**Supplementary materials**

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|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Supplementary Table S1: The position of the sequenced fragment | | | | | | | |
| Target | Chr | Gene | **Gene full name** | **TSS** | **TES** | **Start** | **End** |
| ARHGAP40\_16 | 20 | ARHGAP40 | The RHO Guanosine triphosphatase activating protein 40 | 37230576 | 37279295 | 37274153 | 37274356 |
| C5orf34\_15 | 5 | C5orf34 | Chromosome 5 open reading frame 34 | 43515273 | 43486802 | 43487447 | 43487684 |
| CCDC124\_14 | 19 | CCDC124 | Coiled-coil domain containing 124 | 18045904 | 18054794 | 18054774 | 18054574 |
| COPS8\_11 | 2 | COPS8 | Constitutive photomorphogenic homolog subunit 8 | 237994083 | 238007489 | 237992528 | 237992710 |
| DDR1\_05 | 6 | DDR1 | Discoid in domain receptor tyrosine kinase 1 | 30852756 | 30867933 | 30852639 | 30852815 |
| DNAJB6\_09 | 7 | DNAJB6 | DNAJ homolog, subfamily B, member 6 | 157129710 | 157210133 | 157130190 | 157130031 |
| EIF2AK2\_28 | 2 | EIF2AK2 | Eukaryotic translation initiation factor 2α kinase 2. | 37374965 | 37332283 | 37375038 | 37374822 |
| GCK\_18 | 7 | GCK | Glucokinase | 44185743 | 44182811 | 44185089 | 44185314 |
| HAAO\_13 | 2 | HAAO | 3-hydroxyanthranilate3,4-dioxygenase | 43019751 | 42994228 | 43013714 | 43013885 |
| HAPLN3\_02 | 15 | HAPLN3 | Hyaluronan and proteoglycan link protein 3 | 89438857 | 89420515 | 89438585 | 89438810 |
| HHLA3\_03 | 1 | HHLA3 | HERV-H LTR-associating 3 | 70820492 | 70833705 | 70820116 | 70820310 |
| IFNGR2\_27 | 21 | IFNGR2 | The interferon gamma receptor 2 | 34775201 | 34809828 | 34775191 | 34775397 |
| IL10\_25 | 1 | IL10 | Interleukin 10 | 206945839 | 206940946 | 206945211 | 206945446 |
| IL6\_21 | 7 | IL6 | Interleukin 6 | 22766760 | 22771621 | 22765200 | 22765453 |
| IL6\_22 | 7 | IL6 | Interleukin 6 | 22766760 | 22771621 | 22767361 | 22767112 |
| IL7\_10 | 8 | IL7 | Interleukin 7 | 79717758 | 79645006 | 79717646 | 79717816 |
| MDM2\_08 | 12 | MDM2 | MDM2 oncogene, E3 ubiquitin protein ligase | 69201951 | 69239324 | 69202015 | 69202223 |
| NAGA\_30 | 22 | NAGA | a-N-Acetylgalactosaminidase | 42466846 | 42454337 | 42466437 | 42466229 |
| NDUFC1\_01 | 4 | NDUFC1 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown | 140222364 | 140211070 | 140216838 | 140217048 |
| NFATC4\_17 | 14 | NFATC4 | Nuclear factor of activated T cells 4 | 24838203 | 24848810 | 24837955 | 24837799 |
| PIK3R5\_12 | 17 | PIK3R5 | Phosphoinositide-3-kinase, regulatory subunit 5 | 8815834 | 8782232 | 8792251 | 8792063 |
| PPARG\_20 | 3 | PPARG | peroxisome proliferator‐activated receptor gamma | 12329348 | 12475855 | 12329707 | 12329966 |
| RDH12\_23 | 14 | RDH12 | retinol dehydrogenase 12 | 68168602 | 68201168 | 68166518 | 68166775 |
