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SUPPLEMENTARY DATA

**Supplementary Table 1.** List of Single Nucleotide Variants detected in ADIPOQ in 14002 individuals.

VARIANT_ID	POSITION (NCBI36.3)	RSID	Reference Allele	Variant allele	Variant Type	AA Change	Polyphen Prediction	SIFT Prediction	phyloP
chr3_188043129	188043129		G	A	Flanking				0.143
chr3_188043140	188043140		C	A	Flanking				-0.51
chr3_188043155	188043155		C	T	Flanking				0.161
chr3_188043164	188043164		T	C	UTR				-0.294
chr3_188043179	188043179		T	G	UTR				-0.711
chr3_188043267	188043267		G	C	Intron				0.001
chr3_188043271	188043271		A	G	Intron				-2.163
chr3_188043272	188043272		T	C	Intron				-0.912
chr3_188043274	188043274		C	T	Intron				-0.589
chr3_188043275	188043275		A	C	Intron				-2.126
chr3_188043281	188043281		A	C	Intron				0.501
chr3_188053504	188053504		C	T	Intron				1.163
chr3_188053510	188053510	RS17366653	T	C	Intron				0.441
chr3_188053515	188053515		G	A	Intron				-0.355
chr3_188053522	188053522		T	G	Intron				0.936
chr3_188053533	188053533		G	T	Intron				2.674
chr3_188053554	188053554		G	A	NonSynonymous	G5R	benign	DAMAGING *Warning! Low confidence.	0.753
chr3_188053567	188053567		T	A	NonSynonymous	L9Q	benign	DAMAGING *Warning! Low confidence.	2.16
chr3_188053583	188053583		C	T	Synonymous	P14P			-0.129
chr3_188053586	188053586	RS2241766	T	G	Synonymous	G15G			-0.1
chr3_188053604	188053604		G	A	Synonymous	T21T			-2.321
chr3_188053613	188053613		G	A	Synonymous	G24G			-0.446
chr3_188053617	188053617		G	A	NonSynonymous	G26R	benign	TOLERATE D	0.645
chr3_188053637	188053637		C	T	Synonymous	P32P			0.045

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chr3_188053642	188053642		G	T	Intron			DAMAGING *Warning! Low confidence.	0.262
chr3_188053654	188053654		G	A	NonSynonymous	G38D	possibly damaging	TOLERATE D	2.533
chr3_188053663	188053663		C	T	NonSynonymous	A41V	benign	TOLERATE D	2.616
chr3_188053664	188053664		G	A	Synonymous	A41A			-2.225
chr3_188053674	188053674		G	C	NonSynonymous	G45R	probably damaging	DAMAGING	2.616
chr3_188053682	188053682		G	A	Synonymous	P47P			-0.496
chr3_188053694	188053694		G	A	Synonymous	G51G			0.29
chr3_188053704	188053704		C	T	NonSynonymous	R55C	probably damaging	DAMAGING	2.616
chr3_188053705	188053705		G	A	NonSynonymous	R55H	benign	DAMAGING	2.616
chr3_188053732	188053732		A	G	NonSynonymous	E64G	possibly damaging	DAMAGING	2.198
chr3_188053798	188053798		T	C	Intron				0.21
chr3_188054673	188054673		T	C	NonSynonymous	I74T	benign	TOLERATE D	-0.127
chr3_188054675	188054675		G	T	NonSynonymous	G75C	probably damaging	DAMAGING	1.401
chr3_188054697	188054697		A	G	NonSynonymous	E82G	probably damaging	TOLERATE D	2.211
chr3_188054701	188054701		C	T	Synonymous	T83T			-0.397
chr3_188054702	188054702		G	A	NonSynonymous	G84R	probably damaging	DAMAGING	2.739
chr3_188054710	188054710		C	T	Synonymous	P86P			-0.633
chr3_188054720	188054720		G	A	NonSynonymous	G90S	probably damaging	DAMAGING	2.739
chr3_188054723	188054723		C	T	NonSynonymous	P91S	probably damaging	TOLERATE D	2.739
chr3_188054724	188054724		C	G	NonSynonymous	P91R	probably damaging	DAMAGING	2.739
chr3_188054725	188054725		C	A	Synonymous	P91P			-0.41
chr3_188054775	188054775		C	T	NonSynonymous	A108V	benign	DAMAGING	2.739
chr3_188054778	188054778		A	G	NonSynonymous	Y109C	possibly damaging	DAMAGING	0.39
chr3_188054783	188054783	RS17366743	T	C	NonSynonymous	Y111H	benign	TOLERATE D	0.467

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chr3_188054791	188054791		A	G	Synonymous	S113S			1.015
chr3_188054807	188054807		T	C	Synonymous	L119L			-0.897
chr3_188054811	188054811		A	C	NonSynonymous	E120A	benign	TOLERATE D	1.02
chr3_188054818	188054818		C	T	Synonymous	Y122Y			-0.826
chr3_188054843	188054843		C	T	NonSynonymous	R131C	probably damaging	DAMAGING	2.68
chr3_188054844	188054844		G	A	NonSynonymous	R131H	probably damaging	DAMAGING	2.68
chr3_188054848	188054848		T	C	Synonymous	F132F			0.437
chr3_188054877	188054877		A	T	NonSynonymous	H142L	probably damaging	DAMAGING	2.126
chr3_188054893	188054893		T	C	Synonymous	T147T			-0.202
chr3_188054917	188054917		T	C	Synonymous	P155P			-0.228
chr3_188054920	188054920		G	C	Synonymous	G156G			1.331
chr3_188054943	188054943		T	C	NonSynonymous	I164T	benign	DAMAGING	2.126
chr3_188054959	188054959		G	A	Synonymous	K169K			0.308
chr3_188055020	188055020		C	G	NonSynonymous	Q190E	possibly damaging	DAMAGING	2.777
chr3_188055047	188055047		G	A	NonSynonymous	G199S	benign	DAMAGING	2.628
chr3_188055067	188055067		G	A	Synonymous	L205L			2.409
chr3_188055075	188055075		G	A	NonSynonymous	G208D	benign	TOLERATE D	0.753
chr3_188055076	188055076		C	T	Synonymous	G208G			-2.311
chr3_188055087	188055087		G	A	Nonsense	212			1.367
chr3_188055178	188055178		C	G	NonSynonymous	D234E		DAMAGING	0.448
chr3_188055223	188055223		G	C	UTR				0.083
chr3_188055228	188055228		A	G	UTR				-2.533
chr3_188055242	188055242		G	C	UTR				-0.214
chr3_188055249	188055249		G	C	UTR				-0.194
chr3_188055250	188055250		T	C	UTR				0.494
chr3_188055276	188055276		A	T	UTR				0.065
chr3_188055336	188055336	RS1501298	G	A	UTR				-0.794
chr3_188055366	188055366		T	C	UTR				0.042
chr3_188055390	188055390		A	T	UTR				0.262
chr3_188055419	188055419		T	A	UTR				0.196
chr3_188055444	188055444		A	G	UTR				-0.431

