	67,722,699	67,722,916
17	70,759,627	70,775,877	4	-0.981	0.981	70,759,627	70,767,324
17	79,826,290	79,887,923	29	-0.997	0.997	79,882,473	79,887,923
18	11,489,750	11,493,081	5	-1.000	1.000	11,489,750	11,490,819
18	25,156,004	25,175,957	26	-1.000	1.000	25,156,004	25,157,365
18	40,745,438	42,378,985	1347	-0.976	0.976	41,914,466	41,915,365
18	48,029,093	48,029,879	3	-0.987	0.988	48,029,736	48,029,879
18	51,492,618	51,501,041	3	-0.999	1.000	51,492,618	51,493,288
18	52,473,212	52,494,366	3	-1.000	1.000	52,489,432	52,494,366
18	55,140,378	55,436,867	403	-0.975	0.976	55,262,488	55,266,856
18	62,064,893	62,155,555	83	-0.958	0.982	62,154,982	62,155,555
19	2,681,193	3,137,975	200	-0.997	0.999	2,681,193	2,698,033
19	7,580,557	7,706,046	30	-0.995	0.994	7,612,904	7,613,057
19	20,270,797	20,303,241	19	-0.976	0.976	20,270,797	20,271,532
19	20,983,112	21,277,349	72	-0.973	0.972	20,996,946	20,997,874
19	38,524,709	38,526,386	2	-1.000	1.000	38,524,709	38,525,313
19	38,992,349	39,001,410	3	-0.999	0.999	38,994,650	39,001,410
19	45,745,329	45,748,959	1	-1.000	1.000	45,745,329	45,748,959
19	48,860,884	49,495,518	530	-0.967	0.965	48,860,884	48,862,177
19	56,321,034	56,332,147	5	-0.993	0.993	56,330,078	56,332,147
19	57,677,450	57,683,042	1	-1.000	1.000	57,677,450	57,683,042
19	60,519,669	60,528,783	3	-1.000	1.000	60,526,396	60,527,258
19	63,013,741	63,021,692	3	-1.000	1.000	63,013,741	63,015,210
20	4,482,749	4,499,234	3	-0.982	0.982	4,482,749	4,483,827
20	10,650,821	10,661,001	12	-1.000	1.000	10,659,826	10,661,001
20	11,931,267	11,996,018	78	-0.972	0.973	11,932,461	11,935,635
20	16,153,388	16,155,018	3	-1.000	1.000	16,153,388	16,154,403
20	18,293,048	18,375,219	37	-0.999	1.000	18,293,048	18,294,679
20	30,566,844	30,568,578	1	-1.000	1.000	30,566,844	30,568,578
20	41,116,748	41,127,580	3	-0.985	0.985	41,116,748	41,124,541
20	50,636,037	50,660,509	6	-0.992	0.992	50,659,279	50,660,509
20	53,565,192	53,579,405	8	-0.988	0.988	53,565,192	53,567,667
20	54,825,130	54,834,441	2	-0.998	0.999	54,825,130	54,832,167
20	56,280,471	56,288,277	4	-1.000	1.000	56,280,471	56,282,811
21	2,545,817	2,581,042	61	-0.966	0.968	2,545,817	2,546,686
21	9,989,585	10,006,121	8	-0.992	0.993	9,989,585	9,990,297
21	12,259,502	12,341,005	46	-0.958	0.958	12,259,502	12,259,637
21	17,040,828	17,177,593	162	-0.976	0.975	17,053,649	17,060,743
21	18,231,829	18,257,703	10	-0.976	0.976	18,254,349	18,257,703
21	21,630,893	21,638,700	9	-0.999	0.999	21,630,893	21,632,219
21	29,214,839	29,216,887	1	-1.000	1.000	29,214,839	29,216,887
21	30,545,515	30,552,622	2	-1.000	1.000	30,545,515	30,549,947
22	24,981,166	24,987,525	6	-0.997	0.997	24,981,166	24,981,439
22	31,809,221	31,817,286	3	-0.975	0.976	31,809,335	31,812,362
22	33,534,835	33,539,704	6	-0.996	0.995	33,534,835	33,536,131

22	34,825,691	34,827,264	1	-0.995	0.995	34,825,691	34,827,264
22	37,757,408	37,775,107	3	-0.998	0.998	37,757,408	37,760,872
22	41,001,347	41,012,097	4	-0.994	0.993	41,001,347	41,002,758
22	45,810,157	45,816,503	3	-0.997	0.997	45,810,157	45,810,593
22	47,481,333	47,488,195	2	-0.999	0.999	47,481,333	47,485,269
22	48,279,741	48,280,534	1	-1.000	1.000	48,279,741	48,280,534
22	49,572,377	49,575,651	1	-1.000	1.000	49,572,377	49,575,651

Table S3: The distribution of cross-over breakpoint resolutions. Breakpoint regions were defined as the sequence range containing the 95% credible interval spanning transmission vector switchpoints. Furthermore a 'best guess' range was calculated as the two consecutive sites with the largest change in the posterior probability. This table includes complex events that were resolved over > 1Mb.

	Break point length distribution (bases)				
Interval range percentile	2.50%	20%	50%	80%	97.50%
95% credible interval	754	2,555	8,752	49,328	1,260,462
Best guess SNV interval	54	331	1,230	3,149	10,633

Table S4: Cross-overs detected across five contigs on the pseudoautosomal region (PAR) each with length greater than 20 kb. The panTro3 PAR coordinates were defined as the the interval syntenic with the location of PAR1 in GRCh37 (through liftOver). For children D - I, the number of female (F) and male-specific (M) crossovers are recorded. *# POLY.* records the number of sites that pass filters and are polymorphic. *# MENDEL INCONSISTENT* records the number of sites that are not consistent with Mendel transmission. *LLK TRANS. VEC.* records the log-likelihood of the maxiumum likelihood transmission vector for that contig. *PROP. CONSISTENT W. TRANS. VEC.* represents and the proportion of sites that are consistent with the maximum likelihood transmission vector.

	Contig start (bp)	Contig end (bp)	Number of cross-overs												# POLY.	# MENDEL INCONSISTENT	LLK TRANS. VEC.	PROP. CONSISTENT W. TRANS. VEC
			D		E		F		G		H		I					
			F	M	F	M	F	M	F	M	F	M	F	M				
Contig 1	255,281	277,028													35	0	-3.30	0.94
Contig 2	676,430	700,287				1								1	57	3	-11.80	0.96
Contig 3	2,011,989	2,035,462												1	58	2	-2.13	1.00
Contig 4	2,330,840	2,391,726								1					172	3	-1.15	1.00
Contig 5	2,519,951	2,541,818							1						53	0	-1.51	0.90
Total cross-overs			0	0	0	1	0	0	1	1	0	0	0	2				

Table S5: Sex-specific genetic distance across the pseudo-autosomal region in chimpanzees and humans. Chimpanzee values are calculated using Kosambi mapping function, human values are calculated as the weighted average of studies, which were each computed using the identity mapping function [38-40]. Rates are calculated using the total sequence for PAR1 in human GRCh37 and their liftover to panTro3 coordiantes in chimpanzee. (^) : value from [17].

