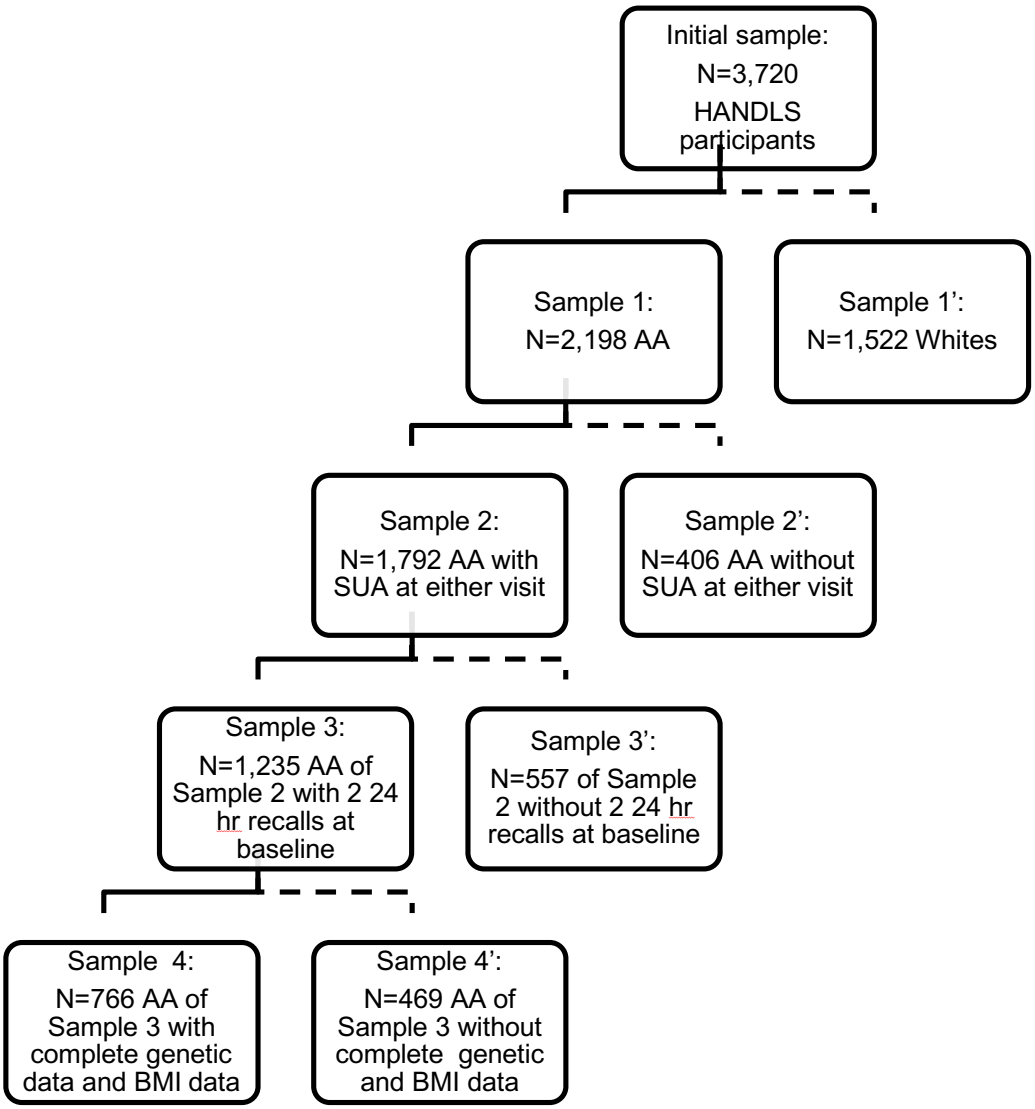
Supplemental Figure 1. Participant flow chart



AA=African-American; BMI=Body Mass Index; HANDLS=Healthy Aging in Neighborhoods of Diversityacross the Life Span; SUA=Serum Uric Acid.

