1   **Supplementary materials**
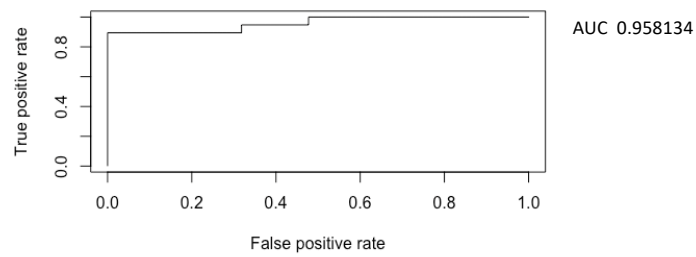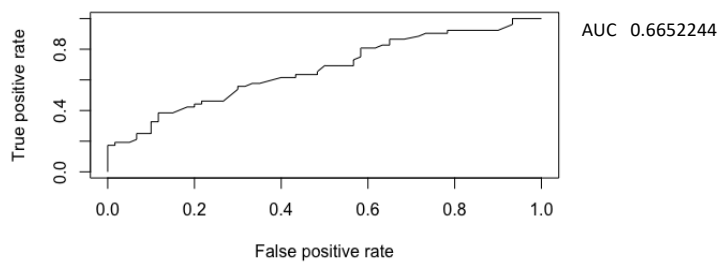
2   <mark>**Figure S1. A.** Roc curve BMI classification random forest for predicting obese status as variable</mark>

3   <mark>that identified the model. **B**. Roc curve GRS classification random forest for predicting high genetic</mark>

4   <mark>risk score as variable that identified the model.</mark>

5   **A.**

True positive rate

AUC 0.958134

False positive rate

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7   **B.**

True positive rate

AUC 0.6652244

False positive rate
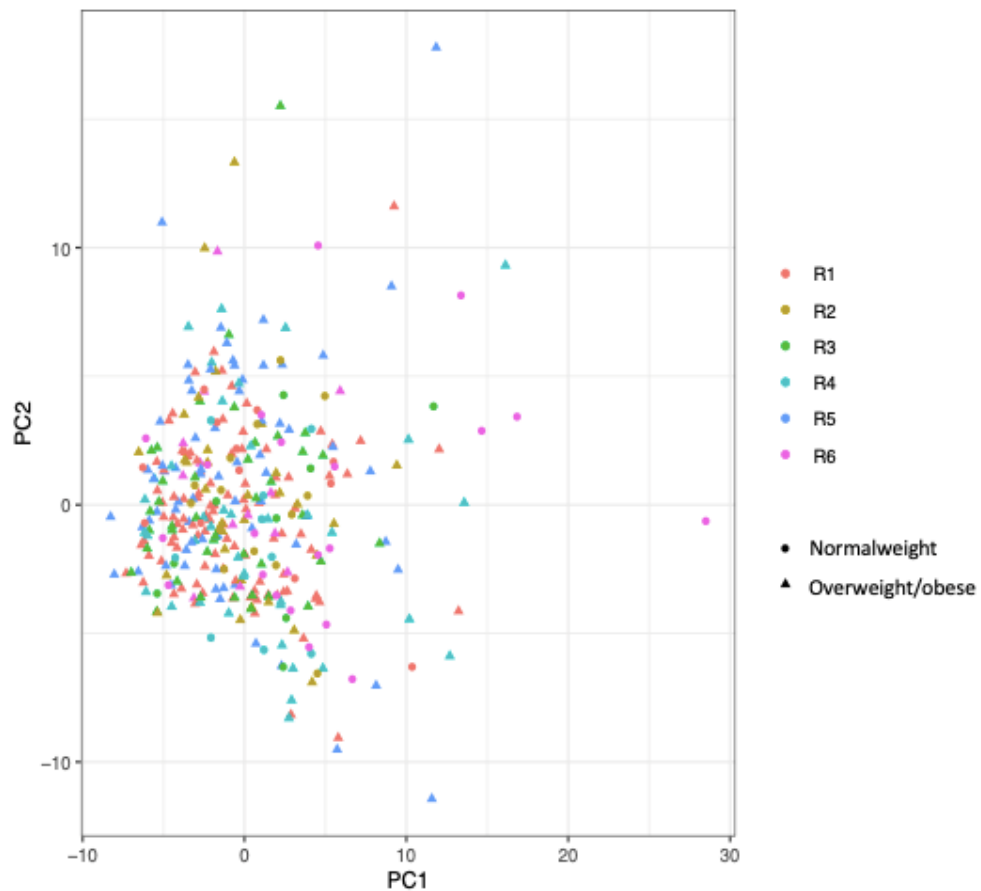
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17 **Figure S2.** Principal component analysis (PCA) scaling based on Euclidean distances.

