# Supplementary Information

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Table 1: S1. 96 Tissue Samples for Illumina MethylationEpic Assay

| No. | Sample.no. | Diagnosis |
| --- | --- | --- |
| 1 | SW103N8 | EM |
| 2 | SW108N3 | FM |
| 3 | SW137NN3 | CM |
| 4 | SW112N3 | FM |
| 5 | SW116N7 | EM |
| 6 | SW108N14 | CM |
| 7 | SW108N10 | EM |
| 8 | SW136NN2 | CM |
| 9 | SW189NN1 | EM |
| 10 | SW150NN4 | EM |
| 11 | SW159NN3 | EM |
| 12 | SW131NN4 | CM |
| 13 | SW148NN2 | FM |
| 14 | SW131NN1 | EM |
| 15 | SW159NN1 | CM |
| 16 | SW159NN2 | FM |
| 17 | SW150NN1 | FM |
| 18 | SW156NN5 | FM |
| 19 | SW94N12 | EM |
| 20 | SW130NN1 | FM |
| 21 | SW160NN1 | EM |
| 22 | SW96N2 | EM |
| 23 | SW160NN2 | CM |
| 24 | SW156NN1 | EM |
| 25 | SW95N4 | EM |
| 26 | SW96N5 | CM |
| 27 | SW156NN4 | CM |
| 28 | SW101N2 | FM |
| 29 | SW197NN1 | EM |
| 30 | SW150NN2 | CM |
| 31 | SW95N2 | FM |
| 32 | SW95N16 | CM |
| 33 | SW94N4 | CM |
| 34 | SW147NN2 | FM |
| 35 | SW173NN4 | FM |
| 36 | SW201NN2 | CM |
| 37 | ZM | uterine carcinosarcoma (MMMT) |
| 38 | SW288T1 | uterine endometrioid |
| 39 | 702TS | uterine serous |
| 40 | DM851T | uterine serous |

Table 1: S1. 96 Tissue Samples for Illumina MethylationEpic Assay *(continued)*

| No. | Sample.no. | Diagnosis |
|---|---|---|
| 41 | KK | uterine endometrioid |
| 42 | PAP54 | uterine endometrioid |
| 43 | SW274T1 | uterine endometrioid |
| 44 | OY | uterine endometrioid |
| 45 | HM | uterine endometrioid |
| 46 | SY | uterine serous |
| 47 | SW190T1 | uterine serous |
| 48 | PAP43 | uterine endometrioid |
| 49 | MT | uterine endometrioid |
| 50 | PAP53 | uterine endometrioid |
| 51 | ST | uterine endometrioid |
| 52 | 650AS | ovarian HGSC = ovarian high grade serous carcinoma |
| 53 | USC6 | ovarian HGSC |
| 54 | 562TS2 | ovarian HGSC |
| 55 | 6407TCS | ovarian poorly differentiated carcinoma |
| 56 | 7491TS2 | ovarian HGSC |
| 57 | 792TCS2 | ovarian HGSC (High grade adenocarcinoma with serous features) |
| 58 | 221TCS | ovarian MMMT (with high-grade serous and endometrioid carcinoma) |
| 59 | 600TCS1 | ovarian HGSC |
| 60 | 376TCS1 | ovarian HGSC |
| 61 | 415TCS2 | ovarian HGSC |
| 62 | 514TCS | oarian MMMT (High grade carcinoma, consistent with malignant mixed mesodermal tumor.) |
| 63 | 1120 | ovarian HGSC |
| 64 | 64212T(JH626) | ovarian HGSC |
| 65 | 541AT | ovarian HGSC |
| 66 | 713 | ovarian HGSC |
| 67 | 120T1 | ovarian HGSC |
| 68 | 1027T(FM312) | ovarian HGSC |
| 69 | 1028T | ovarian HGSC |
| 70 | 7070T | ovarian HGSC |
| 71 | 121T | ovarian HGSC |
| 72 | 125T(FM342) | ovarian HGSC |
| 73 | 126T(FM343) | ovarian HGSC |
| 74 | 199TCS | ovarian HGSC |
| 75 | 633TCS | ovarian HGSC |
| 76 | 810TCS(FM417) | ovarian HGSC |
| 77 | 906T | ovarian HGSC |
| 78 | SW0084T2 | uterine EM = endometrioid endometrial cancer |
| 79 | SW0143T1 | uterine EM |