	Western chimpanzee		Human	
	Distance (cM)	Rate (cM/Mb)	Distance (cM)	Rate (cM/Mb)
PAR male-specific	34.657	16.085	49.528	18.764
PAR female-specifc	8.664	3.217	4.06	1.538
Autosome sex-average		1.28		1.55^

Table S6: Listed are the de novo mutation candidates detected across the pedigree. Locations are defined according to panTro3. Two quality metrics are presented: *pDepth* - the within-chunk combined depth percentile and *p.AB* - the significance for deviation from the expected allele balance given the observed combined coverage. *Sequence context* represents the observed mutated allele flanked by 25 bases of surrounding sequence. *Allele0* and *Allele1* represent the reference and mutant alleles repectively. *Parental origin* indicates the inferred phase of the mutation (both direct read-based and transmission based phasing). *is.cpg* is an indicator variable marking mutations at CpGs. *is.suspicious* is an indicator variable recording our manual curation of the candidates.

Chr	Pos (bp)	p.Depth	p.AB	Sequence context	Allele0	Allele1	Recipient individual	Parental origin	is.cpg	is.validated	is.suspicious
chr1	2700783	0.67	0.96	GGCTTACGTCCGGGGCGGTCCAGCGCGCCCAGGAGCCGGCGAGCTCTCAAT	C	T	E	0	1	0	0
chr1	9649394	0.84	0.22	AGCTGGAATGGTGAGACCAACATCCGTGACACCTGGACTCTTTCAGGTTCT	G	A	D	0	1	0	0
chr1	10890395	0.60	0.98	TCCCCGGAGGCCTTGCAGGAGTGCACGAACCCCTCCCCTCCTGCCTCCCAA	C	T	D	0	1	0	0
chr1	12044708	0.78	0.51	ctctttagatcgtataaatctttcgccttttactaaagatttccgtggaga	C	T	F	PATERNAL	0	0	0
chr1	14537407	0.10	0.95	GATCATATGCAGGACAGAGTATGCAATCCATtaggatgtcatggcctgttt	A	G	D	0	0	0	0
chr1	43336084	0.27	0.29	catgagatatttatgagccaaaagagacagataactcttggtgactgacag	G	A	H	0	0	0	0
chr1	47564020	0.47	0.12	CCTTCTCTACttttttttattttttaatagagacagggtcttactatgttgc	A	G	D	0	0	0	0
chr1	50448804	0.78	0.23	TTGTTCACCAGTTGTAAGTCCTATTGGGGGTAACTGTTCATGTGATTTGTC	G	T	I	0	0	0	0
chr1	73296334	0.65	0.56	cATGCACATGTTCAATTGTTTCATATTGTTCATACCAGTAGGCTAGGTTAT	T	C	I	0	0	0	0
chr1	88113479	0.43	0.74	tagaattatctagtattagacttctaccttgtttctaagtatagaaattac	A	G	H	0	0	0	0
chr1	100011899	0.88	0.05	tactgtacctttctatgttcagatatgtgtagctacatcatgcttaccat	A	G	H	PATERNAL	0	0	0
chr1	124787048	0.07	0.55	CTTCCATCTCAACCAGACAGGCCCCCGCCCTGAGACAGTGTTGCTACCCCC	C	T	H	0	1	0	0
chr1	130945113	0.29	0.23	CCACGCAAGTTAGAAGCATCTGATAATGGAGATTTGAGGGTTGGGGCTGTT	A	G	E	0	0	1	0
chr1	133753133	0.49	0.19	cggctcactgcaagttccgcctcccgggttcatgccattctcctgcctcag	G	A	I	0	1	0	0
chr1	136785165	0.23	0.70	TGTTGATTCAGATGAGAGTTTCTATCTCAAGGCAGCTTCCCTCTCATTTGC	C	A	E	0	0	1	0
chr1	141345608	0.77	0.04	accagtgccttgctcagttagtgaccgataaaatcatctgttattactGTG	C	A	I	0	1	0	1
chr1	141346025	0.38	0.95	atCGACGAAACAGGAATCAAactgccaactctgctaactggtctccctgct	C	T	I	0	0	0	1
chr1	143564354	0.58	0.06	AAGATTCAGGACCTTGGGGAGAGCATTTATTAATGGAAGCTATAGATGGCC	T	C	E	0	0	1	0
chr1	158831324	0.64	0.97	TAAGGGCAATTTCAAAAGAACAGTACTGACCATTATGGCTTAAGACTCATA	C	T	D	0	0	0	0
chr1	161971490	0.57	0.40	cccatctaattattatttttttttgtagagatgaggtctccctatgttgcc	T	C	G	0	0	0	0