| RDH12\_24 | 14 | RDH12 | retinol dehydrogenase 12 | 68168602 | 68201168 | 68167191 | 68167424 |
| RHOG\_04 | 11 | RHOG | ras homolog family member G | 3862213 | 3848207 | 3863137 | 3862904 |
| SEPT11\_07 | 4 | SEPT11 | Septin 11 | 77870866 | 77959768 | 77871462 | 77871255 |
| STAT1\_26 | 2 | STAT1 | The signal transducer and activator of transcription 1 | 191878976 | 191833761 | 191879029 | 191879241 |
| YAP1\_29 | 11 | YAP1 | Yes-associated protein | 101981191 | 102104154 | 101980889 | 101981108 |
| ZAR1\_06 | 4 | ZAR1 | Zygote arrest 1 | 48492268 | 48496406 | 48492464 | 48492222 |
| Notes: Target: Target fragment of DNA sequencing; Chr: Chromosome; Gene: The name of the gene in which the target fragment is located; TSS: mRNA transcription initiation site; TES: mRNA transcription termination sites; Start: Target fragment initiation site; End: Target fragment termination site; Length: Target fragment sequencing length; Distance to TSS: The distance of the target fragment from the TSS. The minus sign indicates that the target is upstream of the transcription start site. | | | | | | | |

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| Supplementary Table S2: Primer information | | | | |
| Target | Length | Distance to TSS | Primer F | Primer R |
| ARHGAP40\_16 | 204 | 43577 | AAAAGGGGAATTTAGAATYGATTTTAGT | ACACCTAAAACAAACTCTACTCTAAAAACC |
| C5orf34\_15 | 238 | 27826 | GGTTTGGTGGTAAGGAGGAAATG | ATTCTATACATTCTCACCCAATTCATCT |
| CCDC124\_14 | 201 | 8870 | GTTATTTTTATTGGGTATTTAGTTTTGAGGT | TCTACACRCCCTTAAACCAAATCAA |
| COPS8\_11 | 183 | -1555 | GAGGTTAGTAAGATTTAAAGTGAGTATAAGGTA | ACCATAACTCATACAATATAATTTCTTCATAC |
| DDR1\_05 | 177 | -117 | TTTYGATGTTTTGGTATATYGTTTGAA | AACTAACTCAATAAAACTACACAAAAACACC |
| DNAJB6\_09 | 160 | 480 | GGTTTYGTYGAGTTTTAGTYGAGTTTTAGT | ATCTAAAACCRAAACCRAAACTAAAATCT |
| EIF2AK2\_28 | 217 | -73 | TAAATTGTATTGGGAAATTTAGATTAAATATGTT | ACAACCTACCTCCTATCATATAAAAATCCTA |
| GCK\_18 | 226 | 654 | GGTTTATTTGGGGTGTAGTTTGT | CAAACAAATCTACAACATCCTAAACA |
| HAAO\_13 | 172 | 6037 | TTATGTGTTTATGGAAATAGGTTTGGAGA | CACCTACCACCTATACTCCACCTACC |
| HAPLN3\_02 | 226 | 272 | GATTTTGTTYGGGAGGTGTGG | AATTTTTCTACTACCRCTTCCTTTCTACC |
| HHLA3\_03 | 195 | -376 | GAATYGGGAGGTTTATYGTTGG | AATTCTAACTTCCCCCAACRAAC |
| IFNGR2\_27 | 207 | -10 | TTTAAAATGGGGTTGATTGGAG | CTCTCCTCTCRAATACTTAATCRCACAATTC |
| IL10\_25 | 236 | 628 | TTTAAATTATTGGTTTTTTAGGTTTGGAA | ATTAAACTAAACCAAATAATACAATAAATATACAAA |
| IL6\_21 | 254 | -1560 | TTATGTAGGAAAGAGAATTTGGTTTAGG | TAAAACAATAACCTCTATTAAACATTTACTCAA |
| IL6\_22 | 250 | 601 | TTAGAATTTAGTAAAGATTTTTTAATGTAGGTAGT | TACTACCTTCCCTACCCCAATACC |
| IL7\_10 | 171 | 112 | GATTGGGAGTTAGAATTATGAGTTGTTAATG | TAACCCTCTTAATCATTCTTCACTTCCTT |
| MDM2\_08 | 209 | 64 | TGTGTYGGAAAGATGGAGTAAGAAGT | AAAACTCCCCAATTTCCTTCAC |