Appendix 1. Genotyping and quality control

HANDLS participants were genotyped using the Illumina 1M genotyping array. A total of 1,024 individuals were successfully genotyped. Sample quality control inclusion criteria were: **(1)** concordance between self-reported sex and X-chromosome based sex; **(2)** >95% call rate per participant (across all equivalent arrays), **(3)** concordance between self-reported African ancestry and genotyped SNPs confirmed ancestry, and **(4)** proportional sharing of genotypes < 15% between samples, excluding close relatives from the final sample. Moreover, SNPs in HANDLS were selected when the following criteria were met: **(1)** Hardy-Weinberg equilibrium (HWE) p-value>10^{-7}; **(2)** Missing by haplotype p-values > 10^{-7}; **(3)** Minor allele frequency>0.01, and **(4)** Call rate > 95%. Basic quality control and data management for each genotype was conducted using PLINKv1.06.(1) Cryptic relatedness was estimated via pairwise identity by descent analyses in PLINK and confirmed using RELPAIR.(2) STRUCTUREv2.3(3-5) and the multidimensional scaling (MDS) function in PLINKv1.06 were used to determine ancestry among HANDLS participants. HANDLS participants with component vector estimates consistent with the HapMap African ancestry samples for the first 4 component vectors were included. Moreover, in our main analyses, we adjusted for all 10 principal components to control for any residual effects of population structure.(6). SNPs that passed the above quality control criteria were used for genotype imputation using MACH and minimac softwares (http://www.sph.umich.edu/csg/abecasis/mach/). The 1000 Genomes Project phase 1 alpha freeze multiethnic panel were used as a reference population to impute SNPs. Imputed SNP with imputation quality measure of R^2<0.3 or minor allele frequency of <1% were excluded from the analysis. Serum uric acid (SUA) associated SNPs identified by genome-wide association and candidate gene studies were selected from those SNPs that passed the imputation quality control criteria.

References:

1. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet 2007;81(3):559-75. doi: S0002-9297(07)61352-4 [pii]

10.1086/519795.
2. Epstein MP, Duren WL, Boehnke M. Improved inference of relationship for pairs of individuals. Am J Hum Genet 2000;67(5):1219-31. doi: S0002-9297(07)62952-8 [pii]

10.1016/S0002-9297(07)62952-8.
3. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. Genetics 2000;155(2):945-59.
4. Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. Genetics 2003;164(4):1567-87.
5. Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: dominant markers and null alleles. Mol Ecol Notes 2007;7(4):574-8. doi: 10.1111/j.1471-8286.2007.01758.x.
6. Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis corrects for stratification in genome-wide association studies. Nature genetics 2006;38(8):904-9. doi: ng1847 [pii]

10.1038/ng1847.

Supplemental Table 1. List of SNP selected from various GWAS and confirmatory studies [1; 2; 3; 4; 5] shown to be associated with high serum uric acid (SNPhsua)

Variant	Location	Risk allele (Higher SUA)	Other allele (Lower SUA)	Population, references	Minor Allele Frequency	Status
SLC2A9 (chromosome 4)						
rs1014290	**Intron 3**	**T**	**C**	**European ancestry[6]**	**G=0.33**	**A**
rs6449213	**Intron 4**	**T**	**C**	**White [6; 7; 8; 9; 10], AA[11; 12], Hispanic[2]**	**C=0.14**	**A**
rs734553	Intron 6	T	G	White,[13; 14; 15] Icelandic,[16] AA[12]	G=0.30	D
rs7442295	**Intron 6**	**A**	**G**	**White[7; 14; 15; 17]**	**G=0.26**	**A**
rs737269	Intron 7	T	C	European ancestry[6; 15]	T=0.41	C
rs6855911	Intron 7	A	G	White, [7; 14; 15; 17] AA[12]	G=0.30	D
rs13129697	**Intron 7**	**T**	**G**	**White,[15; 18] AA[12], Hispanic[2]**	**G=0.48**	**A**
rs2241480	**Intron 8**	**T**	**A/C**	**European ancestry[12]**	**T=0.33**	**B**
rs7663032	Intron 9	T	G/C	AA,[12] Croatian[15]	C=0.37	D
rs3775948	Intron 9	C	G	Croatian,[15] AA[11]	G=0.34	D
rs16890979	Intergenic	C	T	White,[15; 19; 20] AA[12], Amish,[21] Croatian, [15] Pacific Islander,[20] New Zealander[20]	T=0.26	D
rs717615	Intergenic	A	G	Croatian[15]	G=0.43	C
rs6856396	Intergenic	T	A	AA[11]	A=0.14	C
rs11942223	Intergenic	T	C	European[22]	C=0.27	D
rs11723388	Intergenic	G	A	Hispanic[2]	A=0.12	C
rs11721501	Intergenic	G	A	Hispanic[2]	A=0.13	D
rs6843466	Intergenic	G	A	Hispanic[2]	T=0.49	E
rs17251963	Intergenic	A	G	Hispanic[2]	C=0.13	D
rs13113918	Exon 3	G	A	Hispanic[2]	A=0.18	D
rs7683856	Intron	G	A	Hispanic[2]	A=0.18	D
rs9991278	**Intron**	**G**	**A**	**Hispanic[2]**	**T=0.17**	**A**
rs11723439	Intron	G	A	Hispanic[2]	T=0.12	C
rs4697745	Intergenic	G	A	Hispanic[2]	A=0.19	C
rs7675964	Intron	G	A	Hispanic[2]	T=0.47	D
rs938552	Intron	G	A	Hispanic[2]	T=0.26	D
rs12510549	Intergenic	A	G	Hispanic[2]	C=0.17	C
rs11722228	Intron	T	C	Chinese[3]	T=0.31	C
rs12498742	**Intron**	**A**	**G**	**European[5]**	**G=0.30**	**A**
ABCG2 (chromosome 4)						
rs2231137	Exon 2	A	G	Japanese[23]	A= 0.16	D
rs72552713 (Q126X)	Exon 4	T	C	Japanese[23]	A=0.001	F
rs2231142(Q141K)	**Exon 5**	**T**	**G**	**White,[13; 14; 15; 19; 24], European,[5] African, [12; 19]Chinese,[3; 25] Icelandic,[16] Japanese, [23; 26]**	**T=0.12**	**A**