Table 1: S1. 96 Tissue Samples for Illumina MethylationEpic Assay *(continued)*

| No. | Sample.no. | Diagnosis |
|-----|-----------|-----------|
| 80 | SW0114T2 | uterine EM |
| 81 | SW0145T1 | uterine EM |
| 82 | SW0213T4 | uterine EM |
| 83 | PAP44 | FIGO GRADE 1 = endometrioid endometrial cancer grade 1 |
| 84 | PAP45 | FIGO GRADE 2 = endometrioid endometrial cancer grade 2 |
| 85 | PAP46 | FIGO GRADE 1 = endometrioid endometrial cancer grade 1 |
| 86 | PAP47 | FIGO GRADE 2 = endometrioid endometrial cancer grade 2 |
| 87 | PAP48 | FIGO GRADE 1 = endometrioid endometrial cancer grade 1 |
| 88 | PAP49 | FIGO GRADE 1 = endometrioid endometrial cancer grade 1 |
| 89 | PAP50 | FIGO GRADE 1 = endometrioid endometrial cancer grade 1 |
| 90 | PAP52 | FIGO GRADE 2 = endometrioid endometrial cancer grade 2 |
| 91 | 366TS | USC = seours endomerial carcinoma |
| 92 | 340TS | USC |
| 93 | 993TCS | USC |
| 94 | FM474T | USC |
| 95 | FM403T | USC |
| 96 | 900TDNA | USC |

Table 2: S2. Location of Selected 294 Probes within 91 High-confidence DMRs

| No. | loc | probes | genes |
|-----|-----|--------|-------|
| 1 | chr5 178422415:178422431 | cg25423752, cg02229543 | GRM6 |
| 2 | chr5 140753387:140753418 | cg01357507, cg09066326, cg03835609 | PCDHGA6, PCDHGA1, PCDHGA2, PCDHGA3, PCDHGA4, PCDHGA5, PCDHGB1, PCDHGB2, PCDHGB3 |
| 3 | chr1 149784212:149784571 | cg04888113, cg12769994 | HIST2H2BF |
| 4 | chr2 182545768:182545934 | cg02819605, cg01863682, cg20709008 | NEUROD1 |
| 5 | chr1 215255572:215255716 | cg08453036, cg17934948 | KCNK2 |
| 6 | chr2 207506675:207506991 | cg20841047, cg08057136, cg12110911 | LOC200726 |
| 7 | chr14 57278351:57279275 | cg05241355, cg21039708, cg25092838, cg23478293 | OTX2OS1, OTX2 |
| 8 | chr2 220174232:220174325 | cg03970036, cg15119274 | PTPRN |

Table 2: S2. Location of Selected 294 Probes within 91 High-confidence DMRs *(continued)*

