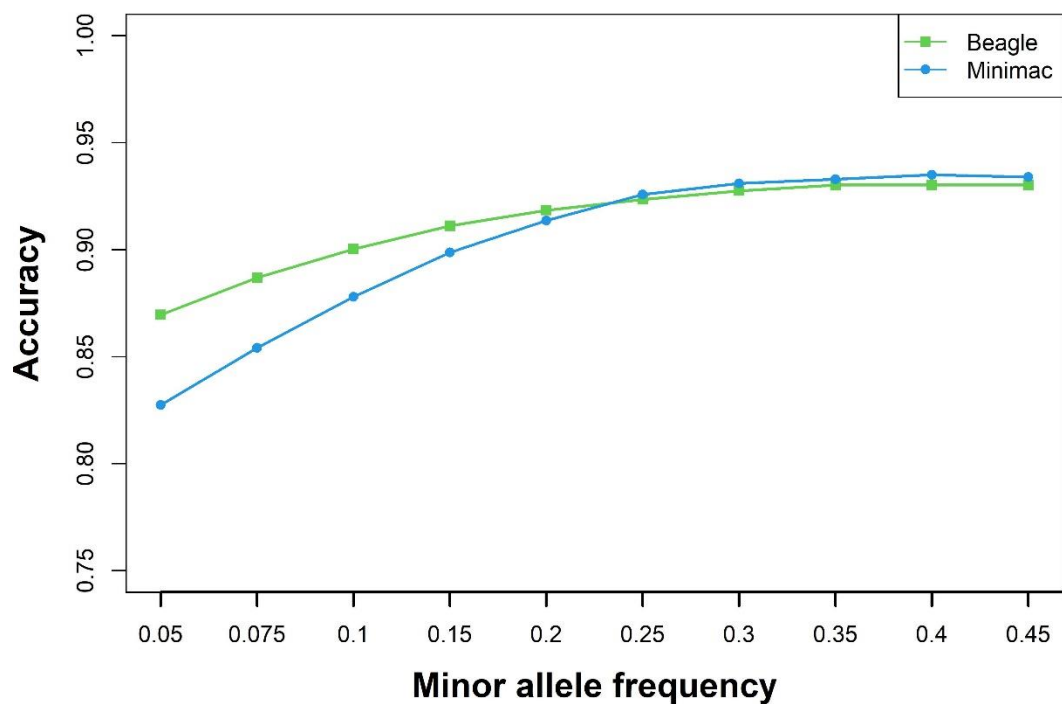


1 **Supplementary Figures 1-9 and Supplementary**
2 **Tables 1-7**

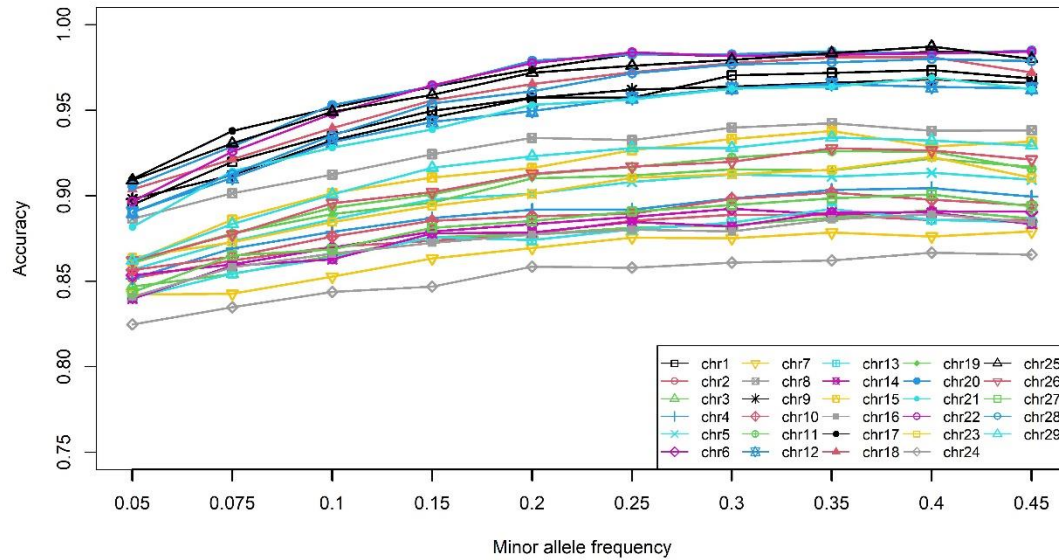
3 **Supplementary Fig. 1: Imputation reliability by MAFs using BEAGLE and**
4 **Minimac.**



5

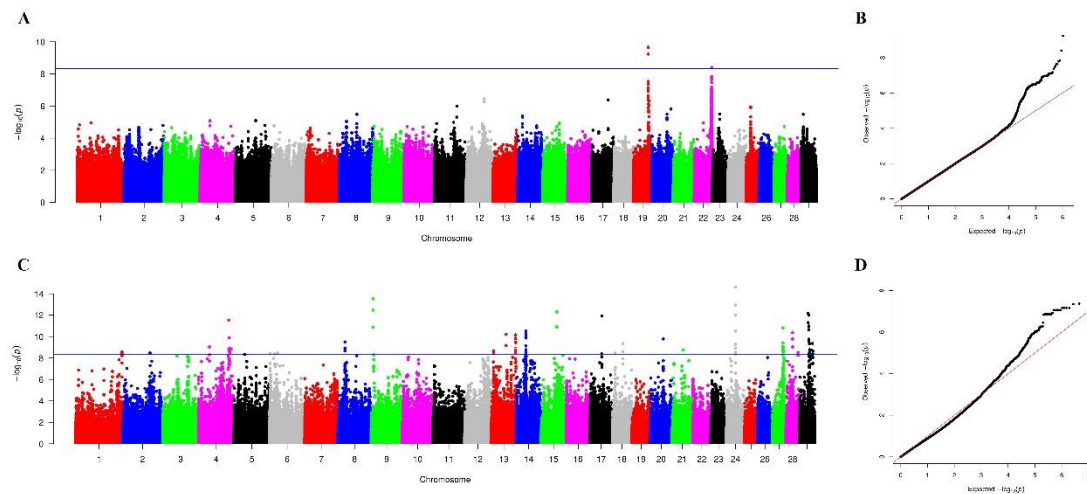
6

7 **Supplementary Fig. 2: MAFs of sequenced SNP versus the imputation**
8 **reliabilities for different chromosomes using Beagle.**