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19 PCA plot showing the absence of batch effect. Different colors indicate different runs (R1-6) in
20 sequencing, while different symbols represent sample types, triangle represent subjects with
21 BMI>25kg/m^2 and circles represent subjects with BMI<24.9kg/m^2. This plot demonstrated that
22 grouping was not caused by batch effect in our samples.

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32 **Table S1.** Genomic characteristics of the 95 obesity-predisposing SNPs.

SNP[a]	Gene[b]	Chromosome position[c]	Alleles
rs17024393	*GNAT2*	Chr1:110154688	T/C
rs1801131	*MTHFR*	Chr1:11854476	T/G
rs1801133	*MTHFR*	Chr1:11856378	G/A
rs543874	*SEC16B*	Chr1:177889480	A/G
rs2605100	*LYPLAL1*	Chr1:219644224	A/G
rs4846567	*LYPLAL1*	Chr1:219750717	G/T
rs3123554	*CNR2*	Chr1:24196401	A/G
rs324420	*FAAH*	Chr1:46870761	C/A
rs8179183/rs1805094	*LEPR*	Chr1:66075952	G/C
rs2815752	*NEGR1*	Chr1:72812440	G/A
rs519887	*ABCB11*	Chr2:169780885	T/C
rs484066	*ABCB11*	Chr2:169782481	A/T
rs569805	*ABCB11*	Chr2:169782880	A/T
rs494874	*ABCB11*	Chr2:169789306	T/C
rs2943641	*IRS1*	Chr2:227093745	T/C
rs10182181	*ADCY3*	Chr2:25150296	A/G
rs713586	*ADCY3*	Chr2:25158008	T/C
rs2860323	*TMEM18*	Chr2:614210	A/G
rs2867125	*TMEM18*	Chr2:622827	T/C
rs13021737	*TMEM18*	Chr2:632348	A/G
rs1801282	*PPARG*	Chr3:12393125	C/G
rs2959272	*PPARG*	Chr3:12442833	T/G
rs1386835	*PPARG*	Chr3:12450918	A/G
rs709158	*PPARG*	Chr3:12463176	A/G
rs1175540	*PPARG*	Chr3:12465243	C/A
rs1175544	*PPARG*	Chr3:12467044	C/T
rs1797912	*PPARG*	Chr3:12470239	A/C
rs1516725	*ETV5*	Chr3:185824004	T/C
rs9816226	*ETV5*	Chr3:185834499	A/T
rs13107325	*SLC39A8*	Chr4:103188709	C/A/T
rs1799883	*FABP2*	Chr4:120241902	T/C
rs6536991	*UCP1*	Chr4:141481581	T/C
rs12502572	*UCP1*	Chr4:141485134	G/A
rs1800592	*UCP1*	Chr4:141493961	T/C
rs8192678	*PPARGC1A*	Chr4:23815662	C/T
rs10938397	*GNPDA2*	Chr4:45182527	A/G
rs1801260	*CLOCK*	Chr4:56301369	A/G
rs1440581	*PPM1K*	Chr4:89226422	T/C
rs1042713	*ADRB2*	Chr5:148206440	G/A
rs1042714	*ADRB2*	Chr5:148206473	G/C
rs6861681	*CPEB4*	Chr5:173362458	G/A
rs1800629	*TNFA*	Chr6:31543031	G/A
rs206936	*NUDT3*	Chr6:34302869	A/G
rs987237	*TFAP2B*	Chr6:50803050	A/G
rs2207139	*TFAP2B*	Chr6:50845490	A/G
rs7799039	*LEP*	Chr7:127878783	G/A
rs4731426	*LEP*	Chr7:127882070	G/C
rs2071045	*LEP*	Chr7:127892980	T/C
rs1055144	*NFE2L3*	Chr7:25871109	C/T
rs4994	*ADRB3*	Chr8:37823798	A/G
rs1800544	*ADRA2A*	Chr10:112836503	G/C
rs2419621	*ACSL5*	Chr10:114135013	C/T
rs7903146	*TCF7L2*	Chr10:114758349	C/T
rs12255372	*TCF7L2*	Chr10:114808902	G/T
rs1800497	*ANKK1*	Chr11:113270828	G/A
rs662799	*APOA5*	Chr11:116663707	G/A
rs6265	*BDNF*	Chr11:27679916	C/T
rs11030104	*BDNF*	Chr11:27684517	A/G
rs10767664	*BDNF*	Chr11:27725986	T/A
rs11605924	*CRY2*	Chr11:45873091	A/C