				Pacific Islander,[27] New Zealander[27; 28]		
rs2199936	Intergenic	A	G	White[13; 15; 18]	N/A	E
rs4148152	Intron	T	C	Chinese[3]	C=0.16	C
rs3114018	Intron	G	T	Chinese[3]	C=0.50	C
SLC22A12 (chromosome 11)						
rs11231825	Exon 1	C	T	Chinese,[29] White,[13; 30] AA[12]	C=0.39	D
rs12800450	Exon 2	G	T	AA[12]	**T=0.01**[12]	E
rs559946	Intron 3	C	T	Chinese[31]	T=0.43	C
rs893006	Intron 4	G	T	Japanese,[32] Chinese[33]	G/T=0.50	C
rs1529909	Intron 4	T	C	Korean[34]	C=0.39	E
rs17300741	Intron 4	A	G	European[13; 35]	G=0.33	C
rs7932775	**Exon 8**	**C**	**T**	**German,[30] Chinese,[29; 31] Solomon Islander[29]**	**C=0.40**	**A**
rs505802	Intergenic	C	T	European,[13; 15] AA[12]	T=0.43	D
rs11602903	Intergenic	A	T	German,[30] Chinese[31]	T=0.39	D
rs3825018	Intergenic	G	A	European[22]	A=0.39	D
SLC16A9 (chromosome 10)						
rs12356193	Intron 1	A	G	European,[13] Icelandic[16]	G=0.09	C
SLC17A1 (chromosome 6)						
rs1165196	Exon 7	A	G	White,[18] Icelandic,[16] Japanese[19; 36]	G=0.28	D
rs1183201	Intron 10	T	A	European[13]	A=0.29	D
rs11751616	Intergenic	A	G	AA[12]	G=0.02	C
rs2051541	Intergenic	G	A	European ancestry[12]	A=0.50	C
rs3799344	**Intergenic**	**C**	**T**	**European[37]**	**T=0.37**	**A**
SLC17A3 (chromosome 6)						
rs1165205	Intron 1	C	T	White[19]	T=0.31	C
SLC22A11 (chromosome 11)						
rs10792443	Intron 4	G	C	European ancestry[12]	C=0.39	C
rs2078267	Intron 6	C	T	European[5], White,[18] Icelandic[16]	T=0.23	C
GCKR (chromosome 2)						
rs780094	Intron 16	T	C	European[13; 35]	T=0.30	C
rs780093	Intron 17	T	C	White,[18] Icelandic[16]	T=0.29	D
rs814295	Intron 17	G	A	AA[12]	G=0.23	C
rs1260326	**Exon 15**	**T**	**C**	**European[5]**	**T=0.29**	**A**
LRRC16A (chromosome 6)						
rs9321453	Intron 12	T	C	AA[12]	T=0.24	C
rs742132	**Intron 30**	**A**	**G**	**European[13; 35]**	**G=0.29**	**A**

		(G increases SUA in our sample)				
PDZK1 (chromosome 1)						
rs882211	Intron 1	C	G	AA[12]	G=0.06	C
rs1967017	Intergenic	T	C	White[18], European[22]	C=0.30	C
R3HDM2-INHBC region (chromosome 12)						
rs1106766	Intergenic	C	T	White, [18] Icelandic[16]	T=0.14	C
RREB1 (chromosome 6)						
rs675209	Intergenic	T	C	White, [18] Icelandic,[16] Croatian[15], European[5; 22]	C=0.45	C
NRXN2 (chromosome 11)						
rs478607	**Intron**	**G**	**A**	**European[5]**	**G=0.28**	**B**
UBE2Q2 (chromosome 15)						
rs1394125	Intron	A	G	European[5]	G=0.26	C
IGF1R (chromosome15)						
rs6598541	Intron	A	G	European[5]	A=0.45	C
NFAT5 (chromosome16)						
rs71931165778	**Intergenic**	**C**	**T**	**European[5]**	**C=0.08**	**B**
HLF (chromosome 17)						
rs7224610	**Intron**	**C**	**A**	**European[5]**	**C=0.22**	**A**

