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14. ABSTRACT
This project tested the hypotheses that inherited and/or acquired differences in telomere length prostate cancer observed in (i) African Americans compared to Caucasians and (ii) affected member (HPC) families. Telomere content, determined by quantitative PCR, in genomic DNA isolated from was assessed for associations with either racial background or prostate cancer in HPC families. isolated blood-derived genomic DNA from 289 members of 39 HPC families, 160 anonymous cord blood of different racial backgrounds and 99 samples from black and white males at mid-life. Analyses on these genomic DNA samples reveals that (i) affected individuals in HPC families tend to have a than the mean telomere lengths of unaffected family members, however, in a subset of families in affected individuals; (ii) no significant differences in telomeres were observed when comparing birth or at mid-life. These results indicate a potential association between telomere length development in a subset of hereditary prostate cancer families, but no evidence of association prostate cancer disparity between black and white males.

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INTRODUCTION

We are submitting this Final Addendum Report for our project entitled "Telomere Length Polymorphisms: a Potential Factor Underlying Increased Risk of Prostate Cancer in African American Men and Familial Prostate Cancer".

In this multidisciplinary project, we investigated whether heritable telomere length polymorphisms may help explain certain unresolved questions in clinical prostate cancer. Specifically, we hypothesized that shorter than average telomeres would be associated with the increased prostate cancer risk observed in (1) African American males compared to Caucasian American males and (2) affected versus unaffected members of hereditary prostate cancer (HPC) predisposition families which lack clear significant linkage between cancer risk and specific genomic loci. This final report communicates our final collected data, statistical analyses and conclusions drawn from these studies.

BODY

The aims of this proposal were to:

1. To test whether mean telomere lengths measured in genomic DNA isolated from peripheral blood mononuclear cells (PBMCs) differs between African Americans and Caucasians at birth and/or at mid-life.

2. To test whether mean telomere lengths measured in genomic DNA from PBMCs differ between affected versus non-affected men within hereditary prostate cancer families displaying an autosomal dominant (AD) mode of transmission, but lacking evidence for strong linkage to specific genomic loci.

3. To test whether X-chromosome specific telomere lengths measured in PBMCs differ between affected and non-affected men in hereditary prostate cancer families displaying an X-linked pattern of disease inheritance.

We proposed that these aims be accomplished by the following tasks:

Task 1: Assessment of telomere lengths in men of differing racial backgrounds

Task 1 was completed. A previously published telomere-specific quantitative polymerase chain reaction (Q-PCR) assay was established in our laboratory and extensively validated for use on genomic DNA purified from blood leukocytes (Cawthon, 2002). Pilot assays were conducted using DNA from normal and prostate cancer cell lines with known absolute mean telomere lengths derived independently by Southern blot analysis, in order to assess assay reliability and reproducibility, as well as create a set of positive control DNA samples for construction of standard curves and QC checks on each assay run. To correct for slight differences in input DNA concentrations, separate Q-PCR reactions were run, in triplicate, on each sample (96 well plate format) for telomere repeats as well as a for a single copy reference gene (beta-globin). In addition to negative (no template) controls, each assay plate also included two 5-point dilution series standard curves selected from the same set of genomic DNAs being assayed. These standard curves served as important quality control indicators and allowed us to determine the PCR efficiency for each separate experimental run, thus verifying correct assay performance. Furthermore, each run included three genomic DNA samples isolated from LNCaP prostate cancer cell lines with known differing absolute telomere lengths (as determined by Southern blot Terminal Restriction Fragment (TRF) analysis (Allsopp, et al., 1992) spanning the expected range of approximately 3 – 15 kilobases (Kbp) of telomere repeats (Meeker, et al., 2002). As well as serving as an additional QC check this sample set allowed us to directly convert our telomere Q-PCR measurements to actual average telomeric DNA lengths, expressed in Kbp. Since different PCR efficiencies were obtained for the telomere and beta-globin PCRs, the Pfaffl method (Pfaffl, 2001) was applied to determine the normalized T/S ratio. For each sample, the following equation was used:

$$\text{T/S Ratio} = (E_{\text{telomere}}^{\Delta Ct,\ \text{telomere (calibrator – test)}}) / (E_{\beta\text{-globin}}^{\Delta Ct,\ \beta\text{-globin (calibrator – test)}})$$

In this equation, E is the amplification efficiencies for the telomere and β-globin reactions. Next, the LNCaP standard curve was used to generate a best fit line equation and the normalized T/S ratio was used to determine the telomere length (in Kb) for each experimental sample. All standard curves had an R^2 value >0.99 (range: 0.991-0.998) for both telomere & beta-globin Q-PCR assays. The coefficient of variation for replicates across multiple assays on the LNCaP series ranged from 1.86% to 7.58%, with the higher CVs obtained from those samples with the lowest telomere DNA content, thus also having the smallest values for mean telomere length.

Racial variation in telomere length 1: telomeres at birth: To assess potential racial variation in telomere length at birth, we obtained neonatal umbilical venous cord blood samples from 160 normal, live, full-term births, including 84 African American neonates (39 male, 45 female) and 76 Caucasian neonates (38 male, 38 female). White blood cell fractions (buffy coat) were isolated and genomic DNA was purified from each sample. For each specimen, 5 ng was assayed for telomere content in triplicate by telomere Q-PCR. Telomere length data is tabulated in Table 1 in the Supporting Data section of this report.

Results: We tested for telomere length differences by race using the t-test for the cord blood study. In this part of the racial disparity study aim, no statistically significant differences were found in mean telomere length between African-American and white neonates at time of birth, nor between male and female neonates in this cohort, regardless of race (see Figure 1 in the Supporting Data section of this report for a summary of these results).

Racial variation in telomere length 2: telomeres at mid-life: To assess potential racial variation in telomere length at mid-life, we utilized buffy coat white blood cell fractions from blood samples collected as part of the Health Professionals Follow-up Study (HPFS), an ongoing prospective cohort study, based at Harvard University, among 51,529 male health professionals, extensively characterized with respect to lifestyle, dietary and medical history, 18,000 of who provided blood samples in 1993-1995. In a previous study, all men without diagnosis of cancer who donated blood and described their major ancestry as African American (n=63), plus a random selection of 75 Caucasian Americans without cancer were invited to donate a second blood sample. (Platz, et al., 1999). From this resource we obtained 99 samples in total, 56 from white donors and 43 from African American donors. Corresponding donor characteristics, including age, BMI, smoking status and family history of prostate cancer are presented in Table 2 in the Supporting Data section of this report. None of these characteristics were found to differ significantly on the basis of racial ancestry. Genomic DNA was purified from each sample and 5 ng was assayed in triplicate by telomere Q-PCR. Telomere length data is presented in Table 3 in the Supporting Data section of this report.

Results: In part two of the racial disparity study aim we used ANOVA to test for telomere length differences by race. No statistically significant differences were found in mean telomere length between African-American and white males at mid-life. This was true both when the two groups were directly compared, as well as when the data were modeled to include adjustment for age using linear regression.

Task 2: Assessment of telomere lengths in men from hereditary prostate cancer families displaying an autosomal dominant (AD) mode of transmission, but lacking evidence for strong linkage to specific genomic loci.

Task 2 was completed.

Quantitative PCR (detailed above) was used to assess telomere DNA repeat content in genomic DNA samples isolated from 128 members of the Johns Hopkins HPC family database, an ongoing familial prostate cancer study begun in 1992 and overseen by Dr, William Issacs. Currently the registry contains 2500 families meeting established accepted criteria for HPC (Carter et al., 1993). A subset of 200 of these families has previously been selected for genetic studies with over 1500 PBMC samples collected. Within this subset the average number of affected individuals per family is 5.1, with an average age at diagnosis of 64.3 years of age. HPC families. Individuals were selected from 17 different HPC families who had PBMC collected and whose pedigrees are consistent with an autosomal dominant (AD) mode of disease inheritance but excluding families with linkage to known AD familial prostate cancer genes. The study cohort included 71 prostate cancer affected men (biopsy-proven prostate cancer) and 57 non-affected relatives (22 male, 35 female family members), with a mean of 7.5 subjects per family. Subjects provided blood samples for research purposes. For cases, the mean time between diagnosis and blood draw was 2.11 years (sd=3.38). For each individual, telomere DNA content was measured in triplicate by Syber green Q-PCR performed on 5 ng of genomic DNA (Cawthon, 2002). Linear and conditional logistic regression were used to estimate adjusted means and odds ratios (ORs), respectively.

Results: In Supporting Data Figure 2, Telomere length data from the initial HPC cohort is plotted as a function of donor age, (excluding a single individual whose telomere

length was >6 standard deviations away form the overall mean for the cohort and was thus considered an extreme outlier). The observed range of telomere lengths observed, the broad inter-individual variation in telomere lengths and the gradual decline in telomere length with increasing age are wholly consistent with previously published series in other studies on PBMC telomere lengths in human subjects.
Mean telomere length data for each of the 128 HPC family members (cases and controls) are presented in Table 4 in the Supporting Data section, while a full dataset including clinical and family parameters is presented in Table 5. Among HPC family members, the mean telomere length for the affected group was 7.86 +/- 2.09 Kbp (median: 7.55, range: 3.66-14.04 Kb); whereas, the mean telomere length for the unaffected group was 8.87 +/- 1.92 Kbp (median: 8.82, range: 3.51-17.58 Kb). After adjusting for age and taking into account within-family correlation, the overall mean telomere length remained shorter in affected compared with unaffected individuals (mean difference = 0.55 Kb), although these results did not reach statistical significance, perhaps due to the relatively small sample size (Table 6, Supporting Data). However, in the subset of families (10 families; 39 affecteds and 38 unaffecteds) in which affecteds tended to have shorter telomeres than unaffecteds, the mean telomere length difference observed between the affected and unaffected groups (mean difference = 1.32 Kb) was statistically significant. In this subset, an inverse association was observed for telomere lengths and prostate cancer (median: OR=3.45, 95% CI: 1.22-9.96, p=0.002).

Overall, mean telomere lengths were shorter in affected versus unaffected members of HPC families, although this telomere length difference was not statistically significant when all members of the 17 HPC families were analyzed together. A subset analysis revealed 10 families which, when analyzed together, displayed a statistically significant inverse relationship between mean telomere length and prostate cancer. We therefore hypothesize that in some HPC families, losses of telomeric DNA on the order of ~1 Kb could cause telomeres within the shorter range of the normal telomere length distribution to become destabilized, thus instigating genomic instability with its inherent risk for tumorigenesis.

In an attempt to validate these results and also to increase the total sample size (and thus the statistical power), we derived a second cohort consisting of 165 members from 22 additional Johns Hopkins HPC families (83 cancer cases, 76 unaffected relatives), using the same selection criteria as was used to generate the original cohort. As with the original cohort, telomere-specific Q-PCR was conducted on genomic DNA purified from PBMC samples, as described above. A complete dataset for HPC set #2 is presented in Supporting Data, Table 7. As with the first HPC set, in this second cohort we also observed an inverse relationship between age at blood donation and white blood cell telomere length. The median telomere length for the cases in set 2 was 7.88 Kbp, very close to the value of 7.55 Kbp observed in set 1. However, the median telomere length value for the unaffected relatives in set 2 was 6.85 Kbp; significantly lower than the median value of 8.54 Kbp observed in set 1. Thus far, we have not identified any methodological source that would reasonably account for this difference between the two HPC sets.

