# DeepMAge: A Methylation Aging Clock Developed with Deep Learning

**Fedor Galkin[1,2], Polina Mamoshina[1], Kirill Kochetov[1], Denis Sidorenko[3], Alex Zhavoronkov[1,3,4*]**

## Supplementary Materials

*Comparing DeepMAge to a de novo linear model*

While Horvath's 353 CpG aging clock is a well-known frame of reference for age predictors, it is not sufficient to show the extra benefits offered by deep learning compared to linear machine learning techniques. Horvath's DNAm clock was trained on a different data collection, and the original paper suggests training models from scratch for new datasets.

Thus, to show deep learning superiority relative to other algorithms, we reproduced an elastic net aging clock as described in Horvath's original paper, using the same data as for DeepMAge. The resulting model contains 348 CpGs, 75 of which overlap with the 353 CpGs originally described by Horvath (Supplementary Table 5). We then verified the obtained linear predictor in the verification set containing 1,293 samples and found that both its MAE = 4.24 and MedAE = 3.23 years were higher than those of DeepMAge in the same set (MAE =3.80, MedAE = 2.77 years). The difference between MAEs, although slight, was deemed significant, with a *p-value* = 0.0001 (Supplementary Fig. 6).

The R script used to reproduce Horvath's method and the corresponding prediction tables can be found in the Supplementary Script section (Supplementary Script 1).

*Comparing DeepMAge to the 71 CpG clock*

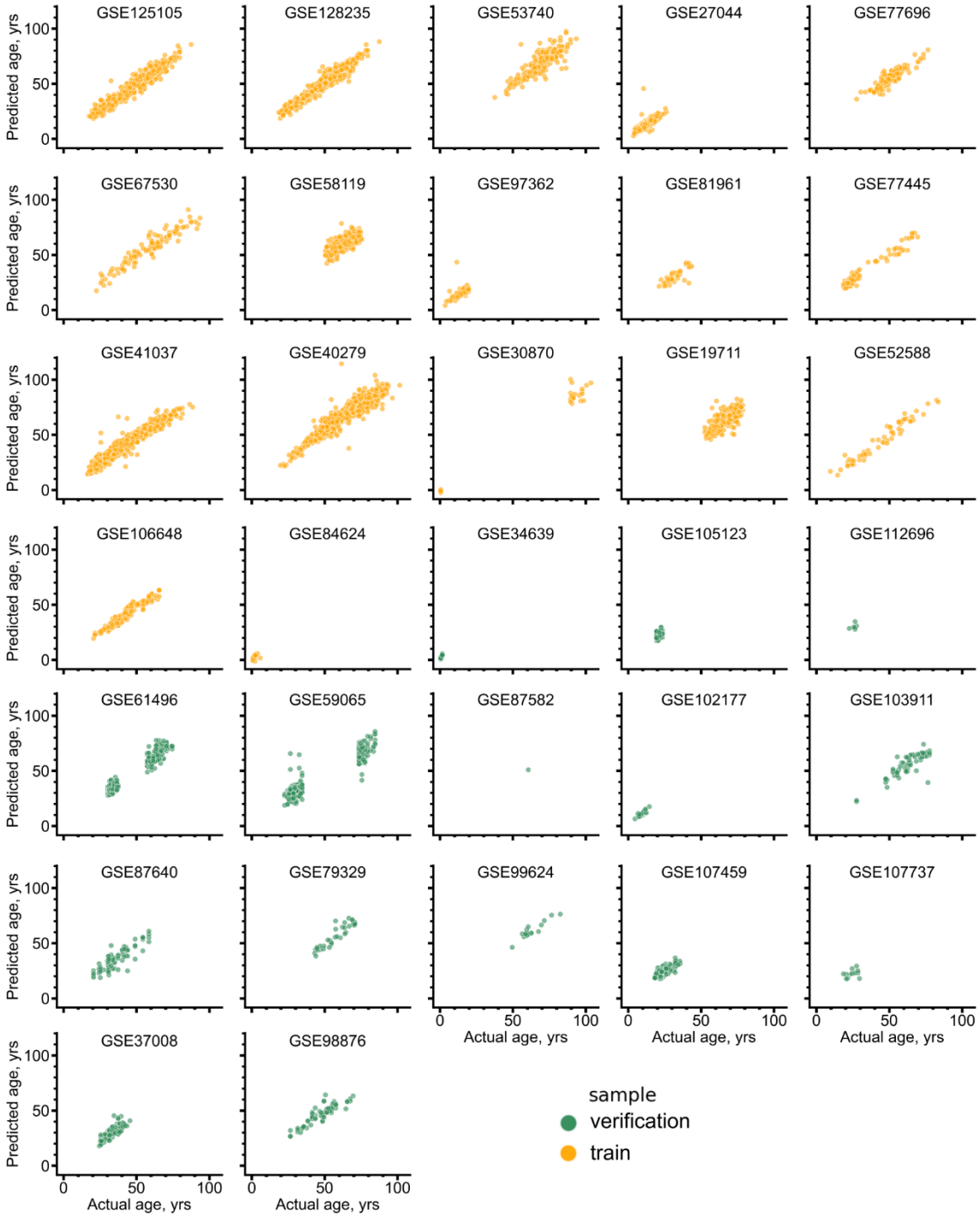
In addition to the 353 CpG clock, we also compared DeepMAge to the 71 CpG and 89 CpG blood DNAm clocks published by Hannum in 2013 [13]. The 71 CpG aging clock was developed using only blood-derived data obtained with the Illumina 450k platform.

We used the coefficients from the original linear regressions and tested these models on studies within the verification set, as defined by the current study. In a set of 1,404 DNAm profiles, both DeepMAge and the 71 CpG clock performed better than the baseline mean age assignment, but DeepMAge showed superior performance in terms of both RMSE and MAE (Supplementary Table 4). The RMSE of the 71 CpG clock (15.12 years) was significantly higher than the accuracy reported in the original paper (3.9 years).

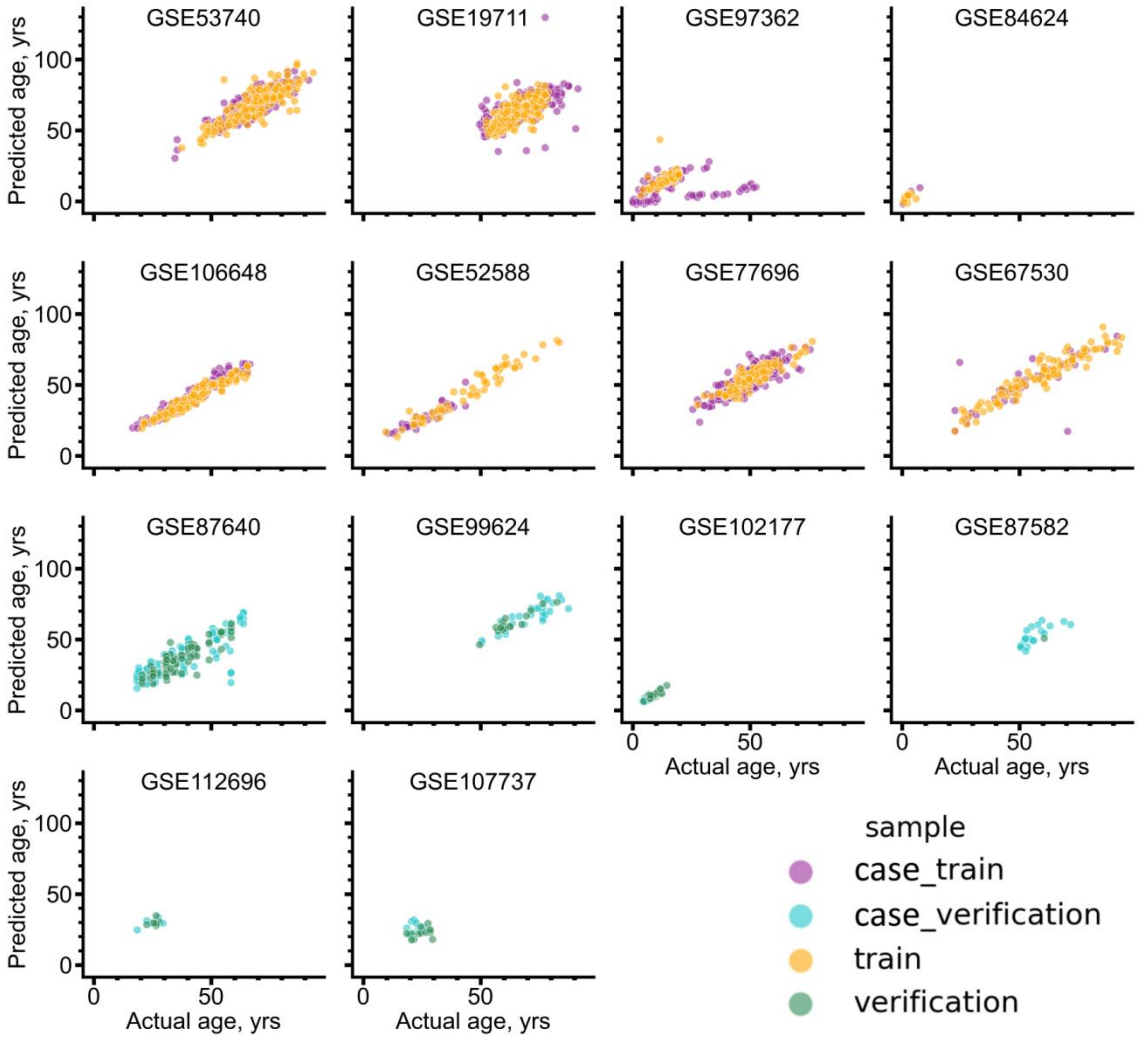
The MedAE achieved by the CpG clock for this set was 7.63 years. The MedAE achieved by DeepMAge for this set was 3.97 years.

The cause of such poor performance of the 71 CpG clock may be its training set size, which contained just 656 individuals. The 353 CpG clock, in turn, was trained on a set containing 7,844 multi-tissue DNAm profiles, and DeepMAge was trained on 4,930 blood samples.

