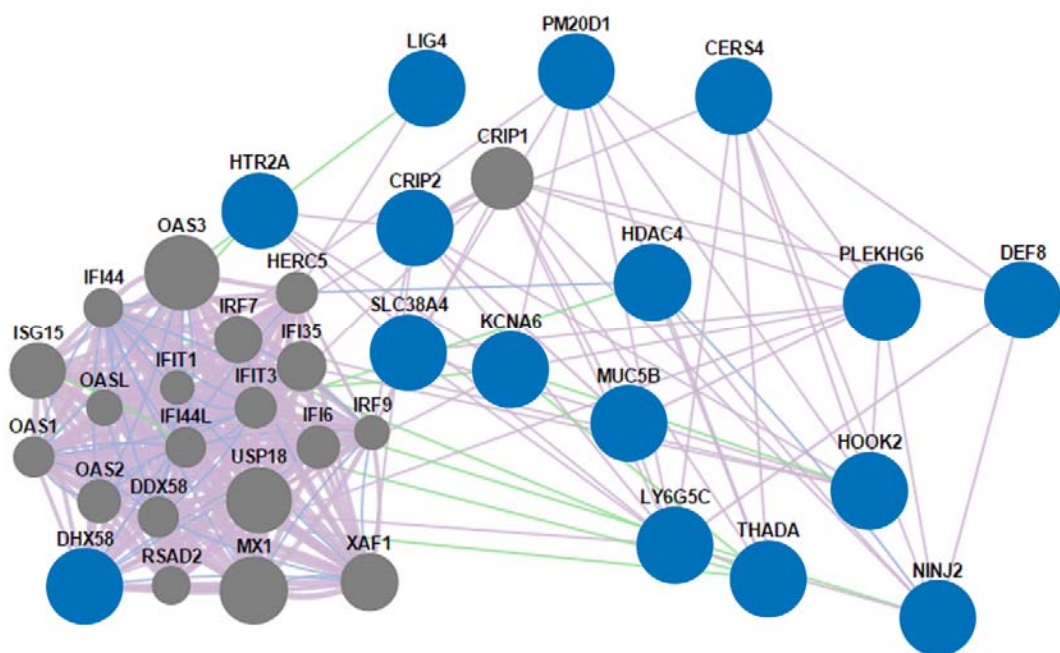


**Supplementary Figure 1:** Network analysis results showing relationships amongst genes with hypermethylated regions (hyper-DMRs) specific to SLE patients with a history of malar rash. Manifestation-specific hyper-DMR genes and network-associated genes are represented by blue and grey nodes, respectively. The lines connecting the nodes depict gene-gene relationships based on co-expression (purple), co-localization (blue), and genetic interactions (green). Line thickness is relative to the strength of the gene-gene relationship. The network analysis was performed using GeneMANIA software.



**Supplementary Table 1:** Demographics of SLE patients with either malar rash, discoid rash, or neither cutaneous involvement and healthy controls matched by age, sex, and ethnicity.

| Patients                        |        |           |     | Controls  |        |           |     |
|---------------------------------|--------|-----------|-----|-----------|--------|-----------|-----|
| Sample ID                       | Sex    | Ethnicity | Age | Sample ID | Sex    | Ethnicity | Age |
| <b>Malar Rash</b>               |        |           |     |           |        |           |     |
| M1                              | Female | EA        | 22  | C1        | Female | EA        | 22  |
| M2                              | Female | EA        | 33  | C2        | Female | EA        | 35  |
| M3                              | Female | EA        | 36  | C3        | Female | EA        | 35  |
| M4                              | Female | AA        | 38  | C4        | Female | AA        | 38  |
| M5                              | Female | EA        | 49  | C5        | Female | EA        | 47  |
| M6                              | Female | EA        | 56  | C6        | Female | EA        | 60  |
| M7                              | Female | AA        | 60  | C7        | Female | AA        | 62  |
| M8                              | Female | EA        | 66  | C8        | Female | EA        | 63  |
| <b>Discoid Rash</b>             |        |           |     |           |        |           |     |
| D1                              | Female | EA        | 58  | C9        | Female | EA        | 53  |
| D2                              | Female | EA        | 56  | C10       | Female | EA        | 57  |
| D3                              | Female | AA        | 56  | C11       | Female | AA        | 56  |
| D4                              | Female | EA        | 47  | C12       | Female | EA        | 43  |
| D5                              | Female | AA        | 54  | C13       | Female | AA        | 58  |
| D6                              | Female | AA        | 25  | C14       | Female | AA        | 26  |
| D7                              | Female | EA        | 56  | C15       | Female | EA        | 60  |
| D8                              | Female | AA        | 62  | C16       | Female | AA        | 57  |
| <b>No Cutaneous Involvement</b> |        |           |     |           |        |           |     |
| N1                              | Female | AA        | 23  | C17       | Female | AA        | 20  |
| N2                              | Female | EA        | 34  | C18       | Female | EA        | 30  |
| N3                              | Female | EA        | 36  | C19       | Female | EA        | 41  |
| N4                              | Female | AA        | 42  | C20       | Female | AA        | 41  |
| N5                              | Female | AA        | 50  | C21       | Female | AA        | 52  |
| N6                              | Female | EA        | 54  | C22       | Female | EA        | 50  |
| N7                              | Female | AA        | 57  | C23       | Female | AA        | 57  |
| N8                              | Female | EA        | 64  | C24       | Female | EA        | 66  |

AA=African-American; EA=European-American.

**Supplementary Table 2:** American College of Rheumatology classification criteria for SLE in patients with either malar rash, discoid rash, or neither cutaneous manifestation.

| Sample ID                       | Age | Ethnicity | Malar Rash | Discoid Rash | Photo-sensitivity | Oral Ulcers | Arthritis | Serositis | Renal Disorder | Neurologic Disorder | Hematologic Disorder | Immunologic Disorder | ANA Presence |
|---------------------------------|-----|-----------|------------|--------------|-------------------|-------------|-----------|-----------|----------------|---------------------|----------------------|----------------------|--------------|
| <b>Malar Rash</b>               |     |           |            |              |                   |             |           |           |                |                     |                      |                      |              |
| M1                              | 22  | EA        | X          |              | X                 |             | X         | X         |                |                     |                      | X                    | X            |
| M2                              | 33  | EA        | X          |              | X                 | X           | X         |           | X              |                     |                      | X                    | X            |
| M3                              | 36  | EA        | X          |              |                   | X           |           |           |                |                     | X                    | X                    | X            |
| M4                              | 38  | AA        | X          |              | X                 |             | X         |           |                |                     | X                    | X                    | X            |
| M5                              | 49  | EA        | X          |              | X                 |             | X         |           | X              |                     | X                    | X                    | X            |
| M6                              | 56  | EA        | X          |              | X                 |             | X         |           |                |                     | X                    | X                    | X            |
| M7                              | 60  | AA        | X          |              | X                 | X           | X         |           |                |                     |                      | X                    | X            |
| M8                              | 66  | EA        | X          |              |                   |             | X         | X         |                |                     |                      | X                    |              |
| <b>Discoid Rash</b>             |     |           |            |              |                   |             |           |           |                |                     |                      |                      |              |
| D1                              | 58  | EA        |            | X            |                   | X           | X         |           |                |                     | X                    | X                    | X            |
| D2                              | 56  | EA        |            | X            | X                 |             | X         |           | X              |                     |                      | X                    | X            |
| D3                              | 56  | AA        |            | X            | X                 |             |           |           |                |                     |                      | X                    | X            |
| D4                              | 47  | EA        |            | X            | X                 | X           |           |           |                |                     |                      | X                    | X            |
| D5                              | 54  | AA        |            | X            |                   |             |           |           | X              | X                   | X                    | X                    | X            |
| D6                              | 25  | AA        |            | X            | X                 | X           | X         | X         |                |                     | X                    | X                    | X            |
| D7                              | 56  | EA        |            | X            |                   |             |           | X         | X              |                     | X                    | X                    | X            |
| D8                              | 62  | AA        |            | X            | X                 | X           | X         |           |                |                     | X                    |                      | X            |
| <b>No Cutaneous Involvement</b> |     |           |            |              |                   |             |           |           |                |                     |                      |                      |              |
| N1                              | 23  | AA        |            |              |                   |             |           |           | X              | X                   |                      | X                    | X            |
| N2                              | 34  | EA        |            |              |                   |             |           |           |                | X                   | X                    | X                    | X            |
| N3                              | 36  | EA        |            |              |                   |             | X         |           |                |                     | X                    | X                    | X            |
| N4                              | 42  | AA        |            |              |                   |             | X         | X         | X              |                     |                      | X                    | X            |
| N5                              | 50  | AA        |            |              |                   | X           | X         |           |                |                     | X                    | X                    | X            |
| N6                              | 54  | EA        |            |              | X                 |             | X         |           |                |                     | X                    | X                    |              |
| N7                              | 57  | AA        |            |              | X                 |             | X         |           |                |                     | X                    |                      | X            |
| N8                              | 64  | EA        |            |              | X                 |             |           | X         |                |                     |                      | X                    | X            |

AA=African-American; EA=European-American.

**Supplementary Table 3:** SLEDAI scores and criteria, and background medications at the time of enrolment of the SLE patients included in this study.

| Sample ID                       | Age | Ethnicity | SLEDAI Score | SLEDAI Criteria at the Time of Blood Draw  | Medications   |
|---------------------------------|-----|-----------|--------------|--|---|
| <b>Malar Rash</b>               |     |           |              |  |   |
| M1                              | 22  | EA        | 10           | New rash, mucosal ulcers, pleurisy, low complement, increased DNA binding        | -   |
| M2                              | 33  | EA        | 6            | Proteinuria, low complement  | Prednisone, Azathioprine, Etanercept  |
| M3                              | 36  | EA        | 4            | Low complement, increased DNA binding  | Hydroxychloroquine  |
| M4                              | 38  | AA        | 0            | -  | Prednisone, Hydroxychloroquine, Methotrexate                                    |
| M5                              | 49  | EA        | 3            | Low complement, thrombocytopenia   | Prednisone, Mycophenolate mofetil   |
| M6                              | 56  | EA        | 0            | -  | Hydroxychloroquine, has been prescribed Cyclophosphamide                        |
| M7                              | 60  | AA        | 8            | Arthritis, new rash, low complement  | Prednisone  |
| M8                              | 66  | EA        | 2            | Increased DNA binding  | -   |
| <b>Discoid Rash</b>             |     |           |              |  |   |
| D1                              | 58  | EA        | 0            | -  | Hydroxychloroquine  |
| D2                              | 56  | EA        | 4            | Low complement, increased DNA binding  | Prednisone, Hydroxychloroquine, Mycophenolate mofetil                           |
| D3                              | 56  | AA        | 2            | Increased DNA binding  | Hydroxychloroquine  |
| D4                              | 47  | EA        | 0            | -  | Prednisone, Mycophenolate mofetil   |
| D5                              | 54  | AA        | 4            | Proteinuria  | Hydroxychloroquine, Mycophenolate mofetil, has been prescribed Cyclophosphamide |
| D6                              | 25  | AA        | 13           | Arthritis, new rash, alopecia, low complement, increased DNA binding, leukopenia | Hydroxychloroquine  |
| D7                              | 56  | EA        | 0            | -  | Prednisone  |
| D8                              | 62  | AA        | 2            | Alopecia   | Prednisone, Hydroxychloroquine  |
| <b>No Cutaneous Involvement</b> |     |           |              |  |   |
| N1                              | 23  | AA        | 0            | -  | Prednisone, Hydroxychloroquine, Mycophenolate mofetil                           |
| N2                              | 34  | EA        | 2            | Low complement   | Hydroxychloroquine  |
| N3                              | 36  | EA        | 0            | -  | Hydroxychloroquine  |
| N4                              | 42  | AA        | 4            | Low complement, increased DNA binding  | Hydroxychloroquine, Azathioprine  |
| N5                              | 50  | AA        | 4            | Arthritis  | Hydroxychloroquine, Mycophenolate mofetil                                       |
| N6                              | 54  | EA        | 10           | Arthritis, hematuria, increased DNA binding                                      | Prednisone, has been prescribed Cyclophosphamide                                |
| N7                              | 57  | AA        | 2            | Alopecia   | Hydroxychloroquine  |
| N8                              | 64  | EA        | 2            | Increased DNA binding  | Hydroxychloroquine  |

AA=African-American; EA=European-American.

**Supplementary Table 4:** Differentially methylated CG sites in naïve CD4+ T cells from SLE patients with **A.** malar rash, **B.** discoid rash, or **C.** neither cutaneous involvement compared to respective healthy matched controls.

**A.**

**Malar Rash**

| CG Site ID             | Mean $\beta$ Case | Mean $\beta$ Control | $\Delta\beta$ | DiffScore | Location (HG19)  | Gene Name  | Gene-Relative Location                            | CGI-Relative Location | Enhancer |
|------------------------|-------------------|----------------------|---------------|-----------|------------------|--|---|-----------------------|----------|
| <b>Hypomethylation</b> |                   |                      |               |           |                  |  |   |                       |          |
| cg21549285             | 0.31              | 0.66                 | -0.35         | -338.82   | Chr21: 42799141  | <i>MX1, MX1</i>  | 5'UTR, 5'UTR                                      | S_Shore               | FALSE    |
| cg14392283             | 0.61              | 0.91                 | -0.30         | -338.82   | Chr8: 144103587  | <i>LY6E, LY6E</i>                                      | 3'UTR, 3'UTR                                      | N_Shelf               | FALSE    |
| cg15065340             | 0.40              | 0.68                 | -0.28         | -289.58   | Chr3: 195632915  | <i>TNK2</i>  | 5'UTR   | N_Shelf               | FALSE    |
| cg11404906             | 0.56              | 0.84                 | -0.27         | -338.82   | Chr6: 32551749   | <i>HLA-DRB1</i>  | Body  | N_Shore               | FALSE    |
| cg06981309             | 0.40              | 0.66                 | -0.27         | -246.35   | Chr3: 146260954  | <i>PLSCR1</i>  | 5'UTR   | N_Shore               | FALSE    |
| cg09885502             | 0.37              | 0.63                 | -0.27         | -242.35   | Chr20: 57463991  | <i>GNAS, GNAS, GNAS, GNAS</i>                          | 3'UTR, TSS200, 3'UTR, Body                        | Island                | FALSE    |
| cg01028142             | 0.59              | 0.85                 | -0.26         | -338.82   | Chr2: 7004578    | <i>CMPK2</i>   | Body  | N_Shore               | FALSE    |
| cg08122652             | 0.50              | 0.76                 | -0.26         | -265.15   | Chr3: 122281939  | <i>PARP9, PARP9, DTX3L, PARP9, PARP9, PARP9, PARP9</i> | 5'UTR, 5'UTR, TSS1500, 5'UTR, 5'UTR, 5'UTR, 5'UTR | N_Shore               | FALSE    |
| cg03607951             | 0.47              | 0.72                 | -0.25         | -221.63   | Chr1: 79085586   | <i>IFI44L</i>  | TSS1500   |                       | FALSE    |
| cg10090844             | 0.27              | 0.51                 | -0.24         | -200.61   | Chr12: 132167226 |  |   | N_Shelf               | TRUE     |
| cg17384323             | 0.47              | 0.71                 | -0.24         | -201.84   | Chr4: 169242366  |  |   | S_Shelf               | FALSE    |
| cg01821018             | 0.60              | 0.84                 | -0.24         | -272.08   | Chr1: 59043280   | <i>TACSTD2</i>   | TSS200  | Island                | TRUE     |
| cg05696877             | 0.30              | 0.54                 | -0.23         | -182.16   | Chr1: 79088769   | <i>IFI44L</i>  | 5'UTR   |                       | FALSE    |
| cg14286514             | 0.36              | 0.58                 | -0.23         | -167.02   | Chr9: 32525315   | <i>DDX58</i>   | Body  | N_Shore               | TRUE     |
| cg14212360             | 0.57              | 0.80                 | -0.23         | -220.29   | Chr4: 89302999   | <i>HERC6, HERC6</i>                                    | Body, Body  | S_Shelf               | FALSE    |
| cg05552874             | 0.56              | 0.79                 | -0.22         | -204.94   | Chr10: 91153143  | <i>IFIT1</i>   | Body  |                       | FALSE    |
| cg02891314             | 0.49              | 0.71                 | -0.22         | -171.35   | Chr5: 179741120  | <i>GFPT2</i>   | Body  | Island                | FALSE    |
| cg23221052             | 0.45              | 0.67                 | -0.22         | -158.78   | Chr5: 179740743  | <i>GFPT2</i>   | Body  | Island                | FALSE    |
| cg22862003             | 0.46              | 0.68                 | -0.22         | -156.59   | Chr21: 42797588  | <i>MX1, MX1</i>  | TSS1500, 5'UTR                                    | N_Shore               | FALSE    |
| cg04863005             | 0.53              | 0.74                 | -0.21         | -158.15   | Chr1: 59043208   | <i>TACSTD2</i>   | TSS200  | Island                | TRUE     |
| cg00274965             | 0.32              | 0.53                 | -0.20         | -130.08   | Chr21: 34405681  |  |   | Island                | FALSE    |
| cg13944838             | 0.52              | 0.73                 | -0.20         | -144.11   | Chr5: 179740914  | <i>GFPT2</i>   | Body  | Island                | FALSE    |
| cg26220594             | 0.28              | 0.48                 | -0.20         | -129.25   | Chr1: 19110978   |  |   | S_Shore               | TRUE     |
| cg18686270             | 0.61              | 0.80                 | -0.19         | -163.85   | Chr3: 146258875  | <i>PLSCR1</i>  | 5'UTR   | N_Shelf               | FALSE    |
| cg24853868             | 0.39              | 0.59                 | -0.19         | -112.67   | Chr1: 146555624  |  |   | N_Shore               | FALSE    |
| cg00855901             | 0.24              | 0.43                 | -0.19         | -118.22   | Chr1: 79085765   | <i>IFI44L</i>  | TSS1500   |                       | FALSE    |
| cg01694488             | 0.78              | 0.96                 | -0.18         | -328.93   | Chr4: 1580172    |  |   | Island                | FALSE    |
| cg16523850             | 0.42              | 0.60                 | -0.18         | -95.04    | Chr6: 54156824   |  |   |                       | TRUE     |
| cg16301894             | 0.53              | 0.71                 | -0.18         | -105.55   | Chr4: 129389744  |  |   |                       | TRUE     |
| cg23549331             | 0.36              | 0.54                 | -0.18         | -89.64    | Chr8: 6189008    |  |   |                       | TRUE     |

|            |      |      |       |         |                  |   |   |         |       |
|------------|------|------|-------|---------|------------------|---|---|---------|-------|
| cg12051710 | 0.25 | 0.43 | -0.17 | -97.68  | Chr12: 2989070   | <i>C12orf32, C12orf32, C12orf32</i>             | Body, Body, Body                            | S_Shelf | FALSE |
| cg16080552 | 0.48 | 0.66 | -0.17 | -89.43  | Chr1: 59043199   | <i>TACSTD2</i>                                  | TSS200                                      | Island  | TRUE  |
| cg01238044 | 0.19 | 0.36 | -0.17 | -106.32 | Chr22: 24384105  | <i>GSTT1</i>                                    | Body  | N_Shore | FALSE |
| cg17980508 | 0.43 | 0.60 | -0.17 | -79.50  | Chr1: 79085713   | <i>IFI44L</i>                                   | TSS1500                                     |         | FALSE |
| cg13200575 | 0.47 | 0.63 | -0.16 | -78.42  | Chr17: 38096571  |   |   |         | FALSE |
| cg06188083 | 0.20 | 0.37 | -0.16 | -96.21  | Chr10: 91093005  | <i>IFIT3, IFIT3</i>                             | Body, Body                                  |         | TRUE  |
| cg27107893 | 0.74 | 0.90 | -0.16 | -169.86 | Chr5: 142776274  | <i>NR3C1, NR3C1, NR3C1, NR3C1, NR3C1, NR3C1</i> | Body, Body, Body, Body, Body                |         | TRUE  |
| cg07833467 | 0.39 | 0.54 | -0.16 | -68.81  | Chr22: 50986511  | <i>KLHDC7B, KLHDC7B</i>                         | 5'UTR, 1stExon                              | Island  | FALSE |
| cg05073382 | 0.70 | 0.86 | -0.16 | -135.21 | Chr8: 2045798    | <i>MYOM2</i>                                    | Body  | N_Shore | FALSE |
| cg16699148 | 0.42 | 0.58 | -0.16 | -67.46  | Chr1: 59043255   | <i>TACSTD2</i>                                  | TSS200                                      | Island  | TRUE  |
| cg16824113 | 0.54 | 0.69 | -0.16 | -76.54  | Chr12: 132166485 |   |   |         | TRUE  |
| cg15708909 | 0.64 | 0.80 | -0.15 | -101.71 | Chr6: 32487314   | <i>HLA-DRB5</i>                                 | Body  | N_Shelf | FALSE |
| cg00639218 | 0.24 | 0.40 | -0.15 | -78.00  | ChrY: 14096487   |   |   | N_Shelf | FALSE |
| cg08822075 | 0.57 | 0.72 | -0.15 | -78.80  | Chr7: 26193607   | <i>NFE2L3</i>                                   | Body  | S_Shore | TRUE  |
| cg04234412 | 0.26 | 0.41 | -0.15 | -73.77  | Chr22: 24373322  | <i>LOC391322</i>                                | Body  | Island  | FALSE |
| cg20053110 | 0.64 | 0.79 | -0.15 | -97.71  | Chr6: 37617864   | <i>MDGA1</i>                                    | Body  | Island  | TRUE  |
| cg21159568 | 0.60 | 0.75 | -0.15 | -83.46  | Chr7: 2445331    | <i>CHST12</i>                                   | 5'UTR                                       | S_Shore | FALSE |
| cg12397463 | 0.63 | 0.78 | -0.15 | -91.02  | Chr6: 33128825   |   |   | N_Shore | FALSE |
| cg13218423 | 0.47 | 0.62 | -0.15 | -63.95  | Chr11: 89735737  | <i>TRIM53</i>                                   | TSS200                                      |         | FALSE |
| cg09768983 | 0.53 | 0.68 | -0.15 | -67.57  | Chr4: 183935060  |   |   |         | FALSE |
| cg25303761 | 0.32 | 0.47 | -0.15 | -62.62  | Chr1: 31256028   |   |   |         | TRUE  |
| cg22992730 | 0.47 | 0.62 | -0.15 | -60.80  | Chr19: 4784940   |   |   | N_Shore | FALSE |
| cg09976051 | 0.47 | 0.62 | -0.15 | -60.65  | Chr4: 178362394  | <i>AGA</i>                                      | Body  | N_Shore | FALSE |
| cg18792536 | 0.30 | 0.45 | -0.15 | -63.09  | Chr7: 76145562   | <i>UPK3B, UPK3B</i>                             | 3'UTR, 3'UTR                                | Island  | FALSE |
| cg12110437 | 0.16 | 0.31 | -0.15 | -90.48  | Chr8: 144098888  | <i>LY6E, LY6E, LOC100133669</i>                 | TSS1500, TSS1500, Body                      | N_Shore | FALSE |
| cg21656205 | 0.37 | 0.51 | -0.15 | -58.86  | Chr20: 43439688  | <i>RIMS4</i>                                    | TSS1500                                     | S_Shore | FALSE |
| cg20790798 | 0.52 | 0.67 | -0.15 | -63.62  | Chr5: 1857306    |   |   | Island  | FALSE |
| cg10213302 | 0.48 | 0.63 | -0.15 | -59.33  | ChrY: 2802975    | <i>ZFY, ZFY, ZFY</i>                            | TSS1500, TSS200, TSS1500                    | Island  | FALSE |
| cg21699330 | 0.36 | 0.51 | -0.14 | -56.52  | Chr7: 26193032   | <i>NFE2L3</i>                                   | Body  | S_Shore | FALSE |
| cg16399632 | 0.67 | 0.81 | -0.14 | -93.05  | Chr4: 1244006    | <i>CTBP1, CTBP1, C4orf42</i>                    | TSS1500, TSS1500, TSS200                    | Island  | FALSE |
| cg26479374 | 0.70 | 0.84 | -0.14 | -103.85 | Chr4: 1243980    | <i>CTBP1, CTBP1, C4orf42</i>                    | TSS1500, TSS1500, TSS200                    | Island  | FALSE |
| cg20062691 | 0.53 | 0.67 | -0.14 | -59.86  | Chr1: 949392     | <i>ISG15</i>                                    | Body  | Island  | TRUE  |
| cg20971158 | 0.50 | 0.64 | -0.14 | -55.90  | Chr11: 35159382  | <i>CD44, CD44, CD44, CD44, CD44</i>             | TSS1500, TSS1500, TSS1500, TSS1500, TSS1500 | N_Shore | FALSE |
| cg18085176 | 0.50 | 0.64 | -0.14 | -55.51  | Chr4: 7939940    | <i>AFAP1, AFAP1</i>                             | 5'UTR, 5'UTR                                | N_Shore | FALSE |
| cg18451016 | 0.50 | 0.64 | -0.14 | -55.93  | Chr1: 38461880   |   |   | Island  | FALSE |

|            |      |      |       |         |                 |   |  |         |       |
|------------|------|------|-------|---------|-----------------|---|--|---------|-------|
| cg27192248 | 0.28 | 0.42 | -0.14 | -58.61  | Chr15: 65285669 |   |  | S_Shelf | FALSE |
| cg24100841 | 0.60 | 0.74 | -0.14 | -68.21  | Chr6: 29649024  |   |  |         | FALSE |
| cg23264429 | 0.52 | 0.66 | -0.14 | -56.65  | Chr10: 90642003 | STAMBPL1  | 5'UTR                                    | S_Shore | FALSE |
| cg21593149 | 0.65 | 0.79 | -0.14 | -81.49  | Chr4: 1300163   | MAEA, MAEA  | Body, Body                               | N_Shelf | FALSE |
| cg24796644 | 0.65 | 0.79 | -0.14 | -78.34  | Chr6: 37617956  | MDGA1   | Body                                     | Island  | TRUE  |
| cg14951497 | 0.26 | 0.40 | -0.14 | -59.69  | Chr2: 191875807 | STAT1, STAT1  | 5'UTR, 5'UTR                             | N_Shelf | FALSE |
| cg06343673 | 0.63 | 0.77 | -0.14 | -72.14  | Chr17: 78778232 | RPTOR, RPTOR  | Body, Body                               | S_Shelf | FALSE |
| cg26227225 | 0.34 | 0.48 | -0.14 | -51.08  | Chr1: 2121039   | C1orf86,<br>LOC100128003,<br>C1orf86                                | Body, Body,<br>3'UTR                     | Island  | FALSE |
| cg27207756 | 0.29 | 0.42 | -0.14 | -54.56  | Chr4: 1607291   |   |  |         | FALSE |
| cg02334775 | 0.49 | 0.62 | -0.14 | -50.98  | Chr15: 89182676 | ISG20   | Body                                     |         | FALSE |
| cg06889571 | 0.75 | 0.88 | -0.14 | -122.45 | Chr10: 1416791  | ADARB2  | Body                                     | S_Shore | FALSE |
| cg08926253 | 0.60 | 0.74 | -0.14 | -62.38  | Chr11: 614761   | IRF7, IRF7, IRF7  | Body, Body, Body                         | Island  | TRUE  |
| cg23942717 | 0.73 | 0.87 | -0.14 | -107.63 | Chr7: 56437746  |   |  | S_Shore | FALSE |
| cg15085883 | 0.47 | 0.60 | -0.14 | -48.22  | Chr12: 68848994 |   |  |         | TRUE  |
| cg00676801 | 0.22 | 0.36 | -0.13 | -60.46  | Chr2: 191876673 | STAT1, STAT1  | 5'UTR, 5'UTR                             | N_Shore | FALSE |
| cg08511818 | 0.37 | 0.50 | -0.13 | -46.91  | Chr20: 30104637 | HM13, HM13,<br>HM13, HM13   | Body, Body,<br>Body, Body                | S_Shore | TRUE  |
| cg10690152 | 0.05 | 0.18 | -0.13 | -140.32 | Chr6: 31698089  | DDAH2   | TSS200                                   | Island  | FALSE |
| cg14964336 | 0.13 | 0.26 | -0.13 | -86.70  | Chr4: 1523275   |   |  | Island  | FALSE |
| cg11222703 | 0.55 | 0.68 | -0.13 | -52.63  | Chr4: 190983569 |   |  | N_Shelf | FALSE |
| cg26328633 | 0.34 | 0.48 | -0.13 | -47.27  | Chr5: 135416394 | MIR886  | TSS200                                   | Island  | FALSE |
| cg18071071 | 0.16 | 0.29 | -0.13 | -75.83  | Chr4: 1558451   |   |  | S_Shore | FALSE |
| cg23066280 | 0.50 | 0.64 | -0.13 | -48.34  | Chr7: 158032496 | PTPRN2, PTPRN2,<br>PTPRN2   | Body, Body, Body                         |         | FALSE |
| cg17251423 | 0.57 | 0.71 | -0.13 | -54.78  | Chr5: 139088815 |   |  | Island  | FALSE |
| cg15935070 | 0.55 | 0.68 | -0.13 | -52.04  | Chr6: 29944146  | HCG9  | Body                                     | N_Shore | FALSE |
| cg26764761 | 0.64 | 0.77 | -0.13 | -66.39  | Chr16: 87682142 | JPH3  | Body                                     | S_Shelf | FALSE |
| cg18367631 | 0.55 | 0.68 | -0.13 | -51.34  | Chr7: 653309    | PRKAR1B,<br>PRKAR1B,<br>PRKAR1B,<br>PRKAR1B,<br>PRKAR1B,<br>PRKAR1B | Body, Body,<br>Body, Body,<br>Body, Body |         | FALSE |
| cg21359950 | 0.52 | 0.65 | -0.13 | -47.41  | Chr12: 94083470 | CRADD   | Body                                     |         | TRUE  |
| cg15287443 | 0.56 | 0.69 | -0.13 | -50.85  | Chr3: 147121229 | ZIC4, ZIC4, ZIC4  | Body, 5'UTR,<br>Body                     |         | TRUE  |
| cg26207766 | 0.47 | 0.60 | -0.13 | -43.31  | Chr2: 242763794 |   |  | N_Shelf | FALSE |
| cg04554929 | 0.19 | 0.32 | -0.13 | -62.68  | Chr8: 105342491 |   |  | Island  | FALSE |
| cg21079003 | 0.53 | 0.66 | -0.13 | -46.69  | Chr15: 93615146 | RGMA, RGMA,<br>RGMA, RGMA,<br>RGMA, RGMA                            | Body, Body,<br>Body, Body,<br>Body, Body | N_Shore | FALSE |
| cg01948202 | 0.10 | 0.23 | -0.13 | -93.53  | Chr3: 122400474 | PARP14  | Body                                     | S_Shore | FALSE |
| cg05600581 | 0.33 | 0.46 | -0.13 | -43.97  | ChrX: 134232907 | NCRNA00087  | TSS200                                   | Island  | FALSE |
| cg13458803 | 0.44 | 0.57 | -0.13 | -42.00  | Chr3: 119276917 | CD80  | 5'UTR                                    |         | FALSE |
| cg25340688 | 0.32 | 0.45 | -0.13 | -44.36  | Chr5: 135416398 | MIR886  | TSS200                                   | Island  | FALSE |
| cg20167074 | 0.61 | 0.74 | -0.13 | -55.45  | Chr1: 151967023 | S100A10   | TSS1500                                  | S_Shore | FALSE |

|            |      |      |       |         |                  |   |                            |         |       |
|------------|------|------|-------|---------|------------------|---|----------------------------|---------|-------|
| cg18025438 | 0.40 | 0.53 | -0.13 | -41.41  | Chr1: 228756789  |   |                            | Island  | FALSE |
| cg21351392 | 0.66 | 0.79 | -0.13 | -65.52  | Chr6: 161607487  | <i>AGPAT4</i>                             | Body                       |         | TRUE  |
| cg16486109 | 0.38 | 0.50 | -0.13 | -41.47  | Chr11: 613632    | <i>IRF7, IRF7, IRF7</i>                   | Body, Body, Body           | N_Shore | FALSE |
| cg07111834 | 0.54 | 0.67 | -0.13 | -46.54  | Chr1: 114402309  | <i>PTPN22, PTPN22</i>                     | Body, Body                 |         | TRUE  |
| cg01079652 | 0.71 | 0.84 | -0.13 | -84.51  | Chr1: 79118191   | <i>IFI44</i>                              | Body                       |         | FALSE |
| cg18749349 | 0.61 | 0.74 | -0.13 | -54.88  | Chr11: 16431523  | <i>SOX6, SOX6</i>                         | 5'UTR, TSS1500             |         | FALSE |
| cg00168785 | 0.29 | 0.42 | -0.13 | -45.26  | Chr2: 160142643  | <i>WDSUB1, WDSUB1, WDSUB1</i>             | 5'UTR, 5'UTR, 5'UTR        | Island  | FALSE |
| cg07971089 | 0.33 | 0.46 | -0.13 | -42.56  | Chr8: 144629702  |   |                            | N_Shelf | FALSE |
| cg12510708 | 0.66 | 0.79 | -0.13 | -64.72  | Chr7: 26193805   | <i>NFE2L3</i>                             | Body                       | S_Shore | TRUE  |
| cg01175610 | 0.21 | 0.33 | -0.13 | -55.52  | Chr12: 12224246  | <i>BCL2L14, BCL2L14, BCL2L14</i>          | 5'UTR, TSS200, TSS200      |         | TRUE  |
| cg14344620 | 0.64 | 0.76 | -0.13 | -57.89  | Chr2: 3418831    | <i>TTC15</i>                              | Body                       |         | FALSE |
| cg11168104 | 0.57 | 0.69 | -0.13 | -46.56  | Chr5: 1857477    |   |                            | Island  | FALSE |
| cg08124030 | 0.71 | 0.84 | -0.13 | -79.71  | Chr3: 149095283  | <i>TM4SF1</i>                             | 1stExon                    |         | FALSE |
| cg10599438 | 0.32 | 0.45 | -0.12 | -40.84  | Chr19: 844589    | <i>PRTN3</i>                              | Body                       | N_Shore | FALSE |
| cg07480608 | 0.22 | 0.34 | -0.12 | -51.62  | Chr3: 15352493   | <i>SH3BP5, SH3BP5</i>                     | Body, 5'UTR                |         | TRUE  |
| cg25606201 | 0.40 | 0.52 | -0.12 | -37.80  | Chr5: 180614858  |   |                            | N_Shore | FALSE |
| cg15798862 | 0.38 | 0.50 | -0.12 | -37.96  | Chr7: 76129360   | <i>DTX2, DTX2, DTX2, DTX2</i>             | Body, Body, Body, Body     | N_Shore | FALSE |
| cg15041044 | 0.76 | 0.88 | -0.12 | -102.79 | Chr7: 23019795   | <i>FAM126A</i>                            | Body                       |         | TRUE  |
| cg13420273 | 0.73 | 0.85 | -0.12 | -82.41  | Chr7: 18810212   | <i>HDAC9, HDAC9, HDAC9, HDAC9</i>         | Body, Body, Body, Body     |         | TRUE  |
| cg24113243 | 0.62 | 0.74 | -0.12 | -50.91  | Chr12: 132882028 | <i>GALNT9</i>                             | Body                       | Island  | FALSE |
| cg00256231 | 0.17 | 0.29 | -0.12 | -59.86  | Chr17: 77916733  | <i>TBC1D16</i>                            | Body                       | Island  | TRUE  |
| cg20529645 | 0.42 | 0.55 | -0.12 | -36.39  | Chr4: 5886898    | <i>CRMP1, CRMP1</i>                       | Body, Body                 | N_Shelf | FALSE |
| cg02253142 | 0.63 | 0.75 | -0.12 | -51.06  | Chr15: 52048211  | <i>TMOD2, TMOD2</i>                       | 5'UTR, 5'UTR               | S_Shelf | FALSE |
| cg11186706 | 0.74 | 0.86 | -0.12 | -83.61  | Chr14: 54815745  |   |                            |         | TRUE  |
| cg17322044 | 0.67 | 0.79 | -0.12 | -60.32  | Chr12: 125140105 |   |                            |         | TRUE  |
| cg08477687 | 0.36 | 0.48 | -0.12 | -36.30  | Chr1: 566570     | <i>MIR1977</i>                            | TSS1500                    |         | FALSE |
| cg23280506 | 0.40 | 0.52 | -0.12 | -35.61  | Chr17: 14201938  |   |                            | Island  | FALSE |
| cg16985233 | 0.65 | 0.77 | -0.12 | -54.17  | Chr15: 43806249  |   |                            | S_Shelf | FALSE |
| cg03513464 | 0.55 | 0.67 | -0.12 | -39.88  | Chr1: 58898672   |   |                            |         | TRUE  |
| cg04122858 | 0.79 | 0.91 | -0.12 | -118.35 | Chr3: 46799010   |   |                            | S_Shore | FALSE |
| cg24550026 | 0.37 | 0.49 | -0.12 | -35.33  | Chr1: 114430031  | <i>BCL2L15, BCL2L15</i>                   | 1stExon, 5'UTR             |         | FALSE |
| cg03142697 | 0.28 | 0.40 | -0.12 | -39.68  | Chr21: 36258497  | <i>RUNX1, RUNX1, RUNX1</i>                | Body, Body, Body           | N_Shore | FALSE |
| cg05276469 | 0.20 | 0.32 | -0.12 | -50.58  | Chr17: 16570473  |   |                            | Island  | FALSE |
| cg07629776 | 0.40 | 0.52 | -0.12 | -34.26  | Chr10: 13972210  | <i>FRMD4A</i>                             | Body                       |         | TRUE  |
| cg13144059 | 0.83 | 0.95 | -0.12 | -168.18 | Chr2: 201245077  | <i>SPATS2L, SPATS2L, SPATS2L, SPATS2L</i> | 5'UTR, 5'UTR, 5'UTR, 5'UTR |         | TRUE  |
| cg25753473 | 0.14 | 0.26 | -0.12 | -64.23  | Chr6: 170532835  |   |                            | S_Shelf | FALSE |
| cg19046167 | 0.78 | 0.90 | -0.12 | -107.68 | Chr17: 80928561  | <i>B3GNTL1</i>                            | Body                       | N_Shore | FALSE |
| cg01911981 | 0.84 | 0.96 | -0.12 | -190.45 | Chr8: 39380341   | <i>ADAM3A, ADAM3A, ADAM3A</i>             | Body, Body, Body           | Island  | FALSE |



|            |      |      |       |         |                  |  |                                       |         |       |
|------------|------|------|-------|---------|------------------|--|---------------------------------------|---------|-------|
| cg24341059 | 0.78 | 0.90 | -0.12 | -103.37 | Chr8: 121604940  | <i>SNTB1</i>                                       | Body                                  |         | TRUE  |
| cg11652636 | 0.08 | 0.19 | -0.12 | -92.05  | Chr2: 55450823   | <i>C2orf63, C2orf63</i>                            | 5'UTR, 5'UTR                          | Island  | FALSE |
| cg00124993 | 0.31 | 0.43 | -0.12 | -36.67  | Chr5: 135416412  | <i>MIR886</i>                                      | TSS200                                | Island  | FALSE |
| cg15115365 | 0.53 | 0.65 | -0.12 | -36.70  | Chr5: 88384656   |  |                                       |         | TRUE  |
| cg03995300 | 0.43 | 0.55 | -0.12 | -33.49  | Chr17: 5019989   | <i>ZNF232</i>                                      | 5'UTR                                 | S_Shore | FALSE |
| cg01636599 | 0.27 | 0.39 | -0.12 | -39.91  | Chr19: 639386    | <i>FGF22</i>                                       | TSS1500                               | Island  | TRUE  |
| cg16717578 | 0.73 | 0.85 | -0.12 | -76.98  | Chr19: 867030    |  |                                       | Island  | FALSE |
| cg13909895 | 0.31 | 0.43 | -0.12 | -36.10  | Chr22: 51066142  | <i>ARSA, ARSA, ARSA, ARSA, ARSA</i>                | 1stExon, Body, Body, Body, 5'UTR      | Island  | FALSE |
| cg14939821 | 0.44 | 0.56 | -0.12 | -33.16  | Chr10: 128947230 | <i>DOCK1, FAM196A</i>                              | Body, Body                            |         | TRUE  |
| cg03168497 | 0.26 | 0.38 | -0.12 | -40.07  | Chr17: 48586147  | <i>MYCBPAP</i>                                     | Body                                  | Island  | FALSE |
| cg11478607 | 0.12 | 0.23 | -0.12 | -69.68  | Chr22: 24384400  | <i>GSTT1</i>                                       | TSS200                                | Island  | FALSE |
| cg25120325 | 0.75 | 0.86 | -0.12 | -80.26  | Chr10: 118380370 | <i>PNLIPRP2</i>                                    | TSS200                                |         | FALSE |
| cg04602696 | 0.57 | 0.68 | -0.12 | -37.87  | Chr16: 88846723  | <i>FAM38A</i>                                      | Body                                  | S_Shore | TRUE  |
| cg25034424 | 0.69 | 0.81 | -0.12 | -59.53  | Chr4: 1513089    |  |                                       | N_Shore | FALSE |
| cg03829194 | 0.71 | 0.83 | -0.12 | -65.77  | Chr16: 875571    |  |                                       | Island  | TRUE  |
| cg16853860 | 0.45 | 0.57 | -0.12 | -32.21  | Chr6: 32823116   | <i>PSMB9, PSMB9, TAP1</i>                          | Body, Body, TSS1500                   | S_Shore | FALSE |
| cg04974804 | 0.69 | 0.80 | -0.12 | -57.37  | Chr1: 23521815   | <i>HTR1D</i>                                       | TSS1500                               |         | FALSE |
| cg02978505 | 0.39 | 0.51 | -0.12 | -31.93  | Chr16: 85292322  |  |                                       |         | TRUE  |
| cg02869559 | 0.32 | 0.44 | -0.12 | -33.96  | Chr21: 36259067  | <i>RUNX1, RUNX1, RUNX1</i>                         | Body, Body, Body                      | Island  | FALSE |
| cg06236987 | 0.79 | 0.90 | -0.12 | -103.21 | Chr6: 114225023  | <i>FLJ34503</i>                                    | TSS1500                               |         | TRUE  |
| cg20481287 | 0.53 | 0.64 | -0.12 | -34.35  | Chr12: 12224457  | <i>BCL2L14, BCL2L14, BCL2L14, BCL2L14, BCL2L14</i> | 5'UTR, 5'UTR, 1stExon, 5'UTR, 1stExon |         | TRUE  |
| cg16379462 | 0.77 | 0.88 | -0.12 | -88.82  | Chr14: 55119082  | <i>SAMD4A, SAMD4A</i>                              | Body, Body                            |         | TRUE  |
| cg02148547 | 0.60 | 0.72 | -0.12 | -40.36  | Chr14: 21457502  | <i>METT11D1, METT11D1</i>                          | TSS1500, TSS1500                      | N_Shore | FALSE |
| cg06536614 | 0.34 | 0.45 | -0.12 | -32.91  | Chr5: 135416381  | <i>MIR886</i>                                      | TSS200                                | Island  | FALSE |
| cg02830749 | 0.70 | 0.82 | -0.11 | -59.50  | Chr4: 154451068  | <i>KIAA0922, KIAA0922</i>                          | Body, Body                            |         | TRUE  |
| cg12463578 | 0.49 | 0.60 | -0.11 | -31.99  | Chr6: 29644756   | <i>ZFP57</i>                                       | 1stExon                               |         | FALSE |
| cg04742550 | 0.43 | 0.54 | -0.11 | -30.80  | Chr16: 31366429  | <i>ITGAX</i>                                       | TSS200                                |         | FALSE |
| cg08534443 | 0.51 | 0.62 | -0.11 | -32.44  | Chr12: 133022550 |  |                                       | N_Shore | FALSE |
| cg00169792 | 0.30 | 0.41 | -0.11 | -34.10  | Chr20: 50418554  | <i>SALL4</i>                                       | Body                                  | Island  | FALSE |
| cg25849281 | 0.30 | 0.42 | -0.11 | -33.71  | Chr1: 8937077    | <i>ENO1</i>  | 5'UTR                                 | N_Shore | FALSE |
| cg05337761 | 0.42 | 0.53 | -0.11 | -30.11  | Chr1: 2121349    | <i>C1orf86, LOC100128003, C1orf86</i>              | Body, Body, Body                      | Island  | FALSE |
| cg25737313 | 0.43 | 0.55 | -0.11 | -29.74  | Chr19: 12899557  |  |                                       | N_Shore | FALSE |
| cg13569486 | 0.49 | 0.60 | -0.11 | -30.47  | Chr11: 8290738   |  |                                       | S_Shore | TRUE  |
| cg08787039 | 0.54 | 0.65 | -0.11 | -32.48  | Chr1: 182921857  | <i>C1orf14</i>                                     | Body                                  | Island  | FALSE |
| cg26876834 | 0.72 | 0.83 | -0.11 | -61.32  | Chr16: 2013573   | <i>SNHG9, SNORA64, SNORA10, RPS2</i>               | TSS1500, TSS1500, TSS1500, Body       | N_Shore | FALSE |
| cg06385583 | 0.20 | 0.31 | -0.11 | -42.72  | Chr2: 12596843   |  |                                       |         | TRUE  |