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chr3_188055463	188055463		A	G	UTR			0.603
chr3_188055474	188055474		A	G	UTR			-1.624
chr3_188055516	188055516		T	G	UTR			-0.71
chr3_188055521	188055521		T	C	UTR			0.516
chr3_188055560	188055560		G	A	UTR			0.935
chr3_188055583	188055583		T	A	UTR			-0.112
chr3_188055629	188055629		T	G	UTR			-1
chr3_188055636	188055636		A	G	UTR			-0.211
chr3_188055652	188055652		G	A	UTR			-0.267
chr3_188055659	188055659		T	C	UTR			0.019
chr3_188055662	188055662		G	T	UTR			-0.036
chr3_188055668	188055668		G	A	UTR			-0.126
chr3_188055679	188055679		C	T	UTR			-0.091
chr3_188055692	188055692		T	C	UTR			-0.253
chr3_188055758	188055758		A	G	UTR			-0.444
chr3_188055765	188055765	RS6444172	C	A	UTR			-1.467
chr3_188055771	188055771		G	A	UTR			-0.79
chr3_188055837	188055837		C	T	UTR			0.757
chr3_188055839	188055839		T	A	UTR			-2.309
chr3_188055853	188055853		A	T	UTR			-0.751
chr3_188055854	188055854		C	T	UTR			0.043
chr3_188055855	188055855		G	A	UTR			-0.379
chr3_188055883	188055883	RS6444174	C	T	UTR			-0.163
chr3_188055905	188055905		G	C	UTR			0.22
chr3_188055906	188055906		G	T	UTR			-1.359
chr3_188055910	188055910		C	T	UTR			0.72
chr3_188055927	188055927		C	G	UTR			-0.24
chr3_188055928	188055928		T	C	UTR			0.025
chr3_188055931	188055931		T	C	UTR			0.87
chr3_188055942	188055942		C	T	UTR			0.406
chr3_188055956	188055956		G	T	UTR			-0.289
chr3_188056000	188056000		C	T	UTR			-0.623
chr3_188056001	188056001		G	A	UTR			-1.249
chr3_188056003	188056003		C	T	UTR			-0.845

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chr3_188056023	188056023		C	T	UTR				0.177
chr3_188056035	188056035		C	T	UTR				-0.42
chr3_188056045	188056045		A	T	UTR				-1.224
chr3_188056052	188056052		C	T	UTR				-0.172
chr3_188056061	188056061		C	T	UTR				0.816
chr3_188056062	188056062		C	T	UTR				-0.002
chr3_188056065	188056065		G	T	UTR				0.3
chr3_188056093	188056093		A	G	UTR				0.836
chr3_188056097	188056097		A	T	UTR				-1.383
chr3_188056124	188056124		A	G	UTR				0.257
chr3_188056129	188056129	RS6796106	G	A	UTR				0.453
chr3_188056136	188056136		T	C	UTR				-0.699
chr3_188056173	188056173		G	A	UTR				0.308
chr3_188056183	188056183		C	T	UTR				0.308
chr3_188056184	188056184		G	A	UTR				-1.808
chr3_188056188	188056188		C	T	UTR				-2.235
chr3_188056202	188056202		G	T	UTR				0.308
chr3_188056217	188056217	RS6414520	A	G	UTR				-0.877
chr3_188056231	188056231		C	A	UTR				-0.645
chr3_188056236	188056236		C	T	UTR				-0.266
chr3_188056245	188056245		A	C	UTR				-0.265
chr3_188056246	188056246		C	T	UTR				0.086
chr3_188056296	188056296		C	T	UTR				-0.065
chr3_188056325	188056325		C	T	UTR				-0.017
chr3_188056329	188056329		G	A	UTR				0.124
chr3_188056367	188056367		A	T	UTR				0.405
chr3_188056372	188056372		C	G	UTR				0.239
chr3_188056467	188056467		A	G	UTR				0.995
chr3_188056491	188056491		G	A	UTR				-1.324
chr3_188056508	188056508		G	A	UTR				-1.082
chr3_188056542	188056542		G	A	UTR				0.278
chr3_188056549	188056549		T	G	UTR				0.133
chr3_188056557	188056557		T	G	UTR				0.303
chr3_188056565	188056565		C	T	UTR				0.148

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chr3_188056577	188056577		T	C	UTR				0.97
chr3_188056582	188056582		C	T	UTR				0.691
chr3_188056600	188056600		C	G	UTR				0.358
chr3_188056606	188056606		T	C	UTR				0.239
chr3_188056640	188056640		C	T	UTR				0.091
chr3_188056646	188056646		G	A	UTR				0.222
chr3_188056674	188056674		G	T	UTR				-0.231
chr3_188056710	188056710		G	A	UTR				-0.509
chr3_188056746	188056746		G	C	UTR				0.278
chr3_188056767	188056767		T	C	UTR				-2.182
chr3_188056769	188056769	RS1063537	C	T	UTR				-1.303
chr3_188056783	188056783	RS17846872	G	T	UTR				0.588
chr3_188056802	188056802		C	G	UTR				-0.507
chr3_188056806	188056806		C	G	UTR				0.482
chr3_188056814	188056814		A	G	UTR				0.408
chr3_188056858	188056858	RS2082940	T	C	UTR				0.351
chr3_188056877	188056877	RS1063538	T	C	UTR				0.029
chr3_188056891	188056891		A	G	UTR				-0.187
chr3_188056913	188056913		C	T	UTR				0.762
chr3_188056945	188056945		G	A	UTR				-0.43
chr3_188056955	188056955		A	G	UTR				0.349
chr3_188056962	188056962		G	A	UTR				-0.199
chr3_188056976	188056976	RS35469083	C	T	UTR				0.183
chr3_188057016	188057016		C	T	UTR				-2.892
chr3_188057033	188057033	RS4686803	C	T	UTR				0.529
chr3_188057042	188057042		C	G	UTR				-1.06
chr3_188057057	188057057		C	T	UTR				0.183
chr3_188057067	188057067		T	A	UTR				0.158
chr3_188057085	188057085		C	T	UTR				-1.258
chr3_188057089	188057089		C	T	UTR				0.596
chr3_188057095	188057095		A	C	UTR				-1.388
chr3_188057109	188057109		A	G	UTR				0.158
chr3_188057115	188057115		A	G	UTR				0.403
chr3_188057119	188057119		A	G	UTR				-1.592

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chr3_188057180	188057180	RS4686804	G	A	UTR				-0.476
chr3_188057210	188057210		A	G	UTR				0.614
chr3_188057219	188057219		T	C	UTR				0.171
chr3_188057223	188057223		G	T	UTR				-0.418
chr3_188057248	188057248		A	C	UTR				-0.205
chr3_188057303	188057303		A	G	UTR				0.537
chr3_188057350	188057350		A	T	UTR				-0.258
chr3_188057353	188057353		G	A	UTR				0.177
chr3_188057363	188057363		A	C	UTR				-1.83
chr3_188057396	188057396		T	G	UTR				0.026
chr3_188057419	188057419		C	T	UTR				-0.74
chr3_188057420	188057420		C	G	UTR				0.069
chr3_188057424	188057424		G	C	UTR				-0.654
chr3_188057425	188057425		C	A	UTR				-0.541
chr3_188057441	188057441		C	T	UTR				0.21
chr3_188057447	188057447		T	C	UTR				0.409
chr3_188057452	188057452		A	G	UTR				-0.476
chr3_188057453	188057453		T	G	UTR				0.45
chr3_188057466	188057466		T	G	UTR				0.023
chr3_188057473	188057473		C	T	UTR				-0.788
chr3_188057484	188057484		C	T	UTR				-0.345
chr3_188057529	188057529		C	T	UTR				-1.317
chr3_188057549	188057549		C	T	UTR				-0.787
chr3_188057563	188057563		G	A	UTR				-1.542
chr3_188057569	188057569		C	T	UTR				-1.048
chr3_188057576	188057576		A	C	UTR				0.429
chr3_188057592	188057592		T	C	UTR				-0.74
chr3_188057617	188057617		C	T	UTR				1.862
chr3_188057629	188057629		G	C	UTR				0.732
chr3_188057677	188057677		C	T	UTR				0.269
chr3_188057719	188057719		T	C	UTR				-1.11
chr3_188057739	188057739		T	C	UTR				-0.156
chr3_188057746	188057746		T	A	UTR				-0.15
chr3_188057763	188057763		A	T	UTR				0.358