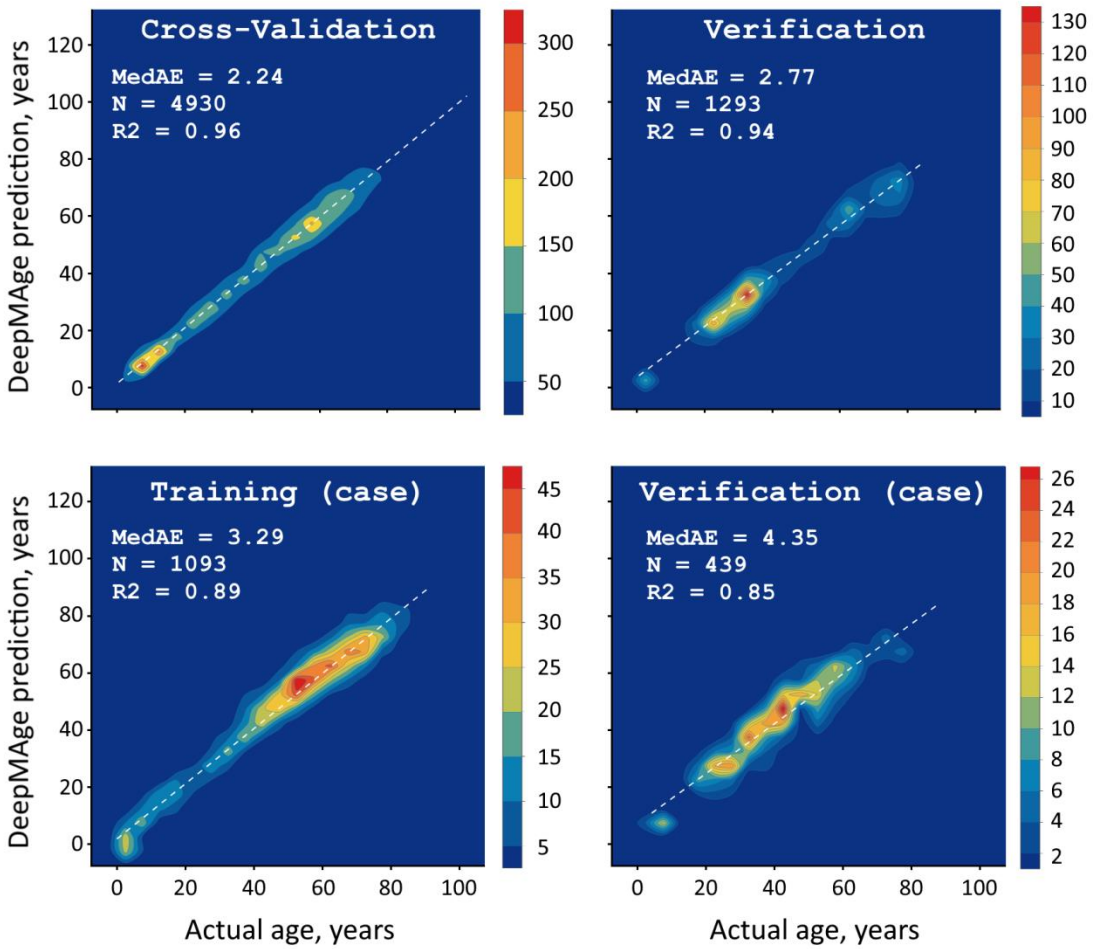
Note: All supplementary tables and the supplementary R script have been uploaded to the Open Science Framework (https://dx.doi.org/10.17605/OSF.IO/74ZGA).



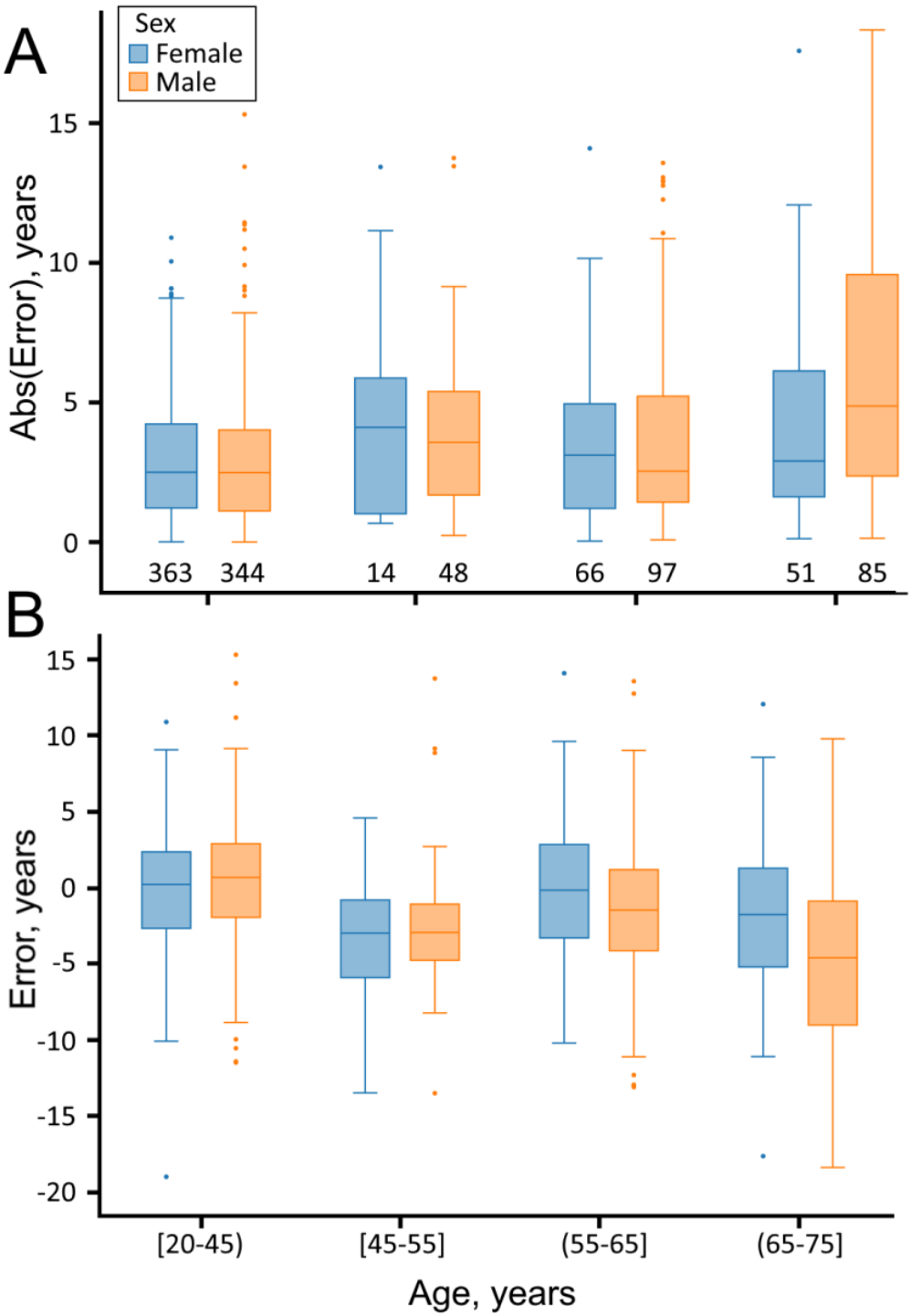

**Supplementary Figure 1. DeepMAge accurately predicted the ages of the healthy blood sample donors of all studies from the training and verification sets.** Training set predictions were obtained during cross-validation.
Yrs = Years



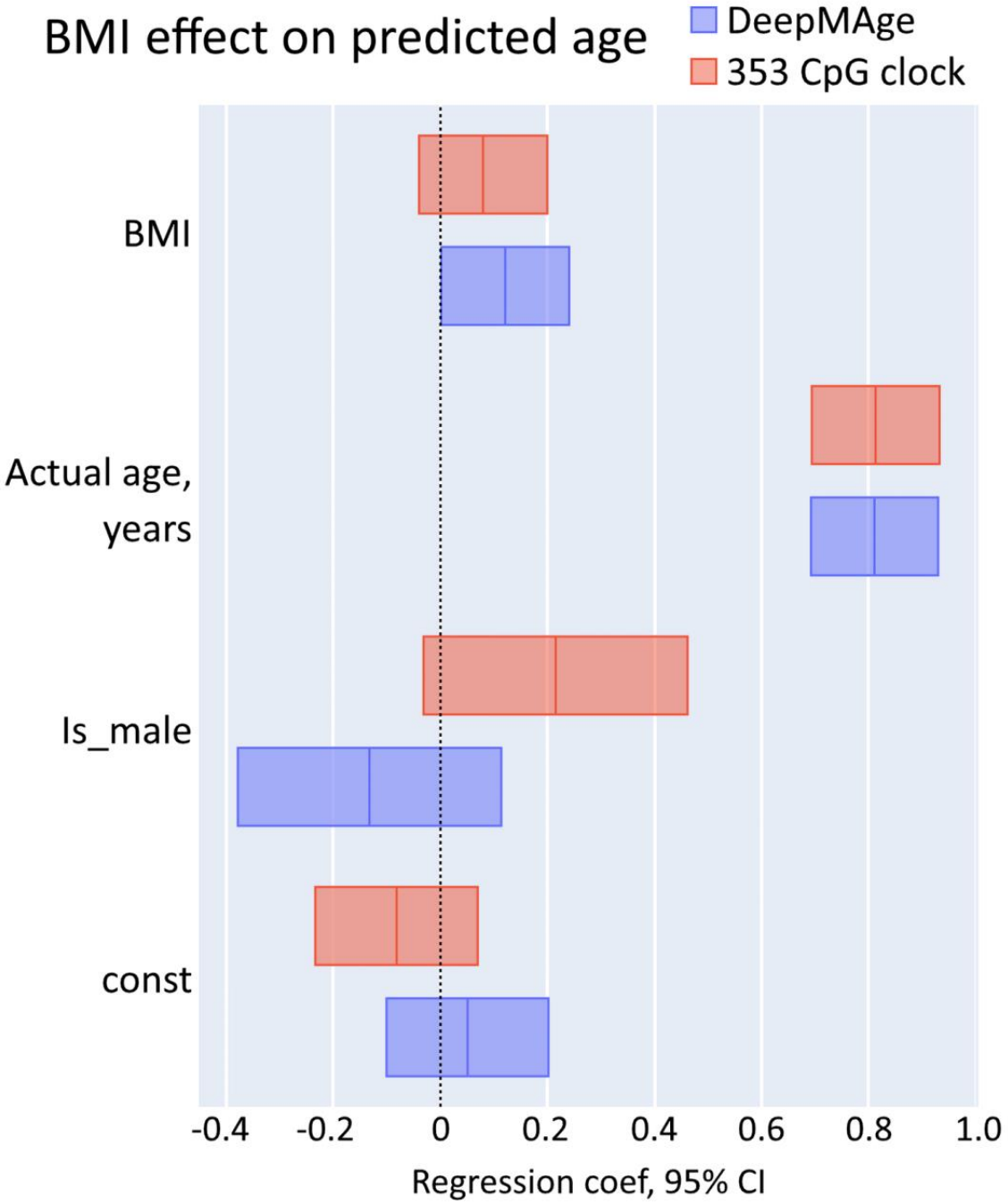

**Supplementary Figure 2. DeepMAge accurately predicted the ages of the blood sample donors of the case-control studies from the training and verification sets.**
Yrs = Years




**Supplementary Figure 3. KDE representation of Fig.1 in the main text. DeepMAge accurately predicted the chronological ages of both healthy individuals (top) and in an aggregation of case cohorts from multiple studies (bottom).** All the cohorts, apart from the "Cross-Validation" cohort, were predicted by the final model. The "Training (case)" cohort refers to the samples that were present in the studies used for training but were excluded from CV because they came from unhealthy donors. Similarly, the "Verification" cohort contains only healthy donors, and the "Verification (case)" cohort contains donors with various health conditions from the same studies. MedAE = Median absolute error measured in years; N = Number of samples in a corresponding cohort; R2 = Coefficient of determination. The white dashed lines are the least squares regressions. The number of counts contained within each contour of the 2D histograms is color-coded according to the color bars to the right of each subplot.

