Supporting Information

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SI Text

The majority of published telomere length (TL) research, as noted above, uses peripheral mononuclear blood cells (PMBCs) from whole blood as a source of DNA. To better understand the relationship between DNA from PMBCs and DNA derived from saliva, we asked 16 healthy adult volunteers (10 females and 6 males) to contribute blood and saliva samples following oral consent. The Institutional Research Board at the Penn State College of Medicine approved this study. In addition to saliva collected following the same protocol as the Fragile Families and Child Wellbeing Study sample, we also collected blood using tubes containing EDTA, followed by Ficoll separation to isolate PBMCs.

After determining TL in the 16 subjects (as described in *Materials and Methods*), a single outlier (by 4 SD) in one of the PBMC samples was removed before analysis. Telomere length was significantly greater in saliva than in blood leukocyte-derived DNA [6.5 kb ± 1.8 SD (saliva) vs. 4.2 kb ± 1.2 SD (PMBCs) $P < 0.001$] (Fig. S2). However, saliva and leukocyte DNA lengths were highly and significantly correlated ($R = 0.72$, $P = 0.002$) (Fig. S3). The difference in absolute TL is not surprising because different cell types have different rates of division and thus different rates of telomere shortening and different microenvironmental exposures. Saliva DNA originates from a number of cell types including white blood cells (21–74%) (1) and bacteria (~12%) (2). However, the fact that TL from saliva- and PMBC-derived DNA are highly correlated in adults suggests that there is no a priori reason to prefer one tissue source over another. Therefore, it may be feasible to compare studies that evaluate telomere lengths across different DNA sources (3). Unless researchers are interested in one particular cell type there is little reason to believe that one tissue TL is a better biomarker than another. Because saliva DNA is derived from several different tissue types, it is plausible that it may be more representative of organism weathering than measurements performed on DNA from a single source, such as circulating PMBCs.

1. Thiede C, Prange-Krex G, Freiberg-Richter J, Bornhäuser M, Ehninger G (2000) Buccal swabs but not mouthwash samples can be used to obtain pretransplant DNA fingerprints from recipients of allogeneic bone marrow transplants. *Bone Marrow Transplant* 25(5):575–577.
2. James C, Iwasiow RM, Birnboim HC (2011) Human genomic DNA content of saliva samples collected with Oragene self-collection kit. Available at www.DNAgenotek.com. Accessed March 1, 2014.
3. Daniali L, et al. (2013) Telomeres shorten at equivalent rates in somatic tissues of adults. *Nat Commun* 4:1597.