| NAGA\_30 | 209 | 409 | TTGAGGGYGGTYGAGTTAGTTAGGTAGT | ACACTCCTTATAACACTCACCCCTACC |
| NDUFC1\_01 | 211 | 5526 | GAGGGGTAATTTGAGGGTYGAGT | AAACTCTACTACAAAACCCTCRAATCC |
| NFATC4\_17 | 157 | -248 | TTTGGYGGYGTTTGGTGTTGTT | AACTAAAAACCCRAACACCACTTTC |
| PIK3R5\_12 | 189 | 23583 | GGGGTTTAGAYGTTTAGATAGTGTTGG | AAACAAAAAATCTCTCTCRACACAATAC |
| PPARG\_20 | 260 | 359 | GGTAGGGTTATGGTTYGGTAGGATT | TCCCCRTATCCCCRACTCC |
| RDH12\_23 | 258 | -2084 | TTGGAATTTTATTTAGATAATTTGGAAGAT | AAACRATTCTCCTACCTCCATCTCC |
| RDH12\_24 | 234 | -1411 | GGGAGGTYGAGGTGGGTAGA | AATCTTACTATATCACCCAAACTAAAATACAATAC |
| RHOG\_04 | 234 | -924 | ATTTGAAAAGTTTTTGGAAGATAGG | CCCAAACCTAAAATCCAACTTAAAC |
| SEPT11\_07 | 208 | 596 | GGGGAGATTGGAGGAAAGTT | CCCAAAAACTCAATTACRTAATACAACAATA |
| STAT1\_26 | 213 | -53 | GTTTYGTTTAYGYGTTGGGGTATT | ATCTATCCTCTACCTAAATTCTCRACRATAA |
| YAP1\_29 | 220 | -302 | GTTYGYGGGGTAGAATAYGGGGTA | CTCCTCTCRACTCTTCCTTCCTCTA |
| ZAR1\_06 | 243 | 196 | GGAGGAGGYGGGAAGGTAGTT | CCCCRCCRAAAACCATCC |
| Notes: Length: Target fragment sequencing length; Distance to TSS: The distance of the target fragment from the TSS. The minus sign indicates that the target is upstream of the transcription start site; Primer F: Target fragment forward primer sequence; Primer R: Target fragment reverse primer sequence. | | | | |

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| Supplementary Table S3: Source of candidate CpG sites | | |
| References | Gene Symbol | Number of CpG islands or cg sites |
| Daniel A. Enquobahrie（2015）1 | HAPLN3 | cg08348496 |
| HHLA3 | cg09735905 |
| RHOG | cg17732521 |
| MDM2 | cg12504957 |
| DNAJB6 | cg13456653 |
| IL7 | cg23512958 |
| YAP1 | cg01442799 |
| NAGA | cg27187881 |
| NDUFC1 | cg15010390 |
| SEPT11 | cg00899086 |
| DDR1 | cg11977634 |
| ZAR1 | cg18342279 |
| Pensee Wu (2018)2 | COPS8 | cg16995742 |
| PIK3R5 | cg02823329 |
| HAAO | cg17283620 |
| CDCC124 | cg14060113 |
| C5orf34 | cg09101062 |
| RDH12 | 2 |
| Ana Laura (2014)3 | GCK | 1 |
| Velosha Naidoo (2018)4 | PPARG | 1 |
| Velosha Naidoo (2018)4 | IL6 | 2 |
| Jessica Kang (2018)5 | IL10 | cg206771801-cg206772098 |
| Enchun Li (2019)6 | STAT1 | cg07052015 |
| IFNGR2 | cg23508786 |
| EIF2AK2 | cg06969118 |
| Bioinformatics Analysis | ARHGAP40 | cg03044376 |
| NFATC4 | cg06111454 |

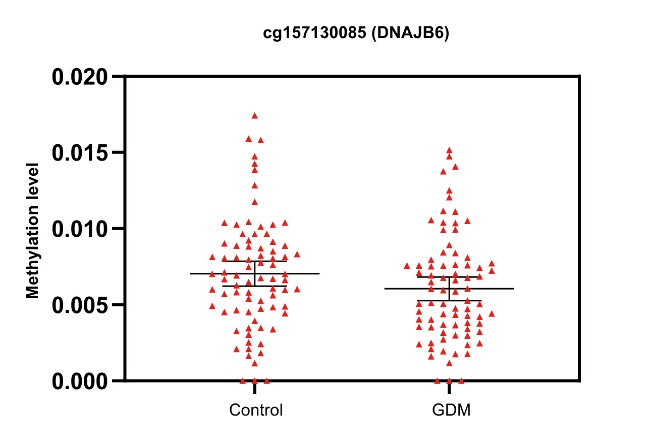
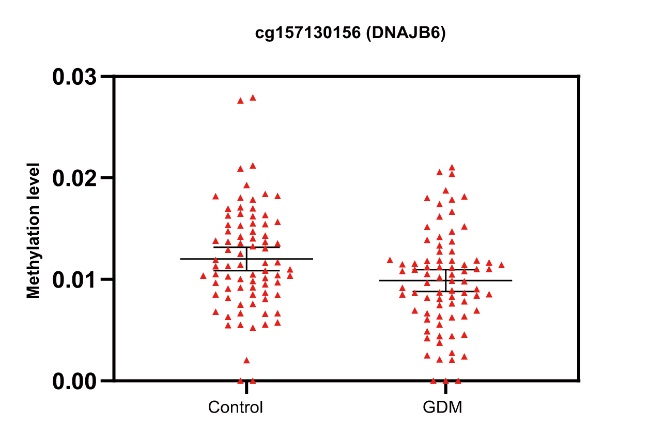
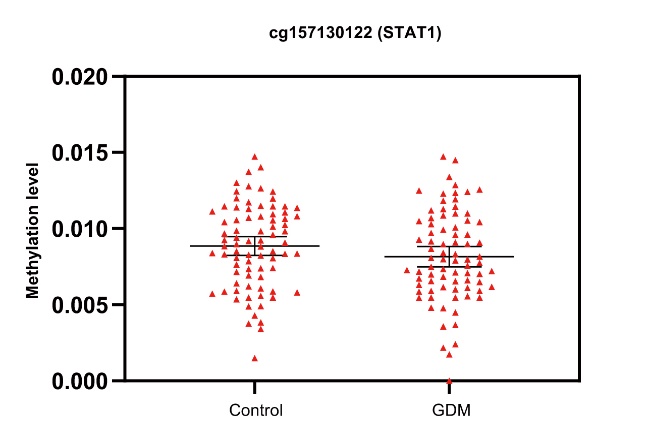
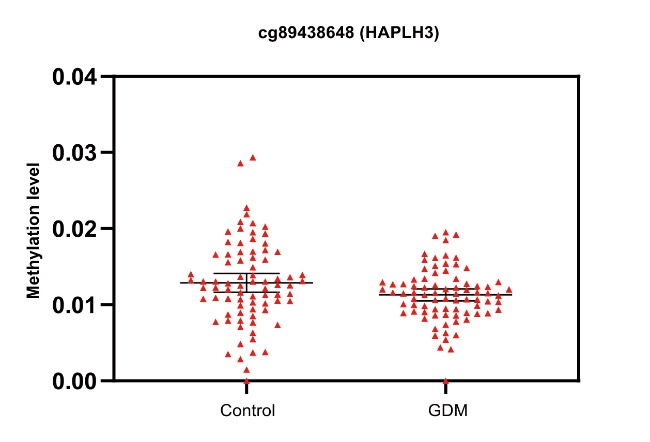
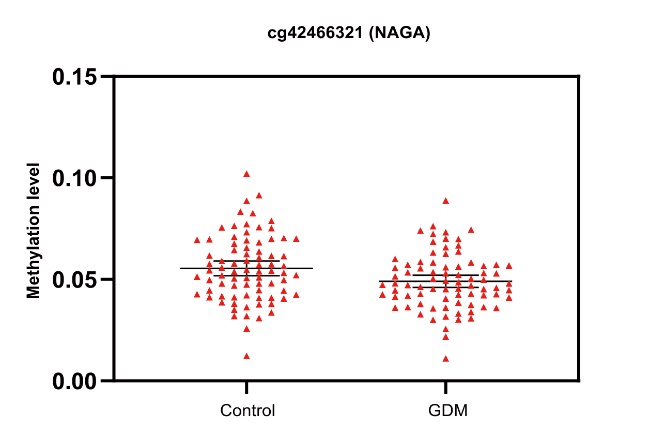
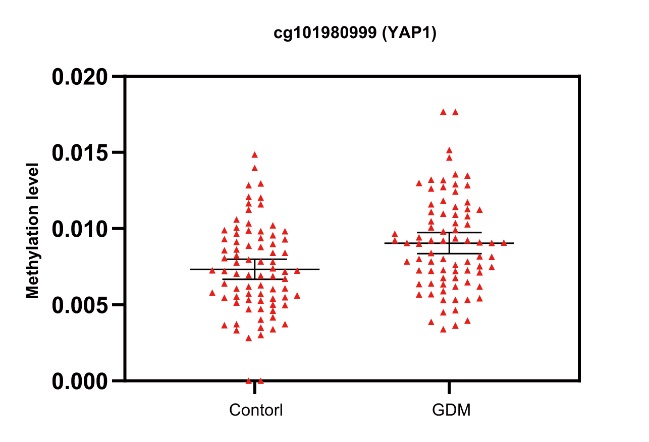
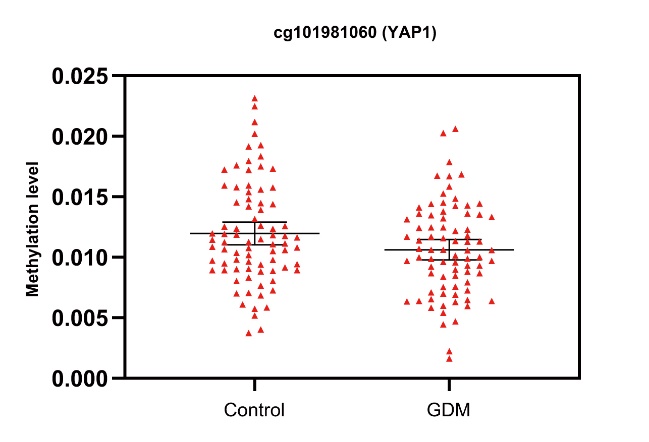
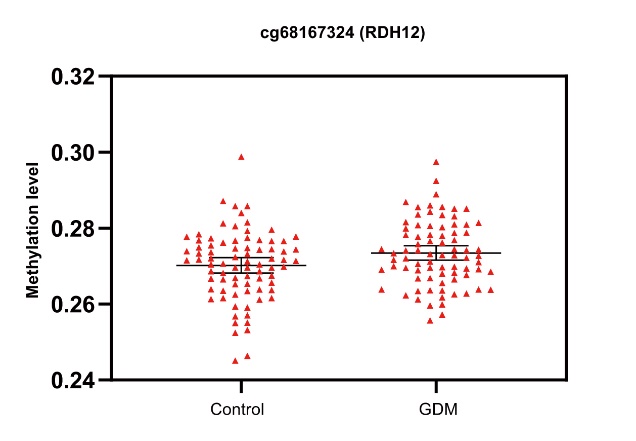
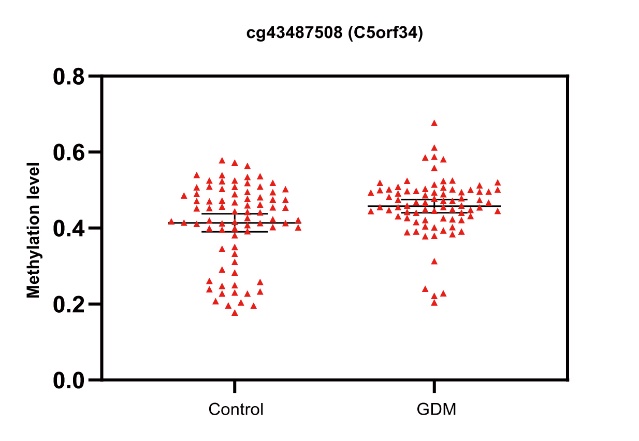
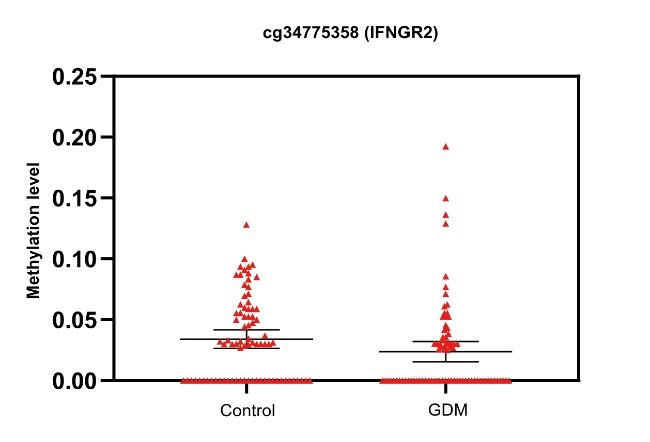
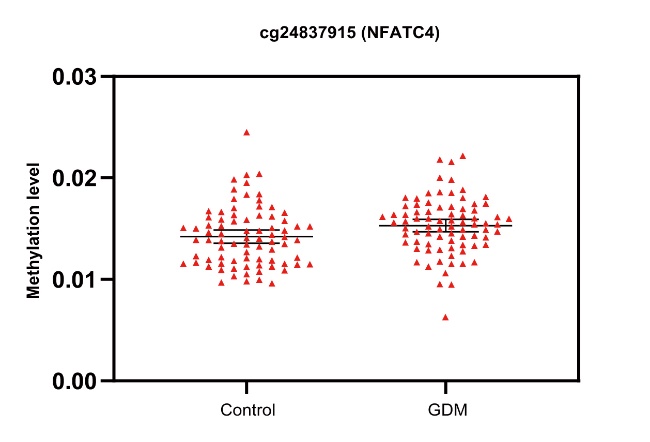
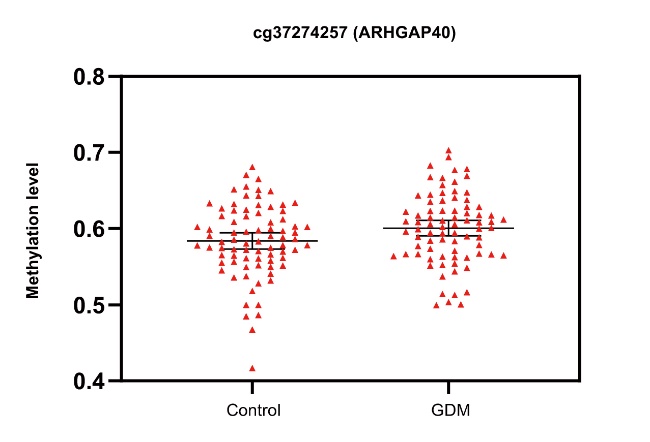