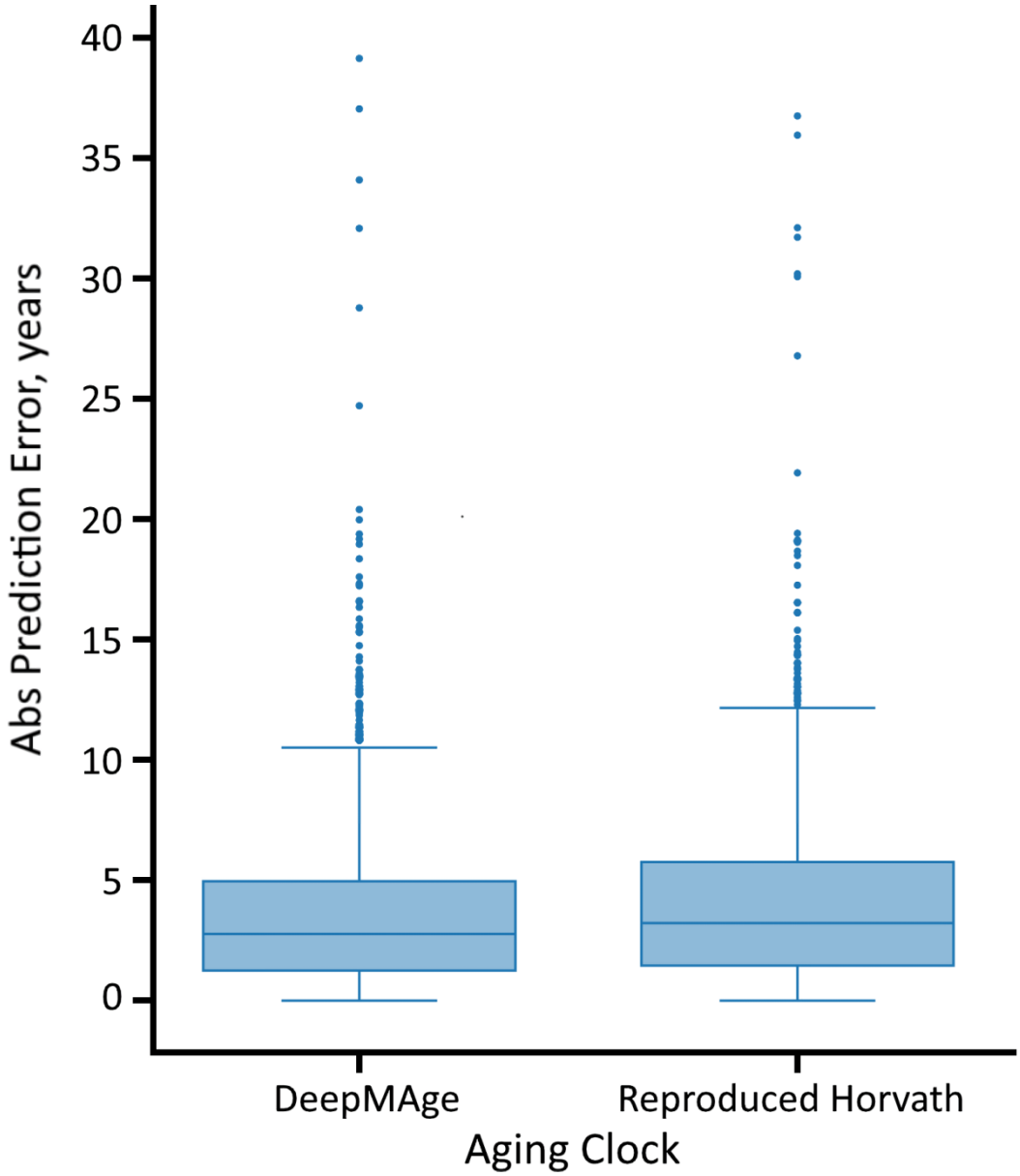



**Supplementary Figure 4. Older adults but not younger adults have significantly different DeepMAge error distributions for males and females (Table 2). (A)** DeepMAge absolute prediction error per age group in the verification set. The number of samples in each age group is marked below the boxes; **(B)** DeepMAge prediction error per age group in the verification set; The middle lines represent the medians; the box edges represent the quartiles; the whiskers reach out no farther than 1.5 times the interquartile distance. Four upper outliers in the [20-45) female age group were removed for presentation purposes. Abs (Error) = absolute error




**Supplementary Figure 5. Scaled BMI effect on age prediction, as observed in [Predicted ~ Real Age + Sex + BMI] ordinary least squares linear regression.** BMI had a significant effect (*p-value* = 0.048) on the predicted age for DeepMAge, but not for Horvath's aging clock (*p-value* = 0.19). Data set used: GSE37008. The middle lines of the boxes represent the point estimate for the regression coefficients; their edges represent the 2.5% and the 97.5% CI borders. BMI = Body mass index; CI = Confidence interval; const = Model intercept

# SUPPLEMENTARY DATA




**Supplementary Figure 6.** Boxplots for absolute prediction errors in the DeepMAge and the *de novo* elastic net regressor reproduced according to Horvath's protocol. The MAE of DeepMAge (3.80 years) was significantly lower (*p-value* = 0.0001) than that of the elastic net (4.24 years). The total number of samples used was 1,293. The middle lines represent the medians; the box edges represent the quartiles; the whiskers reach out no farther than 1.5 times the interquartile distance.
Abs = Absolute; MAE =Mean Absolute Error

# SUPPLEMENTARY DATA

**Supplementary Table 1.** Per-study report containing DeepMAge accuracy (MedAE in years), DeepMAge cohort, male ratio, and age range, as well as the baseline accuracy (median age assignment).

| Study | Cohort | N, samples | Male ratio, % | Age range, years | MedAE, years | Baseline, years | Platform |
|---|---|---|---|---|---|---|---|
| GSE81961 | train | 40 | 0.0 | 21-43 | 2.62 | 3.65 | 450k |
| GSE52588 | train | 58 | 12.0 | 9-83 | 2.72 | 14.0 | 450k |
| GSE52588 | case_train | 29 | 62.0 | 10-43 | 2.82 | 8.0 | 450k |
| GSE97362 | train | 83 | 67.0 | 3-19 | 1.4 | 3.0 | 450k |
| GSE97362 | case_train | 150 | 61.0 | 0-52 | 3.47 | 5.5 | 450k |
| GSE41037 | train | 720 | 62.0 | 16-88 | 2.29 | 10.0 | 27k |
| GSE30870 | train | 39 | 0.0 | 0-103 | 2.96 | 14.0 | 450k |
| GSE61496 | verification | 310 | 53.0 | 30-74 | 2.14 | 16.5 | 450k |
| GSE98876 | verification | 71 | 100.0 | 26-69 | 2.54 | 6.0 | 450k |
| GSE37008 | verification | 99 | 37.0 | 24-45 | 3.74 | 4.0 | 27k |
| GSE128235 | train | 536 | 43.0 | 18-87 | 1.99 | 9.0 | 450k |
| GSE87640 | case_verification | 156 | 65.0 | 18-63 | 3.97 | 8.8 | 450k |
| GSE87640 | verification | 84 | 62.0 | 20-58 | 2.52 | 5.05 | 450k |
| GSE87582 | case_verification | 20 | 90.0 | 50-71 | 4.38 | 2.81 | 450k |
| GSE87582 | verification | 1 | 100.0 | 60-60 | 9.59 | 0.0 | 450k |
| GSE19711 | train | 272 | 0.0 | 52-78 | 4.25 | 6.0 | 27k |
| GSE19711 | case_train | 264 | 0.0 | 49-91 | 3.7 | 8.0 | 27k |
| GSE34639 | verification | 48 | 33.0 | 0-1 | 1.92 | 0.5 | 450k |
| GSE79329 | verification | 34 | 100.0 | 43-70 | 2.63 | 8.7 | 450k |
| GSE67530 | train | 105 | 53.0 | 22-93 | 4.43 | 12.0 | 450k |
| GSE67530 | case_train | 39 | 59.0 | 22-91 | 3.43 | 10.0 | 450k |
| GSE105123 | verification | 107 | 58 | 19-23 | 2.06 | 1.0 | 450k |
| GSE99624 | case_verification | 32 | 12.0 | 50-87 | 3.92 | 7.5 | 450k |
| GSE99624 | verification | 16 | 38.0 | 49-82 | 2.72 | 2.5 | 450k |
| GSE125105 | train | 688 | 45.0 | 17-87 | 2.1 | 11.0 | 450k |
| GSE102177 | case_verification | 18 | 61.0 | 4-10 | 1.84 | 0.53 | 450k |
| GSE102177 | verification | 18 | 56 | 4-14 | 1.87 | 2.0 | 450k |
| GSE20067 | case_verification | 195 | 49.0 | 24-74 | 4.99 | 6.0 | 27k |
| GSE27044 | train | 889 | 100.0 | 3-26 | 1.08 | 3.0 | 27k |
| GSE103911 | verification | 65 | 71.0 | 27-77 | 6.96 | 8.0 | 450k |
| GSE53740 | train | 197 | 32.0 | 37-93 | 2.95 | 7.0 | 450k |
| GSE53740 | case_train | 186 | 35.0 | 34-91 | 3.62 | 4.5 | 450k |
| GSE59065 | verification | 295 | 48.0 | 22-84 | 4.35 | 11.0 | 450k |
| GSE112696 | case_verification | 6 | 67.0 | 18-29 | 5.51 | 3.0 | 450k |
| GSE112696 | verification | 6 | 67.0 | 22-27 | 3.75 | 0.5 | 450k |
| GSE77696 | train | 117 | 88.0 | 27-76 | 4.24 | 5.0 | 450k |
| GSE77696 | case_train | 261 | 96.0 | 25-75 | 4.25 | 6.0 | 450k |
| GSE58119 | train | 282 | 0.0 | 50-75 | 3.89 | 5.0 | 27k |
| GSE106648 | train | 139 | 25.0 | 20-65 | 2.48 | 7.0 | 450k |
| GSE106648 | case_train | 140 | 30.0 | 16-66 | 1.74 | 9.0 | 450k |
| GSE77445 | train | 85 | 51.0 | 18-69 | 2.7 | 4.0 | 450k |
| GSE84624 | train | 24 | 50.0 | 0-5 | 1.32 | 0.42 | 450k |
| GSE84624 | case_train | 24 | 54.0 | 0-7 | 1.27 | 0.9 | 450k |
| GSE107737 | case_verification | 12 | 100.0 | 18-27 | 2.46 | 2.0 | 450k |
| GSE107737 | verification | 12 | 100.0 | 18-29 | 3.03 | 3.5 | 450k |
| GSE40279 | train | 656 | 48.0 | 19-101 | 4.25 | 11.0 | 450k |
| GSE107459 | verification | 127 | 0.0 | 18-35 | 1.63 | 2.72 | 450k |