chr1	173030464	0.00	0.21	CGGCTCTTTAACAAATACCAGAGAAACAGAAATAGCCTTTAATAAAGTTCA	A	G	F	PATERNAL	0	0	0
chr1	180953269	0.11	0.04	GGCCCAGGCCAGTGCCTGGCTGGACGGTGAGTCCCCGCTGGTGGGGAGCAG	G	A	F	PATERNAL	1	0	0
chr1	199424919	0.08	0.08	TGAAATTATAAATGCATGTGTCCACTTTAGTATGCAATGCCTGTGAGGTTT	T	C	F	PATERNAL	0	1	0
chr1	209989089	0.66	0.71	GGGGCTAACTGAAAGAAAAATTCTTCCAGATTATAAGAAGAAACTCAGGGG	C	A	D	PATERNAL	0	0	0
chr10	23138612	0.25	0.45	cacgtgcctagcactgaaatcaatacgcagaatatcagccgcatctcagaa	C	T	G	0	1	0	0
chr10	37391479	0.68	0.02	TGATTTAATTTTTCCTCCTGTTCTATTTCTTCAGTAAACCTGGCAATAGT	A	G	I	0	0	0	0
chr10	57652821	0.77	0.74	ttcaaggtcatcatatgagactagcattattatatctatttcacctaatag	A	C	E	0	0	1	0
chr10	60154190	0.73	0.49	CTTTTTCAAAGATTATGCTACTGGTGCTAATTATTATCTCTCTGTGTGGGT	G	C	D	0	0	0	0
chr10	60351464	0.44	0.54	tcctccagctttgtatataataaacagtgctctcagagacatccctgaag	C	G	D	0	0	0	0
chr10	63206713	0.11	0.37	TCCTATCCCTGCCTGAAAAGGGCTCACATATAACTATCTCAGCTTTCTGGG	A	G	D	0	0	0	0
chr10	80306438	0.56	0.21	tgttgaccggaagccttaccaataacatatagtcgattaacacatatgttg	C	T	E	0	0	1	0
chr10	104051224	0.91	0.35	aacctttagaactataatttcctcacttgtaaaatgggagtaagaatgtc	A	G	H	0	0	0	0
chr10	114595820	0.72	0.76	agatcaatttggagagtattatcctcttaatcaatttggagagtattatct	C	T	H	0	0	0	0
chr10	115657549	0.47	0.06	GTGGCTCCCCTGCTAGGTTAAAACAGACCTATGATGCTTCCATGTGGACAG	G	A	H	MATERNAL	0	0	0
chr10	120057414	0.56	0.28	TCAGTCACATAAAAATGTAGAGCAGGCTGTTTGCAGTCTCCTTTAGGGCTC	G	A	E	0	0	1	0
chr11	18072619	0.33	0.97	TGTggccagagtaggaagatcactgaggccataagtttgaggctgtagtat	A	G	D	0	0	0	0
chr11	24359728	0.96	0.03	attttgaaatatccatctacaactgcatttgtttttgttattttaacggtc	C	T	E	0	0	1	0
chr11	40682961	0.31	0.88	cacttcctgacttcaaaacatattacaaaggtatggtaattaaaatagtat	C	A	D	PATERNAL	0	0	0
chr11	40996823	0.25	0.46	GCCCTTTTTTAGCAGCCTTCTTTTACGATGGCACACATCCTTAAAAATCTA	C	T	H	0	1	0	0
chr11	65829622	0.65	0.08	CCCCATGCTCAACAAGACCCCCTCAGTGGGGAATTCCTCATTGCAGAAGGG	G	A	I	0	0	0	0
chr11	76555883	0.62	0.27	AAAGGGATGATCAAGTGGCAGAGGAGGAGTTGTTAGCTGCTCATCAGGATG	G	A	F	PATERNAL	0	0	0
chr11	76630753	0.71	0.14	GGAAAAAACTAATTTCCCTTGGCACCTCACCAGGATCTACTTCATAGCTTG	C	G	I	0	0	0	0
chr11	84419450	0.45	0.87	TGGGATGAGTAGCAGAGGAGAGATGGAATGGGAGGAGTCCCATTTAGGTTG	G	A	F	MATERNAL	0	1	0
chr11	87881265	0.61	0.19	AATTGGGGTTGTTTTTAGTTTATATTTTTCTTTTTTCTCAGAGATCCTTGT	T	A	H	0	0	0	0
chr11	92012626	0.81	0.15	ACACTGCAAATCCTTGTTGAGTGAGCTCATGCATTTGCTATTATGGGaaga	C	T	G	PATERNAL	0	0	0
chr11	104757364	0.79	0.94	CAAATTTGTATTTAGCTTGAGAATTTAGAAGTTTCTAAAATAAAATTCAAA	T	C	D	0	0	0	0
chr11	120980025	0.87	0.52	attactttaaattcattttatttgtattattaatatattacatagtaagct	A	G	D	0	0	0	0
chr11	127434963	0.07	0.21	CTAGGGGGCGGAGGCGGGAATGTTGGTTGAGAAAGACTACCAAAATGTTAG	G	A	I	PATERNAL	0	0	0
chr11	131535324	0.42	0.43	atataaaagttgatatttatacttacagggtaacaaaatatcctaatcaat	C	T	I	0	0	0	0
chr12	21896743	0.35	0.33	ATCTTTCCCTGACAGTTGTACATACGTGCCCGACTCCCATTTTTCCCAGTC	G	A	D	0	1	0	0
chr12	34462218	0.96	0.99	gtattatttaaatttttctgttgccatagtttccaaatgctaaaaattta	A	G	D	0	0	0	0