Excluded SNPs of n=68	
Reason #1: Missing from database	
4 SNPs were not available in the HANDLS genotype imputed database: Status E.	
AA	rs12800450
Korean	rs1529909
Whites	rs2199936
Hispanic	rs6843466
Reason #2: Poor imputation quality	
SNP rs72552713 has poor imputation quality (imputation quality measure of $R^2 = 0.0073$: Status F	
Reason #3: High linkage disequilibrium with another SNP	
At LD R^2 of 0.8, in 500 kb window, LD pruning was done, regardless of MAF; 20/63 were excluded, resulting in 43 tag SNPs. 12 found to be associated with baseline SUA (Status A)	

3 found to be associated with SUA rate of change (Status B) 28 non-significant (Status C) 20 remaining SNPs (Status D)
Initially selected SNPs: n=43
Finally selected SNPs: N=15 (12 for baseline and 3 for rate of change in SUA)

Note: Minor allele frequency is obtained from: http://www.ncbi.nlm.nih.gov/snp, except when bolded (the MAF is obtained from a study). The risk allele is determined from the largest study. Both risk allele and other allele indicate the direction of reported association with serum uric acid (SUA) in previous studies regardless of their allele frequency in the population. Minor Allele Frequency indicates which allele (risk or other) is the less frequent one.

References

1. Reginato AM, Mount DB, Yang I *et al.* (2012) The genetics of hyperuricaemia and gout. *Nature reviews Rheumatology* **8**, 610-621.
2. Voruganti VS, Laston S, Haack K *et al.* (2015) Serum uric acid concentrations and SLC2A9 genetic variation in Hispanic children: the Viva La Familia Study. *The American Journal of Clinical Nutrition* **101**, 725-732.
3. Yang B, Mo Z, Wu C *et al.* (2014) A genome-wide association study identifies common variants influencing serum uric acid concentrations in a Chinese population. *BMC Medical Genomics* **7**, 10.
4. Li C, Yu Q, Han L *et al.* (2014) The hURAT1 rs559946 polymorphism and the incidence of gout in Han Chinese men. *Scandinavian journal of rheumatology* **43**, 35-42.
5. Kottgen A (2013) Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nat Genet* **45**, 145 - 154.
6. Vitart V (2008) SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. *Nat Genet* **40**, 437 - 442.
7. Doring A (2008) SLC2A9 influences uric acid concentrations with pronounced sex-specific effects. *Nat Genet* **40**, 430 - 436.
8. Wallace C (2008) Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. *Am J Hum Genet* **82**, 139 - 149.
9. Dehghan A (2008) High serum uric acid as a novel risk factor for type 2 diabetes. *Diabetes Care* **31**, 361 - 362.
10. Brandstatter A (2008) Sex-specific association of the putative fructose transporter SLC2A9 variants with uric acid levels is modified by BMI. *Diabetes Care* **31**, 1662 - 1667.
11. Charles BA, Shriner D, Doumatey A *et al.* (2011) A genome-wide association study of serum uric acid in African Americans. *BMC Med Genomics* **4**, 17.
12. Tin A, Woodward OM, Kao WH *et al.* (2011) Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. *Hum Mol Genet* **20**, 4056-4068.
13. Kolz M (2009) Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. *PLoS Genet* **5**, e1000504.
14. Stark K, Reinhard W, Neureuther K *et al.* (2008) Association of common polymorphisms in GLUT9 gene with gout but not with coronary artery disease in a large case-control study. *PloS one* **3**, e1948.