9

10 **Supplementary Fig. 3: Manhattan plots and QQ plot for C14:0 and C20:0.**



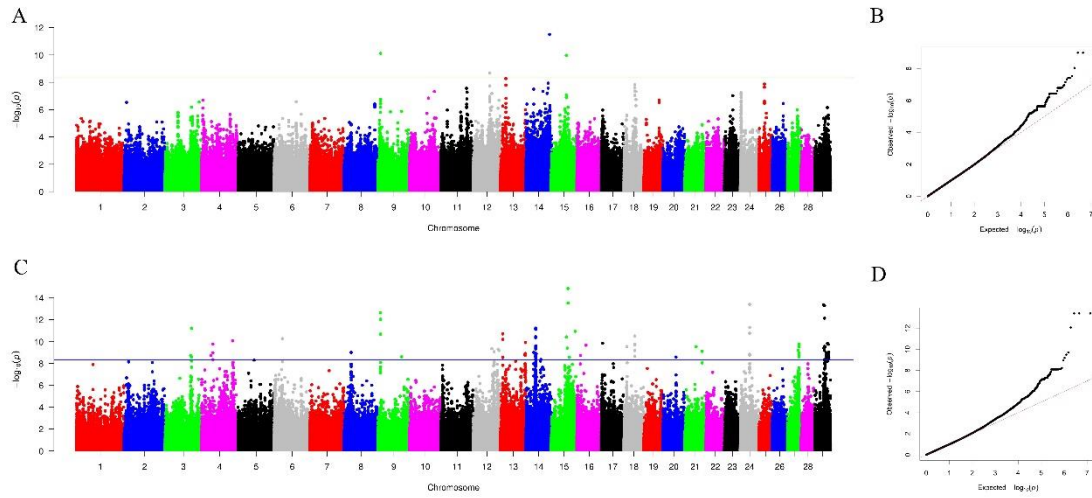
11

12 **A** Genome-wide Manhattan plots showing P-values of association for saturated fatty
13 acids (C14:0) using GRAMMAR-GC approach, expressed as $-\log_{10}(P)$ -value). **B** Q-Q
14 plot shows observed versus expected ordered $-\log_{10}(P)$ values for GWAS analysis of
15 C14:0. **C** Genome-wide manhattan plots showing P-values of association for saturated
16 fatty acids (C20:0) using GRAMMAR-GC approach, expressed as $-\log_{10}(P)$ -value).
17 **D** Q-Q plot shows observed versus expected ordered $-\log_{10}(P)$ values for GWAS
18 analysis of C20:0.

19

20

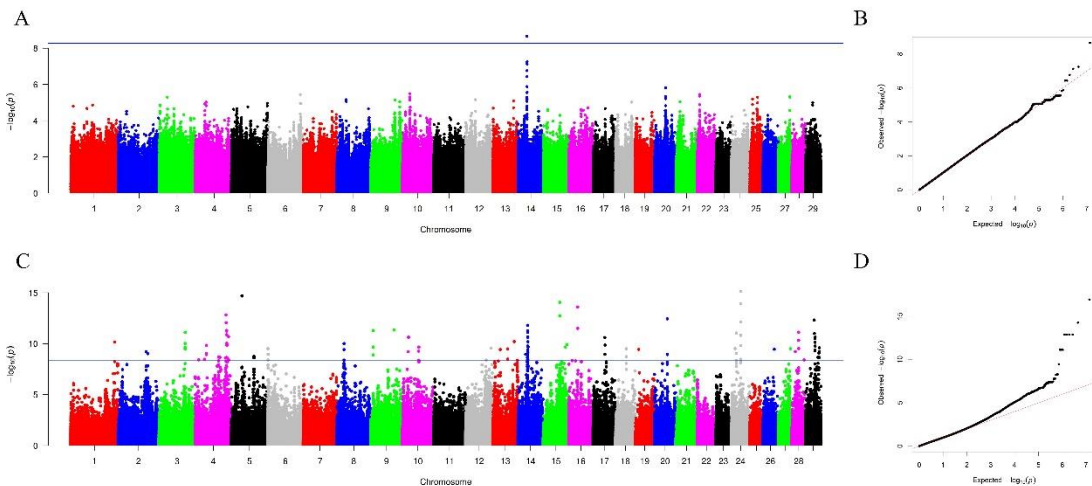
21 **Supplementary Fig. 4: Manhattan plots and QQ plot for C14:1 and C20:1.**



22

23 **A** Genome-wide manhattan plots showing P-values of association for
24 monounsaturated fatty acids (C14:1) using GRAMMAR-GC approach, expressed as -
25 $\log_{10}$ (P-value). **B** Q-Q plot shows observed versus expected ordered $-\log_{10}$ (P)
26 values for GWAS analysis of C14:1. **C** Genome-wide manhattan plots showing P-
27 values of association for monounsaturated fatty acids (C20:1) using GRAMMAR-GC
28 approach, expressed as $-\log_{10}$ (P-value). **D** Q-Q plot shows observed versus expected
29 ordered $-\log_{10}$ (P) values for GWAS analysis of C20:1.