chr12	67025713	0.59	0.29	caagatcaagatgctaatagatttcggtgtctagagaggggtgtttctca	G	A	G	0	1	0	0
chr12	76406428	0.04	0.89	gcaacctctgcctcccaggttcaagcgattctcctgcctcagcctcctcgg	C	T	F	PATERNAL	1	0	0
chr12	80105129	0.29	0.93	TCAGACCTTCAGATAAAGGAGCTCTCGAAATACAACCCATAAGGAATAAAG	C	T	D	PATERNAL	1	0	0
chr12	83875810	0.27	0.58	tgagagtttataaaagatggaataaaacagtaacattggttagagaaaaaa	A	T	H	PATERNAL	0	0	0
chr12	117682609	0.33	0.58	GGGTTCTTTTTAAACCATAAAACAGGAGGAGCTGAAGAAATGTGAGAATAT	G	A	I	0	0	0	0
chr12	132577953	0.55	0.09	cccaaatctcatgtccttacatttcgaaacaaatcatgccttcccaacagt	G	A	F	PATERNAL	1	0	0
chr13	21640458	0.19	0.08	CGGTTGCTTGTCTGTCCCCTGTAATTTCCCCGTCTCCATTTAGACAGCTGT	T	C	F	PATERNAL	0	1	0
chr13	33237421	0.46	0.62	tgcagaagctgaggccacaagagattaaacttctgagttaagttagtatgg	T	G	H	0	0	0	0
chr13	74837893	0.73	0.05	aatgtccacaagagaaagcaggaaagatctgaaatcgacaccctaacatca	G	A	H	0	0	0	0
chr13	76036621	0.05	0.58	TGGAAGCTCTCCTTCCTAAATTCTACCTGCCAAGCCACTGGCTCATGGAGA	C	T	F	PATERNAL	0	1	0
chr13	95270772	0.04	0.17	GCcctgcagcatgccatttctgggggtacagagacgaatataaaatgctc	G	C	E	0	0	1	0
chr13	105056913	0.92	0.44	TGTTCTCATATTAAATGGAGTTAAGAAAATCTAATTTTGAAAAAAATTGGC	A	G	F	MATERNAL	0	0	0
chr13	105786433	0.74	0.64	CATTGGATACACGCATAACAGTGAGCAAGTTTCTCAGCTCCTGCATGGCAG	C	A	I	0	0	0	0
chr13	112088768	0.82	0.30	TCTGATTGGGATGGCACTAAAATATGGGAACCCCCTCATCCCTCTAAATTT	G	A	I	PATERNAL	0	0	0
chr14	39651670	0.40	0.59	ACACTCTAAGCATTAGACTTTGCATCGataatatatataaaatatatttaa	C	T	E	0	1	0	0
chr14	65139282	0.31	0.38	accacactgcctcCAAGGGAACTGACGCATACATTGCAGGCTTTGTGGAAG	C	T	E	0	1	1	0
chr14	80717859	0.06	0.20	gacgtagaccttggtggtagctctgtgtacctgacagtggtggcaccctat	T	A	D	PATERNAL	0	0	0
chr14	83638347	0.44	0.47	ctctgaagcaatggccttgagttgtacattggccccttttggtctgggctgg	C	A	F	PATERNAL	0	1	0
chr14	87560743	1.00	0.17	ACCTAATAAGAATTTATGTGAAAATACTTTATAAATTTTGAAGCACTGTAA	A	G	F	PATERNAL	0	0	0
chr14	93410608	0.98	0.02	AAAGAAAAAGGTGTTAATTTCTGAGATGTCTACAGCCCTGAAATGGATGTG	A	C	G	PATERNAL	0	0	0
chr14	93462276	0.06	0.01	GGTGGAGACGGGCCAGCTGAACACCCCTGCCTAATTGGTGTCCCTCTGCTA	C	A	H	0	0	0	0
chr15	47051860	0.89	0.23	GACTAATGTAACAAAAATCTCCCCAATGAATTTCCCATAAAGAAGAGATAA	A	G	I	0	0	0	0
chr15	78798994	0.92	0.58	CACAATTAAAAACTATTACTAATTCGTATGACAGCAATGTAAGCATTGCAA	G	A	F	PATERNAL	1	0	0
chr15	85354878	0.16	0.10	CCCAAGATATCTCATTCTGGCAACGTCCAGCTCTTTCTAGAAAGAAAGAAT	T	C	F	PATERNAL	0	1	0
chr15	91802628	0.43	0.01	AGAGCCTTTCTTGGAGAAGGAAAAGCGTTTTCACAGTCCAGCTATAAGATA	C	T	E	MATERNAL	1	1	0
chr16	407650	0.02	0.48	cctctgtctccgggcccctgtctccgggcctctgtctccgggcctctgtct	G	A	G	0	1	0	0
chr16	13523624	0.90	0.00	CTATTTCCTCCTGGCTTGTGGTTGAGGTTTTAAGGATTCAGACATCCAGGA	G	C	F	PATERNAL	0	1	0
chr16	31618775	0.13	0.73	gtaatcaagatgaggGACTTCCAAGAGGAGTGCTGGCAATTAAGAGAGCTG	A	G	F	PATERNAL	0	1	0
chr16	48933243	0.11	0.37	tgtgcagggaaactccctttttataaatctatcagatctcatgagatttatt	A	G	D	0	0	0	0
chr16	50735389	0.93	0.00	AATGAGCCTCAGCACGCAGCAGCCCCGACATCAAACGCACTTGTGTTGTAA	C	T	E	0	1	1	0
chr16	57039898	0.69	0.89	CAGGgtggctcagaaggcagaattaggacaagtcaggaagggacagaagcc	G	T	D	0	0	0	0