We combined HPC set 1 and set 2 for further analysis, providing a sample set representing 39 HPC families and including 286 subjects (mean of 7.33 subjects per family, after excluding 3 men who had extreme mean telomere lengths which lay outside of the 99^{th} percentile). Four of the 39 HPC families were African American, with the remainder being Caucasian. As expected, age at blood draw and telomere length were strongly inversely associated with one another, thus highlighting the need to take age into account in subsequent analyses. Telomere lengths were not normally distributed, thus we utilized natural log transformed data which was closer to being normally distributed. In agreement with our results on neonates obtained in Task 1, we did not observe any significant association between telomere length and gender. However, after adjusting for age and gender and taking into account family history we did observe shorter mean telomere length in African American families compared to the Caucasian families and this difference was statistically significant ($p=0.02$; Wilcoxon rank sum, non-parametric, not paired), a finding in contrast to our observations on PBL telomeres in individuals at mid-life where no association by race/ethnicity was found. When comparing cases to controls (unaffecteds), after adjusting for age and conditioning on family, we did see a small but significant difference, in which controls had a shorter mean telomere length than did cases (7.85 Kbp vs. 7.32 Kbp, respectively; $p=0.04$). Essentially the same results were obtained when the analysis was restricted only to male family members.

Task 3: Assessment of X-chromosome specific telomere lengths in hereditary prostate cancer families displaying an X-linked pattern of disease inheritance.

Task 3 was not completed.

We were unable to complete Task 3 due to our inability to establish the required assay in the laboratory in time to fully complete this task. The existing published method, termed STELA, (Baird, 2003) relies on the use of radioisotopic labeling to visualize DNA products generated from individual Xp telomeres, using a technically challenging PCR. In addition to implementing this assay in our laboratory, we decided to also change the labeling strategy from one using radioactivity to one using chemiluminescence, resulting in a safer implementation of the assay. Unfortunately, this turned out to take longer than anticipated. Thus, although we eventually succeeded in converting the assay to a non-radioactive form, we were unable to complete processing of the genomic DNA samples from the X-linked HPC families. The modified version of the STELA assay was presented in April, 2010 at the American Association of Cancer Research (AACR) Annual Meeting in Washington, D.C. (C.M. Heaphy, M.C. Haffner and A.K. Meeker (2010). Development of a chemiluminescence-based single telomere length analysis (STELA) method). We plan to pursue this Aim in the future, as time and funding allows.

Key Research Accomplishments

- Q-PCR telomere content assay validated using control genomic DNA dilution series and genomic DNA from cell lines having known telomere lengths, thus allowing determination of average telomere lengths in kilobase pairs.

- Assessment of average telomere length by race at birth for160 neonates, including both male and female African Americans and 76 Caucasians.

- Assessment of average telomere length by race at mid-life for 99 male subjects - 56 Caucasians and 43 African Americans.

- Assessment of telomere lengths from genomic DNA for 286 members (affected and unaffected) of 39 hereditary prostate cancer families with autosomal dominant hereditary pattern.

- Development of a non-radioactive version of the STELA assay for measuring telomere lengths on specific telomeres.

- Other accomplishments of the research team, which were enhanced by the collaboration funded by DOD, include the implementation of a monthly joint laboratory meeting. Participants include the investigators on this DOD-funded New Investigator award (Dr. Alan Meeker (PI; cancer biology)) and Dr. Elizabeth Platz (epidemiology)), Dr. Angelo De Marzo as well as other prostate cancer principal investigators (Drs. Charles Drake (tumor immunology) and Srinivasan Yegnasubramanian (cancer biology)), doctoral students, and research fellows. We review the status of ongoing projects, brain storm about solutions to problems, and develop new research questions, some of which have culminated in grant application submissions.

Reportable Outcomes

Aim 1 (racial disparity): We assessed Racial variation in telomere length at birth and at mid-life. For the neonatal studies the final sample size was 160, including 84 African Americans (39 male, 45 female) and 76 Caucasians (38 male, 38 female). In this part of the racial disparity study aim, no statistically significant differences were found in mean telomere length between African-American and white neonates at time of birth, nor between male and female neonates (Figure 1, Supporting Data. Potential racial variation in telomere length at mid-life was also assessed. The final sample size was 99 in total, 56 from Caucasian donors and 43 from African American donors, all obtained from the Health Professionals Follow-up Study (HPFS). Telomere length data is presented in Table 3 in the Supporting Data section of this report. As in the neonatal arm, no statistically significant differences were found in mean telomere length between African-American and Caucasian males at mid-life.

Aim 2 (Telomeres in autosomal dominant hereditary prostate cancer): The final sample size was 286 subjects representing 39 AD pattern HPC families. Age at blood draw and telomere length were strongly inversely correlated. No association was found between telomere length and gender. After adjusting for age and gender, and taking into account family history, a statically significant shorter mean telomere length was found in African American families compared to the Caucasian families. After adjusting for age and family, we observed a small but significant difference in mean telomere length between cases and controls (7.85 Kbp vs. 7.32 Kbp, respectively; $p=0.04$). In subset analysis, a portion of HPC families exhibited a pattern in which affected family members possessed significantly shorter telomeres than their unaffected relatives.

Aim 3 (Telomeres in X-linked hereditary prostate cancer): We successfully developed a non-radioactive version of the assay for measuring telomere lengths on specific telomeres. Assessment of X-linked HPC families is pending.

Conclusions:

Telomeres are critical structural DNA elements of chromosomes that serve to maintain chromosomal integrity. Telomere dysfunction, particularly due to loss of telomere repeats, results in genomic instability which can, in turn, foster malignant transformation. We and others have previously published data indicating that telomere shortening is a common characteristic of cancer cells and, notably, most pre-malignant lesions as well, thus supporting a causal role for telomere shortening in human carcinogenesis. In the project described herein, we have utilized a PCR-based approach to examine the telomere length status in genomic DNA isolated from normal blood lymphocytes; thought to serve as a proxy for an individual's constitutional telomere length. By measuring an individual's telomere length in this way, we tested the hypotheses that shorter constitutive telomeres underlie (1) the racial disparity seen in prostate cancer rates between African Americans and Caucasian Americans, and (2) the difference between affected and non-affected individuals within hereditary prostate cancer fillies.

The results presented here on telomere length as a function of race found no statistical differences between African Americans and Caucasians. This was true both for male and female neonates, as well as men at mid-life. The former indicates that there is no appreciable race-associated difference in the telomere lengths an individual inherits at birth, thus, from a telomere length point of view; African Americans do not appear to start life out with telomere lengths that would conceivably place them at elevated risk of developing cancer. Likewise, the observation of no significant, race-dependent telomere length differences at mid-life indicates that racial differences in telomeres do not develop as a result either of environmental influences (e.g. dietary factors, oxidative stress, other lifestyle factors, etc.) or the impact of genetic polymorphisms (e.g. telomere maintenance genes, DNA repair genes, anti-oxidant defenses, etc.) that could have resulted in differing rates of telomere loss over time between the two groups. **We therefore conclude that telomere length changes do not appear to be an underlying contributor to the increased incidence of prostate cancer observed in African American males**. One important limitation of our study is that we were only able to assay average telomere lengths in normal circulating peripheral blood cells. While it is assumed that this measurement is reflective of the telomere lengths in other tissues throughout the body this has yet to be formally proven. Thus the possibility exists that telomere length differences in the prostate itself could still be playing a role in these phenomena. Further research is required to address this issue.

The results presented here on hereditary prostate cancer show a small but significant difference in mean telomere length between cases and controls. However, the trend in this combined analysis was opposite to that we hypothesized, namely that telomeres would be shorter in affected versus non-affected HPC individuals. On theoretical grounds, it is not expected that all HPC families have an increased prostate cancer risk due to inheritance of abnormal telomeres. In this regard it is worth noting that certain families (e.g. families 43, 134, 137, 231, 239 and 244) displayed a significant association between affected individuals and shorter telomeres. This result is in agreement with our initial hypothesis. The affected individuals in these particular families may have inherited relatively shorter telomere lengths and it will be interesting to assay additional individual's samples from these families to explore this possibility further. The results obtained to date support a role for telomere shortening in the development of prostate cancer in a subset of hereditary prostate cancer families and suggest that inheritance of chromosomes with reduced telomere lengths may place men at increased risk of developing the disease. Should further study validate this hypothesis it could provide a relatively simple, non-invasive assay to help with risk assessment in members of HPC families.

Regarding the program goals of the New Investigator Award funding mechanism, support for the PI by the DOD New Investigator Award was critical in enabling a successful early career transition from postdoctoral fellow to junior faculty with a primary focus on prostate cancer research. In addition, experience gained through conducting this study has helped in initiating other research projects aimed at elucidating the role of telomeres (and other biomarker studies) in prostate cancer. Notable milestones are outlined below.

A. As a result of the support and experience received through the DOD New Investigator Award, participation and support for additional prostate cancer projects was advanced:

Patrick C. Walsh Prostate Cancer Research Fund (Alan. Meeker, PI)
04/01/10-03/31/12
Developing Innovative Rat Prostate Cancer Models.
The goal of this project is to develop innovative rat models that more closely mimic key features of human prostate cancer biology than existing mouse or rat models.
Role: PI.

Patrick C. Walsh Prostate Cancer Research Fund (David. Shortle, PI)
04/01/10-03/31/12
Induction of Metabolic Failure in Cancer Cells: A Possible Route to Highly Selective Therapy.
This study will Assess the merits of an unconventional approach to cancer therapy – an multi-directional assault on central metabolism. Implemented by partial inhibition of multiple essential reactions plus temperature and x-irradiation.
Role: Co-investigator.

Patrick C Walsh Prostate Cancer Foundation (Shawn. Lupold, PI)
04/ 01/09-03/31/11
The Oncogenic miR-21 Gene Locus in Advanced Prostate Cancer
The goals of this project is the evaluation of miR-21 and TMEM49 expression and miR-21 gene locus copy number in advanced prostate cancer and their potential role in cancer progression. Role: co-investigator.

Department of Defense W81XWH-05-1-0030 (Elizabeth Platz, PI)
11/01/2004-10/31/2008
Telomere Length as Predictor of Aggressive Prostate Cancer

The goals of this project are to evaluate whether telomere shortening predicts aggressive prostate cancer in cohort of men and to determine whether dietary and lifestyle factors that influence cellular proliferation or oxidative stress predict telomere length in normal appearing prostate and in peripheral blood lymphocytes.
Role: Co-Investigator

NIH/NCI P01CA108964-01A1 (Project 4; Elizabeth Platz, PI)
05/01/2005-04/30/2010
Genotypic and Phenotypic Studies of Inflammation in the PCPT
The goal of this project, which is a component of the program project entitled “Biology of the Prostate Cancer Prevention Trial (PCPT)”, is to examine the contribution of the extent of intra-prostatic inflammation and atrophy as assessed in biopsies, polymorphisms in genes involved in inflammation and response to infection, and presence of antibodies against infectious agents to prostate cancer.
Role: Co-Investigator

P50 CA058236 (William. Nelson, PI)
09/01/08-08/31/13
NIH SPORE in Prostate Cancer Project 3: Blockade of the Immune Checkpoint Medicated by B7-H1 in Men with Prostate Cancer.
The major goal of this grant is to evaluate the role of LAG-3 in the inhibition of immune responses against prostate cancer and its manipulation for treatment in a transgenic mouse model.
Role: co-investigator.

Maryland TEDCO Stem Cell Fund (John Isaacs, PI)
07/01/08-06/30/11
Developing Methods for Identification and Isolation of Prostate Cancer Stem Cells
The major goal of this project is to accelerate rational development of effective therapies for both the prevention and treatment of prostate cancer.
Role: co-investigator.