15. Karns R, Zhang G, Sun G *et al.* (2012) Genome-wide association of serum uric acid concentration: replication of sequence variants in an island population of the Adriatic coast of Croatia. *Ann Hum Genet* **76**, 121-127.
16. Sulem P, Gudbjartsson DF, Walters GB *et al.* (2011) Identification of low-frequency variants associated with gout and serum uric acid levels. *Nat Genet* **43**, 1127-1130.
17. Li S (2007) The GLUT9 gene is associated with serum uric acid levels in Sardinia and Chianti cohorts. *PLoS Genet* **3**, e194.
18. Yang Q, Kottgen A, Dehghan A *et al.* (2010) Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors. *Circulation Cardiovascular genetics* **3**, 523-530.
19. Dehghan A (2008) Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. *Lancet* **372**, 1953 - 1961.
20. Hollis-Moffatt JE, Xu X, Dalbeth N *et al.* (2009) Role of the urate transporter SLC2A9 gene in susceptibility to gout in New Zealand Maori, Pacific Island, and Caucasian case-control sample sets. *Arthritis and rheumatism* **60**, 3485-3492.
21. McArdle PF, Parsa A, Chang YP *et al.* (2008) Association of a common nonsynonymous variant in GLUT9 with serum uric acid levels in old order amish. *Arthritis and rheumatism* **58**, 2874-2881.
22. Phipps-Green AJ, Merriman ME, Topless R *et al.* (2014) Twenty-eight loci that influence serum urate levels: analysis of association with gout. *Ann Rheum Dis*.
23. Matsuo H (2011) Identification of ABCG2 dysfunction as a major factor contributing to gout. *Nucleosides Nucleotides Nucleic Acids* **30**, 1098 - 1104.
24. Woodward O (2009) Identification of a urate transporter, ABCG2, with a common functional polymorphism causing gout. *Proc Natl Acad Sci U S A* **106**, 10338 - 10342.
25. Wang B, Miao Z, Liu S *et al.* (2010) Genetic analysis of ABCG2 gene C421A polymorphism with gout disease in Chinese Han male population. *Human genetics* **127**, 245-246.
26. Yamagishi K (2010) The rs2231142 variant of the ABCG2 gene is associated with uric acid levels and gout among Japanese people. *Rheumatology* **49**, 1461 - 1465.
27. Phipps-Green AJ, Hollis-Moffatt JE, Dalbeth N *et al.* (2010) A strong role for the ABCG2 gene in susceptibility to gout in New Zealand Pacific Island and Caucasian, but not Maori, case and control sample sets. *Hum Mol Genet* **19**, 4813-4819.
28. Caulfield M (2008) SLC2A9 is a high-capacity urate transporter in humans. *PLoS Med* **5**, e197.
29. Tu HP, Chen CJ, Lee CH *et al.* (2010) The SLC22A12 gene is associated with gout in Han Chinese and Solomon Islanders. *Ann Rheum Dis* **69**, 1252-1254.
30. Graessler J, Graessler A, Unger S *et al.* (2006) Association of the human urate transporter 1 with reduced renal uric acid excretion and hyperuricemia in a German Caucasian population. *Arthritis and rheumatism* **54**, 292-300.
31. Li C, Han L, Levin AM *et al.* (2010) Multiple single nucleotide polymorphisms in the human urate transporter 1 (hURAT1) gene are associated with hyperuricaemia in Han Chinese. *Journal of medical genetics* **47**, 204-210.
32. Shima Y, Teruya K, Ohta H (2006) Association between intronic SNP in urate-anion exchanger gene, SLC22A12, and serum uric acid levels in Japanese. *Life sciences* **79**, 2234-2237.
33. Guan M (2011) Association of an intronic SNP of SLC2A9 gene with serum uric acid levels in the Chinese male Han population by high-resolution melting method. *Clin Rheumatol* **30**, 29 - 35.
34. Jang WC, Nam YH, Park SM *et al.* (2008) T6092C polymorphism of SLC22A12 gene is associated with serum uric acid concentrations in Korean male subjects. *Clinica chimica acta; international journal of clinical chemistry* **398**, 140-144.
35. van der Harst P, Bakker SJ, de Boer RA *et al.* (2010) Replication of the five novel loci for uric acid concentrations and potential mediating mechanisms. *Hum Mol Genet* **19**, 387-395.

36. Urano W, Taniguchi A, Anzai N *et al.* (2010) Sodium-dependent phosphate cotransporter type 1 sequence polymorphisms in male patients with gout. *Ann Rheum Dis* **69**, 1232-1234.
37. Hollis-Moffatt JE, Phipps-Green AJ, Chapman B *et al.* (2012) The renal urate transporter SLC17A1 locus: confirmation of association with gout. *Arthritis research & therapy* **14**, R92.

Appendix 2. Mixed-effects regression models

The main multiple mixed-effects regression models can be summarized as follows:

	Multi-level models vs. **Composite models**	
Eq.		
1.1-1.4	$Y_{ij} = \pi_{0i} + \pi_{1i} Time_{ij} + \varepsilon_{ij}$	$\pi_{0i} = \gamma_{00} + \gamma_{0a} X_{aij} + \sum_{k=1}^{l} \gamma_{0k} Z_{ik} + \zeta_{0i}$ $\pi_{1i} = \gamma_{10} + \gamma_{1a} X_{aij} + \sum_{m=1}^{n} \gamma_{1m} Z_{im} + \zeta_{1i}$
		$Y_{ij} = \gamma_{00} + \gamma_{0a} X_{aij} + \sum_{k=1}^{l} \gamma_{0k} Z_{ik} + \gamma_{10} Time_{ij} + \gamma_{1a} X_{aij} Time_{ij} + \sum_{m=1}^{n} \gamma_{1m} Z_{im} Time_{ij} + (\zeta_{0i} + \zeta_{1i} Time_{ij} + \varepsilon_{ij})$

Where Y_{ij} is the outcome (SUA) for each individual "i" and visit "j"; π_{0i} is the level-1 intercept for individual i; π_{1i} is the level-1 slope for individual i; γ_{00} is the level-2 intercept of the random intercept π_{0i}; γ_{10} is the level-2 intercept of the slope π_{1i}; Z_{ik} is a vector of fixed covariates for each individual *i* that are used to predict level-1 intercepts and slopes and included baseline age (Age_{base}) among other covariates. $X_{ija,}$ represents the main predictor variables (8 dietary components or the two dummy variables for GRS tertiles); ζ_{0i} and ζ_{1i} are level-2 disturbances; ε_{ij} is the within-person level-1 disturbance. Of primary interest are the main effects of each exposure X_a (γ_{0a}) and their interaction with *TIME* (γ_{1a}), as described in a previous methodological paper.(1)

Reference

1. Blackwell E, de Leon CF, Miller GE. Applying mixed regression models to the analysis of repeated-measures data in psychosomatic medicine. Psychosom Med 2006;68(6):870-8. doi: 01.psy.0000239144.91689.ca [pii]

10.1097/01.psy.0000239144.91689.ca.

