

Table S1. Participant characteristics for Non-Hispanic Whites only sample.

Characteristic	Total (N= 1,614)	DSE (N=790)	ILI (N=824)	p-value*
Women; n (%)	836 (51.8)	411 (52)	425 (51.6)	0.8572
Age, years; mean (SD)	59.5 (6.9)	59.5 (6.9)	59.4 (6.9)	0.8593
Baseline measurements				
Diabetes Duration, years; median (IQR)	5 (2 to 10)	5 (2 to 10)	5 (2 to 10)	0.3904
HbA1c, %; mean (SD)	7.2 (1.14)	7.2 (1.15)	7.2 (1.13)	0.6672
Insulin use; n (%)	233 (14.4)	119 (15.1)	114 (13.8)	0.4827
BMI, kg/m ² ; mean (SD)	36.2 (6)	36.2 (6)	36.3 (6)	0.6600
Smoking; n (%)				
Year 0	44 (2.7)	23 (2.9)	21 (2.5)	0.6512
Year 1	40 (2.6)	19 (2.5)	21 (2.7)	0.8820
Anti-depressant use; n (%)				
Year 0	331 (20.5)	155 (19.6)	176 (21.4)	0.3871
Year 1	323 (21)	161 (21.4)	162 (20.6)	0.7982
Weight, kg; mean (SD)				
Year 0	103.7 (19.2)	103.3 (18.9)	104 (19.5)	0.4120
Year 1	97.9 (19.7)	101.9 (19)	94 (19.5)	<0.0001
Absolute change from baseline	-5.73 (8.26)	-1.19 (5.51)	-10.08 (8.12)	<0.0001
BDI; mean (SD)				
Year 0	5.3 (4.6)	5.3 (4.4)	5.3 (4.8)	0.9259
Year 1	4.6 (5.2)	5.1 (4.9)	4.2 (5.4)	0.0020
Absolute change from baseline	-0.63 (4.6)	-0.22 (4.45)	-1.02 (4.71)	0.0006

* P-values obtained using: independent samples *t* test results for quantitative variables with reported mean (SD); Wilcoxon rank sum test results for quantitative variables with reported median (IQR); and chi-square test results for categorical variables with reported n (%).

Table S2. SNP Characteristics for *a priori* SNPs in the overall sample and in the three largest racial/ethnic groups, Non-Hispanic White, Non-Hispanic Black, and Hispanic individuals.

SNP	Chr	Position (Build 137)	Nearest Gene	Overall			White (N=1614)			Black (N=215)			Hispanic (N=230)		
				Allele*	MAF	N	Allele*	MAF	HWE p-val	Allele*	MAF	HWE p-val	Allele*	MAF	HWE p-val
rs12240047	1	101181342	VCAM1	A/G	19.1	2118	A/G	20.8	0.821	A/G	5.1	0.094	A/G	20.9	0.048
rs1011319	1	225597846	LBR	G/A	19.7	2118	G/A	16.3	0.202	A/G	48.6	0.892	G/A	13.3	1.000
rs2230419	1	225607144	LBR	A/G	20.0	2118	A/G	16.3	0.202	G/A	45.8	0.891	A/G	13.5	1.000
rs60271	5	104078233	RAB9BP1	C/A	27.8	2118	C/A	32.1	0.361	C/A	7.2	1.000	C/A	18.7	0.515
rs2239110	12	2629143	CACNA1C	G/A	14.8	2118	G/A	12.1	0.294	G/A	35.1	0.765	G/A	13.5	0.776
rs216865	12	6090303	VWF	G/A	35.1	2118	G/A	33.1	0.911	A/G	43.7	0.582	G/A	28.7	0.198
rs216873	12	6095274	VWF	G/A	20.3	2116	G/A	18.7	0.870	G/A	34.7	0.364	G/A	16.3	0.338
rs3125	13	47408851	HTR2A	C/G	15.1	2117	C/G	14.8	0.167	C/G	8.4	0.646	C/G	23.9	0.282