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chr3_188057769	188057769		G	C	UTR				-0.28
chr3_188057770	188057770		G	T	UTR				-0.51
chr3_188057785	188057785		T	G	UTR				0.33
chr3_188057793	188057793		A	G	UTR				1.625
chr3_188057808	188057808		C	T	UTR				0.113
chr3_188057812	188057812		G	T	UTR				0.026
chr3_188057838	188057838		T	C	UTR				-1.367
chr3_188057844	188057844		C	G	UTR				0.03
chr3_188057874	188057874		A	C	UTR				0.491
chr3_188057892	188057892		T	C	UTR				0.572
chr3_188057894	188057894		A	G	UTR				-0.145
chr3_188057898	188057898		G	A	UTR				-0.292
chr3_188057901	188057901		T	C	UTR				0.491
chr3_188057909	188057909		A	G	UTR				0.548
chr3_188057979	188057979		A	T	UTR				0.575
chr3_188057992	188057992		T	G	UTR				0.067
chr3_188058005	188058005		C	T	UTR				0.008
chr3_188058010	188058010		T	C	UTR				0.807
chr3_188058019	188058019		C	T	UTR				-0.908
chr3_188058020	188058020		G	A	UTR				-0.231
chr3_188058054	188058054		G	T	UTR				0.212
chr3_188058055	188058055		T	C	UTR				0.146
chr3_188058109	188058109		C	T	UTR				-0.034
chr3_188058115	188058115		A	G	UTR				1.607
chr3_188058124	188058124		G	A	UTR				0.813
chr3_188058146	188058146		G	A	UTR				-0.509
chr3_188058151	188058151		G	A	UTR				0.01
chr3_188058152	188058152		T	C	UTR				0.067
chr3_188058166	188058166		A	G	UTR				-0.569
chr3_188058174	188058174		G	A	UTR				0.01
chr3_188058176	188058176	RS9842733	A	T	UTR				0.088
chr3_188058183	188058183		C	T	UTR				0.11
chr3_188058186	188058186		T	A	UTR				1.61
chr3_188058190	188058190		C	T	UTR				-0.249

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chr3_188058205	188058205		C	A	UTR				-0.071
chr3_188058223	188058223		T	C	UTR				0.513
chr3_188058226	188058226		C	T	UTR				-0.156
chr3_188058230	188058230		C	G	UTR				-0.055
chr3_188058243	188058243		T	C	UTR				-1.147
chr3_188058249	188058249		T	G	UTR				-0.036
chr3_188058282	188058282		C	G	UTR				1.768
chr3_188058313	188058313		T	C	UTR				0.493
chr3_188058318	188058318		T	C	UTR				0.501
chr3_188058342	188058342		C	T	UTR				0.096
chr3_188058349	188058349		T	C	UTR				0.39
chr3_188058350	188058350		A	G	UTR				-0.522
chr3_188058362	188058362		C	T	UTR				-0.782
chr3_188058363	188058363		G	A	UTR				-0.39
chr3_188058383	188058383		T	C	UTR				0.604
chr3_188058391	188058391		C	T	UTR				-0.785
chr3_188058428	188058428		C	T	UTR				0.202
chr3_188058435	188058435		T	C	UTR				-1.121
chr3_188058475	188058475		C	T	UTR				-1.388
chr3_188058534	188058534	RS7649044	C	T	UTR				0.202
chr3_188058596	188058596		A	G	UTR				0.175
chr3_188058647	188058647		G	A	UTR				-1.029
chr3_188058733	188058733	RS34422369	A	G	UTR				-0.463
chr3_188058737	188058737		G	A	UTR				-1.254
chr3_188058811	188058811		A	G	UTR				-1.542
chr3_188058831	188058831		A	C	UTR				-0.707
chr3_188058842	188058842		C	G	UTR				-0.351
chr3_188058870	188058870		T	C	UTR				-0.075
chr3_188058875	188058875		A	T	UTR				-0.48
chr3_188058976	188058976		T	C	Flanking				0.668
chr3_188056765_C	188056765		T	C	UTR				-0.058
chr3_188056765_A	188056765		T	A	UTR				-0.058
chr3_188055252_T	188055252	RS4068	C	T	UTR				0.004
chr3_188055252_G	188055252		C	G	UTR				0.004

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chr3_188057155_C	188057155		G	C	UTR				0.479
chr3_188057155_A	188057155		G	A	UTR				0.479
chr3_188055113_A	188055113		C	A	NonSynonymous	R221S	benign	TOLERATE D	-1.442
chr3_188055113_T	188055113		C	T	NonSynonymous	R221C	benign	TOLERATE D	-1.442
chr3_188057017_A	188057017		C	A	UTR				
chr3_188056399_G	188056399	RS6773957	A	G	UTR				-0.964
chr3_188056399_C	188056399		A	C	UTR				-0.964
chr3_188057474_T	188057474		G	T	UTR				-1.046
chr3_188057474_A	188057474		G	A	UTR				-1.046
chr3_188058086_C	188058086	RS1063539	G	C	UTR				-0.116
chr3_188058086_A	188058086		G	A	UTR				-0.116
chr3_188055558_A	188055558		C	A	UTR				-0.339
chr3_188055558_T	188055558		C	T	UTR				-0.339

SUPPLEMENTARY DATA

**Supplementary Table 1.** List of Single Nucleotide Variants detected in ADIPOQ in 14002 individuals (continued)

VARIANT_ID	Caucasian			African American			Indian Asian		
	Variant Allele Frequency	Variant Allele Count	N	Variant Allele Frequency	Variant Allele Count	N	Variant Allele Frequency	Variant Allele Count	N
chr3_188043129	8.6E-05	2	11612	0	0	594	0	0	565
chr3_188043140	1.3E-04	3	11611	0	0	594	0	0	566
chr3_188043155	4.3E-05	1	11614	0	0	594	0	0	566
chr3_188043164	3.0E-04	7	11617	0	0	594	0	0	566
chr3_188043179	4.3E-05	1	11616	0	0	593	0	0	566
chr3_188043267	0	0	11580	8.4E-04	1	593	0	0	564
chr3_188043271	4.3E-05	1	11572	0	0	593	0	0	564
chr3_188043272	0	0	11573	8.4E-04	1	593	0	0	564
chr3_188043274	4.3E-05	1	11570	0	0	593	0	0	564
chr3_188043275	1.3E-04	3	11570	0	0	593	0	0	564
chr3_188043281	4.3E-05	1	11560	0	0	593	0	0	564
chr3_188053504	8.6E-05	2	11598	0	0	593	0	0	559
chr3_188053510	1.3E-02	301	11577	3.4E-03	4	593	7.2E-03	8	559
chr3_188053515	4.3E-05	1	11615	0	0	593	0	0	563
chr3_188053522	4.3E-05	1	11617	0	0	593	0	0	562
chr3_188053533	4.3E-05	1	11617	0	0	594	0	0	560
chr3_188053554	0	0	11621	0	0	594	8.9E-04	1	564
chr3_188053567	6.5E-04	15	11621	8.4E-04	1	594	0	0	564
chr3_188053583	4.3E-05	1	11623	0	0	594	0	0	565
chr3_188053586	1.2E-01	2777	11572	4.5E-02	53	594	1.2E-01	135	562
chr3_188053604	1.3E-04	3	11624	0	0	594	0	0	566
chr3_188053613	4.3E-05	1	11622	0	0	594	0	0	566
chr3_188053617	4.3E-05	1	11623	0	0	594	0	0	566
chr3_188053637	8.6E-05	2	11619	0	0	594	0	0	564
chr3_188053642	4.3E-05	1	11618	0	0	594	0	0	563
chr3_188053654	0	0	11613	1.6E-02	19	594	0	0	564
chr3_188053663	4.3E-05	1	11614	0	0	594	0	0	563
chr3_188053664	0	0	11615	0	0	594	0	0	564
chr3_188053674	0	0	11610	0	0	594	0	0	565
chr3_188053682	4.3E-05	1	11613	0	0	594	0	0	565
chr3_188053694	3.0E-04	7	11613	0	0	593	0	0	565
chr3_188053704	8.6E-05	2	11613	8.4E-04	1	593	8.8E-04	1	565
chr3_188053705	2.2E-04	5	11611	0	0	593	0	0	565
chr3_188053732	4.3E-05	1	11616	0	0	594	0	0	565
chr3_188053798	8.7E-05	2	11489	0	0	593	0	0	551
chr3_188054673	1.3E-04	3	11500	0	0	592	0	0	562
chr3_188054675	0	0	11507	0	0	593	8.9E-04	1	562
chr3_188054697	0	0	11556	0	0	593	8.9E-04	1	562
chr3_188054701	5.2E-04	12	11565	0	0	593	0	0	562
chr3_188054702	4.3E-05	1	11565	0	0	593	8.9E-04	1	562
chr3_188054710	4.3E-05	1	11579	0	0	592	0	0	562
chr3_188054720	4.3E-03	100	11595	0	0	592	0	0	564
chr3_188054723	0	0	11596	0	0	592	8.9E-04	1	564
chr3_188054724	4.3E-05	1	11598	0	0	592	0	0	564
chr3_188054725	4.3E-05	1	11596	0	0	592	0	0	564
chr3_188054775	0	0	11626	8.4E-04	1	594	0	0	565

