Supplementary Information for
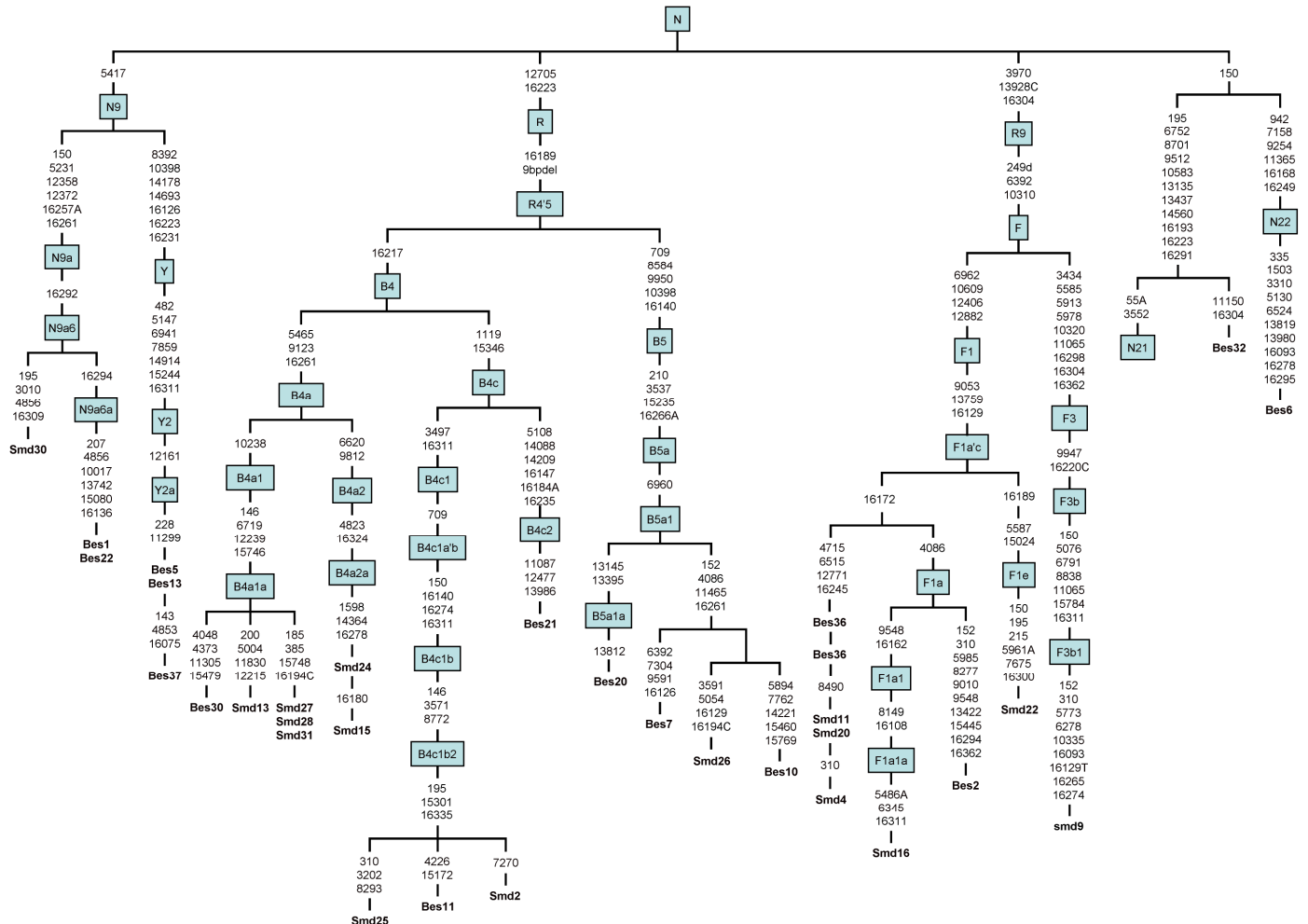
Larger mtDNA than Y-chromosome differences between matrilocal and patrilocal groups from Sumatra

Ellen Dröfn Gunnarsdóttir, Madhusudan R. Nandineni, Mingkun Li, Sean Myles, David Gil, Brigitte Pakendorf and Mark Stoneking.
