Errata

In the November issue of the *Journal,* in the article "Improved Inference of Relationship for Pairs of Individuals," by Epstein et al. (67:1219–1231), the first sentence of the footnote to table 8 is incorrect; the underlined entries are classification rates for MZ twins and parent-offspring pairs (not for 2° relatives).

In the August 2000 issue of the *Journal,* in the article "An Optimized Set of Human Telomere Clones for Studying Telomere Integrity and Architecture," by Knight et al. (67:320–332), the two rows listing data for 18p were inadvertently deleted from the bottom of the first page of table 1 (p. 324); the publisher regrets this error. In addition, the clone type for 5p clone ID GS-24-H17 should be PAC (not BAC), and the source BAC libraries for 22q and XpYp should be CTD-3018-K1 and RPCI-11-839-D20, respectively (not GS-3018-K1 and GS-839-D20); the authors regret these errors. The corrected table (in which the missing rows are indicated by **bold type** and in which the other changes are underlined) is provided below.

Table 1

Second-Generation Telomere Clones and Their Location

Telomere	Clone ID	Clone Type	Maximum Physical Distance from Telomere (kb)	Method	Fiber-FISH (kb)[a]	RH Mapping (cR)[b]	Marker
1p	GS-62-L8	PAC	200	Interphase mapping from subtelomeric sequences		7.69 tel	1PTEL06
	GS-232-B23	BAC	200	Interphase mapping from subtelomeric sequences			CEB108/T7
1q	GS-160-H23	PAC	80	Contig	<50		1QTEL19
	GS-167-K11	BAC	270	RARE from YAC end sequence			1QTEL10, 1QTEL19, VIJ-YRM2123
2p	GS-892-G20	PAC	330	RARE from YAC end sequence			2PTEL27
	GS-8-L3	BAC	330	RARE from YAC end sequence			VIJ-YRM2052
2q	GS-1011-O17	PAC	240	RARE from YAC end sequence			2QTEL47
	RG-172-I13	BAC	240	RARE from YAC end sequence			VIJ-YRM2112
3p	GS-1186-B18	PAC	450	RARE from YAC end sequence	150–250		3PTEL25
	RG-228-K22	BAC	450	RARE from YAC end sequence			3PTEL25
3q	196-F4	PAC	450	YAC clone size			3QTEL06
	GS-56-H22	BAC	450	YAC clone size			3QTEL05
4p	GS-36-P21	PAC	73	Sequence: Z95704	80–100		4PTEL04
	GS-118-B13	BAC	101	Sequence: Z95704; walk from 4PTEL01			GS10K2/T7
4q	GS-963-K6	PAC	275–500	Contig (vanGeel et al. 1999)		2.9 tel	4QTEL11
	GS-31-J3	BAC	300–700[c]	Interphase distance from 4QTEL11			AFMA224XH1
5p	GS-189-N21	PAC	Unknown			16.2 cen	5PTEL48
	GS-24-H17	PAC	Unknown	Distal marker of 5p contig			C84C11/T3
5q	GS-240-G13	PAC	245	YAC clone size			5QTEL70
6p	GS-62-I11	PAC	300	Fiber FISH	<300	19.3 cen	6PTEL48
	GS-196-I5	BAC	300				6PTEL48
6q	GS-57-H24	PAC	280	RARE from YAC end sequence			6QTEL54
7p	GS-164-D18	PAC	255	YAC clone size	~130	5.76 cen	7PTEL03, VIJ-YRM2185
7q	GS-3K-23	PAC	7	Sequence: AF027390			7QTEL20, VIJ-YRM2000
8p	GS-580-L5[d]	PAC	250	YAC clone size	NP		8PTEL91
	GS-77-L23	BAC	250–450[c]	Interphase distance from 8PTEL91			AFM197XG5
8q	GS-489-D14	PAC	170	RARE from YAC end sequence			8QTEL11
	GS-261-I1	BAC	170	RARE from YAC end sequence			VIJ-YRM2053
9p	GS-43-N6	PAC	600	YAC clone size	<600	13.9 tel	9PTEL30
	RG-41-L13	BAC	190	YAC clone size			305J7-T7
9q	GS-112-N13[d]	PAC	65	YAC clone size	NP		9QTEL33
	GS-135-I17	BAC	65	YAC clone size			VIJ-YRM2241
10p	GS-306-F7	PAC	320	YAC clone size	~100		10PTEL45
	GS-23-B11	BAC	320	YAC clone size			10PTEL006
10q	GS-137-E24	PAC	270	YAC clone size	~100		10QTEL24
	GS-261-B16	BAC	270	YAC clone size			10QTEL24

(*continued*)