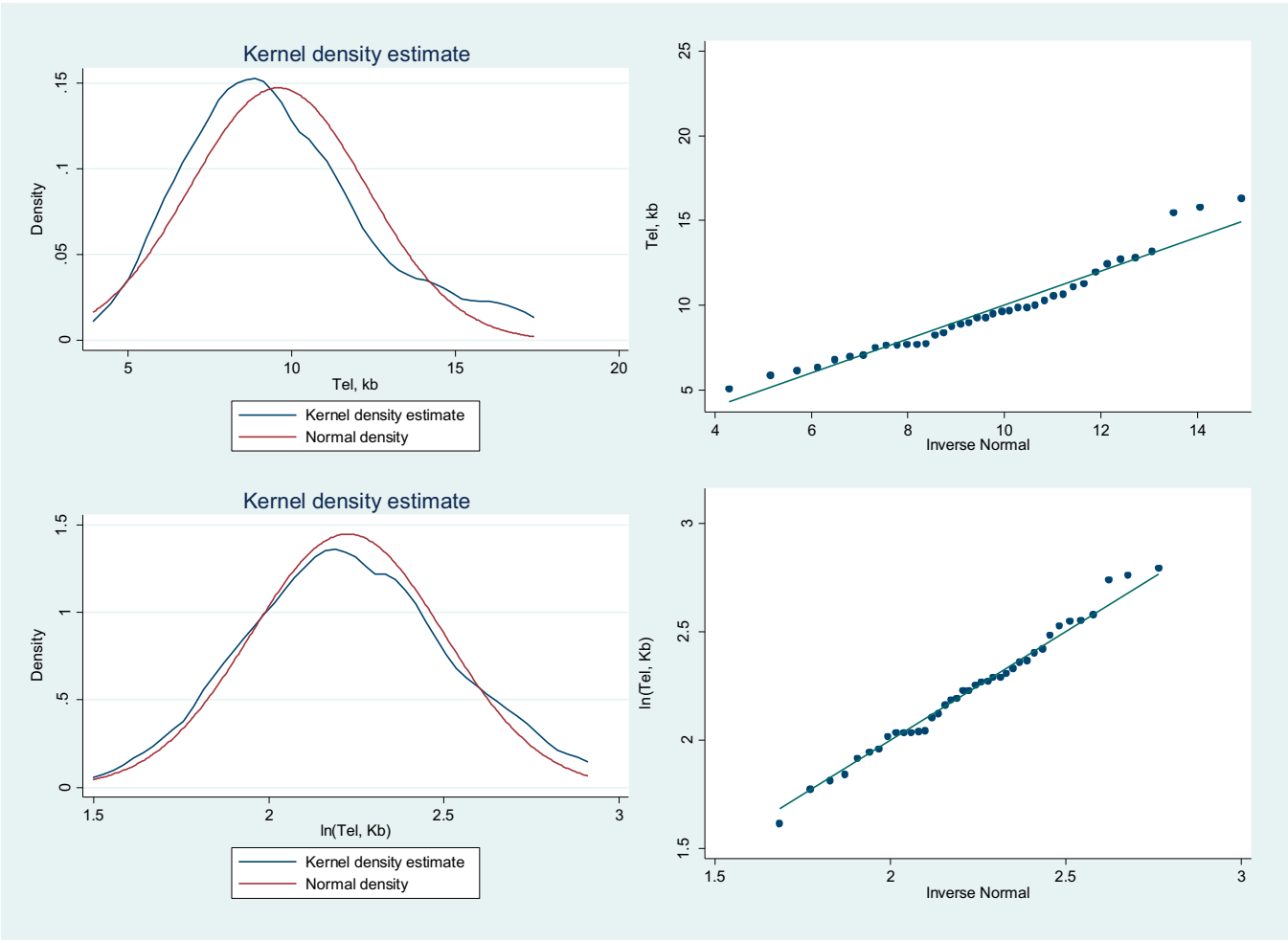

Fig. S1. Distribution of child telomere length: Raw (*Upper*) and Log Transformed (*Lower*) and kernal density (*Left*) and Q-Q plot (*Right*).