chr16	57041959	0.34	0.12	TGTCCCATGACACCTGAGCCCAGACCTGGACTTTCCAACCAAGGCTCAACC	C	G	D	0	0	0	0
chr17	22915263	0.39	0.26	ccaggtggcacattagaaatcacctggagaacattaaaaaaaacatagatg	G	A	D	0	0	0	0
chr18	34126674	0.85	0.81	TTCatcagttatttattcctgtgtaacaaattaccacagacttaaaaatgt	A	G	D	0	0	0	0
chr18	43677840	0.89	0.40	ttaactatgcttgttaaagtttctagggtagccactaaaacgacagaacta	G	C	D	0	0	0	0
chr18	48940031	0.56	0.02	ACCTTTTGTAAAAGAAATAGGATTGATTGCTATAAATTGTCCAAAAGAGAA	A	G	G	0	0	0	0
chr18	68820360	0.80	0.40	gcagccatataaaacagaatgagatcacgtcctttgaaagcacatgggtggag	C	T	D	PATERNAL	1	0	0
chr19	3715608	0.63	0.16	GAGCCTTCCCTGAAATACTGCTCAGGGTCAAAACCGGGatccccgttttac	G	A	E	0	0	1	0
chr19	13923743	0.92	0.21	GAGAGGTGCTATCTTAGCCAGAACAGCTGGCTTGGTCTCTACTCTTTCAAA	G	T	I	0	0	0	0
chr19	15868291	0.46	0.94	GCACTTTTTTTTCTTATATTTCCCTCCACCCCTGAGATATGTCAACGGGCC	C	T	D	0	0	0	0
chr19	34447377	0.96	0.59	atgggaaaaaatttttgcagtctactcatctgacaaagggctaatatccag	T	C	I	0	0	0	0
chr19	41223300	0.27	0.49	CCAGGTGGTGCCCTGGGTTTGGGCTGGAAGTTTGGGCTCACCTCTGAATAC	G	A	F	PATERNAL	0	1	0
chr19	48224431	0.56	0.36	TTCTGGGTCCACAATGCTCCCTTCCCCCTGTAGAGGGCAGGTGAGGACCAT	C	T	H	0	0	0	0
chr20	5689405	0.56	0.88	tcccacctcagcctcctgagtagccgagactacaggcatgtaccaccatgc	G	A	D	0	1	0	0
chr21	12818564	0.81	0.90	taaatttttgacactcatttacattgttgcaggtatcatcattcatgttt	T	G	D	MATERNAL	0	0	0
chr22	45328207	0.91	0.98	aacataaaCATTTAAGACCTACATGGCAAAAGAGACCATTGAGTTAGAATA	G	T	I	PATERNAL	0	0	0
chr2A	12036323	0.30	0.12	aatgcagtggcacggtctcagctcactgcaacctccacctcccgggttcaa	C	A	E	PATERNAL	0	1	0
chr2A	18269979	0.03	0.62	AAAAGATATGAAATTATTCATCTAGGTAAGTTTCAGGACAGCCATCTAGGT	G	A	E	0	0	1	0
chr2A	27752205	0.07	0.22	CCTGATGAAAAGGAACTCCCTTCACTAGCAGATTTCCCCACTTCCTCTACA	T	C	E	0	0	1	0
chr2A	54969559	0.55	0.03	TTTCAAAAGCCAATCTTACTGGGATGgagtagggtgggggacctgggatgg	G	T	I	0	0	0	0
chr2A	59032194	0.66	0.85	aaaacagggtctggaggggacctctagcaaactccaacagacctgcagctg	A	G	D	0	0	0	0
chr2A	86937581	0.53	0.35	gcctcaagggatctacctgcctcagcctctcaaagtgctgggattacagga	C	T	D	0	0	0	0
chr2A	101291619	0.34	0.13	ACCTGGAAGCGCCCCTAGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGG	G	C	F	PATERNAL	0	1	0
chr2A	113292822	0.51	0.41	CCGCCAAGTCGACACCCAGCATCCACTAGGAAGGTCCCTTGTTGGTTCAGA	C	G	F	PATERNAL	0	1	0
chr2A	113293908	0.38	0.45	AGTAGGTATGCAGCTGCGGCAAAAGAGCCAAGAAGGATATGAAAACTGCCA	A	G	F	PATERNAL	0	1	0
chr2B	121355305	0.03	0.84	TGAAGAGGGATGATAGGCCCTGCGCGTCTGTTGTGTGCTTGGGCACAGTAG	G	A	F	PATERNAL	1	1	0
chr2B	127429405	0.24	0.47	gaggaggctatgtggtcaatggagttttatcttagttccatcttacagtgg	T	G	E	MATERNAL	0	1	0
chr2B	143063121	0.64	0.36	CTTTTACCTGTCATATACTGGAGGCATGAAAGATTTTCTGTTCTAAACAAC	A	G	H	PATERNAL	0	0	0
chr2B	154009128	0.65	0.13	TTTTCTCAACACTATTTCCATCTAAGTGAATGCAGATTAGACTTTCAAAGT	G	C	H	0	0	0	0
chr2B	154495987	0.68	0.36	ttaccatttctctgttaatagaaatgccttagaaaccttagaccatttgcc	G	A	H	0	0	0	0
chr2B	154740624	0.01	0.02	actagattagctagatacagagtgtccattggtgtatttacaaactctgagc	CC	TG	E	0	0	0	1
chr2B	154740632	0.01	0.02	agctagatacagagtgtccattggtgtatttacaaactctgagctagacacaga	GTAT	ATAA	E	0	0	0	1
chr2B	155669031	0.30	0.26	TCTGATCTACACTCATCTGAAGAAACGAATACCAAAATGAAAAATTATGAA	C	T	E	PATERNAL	1	1	0
chr2B	176954922	0.58	0.20	TGTTCTTCCCGTAGTTTCTGATTACGGTTAATAGCAAGTTCTTTTTCTCTC	G	A	H	0	1	0	0
chr2B	183825011	0.37	0.04	tcactaggaaagctgtttctcactcgggctttcctacctagAAATAACTT	G	A	G	0	1	0	0
chr2B	193603986	0.95	0.10	CTGCATTTTAGACATGATTTTATTATCCAATGAAAAACTTTAAGAAAGTTT	T	C	H	0	0	0	0
chr2B	226291593	0.66	0.79	caccttcaagtgctccctagctacgtggggctagtggctacattattggg	G	A	D	PATERNAL	1	0	0
chr2B	239281601	0.10	0.62	ATGGTTTTCTTGCTCCAACCTTGACATTAGGCTCACTTGGACTGTTCCCTC	A	G	G	0	0	0	0
chr2B	245221725	0.55	0.51	ATGAGCAGATGGAATCCTAATAGGAGTTGTCAATCTGAGCCTTTGGGGATT	G	A	G	0	0	0	0
chr3	16093871	0.26	0.37	gggagggctgcacatggcttgaactcgtaagttcaaggccagcctgggcaa	C	T	E	0	1	0	0
chr3	17564718	0.72	0.89	ttaaaatatttaaaatgttttaaatgttcaatttttaaaaatgttacaatg	G	A	H	0	0	0	0
chr3	21876518	0.62	0.06	ccaccccaaccaatgtcagtttactgtaactaagcattaagccttatatag	G	A	F	PATERNAL	0	1	0
chr3	23332122	0.32	0.76	agaggacattctagaaagcagatggcaaatgtgtaGCTAACTGATGCCAGA	C	T	I	0	0	0	0
chr3	25530176	0.54	0.14	acccaggaggtgaaagttgcagtgcgccaagatcacgccactgcacttcag	G	A	D	0	1	0	0
chr3	70708139	0.26	0.57	ctaaaaaaaaaaatacaaaaattagccaggtgtggtgatgcacccctgtaa	C	A	G	0	0	0	0