Table 1 Continued

Telomere	Clone ID	Clone Type	Maximum Physical Distance from Telomere (kb)	Method	Fiber-FISH (kb)[a]	RH Mapping (cR)[b]	Marker
11p	GS-908-H22[d]	PAC	125	YAC clone size	NP		11PTEL03
	GS-44-H16	PAC	125	YAC clone size			VIJ-YRM2209
11q	GS-770-G7[d]	PAC	65	YAC clone size	NP		11QTEL38
	GS-26-N8	PAC	65	YAC clone size			VIJ-YRM2072
12p	GS-496-A11[d]	PAC	Unknown	TTAGGG clone	NP	27.8 cen	12PTEL27
	GS-8-M16[d]	BAC	100	YAC clone size			TYAC-14
	GS-124-K20	BAC	100	YAC clone size			8M16/SP6
12q	GS-221-K18	PAC	190	RARE from YAC end sequence	100/600[e]		12QTEL87, VIJ-YRM2196
13q	GS-163-C9	PAC	170	RARE from YAC end sequence	<20		13QTEL56
	GS-1-L16	PAC	170	RARE from YAC end sequence			VIJ-YRM2002
14q	GS-820-M16	PAC	200	RARE from YAC end sequence			14QTEL01
	GS-200-D12	BAC	200	RARE from YAC end sequence			VIJ-YRM2006
15q	GS-124-05[d]	PAC	300[c]	Interphase mapping from 15q YAC	NP	24.46 tel	15QTEL56
	GS-154-P1	PAC	300[c]	Interphase mapping from 15q YAC			WI-5214
16p	GS-121-I4	PAC	160	Sequence: Z84721			16PTEL05
	RG-191-K2	BAC	160	Sequence: Z84721			16PTEL05
16q	GS-240-G10	PAC	200	YAC clone size		17.91 tel	16QTEL48
	GS-191-P24	PAC	200	YAC clone size			16QTEL13
17p	GS-202-L17[d]	PAC	60	Contig (Xiang et al. 1999)	30/100[e]		17PTEL80
	GS-68-F18	BAC	100–200	Walk from 17PTEL80			282M15/SP6
17q	GS-362-K4[d]	PAC	90	YAC clone size	NP		17QTEL13
	GS-50-C4	BAC	100–300	Interphase distance from 17QTEL13			AFM217YD10
18p	**GS-52-M11**	**P1**	**220**	**RARE from YAC end sequence**			**18PTEL02**
	GS-74-G18	**BAC**	**220**	**RARE from YAC end sequence**			**VIJ-YRM2102**
18q	GS-964-M9	PAC	290	RARE from YAC end sequence			18QTEL11
	GS-75-F20	BAC	290	RARE from YAC end sequence			VIJ-YRM2050
19p	GS-546-C11	PAC	250–500	LLNL chromosome 19 contig	NP	16.13 tel	19PTEL29
	RG-129-F16	BAC	250–500	LLNL chromosome 19 contig			129F16/SP6
19q	GS-48-O23	PAC	250–500	LLNL chromosome 19 contig		11.65 tel	19QTEL12
	GS-325-I23	BAC	250–500	LLNL chromosome 19 contig			D19S238E
20p	GS-1061-L1	PAC	180	YAC clone size			20PTHY33
	GS-82-O2	PAC	180	YAC clone size			20PTEL18
20q	GS-81-F12[d]	PAC	50	Fiber FISH	<50	28.2 tel	20QTEL14
21q	GS-63-H24	PAC	175	RARE from YAC end sequence			21QTEL07
	GS-2-H14[d]	P1	175	RARE from YAC end sequence			VIJ-YRM2029
22q	GS-99-K24[d]	PAC	120	Sequence: (Dunham et al. 1999)	150–200	12.6 tel	22QTEL31
	CITD-3018-K1	BAC	155	Sequence: (Dunham et al. 1999)			3018K1/T7
XpYp	GS-98-C4	PAC	490	STS map (Nagaraja et al. 1997)			DXYS28
	RPCI-11-839-D20	BAC	160	STS map (Nagaraja et al. 1997)			DXYS129
XqYq	GS-225-F6	BAC	100				CDY16C07
Xq	GS-202-M24	PAC	500	STS map (Nagaraja et al. 1997)			DXS7059

[a] NP = not possible, because of cross-hybridization.

[b] cen = centromeric; tel = telomeric.

[c] The distance given is the sum of the size of the relevant half-YAC and the estimated interphase FISH distance between the BAC clone and a subtelomeric clone known to be contained within the half-YAC.

[d] Cross-hybridization visible by FISH; see table 3 for details.

[e] Fiber-FISH indicates a size polymorphism.