Supporting Information

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SI Materials and Methods

Study Groups. In 2010 the Mare gang contained *ca*. 63 individuals (including nine adult males); in 2011 it contained *ca*. 55, and the Simenti gang contained *ca*. 60 individuals (both including eight adult males each; see Table S1). Between the two observation periods, two of the focal males disappeared from the Mare gang, and one transferred into another gang. Two males classified as subadult in 2010 were assigned to the adult category in 2011 and then were included in the observations.

Global Positioning System Data. Fourteen of the 18 collared individuals belonged to the two focal gangs (the Mare and Simenti gangs), and three individuals belonged to a third gang, the River gang. One remaining male belonged to a separate gang that we never saw during focal observations. Global Positioning System (GPS) data were downloaded in the field using a UHF download system (RCD-04; Televilt). The error of a fix was given as 10–15 m (Televilt), and the error estimated from the actual data was given as 12.3 m (SD = 18.1; n = 1,112). The number of animals equipped with a GPS collar at any one point in time is indicated in Table S4. We estimated the actual error by comparing night fixes of two GPS collars. Assuming that the baboons move only minimally during the night, we calculated the Euclidian distances between the positions at 21:00 and 00:00 and between the positions at 00:00 and 03:00. Because of limited resources, the considerable effort required to renew the collars, and restricted battery life, not all animals could be equipped with collars at the same time. To calculate association patterns, we used the custom software "at" programmed by C. Franzl (1). The output of the program is a matrix of dyadic frequencies of individuals remaining within a specified distance of each other within a given time frame. To avoid overrepresenting fixes taken at sleeping trees, only data taken between 08:00 and 21:00 were included (i.e., one fix per night at 21:00). GPS data revealed that the male from the unknown party came in proximity with all other collared individuals occasionally [association index (AI) range, 0.01–0.04].

Clustering Method. To determine the most appropriate clustering method, we used the cophenetic correlation coefficient (CCC), which reflects the correlation of the AIs between two individuals in the dendrogram and the actual AIs between two individuals. The CCC thus describes how correctly the real data are represented by the dendrogram (2). We obtained dendrograms using the single, complete, and average linkage methods and compared them with the real data. The results obtained with the average linkage method revealed the highest correlations (CCC_{2010} = 0.981 and CCC_{2011} = 0.987). The other methods yielded only marginally weaker correlations [single link 0.978 (2010) and 0.965 (2011); complete link 0.979 (2010) and 0.975 (2011)]. Additionally, we used an iterative clustering method [Tabu Search provided in UCInet v. 6; Borgatti et al. (3)] to confirm the number of clusters in the dataset obtained from the hierarchical cluster analysis. The program uses a combinatorial optimization algorithm to assign nodes to as many clusters as hypothesized by the user and attempts to find the best fit [i.e., the highest Pearson correlation coefficient (r^2) value]. For each dataset, all possible cluster solutions (i.e., up to the total number of adult males) were tested.

Description of Recorded Behavioral Interactions. ***Affiliation.*** We categorized three types of affiliation: (*i*) close contact: two subjects resting within 0.1 m distance; (*ii*) embrace: one subject puts one or two arm(s) around the other, or both embrace each other; and (*iii*) grooming: one subject combs through the fur of the other subject with one or both hands.

Agonism. We categorized four types of agonism: (*i*) supplanting, in which one animal approaches another subject; the approached subject leaves, and the approaching subject takes the supplanted subject's position; (*ii*) threats, which may consist of a head bob, raised eyelids, lunges, ground slaps, threat-grunt vocalizations, stares, and any combination of these patterns; (*iii*) chase, i.e., pursuing another group member for more than 5 m without body contact; and (iv) a physical fight, including slaps, hitting, and biting.

Greeting. As greeting, we categorized interactions that may include manipulation of the genitals, mounting, hindquarter touch, head bobbing, prancing, tail wrapping, or lean/lying on the partners back; often accompanied by grunts.

Relatedness Analysis. ***Samples and extraction.*** During the capture of the animals, we collected tissue samples by ear punch (*ca*. 0.5 × 0.5 cm^2) from 40 adult males under anesthetic. We stored the samples in 90% ethanol for up to 6 mo at ambient temperature in the field before shipping them to the German Primate Center, Germany. We extracted DNA using the QIAamp DNA Blood and Tissue Mini Kit (Qiagen) following the manufacturer's protocol and stored the extracts at −20 °C.