rs10838738	*MTCH2*	Chr11:47663049	A/G
rs660339	*UCP2*	Chr11:73689104	G/A
rs659366	*UCP2*	Chr11:73694754	C/T
rs2075577	*UCP3*	Chr11:73715542	G/A
rs2734827	*UCP3*	Chr11:73716277	G/A
rs1685325	*UCP3*	Chr11:73717025	T/C
rs2075576	*UCP3*	Chr11:73717121	C/T
rs1800006	*UCP3*	Chr11:73717254	A/G
rs1800849	*UCP3*	Chr11:73720165	G/A
rs4929949	*STK33*	Chr11:8604593	T/C
rs10830963	*MTNR1B*	Chr11:92708710	C/G
rs4769873	*ALOX5AP*	Chr13:31312689	C/T
rs1052700	*PLIN1*	Chr15:90208310	A/T
rs894160	*PLIN1*	Chr15:90211823	C/T
rs2289487	*PLIN1*	Chr15:90217096	C/T
rs7498665	*SH2B1*	Chr16:28883241	A/G
rs7359397	*SH2B1*	Chr16:28885659	C/T
rs1558902	*FTO*	Chr16:53803574	T/A
rs1121980	*FTO*	Chr16:53809247	G/A
rs17817449	*FTO*	Chr16:53813367	T/G
rs8050136	*FTO*	Chr16:53816275	C/A
rs3751812	*FTO*	chr16:53818460	G/T
rs9939609	*FTO*	Chr16:53820527	T/A
rs12452844	*AANAT*	Chr17:74459243	G/A
rs1805081	*NPC1*	Chr18:21140432	T/C
rs6567160	*MC4R*	Chr18:57829135	T/C
rs571312	*MC4R*	Chr18:57839769	C/A
rs17782313	*MC4R*	Chr18:57851097	T/C
rs17066866	*MC4R*	Chr18:58055619	A/T
rs17069904	*TNFRSF11A*	Chr18:60032949	G/A
rs2287019	*QPCTL*	Chr19:46202172	C/T
rs6013029	*CTNNBL1*	Chr20:36399580	G/T
rs6123837	*GNAS*	Chr20:57465571	G/A
rs3813929	*HTR2C*	ChrX:113818520	C/T
rs11091046	*AGTR2*	ChrX:115305126	A/C

33 [a] dbSNP reference, [b] gene assigned by dbSNP and [c] GRCh37, p13 assemb

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Table S2. Mean of abundance for each bacterial taxa obtained from LEfSe analysis between normalweight and overweight+obese subjects.