# SUPPLEMENTARY DATA

**Supplementary Table 2.** 1,000 CpG sites comprising DeepMAge, ranked by feature importance (higher importance features come first).

| Rank | CpG site | Importance | Rank | CpG site | Importance | Rank | CpG site | Importance | Rank | CpG site | Importance |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | cg01580888 | 0.000149323 | 31 | cg15319457 | 7.45E-05 | 61 | cg08209133 | 6.14E-05 | 91 | cg00462994 | 5.47E-05 |
| 2 | cg21801378 | 0.000143596 | 32 | cg11668844 | 7.41E-05 | 62 | cg18182399 | 6.13E-05 | 92 | cg11377136 | 5.45E-05 |
| 3 | cg00343092 | 0.000143059 | 33 | cg07850604 | 7.32E-05 | 63 | cg07388493 | 6.11E-05 | 93 | cg25809905 | 5.44E-05 |
| 4 | cg26394940 | 0.00012294 | 34 | cg27015931 | 7.21E-05 | 64 | cg17729667 | 6.11E-05 | 94 | cg25564800 | 5.43E-05 |
| 5 | cg12024906 | 0.000120211 | 35 | cg19046959 | 7.18E-05 | 65 | cg26372517 | 6.08E-05 | 95 | cg05436231 | 5.42E-05 |
| 6 | cg22736354 | 0.000119079 | 36 | cg08668790 | 7.05E-05 | 66 | cg19885761 | 6.05E-05 | 96 | cg00987379 | 5.42E-05 |
| 7 | cg18815943 | 0.000107798 | 37 | cg01511567 | 6.88E-05 | 67 | cg26842024 | 5.99E-05 | 97 | cg01820374 | 5.40E-05 |
| 8 | cg13269407 | 0.000107461 | 38 | cg00503840 | 6.81E-05 | 68 | cg23303074 | 5.95E-05 | 98 | cg12238343 | 5.39E-05 |
| 9 | cg06493994 | 0.000106796 | 39 | cg20143092 | 6.77E-05 | 69 | cg24826867 | 5.95E-05 | 99 | cg13975369 | 5.36E-05 |
| 10 | cg10523019 | 9.53E-05 | 40 | cg12373771 | 6.76E-05 | 70 | cg10362475 | 5.94E-05 | 100 | cg23887396 | 5.29E-05 |
| 11 | cg27491887 | 9.13E-05 | 41 | cg15957394 | 6.76E-05 | 71 | cg11299964 | 5.92E-05 | 101 | cg04662594 | 5.29E-05 |
| 12 | cg17861230 | 9.11E-05 | 42 | cg18902090 | 6.72E-05 | 72 | cg22947000 | 5.91E-05 | 102 | cg03330058 | 5.27E-05 |
| 13 | cg04836038 | 8.82E-05 | 43 | cg15013019 | 6.70E-05 | 73 | cg06268694 | 5.90E-05 | 103 | cg00930873 | 5.26E-05 |
| 14 | cg09809672 | 8.76E-05 | 44 | cg03623878 | 6.66E-05 | 74 | cg16785344 | 5.88E-05 | 104 | cg08468689 | 5.26E-05 |
| 15 | cg02479575 | 8.66E-05 | 45 | cg18267374 | 6.64E-05 | 75 | cg19724470 | 5.81E-05 | 105 | cg06836772 | 5.25E-05 |
| 16 | cg21296230 | 8.63E-05 | 46 | cg02397514 | 6.57E-05 | 76 | cg07158339 | 5.76E-05 | 106 | cg08694544 | 5.24E-05 |
| 17 | cg19722847 | 8.50E-05 | 47 | cg15804973 | 6.53E-05 | 77 | cg26614073 | 5.75E-05 | 107 | cg13931228 | 5.23E-05 |
| 18 | cg27320127 | 8.47E-05 | 48 | cg16744741 | 6.53E-05 | 78 | cg26845300 | 5.74E-05 | 108 | cg01530101 | 5.22E-05 |
| 19 | cg05675373 | 8.29E-05 | 49 | cg25148589 | 6.44E-05 | 79 | cg05822532 | 5.70E-05 | 109 | cg03975694 | 5.22E-05 |
| 20 | cg18008766 | 8.26E-05 | 50 | cg18055007 | 6.42E-05 | 80 | cg21790626 | 5.65E-05 | 110 | cg08317263 | 5.22E-05 |
| 21 | cg24127874 | 8.09E-05 | 51 | cg00059225 | 6.40E-05 | 81 | cg18660898 | 5.65E-05 | 111 | cg12339802 | 5.19E-05 |
| 22 | cg13663218 | 7.87E-05 | 52 | cg24081819 | 6.35E-05 | 82 | cg02310296 | 5.63E-05 | 112 | cg12946225 | 5.19E-05 |
| 23 | cg19560758 | 7.87E-05 | 53 | cg27544190 | 6.30E-05 | 83 | cg21368354 | 5.62E-05 | 113 | cg04431054 | 5.17E-05 |
| 24 | cg11126134 | 7.77E-05 | 54 | cg18236477 | 6.27E-05 | 84 | cg16313343 | 5.58E-05 | 114 | cg05135156 | 5.13E-05 |
| 25 | cg22407458 | 7.75E-05 | 55 | cg06291867 | 6.26E-05 | 85 | cg16273597 | 5.56E-05 | 115 | cg14918082 | 5.08E-05 |
| 26 | cg18691434 | 7.74E-05 | 56 | cg07211259 | 6.25E-05 | 86 | cg04123409 | 5.56E-05 | 116 | cg08965235 | 5.05E-05 |
| 27 | cg19761273 | 7.66E-05 | 57 | cg13494498 | 6.23E-05 | 87 | cg08090640 | 5.49E-05 | 117 | cg10947146 | 5.04E-05 |
| 28 | cg24891133 | 7.53E-05 | 58 | cg10189695 | 6.21E-05 | 88 | cg18440048 | 5.48E-05 | 118 | cg13460409 | 5.04E-05 |
| 29 | cg04528819 | 7.47E-05 | 59 | cg12422450 | 6.17E-05 | 89 | cg20300246 | 5.47E-05 | 119 | cg06156376 | 5.04E-05 |
| 30 | cg17285325 | 7.47E-05 | 60 | cg24170090 | 6.14E-05 | 90 | cg20761322 | 5.47E-05 | 120 | cg01899253 | 5.03E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 121 | cg08695830 | 5.01E-05 | 151 | cg13921352 | 4.67E-05 | 181 | cg02154074 | 4.40E-05 | 211 | cg07313155 | 4.21E-05 |
| 122 | cg04872689 | 5.00E-05 | 152 | cg21870884 | 4.66E-05 | 182 | cg21448423 | 4.40E-05 | 212 | cg08186362 | 4.20E-05 |
| 123 | cg10734665 | 4.98E-05 | 153 | cg13302154 | 4.65E-05 | 183 | cg09949775 | 4.39E-05 | 213 | cg09626984 | 4.20E-05 |