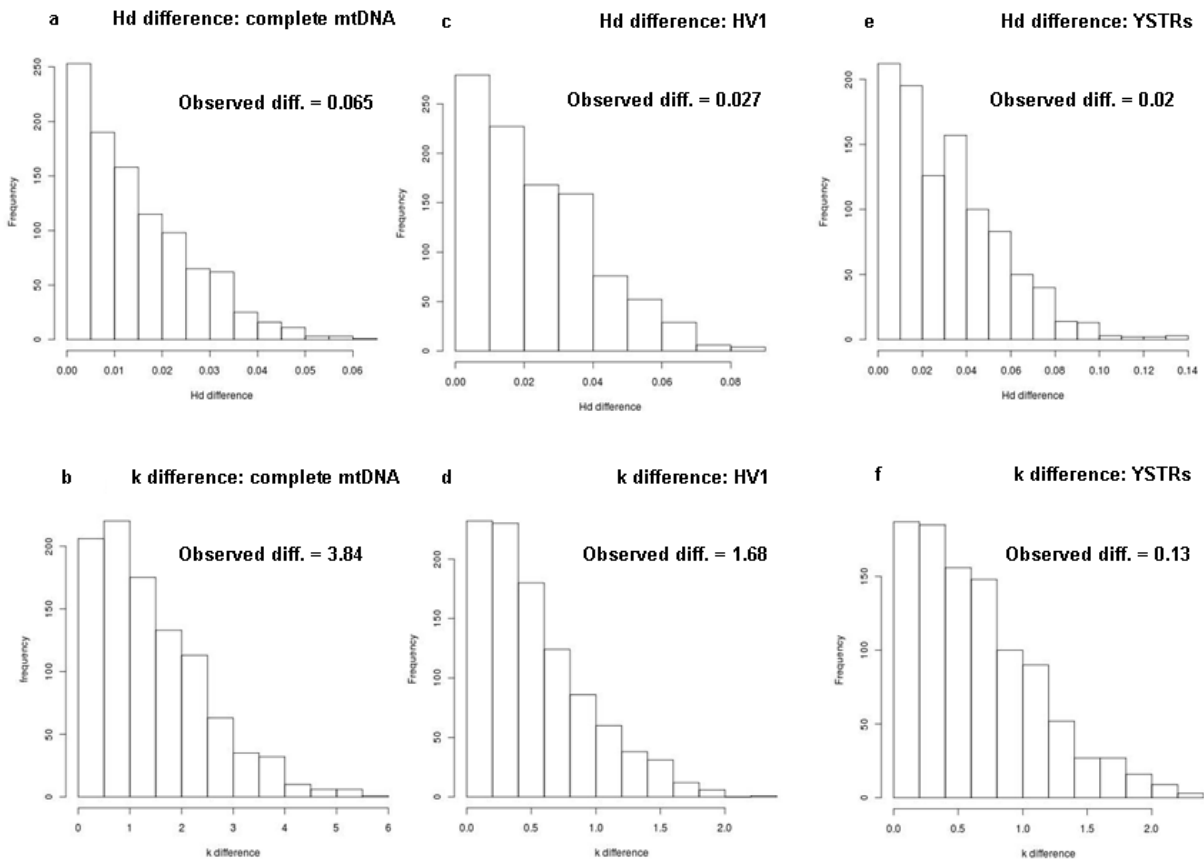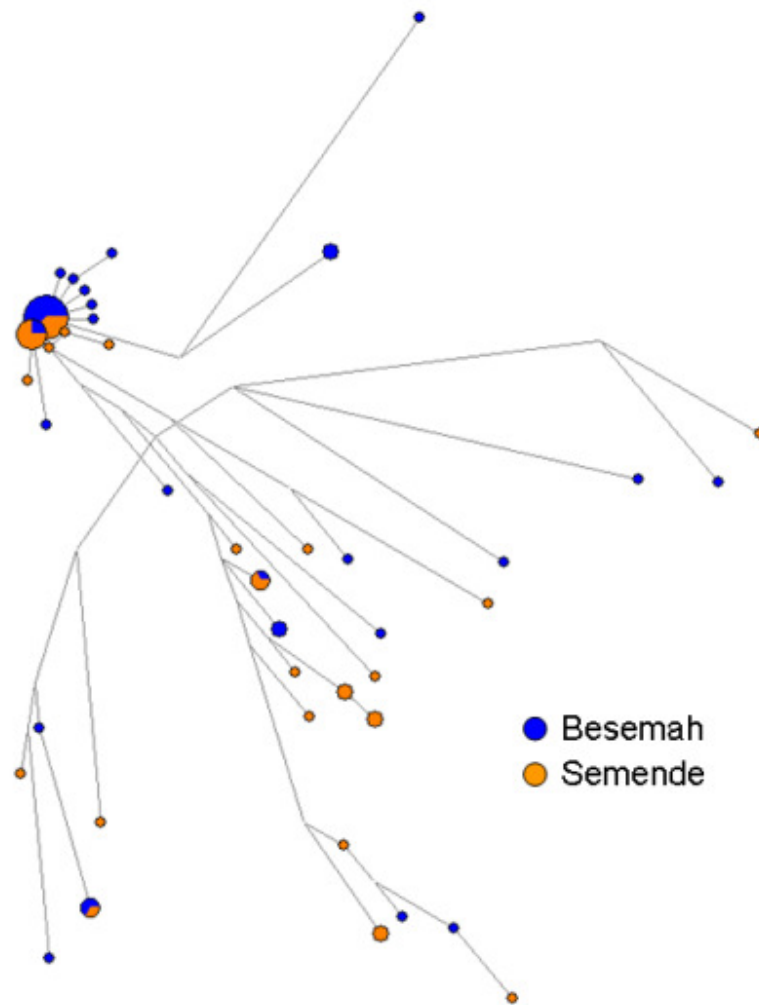
Supplementary Figures:

a

Supplementary Figure S1. Schematic tree of complete mtDNA sequences.
The figure shows the nearest haplogroup affiliation of all complete mtDNA sequences in the study. The individual ID is shown in bold and haplogroup names are shown in blue boxes. Back mutations are shown in italics. Mutations that are transversions are indicated with the associated base. **A)** Complete mtDNA sequences belonging to macrohaplogroup M. **B)** Complete mtDNA sequences belonging to macrohaplogroup N. Positions 309.1C(C), 16182C, 16183C, 16193.1C(C) and 16519 were not used for reconstructing the haplogroup trees.

Supplementary Figure S2. Permutation tests of significance.
Histograms of frequencies of diversity statistics obtained with 1000 permutations. After
each permutation, a diversity statistic was calculated for each random group and then the
difference between the two randomly sampled groups was calculated and compared to the
values obtained from the observed data. The Y-axis shows the frequency of the difference
between the two populations for a given diversity statistic and the X-axis shows the value
of the difference for the summary statistic. **A)** Frequency distribution of the haplotype
diversity difference for mtDNA. **B)** Frequency distribution of the mean number of
pairwise difference for mtDNA. **C)** Frequency distribution of the haplotype diversity
difference for the mtDNA HV1 region . **D)** Frequency distribution of the difference of the
mean number of pairwise differences for the mtDNA HV1 region. **E)** Frequency
distribution of the haplotype diversity difference for the Y-chromosome. **F)** Frequency
distribution of the difference of the mean number of pairwise differences for the Y-
chromosome.

Supplementary Figure S3. Network for all Y-STRs .
The network is based on all 12 YSTRs in the study. Diameters represent YSTR haplotypes and are proportional to the frequency of the haplotype. Branch lengths are proportional to the number of mutation steps. The Semende are depicted in orange and the Besemah are depicted in blue.