**Supplementary Text S1**

Quality control of DNA methylation sequencing results

In order to ensure the consistency of the DNA methylation level detection results of all CpG sites, all our DNA samples are sent in the same batch and tested using the same test method. For the data results after sequencing, we need to evaluate the quality of the original data through Fast QC software. The main evaluation index is the basic quality index (Q value). During sequencing, Q20 indicates that the Q value is greater than or equal to 20, that is, the sequencing error rate (P) during sequencing is less than or equal to 1%; Q30 indicates that the Q value is greater than or equal to 30, that is, the sequencing error rate (P) during sequencing is less than or equal to 0.1%. Generally, Q20 ≥ 90% (ie 90% base sequencing error rate ≤ 1%), and Q30 ≥ 85% (ie 85% base sequencing error rate ≤ 0.1%) are considered as qualified sequencing results. For the raw reads, we eliminated some poor-quality reads according to the standards of sequencing quality evaluation, and finally generated the reads we needed, that is, "clean reads". In this study, the Q value of all base sequencing: Q20≥99.95%, Q30≥96.41%,

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| Supplementary Table S4: Univariate analysis of all CpG sites | | | | | | | | |
| Gene Symbol | CpG site | Missing values | P-value | | Gene Symbol | CpG site | Missing values | P-value |
| ARHGAP40 | cg37274183 | 0 | 0.388 | EIF2AK2\_28 | | cg37374961\* | 0 | 0.222 |
|  | cg34274257\* | 0 | 0.015 |  | | cg37374898 | 0 | 0.231 |
| C5orf34 | cg43487508 | 0 | 0.012 | DDR1\_05 | | cg30852669 | 1 | 0.469 |
|  | cg43487597\* | 0 | 0.612 |  | | cg30852675 | 1 | 0.561 |
| CCDC124 | cg18054733 | 0 | 0.850 |  | | cg30852699 | 1 | 0.988 |
|  | cg18054731 | 0 | 0.673 |  | | cg30852761 | 1 | 0.278 |
|  | cg18054728 | 0 | 0.524 |  | | cg30852777 | 1 | 0.945 |
|  | cg18054699 | 0 | 0.558 | GCK\_18 | | cg 44185115\* | 0 | 0.505 |
|  | cg18054680 | 0 | 0.163 |  | | cg 44185127\* | 0 | 0.797 |
|  | cg18054672 | 00 | 0.130 |  | | cg 44185141 | 0 | 0.407 |
|  | cg18054644 | 0 | 0.708 |  | | cg 44185148 | 0 | 0.160 |
|  | cg18054637 | 0 | 0.248 |  | | cg 44185154 | 0 | 0.096 |
|  | cg18054634 | 0 | 0.844 |  | | cg 44185159 | 0 | 0.777 |
|  | cg18054622 | 0 | 0.312 |  | | cg 44185166 | 0 | 0.555 |
|  | cg18054617 | 0 | 0.380 |  | | cg 44185168 | 0 | 0.863 |
|  | cg18054603 | 0 | 0.822 |  | | cg 44185174 | 0 | 0.698 |
| COPS8\_11 | cg237992563 | 0 | 0.305 |  | | cg 44185184 | 0 | 0.916 |
|  | cg237992612 | 0 | 0.242 |  | | cg 44185188 | 0 | 0.950 |
|  | cg237992645 | 0 | 0.138 |  | | cg 44185197 | 0 | 0.199 |
| DNAJB6\_09 | cg157130160 | 1 | 0.992 |  | | cg 44185200 | 0 | 0.443 |
|  | cg157130156 | 1 | 0.013 |  | | cg 44185212\* | 0 | 0.357 |