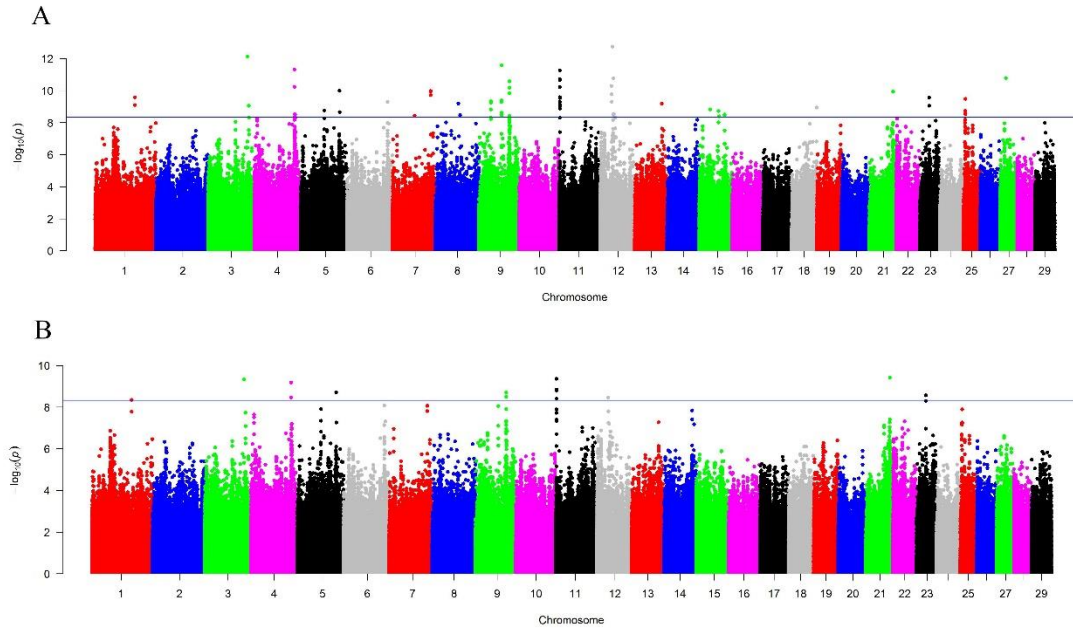
30 **Supplementary Fig. 5: Manhattan plots and QQ plot for C18:3:n-6 and C20:4.**



31

32 **A** Genome-wide manhattan plots showing P-values of association for polyunsaturated
33 fatty acids (C18:3:n-6) using GRAMMAR-GC approach, expressed as $-\log_{10}$ (P-
34 value). **B** Q-Q plot shows observed versus expected ordered $-\log_{10}$ (P) values for
35 GWAS analysis of C18:3:n-6. **C** Genome-wide manhattan plots showing P-values of
36 association for polyunsaturated fatty acids (C20:4) using GRAMMAR-GC approach,
37 expressed as $-\log_{10}$ (P-value). **D** Q-Q plot shows observed versus expected ordered
38 $-\log_{10}$ (P) values for GWAS analysis of C20:4.

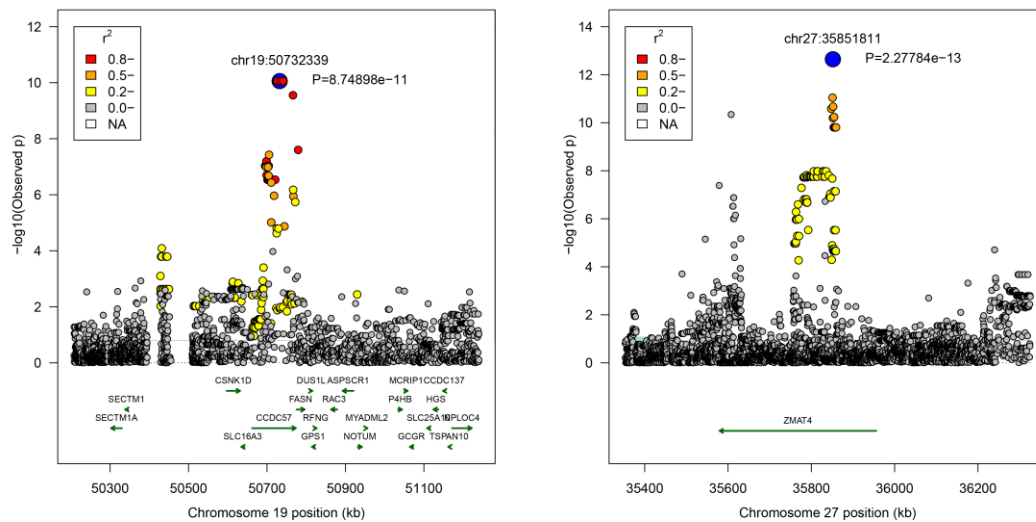
39 **Supplementary Fig. 6: Manhattan plots for C20:0 and C20:1 with MTAG**
 40 **analysis.**



41

42 **A** Genome-wide manhattan plots showing P-values of association forC20:0 using
 43 MTAG approach, expressed as $-\log_{10}(\text{P-value})$. **B** Genome-wide manhattan plots
 44 showing P-values of association forC20:1 using MTAG approach, expressed as $-\log_{10}(\text{P-value})$
 45