|            |      |      |       |         |                  |                                   |                                |         |       |
|------------|------|------|-------|---------|------------------|-----------------------------------|--------------------------------|---------|-------|
| cg18108683 | 0.77 | 0.88 | -0.11 | -81.44  | Chr7: 102477205  | <i>FBXL13, FBXL13</i>             | Body, Body                     |         | TRUE  |
| cg04380118 | 0.48 | 0.59 | -0.11 | -29.42  | Chr1: 45670624   | <i>ZSWIM5</i>                     | Body                           | N_Shore | FALSE |
| cg09704168 | 0.29 | 0.40 | -0.11 | -32.71  | Chr17: 32751554  |                                   |                                |         | TRUE  |
| cg27102141 | 0.65 | 0.76 | -0.11 | -43.78  | Chr10: 131843798 |                                   |                                | Island  | FALSE |
| cg24522654 | 0.66 | 0.77 | -0.11 | -44.14  | Chr12: 19535154  |                                   |                                |         | TRUE  |
| cg16366262 | 0.50 | 0.61 | -0.11 | -29.34  | Chr1: 1118157    | <i>TTL10, TTL10</i>               | Body, Body                     | S_Shelf | FALSE |
| cg15309053 | 0.41 | 0.52 | -0.11 | -28.06  | Chr8: 964076     |                                   |                                | S_Shore | FALSE |
| cg11834066 | 0.65 | 0.76 | -0.11 | -42.74  | ChrX: 145701413  |                                   |                                | Island  | FALSE |
| cg19751990 | 0.76 | 0.87 | -0.11 | -74.33  | Chr11: 5800287   | <i>OR52N5</i>                     | TSS1500                        |         | FALSE |
| cg11979743 | 0.02 | 0.13 | -0.11 | -130.60 | Chr20: 814510    | <i>FAM110A, FAM110A</i>           | 1stExon, 5'UTR                 | Island  | FALSE |
| cg27366964 | 0.54 | 0.65 | -0.11 | -31.17  | Chr10: 77946906  | <i>C10orf11</i>                   | Body                           |         | TRUE  |
| cg01088404 | 0.54 | 0.65 | -0.11 | -30.90  | Chr12: 48214523  | <i>HDAC7, HDAC7</i>               | TSS1500, TSS1500               | S_Shore | FALSE |
| cg17165241 | 0.60 | 0.71 | -0.11 | -36.12  | Chr11: 400385    | <i>PKP3</i>                       | Body                           | Island  | FALSE |
| cg19637330 | 0.34 | 0.45 | -0.11 | -29.30  | Chr1: 19110922   |                                   |                                | Island  | TRUE  |
| cg24506221 | 0.13 | 0.24 | -0.11 | -58.62  | Chr1: 110230401  | <i>GSTM1, GSTM1</i>               | TSS200, TSS200                 | Island  | FALSE |
| cg01664727 | 0.27 | 0.38 | -0.11 | -33.08  | Chr21: 36258423  | <i>RUNX1, RUNX1, RUNX1</i>        | Body, Body, Body               | N_Shore | FALSE |
| cg00599163 | 0.66 | 0.77 | -0.11 | -43.60  | Chr2: 162100495  |                                   |                                | N_Shore | FALSE |
| cg12765123 | 0.51 | 0.62 | -0.11 | -29.09  | Chr10: 132100019 |                                   |                                |         | FALSE |
| cg08381620 | 0.42 | 0.53 | -0.11 | -27.21  | Chr13: 24062873  |                                   |                                |         | TRUE  |
| cg16363586 | 0.22 | 0.33 | -0.11 | -38.50  | Chr19: 17516329  | <i>BST2</i>                       | 1stExon                        |         | TRUE  |
| cg15498134 | 0.68 | 0.79 | -0.11 | -46.75  | Chr1: 25246854   | <i>RUNX3, RUNX3</i>               | Body, Body                     |         | TRUE  |
| cg01406381 | 0.38 | 0.49 | -0.11 | -27.38  | Chr19: 47288263  | <i>SLC1A5, SLC1A5, SLC1A5</i>     | TSS200, Body, 5'UTR            | N_Shelf | FALSE |
| cg07777042 | 0.73 | 0.84 | -0.11 | -61.26  | Chr8: 144702879  |                                   |                                | S_Shelf | FALSE |
| cg26896946 | 0.35 | 0.46 | -0.11 | -27.87  | Chr5: 135416405  | <i>MIR886</i>                     | TSS200                         | Island  | FALSE |
| cg05282260 | 0.77 | 0.88 | -0.11 | -78.90  | Chr6: 156983263  |                                   |                                |         | FALSE |
| cg09033563 | 0.13 | 0.24 | -0.11 | -55.63  | Chr22: 24373618  | <i>LOC391322</i>                  | Body                           | Island  | FALSE |
| cg22094750 | 0.04 | 0.15 | -0.11 | -104.98 | Chr1: 1851056    | <i>TMEM52</i>                     | TSS1500                        | Island  | FALSE |
| cg06952519 | 0.78 | 0.89 | -0.11 | -83.64  | Chr17: 2057234   | <i>SMG6, SMG6</i>                 | Body, Body                     |         | FALSE |
| cg12015615 | 0.60 | 0.71 | -0.11 | -34.11  | Chr7: 55540725   | <i>VOPP1</i>                      | Body                           |         | FALSE |
| cg03834411 | 0.70 | 0.81 | -0.11 | -49.83  | Chr16: 87682036  | <i>JPH3</i>                       | Body                           | S_Shelf | FALSE |
| cg17790273 | 0.45 | 0.56 | -0.11 | -26.63  | Chr17: 49040709  | <i>SPAG9, SPAG9</i>               | 3'UTR, 3'UTR                   |         | TRUE  |
| cg05931119 | 0.65 | 0.76 | -0.11 | -40.03  | Chr6: 168569742  |                                   |                                |         | FALSE |
| cg06603074 | 0.30 | 0.41 | -0.11 | -29.66  | Chr18: 60192893  | <i>ZCCHC2</i>                     | Body                           | N_Shore | FALSE |
| cg10407894 | 0.71 | 0.82 | -0.11 | -54.33  | Chr7: 148517345  | <i>EZH2, EZH2</i>                 | Body, Body                     |         | TRUE  |
| cg23071186 | 0.41 | 0.52 | -0.11 | -26.35  | Chr19: 6669849   | <i>TNFSF14, TNFSF14</i>           | Body, Body                     |         | FALSE |
| cg02018277 | 0.04 | 0.15 | -0.11 | -98.25  | Chr15: 65116255  | <i>PIF1</i>                       | Body                           | Island  | FALSE |
| cg22549408 | 0.63 | 0.74 | -0.11 | -37.35  | Chr18: 57566300  | <i>PMAIP1</i>                     | TSS1500                        | N_Shore | FALSE |
| cg00538591 | 0.61 | 0.72 | -0.11 | -34.43  | Chr16: 89008994  | <i>CBFA2T3, CBFA2T3</i>           | TSS1500, Body                  | S_Shore | FALSE |
| cg25232942 | 0.10 | 0.21 | -0.11 | -63.93  | Chr19: 50194519  | <i>CPT1C, CPT1C, CPT1C, CPT1C</i> | 1stExon, 1stExon, 5'UTR, 5'UTR | Island  | FALSE |

|            |      |      |       |        |                  |   |  |         |       |
|------------|------|------|-------|--------|------------------|---|--|---------|-------|
| cg27366766 | 0.12 | 0.22 | -0.11 | -59.08 | Chr17: 56565286  | <i>HSF5</i>   | 1stExon  | Island  | FALSE |
| cg07252200 | 0.55 | 0.66 | -0.11 | -29.57 | Chr10: 125751941 |   |  | Island  | FALSE |
| cg18735015 | 0.36 | 0.47 | -0.11 | -26.80 | Chr10: 105428506 | <i>SH3PXD2A</i>   | Body   | Island  | TRUE  |
| cg08284263 | 0.36 | 0.46 | -0.11 | -26.81 | Chr10: 92958627  |   |  |         | TRUE  |
| cg23085143 | 0.42 | 0.53 | -0.11 | -25.52 | Chr7: 138349443  | <i>SVOPL, SVOPL</i>                                     | Body, TSS1500  | Island  | FALSE |
| cg13076785 | 0.76 | 0.86 | -0.11 | -67.49 | Chr6: 32520916   | <i>HLA-DRB6</i>   | Body   |         | FALSE |
| cg18678645 | 0.29 | 0.40 | -0.11 | -29.16 | Chr5: 135416331  | <i>MIR886</i>   | TSS200   | Island  | FALSE |
| cg10510935 | 0.33 | 0.44 | -0.11 | -27.22 | Chr1: 4059661    |   |  |         | FALSE |
| cg09438522 | 0.29 | 0.40 | -0.11 | -29.05 | Chr3: 15000765   | <i>NR2C2</i>  | 5'UTR  |         | TRUE  |
| cg03809847 | 0.20 | 0.31 | -0.11 | -38.10 | Chr17: 79093482  | <i>AATK</i>   | Body   | Island  | TRUE  |
| cg00994804 | 0.27 | 0.37 | -0.11 | -30.82 | Chr21: 36259383  | <i>RUNX1, RUNX1, RUNX1</i>                              | 1stExon, 1stExon, Body   | Island  | TRUE  |
| cg23024343 | 0.73 | 0.83 | -0.11 | -54.92 | Chr7: 107201750  | <i>COG5, COG5, COG5</i>                                 | Body, Body, Body   | N_Shelf | FALSE |
| cg16341836 | 0.44 | 0.55 | -0.11 | -24.92 | Chr10: 90641389  | <i>STAMBPL1</i>   | 5'UTR  | S_Shore | FALSE |
| cg26312951 | 0.15 | 0.25 | -0.11 | -47.95 | Chr21: 42797847  | <i>MX1, MX1</i>   | TSS200, 5'UTR  | N_Shore | TRUE  |
| cg18125510 | 0.15 | 0.25 | -0.11 | -47.46 | Chr14: 100841768 | <i>WARS, WDR25, WARS, WARS, WDR25, WARS, WARS, WARS</i> | 1stExon, TSS1500, 5'UTR, 5'UTR, TSS1500, 1stExon, 5'UTR, 5'UTR | N_Shore | FALSE |
| cg12623145 | 0.29 | 0.40 | -0.11 | -28.44 | Chr2: 97778927   | <i>ANKRD36</i>  | TSS1500  | Island  | FALSE |
| cg11025609 | 0.68 | 0.79 | -0.11 | -42.81 | Chr12: 110727072 | <i>ATP2A2, ATP2A2, ATP2A2</i>                           | Body, Body, Body   |         | TRUE  |
| cg12800105 | 0.67 | 0.78 | -0.11 | -41.20 | Chr12: 121972412 | <i>KDM2B, KDM2B</i>                                     | Body, Body   | N_Shelf | FALSE |
| cg05487134 | 0.19 | 0.30 | -0.11 | -37.98 | Chr17: 40489569  | <i>STAT3, STAT3, STAT3</i>                              | Body, Body, Body   |         | FALSE |
| cg17573270 | 0.58 | 0.68 | -0.11 | -29.15 | Chr22: 42950376  | <i>SERHL2</i>   | Body   | S_Shore | FALSE |
| cg06401414 | 0.58 | 0.68 | -0.11 | -29.33 | Chr8: 141599436  | <i>EIF2C2, EIF2C2</i>                                   | Body, Body   |         | FALSE |
| cg12362118 | 0.29 | 0.40 | -0.10 | -28.00 | Chr3: 148995174  |   |  |         | FALSE |
| cg12253071 | 0.65 | 0.75 | -0.10 | -36.28 | Chr4: 19740944   |   |  |         | TRUE  |
| cg08562672 | 0.35 | 0.46 | -0.10 | -25.24 | Chr19: 21860753  |   |  | N_Shore | FALSE |
| cg19735514 | 0.65 | 0.75 | -0.10 | -36.47 | Chr1: 161762739  | <i>ATF6</i>   | Body   |         | FALSE |
| cg20737388 | 0.47 | 0.57 | -0.10 | -24.30 | Chr11: 73668626  | <i>DNAJB13</i>  | Body   |         | FALSE |
| cg27633287 | 0.65 | 0.76 | -0.10 | -36.97 | Chr12: 130766243 |   |  |         | FALSE |
| cg02402208 | 0.27 | 0.38 | -0.10 | -28.87 | ChrY: 9384707    |   |  | N_Shore | FALSE |
| cg26724018 | 0.18 | 0.29 | -0.10 | -39.25 | Chr11: 5716255   | <i>TRIM22</i>   | 5'UTR  |         | FALSE |
| cg13593090 | 0.51 | 0.61 | -0.10 | -25.11 | Chr19: 9546723   | <i>ZNF266, ZNF266</i>                                   | TSS1500, TSS1500   | S_Shore | FALSE |
| cg20376189 | 0.77 | 0.87 | -0.10 | -66.64 | Chr6: 7317168    |   |  | S_Shelf | FALSE |
| cg06546677 | 0.67 | 0.78 | -0.10 | -39.50 | Chr8: 145537504  | <i>HSF1</i>   | Body   |         | TRUE  |
| cg21058822 | 0.75 | 0.86 | -0.10 | -60.28 | Chr8: 30002223   | <i>MBOAT4</i>   | TSS200   |         | FALSE |
| cg13210558 | 0.72 | 0.82 | -0.10 | -49.13 | Chr9: 138369918  |   |  | N_Shore | FALSE |
| cg08010094 | 0.54 | 0.65 | -0.10 | -25.88 | Chr2: 139539001  | <i>NXP2</i>   | TSS1500  | S_Shore | FALSE |
| cg13753488 | 0.34 | 0.44 | -0.10 | -24.71 | Chr9: 136001623  | <i>RALGDS</i>   | Body   |         | TRUE  |
| cg10927178 | 0.25 | 0.35 | -0.10 | -29.76 | Chr20: 56883965  | <i>RAB22A, PPP4R1L</i>                                  | TSS1500, Body  | N_Shore | FALSE |
| cg17329648 | 0.69 | 0.79 | -0.10 | -41.32 | Chr2: 73297389   | <i>SFXN5</i>  | Body   | N_Shore | FALSE |

|            |      |      |       |        |                  |   |                          |         |       |
|------------|------|------|-------|--------|------------------|---|--------------------------|---------|-------|
| cg09084320 | 0.70 | 0.80 | -0.10 | -43.12 | Chr10: 33553435  | <i>NRP1, NRP1, NRP1</i>                           | Body, Body, Body         |         | TRUE  |
| cg15954353 | 0.75 | 0.85 | -0.10 | -57.95 | Chr17: 5403337   | <i>LOC728392</i>                                  | 3'UTR                    | Island  | FALSE |
| cg14628108 | 0.77 | 0.87 | -0.10 | -64.60 | Chr12: 106631875 | <i>CKAP4</i>                                      | 3'UTR                    | N_Shore | TRUE  |
| cg00355656 | 0.61 | 0.72 | -0.10 | -30.72 | Chr1: 229692519  | <i>ABCB10</i>                                     | Body                     | N_Shore | FALSE |
| cg22107533 | 0.49 | 0.59 | -0.10 | -23.62 | Chr15: 45028083  | <i>TRIM69, TRIM69</i>                             | TSS1500, TSS1500         |         | TRUE  |
| cg06679494 | 0.34 | 0.45 | -0.10 | -24.09 | Chr17: 6921295   | <i>MIR497, MIR195</i>                             | Body, TSS1500            | S_Shelf | FALSE |
| cg00269725 | 0.74 | 0.84 | -0.10 | -54.55 | Chr6: 156983315  |   |                          |         | FALSE |
| cg05439368 | 0.62 | 0.72 | -0.10 | -31.06 | Chr15: 45028098  | <i>TRIM69, TRIM69</i>                             | TSS1500, TSS1500         |         | TRUE  |
| cg10184328 | 0.46 | 0.57 | -0.10 | -22.94 | Chr7: 138349158  | <i>SVOPL, SVOPL</i>                               | Body, TSS200             | Island  | FALSE |
| cg00479463 | 0.55 | 0.65 | -0.10 | -25.71 | Chr19: 33726786  |   |                          | Island  | FALSE |
| cg01771247 | 0.67 | 0.77 | -0.10 | -37.21 | Chr16: 61846623  | <i>CDH8</i>                                       | Body                     |         | TRUE  |
| cg05883128 | 0.13 | 0.23 | -0.10 | -49.16 | Chr4: 169239131  | <i>DDX60</i>                                      | 5'UTR                    | N_Shore | FALSE |
| cg23835219 | 0.57 | 0.67 | -0.10 | -26.62 | Chr4: 1244017    | <i>CTBP1, CTBP1, C4orf42</i>                      | TSS1500, TSS1500, TSS200 | Island  | FALSE |
| cg04515608 | 0.65 | 0.75 | -0.10 | -34.24 | Chr11: 48129067  | <i>PTPRJ, PTPRJ</i>                               | Body, Body               |         | TRUE  |
| cg09315878 | 0.71 | 0.81 | -0.10 | -43.74 | Chr1: 1152580    | <i>SDF4, SDF4</i>                                 | 3'UTR, 3'UTR             | Island  | FALSE |
| cg25897951 | 0.62 | 0.72 | -0.10 | -30.76 | Chr4: 1244024    | <i>CTBP1, CTBP1, C4orf42</i>                      | TSS1500, TSS1500, TSS200 | Island  | FALSE |
| cg22544881 | 0.59 | 0.70 | -0.10 | -28.14 | Chr7: 130712346  | <i>FLJ43663, FLJ43663</i>                         | Body, Body               |         | TRUE  |
| cg05992904 | 0.75 | 0.85 | -0.10 | -56.45 | Chr22: 48892994  | <i>FAM19A5</i>                                    | Body                     | N_Shelf | FALSE |
| cg04138046 | 0.70 | 0.80 | -0.10 | -42.09 | Chr5: 112608004  | <i>MCC, MCC</i>                                   | Body, Body               |         | TRUE  |
| cg17502213 | 0.71 | 0.81 | -0.10 | -44.56 | Chr1: 58704335   | <i>DAB1</i>                                       | 5'UTR                    |         | TRUE  |
| cg23084506 | 0.46 | 0.56 | -0.10 | -22.46 | Chr1: 13111908   | <i>PRAMEF5</i>                                    | Body                     |         | FALSE |
| cg05850997 | 0.73 | 0.83 | -0.10 | -50.42 | Chr4: 89207307   | <i>PPM1K</i>                                      | TSS1500                  | S_Shore | FALSE |
| cg16092135 | 0.53 | 0.63 | -0.10 | -24.27 | Chr2: 307058     |   |                          | Island  | FALSE |
| cg24115681 | 0.66 | 0.76 | -0.10 | -35.34 | Chr7: 114566161  | <i>MDFIC, MDFIC</i>                               | Body, Body               | S_Shelf | FALSE |
| cg15411272 | 0.25 | 0.36 | -0.10 | -28.38 | Chr6: 29895187   |   |                          | S_Shore | FALSE |
| cg00343839 | 0.31 | 0.41 | -0.10 | -24.58 | Chr17: 5403516   | <i>LOC728392, LOC728392</i>                       | 1stExon, 3'UTR           | Island  | FALSE |
| cg09318375 | 0.10 | 0.20 | -0.10 | -56.28 | Chr1: 67218090   | <i>TCTEX1D1</i>                                   | TSS200                   | Island  | TRUE  |
| cg21169490 | 0.48 | 0.58 | -0.10 | -22.37 | Chr6: 73135072   |   |                          |         | TRUE  |
| cg07600533 | 0.79 | 0.89 | -0.10 | -75.85 | Chr22: 50986031  | <i>KLHDC7B</i>                                    | TSS1500                  | Island  | FALSE |
| cg24680439 | 0.52 | 0.62 | -0.10 | -23.47 | Chr10: 134778467 |   |                          | N_Shore | FALSE |
| cg12494529 | 0.71 | 0.81 | -0.10 | -44.43 | Chr10: 1082432   | <i>C10orf110, C10orf110, C10orf110, C10orf110</i> | Body, Body, Body, Body   |         | TRUE  |
| cg08575688 | 0.69 | 0.80 | -0.10 | -40.20 | Chr2: 228678500  | <i>CCL20, CCL20</i>                               | TSS200, TSS200           |         | FALSE |
| cg24794857 | 0.20 | 0.30 | -0.10 | -33.99 | Chr4: 187113578  | <i>CYP4V2</i>                                     | Body                     | S_Shore | FALSE |
| cg09987201 | 0.06 | 0.16 | -0.10 | -77.84 | Chr9: 130549116  | <i>CDK9</i>                                       | Body                     | Island  | FALSE |
| cg06357908 | 0.49 | 0.59 | -0.10 | -22.37 | Chr1: 192548609  | <i>RGS1</i>                                       | 3'UTR                    |         | FALSE |
| cg07621803 | 0.63 | 0.73 | -0.10 | -30.28 | Chr18: 76674796  |   |                          | Island  | FALSE |
| cg12115302 | 0.58 | 0.68 | -0.10 | -26.37 | Chr12: 30323676  |   |                          | S_Shore | FALSE |
| cg04242525 | 0.79 | 0.89 | -0.10 | -74.96 | Chr8: 144236576  |   |                          |         | FALSE |

|                         |      |      |       |        |                  |                                  |                           |         |       |
|-------------------------|------|------|-------|--------|------------------|----------------------------------|---------------------------|---------|-------|
| cg20128323              | 0.51 | 0.62 | -0.10 | -23.07 | Chr6: 9503813    |                                  |                           |         | TRUE  |
| cg05617801              | 0.71 | 0.82 | -0.10 | -44.32 | Chr2: 108008839  |                                  |                           |         | FALSE |
| cg05656688              | 0.69 | 0.79 | -0.10 | -39.13 | Chr1: 25254088   | <i>RUNX3, RUNX3</i>              | Body, Body                | N_Shore | TRUE  |
| cg01624173              | 0.32 | 0.42 | -0.10 | -23.73 | Chr14: 75981868  |                                  |                           |         | TRUE  |
| cg06508867              | 0.31 | 0.41 | -0.10 | -23.95 | Chr16: 87814178  |                                  |                           | S_Shore | FALSE |
| cg06904356              | 0.53 | 0.63 | -0.10 | -23.35 | Chr5: 1849983    |                                  |                           | N_Shore | FALSE |
| cg23681866              | 0.25 | 0.35 | -0.10 | -27.67 | Chr6: 29895175   |                                  |                           | S_Shore | FALSE |
| cg02531227              | 0.51 | 0.61 | -0.10 | -22.59 | Chr12: 129460621 | <i>GLT1D1</i>                    | Body                      |         | FALSE |
| <b>Hypermethylation</b> |      |      |       |        |                  |                                  |                           |         |       |
| cg05176970              | 0.75 | 0.35 | 0.40  | 341.10 | Chr17: 724273    | <i>NXN</i>                       | Body                      |         | FALSE |
| cg00256329              | 0.71 | 0.37 | 0.34  | 341.10 | Chr17: 724374    | <i>NXN</i>                       | Body                      |         | FALSE |
| cg19214707              | 0.65 | 0.32 | 0.33  | 341.10 | Chr7: 3157722    |                                  |                           |         | TRUE  |
| cg18402987              | 0.36 | 0.04 | 0.32  | 341.10 | Chr7: 1209562    |                                  |                           |         | FALSE |
| cg03188948              | 0.50 | 0.19 | 0.31  | 341.10 | Chr7: 1209495    |                                  |                           |         | FALSE |
| cg15262954              | 0.40 | 0.09 | 0.30  | 341.10 | Chr20: 62198872  | <i>PRIC285, PRIC285</i>          | Body, 1stExon             | Island  | FALSE |
| cg15591384              | 0.75 | 0.49 | 0.26  | 341.10 | Chr6: 32525960   | <i>HLA-DRB6</i>                  | Body                      |         | FALSE |
| cg17178900              | 0.54 | 0.28 | 0.26  | 341.10 | Chr1: 205818956  | <i>PM20D1</i>                    | Body                      | Island  | TRUE  |
| cg22355889              | 0.33 | 0.08 | 0.25  | 341.10 | Chr11: 107461585 | <i>ELMOD1, LOC643923, ELMOD1</i> | TSS1500, TSS1500, TSS1500 | N_Shore | FALSE |
| cg26354017              | 0.50 | 0.26 | 0.24  | 341.10 | Chr1: 205819088  | <i>PM20D1</i>                    | 1stExon                   | Island  | TRUE  |
| cg14159672              | 0.50 | 0.26 | 0.24  | 341.10 | Chr1: 205819179  | <i>PM20D1</i>                    | 1stExon                   | Island  | TRUE  |
| cg11224582              | 0.39 | 0.15 | 0.24  | 341.10 | Chr12: 4919138   | <i>KCNA6, KCNA6</i>              | 5'UTR, 1stExon            | Island  | FALSE |
| cg19870512              | 0.33 | 0.10 | 0.24  | 341.10 | Chr12: 4919081   | <i>KCNA6, KCNA6</i>              | 5'UTR, 1stExon            | Island  | FALSE |
| cg07167872              | 0.48 | 0.24 | 0.24  | 341.10 | Chr1: 205819463  | <i>PM20D1</i>                    | TSS200                    | S_Shore | FALSE |
| cg10671668              | 0.32 | 0.09 | 0.23  | 341.10 | Chr12: 4919230   | <i>KCNA6</i>                     | 1stExon                   | Island  | FALSE |
| cg24118521              | 0.67 | 0.45 | 0.22  | 341.10 | Chr13: 47472330  | <i>HTR2A, HTR2A</i>              | TSS1500, TSS1500          |         | FALSE |
| cg24503407              | 0.48 | 0.26 | 0.22  | 341.10 | Chr1: 205819492  | <i>PM20D1</i>                    | TSS1500                   | S_Shore | FALSE |
| cg19362774              | 0.87 | 0.66 | 0.21  | 341.10 | Chr8: 6664522    |                                  |                           | S_Shore | FALSE |
| cg26858704              | 0.28 | 0.07 | 0.21  | 341.10 | Chr12: 4918848   | <i>KCNA6, KCNA6</i>              | 5'UTR, 1stExon            | Island  | FALSE |
| cg18803147              | 0.63 | 0.42 | 0.21  | 341.10 | Chr5: 2743124    |                                  |                           | S_Shore | FALSE |
| cg14911689              | 0.48 | 0.27 | 0.20  | 341.10 | Chr12: 739980    | <i>NINJ2</i>                     | Body                      |         | FALSE |
| cg08624648              | 0.75 | 0.54 | 0.20  | 341.10 | Chr6: 31651029   |                                  |                           | Island  | FALSE |
| cg26654770              | 0.49 | 0.29 | 0.20  | 126.71 | Chr12: 740100    | <i>NINJ2</i>                     | Body                      |         | FALSE |
| cg18264486              | 0.71 | 0.52 | 0.19  | 126.71 | Chr6: 31650916   |                                  |                           | Island  | FALSE |
| cg25407410              | 0.77 | 0.58 | 0.19  | 341.10 | Chr6: 143891975  | <i>LOC285740</i>                 | TSS1500                   |         | FALSE |
| cg11965913              | 0.36 | 0.17 | 0.19  | 341.10 | Chr1: 205819406  | <i>PM20D1</i>                    | TSS200                    | S_Shore | FALSE |
| cg12119625              | 0.51 | 0.32 | 0.19  | 108.12 | Chr19: 54106789  | <i>LOC284379</i>                 | TSS200                    |         | FALSE |
| cg14893161              | 0.40 | 0.21 | 0.19  | 126.71 | Chr1: 205819251  | <i>PM20D1, PM20D1</i>            | 5'UTR, 1stExon            | S_Shore | TRUE  |
| cg00101728              | 0.64 | 0.46 | 0.18  | 103.94 | Chr6: 2953027    | <i>SERPINB6</i>                  | Body                      |         | TRUE  |
| cg05380919              | 0.81 | 0.63 | 0.18  | 341.10 | Chr22: 24376252  | <i>GSTT1</i>                     | 3'UTR                     | S_Shelf | FALSE |
| cg11738485              | 0.53 | 0.35 | 0.18  | 94.77  | Chr19: 12877000  | <i>HOOK2, HOOK2</i>              | Body, Body                | Island  | FALSE |
| cg01500431              | 0.83 | 0.66 | 0.18  | 341.10 | Chr22: 24388327  | <i>GSTTP2</i>                    | Body                      | S_Shelf | FALSE |

|            |      |      |      |        |                  |                                      |                                 |         |       |
|------------|------|------|------|--------|------------------|--------------------------------------|---------------------------------|---------|-------|
| cg13679164 | 0.76 | 0.58 | 0.18 | 120.85 | Chr6: 161258479  |                                      |                                 |         | FALSE |
| cg01201512 | 0.58 | 0.40 | 0.18 | 92.49  | Chr12: 740338    | <i>NINJ2</i>                         | Body                            |         | TRUE  |
| cg15242686 | 0.63 | 0.45 | 0.18 | 94.31  | Chr22: 24348715  | <i>GSTTP1</i>                        | TSS1500                         |         | FALSE |
| cg10604476 | 0.35 | 0.18 | 0.18 | 123.79 | Chr19: 10403908  | <i>ICAM5</i>                         | Body                            | Island  | FALSE |
| cg23881368 | 0.61 | 0.43 | 0.18 | 90.87  | Chr13: 47472343  | <i>HTR2A, HTR2A</i>                  | TSS1500,<br>TSS1500             |         | FALSE |
| cg01243072 | 0.54 | 0.37 | 0.18 | 89.99  | Chr2: 43398171   |                                      |                                 | Island  | FALSE |
| cg09584650 | 0.46 | 0.29 | 0.17 | 93.56  | Chr8: 2002012    | <i>MYOM2</i>                         | Body                            | N_Shore | FALSE |
| cg01560476 | 0.49 | 0.31 | 0.17 | 86.56  | Chr16: 24743405  | <i>TNRC6A</i>                        | Body                            | S_Shore | FALSE |
| cg23708337 | 0.26 | 0.09 | 0.17 | 341.10 | Chr7: 1209742    |                                      |                                 |         | FALSE |
| cg09727148 | 0.46 | 0.29 | 0.17 | 87.48  | Chr21: 43560719  | <i>UMODL1,<br/>UMODL1</i>            | 3'UTR, 3'UTR                    |         | FALSE |
| cg05185784 | 0.66 | 0.49 | 0.17 | 86.16  | Chr16: 90016020  | <i>DEF8, DEF8</i>                    | 5'UTR, Body                     | Island  | FALSE |
| cg01517680 | 0.72 | 0.55 | 0.17 | 93.15  | Chr16: 49499006  |                                      |                                 | Island  | TRUE  |
| cg14580085 | 0.62 | 0.45 | 0.17 | 80.09  | Chr2: 239553406  |                                      |                                 |         | TRUE  |
| cg02389040 | 0.76 | 0.59 | 0.17 | 103.50 | Chr6: 31650786   |                                      |                                 | Island  | FALSE |
| cg22240348 | 0.26 | 0.10 | 0.17 | 341.10 | Chr21: 46975805  |                                      |                                 | Island  | FALSE |
| cg05082466 | 0.71 | 0.54 | 0.17 | 90.73  | Chr6: 2953123    | <i>SERPINB6</i>                      | Body                            |         | TRUE  |
| cg08917117 | 0.37 | 0.21 | 0.16 | 99.14  | Chr10: 115059021 |                                      |                                 |         | TRUE  |
| cg18105134 | 0.76 | 0.60 | 0.16 | 100.95 | Chr13: 113819100 | <i>PROZ</i>                          | Body                            |         | FALSE |
| cg00440797 | 0.26 | 0.10 | 0.16 | 341.10 | Chr6: 32493873   | <i>HLA-DRB5</i>                      | Body                            | S_Shelf | FALSE |
| cg01889448 | 0.86 | 0.70 | 0.16 | 341.10 | Chr6: 32635871   | <i>HLA-DQB1</i>                      | TSS1500                         | S_Shelf | FALSE |
| cg18200810 | 0.50 | 0.34 | 0.16 | 72.98  | Chr13: 47472200  | <i>HTR2A, HTR2A</i>                  | TSS1500,<br>TSS1500             |         | FALSE |
| cg06417478 | 0.47 | 0.31 | 0.16 | 70.85  | Chr19: 12876846  | <i>HOOK2, HOOK2</i>                  | Body, Body                      | N_Shore | FALSE |
| cg12064134 | 0.81 | 0.65 | 0.16 | 106.18 | Chr16: 90016061  | <i>DEF8, DEF8</i>                    | 5'UTR, Body                     | Island  | FALSE |
| cg00492070 | 0.62 | 0.46 | 0.16 | 68.49  | Chr3: 107810716  | <i>CD47, CD47, CD47</i>              | TSS1500,<br>TSS1500,<br>TSS1500 | S_Shore | FALSE |
| cg02285791 | 0.55 | 0.40 | 0.15 | 66.17  | Chr6: 27550747   |                                      |                                 |         | FALSE |
| cg16781264 | 0.33 | 0.18 | 0.15 | 93.66  | Chr2: 101087575  | <i>NMS</i>                           | Body                            |         | FALSE |
| cg27084028 | 0.39 | 0.24 | 0.15 | 77.80  | Chr7: 6836436    | <i>RSPH10B,<br/>RSPH10B2</i>         | Body, Body                      |         | FALSE |
| cg20435535 | 0.71 | 0.55 | 0.15 | 75.82  | Chr6: 31651151   |                                      |                                 | Island  | FALSE |
| cg10528576 | 0.63 | 0.47 | 0.15 | 66.07  | Chr14: 101192913 | <i>DLK1</i>                          | TSS1500                         | Island  | FALSE |
| cg02304584 | 0.69 | 0.53 | 0.15 | 71.23  | Chr6: 31650790   |                                      |                                 | Island  | FALSE |
| cg05857999 | 0.66 | 0.51 | 0.15 | 68.44  | Chr6: 31650760   |                                      |                                 | Island  | FALSE |
| cg01274643 | 0.23 | 0.08 | 0.15 | 341.10 | Chr11: 1283946   |                                      |                                 |         | TRUE  |
| cg06460587 | 0.74 | 0.59 | 0.15 | 79.45  | Chr6: 31650930   |                                      |                                 | Island  | FALSE |
| cg01246520 | 0.28 | 0.13 | 0.15 | 106.99 | Chr17: 17644344  | <i>RAI1</i>                          | 5'UTR                           |         | TRUE  |
| cg11141652 | 0.58 | 0.43 | 0.15 | 62.14  | Chr22: 24348549  | <i>GSTTP1</i>                        | TSS1500                         |         | FALSE |
| cg17593958 | 0.30 | 0.15 | 0.15 | 94.68  | Chr20: 62199034  | <i>PRIC285, PRIC285,<br/>PRIC285</i> | 5'UTR, Body,<br>1stExon         | N_Shore | FALSE |
| cg16761754 | 0.44 | 0.29 | 0.15 | 63.91  | Chr14: 105127242 |                                      |                                 | S_Shore | FALSE |
| cg01252526 | 0.49 | 0.34 | 0.15 | 60.04  | Chr16: 711033    | <i>WDR90</i>                         | Body                            | N_Shore | TRUE  |
| cg18576957 | 0.74 | 0.59 | 0.15 | 74.60  | Chr6: 31651020   |                                      |                                 | Island  | FALSE |

|            |      |      |      |        |                  |   |                                |         |       |
|------------|------|------|------|--------|------------------|---|--------------------------------|---------|-------|
| cg14641829 | 0.88 | 0.73 | 0.15 | 341.10 | Chr9: 33270634   | <i>SUGT1P1, CHMP5</i>                     | Body, Body                     |         | FALSE |
| cg07403350 | 0.64 | 0.49 | 0.15 | 59.75  | Chr13: 108867111 | <i>LIG4, LIG4, LIG4, LIG4</i>             | 5'UTR, 1stExon, 5'UTR, 5'UTR   | Island  | FALSE |
| cg05795849 | 0.50 | 0.36 | 0.15 | 57.48  | Chr3: 4794082    | <i>ITPR1, ITPR1, ITPR1, EGOT</i>          | Body, Body, Body, TSS1500      |         | TRUE  |
| cg00813378 | 0.46 | 0.31 | 0.15 | 60.19  | Chr1: 1475209    | <i>C1orf70</i>                            | Body                           | Island  | FALSE |
| cg08083251 | 0.69 | 0.54 | 0.14 | 63.82  | Chr13: 23309930  |   |                                |         | FALSE |
| cg19980771 | 0.46 | 0.31 | 0.14 | 58.77  | Chr6: 110798022  | <i>SLC22A16</i>                           | TSS200                         | Island  | FALSE |
| cg17518825 | 0.80 | 0.65 | 0.14 | 86.46  | Chr2: 46523461   | <i>EPAS1</i>                              | TSS1500                        | N_Shore | FALSE |
| cg25417675 | 0.76 | 0.62 | 0.14 | 76.52  | Chr6: 31651059   |   |                                | Island  | FALSE |
| cg27279301 | 0.65 | 0.50 | 0.14 | 57.27  | Chr14: 105945287 | <i>CRIP2</i>                              | Body                           | Island  | FALSE |
| cg14279856 | 0.52 | 0.38 | 0.14 | 53.72  | Chr6: 30851086   | <i>DDR1, DDR1</i>                         | TSS1500, TSS1500               | N_Shore | TRUE  |
| cg22318514 | 0.54 | 0.40 | 0.14 | 52.87  | Chr6: 31650850   |   |                                | Island  | FALSE |
| cg15529432 | 0.54 | 0.40 | 0.14 | 52.70  | Chr5: 16615750   | <i>FAM134B</i>                            | Body                           | N_Shore | FALSE |
| cg27128560 | 0.73 | 0.59 | 0.14 | 65.51  | Chr10: 105815443 | <i>COL17A1</i>                            | Body                           |         | TRUE  |
| cg11146691 | 0.56 | 0.42 | 0.14 | 51.77  | Chr12: 47219737  | <i>SLC38A4, SLC38A4, SLC38A4, SLC38A4</i> | 1stExon, 5'UTR, 1stExon, 5'UTR |         | FALSE |
| cg18232235 | 0.89 | 0.75 | 0.14 | 341.10 | Chr12: 11700321  |   |                                |         | FALSE |
| cg12367833 | 0.86 | 0.72 | 0.14 | 111.23 | Chr4: 42764094   |   |                                |         | TRUE  |
| cg04227007 | 0.74 | 0.61 | 0.14 | 66.91  | Chr19: 37760583  | <i>LOC284412</i>                          | TSS1500                        | N_Shore | FALSE |
| cg03393996 | 0.33 | 0.19 | 0.14 | 70.02  | Chr4: 1580377    |   |                                | Island  | FALSE |
| cg10430963 | 0.66 | 0.52 | 0.14 | 54.05  | Chr17: 37124558  | <i>FBXO47</i>                             | TSS1500                        |         | FALSE |
| cg18156486 | 0.57 | 0.43 | 0.14 | 49.40  | Chr11: 2884295   |   |                                | Island  | FALSE |
| cg01299579 | 0.29 | 0.15 | 0.14 | 82.11  | Chr2: 10830716   | <i>NOL10</i>                              | TSS1500                        | S_Shore | FALSE |
| cg07618780 | 0.57 | 0.43 | 0.14 | 48.84  | Chr2: 240142806  | <i>HDAC4</i>                              | Body                           |         | FALSE |
| cg05547895 | 0.50 | 0.36 | 0.14 | 48.79  | Chr3: 196705855  |   |                                |         | FALSE |
| cg21434132 | 0.40 | 0.26 | 0.13 | 54.70  | Chr3: 196705742  |   |                                |         | FALSE |
| cg16922644 | 0.71 | 0.58 | 0.13 | 56.99  | Chr10: 45146765  |   |                                |         | TRUE  |
| cg20558320 | 0.47 | 0.34 | 0.13 | 47.85  | Chr2: 235210313  |   |                                |         | TRUE  |
| cg13390570 | 0.32 | 0.19 | 0.13 | 67.57  | Chr5: 1255616    | <i>TERT, TERT</i>                         | Body, Body                     | N_Shore | FALSE |
| cg27182070 | 0.51 | 0.37 | 0.13 | 45.82  | Chr1: 28218282   | <i>RPA2</i>                               | 3'UTR                          |         | FALSE |
| cg21078654 | 0.48 | 0.35 | 0.13 | 46.48  | Chr15: 52130305  | <i>TMOD3</i>                              | 5'UTR                          |         | TRUE  |
| cg15363314 | 0.22 | 0.08 | 0.13 | 108.37 | Chr11: 1283970   |   |                                |         | TRUE  |
| cg10920224 | 0.58 | 0.45 | 0.13 | 45.64  | Chr14: 103367591 | <i>TRAF3, TRAF3, TRAF3</i>                | Body, Body, Body               |         | FALSE |
| cg00739471 | 0.43 | 0.30 | 0.13 | 48.95  | Chr14: 69415588  | <i>ACTN1, ACTN1, ACTN1</i>                | Body, Body, Body               |         | FALSE |
| cg08133631 | 0.56 | 0.42 | 0.13 | 44.11  | Chr1: 26527909   | <i>CATSPER4</i>                           | Body                           |         | TRUE  |
| cg04329125 | 0.50 | 0.37 | 0.13 | 44.31  | Chr14: 105945022 | <i>CRIP2</i>                              | Body                           | Island  | FALSE |
| cg24456340 | 0.52 | 0.39 | 0.13 | 42.97  | Chr17: 47286483  | <i>ABI3, ABI3, GNGT2</i>                  | TSS1500, TSS1500, 5'UTR        |         | FALSE |
| cg14316629 | 0.49 | 0.36 | 0.13 | 43.45  | Chr6: 168436353  | <i>KIF25, KIF25</i>                       | Body, Body                     | S_Shore | TRUE  |
| cg07455790 | 0.86 | 0.73 | 0.13 | 95.92  | Chr6: 31650735   |   |                                | Island  | FALSE |
| cg07371521 | 0.45 | 0.32 | 0.13 | 45.34  | Chr5: 154026371  |   |                                | N_Shore | TRUE  |
| cg04097388 | 0.80 | 0.67 | 0.13 | 69.62  | Chr2: 236671717  | <i>AGAP1, AGAP1</i>                       | Body, Body                     | N_Shore | FALSE |