|  | cg157130145 | 1 | 0.287 |  | | cg 44185217 | 0 | 0.673 |
|  | cg157130128 | 1 | 0.837 |  | | cg 44185219 | 0 | 0.432 |
|  | cg157130125 | 1 | 0.415 |  | | cg 44185221 | 0 | 0.814 |
|  | cg157130122 | 1 | 0.104 |  | | cg 44185229\* | 0 | 0.132 |
|  | cg157130120 | 1 | 0.067 |  | | cg 44185235\* | 0 | 0.188 |
|  | cg157130108 | 1 | 0.844 |  | | cg 44185241 | 0 | 0.056 |
|  | cg157130106 | 1 | 0.345 |  | | cg 44185243 | 0 | 0.240 |
|  | cg157130101 | 1 | 0.594 |  | | cg 44185246\* | 0 | 0.393 |
|  | cg157130092 | 1 | 0.129 |  | | cg 44185250 | 0 | 0.357 |
|  | cg157130089 | 1 | 0.252 |  | | cg 44185256 | 0 | 0.270 |
|  | cg157130085 | 1 | 0.018 |  | | cg 44185262\* | 0 | 0.364 |
|  | cg157130076 | 1 | 0.575 |  | | cg 44185269\* | 0 | 0.517 |
|  | cg157130074 | 1 | 0.966 |  | | cg 44185276\* | 0 | 0.256 |
|  | cg157130070 | 1 | 0.766 |  | | cg 44185287 | 0 | 0.916 |
|  | cg157130066 | 1 | 0.578 | HHLA3\_03 | | cg 70820138 | 0 | 0.539 |
| HAAO\_13 | cg 43013772 | 0 | 0.601 |  | | cg 70820141\* | 0 | 0.982 |
|  | cg 43013785 | 0 | 0.289 |  | | cg 70820150\* | 0 | 0.337 |
|  | cg 43013841 | 0 | 0.759 |  | | cg 70820155\* | 0 | 0.946 |
| HAPLN3\_02 | cg 89438611\* | 1 | 0.471 |  | | cg 70820158\* | 0 | 0.720 |
|  | cg 89438627 | 1 | 0.996 |  | | cg 70820168\* | 0 | 0.074 |
|  | cg 89438643 | 1 | 0.581 |  | | cg 70820177\* | 0 | 0.482 |
|  | cg 89438648 | 1 | 0.048 |  | | cg 70820197\* | 0 | 0.771 |
|  | cg 89438671 | 1 | 0.145 |  | | cg 70820223\* | 0 | 0.484 |
|  | cg 89438685 | 1 | 0.085 |  | | cg 70820238\* | 0 | 0.109 |
|  | cg 89438690 | 1 | 0.708 |  | | cg 70820247\* | 0 | 0.499 |
|  | cg 89438708\* | 1 | 0.889 |  | | cg 70820258\* | 0 | 0.237 |
|  | cg 89438711\* | 1 | 0.791 |  | | cg 70820265\* | 0 | 0.907 |
|  | cg 89438724 | 1 | 0.460 |  | | cg 70820275\* | 0 | 0.762 |
|  | cg 89438731\* | 1 | 0.862 |  | | cg 70820283\* | 0 | 0.316 |
|  | cg 89438733 | 1 | 0.355 |  | | cg 70820285\* | 0 | 0.909 |
|  | cg 89438743 | 1 | 0.401 |  | | cg 70820287 | 0 | 0.878 |
|  | cg 89438767 | 1 | 0.101 | IL10\_25 | | cg 206945241\* | 2 | 0.297 |
| IFNGR2\_27 | cg 34775214 | 8 | 0.958 |  | | cg 206945301\* | 2 | 0.427 |
|  | cg 34775231 | 8 | 0.740 |  | | cg 206945346 | 2 | 0.316 |
|  | cg 34775237 | 8 | 0.361 |  | | cg 206945376 | 2 | 0.912 |
|  | cg 34775266 | 8 | 0.956 |  | | cg 206945386 | 2 | 0.330 |
|  | cg 34775291 | 8 | 0.222 | IL7\_10 | | cg 79717683 | 0 | 0.958 |
|  | cg 34775346 | 8 | 0.490 |  | | cg 79717705\* | 0 | 0.836 |
|  | cg 34775358 | 8 | 0.012 |  | | cg 79717726 | 0 | 0.962 |
|  | cg 34775366 | 8 | 0.191 |  | | cg 79717730\* | 0 | 0.310 |
| IL6\_21 | cg 22767323\* | 1 | 0.889 |  | | cg 79717744\* | 0 | 0.999 |
|  | cg 22767315\* | 1 | 0.406 |  | | cg 79717750 | 0 | 0.638 |