TAXA NAME	Mean of abundance in normalweight subjects	Mean of abundance in overweight+obese subjects
Actinobacteria	10.6 ± 0.2	9.8 ± 0.1
Bacteroidetes	16.8 ± 0.05	16.9 ± 0.02
Firmicutes	16.1 ± 0.7	15.8 ± 0.03
Actinobacteria (class)	10.6 ± 0.2	9.7 ± 0.1
Bacteroidia	16.8 ± 0.05	17.0 ± 0.02
Clostridia	15.8 ± 0.1	15.4 ± 0.05
Negativicutes	11.4 ± 0.2	11.8 ± 0.08
Aeromonadales	0.9 ± 0.2	1.7 ± 0.2
Bacteroidales	16.8 ± 0.05	17.0 ± 0.02
Caulobacterales	0.3 ± 0.1	0.6 ± 0.06
Clostridiales	15.8 ± 0.1	15.4 ± 0.05
Coriobacteriales	9.0 ± 0.2	8.14 ± 0.09
Selenomonadales	11.4 ± 0.2	11.8 ± 0.09
Sphingomonadales	0.17 ± 0.08	0.4 ± 0.04
Aerococcaceae	0.1 ± 0.07	0.4 ± 0.05
Catabacteriaceae	5.7 ± 0.4	4.3 ± 0.2
Christensenellaceae	8.0 ± 0.4	6.9 ± 0.2
Clostrdidiales FamilyXIII_IncertaeSedis	0.06 ± 0.03	0.4 ± 0.06
Coriobacteriaceae	9.0 ± 0.2	8.1 ± 0.1
Lactobacillaceae	2.5 ± 0.3	3.7 ± 0.2
Leuconostocaceae	2.0 ± 0.2	2.4 ± 0.2
Micrococcaceae	1.9 ± 0.2	1.5 ± 0.1
Oscillospiraceae	12.9 ± 0.2	12.4 ± 0.1
Prevotellaceae	11.15 ± 0.5	12.7 ± 0.2
Ruminococcaceae	14.4 ± 0.1	14.0 ± 0.1
Sphingomonadaceae	0.2 ± 0.07	0.4 ± 0.04
Succinivibrionaceae	0.8 ± 0.2	1.7 ± 0.2
Unclassified_Clostridiales	1.8 ± 0.4	2.7 ± 0.2

Values correspond to the mean ± SEM.

Table S3. Mean of abundance for each bacterial taxa obtained from LEfSe analysis between high-GRS and low-GRS subjects.

TAXA NAME	Mean of abundance in high GRS subjects	Mean of abundance in low GRS subjects
Bacteroides	16.0 ± 0.06	16.2 ± 0.05
Caulobacterales	0.6 ± 0.08	0.4 ± 0.06
Bacteroidaceae	16.0 ± 0.06	16.2 ± 0.05
Caulobacteraceae	0.6 ± 0.08	0.4 ± 0.07
Leuconostocaceae	0.8 ± 0.1	0.5 ± 0.07
Peptostreptococcaceae	8.0 ± 0.1	8.4 ± 0.1
Prevotellaceae	13.0 ± 0.3	12.0 ± 0.2
Rikenellaceae	12.1 ± 0.1	12.5 ± 0.1
Acidaminococcus	3.5 ± 0.3	2.8 ± 0.2
Actinomyces	1.5 ± 0.1	1.3 ± 0.09
Alistipes	12.1 ± 0.1	12.5 ± 0.1
Barnesiella	6.4 ± 0.3	7.3 ± 0.2
Celluslostiycum	0.09 ± 0.04	0.5 ± 0.1
Citrobacter	0.6 ± 0.1	1.0 ± 0.2
Prevotella	11.8 ± 0.3	10.5 ± 0.3
Romboutsia	8.0 ± 0.1	8.4 ± 0.1
Weisella	0.6 ± 0.1	0.3 ± 0.07

Values correspond to the mean ± SEM.