# SUPPLEMENTARY DATA

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 124 | cg15361590 | 4.98E-05 | 154 | cg07895149 | 4.64E-05 | 184 | cg02840794 | 4.39E-05 | 214 | cg25141674 | 4.17E-05 |
| 125 | cg15201877 | 4.97E-05 | 155 | cg07715201 | 4.64E-05 | 185 | cg21581873 | 4.39E-05 | 215 | cg16933388 | 4.17E-05 |
| 126 | cg18992688 | 4.97E-05 | 156 | cg01295203 | 4.64E-05 | 186 | cg17410236 | 4.38E-05 | 216 | cg02096633 | 4.17E-05 |
| 127 | cg17051321 | 4.95E-05 | 157 | cg16670497 | 4.62E-05 | 187 | cg25332298 | 4.37E-05 | 217 | cg23843812 | 4.16E-05 |
| 128 | cg03664992 | 4.91E-05 | 158 | cg16786458 | 4.62E-05 | 188 | cg00194146 | 4.37E-05 | 218 | cg17832674 | 4.15E-05 |
| 129 | cg00565688 | 4.89E-05 | 159 | cg13129046 | 4.61E-05 | 189 | cg26599006 | 4.36E-05 | 219 | cg20295671 | 4.15E-05 |
| 130 | cg04425624 | 4.87E-05 | 160 | cg23290344 | 4.61E-05 | 190 | cg27316956 | 4.36E-05 | 220 | cg19423311 | 4.14E-05 |
| 131 | cg21256649 | 4.87E-05 | 161 | cg04474832 | 4.59E-05 | 191 | cg05266781 | 4.36E-05 | 221 | cg23124451 | 4.13E-05 |
| 132 | cg03734874 | 4.87E-05 | 162 | cg22392276 | 4.58E-05 | 192 | cg19357849 | 4.32E-05 | 222 | cg24989962 | 4.13E-05 |
| 133 | cg02844545 | 4.87E-05 | 163 | cg15379633 | 4.58E-05 | 193 | cg24871743 | 4.32E-05 | 223 | cg22809047 | 4.13E-05 |
| 134 | cg20125091 | 4.86E-05 | 164 | cg19211800 | 4.57E-05 | 194 | cg23178308 | 4.31E-05 | 224 | cg04586023 | 4.13E-05 |
| 135 | cg16516400 | 4.84E-05 | 165 | cg20692569 | 4.56E-05 | 195 | cg21700166 | 4.31E-05 | 225 | cg10741760 | 4.13E-05 |
| 136 | cg07408456 | 4.83E-05 | 166 | cg22919728 | 4.54E-05 | 196 | cg16168311 | 4.30E-05 | 226 | cg11065385 | 4.12E-05 |
| 137 | cg12145907 | 4.83E-05 | 167 | cg26369667 | 4.51E-05 | 197 | cg17133388 | 4.30E-05 | 227 | cg03996822 | 4.11E-05 |
| 138 | cg14754581 | 4.82E-05 | 168 | cg27210390 | 4.51E-05 | 198 | cg25499099 | 4.29E-05 | 228 | cg22730004 | 4.11E-05 |
| 139 | cg06263495 | 4.81E-05 | 169 | cg09381003 | 4.51E-05 | 199 | cg18693704 | 4.28E-05 | 229 | cg03336167 | 4.10E-05 |
| 140 | cg12402251 | 4.81E-05 | 170 | cg02164046 | 4.51E-05 | 200 | cg06458239 | 4.28E-05 | 230 | cg07703401 | 4.08E-05 |
| 141 | cg09643544 | 4.80E-05 | 171 | cg25229172 | 4.50E-05 | 201 | cg06738602 | 4.27E-05 | 231 | cg17339202 | 4.08E-05 |
| 142 | cg26005082 | 4.80E-05 | 172 | cg13836627 | 4.50E-05 | 202 | cg01777397 | 4.27E-05 | 232 | cg17497271 | 4.07E-05 |
| 143 | cg16731240 | 4.77E-05 | 173 | cg12620499 | 4.49E-05 | 203 | cg03688818 | 4.26E-05 | 233 | cg01405761 | 4.05E-05 |
| 144 | cg25763788 | 4.75E-05 | 174 | cg13573276 | 4.49E-05 | 204 | cg06204948 | 4.24E-05 | 234 | cg08900043 | 4.05E-05 |
| 145 | cg14166009 | 4.75E-05 | 175 | cg17940013 | 4.48E-05 | 205 | cg25985778 | 4.24E-05 | 235 | cg08529529 | 4.05E-05 |
| 146 | cg02151301 | 4.74E-05 | 176 | cg24199834 | 4.47E-05 | 206 | cg02228185 | 4.24E-05 | 236 | cg17471102 | 4.04E-05 |
| 147 | cg26610808 | 4.71E-05 | 177 | cg04270799 | 4.45E-05 | 207 | cg16363586 | 4.22E-05 | 237 | cg22892904 | 4.03E-05 |
| 148 | cg10316635 | 4.71E-05 | 178 | cg08888956 | 4.44E-05 | 208 | cg26151675 | 4.22E-05 | 238 | cg24968336 | 3.99E-05 |
| 149 | cg22171829 | 4.70E-05 | 179 | cg23710218 | 4.43E-05 | 209 | cg23967169 | 4.22E-05 | 239 | cg00236832 | 3.98E-05 |
| 150 | cg17199483 | 4.69E-05 | 180 | cg11896923 | 4.42E-05 | 210 | cg24921089 | 4.22E-05 | 240 | cg15898840 | 3.97E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 241 | cg24471894 | 3.96E-05 | 271 | cg23828595 | 3.75E-05 | 301 | cg21697134 | 3.58E-05 | 331 | cg15743985 | 3.44E-05 |
| 242 | cg03991512 | 3.96E-05 | 272 | cg14592406 | 3.75E-05 | 302 | cg04601137 | 3.57E-05 | 332 | cg23854009 | 3.43E-05 |
| 243 | cg22285621 | 3.94E-05 | 273 | cg10822172 | 3.75E-05 | 303 | cg24169822 | 3.57E-05 | 333 | cg19008809 | 3.43E-05 |
| 244 | cg23843505 | 3.93E-05 | 274 | cg05064673 | 3.75E-05 | 304 | cg27360098 | 3.56E-05 | 334 | cg23668631 | 3.42E-05 |
| 245 | cg11378686 | 3.92E-05 | 275 | cg09554443 | 3.74E-05 | 305 | cg01968178 | 3.55E-05 | 335 | cg27153400 | 3.42E-05 |
| 246 | cg19515518 | 3.92E-05 | 276 | cg05369142 | 3.74E-05 | 306 | cg02217159 | 3.55E-05 | 336 | cg11946503 | 3.42E-05 |
| 247 | cg23211240 | 3.92E-05 | 277 | cg17274064 | 3.73E-05 | 307 | cg13697378 | 3.55E-05 | 337 | cg00081975 | 3.41E-05 |
| 248 | cg23189044 | 3.92E-05 | 278 | cg23517605 | 3.73E-05 | 308 | cg25044651 | 3.54E-05 | 338 | cg14175438 | 3.41E-05 |
| 249 | cg09118625 | 3.91E-05 | 279 | cg21992250 | 3.73E-05 | 309 | cg16319578 | 3.54E-05 | 339 | cg17688525 | 3.41E-05 |

# SUPPLEMENTARY DATA

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 250 | cg04765422 | 3.91E-05 | 280 | cg20974196 | 3.72E-05 | 310 | cg09067967 | 3.54E-05 | 340 | cg27553955 | 3.41E-05 |
| 251 | cg26911787 | 3.91E-05 | 281 | cg11120551 | 3.72E-05 | 311 | cg12688670 | 3.54E-05 | 341 | cg05767404 | 3.41E-05 |
| 252 | cg11536940 | 3.90E-05 | 282 | cg11919694 | 3.69E-05 | 312 | cg03891319 | 3.53E-05 | 342 | cg27016307 | 3.40E-05 |
| 253 | cg25822709 | 3.90E-05 | 283 | cg14319409 | 3.68E-05 | 313 | cg18919097 | 3.53E-05 | 343 | cg12782180 | 3.40E-05 |
| 254 | cg14456683 | 3.89E-05 | 284 | cg16620032 | 3.67E-05 | 314 | cg09736162 | 3.53E-05 | 344 | cg16465939 | 3.40E-05 |
| 255 | cg15297650 | 3.88E-05 | 285 | cg19789466 | 3.67E-05 | 315 | cg14261309 | 3.53E-05 | 345 | cg03224418 | 3.40E-05 |
| 256 | cg23587449 | 3.88E-05 | 286 | cg25459323 | 3.66E-05 | 316 | cg26500816 | 3.52E-05 | 346 | cg26963271 | 3.39E-05 |
| 257 | cg05881135 | 3.86E-05 | 287 | cg19356189 | 3.66E-05 | 317 | cg25538571 | 3.52E-05 | 347 | cg01407797 | 3.39E-05 |
| 258 | cg01283289 | 3.86E-05 | 288 | cg03544320 | 3.66E-05 | 318 | cg09915099 | 3.51E-05 | 348 | cg08822227 | 3.38E-05 |
| 259 | cg10549973 | 3.83E-05 | 289 | cg02364642 | 3.64E-05 | 319 | cg23428445 | 3.50E-05 | 349 | cg06320982 | 3.38E-05 |
| 260 | cg25256723 | 3.82E-05 | 290 | cg18755783 | 3.64E-05 | 320 | cg16614500 | 3.48E-05 | 350 | cg05535113 | 3.38E-05 |
| 261 | cg03929796 | 3.81E-05 | 291 | cg03030757 | 3.63E-05 | 321 | cg19235307 | 3.47E-05 | 351 | cg21096915 | 3.36E-05 |
| 262 | cg13854874 | 3.80E-05 | 292 | cg09462576 | 3.63E-05 | 322 | cg08876932 | 3.46E-05 | 352 | cg03909500 | 3.36E-05 |
| 263 | cg14332079 | 3.78E-05 | 293 | cg05379350 | 3.63E-05 | 323 | cg10235817 | 3.46E-05 | 353 | cg06147863 | 3.36E-05 |
| 264 | cg01946401 | 3.78E-05 | 294 | cg05158615 | 3.60E-05 | 324 | cg01459453 | 3.46E-05 | 354 | cg20240860 | 3.36E-05 |
| 265 | cg01294695 | 3.78E-05 | 295 | cg24860534 | 3.60E-05 | 325 | cg19055231 | 3.46E-05 | 355 | cg03943081 | 3.35E-05 |
| 266 | cg07123069 | 3.77E-05 | 296 | cg16682903 | 3.60E-05 | 326 | cg24851490 | 3.45E-05 | 356 | cg01154193 | 3.35E-05 |
| 267 | cg18573383 | 3.77E-05 | 297 | cg02489552 | 3.60E-05 | 327 | cg15839448 | 3.45E-05 | 357 | cg06361108 | 3.34E-05 |
| 268 | cg01400401 | 3.77E-05 | 298 | cg22527345 | 3.59E-05 | 328 | cg00489401 | 3.45E-05 | 358 | cg24012925 | 3.33E-05 |
| 269 | cg00047050 | 3.76E-05 | 299 | cg20008332 | 3.59E-05 | 329 | cg04062391 | 3.45E-05 | 359 | cg17791651 | 3.33E-05 |
| 270 | cg23506842 | 3.75E-05 | 300 | cg05442902 | 3.59E-05 | 330 | cg22396353 | 3.45E-05 | 360 | cg20979799 | 3.32E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 361 | cg12365667 | 3.32E-05 | 391 | cg17207590 | 3.22E-05 | 421 | cg27389185 | 3.13E-05 | 451 | cg26297688 | 3.07E-05 |
| 362 | cg17031727 | 3.32E-05 | 392 | cg09072120 | 3.21E-05 | 422 | cg00308665 | 3.13E-05 | 452 | cg25736482 | 3.06E-05 |
| 363 | cg18059933 | 3.32E-05 | 393 | cg10927536 | 3.21E-05 | 423 | cg10150813 | 3.13E-05 | 453 | cg00911351 | 3.06E-05 |
| 364 | cg25947945 | 3.31E-05 | 394 | cg20264732 | 3.20E-05 | 424 | cg06433658 | 3.13E-05 | 454 | cg05010623 | 3.05E-05 |
| 365 | cg25766046 | 3.31E-05 | 395 | cg25282410 | 3.20E-05 | 425 | cg12758687 | 3.13E-05 | 455 | cg11808757 | 3.05E-05 |
| 366 | cg09427311 | 3.31E-05 | 396 | cg14859417 | 3.20E-05 | 426 | cg09262269 | 3.12E-05 | 456 | cg05570980 | 3.05E-05 |
| 367 | cg26304237 | 3.31E-05 | 397 | cg12774845 | 3.20E-05 | 427 | cg13885201 | 3.12E-05 | 457 | cg00426498 | 3.04E-05 |
| 368 | cg22747092 | 3.30E-05 | 398 | cg12741420 | 3.20E-05 | 428 | cg18787975 | 3.12E-05 | 458 | cg05890019 | 3.04E-05 |
| 369 | cg19713196 | 3.30E-05 | 399 | cg04424621 | 3.19E-05 | 429 | cg20973210 | 3.12E-05 | 459 | cg14967066 | 3.04E-05 |
| 370 | cg19402885 | 3.30E-05 | 400 | cg17878972 | 3.19E-05 | 430 | cg06971096 | 3.11E-05 | 460 | cg18074297 | 3.04E-05 |
| 371 | cg19310430 | 3.29E-05 | 401 | cg21530890 | 3.19E-05 | 431 | cg15563382 | 3.11E-05 | 461 | cg19395441 | 3.04E-05 |
| 372 | cg24653181 | 3.29E-05 | 402 | cg25166896 | 3.19E-05 | 432 | cg10281002 | 3.11E-05 | 462 | cg03565323 | 3.03E-05 |
| 373 | cg19945840 | 3.29E-05 | 403 | cg16543027 | 3.18E-05 | 433 | cg15982419 | 3.11E-05 | 463 | cg17453778 | 3.03E-05 |
| 374 | cg21870662 | 3.28E-05 | 404 | cg21057046 | 3.18E-05 | 434 | cg15928398 | 3.10E-05 | 464 | cg24231716 | 3.03E-05 |
| 375 | cg15903421 | 3.28E-05 | 405 | cg09816471 | 3.18E-05 | 435 | cg17992056 | 3.10E-05 | 465 | cg05473871 | 3.03E-05 |