| No. | loc | probes | genes |
|-----|-----|--------|-------|
| 9 | chr18 12307329:12307649 | cg16546503, cg07307078, cg03507241 | TUBB6 |
| 10 | chr8 50822281:50822565 | cg09246637, cg19254369, cg00230631, cg10767350, cg03759824 | SNTG1 |
| 11 | chr5 2751550:2751837 | cg18371475, cg15941948, cg10237977 | IRX2, C5orf38 |
| 12 | chr6 127840616:127840704 | cg25929533, cg12695797 | C6orf174 |
| 13 | chr6 26044204:26044495 | cg15387132, cg07701237, cg26426142, cg02221866, cg21250296, cg11503599 | HIST1H2BB, HIST1H3C |
| 14 | chr2 145277843:145278152 | cg26522240, cg04836221, cg05322294 | ZEB2, LINC01412, ZEB2-AS1 |
| 15 | chr14 60975174:60975199 | cg07747306, cg13769906 | SIX6 |
| 16 | chr5 140624869:140624898 | cg03572772, cg18606364 | PCDHB15 |
| 17 | chr8 102217712:102217722 | cg01767118, cg11878182 | ZNF706 |
| 18 | chr3 62861142:62861245 | cg13491481, cg25947544, cg02719752 | CADPS |
| 19 | chr6 26183508:26183684 | cg21146268, cg22942804, cg22036966, cg07997936, cg26191923 | HIST1H2BE |
| 20 | chr17 58498712:58498977 | cg22191510, cg10179315, cg09695735 | C17orf64 |
| 21 | chr17 48546503:48546620 | cg13764778, cg05180443, cg06818777 | ACSF2, CHAD |
| 22 | chr3 157261004:157261021 | cg15570323, cg24783642, cg03358769 | C3orf55 |
| 23 | chr5 140797092:140797196 | cg03510378, cg13933262, cg14378860 | PCDHGB7, PCDHGA1, PCDHGA10, PCDHGA2, PCDHGA3, PCDHGA4, PCDHGA5, PCDHGA6, PCDHGA7, PCDHGA8, PCDHGA9, PCDHGB1, PCDHGB2, PCDHGB3, PCDHGB4, PCDHGB5, PCDHGB6 |
| 24 | chr14 102026086:102026953 | cg16366843, cg13126530, cg02609127, cg07193553, cg23354716, cg01044961, cg16781205, cg21174533, cg03721993, cg00328051, cg22325330, cg10590512, cg01693026 | DIO3, MIR1247 |
| 25 | chr11 86085694:86085715 | cg18282849, cg10395685 | CCDC81 |
| 26 | chr13 100624130:100624373 | cg12907379, cg23476830 | ZIC5 |

Table 2: S2. Location of Selected 294 Probes within 91 High-confidence DMRs *(continued)*

| No. | loc | probes | genes |
| --- | --- | --- | --- |
| 27 | chr6 31782961:31783196 | cg09085842, cg15185479, cg18846140, cg22715094, cg01639032, cg11353380 | HSPA1A, HSPA1L |
| 28 | chr1 174968334:174968388 | cg13673319, cg01730534, cg13384453 | CACYBP |
| 29 | chr7 27213966:27214201 | cg01397139, cg14649140 | HOXA10 |
| 30 | chr2 43019997:43020169 | cg26360792, cg27299406, cg09480054, cg01561916 | HAAO |
| 31 | chr12 25055967:25056127 | cg20399616, cg23424146, cg10072115, cg23930313, cg08598454 | BCAT1 |
| 32 | chr6 73330106:73330297 | cg15120732, cg05350268, cg04290119, cg03922126 | KCNQ5 |
| 33 | chr5 75377968:75378102 | cg25025437, cg24794347 | SV2C |
| 34 | chr5 140787504:140787507 | cg18617005, cg18507379 | PCDHGB6, PCDHGA1, PCDHGA2, PCDHGA3, PCDHGA4, PCDHGA5, PCDHGA6, PCDHGA7, PCDHGA8, PCDHGA9, PCDHGB1, PCDHGB2, PCDHGB3, PCDHGB4, PCDHGB5 |
| 35 | chr3 147124417:147124543 | cg21127068, cg06369327, cg05548555 | ZIC4 |
| 36 | chr2 216300268:216300292 | cg10692870, cg21314106 | FN1 |
| 37 | chr11 116706372:116706520 | cg13090478, cg10753889 | APOA1 |
| 38 | chr6 25652390:25652407 | cg04200224, cg10721149, cg13834623 | SCGN |
| 39 | chr11 76381971:76382149 | cg01691530, cg25717182 | LRRC32 |
| 40 | chr15 83953744:83953780 | cg18952647, cg09180848 | BNC1 |
| 41 | chr17 16283974:16284678 | cg10262404, cg06537829, cg23752691, cg14349843, cg13425712, cg05090851, cg01286555, cg24668364, cg25745651, cg07587433, cg03954587, cg10637938 | UBB |
| 42 | chr7 27205381:27205504 | cg26365299, cg03464573 | HOXA9 |
| 43 | chr11 31840628:31840698 | cg06312283, cg07434271 | PAX6 |
| 44 | chr19 13135333:13135494 | cg26581012, cg19611364 | NFIX |
| 45 | chr20 25129184:25129562 | cg01505767, cg04299389, cg22273939, cg18009321, cg05908371, cg16265348, cg08941457 | LOC284798 |
| 46 | chr11 131780492:131780894 | cg15617814, cg11473001, cg06931179, cg26918812, cg17683427 | NTM |
| 47 | chr11 31827899:31827998 | cg13596833, cg04504066 | PAX6 |

