

Supplementary Table S6: Risk allele, frequency and functional annotation of the SNPs associated with anthropometric traits in GCAT and UK Biobank cohorts. Green color: unreported/new loci/locus. Magenta color: no association in UK Biobank. Yellow color: univariate association in GCAT and UKBiobank. Blue color: multitrait p-value.

| gene | chr_pos | snp | risk allele | frequency | consequence: Variant Effect Predictor tool | beta_b mi | se_bmi | z_bmi | P_bmi | beta_hei ght | se_heigh t | z_height | P_height |
|-------------------------|-------------|-------------|-------------|-----------|---------------------------------------------------------------------------------------------------------------------------|-----------|---------|---------|---------|--------------|------------|----------|-----------|
| SF3B4, SV2A | 1:149892872 | rs11205277 | G | 0,44 | downstream_gene_variant, upstream_gene_variant | -0,0645 | 0,0928 | -0,6948 | 0,4872 | 0,5492 | 0,1236 | 4,442 | 9,114E-06 |
| | | | | 0,44 | | -0,0017 | 0,00242 | -0,7161 | 0,47393 | 0,03407 | 0,00174 | 19,6221 | 1,119E-85 |
| ZRANB2-AS2 | 1:71702511 | rs115213730 | C | 0,016 | intron_variant,non_coding_transcript_ variant | 1,693 | 0,3677 | 4,605 | 4,2E-06 | -0,7731 | 0,4915 | -1,573 | 0,1158 |
| | | | | 0,033 | | 0,0206 | 0,00683 | 3,01381 | 0,00258 | 0,00438 | 0,00491 | 0,89302 | 0,371849 |
| DPYD, DPYD-IT1 | 1:97884058 | rs140281723 | A | 0,011 | intron_variant, intron_variant,non_coding_transcript_ variant | 1,91 | 0,4477 | 4,267 | 2E-05 | 1,08 | 0,5989 | 1,803 | 0,07143 |
| | | | | 0,022 | | 0,01064 | 0,00857 | 1,24126 | 0,21451 | -0,0155 | 0,00616 | -2,5117 | 0,012015 |
| PRELID1, RAB24, MXD3 | 5:176735612 | rs111251222 | G | 0,192 | downstream_gene_variant, upstream_gene_variant, intron_variant, intron_variant,non_coding_transcript_ variant | 0,05993 | 0,1193 | 0,5024 | 0,6154 | 0,7772 | 0,1588 | 4,894 | 1,019E-06 |
| | | | | 0,261 | | -0,0084 | 0,00275 | -3,0393 | 0,00237 | 0,03424 | 0,00198 | 17,3356 | 2,709E-67 |
| LMAN2, AC146507.1 | 5:176772736 | rs4976686 | G | 0,305 | intron_variant, upstream_gene_variant, intron_variant,non_coding_transcript_ variant | 0,04921 | 0,1013 | 0,4859 | 0,6271 | 0,7093 | 0,1348 | 5,261 | 1,493E-07 |
| | | | | 0,448 | | -0,0056 | 0,00262 | -2,1239 | 0,03368 | 0,02757 | 0,00188 | 14,6738 | 9,82E-49 |
| PIK3R1 | 5:67579576 | rs12657050 | T | 0,237 | upstream_gene_variant, downstream_gene_variant, intron_variant | -0,2893 | 0,1095 | -2,641 | 0,0083 | -0,3334 | 0,146 | -2,284 | 0,02242 |
| | | | | 0,24 | | -0,0043 | 0,00283 | -1,5306 | 0,12587 | -0,014 | 0,00203 | -6,9074 | 4,945E-12 |
| PIK3R1 | 5:67604628 | rs695166 | C | 0,28 | intergenic_variant | -0,2651 | 0,1036 | -2,558 | 0,01055 | -0,4112 | 0,1378 | -2,984 | 0,002859 |
| | | | | 0,277 | | -0,0031 | 0,00268 | -1,1728 | 0,24089 | -0,0147 | 0,00193 | -7,6349 | 2,265E-14 |