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chr3_188054778	0	0	11627	0	0	594	0	0	565
chr3_188054783	3.0E-02	697	11621	5.1E-03	6	594	1.2E-02	14	565
chr3_188054791	4.3E-05	1	11627	0	0	594	0	0	566
chr3_188054807	1.3E-04	3	11626	0	0	594	0	0	566
chr3_188054811	4.3E-05	1	11626	0	0	594	0	0	566
chr3_188054818	1.7E-04	4	11629	0	0	594	8.8E-04	1	566
chr3_188054843	0	0	11629	0	0	594	1.8E-03	2	565
chr3_188054844	4.3E-05	1	11629	0	0	594	0	0	565
chr3_188054848	4.3E-05	1	11628	0	0	594	8.8E-04	1	565
chr3_188054877	4.3E-05	1	11623	0	0	594	0	0	564
chr3_188054893	0	0	11620	0	0	594	0	0	566
chr3_188054917	4.3E-05	1	11621	0	0	594	0	0	564
chr3_188054920	8.6E-05	2	11618	0	0	594	0	0	564
chr3_188054943	0	0	11617	0	0	594	0	0	565
chr3_188054959	8.6E-05	2	11618	0	0	594	0	0	564
chr3_188055020	0	0	11612	0	0	594	0	0	563
chr3_188055047	2.2E-04	5	11616	0	0	594	0	0	565
chr3_188055067	0	0	11612	8.4E-04	1	594	0	0	564
chr3_188055075	8.6E-05	2	11612	0	0	594	0	0	562
chr3_188055076	4.3E-05	1	11608	0	0	594	0	0	562
chr3_188055087	8.6E-05	2	11609	0	0	594	0	0	563
chr3_188055178	0	0	11522	0	0	594	8.9E-04	1	562
chr3_188055223	0	0	11494	8.4E-04	1	593	0	0	563
chr3_188055228	4.4E-05	1	11488	0	0	593	0	0	564
chr3_188055242	4.4E-05	1	11478	0	0	594	0	0	563
chr3_188055249	4.4E-05	1	11463	0	0	594	0	0	564
chr3_188055250	4.4E-05	1	11453	0	0	594	0	0	564
chr3_188055276	8.8E-05	2	11408	4.2E-03	5	594	0	0	562
chr3_188055336	1.3E-04	3	11169	5.9E-02	70	592	0	0	551
chr3_188055366	0	0	11569	8.4E-04	1	593	0	0	562
chr3_188055390	0	0	11594	1.7E-03	2	594	0	0	563
chr3_188055419	2.2E-04	5	11608	0	0	594	0	0	564
chr3_188055444	4.3E-05	1	11603	0	0	594	0	0	562
chr3_188055463	4.3E-05	1	11609	0	0	594	0	0	563
chr3_188055474	4.3E-05	1	11606	0	0	594	0	0	565
chr3_188055516	4.3E-05	1	11513	0	0	594	0	0	562
chr3_188055521	8.7E-05	2	11476	0	0	594	0	0	562
chr3_188055560	1.5E-02	222	7415	1.2E-02	11	463	2.2E-02	14	323
chr3_188055583	4.5E-05	1	11181	0	0	591	0	0	538
chr3_188055629	8.7E-05	2	11565	0	0	594	0	0	563
chr3_188055636	0	0	11561	0	0	594	8.8E-04	1	565
chr3_188055652	4.3E-05	1	11576	0	0	594	0	0	565
chr3_188055659	4.3E-05	1	11590	0	0	594	0	0	565
chr3_188055662	3.0E-04	7	11590	0	0	594	8.8E-04	1	565
chr3_188055668	4.3E-05	1	11586	0	0	594	0	0	566
chr3_188055679	4.3E-05	1	11590	0	0	594	0	0	566
chr3_188055692	8.6E-05	2	11592	0	0	594	0	0	564
chr3_188055758	0	0	11560	0	0	594	0	0	566
chr3_188055765	4.4E-05	1	11507	4.3E-02	51	593	0	0	565
chr3_188055771	4.3E-05	1	11559	0	0	594	0	0	566
chr3_188055837	4.4E-05	1	11450	0	0	593	0	0	559
chr3_188055839	4.4E-04	10	11435	0	0	593	0	0	559
chr3_188055853	8.8E-05	2	11325	0	0	593	0	0	553
chr3_188055854	1.8E-04	4	11329	1.1E-02	13	592	9.1E-04	1	552

SUPPLEMENTARY DATA

chr3_188055855	0	0	11344	0	0	593	0	0	555
chr3_188055883	3.4E-03	78	11436	1.6E-01	189	591	1.4E-02	16	560
chr3_188055905	4.4E-05	1	11333	0	0	594	0	0	555
chr3_188055906	4.4E-05	1	11320	0	0	594	0	0	555
chr3_188055910	4.4E-05	1	11271	0	0	594	0	0	552
chr3_188055927	4.6E-05	1	10771	0	0	590	0	0	529
chr3_188055928	0	0	10714	2.5E-03	3	589	0	0	529
chr3_188055931	4.8E-05	1	10375	0	0	586	0	0	506
chr3_188055942	4.2E-04	6	7070	1.1E-03	1	471	0	0	400
chr3_188055956	1.6E-02	75	2351	1.9E-03	1	268	8.5E-03	2	117
chr3_188056000	6.1E-05	1	8222	0	0	510	0	0	378
chr3_188056001	6.0E-05	1	8332	0	0	514	0	0	380
chr3_188056003	5.9E-05	1	8411	0	0	513	0	0	382
chr3_188056023	0	0	8642	3.9E-03	4	512	0	0	391
chr3_188056035	6.0E-05	1	8317	0	0	505	0	0	363
chr3_188056045	6.1E-05	1	8249	0	0	499	0	0	363
chr3_188056052	6.2E-05	1	8103	0	0	499	0	0	353
chr3_188056061	6.1E-05	1	8193	0	0	494	0	0	341
chr3_188056062	0	0	8235	0	0	496	0	0	342
chr3_188056065	0	0	8311	5.0E-03	5	497	0	0	349
chr3_188056093	5.7E-05	1	8819	0	0	509	0	0	381
chr3_188056097	5.6E-05	1	8944	0	0	508	0	0	390
chr3_188056124	0	0	10383	0	0	565	1.0E-03	1	495
chr3_188056129	7.1E-03	150	10541	2.3E-01	259	564	0	0	510
chr3_188056136	4.6E-05	1	10822	0	0	580	0	0	524
chr3_188056173	4.4E-05	1	11384	0	0	591	0	0	557
chr3_188056183	0	0	11410	8.5E-04	1	590	0	0	556
chr3_188056184	8.8E-05	2	11421	0	0	589	0	0	555
chr3_188056188	4.4E-05	1	11453	0	0	592	0	0	559
chr3_188056202	8.7E-05	2	11487	0	0	592	0	0	560
chr3_188056217	3.4E-01	7700	11323	3.3E-01	389	590	3.0E-01	333	555
chr3_188056231	0	0	11552	0	0	594	8.9E-04	1	564
chr3_188056236	1.3E-04	3	11568	2.3E-02	27	594	0	0	565
chr3_188056245	4.3E-05	1	11592	0	0	594	0	0	566
chr3_188056246	4.3E-05	1	11591	0	0	594	0	0	566
chr3_188056296	4.3E-05	1	11624	0	0	594	0	0	566
chr3_188056325	0	0	11622	0	0	594	8.8E-04	1	566
chr3_188056329	4.3E-05	1	11621	0	0	594	0	0	566
chr3_188056367	8.6E-05	2	11613	4.2E-03	5	594	0	0	566
chr3_188056372	4.3E-05	1	11606	0	0	594	0	0	566
chr3_188056467	0	0	11566	0	0	594	4.4E-03	5	566
chr3_188056491	0	0	11574	0	0	594	0	0	566
chr3_188056508	0	0	11567	8.4E-04	1	594	0	0	565
chr3_188056542	0	0	11562	1.7E-03	2	594	0	0	563
chr3_188056549	4.3E-05	1	11558	0	0	594	0	0	563
chr3_188056557	4.3E-05	1	11543	0	0	594	0	0	562
chr3_188056565	1.3E-04	3	11544	0	0	594	0	0	562
chr3_188056577	4.3E-05	1	11532	0	0	594	0	0	563
chr3_188056582	4.3E-05	1	11528	0	0	594	3.6E-03	4	563
chr3_188056600	4.3E-05	1	11515	0	0	594	0	0	563
chr3_188056606	4.3E-05	1	11519	0	0	594	0	0	563
chr3_188056640	0	0	11497	0	0	594	8.9E-04	1	564
chr3_188056646	1.3E-02	299	11498	6.7E-03	8	594	2.7E-03	3	563
chr3_188056674	0	0	11405	0	0	593	8.9E-04	1	563

