

July 7, 2009

Sample Selection Results for Ancillary Study #254:

Telomere and its biochemical and genetic regulators as predictors for clinical diabetes in women

Sample Selection:

All selected case control pairs (among white participants) and triads (among minority participants) selected for WHI ancillary study #132 (AS 132) were selected for entry.

Ethnicity	Cases	Controls	Total
White	1,100	1,100	2,200
Black	417	834	1,251
Hispanic	174	348	522
Asian	109	218	327

Figure 1. Ancillary study #132 Case*Ethnicity

From this original sample of 4300 participants were excluded if they had inadequate baseline DNA ($< 2 \mu\text{g}$ previously extracted and no available buffy coats for extraction) or a new genetic refusal in the time since the matching for AS 132. This resulted in the exclusion of 72 cases and 34 controls. The remaining pairs/triads were defined as follows:

Grouping	White pairs	Minority triads
Complete pair/triad	1042	657
Case DNA, single control DNA	-	16
Case DNA, no control DNA	13	0
No case DNA, full control DNA	41	26
No case DNA, single control DNA	-	1
No case DNA, no control DNA	4	0

Figure 2. Ancillary study #254 DNA availability

The remaining 4194 participants are included in the final AS 254 sample. Of the remaining 4194 participants, 199 needed DNA extraction for baseline DNA.

For the year 3 portion of the study, 120 control participants, made up of 30 of each ethnicity, were selected from among the AS 132 controls with available DNA at both baseline ($\geq 4 \mu\text{g}$ extracted, includes DNA needed for phase 1 above) and year 3 ($\geq 2 \mu\text{g}$ extracted or at least one buffy coat available for extraction). Participants with previously extracted DNA at year 3 were prioritized for the sample, with participants randomly selected first from this group and then, if necessary, from controls who required DNA extraction. Out of the 120 controls selected, 12 required DNA extraction.

The final total for AS 254 selection is 4194 baseline and 120 year 3 DNA samples of $2 \mu\text{g}$ each for a total of 4314 samples (not including blind duplicates). Out of the 4314 participants, 211 (199 at baseline, 12 at year 3) require DNA extraction.