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|---------------------------------|-------------|-------------|---|----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|------------------------|
| GMDS | 6:1944345 | rs62391629 | A | 0,082 | intron_variant, intron_variant,non_coding_transcript_ variant | 0,5392 0,01329 | 0,1714 0,00505 | 3,146 2,63088 | 0,00166 0,00852 | 0,5196 0,00845 | 0,2289 0,00363 | 2,27 2,3287 | 0,02326 0,0198756 |
| ID4, AL022068.1, - | 6:19839415 | rs41271299 | T | 0,048 0,052 | intron_variant, upstream_gene_variant, | -0,109 -0,0032 | 0,2227 0,00543 | -0,4896 -0,5964 | 0,6245 0,55094 | 1,408 0,09443 | 0,2957 0,0039 | 4,761 24,2311 | 1,987E-06 1,35E-129 |
| GRM4-HMGA1 | 6:34199092 | rs2780226 | C | 0,107 0,089 | intergenic_variant | 0,0295 0,00064 | 0,1511 0,00422 | 0,1953 0,15197 | 0,8452 0,87921 | 0,9147 0,06723 | 0,2012 0,00303 | 4,546 22,1736 | 5,601E-06 7,39E-109 |
| HMGA1, SMIM29, AL354740.1 | 6:34214322 | rs1150781 | C | 0,106 0,09 | downstream_gene_variant, missense_variant, 3_prime_UTR_variant, 3_prime_UTR_variant,NMD_transcript_ variant, non_coding_transcript_exon_variant, | 0,02943 0,00227 | 0,152 0,0042 | 0,1936 0,54029 | 0,8465 0,58899 | 0,895 0,0661 | 0,2022 0,00302 | 4,427 21,9119 | 9,777E-06 2,38E-106 |
| EPHA7 | 6:94075927 | rs143547391 | T | 0,014 0,02 | intron_variant | 1,237 -0,0218 | 0,398 0,00884 | 3,109 -2,4622 | 0,00189 0,01381 | 1,714 -0,0104 | 0,5317 0,00635 | 3,223 -1,6404 | 0,001275 0,100928 |
| AOC1-KCNH | 7:150599205 | rs10216051 | G | 0,354 0,353 | intergenic_variant | -0,4364 0,00732 | 0,09864 0,00253 | -4,424 2,88912 | 9,9E-06 0,00386 | 0,08893 0,01211 | 0,1319 0,00182 | 0,6744 6,65972 | 0,5001 2,748E-11 |
| MAD1L1, - | 7:2068330 | rs62444886 | T | 0,068 0,057 | intron_variant, regulatory_region_variant | -0,7583 -0,0258 | 0,1842 0,0052 | -4,118 -4,9531 | 3,9E-05 7,3E-07 | -0,2341 0,00513 | 0,2463 0,00374 | -0,9506 1,37294 | 0,3419 0,169772 |
| FUBP3 | 9:133482006 | rs11792294 | G | 0,447 0,425 | intron_variant, intron_variant,non_coding_transcript_ variant | -0,0749 0,00212 | 0,09942 0,00248 | -0,7534 0,85457 | 0,4513 0,39279 | -0,5945 -0,02 | 0,1322 0,00178 | -4,496 -11,262 | 7,101E-06 2,043E-29 |

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|-----------------------|--------------|-------------|---|----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|------------------------|
| CACUL1 | 10:120465796 | rs12414412 | G | 0,079 0,084 | intron_variant, intron_variant,non_coding_transcript_ variant, intron_variant,NMD_transcript_variant | 0,05409 0,02193 | 0,1718 0,00434 | 0,3149 5,05553 | 0,7529 4,3E-07 | 1,036 0,00742 | 0,2285 0,00312 | 4,533 2,38095 | 5,941E-06 0,0172685 |
| INS-IGF2, IGF2-AS, - | 11:2172830 | rs7948458 | A | 0,258 0,19 | intron_variant,NMD_transcript_variant , downstream_gene_variant, intron_variant, intron_variant,non_coding_transcript_ variant, upstream_gene_variant, regulatory_region_variant | -0,3723 -0,002 | 0,1059 0,00306 | -3,518 -0,6672 | 0,00044 0,50466 | -0,4247 -0,0223 | 0,1416 0,0022 | -2,999 -10,129 | 0,002725 4,16E-24 |