Patrick C. Walsh Prostate Cancer Research Fund (Alan Meeker, PI)

04/01/2007-03/31/2008
Specific Detection of Prostate Cancer in Urine by Multiplex Immunofluorescence and Telomere FISH – Guiding Clinical Decisions Following Negative Prostate Biopsy
The goal of this project is to develop a novel cell-based assay involving simultaneous staining of telomeres and a set of protein molecular markers to allow specific identification of prostate cancer cells in urine cytology specimens.
Role: PI

Patrick C. Walsh Prostate Cancer Research Fund (Bruce Trock, PI)
04/01/2007-03/31/2008

The Senescent Phenotype in Human Prostate Cancer: Pilot Characterization Study and Association with Aging and Cellular Stress
The goal of this project is to characterize the senescent phenotype in the human prostate, its relationship to age, modulation of the phenotype by dietary factors and oxidative damage, and how it relates to risk of prostate cancer.
Role: Co-investigator

B. Experience gained while supported by the DOD New Investigator Award contributed to publication of the following peer-reviewed manuscripts related to prostate cancer and telomere cancer biology with which the applicant was directly involved:

1. Palapattu GS, **Meeker AK**, Harris T, Collector MI, Sharkis SJ, DeMarzo AM, Warlick C, Drake CG, Nelson WG. Epithelial architectural destruction is necessary for bone marrow derived cell contribution to regenerating prostate epithelium. *Journal of Urology.* 176:813-818. 2006. (Featured cover article).

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7. Albadine R, Latour M, Toubaji A, Haffner M, Isaacs WB, Platz EA, **Meeker AK**, Demarzo AM, Epstein JI, Netto GJ. TMPRSS2-ERG gene fusion status in minute (minimal) prostatic adenocarcinoma. Mod Pathol 2009;22:1415-1422. PMID: 19734849

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12. Subhawong AP, Heaphy CM, Argani P, Konishi Y, Kouprina N, Nassar H, Vang R, **Meeker AK**. The alternative lengthening of telomeres phenotype in breast carcinoma is associated with HER-2 overexpression. Mod Pathol 2009;22:1423-1431. PMID: 19734843

13. Vander Griend DJ, Konishi Y, De Marzo AM, Isaacs JT, **Meeker AK**. Dual-label centromere and telomere FISH identifies human, rat, and mouse cell contribution to Multispecies recombinant urogenital sinus xenografts. Prostate 2009;69:1557-1564. PMID: 19562732

14. Kuhn E, **Meeker A**, Wang TL, Sehdev AS, Kurman RJ, Shih IM. Shortened Telomeres in Serous Tubal Intraepithelial Carcinoma: An Early Event in Ovarian High-grade Serous Carcinogenesis. Am. J. Surg. Pathol. 2010 Apr 28. [Epub ahead of print]

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16. Shira P, Kushner J, Buchholz B, **Meeker AK**, Stein GM, Hsieh M, Kirby M, Pechhold S, Liu EH, Harlan DM, Tisdale JF. Adult human pancreatic islet beta-cells display limited turnover and long lifespan as determined by in-vivo thymidine analog incorporation and radiocarbon dating. Journal of Clinical Endocrinology & Metabolism; In press.

C. Published abstracts from presentations at national scientific meetings

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2. **Meeker AK**, Hicks JL, Smearman E, De Marzo AM. A chromogenic in situ hybridization (CISH) technique for visualizing telomeric DNA in fixed tissue sections. Lab. Invest.86: 331A-331A 1544 Suppl. 1 Jan. 2006.

3. Iwata T, **Meeker AK**, Smearman E, De Marzo AM. The telomere shortening in prostatic atrophy lesions Lab. Invest.88: 162A-162A 738 Suppl. 1 Jan. 2008.

4. Bechan GI, **Meeker AK**, DeMarzo AM, Racke F, Jaffe R ,Sugar E, Arceci RJ.Telomere length shortening in langerhans cell histiocytosis. BLOOD 110 (11): 711A-711A 2411 Part 1 Nov. 16 2007.

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7. Iwata T, **Meeker AK**, Smearman E, De Marzo AM. The telomere shortening in prostatic atrophy lesions Modern Pathology 21: 162A-162A 738 Suppl. 1 Jan. 2008.

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9. Toubaji A, Albadine R, **Meeker A**, Fedor H, DeMarzo A, Epstein JI, Platz E, Netto GJ. Chromosome 21 Copy Number but Not TMPRSS2-ERG Fusion Predicts Outcome in Prostatic Adenocacrcinoma: A Large Case-Control Radical Prostatectomy Cohort Analysis. Modern Pathology 22:197A-197A Suppl. 1 Jan. 2009.

10. Toubaji A, **Meeker A**, Albadine R, Fedor H, De Marzo AM, Netto GJ. Prognostic Significance of TMPRSS2-ERG Fusion in Prostate Cancer Progression. Jol. Mol. Diag: 10 Issue: 6, 609-609 Nov. 2008.

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12. Murray-Stewart T, Wang Y, Goodwin A, Hacker A, **Meeker A**, Casero RA. Nuclear localization of human spermine oxidase isoforms - possible implications in drug response and disease etiology. FEBS Journal 275: 11 2795-2806 Jun. 2008.

13. Sivajothi Kanagalingam, Marc K Halushka, Yuko Konishi, James Morgan, and **Alan K Meeker** Telomere Length in Diabetic Vascular Tissues Conference Information: 69th Annual Meeting of the American-Diabetes-Association, JUN 05-09, 2009 New Orleans, LA Source: DIABETES Volume: 58 Pages: A196-A196 Supplement: Suppl. 1 Published: JUN 2009.

14. Lotan TL, Toubaji A, Albadine R, Mathieu Latour, Mehsati Herawi, **Alan K Meeker**, Jonathan I Epstein and George J Netto TMPRSS2-ERG GENE FUSIONS ARE INFREQUENT IN PROSTATIC DUCTAL ADENOCARCINOMAS Conference Information: 104th Annual Meeting of the American-Urological-Association, APR 25-30, 2009 Chicago, IL. Source: JOURNAL OF UROLOGY Volume: 181 Issue: 4 Pages: 260-260 Supplement: Suppl. S Meeting Abstract: 728 Published: APR 2009.

15. Hansel DE, Konishi Y, **Meeker AK**. "Telomere Variability Is Common in Neoplastic Urothelium and Associated Morphologically Normal Urothelium" Conference Information: 98th Annual Meeting of the United-States-and-Canadian-Academy-of-Pathology, MAR 07-13, 2009 Boston, MA. Source: LABORATORY INVESTIGATION Volume: 89 Pages: 172A-172A Supplement: Suppl. 1 Meeting Abstract: 775 Published: JAN 2009.

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Recently presented abstracts:

1. G. Yun, T. Lee, C.M. Heaphy, E. Giovannucci, L.A. Mucci, S.A. Kenfield, M.J. Stampfer, W.C. Willett, J.L. Hicks, A.M. De Marzo, E.A. Platz and **A.K. Meeker** (2010). Greater variability in telomeres in cancer cells and shorter telomeres in cancer-associated stromal cells are associated with a higher risk of prostate cancer death in surgically-treated men. American Association of Cancer Research (AACR) Special Topic Conference: Role of telomeres and telomerase in cancer. Fort Worth, TX.

2. C.M. Heaphy, M.C. Haffner and **A.K. Meeker** (2010). Development of a chemiluminescence-based single telomere length analysis (STELA) method. American Association of Cancer Research (AACR) Annual Meeting, Washington, D.C.

3. C.M. Heaphy, W.B. Isaacs, S. Isaacs, K. Wiley, Y. Konishi, A. Mondul, S. Rohrmann, J.L. Bienstock, T. Agurs-Collins, E. Giovannucci, A.M. De Marzo, E.A. Platz and **A.K. Meeker** (2009). Telomere Length Polymorphisms: a Potential Factor Underlying Increased Risk of Prostate Cancer within Hereditary Prostate Cancer Families and in

African American Men. American Association of Cancer Research (AACR) Annual Meeting, Denver, CO.

D. Invited Review articles and book chapters

1. Meeker, A.K. Telomeres and telomerase in prostatic intraepithelial neoplasia and prostate cancer biology. *Urologic Oncology.* 24:122-130, 2006.

2. **Meeker, A.K.**, Gage, W.R., DeMarzo, A.M., and Maitra, A. Direct, in situ Assessment of Telomere Length Variation in Human Cancers and Preneoplastic Lesions. In Handbook of Immunochemistry and In Situ Hybridization of Human Carcinomas, Volume 2: Hayat, M.A., editor. Elsevier Academic Press. pp. 83-89, 2005.

3. **Meeker, A.K.,** and Coffey, D.S. Cellular Proliferation and Senescence in Prostate Cancer. In Prostate Cancer Principles and Practice: Roger Kirby, Alan Partin, Mark Feneley, and J. Kellogg Parsons, editors. Taylor and Francis. pp. 333-345, 2006.

4. **Meeker, A.K.** Telomeres, Telomerase and Chromosome Stability and Prostate Cancer. In Prostate Cancer Biology, Genetics, and the New Therapeutics, 2nd Edition, L. Chung, J. Simons, and W. Isaacs, editors. Humana Press. pp.317-352, 2007.

5. Gonzalgo, M and **Meeker, AK** Molecular Genetics and Cancer Biology. In *Campbell-Walsh Urology*, 10th edition. Elsevier Press, in press.

Appendices

Abbrevaitions

AD – Autosomal Dominant
APC – Adenomatous Polyposis Coli gene
BRCA1, BRCA2 –
CIN– Chromosomal Instability
CV – Coefficient of Variation
DZ – Dizygotic
FISH – Fluorescent In Situ Hybridization
HPC – Hereditary Prostate Cancer
HPFS – Health Professionals Follow-up Study
MZ – Monozygotic
OR – Odds Ratio
PBMC – Peripheral Blood Mononuclear Cell
PCR – Polymerase Chain Reaction
PIN – Prostatic Intraepithelial Neoplasia
PNA – Peptide Nucleic Acid
PSA – Prostate Specific Antigen
RR – Relative Risk
STELA – Single Telomere Length Analysis
Xp – petite (short) arm of X chromosome
Yp – petite (short) arm of Y chromosome

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Supporting Data

Table 1 Neonatal cord blood telomere length (Kbp) by race and gender				
Male			**Female**	
African American	**Caucasian**		**African American**	**Caucasian**
5.1	5.5		6.0	3.7
3.9	9.6		9.8	6.4
6.9	5.5		4.0	8.3
7.3	6.4		7.0	4.5
6.7	12.1		3.8	4.3
5.7	9.3		9.5	5.5
5.0	7.0		7.4	4.9
8.8	5.2		3.1	6.2
7.2	5.0		8.2	5.4
6.6	7.1		6.7	4.2
6.2	7.4		6.7	6.3
10.9	4.4		5.6	7.3
4.7	7.3		9.6	3.7
7.5	5.2		4.2	4.2
9.9	5.6		5.3	5.4
8.4	4.3		5.5	8.6
5.7	4.3		5.2	4.4
11.2	6.3		9.2	5.3
7.3	7.9		7.7	4.5
10.2	5.3		4.1	5.5
6.0	3.9		13.4	9.0
5.7	4.6		6.2	6.4
5.4	5.4		6.1	6.3
4.6	6.2		7.8	4.6
6.5	5.6		5.4	12.3

5.7	7.9		6.2	8.4
6.9	6.5		9.6	8.7
7.4	5.8		4.8	6.1
5.9	14.6		7.3	11.0
5.7	5.5		5.3	6.0
6.5	6.2		11.0	8.1
6.1	6.5		6.2	5.3
6.7	12.7		6.1	6.6
8.7	5.9		6.7	6.0
4.4	5.2		6.8	5.1
10.0	5.4		4.1	9.8
5.0	10.7		4.1	11.3
6.5	7.9		3.2	5.1
			9.5	9.9
			4.4	
			5.3	
			5.0	
			4.3	
			4.9	
			5.1	

Table 2 – Age-adjusted† characteristics‡ of men by major ancestry among a subset of members of the Health Professionals Follow-up Study

	White	African-American	*p-value*§
N	56	43	
Age (years)			
mean	54.1	54.4	*0.86*
Body Mass Index (kg/m^2)			
mean	25.2	26.7	*0.09*
Cigarette Smoking (%)			
never	52.0	36.7	
former	43.4	57.5	
current	0.00	0.00	
missing	0.00	3.6	*0.43*
Family History of Prostate Cancer (%)			
Yes	17.9	18.3	*0.99*

† - Standardized to the age distribution of the study population
‡ - All characteristics are from the 1994 questionnaire, except: age is from the 1986 questionnaire and 1st degree family history of prostate cancer is cumulative and is derived from the 1990, 1992, and 1996 questionnaires.
§ - Calculated using a 2-sample t-test for age, the Wald test for cigarette smoking and family history of prostate cancer, and using linear modeling for BMI.