Genotyping. We genotyped individuals at 25 polymorphic autosomal microsatellites in five multiplex PCR reactions (mean number of alleles per locus, 4.08 ± 1.19 SD). Loci were amplified using human map pair primers. Multiplex PCR amplifications were performed on a SensoQuest Labcycler in a total volume of 10 μL, composed of 1.2 μL DNA extract, 2.65 μL H_2O, 5.0 μL Qiagen Multiplex PCR Kit Mastermix [containing HotStartTaq DNA Polymerase, Multiplex PCR Buffer (which contains 6 mM $MgCl_2$)], dNTP Mix, 1.0 μL Primer Mix (containing 0.07–0.9 μM of four to six primer pairs), and 0.15 μL bovine serum albumin and Triton X-100. PCR conditions comprised a predenaturation and polymerase activation step at 95 °C for 15 min, followed by 35 cycles at 94 °C for 30 s, optimal annealing temperature (T_a) for 40 s, 72 °C for 40 s, and a single final extension step at 72 °C for 30 min. All sets of amplifications contained negative controls with HPLC water to monitor contamination. The success of PCR amplification was confirmed by visualization of 2 μL of product under UV light after electrophoresis on 2.5% agarose gels containing ethidium bromide. The DNA concentration was estimated by comparison with 1 μL pUC19 DNA (Fermentas) with known concentrations of 5, 10, 25, and 50 ng/μL, respectively. We mixed 0.5 μL appropriately diluted PCR product with 9.9 μL Hi-Di (Applied Biosystems) and 0.1 μL GeneScan-400HD ROX Size Standard (Applied Biosystems) and analyzed it further by capillary electrophoresis on an ABI 3130xL Genetic Analyzer (16-capillary sequencer; Applied Biosystems). Fragment length was rated relative to the size standard using Peak Scanner Software v1.0 (Applied Biosystems). To assure accuracy, we repeated the genotyping, and two investigators called the alleles independently. Details on loci and the protocol are summarized in Table S5.

Relatedness estimation. We estimated dyadic relatedness coefficients (4) in COANCESTRY v. 1.0 (5). The estimator may range from −1.0 to 1.0; negative values indicate that individuals share fewer alleles than the mean level of the population. We then examined the average genetic relatedness of male–male dyads in relation to their social affiliation. Dyads that could not be assigned to any category of social affiliation (i.e., were never seen again) were excluded from the analysis; 175 of 703 dyads were removed. We examined differences in average dyadic relatedness between the

pairs of social levels by bootstrapping the individuals 10,000 times using the program COANCESTRY v. 1.0 (5). Because of the lack of information about mother–offspring pairs, we refrained from parentage analyses.

We assessed the number of loci needed to provide consistent estimates of relatedness by simulating full-sib dyads ($r = 0.5$) at a given number of loci based on the allele frequency distribution in the real dataset. We estimated dyadic relatedness for each dyad ($n = 2{,}000$) adding one locus in each step (range, 2–25 loci). We used 10,000 bootstraps and calculated mean difference values. Results revealed that when using ≥17 microsatellite loci, there are no important changes in estimates or in the respective error.

1. Custom software "at." Available from the authors upon request.
2. Sokal RR, Rohlf FJ (1962) The comparison of dendrograms by objective methods. *Taxon* 11(2):33–40.
3. Borgatti SP, Everett MG, Freeman LC (2002) Ucinet for Windows: Software for social network analysis. Available at https://sites.google.com/site/ucinetsoftware/home. Accessed August 26, 2014.
4. Queller DC, Goodnight KF (1989) Estimating relatedness using genetic markers. *Evolution (N Y)* 43(2):258–275.
5. Wang J (2011) COANCESTRY: A program for simulating, estimating and analysing relatedness and inbreeding coefficients. *Mol Ecol Resour* 11(1):141–145.

Table S1. Gang compositions for the two study periods

Gang	Year	No. of individuals	Adult males	Adult females	Subadult males	Juveniles	Infants
Mare	2010	*ca*. 63	9	*ca*. 19	3	*ca*. 22	10
Mare	2011	*ca*. 55	8	16–17	2	19–20	9
Simenti	2011	*ca*. 60	8 (+2*)	*ca*. 18	4	*ca*. 20	8+

In 2011 the composition of the Mare gang changed because two males (CSS and MBY) disappeared, one (ANT) changed into another gang, and two subadults (BAA and NDR) became adult and were included in the analysis of 2011. Thus, six males were included in the analyses of both years (HOK, SNE, SML, PTR, OSM, and DTM).
*The Simenti gang contained two older subadult/young adult males that were seen occasionally and were not well habituated to observers. Therefore they were not included as focal subjects rather as but as unspecified subadult male partners in interactions. The remaining male-interaction partners either could not be identified or were members of a different gang.

Table S2. Dyadic relatedness estimates in the Simenti gang according to Queller and Goodnight (4)

	ASN	JKY	MSA	TBS	MST	CLV	ADM	IBR
ASN								
JKY	0.51							
MSA	−0.07	−0.12						
TBS	−0.08	−0.36	0.07					
MST	*0.02*	*0.00*	*0.02*	*0.09*				
CLV	*0.13*	*−0.21*	*-0.01*	*0.17*	−0.20			
ADM	*0.09*	*0.00*	*0.20*	*−0.11*	−0.17	0.04		
IBR	*0.14*	*0.08*	*0.22*	*−0.21*	−0.41	−0.08	0.43	