|            |      |      |      |        |                  |                                     |                           |         |       |
|------------|------|------|------|--------|------------------|-------------------------------------|---------------------------|---------|-------|
| cg27425314 | 0.40 | 0.28 | 0.13 | 46.83  | Chr1: 26797619   | <i>DHDDS, HMG2, DHDDS</i>           | 3'UTR, TSS1500, 3'UTR     | N_Shore | TRUE  |
| cg00058449 | 0.49 | 0.36 | 0.13 | 40.92  | Chr6: 31867956   | <i>ZBTB12</i>                       | Body                      | Island  | FALSE |
| cg13661648 | 0.71 | 0.58 | 0.13 | 49.46  | Chr6: 33035284   | <i>HLA-DPA1</i>                     | 3'UTR                     |         | FALSE |
| cg26751588 | 0.78 | 0.65 | 0.13 | 61.24  | Chr17: 14109671  | <i>COX10</i>                        | Body                      | N_Shore | FALSE |
| cg03259126 | 0.88 | 0.76 | 0.13 | 104.07 | Chr7: 56029683   |                                     |                           | N_Shelf | FALSE |
| cg09971646 | 0.66 | 0.54 | 0.13 | 43.37  | Chr14: 101194145 | <i>DLK1</i>                         | Body                      | S_Shore | FALSE |
| cg04118910 | 0.58 | 0.46 | 0.13 | 39.31  | Chr13: 114875170 | <i>RASA3</i>                        | Body                      | N_Shore | FALSE |
| cg18522231 | 0.45 | 0.32 | 0.13 | 41.31  | Chr3: 196705629  |                                     |                           |         | FALSE |
| cg27216937 | 0.67 | 0.55 | 0.12 | 43.39  | Chr11: 6425978   | <i>APBB1, APBB1</i>                 | Body, Body                |         | TRUE  |
| cg03441844 | 0.46 | 0.33 | 0.12 | 39.85  | Chr1: 161368947  |                                     |                           | Island  | FALSE |
| cg24544490 | 0.33 | 0.20 | 0.12 | 53.71  | Chr1: 155290961  | <i>RUSC1, RUSC1, C1orf104</i>       | 5'UTR, 5'UTR, Body        | Island  | FALSE |
| cg09253696 | 0.32 | 0.20 | 0.12 | 53.99  | Chr17: 73873529  | <i>TRIM47</i>                       | Body                      | Island  | TRUE  |
| cg02341556 | 0.37 | 0.24 | 0.12 | 46.88  | Chr11: 118781978 | <i>BCL9L</i>                        | TSS1500                   | S_Shore | FALSE |
| cg02355304 | 0.59 | 0.47 | 0.12 | 38.03  | Chr7: 5536984    | <i>MIR589, FBXL18</i>               | TSS1500, Body             | N_Shelf | FALSE |
| cg27665146 | 0.44 | 0.31 | 0.12 | 40.03  | Chr15: 51369926  | <i>TNFAIP8L3</i>                    | Body                      |         | TRUE  |
| cg10424681 | 0.61 | 0.49 | 0.12 | 38.45  | Chr6: 4079350    | <i>C6orf201, C6orf146, C6orf146</i> | TSS200, 5'UTR, 1stExon    | Island  | TRUE  |
| cg17052675 | 0.71 | 0.58 | 0.12 | 45.59  | Chr2: 3827356    |                                     |                           |         | TRUE  |
| cg26922780 | 0.39 | 0.26 | 0.12 | 43.91  | Chr16: 88769443  | <i>RNF166</i>                       | Body                      | N_Shelf | FALSE |
| cg07115206 | 0.66 | 0.54 | 0.12 | 40.99  | Chr16: 6425686   | <i>A2BP1, A2BP1</i>                 | 5'UTR, 5'UTR              |         | TRUE  |
| cg15556709 | 0.61 | 0.49 | 0.12 | 37.82  | Chr7: 43739176   | <i>C7orf44</i>                      | 5'UTR                     |         | TRUE  |
| cg06223736 | 0.77 | 0.65 | 0.12 | 55.93  | Chr2: 240142694  | <i>HDAC4</i>                        | Body                      |         | FALSE |
| cg04248271 | 0.35 | 0.23 | 0.12 | 47.47  | Chr5: 158524404  | <i>EBF1</i>                         | Body                      | Island  | TRUE  |
| cg27119456 | 0.34 | 0.22 | 0.12 | 48.19  | Chr10: 42863173  | <i>LOC441666</i>                    | Body                      | Island  | FALSE |
| cg13286582 | 0.43 | 0.31 | 0.12 | 38.03  | Chr2: 37883934   | <i>CDC42EP3</i>                     | 5'UTR                     |         | TRUE  |
| cg13682187 | 0.50 | 0.38 | 0.12 | 35.23  | Chr1: 196946512  | <i>CFHR5</i>                        | TSS200                    |         | FALSE |
| cg19383211 | 0.62 | 0.50 | 0.12 | 36.20  | Chr6: 32527588   | <i>HLA-DRB6</i>                     | Body                      |         | FALSE |
| cg02228675 | 0.39 | 0.27 | 0.12 | 40.83  | Chr17: 40259724  | <i>DHX58</i>                        | Body                      | Island  | TRUE  |
| cg26429520 | 0.25 | 0.13 | 0.12 | 67.09  | Chr11: 1283875   |                                     |                           |         | TRUE  |
| cg11236515 | 0.32 | 0.20 | 0.12 | 49.28  | Chr2: 74213762   |                                     |                           | S_Shore | FALSE |
| cg12108912 | 0.76 | 0.64 | 0.12 | 49.43  | Chr2: 120435949  | <i>TMEM177, TMEM177, TMEM177</i>    | TSS1500, TSS1500, TSS1500 | N_Shore | FALSE |
| cg10428938 | 0.40 | 0.28 | 0.12 | 39.53  | Chr7: 98990837   | <i>ARPC1B</i>                       | Body                      | Island  | TRUE  |
| cg13298116 | 0.41 | 0.30 | 0.12 | 37.89  | Chr11: 62369859  | <i>EML3, MTA2</i>                   | 3'UTR, TSS1500            | Island  | FALSE |
| cg13374304 | 0.81 | 0.69 | 0.12 | 62.46  | Chr7: 63016648   |                                     |                           | N_Shore | FALSE |
| cg17681079 | 0.59 | 0.47 | 0.12 | 34.17  | Chr7: 27556963   |                                     |                           |         | TRUE  |
| cg00253658 | 0.56 | 0.45 | 0.12 | 33.65  | Chr16: 54210496  |                                     |                           |         | FALSE |
| cg26893861 | 0.38 | 0.27 | 0.12 | 39.88  | Chr17: 41843967  | <i>DUSP3</i>                        | 3'UTR                     |         | FALSE |
| cg06022607 | 0.67 | 0.56 | 0.12 | 38.49  | Chr12: 133412002 |                                     |                           | N_Shore | FALSE |
| cg12548638 | 0.57 | 0.45 | 0.12 | 33.40  | Chr1: 38226812   | <i>EPHA10, EPHA10</i>               | 3'UTR, Body               | N_Shore | FALSE |
| cg03898365 | 0.64 | 0.53 | 0.12 | 35.99  | Chr11: 6897491   | <i>OR10A4</i>                       | TSS1500                   |         | FALSE |



|            |      |      |      |        |                  |  |                                       |         |       |
|------------|------|------|------|--------|------------------|--|---------------------------------------|---------|-------|
| cg26843498 | 0.54 | 0.42 | 0.12 | 32.96  | Chr19: 2361574   |  |                                       | S_Shore | FALSE |
| cg08754654 | 0.41 | 0.29 | 0.12 | 37.13  | Chr5: 154026448  |  |                                       | N_Shore | TRUE  |
| cg20557159 | 0.57 | 0.45 | 0.12 | 32.95  | Chr17: 75445261  | <i>SEPT9, SEPT9, SEPT9, SEPT9, SEPT9</i> | Body, Body, Body, Body, TSS1500, Body | N_Shelf | FALSE |
| cg05185038 | 0.70 | 0.59 | 0.12 | 40.44  | Chr14: 105945685 | <i>CRIP2</i>                             | Body                                  | Island  | FALSE |
| cg04657146 | 0.43 | 0.32 | 0.12 | 35.29  | Chr19: 12876947  | <i>HOOK2, HOOK2</i>                      | Body, Body                            | Island  | FALSE |
| cg23691894 | 0.67 | 0.55 | 0.12 | 37.17  | Chr10: 111765904 | <i>ADD3, ADD3</i>                        | 1stExon, 5'UTR                        | N_Shore | FALSE |
| cg08109568 | 0.80 | 0.68 | 0.12 | 55.91  | Chr15: 31115862  |  |                                       |         | FALSE |
| cg00638631 | 0.91 | 0.79 | 0.12 | 108.58 | Chr21: 39039777  | <i>KCNJ6</i>                             | Body                                  | Island  | FALSE |
| cg15205435 | 0.30 | 0.19 | 0.12 | 49.15  | Chr1: 6187920    | <i>CHD5</i>                              | Body                                  | Island  | TRUE  |
| cg03816370 | 0.67 | 0.55 | 0.12 | 36.58  | Chr2: 190616071  | <i>OSGEPL1</i>                           | Body                                  |         | FALSE |
| cg08017858 | 0.17 | 0.06 | 0.12 | 101.53 | Chr11: 74022642  | <i>PAHA3</i>                             | 1stExon                               | Island  | TRUE  |
| cg08280368 | 0.24 | 0.12 | 0.12 | 65.33  | Chr14: 71110536  | <i>TTC9</i>                              | Body                                  | S_Shore | FALSE |
| cg16777618 | 0.56 | 0.45 | 0.12 | 31.75  | Chr11: 128694184 |  |                                       | Island  | FALSE |
| cg05662444 | 0.48 | 0.37 | 0.12 | 32.00  | Chr5: 154026397  |  |                                       | N_Shore | TRUE  |
| cg04246864 | 0.80 | 0.69 | 0.12 | 56.39  | Chr16: 33357426  |  |                                       | Island  | FALSE |
| cg25019722 | 0.46 | 0.34 | 0.12 | 32.68  | Chr6: 37503610   |  |                                       | Island  | TRUE  |
| cg04255230 | 0.45 | 0.33 | 0.11 | 32.76  | Chr2: 74727010   | <i>LBX2</i>                              | Body                                  | Island  | FALSE |
| cg25071634 | 0.41 | 0.30 | 0.11 | 34.61  | ChrY: 9172441    | <i>TTY20</i>                             | TSS200                                | N_Shore | FALSE |
| cg12770425 | 0.69 | 0.57 | 0.11 | 36.94  | Chr6: 33585071   |  |                                       | N_Shelf | FALSE |
| cg26371957 | 0.72 | 0.60 | 0.11 | 40.03  | Chr12: 739280    | <i>NINJ2</i>                             | Body                                  |         | FALSE |
| cg18848287 | 0.37 | 0.26 | 0.11 | 37.73  | Chr7: 5111641    | <i>LOC389458</i>                         | TSS200                                | Island  | FALSE |
| cg09553982 | 0.63 | 0.51 | 0.11 | 32.56  | Chr10: 77875676  | <i>C10orf11</i>                          | Body                                  | S_Shelf | FALSE |
| cg24573207 | 0.50 | 0.39 | 0.11 | 30.70  | Chr3: 75661206   |  |                                       |         | FALSE |
| cg23774988 | 0.28 | 0.16 | 0.11 | 52.00  | Chr11: 128419199 | <i>ETS1</i>                              | Body                                  | Island  | FALSE |
| cg07502661 | 0.46 | 0.35 | 0.11 | 31.65  | Chr2: 43398339   |  |                                       | S_Shore | FALSE |
| cg09119854 | 0.63 | 0.51 | 0.11 | 32.33  | Chr17: 63550766  | <i>AXIN2</i>                             | Body                                  |         | TRUE  |
| cg26450717 | 0.49 | 0.38 | 0.11 | 30.65  | Chr6: 31650835   |  |                                       | Island  | FALSE |
| cg21139150 | 0.45 | 0.33 | 0.11 | 32.12  | Chr21: 46976175  |  |                                       | Island  | FALSE |
| cg01744331 | 0.98 | 0.86 | 0.11 | 341.10 | Chr11: 2722358   | <i>KCNQ1OT1, KCNQ1, KCNQ1</i>            | TSS1500, Body, Body                   | S_Shore | FALSE |
| cg07639376 | 0.39 | 0.28 | 0.11 | 35.11  | Chr16: 1584516   | <i>IFT140, TMEM204</i>                   | Body, 1stExon                         | Island  | TRUE  |
| cg01139861 | 0.29 | 0.18 | 0.11 | 47.76  | Chr7: 50343298   | <i>IKZF1</i>                             | TSS1500                               | Island  | FALSE |
| cg02965712 | 0.52 | 0.41 | 0.11 | 29.59  | Chr1: 77746028   |  |                                       | N_Shore | FALSE |
| cg27271937 | 0.43 | 0.32 | 0.11 | 32.11  | Chr12: 6419570   | <i>PLEKHG6, PLEKHG6</i>                  | TSS1500, TSS200                       | N_Shore | FALSE |
| cg04192168 | 0.29 | 0.18 | 0.11 | 48.07  | Chr15: 64806741  | <i>ZNF609</i>                            | Body                                  |         | TRUE  |
| cg04880091 | 0.56 | 0.45 | 0.11 | 29.65  | Chr8: 43132451   |  |                                       | Island  | FALSE |
| cg06202470 | 0.92 | 0.80 | 0.11 | 112.28 | Chr12: 11700489  |  |                                       |         | FALSE |
| cg05825244 | 0.54 | 0.43 | 0.11 | 29.45  | Chr20: 2730488   | <i>EBF4</i>                              | Body                                  | Island  | FALSE |
| cg27102737 | 0.77 | 0.66 | 0.11 | 46.87  | Chr8: 59468814   | <i>SDCBP, SDCBP, SDCBP, SDCBP</i>        | 5'UTR, 5'UTR, 5'UTR, 5'UTR            | S_Shelf | FALSE |
| cg00547480 | 0.49 | 0.38 | 0.11 | 29.68  | Chr10: 103875961 | <i>LDB1, LDB1</i>                        | Body, TSS1500                         | N_Shelf | FALSE |

|            |      |      |      |       |                  |                            |                        |         |       |
|------------|------|------|------|-------|------------------|----------------------------|------------------------|---------|-------|
| cg00647820 | 0.27 | 0.16 | 0.11 | 51.90 | Chr17: 40259828  | <i>DHX58</i>               | Body                   | Island  | TRUE  |
| cg20824294 | 0.61 | 0.50 | 0.11 | 30.38 | Chr3: 142316082  | <i>PLS1</i>                | 5'UTR                  | S_Shore | FALSE |
| cg10169515 | 0.74 | 0.63 | 0.11 | 41.02 | Chr12: 123707536 | <i>MPHOSPH9</i>            | TSS1500                |         | FALSE |
| cg14675881 | 0.43 | 0.32 | 0.11 | 31.41 | Chr2: 43396331   |                            |                        | N_Shore | TRUE  |
| cg16553589 | 0.72 | 0.61 | 0.11 | 38.32 | Chr5: 122766566  |                            |                        |         | FALSE |
| cg12583076 | 0.39 | 0.28 | 0.11 | 33.63 | Chr12: 65082713  | <i>RASSF3</i>              | Body                   |         | TRUE  |
| cg20386487 | 0.31 | 0.20 | 0.11 | 42.64 | Chr15: 96898045  |                            |                        | Island  | FALSE |
| cg26280976 | 0.46 | 0.34 | 0.11 | 30.09 | Chr14: 69660603  |                            |                        | S_Shore | FALSE |
| cg18470780 | 0.36 | 0.25 | 0.11 | 35.90 | Chr14: 59064969  |                            |                        |         | TRUE  |
| cg13153942 | 0.78 | 0.67 | 0.11 | 46.58 | ChrX: 12924247   | <i>TLR8, LOC349408</i>     | TSS1500, Body          |         | FALSE |
| cg01863042 | 0.63 | 0.52 | 0.11 | 30.63 | Chr13: 23309892  |                            |                        |         | FALSE |
| cg02322400 | 0.36 | 0.25 | 0.11 | 36.37 | Chr11: 95980186  | <i>MAML2</i>               | Body                   |         | TRUE  |
| cg01297670 | 0.57 | 0.46 | 0.11 | 28.71 | Chr6: 31651070   |                            |                        | Island  | FALSE |
| cg22063654 | 0.42 | 0.31 | 0.11 | 31.30 | Chr8: 72758701   |                            |                        | S_Shelf | FALSE |
| cg02396126 | 0.89 | 0.78 | 0.11 | 88.34 | Chr13: 42536640  | <i>KIAA0564, KIAA0564</i>  | TSS1500, TSS1500       | S_Shore | FALSE |
| cg01950479 | 0.71 | 0.60 | 0.11 | 35.85 | Chr22: 23528162  | <i>BCR, BCR</i>            | Body, Body             | S_Shelf | FALSE |
| cg04730355 | 0.22 | 0.11 | 0.11 | 65.53 | Chr14: 51134070  | <i>SAV1</i>                | Body                   | N_Shore | FALSE |
| cg14216940 | 0.31 | 0.20 | 0.11 | 41.74 | Chr7: 50343131   | <i>IKZF1</i>               | TSS1500                | Island  | FALSE |
| cg06307913 | 0.39 | 0.28 | 0.11 | 32.63 | Chr4: 81118794   | <i>PRDM8, PRDM8, PRDM8</i> | 5'UTR, 1stExon, 5'UTR  | N_Shore | FALSE |
| cg19093370 | 0.83 | 0.72 | 0.11 | 59.10 | Chr17: 17110180  | <i>PLD6</i>                | TSS1500                | Island  | TRUE  |
| cg07778180 | 0.68 | 0.56 | 0.11 | 32.52 | Chr17: 34641309  | <i>CCL4L1, CCL4L2</i>      | Body, Body             |         | FALSE |
| cg15201545 | 0.25 | 0.13 | 0.11 | 55.83 | Chr4: 675137     | <i>MYL5</i>                | Body                   | Island  | FALSE |
| cg24895155 | 0.48 | 0.37 | 0.11 | 27.93 | Chr8: 127837199  |                            |                        |         | TRUE  |
| cg05506829 | 0.67 | 0.56 | 0.11 | 31.44 | Chr13: 47472349  | <i>HTR2A, HTR2A</i>        | TSS1500, TSS1500       |         | FALSE |
| cg12883014 | 0.39 | 0.28 | 0.11 | 31.86 | Chr12: 104855500 | <i>CHST11</i>              | Body                   | S_Shelf | FALSE |
| cg13713218 | 0.77 | 0.66 | 0.11 | 43.17 | Chr9: 100000033  | <i>KIAA1529</i>            | TSS1500                | N_Shore | FALSE |
| cg06020661 | 0.66 | 0.55 | 0.11 | 31.01 | Chr13: 47472138  | <i>HTR2A, HTR2A</i>        | TSS1500, TSS1500       |         | FALSE |
| cg13924996 | 0.49 | 0.38 | 0.11 | 27.30 | Chr11: 67053829  | <i>ADRBK1</i>              | 3'UTR                  | S_Shore | FALSE |
| cg13117948 | 0.55 | 0.44 | 0.11 | 26.94 | Chr4: 16086051   | <i>PROM1, PROM1</i>        | TSS1500, TSS1500       | S_Shore | FALSE |
| cg04553307 | 0.87 | 0.76 | 0.11 | 71.36 | Chr7: 922775     | <i>C7orf20</i>             | Body                   |         | FALSE |
| cg13405775 | 0.55 | 0.44 | 0.11 | 26.82 | Chr22: 32599648  | <i>RFPL2, RFPL2, RFPL2</i> | TSS200, 5'UTR, TSS1500 |         | FALSE |
| cg13320138 | 0.37 | 0.26 | 0.11 | 32.71 | Chr12: 6419575   | <i>PLEKHG6, PLEKHG6</i>    | TSS1500, TSS200        | N_Shore | FALSE |
| cg14884931 | 0.84 | 0.73 | 0.11 | 59.27 | Chr22: 42323359  | <i>TNFRSF13C</i>           | TSS1500                | S_Shore | FALSE |
| cg06307939 | 0.87 | 0.76 | 0.11 | 72.16 | Chr19: 12984645  | <i>MAST1</i>               | Body                   | Island  | FALSE |
| cg07690882 | 0.54 | 0.43 | 0.11 | 26.64 | Chr11: 128694303 |                            |                        | Island  | FALSE |
| cg14929208 | 0.40 | 0.29 | 0.11 | 30.32 | Chr3: 156273297  | <i>SSR3</i>                | TSS1500                | S_Shore | FALSE |
| cg26917640 | 0.62 | 0.51 | 0.11 | 28.07 | Chr15: 67204380  |                            |                        |         | FALSE |
| cg10928544 | 0.72 | 0.62 | 0.11 | 35.65 | Chr14: 91862864  | <i>CCDC88C</i>             | Body                   |         | FALSE |
| cg12636607 | 0.45 | 0.34 | 0.11 | 27.88 | Chr6: 112154581  | <i>FYN</i>                 | 5'UTR                  |         | TRUE  |

|            |      |      |      |       |                  |                                  |                     |         |       |
|------------|------|------|------|-------|------------------|----------------------------------|---------------------|---------|-------|
| cg13064658 | 0.24 | 0.13 | 0.11 | 54.41 | Chr1: 212003989  | <i>LPGAT1, LPGAT1</i>            | 5'UTR, 1stExon      | Island  | FALSE |
| cg26256630 | 0.51 | 0.40 | 0.11 | 26.21 | Chr6: 30070738   | <i>TRIM31</i>                    | 3'UTR               | N_Shore | FALSE |
| cg24404329 | 0.60 | 0.49 | 0.11 | 26.99 | Chr7: 115849899  | <i>TES</i>                       | TSS1500             | N_Shore | FALSE |
| cg17551891 | 0.60 | 0.49 | 0.11 | 26.88 | Chr7: 1960795    | <i>MAD1L1, MAD1L1, MAD1L1</i>    | Body, Body, Body    |         | FALSE |
| cg08006309 | 0.29 | 0.19 | 0.11 | 41.61 | Chr16: 1587810   | <i>IFT140, TMEM204</i>           | Body, Body          | Island  | FALSE |
| cg15506703 | 0.68 | 0.57 | 0.11 | 31.11 | Chr2: 242844601  |                                  |                     | Island  | TRUE  |
| cg08846011 | 0.89 | 0.79 | 0.11 | 85.66 | Chr1: 117318133  |                                  |                     |         | FALSE |
| cg05837990 | 0.71 | 0.60 | 0.11 | 33.67 | Chr7: 105596483  |                                  |                     |         | FALSE |
| cg14981532 | 0.23 | 0.12 | 0.11 | 56.99 | Chr1: 17215477   |                                  |                     | Island  | TRUE  |
| cg12440927 | 0.78 | 0.68 | 0.11 | 43.60 | Chr7: 157791721  | <i>PTPRN2, PTPRN2, PTPRN2</i>    | Body, Body, Body    |         | TRUE  |
| cg26582789 | 0.51 | 0.41 | 0.11 | 25.73 | ChrX: 19531688   | <i>MAP3K15</i>                   | Body                | N_Shore | FALSE |
| cg11488033 | 0.70 | 0.59 | 0.11 | 32.00 | Chr3: 196705898  |                                  |                     |         | FALSE |
| cg22968622 | 0.19 | 0.08 | 0.11 | 71.50 | Chr17: 43663579  |                                  |                     | Island  | FALSE |
| cg19584649 | 0.41 | 0.30 | 0.11 | 28.72 | Chr7: 158607898  | <i>ESYT2</i>                     | Body                |         | TRUE  |
| cg27527630 | 0.32 | 0.22 | 0.11 | 36.25 | Chr7: 29923538   | <i>WIPF3</i>                     | Body                | N_Shore | FALSE |
| cg27663938 | 0.33 | 0.22 | 0.11 | 35.27 | Chr12: 103696381 | <i>C12orf42, C12orf42</i>        | Body, Body          | Island  | FALSE |
| cg03277819 | 0.29 | 0.18 | 0.11 | 40.92 | Chr12: 772529    | <i>NINJ2</i>                     | 1stExon             |         | TRUE  |
| cg21877680 | 0.49 | 0.38 | 0.11 | 25.56 | Chr8: 43132507   |                                  |                     | S_Shore | FALSE |
| cg23187316 | 0.50 | 0.39 | 0.11 | 25.30 | Chr7: 1099788    | <i>C7orf50, C7orf50, C7orf50</i> | Body, Body, Body    | S_Shore | TRUE  |
| cg16474696 | 0.48 | 0.37 | 0.11 | 25.59 | Chr19: 13875014  | <i>MRI1, MRI1</i>                | TSS1500, TSS1500    | N_Shore | FALSE |
| cg13765957 | 0.60 | 0.50 | 0.11 | 26.03 | ChrY: 21208621   | <i>TTY14</i>                     | Body                |         | FALSE |
| cg06686742 | 0.80 | 0.69 | 0.11 | 44.82 | Chr19: 8273505   | <i>LASS4</i>                     | TSS1500             | N_Shore | FALSE |
| cg13670957 | 0.80 | 0.69 | 0.11 | 44.93 | Chr19: 18329801  | <i>PDE4C, PDE4C, PDE4C</i>       | Body, Body, Body    | N_Shore | FALSE |
| cg10636447 | 0.47 | 0.36 | 0.11 | 25.57 | Chr20: 826023    | <i>FAM110A, FAM110A, FAM110A</i> | Body, Body, 1stExon | Island  | FALSE |
| cg14632729 | 0.28 | 0.18 | 0.11 | 41.19 | Chr7: 105755441  |                                  |                     | S_Shelf | FALSE |
| cg27519958 | 0.44 | 0.33 | 0.11 | 26.43 | Chr1: 161735129  | <i>ATF6</i>                      | TSS1500             |         | FALSE |
| cg23876832 | 0.34 | 0.23 | 0.11 | 33.55 | Chr11: 62092739  |                                  |                     |         | TRUE  |
| cg02385173 | 0.63 | 0.53 | 0.11 | 26.64 | Chr11: 76571534  | <i>ACER3</i>                     | TSS1500             | N_Shore | FALSE |
| cg22996170 | 0.55 | 0.45 | 0.11 | 24.65 | Chr19: 12895529  |                                  |                     | S_Shore | TRUE  |
| cg15896696 | 0.57 | 0.46 | 0.11 | 24.64 | Chr7: 2059921    | <i>MAD1L1, MAD1L1, MAD1L1</i>    | Body, Body, Body    | Island  | FALSE |
| cg01249544 | 0.34 | 0.24 | 0.11 | 32.41 | Chr10: 69372655  | <i>CTNNA3, CTNNA3</i>            | Body, Body          |         | TRUE  |
| cg06777732 | 0.41 | 0.31 | 0.11 | 27.00 | Chr12: 131118426 |                                  |                     |         | TRUE  |
| cg06106484 | 0.58 | 0.47 | 0.10 | 24.63 | Chr8: 32985289   |                                  |                     |         | TRUE  |
| cg13546858 | 0.57 | 0.46 | 0.10 | 24.45 | Chr1: 869346     | <i>SAMD11</i>                    | Body                | Island  | FALSE |
| cg04838988 | 0.22 | 0.11 | 0.10 | 56.38 | Chr8: 70984437   | <i>PRDM14</i>                    | TSS1500             | Island  | FALSE |
| cg18919209 | 0.39 | 0.29 | 0.10 | 27.96 | Chr11: 96012039  | <i>MAML2</i>                     | Body                |         | TRUE  |
| cg17501823 | 0.35 | 0.25 | 0.10 | 31.13 | Chr12: 47219793  | <i>SLC38A4, SLC38A4</i>          | TSS200, TSS200      |         | FALSE |
| cg00088688 | 0.65 | 0.55 | 0.10 | 26.97 | Chr6: 167560504  |                                  |                     |         | TRUE  |
| cg25061701 | 0.53 | 0.43 | 0.10 | 23.99 | Chr17: 62608856  | <i>SMURF2</i>                    | Body                |         | TRUE  |

|            |      |      |      |       |                  |                                       |                                 |         |       |
|------------|------|------|------|-------|------------------|---------------------------------------|---------------------------------|---------|-------|
| cg24413781 | 0.34 | 0.23 | 0.10 | 32.44 | Chr19: 8273693   | LASS4                                 | TSS1500                         | Island  | FALSE |
| cg06180910 | 0.79 | 0.69 | 0.10 | 43.07 | Chr22: 24382663  | GSTT1                                 | Body                            | N_Shore | FALSE |
| cg15837308 | 0.55 | 0.45 | 0.10 | 24.04 | Chr6: 32427751   |                                       |                                 |         | FALSE |
| cg21156386 | 0.54 | 0.44 | 0.10 | 23.92 | Chr11: 692983    | DEAF1                                 | Body                            | N_Shore | FALSE |
| cg09913449 | 0.76 | 0.65 | 0.10 | 36.69 | Chr8: 42400586   | C8orf40, C8orf40,<br>C8orf40, C8orf40 | 5'UTR, 5'UTR,<br>5'UTR, 5'UTR   | S_Shelf | FALSE |
| cg19318393 | 0.63 | 0.52 | 0.10 | 25.54 | Chr1: 223936508  | CAPN2, CAPN2                          | Body, Body                      | Island  | TRUE  |
| cg00330518 | 0.52 | 0.42 | 0.10 | 23.67 | Chr1: 2228160    | SKI                                   | Body                            |         | FALSE |
| cg03227037 | 0.40 | 0.30 | 0.10 | 26.76 | Chr20: 62212228  |                                       |                                 | S_Shelf | FALSE |
| cg25345738 | 0.51 | 0.40 | 0.10 | 23.50 | Chr12: 108078835 | PWP1                                  | TSS1500                         | N_Shore | FALSE |
| cg13912224 | 0.76 | 0.66 | 0.10 | 36.32 | Chr6: 52172083   |                                       |                                 | Island  | FALSE |
| cg04349084 | 0.19 | 0.09 | 0.10 | 64.30 | Chr8: 23602677   |                                       |                                 |         | TRUE  |
| cg08926642 | 0.85 | 0.75 | 0.10 | 58.42 | Chr1: 7887455    | PER3                                  | Body                            | Island  | FALSE |
| cg01890417 | 0.49 | 0.39 | 0.10 | 23.63 | Chr1: 91488275   | ZNF644, ZNF644,<br>ZNF644             | TSS1500,<br>TSS1500,<br>TSS1500 | S_Shore | FALSE |
| cg02580986 | 0.56 | 0.46 | 0.10 | 23.40 | ChrX: 105421602  | MUM1L1                                | 5'UTR                           |         | TRUE  |
| cg10555744 | 0.36 | 0.25 | 0.10 | 29.37 | Chr1: 25946258   | MAN1C1                                | Body                            | S_Shore | TRUE  |
| cg15436354 | 0.49 | 0.39 | 0.10 | 23.29 | Chr19: 8117875   | CCL25                                 | TSS200                          | S_Shelf | TRUE  |
| cg26853458 | 0.52 | 0.42 | 0.10 | 23.06 | Chr17: 9805074   | RCVRN                                 | Body                            | N_Shelf | FALSE |
| cg19536401 | 0.55 | 0.44 | 0.10 | 23.03 | Chr19: 6504797   |                                       |                                 | S_Shelf | FALSE |
| cg26485825 | 0.32 | 0.22 | 0.10 | 32.89 | Chr18: 21452895  | LAMA3, LAMA3,<br>LAMA3, LAMA3         | TSS200, TSS200,<br>Body, Body   |         | FALSE |
| cg00017826 | 0.33 | 0.23 | 0.10 | 31.47 | Chr2: 30644955   |                                       |                                 |         | TRUE  |
| cg05388281 | 0.30 | 0.20 | 0.10 | 34.74 | Chr4: 125504     | ZNF718                                | Body                            | S_Shore | FALSE |
| cg14588003 | 0.48 | 0.37 | 0.10 | 23.32 | Chr15: 93361889  |                                       |                                 |         | TRUE  |
| cg23829949 | 0.44 | 0.33 | 0.10 | 24.37 | Chr1: 244214679  | ZNF238, ZNF238                        | 1stExon, 5'UTR                  | S_Shore | FALSE |
| cg27316811 | 0.53 | 0.42 | 0.10 | 22.73 | Chr16: 1576146   | IFT140                                | Body                            | S_Shore | FALSE |
| cg25481160 | 0.52 | 0.42 | 0.10 | 22.69 | Chr3: 71111489   | FOXP1                                 | Body                            | N_Shelf | FALSE |
| cg24769830 | 0.60 | 0.49 | 0.10 | 23.47 | Chr3: 108041508  | HHLA2                                 | 5'UTR                           |         | FALSE |
| cg00821186 | 0.89 | 0.79 | 0.10 | 74.33 | Chr1: 248790981  | OR2T11                                | TSS1500                         |         | FALSE |
| cg07116010 | 0.18 | 0.08 | 0.10 | 67.12 | Chr9: 35646325   |                                       |                                 | N_Shore | FALSE |
| cg22485298 | 0.42 | 0.32 | 0.10 | 24.68 | Chr6: 30853333   | DDR1, DDR1                            | 5'UTR, 5'UTR                    | S_Shore | FALSE |
| cg25810247 | 0.37 | 0.26 | 0.10 | 27.98 | Chr13: 108867154 | LIG4, LIG4, LIG4                      | 5'UTR, TSS200,<br>5'UTR         | Island  | FALSE |
| cg08787988 | 0.56 | 0.46 | 0.10 | 22.68 | Chr2: 27713044   | IFT172                                | TSS1500                         | S_Shore | FALSE |
| cg18422587 | 0.20 | 0.10 | 0.10 | 59.61 | Chr7: 3134670    |                                       |                                 |         | FALSE |
| cg24127061 | 0.29 | 0.19 | 0.10 | 35.95 | Chr11: 65839402  | PACS1                                 | Body                            | S_Shore | FALSE |
| cg01366941 | 0.24 | 0.14 | 0.10 | 44.99 | Chr16: 12172962  | SNX29                                 | Body                            |         | FALSE |
| cg24549702 | 0.62 | 0.51 | 0.10 | 23.72 | Chr2: 235364440  |                                       |                                 |         | FALSE |
| cg23743554 | 0.61 | 0.51 | 0.10 | 23.62 | Chr11: 65321226  | LTBP3, LTBP3,<br>LTBP3                | Body, Body, Body                | Island  | FALSE |
| cg20737812 | 0.49 | 0.39 | 0.10 | 22.60 | Chr15: 86336631  | KLHL25                                | 5'UTR                           | N_Shore | FALSE |
| cg23525438 | 0.28 | 0.18 | 0.10 | 37.34 | Chr6: 17016226   |                                       |                                 |         | FALSE |

|            |      |      |      |       |                 |                                       |                                    |         |       |
|------------|------|------|------|-------|-----------------|---------------------------------------|------------------------------------|---------|-------|
| cg05195017 | 0.43 | 0.33 | 0.10 | 23.87 | Chr2: 242758725 | <i>NEU4, NEU4, NEU4, NEU4, NEU4</i>   | 3'UTR, 3'UTR, 3'UTR, 3'UTR, 3'UTR  | N_Shore | FALSE |
| cg11251470 | 0.54 | 0.43 | 0.10 | 22.12 | Chr7: 30008931  | <i>SCRN1, SCRN1, SCRN1, SCRN1</i>     | 5'UTR, Body, 5'UTR, 5'UTR          |         | TRUE  |
| cg19950606 | 0.42 | 0.32 | 0.10 | 24.40 | Chr17: 76121276 | <i>TMC6, TMC6</i>                     | Body, Body                         |         | FALSE |
| cg11779113 | 0.17 | 0.07 | 0.10 | 73.76 | Chr20: 62199156 | <i>PRIC285, PRIC285</i>               | Body, TSS200                       | N_Shore | FALSE |
| cg17624673 | 0.58 | 0.48 | 0.10 | 22.54 | Chr5: 140596187 | <i>PCDHB13, PCDHB13</i>               | 3'UTR, 1stExon                     | S_Shore | FALSE |
| cg01565314 | 0.77 | 0.67 | 0.10 | 35.76 | Chr19: 45737610 | <i>EXOC3L2</i>                        | TSS200                             | Island  | FALSE |
| cg11900509 | 0.69 | 0.59 | 0.10 | 27.26 | Chr10: 81946545 | <i>ANXA11, ANXA11, ANXA11</i>         | 5'UTR, 5'UTR, 5'UTR                |         | TRUE  |
| cg21171339 | 0.45 | 0.35 | 0.10 | 23.13 | Chr9: 79791169  | <i>VPS13A, VPS13A, VPS13A, VPS13A</i> | TSS1500, TSS1500, TSS1500, TSS1500 | N_Shore | FALSE |
| cg20594982 | 0.88 | 0.78 | 0.10 | 65.63 | Chr1: 976707    | <i>AGRN</i>                           | Body                               | Island  | FALSE |
| cg20970205 | 0.41 | 0.31 | 0.10 | 24.33 | Chr17: 77766040 |                                       |                                    | Island  | FALSE |
| cg07420362 | 0.59 | 0.49 | 0.10 | 22.33 | Chr11: 3647419  | <i>TRPC2</i>                          | TSS1500                            |         | FALSE |
| cg20245116 | 0.84 | 0.74 | 0.10 | 51.70 | Chr1: 55522013  | <i>PCSK9</i>                          | Body                               |         | FALSE |
| cg05313153 | 0.44 | 0.34 | 0.10 | 22.65 | Chr8: 119122430 | <i>EXT1</i>                           | 1stExon                            | N_Shore | FALSE |