# SUPPLEMENTARY DATA

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 376 | cg04289385 | 3.28E-05 | 406 | cg10193817 | 3.18E-05 | 436 | cg11981599 | 3.10E-05 | 466 | cg22187630 | 3.02E-05 |
| 377 | cg12870705 | 3.28E-05 | 407 | cg25802093 | 3.17E-05 | 437 | cg00168942 | 3.09E-05 | 467 | cg05250458 | 3.02E-05 |
| 378 | cg04329454 | 3.27E-05 | 408 | cg01519742 | 3.16E-05 | 438 | cg25375711 | 3.09E-05 | 468 | cg07935568 | 3.02E-05 |
| 379 | cg20158248 | 3.26E-05 | 409 | cg12941369 | 3.16E-05 | 439 | cg12532500 | 3.09E-05 | 469 | cg02620013 | 3.02E-05 |
| 380 | cg10319505 | 3.26E-05 | 410 | cg25511429 | 3.16E-05 | 440 | cg10044101 | 3.09E-05 | 470 | cg21016177 | 3.02E-05 |
| 381 | cg12078929 | 3.25E-05 | 411 | cg09660171 | 3.15E-05 | 441 | cg00201234 | 3.08E-05 | 471 | cg03848555 | 3.01E-05 |
| 382 | cg15377518 | 3.25E-05 | 412 | cg22705225 | 3.15E-05 | 442 | cg07139440 | 3.08E-05 | 472 | cg18016365 | 3.01E-05 |
| 383 | cg07099407 | 3.24E-05 | 413 | cg15415507 | 3.15E-05 | 443 | cg22909609 | 3.08E-05 | 473 | cg21908259 | 3.01E-05 |
| 384 | cg08570521 | 3.24E-05 | 414 | cg03641225 | 3.15E-05 | 444 | cg20449692 | 3.08E-05 | 474 | cg24739326 | 3.01E-05 |
| 385 | cg12261786 | 3.24E-05 | 415 | cg14386691 | 3.15E-05 | 445 | cg15473868 | 3.08E-05 | 475 | cg18303397 | 3.01E-05 |
| 386 | cg02789485 | 3.23E-05 | 416 | cg08896945 | 3.14E-05 | 446 | cg02197293 | 3.07E-05 | 476 | cg10756887 | 3.00E-05 |
| 387 | cg19759064 | 3.23E-05 | 417 | cg25983380 | 3.14E-05 | 447 | cg22449114 | 3.07E-05 | 477 | cg17838026 | 3.00E-05 |
| 388 | cg24384676 | 3.23E-05 | 418 | cg22115808 | 3.14E-05 | 448 | cg05228408 | 3.07E-05 | 478 | cg13666340 | 3.00E-05 |
| 389 | cg02564523 | 3.22E-05 | 419 | cg18678185 | 3.13E-05 | 449 | cg16924616 | 3.07E-05 | 479 | cg10722799 | 3.00E-05 |
| 390 | cg06810647 | 3.22E-05 | 420 | cg11438428 | 3.13E-05 | 450 | cg12259537 | 3.07E-05 | 480 | cg01200177 | 3.00E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 481 | cg03852144 | 2.99E-05 | 511 | cg15037004 | 2.94E-05 | 541 | cg13500819 | 2.88E-05 | 571 | cg16776350 | 2.82E-05 |
| 482 | cg18511007 | 2.99E-05 | 512 | cg23833896 | 2.94E-05 | 542 | cg06824727 | 2.88E-05 | 572 | cg23265096 | 2.82E-05 |
| 483 | cg00202702 | 2.99E-05 | 513 | cg10865119 | 2.94E-05 | 543 | cg00563926 | 2.88E-05 | 573 | cg00548268 | 2.81E-05 |
| 484 | cg26824091 | 2.99E-05 | 514 | cg14865868 | 2.94E-05 | 544 | cg08655844 | 2.88E-05 | 574 | cg12052765 | 2.81E-05 |
| 485 | cg02848777 | 2.99E-05 | 515 | cg10281478 | 2.93E-05 | 545 | cg07903918 | 2.88E-05 | 575 | cg25302419 | 2.81E-05 |
| 486 | cg25054311 | 2.98E-05 | 516 | cg25942450 | 2.93E-05 | 546 | cg04460372 | 2.87E-05 | 576 | cg18765542 | 2.81E-05 |
| 487 | cg08022502 | 2.98E-05 | 517 | cg22613010 | 2.93E-05 | 547 | cg16483916 | 2.87E-05 | 577 | cg21289015 | 2.81E-05 |
| 488 | cg02085507 | 2.98E-05 | 518 | cg22901840 | 2.93E-05 | 548 | cg11279021 | 2.87E-05 | 578 | cg20043466 | 2.80E-05 |
| 489 | cg10682057 | 2.98E-05 | 519 | cg20001829 | 2.93E-05 | 549 | cg11189837 | 2.87E-05 | 579 | cg02071305 | 2.80E-05 |
| 490 | cg10084993 | 2.98E-05 | 520 | cg25604883 | 2.93E-05 | 550 | cg27601516 | 2.87E-05 | 580 | cg01805282 | 2.80E-05 |
| 491 | cg20994801 | 2.98E-05 | 521 | cg12513481 | 2.92E-05 | 551 | cg24056567 | 2.86E-05 | 581 | cg07442479 | 2.80E-05 |
| 492 | cg15156836 | 2.98E-05 | 522 | cg13899108 | 2.92E-05 | 552 | cg20279283 | 2.86E-05 | 582 | cg17431739 | 2.80E-05 |
| 493 | cg06269753 | 2.98E-05 | 523 | cg05871136 | 2.92E-05 | 553 | cg16063112 | 2.86E-05 | 583 | cg24642523 | 2.80E-05 |
| 494 | cg22680204 | 2.98E-05 | 524 | cg05483509 | 2.92E-05 | 554 | cg24986868 | 2.86E-05 | 584 | cg10240853 | 2.80E-05 |
| 495 | cg26036443 | 2.97E-05 | 525 | cg16254309 | 2.91E-05 | 555 | cg00431114 | 2.86E-05 | 585 | cg09595479 | 2.79E-05 |
| 496 | cg02828104 | 2.97E-05 | 526 | cg27281093 | 2.91E-05 | 556 | cg00563932 | 2.86E-05 | 586 | cg23320649 | 2.79E-05 |
| 497 | cg16270890 | 2.97E-05 | 527 | cg12556134 | 2.91E-05 | 557 | cg19706682 | 2.85E-05 | 587 | cg08996521 | 2.79E-05 |
| 498 | cg17324128 | 2.97E-05 | 528 | cg20900524 | 2.91E-05 | 558 | cg15747595 | 2.85E-05 | 588 | cg15776355 | 2.79E-05 |
| 499 | cg08303146 | 2.97E-05 | 529 | cg11584690 | 2.91E-05 | 559 | cg16352283 | 2.85E-05 | 589 | cg20654468 | 2.79E-05 |
| 500 | cg07195577 | 2.97E-05 | 530 | cg03600687 | 2.91E-05 | 560 | cg26131019 | 2.85E-05 | 590 | cg09429111 | 2.79E-05 |
| 501 | cg25713185 | 2.97E-05 | 531 | cg19283196 | 2.91E-05 | 561 | cg06638433 | 2.84E-05 | 591 | cg23850212 | 2.79E-05 |