SUPPLEMENTARY DATA

chr3_188056710	1.8E-04	4	11291	0	0	594	0	0	559
chr3_188056746	8.9E-05	2	11262	0	0	594	0	0	559
chr3_188056767	0	0	11123	0	0	594	8.9E-04	1	559
chr3_188056769	1.2E-01	2650	11043	3.5E-02	41	592	1.2E-01	134	559
chr3_188056783	9.6E-04	21	10951	8.5E-04	1	590	1.8E-03	2	551
chr3_188056802	9.4E-05	2	10599	0	0	586	0	0	537
chr3_188056806	4.8E-05	1	10511	0	0	586	0	0	534
chr3_188056814	4.9E-05	1	10241	0	0	584	0	0	521
chr3_188056858	1.2E-01	2274	9476	2.1E-01	233	555	1.1E-01	98	445
chr3_188056877	4.0E-01	7377	9221	5.3E-01	577	544	3.3E-01	291	441
chr3_188056891	1.6E-04	3	9152	0	0	539	0	0	432
chr3_188056913	0	0	8048	0	0	500	0	0	365
chr3_188056945	8.4E-05	1	5946	0	0	372	0	0	275
chr3_188056955	1.8E-04	2	5451	0	0	343	0	0	249
chr3_188056962	0	0	5244	0	0	328	2.1E-03	1	238
chr3_188056976	5.7E-02	551	4833	8.2E-03	5	306	9.8E-02	48	246
chr3_188057016	2.4E-04	2	4184	0	0	292	0	0	211
chr3_188057033	1.2E-01	1048	4365	7.4E-02	43	291	1.4E-01	60	214
chr3_188057042	1.1E-04	1	4682	0	0	301	0	0	213
chr3_188057057	9.1E-05	1	5482	0	0	331	0	0	240
chr3_188057067	0	0	6448	0	0	391	1.8E-03	1	280
chr3_188057085	0	0	7253	0	0	429	0	0	298
chr3_188057089	0	0	7570	0	0	440	0	0	325
chr3_188057095	0	0	8069	0	0	455	0	0	348
chr3_188057109	5.5E-05	1	9031	0	0	504	0	0	424
chr3_188057115	0	0	9349	0	0	527	1.1E-03	1	443
chr3_188057119	5.2E-05	1	9707	0	0	543	0	0	473
chr3_188057180	4.6E-01	9766	10615	5.4E-01	616	570	4.4E-01	458	521
chr3_188057210	4.4E-05	1	11433	0	0	592	0	0	560
chr3_188057219	8.7E-05	2	11500	0	0	594	0	0	562
chr3_188057223	0	0	11530	0	0	594	1.8E-03	2	564
chr3_188057248	4.3E-05	1	11568	0	0	594	0	0	566
chr3_188057303	0	0	11524	0	0	594	0	0	564
chr3_188057350	8.7E-05	2	11525	8.2E-02	97	594	0	0	566
chr3_188057353	4.3E-05	1	11524	0	0	594	0	0	566
chr3_188057363	4.3E-05	1	11521	0	0	594	0	0	566
chr3_188057396	4.3E-05	1	11540	0	0	594	0	0	566
chr3_188057419	1.3E-04	3	11553	0	0	594	0	0	566
chr3_188057420	4.3E-05	1	11554	0	0	594	0	0	566
chr3_188057424	8.7E-05	2	11554	0	0	593	0	0	566
chr3_188057425	0	0	11556	8.4E-04	1	593	0	0	566
chr3_188057441	1.3E-03	30	11559	0	0	594	0	0	566
chr3_188057447	0	0	11561	3.4E-03	4	594	0	0	566
chr3_188057452	4.3E-05	1	11563	0	0	594	0	0	566
chr3_188057453	4.3E-05	1	11566	0	0	594	0	0	566
chr3_188057466	0	0	11568	2.9E-02	34	594	0	0	566
chr3_188057473	0	0	11570	8.4E-04	1	594	0	0	566
chr3_188057484	4.3E-05	1	11577	0	0	594	0	0	565
chr3_188057529	0	0	11577	0	0	594	1.8E-03	2	565
chr3_188057549	0	0	11591	0	0	594	0	0	563
chr3_188057563	4.3E-05	1	11596	8.4E-04	1	594	0	0	562
chr3_188057569	4.3E-05	1	11605	0	0	594	0	0	564
chr3_188057576	4.3E-05	1	11608	0	0	593	0	0	564
chr3_188057592	4.3E-05	1	11616	0	0	593	0	0	564

SUPPLEMENTARY DATA

chr3_188057617	4.3E-05	1	11615	0	0	594	0	0	564
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chr3_188057677	2.2E-03	51	11621	0	0	594	8.8E-04	1	565
chr3_188057719	0	0	11615	8.4E-04	1	594	0	0	564
chr3_188057739	8.6E-05	2	11609	0	0	594	0	0	562
chr3_188057746	8.6E-05	2	11606	0	0	594	0	0	562
chr3_188057763	0	0	11596	0	0	594	8.9E-04	1	563
chr3_188057769	1.3E-04	3	11593	0	0	594	0	0	563
chr3_188057770	0	0	11594	1.7E-03	2	594	0	0	563
chr3_188057785	0	0	11602	0	0	594	8.9E-04	1	564
chr3_188057793	4.3E-05	1	11604	0	0	594	0	0	565
chr3_188057808	4.3E-05	1	11602	0	0	594	0	0	565
chr3_188057812	4.3E-05	1	11606	0	0	594	0	0	566
chr3_188057838	4.3E-05	1	11600	8.4E-04	1	594	0	0	565
chr3_188057844	0	0	11596	8.4E-04	1	594	0	0	565
chr3_188057874	0	0	11578	0	0	594	6.2E-03	7	564
chr3_188057892	4.3E-05	1	11567	0	0	594	1.2E-02	13	562
chr3_188057894	0	0	11567	1.7E-03	2	594	0	0	562
chr3_188057898	4.3E-05	1	11566	0	0	594	0	0	562
chr3_188057901	8.7E-05	2	11564	0	0	594	0	0	564
chr3_188057909	4.3E-05	1	11559	0	0	594	0	0	563
chr3_188057979	4.3E-05	1	11534	0	0	594	0	0	561
chr3_188057992	4.3E-05	1	11541	0	0	594	0	0	563
chr3_188058005	1.3E-04	3	11527	0	0	594	0	0	562
chr3_188058010	4.3E-05	1	11527	0	0	594	0	0	563
chr3_188058019	4.3E-05	1	11516	0	0	594	0	0	562
chr3_188058020	0	0	11513	8.4E-04	1	594	0	0	562
chr3_188058054	0	0	11492	8.4E-04	1	594	0	0	565
chr3_188058055	4.4E-05	1	11486	0	0	594	0	0	564
chr3_188058109	1.7E-04	4	11489	0	0	594	0	0	564
chr3_188058115	0	0	11487	2.5E-03	3	594	0	0	565
chr3_188058124	2.2E-02	505	11471	6.7E-03	8	594	8.0E-03	9	564
chr3_188058146	4.4E-05	1	11455	0	0	594	0	0	566
chr3_188058151	4.4E-05	1	11456	0	0	594	0	0	566
chr3_188058152	0	0	11460	0	0	594	1.8E-03	2	565
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chr3_188058174	1.3E-04	3	11456	0	0	592	0	0	566
chr3_188058176	3.1E-04	7	11449	9.0E-02	107	592	0	0	566
chr3_188058183	4.4E-05	1	11455	0	0	594	0	0	566
chr3_188058186	4.4E-05	1	11455	0	0	593	0	0	566
chr3_188058190	0	0	11436	1.7E-03	2	592	0	0	565
chr3_188058205	4.4E-05	1	11391	0	0	591	0	0	565
chr3_188058223	0	0	11344	1.7E-03	2	593	0	0	566
chr3_188058226	4.4E-05	1	11318	0	0	593	0	0	566
chr3_188058230	0	0	11275	8.4E-04	1	594	0	0	564
chr3_188058243	4.5E-05	1	11195	0	0	594	0	0	565
chr3_188058249	0	0	11155	8.4E-04	1	594	0	0	565
chr3_188058282	0	0	10932	8.4E-04	1	593	0	0	552
chr3_188058313	4.6E-05	1	10775	0	0	592	0	0	547
chr3_188058318	9.3E-05	2	10732	0	0	589	0	0	545
chr3_188058342	0	0	10528	8.5E-04	1	586	0	0	530
chr3_188058349	0	0	10413	0	0	584	0	0	531
chr3_188058350	0	0	10404	0	0	584	0	0	531
chr3_188058362	2.0E-04	4	10164	8.7E-04	1	575	0	0	516