**B.**

**Discoid Rash**

| CG Site ID             | Mean $\beta$ Case | Mean $\beta$ Control | $\Delta\beta$ | DiffScore | Location (HG19)  | Gene Name  | Gene-Relative Location                     | CGI-Relative Location | Enhancer |
|------------------------|-------------------|----------------------|---------------|-----------|------------------|--|--|-----------------------|----------|
| <b>Hypomethylation</b> |                   |                      |               |           |                  |  |  |                       |          |
| cg11404906             | 0.42              | 0.76                 | -0.34         | -338.91   | Chr6: 32551749   | <i>HLA-DRB1</i>  | Body                                       | N_Shore               | FALSE    |
| cg21549285             | 0.38              | 0.63                 | -0.25         | -215.39   | Chr21: 42799141  | <i>MX1, MX1</i>  | 5'UTR, 5'UTR                               | S_Shore               | FALSE    |
| cg14392283             | 0.64              | 0.90                 | -0.25         | -338.91   | Chr8: 144103587  | <i>LY6E, LY6E</i>                                      | 3'UTR, 3'UTR                               | N_Shelf               | FALSE    |
| cg08122652             | 0.53              | 0.75                 | -0.22         | -188.13   | Chr3: 122281939  | <i>PARP9, PARP9, DTX3L, PARP9, PARP9, PARP9, PARP9</i> | 5'UTR, 5'UTR, TSS1500, 5'UTR, 5'UTR, 5'UTR | N_Shore               | FALSE    |
| cg24668570             | 0.09              | 0.30                 | -0.21         | -254.37   | Chr10: 134973778 | <i>KNDC1</i>   | TSS200                                     | Island                | FALSE    |
| cg23066280             | 0.42              | 0.64                 | -0.21         | -144.59   | Chr7: 158032496  | <i>PTPRN2, PTPRN2</i>                                  | Body, Body, Body                           |                       | FALSE    |
| cg18480627             | 0.42              | 0.63                 | -0.21         | -137.10   | Chr2: 130795582  | <i>LOC440905</i>                                       | Body                                       | Island                | FALSE    |
| cg24088508             | 0.26              | 0.47                 | -0.21         | -146.58   | Chr1: 38156462   | <i>C1orf109</i>  | TSS1500                                    | N_Shore               | FALSE    |
| cg19214707             | 0.31              | 0.52                 | -0.21         | -133.32   | Chr7: 3157722    |  |  |                       | TRUE     |
| cg03607951             | 0.47              | 0.68                 | -0.20         | -136.47   | Chr1: 79085586   | <i>IFI44L</i>  | TSS1500                                    |                       | FALSE    |
| cg05696877             | 0.27              | 0.48                 | -0.20         | -133.32   | Chr1: 79088769   | <i>IFI44L</i>  | 5'UTR                                      |                       | FALSE    |
| cg26762873             | 0.68              | 0.88                 | -0.20         | -228.93   | Chr11: 5879799   | <i>OR52E8</i>  | TSS1500                                    |                       | FALSE    |
| cg05552874             | 0.57              | 0.76                 | -0.19         | -132.81   | Chr10: 91153143  | <i>IFIT1</i>   | Body                                       |                       | FALSE    |
| cg01797371             | 0.18              | 0.36                 | -0.19         | -139.72   | Chr3: 195578240  |  |  |                       | FALSE    |
| cg20917491             | 0.15              | 0.34                 | -0.19         | -149.47   | Chr3: 195578259  |  |  |                       | FALSE    |
| cg08103988             | 0.49              | 0.67                 | -0.19         | -109.96   | Chr17: 6558365   |  |  | Island                | FALSE    |
| cg06981309             | 0.44              | 0.62                 | -0.18         | -95.19    | Chr3: 146260954  | <i>PLSCR1</i>  | 5'UTR                                      | N_Shore               | FALSE    |
| cg07157030             | 0.45              | 0.63                 | -0.18         | -95.79    | Chr14: 63671356  | <i>RHOJ, RHOJ</i>                                      | 5'UTR, 1stExon                             |                       | TRUE     |
| cg01028142             | 0.67              | 0.85                 | -0.18         | -160.34   | Chr2: 7004578    | <i>CMPK2</i>   | Body                                       | N_Shore               | FALSE    |
| cg05779406             | 0.37              | 0.54                 | -0.18         | -90.21    | Chr7: 1198841    | <i>ZFAND2A</i>   | 5'UTR                                      | N_Shore               | FALSE    |
| cg17384323             | 0.54              | 0.71                 | -0.17         | -93.18    | Chr4: 169242366  |  |  | S_Shelf               | FALSE    |
| cg18771300             | 0.42              | 0.58                 | -0.16         | -73.27    | Chr14: 63671737  | <i>RHOJ</i>  | 1stExon                                    |                       | TRUE     |
| cg04554929             | 0.22              | 0.38                 | -0.16         | -90.54    | Chr8: 105342491  |  |  | Island                | FALSE    |
| cg11478607             | 0.03              | 0.18                 | -0.16         | -216.49   | Chr22: 24384400  | <i>GSTT1</i>   | TSS200                                     | Island                | FALSE    |
| cg22862003             | 0.54              | 0.70                 | -0.16         | -80.16    | Chr21: 42797588  | <i>MX1, MX1</i>  | TSS1500, 5'UTR                             | N_Shore               | FALSE    |
| cg23804921             | 0.36              | 0.52                 | -0.16         | -69.85    | Chr15: 30861172  |  |  | N_Shelf               | FALSE    |
| cg00555438             | 0.12              | 0.28                 | -0.16         | -122.81   | Chr3: 195578280  |  |  |                       | FALSE    |
| cg24858233             | 0.10              | 0.26                 | -0.16         | -130.18   | Chr3: 195578055  |  |  |                       | FALSE    |
| cg14687298             | 0.24              | 0.39                 | -0.15         | -78.39    | Chr12: 31272119  |  |  |                       | FALSE    |
| cg03299990             | 0.34              | 0.50                 | -0.15         | -64.48    | Chr20: 1757570   |  |  | N_Shore               | FALSE    |
| cg04234412             | 0.21              | 0.36                 | -0.15         | -81.66    | Chr22: 24373322  | <i>LOC391322</i>                                       | Body                                       | Island                | FALSE    |
| cg06188083             | 0.22              | 0.37                 | -0.15         | -79.72    | Chr10: 91093005  | <i>IFIT3, IFIT3</i>                                    | Body, Body                                 |                       | TRUE     |
| cg14951497             | 0.27              | 0.42                 | -0.15         | -70.16    | Chr2: 191875807  | <i>STAT1, STAT1</i>                                    | 5'UTR, 5'UTR                               | N_Shelf               | FALSE    |
| cg01394167             | 0.45              | 0.60                 | -0.15         | -62.69    | Chr4: 9479622    |  |  |                       | FALSE    |
| cg24898914             | 0.56              | 0.71                 | -0.15         | -71.77    | Chr6: 32810706   | <i>PSMB8, PSMB8</i>                                    | Body, Body                                 | N_Shore               | FALSE    |
| cg14212360             | 0.62              | 0.77                 | -0.15         | -82.94    | Chr4: 89302999   | <i>HERC6, HERC6</i>                                    | Body, Body                                 | S_Shelf               | FALSE    |
| cg02380802             | 0.40              | 0.55                 | -0.15         | -58.79    | Chr16: 53407808  |  |  | S_Shore               | FALSE    |
| cg15708909             | 0.55              | 0.70                 | -0.15         | -67.07    | Chr6: 32487314   | <i>HLA-DRB5</i>  | Body                                       | N_Shelf               | FALSE    |
| cg10384133             | 0.43              | 0.58                 | -0.15         | -57.61    | Chr9: 45733081   |  |  | N_Shore               | FALSE    |
| cg00855901             | 0.27              | 0.41                 | -0.15         | -65.47    | Chr1: 79085765   | <i>IFI44L</i>  | TSS1500                                    |                       | FALSE    |
| cg10819238             | 0.77              | 0.92                 | -0.15         | -176.55   | Chr19: 1155184   | <i>SBNO2</i>   | 5'UTR                                      | Island                | TRUE     |
| cg23733394             | 0.38              | 0.53                 | -0.15         | -56.94    | Chr1: 839752     |  |  | Island                | FALSE    |
| cg21358336             | 0.52              | 0.66                 | -0.14         | -59.58    | Chr17: 6558440   |  |  | Island                | FALSE    |
| cg14926196             | 0.39              | 0.53                 | -0.14         | -54.74    | Chr6: 37616482   | <i>MDGA1</i>   | Body                                       | Island                | FALSE    |
| cg00676801             | 0.24              | 0.39                 | -0.14         | -65.71    | Chr2: 191876673  | <i>STAT1, STAT1</i>                                    | 5'UTR, 5'UTR                               | N_Shore               | FALSE    |
| cg06917450             | 0.30              | 0.44                 | -0.14         | -56.40    | Chr1: 38156652   | <i>C1orf109</i>  | TSS1500                                    | N_Shore               | FALSE    |
| cg15448220             | 0.63              | 0.77                 | -0.14         | -73.50    | Chr1: 150897856  | <i>SETDB1, SETDB1, SETDB1</i>                          | TSS1500, TSS1500, TSS1500                  | N_Shore               | FALSE    |
| cg21656205             | 0.43              | 0.57                 | -0.14         | -51.42    | Chr20: 43439688  | <i>RIMS4</i>   | TSS1500                                    | S_Shore               | FALSE    |
| cg03913456             | 0.20              | 0.34                 | -0.14         | -70.33    | Chr2: 97000924   | <i>NCAPH</i>   | TSS1500                                    | N_Shore               | FALSE    |
| cg13405775             | 0.42              | 0.56                 | -0.14         | -50.75    | Chr22: 32599648  | <i>RFPL2, RFPL2, RFPL2</i>                             | TSS200, 5'UTR, TSS1500                     |                       | FALSE    |
| cg25100880             | 0.60              | 0.74                 | -0.14         | -63.16    | Chr11: 5878019   | <i>OR52E8</i>  | 1stExon                                    |                       | FALSE    |
| cg26983430             | 0.11              | 0.25                 | -0.14         | -95.61    | Chr7: 24549675   | <i>RBMY1J, RBMY1J</i>                                  | 5'UTR, 1stExon,                            | Island                | FALSE    |

|            |      |      |       |         |                  |                                     |                        |         |       |
|------------|------|------|-------|---------|------------------|-------------------------------------|------------------------|---------|-------|
| cg08624648 | 0.60 | 0.73 | -0.14 | -62.04  | Chr6: 31651029   | <i>RBMY1F</i>                       | 5'UTR                  | Island  | FALSE |
| cg08937107 | 0.57 | 0.70 | -0.14 | -57.47  | Chr16: 3136857   |                                     |                        | N_Shelf | FALSE |
| cg08159663 | 0.42 | 0.55 | -0.14 | -47.05  | Chr16: 57022486  | <i>NLRC5</i>                        | TSS1500                | N_Shore | TRUE  |
| cg24247231 | 0.48 | 0.61 | -0.13 | -48.47  | Chr15: 67904302  | <i>MAP2K5, MAP2K5</i>               | Body, Body             |         | TRUE  |
| cg10044179 | 0.39 | 0.53 | -0.13 | -46.86  | Chr21: 15352983  | <i>C21orf81</i>                     | TSS1500                | S_Shore | FALSE |
| cg01238044 | 0.12 | 0.26 | -0.13 | -88.87  | Chr22: 24384105  | <i>GSTT1</i>                        | Body                   | N_Shore | FALSE |
| cg17980508 | 0.46 | 0.59 | -0.13 | -47.10  | Chr1: 79085713   | <i>IFI44L</i>                       | TSS1500                |         | FALSE |
| cg14554813 | 0.64 | 0.77 | -0.13 | -68.78  | Chr9: 69092015   | <i>PGM5P2</i>                       | Body                   |         | FALSE |
| cg03671052 | 0.24 | 0.38 | -0.13 | -56.62  | Chr5: 180086260  |                                     |                        |         | FALSE |
| cg16920502 | 0.56 | 0.69 | -0.13 | -54.24  | Chr8: 133141439  | <i>KCNQ3</i>                        | 3'UTR                  | N_Shore | FALSE |
| cg09592244 | 0.30 | 0.43 | -0.13 | -49.37  | Chr17: 37024020  |                                     |                        | N_Shore | FALSE |
| cg25125450 | 0.64 | 0.77 | -0.13 | -65.54  | Chr22: 32601274  | <i>RFPL2</i>                        | TSS1500                |         | FALSE |
| cg18686270 | 0.67 | 0.80 | -0.13 | -72.63  | Chr3: 146258875  | <i>PLSCR1</i>                       | 5'UTR                  | N_Shelf | FALSE |
| cg17052675 | 0.59 | 0.72 | -0.13 | -53.28  | Chr2: 3827356    |                                     |                        |         | TRUE  |
| cg03278514 | 0.42 | 0.54 | -0.13 | -41.69  | Chr15: 70779346  |                                     |                        |         | TRUE  |
| cg06161600 | 0.44 | 0.57 | -0.13 | -41.91  | Chr16: 1393797   | <i>BAIAP3</i>                       | Body                   | Island  | FALSE |
| cg08750459 | 0.43 | 0.56 | -0.13 | -41.38  | Chr17: 6558815   |                                     |                        | N_Shore | FALSE |
| cg17393016 | 0.51 | 0.64 | -0.13 | -43.04  | Chr17: 79283390  | <i>C17orf55</i>                     | TSS1500                | N_Shore | TRUE  |
| cg04335523 | 0.68 | 0.81 | -0.13 | -71.87  | Chr10: 53790078  | <i>PRKG1, PRKG1</i>                 | Body, Body             |         | TRUE  |
| cg00274965 | 0.40 | 0.52 | -0.13 | -39.36  | Chr21: 34405681  |                                     |                        | Island  | FALSE |
| cg06442240 | 0.65 | 0.78 | -0.13 | -60.02  | Chr16: 19129228  | <i>ITPRIPL2, ITPRIPL2, ITPRIPL2</i> | 1stExon, Body, 3'UTR   | S_Shore | FALSE |
| cg14582100 | 0.45 | 0.58 | -0.13 | -38.96  | Chr15: 45693742  | <i>SPATA5L1, SPATA5L1</i>           | TSS1500, TSS1500       | N_Shore | FALSE |
| cg14126601 | 0.45 | 0.57 | -0.12 | -38.23  | Chr2: 37384708   | <i>EIF2AK2, EIF2AK2</i>             | TSS1500, TSS1500       | S_Shore | FALSE |
| cg08284263 | 0.40 | 0.52 | -0.12 | -37.96  | Chr10: 92958627  |                                     |                        |         | TRUE  |
| cg06623899 | 0.82 | 0.94 | -0.12 | -165.71 | Chr8: 142161840  | <i>DENND3</i>                       | Body                   |         | FALSE |
| cg09232555 | 0.56 | 0.68 | -0.12 | -44.05  | Chr8: 11619866   |                                     |                        |         | FALSE |
| cg01124132 | 0.41 | 0.53 | -0.12 | -37.38  | Chr22: 32599511  | <i>RFPL2, RFPL2, RFPL2</i>          | TSS200, 5'UTR, TSS1500 |         | FALSE |
| cg00807871 | 0.30 | 0.43 | -0.12 | -41.06  | Chr6: 37617124   | <i>MDGA1</i>                        | Body                   | Island  | TRUE  |
| cg22886393 | 0.86 | 0.98 | -0.12 | -239.39 | Chr10: 8006646   | <i>TAF3</i>                         | Body                   |         | FALSE |
| cg00566515 | 0.31 | 0.43 | -0.12 | -39.53  | Chr21: 15352608  | <i>C21orf81</i>                     | Body                   | Island  | FALSE |
| cg27295118 | 0.25 | 0.37 | -0.12 | -45.01  | Chr14: 22902226  |                                     |                        |         | FALSE |
| cg03453431 | 0.19 | 0.31 | -0.12 | -53.27  | Chr7: 157225567  |                                     |                        |         | TRUE  |
| cg04506728 | 0.61 | 0.73 | -0.12 | -47.16  | Chr16: 53407722  |                                     |                        | Island  | FALSE |
| cg04387835 | 0.58 | 0.70 | -0.12 | -43.62  | Chr17: 4649076   | <i>ZMYND15, ZMYND15</i>             | Body, Body             |         | FALSE |
| cg07839457 | 0.14 | 0.26 | -0.12 | -65.78  | Chr16: 57023022  | <i>NLRC5</i>                        | TSS1500                | N_Shore | TRUE  |
| cg06715136 | 0.73 | 0.85 | -0.12 | -77.75  | Chr7: 158046025  | <i>PTPRN2, PTPRN2, PTPRN2</i>       | Body, Body, Body       |         | FALSE |
| cg06614118 | 0.73 | 0.85 | -0.12 | -78.52  | Chr5: 180414906  | <i>BTNL3</i>                        | TSS1500                |         | FALSE |
| cg19637330 | 0.47 | 0.59 | -0.12 | -34.92  | Chr1: 19110922   |                                     |                        | Island  | TRUE  |
| cg17251423 | 0.59 | 0.71 | -0.12 | -42.92  | Chr5: 139088815  |                                     |                        | Island  | FALSE |
| cg11940040 | 0.32 | 0.44 | -0.12 | -36.77  | Chr17: 154420    | <i>RPH3AL</i>                       | Body                   | S_Shore | TRUE  |
| cg02181920 | 0.49 | 0.61 | -0.12 | -35.04  | Chr6: 32820029   | <i>TAP1</i>                         | Body                   | N_Shore | FALSE |
| cg01754423 | 0.37 | 0.49 | -0.12 | -34.13  | Chr16: 51465744  |                                     |                        |         | TRUE  |
| cg01842774 | 0.84 | 0.96 | -0.12 | -176.89 | Chr14: 106806179 |                                     |                        |         | FALSE |
| cg08808788 | 0.65 | 0.76 | -0.12 | -50.32  | Chr6: 168780797  |                                     |                        |         | FALSE |
| cg20826740 | 0.29 | 0.41 | -0.12 | -37.63  | Chr17: 37024042  |                                     |                        | N_Shore | FALSE |
| cg08859406 | 0.31 | 0.43 | -0.12 | -35.77  | Chr5: 147699718  |                                     |                        |         | FALSE |
| cg09848508 | 0.67 | 0.79 | -0.12 | -54.81  | Chr16: 1393584   | <i>BAIAP3</i>                       | Body                   | Island  | TRUE  |
| cg21159568 | 0.61 | 0.73 | -0.12 | -43.82  | Chr7: 2445331    | <i>CHST12</i>                       | 5'UTR                  | S_Shore | FALSE |
| cg21649277 | 0.05 | 0.17 | -0.12 | -104.77 | Chr19: 18117794  | <i>ARRDC2, ARRDC2</i>               | Body, TSS1500          | N_Shore | FALSE |
| cg03086067 | 0.58 | 0.70 | -0.12 | -38.57  | Chr10: 82368399  | <i>SH2D4B, SH2D4B</i>               | Body, Body             |         | FALSE |
| cg17573270 | 0.53 | 0.64 | -0.12 | -34.18  | Chr22: 42950376  | <i>SERHL2</i>                       | Body                   | S_Shore | FALSE |
| cg20053110 | 0.47 | 0.58 | -0.12 | -31.74  | Chr6: 37617864   | <i>MDGA1</i>                        | Body                   | Island  | TRUE  |
| cg23024343 | 0.61 | 0.73 | -0.12 | -42.14  | Chr7: 107201750  | <i>COG5, COG5, COG5</i>             | Body, Body, Body       | N_Shelf | FALSE |
| cg02025737 | 0.66 | 0.78 | -0.12 | -50.49  | Chr15: 33384751  |                                     |                        |         | TRUE  |
| cg26383138 | 0.59 | 0.70 | -0.12 | -38.63  | Chr2: 2119533    | <i>MYT1L</i>                        | 5'UTR                  |         | FALSE |
| cg11445109 | 0.10 | 0.22 | -0.12 | -74.12  | Chr10: 135343248 | <i>CYP2E1</i>                       | Body                   | S_Shore | FALSE |
| cg13012494 | 0.14 | 0.26 | -0.12 | -58.37  | Chr21: 47604986  | <i>C21orf56, C21orf56</i>           | TSS1500, TSS1500       | S_Shelf | FALSE |

|            |      |      |       |         |                  |  |   |         |       |
|------------|------|------|-------|---------|------------------|--|---|---------|-------|
| cg26706759 | 0.71 | 0.83 | -0.12 | -62.51  | Chr5: 169011746  | <i>CCDC99</i>                                  | 5'UTR   | S_Shore | FALSE |
| cg07011961 | 0.71 | 0.82 | -0.11 | -60.88  | Chr5: 23507594   | <i>PRDM9</i>                                   | TSS200  |         | FALSE |
| cg02452435 | 0.31 | 0.43 | -0.11 | -33.42  | Chr17: 71188192  | <i>COG1</i>                                    | TSS1500   | N_Shore | FALSE |
| cg10440639 | 0.38 | 0.49 | -0.11 | -30.78  | Chr17: 154499    | <i>RPH3AL</i>                                  | Body  | N_Shelf | TRUE  |
| cg16186435 | 0.44 | 0.55 | -0.11 | -30.34  | Chr6: 32810833   | <i>PSMB8, PSMB8</i>                            | Body, Body  | N_Shore | FALSE |
| cg03263543 | 0.64 | 0.75 | -0.11 | -44.20  | Chr2: 236673440  | <i>AGAP1, AGAP1</i>                            | Body, Body  | Island  | FALSE |
| cg25288140 | 0.70 | 0.82 | -0.11 | -58.41  | Chr17: 41278341  | <i>BRCA1, NBR2, BRCA1, BRCA1, BRCA1, BRCA1</i> | TSS1500, Body, TSS1500, TSS1500, TSS1500, TSS1500 | Island  | FALSE |
| cg06047990 | 0.05 | 0.16 | -0.11 | -105.00 | Chr3: 195578040  |  |   |         | FALSE |
| cg23264429 | 0.55 | 0.66 | -0.11 | -33.92  | Chr10: 90642003  | <i>STAMBPL1</i>                                | 5'UTR   | S_Shore | FALSE |
| cg25532627 | 0.86 | 0.98 | -0.11 | -209.20 | Chr17: 77997833  | <i>TBC1D16</i>                                 | 5'UTR   | Island  | FALSE |
| cg16853860 | 0.53 | 0.65 | -0.11 | -32.65  | Chr6: 32823116   | <i>PSMB9, PSMB9, TAP1</i>                      | Body, Body, TSS1500                               | S_Shore | FALSE |
| cg06376949 | 0.41 | 0.52 | -0.11 | -29.38  | Chr10: 91173811  | <i>IFIT5</i>                                   | TSS1500   | N_Shore | FALSE |
| cg08080396 | 0.51 | 0.63 | -0.11 | -31.22  | Chr3: 11102832   |  |   |         | FALSE |
| cg21494379 | 0.58 | 0.69 | -0.11 | -35.26  | Chr5: 88275243   |  |   |         | TRUE  |
| cg05896524 | 0.22 | 0.33 | -0.11 | -39.67  | Chr21: 47604654  | <i>C21orf56, C21orf56</i>                      | TSS1500, TSS1500                                  | S_Shore | FALSE |
| cg14172108 | 0.59 | 0.70 | -0.11 | -35.58  | Chr21: 34405553  | <i>NFE2L3</i>                                  | Body  | N_Shore | FALSE |
| cg12510708 | 0.70 | 0.82 | -0.11 | -55.96  | Chr7: 26193805   | <i>RNH1, RNH1, RNH1, RNH1, RNH1, RNH1</i>      | 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR          | S_Shore | TRUE  |
| cg23927970 | 0.77 | 0.89 | -0.11 | -85.62  | Chr11: 504933    | <i>RNH1, RNH1, RNH1, RNH1, RNH1, RNH1</i>      | 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR          | N_Shore | FALSE |
| cg26234900 | 0.25 | 0.36 | -0.11 | -36.20  | Chr6: 32820214   | <i>TAP1</i>                                    | Body  | N_Shore | FALSE |
| cg00225902 | 0.41 | 0.52 | -0.11 | -28.11  | Chr3: 66444122   | <i>LRIG1</i>                                   | Body  |         | TRUE  |
| cg06168204 | 0.41 | 0.52 | -0.11 | -28.10  | Chr6: 27570548   |  |   |         | FALSE |
| cg24704287 | 0.59 | 0.70 | -0.11 | -34.65  | Chr19: 13951481  |  |   | N_Shore | FALSE |
| cg08356262 | 0.62 | 0.73 | -0.11 | -38.64  | Chr5: 75838704   | <i>IQGAP2</i>                                  | Body  |         | TRUE  |
| cg24617313 | 0.37 | 0.48 | -0.11 | -28.30  | Chr20: 57427146  | <i>GNAS, GNAS, GNAS, GNASAS</i>                | TSS1500, 3'UTR, TSS1500                           | N_Shore | TRUE  |
| cg16341836 | 0.46 | 0.57 | -0.11 | -27.68  | Chr10: 90641389  | <i>STAMBPL1</i>                                | 5'UTR   | S_Shore | FALSE |
| cg24506221 | 0.11 | 0.22 | -0.11 | -65.11  | Chr1: 110230401  | <i>GSTM1, GSTM1</i>                            | TSS200, TSS200                                    | Island  | FALSE |
| cg17626301 | 0.21 | 0.32 | -0.11 | -39.22  | Chr6: 32820201   | <i>TAP1</i>                                    | Body  | N_Shore | FALSE |
| cg19650706 | 0.49 | 0.60 | -0.11 | -28.25  | Chr5: 140594406  | <i>PCDHB13</i>                                 | 1stExon   | N_Shore | FALSE |
| cg25087499 | 0.64 | 0.75 | -0.11 | -39.86  | Chr5: 177592761  |  |   | Island  | FALSE |
| cg23246911 | 0.44 | 0.55 | -0.11 | -27.14  | Chr17: 154671    | <i>RPH3AL</i>                                  | Body  | N_Shelf | TRUE  |
| cg20045320 | 0.21 | 0.32 | -0.11 | -39.34  | Chr11: 319555    |  |   | S_Shore | FALSE |
| cg07244098 | 0.50 | 0.61 | -0.11 | -28.15  | Chr11: 4415203   | <i>TRIM21</i>                                  | TSS1500   |         | FALSE |
| cg24749559 | 0.23 | 0.34 | -0.11 | -36.12  | Chr5: 141616065  |  |   |         | FALSE |
| cg12494166 | 0.81 | 0.92 | -0.11 | -104.71 | Chr4: 31998088   |  |   |         | FALSE |
| cg07059402 | 0.42 | 0.53 | -0.11 | -26.50  | Chr22: 38244781  | <i>MIR659, EIF3L</i>                           | TSS1500, TSS1500                                  | N_Shore | FALSE |
| cg06459104 | 0.42 | 0.52 | -0.11 | -26.51  | Chr18: 5456880   | <i>EPB41L3</i>                                 | Body  |         | TRUE  |
| cg26724018 | 0.22 | 0.33 | -0.11 | -37.70  | Chr11: 5716255   | <i>TRIM22</i>                                  | 5'UTR   |         | FALSE |
| cg24508426 | 0.31 | 0.42 | -0.11 | -29.48  | Chr10: 124578209 |  |   | Island  | FALSE |
| cg02167713 | 0.38 | 0.49 | -0.11 | -26.80  | Chr17: 79630115  |  |   | N_Shelf | FALSE |
| cg13916469 | 0.60 | 0.71 | -0.11 | -33.83  | Chr9: 95834820   | <i>SUSD3</i>                                   | Body  |         | TRUE  |
| cg04623458 | 0.77 | 0.87 | -0.11 | -74.46  | Chr16: 871165    |  |   | N_Shelf | FALSE |
| cg26702039 | 0.62 | 0.73 | -0.11 | -36.66  | Chr16: 66170991  |  |   |         | TRUE  |
| cg07833467 | 0.46 | 0.56 | -0.11 | -26.21  | Chr22: 50986511  | <i>KLHDC7B, KLHDC7B</i>                        | 5'UTR, 1stExon                                    | Island  | FALSE |
| cg26551200 | 0.84 | 0.95 | -0.11 | -144.32 | Chr7: 2681369    | <i>TTYH3</i>                                   | Body  |         | FALSE |
| cg20282814 | 0.49 | 0.60 | -0.11 | -26.71  | Chr1: 43423072   | <i>SLC2A1</i>                                  | Body  | N_Shore | FALSE |
| cg13937627 | 0.14 | 0.25 | -0.11 | -51.11  | ChrX: 153236838  | <i>TMEM187, HCFC1</i>                          | TSS1500, TSS200                                   | Island  | FALSE |
| cg21048763 | 0.80 | 0.91 | -0.11 | -99.30  | Chr17: 77997997  | <i>TBC1D16</i>                                 | 5'UTR   | S_Shore | FALSE |
| cg11819121 | 0.79 | 0.89 | -0.11 | -85.18  | Chr21: 37664031  | <i>DOPEY2</i>                                  | Body  | N_Shelf | FALSE |
| cg04610450 | 0.77 | 0.88 | -0.11 | -77.69  | Chr19: 18280601  | <i>PIK3R2</i>                                  | 3'UTR   | S_Shore | FALSE |
| cg04206742 | 0.29 | 0.40 | -0.11 | -29.51  | Chr13: 95248882  | <i>TGDS</i>                                    | TSS1500   | S_Shore | FALSE |
| cg17051704 | 0.11 | 0.21 | -0.11 | -62.45  | Chr15: 29424197  | <i>FAM189A1</i>                                | Body  |         | FALSE |
| cg12427303 | 0.34 | 0.45 | -0.11 | -26.73  | Chr22: 32599613  | <i>RFPL2, RFPL2, RFPL2</i>                     | TSS200, 5'UTR, TSS1500                            |         | FALSE |



|                         |      |      |       |         |                  |   |  |         |       |  |
|-------------------------|------|------|-------|---------|------------------|---|--|---------|-------|--|
| cg10854819              | 0.74 | 0.85 | -0.11 | -60.92  | Chr15: 31515852  |   |  |         | TRUE  |  |
| cg20811988              | 0.26 | 0.36 | -0.11 | -31.91  | Chr20: 29611924  | <i>FRG1B</i>  | Body   | Island  | FALSE |  |
| cg20169823              | 0.19 | 0.30 | -0.11 | -40.08  | Chr12: 116354837 |   |  | Island  | TRUE  |  |
| cg05856321              | 0.36 | 0.47 | -0.11 | -25.49  | Chr17: 1133546   |   |  | Island  | FALSE |  |
| cg19985056              | 0.09 | 0.19 | -0.11 | -70.05  | Chr5: 56595244   |   |  |         | FALSE |  |
| cg13368983              | 0.39 | 0.50 | -0.11 | -24.89  | Chr2: 201995729  | <i>CFLAR, CFLAR, CFLAR</i>  | Body, Body, Body   |         | FALSE |  |
| cg21265404              | 0.54 | 0.64 | -0.11 | -27.33  | Chr9: 90531866   | <i>FAM75C1</i>  | TSS1500  |         | FALSE |  |
| cg25472530              | 0.60 | 0.71 | -0.11 | -32.31  | Chr5: 23507617   | <i>PRDM9</i>  | TSS200   |         | FALSE |  |
| cg16273546              | 0.59 | 0.69 | -0.11 | -30.70  | Chr10: 123070392 |   |  |         | TRUE  |  |
| cg00481159              | 0.72 | 0.83 | -0.11 | -53.48  | Chr12: 96353086  | <i>AMDHD1</i>   | Body   | S_Shelf | FALSE |  |
| cg12906381              | 0.44 | 0.55 | -0.11 | -24.27  | Chr22: 32599516  | <i>RFPL2, RFPL2, RFPL2</i>  | TSS200, 5'UTR, TSS1500   |         | FALSE |  |
| cg00034336              | 0.63 | 0.73 | -0.11 | -34.16  | Chr2: 8684126    |   |  |         | TRUE  |  |
| cg19649900              | 0.85 | 0.95 | -0.11 | -138.39 | Chr19: 1155030   | <i>SBNO2</i>  | 5'UTR  | Island  | TRUE  |  |
| cg00601042              | 0.28 | 0.39 | -0.11 | -28.59  | Chr12: 132900274 | <i>GALNT9</i>   | Body   | Island  | FALSE |  |
| cg14020285              | 0.50 | 0.61 | -0.11 | -25.22  | Chr2: 119401665  |   |  |         | TRUE  |  |
| cg12675714              | 0.07 | 0.18 | -0.11 | -75.48  | Chr4: 159592618  | <i>C4orf46, ETFDH</i>   | Body, TSS1500  | Island  | FALSE |  |
| cg02334775              | 0.49 | 0.59 | -0.11 | -24.67  | Chr15: 89182676  | <i>ISG20</i>  | Body   |         | FALSE |  |
| cg01673307              | 0.39 | 0.49 | -0.10 | -23.98  | Chr6: 32819911   | <i>TAP1</i>   | Body   | N_Shore | FALSE |  |
| cg01219135              | 0.44 | 0.55 | -0.10 | -23.57  | Chr7: 158766336  |   |  | Island  | FALSE |  |
| cg11572942              | 0.75 | 0.85 | -0.10 | -58.72  | Chr1: 1656592    | <i>CDK11A, CDK11B, CDK11B, CDK11B, CDK11A, CDK11B, CDK11B, CDK11B</i> | TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500 | S_Shore | FALSE |  |
| cg18576957              | 0.64 | 0.74 | -0.10 | -34.32  | Chr6: 31651020   |   |  | Island  | FALSE |  |
| cg04700648              | 0.81 | 0.91 | -0.10 | -93.37  | Chr19: 52888958  | <i>ZNF880</i>   | 3'UTR  |         | FALSE |  |
| cg23400446              | 0.13 | 0.23 | -0.10 | -51.94  | Chr10: 135342560 | <i>CYP2E1</i>   | Body   | Island  | FALSE |  |
| cg17190781              | 0.76 | 0.86 | -0.10 | -62.73  | Chr6: 40387783   | <i>LRFN2</i>  | Body   |         | TRUE  |  |
| cg19651115              | 0.44 | 0.55 | -0.10 | -23.17  | Chr12: 11700343  |   |  |         | FALSE |  |
| cg27313577              | 0.75 | 0.86 | -0.10 | -59.81  | Chr7: 157260021  |   |  | N_Shore | FALSE |  |
| cg13022905              | 0.65 | 0.75 | -0.10 | -34.42  | Chr5: 147699892  |   |  |         | FALSE |  |
| cg05915866              | 0.41 | 0.51 | -0.10 | -22.40  | Chr16: 73090838  | <i>ZFH3</i>   | 5'UTR  | N_Shore | FALSE |  |
| cg04742550              | 0.50 | 0.61 | -0.10 | -23.45  | Chr16: 31366429  | <i>ITGAX</i>  | TSS200   |         | FALSE |  |
| cg07405182              | 0.67 | 0.77 | -0.10 | -36.66  | Chr1: 40598455   |   |  | N_Shore | TRUE  |  |
| cg01948202              | 0.14 | 0.25 | -0.10 | -44.30  | Chr3: 122400474  | <i>PARP14</i>   | Body   | S_Shore | FALSE |  |
| cg12789884              | 0.60 | 0.70 | -0.10 | -27.75  | Chr3: 175554437  |   |  |         | TRUE  |  |
| cg20971158              | 0.55 | 0.65 | -0.10 | -24.43  | Chr11: 35159382  | <i>CD44, CD44, CD44, CD44, CD44</i>                                   | TSS1500, TSS1500, TSS1500, TSS1500, TSS1500                            | N_Shore | FALSE |  |
| cg01973676              | 0.70 | 0.80 | -0.10 | -42.56  | Chr7: 101596404  | <i>CUX1, CUX1, CUX1</i>   | Body, Body, Body   |         | TRUE  |  |
| cg17888390              | 0.20 | 0.30 | -0.10 | -33.73  | Chr10: 101282816 |   |  | Island  | FALSE |  |
| cg24104616              | 0.78 | 0.89 | -0.10 | -71.24  | Chr6: 28969099   | <i>ZNF311</i>   | Body   |         | FALSE |  |
| cg01741372              | 0.69 | 0.79 | -0.10 | -38.76  | Chr11: 783889    |   |  |         | TRUE  |  |
| cg13732083              | 0.14 | 0.24 | -0.10 | -44.38  | Chr21: 47605072  | <i>C21orf56, C21orf56</i>   | TSS1500, TSS1500   | S_Shelf | FALSE |  |
| cg13298116              | 0.33 | 0.43 | -0.10 | -23.31  | Chr11: 62369859  | <i>EML3, MTA2</i>   | 3'UTR, TSS1500   | Island  | FALSE |  |
| cg19909865              | 0.12 | 0.22 | -0.10 | -50.04  | Chr4: 134074421  | <i>PCDH10</i>   | Body   | S_Shore | TRUE  |  |
| cg04031093              | 0.57 | 0.67 | -0.10 | -25.13  | Chr1: 233027124  |   |  |         | TRUE  |  |
| cg27473997              | 0.72 | 0.82 | -0.10 | -44.91  | Chr4: 9355351    | <i>USP17</i>  | TSS200   |         | FALSE |  |
| cg00916680              | 0.54 | 0.64 | -0.10 | -23.62  | ChrX: 152529487  |   |  | N_Shore | FALSE |  |
| cg01961752              | 0.23 | 0.33 | -0.10 | -30.00  | Chr1: 1109012    | <i>TLL10</i>  | TSS1500  | N_Shore | TRUE  |  |
| cg09166973              | 0.76 | 0.86 | -0.10 | -57.64  | Chr5: 23507573   | <i>PRDM9</i>  | TSS200   |         | FALSE |  |
| cg01190666              | 0.59 | 0.69 | -0.10 | -26.78  | Chr20: 62204908  | <i>PRIC285</i>  | 5'UTR  | N_Shore | FALSE |  |
| cg13051013              | 0.75 | 0.85 | -0.10 | -55.32  | Chr1: 149684418  |   |  |         | FALSE |  |
| cg13979884              | 0.73 | 0.83 | -0.10 | -47.00  | Chr9: 74061171   |   |  | N_Shore | FALSE |  |
| <b>Hypermethylation</b> |      |      |       |         |                  |   |  |         |       |  |
| cg05380919              | 0.89 | 0.62 | 0.27  | 341.63  | Chr22: 24376252  | <i>GSTT1</i>  | 3'UTR  | S_Shelf | FALSE |  |
| cg15262954              | 0.39 | 0.12 | 0.27  | 341.63  | Chr20: 62198872  | <i>PRIC285, PRIC285</i>   | Body, 1stExon  | Island  | FALSE |  |