Table 3 – Mean telomere length (Kbp) by major ancestry among a subset of members of the Health Professionals Follow-up Study

	White	African-American
T-test†		
mean (95% CI)	3.44 (3.25 – 3.64)	3.57 (3.24 – 3.93)
p-value	*0.50*	
Modeled‡		
mean (95% CI)	3.43 (3.22- 3.67)	3.57 (3.31 – 3.85)
p-value	*0.59*	

† - 2-sided 2-sample t-test
‡ - Adjusted for age

Table 4 Telomere lengths measured by Q-PCR in samples from 128 HPC family members from 17 AD pattern HPC families

HPC Family	Mean Telomere Length*	Gender	Race	Disease Status	HPC Family	Mean Telomere Length*	Gender	Race	Disease Status
29	3.51	F	C		84	4.79	M	C	PCa
	5.39	M	C	PCa		5.27	F	C	
	5.41	F	C			6.80	M	C	PCa
	5.53	F	C			7.87	F	C	
	6.57	M	C	PCa		8.39	M	C	PCa
	7.17	M	C			8.41	M	C	PCa
	7.45	M	C	PCa					
	7.55	M	C	PCa	97	4.21	F	AA	
	8.28	M	C			6.07	M	AA	PCa
	8.34	M	C			6.17	M	AA	PCa
	9.25	M	C			6.90	M	AA	PCa
	9.45	F	C			7.52	F	AA	
	9.90	M	C	PCa		8.54	F	AA	
	9.98	M	C	PCa		8.55	M	AA	PCa
	12.51	M	C			8.65	M	AA	PCa
	12.68	M	C	PCa		9.93	M	AA	PCa
	31.72	M	C	PCa					
					113	5.23	F	C	
43	5.68	F	C			5.34	M	C	PCa
	6.11	M	C	PCa		6.18	M	C	PCa
	6.18	F	C			6.19	M	C	PCa
	7.13	M	C	PCa		6.35	M	C	PCa
	8.51	M	C	PCa		7.20	F	C	
	8.82	M	C			7.38	M	C	
	12.53	M	C			7.42	F	C	
	12.73	F	C			7.53	M	C	PCa
						9.26	M	C	
77	3.66	M	C	PCa		9.52	M	C	
	4.33	F	C			9.65	M	C	PCa
	5.45	M	C	PCa		10.10	M	C	PCa
	5.78	M	C	PCa		10.85	M	C	
	6.70	M	C	PCa		11.55	F	C	
	6.85	M	C						
	7.67	M	C	PCa	119	5.83	F	C	
						5.85	M	C	PCa
						6.66	M	C	PCa
						8.39	M	C	PCa

134	6.23	M	C	PCa
	6.54	M	C	PCa
	6.60	M	C	PCa
	7.76	F	C	
	8.63	M	C	
137	5.59	M	AA	PCa
	6.59	M	AA	PCa
	7.67	M	AA	PCa
	8.18	M	AA	PCa
	9.05	M	AA	
	11.29	M	AA	
210	4.79	M	C	PCa
	4.82	M	C	
	5.06	M	C	PCa
	6.22	M	C	
	6.31	F	C	
	6.53	F	C	
	6.76	F	C	
	6.85	M	C	PCa
214	5.87	M	C	PCa
	5.91	F	C	
	7.20	M	C	PCa
	8.29	M	C	PCa
227	8.57	M	C	PCa
	9.25	M	C	PCa
	10.33	M	C	PCa
	10.79	M	C	PCa
230	8.55	M	C	
	9.22	M	C	PCa
	10.51	M	C	PCa
	11.29	M	C	PCa
	9.34	M	C	PCa
	11.80	F	C	
231	7.74	M	C	
	7.85	M	C	PCa
	7.98	M	C	PCa
	8.05	M	C	PCa
	8.66	F	C	
	9.16	F	C	
239	6.36	M	C	PCa
	9.43	M	C	PCa
	11.18	M	C	PCa
	11.37	M	C	PCa
	12.23	F	C	
	14.04	M	C	PCa
	17.58	F	C	
241	8.74	M	C	PCa
	10.08	F	C	
	10.11	M	C	
	10.39	M	C	PCa
	10.85	F	C	
	11.09	F	C	
	11.38	F	C	
	13.07	F	C	
	13.12	M	C	PCa
	13.63	F	C	
	13.93	F	C	
244	6.19	M	C	PCa
	6.56	M	C	PCa
	6.59	M	C	PCa
	8.31	M	C	PCa
	9.06	M	C	

*Telomere lengths listed are averages of at least 3 separate measurements.

Abbreviations: M = Male, F= Female, C= Caucasian, AA= African American, PCa= Prostate Cancer.

Table 5: Telomere lengths, clinical and familial data for HPC set# 1

#	Sample	Mean Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
1	029-015	9.90	1945	M	C	F		
2	029-016	3.51	1908	F	C	T	2002	
3	029-019	9.98	1913	M	C	T	1994	81
4	029-021	5.39	1919	M	C	T	1995	75
5	029-022	7.55	1914	M	C	T	2000	86
6	029-023	31.72	1917	M	C	T	1996	79
7	029-024	5.41	1926	F	C	T	2006	80
8	029-027	9.45	1918	F	C	F		
9	029-033	9.25	1951	M	C	F		
10	029-037	7.45	1946	M	C	F		
11	029-039	7.17	1946	M	C	F		
12	029-045	6.57	1946	M	C	F		
13	029-049	12.68	1954	M	C	F		
14	029-051	8.28	1944	M	C	F		
15	029-059	12.51	1943	M	C	F		
16	029-062	8.34	1950	M	C	F		
17	029-066	5.53	1956	F	C	F		
18	043-014	12.53	1922	M	C	F		
19	043-016	6.18	1919	F	C	F		
20	043-021	7.13	1923	M	C	T		
21	043-022	6.11	1924	M	C	T		75
22	043-025	12.73	1942	F	C	F		
23	043-026	8.51	1944	M	C	F		
24	043-032	5.68	1900	F	C	F		
25	043-034	8.82	1956	M	C	F		
26	077-001	5.78	1907	M	C	T	1997	90
27	077-004	4.33	1927	F	C	F		
28	077-008	3.66	1932	M	C	F		
29	077-010	6.70	1935	M	C	F		
30	077-012	7.67	1941	M	C	F		
31	077-014	5.45	1941	M	C	F		
32	077-030	6.85	1955	M	C	F		
33	084-005	5.27	1929	F	C	F		
34	084-006	4.79	1931	M	C	F		
35	084-009	6.80	1931	M	C	F		
36	084-011	8.41	1935	M	C	F		
37	084-013	8.39	1942	M	C	T	2001	58
38	084-015	7.87	1934	F	C	F		
39	097-002	4.21	1904	F	AA	T	1996	91
40	097-008	6.90	1928	M	AA	F		
41	097-010	7.52	1930	F	AA	F		
42	097-012	8.55	1932	M	AA	F		
43	097-014	6.07	1935	M	AA	F		
44	097-016	8.65	1938	M	AA	F		
45	097-020	8.54	1940	F	AA	F		

#	Sample	Mean Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
46	097-023	6.17	1945	M	AA	F		
47	097-033	9.93	1960	M	AA	F		
48	113-040	5.34	1927	M	C	F		
49	113-043	7.53	1929	M	C	T	2001	71
50	113-044	6.19	1933	M	C	F		
51	113-045	6.35	1923	M	C	T	2004	81
52	113-046	7.42	1925	F	C	T	2003	77
53	113-047	11.55	1931	F	C	F		
54	113-048	6.18	1930	M	C	F		
55	113-050	10.10	1931	M	C	F		
56	113-054	5.23	1923	F	C	F		
57	113-062	7.20	1921	F	C	T	2003	82
58	113-077	10.85	1961	M	C	F		
59	113-087	7.38	1961	M	C	F		
60	113-090	9.52	1958	M	C	F		
61	113-100	9.65	1962	M	C	F		
62	113-130	9.26	1934	M	C	T	2006	72
63	119-024	6.66	1938	M	C	F		
64	119-027	5.83	1916	F	C	F		
65	119-028	5.85	1941	M	C	F		
66	119-029	8.39	1948	M	C	F		
67	119-030	11.80	1944	F	C	F		
68	119-031	9.34	1942	M	C	F		
69	134-009	7.76	1928	F	C	F		
70	134-012	8.63	1952	M	C	F		
71	134-026	6.54	1932	M	C	F		
72	134-027	6.23	1938	M	C	F		
73	134-028	6.60	1939	M	C	T	2005	66
74	137-027	7.67	1941	M	AA	T	1998	56
75	137-028	8.18	1939	M	AA	F		
76	137-033	5.59	1966	M	AA	F		
77	137-034	9.05	1963	M	AA	F		
78	137-035	11.29	1961	M	AA	F		
79	137-051	6.59	1934	M	AA	F		
80	210-003	6.53	1926	F	C	F		
81	210-007	4.82	1919	M	C	F		
82	210-008	6.85	1931	M	C	F		
83	210-010	5.06	1928	M	C	F		
84	210-016	4.79	1953	M	C	F		
85	210-022	6.76	1961	F	C	F		
86	210-024	6.31	1951	F	C	F		
87	210-040	6.22	1950	M	C	F		
88	214-013	5.91	1925	F	C	F		
89	214-017	8.29	1931	M	C	F		