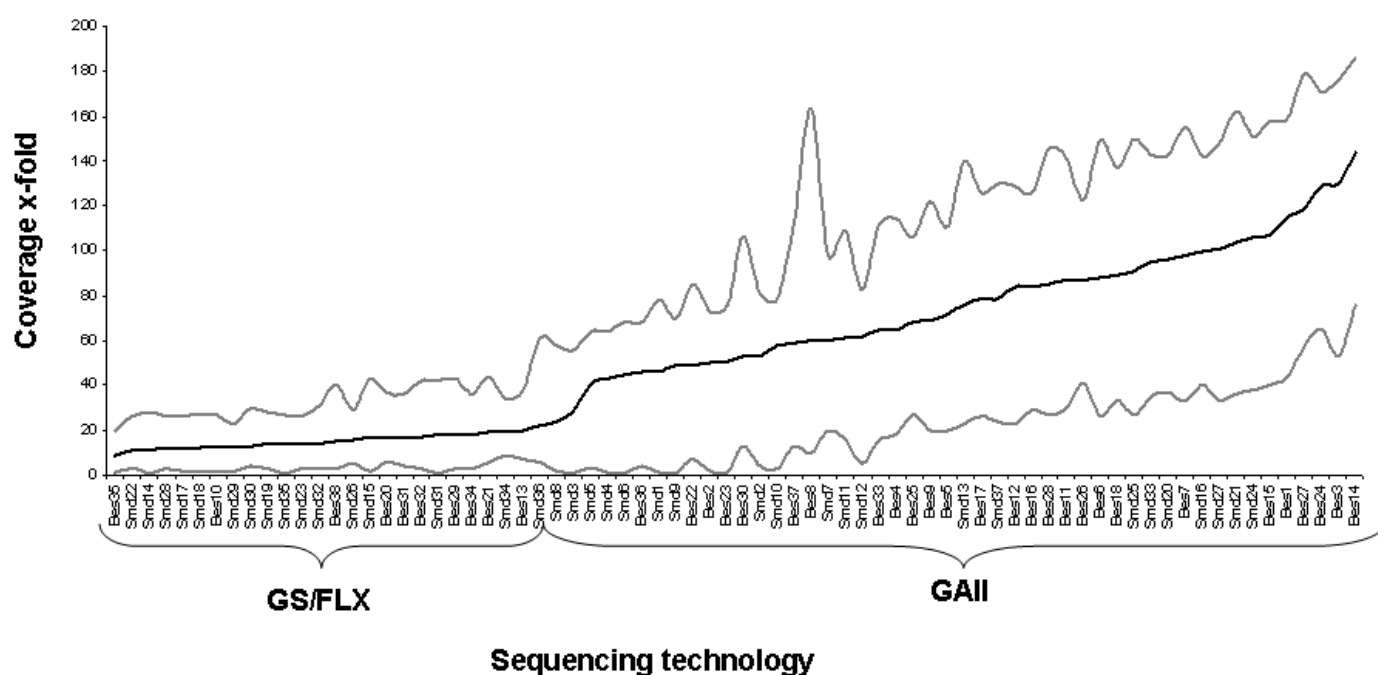
Supplementary Figure S4. Coverage for complete mtDNA sequences.
The plot shows the maximum, minimum and average coverage of complete mtDNA
sequences in the study and the proportion of individuals sequenced with each technology
used. X-axis shows all the individuals in the study, Y-axis shows the coverage. GS/FLX:
Genome Sequencer FLX, GAII: Genome Analyzer II Technology.
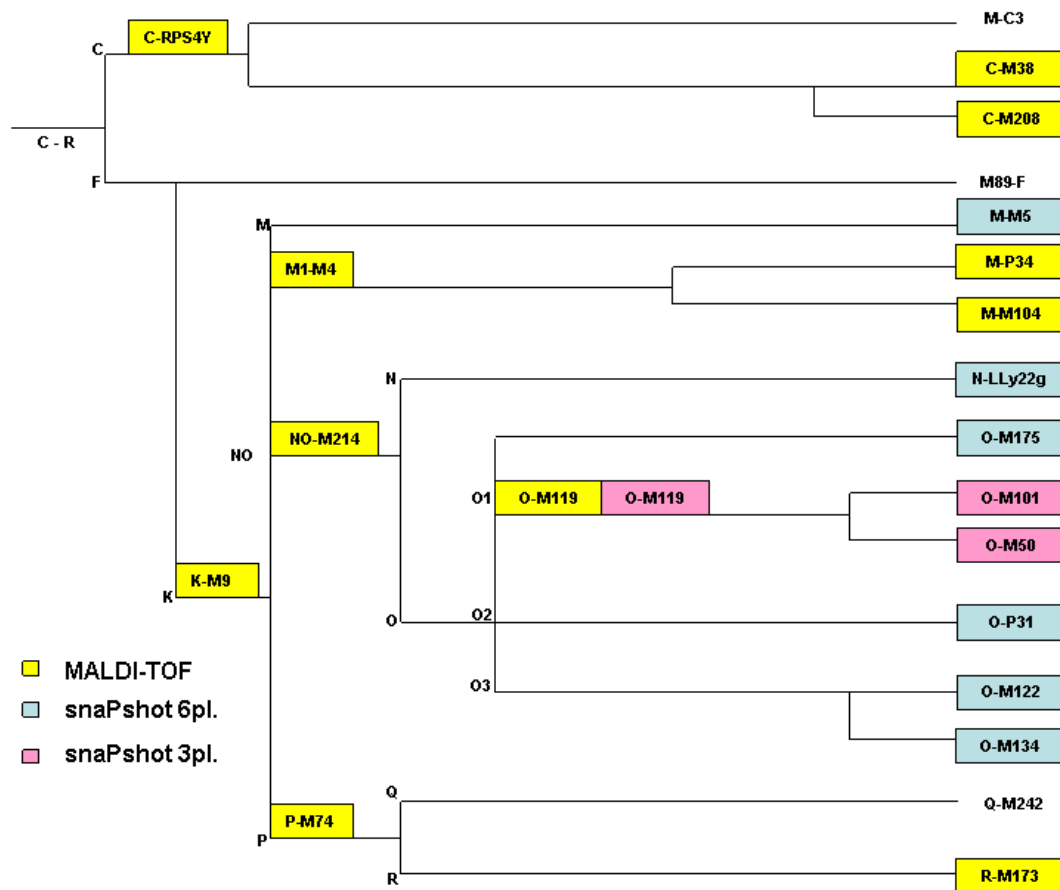
Supplementary Figure S5. A schematic representation of the Y-SNP haplogroup tree.
The figure shows a tree with the phylogenetic relationships of Y-SNPs used in this study. Y-SNPs indicated in yellow boxes were typed using the MALDI-TOF assay for 11 SNPs. Y-SNPs indicated in blue boxes were typed with a snapshot multiplex of 6 SNPs. Y-SNPs indicated in pink boxes were typed with a snapshot multiplex of 3 SNPs.

Supplementary Tables:

SampleID	DYS391	DYS389I	DYS439	DYS389II	DYS438	DYS437	DYS19	DYS392	DYS393	DYS390	DYS385a	DYS385b	Y-hg
Smd1	11	13	13	28	10	14	16	13	14	24	15	22	O2
Smd2	11	13	11	29	10	14	15	13	14	24	15	16	O2
Smd3	10	13	12	29	10	14	15	13	13	24	14	20	O2
Smd4	11	13	11	29	10	14	15	13	14	24	15	15	O2
Smd5	10	14	11	29	10	15	13	13	13	25	13	14	O2
Smd6	11	13	11	29	10	14	15	13	14	24	15	15	O2
Smd7	10	13	12	29	10	15	15	13	13	25	15	20	O2
Smd8	11	13	12	30	10	14	15	13	13	25	14	20	O2
Smd9	11	13	12	30	10	14	16	13	13	25	14	20	O2
Smd10	10	13	11	29	10	15	13	15	13	25	13	13	O3
Smd11	10	13	12	29	10	14	15	13	14	24	15	15	O2
Smd12	10	12	11	27	10	14	15	14	13	23	13	13	O1a2
