Supplemental Figure 1. Flow Diagram of the Study Population

The MEC includes participants from five ethnic groups (African American, Japanese American, Latino, Native Hawaiian, and white) recruited in Hawaii and Los Angeles, LA. The mGWAS and APS are subset groups of the MEC. All participants completed the same validated quantitative food frequency questionnaire (QFFQ) at cohort entry (Qx1), at follow-up (Qx3), and at a second follow-up (APS). All used the same stool protocol and provided a stool sample in 2013-2016. Fecal microbial composition was obtained from 16S rRNA gene sequencing (V1-V3 region).

**Multiethnic Cohort Study (MEC)**

N=215,000

**Adiposity Phenotype Study (APS)**

N=1,861

(23% overall participation rate among eligible individuals)

**Microbiome Genome-Wide Association Study (mGWAS)**

N=4,502

(43% overall participation rate among eligible individuals)

**Excluded N=158**

(Missing BMI, invalid dietary info, and or missing microbiome)

N= 6,094

**Study Population**

N= 5,936

**APS**

(2013-2016)

N=1,685

**Qx3**

(2003-2008)

N=5,280

**Qx1**

(1993-1996)

N=5,936