*Major/minor allele

MAF: Minor allele frequency

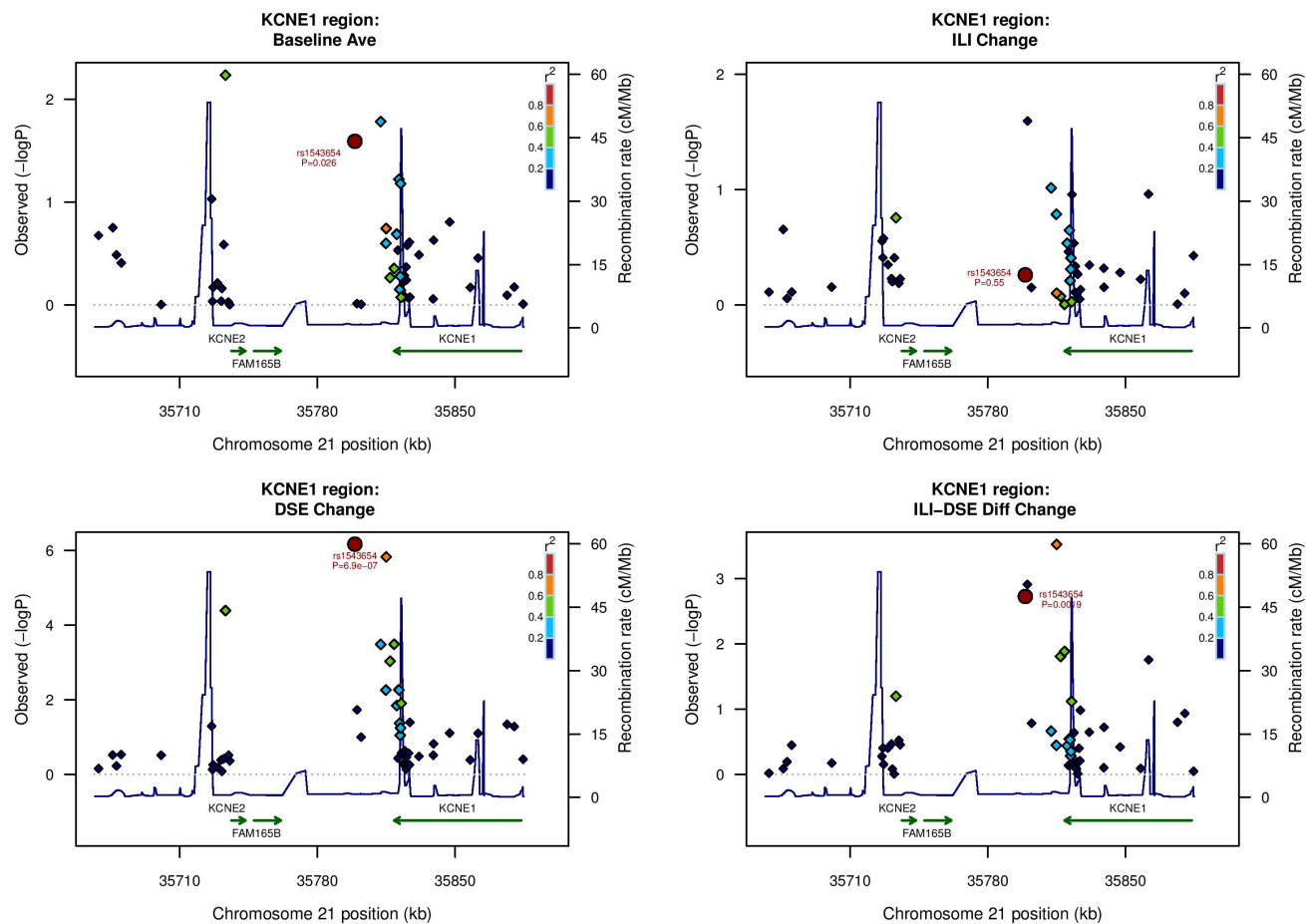
HWE: Hardy-Weinberg Equilibrium, or deviation of genotypic frequencies from $p^2 + 2pq + q^2$, where p = the frequency of the major allele and q = the frequency of the minor allele in a given population.

Table S3. Top hits for baseline depressive symptoms in the full cohort and the Non-Hispanic White subsample for BDI scores without medication adjustment (FDR q-value < 0.30). Note: that no adjusted baseline results met the FDR criteria.)