Smd13	11	13	11	29	10	14	15	13	14	23	15	16	O2
Smd14	11	13	11	29	10	14	15	13	14	24	15	16	O2
Smd15	10	14	11	29	10	15	13	13	13	25	13	21	O3
Smd16	11	13	12	30	10	14	16	13	13	25	14	20	O2
Smd17	10	14	11	30	10	15	13	13	13	27	13	20	O3
Smd18	11	13	11	29	10	14	15	13	14	24	15	16	O2
Smd19	10	13	12	29	10	14	15	13	13	24	14	19	O2
Smd20	10	12	12	27	9	14	16	14	13	22	13	14	O1a2
Smd21	11	13	11	29	10	14	15	13	14	24	15	15	O2
Smd22	10	13	11	29	10	14	15	13	14	24	15	16	O2
Smd23	11	13	11	29	10	14	15	13	14	24	15	16	O2
Smd24	11	13	12	30	10	14	15	13	13	25	14	20	O2
Smd25	11	13	11	29	10	14	15	13	14	24	15	15	O2
Smd26	10	13	12	29	10	14	15	13	13	24	14	20	O2
Smd27	11	13	11	29	10	14	15	13	14	24	15	16	O2
Smd28	10	13	11	31	11	14	17	11	13	27	11	14	O*
Smd29	11	13	11	29	10	14	15	13	14	24	15	15	O3
Smd30	11	13	11	29	10	14	15	13	14	24	15	16	O2
Smd31	11	13	11	29	10	14	15	13	14	24	15	15	O2
Smd32	10	13	12	30	10	14	15	13	13	25	14	20	O2
Smd33	10	13	11	29	10	14	15	13	14	24	15	15	O2
Smd34	11	13	12	29	10	15	15	13	13	24	15	21	O3
Smd35	10	14	12	30	10	14	15	13	14	25	15	19	O2
Smd36	10	14	11	30	10	15	13	13	13	27	13	20	O3
Smd37	11	15	11	30	10	15	13	13	13	25	14	20	O3
Bes1	10	14	10	31	11	14	15	11	13	25	9	14	O*
Bes2	11	13	11	25	8	14	15	13	14	24	12	12	O2
Bes3	11	13	10	29	10	14	15	13	14	24	15	15	O2
Bes4	10	12	13	28	10	14	15	15	13	23	12	12	O*
Bes5	10	13	12	29	10	14	15	13	14	25	15	22	O2
Bes6	11	14	11	30	10	15	13	13	13	25	14	21	O3
Bes7	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes8	10	12	12	27	9	14	16	14	13	22	13	14	O1a2
Bes9	10	13	12	30	10	14	15	13	13	24	16	16	O2