chr3	130786980	0.57	0.11	GGTTGCAGAGTGATATAGAAGCAGATGCCCTGCAAGACAGAAGTAGGTGGC	T	G	D	0	0	0	0
chr3	149461032	0.65	0.17	tatttaatgtaattattcctgtgttcgcatctatgtctacaattttaagag	C	T	H	0	1	0	0
chr3	154089795	0.70	0.86	TTAAACATAGCCTGAATGATATTCCGTAAGTAATTCCTTAATTGGAAAAGC	G	A	G	0	1	0	0
chr3	158138958	0.52	0.55	tcttgatccacaatcaacggtttggatagaaacatgaaggataacttatta	A	C	E	0	0	1	0
chr3	175043577	0.38	0.16	TAAGCTTCACCTACAGAAATTCAGTAAGACAGAAATAGGAATTCAGTGAAG	A	G	E	PATERNAL	0	1	0
chr3	189709073	0.55	0.14	gtgcttgtagtcccagttattgaggaggctgaggtgggaggattgcttgag	A	C	E	PATERNAL	0	1	0
chr3	196558346	0.53	0.54	gtgaaaagagcaagctggaaaactgtagttatataaatcccCAGGTATAG	T	C	I	0	0	0	0
chr3	198345852	0.58	0.64	cggagtttgagaccagcctgggaaacgtagcaagaccccaactcatttaaa	C	T	F	PATERNAL	1	0	0
chr4	12003755	0.87	0.35	TAAAAAGACTAAGATGAACAAAAATTCAAGAGTAGGCCTATGTCCTCTAGT	T	C	H	0	0	0	0
chr4	14340935	0.24	0.40	tcagtgctagaaaatgtttgggtgtcgaccagcctgagtaacaagtattca	C	T	E	0	1	1	0
chr4	18640776	0.57	0.62	AAGTATTAGTTCAGGGAAGTGTTAATTTTAATAATATTTCTTACGGCATGA	T	C	D	PATERNAL	0	0	0
chr4	26839240	0.48	0.30	GTGTATGACTAGTGCTTTCTTTTATGATTCTATTTGTAAATGTTATGCAAA	G	A	E	0	0	1	0
chr4	57611480	0.41	0.18	aacagtagaaactacaaagcaaccagtcaacaacttcatgataggatcaaa	G	T	D	MATERNAL	0	0	0
chr4	72031010	0.61	0.22	ggggacctgccctttttgaagccatcggatctcgtgagatttattcactat	C	T	D	PATERNAL	1	0	0
chr4	76952784	0.53	0.72	AACTGTGGGTTTGCATGATTCATTCGAAAACATCATTTGGGGGTCGTGGTG	G	A	E	0	1	1	0
chr4	84135550	0.72	0.99	CCTTTGAAAGGACTTTCAATTTTCTGTAGGACTGAGAATCATTCATAATTC	G	T	I	0	0	0	1
chr4	84135575	0.65	0.60	GTAGGACTGAGAATCATTCATAATTCTGATCTTCTTGTCCAGAATTCTATG	C	G	I	0	0	0	1
chr4	84732820	0.31	0.33	aatttccagaggaggaagaaagagatggaattctaagcacagcgggcaggg	T	C	E	0	0	1	0
chr4	95208144	0.98	0.38	ACAGAATTTAAATCATAAACATTCTAGTCCATAATATTTTTTTCTCAGTGA	A	G	I	MATERNAL	0	0	0
chr4	98504146	0.49	0.04	CTTCAAACAGCTAGGAATTAATCAGCCAGCTTGGCTTCAAGCTCGGTGTTA	C	A	E	0	0	0	0
chr4	119767460	0.46	0.45	taagccaccactcctggccttggaatgattttaacaagacaaatgtgatat	T	C	E	0	0	0	0
chr4	143009230	0.09	0.07	TCCTGGCTGCCCTCTCTTGTTTCAGATTTTGTGATGGACTGGAACACTTAG	A	G	D	0	0	0	0
chr4	165560949	0.62	0.06	TTCAGCATAGTTTTAGTGTAAAGTGCATTGCATTTTTTCACCTCATACGCT	C	A	G	0	0	0	0
chr4	180521689	0.10	0.76	ggagtcacagacacccccctctcagacagcagagctaaaagagcattgtaac	C	T	D	0	0	0	0
chr4	182152047	0.88	0.00	ggcatgatttggcagcggctggtaccgcttgttccttccatgtttagcgc	C	T	E	0	1	0	0
chr4	182283692	0.42	0.77	CAACTTTCAGATATATTTGTTATACCGTTTTCACATAGCTCTATATTTTCT	C	T	E	0	1	1	0
chr4	189118774	0.39	0.20	AGAGCTggccgggcgcggtggctcaggcctgtaatcccagcactttgggag	G	C	F	PATERNAL	0	0	0
chr5	8099370	0.60	0.19	tttattgatttccatatgttaaatccgccttgcatcccagagacaaatcct	C	T	F	MATERNAL	1	0	0
chr5	8191332	0.89	0.43	tatgacctcatttaaccttaattaacgttttaaataaccATTGAAGAAGCT	C	A	G	0	1	0	0
chr5	13519851	0.68	0.89	aaagaatatacaaagaaatgcattttaaatgcattttaaatTTTAAATGCA	T	A	D	PATERNAL	0	0	0
chr5	30381378	0.11	0.08	tgtatttacccaatgcctgtgcccccgttgtagacaagaagtaactaacttt	C	T	E	0	1	0	0
chr5	31583344	0.64	0.47	AGTGTTGGGGCAGGGGAGGGGGGAGAAAAAGGGAGTTTACAAAAAGAAATA	A	G	E	0	0	1	0
chr5	51269690	0.90	0.06	TTTTATACCTTCCTGTAATTTTTCAATGCTAGCTTTCATTGTTACTGTATT	A	T	H	0	0	0	0
chr5	76356538	0.84	0.72	ACATTTGCAACCACAATTTGAGGGGGAAAGAAGGTAAATATGTTGCATATC	G	A	D	0	0	0	0
chr5	84287684	0.45	0.84	CCTTCATGCATAACATTAATTTGGCGAAGACCACAAAAATATGTGAGTCAC	G	A	I	PATERNAL	1	0	0
chr5	111883216	0.83	0.12	GTTGATATATACCAGAAATACTCATTTAGCTCATAATTCCAGTCATTCATT	T	G	F	PATERNAL	0	1	0
chr5	113309277	0.79	0.88	GAAGTGAATCTGATAGATCAGAAAGACCTGTATTAGTACGCCAGTCAACTT	A	G	E	0	0	1	0
chr5	116781586	0.89	0.03	GTTAAAAAAGCTTCAAATAATCATATTCAAAACCTCTTAACTTGCTGAGTA	T	C	E	PATERNAL	0	1	0
chr5	129805166	0.42	0.05	tgaaaagagtcttatttccctttcacttatgaagcttagtttggctagata	C	T	E	0	0	1	0
chr5	133233606	0.79	0.21	aaaGGAattgaagttaataccctccgtaatgagataaatggaaatgatgtc	G	A	F	PATERNAL	1	1	0
chr5	153116953	0.89	0.36	CTGGTCTCCCTGAGATGTTGCAGCTGATAGCATGTTGGAAGTTAGTTATGT	G	A	H	0	0	0	0
chr6	168304	0.10	0.11	cctggaaacctgcagccctacacgagaacgagcattctcattttcatgccc	G	C	F	PATERNAL	0	1	0
chr6	4529707	0.42	0.03	TCTGTTTGCCAGCAGCACCTTCCCGCATGGAACACCTCCCAGGCCAGATAC	C	T	H	0	0	0	0
chr6	9680705	0.20	0.11	ATTAATATTAACATAATTCCAAAATGCACCAAAATATTTTCATATTTCCAT	G	C	F	PATERNAL	0	0	0
chr6	14157189	0.48	0.50	cccacaaaaatcaactaggggataatttgagggtggacttagttctagggtc	T	A	E	0	0	1	0