|            |      |      |      |        |                  |                                     |                                 |         |       |
|------------|------|------|------|--------|------------------|-------------------------------------|---------------------------------|---------|-------|
| cg01079515 | 0.94 | 0.68 | 0.26 | 341.63 | Chr3: 195576629  |                                     |                                 |         | FALSE |
| cg00103771 | 0.67 | 0.41 | 0.26 | 341.63 | Chr6: 32525805   | <i>HLA-DRB6</i>                     | Body                            |         | FALSE |
| cg23350716 | 0.72 | 0.47 | 0.25 | 341.63 | Chr1: 147956744  | <i>PPIAL4B, PPIAL4A</i>             | TSS1500,<br>TSS1500             |         | FALSE |
| cg05357209 | 0.42 | 0.17 | 0.25 | 341.63 | Chr7: 872208     | <i>UNC84A, UNC84A</i>               | 5'UTR, Body                     |         | TRUE  |
| cg06550200 | 0.92 | 0.69 | 0.23 | 341.63 | Chr5: 1325588    | <i>CLPTM1L</i>                      | Body                            |         | FALSE |
| cg00440797 | 0.31 | 0.09 | 0.22 | 341.63 | Chr6: 32493873   | <i>HLA-DRB5</i>                     | Body                            | S_Shelf | FALSE |
| cg08477687 | 0.57 | 0.35 | 0.22 | 341.63 | Chr1: 566570     | <i>MIR1977</i>                      | TSS1500                         |         | FALSE |
| cg01694488 | 0.95 | 0.73 | 0.22 | 341.63 | Chr4: 1580172    |                                     |                                 | Island  | FALSE |
| cg01500431 | 0.91 | 0.69 | 0.22 | 341.63 | Chr22: 24388327  | <i>GSTTP2</i>                       | Body                            | S_Shelf | FALSE |
| cg02239258 | 0.58 | 0.36 | 0.22 | 341.63 | Chr8: 8241752    |                                     |                                 | N_Shore | FALSE |
| cg12303247 | 0.88 | 0.67 | 0.21 | 341.63 | Chr1: 155853542  | <i>SYT11</i>                        | 3'UTR                           |         | TRUE  |
| cg03188948 | 0.40 | 0.19 | 0.21 | 341.63 | Chr7: 1209495    |                                     |                                 |         | FALSE |
| cg03213289 | 0.52 | 0.32 | 0.19 | 114.27 | Chr20: 61660250  |                                     |                                 | Island  | FALSE |
| cg06301252 | 0.90 | 0.71 | 0.19 | 341.63 | Chr7: 157504143  | <i>PTPRN2, PTPRN2, PTPRN2</i>       | Body, Body, Body                | Island  | FALSE |
| cg00638631 | 0.90 | 0.72 | 0.19 | 341.63 | Chr21: 39039777  | <i>KCNJ6</i>                        | Body                            | Island  | FALSE |
| cg13185413 | 0.43 | 0.25 | 0.18 | 109.95 | Chr6: 30039202   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg12633154 | 0.56 | 0.38 | 0.18 | 95.16  | Chr6: 30039435   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg00947782 | 0.36 | 0.18 | 0.18 | 123.86 | Chr6: 30039142   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg10568066 | 0.59 | 0.42 | 0.18 | 92.38  | Chr6: 30039442   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg20021790 | 0.45 | 0.28 | 0.17 | 94.32  | Chr17: 181288    | <i>RPH3AL</i>                       | 5'UTR                           | N_Shelf | TRUE  |
| cg10930308 | 0.43 | 0.26 | 0.17 | 94.18  | Chr6: 30039476   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg20866694 | 0.37 | 0.20 | 0.17 | 108.72 | Chr6: 27181670   |                                     |                                 |         | FALSE |
| cg09279736 | 0.51 | 0.34 | 0.17 | 84.57  | Chr6: 30039403   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg03847896 | 0.55 | 0.38 | 0.17 | 80.83  | Chr1: 112154295  |                                     |                                 |         | TRUE  |
| cg06675417 | 0.79 | 0.62 | 0.17 | 113.88 | Chr18: 77292443  |                                     |                                 | Island  | FALSE |
| cg03343571 | 0.44 | 0.28 | 0.17 | 87.26  | Chr6: 30039175   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg19418458 | 0.56 | 0.40 | 0.16 | 75.44  | Chr7: 158789849  |                                     |                                 | Island  | FALSE |
| cg09885502 | 0.51 | 0.35 | 0.16 | 74.06  | Chr20: 57463991  | <i>GNAS, GNAS, GNAS, GNAS</i>       | 3'UTR, TSS200,<br>3'UTR, Body   | Island  | FALSE |
| cg01717482 | 0.78 | 0.62 | 0.16 | 102.34 | Chr3: 75657183   |                                     |                                 |         | FALSE |
| cg06249604 | 0.30 | 0.14 | 0.16 | 114.27 | Chr6: 30039206   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg11141652 | 0.74 | 0.58 | 0.16 | 89.39  | Chr22: 24348549  | <i>GSTTP1</i>                       | TSS1500                         |         | FALSE |
| cg14279361 | 0.59 | 0.44 | 0.16 | 69.00  | Chr19: 6721955   | <i>C3</i>                           | TSS1500                         |         | FALSE |
| cg26970113 | 0.89 | 0.74 | 0.16 | 341.63 | Chr5: 133710892  | <i>UBE2B</i>                        | Body                            | S_Shelf | FALSE |
| cg02524205 | 0.64 | 0.48 | 0.16 | 69.75  | Chr6: 167559851  |                                     |                                 |         | FALSE |
| cg13401893 | 0.57 | 0.41 | 0.15 | 66.02  | Chr6: 30039432   | <i>RNF39, RNF39</i>                 | Body, Body                      | Island  | FALSE |
| cg06758191 | 0.87 | 0.72 | 0.15 | 341.63 | Chr4: 7812988    | <i>AFAP1, AFAP1</i>                 | Body, Body                      |         | FALSE |
| cg04097388 | 0.81 | 0.66 | 0.15 | 106.29 | Chr2: 236671717  | <i>AGAP1, AGAP1</i>                 | Body, Body                      | N_Shore | FALSE |
| cg06343673 | 0.73 | 0.58 | 0.15 | 78.99  | Chr17: 78778232  | <i>RPTOR, RPTOR</i>                 | Body, Body                      | S_Shelf | FALSE |
| cg10920224 | 0.57 | 0.42 | 0.15 | 63.03  | Chr14: 103367591 | <i>TRAF3, TRAF3, TRAF3</i>          | Body, Body, Body                |         | FALSE |
| cg00035636 | 0.53 | 0.38 | 0.15 | 62.62  | Chr13: 21900591  |                                     |                                 | Island  | FALSE |
| cg11202023 | 0.77 | 0.62 | 0.15 | 86.03  | Chr4: 73437692   |                                     |                                 | S_Shelf | FALSE |
| cg26280976 | 0.41 | 0.26 | 0.15 | 71.31  | Chr14: 69660603  |                                     |                                 | S_Shore | FALSE |
| cg10599438 | 0.41 | 0.26 | 0.15 | 69.95  | Chr19: 844589    | <i>PRTN3</i>                        | Body                            | N_Shore | FALSE |
| cg17624673 | 0.67 | 0.52 | 0.15 | 66.74  | Chr5: 140596187  | <i>PCDHB13, PCDHB13</i>             | 3'UTR, 1stExon                  | S_Shore | FALSE |
| cg11775292 | 0.40 | 0.26 | 0.15 | 67.89  | Chr15: 33487631  |                                     |                                 | S_Shore | TRUE  |
| cg01252526 | 0.51 | 0.37 | 0.15 | 58.75  | Chr16: 711033    | <i>WDR90</i>                        | Body                            | N_Shore | TRUE  |
| cg15242686 | 0.70 | 0.55 | 0.15 | 66.54  | Chr22: 24348715  | <i>GSTTP1</i>                       | TSS1500                         |         | FALSE |
| cg17014757 | 0.49 | 0.34 | 0.15 | 58.65  | Chr1: 203156097  | <i>CHI3L1</i>                       | TSS200                          |         | TRUE  |
| cg08045932 | 0.64 | 0.50 | 0.14 | 59.75  | Chr20: 61659980  |                                     |                                 | N_Shore | FALSE |
| cg26642960 | 0.79 | 0.64 | 0.14 | 85.82  | Chr19: 54747789  | <i>LILRA6</i>                       | TSS1500                         |         | FALSE |
| cg15948536 | 0.44 | 0.29 | 0.14 | 60.69  | Chr4: 169770092  | <i>PALLD, PALLD, PALLD, PALLD</i>   | 5'UTR, Body,<br>Body, Body      |         | TRUE  |
| cg17416644 | 0.67 | 0.53 | 0.14 | 61.00  | Chr11: 1474841   | <i>BRSK2</i>                        | Body                            | S_Shelf | FALSE |
| cg02996355 | 0.48 | 0.34 | 0.14 | 56.55  | Chr14: 81879375  |                                     |                                 |         | FALSE |
| cg19537719 | 0.49 | 0.35 | 0.14 | 55.13  | Chr8: 41583498   | <i>ANK1, ANK1, ANK1, ANK1, ANK1</i> | Body, Body,<br>Body, Body, Body | Island  | FALSE |
| cg12310025 | 0.54 | 0.39 | 0.14 | 53.46  | Chr6: 25882481   |                                     |                                 | Island  | FALSE |
| cg14017402 | 0.40 | 0.26 | 0.14 | 62.11  | Chr2: 86225602   |                                     |                                 |         | TRUE  |
| cg15690347 | 0.40 | 0.26 | 0.14 | 61.52  | Chr19: 50931515  | <i>SPIB</i>                         | Body                            | Island  | FALSE |
| cg09352518 | 0.38 | 0.24 | 0.14 | 63.50  | Chr19: 21265421  | <i>ZNF714</i>                       | 5'UTR                           | Island  | FALSE |

|            |      |      |      |        |                  |   |  |         |       |
|------------|------|------|------|--------|------------------|---|--|---------|-------|
| cg09584650 | 0.49 | 0.35 | 0.14 | 52.33  | Chr8: 2002012    | <i>MYOM2</i>  | Body   | N_Shore | FALSE |
| cg02188185 | 0.57 | 0.44 | 0.14 | 50.92  | Chr6: 30039524   | <i>RNF39, RNF39</i>   | Body, Body   | S_Shore | FALSE |
| cg23221052 | 0.57 | 0.43 | 0.14 | 50.45  | Chr5: 179740743  | <i>GFPT2</i>  | Body   | Island  | FALSE |
| cg02174092 | 0.36 | 0.22 | 0.14 | 65.09  | Chr10: 43846539  |   |  | Island  | FALSE |
| cg17751872 | 0.47 | 0.34 | 0.14 | 50.86  | Chr19: 21264982  | <i>ZNF714, ZNF714</i>   | 5'UTR, 1stExon   | N_Shore | FALSE |
| cg07512361 | 0.75 | 0.61 | 0.14 | 65.51  | Chr7: 101944430  | <i>SH2B2</i>  | Body   | Island  | FALSE |
| cg27171569 | 0.70 | 0.57 | 0.13 | 56.38  | Chr16: 83987465  | <i>OSGIN1, OSGIN1, OSGIN1</i>   | 5'UTR, Body, 5'UTR   |         | TRUE  |
| cg12709009 | 0.80 | 0.67 | 0.13 | 77.78  | Chr6: 170557582  |   |  |         | FALSE |
| cg16338365 | 0.55 | 0.41 | 0.13 | 46.18  | Chr6: 167559913  |   |  |         | FALSE |
| cg05867499 | 0.27 | 0.13 | 0.13 | 83.27  | Chr7: 4848814    | <i>RADIL</i>  | Body   | Island  | FALSE |
| cg24441899 | 0.54 | 0.40 | 0.13 | 44.81  | Chr7: 4244372    | <i>SDK1, SDK1</i>   | Body, Body   |         | FALSE |
| cg10555744 | 0.37 | 0.24 | 0.13 | 56.16  | Chr1: 25946258   | <i>MAN1C1</i>   | Body   | S_Shore | TRUE  |
| cg06423211 | 0.77 | 0.64 | 0.13 | 65.39  | Chr19: 551401    |   |  | Island  | FALSE |
| cg02779037 | 0.20 | 0.07 | 0.13 | 115.46 | Chr7: 4848683    | <i>RADIL</i>  | Body   | Island  | FALSE |
| cg10277872 | 0.78 | 0.65 | 0.13 | 67.71  | Chr4: 4136918    |   |  |         | FALSE |
| cg26893861 | 0.45 | 0.32 | 0.13 | 46.81  | Chr17: 41843967  | <i>DUSP3</i>  | 3'UTR  |         | FALSE |
| cg04111992 | 0.57 | 0.44 | 0.13 | 43.32  | Chr7: 158790115  |   |  | S_Shore | FALSE |
| cg20381404 | 0.15 | 0.02 | 0.13 | 341.63 | Chr5: 34008215   | <i>AMACR, AMACR, AMACR, AMACR, AMACR, AMACR, AMACR, AMACR, AMACR, AMACR</i> | 5'UTR, 1stExon, 5'UTR, 1stExon, 1stExon, 5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR | S_Shore | FALSE |
| cg13448197 | 0.33 | 0.20 | 0.13 | 60.33  | Chr10: 43846281  |   |  | Island  | FALSE |
| cg01483656 | 0.32 | 0.19 | 0.13 | 62.84  | Chr19: 21264896  | <i>ZNF714</i>   | TSS200   | N_Shore | FALSE |
| cg26576544 | 0.48 | 0.35 | 0.13 | 43.59  | Chr7: 38316654   |   |  |         | FALSE |
| cg18451016 | 0.71 | 0.58 | 0.13 | 52.53  | Chr1: 38461880   |   |  | Island  | FALSE |
| cg11236515 | 0.33 | 0.20 | 0.13 | 59.15  | Chr2: 74213762   |   |  | S_Shore | FALSE |
| cg21809927 | 0.61 | 0.48 | 0.13 | 42.90  | Chr6: 30079265   | <i>TRIM31</i>   | Body   |         | FALSE |
| cg16767506 | 0.28 | 0.15 | 0.13 | 71.94  | Chr7: 142494244  |   |  | N_Shore | TRUE  |
| cg05552543 | 0.29 | 0.16 | 0.13 | 67.34  | Chr16: 75322715  |   |  |         | TRUE  |
| cg08858441 | 0.43 | 0.31 | 0.13 | 44.38  | Chr1: 569427     |   |  |         | FALSE |
| cg15942979 | 0.21 | 0.08 | 0.13 | 103.74 | Chr8: 22497061   | <i>BIN3</i>   | Body   |         | FALSE |
| cg12086421 | 0.87 | 0.74 | 0.13 | 95.11  | Chr6: 68535378   |   |  |         | FALSE |
| cg13318129 | 0.34 | 0.21 | 0.13 | 54.83  | Chr22: 45737514  | <i>FAM118A, FAM118A</i>   | 3'UTR, 3'UTR   |         | FALSE |
| cg17593958 | 0.30 | 0.18 | 0.13 | 60.45  | Chr20: 62199034  | <i>PRIC285, PRIC285, PRIC285</i>  | 5'UTR, Body, 1stExon   | N_Shore | FALSE |
| cg19052272 | 0.80 | 0.67 | 0.13 | 65.18  | Chr2: 3704530    | <i>ALLC</i>   | TSS1500  |         | FALSE |
| cg18930910 | 0.36 | 0.24 | 0.13 | 49.11  | Chr6: 30039151   | <i>RNF39, RNF39</i>   | Body, Body   | Island  | FALSE |
| cg18805164 | 0.75 | 0.62 | 0.13 | 54.08  | Chr19: 36265700  | <i>SNX26</i>  | TSS1500  | N_Shore | FALSE |
| cg10686758 | 0.38 | 0.26 | 0.13 | 46.73  | Chr17: 39279735  | <i>KRTAP4-12, KRTAP4-12</i>   | 3'UTR, 1stExon   |         | FALSE |
| cg04349084 | 0.29 | 0.17 | 0.12 | 62.63  | Chr8: 23602677   |   |  |         | TRUE  |
| cg24838063 | 0.82 | 0.70 | 0.12 | 71.75  | Chr12: 130822603 | <i>PIWIL1</i>   | TSS200   | Island  | FALSE |
| cg07390013 | 0.81 | 0.68 | 0.12 | 67.71  | Chr1: 230838294  | <i>AGT</i>  | 3'UTR  |         | FALSE |
| cg17920646 | 0.51 | 0.39 | 0.12 | 37.85  | Chr8: 216578     |   |  | Island  | FALSE |
| cg00758881 | 0.34 | 0.22 | 0.12 | 50.90  | Chr16: 58534681  | <i>NDRG4, NDRG4, NDRG4</i>  | Body, Body, Body   | N_Shore | FALSE |
| cg09640425 | 0.53 | 0.41 | 0.12 | 37.17  | Chr7: 158790006  |   |  | Island  | FALSE |
| cg18402987 | 0.20 | 0.08 | 0.12 | 97.75  | Chr7: 1209562    |   |  |         | FALSE |
| cg17542795 | 0.73 | 0.61 | 0.12 | 48.81  | Chr4: 178518017  |   |  |         | TRUE  |
| cg04255230 | 0.45 | 0.32 | 0.12 | 39.22  | Chr2: 74727010   | <i>LBX2</i>   | Body   | Island  | FALSE |
| cg26099834 | 0.41 | 0.29 | 0.12 | 41.06  | Chr15: 66947568  |   |  | Island  | FALSE |
| cg09425279 | 0.54 | 0.42 | 0.12 | 36.04  | Chr16: 31188401  |   |  | N_Shelf | FALSE |
| cg11062466 | 0.46 | 0.34 | 0.12 | 37.52  | Chr8: 58055876   |   |  | N_Shore | FALSE |
| cg27387030 | 0.44 | 0.32 | 0.12 | 38.23  | Chr1: 203320541  | <i>FMOD</i>   | TSS1500  |         | FALSE |
| cg02385173 | 0.66 | 0.54 | 0.12 | 39.41  | Chr11: 76571534  | <i>ACER3</i>  | TSS1500  | N_Shore | FALSE |
| cg13944838 | 0.63 | 0.51 | 0.12 | 37.52  | Chr5: 179740914  | <i>GFPT2</i>  | Body   | Island  | FALSE |
| cg08779649 | 0.61 | 0.49 | 0.12 | 36.56  | Chr13: 50194554  |   |  |         | FALSE |
| cg18816397 | 0.56 | 0.44 | 0.12 | 34.96  | Chr6: 32489555   | <i>HLA-DRB5</i>   | Body   | N_Shore | FALSE |
| cg15145296 | 0.31 | 0.19 | 0.12 | 52.85  | Chr3: 125709740  |   |  | S_Shore | FALSE |
| cg14522718 | 0.19 | 0.07 | 0.12 | 98.71  | Chr9: 130868874  | <i>SLC25A25, SLC25A25, SLC25A25,</i>  | Body, Body, Body, Body   |         | FALSE |

|            |      |      |      |        |                  |   |   |         |       |
|------------|------|------|------|--------|------------------|---|---|---------|-------|
| cg00739471 | 0.33 | 0.21 | 0.12 | 47.75  | Chr14: 69415588  | <i>SLC25A25</i><br><i>ACTN1, ACTN1,</i><br><i>ACTN1</i>             | Body, Body, Body                                |         | FALSE |
| cg20290983 | 0.21 | 0.09 | 0.12 | 83.12  | Chr6: 43655470   | <i>MRPS18A</i>  | 1stExon   | Island  | FALSE |
| cg19035788 | 0.43 | 0.31 | 0.12 | 36.68  | Chr2: 242881634  |   |   | S_Shelf | FALSE |
| cg19453686 | 0.45 | 0.33 | 0.12 | 35.18  | Chr14: 92334271  | <i>TC2N</i>   | TSS1500   |         | FALSE |
| cg08474748 | 0.44 | 0.32 | 0.12 | 35.58  | Chr5: 74350214   |   |   | Island  | FALSE |
| cg05600342 | 0.27 | 0.15 | 0.12 | 59.39  | Chr11: 250989    | <i>PSMD13, PSMD13</i>   | Body, Body                                      |         | TRUE  |
| cg13469425 | 0.79 | 0.67 | 0.12 | 54.98  | Chr4: 48175353   | <i>TEC</i>  | Body  |         | TRUE  |
| cg06180910 | 0.85 | 0.73 | 0.12 | 74.57  | Chr22: 24382663  | <i>GSTT1</i>  | Body  | N_Shore | FALSE |
| cg08071329 | 0.93 | 0.81 | 0.12 | 126.76 | Chr6: 170555857  |   |   |         | FALSE |
| cg11949518 | 0.44 | 0.32 | 0.12 | 35.17  | Chr17: 78912765  | <i>RPTOR, RPTOR</i>   | Body, Body                                      | N_Shelf | FALSE |
| cg21873524 | 0.43 | 0.31 | 0.12 | 35.60  | Chr4: 190942744  |   |   | Island  | FALSE |
| cg15529432 | 0.51 | 0.40 | 0.12 | 32.40  | Chr5: 16615750   | <i>FAM134B</i>  | Body  | N_Shore | FALSE |
| cg14047540 | 0.86 | 0.74 | 0.12 | 77.48  | Chr11: 133829660 |   |   | S_Shelf | FALSE |
| cg19595760 | 0.29 | 0.17 | 0.12 | 53.86  | Chr1: 25948511   | <i>MANIC1</i>   | Body  | S_Shelf | TRUE  |
| cg01050736 | 0.79 | 0.67 | 0.12 | 53.73  | Chr6: 32710583   | <i>HLA-DQA2</i>   | Body  |         | FALSE |
| cg21724239 | 0.54 | 0.42 | 0.12 | 31.56  | Chr8: 58056113   |   |   | Island  | FALSE |
| cg13390570 | 0.28 | 0.16 | 0.12 | 54.03  | Chr5: 1255616    | <i>TERT, TERT</i>   | Body, Body                                      | N_Shore | FALSE |
| cg07970799 | 0.21 | 0.10 | 0.11 | 74.92  | Chr6: 6614719    | <i>LOC285780, LY86</i>  | Body, Body                                      |         | FALSE |
| cg12420107 | 0.42 | 0.31 | 0.11 | 33.11  | Chr5: 140090300  | <i>VTRNA1-1</i>   | TSS1500   |         | FALSE |
| cg02486855 | 0.73 | 0.62 | 0.11 | 40.72  | Chr15: 67356942  | <i>SMAD3</i>  | TSS1500   | N_Shore | FALSE |
| cg23939001 | 0.66 | 0.54 | 0.11 | 33.64  | Chr4: 940644     | <i>TMEM175</i>  | 5'UTR   | Island  | FALSE |
| cg16192197 | 0.26 | 0.14 | 0.11 | 56.75  | Chr6: 112301106  |   |   |         | TRUE  |
| cg23917638 | 0.42 | 0.31 | 0.11 | 32.95  | Chr1: 567501     | <i>MIR1977</i>  | TSS1500   |         | FALSE |
| cg21167269 | 0.41 | 0.30 | 0.11 | 33.73  | Chr9: 98981500   |   |   | Island  | FALSE |
| cg12196389 | 0.88 | 0.76 | 0.11 | 82.79  | Chr10: 35504007  |   |   | Island  | FALSE |
| cg01768001 | 0.34 | 0.22 | 0.11 | 40.63  | Chr1: 24831147   | <i>RCAN3</i>  | 5'UTR   | S_Shore | FALSE |
| cg12893697 | 0.36 | 0.25 | 0.11 | 37.02  | Chr11: 970389    | <i>AP2A2</i>  | Body  |         | FALSE |
| cg03396347 | 0.67 | 0.56 | 0.11 | 33.66  | Chr1: 1875803    |   |   | Island  | FALSE |
| cg13719246 | 0.87 | 0.76 | 0.11 | 76.52  | Chr8: 7639801    |   |   |         | FALSE |
| cg23159337 | 0.55 | 0.44 | 0.11 | 28.41  | Chr3: 193272778  | <i>ATP13A4</i>  | TSS200  |         | TRUE  |
| cg20557159 | 0.56 | 0.45 | 0.11 | 28.33  | Chr17: 75445261  | <i>SEPT9, SEPT9,</i><br><i>SEPT9, SEPT9,</i><br><i>SEPT9, SEPT9</i> | Body, Body,<br>Body, Body,<br>TSS1500, Body     | N_Shelf | FALSE |
| cg10598596 | 0.61 | 0.50 | 0.11 | 29.52  | Chr19: 51517212  | <i>KLK10, KLK10,</i><br><i>KLK10</i>                                | 3'UTR, 3'UTR,<br>3'UTR                          | N_Shelf | FALSE |
| cg04682580 | 0.65 | 0.54 | 0.11 | 31.65  | Chr1: 53016396   | <i>ZCCHC11,</i><br><i>ZCCHC11,</i><br><i>ZCCHC11</i>                | 5'UTR, 5'UTR,<br>5'UTR                          | N_Shore | FALSE |
| cg12044599 | 0.31 | 0.20 | 0.11 | 42.35  | Chr11: 67206308  | <i>CORO1B,</i><br><i>CORO1B,</i><br><i>PTPRCAP</i>                  | Body, Body,<br>TSS1500                          | S_Shelf | FALSE |
| cg05262463 | 0.24 | 0.12 | 0.11 | 60.01  | Chr19: 50056081  |   |   | N_Shelf | FALSE |
| cg27366766 | 0.29 | 0.18 | 0.11 | 45.12  | Chr17: 56565286  | <i>HSF5</i>   | 1stExon   | Island  | FALSE |
| cg27182070 | 0.52 | 0.41 | 0.11 | 27.73  | Chr1: 28218282   | <i>RPA2</i>   | 3'UTR   |         | FALSE |
| cg18566515 | 0.40 | 0.29 | 0.11 | 31.84  | Chr10: 123356236 | <i>FGFR2, FGFR2,</i><br><i>FGFR2, FGFR2,</i><br><i>FGFR2, FGFR2</i> | 5'UTR, 5'UTR,<br>5'UTR, 5'UTR,<br>5'UTR, TSS200 | N_Shore | FALSE |
| cg06287775 | 0.38 | 0.27 | 0.11 | 33.47  | Chr7: 4784174    | <i>FOXX1</i>  | Body  | N_Shore | TRUE  |
| cg21177396 | 0.54 | 0.43 | 0.11 | 27.33  | Chr9: 126888124  |   |   |         | TRUE  |
| cg02493602 | 0.65 | 0.54 | 0.11 | 30.17  | Chr11: 86383696  | <i>ME3, ME3, ME3</i>  | TSS1500, TSS200,<br>TSS1500                     | S_Shore | FALSE |
| cg15009294 | 0.37 | 0.26 | 0.11 | 33.24  | Chr1: 214813712  | <i>CENPF</i>  | Body  |         | TRUE  |
| cg08154612 | 0.42 | 0.31 | 0.11 | 29.53  | Chr17: 7037098   |   |   |         | FALSE |
| cg09086987 | 0.44 | 0.33 | 0.11 | 28.47  | Chr3: 18470432   | <i>SATB1</i>  | 5'UTR   | S_Shelf | FALSE |
| cg06159404 | 0.36 | 0.25 | 0.11 | 34.21  | Chr10: 43846376  |   |   | Island  | FALSE |
| cg02090762 | 0.21 | 0.10 | 0.11 | 65.28  | Chr17: 79503859  | <i>FSCN2, FSCN2</i>   | Body, Body                                      | Island  | TRUE  |
| cg12131419 | 0.46 | 0.35 | 0.11 | 27.64  | Chr15: 49353073  |   |   |         | TRUE  |
| cg10411590 | 0.71 | 0.60 | 0.11 | 34.14  | Chr13: 21900810  |   |   | S_Shore | FALSE |
| cg08477332 | 0.35 | 0.24 | 0.11 | 35.20  | Chr1: 153590243  | <i>S100A14</i>  | TSS1500   |         | FALSE |
| cg03227037 | 0.43 | 0.32 | 0.11 | 28.90  | Chr20: 62212228  |   |   | S_Shelf | FALSE |
| cg05460226 | 0.29 | 0.18 | 0.11 | 42.86  | Chr17: 8804279   | <i>PIK3R5, PIK3R5</i>   | Body, Body                                      |         | TRUE  |
| cg27554954 | 0.72 | 0.61 | 0.11 | 35.17  | Chr15: 60691595  | <i>ANXA2, ANXA2,</i><br><i>ANXA2, ANXA2</i>                         | TSS1500,<br>TSS1500,<br>TSS1500,                | S_Shore | TRUE  |

|            |      |      |      |       |                  |   |   |  |         |       |
|------------|------|------|------|-------|------------------|---|---|--|---------|-------|
| cg05406088 | 0.33 | 0.22 | 0.11 | 36.81 | Chr15: 66947617  |   | TSS1500   |  |         | TRUE  |
| cg24885723 | 0.35 | 0.24 | 0.11 | 35.06 | Chr1: 9030439    | CA6   | Body  |  | S_Shore | FALSE |
| cg00106345 | 0.53 | 0.42 | 0.11 | 26.22 | Chr7: 27138396   |   |   |  | S_Shore | FALSE |
| cg21565496 | 0.38 | 0.27 | 0.11 | 31.86 | Chr13: 40762150  |   |   |  |         | FALSE |
| cg18489755 | 0.56 | 0.45 | 0.11 | 26.21 | Chr3: 183533873  | MAP6D1  | 3'UTR   |  |         | FALSE |
| cg26485825 | 0.32 | 0.21 | 0.11 | 37.65 | Chr18: 21452895  | LAMA3, LAMA3,<br>LAMA3, LAMA3<br>FGFR2, FGFR2,<br>FGFR2, FGFR2,<br>FGFR2, FGFR2 | TSS200, TSS200,<br>Body, Body<br>5'UTR, 5'UTR,<br>5'UTR, 5'UTR,<br>5'UTR, 5'UTR |  |         | FALSE |
| cg22633036 | 0.36 | 0.25 | 0.11 | 33.58 | Chr10: 123355576 |   |   |  | N_Shore | FALSE |
| cg01322142 | 0.30 | 0.19 | 0.11 | 40.73 | Chr4: 786718     | CPLX1   | Body  |  | S_Shore | FALSE |
| cg06872548 | 0.30 | 0.19 | 0.11 | 41.06 | Chr17: 78716983  | RPTOR, RPTOR  | Body, Body  |  | N_Shelf | TRUE  |
| cg19348272 | 0.80 | 0.70 | 0.11 | 49.06 | Chr7: 77044158   | PION  | Body  |  | N_Shore | FALSE |
| cg20814179 | 0.60 | 0.49 | 0.11 | 26.73 | Chr4: 940893     | TMEM175   | 5'UTR   |  | Island  | FALSE |
| cg13684379 | 0.88 | 0.77 | 0.11 | 76.13 | Chr10: 1511173   | ADARB2  | Body  |  |         | FALSE |
| cg04632378 | 0.56 | 0.45 | 0.11 | 25.90 | Chr13: 21900426  |   |   |  | Island  | FALSE |
| cg16620160 | 0.78 | 0.68 | 0.11 | 44.59 | Chr5: 174825074  |   |   |  |         | FALSE |
| cg23104954 | 0.27 | 0.17 | 0.11 | 45.58 | Chr13: 50701501  |   |   |  | Island  | FALSE |
| cg20070768 | 0.59 | 0.49 | 0.11 | 26.55 | Chr15: 74285128  | STOML1  | TSS1500   |  | S_Shore | FALSE |
| cg10973622 | 0.69 | 0.59 | 0.11 | 31.96 | Chr2: 86423274   | IMMT, IMMT,<br>IMMT   | TSS1500,<br>TSS1500,<br>TSS1500,<br>TSS1500                                     |  | S_Shore | FALSE |
| cg02299497 | 0.43 | 0.32 | 0.11 | 27.48 | Chr14: 69095570  |   |   |  | S_Shore | TRUE  |
| cg14270590 | 0.42 | 0.31 | 0.11 | 27.91 | Chr14: 105499706 |   |   |  | N_Shore | FALSE |
| cg26094651 | 0.71 | 0.61 | 0.11 | 33.32 | Chr2: 1802045    | MYT1L   | Body  |  | Island  | FALSE |
| cg08310519 | 0.91 | 0.81 | 0.11 | 98.57 | Chr11: 86305199  | ME3, ME3, ME3   | Body, Body, Body  |  |         | TRUE  |
| cg21862353 | 0.68 | 0.58 | 0.11 | 30.54 | Chr2: 1801628    | MYT1L   | Body  |  | Island  | FALSE |
| cg12178432 | 0.44 | 0.34 | 0.11 | 26.77 | Chr1: 26049105   | MAN1C1  | Body  |  |         | FALSE |
| cg24755459 | 0.21 | 0.10 | 0.11 | 64.42 | Chr14: 101908865 |   |   |  | Island  | FALSE |
| cg18110333 | 0.51 | 0.40 | 0.11 | 25.06 | Chr6: 292329     | DUSP22, DUSP22  | 1stExon, 5'UTR  |  | Island  | FALSE |
| cg27134251 | 0.73 | 0.62 | 0.11 | 34.30 | Chr8: 1365049    |   |   |  | N_Shore | FALSE |
| cg04658243 | 0.57 | 0.47 | 0.11 | 25.17 | Chr17: 78865755  | RPTOR, RPTOR  | Body, Body  |  | S_Shore | TRUE  |
| cg03961283 | 0.41 | 0.30 | 0.11 | 28.01 | Chr1: 223566761  | C1orf65, C1orf65  | 5'UTR, 1stExon  |  | Island  | TRUE  |
| cg02722613 | 0.20 | 0.10 | 0.11 | 64.72 | Chr4: 25162898   | SEPSECS,<br>SEPSECS, SEPSECS  | TSS1500,<br>TSS1500,<br>TSS1500   |  | S_Shore | FALSE |
| cg14216940 | 0.37 | 0.26 | 0.11 | 30.94 | Chr7: 50343131   | IKZF1   | TSS1500   |  | Island  | FALSE |
| cg22052514 | 0.38 | 0.27 | 0.11 | 29.91 | Chr8: 142401722  |   |   |  | Island  | FALSE |
| cg19204924 | 0.65 | 0.54 | 0.11 | 27.32 | Chr19: 20576478  | ZNF826  | 3'UTR   |  |         | FALSE |
| cg06476926 | 0.58 | 0.47 | 0.11 | 24.69 | Chr17: 80867707  | TBCD  | Body  |  | N_Shelf | FALSE |
| cg04116354 | 0.35 | 0.24 | 0.11 | 32.37 | Chr1: 26003643   | MAN1C1  | Body  |  |         | TRUE  |
| cg11227278 | 0.31 | 0.20 | 0.11 | 36.74 | Chr2: 23749277   | KLHL29  | 5'UTR   |  | Island  | FALSE |
| cg22668906 | 0.39 | 0.28 | 0.11 | 28.68 | Chr11: 128180077 |   |   |  |         | TRUE  |
| cg15052335 | 0.70 | 0.59 | 0.11 | 30.40 | Chr18: 3011810   | LPIN2, LPIN2  | 5'UTR, 1stExon  |  | N_Shore | FALSE |
| cg04548204 | 0.44 | 0.33 | 0.11 | 25.79 | Chr12: 9162872   | KLRG1   | 3'UTR   |  |         | FALSE |
| cg08222513 | 0.65 | 0.55 | 0.11 | 27.14 | Chr6: 30079280   | TRIM31  | Body  |  |         | FALSE |
| cg23731272 | 0.66 | 0.55 | 0.11 | 27.43 | Chr15: 67356838  | SMAD3   | TSS1500   |  | N_Shore | FALSE |
| cg00693583 | 0.87 | 0.76 | 0.11 | 66.52 | Chr4: 25160982   | SEPSECS,<br>SEPSECS, SEPSECS  | Body, Body, Body  |  | N_Shore | FALSE |
| cg03906434 | 0.35 | 0.25 | 0.10 | 30.91 | Chr7: 27231819   |   |   |  | Island  | FALSE |
| cg17346246 | 0.34 | 0.24 | 0.10 | 31.99 | Chr12: 123214864 | GPR81   | 1stExon<br>5'UTR, 5'UTR,  |  |         | FALSE |
| cg25700686 | 0.45 | 0.35 | 0.10 | 24.57 | Chr8: 72268832   | EYA1, EYA1, EYA1,<br>EYA1, EYA1, EYA1,<br>EYA1                                  | 1stExon,<br>1stExon,<br>1stExon, 5'UTR,<br>5'UTR                                |  |         | TRUE  |
| cg02398342 | 0.73 | 0.62 | 0.10 | 32.37 | Chr17: 80708632  | TBCD, FN3K  | TSS1500, 3'UTR  |  | N_Shore | FALSE |
| cg04597393 | 0.26 | 0.15 | 0.10 | 44.62 | Chr8: 142276533  |   |   |  |         | FALSE |
| cg13578160 | 0.45 | 0.35 | 0.10 | 24.62 | Chr7: 72813978   |   |   |  |         | FALSE |
| cg19383211 | 0.72 | 0.62 | 0.10 | 32.29 | Chr6: 32527588   | HLA-DRB6  | Body  |  |         | FALSE |
| cg27064063 | 0.17 | 0.07 | 0.10 | 74.56 | Chr6: 117869287  | DCBLD1  | Body  |  | Island  | TRUE  |
| cg18766900 | 0.65 | 0.55 | 0.10 | 26.23 | Chr10: 11574616  | USP6NL, USP6NL  | Body, TSS1500   |  |         | FALSE |
| cg19001909 | 0.24 | 0.14 | 0.10 | 47.76 | Chr17: 26205940  | C17orf108   | 3'UTR   |  |         | FALSE |
| cg27257987 | 0.84 | 0.74 | 0.10 | 54.60 | Chr19: 43709360  | PSG4, PSG4  | Body, Body  |  |         | FALSE |
| cg24044478 | 0.78 | 0.67 | 0.10 | 39.45 | Chr8: 145035191  | PLEC1, PLEC1  | Body, Body  |  |         | FALSE |

|            |      |      |      |       |                  |   |   |         |       |
|------------|------|------|------|-------|------------------|---|---|---------|-------|
| cg27216937 | 0.64 | 0.53 | 0.10 | 25.17 | Chr11: 6425978   | <i>APBB1, APBB1</i>   | Body, Body  |         | TRUE  |
| cg01154505 | 0.34 | 0.23 | 0.10 | 31.52 | Chr2: 112940409  | <i>FBLN7, FBLN7</i>   | Body, Body  | S_Shore | TRUE  |
| cg13260278 | 0.31 | 0.21 | 0.10 | 33.97 | Chr10: 121265587 | <i>RGS10, RGS10</i>   | Body, Body  |         | FALSE |
| cg10528576 | 0.64 | 0.54 | 0.10 | 25.17 | Chr14: 101192913 | <i>DLK1</i>   | TSS1500   | Island  | FALSE |
| cg13318241 | 0.41 | 0.31 | 0.10 | 25.47 | Chr6: 3455537    | <i>SLC22A23</i>   | Body  | N_Shore | TRUE  |
| cg06221963 | 0.70 | 0.60 | 0.10 | 29.32 | Chr1: 154839813  | <i>KCNN3</i>  | Body  |         | FALSE |
| cg10730425 | 0.80 | 0.70 | 0.10 | 44.04 | Chr19: 1035093   | <i>CNN2, CNN2</i>   | Body, Body  | Island  | FALSE |
| cg15007959 | 0.24 | 0.13 | 0.10 | 48.46 | Chr19: 50931432  | <i>SPIB</i>   | Body  | Island  | FALSE |
| cg21123519 | 0.42 | 0.32 | 0.10 | 24.78 | Chr14: 69095679  |   |   | S_Shore | TRUE  |
| cg01788113 | 0.47 | 0.37 | 0.10 | 23.10 | Chr3: 46759472   | <i>PRSS50</i>   | TSS200  | Island  | FALSE |
| cg12000995 | 0.79 | 0.69 | 0.10 | 41.16 | Chr2: 27665139   | <i>KRTCAP3, KRTCAP3</i>                                     | TSS200, TSS200  | Island  | FALSE |
| cg06307913 | 0.36 | 0.26 | 0.10 | 28.26 | Chr4: 81118794   | <i>PRDM8, PRDM8, PRDM8</i>                                  | 5'UTR, 1stExon, 5'UTR                                   | N_Shore | FALSE |
| cg00376816 | 0.27 | 0.17 | 0.10 | 39.80 | Chr19: 39332571  | <i>HNRNPL, HNRNPL</i>                                       | Body, Body  |         | FALSE |
| cg13963793 | 0.38 | 0.28 | 0.10 | 26.50 | Chr1: 223567173  | <i>C1orf65</i>  | 1stExon   | Island  | TRUE  |
| cg00119778 | 0.23 | 0.13 | 0.10 | 48.01 | Chr6: 32466447   |   |   |         | FALSE |
| cg20581490 | 0.71 | 0.61 | 0.10 | 29.52 | Chr18: 12775841  |   |   | N_Shore | FALSE |
| cg09891288 | 0.80 | 0.70 | 0.10 | 42.39 | Chr17: 78863674  | <i>RPTOR, RPTOR</i>   | Body, Body  | Island  | FALSE |
| cg25407410 | 0.84 | 0.74 | 0.10 | 53.05 | Chr6: 143891975  | <i>LOC285740</i>  | TSS1500   |         | FALSE |
| cg11370814 | 0.27 | 0.17 | 0.10 | 40.02 | Chr2: 242927418  |   |   | N_Shore | FALSE |
| cg15950273 | 0.58 | 0.48 | 0.10 | 22.31 | Chr14: 103367306 | <i>TRAF3, TRAF3, TRAF3</i>                                  | Body, Body, Body  |         | FALSE |
| cg11480019 | 0.23 | 0.13 | 0.10 | 48.16 | Chr10: 75936982  | <i>ADK, ADK</i>   | Body, Body  | S_Shore | FALSE |
| cg10911276 | 0.84 | 0.74 | 0.10 | 51.97 | Chr4: 4142417    |   |   | N_Shelf | FALSE |
| cg11677105 | 0.37 | 0.27 | 0.10 | 26.66 | Chr22: 42078707  | <i>NHP2L1, NHP2L1</i>                                       | Body, TSS200  | S_Shore | FALSE |
| cg06791446 | 0.59 | 0.49 | 0.10 | 22.12 | Chr10: 123355268 | <i>FGFR2, FGFR2, FGFR2, FGFR2, FGFR2</i>                    | 5'UTR, 5'UTR, 5'UTR, 5'UTR, TSS1500, 5'UTR, 5'UTR       | N_Shore | FALSE |
| cg00356916 | 0.61 | 0.51 | 0.10 | 22.77 | Chr1: 116256618  | <i>CASQ2</i>  | Body  |         | TRUE  |
| cg17446339 | 0.36 | 0.26 | 0.10 | 27.54 | Chr11: 20385254  | <i>HTATIP2, HTATIP2, HTATIP2, HTATIP2, HTATIP2, HTATIP2</i> | TSS200, 1stExon, TSS1500, 1stExon, 5'UTR, 5'UTR, TSS200 | Island  | FALSE |
| cg06712767 | 0.64 | 0.54 | 0.10 | 23.65 | Chr12: 131118561 |   |   |         | TRUE  |
| cg06226386 | 0.25 | 0.15 | 0.10 | 42.35 | Chr8: 22500449   | <i>FLJ14107, BIN3</i>                                       | TSS1500, Body   |         | FALSE |
| cg18405330 | 0.30 | 0.20 | 0.10 | 34.26 | Chr6: 164171960  |   |   |         | FALSE |
| cg24659858 | 0.39 | 0.28 | 0.10 | 25.39 | Chr13: 24270321  |   |   | S_Shore | TRUE  |
| cg21111256 | 0.34 | 0.23 | 0.10 | 29.33 | Chr19: 41386507  | <i>CYP2A7, CYP2A7</i>                                       | Body, Body  | Island  | FALSE |
| cg17804342 | 0.77 | 0.67 | 0.10 | 35.10 | Chr10: 121271663 | <i>RGS10, RGS10</i>   | Body, Body  |         | FALSE |
| cg11559192 | 0.83 | 0.73 | 0.10 | 49.64 | Chr12: 25357592  | <i>LYRM5</i>  | 3'UTR   |         | FALSE |
| cg16704958 | 0.23 | 0.12 | 0.10 | 48.66 | Chr21: 38630728  | <i>DSCR3</i>  | Body  | S_Shore | TRUE  |
| cg01466164 | 0.41 | 0.31 | 0.10 | 23.63 | Chr8: 2481226    |   |   | S_Shore | FALSE |
| cg14279856 | 0.45 | 0.34 | 0.10 | 22.26 | Chr6: 30851086   | <i>DDR1, DDR1</i>   | TSS1500, TSS1500  | N_Shore | TRUE  |
| cg18681853 | 0.25 | 0.15 | 0.10 | 42.69 | Chr2: 224889133  | <i>SERPINE2, SERPINE2, SERPINE2, SERPINE2</i>               | 5'UTR, Body, 5'UTR, 5'UTR                               |         | TRUE  |
| cg13692134 | 0.32 | 0.22 | 0.10 | 29.91 | Chr5: 74350132   |   |   | Island  | FALSE |

C.