|  | cg 22767298\* | 1 | 0.183 |  | | cg 79717752 | 0 | 0.412 |
|  | cg 22767292 | 1 | 0.454 |  | | cg 79717765 | 0 | 0.715 |
|  | cg 22767287 | 1 | 0.408 |  | | cg 79717776 | 0 | 0.645 |
|  | cg 22767269 | 1 | 0.615 | MDM2\_08 | | cg 69202041\* | 0 | 0.143 |
|  | cg 22767230\* | 1 | 0.921 |  | | cg 69202047\* | 0 | 0.060 |
|  | cg 22767227\* | 1 | 0.699 |  | | cg 69202054 | 0 | 0.484 |
|  | cg 22767216\* | 1 | 0.684 |  | | cg 69202058\* | 0 | 0.365 |
|  | cg 22767198\* | 1 | 0.668 |  | | cg 69202060 | 0 | 0.618 |
|  | cg 22767164\* | 1 | 0.283 |  | | cg 69202073 | 0 | 0.741 |
| NAGA\_30 | cg42466409 | 1 | 0.631 |  | | cg 69202090\* | 0 | 0.834 |
|  | cg 42466387 | 1 | 0.133 |  | | cg 69202105 | 0 | 0.499 |
|  | cg 42466346 | 1 | 0.575 |  | | cg 69202115 | 0 | 0.426 |
|  | cg 42466321\* | 1 | 0.008 |  | | cg 69202125 | 0 | 0.897 |
|  | cg 42466303 | 1 | 0.145 |  | | cg 69202129 | 0 | 0.581 |
|  | cg 42466275 | 1 | 0.209 |  | | cg 69202133\* | 0 | 0.918 |
| NDUFC1\_01 | cg 140216861 | 0 | 0.916 |  | | cg 69202150\* | 0 | 0.301 |
|  | cg 140216870\* | 0 | 0.279 |  | | cg 69202169 | 0 | 0.604 |
|  | cg 140216885 | 0 | 0.719 |  | | cg 69202181 | 0 | 0.316 |
|  | cg 140216889\* | 0 | 0.258 |  | | cg 69202184\* | 0 | 0.346 |
|  | cg 140216893\* | 0 | 0.902 |  | | cg 69202192\* | 0 | 0.844 |
|  | cg 140216904 | 0 | 0.740 |  | | cg 69202194\* | 0 | 0.621 |
|  | cg 140216918 | 0 | 0.943 |  | | cg 69202196 | 0 | 0.989 |
|  | cg 140216930 | 0 | 0.101 |  | | cg 69202201 | 0 | 0.350 |
|  | cg 140216940 | 0 | 0.807 | NFATC4\_17 | | cg 24837928\* | 0 | 0.577 |
|  | cg 140216944 | 0 | 0.635 |  | | cg 24837919 | 0 | 0.502 |
|  | cg 140216947 | 0 | 0.663 |  | | cg 24837915\* | 0 | 0.018 |
|  | cg 140216957 | 0 | 0.777 |  | | cg 24837893\* | 0 | 0.055 |
|  | cg 140216978\* | 0 | 0.784 |  | | cg 24837884\* | 0 | 0.163 |
|  | cg 140216998 | 0 | 0.601 |  | | cg 24837877\* | 0 | 0.864 |
|  | cg 140217008 | 0 | 0.266 |  | | cg 24837874\* | 0 | 0.102 |
|  | cg 140217012 | 0 | 0.931 |  | | cg 24837837\* | 0 | 0.098 |
|  | cg 140217020 | 0 | 0.401 | PIK3R5\_12 | | cg 8792093 | 0 | 0.825 |
| RDH12 | cg 68166584\* | 0 | 0.383 | PPARG\_20 | | cg 12329732\* | 0 | 0.732 |
|  | cg 68166586\* | 0 | 0.895 |  | | cg 12329740\* | 0 | 0.658 |
|  | cg 68166596 | 0 | 0.848 |  | | cg 12329745\* | 0 | 0.523 |
|  | cg 68166624\* | 0 | 0.981 |  | | cg 12329747\* | 0 | 0.974 |
|  | cg 68166633 | 0 | 0.830 |  | | cg 12329751 | 0 | 0.342 |
|  | cg 68166654\* | 0 | 0.301 |  | | cg 12329755 | 0 | 0.698 |
|  | cg 68166685\* | 0 | 0.970 |  | | cg 12329762 | 0 | 0.372 |
|  | cg 68166717\* | 0 | 0.748 |  | | cg 12329770 | 0 | 0.640 |
|  | cg 68166727\* | 0 | 0.758 |  | | cg 12329800 | 0 | 0.673 |
|  | cg 68167214\* | 0 | 0.569 |  | | cg 12329812 | 0 | 0.536 |
|  | cg 68167228 | 0 | 0.924 |  | | cg 12329814 | 0 | 0.481 |
