TOPMed Omics Survey Updated: 6/12/2017

Study name	Study PI	Methylation	RNAseq	Other transcriptional profiling	Other transcriptional profiling type	Metabolomics	Proteomics	Are data in dbGaP?	If not, will data be submitted to dbGaP?
AA CAC - DHS	Allred/Bowden	0	0	0		0	0	No data	No current plans, but would submit to dbGaP if NIH funding is acquired
AA CAC - MESA Family	Rotter	0	0	0		0	0		
AFGen HVH	Heckbert	0	0	0		0	0		
AFGen MGH	Ellinor/Lubitz	0	0	0		0	0	No data	Add'l data will be submitted to dbGaP, but no other relevant studies are pending
AFGen Partners	Ellinor/Lubitz	0	0	0		0	0	No data	Add'l data will be submitted to dbGaP, but no other relevant studies are pending
Amish (full cohort n) Amish (TOPMed subset n)	Mitchell	384 279	102 24	0 0		324 209	0 0	 No	Methylomics was not fully funded by NIH, but PI is receptive to posting all data onto dbGaP RNAseq data expected back in 1-2 mos; study needs a
BAGS Asthma	Barnes	0	200 (after 2018)	0		0	0	No data	Yes
CARDIA	Fornage	0	0	0		0	0	No	
CFS Sleep Apnea	Redline	0	0	0		0	0	No data	Yes
COPDGene	Silverman	Small # of control subjects	700	26		543	824	Protein biomarker data in submission process	Gene expression (microarray) data submitted to GEO (accession GSE42057) RNAseq data will be submitted to dbGaP if it can be accommodated; otherwise will be submitted to public repository (e.g. GEO) Metabolomics data could not be deposited to dbGaP; instead submitted to NIH-funded Metabolomics Workbench
CRA Asthma	Weiss	0	300 trios	300 trios		300 trios	0	No	Yes, after initial papers on this data are published
FHS (full cohort n) FHS (TOPMed subset n)	Ramachandran	4152 2091	202 123	overall n=6425 overall n=2898		overall n=3950 overall n= 1979	overall n=1297 overall n=783	Yes except * Yes except *	3rd gen methylation and RNAseq to be submitted for next release 3rd gen methylation and RNAseq to be submitted for next release
GeneSTAR	Mathias	0	~250 samples for iPSC derived megakaryocytes and ~250 samples for platelet RNA	0		0	0	No	Yes
GENOA (also includes AA CAC contribution)	Bielak/Kardia	727	0	(gene expression) 964		0	0		
GenSalt	He	0	0	0		0	0		
GOLDN	Arnett	Illumina 450k on 991 individuals	Available on ~100 individuals	n/a		pre-/post-fat meal challenge, expected to be available on all participants in 2016	n/a	Yes, the data are now in DbGAP except for the metabolomics (it is still being measured).	Yes
IPF	Schwartz	58	44	129	Affymetric Arrays			No	No - Expression and methylation data only
JHS (full cohort n) JHS (TOPMed subset n)	Correa/Wilson	96 participants ~60 participants	none none	none none		in progress for 3420 participants in progress for 3420 participants	application under review for 3420 participants application under review for 3420 participants	No; small methylation dataset was pilot for larger study, intrinsically not useful	Metabolomics analysis just begun, to be completed over ~3 years; data will be submitted Proteomics application is under review; if funded, data will be submitted
MESA	Rotter/Rich	(of monocytes) 1200	0	chip (of monocytes) 1200		(untargeted) 4000; 2950 with WGS	0		
MLOF Hemophilia	Konkle/Johnsen	0	0	0		0	0	No data	Currently no funding for other omics; if NIH funding is acquired, will submit to dbGaP
REDS-III Brazil SCD Substudy on transfusion	Custer/Kelly	0 0	Tempus tube samples for >100; 2000 when last f/u visits are concluded Tempus tube samples for 100 (chronic transfusion), 70 (hydroxyurea), 65 (neither)	0 0		0 0	0 0		
SAPPHIRE	Williams	0	~480	0	0	0	0	No	Yes
Sarcoidosis AA	Montgomery	0	0	0		0	0	No data	Add'l omics data doubtful as contact w/participants is unavailable and only serum and limited DNA remain
SARP Asthma	Meyers	0	0	(gene expression) ~130		0	0	No	Data are in NCBI GEO database (series accession number: GSE67940)
SAFS CVD	Blangero/Curran	0	0	1240	Array based, PBMCs	0	0	No	
SAS	McGarvey	92 participants	0	0		0	0	1st pilot study: flawed design, would share only with strong caveats 2nd pilot study: much better; good raw data, will be cleaned when Dan and his colleagues finalize pipeline; effort to post to dbGaP will be non-trivial	See "Are data in dbGaP?" column
THRV	Rao/Chen	0	0	0		0	0		
VTE CHS	Heckbert	4	0	0		0	0	No	This methylation work is a pilot study and is being done on a very small number of participants who qualify for the TOPMed VTE study (n=10). The work is funded by projects that predated the new genomic data sharing policy. Submission to dbGaP is not planned.
VTE Mayo	de Andrade	0	0	0		0	0	No data	Yes
walk-PHaSST	Gladwin/Zhang	0	0	0		0	0	No data	Unlikely to submit to dbGaP as these will be investigator-driven efforts and PIs do not have full control
WHI	Kooperberg	~2000	0	0		0	0	No	Yes, but timeline for submission is not controlled by PI

TOPMed Omics Survey - FHS Detail Updated: 6/12/2017

Study name	Study PI	Methylation	RNAseq	Other transcriptional profiling	Other transcriptional profiling type	Metabolomics	Metabolic type	Proteomics	proteomic type	other	other type	Are data in dbGaP?	If not, will data be submitted to dbGaP?	
FHS (full cohort n)	Ramachandran	4152	202	overall n=6425		overall n=3950		overall n=1297		7302	N	Yes except *	3rd gen methylation and RNAseq to be submitted for next release	
				5712	A	649	D	873	K			Yes		
				2216	B	2012	E	268	L			Yes		
				5619	C	2456	F	662	M			yes		
						2014	G					yes		
						992	H					yes		
						990	I					yes		
						385	J					yes		
FHS (TOPMed subset n)		2091	123	overall n=2898		overall n= 1979		overall n= 783		3436	N	Yes except *	3rd gen methylation and RNAseq to be submitted for next release	
				2681	A	285	D	507	K			Yes		
				1153	B	1156	E	177	L			Yes		
				2632	C	1391	F	419	M			yes		
						1157	G					yes		
						355	H					yes		
						354	I					yes		
						253	J					yes		

Key

Letter	Description of data type
A	MicroRNA profiling of WBC derived RNA
B	RTPCR Gene Expression
C	gene expression profiling of WBC derived RNA
D	Metabolomics - Risk Factor Study: GC/MS - BMI/Lipids/Glucose Factorial Design
E	Central Metabolomics - Hilic -Installments 1&2
F	Metabolomics data - Hilic - Installments 1-3
G	Metabolomics - Lipid Platform - Installment 1&2
H	Negatively Charged Polar Metabolomics - Amide - Installment 1
I	Targeted and Untargeted Metabolomics - HILIC - Installment 1
J	urine metabolomics
K	Aptamer Proteomic Profiling: Lab Assay (blood)
L	iTRAQ Px data set 135 case/control pairs ;
M	Targeted MRM Px of 33 targets measured in the CVD study; Multiple reaction monitoring (MRM)
N	Immunoassays of 85 circulating protein biomarkers of atherosclerosis and metabolic syndrome