#	Sample	Mean Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
90	214-021	5.87	1942	M	C	F		
91	214-023	7.20	1942	M	C	F		
92	227-020	9.25	1939	M	C	F		
93	227-021	10.79	1937	M	C	F		
94	227-022	8.57	1935	M	C	F		
95	227-023	10.33	1932	M	C	F		
96	230-008	10.51	1950	M	C	F		
97	230-009	9.22	1952	M	C	F		
98	230-010	11.29	1956	M	C	F		
99	230-011	8.55	1958	M	C	F		
100	231-020	8.05	1940	M	C	F		
101	231-022	7.98	1939	M	C	F		
102	231-024	7.85	1936	M	C	F		
103	231-026	7.74	1936	M	C	F		
104	231-027	9.16	1932	F	C	F		
105	231-028	8.66	1940	F	C	F		
106	239-008	9.43	1918	M	C	F		
107	239-010	6.36	1919	M	C	F		
108	239-019	11.18	1947	M	C	F		
109	239-021	14.04	1948	M	C	F		
110	239-023	12.23	1950	F	C	F		
111	239-025	11.37	1953	M	C	F		
112	239-027	17.58	1955	F	C	F		
113	241-008	10.11	1913	M	C	F		
114	241-016	10.85	1931	F	C	F		
115	241-018	13.12	1932	M	C	F		
116	241-020	10.08	1934	F	C	F		
117	241-024	10.39	1938	M	C	F		
118	241-026	13.93	1936	F	C	T	2007	70
119	241-028	8.74	1941	M	C	F		
120	241-030	11.09	1944	F	C	F		
121	241-032	11.38	1946	F	C	F		
122	241-034	13.07	1949	F	C	F		
123	241-036	13.63	1951	F	C	F		
124	244-007	6.19	1922	M	C	F		
125	244-009	6.59	1922	M	C	T	2000	78
126	244-016	8.31	1943	M	C	F		
127	244-020	6.56	1951	M	C	F		
128	244-018	9.06	1947	M	C	F		

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother
1	NA	T	2003	58			2005	NEP	029-021	029-064
2	NA	FF					1993	SIS	029-003	029-004
3	T	T	1977	64			1992	BRO	029-003	029-004
4	T	T	1984	65			1993	BRO	029-003	029-004
5	UNK	T	1990	76	B	7	1992	BRO	029-003	029-004
6	T	T	1987	70			1992	BRO	029-003	029-004
7	NA	FF					1993	SIS	029-003	029-004
8	NA	FF					1993	SIS	029-003	029-004
9	NA	F					1998	SON	029-025	029-026
10	NA	T	2004	57			2004	NEP	029-021	029-064
11	NA	F					1998	NEP	029-019	029-046
12	NA	T	2001	55	T2c	5	2001	NEP	029-044	029-024
13	NA	T	1996	42		4	1997	NEP	029-050	029-027
14	NA	F					1998	NEP	029-019	029-046
15	NA	F					1998	NEP	029-020	029-058
16	NA	F					2004	NEP	029-021	029-064
17	NA	FF					2004	NIE	029-021	029-064
18	NA	F					1993	PCO	043-001	043-036
19	NA	FF					1992	SIS	043-007	043-008
20	UNK	T	1988	65	T2b		1992	BRO	043-007	043-008
21	T	T	1987	63	T2b	5	1993	BRO	043-007	043-008
22	NA	FF					1993	NIE	043-015	043-032
23	NA	T	2001	57			1993	NEP	043-015	043-032
24	NA	FF					1993	LAW	043-051	043-052
25	NA	F					1998	NEP	043-033	043-023
26	T	T	1992	84		7	1994	FAT	077-27	077-28
27	NA	FF					1994	SIS	077-01	077-02
28	NA	T	1992	60			1994	BRO	077-01	077-02
29	NA	T	1999	64			1994	BRO	077-01	077-02
30	NA	T	1993	52			1995	BRO	077-01	077-02
31	NA	T	1994	52	T1c	6	1994	BRO	077-01	077-02
32	NA	F					1998	NEP	077-03	077-04
33	NA	FF					1995	PCO	084-002	084-001
34	NA	T	1994	62	T2b	6	1995	PCO	084-002	084-001
35	NA	T	1988	56			1994	PRO	084-003	084-004
36	NA	T	1992	56			1995	BRO	084-003	084-004
37	T	T	1994	51		7	1995	BRO	084-003	084-004
38	NA	FF					1995	SIS	084-003	084-004
39	NA	FF					1995	MOT	097-062	097-063
40	NA	T	1992	63	T1c	5	1995	BRO	097-001	097-002
41	NA	FF					1995	SIS	097-001	097-002
42	NA	T	1995	63	T1c	6	1995	BRO	097-001	097-002
43	NA	T	1995	61		4	1995	BRO	097-001	097-002
44	NA	T	1998	59		6	1995	BRO	097-001	097-002
45	NA	FF					1995	SIS	097-001	097-002
46	NA	T	1995	49		6	1995	PRO	097-001	097-002
47	NA	T	2000	40			1998	NEP	097-014	097-015

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother
48	NA	T	1994	67		7	1995	BRO	113-001	113-002
49	P	T	1992	62	T2	7	1996	MCO	113-003	113-004
50	NA	T	1993	60		5	1996	MCO	113-003	113-004
51	P	T	1989	66	T1		1996	MCO	113-005	113-006
52	NA	FF					1996	SIS	113-001	113-002
53	NA	FF					1997	SIS	113-001	113-002
54	NA	T	1997	66	T1c	6	1996	MCO	113-005	113-006
55	NA	T	1993	62	T1	4	1996	MCO	113-007	113-008
56	NA	FF					1996	MCO	113-003	113-004
57	NA	FF					1996	MCO	113-005	113-006
58	NA	F					1998	NEP	113-162	113-063
59	NA	F					2002	MCO	113-050	113-025
60	NA	F					1998	MCO	113-048	113-069
61	NA	T	2004	42		6	2005	MCO	113-043	113-023
62	F	F					1998	PCO	113-128	113-129
63	NA	T	1995	56		5	1999	NEP	119-007	119-027
64	NA	FF					1999	SIS	119-021	119-003
65	NA	T	1998	56			1999	NEP	119-007	119-027
66	NA	T	1998	49			1999	NEP	119-007	119-027
67	NA	FF					1999	NIE	119-007	119-027
68	NA	T	1999	56			1999	LAW	119-008	119-009
69	NA	FF					1997	SIS	134-020	134-003
70	NA	F					1996	NEP	134-008	134-009
71	NA	T	1994	62	T2b	7	1996	PCO	134-007	134-006
72	NA	T	1996	58			1996	BRO	134-020	134-003
73	F	T	1998	59			1997	PCO	134-007	134-006
74	F	T	1996	54	T1c	6	1997	BRO	137-020	137-003
75	NA	T	2001	61	T1c	7	2005	BRO	137-020	137-003
76	NA	T	2005	39	T1c	6	2005	SON	137-026	137-032
77	NA	F					2005	SON	137-026	137-032
78	NA	F					2006	SON	137-026	137-032
79	NA	T	2002	68			2005	PCO	137-008	137-007
80	NA	FF					1999	PAN	210-050	210-051
81	NA	F					1999	PUN	210-050	210-051
82	NA	T	1999	67		8	1999	PUN	210-050	210-051
83	NA	T	1995	67		7	1999	PUN	210-050	210-051
84	NA	T	2001	48		6	1999	BRO	210-001	210-002
85	NA	FF					1999	SIS	210-001	210-002
86	NA	FF					1999	SIS	210-001	210-002
87	NA	F					2000	PCO	210-010	210-011
88	NA	FF					1999	SIS	214-001	214-002
89	NA	T	1994	63			1999	BRO	214-001	214-002
90	NA	T	1992	50			1999	PRO	214-001	214-002
91	NA	T	1993	50	T2c	4	1999	NEP	214-003	214-004

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother
92	NA	T	1993	54			2000	PRO	227-001	227-002
93	NA	T	1993	56			2000	BRO	227-001	227-002
94	NA	T	1992	57			2000	BRO	227-001	227-002
95	NA	T	1995	62			1999	BRO	227-001	227-002
96	NA	T	1999	49		7	1999	BRO	230-005	230-006
97	NA	T	2000	47	T1c	6	1999	BRO	230-005	230-006
98	NA	T	1999	43		6	1999	PRO	230-005	230-006
99	NA	F					1999	BRO	230-005	230-006
100	NA	T	1999	59	T1c	6	2000	BRO	231-004	231-005
101	NA	T	1999	60	T2b	6	2000	PRO	231-004	231-005
102	NA	T	1993	57			2000	BRO	231-004	231-005
103	NA	F					2000	PCO	231-016	231-019
104	NA	FF					2000	PCO	231-016	231-019
105	NA	FF					2000	PCO	231-016	231-019
106	NA	T	1995	77	B	8	2000	PUN	239-001	239-002
107	NA	T	1994	74	B	6	2000	FAT	239-001	239-002
108	NA	T	1997	50	T2a	7	2000	PRO	239-010	239-011
109	NA	T	2000	52	T1c	6	2000	BRO	239-010	239-011
110	NA	FF					2000	SIS	239-010	239-011
111	NA	T	2000	47		6	2000	BRO	239-010	239-011
112	NA	FF					2000	SIS	239-010	239-011
113	NA	F					2000	PUN	241-001	241-002
114	NA	FF					2000	SIS	241-012	241-013
115	NA	T	1999	67		6	2000	BRO	241-012	241-013
116	NA	FF					2000	SIS	241-012	241-013
117	NA	T	1997	59	T1c	4	2000	BRO	241-012	241-013
118	F	FF					2000	SIS	241-012	241-013
119	NA	T	1999	57	T1c	5	2000	PRO	241-012	241-013
120	NA	FF					2000	SIS	241-012	241-013
121	NA	FF					2000	SIS	241-012	241-013
122	NA	FF					2000	SIS	241-012	241-013
123	NA	FF					2000	SIS	241-012	241-013
124	NA	T	1999	77	T2a	5	2000	PUN	244-001	244-002
125	UNK	T	2000	77	T2b	6	2000	FAT	244-001	244-002
126	NA	T	1998	55		5	2000	BRO	244-009	244-010
127	NA	T	2000	48		6	2000	BRO	244-009	244-010
128	NA	F					2000	BRO	244-009	244-010

#	RRP	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
1	2003	48	4.4	T1a	3	3	6
2							
3							
4							
5							
6							
7							
8							
9							
10	2004		3.8				
11							
12		40	5.4				
13	1996		6.8				
14							
15							
16							
17							
18							
19							
20	1988	32	37	T2c			5
21							
22							
23							
24							
25							
26	1992	39		T3			7
27							
28	1992		19.2				
29							
30							
31	1994		3.9	T1c			6
32							
33							
34	1994	54	8.5	T2b	3	3	6
35	1988			T2b			
36							
37		17	8				
38							
39							
40		49	8.3				
41							
42	1995	53	4.7				7
43			6.1				
44	1998	37	3.2				5
45							
46	1995	55	4.3	T2	3	3	6
47	2000		2				

#	RRP	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
48	1994	55	22.7				7
49			27				
50	1993	37	14.6	T2			6
51			5.9				
52							
53							
54			9.2				
55			11				
56							
57							
58							
59							
60							
61	2005		1.2	T2	3	3	6
62							
63	1995		13.2				5
64							
65	1998						
66	1998						
67							
68	1999		8.2				7
69							
70							
71			13				6
72	1996		6.1				
73			9				
74	1996	43	9.9	T2	3	3	6
75		64	4.5				
76	2005		4.6	T2	3	3	6
77							
78							
79							
80							
81							
82	1999						
83	1999	69		T3			7
84	2002	51	4	T2	3	3	6
85							
86							
87							
88							
89							
90	1992		8				
91		30	7.2				