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chr3_188058363	5.0E-05	1	10100	0	0	574	0	0	514
chr3_188058383	0	0	8766	9.7E-04	1	516	0	0	455
chr3_188058391	6.2E-05	1	8030	0	0	476	0	0	422
chr3_188058428	2.3E-04	2	4385	0	0	290	0	0	246
chr3_188058435	3.2E-03	24	3759	0	0	248	2.1E-02	9	219
chr3_188058475	1.5E-03	3	1009	0	0	49	0	0	55
chr3_188058534	0	0	242	1.5E-01	3	10	0	0	20
chr3_188058596	1.5E-03	1	328	0	0	12	0	0	21
chr3_188058647	0	0	1232	7.9E-03	1	63	0	0	67
chr3_188058733	3.2E-04	2	3152	0	0	230	0	0	172
chr3_188058737	0	0	3228	4.3E-03	2	234	0	0	174
chr3_188058811	7.7E-05	1	6531	0	0	458	0	0	328
chr3_188058831	0	0	7164	0	0	499	0	0	359
chr3_188058842	6.7E-05	1	7415	0	0	510	0	0	369
chr3_188058870	0	0	7408	9.7E-04	1	514	0	0	363
chr3_188058875	6.9E-05	1	7225	0	0	512	0	0	353
chr3_188058976	2.5E-04	2	3975	0	0	292	0	0	183
chr3_188056765_C	9.0E-05	2	11128	0	0	594	0	0	560
chr3_188056765_A	4.5E-05	1	11128	0	0	594	0	0	560
chr3_188055252_T	5.4E-03	124	11438	4.2E-03	5	594	8.9E-04	1	562
chr3_188055252_G	4.4E-05	1	11438	0	0	594	0	0	562
chr3_188057155_C	9.2E-05	2	10873	0	0	584	9.5E-04	1	528
chr3_188057155_A	4.6E-05	1	10873	0	0	584	0	0	528
chr3_188055113_A	0	0	11589	0	0	594	0	0	562
chr3_188055113_T	4.3E-05	1	11589	0	0	594	0	0	562
chr3_188057017_A	2.4E-04	2	4212	0	0	292	0	0	209
chr3_188056399_G	3.9E-01	8984	11518	5.3E-01	628	592	3.3E-01	372	564
chr3_188056399_C	4.3E-05	1	11518	0	0	592	0	0	564
chr3_188057474_T	0	0	11570	0	0	594	3.5E-03	4	565
chr3_188057474_A	4.3E-05	1	11570	0	0	594	0	0	565
chr3_188058086_C	1.2E-01	2753	11470	4.6E-02	55	594	1.2E-01	135	562
chr3_188058086_A	4.4E-05	1	11470	0	0	594	0	0	562
chr3_188055558_A	2.6E-02	389	7479	2.2E-02	20	460	4.9E-02	32	328
chr3_188055558_T	2.7E-04	4	7479	1.6E-02	15	460	0	0	328

**Supplementary Table 2.** SNPs selected from joint stepwise regression analysis of GWAS and resequence SNPs based on GEMS and CoLaus combined data

SNP	Position	MAF	Partial R Square	Model R Square	Stepwise Selection P-value	Conditional analysis P-value*
rs17366653	188053510	0.02	1.52E-02	0.02	5.38E-13	1.00E-12
rs1354091	187988594	0.24	8.05E-03	0.03	1.06E-07	1.56E-05
rs3774261	188054253	0.40	4.47E-03	0.04	7.15E-05	3.70E-20
rs3821799	188054180	0.46	8.16E-03	0.05	7.21E-08	3.70E-13
rs17366743	188054783	0.03	3.80E-03	0.05	2.27E-04	4.16E-04
rs16848727	188195657	0.25	3.42E-03	0.05	4.61E-04	4.98E-04
rs1868146	187704565	0.11	2.96E-03	0.06	1.09E-03	1.09E-03

\* P-value correspond to conditional analysis on all other SNPs in the model

SUPPLEMENTARY DATA

**Supplementary Table 3.** Statistical power to detect association between *ADIPOQ* SNPs and *type 2 diabetes* risk in the GO-DARTS study.

SNP	Effect (log ug/ml)	Partial R Square	Model R Square	Relative Risk on <i>Type 2 diabetes</i> *	Power ( <i>type 2 diabetes</i> )
rs17366653	-0.24	1.52E-02	0.02	1.09	0.17
rs1354091	-0.05	8.05E-03	0.03	1.02	0.10
rs3774261	0.40	4.47E-03	0.04	0.98	0.12
rs3821799	0.46	8.16E-03	0.05	0.99	0.07
rs17366743	0.03	3.80E-03	0.05	0.96	0.08
rs16848727	0.25	3.42E-03	0.05	0.99	0.06
rs1868146	0.11	2.96E-03	0.06	0.99	0.06
Combined					0.42

\* relative risk of each SNP on *type 2 diabetes* risk was calculated based on the effect of SNP on adiponectin levels and the effect estimate of per 1-log µg/ml adiponectin level change on *type 2 diabetes* risk from the study by Li et al. (Adiponectin levels and risk of *type 2 diabetes*: a systematic review and meta-analysis, *JAMA* 2009).