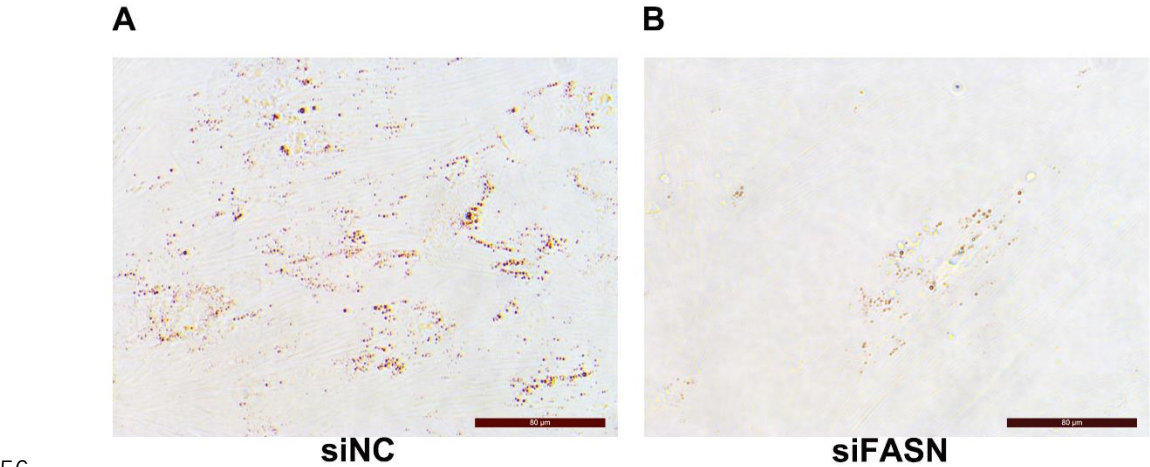
46 **Supplementary Fig. 7: Region plots around 50.7 Mb for chromosome19 and around**
 47 **35.8 Mb for chromosome27.**



48

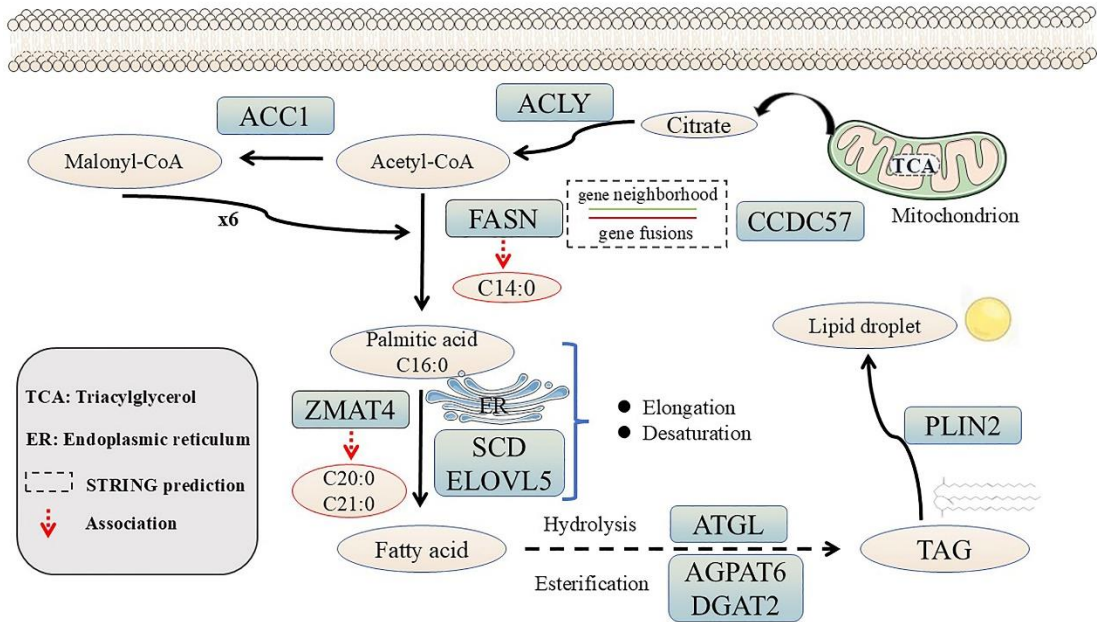
49 **A** Regional zoom plot around 50.7 Mb on chr19. This regional zoom plot shows the
 50 positions (X-axis) and $-\log_{10}(\text{P})$ values (Y-axis) for variants, LD among variants
 51 (colors of dots). **B** Regional zoom plot around 35.8 Mb region on chr27. This regional
 52 zoom plot shows the positions (X-axis) and $-\log_{10}(\text{P})$ values (Y-axis) for variants,
 53 and LD among variants (colors of dots).

Supplementary Fig. 8: Effects of *FASN* gene on fatty acid components and lipid droplet synthesis in preadipocytes.



A Oil Red O staining of preadipocytes after transfected with si-NC. **B** Oil Red O staining of preadipocytes after transfected with si-*FASN*

Supplementary Fig. 9: The regulation of candidate genes of FAs in fatty acid metabolism.



63 **Supplementary Table 1: Predictive reliabilities for different allelic R2 threshold per SNPs of whole autosomes using BEAGLE.**

	number	ar2>0	number	ar2>0.1	number	ar2>0.3	number	ar2>0.5	number	ar2>0.8
chr1	909829	0.82	671798	0.91	582940	0.93	510985	0.95	382666	0.98
chr2	727337	0.74	537050	0.84	476875	0.90	446204	0.91	329405	0.94
chr3	674195	0.74	497811	0.83	440067	0.88	403273	0.92	288608	0.95
chr4	710321	0.76	524486	0.85	460874	0.89	409757	0.90	285393	0.94
chr5	670549	0.78	495119	0.86	435105	0.90	391259	0.93	282058	0.96
chr6	636051	0.75	469647	0.84	416187	0.88	393227	0.91	302673	0.94
chr7	620071	0.73	457847	0.83	399623	0.87	353435	0.90	244591	0.94
chr8	620906	0.81	458464	0.88	409410	0.92	367708	0.94	265690	0.97
chr9	553428	0.82	408639	0.91	362001	0.93	324199	0.94	234677	0.96
chr10	561713	0.75	414757	0.85	368432	0.89	330071	0.91	228598	0.94
chr11	599827	0.78	442900	0.87	390961	0.90	346609	0.93	248978	0.96
chr12	521499	0.81	385064	0.90	337736	0.93	304112	0.94	203188	0.96
chr13	510804	0.75	377167	0.83	332972	0.88	281469	0.91	191796	0.94
chr14	485961	0.74	358823	0.83	312867	0.88	260308	0.91	189290	0.94
chr15	523336	0.78	386420	0.87	339512	0.92	296633	0.95	210610	0.97
chr16	450944	0.75	332967	0.83	294015	0.88	256869	0.91	180373	0.94
chr17	416150	0.84	307276	0.93	268430	0.94	238510	0.95	176411	0.96
chr18	379280	0.83	280052	0.92	249293	0.93	231198	0.94	164104	0.96
chr19	370323	0.78	273439	0.86	243171	0.89	213272	0.93	143941	0.97
chr20	408517	0.84	301640	0.93	269107	0.94	247550	0.95	176142	0.98
chr21	394253	0.81	291108	0.90	252900	0.93	221370	0.94	161089	0.96
chr22	340342	0.85	251301	0.93	222743	0.94	200157	0.95	143787	0.98
chr23	358809	0.78	264937	0.86	234351	0.89	211784	0.93	136395	0.96
chr24	395492	0.72	292023	0.81	253074	0.87	211169	0.91	152210	0.95