Bes10	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes11	10	12	12	27	9	14	16	14	13	22	13	14	O1a2
Bes12	11	13	11	30	10	14	15	13	14	24	15	15	O2
Bes13	11	13	11	29	10	14	15	13	14	24	15	16	O2
Bes14	10	13	12	28	10	14	15	11	13	25	13	20	O2
Bes15	11	10	11	26	10	15	15	13	14	24	15	15	O2

Bes16	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes17	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes18	11	10	11	26	10	15	15	13	14	24	15	15	O2
Bes19	10	12	13	28	10	15	15	13	13	24	12	16	O3
Bes20	11	13	11	29	10	14	15	13	15	24	15	15	O2
Bes21	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes22	11	14	11	29	10	15	13	13	13	25	13	22	O3
Bes23	10	14	11	30	10	14	15	11	15	24	11	17	O*
Bes24	11	13	12	29	10	14	15	13	14	24	16	16	O2
Bes25	11	13	12	29	10	14	15	13	13	24	14	20	O2
Bes26	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes27	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes28	11	13	12	29	10	14	15	13	13	24	14	20	O2
Bes29	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes30	10	13	12	29	10	14	15	13	13	24	14	20	O3
Bes31	11	13	11	29	10	14	15	13	14	24	15	15	O2
Bes32	11	14	11	30	10	14	15	13	14	24	15	15	O2
Bes33	10	12	11	28	10	14	16	14	13	23	13	14	O1a2
Bes35	11	13	12	29	10	14	15	13	14	24	15	15	O2
Bes36	11	13	11	29	10	14	15	13	14	24	15	16	O2
Bes37	11	13	11	29	10	14	15	13	14	24	14	15	O3
Bes38	11	13	11	29	10	14	15	13	14	24	15	15	O2

Supplementary Table S1. Results for Y-STRs and Y-SNPs.
The table shows the number of repeats for each YSTR in the study and the associated Y-chromosome haplogroup for each individual.