Table 2: S2. Location of Selected 294 Probes within 91 High-confidence DMRs *(continued)*

| No. | loc | probes | genes |
| --- | --- | --- | --- |
| 48 | chr5 140529580:140529627 | cg09178190, cg15038110 | PCDHB6 |
| 49 | chr6 31783272:31783545 | cg21122656, cg26616261, cg02704535, cg19677203, cg22847691, cg00929855, cg15174834, cg12883479, cg10598353, cg13413286, cg17494781, cg18466674 | HSPA1A, HSPA1L |
| 50 | chr12 39299326:39299844 | cg13603508, cg01963134, cg07300451, cg26510017, cg11824397, cg13509195, cg21784036, cg24182470 | CPNE8 |
| 51 | chr2 198650987:198651111 | cg13356896, cg07495363, cg17565627 | BOLL |
| 52 | chr10 133110244:133110646 | cg23632875, cg03109827, cg03943081 | TCERG1L |
| 53 | chr4 90757398:90757533 | cg20003494, cg26578617 | SNCA |
| 54 | chr5 10308246:10308250 | cg16575104, cg10178203 | CMBL |
| 55 | chr2 223163677:223163679 | cg18352427, cg20372045 | PAX3, CCDC140 |
| 56 | chr7 27282005:27282233 | cg10188985, cg11640378 | EVX1, EVX1-AS |
| 57 | chr9 36258661:36258825 | cg21042356, cg14447369 | GNE |
| 58 | chr10 43892790:43893073 | cg04424930, cg17824240, cg04990571, cg27641141, cg02169113, cg19029378, cg09936190, cg05525499, cg16042558 | HNRNPF |
| 59 | chr5 140248390:140248424 | cg12091708, cg26023680 | PCDHA11, PCDHA1, PCDHA10, PCDHA6, PCDHA2, PCDHA3, PCDHA4, PCDHA5, PCDHA7, PCDHA8, PCDHA9 |
| 60 | chr15 53083518:53083532 | cg20056542, cg13877670 | ONECUT1 |
| 61 | chr5 140588221:140588231 | cg17047981, cg05827573, cg12343638 | PCDHB12 |
| 62 | chr2 154728202:154728210 | cg26983710, cg07547000 | GALNT13 |
| 63 | chr10 102899949:102900262 | cg02167020, cg16130857 | |
| 64 | chr1 235814188:235814201 | cg02023150, cg21895505 | GNG4, MIR5096 |
| 65 | chr18 76740101:76740258 | cg07382554, cg14007067 | SALL3 |
| 66 | chr8 144650730:144651002 | cg05191879, cg13671044, cg19951303 | MROH6, C8orf73 |
| 67 | chr15 45421578:45421749 | cg06904403, cg13605988, cg17438432 | DUOX1, DUOXA1 |
| 68 | chr10 23982350:23982480 | cg06251764, cg18633693, cg04063945 | KIAA1217 |
| 69 | chr12 95942907:95942964 | cg13879483, cg07783282 | USP44 |
| 70 | chr1 165326069:165326082 | cg02885925, cg26436962 | LMX1A |
| 71 | chr2 176993643:176993841 | cg20732478, cg21815667 | HOXD8 |
| 72 | chr20 25566470:25566563 | cg03522245, cg16686733 | NINL |