|  | cg 68167248 | 0 | 0.601 |  | | cg 12329821\* | 0 | 0.892 |
|  | cg 68167259 | 0 | 0.157 |  | | cg 12329826 | 0 | 0.730 |
|  | cg 68167288 | 0 | 0.119 |  | | cg 12329828 | 0 | 0.770 |
|  | cg 68167292 | 0 | 0.770 |  | | cg 12329839 | 0 | 0.502 |
|  | cg 68167300\* | 0 | 0.605 |  | | cg 12329846\* | 0 | 0.786 |
|  | cg 68167304 | 0 | 0.472 |  | | cg 12329848\* | 0 | 0.502 |
|  | cg 68167324\* | 0 | 0.019 |  | | cg 12329862 | 0 | 0.305 |
|  | cg 68167348\* | 0 | 0.352 |  | | cg 12329864\* | 0 | 0.364 |
|  | cg 68167363 | 0 | 0.642 |  | | cg 12329868\* | 0 | 0.630 |
|  | cg 68167386 | 0 | 0.042 |  | | cg 12329874\* | 0 | 0.692 |
|  | cg 68167388 | 0 | 0.818 |  | | cg 12329879\* | 0 | 0.330 |
| RHOG\_04 | cg 3863098\* | 0 | 0.913 |  | | cg 12329887 | 0 | 0.792 |
|  | cg 3863057\* | 0 | 0.771 |  | | cg 12329889\* | 0 | 0.240 |
|  | cg 3863048 | 0 | 0.737 |  | | cg 12329894\* | 0 | 0.716 |
|  | cg 3863026\* | 0 | 0.383 |  | | cg 12329899 | 0 | 0.054 |
|  | cg 3862996 | 0 | 0.946 |  | | cg 12329904 | 0 | 0.822 |
|  | cg 3862992 | 0 | 0.236 |  | | cg 12329926\* | 0 | 0.291 |
|  | cg 3862977\* | 0 | 0.789 |  | | cg 12329934 | 0 | 0.981 |
|  | cg 3862962 | 0 | 0.352 |  | | cg 12329937\* | 0 | 0.574 |
|  | cg 3862950\* | 0 | 0.423 |  | | cg 12329945 | 0 | 0.870 |
|  | cg 3862942 | 0 | 0.181 |  | | cg 12329947\* | 0 | 0.571 |
|  | cg 3862940 | 0 | 0.562 | SEPT11\_ | | cg 77871441 | 0 | 0.973 |
|  | cg 3862935 | 0 | 0.927 |  | | cg 77871435\* | 0 | 0.945 |
|  | cg 3862932 | 0 | 0.852 |  | | cg 77871432\* | 0 | 0.628 |
| STAT1\_26 | cg 191879055\* | 0 | 0.264 |  | | cg 77871415 | 0 | 0.05 |
|  | cg 191879058 | 0 | 0.309 |  | | cg 77871401 | 0 | 0.752 |
|  | cg 191879065\* | 0 | 0.925 |  | | cg 77871399 | 0 | 0.496 |
|  | cg 191879068 | 0 | 0.676 |  | | cg 77871385 | 0 | 0.822 |
|  | cg 191879075 | 0 | 0.870 |  | | cg 77871374 | 0 | 0.487 |
|  | cg 191879078\* | 0 | 0.625 |  | | cg 77871371 | 0 | 0.601 |
|  | cg 191879104 | 0 | 0.037 |  | | cg 77871369\* | 0 | 0.781 |
|  | cg 191879114 | 0 | 0.205 |  | | cg 77871319 | 0 | 0.211 |
|  | cg 191879127 | 0 | 0.588 |  | | cg 77871300 | 0 | 0.708 |
|  | cg 191879152 | 0 | 0.837 |  | | cg 77871298 | 0 | 0.195 |
|  | cg 191879164 | 0 | 0.161 |  | | cg 77871295 | 0 | 0.781 |
| ZAR1\_06 | cg 48492438\* | 0 | 0.977 |  | | cg 77871290\* | 0 | 0.914 |
|  | cg 48492436 | 0 | 0.992 | YAP1\_29 | | cg 101980913\* | 0 | 0.145 |
|  | cg 48492420 | 0 | 0.604 |  | | cg 101980918 | 0 | 0.837 |
|  | cg 48492416\* | 0 | 0.558 |  | | cg 101980930\* | 0 | 0.203 |
|  | cg 48492413 | 0 | 0.874 |  | | cg 101980938 | 0 | 0.870 |
|  | cg 48492411\* | 0 | 0.651 |  | | cg 101980940 | 0 | 0.412 |
|  | cg 48492392\* | 0 | 0.306 |  | | cg 101980944\* | 0 | 0.176 |
|  | cg 48492390 | 0 | 0.135 |  | | cg 101980951\* | 0 | 0.964 |
