- In about 2608 examination 8 Offspring participants Buffy coat DNA methylation is available and was examined with the Illumina Infinium 450K probe. The same chip was also run on ~3180 Gen 3 participants (total 5788 persons)
- Additional DNA is available for follow up pyrosequencing and Dr. Debette is funding a grant to do this for cerebral SVD association methylation sites.

Omics data at FHS.

Table 1. Number and percent[1] of Framingham participants overall and within each generation with genetic/OMICs resource listed

RESOURCE	GROUP			
	ALL IDTYPES	IDTYPE 0	IDTYPE 1	IDTYPE 3
	ALL GEN	GEN1[§]	GEN2	GEN3
TOTAL PARTICIPANTS(%total)	14169 (100)	5079(36)	5012(35)	4078(29)
	N(%)	N(%)	N(%)	N(%)
Genotypes				
CARE GENOTYPES (candidate genes chip)	7546 (53)	647 (12.7)	3022 (60.3)	3877 (95.1)
CARE IMPUTED GENOTYPES	7544 (53)	647 (12.7)	3021 (60.3)	3876 (95.0)
CHARGE-S EXOME SEQ	621 (4)	13 (0.3)	487 (9.7)	121 (3.0)
CHARGE-S TARGETED SEQ	1095 (8)	36 (0.7)	957 (19.1)	102 (2.5)
CHARGE-S WHOLE GENOME SEQ*	846 (6)	12 (0.2)	713 (14.2)	121 (3.0)
ESP Whole EXOME SEQ**	464 (3)		291 (5.8)	173 (4.2)
ADSP Whole exome SEQ**	1927 (1.4)	475 (9.4)	1452 (29.0)	
EXOME CHIP (Illumina v 1.0)	8051 (57)	655 (12.9)	3377 (67.4)	4019 (98.6)
MICROSATELLITE MARKERS	4112 (29)	454 (8.9)	1400 (27.9)	2258 (55.4)
NHGRI MEDSEQ***	1703 (12)		1703 (34.0)	
OMNI 5 CHIP (Illumina)	2472 (17)		2472 (49.3)	
100K GENOTYPES	1341 (9)	258 (5.1)	1083 (21.6)	
PERLEGEN GENOTYPES	1649 (12)		1649 (32.9)	
PGA GENOTYPES	1748 (12)		1748 (34.9)	
SHARE (550K GENOTYPES)	9163 (65)	1529 (30.1)	3746 (74.7)	3888 (95.3)
SHARE IMPUTED GENOTYPES	8372 (59)	954 (18.8)	3558 (71.0)	3860 (94.7)
SHARE FOLLOWUP GENOTYPES	7974 (56)	659 (13)	3295 (65.7)	4020 (98.6)
OMICS				
Whole blood gene expression (Affymetrix GeneChip Human Exon 1.0 ST Array)			2446 (48.8)	3180 (80)
DNA methylation- whole blood			2608	3180
Whole blood microRNA			3500 (69.8)	3500 (85.8)
Metabolome (350 metabolites)			2500 (49.9)	

TOPMed: For the WGS funded by TOPMed, we selected 4086 participants from 463 of the largest FHS families, using ExomePicks to identify who would be maximally informative for imputation, and also sequenced an additional 129 persons (controls for a study of atrial fibrillation). We expect to be able to reliably impute from these 4197 persons to 6554 FHS participants, using family-based imputation strategies.