Table 2: S2. Location of Selected 294 Probes within 91 High-confidence DMRs *(continued)*

| No. | loc | probes | genes |
|---|---|---|---|
| 73 | chr1 206223241:206224027 | cg18992688, cg17587023, cg00761787, cg26795730, cg16368479, cg17940251, cg04633513 | AVPR1B |
| 74 | chr3 160167746:160167789 | cg26856080, cg26433838, cg02723904, cg12479674 | TRIM59 |
| 75 | chr19 51170816:51171061 | cg08447324, cg16658931 | SHANK1 |
| 76 | chr20 21378045:21378211 | cg11667020, cg21200408 | NKX2-4 |
| 77 | chr3 187455371:187455734 | cg00480331, cg18562663, cg07091593, cg12942328 | BCL6 |
| 78 | chr4 41751886:41752452 | cg11046315, cg05994794, cg11777515 | PHOX2B |
| 79 | chr6 27782126:27782541 | cg21771891, cg20478264, cg04024413 | HIST1H2AJ, HIST1H2BM |
| 80 | chr11 2292428:2292447 | cg20912770, cg05309948 | ASCL2 |
| 81 | chr6 10426637:10426657 | cg26987855, cg21080336 | |
| 82 | chr5 176559881:176560001 | cg08369368, cg18016826 | NSD1 |
| 83 | chr7 99517369:99517378 | cg12914047, cg13822726 | TRIM4 |
| 84 | chr19 58280801:58280832 | cg27046034, cg03584535 | ZNF586 |
| 85 | chr6 6004207:6004337 | cg13021333, cg13237002, cg24720571, cg09555118 | NRN1 |
| 86 | chr6 30711796:30711835 | cg13804182, cg16493531, cg10916998, cg16331823 | FLOT1, IER3 |
| 87 | chr3 139653545:139653573 | cg01755562, cg00134776 | CLSTN2 |
| 88 | chr8 33371996:33372188 | cg11755107, cg00425988 | C8orf41 |
| 89 | chr7 121943990:121944282 | cg16392213, cg24934063, cg16197925 | FEZF1 |
| 90 | chr9 36258587:36258600 | cg22766783, cg21210985 | GNE |
| 91 | chr17 36103953:36104218 | cg05110178, cg11862993, cg09463047 | HNF1B |

Table 3: S3. 93 DNA methylation Genes Grouped into Four Clusters

| genes | probes | auc | NMF_cluster |
|---|---|---|---|
| GRM6 | cg25423752, cg02229543 | 0.98 | 1, 4 |
| PCDHGA4 | cg09066326, cg03835609, cg13933262, cg18617005, cg18507379 | 0.97 | 1, 2, 3 |
| HIST1H2BB | cg15387132, cg07701237, cg26426142, cg02221866, cg21250296, cg11503599 | 0.93 | 1 |
| HIST1H2BE | cg21146268, cg22036966, cg22942804, cg07997936, cg26191923 | 0.91 | 1, 3 |
| UBB | cg10262404, cg06537829, cg23752691, cg14349843, cg13425712, cg05090851, cg01286555, cg24668364, cg25745651, cg07587433, cg03954587, cg10637938 | 0.84 | 1 |

