

Supplementary Figure 1 - Histogram of beta values after filtering for standard deviations across all samples.



Supplementary Figure 2 – Histogram of the samples’ ages.

Supplementary Table 1 - Top 5 rules classifying the 'fetus' class.

|  |  |  |
| --- | --- | --- |
| If part | Accuracy | Support |
| cg07830847(KCNA10\_exonic)=methylated | 1 | 30 |
| cg00658007(RD3\_UTR5)=methylated | 1 | 30 |
| cg01561916(HAAO\_upstream)=unmethylated | 1 | 30 |
| cg24178740(FEV\_upstream)=unmethylated | 1 | 30 |
| cg04716261(ACTRT2\_upstream)=unmethylated | 1 | 30 |

Supplementary Table 2 - top 5 rules classifying the 'Age 0To4' class.

|  |  |  |
| --- | --- | --- |
| If part | Accuracy | Support |
| cg08970446(SLC1A7\_UTR5)=methylated AND cg06144905(PIPOX\_upstream)=unmethylated | 1 | 12 |
| cg26227005(ELAVL4\_intronic)=intermediate AND cg06144905(PIPOX\_upstream)=unmethylated \* | 1 | 12 |
| cg08970446(SLC1A7\_UTR5)=methylated AND cg23283495(IRF6\_upstream)=unmethylated AND cg27554782(CHRNB4\_intronic)=unmethylated \*\* | 1 | 11 |
| cg08970446(SLC1A7\_UTR5)=methylated AND cg27554782(CHRNB4\_intronic)=unmethylated AND cg19224278(ALDH1A3\_upstream)=unmethylated | 1 | 11 |
| cg08970446(SLC1A7\_UTR5)=methylated AND cg04428453(ACSM5\_upstream)=methylated | 1 | 10 |

\* The condition ‘cg06144905(PIPOX\_upstream)=unmethylated’ appears in combination with other CpG sites all with an ‘intermediate’ status, annotated to genes such as: ANGPTL1, RD3, LIMS2, DISP1, RPE65, HAPLN2, SULT1C2, HAAO, KRTCAP3, FEV and SCN5A, with the same accuracy and support.

\*\* The conjunctive rules in red are the ones that could not be identified using a multiple linear regression model.

Supplementary Table 3 - top 5 rules classifying the 'Age 5To27' class.

|  |  |  |
| --- | --- | --- |
| If part | Accuracy | Support |
| cg02525756(RAB42\_intronic)=unmethylated AND cg00548268(NPTX2\_upstream)=unmethylated AND cg26538442(CES3\_upstream)=methylated | 1 | 12 |
| cg02525756(RAB42\_intronic)=unmethylated AND cg25462291(HEYL\_intronic)=intermediate AND cg24691453(S100A4\_upstream)=intermediate \* | 1 | 11 |
| cg02525756(RAB42\_intronic)=unmethylated AND cg25462291(HEYL\_intronic)=intermediate AND cg00548268(NPTX2\_upstream)=unmethylated | 0.93 | 14 |
| cg02525756(RAB42\_intronic)=unmethylated AND cg25462291(HEYL\_intronic)=intermediate AND cg20264732(ESRP2\_exonic)=unmethylated | 0.93 | 14 |
| cg02525756(RAB42\_intronic)=unmethylated AND cg00548268(NPTX2\_upstream)=unmethylated AND cg19224278(ALDH1A3\_upstream)=intermediate | 0.92 | 13 |

\* The conjunctive rules in red are the ones that could not be identified using a multiple linear regression model.

Supplementary Table 4 - top 5 rules classifying the 'Age 28plus' class.

|  |  |  |
| --- | --- | --- |
| If part | Accuracy | Support |
| cg02525756(RAB42\_intronic)= intermediate AND cg24691453(S100A4\_upstream)=methylated \* | 1 | 34 |
| cg24691453(S100A4\_upstream)=methylated AND cg00548268(NPTX2\_upstream)=intermediate | 1 | 31 |
| cg24691453(S100A4\_upstream)=methylated AND cg27337148(CAMK1G\_upstream)= intermediate AND cg20264732(ESRP2\_exonic)= intermediate \*\* | 1 | 34 |
| cg18486150(KIF17\_upstream)=intermediate AND cg24691453(S100A4\_upstream)=methylated | 0.95 | 40 |
| cg24691453(S100A4\_upstream)=methylated AND cg21104946(WNT7B\_upstream)= intermediate | 0.95 | 40 |

\* The conjunctive rules in red are the ones that could not be identified using a multiple linear regression model.

\*\* The conjunct of “cg24691453(S100A4\_upstream)=methylated AND cg20264732(ESRP2\_exonic) = intermediate” appear in the rules in combination with other CpG sites annotated to different genes with the same accuracy and support.