	SNP	Chip	Chr	Nearest		SE	p-value	FDR Q*
				Gene	Beta			
OVERALL SAMPLE	rs242037	MTC	12	EFCAB4B	-0.73	0.16	4.77E-06	0.249
	rs11826956	MTC	11	LUZP2	-0.69	0.16	8.32E-06	0.249
	rs7633228	IBC	3	GBE1	-1.45	0.32	6.86E-06	0.249
	rs1503930	MTC	11	GALNTL4	-0.64	0.15	1.55E-05	0.290
	rs10241252	MTC	7	VWC2	-0.64	0.15	1.98E-05	0.290
	rs10265687	MTC	7	VWC2	-0.64	0.15	1.98E-05	0.290
	rs2941878	MTC	5	GPR98	0.83	0.20	2.66E-05	0.290
	rs10838650	MTC	11	C11orf49	-0.64	0.15	3.23E-05	0.290
	rs10142105	MTC	14	STXBP6	-0.87	0.21	3.07E-05	0.290
	rs16870433	MTC	6	EPHA7	-1.41	0.33	2.44E-05	0.290
	rs1432622	IBC	5	ADRB2	0.63	0.15	3.91E-05	0.292
	rs12201251	IBC	6	COL9A1	-0.66	0.16	3.85E-05	0.292
NON-HISPANIC WHITE SAMPLE	rs10838650	MTC	11	C11orf49	-0.76	0.16	2.24E-06	0.191
	rs4587689	MTC	11	C11orf49	-0.78	0.17	7.71E-06	0.225
	rs5896	IBC	11	F2	-0.91	0.21	1.08E-05	0.225
	rs11826956	MTC	11	LUZP2	-0.72	0.17	1.39E-05	0.225
	rs3136447	IBC	11	F2	-0.76	0.17	1.58E-05	0.225
	rs2070851	IBC	11	F2	-0.75	0.17	1.59E-05	0.225
	rs3136457	IBC	11	F2	-0.88	0.21	2.26E-05	0.263
	rs8043583	MTC	16	ZCCHC14	-1.18	0.28	2.48E-05	0.263
	rs2070850	IBC	11	F2	-0.87	0.21	3.03E-05	0.279
	rs12574081	MTC	11	NR1H3	-0.84	0.20	3.81E-05	0.279
	rs1054736	MTC	3	PLSCR2	0.71	0.17	4.12E-05	0.279
	rs363598	MTC	21	GRIK1	-0.69	0.17	4.23E-05	0.279
	rs13266756	MTC	8	NSMCE2	-0.96	0.23	4.47E-05	0.279
	rs2275801	IBC	20	PRKCBP1	-1.20	0.29	4.60E-05	0.279

* Calculated from the chip-wide results of each group. All p-values are derived from Generalized Estimating Equations models with robust standard errors. False discovery rate (FDR) Q-values calculated using the Q value package (30).

Figure S1. Regional Manhattan plots for the association of *KCNE1* with BDI scores without medication adjustment.



Supplemental Digital Content 5.

Appendix: Look AHEAD Research Group at Year 1

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Clinical Sites

The Johns Hopkins Medical Institutions Frederick L. Brancati, MD, MHS¹; Jeff Honas, MS²; Lawrence Cheskin, MD³; Jeanne M. Clark, MD, MPH³; Kerry Stewart, EdD³; Richard Rubin, PhD³; Jeanne Charleston, RN; Kathy Horak, RD

Pennington Biomedical Research Center George A. Bray, MD¹; Kristi Rau²; Allison Strate, RN²; Brandi Armand, LPN²; Frank L. Greenway, MD³; Donna H. Ryan, MD³; Donald Williamson, PhD³; Amy Bachand; Michelle Begnaud; Betsy Berhard; Elizabeth Caderette; Barbara Cerniauskas; David Creel; Diane Crow; Helen Guay; Nancy Kora; Kelly LaFleur; Kim Landry; Missy Lingle; Jennifer Perault; Mandy Shipp, RD; Marisa Smith; Elizabeth Tucker

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Harvard Center

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Joslin Diabetes Center: Edward S. Horton, MD¹; Sharon D. Jackson, MS, RD, CDE²; Osama Hamdy, MD, PhD³; A. Enrique Caballero, MD³; Sarah Bain, BS; Elizabeth Bovaird, BSN, RN; Ann Goebel-Fabbri, PhD; Lori Lambert, MS, RD; Sarah Ledbury, MEd, RD; Maureen Malloy, BS; Kerry Ovalle, MS, RCEP, CDE