chr6	28019988	0.60	0.72	ttgatgattagtgacattgaacattgttgctcatttgcatgtctcctttgg	G	A	D	0	0	0	0
chr6	33115306	0.42	0.70	gattataggcatgcgccaccatgcccggctaatttgcatttttagtagag	C	T	D	0	1	0	0
chr6	42794716	0.82	0.45	TAAGCCCTGGCATGTCAAGTGTGCACGCATACACACACACCTGCTGCTTTT	C	T	E	0	1	1	0
chr6	46532762	0.13	0.09	GGAAGTAGAGCATGGGAGGATGAAAGGCTAAGAGAAGGGCTTGAGCTGTGC	G	T	F	PATERNAL	0	1	0
chr6	98622075	0.22	0.16	tcttctcattgcatgctagagcagattcattgtaggagaggtgctaaataa	T	C	I	PATERNAL	0	0	0
chr6	103686436	0.41	0.57	ttgactggacggagggatgcctaaaaggctggtaaagtattgtttctgggt	A	C	F	PATERNAL	0	1	0
chr6	116396228	0.17	0.04	AAATGAGTTAGCTCTCCTCGGGAGAGTGTAGGCAATAAGAATATAATTTGC	G	A	F	PATERNAL	0	1	0
chr6	119291966	0.46	0.04	gttactaggctgtgagggcttcaccgtcctgaatagattaatgccattatc	G	A	F	MATERNAL	1	1	0
chr6	164458948	0.64	0.97	gacttccaaattctctaaggcctctgatctggtaagaaatcataccttctg	G	A	D	0	0	0	0
chr6	164715045	0.30	0.92	gaactgtaggcagctacaggatatggcctgtctgttcttcaccagtgtagc	G	T	D	0	0	0	0
chr7	34126065	0.93	0.87	ctatgaagaatgaagagacaacctacggatcgggagaaaatatttgcaaGT	C	T	D	0	1	0	0
chr7	40459857	0.56	0.09	GTGTCAAACTCAGACTAGATCATATTTGTTGTAATTACTATGGAAAAATAT	T	A	H	0	0	0	0
chr7	64328365	0.27	0.85	TTTGCTTGTATGGAATTTTGCCCAAGAGACCTCATTACAGTTTCTAATCTG	G	A	D	0	0	0	0
chr7	66260437	0.76	0.15	GCGTATTGCACGGGAATGTGTTTAAGTGTCAGCAGAGGTGGCCTGGAGTAA	G	C	E	PATERNAL	0	1	0
chr7	82509177	0.19	0.05	CATTTAACTTAGCAAAGAAAATCTAGATAATTGAGACTAAAATACATAAAG	G	T	E	PATERNAL	0	0	0
chr7	108891080	0.99	0.00	actaagtgcgtaatcattcatgaatgcaatagtacttcaaagttaaaatac	G	C	F	PATERNAL	0	0	0
chr7	110859669	0.62	0.18	tttgattatggccattcttgcaggagtaaggtggggtatgacattgtggtt	G	A	I	0	0	0	0
chr7	122154686	0.27	0.26	ATTAACATCTAACTATAGTATATAGCTGCCATAAAATTAACCGAGGAGTAG	C	A	G	PATERNAL	0	0	0
chr7	125884105	0.22	0.53	GCCAAGGAAGGTAGATTTCCAAGTACGGTGGGTGGCTCTCCTGTCAGAGTT	C	T	F	PATERNAL	1	1	0
chr7	137493791	0.98	0.24	ataaaataaaataaTAACAGAGTACGTGTAACTATATATAGAAATACTATG	G	A	E	PATERNAL	1	0	0
chr7	144765721	0.85	0.12	ccatggtggttaatagagctcattactacatctaagtattactaaatatgt	C	A	E	0	0	1	0
chr8	2397243	0.55	0.37	CTTACGATGGGAGATTCTAACATGCGGGTTCTACGGCACAGAATAAGACGG	G	A	G	0	1	0	0
chr8	32850682	0.17	0.69	AGCACTGATGTCAAGGCAGTGTAAGGAATGAGAAAGTGGGCAGTGGGGTCA	G	T	I	0	0	0	0
chr8	35631990	0.37	0.28	tcatctctacagaaaatacaaaaactagccagtgtggtggtgcatgcctgt	T	G	D	0	0	0	0
chr8	48540468	0.10	0.63	ATGCATACTTTGATGACATTTGTTTGCCCTCAGAGCAGGTCTATGAATTTT	G	T	H	0	0	0	0
chr8	50297463	0.77	0.00	ATTACCTGtacttatagttagtatgttaccattttaagtagaaaattgaag	T	G	F	PATERNAL	0	1	0
chr8	58859704	0.96	0.38	GTTTTTGAGTTCTTTCTGTATGTGACCATGTAAATCTAATATCTCTAAAGC	C	A	D	0	0	0	0
chr8	69325294	0.51	0.69	TATGGGTTTTCCTTTTAAATGATAACAATTAAAAACAAGAGAGAATAAATG	C	A	F	PATERNAL	0	1	0
chr8	89412220	0.01	0.07	TAATAGAAGTGGGGCACAGAGACTTGGTAGTGAAAGACACCTGTCTTTGCC	G	T	D	0	0	0	0
chr8	108198400	0.80	0.19	gaattccatagttgaagccattagatacaaagattttctttactgggagat	T	A	H	0	0	0	0
chr8	111018450	0.60	0.07	catacgtaacttacctgcacattgtgcacatgtaccctaaaacttaaagta	G	A	F	MATERNAL	0	1	0
chr8	119452016	0.69	0.38	TTTCAAAGGCCAGAGCTTTGCTTAACGTAAATGAATATATGTCACACATAC	C	T	D	PATERNAL	1	0	0
chr8	134547824	0.69	0.64	TTCTTTAATTAAAATAGGGAATATAAGATGAGAGTAGAATGGGACTGGGAG	A	G	I	0	0	0	0
chr9	8520550	0.08	0.97	gtagctgtcgtaacgtcctagcacagtgcattcattactcctgtggttgca	G	C	D	0	0	0	0
chr9	8525670	0.71	0.99	GTGGTGGTTTAGTTTTTATGGCTATGAAGGTCTGCTTCCAGTCAGCTAAAA	G	A	D	0	0	0	0
chr9	9344875	0.34	0.79	aacagtcctccaaagtgttagctcattccagcattaacccaaaagtccaag	T	A	I	0	0	0	0
chr9	9965284	0.68	0.44	TTGGGAACAAAAAAGAGAGACTAGACGTCAGTATTAATTATAAAACTAGTA	C	T	E	0	1	1	0
chr9	67645020	0.57	0.39	ATGGTGGGCTAAGCACTGTGCCAGCGTTCAATAAGTCACTGCAGATTCTCC	G	A	H	PATERNAL	1	0	0
chr9	91485173	0.38	0.76	aattagcagggtgtggtatctgtgcctgtagccccagctacttgcggggct	C	G	D	0	0	0	0
chr9	98370161	0.48	0.76	gtcatggaggcagatccctcatgaacagatgaatgccctccctttgcggga	C	T	D	0	0	0	0
chr9	108164639	0.48	0.15	AAACTGAATCTAGAAGTCACATGGTGGTCAGTGTCCTACTCACAGTATGAT	G	A	I	0	0	0	0
chr9	110484253	0.48	0.68	ccaaccaacttgctgtatacaccttggacaagtcatttgacctttcagaat	G	A	E	PATERNAL	0	1	0
chr9	116982481	0.60	0.89	AGAGTAGTAAAAAGCATATAGAACTGCCTTCTGCAGCACTCTTAGATCCAA	G	C	H	0	0	0	0
chr9	117602998	0.15	0.67	TTTAAAGTCCAAGGAACCACCTTACACTCCAATTTTCCTGTGACCCAGCCT	A	G	H	0	0	0	0
chr9	132379093	0.99	0.85	TAAAATGTATCAGCAGGATTCTAGTGGCTCTAAAGTCAATCTCTTCTTTCT	G	A	I	0	0	0	0
chr9	134833682	0.96	0.88	tgctgatgttaatttcccctgaaatgacctacaatttttttcctaattttac	G	A	D	0	0	0	0
chrX	9149290	0.42	0.011	caaatatccatccaactgaatactcccaagggatagaaagaaaagaatgac	C	T	E	0	0	0	0
chrX	32889792	0.34	0.54	AACTTCATAAATAATAGTTGAATAAACTTAAGGCATTTGGACAATTTTTTT	A	C	F	0	0	0	0
chrX	126947832	0.49	0.22	gtCTAAGGAAGTCAGGCGCCAATTTTAATCATAAACATTTAAGAAATGGTA	T	C	E	0	0	0	0