Supplemental Table 2. Mixed-effects regression models of SUA by each of the 15 selected SNP[1,2]

	Gene locus	Risk allele Dosage	γ±SEE	p-value
Serum Uric Acid			**n=766[3]**	**n'=1,341[3]**
Model 1: rs1260326	*GCKR*	T(0,1,2)		
rs1260326 (γ_{01} for π_{0i})			**+0.204±0.099**	**0.041**
rs1260326×Time (γ_{11} for π_{1i})			+0.027±0.024	0.26
Model 2: rs1312969	*SLC2A9*	T(0,1,2)		
rs1312969 (γ_{01} for π_{0i})			**+0.195±0.069**	**0.005**
rs1312969×Time (γ_{11} for π_{1i})			+0.003±0.016	0.86
Model 3: rs1249874	*SLC2A9*	A(0,1,2)		
rs1249874 (γ_{01} for π_{0i})			**+0.211±0.068**	**0.002**
rs1249874×Time (γ_{11} for π_{1i})			+0.012±0.016	0.47
Model 4: rs7442295	*SLC2A9*	A(0,1,2)		
rs7442295 (γ_{01} for π_{0i})			**+0.142±0.069**	**0.038**
rs7442295×Time (γ_{11} for π_{1i})			+0.014±0.016	0.38
Model 5: rs6449213	*SLC2A9*	T(0,1,2)		
rs6449213 (γ_{01} for π_{0i})			**+0.256±0.095**	**0.007**
rs6449213×Time (γ_{11} for π_{1i})			+0.025±0.023	0.27
Model 6: rs1014290	*SLC2A9*	T(0,1,2)		
rs1014290 (γ_{01} for π_{0i})			**+0.199±0.073**	**0.007**
rs1014290×Time (γ_{11} for π_{1i})			+0.000±0.017	0.98
Model 7: rs9991278	*SLC2A9*	G(0,1,2)		
rs9991278 (γ_{01} for π_{0i})			**+0.213±0.084**	**0.011**
rs9991278×Time (γ_{11} for π_{1i})			+0.014±0.020	0.46