No Malar or Discoid Rash

| CG Site ID             | Mean $\beta$ Case | Mean $\beta$ Control | $\Delta\beta$ | DiffScore | Location (HG19)  | Gene Name  | Gene-Relative Location                     | CGI-Relative Location | Enhancer |
|------------------------|-------------------|----------------------|---------------|-----------|------------------|--|--|-----------------------|----------|
| <b>Hypomethylation</b> |                   |                      |               |           |                  |  |  |                       |          |
| cg21549285             | 0.36              | 0.65                 | -0.29         | -301.97   | Chr21: 42799141  | <i>MX1, MX1</i>  | 5'UTR, 5'UTR                               | S_Shore               | FALSE    |
| cg04346459             | 0.71              | 0.99                 | -0.28         | -338.22   | Chr6: 41068666   | <i>NFYA, NFYA, LOC221442</i>                           | 3'UTR, 3'UTR, TSS200                       | Island                | TRUE     |
| cg25110423             | 0.70              | 0.96                 | -0.26         | -338.22   | Chr6: 41068646   | <i>NFYA, NFYA, LOC221442</i>                           | 3'UTR, 3'UTR, TSS200                       | Island                | TRUE     |
| cg14392283             | 0.63              | 0.89                 | -0.26         | -338.22   | Chr8: 144103587  | <i>LY6E, LY6E</i>                                      | 3'UTR, 3'UTR                               | N_Shelf               | FALSE    |
| cg15065340             | 0.49              | 0.72                 | -0.22         | -174.57   | Chr3: 195632915  | <i>TNK2</i>  | 5'UTR                                      | N_Shelf               | FALSE    |
| cg26893861             | 0.26              | 0.49                 | -0.22         | -167.87   | Chr17: 41843967  | <i>DUSP3</i>   | 3'UTR                                      |                       | FALSE    |
| cg19418458             | 0.42              | 0.64                 | -0.22         | -154.86   | Chr7: 158789849  |  |  | Island                | FALSE    |
| cg23066280             | 0.43              | 0.64                 | -0.21         | -147.50   | Chr7: 158032496  | <i>PTPRN2, PTPRN2, PTPRN2</i>                          | Body, Body, Body                           |                       | FALSE    |
| cg10890302             | 0.28              | 0.49                 | -0.21         | -142.85   | Chr6: 32064246   | <i>TNXB</i>  | Body                                       | Island                | FALSE    |
| cg06715136             | 0.67              | 0.88                 | -0.21         | -255.48   | Chr7: 158046025  | <i>PTPRN2, PTPRN2, PTPRN2</i>                          | Body, Body, Body                           |                       | FALSE    |
| cg14911689             | 0.33              | 0.54                 | -0.21         | -135.21   | Chr12: 739980    | <i>NINJ2</i>   | Body                                       |                       | FALSE    |
| cg22531183             | 0.03              | 0.24                 | -0.20         | -302.51   | Chr19: 50554451  | <i>FLJ26850</i>  | Body                                       | Island                | FALSE    |
| cg05696877             | 0.29              | 0.49                 | -0.20         | -135.33   | Chr1: 79088769   | <i>IFI44L</i>  | 5'UTR                                      |                       | FALSE    |
| cg01079515             | 0.73              | 0.93                 | -0.20         | -312.22   | Chr3: 195576629  |  |  |                       | FALSE    |
| cg08122652             | 0.58              | 0.78                 | -0.20         | -164.14   | Chr3: 122281939  | <i>PARP9, PARP9, DTX3L, PARP9, PARP9, PARP9, PARP9</i> | 5'UTR, 5'UTR, TSS1500, 5'UTR, 5'UTR, 5'UTR | N_Shore               | FALSE    |
| cg01992382             | 0.24              | 0.44                 | -0.20         | -140.47   | Chr6: 32064212   | <i>TNXB</i>  | Body                                       | Island                | FALSE    |
| cg05357209             | 0.15              | 0.34                 | -0.20         | -175.62   | Chr7: 872208     | <i>UNC84A, UNC84A</i>                                  | 5'UTR, Body                                |                       | TRUE     |
| cg26058907             | 0.52              | 0.71                 | -0.19         | -130.32   | ChrY: 22917942   | <i>RPS4Y2</i>  | TSS200                                     |                       | FALSE    |
| cg14003022             | 0.42              | 0.61                 | -0.19         | -115.72   | Chr4: 3043019    |  |  | Island                | FALSE    |
| cg00525277             | 0.37              | 0.56                 | -0.19         | -113.90   | Chr6: 32064239   | <i>TNXB</i>  | Body                                       | Island                | FALSE    |
| cg00872984             | 0.38              | 0.57                 | -0.19         | -112.22   | Chr6: 32063991   | <i>TNXB</i>  | Body                                       | Island                | FALSE    |
| cg26654770             | 0.35              | 0.54                 | -0.19         | -112.28   | Chr12: 740100    | <i>NINJ2</i>   | Body                                       |                       | FALSE    |
| cg07524919             | 0.42              | 0.61                 | -0.19         | -108.05   | Chr6: 32063901   | <i>TNXB</i>  | Body                                       | Island                | FALSE    |
| cg16834823             | 0.30              | 0.49                 | -0.19         | -111.44   | Chr6: 32064218   | <i>TNXB</i>  | Body                                       | Island                | FALSE    |
| cg01201512             | 0.46              | 0.65                 | -0.19         | -109.83   | Chr12: 740338    | <i>NINJ2</i>   | Body                                       |                       | TRUE     |
| cg06118351             | 0.66              | 0.84                 | -0.19         | -175.88   | Chr16: 4788808   | <i>C16orf71</i>  | Body                                       | N_Shore               | FALSE    |
| cg14212360             | 0.58              | 0.76                 | -0.18         | -131.39   | Chr4: 89302999   | <i>HERC6, HERC6</i>                                    | Body, Body                                 | S_Shelf               | FALSE    |
| cg22862003             | 0.53              | 0.72                 | -0.18         | -115.18   | Chr21: 42797588  | <i>MX1, MX1</i>  | TSS1500, 5'UTR                             | N_Shore               | FALSE    |
| cg03644281             | 0.81              | 0.99                 | -0.18         | -338.22   | Chr6: 41068752   | <i>NFYA, NFYA, LOC221442</i>                           | 3'UTR, 3'UTR, TSS200                       | Island                | TRUE     |
| cg11478607             | 0.09              | 0.27                 | -0.18         | -187.48   | Chr22: 24384400  | <i>GSTT1</i>   | TSS200                                     | Island                | FALSE    |
| cg09640425             | 0.40              | 0.59                 | -0.18         | -96.88    | Chr7: 158790006  |  |  | Island                | FALSE    |
| cg14126601             | 0.44              | 0.61                 | -0.18         | -92.12    | Chr2: 37384708   | <i>EIF2AK2, EIF2AK2</i>                                | TSS1500, TSS1500                           | S_Shore               | FALSE    |
| cg06188083             | 0.19              | 0.36                 | -0.17         | -117.25   | Chr10: 91093005  | <i>IFIT3, IFIT3</i>                                    | Body, Body                                 |                       | TRUE     |
| cg02770061             | 0.64              | 0.81                 | -0.17         | -126.84   | Chr7: 158046166  | <i>PTPRN2, PTPRN2, PTPRN2</i>                          | Body, Body, Body                           |                       | FALSE    |
| cg01624173             | 0.35              | 0.52                 | -0.17         | -83.77    | Chr14: 75981868  |  |  |                       | TRUE     |
| cg03607951             | 0.53              | 0.70                 | -0.17         | -91.33    | Chr1: 79085586   | <i>IFI44L</i>  | TSS1500                                    |                       | FALSE    |
| cg18838701             | 0.31              | 0.47                 | -0.17         | -83.54    | Chr19: 55668612  | <i>TNNI3</i>   | Body                                       | S_Shore               | FALSE    |
| cg24419602             | 0.74              | 0.91                 | -0.17         | -202.91   | Chr19: 5510310   |  |  | S_Shelf               | FALSE    |
| cg00274965             | 0.40              | 0.57                 | -0.17         | -78.54    | Chr21: 34405681  |  |  | Island                | FALSE    |
| cg07777042             | 0.69              | 0.86                 | -0.17         | -150.25   | Chr8: 144702879  |  |  | S_Shelf               | FALSE    |
| cg26287152             | 0.63              | 0.79                 | -0.16         | -112.49   | Chr17: 77923675  | <i>TBC1D16</i>   | Body                                       | N_Shore               | TRUE     |
| cg06981309             | 0.46              | 0.63                 | -0.16         | -78.24    | Chr3: 146260954  | <i>PLSCR1</i>  | 5'UTR                                      | N_Shore               | FALSE    |
| cg10815657             | 0.76              | 0.92                 | -0.16         | -215.62   | Chr19: 289902    | <i>PPAP2C, PPAP2C, PPAP2C</i>                          | Body, Body, 5'UTR                          | N_Shore               | TRUE     |
| cg19495714             | 0.56              | 0.72                 | -0.16         | -89.02    | Chr14: 105218551 | <i>SIVA1, SIVA1</i>                                    | TSS1500, TSS1500                           | Island                | FALSE    |
| cg05834845             | 0.61              | 0.77                 | -0.16         | -102.34   | Chr3: 195489306  | <i>MUC4, MUC4, MUC4</i>                                | Body, Body, Body                           | Island                | FALSE    |
| cg06400119             | 0.72              | 0.89                 | -0.16         | -168.78   | Chr7: 158046222  | <i>PTPRN2, PTPRN2, PTPRN2</i>                          | Body, Body, Body                           |                       | FALSE    |
| cg05401945             | 0.34              | 0.50                 | -0.16         | -75.30    | Chr3: 56590734   | <i>CCDC66, CCDC66, CCDC66</i>                          | TSS1500, TSS1500,                          | N_Shore               | FALSE    |

|            |      |      |       |         |                  |  |   |         |       |
|------------|------|------|-------|---------|------------------|--|---|---------|-------|
| cg13909895 | 0.35 | 0.51 | -0.16 | -74.55  | Chr22: 51066142  | ARSA, ARSA,<br>ARSA, ARSA, ARSA                          | TSS1500<br>1stExon, Body,<br>Body, Body,<br>5'UTR | Island  | FALSE |
| cg22000984 | 0.26 | 0.42 | -0.16 | -83.94  | Chr5: 150226278  | IRGM, IRGM   | 1stExon, 5'UTR                                    |         | FALSE |
| cg09580153 | 0.83 | 0.99 | -0.16 | -338.22 | Chr6: 41068724   | NFYA, NFYA,<br>LOC221442                                 | 3'UTR, 3'UTR,<br>TSS200                           | Island  | TRUE  |
| cg19665696 | 0.26 | 0.41 | -0.16 | -82.06  | Chr7: 949154     | ADAP1  | Body  | Island  | FALSE |
| cg19590115 | 0.66 | 0.82 | -0.16 | -115.67 | Chr7: 157632890  | PTPRN2, PTPRN2,<br>PTPRN2                                | Body, Body, Body                                  | S_Shore | FALSE |
| cg04431054 | 0.29 | 0.45 | -0.16 | -76.26  | Chr5: 126853024  | PRRC1  | TSS1500   | N_Shore | FALSE |
| cg20744362 | 0.66 | 0.82 | -0.16 | -116.94 | Chr22: 50050164  | C22orf34   | Body  |         | FALSE |
| cg14951497 | 0.27 | 0.43 | -0.16 | -78.21  | Chr2: 191875807  | STAT1, STAT1   | 5'UTR, 5'UTR                                      | N_Shelf | FALSE |
| cg13185413 | 0.24 | 0.40 | -0.16 | -82.25  | Chr6: 30039202   | RNF39, RNF39   | Body, Body  | Island  | FALSE |
| cg17384323 | 0.55 | 0.70 | -0.16 | -78.22  | Chr4: 169242366  |  |   | S_Shelf | FALSE |
| cg03393996 | 0.17 | 0.32 | -0.15 | -96.90  | Chr4: 1580377    |  |   | Island  | FALSE |
| cg14286514 | 0.42 | 0.57 | -0.15 | -65.75  | Chr9: 32525315   | DDX58  | Body  | N_Shore | TRUE  |
| cg15848685 | 0.34 | 0.50 | -0.15 | -65.54  | Chr6: 30882641   | VARS2, VARS2,<br>VARS2                                   | Body, 5'UTR,<br>Body                              | S_Shore | TRUE  |
| cg12694372 | 0.23 | 0.38 | -0.15 | -79.07  | Chr6: 32064582   | TNXB   | Body  | Island  | FALSE |
| cg01097406 | 0.38 | 0.53 | -0.15 | -63.67  | Chr16: 89675127  |  |   |         | FALSE |
| cg12016809 | 0.23 | 0.38 | -0.15 | -78.64  | Chr21: 47604291  | C21orf56,<br>C21orf56,<br>C21orf56,<br>C21orf56          | 5'UTR, 5'UTR,<br>1stExon, 1stExon                 | S_Shore | FALSE |
| cg02299497 | 0.30 | 0.46 | -0.15 | -67.57  | Chr14: 69095570  |  |   | S_Shore | TRUE  |
| cg25443613 | 0.17 | 0.32 | -0.15 | -92.92  | ChrY: 2709605    | RPS4Y1   | TSS200  |         | FALSE |
| cg24336839 | 0.05 | 0.20 | -0.15 | -163.25 | Chr22: 24384397  | GSTT1  | TSS200  | Island  | FALSE |
| cg14531026 | 0.73 | 0.88 | -0.15 | -137.01 | Chr3: 184043286  | EIF4G1, EIF4G1,<br>SNORD66,<br>EIF4G1, EIF4G1,<br>EIF4G1 | Body, Body,<br>TSS200, Body,<br>Body, Body        | N_Shore | FALSE |
| cg21159568 | 0.59 | 0.74 | -0.15 | -74.98  | Chr7: 2445331    | CHST12   | 5'UTR   | S_Shore | FALSE |
| cg14573478 | 0.27 | 0.41 | -0.15 | -66.87  | Chr3: 140730858  |  |   |         | TRUE  |
| cg09350919 | 0.25 | 0.40 | -0.15 | -68.07  | ChrY: 9365070    | TSPY3, TSPY4   | TSS1500, Body                                     | N_Shore | FALSE |
| cg00855901 | 0.30 | 0.44 | -0.15 | -62.15  | Chr1: 79085765   | IFI44L   | TSS1500   |         | FALSE |
| cg15254640 | 0.06 | 0.20 | -0.15 | -151.39 | Chr22: 24384393  | GSTT1  | TSS200  | Island  | FALSE |
| cg16565409 | 0.47 | 0.62 | -0.15 | -58.40  | Chr17: 27048223  | RPL23A,<br>SNORD4A                                       | Body, TSS1500                                     | S_Shore | FALSE |
| cg02163885 | 0.57 | 0.71 | -0.14 | -67.24  | Chr6: 27729346   |  |   |         | FALSE |
| cg14089503 | 0.56 | 0.71 | -0.14 | -66.50  | Chr8: 37755555   | RAB11FIP1,<br>RAB11FIP1                                  | Body, Body  | N_Shore | FALSE |
| cg20088245 | 0.39 | 0.54 | -0.14 | -55.37  | Chr8: 1321375    |  |   | Island  | FALSE |
| cg19870512 | 0.23 | 0.37 | -0.14 | -68.75  | Chr12: 4919081   | KCNA6, KCNA6   | 5'UTR, 1stExon                                    | Island  | FALSE |
| cg12319143 | 0.57 | 0.71 | -0.14 | -66.62  | Chr10: 134726771 |  |   | N_Shelf | FALSE |
| cg25932599 | 0.22 | 0.37 | -0.14 | -70.16  | Chr4: 1005201    | FGFRL1, FGFRL1,<br>FGFRL1                                | TSS1500,<br>TSS1500,<br>TSS1500                   | Island  | FALSE |
| cg27192248 | 0.31 | 0.46 | -0.14 | -58.02  | Chr15: 65285669  |  |   | S_Shelf | FALSE |
| cg20398880 | 0.73 | 0.88 | -0.14 | -127.11 | Chr6: 41068722   | NFYA, NFYA,<br>LOC221442                                 | 3'UTR, 3'UTR,<br>TSS200                           | Island  | TRUE  |
| cg05552874 | 0.64 | 0.79 | -0.14 | -81.81  | Chr10: 91153143  | IFIT1  | Body  |         | FALSE |
| cg14926196 | 0.40 | 0.55 | -0.14 | -53.84  | Chr6: 37616482   | MDGA1  | Body  | Island  | FALSE |
| cg14785464 | 0.52 | 0.66 | -0.14 | -58.33  | Chr21: 38362725  | HLCS   | TSS200  | Island  | FALSE |
| cg01028142 | 0.72 | 0.86 | -0.14 | -115.11 | Chr2: 7004578    | CMPK2  | Body  | N_Shore | FALSE |
| cg23804921 | 0.44 | 0.58 | -0.14 | -52.55  | Chr15: 30861172  |  |   | N_Shelf | FALSE |
| cg17980508 | 0.49 | 0.63 | -0.14 | -54.27  | Chr1: 79085713   | IFI44L   | TSS1500   |         | FALSE |
| cg01996567 | 0.37 | 0.51 | -0.14 | -52.33  | Chr7: 149484880  | SSPO   | Body  | N_Shelf | FALSE |
| cg00843105 | 0.06 | 0.20 | -0.14 | -135.54 | Chr19: 44645597  | ZNF234, ZNF234   | TSS200, TSS200                                    | Island  | FALSE |
| cg11224582 | 0.29 | 0.43 | -0.14 | -56.24  | Chr12: 4919138   | KCNA6, KCNA6   | 5'UTR, 1stExon                                    | Island  | FALSE |
| cg01238044 | 0.20 | 0.34 | -0.14 | -70.74  | Chr22: 24384105  | GSTT1  | Body  | N_Shore | FALSE |
| cg25849281 | 0.43 | 0.57 | -0.14 | -51.37  | Chr1: 8937077    | ENO1   | 5'UTR   | N_Shore | FALSE |
| cg19106932 | 0.22 | 0.36 | -0.14 | -66.89  | Chr17: 61926700  |  |   | Island  | FALSE |
| cg03482458 | 0.13 | 0.27 | -0.14 | -92.49  | Chr22: 46692211  | CN5H6.4, GTSE1   | Body, TSS1500                                     | Island  | FALSE |
| cg13012494 | 0.20 | 0.34 | -0.14 | -68.92  | Chr21: 47604986  | C21orf56,<br>C21orf56                                    | TSS1500,<br>TSS1500                               | S_Shelf | FALSE |



|            |      |      |       |         |                  |                                       |                           |         |       |
|------------|------|------|-------|---------|------------------|---------------------------------------|---------------------------|---------|-------|
| cg12110437 | 0.21 | 0.35 | -0.14 | -67.89  | Chr8: 144098888  | <i>LY6E, LY6E, LOC100133669</i>       | TSS1500, TSS1500, Body    | N_Shore | FALSE |
| cg08133631 | 0.51 | 0.64 | -0.14 | -53.64  | Chr1: 26527909   | <i>CATSPER4</i>                       | Body                      |         | TRUE  |
| cg05896524 | 0.29 | 0.43 | -0.14 | -55.21  | Chr21: 47604654  | <i>C21orf56, C21orf56</i>             | TSS1500, TSS1500          | S_Shore | FALSE |
| cg01175610 | 0.24 | 0.38 | -0.14 | -61.03  | Chr12: 12224246  | <i>BCL2L14, BCL2L14</i>               | 5'UTR, TSS200, TSS200     |         | TRUE  |
| cg06167719 | 0.62 | 0.76 | -0.14 | -69.63  | Chr21: 38362727  | <i>HLCS</i>                           | TSS200                    | Island  | FALSE |
| cg18955367 | 0.58 | 0.72 | -0.14 | -61.35  | Chr19: 49002338  | <i>LMTK3</i>                          | Body                      | Island  | FALSE |
| cg18085787 | 0.28 | 0.42 | -0.14 | -55.44  | ChrY: 14646665   |                                       |                           | N_Shelf | FALSE |
| cg12397463 | 0.66 | 0.80 | -0.14 | -81.11  | Chr6: 33128825   |                                       |                           | N_Shore | FALSE |
| cg10909185 | 0.25 | 0.39 | -0.14 | -58.77  | Chr11: 75139736  | <i>KLHL35</i>                         | Body                      | Island  | FALSE |
| cg08742575 | 0.24 | 0.38 | -0.14 | -58.93  | Chr21: 47604166  | <i>C21orf56, C21orf56</i>             | 5'UTR, 5'UTR              | S_Shore | FALSE |
| cg05487134 | 0.23 | 0.37 | -0.13 | -59.65  | Chr17: 40489569  | <i>STAT3, STAT3, STAT3</i>            | Body, Body, Body          |         | FALSE |
| cg03206401 | 0.51 | 0.65 | -0.13 | -50.60  | Chr2: 130956119  | <i>TUBA3E</i>                         | TSS200                    | Island  | FALSE |
| cg00676801 | 0.25 | 0.38 | -0.13 | -56.80  | Chr2: 191876673  | <i>STAT1, STAT1</i>                   | 5'UTR, 5'UTR              | N_Shore | FALSE |
| cg06614118 | 0.78 | 0.92 | -0.13 | -148.68 | Chr5: 180414906  | <i>BTNL3</i>                          | TSS1500                   |         | FALSE |
| cg13516209 | 0.46 | 0.59 | -0.13 | -46.30  | Chr6: 29855302   | <i>HLA-H</i>                          | TSS200                    | Island  | FALSE |
| cg01677628 | 0.52 | 0.66 | -0.13 | -49.80  | Chr11: 8361190   |                                       |                           |         | FALSE |
| cg24238852 | 0.07 | 0.20 | -0.13 | -117.22 | Chr22: 24384340  | <i>GSTT1</i>                          | TSS200                    | Island  | FALSE |
| cg04234412 | 0.30 | 0.44 | -0.13 | -49.32  | Chr22: 24373322  | <i>LOC391322</i>                      | Body                      | Island  | FALSE |
| cg00576139 | 0.38 | 0.51 | -0.13 | -45.54  | ChrY: 6312218    | <i>LOC100101115, TTTY21</i>           | Body, Body                |         | FALSE |
| cg12622242 | 0.46 | 0.59 | -0.13 | -45.87  | Chr8: 19203257   | <i>SH2D4A</i>                         | Body                      |         | TRUE  |
| cg08596608 | 0.22 | 0.36 | -0.13 | -58.52  | ChrY: 14533505   |                                       |                           | Island  | FALSE |
| cg26536949 | 0.59 | 0.72 | -0.13 | -56.24  | Chr17: 57053     |                                       |                           | Island  | TRUE  |
| cg00737841 | 0.68 | 0.81 | -0.13 | -79.15  | Chr10: 130726624 |                                       |                           |         | FALSE |
| cg07971089 | 0.40 | 0.54 | -0.13 | -44.48  | Chr8: 144629702  |                                       |                           | N_Shelf | FALSE |
| cg13732083 | 0.22 | 0.35 | -0.13 | -58.24  | Chr21: 47605072  | <i>C21orf56, C21orf56</i>             | TSS1500, TSS1500          | S_Shelf | FALSE |
| cg23613051 | 0.29 | 0.42 | -0.13 | -49.08  | Chr4: 2820428    | <i>SH3BP2, SH3BP2, SH3BP2, SH3BP2</i> | Body, Body, 5'UTR, TSS200 | Island  | FALSE |
| cg01066472 | 0.36 | 0.49 | -0.13 | -44.48  | Chr1: 75591029   |                                       |                           | Island  | FALSE |
| cg01022117 | 0.73 | 0.86 | -0.13 | -98.59  | Chr1: 201258280  | <i>PKP1, PKP1</i>                     | Body, Body                |         | TRUE  |
| cg06046490 | 0.24 | 0.38 | -0.13 | -53.70  | Chr11: 320940    | <i>IFITM3</i>                         | TSS200                    | S_Shore | FALSE |
| cg24124284 | 0.59 | 0.72 | -0.13 | -54.33  | Chr11: 18476081  | <i>LDHAL6A, LDHAL6A</i>               | TSS1500, TSS1500          | N_Shore | FALSE |
| cg25606201 | 0.46 | 0.59 | -0.13 | -43.38  | Chr5: 180614858  |                                       |                           | N_Shore | FALSE |
| cg05852568 | 0.45 | 0.58 | -0.13 | -42.91  | Chr2: 95537405   | <i>TEKT4</i>                          | 1stExon                   | Island  | FALSE |
| cg16677019 | 0.19 | 0.32 | -0.13 | -62.77  | Chr17: 44847268  | <i>WNT3</i>                           | Body                      | Island  | FALSE |
| cg11222703 | 0.49 | 0.62 | -0.13 | -44.03  | Chr4: 190983569  |                                       |                           | N_Shelf | FALSE |
| cg24312520 | 0.23 | 0.36 | -0.13 | -53.27  | Chr17: 40489584  | <i>STAT3, STAT3, STAT3</i>            | Body, Body, Body          |         | FALSE |
| cg11685843 | 0.59 | 0.71 | -0.13 | -52.12  | Chr4: 176349171  |                                       |                           |         | FALSE |
| cg13626582 | 0.52 | 0.65 | -0.13 | -45.00  | Chr15: 57592083  | <i>LOC283663</i>                      | TSS1500                   |         | FALSE |
| cg14586373 | 0.46 | 0.58 | -0.13 | -41.92  | Chr22: 37447398  | <i>KCTD17</i>                         | TSS1500                   | N_Shore | FALSE |
| cg26968378 | 0.30 | 0.43 | -0.13 | -45.52  | Chr6: 28447087   |                                       |                           |         | FALSE |
| cg17052170 | 0.65 | 0.77 | -0.13 | -62.10  | Chr8: 144099482  | <i>LY6E, LY6E, LOC100133669</i>       | TSS1500, TSS1500, Body    | Island  | FALSE |
| cg01828798 | 0.35 | 0.48 | -0.13 | -42.33  | ChrY: 8571457    | <i>TTY19</i>                          | TSS1500                   |         | FALSE |
| cg16031515 | 0.28 | 0.40 | -0.13 | -47.01  | Chr1: 205743344  | <i>RAB7L1, RAB7L1, RAB7L1, RAB7L1</i> | Body, Body, Body, 5'UTR   | N_Shore | FALSE |
| cg14931215 | 0.50 | 0.63 | -0.13 | -42.29  | ChrY: 21867702   | <i>KDM5D, KDM5D, KDM5D</i>            | 3'UTR, 3'UTR, 3'UTR       |         | FALSE |
| cg17437770 | 0.35 | 0.48 | -0.13 | -41.24  | Chr10: 43250800  |                                       |                           | Island  | FALSE |
| cg08284263 | 0.39 | 0.52 | -0.13 | -40.20  | Chr10: 92958627  |                                       |                           |         | TRUE  |
| cg25319279 | 0.65 | 0.78 | -0.13 | -61.67  | Chr11: 5960081   |                                       |                           |         | FALSE |
| cg09125754 | 0.65 | 0.77 | -0.13 | -60.95  | Chr2: 130886714  | <i>POTEF, POTEF</i>                   | 1stExon, 5'UTR            |         | FALSE |
| cg16006841 | 0.44 | 0.57 | -0.13 | -39.42  | Chr5: 176797999  | <i>RGS14</i>                          | Body                      | S_Shelf | FALSE |
| cg08433110 | 0.77 | 0.89 | -0.13 | -112.66 | Chr6: 1684468    | <i>GMDS</i>                           | Body                      |         | FALSE |
| cg03062944 | 0.70 | 0.82 | -0.13 | -73.06  | Chr10: 6183455   |                                       |                           | N_Shelf | FALSE |
| cg14133106 | 0.38 | 0.51 | -0.13 | -39.23  | ChrY: 14652924   |                                       |                           | S_Shelf | FALSE |
| cg02090762 | 0.10 | 0.23 | -0.13 | -85.57  | Chr17: 79503859  | <i>FSCN2, FSCN2</i>                   | Body, Body                | Island  | TRUE  |
| cg13469590 | 0.23 | 0.36 | -0.13 | -49.71  | Chr9: 19229767   |                                       |                           | N_Shore | FALSE |

|            |      |      |       |         |                 |   |                        |         |       |
|------------|------|------|-------|---------|-----------------|---|------------------------|---------|-------|
| cg13752114 | 0.71 | 0.84 | -0.12 | -78.36  | Chr3: 195489708 | <i>MUC4, MUC4, MUC4</i>                   | Body, Body, Body       | Island  | FALSE |
| cg01819759 | 0.10 | 0.23 | -0.12 | -84.76  | Chr13: 79234251 | <i>RNF219</i>                             | TSS1500                | S_Shore | FALSE |
| cg18286997 | 0.56 | 0.69 | -0.12 | -44.72  | Chr1: 121448638 |   |                        |         | FALSE |
| cg09611599 | 0.40 | 0.53 | -0.12 | -37.85  | Chr11: 20382497 |   |                        | N_Shelf | FALSE |
| cg02784823 | 0.63 | 0.75 | -0.12 | -53.51  | Chr19: 49000897 | <i>LMTK3</i>                              | Body                   | Island  | FALSE |
| cg02219949 | 0.65 | 0.77 | -0.12 | -56.71  | Chr17: 45927392 | <i>SP6</i>                                | 5'UTR                  | N_Shore | FALSE |
| cg20167074 | 0.62 | 0.74 | -0.12 | -51.09  | Chr1: 151967023 | <i>S100A10</i>                            | TSS1500                | S_Shore | FALSE |
| cg04111992 | 0.50 | 0.62 | -0.12 | -39.06  | Chr7: 158790115 |   |                        | S_Shore | FALSE |
| cg17833746 | 0.31 | 0.44 | -0.12 | -40.06  | Chr17: 40489785 | <i>STAT3, STAT3, STAT3</i>                | Body, Body, Body       |         | FALSE |
| cg15059639 | 0.61 | 0.74 | -0.12 | -49.92  | Chr2: 171220061 | <i>MYO3B, MYO3B, MYO3B</i>                | Body, Body, Body       |         | FALSE |
| cg05180887 | 0.57 | 0.69 | -0.12 | -43.84  | Chr2: 1817263   | <i>MYT1L</i>                              | Body                   |         | FALSE |
| cg08822897 | 0.31 | 0.43 | -0.12 | -39.59  | Chr11: 64258103 |   |                        |         | FALSE |
| cg26280727 | 0.67 | 0.79 | -0.12 | -60.99  | Chr19: 49000998 | <i>LMTK3</i>                              | Body                   | Island  | FALSE |
| cg16580985 | 0.78 | 0.90 | -0.12 | -111.78 | Chr4: 1550194   |   |                        |         | FALSE |
| cg07138768 | 0.71 | 0.83 | -0.12 | -71.32  | Chr7: 917805    | <i>C7orf20</i>                            | Body                   | Island  | FALSE |
| cg18650626 | 0.85 | 0.97 | -0.12 | -208.33 | Chr7: 1914073   | <i>MAD1L1, MAD1L1, MAD1L1</i>             | Body, Body, Body       | Island  | FALSE |
| cg21827317 | 0.33 | 0.45 | -0.12 | -38.21  | Chr3: 136751795 |   |                        | S_Shore | FALSE |
| cg03604322 | 0.46 | 0.58 | -0.12 | -36.42  | Chr22: 32439052 | <i>SLC5A1, SLC5A1</i>                     | 5'UTR, 1stExon         | Island  | FALSE |
| cg10016788 | 0.38 | 0.50 | -0.12 | -36.24  | Chr19: 55599029 | <i>EPS8L1, EPS8L1</i>                     | 3'UTR, 3'UTR           | S_Shore | TRUE  |
| cg22730047 | 0.24 | 0.36 | -0.12 | -46.32  | Chr1: 161410551 |   |                        | Island  | FALSE |
| cg08750459 | 0.53 | 0.65 | -0.12 | -39.27  | Chr17: 6558815  |   |                        | N_Shore | FALSE |
| cg21132536 | 0.66 | 0.79 | -0.12 | -57.95  | Chr20: 33465180 | <i>ACSS2, ACSS2, ACSS2</i>                | Body, Body, Body       | S_Shore | FALSE |
| cg08570243 | 0.14 | 0.26 | -0.12 | -67.60  | Chr2: 110969853 | <i>NCRNA00116</i>                         | Body                   | Island  | FALSE |
| cg15085883 | 0.53 | 0.65 | -0.12 | -39.25  | Chr12: 68848994 |   |                        |         | TRUE  |
| cg08985785 | 0.55 | 0.67 | -0.12 | -40.52  | Chr6: 39196340  | <i>KCNK5</i>                              | Body                   | N_Shore | FALSE |
| cg16474696 | 0.39 | 0.51 | -0.12 | -35.36  | Chr19: 13875014 | <i>MRI1, MRI1</i>                         | TSS1500, TSS1500       | N_Shore | FALSE |
| cg19980771 | 0.23 | 0.35 | -0.12 | -46.09  | Chr6: 110798022 | <i>SLC22A16</i>                           | TSS200                 | Island  | FALSE |
| cg09584650 | 0.49 | 0.61 | -0.12 | -36.60  | Chr8: 2002012   | <i>MYOM2</i>                              | Body                   | N_Shore | FALSE |
| cg00325531 | 0.28 | 0.40 | -0.12 | -40.72  | Chr1: 75591353  |   |                        | Island  | FALSE |
| cg26783481 | 0.77 | 0.89 | -0.12 | -101.56 | Chr5: 93125895  | <i>FAM172A, FAM172A, FAM172A, FAM172A</i> | Body, Body, Body, Body |         | TRUE  |
| cg15546638 | 0.48 | 0.60 | -0.12 | -35.96  | Chr15: 93277793 |   |                        |         | FALSE |
| cg12850892 | 0.47 | 0.59 | -0.12 | -35.72  | Chr11: 75945585 |   |                        | N_Shore | FALSE |
| cg07341007 | 0.62 | 0.74 | -0.12 | -48.23  | Chr3: 195489909 | <i>MUC4, MUC4, MUC4</i>                   | Body, Body, Body       | Island  | FALSE |
| cg08516507 | 0.17 | 0.29 | -0.12 | -56.68  | Chr6: 32064206  | <i>TNXB</i>                               | Body                   | Island  | FALSE |
| cg01116956 | 0.70 | 0.82 | -0.12 | -64.97  | Chr2: 4048824   |   |                        | N_Shore | FALSE |
| cg03438552 | 0.59 | 0.71 | -0.12 | -42.34  | Chr6: 32805548  | <i>TAP2, TAP2</i>                         | Body, Body             | N_Shore | FALSE |
| cg04887076 | 0.49 | 0.61 | -0.12 | -35.00  | Chr19: 55477653 | <i>NLRP2</i>                              | TSS200                 |         | FALSE |
| cg14213105 | 0.59 | 0.71 | -0.12 | -42.66  | Chr9: 126980322 |   |                        |         | TRUE  |
| cg16194588 | 0.61 | 0.73 | -0.12 | -44.72  | Chr19: 49002477 | <i>LMTK3</i>                              | Body                   | Island  | FALSE |
| cg18918831 | 0.59 | 0.71 | -0.12 | -42.22  | Chr3: 195489782 | <i>MUC4, MUC4, MUC4</i>                   | Body, Body, Body       | Island  | FALSE |
| cg27387193 | 0.46 | 0.57 | -0.12 | -33.65  | Chr6: 32064032  | <i>TNXB</i>                               | Body                   | Island  | FALSE |
| cg21903646 | 0.25 | 0.37 | -0.12 | -41.06  | Chr6: 28447115  |   |                        |         | FALSE |
| cg11704005 | 0.40 | 0.52 | -0.12 | -33.27  | Chr1: 19002948  | <i>PAX7, PAX7, PAX7</i>                   | Body, Body, Body       |         | TRUE  |
| cg19901940 | 0.37 | 0.48 | -0.12 | -33.82  | Chr14: 22689870 |   |                        |         | FALSE |
| cg12813394 | 0.33 | 0.44 | -0.12 | -35.25  | Chr14: 69095057 |   |                        | Island  | FALSE |
| cg12584458 | 0.34 | 0.46 | -0.12 | -34.20  | Chr6: 28447107  |   |                        |         | FALSE |
| cg08998192 | 0.51 | 0.63 | -0.12 | -34.78  | Chr6: 32805570  | <i>TAP2, TAP2</i>                         | Body, Body             | N_Shore | FALSE |
| cg13565129 | 0.56 | 0.68 | -0.12 | -38.29  | Chr6: 28601419  |   |                        | N_Shore | FALSE |
| cg04850017 | 0.55 | 0.67 | -0.12 | -37.03  | Chr11: 63683019 | <i>RCOR2</i>                              | Body                   | N_Shore | FALSE |
| cg06862049 | 0.58 | 0.70 | -0.12 | -39.56  | Chr19: 49001890 | <i>LMTK3</i>                              | Body                   | Island  | FALSE |
| cg13916469 | 0.62 | 0.74 | -0.12 | -45.04  | Chr9: 95834820  | <i>SUSD3</i>                              | Body                   |         | TRUE  |
| cg20528787 | 0.46 | 0.58 | -0.12 | -32.74  | Chr7: 158032352 | <i>PTPRN2, PTPRN2, PTPRN2</i>             | Body, Body, Body       |         | FALSE |
| cg09826364 | 0.39 | 0.51 | -0.12 | -32.24  | Chr7: 158789723 |   |                        | Island  | FALSE |
| cg21123519 | 0.30 | 0.42 | -0.12 | -35.60  | Chr14: 69095679 |   |                        | S_Shore | TRUE  |

|            |      |      |       |         |                  |  |  |         |       |
|------------|------|------|-------|---------|------------------|--|--|---------|-------|
| cg25323841 | 0.59 | 0.71 | -0.12 | -40.04  | Chr6: 108444506  |  |  | S_Shelf | FALSE |
| cg10152449 | 0.65 | 0.77 | -0.12 | -48.23  | Chr7: 2444534    | <i>CHST12</i>  | 5'UTR                                    | S_Shore | FALSE |
| cg19317226 | 0.67 | 0.79 | -0.12 | -52.18  | Chr10: 130726701 |  |  |         | FALSE |
| cg18756179 | 0.09 | 0.21 | -0.11 | -77.22  | Chr19: 50554510  | <i>FLJ26850</i>  | Body                                     | S_Shore | FALSE |
| cg07026904 | 0.55 | 0.67 | -0.11 | -35.34  | Chr11: 114832606 |  |  | S_Shore | FALSE |
| cg08889243 | 0.78 | 0.89 | -0.11 | -95.56  | Chr1: 57892830   | <i>DAB1</i>  | 5'UTR                                    | S_Shelf | FALSE |
| cg18052511 | 0.44 | 0.55 | -0.11 | -30.81  | Chr3: 46410222   | <i>CCR5, CCR5</i>  | TSS1500,<br>TSS1500                      |         | FALSE |
| cg00600477 | 0.52 | 0.63 | -0.11 | -33.02  | Chr8: 144715010  |  |  | N_Shelf | FALSE |
| cg17542795 | 0.70 | 0.81 | -0.11 | -57.96  | Chr4: 178518017  |  |  |         | TRUE  |
| cg09359103 | 0.46 | 0.57 | -0.11 | -30.95  | Chr1: 154839909  | <i>KCNN3</i>   | Body                                     |         | FALSE |
| cg12119625 | 0.43 | 0.54 | -0.11 | -30.48  | Chr19: 54106789  | <i>LOC284379</i>   | TSS200                                   |         | FALSE |
| cg04819497 | 0.67 | 0.78 | -0.11 | -49.33  | Chr11: 58598444  |  |  |         | FALSE |
| cg07684519 | 0.47 | 0.59 | -0.11 | -31.09  | Chr12: 29303184  |  |  | S_Shore | FALSE |
| cg25582488 | 0.31 | 0.43 | -0.11 | -33.17  | Chr14: 69095171  |  |  | Island  | FALSE |
| cg06237805 | 0.32 | 0.44 | -0.11 | -32.71  | ChrY: 8147958    |  |  | Island  | FALSE |
| cg17566325 | 0.28 | 0.39 | -0.11 | -35.32  | Chr12: 133022423 |  |  | N_Shore | FALSE |
| cg09253696 | 0.17 | 0.28 | -0.11 | -50.80  | Chr17: 73873529  | <i>TRIM47</i>  | Body                                     | Island  | TRUE  |
| cg20737388 | 0.54 | 0.66 | -0.11 | -33.37  | Chr11: 73668626  | <i>DNAJB13</i>   | Body                                     |         | FALSE |
| cg05067427 | 0.58 | 0.69 | -0.11 | -36.01  | Chr16: 54227914  |  |  | N_Shore | TRUE  |
| cg01574481 | 0.45 | 0.56 | -0.11 | -29.82  | Chr14: 24641852  | <i>REC8, REC8</i>  | Body, Body                               | Island  | TRUE  |
| cg15931850 | 0.54 | 0.65 | -0.11 | -32.66  | Chr4: 1550089    |  |  |         | FALSE |
| cg10646950 | 0.30 | 0.41 | -0.11 | -32.85  | ChrY: 20748782   | <i>HSFY1, TTTY9B,<br/>HSFY2, HSFY2,<br/>TTY9A, HSFY1</i> | Body, Body,<br>Body, Body,<br>Body, Body |         | FALSE |
| cg02061626 | 0.84 | 0.96 | -0.11 | -161.00 | Chr2: 233274167  | <i>ALPL2</i>   | Body                                     | Island  | FALSE |
| cg12584960 | 0.55 | 0.66 | -0.11 | -33.08  | Chr13: 114965839 |  |  | Island  | TRUE  |
| cg04863892 | 0.65 | 0.76 | -0.11 | -44.10  | Chr7: 27183375   | <i>HOXA5</i>   | TSS200                                   | Island  | FALSE |
| cg03533500 | 0.20 | 0.31 | -0.11 | -43.79  | ChrY: 21668420   |  |  | S_Shelf | FALSE |
| cg22757362 | 0.45 | 0.57 | -0.11 | -29.22  | Chr10: 43721445  | <i>RASGEF1A</i>  | 5'UTR                                    | N_Shelf | FALSE |
| cg08265926 | 0.62 | 0.73 | -0.11 | -39.05  | Chr16: 81039227  | <i>CENPN, CENPN,<br/>CENPN, C16orf61</i>                 | TSS1500,<br>TSS1500,<br>TSS1500, 5'UTR   | N_Shore | FALSE |
| cg10365886 | 0.64 | 0.75 | -0.11 | -41.58  | Chr6: 32063874   | <i>TNXB</i>  | Body                                     | Island  | FALSE |
| cg00495303 | 0.67 | 0.78 | -0.11 | -47.19  | Chr18: 3771110   | <i>DLGAP1, DLGAP1</i>                                    | Body, Body                               | N_Shore | FALSE |
| cg10881225 | 0.60 | 0.71 | -0.11 | -36.33  | Chr2: 9984929    | <i>TAF1B</i>   | Body                                     | S_Shore | FALSE |
| cg02964324 | 0.55 | 0.66 | -0.11 | -32.38  | Chr7: 43291318   | <i>HECW1</i>   | Body                                     | S_Shelf | FALSE |
| cg25307665 | 0.70 | 0.81 | -0.11 | -54.31  | Chr7: 27183694   | <i>HOXA5</i>   | TSS1500                                  | Island  | FALSE |
| cg24882324 | 0.10 | 0.21 | -0.11 | -69.80  | Chr6: 32064508   | <i>TNXB</i>  | Body                                     | Island  | FALSE |
| cg16958594 | 0.54 | 0.65 | -0.11 | -31.52  | Chr6: 30882708   | <i>VARS2, VARS2,<br/>VARS2</i>                           | Body, 5'UTR,<br>Body                     | S_Shore | TRUE  |
| cg22462983 | 0.08 | 0.19 | -0.11 | -79.52  | Chr6: 133561756  | <i>EYA4, EYA4, EYA4</i>                                  | TSS1500,<br>TSS1500                      | N_Shore | FALSE |
| cg11693285 | 0.26 | 0.37 | -0.11 | -34.69  | Chr10: 131927345 |  |  | Island  | TRUE  |
| cg13773741 | 0.74 | 0.85 | -0.11 | -67.26  | Chr17: 9967499   | <i>GAS7</i>  | Body                                     |         | FALSE |
| cg01337207 | 0.52 | 0.63 | -0.11 | -30.09  | Chr6: 32063835   | <i>TNXB</i>  | Body                                     | Island  | FALSE |
| cg01496720 | 0.41 | 0.52 | -0.11 | -27.97  | Chr10: 3825398   | <i>KLF6, KLF6, KLF6,<br/>KLF6</i>                        | Body, Body,<br>Body, Body                | N_Shore | FALSE |
| cg03556669 | 0.19 | 0.30 | -0.11 | -43.12  | Chr6: 32064497   | <i>TNXB</i>  | Body                                     | Island  | FALSE |
| cg13457410 | 0.66 | 0.77 | -0.11 | -43.88  | Chr1: 9762510    | <i>PIK3CD</i>  | 5'UTR                                    |         | FALSE |
| cg23118561 | 0.76 | 0.87 | -0.11 | -72.62  | Chr13: 51565237  |  |  |         | TRUE  |
| cg18113731 | 0.51 | 0.62 | -0.11 | -28.96  | ChrY: 16636984   | <i>NLGN4Y, NLGN4Y,<br/>NLGN4Y</i>                        | Body, 5'UTR,<br>Body                     | Island  | FALSE |
| cg02160608 | 0.72 | 0.83 | -0.11 | -58.35  | Chr2: 113956634  | <i>PSD4, LOC440839</i>                                   | Body, Body                               | Island  | FALSE |
| cg05263479 | 0.18 | 0.29 | -0.11 | -44.73  | Chr7: 47092529   |  |  | Island  | FALSE |
| cg27436995 | 0.47 | 0.58 | -0.11 | -27.52  | Chr16: 743998    | <i>FBXL16</i>  | 3'UTR                                    | Island  | FALSE |
| cg17430262 | 0.36 | 0.47 | -0.11 | -27.98  | ChrY: 14649051   |  |  | Island  | FALSE |
| cg10612560 | 0.59 | 0.70 | -0.11 | -33.41  | Chr17: 8019912   | <i>ALOXE3, ALOXE3</i>                                    | Body, Body                               | N_Shelf | FALSE |
| cg08291996 | 0.17 | 0.28 | -0.11 | -46.59  | Chr19: 58791159  | <i>ZNF8</i>  | Body                                     | S_Shore | FALSE |
| cg22973012 | 0.74 | 0.85 | -0.11 | -63.43  | Chr6: 168760457  |  |  |         | FALSE |
| cg06060754 | 0.47 | 0.58 | -0.11 | -27.37  | Chr5: 176797920  | <i>RGS14</i>   | Body                                     | S_Shelf | FALSE |
| cg17076635 | 0.12 | 0.22 | -0.11 | -60.26  | Chr8: 144484205  |  |  |         | TRUE  |
| cg09757644 | 0.68 | 0.79 | -0.11 | -45.53  | Chr6: 447497     |  |  |         | FALSE |
| cg25970575 | 0.49 | 0.60 | -0.11 | -27.52  | Chr4: 6010164    |  |  | S_Shore | TRUE  |
| cg05250380 | 0.82 | 0.93 | -0.11 | -117.61 | Chr9: 140735359  |  |  | N_Shore | FALSE |