Sample ID	Seq Tech	#Reads	#Mapped Reads	Seq.len	Av.cov.	Min.cov	Max.cov	Ns	mtHap	GenBank ID	Sample Location
Bes1	GAII/Cap	183912	25406	16570	115	44	159	0	N9a6a	HM596644	Padang
Bes10	GS/FLX	1446	1012	16560	13	2	27	1	B5a1	HM596645	Merpayang
Bes11	GAII/Cap	174995	19032	16562	87	30	141	0	B4c1b2	HM596646	Pauna Salak
Bes12	GAII/Cap	161661	18427	16571	84	23	129	1	E1a1a	HM596647	Pelagaran
Bes13	GS/FLX	2108	1475	16569	20	7	38	2	Y2a	HM596648	Pelagaran
Bes14	GAII/Cap	352424	31621	16568	144	76	186	0	M7c3c	HM596649	Pelagaran
Bes15	GAII/Cap	270865	23583	16568	107	40	158	0	M7c3c	HM596650	Pelagaran
Bes16	GAII/Cap	193494	18459	16570	84	29	126	0	E1a1a	HM596651	Pelagaran
Bes17	GAII/Cap	193287	17368	16570	79	26	126	0	E2a	HM596652	Pelagaran
Bes18	GAII/Cap	190980	19660	16574	89	33	137	0	M	HM596653	Pelagaran
Bes19	na	na	na	na	na	na	na	na	na	na	Pelagaran
Bes2	GAII/PCR	50421	20750	16563	50	2	73	4	F1a	HM596654	Jambat Akar
Bes20	GS/FLX	1795	1231	16558	17	6	37	1	B5a1a	HM596655	Jambat Akar
Bes21	GS/FLX	2148	1444	16560	19	6	44	2	B4c2	HM596656	Pelagaran
Bes22	GAII/Cap	151490	10806	16570	49	7	85	0	N9a6a	HM596657	Jambat Akar
Bes23	GAII/PCR	63318	21230	16568	51	2	76	2	E1a1a	HM596658	Jambat Akar
Bes24	na	na	na	na	na	na	na	na	na	na	Jangkar
Bes25	GAII/Cap	149942	14930	16568	68	27	106	0	M7c3c	HM596659	Pelagaran
Bes26	GAII/Cap	274861	19155	16570	87	41	123	1	E1a1a	HM596660	Pelagaran
Bes27	GAII/Cap	233407	26377	16570	119	58	179	0	E1a1a	HM596661	Pelagaran
Bes28	GAII/Cap	134707	18614	16568	85	27	146	1	M7c3c	HM596662	Pelagaran
Bes29	GS/FLX	1896	1336	16566	18	3	43	4	M7c3c	HM596663	Pelagaran
Bes3	GAII/Cap	285995	28511	16567	130	53	176	0	M7c3c	HM596664	Pelagaran
Bes30	GAII/Cap	152833	11614	16557	53	13	106	1	B4a1a	HM596665	Semende
Bes31	GS/FLX	1827	1251	16569	17	4	36	3	E1a1a1	HM596666	Semende
Bes32	GS/FLX	1792	1251	16567	17	3	42	0	N	HM596667	Semende
Bes33	GAII/Cap	144221	14351	16567	65	16	112	1	M7c3c	HM596668	Semende
Bes34	GS/FLX	1906	1336	16566	18	3	36	0	M7c3c	HM596669	Semende
Bes35	GS/FLX	1077	706	16569	9	2	20	2	M	HM596670	Semende
Bes36	GAII/PCR	45020	19356	16566	46	4	68	0	F1a'c	HM596671	Semende
Bes37	GAII/Cap	130263	12993	16570	59	13	113	1	Y2a	HM596672	Semende
Bes38	GS/FLX	1665	1153	16568	15	3	40	2	M7c3c	HM596673	Semende
Bes4	GAII/Cap	149504	14354	16569	65	18	114	0	M7c3c	HM596674	Semende
Bes5	GAII/Cap	148433	15859	16569	72	20	111	0	Y2a	HM596675	Semende
Bes6	GAII/Cap	150795	19523	16569	88	26	149	0	N22	HM596676	Pagaralam
Bes7	GAII/Cap	140204	21575	16554	98	33	155	2	B5a1	HM596677	Pelagaran
Bes8	GAII/Cap	167707	13186	16568	60	10	163	1	M7c3c	HM596678	Jangkar
Bes9	GAII/Cap	111711	15202	16571	69	20	122	0	M4	HM596679	Semende
Smd1	GAII/PCR	52311	19050	16566	46	2	78	26	M1'51	HM596680	Semende