|  | cg 48492376\* | 0 | 0.399 |  | | cg 101980956\* | 0 | 0.458 |
|  | cg 48492371\* | 0 | 0.347 |  | | cg 101980966 | 0 | 0.807 |
|  | cg 48492356 | 0 | 0.254 |  | | cg 101980970\* | 0 | 0.596 |
|  | cg 48492353 | 0 | 0.159 |  | | cg 101980977\* | 0 | 0.970 |
|  | cg 48492345\* | 0 | 0.860 |  | | cg 101980981\* | 0 | 0.831 |
|  | cg 48492339\* | 0 | 0.841 |  | | cg 101980985\* | 0 | 0.157 |
|  | cg 48492327\* | 0 | 0.617 |  | | cg 101980994\* | 0 | 0.962 |
|  | cg 48492314\* | 0 | 0.121 |  | | cg 101980997\* | 0 | 0.475 |
|  | cg 48492305 | 0 | 0.252 |  | | cg 101980999\* | 0 | 0.001 |
|  | cg 48492294\* | 0 | 0.543 |  | | cg 101981004\* | 0 | 0.191 |
|  | cg 48492290 | 0 | 0.321 |  | | cg 101981035 | 0 | 0.840 |
|  | cg 48492287 | 4 | 0.848 |  | | cg 101981050 | 0 | 0.107 |
|  | cg 48492284\* | 0 | 0.252 |  | | cg 101981056\* | 0 | 0.519 |
|  | cg 48492269\* | 0 | 0.604 |  | | cg 101981060\* | 0 | 0.028 |
|  | cg 48492260 | 0 | 0.807 |  | | cg 101981065 | 0 | 0.912 |
|  | cg 48492256\* | 0 | 0.318 |  | | cg 101981067 | 0 | 0.135 |
|  | cg 48492252\* | 0 | 0.747 |  | | cg 101981072 | 0 | 0.077 |
|  | cg 48492248\* | 0 | 0.468 |  | | cg 101981076 | 0 | 0.120 |
|  | cg 48492242 | 0 | 0.524 |  | | cg 101981080\* | 0 | 0.593 |
|  |  |  |  |  | | cg 101981082 | 0 | 0.908 |
| \*: Normal distribution | | | | | | | | |

|  |  |
| --- | --- |
| Supplementary Table S5: Introduction to the gene where the differential CpG locus is located | |
| Gene Symbol | Function summary |
| ARHGAP40 | It involved in cell cycle progression, cytoskeleton reorganization, cell polarity, migration, and invasion. |
| C5orf34 | It involved in gene regulation and cell proliferation. |
| RDH12 | It participates in the metabolism of steroids and retinol. |
| YAP1 | It interacts with DNA-binding proteins to promote proliferation and inhibit cell apoptosis. |
| NAGA | It hydrolyzes the α-N-acetylglucosamine bond in glycoconjugates. |
| HAPLN3 | Aggregation of proteoglycan and hyaluronic acid, cell adhesion. |
| DNAJB6 | Acts as a molecular chaperone for various cellular processes. |
| IFNGR2 | Participates in the JAK2-Signal transducer and activators of transcription proteins (STAT) signaling pathway (JAK2-STAT) via signal transduction. |
| NFATC4 | The product of this gene induces the expression of cytokine genes in T cells. |
| STAT1 | Participate in a variety of immune pathways and play an important role in mediating type I interferon (IFN-α/β) and type II interferon (IFN-γ). |



**Supplementary Figure S1:** DNA methylation level of different CpG sites in GDM and Control group.

**Notes:** Little red triangle means the methylation levels of samples and the three black lines means the mean±95%CI.

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