chr25	260835	0.84	192595	0.92	170856	0.93	160050	0.94	111274	0.96
chr26	323213	0.78	238654	0.87	205685	0.91	174037	0.93	121116	0.96
chr27	264563	0.75	195348	0.84	171397	0.89	149308	0.92	107408	0.95
chr28	306538	0.82	226342	0.91	194278	0.93	154990	0.94	109449	0.95
chr29	350652	0.78	258914	0.87	223392	0.92	183972	0.95	130761	0.97
	14345738	0.78	10592588	0.87	9318254	0.91	8273481	0.93	5902681	0.96

64

65 **Supplementary Table 2:** Average imputation reliabilities of different MAF bins.

MAF bins	Beagle	Minimac
0.05-0.075	0.87	0.83
0.075-0.1	0.89	0.85
0.1-0.15	0.90	0.88
0.15-0.2	0.91	0.90
0.2-0.25	0.92	0.91
0.25-0.3	0.92	0.93
0.3-0.35	0.93	0.93
0.35-0.4	0.93	0.93
0.4-0.45	0.93	0.93
0.45-0.5	0.93	0.93

66

67 **Supplementary Table 3:** Imputation reliability of different MAF classes using Beagle.

Chr	0.05-0.075	0.075-0.1	0.1-0.15	0.15-0.2	0.2-0.25	0.25-0.3	0.3-0.35	0.35-0.4	0.4-0.45	0.45-0.5
chr1	0.89	0.92	0.94	0.95	0.96	0.96	0.97	0.97	0.97	0.97
chr2	0.85	0.86	0.87	0.87	0.88	0.89	0.89	0.89	0.89	0.89
chr3	0.85	0.85	0.86	0.88	0.88	0.88	0.88	0.89	0.89	0.89
chr4	0.85	0.87	0.88	0.89	0.89	0.89	0.90	0.90	0.90	0.90
chr5	0.86	0.87	0.89	0.90	0.90	0.91	0.91	0.91	0.91	0.91
chr6	0.85	0.86	0.87	0.88	0.88	0.89	0.89	0.89	0.89	0.89
chr7	0.84	0.84	0.85	0.86	0.87	0.88	0.88	0.88	0.88	0.88
chr8	0.89	0.90	0.91	0.92	0.93	0.93	0.94	0.94	0.94	0.94
chr9	0.90	0.91	0.93	0.95	0.96	0.96	0.96	0.97	0.97	0.97
chr10	0.86	0.86	0.88	0.89	0.89	0.89	0.90	0.90	0.90	0.89
chr11	0.86	0.88	0.89	0.90	0.91	0.92	0.92	0.93	0.93	0.92
chr12	0.89	0.91	0.93	0.94	0.95	0.96	0.96	0.97	0.96	0.96
chr13	0.84	0.85	0.86	0.88	0.87	0.88	0.88	0.89	0.89	0.88
chr14	0.84	0.86	0.86	0.88	0.88	0.88	0.88	0.89	0.89	0.88
chr15	0.86	0.89	0.90	0.91	0.92	0.93	0.93	0.94	0.93	0.93
chr16	0.84	0.86	0.87	0.87	0.88	0.88	0.88	0.89	0.89	0.88
chr17	0.91	0.94	0.95	0.96	0.97	0.98	0.98	0.98	0.98	0.98
chr18	0.90	0.92	0.94	0.96	0.97	0.97	0.98	0.98	0.98	0.97
chr19	0.86	0.88	0.89	0.90	0.91	0.91	0.92	0.91	0.92	0.92
chr20	0.91	0.93	0.95	0.96	0.98	0.98	0.98	0.98	0.98	0.98
chr21	0.88	0.91	0.93	0.94	0.95	0.96	0.96	0.96	0.97	0.96
chr22	0.90	0.93	0.95	0.96	0.98	0.98	0.98	0.98	0.98	0.98

chr23	0.86	0.87	0.88	0.89	0.90	0.91	0.91	0.92	0.92	0.91
chr24	0.82	0.83	0.84	0.85	0.86	0.86	0.86	0.86	0.87	0.87
chr25	0.91	0.93	0.95	0.96	0.97	0.98	0.98	0.98	0.99	0.98
chr26	0.86	0.88	0.90	0.90	0.91	0.92	0.92	0.93	0.93	0.92
chr27	0.84	0.87	0.87	0.88	0.89	0.89	0.89	0.90	0.90	0.89
chr28	0.89	0.91	0.94	0.95	0.96	0.97	0.98	0.98	0.98	0.98
chr29	0.86	0.88	0.90	0.92	0.92	0.93	0.93	0.93	0.93	0.93
Mean	0.89	0.92	0.94	0.95	0.96	0.96	0.97	0.97	0.97	0.97

68

69 **Supplementary Table 4:** Significant SNPs identified by step II genome-wide association tests.