|            |      |      |       |        |                  |   |   |         |       |
|------------|------|------|-------|--------|------------------|---|---|---------|-------|
| cg02482603 | 0.40 | 0.51 | -0.11 | -26.66 | Chr1: 174843754  | <i>RABGAP1L</i> ,<br><i>RABGAP1L</i>  | TSS1500, Body   |         | FALSE |
| cg08288016 | 0.70 | 0.81 | -0.11 | -49.78 | Chr4: 187590536  | <i>FAT1</i>   | Body  |         | TRUE  |
| cg16274205 | 0.40 | 0.51 | -0.11 | -26.60 | Chr3: 94243571   |   |   |         | TRUE  |
| cg27505492 | 0.22 | 0.33 | -0.11 | -36.09 | Chr12: 133187045 |   |   | Island  | TRUE  |
| cg00412772 | 0.55 | 0.66 | -0.11 | -29.53 | Chr19: 38794845  | <i>YIF1B</i> , <i>YIF1B</i> ,<br><i>C19orf33</i> , <i>YIF1B</i> ,<br><i>YIF1B</i> , <i>YIF1B</i> ,<br><i>YIF1B</i> , <i>YIF1B</i> ,<br><i>C19orf33</i>          | 3'UTR, 3'UTR,<br>1stExon, 3'UTR,<br>3'UTR, 3'UTR,<br>3'UTR, 3'UTR,<br>5'UTR                             |         | TRUE  |
| cg13799081 | 0.57 | 0.68 | -0.11 | -30.71 | Chr10: 112410313 | <i>RBM20</i>  | Body  |         | TRUE  |
| cg20092122 | 0.07 | 0.18 | -0.11 | -76.58 | Chr19: 17517221  | <i>BST2</i>   | TSS1500   |         | TRUE  |
| cg02251754 | 0.50 | 0.61 | -0.11 | -27.01 | Chr1: 28572299   |   |   | N_Shore | FALSE |
| cg16288318 | 0.58 | 0.68 | -0.11 | -30.86 | Chr13: 112986927 |   |   | S_Shore | FALSE |
| cg19650706 | 0.59 | 0.70 | -0.11 | -32.01 | Chr5: 140594406  | <i>PCDHB13</i>  | 1stExon   | N_Shore | FALSE |
| cg13661648 | 0.50 | 0.61 | -0.11 | -26.98 | Chr6: 33035284   | <i>HLA-DPA1</i>   | 3'UTR   |         | FALSE |
| cg00044354 | 0.36 | 0.47 | -0.11 | -26.33 | Chr1: 67389884   | <i>MIER1</i> , <i>WDR78</i> ,<br><i>MIER1</i> , <i>MIER1</i> ,<br><i>MIER1</i> , <i>MIER1</i> ,<br><i>MIER1</i> , <i>WDR78</i> ,<br><i>MIER1</i> , <i>MIER1</i> | TSS1500, Body,<br>TSS1500,<br>TSS1500,<br>TSS1500,<br>TSS1500,<br>TSS1500, Body,<br>TSS1500,<br>TSS1500 | N_Shore | FALSE |
| cg02916272 | 0.45 | 0.56 | -0.11 | -25.62 | Chr11: 1769443   | <i>HCCA2</i> ,<br><i>LOC402778</i>  | Body, TSS200  | Island  | FALSE |
| cg22094750 | 0.05 | 0.15 | -0.11 | -95.17 | Chr1: 1851056    | <i>TMEM52</i>   | TSS1500   | Island  | FALSE |
| cg15971518 | 0.67 | 0.78 | -0.11 | -41.84 | Chr11: 57159174  | <i>PRG2</i>   | TSS1500   |         | FALSE |
| cg06201514 | 0.59 | 0.70 | -0.11 | -31.70 | Chr2: 1817409    | <i>MYT1L</i>  | Body  |         | FALSE |
| cg07330481 | 0.68 | 0.78 | -0.11 | -42.51 | Chr17: 37322330  | <i>ARL5C</i> , <i>ARL5C</i>   | 1stExon, 5'UTR  | S_Shore | TRUE  |
| cg25436886 | 0.24 | 0.35 | -0.11 | -32.78 | Chr3: 127056972  |   |   | Island  | FALSE |
| cg16824113 | 0.50 | 0.60 | -0.11 | -25.88 | Chr12: 132166485 |   |   |         | TRUE  |
| cg00791851 | 0.40 | 0.50 | -0.11 | -24.99 | Chr1: 76518896   |   |   |         | TRUE  |
| cg02698668 | 0.46 | 0.57 | -0.11 | -24.99 | Chr19: 44261472  |   |   | S_Shelf | FALSE |
| cg13593090 | 0.47 | 0.58 | -0.11 | -25.19 | Chr19: 9546723   | <i>ZNF266</i> , <i>ZNF266</i>   | TSS1500,<br>TSS1500   | S_Shore | FALSE |
| cg24040502 | 0.52 | 0.63 | -0.11 | -26.61 | Chr19: 55477810  | <i>NLRP2</i> , <i>NLRP2</i>   | 5'UTR, 1stExon  |         | FALSE |
| cg20481287 | 0.56 | 0.66 | -0.11 | -28.26 | Chr12: 12224457  | <i>BCL2L14</i> ,<br><i>BCL2L14</i> ,<br><i>BCL2L14</i> ,<br><i>BCL2L14</i> , <i>BCL2L14</i>   | 5'UTR, 5'UTR,<br>1stExon, 5'UTR,<br>1stExon   |         | TRUE  |
| cg07676361 | 0.45 | 0.56 | -0.11 | -24.70 | Chr16: 80966860  |   |   | S_Shore | FALSE |
| cg26056498 | 0.45 | 0.55 | -0.11 | -24.57 | Chr8: 1030319    |   |   |         | FALSE |
| cg25099892 | 0.43 | 0.53 | -0.11 | -24.43 | Chr13: 113313905 | <i>C13orf35</i>   | 5'UTR   |         | FALSE |
| cg15788369 | 0.53 | 0.63 | -0.11 | -26.66 | Chr19: 15833777  |   |   | Island  | FALSE |
| cg12048965 | 0.32 | 0.43 | -0.10 | -26.39 | Chr10: 3848384   |   |   |         | TRUE  |
| cg15015639 | 0.51 | 0.61 | -0.10 | -25.62 | Chr2: 220282977  | <i>DES</i>  | TSS200  | N_Shore | TRUE  |
| cg25987564 | 0.42 | 0.53 | -0.10 | -24.17 | Chr4: 6010075    |   |   | Island  | FALSE |
| cg14005211 | 0.36 | 0.46 | -0.10 | -25.13 | Chr2: 171676925  | <i>GAD1</i> , <i>GAD1</i>   | Body, Body  | Island  | FALSE |
| cg20045320 | 0.24 | 0.34 | -0.10 | -32.45 | Chr11: 319555    |   |   | S_Shore | FALSE |
| cg26535992 | 0.49 | 0.60 | -0.10 | -24.80 | Chr6: 166671495  |   |   | S_Shelf | FALSE |
| cg17842918 | 0.48 | 0.59 | -0.10 | -24.63 | Chr13: 113540400 | <i>ATP11A</i> , <i>ATP11A</i>   | 3'UTR, 3'UTR  | Island  | TRUE  |
| cg20583945 | 0.26 | 0.36 | -0.10 | -30.23 | Chr8: 144636462  | <i>GSDMD</i>  | 5'UTR   | S_Shore | FALSE |
| cg24516106 | 0.60 | 0.70 | -0.10 | -30.42 | Chr2: 72079413   |   |   | Island  | FALSE |
| cg03128011 | 0.42 | 0.52 | -0.10 | -23.77 | Chr8: 1321333    |   |   | Island  | FALSE |
| cg25396728 | 0.36 | 0.46 | -0.10 | -24.67 | Chr12: 248500    | <i>IQSEC3</i> , <i>IQSEC3</i>   | Body, Body  | Island  | TRUE  |
| cg02002345 | 0.10 | 0.20 | -0.10 | -62.50 | ChrY: 6777855    | <i>TBL1Y</i> , <i>TBL1Y</i> ,<br><i>TBL1Y</i>   | TSS1500,<br>TSS1500,<br>TSS1500   | N_Shore | FALSE |
| cg12526471 | 0.61 | 0.72 | -0.10 | -31.31 | Chr11: 113929188 | <i>ZBTB16</i>   | TSS1500   | N_Shore | FALSE |
| cg23141851 | 0.57 | 0.67 | -0.10 | -27.68 | Chr3: 14615941   |   |   | Island  | FALSE |
| cg01219135 | 0.51 | 0.62 | -0.10 | -25.06 | Chr7: 158766336  |   |   | Island  | FALSE |
| cg02002217 | 0.67 | 0.78 | -0.10 | -39.34 | Chr13: 24520348  |   |   |         | FALSE |
| cg20474581 | 0.44 | 0.55 | -0.10 | -23.48 | ChrY: 14812997   | <i>USP9Y</i>  | TSS200  |         | FALSE |
| cg01428095 | 0.49 | 0.59 | -0.10 | -24.09 | Chr1: 228134229  | <i>WNT9A</i>  | Body  | N_Shore | FALSE |
| cg10568066 | 0.40 | 0.50 | -0.10 | -23.50 | Chr6: 30039442   | <i>RNF39</i> , <i>RNF39</i>   | Body, Body  | Island  | FALSE |

|                         |      |      |       |        |                  |   |  |         |       |
|-------------------------|------|------|-------|--------|------------------|---|--|---------|-------|
| cg21871091              | 0.64 | 0.74 | -0.10 | -34.10 | Chr21: 38349937  | <i>HLCS</i>   | 5'UTR                                    | N_Shelf | TRUE  |
| cg22771759              | 0.23 | 0.33 | -0.10 | -32.34 | Chr13: 24902376  |   |  | Island  | FALSE |
| cg03031988              | 0.77 | 0.88 | -0.10 | -67.82 | Chr6: 31510729   | <i>BAT1, BAT1</i>                                       | TSS1500,<br>TSS1500                      | S_Shore | FALSE |
| cg06904356              | 0.57 | 0.67 | -0.10 | -27.09 | Chr5: 1849983    |   |  | N_Shore | FALSE |
| cg02649063              | 0.55 | 0.65 | -0.10 | -25.90 | Chr16: 55794731  | <i>CES4</i>   | Body                                     | Island  | FALSE |
| cg06065495              | 0.16 | 0.26 | -0.10 | -42.12 | ChrY: 21666309   | <i>BCORL2</i>   | TSS1500                                  | S_Shore | FALSE |
| cg15196197              | 0.10 | 0.20 | -0.10 | -60.37 | Chr6: 32064573   | <i>TNXB</i>   | Body                                     | Island  | FALSE |
| cg26695758              | 0.72 | 0.83 | -0.10 | -49.67 | Chr6: 32063607   | <i>TNXB</i>   | Body                                     | Island  | FALSE |
| cg08475194              | 0.06 | 0.16 | -0.10 | -77.70 | Chr5: 111755481  | <i>FLJ11235,<br/>EPB41L4A</i>                           | Body, TSS1500                            | Island  | FALSE |
| cg13968390              | 0.67 | 0.77 | -0.10 | -37.08 | Chr2: 108904812  | <i>SULT1C2,<br/>SULT1C2</i>                             | TSS1500,<br>TSS1500                      |         | TRUE  |
| cg17651935              | 0.52 | 0.62 | -0.10 | -24.22 | ChrY: 14078666   |   |  | S_Shore | FALSE |
| cg08364137              | 0.10 | 0.21 | -0.10 | -57.46 | Chr7: 156400990  |   |  | S_Shore | FALSE |
| cg08895590              | 0.53 | 0.64 | -0.10 | -24.82 | Chr1: 91227319   |   |  |         | TRUE  |
| cg03486986              | 0.30 | 0.40 | -0.10 | -25.92 | Chr13: 112986285 |   |  | S_Shore | TRUE  |
| cg09315878              | 0.72 | 0.82 | -0.10 | -46.96 | Chr1: 1152580    | <i>SDF4, SDF4</i>                                       | 3'UTR, 3'UTR                             | Island  | FALSE |
| cg10671668              | 0.23 | 0.33 | -0.10 | -30.99 | Chr12: 4919230   | <i>KCNA6</i>  | 1stExon                                  | Island  | FALSE |
| cg16582517              | 0.38 | 0.49 | -0.10 | -22.81 | Chr3: 5025885    | <i>BHLHE40</i>  | 3'UTR                                    | S_Shore | FALSE |
| cg13686059              | 0.79 | 0.90 | -0.10 | -77.46 | Chr2: 11101549   |   |  | S_Shore | FALSE |
| cg09115713              | 0.76 | 0.86 | -0.10 | -59.30 | Chr16: 88832476  | <i>FAM38A</i>   | Body                                     |         | FALSE |
| cg21119074              | 0.61 | 0.72 | -0.10 | -29.79 | Chr6: 20211654   | <i>MBOAT1</i>   | Body                                     | N_Shore | FALSE |
| cg19460095              | 0.26 | 0.36 | -0.10 | -28.16 | Chr11: 34672025  | <i>EHF</i>  | Body                                     |         | FALSE |
| cg00290607              | 0.51 | 0.61 | -0.10 | -23.50 | Chr11: 67383545  |   |  | Island  | TRUE  |
| cg20724680              | 0.64 | 0.74 | -0.10 | -32.38 | Chr19: 49000743  | <i>LMTK3</i>  | Body                                     | Island  | FALSE |
| cg21052687              | 0.54 | 0.64 | -0.10 | -24.53 | Chr11: 55561545  | <i>OR5D14</i>   | TSS1500                                  |         | FALSE |
| cg10557773              | 0.32 | 0.42 | -0.10 | -24.37 | ChrY: 2801877    | <i>ZFY</i>  | TSS1500                                  | N_Shore | FALSE |
| cg25737313              | 0.45 | 0.55 | -0.10 | -22.23 | Chr19: 12899557  |   |  | N_Shore | FALSE |
| cg26974214              | 0.16 | 0.26 | -0.10 | -41.30 | Chr10: 91151885  | <i>IFIT1</i>  | TSS1500                                  |         | FALSE |
| cg08900409              | 0.61 | 0.71 | -0.10 | -28.73 | Chr19: 18475669  | <i>PGPEP1</i>   | 3'UTR                                    |         | TRUE  |
| cg10510935              | 0.45 | 0.55 | -0.10 | -22.10 | Chr1: 4059661    |   |  |         | FALSE |
| cg14741691              | 0.54 | 0.64 | -0.10 | -24.30 | Chr19: 40855329  | <i>PLD3, PLD3,<br/>C19orf47</i>                         | 5'UTR, 5'UTR,<br>TSS1500                 | S_Shore | FALSE |
| cg15473346              | 0.30 | 0.40 | -0.10 | -25.11 | Chr1: 165798420  | <i>UCK2</i>   | Body                                     | S_Shore | FALSE |
| cg23099319              | 0.53 | 0.63 | -0.10 | -23.70 | Chr10: 1517224   | <i>ADARB2</i>   | Body                                     | Island  | TRUE  |
| cg06351537              | 0.75 | 0.85 | -0.10 | -55.17 | Chr22: 49798750  |   |  | Island  | FALSE |
| cg02297043              | 0.37 | 0.47 | -0.10 | -22.25 | Chr1: 75590912   |   |  | Island  | FALSE |
| cg12154045              | 0.56 | 0.66 | -0.10 | -24.90 | Chr19: 1465556   | <i>APC2</i>   | Body                                     | Island  | FALSE |
| cg16761754              | 0.32 | 0.42 | -0.10 | -23.75 | Chr14: 105127242 |   |  | S_Shore | FALSE |
| cg07021523              | 0.78 | 0.88 | -0.10 | -67.28 | Chr1: 16810670   | <i>CROCCL2</i>  | Body                                     | Island  | FALSE |
| cg17723710              | 0.49 | 0.59 | -0.10 | -22.27 | Chr5: 34621927   |   |  |         | TRUE  |
| cg20857253              | 0.56 | 0.66 | -0.10 | -24.80 | Chr21: 33957290  | <i>TCP10L</i>   | 5'UTR                                    |         | FALSE |
| cg05234568              | 0.72 | 0.82 | -0.10 | -45.76 | Chr11: 5960015   |   |  |         | FALSE |
| cg11955878              | 0.32 | 0.42 | -0.10 | -23.65 | Chr4: 165898967  | <i>TRIM61</i>   | TSS200                                   |         | FALSE |
| cg13978347              | 0.71 | 0.81 | -0.10 | -42.66 | Chr9: 120140243  | <i>ASTN2, ASTN2,<br/>ASTN2</i>                          | Body, Body, Body                         |         | FALSE |
| cg22716280              | 0.64 | 0.74 | -0.10 | -31.46 | Chr10: 134727319 |   |  | N_Shelf | FALSE |
| cg08879910              | 0.07 | 0.17 | -0.10 | -67.34 | Chr6: 29974319   | <i>HLA-J,<br/>NCRNA00171</i>                            | Body, Body                               | Island  | TRUE  |
| cg04789475              | 0.66 | 0.76 | -0.10 | -33.13 | Chr4: 186960991  |   |  |         | FALSE |
| <b>Hypermethylation</b> |      |      |       |        |                  |   |  |         |       |
| cg09885502              | 0.57 | 0.16 | 0.41  | 340.66 | Chr20: 57463991  | <i>GNAS, GNAS,<br/>GNAS, GNAS</i>                       | 3'UTR, TSS200,<br>3'UTR, Body            | Island  | FALSE |
| cg05176970              | 0.79 | 0.41 | 0.37  | 340.66 | Chr17: 724273    | <i>NXN</i>  | Body                                     |         | FALSE |
| cg00256329              | 0.77 | 0.41 | 0.36  | 340.66 | Chr17: 724374    | <i>NXN</i>  | Body                                     |         | FALSE |
| cg26287080              | 0.85 | 0.52 | 0.33  | 340.66 | Chr17: 74086286  | <i>EXOC7, EXOC7,<br/>EXOC7, EXOC7,<br/>EXOC7, EXOC7</i> | Body, Body,<br>Body, Body,<br>Body, Body |         | FALSE |
| cg08479752              | 0.67 | 0.37 | 0.30  | 340.66 | Chr19: 54567279  | <i>VSTM1</i>  | TSS200                                   |         | FALSE |
| cg16066505              | 0.84 | 0.55 | 0.29  | 340.66 | Chr2: 171316530  | <i>MYO3B, MYO3B,<br/>MYO3B</i>                          | Body, Body, Body                         |         | FALSE |
| cg25225073              | 0.30 | 0.06 | 0.24  | 340.66 | Chr14: 90528983  | <i>KCNK13</i>   | Body                                     | S_Shore | FALSE |
| cg18025438              | 0.63 | 0.39 | 0.24  | 340.66 | Chr1: 228756789  |   |  | Island  | FALSE |
| cg16154810              | 0.41 | 0.18 | 0.23  | 340.66 | Chr22: 47135258  | <i>CERK</i>   | TSS1500                                  |         | FALSE |
| cg13830619              | 0.93 | 0.71 | 0.22  | 340.66 | Chr12: 9555480   |   |  |         | FALSE |

|            |      |      |      |        |                  |   |  |         |       |
|------------|------|------|------|--------|------------------|---|--|---------|-------|
| cg17783317 | 0.53 | 0.31 | 0.22 | 340.66 | Chr19: 54567123  | <i>VSTM1, VSTM1</i>   | 1stExon, 5'UTR                                 |         | FALSE |
| cg24247231 | 0.52 | 0.31 | 0.21 | 340.66 | Chr15: 67904302  | <i>MAP2K5, MAP2K5</i>   | Body, Body                                     |         | TRUE  |
| cg07784793 | 0.91 | 0.70 | 0.20 | 340.66 | Chr5: 33794720   | <i>ADAMTS12</i>   | Body   |         | TRUE  |
| cg21139150 | 0.54 | 0.34 | 0.20 | 123.60 | Chr21: 46976175  |   |  | Island  | FALSE |
| cg01500431 | 0.88 | 0.68 | 0.20 | 340.66 | Chr22: 24388327  | <i>GSTTP2</i>   | Body   | S_Shelf | FALSE |
| cg03086067 | 0.66 | 0.47 | 0.19 | 118.36 | Chr10: 82368399  | <i>SH2D4B, SH2D4B</i>   | Body, Body                                     |         | FALSE |
| cg16316162 | 0.28 | 0.09 | 0.19 | 340.66 | Chr8: 144660157  | <i>NAPRT1</i>   | Body   | Island  | FALSE |
| cg24265076 | 0.72 | 0.54 | 0.19 | 120.70 | Chr10: 1939618   |   |  |         | FALSE |
| cg05617307 | 0.43 | 0.26 | 0.18 | 103.00 | Chr10: 121413182 | <i>BAG3</i>   | Body   | S_Shore | FALSE |
| cg20811988 | 0.43 | 0.25 | 0.18 | 103.09 | Chr20: 29611924  | <i>FRG1B</i>  | Body   | Island  | FALSE |
| cg06301252 | 0.83 | 0.65 | 0.18 | 340.66 | Chr7: 157504143  | <i>PTPRN2, PTPRN2, PTPRN2</i>   | Body, Body, Body                               | Island  | FALSE |
| cg09191173 | 0.47 | 0.30 | 0.18 | 94.97  | Chr11: 108090159 | <i>NPAT</i>   | Body   | N_Shelf | FALSE |
| cg18391209 | 0.54 | 0.36 | 0.17 | 88.48  | Chr1: 223747670  | <i>CAPN8</i>  | Body   | S_Shelf | FALSE |
| cg12327866 | 0.65 | 0.48 | 0.17 | 88.63  | Chr10: 1939663   |   |  |         | FALSE |
| cg27182070 | 0.58 | 0.41 | 0.17 | 84.03  | Chr1: 28218282   | <i>RPA2</i>   | 3'UTR  |         | FALSE |
| cg11141652 | 0.57 | 0.40 | 0.17 | 79.82  | Chr22: 24348549  | <i>GSTTP1</i>   | TSS1500  |         | FALSE |
| cg22240348 | 0.27 | 0.10 | 0.17 | 340.66 | Chr21: 46975805  |   |  | Island  | FALSE |
| cg05380919 | 0.82 | 0.65 | 0.17 | 126.50 | Chr22: 24376252  | <i>GSTT1</i>  | 3'UTR  | S_Shelf | FALSE |
| cg02691506 | 0.43 | 0.27 | 0.16 | 84.76  | Chr3: 8685827    | <i>C3orf32</i>  | 5'UTR  |         | FALSE |
| cg24647015 | 0.55 | 0.38 | 0.16 | 74.51  | Chr11: 114191367 |   |  |         | TRUE  |
| cg02398342 | 0.76 | 0.60 | 0.16 | 98.43  | Chr17: 80708632  | <i>TBCD, FN3K</i>   | TSS1500, 3'UTR                                 | N_Shore | FALSE |
| cg02167713 | 0.44 | 0.28 | 0.16 | 80.30  | Chr17: 79630115  |   |  | N_Shelf | FALSE |
| cg15039826 | 0.31 | 0.15 | 0.16 | 110.75 | ChrX: 39958196   | <i>BCOR, BCOR, BCOR, BCOR</i>   | TSS1500, 5'UTR, TSS1500, 5'UTR                 | Island  | FALSE |
| cg10555744 | 0.38 | 0.22 | 0.16 | 85.26  | Chr1: 25946258   | <i>MAN1C1</i>   | Body   | S_Shore | TRUE  |
| cg27433982 | 0.41 | 0.26 | 0.16 | 77.71  | ChrY: 2802985    | <i>ZFY, ZFY, ZFY</i>  | TSS1500, TSS200, TSS1500                       | Island  | FALSE |
| cg16662477 | 0.26 | 0.11 | 0.15 | 126.50 | Chr17: 33401430  | <i>RFLL</i>   | 5'UTR  |         | TRUE  |
| cg26046487 | 0.43 | 0.28 | 0.15 | 73.20  | ChrY: 20736147   | <i>HSFY1, HSFY2, HSFY2, HSFY1</i>   | Body, Body, Body, Body                         |         | FALSE |
| cg15242686 | 0.55 | 0.39 | 0.15 | 64.32  | Chr22: 24348715  | <i>GSTTP1</i>   | TSS1500  |         | FALSE |
| cg06180910 | 0.87 | 0.71 | 0.15 | 340.66 | Chr22: 24382663  | <i>GSTT1</i>  | Body   | N_Shore | FALSE |
| cg17099656 | 0.23 | 0.08 | 0.15 | 340.66 | Chr22: 47135171  | <i>CERK</i>   | TSS1500  |         | FALSE |
| cg08835041 | 0.80 | 0.65 | 0.15 | 95.94  | Chr19: 37461278  |   |  | N_Shelf | FALSE |
| cg17524265 | 0.44 | 0.29 | 0.15 | 67.37  | Chr8: 144659883  | <i>NAPRT1</i>   | Body   | Island  | FALSE |
| cg01053087 | 0.23 | 0.08 | 0.15 | 340.66 | Chr8: 637909     | <i>ERICH1</i>   | Body   | Island  | FALSE |
| cg02032872 | 0.90 | 0.75 | 0.15 | 340.66 | Chr19: 44260537  | <i>C19orf61</i>   | TSS1500  | S_Shore | FALSE |
| cg13116946 | 0.87 | 0.72 | 0.15 | 126.50 | Chr22: 38479732  | <i>SLC16A8</i>  | TSS1500  | S_Shore | FALSE |
| cg22681495 | 0.83 | 0.69 | 0.15 | 102.92 | Chr15: 86058755  | <i>AKAP13, AKAP13</i>   | Body, Body                                     |         | TRUE  |
| cg01479768 | 0.80 | 0.65 | 0.15 | 88.58  | Chr2: 731298     |   |  | N_Shore | FALSE |
| cg06343673 | 0.78 | 0.63 | 0.14 | 81.99  | Chr17: 78778232  | <i>RPTOR, RPTOR</i>   | Body, Body                                     | S_Shelf | FALSE |
| cg18679504 | 0.37 | 0.22 | 0.14 | 70.50  | ChrX: 40439984   | <i>ATPGAP2</i>  | TSS1500  | Island  | FALSE |
| cg09107344 | 0.36 | 0.22 | 0.14 | 70.51  | Chr12: 53612734  | <i>RARG, RARG</i>   | Body, Body                                     | N_Shore | FALSE |
| cg02025737 | 0.82 | 0.67 | 0.14 | 92.53  | Chr15: 33384751  |   |  |         | TRUE  |
| cg25593510 | 0.54 | 0.40 | 0.14 | 53.19  | Chr1: 110254662  | <i>GSTM5</i>  | TSS1500  |         | FALSE |
| cg05095590 | 0.26 | 0.12 | 0.14 | 101.00 | Chr7: 2139259    | <i>MAD1L1, MAD1L1, MAD1L1</i>   | Body, Body, Body                               |         | FALSE |
| cg20916523 | 0.24 | 0.10 | 0.14 | 109.67 | Chr3: 10184584   | <i>VHL, VHL</i>   | Body, Body                                     | S_Shore | FALSE |
| cg09381666 | 0.59 | 0.45 | 0.14 | 52.32  | Chr16: 88757816  |   |  |         | FALSE |
| cg15171154 | 0.65 | 0.51 | 0.14 | 54.85  | Chr3: 30722557   | <i>TGFBR2, TGFBR2</i>   | Body, Body                                     |         | TRUE  |
| cg07598341 | 0.67 | 0.53 | 0.14 | 55.49  | Chr1: 44344466   | <i>ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3</i> | Body, Body, Body, Body, Body, Body, Body, Body |         | TRUE  |
| cg02836135 | 0.30 | 0.17 | 0.14 | 77.47  | Chr6: 108052093  | <i>SCML4</i>  | Body   |         | TRUE  |
| cg23971987 | 0.62 | 0.49 | 0.14 | 51.60  | Chr4: 11652505   |   |  |         | TRUE  |
| cg05026884 | 0.44 | 0.30 | 0.14 | 53.43  | ChrX: 40032180   | <i>BCOR, BCOR</i>   | 5'UTR, 5'UTR                                   | Island  | FALSE |
| cg26720010 | 0.32 | 0.18 | 0.14 | 71.52  | Chr7: 45147131   | <i>TBRG4, SNORA5B, TBRG4, TBRG4</i>   | Body, TSS1500, Body, Body                      | N_Shelf | FALSE |



|            |      |      |      |        |                  |                               |  |         |       |
|------------|------|------|------|--------|------------------|-------------------------------|--|---------|-------|
| cg08017634 | 0.47 | 0.35 | 0.12 | 37.32  | Chr8: 144659831  | <i>NAPRT1</i>                 | Body   | Island  | FALSE |
| cg23352942 | 0.53 | 0.41 | 0.12 | 35.88  | Chr3: 46931381   | <i>PTH1R</i>                  | Body   | N_Shelf | FALSE |
| cg07234876 | 0.76 | 0.64 | 0.12 | 52.92  | Chr8: 600039     |                               |  | Island  | FALSE |
| cg06937882 | 0.81 | 0.69 | 0.12 | 65.56  | Chr20: 24974362  | <i>C20orf3</i>                | TSS1500                                      | S_Shore | FALSE |
| cg25835179 | 0.43 | 0.31 | 0.12 | 38.50  | Chr11: 67418291  | <i>ACY3</i>                   | TSS200                                       |         | FALSE |
| cg02771260 | 0.61 | 0.49 | 0.12 | 36.56  | Chr11: 59836817  | <i>MS4A3, MS4A3, MS4A3</i>    | Body, Body, Body                             |         | FALSE |
| cg23496314 | 0.37 | 0.25 | 0.12 | 44.13  | ChrX: 39956534   | <i>BCOR, BCOR, BCOR, BCOR</i> | 5'UTR, 5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR | Island  | FALSE |
| cg25393323 | 0.15 | 0.03 | 0.12 | 340.66 | Chr15: 42565830  | <i>GANC, TMEM87A, TMEM87A</i> | TSS1500, TSS200, TSS200                      | N_Shore | FALSE |
| cg26921093 | 0.29 | 0.17 | 0.12 | 58.26  | Chr17: 63534688  | <i>AXIN2</i>                  | Body   | S_Shore | FALSE |
| cg05002314 | 0.97 | 0.85 | 0.12 | 340.66 | Chr20: 54978854  | <i>CSTF1, CSTF1, CSTF1</i>    | 3'UTR, 3'UTR, 3'UTR                          | S_Shore | FALSE |
| cg10430963 | 0.67 | 0.55 | 0.12 | 39.79  | Chr17: 37124558  | <i>FBXO47</i>                 | TSS1500                                      |         | FALSE |
| cg02824443 | 0.60 | 0.48 | 0.12 | 35.63  | Chr7: 108093448  | <i>NRCAM, NRCAM</i>           | 5'UTR, 5'UTR                                 | N_Shore | FALSE |
| cg08945443 | 0.39 | 0.27 | 0.12 | 41.10  | Chr10: 75193254  | <i>ZMYND17</i>                | 5'UTR  |         | FALSE |
| cg07493435 | 0.48 | 0.36 | 0.12 | 35.17  | Chr7: 128556140  |                               |  | Island  | FALSE |
| cg02498120 | 0.69 | 0.57 | 0.12 | 41.34  | Chr21: 15095903  |                               |  | Island  | FALSE |
| cg25189608 | 0.70 | 0.58 | 0.12 | 42.39  | Chr11: 96117844  | <i>CCDC82</i>                 | Body   |         | FALSE |
| cg04192168 | 0.27 | 0.15 | 0.12 | 60.23  | Chr15: 64806741  | <i>ZNF609</i>                 | Body   |         | TRUE  |
| cg22772691 | 0.36 | 0.24 | 0.12 | 43.50  | Chr5: 1104195    | <i>SLC12A7</i>                | Body   | S_Shelf | FALSE |
| cg26597838 | 0.54 | 0.43 | 0.12 | 33.91  | Chr10: 835615    |                               |  | N_Shelf | TRUE  |
| cg03092399 | 0.73 | 0.61 | 0.12 | 45.32  | Chr11: 108149307 | <i>ATM</i>                    | Body   |         | TRUE  |
| cg26476930 | 0.81 | 0.69 | 0.12 | 61.73  | Chr2: 731519     |                               |  | N_Shore | FALSE |
| cg13286116 | 0.67 | 0.55 | 0.12 | 37.80  | Chr11: 13302098  | <i>ARNTL, ARNTL, ARNTL</i>    | 5'UTR, 5'UTR, 5'UTR                          | S_Shore | FALSE |
| cg15241074 | 0.29 | 0.18 | 0.12 | 52.81  | Chr2: 12860614   | <i>TRIB2, TRIB2</i>           | Body, Body                                   | S_Shore | FALSE |
| cg00208274 | 0.52 | 0.41 | 0.12 | 32.96  | Chr7: 4779342    | <i>FOKK1</i>                  | Body   |         | FALSE |
| cg06892679 | 0.59 | 0.47 | 0.12 | 32.96  | Chr14: 68008964  | <i>PLEKHH1</i>                | Body   |         | FALSE |
| cg00859178 | 0.76 | 0.64 | 0.12 | 47.55  | Chr1: 162467208  | <i>UHMK1</i>                  | TSS1500                                      | N_Shore | FALSE |
| cg14287022 | 0.27 | 0.15 | 0.12 | 57.88  | Chr12: 19557343  |                               |  |         | FALSE |
| cg07110949 | 0.35 | 0.24 | 0.12 | 41.53  | Chr4: 1309878    | <i>MAEA, MAEA</i>             | Body, Body                                   | S_Shore | FALSE |
| cg26003388 | 0.55 | 0.44 | 0.12 | 31.95  | Chr17: 76129533  | <i>TMC8, TMC6</i>             | Body, TSS1500                                | S_Shore | FALSE |
| cg24004368 | 0.62 | 0.51 | 0.12 | 33.72  | Chr6: 30706647   | <i>FLOT1</i>                  |  | N_Shelf | FALSE |
| cg12277366 | 0.40 | 0.28 | 0.12 | 36.93  | Chr8: 54931229   | <i>TCEA1, TCEA1</i>           | Body, Body                                   | N_Shelf | FALSE |
| cg26764761 | 0.85 | 0.73 | 0.12 | 70.78  | Chr16: 87682142  | <i>JPH3</i>                   | Body   | S_Shelf | FALSE |
| cg10296062 | 0.56 | 0.44 | 0.12 | 31.67  | Chr11: 64528569  | <i>PYGM, PYGM</i>             | TSS1500, TSS1500                             |         | FALSE |
| cg18470780 | 0.39 | 0.28 | 0.12 | 36.72  | Chr14: 59064969  |                               |  |         | TRUE  |
| cg18808929 | 0.48 | 0.37 | 0.12 | 31.88  | Chr8: 61825469   |                               |  | S_Shelf | TRUE  |
| cg26280976 | 0.42 | 0.30 | 0.11 | 34.50  | Chr14: 69660603  |                               |  | S_Shore | FALSE |
| cg19528654 | 0.36 | 0.24 | 0.11 | 39.45  | Chr11: 67251154  |                               |  | S_Shore | TRUE  |
| cg15469871 | 0.39 | 0.27 | 0.11 | 36.61  | Chr10: 27541418  | <i>AIP</i>                    | Body   | S_Shore | FALSE |
| cg11900328 | 0.34 | 0.22 | 0.11 | 42.01  | Chr8: 2263331    | <i>LOC387646</i>              | TSS200                                       | Island  | FALSE |
| cg03450844 | 0.77 | 0.65 | 0.11 | 46.95  | Chr7: 150416671  | <i>GIMAP1</i>                 | Body   | N_Shore | FALSE |
| cg09417038 | 0.56 | 0.45 | 0.11 | 30.62  | Chr21: 47716443  | <i>C21orf57</i>               | Body   | N_Shore | FALSE |
| cg10008347 | 0.36 | 0.25 | 0.11 | 38.36  | ChrX: 39958040   | <i>BCOR, BCOR, BCOR, BCOR</i> | TSS1500, 5'UTR, TSS1500, 5'UTR               | Island  | FALSE |
| cg20803293 | 0.34 | 0.23 | 0.11 | 40.64  | Chr1: 110254709  | <i>GSTM5</i>                  | TSS200                                       |         | FALSE |
| cg26702039 | 0.81 | 0.69 | 0.11 | 55.36  | Chr16: 66170991  |                               |  |         | TRUE  |
| cg25472530 | 0.68 | 0.57 | 0.11 | 35.67  | Chr5: 23507617   | <i>PRDM9</i>                  | TSS200                                       |         | FALSE |
| cg24139837 | 0.29 | 0.18 | 0.11 | 48.98  | ChrX: 3730151    |                               |  | N_Shelf | FALSE |
| cg04850148 | 0.67 | 0.56 | 0.11 | 34.10  | Chr17: 34539744  | <i>CCL4L2, CCL4L1</i>         | Body, Body                                   |         | FALSE |
| cg24370881 | 0.58 | 0.47 | 0.11 | 29.17  | Chr4: 10112059   | <i>WDR1, WDR1</i>             | Body, Body                                   |         | TRUE  |
| cg05914034 | 0.51 | 0.40 | 0.11 | 28.78  | Chr7: 5528179    | <i>FBXL18</i>                 | Body   | Island  | FALSE |
| cg14124261 | 0.31 | 0.20 | 0.11 | 42.84  | Chr9: 116262291  | <i>RGS3, RGS3, RGS3</i>       | TSS1500, Body, Body                          |         | FALSE |
| cg04691264 | 0.47 | 0.36 | 0.11 | 29.11  | Chr10: 29697905  | <i>LOC387647</i>              | TSS1500                                      | N_Shore | FALSE |
| cg06211550 | 0.35 | 0.23 | 0.11 | 37.39  | Chr16: 3230726   |                               |  | N_Shelf | FALSE |
| cg10265387 | 0.30 | 0.19 | 0.11 | 44.04  | ChrX: 20009123   | <i>LOC729609</i>              | TSS1500                                      | Island  | FALSE |
| cg11861406 | 0.89 | 0.78 | 0.11 | 85.32  | Chr13: 21749154  | <i>SKA3, SKA3, MRP63</i>      | Body, Body, TSS1500                          | N_Shore | FALSE |
| cg15667493 | 0.36 | 0.25 | 0.11 | 35.38  | Chr5: 55404179   | <i>ANKRD55, ANKRD55</i>       | Body, Body                                   |         | TRUE  |