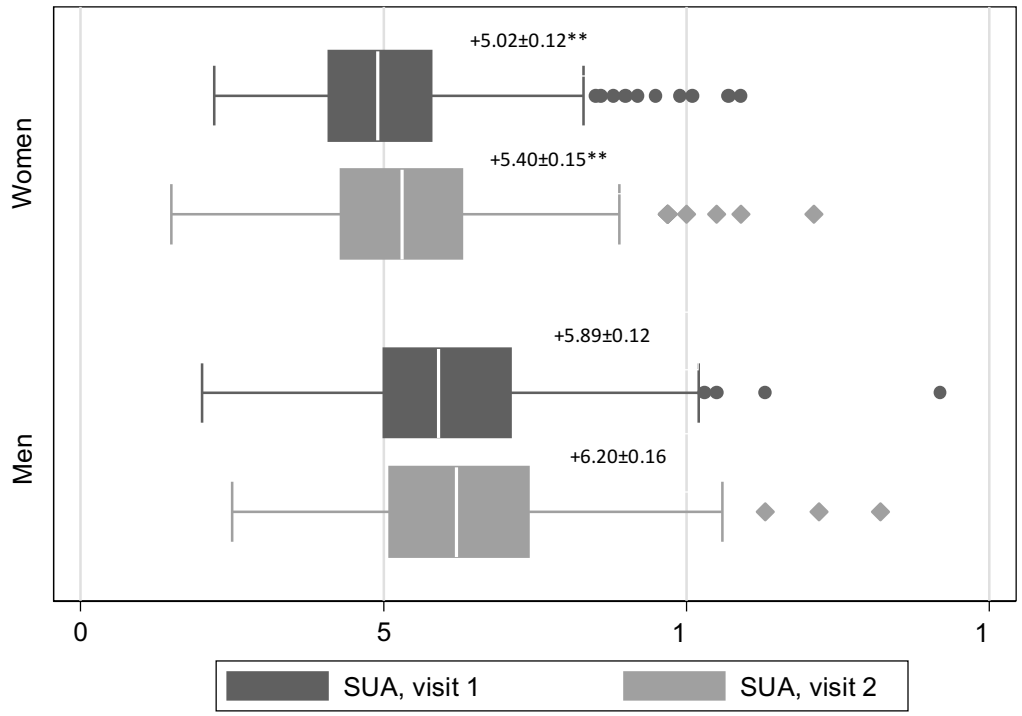
Model 8: rs2231142	*ABCG2*	T(0,1,2)		
rs2231142 (γ_{01} for π_{0i})			**+0.581±0.229**	**0.011**[3]
rs2231142×Time (γ_{11} for π_{1i})			+0.039±0.055	0.47[3]
Model 9: rs742132	*LRRC16A*	G(0,1,2)		
rs742132 (γ_{01} for π_{0i})			*+0.132±0.074*	*0.076*
rs742132×Time (γ_{11} for π_{1i})			-0.002±0.018	0.89[4]
Model 10: rs3799344	*SLC17A1*	C(0,1,2)		
rs3799344 (γ_{01} for π_{0i})			**+0.185±0.072**	**0.010**
rs3799344×Time (γ_{11} for π_{1i})			-0.008±0.017	0.63
Model 11: rs7932775	*SLC22A12*	C(0,1,2)		
rs7932775 (γ_{01} for π_{0i})			**+0.145±0.072**	**0.045**[3]
rs7932775×Time (γ_{11} for π_{1i})			+0.013±0.017	0.444
Model 12: rs7224610	*HLF*	C(0,1,2)		
rs7224610 (γ_{01} for π_{0i})			**+0.237±0.117**	**0.042**
rs7224610×Time (γ_{11} for π_{1i})			-0.043±0.028	0.13
Model 13: rs2241480	*SLC2A9*	T(0,1,2)		
rs2241480 (γ_{01} for π_{0i})			-0.085±0.081	0.30
rs2241480×Time (γ_{11} for π_{1i})			*+0.032±0.018*	*0.096*
Model 14: rs478607	*NRXN2*	G(0,1,2)		
rs478607 (γ_{01} for π_{0i})			-0.030±0.069	0.66
rs478607×Time (γ_{11} for π_{1i})			*+0.027±0.016*	*0.094*
Model 15: rs71931165778	*NFAT5*	C(0,1,2)		
rs71931165778 (γ_{01} for π_{0i})			+0.270±0.213	0.21
rs71931165778×Time (γ_{11} for π_{1i})			*+0.080±0.047*	*0.090*

Abbreviations: Age_{base}=Baseline age at visit 1, SUA=Serum Uric Acid.

[1] Each of the models' intercepts and slopes were further adjusted for Age_{base}, for marital status, poverty status, education (years), baseline current smoking status, current illicit drug use and baseline body mass index, BMI centered at 30 $kg.m^{-2}$, the

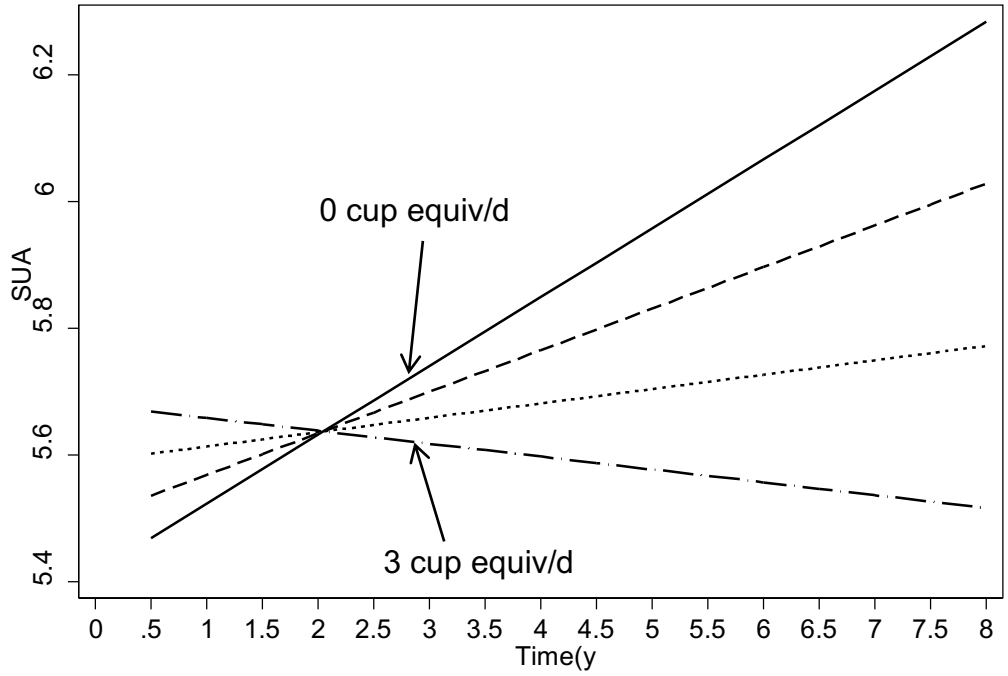
10 principal components for population structure, and 8 key dietary factors factors in addition to total grains, total fruits, total vegetables, other meats, discretionary solid fat and discretionary oils, and the inverse mills ratio. Age_{base} was centered at 50y, and all dietary factors were centered at their weighted means (See Table 1, Total). [2]Values are regression coefficients $\gamma \pm$ standard error of the estimate (SEE). n=number of participants in the analysis; n'=total number of visits included in the analysis. [3] $P<0.05$ for interaction with sex, suggestive of a stronger positive effect among men. [4] $P<0.05$ for interaction with sex, suggestive of a stronger positive effect among women.