Table 3: S3. 93 DNA methylation Genes Grouped into Four Clusters
*(continued)*

| genes | probes | auc | NMF_cluster |
|---|---|---|---|
| NFIX | cg26581012, cg19611364 | 0.84 | 1 |
| C8orf73 | cg05191879 | 0.80 | 1 |
| MROH6 | cg13671044, cg19951303 | 0.78 | 1 |
| HSPA1A | cg09085842, cg15185479, cg18846140, cg22715094, cg01639032, cg11353380, cg21122656, cg02704535, cg19677203, cg22847691, cg00929855, cg15174834, cg12883479, cg10598353, cg13413286, cg17494781, cg18466674 | 0.84 | 1 |
| ZNF586 | cg27046034, cg03584535 | 0.63 | 1 |
| HSPA1L | cg26616261 | 0.88 | 1 |
| HIST1H2AJ | cg21771891, cg20478264 | 0.69 | 1 |
| HIST1H2BM | cg04024413 | 0.70 | 1 |
| GNE | cg21042356, cg14447369, cg22766783, cg21210985 | 0.70 | 2 |
| PCDHGA6 | cg01357507 | 0.96 | 2 |
| C17orf64 | cg22191510, cg10179315, cg09695735 | 0.91 | 2, 3 |
| CACYBP | cg13673319, cg01730534, cg13384453 | 0.88 | 2 |
| HNRNPF | cg04424930, cg17824240, cg04990571, cg27641141, cg02169113, cg19029378, cg09936190, cg05525499, cg16042558 | 0.79 | 2 |
| DUOX1 | cg06904403, cg13605988, cg17438432 | 0.78 | 2 |
| CPNE8 | cg13603508, cg01963134, cg07300451, cg26510017, cg11824397, cg13509195, cg21784036, cg24182470 | 0.82 | 2 |
| BCL6 | cg00480331, cg18562663, cg07091593, cg12942328 | 0.71 | 2 |
| PCDHGB7 | cg03510378, cg14378860 | 0.91 | 2, 3 |
| TRIM59 | cg26856080, cg26433838, cg02723904, cg12479674 | 0.74 | 2 |
| CMBL | cg16575104, cg10178203 | 0.81 | 2 |
| BCAT1 | cg23424146, cg10072115, cg23930313, cg08598454, cg20399616 | 0.86 | 2, 3 |
| PCDHA11 | cg12091708, cg26023680 | 0.79 | 2 |
| C8orf41 | cg11755107, cg00425988 | 0.54 | 2, 4 |
| HNF1B | cg05110178, cg11862993, cg09463047 | 0.42 | 2 |
| PCDHB12 | cg17047981, cg05827573, cg12343638 | 0.79 | 2, 3 |
| NSD1 | cg08369368, cg18016826 | 0.68 | 2 |
| LOC200726 | cg20841047, cg08057136, cg12110911 | 0.96 | 3 |
| OTX2OS1 | cg23478293, cg21039708, cg25092838 | 0.95 | 3, 4 |
| HIST2H2BF | cg04888113, cg12769994 | 0.97 | 3 |
| PTPRN | cg03970036, cg15119274 | 0.95 | 3 |
| NEUROD1 | cg02819605, cg01863682, cg20709008 | 0.96 | 3 |
| SNTG1 | cg09246637, cg19254369, cg00230631 | 0.93 | 3 |
| IRX2 | cg18371475, cg15941948 | 0.95 | 3 |
| C5orf38 | cg10237977 | 0.84 | 3 |