Trait	SNP	Chr	Position ^a	P_value ^b	Nearest gene ^c	MAF	R ²
C14:0	chr19:50724699	19	50724699	5.11E-11	CCDC57	0.24	0.98
	chr19:50724757	19	50724757	5.11E-11	CCDC57	0.24	0.98
	chr19:50726437	19	50726437	5.11E-11	CCDC57	0.24	0.98
	chr19:50732339	19	50732339	5.11E-11	CCDC57	0.24	1
	chr19:50734637	19	50734637	5.11E-11	CCDC57	0.24	1
	chr19:50741020	19	50741020	5.11E-11	CCDC57	0.24	1
	chr19:50766239	19	50766239	7.85E-11	FASN	0.27	0.97
	chr19:50779529	19	50779529	9.78E-09	FASN	0.27	0.98
	chr19:50705362	19	50705362	2.70E-08	CCDC57	0.2	0.96
	chr19:50698782	19	50698782	2.94E-08	CCDC57	0.22	0.98
	chr19:50698797	19	50698797	2.94E-08	CCDC57	0.22	0.98
	chr19:50695215	19	50695215	4.05E-08	CCDC57	0.22	0.98
	chr19:50696161	19	50696161	4.05E-08	CCDC57	0.22	0.98
	chr19:50696545	19	50696545	4.05E-08	CCDC57	0.22	0.98
	chr19:50697546	19	50697546	4.05E-08	CCDC57	0.22	0.98
	chr19:50701151	19	50701151	4.05E-08	CCDC57	0.22	0.98
	chr19:50702881	19	50702881	4.05E-08	CCDC57	0.22	0.98
	chr19:50704457	19	50704457	4.05E-08	CCDC57	0.22	0.98
	chr22:58427069	22	58427069	4.16E-08	HDAC11	0.28	0.88
	chr19:50697929	19	50697929	4.34E-08	CCDC57	0.22	0.99
	chr19:50702681	19	50702681	4.34E-08	CCDC57	0.22	0.99
C14:1	chr12:54714669	12	54714669	3.67E-10		0.05	0.93
	chr12:54717553	12	54717553	3.67E-10		0.05	0.93

C18:3 n-6	chr12:54718423	12	54718423	3.67E-10		0.05	0.93
	chr12:54677836	12	54677836	5.82E-09		0.06	0.94
	chr14:28740444	14	28740444	8.13E-10		0.05	0.88
	chr14:28747129	14	28747129	1.19E-08		0.06	0.92
	chr14:28612750	14	28612750	5.09E-08		0.05	0.91
C18:2 t-9c-11	chr3:48428579	3	48428579	1.95E-08	ALG14	0.08	0.84
C18:2 t-12c-10	chr3:48428579	3	48428579	7.41E-09	ALG14	0.08	0.84
C20:0	chr3:48428579	3	48428579	1.17E-09	ALG14	0.08	0.84
	chr27:35805955	27	35805955	9.92E-09	ZMAT4	0.06	0.94
	chr27:35814687	27	35814687	9.92E-09	ZMAT4	0.06	0.93
	chr27:35815414	27	35815414	9.92E-09	ZMAT4	0.06	0.93
	chr27:35815496	27	35815496	9.92E-09	ZMAT4	0.06	0.93
	chr27:35828077	27	35828077	9.92E-09	ZMAT4	0.06	0.91
	chr27:35831468	27	35831468	9.92E-09	ZMAT4	0.06	0.91
	chr27:35835745	27	35835745	9.92E-09	ZMAT4	0.06	0.88
	chr27:35841994	27	35841994	1.30E-08	ZMAT4	0.06	0.88
	chr14:30804644	14	30804644	1.52E-08		0.05	0.9
	chr27:35783752	27	35783752	2.17E-08	ZMAT4	0.06	0.9
	chr27:35791484	27	35791484	2.17E-08	ZMAT4	0.06	0.91
	chr27:35791630	27	35791630	2.17E-08	ZMAT4	0.06	0.91
	chr27:35795581	27	35795581	2.17E-08	ZMAT4	0.06	0.91
	chr27:35798458	27	35798458	2.17E-08	ZMAT4	0.06	0.91
	chr27:35800041	27	35800041	2.17E-08	ZMAT4	0.06	0.91
	chr27:35803911	27	35803911	2.17E-08	ZMAT4	0.06	0.91
	chr27:35805747	27	35805747	2.17E-08	ZMAT4	0.06	0.92
	chr27:35813644	27	35813644	2.17E-08	ZMAT4	0.06	0.92

C20:1	chr27:35814445	27	35814445	2.17E-08	ZMAT4	0.06	0.92
	chr27:35826374	27	35826374	2.17E-08	ZMAT4	0.06	0.92
	chr27:35832138	27	35832138	2.17E-08	ZMAT4	0.06	0.92
	chr27:35832564	27	35832564	2.17E-08	ZMAT4	0.06	0.92
	chr27:35781352	27	35781352	2.90E-08	ZMAT4	0.06	0.85
	chr27:35783020	27	35783020	2.90E-08	ZMAT4	0.06	0.85
	chr27:35789498	27	35789498	2.90E-08	ZMAT4	0.06	0.85
	chr27:35788247	27	35788247	3.36E-08	ZMAT4	0.07	0.85
	chr27:35805955	27	35805955	3.94E-09	ZMAT4	0.06	0.94
	chr27:35814687	27	35814687	3.94E-09	ZMAT4	0.06	0.93
	chr27:35815414	27	35815414	3.94E-09	ZMAT4	0.06	0.93
	chr27:35815496	27	35815496	3.94E-09	ZMAT4	0.06	0.93
	chr27:35828077	27	35828077	3.94E-09	ZMAT4	0.06	0.91
	chr27:35831468	27	35831468	3.94E-09	ZMAT4	0.06	0.91
	chr27:35835745	27	35835745	3.94E-09	ZMAT4	0.06	0.88
	chr27:35841994	27	35841994	4.76E-09	ZMAT4	0.06	0.88
	chr27:35783752	27	35783752	1.15E-08	ZMAT4	0.06	0.9
	chr27:35791484	27	35791484	1.15E-08	ZMAT4	0.06	0.91
	chr27:35791630	27	35791630	1.15E-08	ZMAT4	0.06	0.91
	chr27:35795581	27	35795581	1.15E-08	ZMAT4	0.06	0.91
	chr27:35798458	27	35798458	1.15E-08	ZMAT4	0.06	0.91
	chr27:35800041	27	35800041	1.15E-08	ZMAT4	0.06	0.91
	chr27:35803911	27	35803911	1.15E-08	ZMAT4	0.06	0.91
	chr27:35805747	27	35805747	1.15E-08	ZMAT4	0.06	0.92
	chr27:35813644	27	35813644	1.15E-08	ZMAT4	0.06	0.92
	chr27:35814445	27	35814445	1.15E-08	ZMAT4	0.06	0.92