#	RRP	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
92	Y						
93	2000	28	9.8	T2c			5
94	1993						
95	1995	60	6.4				7
96	2000	37	3.9	T2c			7
97	2000		3.4	T2c			6
98	1999	51	3.8	T2c	3	3	6
99							
100	2000	48	4.3	T1c			6
101	1999		2.9	T2b			6
102	2000	46					6
103							
104							
105							
106			2				
107			3.8				
108	1997	56	3.3	T2			6
109	2001		1.8	T2			6
110							
111	2000		3.6				
112							
113							
114							
115	2000	102	11				
116							
117	1997	35	5.1		2	3	5
118							
119	1999	43	2.8	T2c			6
120							
121							
122							
123							
124			2.3				
125		21	3.6				
126	1998	38	4.7	T2			7
127	2000	44.5	3.8	T1c			6
128							

Table 6 Telomere lengths in non-affected and affected individuals of an initial cohort of 17 HPC families (n=128 individuals)

	Non-affected	Affected
Mean	8.87	7.86
SD	1.92	2.10
Median	8.82	7.55

Table 7: HPC set# 2 complete data set

#	Sample	MEAN Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
1	006-004	14.24	1916	M	C	F	NA	NA
2	006-005	12.28	1912	M	C	T	1993	81
3	006-006	14.79	1920	M	C	T	1997	77
4	009-014	8.38	1935	M	C	F	NA	NA
5	009-016	7.52	1932	M	C	T	2002	70
6	009-017	10.34	1932	M	C	T	1991	59
7	009-019	4.15	1930	F	C	T	2005	75
8	011-017	5.81	1920	M	C	T	2003	83
9	011-018	5.96	1922	M	C	F	NA	NA
10	011-020	7.88	1924	M	C	T	1994	70
11	011-021	4.63	1926	M	C	F	NA	NA
12	011-022	5.90	1928	M	C	F	NA	NA
13	018-012	6.85	1920	F	C	T	1997	77
14	018-014	7.16	1922	M	C	T	1999	77
15	018-015	5.07	1924	F	C	F	NA	NA
16	018-018	11.04	1928	M	C	F	NA	NA
17	018-019	5.85	1930	M	C	F	NA	NA
18	018-021	6.51	1938	M	C	F	NA	NA
19	018-022	9.90	1942	M	C	F	NA	NA
20	018-026	6.40	1948	M	C	F	NA	NA
21	018-031	8.11	1951	M	C	F	NA	NA
22	018-033	7.25	1960	M	C	F	NA	NA
23	019-013	13.23	1923	M	C	F	NA	NA
24	019-015	20.57	1926	M	C	F	NA	NA
25	019-017	12.51	1931	M	C	F	NA	NA
26	019-018	10.81	1938	M	C	T	UNK	UNK
27	019-022	6.89	1949	M	C	F	NA	NA
28	019-023	7.21	1952	M	C	F	NA	NA
29	020-017	8.17	1910	M	C	T	2005	95
30	020-018	5.74	1917	M	C	T	2003	86
31	020-019	8.76	1923	M	C	F	NA	NA
32	020-021	13.26	1912	M	C	T	2004	92
33	020-023	5.86	1914	F	C	F	NA	NA
34	020-024	5.25	1920	F	C	F	NA	NA
35	020-025	8.02	1950	M	C	F	NA	NA
36	020-026	8.23	1937	M	C	F	NA	NA
37	020-027	7.60	1944	M	C	F	NA	NA
38	020-047	7.03	1942	M	C	F	NA	NA
39	020-065	7.86	1937	M	C	F	NA	NA
40	031-023	7.28	1918	M	C	F	NA	NA
41	031-025	5.45	1921	M	C	F	NA	NA
42	031-026	6.04	1922	M	C	T	2009	87
43	031-027	8.16	1925	M	C	F	NA	NA

#	Sample	MEAN Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
44	031-028	7.22	1930	F	C	F	NA	NA
45	031-045	6.83	1915	M	C	T	2005	90
46	031-054	7.34	1947	M	C	F	NA	NA
47	031-058	6.67	1953	M	C	F	NA	NA
48	032-003	12.26	1927	M	C	F	NA	NA
49	032-004	11.38	1929	M	C	T	2008	79
50	032-007	11.08	1939	M	C	F	NA	NA
51	032-018	11.19	1956	M	C	F	NA	NA
52	032-019	8.89	1958	M	C	F	NA	NA
53	032-023	9.81	1966	M	C	F	NA	NA
54	033-011	11.80	1926	M	C	F	NA	NA
55	033-013	9.35	1928	M	C	F	NA	NA
56	033-014	13.90	1930	M	C	F	NA	NA
57	033-015	6.88	1931	F	C	F	NA	NA
58	033-016	7.45	1933	M	C	F	NA	NA
59	033-017	6.84	1941	F	C	F	NA	NA
60	033-020	11.20	1958	M	C	F	NA	NA
61	034-010	5.22	1913	M	C	T	2004	91
62	034-011	10.41	1918	F	C	T	UNK	UNK
63	034-012	8.59	1920	M	C	F	NA	NA
64	034-013	12.13	1924	M	C	F	NA	NA
65	034-016	4.24	1929	F	C	F	NA	NA
66	034-026	9.61	1957	M	C	F	NA	NA
67	036-017	5.52	1909	M	C	T	1995	86
68	036-019	10.79	1912	M	C	T	1995	83
69	036-022	6.65	1914	M	C	T	1996	82
70	036-024	9.71	1916	M	C	T	1999	83
71	036-026	8.65	1921	F	C	T	2005	84
72	037-016	7.26	1922	M	C	T	2002	80
73	037-018	7.35	1925	M	C	F	NA	NA
74	037-019	9.10	1928	M	C	F	NA	NA
75	037-020	6.26	1930	F	C	F	NA	NA
76	037-021	14.51	1932	F	C	F	NA	NA
77	038-014	11.08	1911	F	C	T	1998	87
78	038-017	10.35	1911	F	C	T	1998	87
79	038-018	6.52	1920	M	C	F	NA	NA
80	038-021	8.45	1923	M	C	F	NA	NA
81	038-025	10.94	1927	M	C	F	NA	NA
82	044-012	5.27	1915	M	C	T	2008	93
83	044-018	7.87	1918	M	C	F	NA	NA
84	044-019	16.09	1923	M	C	F	NA	NA
85	044-020	8.48	1927	M	C	F	NA	NA
86	044-021	8.22	1931	M	C	F	NA	NA

#	Sample	MEAN Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
87	045-003	7.89	1921	M	C	T	1996	75
88	045-004	8.79	1923	M	C	F	NA	NA
89	045-006	4.26	1930	M	C	F	NA	NA
90	045-010	6.38	1953	M	C	F	NA	NA
91	045-026	6.18	1911	M	C	F	NA	NA
92	045-029	7.39	1954	M	C	F	NA	NA
93	045-040	6.08	1900	M	C	F	NA	NA
94	045-041	6.25	1922	M	C	F	NA	NA
95	045-042	9.16	1927	M	C	F	NA	NA
96	045-064	7.00	1945	M	C	F	NA	NA
97	048-012	2.76	1919	F	AA	F	NA	NA
98	048-019	7.63	1936	F	AA	T	2002	66
99	048-020	6.86	1943	M	AA	F	NA	NA
100	048-022	4.85	1937	F	AA	F	NA	NA
101	048-026	6.48	1938	F	AA	F	NA	NA
102	048-028	8.77	1948	M	AA	F	NA	NA
103	048-029	12.46	1900	F	AA	F	NA	NA
104	048-030	21.67	1945	M	AA	F	NA	NA
105	048-031	6.12	1960	F	AA	F	NA	NA
106	048-032	5.00	1951	M	AA	F	NA	NA
107	048-044	3.40	1937	M	AA	F	NA	NA
108	051-009	7.64	1915	M	AA	T	2001	86
109	051-012	4.98	1926	F	AA	T	2007	81
110	051-013	3.85	1932	F	AA	T	1997	65
111	051-014	5.20	1953	M	AA	T	2007	54
112	051-015	6.81	1924	M	AA	T	1994	70
113	051-016	8.70	1931	F	AA	F	NA	NA
116	055-005	5.96	1915	M	C	F	NA	NA
117	055-006	7.89	1908	M	C	T	UNK	UNK
118	055-008	5.73	1917	M	C	T	2002	85
119	055-013	5.62	1914	M	C	T	2005	91
120	055-017	10.11	1920	M	C	F	NA	NA
121	055-023	6.95	1927	M	C	F	NA	NA
122	055-025	9.13	1945	M	C	F	NA	NA
123	055-027	8.85	1957	M	C	F	NA	NA
124	055-060	4.52	1954	M	C	F	NA	NA
125	070-020	8.33	1918	F	C	T	UNK	UNK
126	070-022	8.42	1921	M	C	T	2008	87
127	070-023	7.46	1922	M	C	F	NA	NA
128	070-024	7.68	1924	M	C	T	2009	85
129	070-026	6.94	1925	M	C	T	2005	80
130	070-027	4.19	1927	F	C	F	NA	NA
131	070-029	7.79	1934	F	C	F	NA	NA
132	072-011	7.84	1921	M	C	T	2008	87
133	072-013	5.19	1928	M	C	T	2008	80
134	072-016	5.78	1918	F	C	F	NA	NA

#	Sample	MEAN Telomere	Birth Year	Gender	Race	deceased	Yr. died	Age @ death
135	072-020	6.82	1927	F	C	F	NA	NA
136	072-037	8.15	1947	M	C	F	NA	NA
137	072-038	9.55	1950	M	C	F	NA	NA
138	072-041	6.39	1948	M	C	F	NA	NA
139	072-044	6.84	1961	M	C	F	NA	NA
141	072-067	5.13	1920	M	C	F	NA	NA
142	072-071	5.27	1913	M	C	T	1997	84
143	072-072	5.57	1918	M	C	T	2002	84
144	072-073	6.10	1923	M	C	T	2006	83
145	072-074	5.73	1928	M	C	T	2000	72
146	072-075	6.89	1914	F	C	F	NA	NA
147	072-077	6.87	1924	M	C	T	2000	76
148	072-079	5.62	1926	M	C	F	NA	NA
149	072-084	9.12	1956	M	C	F	NA	NA
150	072-087	6.15	1950	M	C	F	NA	NA
151	072-090	4.68	1911	F	C	T	2001	90
152	072-091	6.00	1918	F	C	F	NA	NA
153	072-093	5.85	1939	M	C	F	NA	NA
155	075-004	5.18	1923	M	C	T	2003	80
156	075-006	6.18	1925	M	C	F	NA	NA
157	075-010	5.79	1927	M	C	F	NA	NA
158	075-012	7.82	1931	F	C	F	NA	NA
159	075-014	10.09	1935	M	C	F	NA	NA
160	075-016	10.03	1941	M	C	F	NA	NA
161	075-044	12.82	1957	F	C	F	NA	NA
162	076-004	5.76	1926	M	C	F	NA	NA
163	076-006	8.10	1928	M	C	F	NA	NA
164	076-008	6.37	1929	M	C	T	2003	74
165	076-010	6.02	1931	M	C	F	NA	NA