| MAP3K9 | 14:71268446 | rs7151024 | C | 0,246 0,23 | intron_variant | -0,4864 -0,0097 | 0,1076 0,00286 | -4,521 -3,3791 | 6,3E-06 0,00073 | 0,3444 0,00541 | 0,1438 0,00205 | 2,395 2,63402 | 0,01664 0,0084385 |
| GABRG3-AS1, GABRG3 | 15:27398499 | rs184405367 | C | 0,022 0,007 | downstream_gene_variant, intron_variant | 1,511 -0,0027 | 0,3152 0,01566 | 4,795 -0,1755 | 1,7E-06 0,8607 | 0,6705 -0,0015 | 0,4225 0,01125 | 1,587 -0,1332 | 0,1125 0,894064 |
| SEMA6D | 15:47923520 | rs10220751 | G | 0,469 0,405 | intron_variant | -0,4405 -0,0115 | 0,09258 0,00245 | -4,757 -4,6896 | 2E-06 2,7E-06 | 0,2124 0,00431 | 0,1237 0,00176 | 1,717 2,45467 | 0,08601 0,0141018 |
| GPRC5B- GPR139 | 16:19988852 | rs9940317 | G | 0,189 0,225 | intergenic_variant | 0,4314 0,01188 | 0,1199 0,00288 | 3,597 4,11762 | 0,00033 3,8E-05 | 0,4215 0,00684 | 0,1602 0,00207 | 2,631 3,30334 | 0,008549 0,0009555 |
| GPR139 | 16:20046115 | rs2045457 | G | 0,316 0,303 | intron_variant,NMD_transcript_variant , intron_variant | 0,3811 0,01297 | 0,1008 0,00262 | 3,783 4,94518 | 0,00016 7,6E-07 | 0,2445 0,00571 | 0,1345 0,00188 | 1,818 3,03287 | 0,06908 0,0024226 |
| ECl1, AC009065.8 | 16:2296197 | rs77407216 | C | 0,14 0,14 | intron_variant, intron_variant,non_coding_transcript_ variant, upstream_gene_variant, downstream_gene_variant | -0,3922 -0,0021 | 0,1349 0,0035 | -2,908 -0,5925 | 0,00365 0,55354 | -0,7026 -0,0157 | 0,18 0,00251 | -3,903 -6,241 | 9,628E-05 4,354E-10 |

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|----------------------|-------------|------------|---|------------------------------------------------------------------------------------------------------------------------------------|----------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|------------------------|
| ATAD5, AC130324.2 | 17:29165934 | rs9890032 | G | intron_variant, intron_variant,non_coding_transcript_ variant | 0,429 0,381 | -0,098 -7E-05 | 0,09489 0,00248 | -1,032 -0,027 | 0,302 0,97848 | -0,6091 -0,0318 | 0,126 0,00178 | -4,833 -17,881 | 1,388E-06 1,804E-71 |
| TBX2 | 17:59498052 | rs7214743 | A | intergenic_variant | 0,371 0,33 | 0,08425 -0,0093 | 0,09482 0,00255 | 0,8885 -3,6408 | 0,3743 0,00027 | 0,6568 0,0344 | 0,1262 0,00183 | 5,205 18,777 | 2,017E-07 1,277E-78 |
| CABLES1 | 18:20758310 | rs34302357 | G | intron_variant, intron_variant,non_coding_transcript_ variant, intron_variant,NMD_transcript_variant | 0,196 0,184 | 0,2156 -0,0024 | 0,1196 0,0031 | 1,803 -0,7868 | 0,07142 0,43139 | -0,7454 -0,0422 | 0,1593 0,00222 | -4,68 -18,971 | 2,943E-06 3,281E-80 |
| RIOK3, Y_RNA | 18:21039393 | rs9954741 | C | intron_variant, downstream_gene_variant, intron_variant,non_coding_transcript_ variant | 0,3 0,351 | 0,1989 -0,01 | 0,1013 0,00252 | 1,963 -3,9741 | 0,04965 7,1E-05 | -0,6011 -0,0134 | 0,135 0,00181 | -4,452 -7,4229 | 8,714E-06 1,148E-13 |