**Supplementary Table 4.** Association analysis between the seven independent SNPs associated with adiponectin levels and other metabolic traits (add homa-IR, then order by trait and order by SNP)

SNP	Trait	GEMS		CoLaus	
		Beta (S.E.)	P-value	Beta (S.E.)	P-value
rs17366653	BMI	-0.09 (0.15)	0.53	-0.05 (0.11)	0.63
	Systolic BP	-0.17 (0.15)	0.25	0.11 (0.11)	0.30
	Diastolic BP	-0.03 (0.15)	0.85	-0.05 (0.11)	0.64
	Total Cholesterol	0.00 (0.15)	0.98	0.08 (0.11)	0.49
	HDL	-0.28 (0.15)	0.07	0.00 (0.11)	0.99
	LDL	0.13 (0.16)	0.44	0.01 (0.12)	0.92
	Triglycerides	-0.25 (0.15)	0.10	0.20 (0.11)	0.08
	APOB	-0.08 (0.15)	0.62	0.09 (0.12)	0.45
	Glucose	0.10 (0.17)	0.56	0.05 (0.12)	0.70
	Insulin	0.02 (0.15)	0.89	0.09 (0.12)	0.46
	Leptin	0.15 (0.16)	0.34	-0.13 (0.14)	0.35
HOMA-IR	-0.02 (0.17)	0.93	0.08 (0.12)	0.54	
rs1354091	BMI	-0.01 (0.04)	0.77	0.01 (0.04)	0.88
	Systolic BP	-0.05 (0.04)	0.24	-0.02 (0.04)	0.53
	Diastolic BP	-0.07 (0.04)	0.08	-0.06 (0.04)	0.14
	Total Cholesterol	0.03 (0.04)	0.44	-0.01 (0.04)	0.86
	HDL	0.01 (0.04)	0.88	-0.06 (0.04)	0.14
	LDL	0.01 (0.04)	0.77	0.02 (0.04)	0.70
	Triglycerides	0.05 (0.04)	0.22	0.03 (0.04)	0.52
	APOB	0.02 (0.04)	0.64	-0.01 (0.04)	0.73
	Glucose	-0.02 (0.04)	0.63	0.04 (0.04)	0.33
	Insulin	-0.05 (0.04)	0.29	0.07 (0.04)	0.10
	Leptin	-0.03 (0.04)	0.51	0.06 (0.05)	0.19
HOMA-IR	-0.07 (0.04)	0.12	0.06 (0.04)	0.15	
rs3774261	BMI	-0.14 (0.08)	0.07	-0.11 (0.07)	0.12

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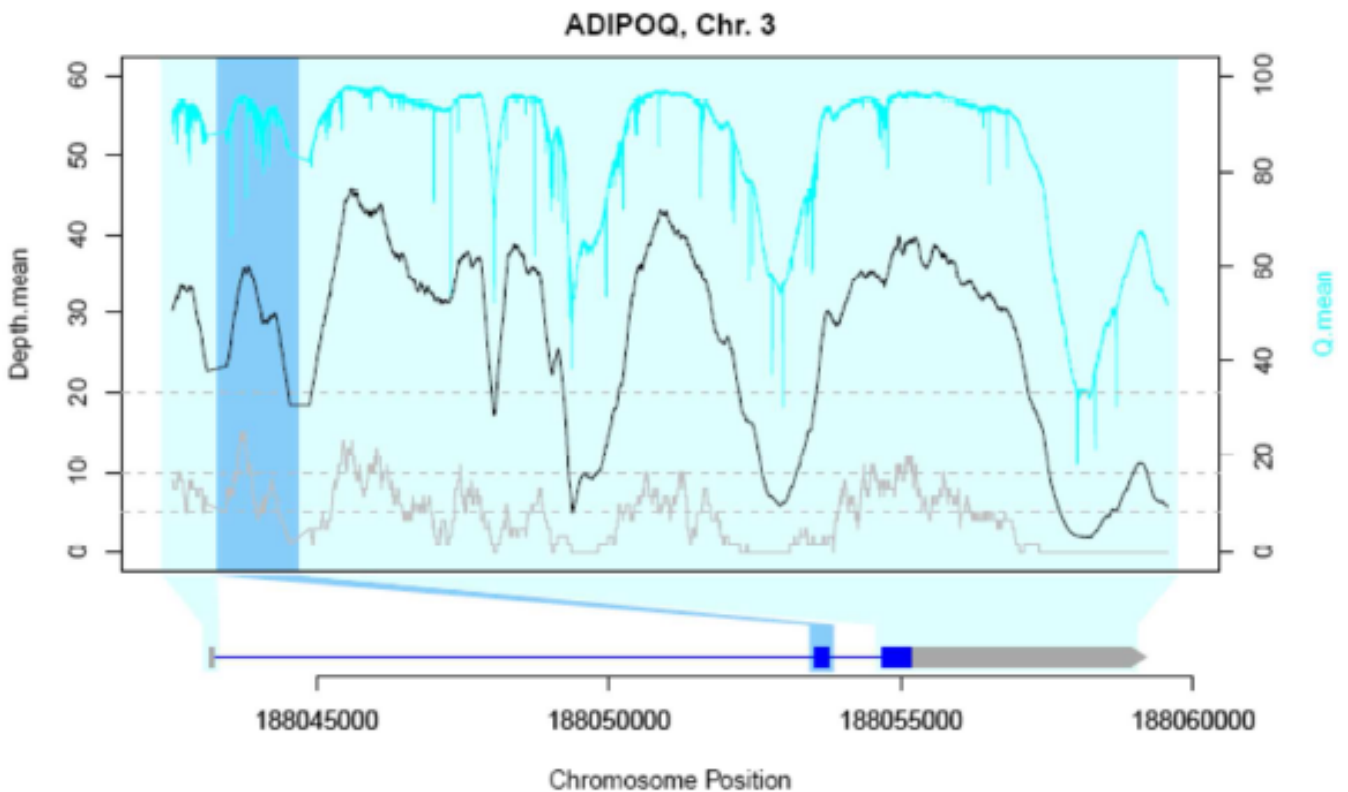
	Systolic BP	-0.14 (0.08)	0.07	0.08 (0.07)	0.25
	Diastolic BP	-0.04 (0.08)	0.61	0.09 (0.07)	0.20
	Total Cholesterol	0.17 (0.08)	0.03	0.16 (0.07)	0.03
	HDL	0.02 (0.08)	0.83	0.05 (0.07)	0.51
	LDL	0.12 (0.08)	0.13	0.11 (0.07)	0.12
	Triglycerides	0.18 (0.08)	0.02	0.13 (0.07)	0.07
	APOB	0.14 (0.08)	0.07	0.15 (0.07)	0.04
	Glucose	-0.02 (0.08)	0.84	-0.06 (0.08)	0.43
	Insulin	-0.05 (0.08)	0.52	-0.02 (0.08)	0.85
	Leptin	-0.02 (0.08)	0.81	0.04 (0.09)	0.64
	HOMA-IR	-0.06 (0.08)	0.47	-0.02 (0.08)	0.76
rs17366743	BMI	-0.00 (0.11)	0.97	-0.01 (0.10)	0.91
	Systolic BP	0.02 (0.11)	0.87	-0.07 (0.10)	0.49
	Diastolic BP	-0.05 (0.11)	0.61	-0.03 (0.10)	0.78
	Total Cholesterol	0.13 (0.11)	0.23	0.14 (0.11)	0.17
	HDL	-0.02 (0.11)	0.84	0.15 (0.11)	0.16
	LDL	0.13 (0.11)	0.24	0.14 (0.11)	0.20
	Triglycerides	0.07 (0.11)	0.55	-0.01 (0.11)	0.92
	APOB	0.10 (0.11)	0.39	-0.05 (0.11)	0.64
	Glucose	0.22 (0.11)	0.06	0.10 (0.11)	0.36
	Insulin	0.02 (0.11)	0.89	-0.25 (0.11)	0.02
	Leptin	0.03 (0.12)	0.81	0.08 (0.14)	0.59
HOMA-IR	-0.00 (0.12)	0.98	-0.18 (0.11)	0.10	
rs16848727	BMI	-0.06 (0.04)	0.13	0.05 (0.04)	0.21
	Systolic BP	0.01 (0.04)	0.79	-0.01 (0.04)	0.81
	Diastolic BP	-0.04 (0.04)	0.32	-0.01 (0.04)	0.85
	Total Cholesterol	-0.02 (0.04)	0.61	-0.02 (0.04)	0.52
	HDL	-0.03 (0.04)	0.42	-0.01 (0.04)	0.79
	LDL	-0.01 (0.04)	0.87	-0.03 (0.04)	0.36
	Triglycerides	0.03 (0.04)	0.52	-0.00 (0.04)	0.97
	APOB	-0.08 (0.04)	0.08	-0.05 (0.04)	0.22
	Glucose	-0.07 (0.04)	0.11	0.01 (0.04)	0.75
	Insulin	0.01 (0.04)	0.90	-0.02 (0.04)	0.69
	Leptin	-0.02 (0.04)	0.58	-0.04 (0.05)	0.38
HOMA-IR	-0.02 (0.05)	0.73	-0.01 (0.04)	0.72	
rs1868146	BMI	0.03 (0.06)	0.58	-0.07 (0.05)	0.22
	Systolic BP	-0.00 (0.06)	0.98	0.01 (0.05)	0.78
	Diastolic BP	-0.01 (0.06)	0.92	0.05 (0.05)	0.32
	Total Cholesterol	0.04 (0.06)	0.53	0.02 (0.05)	0.68
	HDL	0.10 (0.06)	0.09	-0.02 (0.05)	0.70
	LDL	-0.01 (0.06)	0.86	0.05 (0.05)	0.33
	Triglycerides	0.06 (0.06)	0.34	-0.01 (0.05)	0.89
	APOB	0.01 (0.06)	0.88	-0.02 (0.06)	0.79
	Glucose	0.01 (0.06)	0.84	-0.00 (0.06)	0.93
	Insulin	0.11 (0.06)	0.08	-0.02 (0.06)	0.67
	Leptin	0.03 (0.06)	0.66	-0.02 (0.07)	0.79
HOMA-IR	0.12 (0.06)	0.06	-0.02 (0.06)	0.72	
rs3821799	BMI	0.09 (0.08)	0.24	0.10 (0.07)	0.14
	Systolic BP	0.06 (0.07)	0.44	-0.12 (0.07)	0.08
	Diastolic BP	-0.02 (0.08)	0.82	-0.14 (0.07)	0.05
	Total Cholesterol	-0.14 (0.07)	0.07	-0.11 (0.07)	0.12
	HDL	-0.04 (0.08)	0.58	-0.02 (0.07)	0.83
	LDL	-0.13 (0.08)	0.10	-0.08 (0.07)	0.25
Triglycerides	-0.13 (0.08)	0.09	-0.09 (0.07)	0.20	