Table 3: S3. 93 DNA methylation Genes Grouped into Four Clusters *(continued)*

| genes | probes | auc | NMF_cluster |
|---|---|---|---|
| DIO3 | cg13126530, cg02609127, cg07193553, cg23354716, cg01044961, cg16781205, cg21174533, cg03721993, cg00328051, cg22325330, cg10590512, cg01693026 | 0.89 | 3, 4 |
| ZNF706 | cg01767118, cg11878182 | 0.93 | 3, 4 |
| CHAD | cg13764778, cg05180443, cg06818777 | 0.91 | 3 |
| CADPS | cg13491481, cg25947544, cg02719752 | 0.92 | 3 |
| PCDHB15 | cg03572772, cg18606364 | 0.93 | 3 |
| PAX6 | cg13596833, cg04504066, cg06312283, cg07434271 | 0.88 | 3, 4 |
| CCDC81 | cg18282849, cg10395685 | 0.89 | 3 |
| C3orf55 | cg15570323, cg24783642, cg03358769 | 0.90 | 3 |
| HAAO | cg26360792, cg27299406, cg09480054, cg01561916 | 0.87 | 3 |
| USP44 | cg13879483, cg07783282 | 0.77 | 3, 4 |
| PCDHB6 | cg09178190, cg15038110 | 0.83 | 3 |
| NTM | cg15617814, cg11473001, cg06931179, cg26918812, cg17683427 | 0.83 | 3 |
| GALNT13 | cg26983710, cg07547000 | 0.79 | 3 |
| PAX3 | cg18352427, cg20372045 | 0.81 | 3 |
| BOLL | cg13356896, cg07495363, cg17565627 | 0.82 | 3 |
| TCERG1L | cg23632875, cg03109827, cg03943081 | 0.82 | 3 |
| SALL3 | cg07382554, cg14007067 | 0.79 | 3 |
| ASCL2 | cg20912770, cg05309948 | 0.68 | 3 |
| TUBB6 | cg16546503, cg07307078, cg03507241 | 0.94 | 4 |
| C6orf174 | cg25929533, cg12695797 | 0.94 | 4 |
| OTX2 | cg05241355 | 0.88 | 4 |
| KCNK2 | cg08453036, cg17934948 | 0.96 | 4 |
| APOA1 | cg10753889 | 0.92 | 4 |
| LRRC32 | cg01691530, cg25717182 | 0.85 | 4 |
| ZEB2 | cg26522240, cg04836221 | 0.79 | 4 |
| ZEB2-AS1 | cg05322294 | 0.91 | 4 |
| SV2C | cg25025437, cg24794347 | 0.86 | 4 |
| HOXA10 | cg01397139, cg14649140 | 0.88 | 4 |
| ZIC5 | cg12907379, cg23476830 | 0.89 | 4 |
| SIX6 | cg07747306, cg13769906 | 0.93 | 4 |
| ZIC4 | cg21127068, cg06369327, cg05548555 | 0.86 | 4 |
| FN1 | cg10692870, cg21314106 | 0.86 | 4 |
| LOC284798 | cg01505767, cg04299389, cg22273939, cg18009321, cg05908371, cg16265348, cg08941457 | 0.83 | 4 |
| HOXD8 | cg20732478, cg21815667 | 0.75 | 4 |
| PHOX2B | cg11046315, cg05994794, cg11777515 | 0.71 | 4 |
| EVX1-AS | cg10188985 | 0.83 | 4 |
| EVX1 | cg11640378 | 0.73 | 4 |

Table 3: S3. 93 DNA methylation Genes Grouped into Four Clusters *(continued)*

| genes | probes | auc | NMF_cluster |
|---|---|---|---|
| HOXA9 | cg26365299, cg03464573 | 0.84 | 4 |
| BNC1 | cg18952647, cg09180848 | 0.85 | 4 |
| KCNQ5 | cg15120732, cg05350268, cg04290119, cg03922126 | 0.86 | 4 |
| SNCA | cg20003494, cg26578617 | 0.82 | 4 |
| SCGN | cg04200224, cg10721149, cg13834623 | 0.85 | 4 |
| AVPR1B | cg18992688, cg17587023, cg00761787, cg26795730, cg16368479, cg17940251, cg04633513 | 0.74 | 4 |
| FEZF1 | cg16392213, cg24934063, cg16197925 | 0.52 | 4 |
| LMX1A | cg02885925, cg26436962 | 0.75 | 4 |
| GNG4 | cg02023150, cg21895505 | 0.79 | 4 |
| SHANK1 | cg08447324, cg16658931 | 0.74 | 4 |
| NINL | cg03522245, cg16686733 | 0.75 | 4 |
| ONECUT1 | cg20056542, cg13877670 | 0.79 | 4 |
| KIAA1217 | cg06251764, cg18633693, cg04063945 | 0.78 | 4 |
| TRIM4 | cg12914047, cg13822726 | 0.67 | 4 |
| FLOT1 | cg13804182, cg16493531, cg10916998, cg16331823 | 0.58 | 4 |
| CLSTN2 | cg01755562, cg00134776 | 0.57 | 4 |
| NKX2-4 | cg11667020, cg21200408 | 0.73 | 4 |
| NRN1 | cg13021333, cg13237002, cg24720571, cg09555118 | 0.59 | 4 |