| ADAMTS10, - | 19:8670147 | rs62621197 | T | missense_variant, non_coding_transcript_exon_variant, missense_variant,NMD_transcript_vari ant, regulatory_region_variant | 0,064 0,036 | 0,4839 0,01398 | 0,1892 0,00665 | 2,557 2,10163 | 0,01059 0,03559 | -1,193 -0,1117 | 0,2523 0,00478 | -4,729 -23,4 | 2,321E-06 5,35E-121 |
| GDF5, GDF5OS, - | 20:34025756 | rs143384 | G | 5_prime_UTR_variant, downstream_gene_variant, regulatory_region_variant | 0,441 0,403 | 0,07187 -0,0014 | 0,09433 0,00245 | 0,7619 -0,5565 | 0,4462 0,57784 | 0,5904 0,06411 | 0,1256 0,00175 | 4,699 36,5424 | 2,686E-06 8,85E-292 |
| HORMAN-LIF | 22:30610546 | rs9608851 | T | intergenic_variant | 0,462 0,439 | 0,4508 0,00503 | 0,0948 0,00242 | 4,755 2,07922 | 2E-06 0,0376 | -0,2913 0,00619 | 0,1268 0,00174 | -2,297 3,56052 | 0,02168 0,0003702 |

| gene | chr_pos | snp | beta_weight | se_weight | z_weight | P_weight | beta_waist | se_waist | z_waist | P_waist |
|-------------------------|-------------|-------------|----------------------|----------------------|--------------------|--------------------------|-----------------------|----------------------|--------------------|----------------------------|
| SF3B4, SV2A | 1:149892872 | rs11205277 | 0,2943 0,0173643 | 0,2681 0,00213579 | 1,098 8,13013 | 0,2722 4,30256E-16 | 0,2021 0,00899567 | 0,2394 0,00216508 | 0,8442 4,15489 | 0,3986 0,000032553 |
| ZRANB2-AS2 | 1:71702511 | rs115213730 | 3,817 0,0190109 | 1,063 0,00603745 | 3,593 3,14883 | 0,0003304 0,00163942 | 3,793 0,0167197 | 0,9485 0,00611993 | 3,999 2,732 | 0,00006452 0,00629537 |
| DPYD, DPYD-IT1 | 1:97884058 | rs140281723 | 6,54 0,000408534 | 1,292 0,00757227 | 5,062 0,0539513 | 4,293E-07 0,956974 | 5,626 0,0125187 | 1,154 0,0076726 | 4,874 1,63161 | 0,000001126 0,102763 |
| PRELID1, RAB24, MXD3 | 5:176735612 | rs111251222 | 0,8442 0,0118091 | 0,3445 0,00242996 | 2,451 4,85978 | 0,01429 1,17569E-06 | 0,3323 0,00842181 | 0,3073 0,00246309 | 1,082 3,41921 | 0,2795 0,00062811 |
| LMAN2, AC146507.1 | 5:176772736 | rs4976686 | 0,7868 0,0102822 | 0,2923 0,00231099 | 2,691 4,44925 | 0,007141 8,61974E-06 | 0,2924 0,00419927 | 0,2612 0,00234244 | 1,12 1,79269 | 0,263 0,0730238 |
| PIK3R1 | 5:67579576 | rs12657050 | -1,033 -0,0111662 | 0,3161 0,0024963 | -3,268 -4,47309 | 0,001089 7,71231E-06 | -1,255 -0,0090435 | 0,2821 0,00253059 | -4,448 -3,57368 | 0,000008851 0,000352054 |
| PIK3R1 | 5:67604628 | rs695166 | -1,055 -0,01046 | 0,2992 0,00237074 | -3,526 -4,41211 | 0,0004263 1,02401E-05 | -1,199 -0,00834958 | 0,2671 0,00240319 | -4,488 -3,47437 | 0,000007354 0,000512123 |
| GMDS | 6:1944345 | rs62391629 | 1,954 0,0156476 | 0,4948 0,00446268 | 3,95 3,50632 | 0,0000793 0,000454408 | 1,352 0,0144837 | 0,4421 0,00452316 | 3,057 3,20212 | 0,002248 0,00136435 |
| ID4, AL022068.1, - | 6:19839415 | rs41271299 | 0,9637 0,0489412 | 0,6418 0,00479425 | 1,502 10,2083 | 0,1333 1,83515E-24 | 0,08072 0,0273215 | 0,576 0,00486093 | 0,1401 5,62062 | 0,8886 1,90418E-08 |