Smd10	GAII/PCR	66518	24110	16566	58	3	79	1	M1'51	HM596681	Semende
Smd11	GAII/Cap	112792	13476	16566	61	16	109	0	F1a'c	HM596682	Semende
Smd12	GAII/PCR	84471	25971	16566	62	5	83	1	M1'51	HM596683	Semende
Smd13	GAII/Cap	161582	16662	16557	76	23	140	1	B4a1a	HM596684	Semende
Smd14	GS/FLX	1158	851	16567	11	2	28	0	M7c3c	HM596685	Semende
Smd15	GS/FLX	1707	1215	16559	17	2	43	2	B4a2a	HM596686	Semende
Smd16	GAII/Cap	158439	21895	16566	100	40	142	0	F1a1a	HM596687	Semende

Smd17	GS/FLX	1265	906	16569	12	2	26	3	E1a1a1	HM596688	Pelagaran
Smd18	GS/FLX	1298	900	16569	12	2	27	2	M	HM596689	Jemaring
Smd19	GS/FLX	1543	1070	16569	14	3	28	1	M13'46'61	HM596690	Jemaring
Smd2	GAII/PCR	75283	22247	16567	53	4	81	4	B4c1b	HM596691	Pelagaran
Smd20	GAII/Cap	209424	21260	16566	96	37	143	0	F1a'c	HM596692	Jambat Akar
Smd21	GAII/Cap	214875	23004	16568	104	36	162	0	M1'51	HM596693	Jambat Akar
Smd22	GS/FLX	1167	852	16563	11	3	26	5	F1e	HM596694	Jambat Akar
Smd23	GS/FLX	1540	1049	16566	14	3	26	3	M1'51	HM596695	Jambat Akar
Smd24	GAII/Cap	271035	23501	16560	106	38	151	1	B4a2a	HM596696	Jangkar
Smd25	GAII/Cap	171890	20125	16558	91	27	150	0	B4c1b2	HM596697	Pagaralam
Smd26	GS/FLX	1768	1158	16559	16	5	29	0	B5a1	HM596698	Semende
Smd27	GAII/Cap	239721	22269	16556	101	33	148	0	B4a1a	HM596699	Semende
Smd28	GS/FLX	1331	911	16557	12	3	26	1	B4a1a	HM596700	Semende
Smd29	GS/FLX	1389	960	16569	13	2	23	2	M	HM596701	Semende
Smd3	GAII/PCR	23689	12297	16568	29	2	56	7	M	HM596702	Semende
Smd30	GS/FLX	1558	1007	16571	13	4	30	0	N9a6	HM596703	Semende
Smd31	GS/FLX	1878	1337	16557	18	2	42	0	B4a1a	HM596704	Semende
Smd32	GS/FLX	1491	1071	16567	14	3	31	2	M1'51	HM596705	Semende
Smd33	GAII/Cap	180904	20918	16568	95	35	143	0	M1'51	HM596706	Semende
Smd34	GS/FLX	2106	1410	16568	19	9	34	0	M1'51	HM596707	Semende
Smd35	GS/FLX	1553	1046	16569	14	2	27	2	M4	HM596708	Semende
Smd36	GS/FLX	2150	1654	16568	22	6	61	0	M1'51	HM596709	Semende
Smd37	GAII/Cap	232335	17429	16569	79	24	130	0	M13'46'61	HM596710	Semende
Smd4	GAII/PCR	39505	17893	16565	43	2	64	3	F1a'c	HM596711	Semende
Smd5	GAII/PCR	36677	17013	16568	41	3	64	4	M	HM596712	Semende
Smd6	GAII/PCR	47174	18823	16568	45	2	68	24	M	HM596713	Semende
Smd8	GAII/Cap	31502	5354	16568	24	2	58	2	M7c3c	HM596714	Jemaring
Smd9	GAII/PCR	53760	20310	16558	49	2	70	7	F3b1	HM596715	Pelagaran
Smd7	na	na	na	na	na	na	na	na	na	na	Semende

Supplementary Table S2. Sample information.
The table give information on the sequencing technology used, number of reads from tags, number of reads that mapped to the reference genome, sequence length, maximum, minimum and average coverage, number of Ns in sequences, mtDNA haplogroup affiliation, GenBank accession number and sample location.