	chr27:35826374	27	35826374	1.15E-08	ZMAT4	0.06	0.920
	chr27:35832138	27	35832138	1.15E-08	ZMAT4	0.06	0.92
	chr27:35832564	27	35832564	1.15E-08	ZMAT4	0.06	0.92
	chr27:35781352	27	35781352	1.36E-08	ZMAT4	0.06	0.85
	chr27:35783020	27	35783020	1.36E-08	ZMAT4	0.06	0.85
	chr27:35789498	27	35789498	1.36E-08	ZMAT4	0.06	0.85
	chr27:35833204	27	35833204	2.36E-08	ZMAT4	0.08	0.89
	chr27:35776413	27	35776413	3.52E-08	ZMAT4	0.06	0.88
C20:2	chr3:48428579	3	48428579	7.09E-09	ALG14	0.08	0.84
C20:4	chr3:48428579	3	48428579	2.68E-08	ALG14	0.08	0.84
	chr16:41332960	16	41332960	5.02E-08		0.06	0.89
	chr14:77505817	14	77505817	4.92E-09		0.05	0.91
	chr14:77508286	14	77508286	4.92E-09		0.05	0.91
C24:0	chr14:77513512	14	77513512	4.92E-09		0.05	0.91
	chr14:77514078	14	77514078	4.92E-09		0.05	0.91
	chr14:77514157	14	77514157	4.92E-09		0.05	0.91
	chr14:77517587	14	77517587	4.92E-09		0.05	0.91
C22:6 n-3	chr29:33775946	29	33775946	4.90E-08		0.08	0.93

71 **Supplementary Table 5:** Significant SNPs and its nearest genes identified by multiple traits GWAS analysis using MTAG.

Trait	SNP	Chr	Position ^a	P_value ^b	Nearest gene ^c	MAF	R ²
C14:0	chr19:50726437	19	50726437	5.07E-15	CCDC57	0.24	0.98
	chr19:50779529	19	50779529	2.3E-14	FASN	0.27	0.98
	chr19:50766239	19	50766239	7.16E-14	CCDC57	0.27	0.97
	chr19:50704213	19	50704213	1.13E-13	CCDC57	0.25	0.98
	chr19:50698782	19	50698782	3.27E-13	CCDC57	0.22	0.98
	chr19:50705362	19	50705362	3.74E-13	CCDC57	0.2	0.96
	chr19:50718075	19	50718075	5.79E-13	CCDC57	0.22	0.98
	chr19:50697929	19	50697929	6.76E-13	CCDC57	0.22	0.99
	chr19:50698916	19	50698916	9.6E-13	CCDC57	0.22	0.98
	chr19:50701293	19	50701293	1.81E-12	CCDC57	0.22	0.98
	chr19:50715174	19	50715174	1.81E-12	CCDC57	0.22	0.98
	chr19:50705700	19	50705700	1.81E-12	CCDC57	0.22	0.98
	chr19:50710999	19	50710999	6.09E-12	CCDC57	0.22	0.98
	chr19:50766772	19	50766772	5.43E-11	CCDC57	0.43	0.99
	chr19:50767356	19	50767356	6.49E-11	CCDC57	0.39	0.99
	chr19:50710923	19	50710923	9.32E-11	CCDC57	0.23	0.99
C20:0	chr12:32110328	12	32110328	1.05E-13	PDX1	0.05	0.92
	chr3:102629378	3	102629378	4.36E-13	MED8	0.05	0.92

chr4:103896099	4	103896099	2.82E-12	DENND2A	0.05	0.93
chr11:1973296	11	1973296	3.13E-12	ZNF514	0.07	0.94
chr27:16523997	27	16523997	9.46E-12	FAT1	0.05	0.92
chr12:34733359	12	34733359	9.77E-12	SGCG	0.05	0.92
chr11:1966257	11	1966257	1.12E-11	ZNF514	0.08	0.93
chr11:1969792	11	1969792	1.14E-11	ZNF514	0.08	0.94
chr11:1969618	11	1969618	1.27E-11	ZNF514	0.08	0.95
chr4:103824797	4	103824797	3.34E-11	RAB19	0.05	0.93
chr11:1961687	11	1961687	3.49E-11	ZNF514	0.07	0.94
chr5:101175254	5	101175254	5.92E-11	MFAP5	0.21	0.98
chr21:61626059	21	61626059	6.64E-11	VRK1	0.05	0.919
chr12:30609779	12	30609779	9.87E-11	SNORA70	0.05	0.918667
chr11:1964062	11	1964062	1.47E-10	ZNF514	0.07	0.92
chr23:25167448	23	25167448	1.59E-10	GSTA5	0.06	0.918167
chr11:1958493	11	1958493	1.71E-10	ZNF514	0.07	0.91
chr11:1969993	11	1969993	1.71E-10	ZNF514	0.07	0.91
chr12:30593748	12	30593748	2.91E-10	SNORA70	0.05	0.917667
chr11:1966968	11	1966968	2.92E-10	ZNF514	0.08	0.94
chr6:114654025	6	114654025	3.02E-10	ACOX3	0.12	0.97
chr8:59203614	8	59203614	3.73E-10	FAM205C	0.05	0.917167
chr13:69674402	13	69674402	3.78E-10	TOP1	0.05	0.94