| GRM4-HMGA1 | 6:34199092 | rs2780226 | 0,886 0,0366939 | 0,4362 0,00373042 | 2,031 9,83641 | 0,04228 7,90238E-23 | 0,1369 0,0334893 | 0,3896 0,00378108 | 0,3514 8,85708 | 0,7253 8,25245E-19 |

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|------------------------------|--------------|-------------|------------------------|----------------------|--------------------|----------------------------|-------------------------|----------------------|---------------------|----------------------------|
| HMGA1, SMIM29, AL354740.1 | 6:34214322 | rs1150781 | 0,8622 0,0374785 | 0,4388 0,00371174 | 1,965 10,0973 | 0,04949 5,72332E-24 | 0,07992 0,0343297 | 0,3921 0,00376215 | 0,2038 9,12502 | 0,8385 7,21039E-20 |
| EPHA7 | 6:94075927 | rs143547391 | 5,202 -0,0249075 | 1,148 0,00780417 | 4,532 -3,19156 | 0,000005972 0,0014152 | 3,511 -0,0266055 | 1,027 0,00791186 | 3,419 -3,36274 | 0,0006327 0,000771807 |
| AOC1-KCNH | 7:150599205 | rs10216051 | -1,049 0,0124664 | 0,284 0,00223657 | -3,693 5,57392 | 0,0002238 2,49262E-08 | -1,066 0,00821204 | 0,2533 0,00226688 | -4,208 3,62261 | 0,00002627 0,000291683 |
| MAD1L1, - | 7:2068330 | rs62444886 | -2,301 -0,0187147 | 0,5319 0,00459653 | -4,326 -4,07149 | 0,00001552 0,000046725 | -2,193 -0,0205616 | 0,475 0,00465786 | -4,617 -4,41439 | 0,000003986 1,01325E-05 |
| FUBP3 | 9:133482006 | rs11792294 | -0,6907 -0,00923225 | 0,2858 0,00218848 | -2,417 -4,21857 | 0,01569 2,45918E-05 | -0,07927 -0,00242781 | 0,2564 0,00221827 | -0,3091 -1,09446 | 0,7572 0,273752 |
| CACUL1 | 10:120465796 | rs12414412 | 1,084 0,0222561 | 0,496 0,0038325 | 2,186 5,80721 | 0,02888 6,358E-09 | 0,151 0,015499 | 0,4426 0,00388501 | 0,3411 3,98944 | 0,733 6,62429E-05 |
| INS-IGF2, IGF2-AS, - | 11:2172830 | rs7948458 | -1,387 -0,0137686 | 0,3057 0,00270564 | -4,537 -5,08884 | 0,00000585 3,6046E-07 | -0,9066 -0,00444939 | 0,2732 0,00274244 | -3,319 -1,62242 | 0,0009093 0,104714 |
| MAP3K9 | 14:71268446 | rs7151024 | -0,9997 -0,00512978 | 0,3111 0,00252569 | -3,213 -2,03104 | 0,001321 0,0422518 | -1,134 -0,00646628 | 0,2774 0,00256002 | -4,088 -2,52587 | 0,00004418 0,0115415 |
| GABRG3-AS1, GABRG3 | 15:27398499 | rs184405367 | 4,708 -0,00405344 | 0,9096 0,0138321 | 5,176 -0,293045 | 2,358E-07 0,769488 | 3,612 -0,0049679 | 0,8129 0,0140211 | 4,443 -0,354315 | 0,000009051 0,723103 |
| SEMA6D | 15:47923520 | rs10220751 | -1,015 -0,00708755 | 0,2676 0,0021598 | -3,793 -3,28157 | 0,0001507 0,00103241 | -0,7963 -0,00452462 | 0,2389 0,0021891 | -3,334 -2,06689 | 0,0008633 0,0387456 |
| GPRC5B-GPR139 | 16:19988852 | rs9940317 | 1,564 0,0134204 | 0,346 0,00254788 | 4,522 5,26728 | 0,000006275 1,38544E-07 | 1,355 0,0079057 | 0,3086 0,00258274 | 4,391 3,06098 | 0,00001152 0,00220633 |
| GPR139 | 16:20046115 | rs2045457 | 1,262 0,0138953 | 0,2906 0,00231694 | 4,343 5,99724 | 0,00001431 2,00897E-09 | 1,209 0,00679946 | 0,2596 0,00234854 | 4,657 2,89519 | 0,000003294 0,00378951 |