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother	RRP
1	NA	T	1987	71			1991	Pro	006-002	006-003	T
2	T	T	1980	68			1991	Bro	006-002	006-003	UNK
3	T	T	1990	70			1991	Bro	006-002	006-003	T
				0							
4	NA	T	1989	54	T2b	6	1990	Bro	009-006	009-007	T
5	UNK	T	1987	55	T2b	4	1990	Pro	009-006	009-007	T
6	T	T	1986	54			1991	Bro	009-006	009-007	T
7	NA	NA	NA	NA	NA	NA	1993	Sis	009-006	009-007	NA
8	UNK	T	1995	75	B2	2	1993	Bro	011-014	011-015	F
9	NA	T	1984	62	T2c	6	1990	Pro	011-014	011-015	T
10	T	T	1982	58			1990	Bro	011-014	011-015	F
11	NA	F	NA	NA	NA	NA	1993	Bro	011-014	011-015	NA
12	NA	F	NA	NA	NA	NA	1993	Bro	011-014	011-015	NA
13	NA	NA	NA	NA	NA	NA	1992	Sis	018-001	018-002	NA
14	T	T	1990	68			1992	Bro	018-001	018-002	F
15	NA	NA	NA	NA	NA	NA	1993	Sis	018-001	018-002	NA
16	NA	T	1991	63			1991	Pro	018-001	018-002	T
17	NA	T	1992	62			1992	Bro	018-001	018-002	T
18	NA	F	NA	NA	NA	NA	1992	Nep	018-005	018-004	NA
19	NA	F	NA	NA	NA	NA	1992	Nep	018-005	018-004	NA
20	NA	F	NA	NA	NA	NA	1998	Nep	018-042	018-012	NA
21	NA	T	2005	54		6	2005	Nep	018-014	018-013	T
22	NA	F	NA	NA	NA	NA	1998	Son	018-018	018-017	NA
23	NA	T	1991	68			1991	Pro	019-005	019-006	F
24	NA	T	1991	65			1991	Bro	019-005	019-006	T
25	NA	T	1991	60	T2c	6	1991	Bro	019-005	019-006	T
26	UNK	T	1991	53			1991	Bro	019-005	019-006	T
27	NA	F	NA	NA	NA	NA	1998	Son	019-013	019-014	NA
28	NA	F	NA	NA	NA	NA	1998	Son	019-013	019-014	NA
29	UNK	T	1980	70		5	1992	Pro	020-008	020-009	F
30	UNK	T	1980	63	B		1992	Bro	020-008	020-009	F
31	NA	T	1978	55			1992	Bro	020-008	020-009	T
32	UNK	T	1991	79	T2		1992	Bro	020-008	020-009	F
33	NA	NA	NA	NA	NA	NA	1993	Sis	020-008	020-009	NA
34	NA	NA	NA	NA	NA	NA	1994	Sis	020-008	020-009	NA
35	NA	F	NA	NA	NA	NA	1998	Nep	020-019	020-052	NA
36	NA	F	NA	NA	NA	NA	2004	Mco	020-066	020-069	NA
37	NA	F	NA	NA	NA	NA	1998	Nep	020-021	020-022	NA
38	NA	F	NA	NA	NA	NA	1998	Son	020-017	020-029	NA
39	NA	F	NA	NA	NA	NA	2004	Mco	020-066	020-069	NA
40	NA	T	1991	73			1992	Pro	031-012	031-013	T
41	NA	T	1984	63			1992	Bro	031-012	031-013	T
42	UNK	T	1984	62	B2		1992	Bro	031-012	031-013	T
43	NA	T	2001	76	T2b	7	1992	Bro	031-012	031-013	T
44	NA	NA	NA	NA	NA	NA	1993	Sis	031-012	031-013	NA
45	UNK	T	1990	75			1993	Pco	031-010	031-062	F

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother	RRP
46	NA	F	NA	NA	NA	NA	1998	Son	031-023	031-022	NA
47	NA	F	NA	NA	NA	NA	1998	Nep	031-026	031-030	NA
48	NA	T	1992	65	B2	6	1992	Bro	032-001	032-002	T
49	T	T	1992	63			1992	Pro	032-001	032-002	F
50	NA	T	1991	52	B	5	1992	Bro	032-001	032-002	T
51	NA	F	NA	NA	NA	NA	1998	Nep	032-003	032-008	NA
52	NA	F	NA	NA	NA	NA	1998	Nep	032-003	032-008	NA
53	NA	F	NA	NA	NA	NA	1998	Nep	032-006	032-009	NA
54	NA	T	1992	66			1992	Bro	033-006	033-007	T
55	NA	T	1991	63		8	1992	Bro	033-006	033-007	T
56	NA	T	1992	62			1992	Bro	033-006	033-007	T
57	NA	NA	NA	N	NA	NA	1993	Sis	033-006	033-007	NA
58	NA	T	1992	59			1992	Pro	033-006	033-007	T
59	NA	NA	NA	NA	NA	NA	1993	Sis	033-006	033-007	NA
60	NA	F	NA	NA	NA	NA	1998	Nep	033-011	033-012	NA
61	UNK	T	1992	79			1992	Bro	034-006	034-007	
62	NA	NA	NA	NA	NA	NA	1993	Sis	034-006	034-007	NA
63	NA	T	1984	64			1992	Bro	034-006	034-007	T
64	NA	T	1991	67			1992	Bro	034-006	034-007	T
65	NA	NA	NA	NA	NA	NA	1993	Sis	034-006	034-007	NA
66	NA	F	NA	NA	NA	NA	1998	Nep	034-012	034-024	NA
67	F	F	NA	NA	NA	NA	1992	Bro	036-008	036-009	NA
68	F	T	1987	75			1992	Pro	036-008	036-009	
69	F	T	1989	75			1992	Bro	036-008	036-009	NA
70	F	T	1987	71			1992	Bro	036-008	036-009	T
71	NA	NA	NA	NA	NA	NA	1992	Sis	036-008	036-009	NA
72	T	T	1995	73	T2b		1992	Bro	037-006	037-007	NA
73	NA	T	1992	67		5	1992	Bro	037-006	037-007	T
74	NA	T	1991	63	T1a	4	1992	Bro	037-006	037-007	T
75	NA	NA	NA	NA	NA	NA	1993	Sis	037-006	037-007	NA
76	NA	NA	NA	NA	NA	NA	1992	Sis	037-006	037-007	NA
77	NA	NA	NA	NA	NA	NA	1992	Sis	038-010	038-011	NA
78	NA	NA	NA	NA	NA	NA	1992	Sis	038-010	038-011	NA
79	NA	T	1991	71			1992	Bro	038-010	038-011	T
80	NA	T	1992	69		5	1992	Pro	038-010	038-011	T
81	NA	F	NA	NA	NA	NA	1993	Pco	038-040	038-008	NA
82	F	F	NA	NA	NA	NA	1992	Bro	044-005	044-006	NA
83	NA	T	1990	72	C		1992	Bro	044-005	044-006	F
84	NA	T	1998	75	T1c		1992	Bro	044-005	044-006	F
85	NA	T	1989	62			1992	Bro	044-005	044-006	F
86	NA	T	1991	60			1992	Pro	044-005	044-006	T
87	T	T	1982	61	T2b	4	1993	Pro	045-001	045-002	T
88	NA	T	1990	67			1995	Bro	045-001	045-002	F

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother	RRP
89	NA	F	NA	NA	NA	NA	1995	Bro	045-001	045-002	NA
90	NA	F	NA	NA	NA	NA	1998	Son	045-003	045-008	NA
91	NA	T	1994	83	UNK	5	2004	Mco	045-024	045-025	F
92	NA	F	NA	NA	NA	NA	1998	Nep	045-006	045-016	NA
93	NA	F	NA	NA	NA	NA	2004	Mco	045-024	045-025	NA
94	NA	F	NA	NA	NA	NA	2004	Mco	045-024	045-025	NA
95	NA	T	1998	71	T1c	6	2004	Mco	045-024	045-025	F
96	NA	T	2006	61		6	2007	Nep	045-005	045-015	T
97	NA	NA	NA	NA	NA	NA	1993	Mot	048-003	048-004	NA
98	NA	NA	NA	NA	NA	NA	1993	Pco	048-080	048-007	NA
99	NA	F	NA	NA	NA	NA	1993	Pco	048-080	048-007	NA
100	NA	NA	NA	NA	NA	NA	1993	Pco	048-038	048-013	NA
101	NA	NA	NA	NA	NA	NA	1993	Sis	048-011	048-012	NA
102	NA	T	1991	43	B3	4	1993	Pro	048-011	048-012	T
103	NA	NA	NA	NA	NA	NA	1993	Sis	048-011	048-012	NA
104	NA	F	NA	NA	NA	NA	1993	Bro	048-011	048-012	NA
105	NA	NA	NA	NA	NA	NA	1993	Sis	048-011	048-012	NA
106	NA	T	1995	44			1993	Bro	048-011	048-012	T
107	NA	F	NA	NA	NA	NA	1993	Pco	048-037	048-014	NA
108	UNK	T	1992	77		5	1993	Pun	051-001	051-002	F
109	NA	NA	NA	NA	NA	NA	1993	Pan	051-001	051-002	NA
110	NA	NA	NA	NA	NA	NA	1993	Pan	051-001	051-002	NA
111	F	T	1993	40		6	1993	Pro	051-015	051-016	T
112	UNK	T	1992	68		8	1993	Fat	051-001	051-002	F
113	NA	NA	NA	NA	NA	NA	1993	Mot	051-020	051-021	NA
116	NA	T	1986	71	T1c		1993	Pro	055-001	055-002	F
117	NA	F	NA	NA	NA	NA	1993	Bro	055-001	055-002	NA
118	UNK	T	1992	75		8	1993	Bro	055-001	055-002	F
119	F	F	NA	NA	NA	NA	1993	Bro	055-001	055-002	NA
120	NA	T	1996	76	T1a	6	1993	Bro	055-001	055-002	T
121	NA	F	NA	NA	NA	NA	1993	Bro	055-001	055-002	NA
122	N	T	2001	56			1998	Son	055-005	055-010	T
123	NA	F	NA	NA	NA	NA	1999	Son	055-005	055-010	NA
124	N	F	NA	NA	NA	NA	1998	Nep	055-019	055-018	NA
125	NA	NA	NA	NA	NA	NA	1994	Sis	070-014	070-015	NA
126	UNK	T	1990	69	T2b		1994	Bro	070-014	070-015	T
127	F	T	1989	67			1994	Bro	070-014	070-015	T
128	UNK	T	1991	67	T2b	5	1994	Pro	070-014	070-015	T
129	F	F	NA	NA	NA	NA	1994	Bro	070-014	070-015	NA
130	NA	NA	NA	NA	NA	NA	1994	Sis	070-014	070-015	NA
131	NA	NA	NA	NA	NA	NA	1994	Sis	070-014	070-015	NA
132	UNK	T	1994	73	T1c	6	1994	Bro	072-008	072-009	F
133	T	T	1984	56	T2		1995	Bro	072-008	072-009	F
134	NA	NA	NA	NA	NA	NA	1994	Sis	072-008	072-009	NA
135	NA	NA	NA	NA	NA	NA	1995	Sis	072-008	072-009	NA
136	NA	T	2006	59	T1c	6	1998	Nep	072-011	072-010	F