Beth Israel Deaconess Medical Center: George Blackburn, MD, PhD¹; Christos Mantzoros, MD, DSc³; Kristinia Day, RD; Ann McNamara, RN

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TRS; Kristin Wallace, MPH; Terra Worley, BA

Baylor College of Medicine John P. Foreyt, PhD¹; Rebecca S. Reeves, DrPH, RD²; Henry Pownall, PhD³; Ashok Balasubramanyam, MBBS³; Peter Jones, MD³; Michele Burrington, RD; Chu-Huang Chen, MD, PhD³; Allyson Clark, RD; Molly Gee, MEd, RD; Sharon Griggs; Michelle Hamilton; Veronica Holley; Jayne Joseph, RD; Patricia Pace, RD; Julieta Palencia, RN; Olga Satterwhite, RD; Jennifer Schmidt; Devin Volding, LMSW; Carolyn White

University of California at Los Angeles School of Medicine Mohammed F. Saad, MD¹; Siran Ghazarian, MD²; Ken C. Chiu, MD³; Medhat Botrous; Michelle Chan, BS; Kati Konersman, MA, RD, CDE; Magpuri Perpetua, RD

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University of Tennessee East. Karen C. Johnson, MD, MPH; Carolyn Gresham, RN; Stephanie Connelly, MD, MPH; Amy Brewer, RD, MS; Mace Coday, PhD; Lisa Jones, RN; Lynne Lichtermann, RN, BSN; Shirley Vosburg, RD, MPH; and J. Lee Taylor, MEd, MBA

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Nayyar Iqbal, MD

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The University of Texas Health Science Center at San Antonio Steven M. Haffner, MD¹; Maria G. Montez, RN, MSHP, CDE²; Carlos Lorenzo, MD³

University of Washington / VA Puget Sound Health Care System Steven E.

Kahn, MB, ChB¹; Brenda Montgomery, RN, MS, CDE²; Robert Knopp, MD³;
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BS²; Cathy Manus, LPN³; Jonathan Krakoff, MD³; Jeffrey M. Curtis, MD, MPH³;
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Janelia Smiley; Katie Toledo, MS, LPC; Christina Tomchee, BA; Darryl Tonemah
PhD

University of Southern California Anne Peters, MD¹; Valerie Ruelas, MSW,

LCSW²; Siran Ghazarian Sengardi, MD²; Kathryn Graves, MPH, RD, CDE;
Kati Konersman, MA, RD, CDE; Sara Serafin-Dokhan

Coordinating Center

Wake Forest University Mark A. Espeland, PhD¹; Judy L. Bahnson, BA²; Lynne Wagenknecht, DrPH³; David Reboussin, PhD³; W. Jack Rejeski, PhD³; Alain Bertoni, MD, MPH³; Wei Lang, PhD³; Gary Miller, PhD³; David Lefkowitz, MD³; Patrick S. Reynolds, MD³; Paul Ribisl, PhD³; Mara Vitolins, DrPH³; Michael Booth, MBA²; Kathy M. Dotson, BA²; Amelia Hodges, BS²; Carrie C. Williams, MA²; Jerry M. Barnes, MA; Patricia A. Feeney, MS; Jason Griffin, BS; Lea Harvin, BS; William Herman, MD, MPH; Patricia Hogan, MS; Sarah Jaramillo, MS; Mark King, BS; Kathy Lane, BS; Rebecca Neiberg, MS; Andrea Ruggiero, MS; Christian Speas, BS; Michael P. Walkup, MS; Karen Wall; Michelle Ward; Delia S. West, PhD; Terri Windham

Central Resources Centers

DXA Reading Center, University of California at San Francisco Michael Nevitt, PhD¹; Susan Ewing, MS; Cynthia Hayashi; Jason Maeda, MPH; Lisa Palermo, MS, MA; Michaela Rahorst; Ann Schwartz, PhD; John Shepherd, PhD

Central Laboratory, Northwest Lipid Research Laboratories Santica M.

Marcovina, PhD, ScD¹; Greg Strylewicz, MS

ECG Reading Center, EPICARE, Wake Forest University School of Medicine

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Williamson, PhD; Ping Zhang, PhD

¹ Principal Investigator

² Program Coordinator

³ Co-Investigator

All other Look AHEAD staff members are listed alphabetically by site.