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	APOB	-0.13 (0.08)	0.08	-0.07 (0.07)	0.37
	Glucose	0.03 (0.08)	0.71	0.09 (0.07)	0.22
	Insulin	0.08 (0.08)	0.32	-0.01 (0.08)	0.85
	Leptin	0.06 (0.08)	0.43	-0.08 (0.09)	0.39
	HOMA-IR	0.09 (0.08)	0.25	0.01 (0.08)	0.87

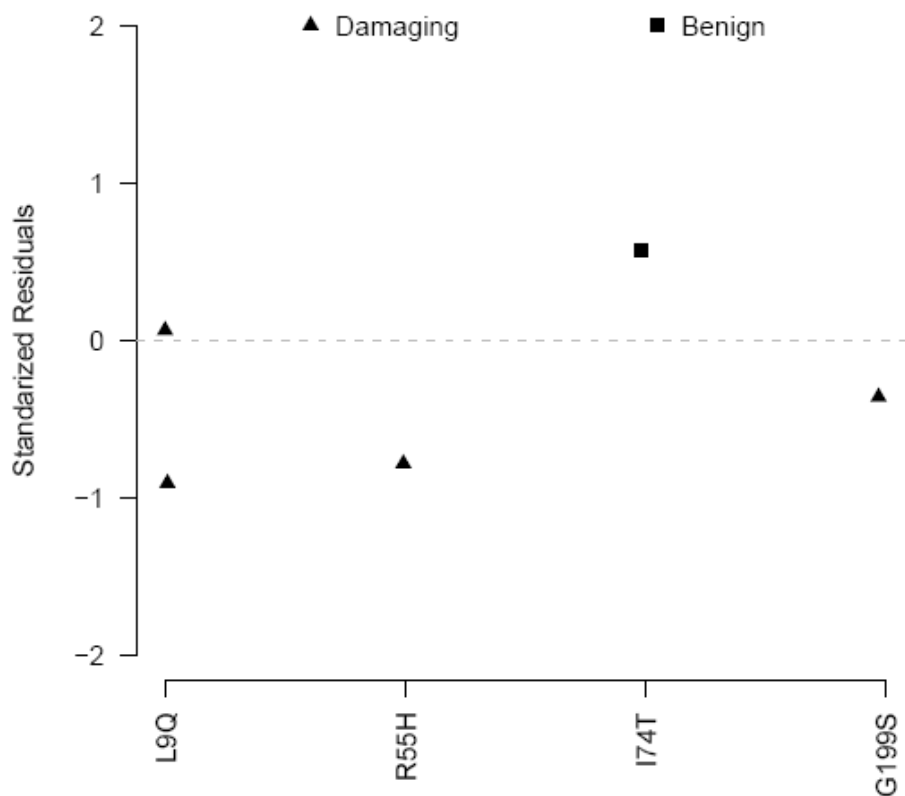
Data were natural log transformed and analyzed via linear regression under an additive model with the adjustment for covariates including center, age, gender, alcohol use, smoking status, medication when appropriate. Standardized residuals were analyzed to assess genetic association under an additive model.

**Supplementary Figure 1.** Sequence depth and quality plot of ADIPOQ



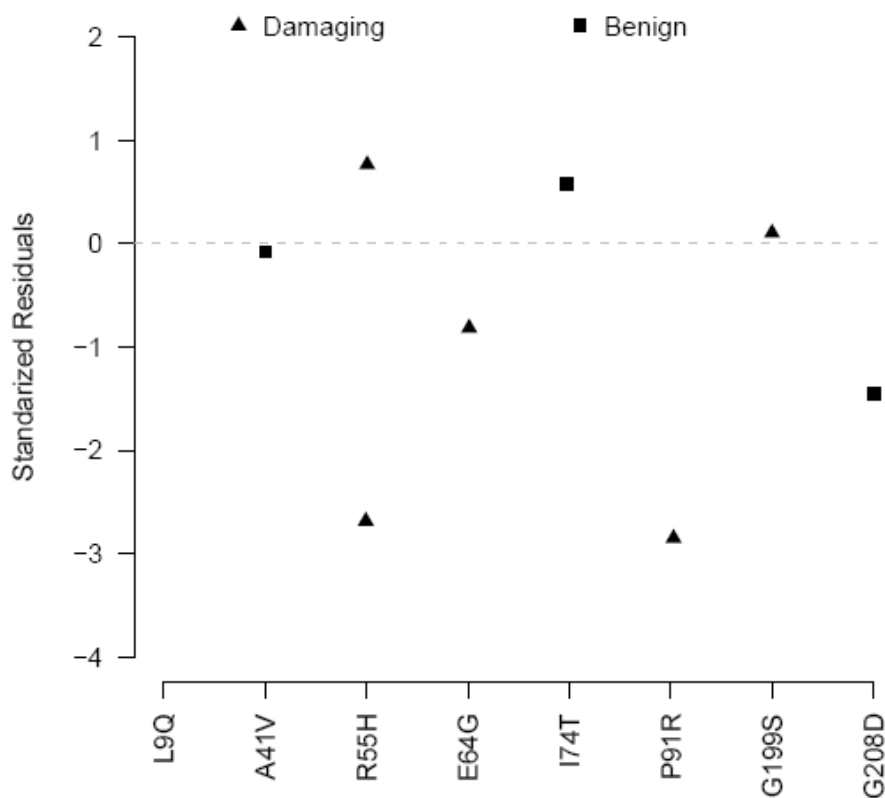
SUPPLEMENTARY DATA

**Supplementary Figure 2.** Effect of aggregated rare non-synonymous SNPs on log<sub>10</sub>(adiponectin) after adjusting for covariates in GEMS.



SUPPLEMENTARY DATA

**Supplementary Figure 3.** Effect of aggregated rare non-synonymous SNPs on log<sub>10</sub>(adiponectin) after adjusting for covariates in CoLaus



**Supplementary Figure 4.** Posterior density distribution of  $K$ , the number of independent SNPs, based on bayes variable selection analysis using WinBUGS