Table S7: False positive rates estimated through re-genotyping at de novo mutation candidates in two non-founders E and F. Fractions represent the number of conflicting genotypes (assumed to be sequencing errors) over the total number of assayed sites; the rate is represented in brackets. *Trio consistency* denotes that the parental and the recipient child genotypes were consistent with the inferred mutation. *Pedigree consistency* denotes that the genotypes across the entire pedigree were consistent with the inferred genotypes.

Individual	Trio consistency	Pedigree consistency
E	1/36 (0.028)	1/35 (0.029)
F	0/25 (0)	0/24 (0)

Table S8: The estimated rate of false negatives in the point mutation detection approach, estimated through simulation on alignments (see Supplementary Text).

Individual	Transmission to F2	Number of missed simulated mutations	Total simulated	FNR
D		6	138	0.044
E		4	162	0.025
F		7	163	0.043
F[a]	{}	0	16	0.000
F[b]	{I}	1	16	0.063
F[b]	{H}	0	23	0.000
F[b]	{H,I}	1	20	0.050
F[b]	{G}	2	32	0.063
F[b]	{G,I}	0	18	0.000
F[b]	{I,H}	1	19	0.053
F[b]	{G,H,I}	2	19	0.105
G		35	153	0.229
H		36	152	0.237
I		34	152	0.224

[a]Aggregate values for F

[b]Values for F marginalized over transmission to F2

Table S9: The total sequence of each individual's genome (unless otherwise specified) accessible to variation calling. The intersection mask was generated by taking the intersection of the sequence accessible to calling across the family. *Genome accessible to calling* represents the total sequence passing filters on minimum coverage and mapping quality. The three remaing columns indicate the sequence failing each applied filter.

	Sequence accessible to variation calling (bp, %)		Sequence failing filters					
			No coverage (bp,%)		Coverage < 4 reads (bp,%)		Proportion of reads with mapping quality < 1 exceeds 0.1 (bp,%)	
A	2,625,654,085	95.354%	11,776,453	0.428%	11,461,457	0.416%	104,702,931	3.802%
B	2,611,551,977	94.842%	29,855,103	1.084%	15,555,201	0.565%	96,632,645	3.509%
C	2,622,647,354	95.244%	14,435,474	0.524%	31,864,036	1.157%	84,648,062	3.074%
D	2,623,685,945	95.282%	12,565,515	0.456%	20,481,221	0.744%	96,862,245	3.518%
E	2,623,912,927	95.290%	15,049,588	0.547%	36,213,785	1.315%	78,418,626	2.848%
F	2,614,415,878	94.946%	33,653,521	1.222%	20,698,310	0.752%	84,827,217	3.081%
G	2,621,362,476	95.198%	14,375,769	0.522%	34,117,425	1.239%	83,739,256	3.041%
H	2,621,596,116	95.206%	14,212,212	0.516%	33,167,882	1.205%	84,618,716	3.073%
I	2,619,595,151	95.134%	14,436,389	0.524%	29,333,844	1.065%	90,229,542	3.277%
Intersection	2,537,740,297	92.161%						
Intersection (Autosomes)	2,537,474,219							
Intersection (X)	114,284,786							
Intersection (Y)	266,078							

Bases assiged N	390,678,468
Bases not gaps or N, i.e. mappable genome	2,753,594,926

Table S10: Estimates of the number of point mutations in human and chimpanzees. The intercept and slope coefficients are estimated through Bayesian linear regression and are the posterior mean values.

	Western Chimpanzee	Human
Male intercept (mutations per generation)[a]	-23.80	-14.20
Female intercept (mutations per generation)[a]	6.65	14.20
Male slope (mutations per generation per paternal year)[a]	2.95	1.93
Female slope (mutations per generation per maternal year)[a]	0.00	0.00
Average paternal age (years)[b]	24.30	31.50
Average maternal age (years)[b]	26.30	25.60
Average mutations per generation (autosomes, haploid)	27.27	30.40
Average mutations per generation (X chromosome)[c]	20.40	25.00
Autosomal rate of divergence (mutations per year per genome)	1.08	1.06
X chromosome rate of divergence (mutations per year per genome equivalent)	0.80	0.91
Predicted X:A divergence	0.74	0.85
Autosomal diversity[d] (relative)	54.54	60.80
X chromosome diversity (relative)	30.59	37.50
Predicted X:A diversity	0.56	0.62
Proportion X chromosome mutations in female	**0.22**	**0.38**
Proportion A chromosome mutations in female	**0.12**	**0.23**
Alpha	**7.20**	**3.28**

[a]Human data from [16]
[b]Generation times from [20]
[c]Scaling male and female contributions by 1/3 and 2/3 respectively. Length of X scaled to be comparable to autosomes.
[d]Assuming female and male effective population sizes are comparable.

Table S11: Analyses of point substitution divergence between human and chimpanzee. Spontaneous mutatition estimates corrected for genomic regions where human and chimpanzee alignments are possible (see Supplement)

Divergence calculations for substituitions in the combined mask	
Autosomal substitutions (bases)	26,402,946
X chromosome substitutions (bases)	437,524
Autosomal sequence in combined mask (bases)	2,193,451,330
X Chromosome sequence in combined mask (bases)	44,039,427
Autosomal rate of divergence (substitution/base)	0.012
X chromosome rate of divergence (substitution/base)	0.010
X:A divergence	0.825
Estimated autosomal divergence time (using 2 x the chimpanzee muation rate) (Million years)	13.331
Estimated autosomal divergence time (using chimpanzee and human mutation rates) (Million years)	11.323
Estimated autosomal divergence time (using 2 x the chimpanzee muation rate) (Million years)	14.928

Spontaneous mutation esimtates for mutations in the combined mask	Chimpanzee	Human*
Male intercept (mutations per generation)[a]	-18.263	-14.200
Female intercept (mutations per generation)[a]	6.019	14.200
Male slope (mutations per generation per paternal year)[a]	2.566	1.930
Female slope (mutations per generation per maternal year)[a]	0.000	0.000
Average paternal age (years)[b]	24.300	31.500
Average maternal age (years)[b]	26.300	25.600
Average mutations per generation (autosomes, haploid)	34.268	36.477
Average mutations per year per genome (autosomes, haploid)	1.354	1.278
Average muations per year per base	4.515E-10	4.259E-10
Average mutations per generation (X chromosome, haploid)[c]. autosome equivalent	18.710	24.998
Average mutations per year (X chromosome, haploid)[c]; autosome equivalent	0.998	1.088
Average mutations per year per base (X chromosome)[c]	3.33E-10	3.63E-10

[a]Human data from [16]; all mutations are assumed to lie in the mask

[b]Generation times from [20]

[c]Scaling male and female contributions by 1/3 and 2/3 respectively. Length of X scaled to be comparable to autosomes.

[d]Assuming female and male effective population sizes are comparable.

*Since only summary data was available, we were unable to apply the mask to the human mutation counts.

Table S12: Comparison of paternal and maternal spontaneous mutation coefficients for the callable genome mask (constructed from pedigree sequencing alignments) and the combined mask (intersection of the callable genome mask and divergence mask).

Poisson regression modelling paternal affect only	Callable genome mask	Combined mask
Mean paternal age effect (mutations/year)	3.02 (1.35 - 4.68)	2.74 (1.12 - 4.34)
Poisson regression including parent of origin information		
Mean maternal effect (mutations)	6.5 (3.5 - 10.3)	6.50 (3.49 - 10.20)
Mean paternal age effect (mutations/year)	2.9 (1.2 - 4.4)	2.54 (0.957 - 4.13)
Mean onset paternal mutation (years)	5.6 (0 - 12)	4.99 (-13.5 - 11.7)
Alpha		
All	5.5 (3.0 - 10.0)	5.01 (2.84 - 9.90)
non-CpG	5.60	5.25
CpG	5.30	5.33
Clustering		
Observed mutations within 2e+06 bp of 1 or more other event (%)	17	12
Clustered mutations with all neighbours from the same individual (%)	41	52
Expectation for clustered mutations in the same individual across simulations (%)	13 (P = 0.001)	15 (P = 0.002)