Supplemental Figure 2. Boxplot of serum uric acid (SUA) at baseline and follow-up, by sex



**P<0.001 based on design-based F-test from linear regression models accounting for sampling weight, with SUA (visits 1 and 2) as outcome and sex as the only predictor. Values are means±standard error.

Supplemental Figure 4. Predictive margins of SUA by Time and dairy intake, from mixed-effects regression model, total population[1]



[1] Predictive margins obtained from mixed-effects regression model with SUA as the outcome, random effects added to slope and intercept, and both slopes and intercept adjusted for multiple factors including age, sex, poverty status, marital status, education, smoking and drug use, several dietary factors, BMI, 10 principal components for population structure and an inverse mills ratio. The Figure simulates the trajectory of a population with comparable characteristics (covariates set at their observed values in the sample) when exposed alternatively to 4 levels of dairy intakes (0,1,2,3 cups equiv./d, bottom to top) (See Table 2, Model 1).

Supplementary Table 3. Genotype call rate and imputation quality score of serum uric acid linked genetic variants in the HANDLS study.

Variant	Imputed or Genotyped	Genotype call rate	R-squared*
rs1014290	Genotyped	0.99	-
rs10792443	Imputed	-	0.99
rs1106766	Imputed	-	0.99
rs11231825	Genotyped	0.99	-
rs11602903	Imputed	-	0.99
rs1165196	Genotyped	0.99	-
rs1165205	Imputed	-	0.97
rs11721501	Imputed	-	0.91
rs11722228	Imputed	-	0.99
rs11723388	Imputed	-	0.91
rs11723439	Genotyped	0.99	-
rs11751616	Genotyped	0.99	-
rs1183201	Imputed	-	0.99
rs11942223	Imputed	-	0.99
rs12356193	Genotyped	0.99	-
rs12498742	Imputed	-	0.99
rs12510549	Imputed	-	0.95
rs1260326	Genotyped	0.99	-
rs12800450	NA	NA	NA
rs13113918	Genotyped	1	-
rs13129697	Genotyped	0.99	-
rs1394125	Genotyped	0.98	-
rs1529909	NA	NA	NA
rs16890979	Genotyped	0.99	-
rs17251963	Imputed	-	0.97
rs17300741	Genotyped	0.99	-
rs1967017	Genotyped	0.99	-
rs2051541	Genotyped	0.99	-
rs2078267	Genotyped	0.99	-
rs2199936	NA	NA	NA
rs2231137	Imputed	-	0.99
rs2231142	Genotyped	0.99	-
rs2241480	Genotyped	0.98	-
rs3114018	Genotyped	0.99	-
rs3775948	Imputed	-	0.99
rs3799344	Genotyped	1	-
rs3825018	Imputed	-	0.99

rs4148152	Genotyped	1	-
rs4697745	Imputed	-	0.97
rs478607	Imputed	-	0.99
rs505802	Genotyped	0.99	-
rs559946	Imputed	-	0.98
rs6449213	Genotyped	0.99	-
rs6598541	Imputed	-	0.93
rs675209	Genotyped	0.99	-
rs6843466	NA	NA	NA
rs6855911	Imputed	-	0.99
rs6856396	Imputed	-	0.71
rs717615	Genotyped	0.99	-
rs7193778	Imputed	-	0.97
rs7224610	Genotyped	1	-
rs72552713	Imputed	-	0.0073
rs734553	Genotyped	0.99	-
rs737269	Imputed	-	0.98
rs742132	Imputed	-	0.99
rs7442295	Imputed	-	0.99
rs7663032	Genotyped	0.99	-
rs7675964	Imputed	-	0.98
rs7683856	Imputed	-	0.98
rs780093	Genotyped	0.99	-
rs780094	Genotyped	0.99	-
rs7932775	Genotyped	0.99	-
rs814295	Imputed	-	0.99
rs882211	Imputed	-	0.82
rs893006	Genotyped	0.96	-
rs9321453	Imputed	-	0.99
rs938552	Imputed	-	0.99
rs9991278	Imputed	-	0.98

NA, SNP not available in the HANDLS study participants.

* Variant imputation quality score, R square, was from MACH/minimac.