#	Died of PCa	Affected	Diag Year	Age @ Dx	Stage	Bx G	Blood	Rel	Father	Mother	RRP
137	NA	F	NA	NA	NA	NA	1998	Nep	072-011	072-010	NA
138	NA	F	NA	NA	NA	NA	1999	Nep	072-029	072-020	NA
139	NA	F	NA	NA	NA	NA	1998	Son	072-015	072-014	NA
141	NA	T	1991	71		6	1994	Pco	072-005	072-065	T
142	T	T	1987	74		7	1995	Pco	072-006	072-068	F
143	UNK	T	1987	69	T2	4	1995	Pco	072-007	072-069	F
144	UNK	T	1992	69		5	1994	Pco	072-006	072-068	T
145	UNK	T	1987	59	T2		1994	Pco	072-006	072-068	F
146	NA	NA	NA	NA	NA	NA	1994	Pco	072-006	072-068	NA
147	UNK	T	1998	74			1994	Pco	072-007	072-076	F
148	NA	T	1993	67	T2c	4	1994	Pco	072-007	072-076	T
149	NA	T	2007	51		7	2008	Pco	072-066	072-081	T
150	NA	F	NA	NA	NA	NA	1994	Pco	072-067	072-088	NA
151	NA	NA	NA	NA	NA	NA	1994	Pco	072-053	072-001	NA
152	NA	NA	NA	NA	NA	NA	1994	Pco	072-053	072-001	NA
153	NA	F	NA	NA	NA	NA	1994	Pco	072-092	072-090	NA
155	UNK	T	1993	70			1994	Bro	075-001	075-002	T
156	NA	T	1993	68		6	1994	Bro	075-001	075-002	T
157	NA	F	NA	NA	NA	NA	1995	Bro	075-001	075-002	NA
158	NA	NA	NA	NA	NA	NA	1994	Sis	075-001	075-002	NA
159	NA	T	2000	65		5	1994	Bro	075-001	075-002	T
160	NA	T	1999	58		5	2001	Bro	075-001	075-002	T
161	NA	NA	NA	NA	NA	NA	2006	Nie	075-010	075-009	NA
162	NA	T	1987	61	T2b	4	1994	Pro	076-001	076-002	T
163	NA	T	1992	64	T2b	6	1994	Bro	076-001	076-002	T
164	UNK	T	1994	65	T2b	4	1994	Bro	076-001	076-002	T
165	NA	T	1991	60			1994	Bro	076-001	076-002	T

#	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
1	55	2	T3b			7
2						
3						
4	45	3.6	T2c			6
5	43	1.5	T2c			5
6	38	UNK	T2c			6
7	NA	NA	NA			NA
8	NA	13				
9		36	T2x	3	3	6
10	NA					
11	NA					
12	NA					
13	NA	NA	NA	NA	NA	NA
14	NA	NA				NA
15	NA	NA	NA	NA	NA	NA
16	54	6.9	T2	3	3	6
17		7.9	T2c			7
18	NA	NA	NA	NA	NA	NA
19	NA	NA	NA	NA	NA	NA
20	NA	NA	NA	NA	NA	NA
21	55	3.9	T2c	3	3	6
22	NA	NA	NA	NA	NA	NA
23	NA	25	NA	NA	NA	NA
24						
25	56	15.8	T2a	4	3	7
26		2.7				
27	NA	NA	NA	NA	NA	NA
28	NA	NA	NA	NA	NA	NA
29	NA	25	NA	NA	NA	NA
30	NA					
31	120		T2	2	2	4
32	NA	5.9	NA	NA	NA	NA
33	NA	NA	NA	NA	NA	NA
34	NA	NA	NA	NA	NA	NA
35	NA	NA	NA	NA	NA	NA
36	NA	NA	NA	NA	NA	NA
37	NA	NA	NA	NA	NA	NA
38	NA	NA	NA	NA	NA	NA
39	NA	NA	NA	NA	NA	NA
40	60	7.5	T2			7
41			B2			
42			B3			5
43		21				7
44	NA	NA	NA	NA	NA	NA
45	NA	8				

#	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
46	NA	NA	NA	NA	NA	NA
47	NA	NA	NA	NA	NA	NA
48	51	7.5				5
49	NA	5.8				
50		5				5
51	NA					
52	NA					
53	NA					
54		9				
55	44		T3c			8
56						
57	NA	NA	NA	NA	NA	NA
58	40	3.2	B1			6
59	NA	NA	NA	NA	NA	NA
60	NA	NA	NA	NA	NA	NA
61						
62	NA	NA	NA	NA	NA	NA
63		12.2				
64	32		T2c			5
65	NA	NA	NA	NA	NA	NA
66	NA	NA	NA	NA	NA	NA
67	NA	NA	NA	NA	NA	NA
68						
69	NA	NA	NA	NA	NA	NA
70	77		C			
71	NA	NA	NA	NA	NA	NA
72	NA	80	NA	NA	NA	NA
73	40	6.6		2	3	5
74	45	2.2	T2	2	2	4
75	NA	NA	NA	NA	NA	NA
76	NA	NA	NA	NA	NA	NA
77	NA	NA	NA	NA	NA	NA
78	NA	NA	NA	NA	NA	NA
79		5				
80	74	7.1	T2			6
81	NA	NA	NA	NA	NA	NA
82	NA					
83	NA	17	B			
84	34	9.2				
85	NA		A2			4
86	66	5.8	T2	3	2	5
87	107	10	T3a	3	2	5
88	NA	NA	NA	NA	NA	NA

#	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
89	NA	8	NA	NA	NA	NA
90	NA	NA	NA	NA	NA	NA
91	NA	6.6	NA	NA	NA	NA
92	NA	NA	NA	NA	NA	NA
93	NA	NA	NA	NA	NA	NA
94	NA	NA	NA	NA	NA	NA
95	NA	5.7	NA	NA	NA	NA
96	45.9	3.4	T2	3	3	6
97	NA	NA	NA	NA	NA	NA
98	NA	NA	NA	NA	NA	NA
99	NA	NA	NA	NA	NA	NA
100	NA	NA	NA	NA	NA	NA
101	NA	NA	NA	NA	NA	NA
102	45	14.7	C1			5
103	NA	NA	NA	NA	NA	NA
104	NA	NA	NA	NA	NA	NA
105	NA	NA	NA	NA	NA	NA
106		2.4				
107	NA	NA	NA	NA	NA	NA
108	NA		NA	NA	NA	NA
109	NA	NA	NA	NA	NA	NA
110	NA	NA	NA	NA	NA	NA
111	43	4.4	T2c	3	4	7
112	NA	NA	NA	NA	NA	NA
113	NA	NA	NA	NA	NA	NA
116	NA	3.5	NA	NA	NA	NA
117	NA	NA	NA	NA	NA	NA
118	NA	58.4	NA	NA	NA	NA
119	NA	NA	NA	NA	NA	NA
120	52	6.8	T1c	3	3	6
121	NA	NA	NA	NA	NA	NA
122		1.5				
123	NA	NA	NA	NA	NA	NA
124	NA	NA	NA	NA	NA	NA
125	NA	NA	NA	NA	NA	NA
126		11.2	T2b			5
127						
128	30	1.3	T2			5
129	NA	NA	NA	NA	NA	NA
130	NA	NA	NA	NA	NA	NA
131	NA	NA	NA	NA	NA	NA
132	NA	5.6	NA	NA	NA	NA
133	NA		NA	NA	NA	NA
134	NA	NA	NA	NA	NA	NA
135	NA	NA	NA	NA	NA	NA
136	NA	4.2	NA	NA	NA	NA

#	Pros Wt.(g)	PreTx PSA	Stage	Primary Gleason	Secondary Gleason	Gleason sum
137	NA	NA	NA	NA	NA	NA
138	NA	NA	NA	NA	NA	NA
139	NA	NA	NA	NA	NA	NA
141	43					5
142	NA	68.1	NA	NA	NA	NA
143	NA		NA	NA	NA	NA
144	86		T2			5
145	33	3.9	NA	NA	NA	NA
146	NA	NA	NA	NA	NA	NA
147	NA	3500	NA	NA	NA	NA
148	38	12.5	T2			4
149	30	2.5	T2c	4	3	7
150	NA	NA	NA	NA	NA	NA
151	NA	NA	NA	NA	NA	NA
152	NA	NA	NA	NA	NA	NA
153	NA	NA	NA	NA	NA	NA
155		5.2				
156	48	6.6	T2	3	3	6
157	NA	NA	NA	NA	NA	NA
158	NA	NA	NA	NA	NA	NA
159	24	4.6		3	3	6
160	41	2.7	T2b	3	3	6
161	NA	NA	NA	NA	NA	NA
162	76		T2			5
163		10.8				
164	61	15.8	T2			4
165		10				

Figure 1 Summary boxplot for data collected on telomere DNA content in neonates as a function of race and gender.

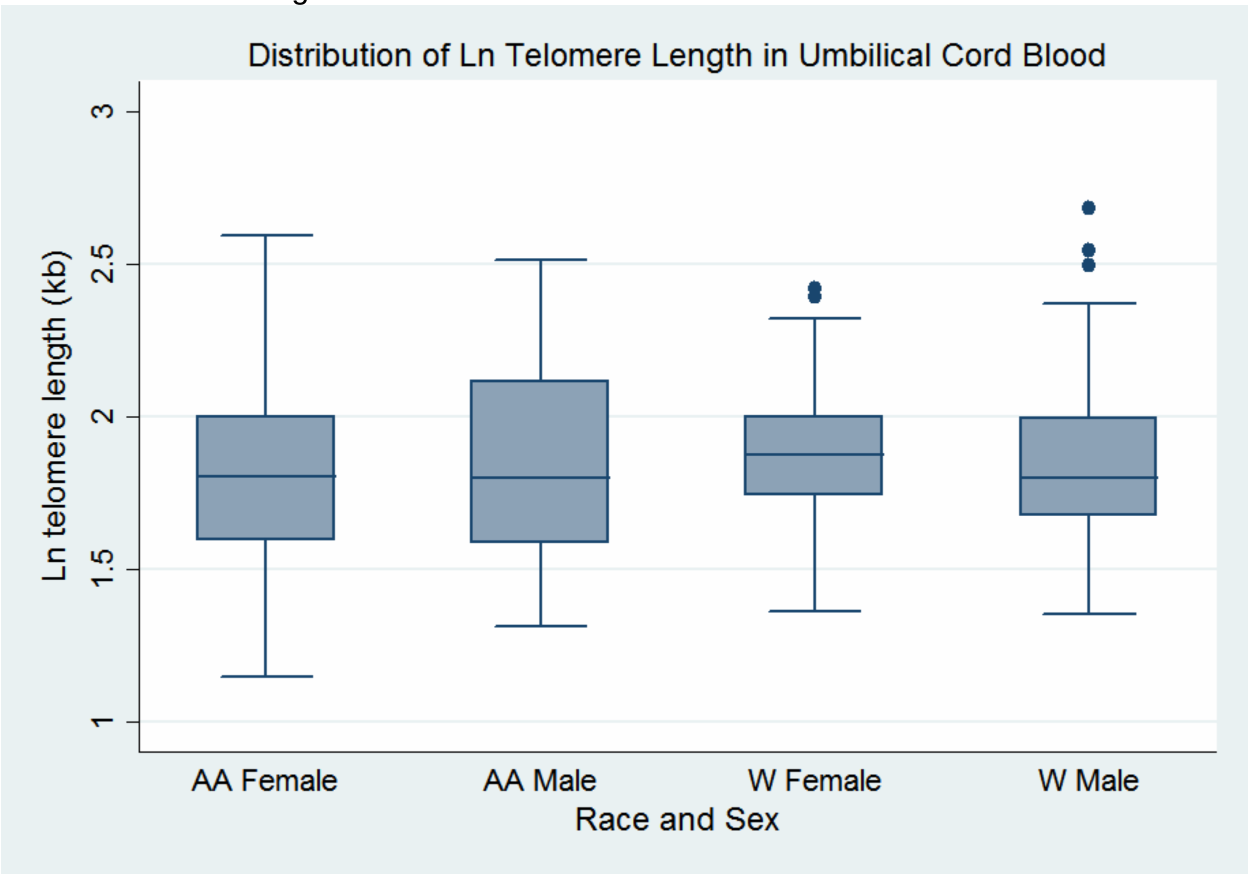

Figure 2 Telomere length as a function of donor age for 128 HPC family members from 17 AD HPC families