chr11:1972055	11	1972055	4.25E-10	ZNF514	0.07	0.93
chr23:25168889	23	25168889	5.07E-10	GSTA5	0.05	0.93
chr3:105687830	3	105687830	5.07E-10	ZFP69	0.06	0.92
chr11:1971016	11	1971016	5.6E-10	ZNF514	0.07	0.93
chr18:65071254	18	65071254	6.58E-10	ZSCAN4	0.05128	0.915167
chr18:65071254	18	65071254	6.58E-10	ZNF551	0.05128	0.915167
chr11:1973149	11	1973149	7.66E-10	ZNF514	0.07	0.93
chr15:27993751	15	27993751	8.81E-10	BACE1	0.05128	0.914167
chr25:3756265	25	3756265	1.05E-09	MGRN1	0.06	0.913667
chr12:35833371	12	35833371	1.64E-09	IL17D	0.05128	0.922167
chr12:36153394	12	36153394	1.64E-09	ZMYM2	0.05128	0.922167
chr12:36222951	12	36222951	1.64E-09	ZMYM5	0.05128	0.922167
chr4:105271796	4	105271796	1.74E-09	MGAM	0.05128	0.93
chr4:105295283	4	105295283	1.79E-09	MGAM	0.05128	0.93
chr15:51027496	15	51027496	2.31E-09	STIM1	0.05128	0.910667
chr4:105283526	4	105283526	2.39E-09	MGAM	0.05128	0.93
chr4:105274903	4	105274903	2.79E-09	MGAM	0.05128	0.93
chr3:106470142	3	106470142	2.83E-09	HEYL	0.05128	0.92
chr11:1961017	11	1961017	2.85E-09	ZNF514	0.07	0.94
chr4:105295268	4	105295268	3.06E-09	MGAM	0.05128	0.93
chr4:7303962	4	7303962	3.19E-09	ABCA13	0.36	0.98

	chr4:7304904	4	7304904	3.21E-09	ABCA13	0.36	0.98
	chr22:2072272	22	2072272	3.28E-09	EOMES	0.05128	0.908167
	chr22:2076783	22	2076783	3.28E-09	EOMES	0.05128	0.93
	chr25:3154184	25	3154184	3.76E-09	CREBBP	0.04827	0.93
	chr25:3171798	25	3171798	3.76E-09	CREBBP	0.04827	0.93
	chr4:103818436	4	103818436	3.81E-09	RAB19	0.06	0.93
	chr14:77014201	14	77014201	3.85E-09	CA3	0.07	0.905667
	chr12:33780929	12	33780929	3.91E-09	ATP8A2	0.07	0.905167
	chr25:3136722	25	3136722	4.14E-09	CREBBP	0.04827	0.93
	chr4:7303902	4	7303902	4.29E-09	ABCA13	0.36	0.98
	chr11:69593714	11	69593714	5.22E-09	LBH	0.36	0.98
C20:1	chr21:61626059	21	61626059	2.22E-10	VRK1	0.048	0.94
	chr11:1973296	11	1973296	2.51E-10	ZNF514	0.07	0.94
	chr3:102629378	3	102629378	2.7E-10	MED8	0.05	0.92
	chr4:103896099	4	103896099	3.85E-10	DENND2A	0.05	0.93
	chr11:1966257	11	1966257	8.34E-10	ZNF514	0.08	0.93
	chr11:1969792	11	1969792	9.13E-10	ZNF514	0.08	0.94
	chr11:1969618	11	1969618	9.29E-10	ZNF514	0.08	0.95
	chr11:1969618	11	1969618	9.29E-10	PROM2	0.08	0.95
	chr5:101175254	5	101175254	1.14E-09	MFAP5	0.21	0.98
	chr23:25167448	23	25167448	1.57E-09	GSTA5	0.05	0.92

chr4:103824797	4	103824797	1.99E-09	RAB19	0.05	0.93
chr11:1961687	11	1961687	2.24E-09	ZNF514	0.07	0.94
chr23:25168889	23	25168889	2.95E-09	GSTA5	0.05	0.93
chr6:114654025	6	114654025	4.74E-09	ACOX3	0.12	0.97

72 ^a Position (bp) on ARS-UCD1.2.

73 ^b P-value after Bonferroni correction.

74 ^c Nearest gene found on the Ensembl (www.ensembl.org)

75 **Supplementary Table 6:** The sequence of siRNA for interference *FASN*.

Name	Sequence
FASN-1	GCAACTCAACGGGAACCTTA
FASN-2	CCATCCTTCTGACCAAGAA
FASN-3	CCTACTTCATGGACGCTAT

76 **Supplementary Table 7:** Sequence of primers for qPCR.

Gene	Forward (5'to 3')	Reverse (5'to 3')	production (bp)	Accession number
<i>GAPDH</i>	CCTGCCCCGTTTCGACAGATA	GGCGACGATGTCCACTTTG	201	NM_001034034.2
<i>FASN</i>	CTGGAGCGTGAGCACAACCTG	GTGTGGAGTCCGTCAGCTCAT	118	NM_001012669.1
<i>DGAT2</i>	GTCCTGTCTTTCCTCGTGCT	CCTCCTGCCACCTTTCTT	141	NM_205793.2
<i>AGPAT6</i>	AACCTGCATCAATAATACATCA	GGTAGGTCACCATTCCGTA	146	XM_024986242.1
<i>ATGL</i>	TGCTGATTGCTATGAGTGTGCC	CCTCTTTGGAGTTGAAGTGGGT	101	NM_001046005.2
<i>PLIN2</i>	AGTGAACTTGCCAGGAAGAATG	TTCATCTGTATCATCGTAGCCG	120	NM_173980.2

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