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|----------------------|-------------|------------|------------------------|----------------------|----------------------|---------------------------|------------------------|----------------------|--------------------|-------------------------|
| ECI1, AC009065.8 | 16:2296197 | rs77407216 | -1,748 -0,010062 | 0,3885 0,00308886 | -4,501 -3,2575 | 0,000006917 0,00112409 | -0,8244 -0,00756436 | 0,348 0,00313116 | -2,369 -2,41583 | 0,01788 0,0156997 |
| ATAD5, AC130324.2 | 17:29165934 | rs9890032 | -0,8345 -0,0174232 | 0,2734 0,00218618 | -3,052 -7,96971 | 0,002288 1,59541E-15 | -0,4922 -0,0105009 | 0,2445 0,00221596 | -2,013 -4,73875 | 0,04416 2,15132E-06 |
| TBX2 | 17:59498052 | rs7214743 | 0,8188 0,0114426 | 0,2738 0,00225369 | 2,991 5,07726 | 0,002794 3,83119E-07 | 0,4251 0,00636958 | 0,2446 0,00228442 | 1,738 2,78827 | 0,08235 0,00529926 |
| CABLES1 | 18:20758310 | rs34302357 | -0,131 -0,0244692 | 0,3454 0,00273579 | -0,3792 -8,94411 | 0,7046 3,76783E-19 | 0,211 -0,0175178 | 0,3082 0,00277319 | 0,6847 -6,31685 | 0,4936 2,67282E-10 |
| RIOK3, Y_RNA | 18:21039393 | rs9954741 | -0,02502 -0,0156043 | 0,2928 0,00222174 | -0,08547 -7,02345 | 0,9319 2,16866E-12 | 0,1437 -0,0152915 | 0,2614 0,00225188 | 0,5496 -6,79057 | 0,5826 1,11875E-11 |
| ADAMTS10, - | 19:8670147 | rs62621197 | 0,2932 -0,0497392 | 0,5469 0,00587654 | 0,5362 -8,46403 | 0,5918 2,593E-17 | 0,371 -0,0355763 | 0,4881 0,00595756 | 0,7602 -5,97162 | 0,4472 2,35148E-09 |
| GDF5, GDF5OS, - | 20:34025756 | rs143384 | 0,7418 0,033259 | 0,2723 0,0021608 | 2,724 15,392 | 0,00647 1,93191E-53 | 0,3053 0,00705718 | 0,2433 0,0021909 | 1,255 3,22114 | 0,2096 0,00127695 |
| HORMAN-LIF | 22:30610546 | rs9608851 | 0,9996 0,00768726 | 0,2741 0,0021381 | 3,647 3,59537 | 0,0002678 0,000323976 | 0,8169 0,00583982 | 0,2449 0,00216719 | 3,336 2,69465 | 0,0008571 0,00704664 |

| gene | chr_pos | snp | beta_hip | se_hip | z_hip | P_hip | P_multi | cohort | GWAS catalog |
|-------------------------|-------------|-------------|------------------------|---------------------|--------------------|----------------------------|--------------------------|------------|------------------|
| SF3B4, SV2A | 1:149892872 | rs11205277 | 0,2035 0,0189385 | 0,1919 0,0024207 | 1,06 7,82375 | 0,289 5,14209E-15 | 0,00092082 3,8288E-53 | GCAT UK | reported SNP |
| ZRANB2-AS2 | 1:71702511 | rs115213730 | 2,83 0,0162759 | 0,7605 0,0068431 | 3,721 2,37845 | 0,0002004 0,017386 | 1,6093E-08 0,00015148 | GCAT UK | new loci |
| DPYD, DPYD-IT1 | 1:97884058 | rs140281723 | 3,772 0,00229719 | 0,9254 0,0085796 | 4,076 0,26775 | 0,00004657 0,788891 | 8,6185E-11 0,03545792 | GCAT UK | no association |
| PRELID1, RAB24, MXD3 | 5:176735612 | rs111251222 | 0,1324 0,000697939 | 0,2465 0,002754 | 0,537 0,25343 | 0,5913 0,79994 | 0,0001041 3,4587E-35 | GCAT UK | reported loci |