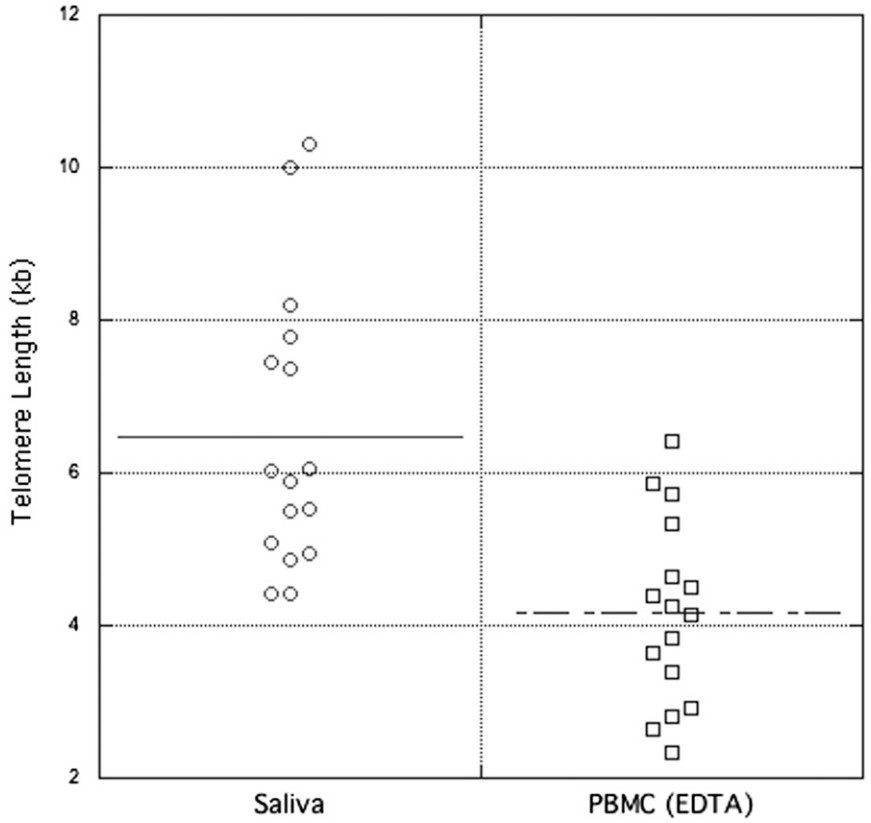

Fig. S2. Telomere length in DNA from saliva and DNA from PMBCs. Saliva DNA TL was greater than PMBC DNA [6.5 kb ± 1.8 SD (saliva) vs. 4.2 kb ± 1.2 SD (PMBCs) $P < 0.001$].

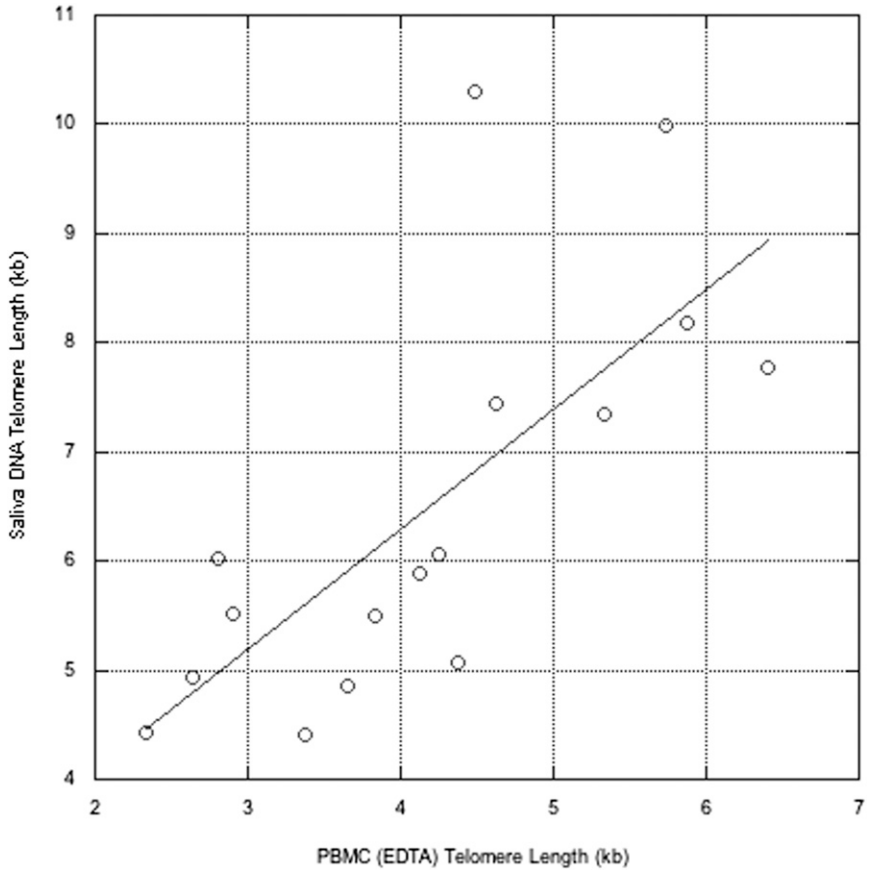

Fig. S3. Association between telomere length in saliva DNA and DNA from PBMCs. Saliva DNA TL was highly correlated with PMBC TL ($r = 0.72$, $P < 0.002$).

Table S1. Distribution of genotypes

Genotypes	Harsh environment	Nurturing environment
DRD4		
4R/4R	55	45
4R/7R	35	50
7R/7R	10	5
DRD2		
CC	55	40
CT	45	50
TT	0	10
DAT1		
TT	15	25
CT	65	40
CC	20	35
COMT		
Val/Val	35	50
Val/Met	45	35
Met/Met	20	15
5-HTT		
LL	35	60
LS	40	25
SS	25	15
Stin2		
10/10	10	5
12/10	30	50
12/12	60	45
TPH2-A		
TT	5	25
GT	50	40
GG	45	35
TPH2-B		
CC	60	45
CT	30	40
TT	10	15

The homozygous putative sensitizing genotype is in boldface type. The distributions did not differ significantly between harsh and nourishing environments.