# SUPPLEMENTARY DATA

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 502 | cg14826456 | 2.96E-05 | 532 | cg03883519 | 2.90E-05 | 562 | cg00689340 | 2.84E-05 | 592 | cg16240480 | 2.79E-05 |
| 503 | cg27169020 | 2.95E-05 | 533 | cg19594666 | 2.90E-05 | 563 | cg27187881 | 2.84E-05 | 593 | cg07185695 | 2.78E-05 |
| 504 | cg07430605 | 2.95E-05 | 534 | cg10515956 | 2.90E-05 | 564 | cg11879514 | 2.83E-05 | 594 | cg12073594 | 2.78E-05 |
| 505 | cg09492887 | 2.95E-05 | 535 | cg16362133 | 2.90E-05 | 565 | cg13593287 | 2.83E-05 | 595 | cg15201635 | 2.78E-05 |
| 506 | cg05010058 | 2.95E-05 | 536 | cg07737781 | 2.89E-05 | 566 | cg06948294 | 2.83E-05 | 596 | cg23762517 | 2.78E-05 |
| 507 | cg10226744 | 2.95E-05 | 537 | cg11314684 | 2.89E-05 | 567 | cg03565081 | 2.83E-05 | 597 | cg15352829 | 2.78E-05 |
| 508 | cg02206259 | 2.95E-05 | 538 | cg14377791 | 2.89E-05 | 568 | cg06161930 | 2.82E-05 | 598 | cg20346726 | 2.78E-05 |
| 509 | cg17471928 | 2.94E-05 | 539 | cg19355190 | 2.89E-05 | 569 | cg11010122 | 2.82E-05 | 599 | cg11738543 | 2.77E-05 |
| 510 | cg20637307 | 2.94E-05 | 540 | cg11747499 | 2.88E-05 | 570 | cg24512400 | 2.82E-05 | 600 | cg00208967 | 2.77E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 601 | cg03782453 | 2.77E-05 | 631 | cg01654582 | 2.71E-05 | 661 | cg09325711 | 2.64E-05 | 691 | cg09563216 | 2.60E-05 |
| 602 | cg19713460 | 2.77E-05 | 632 | cg00340102 | 2.71E-05 | 662 | cg23239396 | 2.64E-05 | 692 | cg06144905 | 2.59E-05 |
| 603 | cg05600717 | 2.77E-05 | 633 | cg03826976 | 2.70E-05 | 663 | cg14155397 | 2.64E-05 | 693 | cg09706243 | 2.59E-05 |
| 604 | cg04786857 | 2.76E-05 | 634 | cg14870271 | 2.70E-05 | 664 | cg17029151 | 2.64E-05 | 694 | cg01919208 | 2.59E-05 |
| 605 | cg02335441 | 2.76E-05 | 635 | cg02654291 | 2.70E-05 | 665 | cg13620770 | 2.64E-05 | 695 | cg11428724 | 2.59E-05 |
| 606 | cg16127845 | 2.76E-05 | 636 | cg04036898 | 2.70E-05 | 666 | cg15974053 | 2.64E-05 | 696 | cg12928668 | 2.59E-05 |
| 607 | cg22631938 | 2.76E-05 | 637 | cg14992253 | 2.69E-05 | 667 | cg01161216 | 2.64E-05 | 697 | cg00090147 | 2.59E-05 |
| 608 | cg21426387 | 2.76E-05 | 638 | cg12613383 | 2.69E-05 | 668 | cg08849574 | 2.64E-05 | 698 | cg00630583 | 2.59E-05 |
| 609 | cg22472290 | 2.76E-05 | 639 | cg10917602 | 2.69E-05 | 669 | cg00152644 | 2.63E-05 | 699 | cg14958635 | 2.59E-05 |
| 610 | cg09340639 | 2.76E-05 | 640 | cg07652213 | 2.68E-05 | 670 | cg17966619 | 2.63E-05 | 700 | cg26083396 | 2.59E-05 |
| 611 | cg08587864 | 2.76E-05 | 641 | cg21820677 | 2.68E-05 | 671 | cg26780333 | 2.63E-05 | 701 | cg20080624 | 2.58E-05 |
| 612 | cg19168338 | 2.76E-05 | 642 | cg14681055 | 2.68E-05 | 672 | cg20419410 | 2.63E-05 | 702 | cg08370996 | 2.58E-05 |
| 613 | cg25725843 | 2.75E-05 | 643 | cg19635712 | 2.68E-05 | 673 | cg20227766 | 2.63E-05 | 703 | cg23430664 | 2.58E-05 |
| 614 | cg20616414 | 2.75E-05 | 644 | cg13726191 | 2.68E-05 | 674 | cg24127989 | 2.63E-05 | 704 | cg19889780 | 2.58E-05 |
| 615 | cg06675478 | 2.75E-05 | 645 | cg05164634 | 2.67E-05 | 675 | cg23752923 | 2.63E-05 | 705 | cg24200059 | 2.58E-05 |
| 616 | cg20209009 | 2.75E-05 | 646 | cg19155599 | 2.67E-05 | 676 | cg15456206 | 2.63E-05 | 706 | cg14100184 | 2.58E-05 |
| 617 | cg04598121 | 2.75E-05 | 647 | cg01269795 | 2.67E-05 | 677 | cg24727203 | 2.62E-05 | 707 | cg13047892 | 2.58E-05 |
| 618 | cg00564163 | 2.75E-05 | 648 | cg19764555 | 2.67E-05 | 678 | cg04739570 | 2.62E-05 | 708 | cg04457979 | 2.58E-05 |
| 619 | cg20496643 | 2.75E-05 | 649 | cg22236626 | 2.67E-05 | 679 | cg05056120 | 2.61E-05 | 709 | cg14056644 | 2.57E-05 |
| 620 | cg01027739 | 2.74E-05 | 650 | cg11260848 | 2.66E-05 | 680 | cg17692403 | 2.61E-05 | 710 | cg19669036 | 2.57E-05 |
| 621 | cg02503850 | 2.74E-05 | 651 | cg07621046 | 2.66E-05 | 681 | cg17914753 | 2.60E-05 | 711 | cg04597449 | 2.57E-05 |
| 622 | cg12902039 | 2.74E-05 | 652 | cg22719623 | 2.66E-05 | 682 | cg27493997 | 2.60E-05 | 712 | cg07979752 | 2.56E-05 |
| 623 | cg06238491 | 2.73E-05 | 653 | cg09083627 | 2.66E-05 | 683 | cg02988947 | 2.60E-05 | 713 | cg00685836 | 2.56E-05 |
| 624 | cg24587268 | 2.73E-05 | 654 | cg11833861 | 2.65E-05 | 684 | cg02016419 | 2.60E-05 | 714 | cg09079275 | 2.56E-05 |
| 625 | cg04880063 | 2.73E-05 | 655 | cg01580044 | 2.65E-05 | 685 | cg10362591 | 2.60E-05 | 715 | cg04726200 | 2.56E-05 |
| 626 | cg26711820 | 2.72E-05 | 656 | cg05546044 | 2.65E-05 | 686 | cg22521310 | 2.60E-05 | 716 | cg26673195 | 2.56E-05 |
| 627 | cg25655096 | 2.72E-05 | 657 | cg13745346 | 2.64E-05 | 687 | cg06051311 | 2.60E-05 | 717 | cg12069309 | 2.56E-05 |

# SUPPLEMENTARY DATA

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 628 | cg09601629 | 2.72E-05 | 658 | cg20831708 | 2.64E-05 | 688 | cg02515725 | 2.60E-05 | 718 | cg23283875 | 2.56E-05 |
| 629 | cg19233923 | 2.72E-05 | 659 | cg08555657 | 2.64E-05 | 689 | cg22321558 | 2.60E-05 | 719 | cg02994956 | 2.55E-05 |
| 630 | cg25629694 | 2.72E-05 | 660 | cg19573166 | 2.64E-05 | 690 | cg07588779 | 2.60E-05 | 720 | cg21480743 | 2.55E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 721 | cg11896271 | 2.55E-05 | 751 | cg22971191 | 2.52E-05 | 781 | cg02776251 | 2.48E-05 | 811 | cg16761581 | 2.45E-05 |
| 722 | cg02181506 | 2.55E-05 | 752 | cg22436229 | 2.52E-05 | 782 | cg10104451 | 2.48E-05 | 812 | cg07314414 | 2.45E-05 |
| 723 | cg00497251 | 2.55E-05 | 753 | cg01600189 | 2.52E-05 | 783 | cg15945417 | 2.48E-05 | 813 | cg03945800 | 2.45E-05 |
| 724 | cg21808053 | 2.55E-05 | 754 | cg00651216 | 2.51E-05 | 784 | cg17589341 | 2.48E-05 | 814 | cg26512148 | 2.44E-05 |
| 725 | cg15316334 | 2.55E-05 | 755 | cg24076884 | 2.51E-05 | 785 | cg06253072 | 2.47E-05 | 815 | cg23047271 | 2.44E-05 |
| 726 | cg16408970 | 2.55E-05 | 756 | cg12955583 | 2.51E-05 | 786 | cg24173049 | 2.47E-05 | 816 | cg02774439 | 2.44E-05 |
| 727 | cg15261665 | 2.54E-05 | 757 | cg03760483 | 2.51E-05 | 787 | cg02062650 | 2.47E-05 | 817 | cg06621358 | 2.43E-05 |
| 728 | cg05373457 | 2.54E-05 | 758 | cg06392241 | 2.51E-05 | 788 | cg03138091 | 2.47E-05 | 818 | cg05898524 | 2.43E-05 |
| 729 | cg25483003 | 2.54E-05 | 759 | cg14913925 | 2.51E-05 | 789 | cg07973967 | 2.47E-05 | 819 | cg01346152 | 2.43E-05 |
| 730 | cg01114088 | 2.54E-05 | 760 | cg24429836 | 2.51E-05 | 790 | cg15853125 | 2.47E-05 | 820 | cg20557202 | 2.43E-05 |
| 731 | cg19037167 | 2.54E-05 | 761 | cg23758485 | 2.50E-05 | 791 | cg06236061 | 2.47E-05 | 821 | cg17943999 | 2.43E-05 |
| 732 | cg02255609 | 2.54E-05 | 762 | cg07846167 | 2.50E-05 | 792 | cg18555440 | 2.47E-05 | 822 | cg00398048 | 2.43E-05 |
| 733 | cg11648289 | 2.54E-05 | 763 | cg22101147 | 2.50E-05 | 793 | cg00282347 | 2.46E-05 | 823 | cg08441806 | 2.43E-05 |
| 734 | cg09582042 | 2.54E-05 | 764 | cg19728223 | 2.50E-05 | 794 | cg11223252 | 2.46E-05 | 824 | cg12600197 | 2.43E-05 |
| 735 | cg21353232 | 2.54E-05 | 765 | cg07469792 | 2.50E-05 | 795 | cg01017147 | 2.46E-05 | 825 | cg00187380 | 2.43E-05 |
| 736 | cg26018901 | 2.53E-05 | 766 | cg13311440 | 2.49E-05 | 796 | cg06117855 | 2.46E-05 | 826 | cg16998353 | 2.43E-05 |
| 737 | cg21818252 | 2.53E-05 | 767 | cg07482936 | 2.49E-05 | 797 | cg24768561 | 2.46E-05 | 827 | cg26509022 | 2.43E-05 |
| 738 | cg14348532 | 2.53E-05 | 768 | cg24646414 | 2.49E-05 | 798 | cg02276665 | 2.46E-05 | 828 | cg04466273 | 2.43E-05 |
| 739 | cg13565157 | 2.53E-05 | 769 | cg26928682 | 2.49E-05 | 799 | cg21509097 | 2.46E-05 | 829 | cg14093936 | 2.43E-05 |
| 740 | cg02764611 | 2.53E-05 | 770 | cg16386080 | 2.49E-05 | 800 | cg18972811 | 2.46E-05 | 830 | cg00472814 | 2.43E-05 |
| 741 | cg05488632 | 2.53E-05 | 771 | cg03547797 | 2.49E-05 | 801 | cg00576250 | 2.46E-05 | 831 | cg27236973 | 2.43E-05 |
| 742 | cg21120249 | 2.53E-05 | 772 | cg06630241 | 2.49E-05 | 802 | cg09155852 | 2.46E-05 | 832 | cg23786576 | 2.42E-05 |
| 743 | cg08569678 | 2.53E-05 | 773 | cg08097882 | 2.48E-05 | 803 | cg02254649 | 2.46E-05 | 833 | cg12457773 | 2.42E-05 |
| 744 | cg26624134 | 2.53E-05 | 774 | cg08646988 | 2.48E-05 | 804 | cg07495664 | 2.46E-05 | 834 | cg09863772 | 2.42E-05 |
| 745 | cg13163729 | 2.52E-05 | 775 | cg17830308 | 2.48E-05 | 805 | cg24450312 | 2.46E-05 | 835 | cg26209676 | 2.42E-05 |
| 746 | cg07753644 | 2.52E-05 | 776 | cg20028470 | 2.48E-05 | 806 | cg15271616 | 2.46E-05 | 836 | cg10194829 | 2.42E-05 |
| 747 | cg06154570 | 2.52E-05 | 777 | cg15720535 | 2.48E-05 | 807 | cg26968812 | 2.45E-05 | 837 | cg21073927 | 2.42E-05 |
| 748 | cg05294243 | 2.52E-05 | 778 | cg21604042 | 2.48E-05 | 808 | cg05786809 | 2.45E-05 | 838 | cg27626102 | 2.42E-05 |
| 749 | cg22580512 | 2.52E-05 | 779 | cg24801210 | 2.48E-05 | 809 | cg11469321 | 2.45E-05 | 839 | cg21402071 | 2.42E-05 |
| 750 | cg00107187 | 2.52E-05 | 780 | cg14973995 | 2.48E-05 | 810 | cg07558455 | 2.45E-05 | 840 | cg17165284 | 2.42E-05 |
| **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** | **Rank** | **CpG site** | **Importance** |
| 841 | cg16332577 | 2.41E-05 | 871 | cg23748737 | 2.39E-05 | 901 | cg01655355 | 2.36E-05 | 931 | cg04409945 | 2.33E-05 |
| 842 | cg14540297 | 2.41E-05 | 872 | cg19464016 | 2.39E-05 | 902 | cg03775422 | 2.36E-05 | 932 | cg08654655 | 2.32E-05 |