| LMAN2, AC146507.1 | 5:176772736 | rs4976686 | 0,1407 0,00212588 | 0,2094 0,0026191 | 0,6718 0,81168 | 0,5017 0,416977 | 2,7571E-05 2,6816E-25 | GCAT UK | reported loci |
| PIK3R1 | 5:67579576 | rs12657050 | -0,5919 -0,00674386 | 0,2264 0,0028296 | -2,615 -2,38335 | 0,008958 0,0171566 | 1,1231E-06 4,0687E-10 | GCAT UK | unreported locus |
| PIK3R1 | 5:67604628 | rs695166 | -0,6947 -0,00541977 | 0,2141 0,0026871 | -3,244 -2,01699 | 0,001186 0,0436976 | 1,1554E-07 8,7375E-11 | GCAT UK | |
| GMDS | 6:1944345 | rs62391629 | 1,658 0,0171762 | 0,3539 0,0050575 | 4,685 3,39619 | 0,000002881 0,000683385 | 4,9309E-08 6,4095E-06 | GCAT UK | reported locus |
| ID4, AL022068.1, - | 6:19839415 | rs41271299 | 0,3465 0,0407137 | 0,4609 0,0054349 | 0,7519 7,49113 | 0,4521 6,84504E-14 | 0,00048078 2,6565E-77 | GCAT UK | reported loci |
| GRM4-HMGA1 | 6:34199092 | rs2780226 | 0,3394 0,0198438 | 0,3123 0,0042281 | 1,087 4,69329 | 0,2772 2,6895E-06 | 0,00043484 1,5502E-68 | GCAT UK | reported SNP |
| HMGA1, SMIM29, AL35474C | 6:34214322 | rs1150781 | 0,3727 0,0211274 | 0,3143 0,004207 | 1,186 5,02202 | 0,2356 5,11577E-07 | 0,00059245 1,0047E-68 | GCAT UK | reported SNP |
| | | | | | | | 2,2693E-69 | UK-GCAT | |

| | | | | | | | | | |
|----------------------|--------------|-------------|-------------|-----------|----------|-------------|------------|---------|------------------|
| EPHA7 | 6:94075927 | rs143547391 | 2,757 | 0,8234 | 3,348 | 0,0008195 | 3,3515E-08 | GCAT | new locus |
| | | | -0,0267556 | 0,0088463 | -3,0245 | 0,00249061 | 3,3033E-05 | UK | |
| | | | | | | | 6,5456E-10 | UK-GCAT | |
| AOC1-KCNH | 7:150599205 | rs10216051 | -0,8431 | 0,2035 | -4,142 | 0,00003502 | 9,5279E-09 | GCAT | reported loci |
| | | | 0,00867418 | 0,0025347 | 3,42219 | 0,000621268 | 4,2346E-12 | UK | |
| | | | | | | | 4,769E-17 | UK-GCAT | |
| MAD1L1, - | 7:2068330 | rs62444886 | -1,577 | 0,3812 | -4,138 | 0,00003562 | 1,8925E-09 | GCAT | unreported locus |
| | | | -0,0245014 | 0,0052084 | -4,70422 | 2,54945E-06 | 9,9041E-10 | UK | |
| | | | | | | | 2,3233E-15 | UK-GCAT | |
| FUBP3 | 9:133482006 | rs11792294 | -0,2049 | 0,2057 | -0,9957 | 0,3194 | 0,00028897 | GCAT | reported locus |
| | | | -0,00316976 | 0,0024803 | -1,27797 | 0,201262 | 5,4697E-16 | UK | |
| | | | | | | | 6,36E-017 | UK-GCAT | |
| CACUL1 | 10:120465796 | rs12414412 | 0,4539 | 0,3548 | 1,279 | 0,2009 | 0,00033169 | GCAT | unreported locus |
| | | | 0,0231133 | 0,0043437 | 5,32107 | 1,03222E-07 | 3,7141E-12 | UK | |
| | | | | | | | 4,0336E-13 | UK-GCAT | |
| INS-IGF2, IGF2-AS, - | 11:2172830 | rs7948458 | -0,943 | 0,219 | -4,306 | 0,00001694 | 4,5283E-09 | GCAT | reported loci |
| | | | -0,0139008 | 0,0030664 | -4,53327 | 5,80974E-06 | 2,2587E-16 | UK | |
| | | | | | | | 1,5356E-21 | UK-GCAT | |
| MAP3K9 | 14:71268446 | rs7151024 | -0,9265 | 0,2224 | -4,166 | 0,00003148 | 5,7321E-09 | GCAT | new locus |
| | | | -0,00577888 | 0,0028624 | -2,01886 | 0,0435025 | 0,00015074 | UK | |
| | | | | | | | 5,7139E-10 | UK-GCAT | |