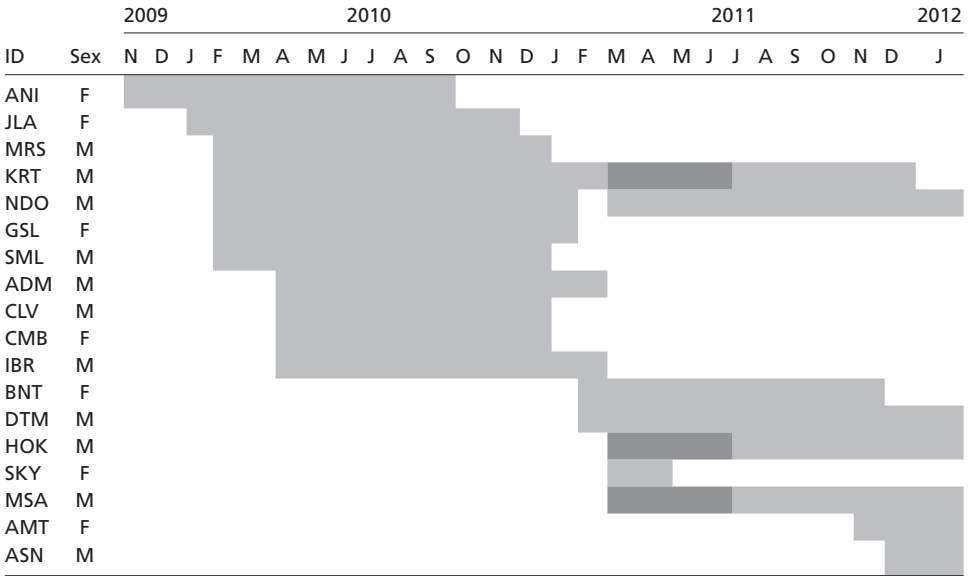
Values range from −1 to 1. Negative values reflect dyads that are less related than the average population. Between-party dyads are shown in italics.

Table S3. Dyadic relatedness estimates in the Mare gang according to Queller and Goodnight (4)

	OSM	PTR	NDR	DTM	SML	SNE	BAA	HOK
OSM								
PTR	0.28							
NDR	−0.25	−0.28						
DTM	−0.13	0.08	−0.19					
SML	*0.02*	*0.20*	*−0.11*	*0.13*				
SNE	*0.11*	*0.16*	*−0.13*	*−0.19*	−0.01			
BAA	*−0.26*	*−0.25*	*0.12*	*−0.24*	0.25	−0.17		
HOK	*0.24*	*−0.03*	*0.07*	*−0.21*	0.05	0.06	−0.01	

Values range from −1 to 1. Negative values reflect dyads that are less related than the average population. Between-party dyads are shown in italics.

Table S4. Times during which GPS data were collected from different individuals



Gray areas indicate periods during which data were collected for each animal. Dark gray areas indicate the times during which the home range areas depicted in Fig. 2 were calculated.

Table S5. Multiplex-PCR–relevant information and summary statistics for 25 microsatellite loci used to estimate dyadic relatedness

	Multiplex-PCR–relevant information		Summary statistics				
Locus	T_a, °C	Primer concentration, μM	Allele range, bp	No. of alleles	H observed	H expected	Fis
D6s264	57	0.07	94–100	4	0.55	0.51	−0.08
D7s503	54	0.7	144–158	5	0.81	0.75	−0.08
D12s375	57	0.1	165–181	5	0.73	0.78	0.06
D3s1766	58	0.05	194–202	3	0.30	0.28	−0.07
D13s765	58	0.15	197–213	5	0.42	0.46	0.10
D5s1457	58	0.08	121–133	2	0.36	0.38	0.06
D8s505	57	0.1	139–151	2	0.25	0.25	−0.04
D10s1432	56	0.3	159–171	4	0.57	0.54	−0.04
D5s820	53	0.4	178–198	6	0.84	0.76	−0.10
D3s1768	56	0.08	193–209	4	0.43	0.50	0.13
D7s2204	57	0.4	232–248	5	0.72	0.76	0.06
D14s306	62	0.08	157–177	4	0.57	0.55	−0.04
D1s533	55	0.05	187–203	4	0.69	0.67	−0.02
D2s1329	50	0.9	210–226	5	0.60	0.60	0.01
D2s1326	56	0.08	239–263	4	0.42	0.39	−0.08
D10s611	60	0.1	133–141	3	0.57	0.55	−0.03
D8s1106	58	0.1	144–160	4	0.51	0.46	−0.09
D17s791	57	0.3	164–170	4	0.46	0.50	0.07
D6s501	58	0.3	172–192	5	0.72	0.71	−0.01
D17s1290	56	0.25	194–206	4	0.57	0.58	0.03
D6s311	54	0.3	226–228	2	0.36	0.37	0.02
D1s207	57	0.1	133–135	2	0.55	0.46	−0.21
D4s243	60	0.1	147–171	5	0.75	0.65	−0.15
D1s548	57	0.1	192–208	5	0.85	0.76	−0.12
D21s1142	58	0.5	226–246	6	0.78	0.71	−0.09
Mean				4.08	0.57	0.56	−0.03
SD				1.19	0.17	0.16	

bp, base pair; Fis, inbreeding coefficient; H, heterozygosity.