|            |      |      |      |        |                  |   |                                       |         |       |
|------------|------|------|------|--------|------------------|---|---------------------------------------|---------|-------|
| cg15935877 | 0.28 | 0.17 | 0.11 | 47.39  | ChrY: 9303715    | <i>TSPY1, TSPY4</i>                             | TSS1500, Body                         | Island  | FALSE |
| cg13282195 | 0.46 | 0.35 | 0.11 | 28.96  | Chr8: 144660772  | <i>NAPRT1</i>                                   | TSS1500                               | S_Shore | FALSE |
| cg17939040 | 0.47 | 0.36 | 0.11 | 28.58  | Chr17: 35503956  | <i>ACACA, ACACA, ACACA, ACACA</i>               | Body, Body, Body, Body, Body          |         | TRUE  |
| cg22068400 | 0.50 | 0.39 | 0.11 | 28.01  | Chr2: 90016264   |   |                                       |         | FALSE |
| cg13390570 | 0.27 | 0.16 | 0.11 | 49.76  | Chr5: 1255616    | <i>TERT, TERT</i>                               | Body, Body                            | N_Shore | FALSE |
| cg02125365 | 0.33 | 0.22 | 0.11 | 38.43  | Chr5: 78813058   |   |                                       | S_Shelf | FALSE |
| cg12417549 | 0.36 | 0.25 | 0.11 | 34.88  | Chr4: 70697416   |   |                                       |         | TRUE  |
| cg04548204 | 0.48 | 0.37 | 0.11 | 27.99  | Chr12: 9162872   | <i>KLRG1</i>                                    | 3'UTR                                 |         | FALSE |
| cg24168538 | 0.83 | 0.72 | 0.11 | 58.09  | Chr4: 35527016   |   |                                       |         | TRUE  |
| cg07165260 | 0.39 | 0.28 | 0.11 | 31.44  | Chr16: 85062881  | <i>KIAA0513</i>                                 | 5'UTR                                 | S_Shore | TRUE  |
| cg09508730 | 0.50 | 0.39 | 0.11 | 27.02  | Chr6: 27706275   |   |                                       |         | FALSE |
| cg05509777 | 0.19 | 0.08 | 0.11 | 73.25  | Chr11: 2322517   | <i>C11orf21, TSPAN32, C11orf21</i>              | Body, TSS1500, Body                   |         | FALSE |
| cg02713832 | 0.17 | 0.07 | 0.11 | 83.30  | Chr11: 60772559  | <i>CD6</i>                                      | Body                                  | N_Shelf | FALSE |
| cg15454820 | 0.31 | 0.20 | 0.11 | 39.80  | Chr10: 96990858  |   |                                       |         | FALSE |
| cg05600342 | 0.26 | 0.16 | 0.11 | 48.07  | Chr11: 250989    | <i>PSMD13, PSMD13</i>                           | Body, Body                            |         | TRUE  |
| cg09926364 | 0.43 | 0.32 | 0.11 | 28.32  | Chr14: 73137242  | <i>DPF3</i>                                     | 3'UTR                                 |         | FALSE |
| cg20894640 | 0.23 | 0.12 | 0.11 | 57.70  | Chr12: 19557334  |   |                                       |         | FALSE |
| cg02640489 | 0.35 | 0.25 | 0.11 | 33.46  | Chr2: 219153935  | <i>PNKD, TMBIM1</i>                             | Body, 5'UTR                           | N_Shelf | FALSE |
| cg24508426 | 0.38 | 0.27 | 0.11 | 31.19  | Chr10: 124578209 |   |                                       | Island  | FALSE |
| cg11766577 | 0.64 | 0.53 | 0.11 | 28.17  | Chr21: 47581405  | <i>C21orf56, C21orf56</i>                       | Body, Body                            | Island  | FALSE |
| cg24885723 | 0.39 | 0.28 | 0.11 | 30.54  | Chr1: 9030439    | <i>CA6</i>                                      | Body                                  |         | FALSE |
| cg22668906 | 0.41 | 0.30 | 0.11 | 28.99  | Chr11: 128180077 |   |                                       |         | TRUE  |
| cg08537890 | 0.50 | 0.39 | 0.11 | 25.96  | Chr12: 31272865  |   |                                       |         | FALSE |
| cg22968622 | 0.14 | 0.03 | 0.11 | 111.73 | Chr17: 43663579  |   |                                       | Island  | FALSE |
| cg05200811 | 0.58 | 0.47 | 0.11 | 26.06  | Chr21: 47581042  |   |                                       | Island  | FALSE |
| cg20557159 | 0.56 | 0.45 | 0.11 | 25.39  | Chr17: 75445261  | <i>SEPT9, SEPT9, SEPT9, SEPT9, SEPT9, SEPT9</i> | Body, Body, Body, Body, TSS1500, Body | N_Shelf | FALSE |
| cg01768001 | 0.34 | 0.23 | 0.11 | 33.98  | Chr1: 24831147   | <i>RCAN3</i>                                    | 5'UTR                                 | S_Shore | FALSE |
| cg15493018 | 0.87 | 0.76 | 0.11 | 67.94  | Chr1: 108710337  | <i>SLC25A24, SLC25A24</i>                       | Body, Body                            |         | FALSE |
| cg17346246 | 0.28 | 0.18 | 0.11 | 41.70  | Chr12: 123214864 | <i>GPR81</i>                                    | 1stExon                               |         | FALSE |
| cg00101728 | 0.64 | 0.53 | 0.11 | 27.32  | Chr6: 2953027    | <i>SERPINB6</i>                                 | Body                                  |         | TRUE  |
| cg23733394 | 0.43 | 0.33 | 0.11 | 27.06  | Chr1: 839752     |   |                                       | Island  | FALSE |
| cg15009294 | 0.39 | 0.28 | 0.11 | 29.57  | Chr1: 214813712  | <i>CENPF</i>                                    | Body                                  |         | TRUE  |
| cg22715764 | 0.48 | 0.38 | 0.11 | 25.36  | Chr1: 10556294   | <i>PEX14</i>                                    | Body                                  |         | FALSE |
| cg00568384 | 0.67 | 0.56 | 0.11 | 28.90  | Chr2: 173539262  |   |                                       |         | TRUE  |
| cg23088126 | 0.32 | 0.21 | 0.11 | 35.91  | Chr1: 207078912  | <i>FAIM3, FAIM3, FAIM3</i>                      | Body, Body, Body                      | N_Shelf | TRUE  |
| cg06828418 | 0.74 | 0.64 | 0.11 | 35.81  | Chr6: 30706654   | <i>FLOT1</i>                                    | Body                                  | N_Shelf | FALSE |
| cg07544796 | 0.37 | 0.26 | 0.11 | 30.74  | Chr6: 36817048   |   |                                       |         | TRUE  |
| cg22761176 | 0.33 | 0.23 | 0.11 | 33.76  | Chr2: 173539542  |   |                                       |         | TRUE  |
| cg00141688 | 0.76 | 0.66 | 0.10 | 37.70  | Chr2: 10517352   | <i>HPCAL1, HPCAL1</i>                           | 5'UTR, 5'UTR                          |         | FALSE |
| cg20208600 | 0.34 | 0.24 | 0.10 | 32.43  | Chr11: 61159687  | <i>TMEM216</i>                                  | TSS200                                | N_Shore | FALSE |
| cg04681579 | 0.83 | 0.72 | 0.10 | 52.27  | Chr7: 75027559   | <i>TRIM73, TRIM74</i>                           | 5'UTR, 5'UTR                          | S_Shelf | FALSE |
| cg12149986 | 0.93 | 0.82 | 0.10 | 105.58 | Chr19: 50059027  | <i>NOSIP</i>                                    | Body                                  | Island  | FALSE |
| cg02402882 | 0.36 | 0.26 | 0.10 | 30.40  | Chr5: 56620429   |   |                                       |         | TRUE  |
| cg21238284 | 0.66 | 0.56 | 0.10 | 27.66  | Chr8: 127889295  |   |                                       |         | TRUE  |
| cg13937905 | 0.70 | 0.60 | 0.10 | 30.56  | Chr12: 53612551  | <i>RARG, RARG</i>                               | Body, Body                            | N_Shore | FALSE |
| cg15506890 | 0.79 | 0.69 | 0.10 | 42.19  | Chr2: 3487001    |   |                                       |         | TRUE  |
| cg16906964 | 0.71 | 0.60 | 0.10 | 30.71  | Chr1: 4660171    |   |                                       |         | FALSE |
| cg25709050 | 0.43 | 0.32 | 0.10 | 25.96  | Chr17: 29817279  | <i>RAB11FIP4</i>                                | Body                                  | S_Shore | TRUE  |
| cg12421110 | 0.57 | 0.47 | 0.10 | 24.14  | Chr13: 42035731  | <i>C13orf15</i>                                 | Body                                  | S_Shelf | FALSE |
| cg11909526 | 0.50 | 0.39 | 0.10 | 24.01  | Chr17: 33519851  | <i>AMAC1, AMAC1</i>                             | 3'UTR, 1stExon                        |         | FALSE |
| cg12419766 | 0.80 | 0.69 | 0.10 | 43.73  | Chr7: 157620445  | <i>PTPRN2, PTPRN2, PTPRN2</i>                   | Body, Body, Body                      | S_Shore | FALSE |
| cg03209332 | 0.26 | 0.15 | 0.10 | 44.95  | Chr12: 132670372 |   |                                       | N_Shelf | FALSE |
| cg15973818 | 0.54 | 0.44 | 0.10 | 23.59  | Chr8: 53623995   | <i>RB1CC1, RB1CC1</i>                           | 5'UTR, 5'UTR                          | N_Shelf | FALSE |
| cg01560476 | 0.50 | 0.39 | 0.10 | 23.70  | Chr16: 24743405  | <i>TNRC6A</i>                                   | Body                                  | S_Shore | FALSE |
| cg14789911 | 0.72 | 0.62 | 0.10 | 31.46  | Chr21: 47582049  | <i>C21orf56, C21orf56</i>                       | Body, Body                            | Island  | FALSE |

|            |      |      |      |        |                  |   |   |         |       |
|------------|------|------|------|--------|------------------|---|---|---------|-------|
| cg25130381 | 0.42 | 0.31 | 0.10 | 26.01  | Chr1: 27440721   | <i>SLC9A1</i>   | Body  |         | FALSE |
| cg12850078 | 0.13 | 0.03 | 0.10 | 106.79 | Chr15: 89922071  | <i>LOC254559</i>  | Body  | Island  | TRUE  |
| cg09027133 | 0.35 | 0.25 | 0.10 | 30.28  | Chr1: 25945042   | <i>MAN1C1</i>   | Body  | S_Shore | FALSE |
| cg01567509 | 0.34 | 0.24 | 0.10 | 31.15  | Chr1: 15104223   | <i>KIAA1026, KIAA1026</i>   | Body, Body  |         | FALSE |
| cg19863426 | 0.30 | 0.20 | 0.10 | 36.01  | Chr10: 124138853 | <i>PLEKHA1</i>  | 5'UTR   | S_Shelf | FALSE |
| cg13600149 | 0.16 | 0.06 | 0.10 | 79.42  | Chr9: 98079129   | <i>FANCC</i>  | 5'UTR   | N_Shore | FALSE |
| cg09035699 | 0.37 | 0.26 | 0.10 | 29.02  | Chr5: 131310461  | <i>ACSL6, ACSL6</i>   | Body, Body  |         | TRUE  |
| cg08113187 | 0.40 | 0.30 | 0.10 | 26.63  | Chr16: 87469329  | <i>ZCCHC14</i>  | Body  |         | FALSE |
| cg01540386 | 0.30 | 0.20 | 0.10 | 36.10  | ChrX: 39873535   |   |   | Island  | FALSE |
| cg04284196 | 0.33 | 0.23 | 0.10 | 31.89  | Chr14: 22975248  |   |   |         | FALSE |
| cg16969872 | 0.56 | 0.46 | 0.10 | 23.46  | Chr13: 79968324  | <i>RBM26</i>  | Body  |         | FALSE |
| cg22211507 | 0.57 | 0.46 | 0.10 | 23.46  | Chr3: 108564871  | <i>TRAT1</i>  | Body  |         | FALSE |
| cg27554954 | 0.80 | 0.69 | 0.10 | 42.44  | Chr15: 60691595  | <i>ANXA2, ANXA2, ANXA2, ANXA2</i>   | TSS1500, TSS1500, TSS1500, TSS1500  | S_Shore | TRUE  |
| cg06329392 | 0.29 | 0.18 | 0.10 | 38.19  | Chr13: 40762435  |   |   |         | TRUE  |
| cg08560373 | 0.38 | 0.27 | 0.10 | 28.12  | Chr15: 25123381  | <i>SNRPN, SNRPN, SNRPN, SNRPN</i>   | 5'UTR, 5'UTR, 5'UTR, 5'UTR  | Island  | FALSE |
| cg01052065 | 0.22 | 0.11 | 0.10 | 54.54  | ChrX: 110339654  | <i>PAK3, PAK3, PAK3</i>   | 5'UTR, 5'UTR, 5'UTR   | Island  | FALSE |
| cg05376982 | 0.52 | 0.41 | 0.10 | 23.13  | Chr1: 110254692  | <i>GSTM5</i>  | TSS200  |         | FALSE |
| cg01890417 | 0.46 | 0.35 | 0.10 | 23.85  | Chr1: 91488275   | <i>ZNF644, ZNF644, ZNF644</i>   | TSS1500, TSS1500, TSS1500   | S_Shore | FALSE |
| cg20306694 | 0.34 | 0.24 | 0.10 | 30.54  | Chr12: 51718251  | <i>BIN2</i>   | TSS1500   |         | FALSE |
| cg06758191 | 0.92 | 0.82 | 0.10 | 95.94  | Chr4: 7812988    | <i>AFAP1, AFAP1</i>   | Body, Body  |         | FALSE |
| cg21436572 | 0.73 | 0.63 | 0.10 | 31.88  | Chr8: 70623422   | <i>SLCO5A1, SLCO5A1, SLCO5A1</i>  | Body, Body, Body  |         | FALSE |
| cg15576492 | 0.23 | 0.13 | 0.10 | 48.31  | Chr1: 1015447    |   |   | N_Shore | TRUE  |
| cg02540440 | 0.58 | 0.48 | 0.10 | 23.17  | ChrX: 39866758   |   |   | Island  | FALSE |
| cg23737407 | 0.17 | 0.07 | 0.10 | 70.89  | ChrX: 40029094   | <i>BCOR, BCOR</i>   | 5'UTR, 5'UTR  | Island  | FALSE |
| cg02952635 | 0.86 | 0.75 | 0.10 | 57.81  | Chr2: 178741216  | <i>PDE11A, PDE11A, PDE11A, PDE11A, PCDHA2, PCDHA1, PCDHA1, PCDHA6, PCDHA5, PCDHA6, PCDHA3, PCDHA4, PCDHA6</i> | Body, 5'UTR, Body, Body, Body, Body, TSS200, Body, TSS200, Body, Body, TSS200 |         | FALSE |
| cg16987900 | 0.30 | 0.20 | 0.10 | 34.42  | Chr5: 140207609  | <i>CCDC52</i>   | TSS1500   | N_Shore | FALSE |
| cg18753928 | 0.40 | 0.30 | 0.10 | 25.37  | Chr3: 113234510  | <i>TMEM164, TMEM164</i>   | TSS200, 5'UTR   | S_Shore | FALSE |
| cg20589243 | 0.39 | 0.29 | 0.10 | 25.91  | ChrX: 109246229  | <i>ITGA6, ITGA6</i>   | Body, Body  | Island  | FALSE |
| cg22061832 | 0.29 | 0.19 | 0.10 | 35.80  | Chr2: 173293627  | <i>HPCAL1, HPCAL1</i>   | 5'UTR, 5'UTR  | S_Shore | TRUE  |
| cg04618171 | 0.44 | 0.34 | 0.10 | 23.68  | Chr2: 10470465   |   |   |         | TRUE  |
| cg08964643 | 0.75 | 0.65 | 0.10 | 33.20  | Chr7: 63560420   | <i>DNMT3A, DNMT3A, DNMT3A</i>   | 5'UTR, 5'UTR, 5'UTR   | Island  | FALSE |
| cg15302376 | 0.26 | 0.16 | 0.10 | 41.37  | Chr2: 25560263   | <i>PRDM9</i>  | TSS200  | N_Shelf | FALSE |
| cg07011961 | 0.80 | 0.70 | 0.10 | 42.66  | Chr5: 23507594   | <i>CORO1B, CORO1B, PTPRCAP</i>  | Body, Body, TSS1500   |         | FALSE |
| cg12044599 | 0.30 | 0.19 | 0.10 | 34.86  | Chr11: 67206308  | <i>EPGN</i>   | TSS200  | S_Shelf | FALSE |
| cg07643762 | 0.29 | 0.19 | 0.10 | 36.03  | Chr4: 75174080   | <i>USP11</i>  | Body  |         | FALSE |
| cg14699257 | 0.28 | 0.18 | 0.10 | 37.23  | ChrX: 47092993   | <i>ZNF445</i>   | 5'UTR   | Island  | FALSE |
| cg11619648 | 0.85 | 0.75 | 0.10 | 54.77  | Chr3: 44515242   | <i>SH3BP5L</i>  | Body  | N_Shelf | FALSE |
| cg00804354 | 0.35 | 0.25 | 0.10 | 28.62  | Chr1: 249111407  |   |   |         | FALSE |
| cg26118221 | 0.67 | 0.57 | 0.10 | 25.83  | Chr4: 8262589    |   |   |         | FALSE |
| cg14780427 | 0.61 | 0.51 | 0.10 | 23.14  | Chr17: 78754372  | <i>RPTOR, RPTOR</i>   | Body, Body  |         | TRUE  |
| cg08639389 | 0.33 | 0.22 | 0.10 | 30.77  | Chr4: 26995889   | <i>STIM2, STIM2, STIM2</i>  | Body, Body, Body  |         | TRUE  |
| cg00876757 | 0.65 | 0.55 | 0.10 | 24.58  | Chr16: 33483591  |   |   | S_Shore | FALSE |
| cg18015035 | 0.45 | 0.35 | 0.10 | 22.88  | ChrX: 19002577   | <i>PHKA2</i>  | TSS200  | Island  | FALSE |
| cg21191275 | 0.36 | 0.26 | 0.10 | 27.72  | Chr9: 135907982  | <i>GTF3C5, GTF3C5</i>   | Body, Body  | S_Shore | FALSE |
| cg13568659 | 0.40 | 0.30 | 0.10 | 24.80  | Chr6: 159438801  |   |   |         | FALSE |

|            |      |      |      |       |                 |                       |                |         |       |
|------------|------|------|------|-------|-----------------|-----------------------|----------------|---------|-------|
| cg02188048 | 0.34 | 0.24 | 0.10 | 28.85 | ChrX: 39871543  |                       |                | Island  | TRUE  |
| cg23486701 | 0.27 | 0.17 | 0.10 | 38.55 | Chr2: 54789491  | <i>SPTBN1, SPTBN1</i> | Body, Body     | S_Shelf | FALSE |
| cg11909467 | 0.28 | 0.18 | 0.10 | 35.96 | Chr8: 132912348 |                       |                | N_Shelf | FALSE |
| cg20197861 | 0.31 | 0.21 | 0.10 | 31.74 | ChrX: 39964229  | <i>BCOR, BCOR</i>     | 5'UTR, 5'UTR   | Island  | FALSE |
| cg23953831 | 0.18 | 0.08 | 0.10 | 62.38 | Chr1: 117544416 | <i>CD101, CD101</i>   | 5'UTR, 1stExon |         | FALSE |
| cg07129803 | 0.76 | 0.66 | 0.10 | 33.98 | Chr16: 88370583 |                       |                |         | FALSE |
| cg10288578 | 0.88 | 0.78 | 0.10 | 65.53 | Chr2: 16816994  | <i>FAM49A</i>         | 5'UTR          |         | TRUE  |

**Supplementary Table 5:** Shared differentially methylated regions (DMRs) in naïve CD4+ T cells from patients with a history of **A.** malar rash and discoid rash, or **B.** malar rash, discoid rash, and neither cutaneous involvement.

**A.**

Shared DMRs Between Malar Rash and Discoid Rash

| DMR Gene         | Malar Rash               |                   |                   |                      |                    | Discoid Rash             |                   |                   |                      |                    | No Cutaneous Involvement |                  |                   |                      |                    |
|------------------|--------------------------|-------------------|-------------------|----------------------|--------------------|--------------------------|-------------------|-------------------|----------------------|--------------------|--------------------------|------------------|-------------------|----------------------|--------------------|
|                  | DMR Location             | # DM Sites in DMR | Mean $\beta$ Case | Mean $\beta$ Control | Mean $\Delta\beta$ | DMR Location             | # DM Sites in DMR | Mean $\beta$ Case | Mean $\beta$ Control | Mean $\Delta\beta$ | DMR Location             | #DM Sites in DMR | Mean $\beta$ Case | Mean $\beta$ Control | Mean $\Delta\beta$ |
| <b>Hyper-DMR</b> |                          |                   |                   |                      |                    |                          |                   |                   |                      |                    |                          |                  |                   |                      |                    |
| (Intergenic)     | Chr7: 1209495-1209562    | 3                 | 0.37              | 0.11                 | 0.27               | Chr7: 1209495-1209742    | 2                 | 0.30              | 0.14                 | 0.16               | NA                       | NA               | 0.18              | 0.24                 | -0.06              |
| <i>PRIC285</i>   | Chr20: 62198872-62199034 | 3                 | 0.29              | 0.10                 | 0.18               | Chr20: 62198872-62199156 | 2                 | 0.35              | 0.15                 | 0.20               | NA                       | NA               | 0.24              | 0.16                 | 0.07               |

**B.**

Shared DMRs Between Cutaneous and No Cutaneous Involvement

| DMR Gene         | Malar Rash               |                   |                   |                      |                    | Discoid Rash             |                   |                   |                      |                    | No Cutaneous Involvement |                  |                   |                      |                    |
|------------------|--------------------------|-------------------|-------------------|----------------------|--------------------|--------------------------|-------------------|-------------------|----------------------|--------------------|--------------------------|------------------|-------------------|----------------------|--------------------|
|                  | DMR Location             | # DM Sites in DMR | Mean $\beta$ Case | Mean $\beta$ Control | Mean $\Delta\beta$ | DMR Location             | # DM Sites in DMR | Mean $\beta$ Case | Mean $\beta$ Control | Mean $\Delta\beta$ | DMR Location             | #DM Sites in DMR | Mean $\beta$ Case | Mean $\beta$ Control | Mean $\Delta\beta$ |
| <b>Hypo-DMR</b>  |                          |                   |                   |                      |                    |                          |                   |                   |                      |                    |                          |                  |                   |                      |                    |
| <i>IFI44L</i>    | Chr1: 79085586-79085765  | 3                 | 0.38              | 0.58                 | -0.20              | Chr1: 79085586-79085765  | 3                 | 0.40              | 0.56                 | -0.16              | Chr1: 79085586-79085765  | 3                | 0.44              | 0.59                 | -0.15              |
| <i>GSTT1</i>     | Chr22: 24384105-24384400 | 2                 | 0.16              | 0.30                 | -0.14              | Chr22: 24384105-24384400 | 2                 | 0.07              | 0.22                 | -0.15              | Chr22: 24384105-24384400 | 5                | 0.09              | 0.24                 | -0.15              |
| <b>Hyper-DMR</b> |                          |                   |                   |                      |                    |                          |                   |                   |                      |                    |                          |                  |                   |                      |                    |
| <i>GSTTP1</i>    | Chr22: 24348549-24348715 | 2                 | 0.61              | 0.44                 | 0.16               | Chr22: 24348549-24348715 | 2                 | 0.72              | 0.57                 | 0.15               | Chr22: 24348549-24348715 | 2                | 0.56              | 0.40                 | 0.16               |

**Supplementary Table 6:** Network analysis results are depicted for genes with unique

hypomethylated regions (hypo-DMRs) in naïve CD4+ T cells from SLE patients with a history of

**A.** malar rash, **B.** discoid rash, or **C.** neither cutaneous involvement. All network analyses were performed using GeneMANIA software.

**A.**

**Malar Rash**

| <b>Enriched Function</b>  | <b>P Value</b> |
|---|----------------|
| Antigen processing and presentation of exogenous peptide antigen via MHC class I                | 3.66E-18       |
| Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 3.66E-18       |
| Antigen processing and presentation of peptide antigen via MHC class I                          | 2.65E-17       |
| Peptide antigen binding   | 1.87E-15       |
| Antigen processing and presentation of exogenous peptide antigen                                | 1.91E-14       |
| Antigen processing and presentation of exogenous antigen  | 2.29E-14       |
| Antigen processing and presentation of peptide antigen  | 3.21E-14       |
| Antigen processing and presentation   | 2.97E-13       |
| Interferon-gamma-mediated signaling pathway   | 1.77E-12       |
| Cellular response to type I interferon  | 1.77E-12       |
| Type I interferon signaling pathway   | 1.77E-12       |
| Response to type I interferon   | 1.85E-12       |
| Phagocytic vesicle membrane   | 1.90E-12       |
| Antigen processing and presentation of endogenous antigen                                       | 1.90E-12       |
| Cellular response to interferon-gamma   | 7.37E-12       |
| Antigen binding   | 2.27E-11       |
| ER to Golgi transport vesicle membrane  | 2.29E-11       |
| Response to interferon-gamma  | 2.86E-11       |
| ER to Golgi transport vesicle   | 4.95E-11       |
| Early endosome membrane   | 4.95E-11       |
| Transport vesicle membrane  | 5.94E-10       |
| Transport vesicle   | 6.73E-10       |
| Integral component of endoplasmic reticulum membrane  | 7.68E-10       |
| Intrinsic component of endoplasmic reticulum membrane   | 8.03E-10       |
| Luminal side of membrane  | 1.32E-09       |
| Peptide binding   | 1.32E-09       |
| Integral component of luminal side of endoplasmic reticulum membrane                            | 1.32E-09       |
| Luminal side of endoplasmic reticulum membrane  | 1.32E-09       |
| Amide binding   | 1.46E-09       |
| Phagocytic vesicle  | 1.46E-09       |
| T cell mediated immunity  | 2.41E-08       |
| Lymphocyte mediated immunity  | 4.44E-08       |
| Endocytic vesicle membrane  | 4.64E-08       |
| Integral component of organelle membrane  | 6.05E-08       |
| Coated vesicle membrane   | 6.31E-08       |
| Intrinsic component of organelle membrane   | 9.05E-08       |
| Regulation of leukocyte mediated cytotoxicity   | 2.65E-07       |
| Leukocyte mediated immunity   | 2.67E-07       |
| Early endosome  | 3.63E-07       |
| Regulation of cell killing  | 4.23E-07       |
| Positive regulation of lymphocyte mediated immunity   | 5.75E-07       |

|  |          |
|--|----------|
| Positive regulation of leukocyte mediated immunity   | 7.67E-07 |
| Positive regulation of T cell mediated cytotoxicity  | 1.82E-06 |
| Endosome membrane  | 2.19E-06 |
| Coated vesicle   | 2.23E-06 |
| Endocytic vesicle  | 2.46E-06 |
| Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains                        | 2.59E-06 |
| Leukocyte mediated cytotoxicity  | 2.74E-06 |
| Endosomal part   | 2.74E-06 |
| Regulation of T cell mediated cytotoxicity   | 3.71E-06 |
| Cell killing   | 5.37E-06 |
| Regulation of lymphocyte mediated immunity   | 5.37E-06 |
| T cell mediated cytotoxicity   | 8.61E-06 |
| Positive regulation of leukocyte mediated cytotoxicity   | 8.61E-06 |
| Positive regulation of cell killing  | 1.25E-05 |
| Cytoplasmic vesicle membrane   | 1.37E-05 |
| Positive regulation of immune effector process   | 1.39E-05 |
| Adaptive immune response   | 1.44E-05 |
| Regulation of leukocyte mediated immunity  | 1.57E-05 |
| Vesicle membrane   | 1.57E-05 |
| Positive regulation of T cell mediated immunity  | 1.89E-05 |
| Positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 3.90E-05 |
| Side of membrane   | 3.93E-05 |
| Regulation of T cell mediated immunity   | 4.91E-05 |
| Golgi membrane   | 5.20E-05 |
| Positive regulation of adaptive immune response  | 5.39E-05 |
| Regulation of immune effector process  | 7.60E-05 |
| MHC class I protein binding  | 3.11E-04 |
| Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains          | 4.60E-04 |
| Regulation of adaptive immune response   | 7.63E-04 |
| MHC protein binding  | 9.27E-04 |
| Dendritic cell differentiation   | 1.23E-03 |
| Proteasome complex   | 1.60E-02 |
| Regulation of cellular amino acid metabolic process  | 2.20E-02 |
| Protein polyubiquitination   | 2.42E-02 |
| Tolerance induction  | 2.47E-02 |
| RNA polymerase II core promoter sequence-specific DNA binding  | 2.98E-02 |
| DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest  | 3.17E-02 |
| Signal transduction involved in DNA integrity checkpoint   | 3.17E-02 |
| Signal transduction involved in mitotic G1 DNA damage checkpoint   | 3.17E-02 |
| Signal transduction involved in mitotic cell cycle checkpoint  | 3.17E-02 |
| Signal transduction involved in DNA damage checkpoint  | 3.17E-02 |
| Signal transduction involved in mitotic DNA damage checkpoint  | 3.17E-02 |
| Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle  | 3.17E-02 |
| Signal transduction involved in mitotic DNA integrity checkpoint   | 3.17E-02 |
| Regulation of cellular amine metabolic process   | 3.17E-02 |
| Intracellular signal transduction involved in G1 DNA damage checkpoint   | 3.17E-02 |
| Signal transduction involved in cell cycle checkpoint  | 3.27E-02 |
| Negative regulation of ubiquitin-protein ligase activity   | 3.48E-02 |
| Negative regulation of ligase activity   | 3.48E-02 |
| Positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle  | 3.58E-02 |
| Defense response to other organism   | 3.58E-02 |
| Mitotic G1 DNA damage checkpoint   | 3.77E-02 |
| Mitotic G1/S transition checkpoint   | 3.77E-02 |
| G1 DNA damage checkpoint   | 3.88E-02 |
| Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle   | 4.32E-02 |

|  |          |
|--|----------|
| Detection of bacterium   | 4.49E-02 |
| Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process | 4.98E-02 |
| Positive regulation of cell cycle arrest   | 4.98E-02 |
| Detection of other organism  | 4.98E-02 |
| Positive regulation of ubiquitin-protein ligase activity                                       | 5.06E-02 |
| Mitotic DNA damage checkpoint  | 5.06E-02 |
| Mitotic DNA integrity checkpoint   | 5.50E-02 |
| Positive regulation of ligase activity   | 5.50E-02 |
| Proteasome core complex  | 6.03E-02 |
| Negative regulation of G1/S transition of mitotic cell cycle                                   | 6.11E-02 |
| Proteasome-mediated ubiquitin-dependent protein catabolic process                              | 6.11E-02 |
| Leukocyte differentiation  | 6.16E-02 |
| Detection of external biotic stimulus  | 6.49E-02 |
| Negative regulation of protein ubiquitination  | 6.95E-02 |
| Regulation of ubiquitin-protein ligase activity  | 7.10E-02 |
| Regulation of ligase activity  | 7.56E-02 |
| Proteasomal protein catabolic process  | 7.56E-02 |
| Regulation of cell cycle arrest  | 7.56E-02 |
| Detection of biotic stimulus   | 8.14E-02 |
| Regulation of interferon-gamma-mediated signaling pathway                                      | 8.14E-02 |
| Modulation by virus of host morphology or physiology   | 8.14E-02 |
| Regulation of response to interferon-gamma   | 8.84E-02 |
| DNA damage response, signal transduction by p53 class mediator                                 | 9.23E-02 |
| Regulation of leukocyte differentiation  | 9.23E-02 |
| Negative regulation of cell morphogenesis involved in differentiation                          | 9.39E-02 |
| Regulation of G1/S transition of mitotic cell cycle  | 9.58E-02 |
| Negative regulation of cell differentiation  | 9.99E-02 |

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**B.****Discoid Rash**

| <b>Enriched Function</b>  | <b>P Value</b> |
|---|----------------|
| Antigen processing and presentation of exogenous peptide antigen via MHC class I                | 3.67E-13       |
| Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 3.67E-13       |
| Antigen processing and presentation of peptide antigen via MHC class I                          | 1.73E-12       |
| Peptide antigen binding   | 2.57E-12       |
| Antigen processing and presentation   | 1.07E-10       |
| Antigen processing and presentation of exogenous peptide antigen                                | 2.94E-10       |
| Antigen processing and presentation of exogenous antigen  | 3.40E-10       |
| Antigen processing and presentation of peptide antigen  | 4.47E-10       |
| Antigen binding   | 1.17E-08       |
| Intrinsic component of endoplasmic reticulum membrane   | 2.97E-07       |
| Integral component of endoplasmic reticulum membrane  | 2.97E-07       |
| Peptide binding   | 4.51E-07       |
| Amide binding   | 5.11E-07       |
| Luminal side of membrane  | 8.53E-07       |
| Integral component of luminal side of endoplasmic reticulum membrane                            | 8.53E-07       |
| Luminal side of endoplasmic reticulum membrane  | 8.53E-07       |
| Antigen processing and presentation of endogenous antigen                                       | 1.47E-06       |
| Interferon-gamma-mediated signaling pathway   | 2.08E-06       |
| Cellular response to type I interferon  | 2.08E-06       |
| Type I interferon signaling pathway   | 2.08E-06       |
| Response to type I interferon   | 2.15E-06       |
| MHC class I protein binding   | 5.38E-06       |
| Cellular response to interferon-gamma   | 5.57E-06       |
| Integral component of organelle membrane  | 7.79E-06       |
| Intrinsic component of organelle membrane   | 1.11E-05       |
| Response to interferon-gamma  | 1.34E-05       |
| MHC protein binding   | 2.11E-05       |
| Phagocytic vesicle membrane   | 3.06E-05       |
| Regulation of leukocyte mediated cytotoxicity   | 8.22E-05       |
| Regulation of cell killing  | 1.18E-04       |
| ER to Golgi transport vesicle membrane  | 1.18E-04       |
| Positive regulation of lymphocyte mediated immunity   | 1.48E-04       |
| ER to Golgi transport vesicle   | 1.73E-04       |
| Positive regulation of leukocyte mediated immunity  | 1.73E-04       |
| Early endosome membrane   | 1.73E-04       |
| Transport vesicle   | 2.14E-04       |
| Lymphocyte mediated immunity  | 2.32E-04       |
| T cell mediated immunity  | 3.72E-04       |
| Leukocyte mediated cytotoxicity   | 4.77E-04       |
| Transport vesicle membrane  | 6.02E-04       |
| Positive regulation of T cell mediated cytotoxicity   | 6.99E-04       |
| Cell killing  | 7.70E-04       |
| Regulation of lymphocyte mediated immunity  | 7.70E-04       |
| Leukocyte mediated immunity   | 7.73E-04       |
| Phagocytic vesicle  | 1.06E-03       |
| Regulation of T cell mediated cytotoxicity  | 1.16E-03       |
| Positive regulation of immune effector process  | 1.61E-03       |
| Regulation of leukocyte mediated immunity   | 1.78E-03       |
| T cell mediated cytotoxicity  | 2.08E-03       |
| Positive regulation of leukocyte mediated cytotoxicity  | 2.08E-03       |
| Side of membrane  | 2.47E-03       |
| Positive regulation of cell killing   | 2.66E-03       |
| Endosome membrane   | 3.10E-03       |
| Coated vesicle  | 3.13E-03       |



|  |          |
|--|----------|
| Positive regulation of T cell mediated immunity  | 3.66E-03 |
| Endosomal part   | 3.66E-03 |
| Positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 5.99E-03 |
| Endocytic vesicle membrane   | 5.99E-03 |
| Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains                        | 6.57E-03 |
| Regulation of T cell mediated immunity   | 6.89E-03 |
| Coated vesicle membrane  | 6.89E-03 |
| Positive regulation of adaptive immune response  | 7.43E-03 |
| ATPase activity, coupled to transmembrane movement of substances   | 1.27E-02 |
| Hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances   | 1.27E-02 |
| P-P-bond-hydrolysis-driven transmembrane transporter activity  | 1.33E-02 |
| Primary active transmembrane transporter activity  | 1.33E-02 |
| ATPase activity, coupled to movement of substances   | 1.72E-02 |
| Early endosome   | 1.73E-02 |
| Adaptive immune response   | 1.97E-02 |
| Proteasome complex   | 2.25E-02 |
| Golgi membrane   | 2.75E-02 |
| Regulation of cellular amino acid metabolic process  | 3.05E-02 |
| Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains          | 3.17E-02 |
| DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest  | 4.37E-02 |
| Regulation of adaptive immune response   | 4.37E-02 |
| Signal transduction involved in DNA integrity checkpoint   | 4.37E-02 |
| Signal transduction involved in mitotic G1 DNA damage checkpoint   | 4.37E-02 |
| Signal transduction involved in mitotic cell cycle checkpoint  | 4.37E-02 |
| Signal transduction involved in DNA damage checkpoint  | 4.37E-02 |
| Endocytic vesicle  | 4.37E-02 |
| Signal transduction involved in mitotic DNA damage checkpoint  | 4.37E-02 |
| Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle  | 4.37E-02 |
| Signal transduction involved in mitotic DNA integrity checkpoint   | 4.37E-02 |
| Regulation of cellular amine metabolic process   | 4.37E-02 |
| Intracellular signal transduction involved in G1 DNA damage checkpoint   | 4.37E-02 |
| Signal transduction involved in cell cycle checkpoint  | 4.46E-02 |
| Positive regulation of cell cycle process  | 4.46E-02 |
| Negative regulation of ubiquitin-protein ligase activity   | 4.74E-02 |
| Negative regulation of ligase activity   | 4.74E-02 |
| Positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle  | 4.84E-02 |
| Regulation of immune effector process  | 4.84E-02 |
| Mitotic G1 DNA damage checkpoint   | 5.13E-02 |
| Mitotic G1/S transition checkpoint   | 5.13E-02 |
| G1 DNA damage checkpoint   | 5.28E-02 |
| Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle   | 5.87E-02 |
| Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process   | 6.90E-02 |
| Positive regulation of cell cycle arrest   | 6.90E-02 |
| Positive regulation of ubiquitin-protein ligase activity   | 7.01E-02 |
| Mitotic DNA damage checkpoint  | 7.01E-02 |
| Proteasome core complex  | 7.58E-02 |
| Mitotic DNA integrity checkpoint   | 7.58E-02 |
| Positive regulation of ligase activity   | 7.58E-02 |
| Negative regulation of G1/S transition of mitotic cell cycle   | 8.52E-02 |
| Negative regulation of protein ubiquitination  | 9.87E-02 |

**C.**

**No Malar or Discoid Rash**

| <b>Enriched Function</b>  | <b>P Value</b> |
|---|----------------|
| Protein trimerization   | 1.60E-03       |
| Type I interferon signaling pathway   | 5.85E-02       |
| Cellular response to type I interferon  | 5.85E-02       |
| Response to type I interferon   | 5.85E-02       |
| Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 5.85E-02       |
| Antigen processing and presentation of exogenous peptide antigen via MHC class I                | 5.85E-02       |
| Antigen processing and presentation of peptide antigen via MHC class I                          | 1.05E-01       |
| Antigen processing and presentation of endogenous antigen                                       | 4.27E-01       |
| Antigen processing and presentation of exogenous peptide antigen                                | 4.58E-01       |
| MHC class I protein binding   | 4.58E-01       |

**Supplementary Table 7: Network analysis results for genes with unique hypermethylated**

regions (hyper-DMRs) in naïve CD4+ T cells from SLE patients with a history of malar rash. The network analysis was performed using GeneMANIA software.

| <b>Malar Rash</b>   |                |
|---|----------------|
| <b>Enriched Function</b>  | <b>P Value</b> |
| Response to type I interferon   | 1.11E-21       |
| Cellular response to type I interferon  | 1.11E-21       |
| Type I interferon signaling pathway   | 1.11E-21       |
| Response to virus   | 3.20E-17       |
| Defense response to virus   | 3.53E-11       |
| Regulation of multiorganism process   | 3.80E-10       |
| Negative regulation of viral genome replication                                 | 1.40E-09       |
| Defense response to other organism  | 2.95E-09       |
| Negative regulation of multiorganism process                                    | 3.22E-09       |
| Regulation of viral genome replication  | 8.85E-09       |
| Viral genome replication  | 4.24E-08       |
| Negative regulation of viral process  | 4.35E-08       |
| Regulation of viral process   | 1.66E-07       |
| Regulation of symbiosis, encompassing mutualism through parasitism              | 2.45E-07       |
| Doublestranded RNA binding  | 2.69E-07       |
| Interferongammamediated signaling pathway                                       | 5.07E-06       |
| Cellular response to interferongamma  | 1.60E-05       |
| Response to interferongamma   | 4.08E-05       |
| Regulation of defense response to virus   | 1.41E-04       |
| Negative regulation of type I interferon production                             | 4.83E-04       |
| Regulation of response to biotic stimulus                                       | 4.83E-04       |
| Regulation of immune effector process   | 8.98E-04       |
| Cytoplasmic pattern recognition receptor signaling pathway in response to virus | 9.60E-04       |
| Regulation of type I interferon production                                      | 9.60E-04       |
| Type I interferon production  | 9.60E-04       |
| Cellular response to virus  | 9.60E-04       |
| Zinc ion binding  | 2.31E-03       |
| Adenylyltransferase activity  | 3.28E-03       |
| Regulation of defense response to virus by host                                 | 7.80E-03       |
| Transition metal ion binding  | 1.11E-02       |
| Negative regulation of cytokine production                                      | 3.17E-02       |
| Cytoplasmic pattern recognition receptor signaling pathway                      | 3.38E-02       |
| Regulation of innate immune response  | 4.85E-02       |
| Establishment of viral latency  | 8.55E-02       |
| Positive regulation of interferonalphaproduction                                | 9.86E-02       |
| Viral latency   | 9.86E-02       |