| GABRG3-AS1, GABRG3 | 15:27398499 | rs184405367 | 3,112 | 0,6504 | 4,785 | 0,000001763 | 1,3485E-11 | GCAT | no association |
| | | | 0,00239918 | 0,0156784 | 0,15302 | 0,878379 | 1 | UK | |
| | | | | | | | 3,5351E-09 | UK-GCAT | |
| SEMA6D | 15:47923520 | rs10220751 | -0,5882 | 0,1916 | -3,069 | 0,002156 | 7,0858E-08 | GCAT | reported locus |
| | | | -0,0107556 | 0,0024476 | -4,39428 | 1,11172E-05 | 1,6109E-07 | UK | |
| | | | | | | | 7,9733E-12 | UK-GCAT | |
| GPRC5B-GPR139 | 16:19988852 | rs9940317 | 1,161 | 0,2473 | 4,694 | 0,000002748 | 3,6608E-10 | GCAT | reported loci |
| | | | 0,0111159 | 0,0028878 | 3,84926 | 0,000118498 | 2,9711E-09 | UK | |
| | | | | | | | 1,5605E-15 | UK-GCAT | |
| GPR139 | 16:20046115 | rs2045457 | 0,9268 | 0,2081 | 4,454 | 0,000008603 | 9,0001E-10 | GCAT | reported locus |
| | | | 0,0106063 | 0,0026259 | 4,03912 | 5,36642E-05 | 1,0863E-10 | UK | |
| | | | | | | | 1,3882E-16 | UK-GCAT | |
| ECI1, AC009065.8 | 16:2296197 | rs77407216 | -0,9674 | 0,279 | -3,467 | 0,0005304 | 5,4038E-08 | GCAT | reported loci |
| | | | -0,0068188 | 0,0035011 | -1,94762 | 0,0514616 | 3,0872E-07 | UK | |
| | | | | | | | 1,1721E-11 | UK-GCAT | |
| ATAD5, AC130324.2 | 17:29165934 | rs9890032 | -0,4148 | 0,1962 | -2,114 | 0,03453 | 6,9906E-06 | GCAT | reported SNP |
| | | | -0,0125827 | 0,0024777 | -5,07851 | 3,80612E-07 | 1,4203E-43 | UK | |
| | | | | | | | 8,2115E-46 | UK-GCAT | |

| | | | | | | | | | |
|-----------------|-------------|------------|-------------|-----------|----------|-------------|------------|---------|----------------|
| TBX2 | 17:59498052 | rs7214743 | 0,4702 | 0,196 | 2,399 | 0,01647 | 2,9981E-06 | GCAT | reported locus |
| | | | 0,000262197 | 0,0025544 | 0,10265 | 0,918243 | 1,8515E-40 | UK | |
| | | | | | | | 5,1119E-43 | UK-GCAT | |
| CABLES1 | 18:20758310 | rs34302357 | -0,03673 | 0,2471 | -0,1486 | 0,8819 | 0,00047579 | GCAT | reported locus |
| | | | -0,0170757 | 0,0031008 | -5,50684 | 3,65602E-08 | 2,9023E-51 | UK | |
| | | | | | | | 6,4314E-52 | UK-GCAT | |
| RIOK3, Y_RNA | 18:21039393 | rs9954741 | -0,0315 | 0,2096 | -0,1503 | 0,8805 | 0,00075696 | GCAT | reported loci |
| | | | -0,0139768 | 0,0025179 | -5,55094 | 2,84352E-08 | 8,909E-21 | UK | |
| | | | | | | | 2,6636E-21 | UK-GCAT | |
| ADAMTS10, - | 19:8670147 | rs62621197 | 0,1977 | 0,3916 | 0,5048 | 0,6137 | 0,00015908 | GCAT | reported locus |
| | | | -0,0416637 | 0,0066606 | -6,25528 | 3,97268E-10 | 1,8707E-69 | UK | |
| | | | | | | | 1,3415E-70 | UK-GCAT | |
| GDF5, GDF5OS, - | 20:34025756 | rs143384 | 0,5451 | 0,1949 | 2,797 | 0,005182 | 1,4156E-05 | GCAT | reported SNP |
| | | | 0,0281276 | 0,0024492 | 11,4842 | 1,60444E-30 | 8,334E-168 | UK | |
| | | | | | | | 1,259E-170 | UK-GCAT | |
| HORMAN-LIF | 22:30610546 | rs9608851 | 0,6614 | 0,1961 | 3,372 | 0,0007518 | 3,1922E-08 | GCAT | reported locus |
| | | | 0,00544783 | 0,0024232 | 2,24821 | 0,0245636 | 1,6979E-05 | UK | |
| | | | | | | | 3,3486E-10 | UK-GCAT | |