# SUPPLEMENTARY DATA

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 843 | cg17421623 | 2.41E-05 | 873 | cg23002907 | 2.39E-05 | 903 | cg01441777 | 2.36E-05 | 933 | cg21176048 | 2.32E-05 |
| 844 | cg21974766 | 2.41E-05 | 874 | cg16427670 | 2.39E-05 | 904 | cg20723355 | 2.36E-05 | 934 | cg12331389 | 2.32E-05 |
| 845 | cg02196655 | 2.41E-05 | 875 | cg06385087 | 2.39E-05 | 905 | cg01791232 | 2.36E-05 | 935 | cg27631256 | 2.32E-05 |
| 846 | cg26202340 | 2.41E-05 | 876 | cg10648908 | 2.38E-05 | 906 | cg22215728 | 2.36E-05 | 936 | cg18081258 | 2.32E-05 |
| 847 | cg26374101 | 2.41E-05 | 877 | cg18464137 | 2.38E-05 | 907 | cg24207176 | 2.36E-05 | 937 | cg07991621 | 2.32E-05 |
| 848 | cg11480873 | 2.41E-05 | 878 | cg06288351 | 2.38E-05 | 908 | cg13262687 | 2.36E-05 | 938 | cg22799850 | 2.32E-05 |
| 849 | cg07349094 | 2.41E-05 | 879 | cg04114315 | 2.38E-05 | 909 | cg12564453 | 2.36E-05 | 939 | cg08097755 | 2.32E-05 |
| 850 | cg15364618 | 2.41E-05 | 880 | cg04032226 | 2.38E-05 | 910 | cg11296937 | 2.36E-05 | 940 | cg24874111 | 2.31E-05 |
| 851 | cg25050026 | 2.41E-05 | 881 | cg23146358 | 2.38E-05 | 911 | cg14972143 | 2.35E-05 | 941 | cg08587542 | 2.31E-05 |
| 852 | cg05724065 | 2.40E-05 | 882 | cg11108890 | 2.38E-05 | 912 | cg11041457 | 2.35E-05 | 942 | cg25713309 | 2.31E-05 |
| 853 | cg10175795 | 2.40E-05 | 883 | cg11158729 | 2.38E-05 | 913 | cg24107665 | 2.35E-05 | 943 | cg01353448 | 2.31E-05 |
| 854 | cg17338403 | 2.40E-05 | 884 | cg10080004 | 2.38E-05 | 914 | cg00653387 | 2.35E-05 | 944 | cg20506783 | 2.31E-05 |
| 855 | cg05001145 | 2.40E-05 | 885 | cg10052840 | 2.38E-05 | 915 | cg05073035 | 2.35E-05 | 945 | cg04588079 | 2.31E-05 |
| 856 | cg17169998 | 2.40E-05 | 886 | cg00399483 | 2.38E-05 | 916 | cg16404106 | 2.35E-05 | 946 | cg26898166 | 2.31E-05 |
| 857 | cg13234863 | 2.40E-05 | 887 | cg05769161 | 2.38E-05 | 917 | cg16954341 | 2.35E-05 | 947 | cg05157725 | 2.31E-05 |
| 858 | cg05868799 | 2.40E-05 | 888 | cg08572611 | 2.38E-05 | 918 | cg21926138 | 2.35E-05 | 948 | cg08197122 | 2.31E-05 |
| 859 | cg21949781 | 2.40E-05 | 889 | cg26270746 | 2.37E-05 | 919 | cg02755525 | 2.34E-05 | 949 | cg00565075 | 2.31E-05 |
| 860 | cg17252960 | 2.40E-05 | 890 | cg06911084 | 2.37E-05 | 920 | cg26093148 | 2.34E-05 | 950 | cg10331779 | 2.30E-05 |
| 861 | cg13548361 | 2.40E-05 | 891 | cg18678763 | 2.37E-05 | 921 | cg03889226 | 2.34E-05 | 951 | cg02782630 | 2.30E-05 |
| 862 | cg15003434 | 2.40E-05 | 892 | cg10989517 | 2.37E-05 | 922 | cg16984944 | 2.34E-05 | 952 | cg20083676 | 2.30E-05 |
| 863 | cg10287137 | 2.40E-05 | 893 | cg16721845 | 2.37E-05 | 923 | cg14913610 | 2.34E-05 | 953 | cg12478185 | 2.30E-05 |
| 864 | cg08724517 | 2.40E-05 | 894 | cg07845392 | 2.37E-05 | 924 | cg10893437 | 2.34E-05 | 954 | cg05824484 | 2.30E-05 |
| 865 | cg27376271 | 2.40E-05 | 895 | cg13438834 | 2.37E-05 | 925 | cg13526007 | 2.34E-05 | 955 | cg24641352 | 2.30E-05 |
| 866 | cg03379131 | 2.40E-05 | 896 | cg16284292 | 2.36E-05 | 926 | cg16718678 | 2.33E-05 | 956 | cg08162780 | 2.30E-05 |
| 867 | cg26261431 | 2.39E-05 | 897 | cg04887278 | 2.36E-05 | 927 | cg19596204 | 2.33E-05 | 957 | cg02260587 | 2.30E-05 |
| 868 | cg21547708 | 2.39E-05 | 898 | cg13904493 | 2.36E-05 | 928 | cg06885782 | 2.33E-05 | 958 | cg24649713 | 2.30E-05 |
| 869 | cg11368643 | 2.39E-05 | 899 | cg05924583 | 2.36E-05 | 929 | cg05507459 | 2.33E-05 | 959 | cg20051033 | 2.30E-05 |
| 870 | cg16474696 | 2.39E-05 | 900 | cg24125648 | 2.36E-05 | 930 | cg19192120 | 2.33E-05 | 960 | cg05697231 | 2.30E-05 |

| Rank | CpG site | Importance | Rank | CpG site | Importance |
|---|---|---|---|---|---|
| 961 | cg21092687 | 2.30E-05 | 991 | cg13818573 | 2.26E-05 |
| 962 | cg14244577 | 2.30E-05 | 992 | cg26581729 | 2.26E-05 |
| 963 | cg14329157 | 2.30E-05 | 993 | cg10521852 | 2.26E-05 |
| 964 | cg18809289 | 2.29E-05 | 994 | cg11386746 | 2.26E-05 |
| 965 | cg13150977 | 2.29E-05 | 995 | cg13806135 | 2.26E-05 |
| 966 | cg10986043 | 2.29E-05 | 996 | cg21053529 | 2.26E-05 |
| 967 | cg21152671 | 2.29E-05 | 997 | cg00650762 | 2.25E-05 |
| 968 | cg26984624 | 2.29E-05 | 998 | cg22183706 | 2.25E-05 |
| 969 | cg24101578 | 2.29E-05 | 999 | cg20537629 | 2.25E-05 |
| 970 | cg20716064 | 2.29E-05 | 1000 | cg08331960 | 2.25E-05 |

| | | |
|---|---|---|
| 971 | cg02994974 | 2.29E-05 |
| 972 | cg17655614 | 2.29E-05 |
| 973 | cg22799321 | 2.28E-05 |
| 974 | cg16413777 | 2.28E-05 |
| 975 | cg17775235 | 2.28E-05 |
| 976 | cg21972382 | 2.28E-05 |
| 977 | cg10064162 | 2.28E-05 |
| 978 | cg08858521 | 2.28E-05 |
| 979 | cg24596472 | 2.28E-05 |
| 980 | cg16774604 | 2.28E-05 |
| 981 | cg10106284 | 2.28E-05 |
| 982 | cg18993334 | 2.27E-05 |
| 983 | cg16519321 | 2.27E-05 |
| 984 | cg00582628 | 2.27E-05 |
| 985 | cg05194726 | 2.27E-05 |
| 986 | cg24715735 | 2.27E-05 |
| 987 | cg04587910 | 2.27E-05 |
| 988 | cg17241310 | 2.27E-05 |
| 989 | cg14380517 | 2.27E-05 |
| 990 | cg23771661 | 2.27E-05 |

**Supplementary Table 3.** Gene enrichment report obtained with Gene Ontology.

| GO biological process complete | Homo sapiens - REFLIST (20851) | # (out of 849 uploaded) | # (expected) | over/under | Fold Enrichment | raw P-value | FDR |
|---|---|---|---|---|---|---|---|
| system development (GO:0048731) | 4460 | 302 | 181.6 | + | 1.66 | 2.52E-20 | 4.02E-16 |
| neurogenesis (GO:0022008) | 1669 | 152 | 67.96 | + | 2.24 | 1.41E-19 | 1.12E-15 |
| multicellular organism development (GO:0007275) | 5080 | 328 | 206.84 | + | 1.59 | 2.51E-19 | 1.33E-15 |
| generation of neurons (GO:0048699) | 1565 | 145 | 63.72 | + | 2.28 | 2.60E-19 | 1.04E-15 |
| anatomical structure development (GO:0048856) | 5469 | 346 | 222.68 | + | 1.55 | 2.85E-19 | 9.09E-16 |
| nervous system development (GO:0007399) | 2395 | 191 | 97.52 | + | 1.96 | 9.46E-19 | 2.52E-15 |
| regulation of multicellular organismal process (GO:0051239) | 3211 | 233 | 130.74 | + | 1.78 | 2.50E-18 | 5.70E-15 |
| developmental process (GO:0032502) | 5918 | 363 | 240.97 | + | 1.51 | 2.83E-18 | 5.64E-15 |
| biological regulation (GO:0065007) | 12525 | 633 | 509.99 | + | 1.24 | 3.51E-18 | 6.22E-15 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| neuron differentiation (GO:0030182) | 1021 | 107 | 41.57 | + | 2.57 | 1.10E-17 | 1.76E-14 |
| multicellular organismal process (GO:0032501) | 7037 | 410 | 286.53 | + | 1.43 | 1.33E-17 | 1.94E-14 |
| cellular process (GO:0009987) | 15458 | 732 | 629.41 | + | 1.16 | 4.76E-17 | 6.33E-14 |
| Unclassified (UNCLASSIFIED) | 3041 | 46 | 123.82 | - | 0.37 | 8.99E-17 | 1.10E-13 |
| biological_process (GO:0008150) | 17810 | 803 | 725.18 | + | 1.11 | 8.99E-17 | 1.02E-13 |
| animal organ development (GO:0048513) | 3225 | 227 | 131.31 | + | 1.73 | 2.04E-16 | 2.17E-13 |
| cell differentiation (GO:0030154) | 3744 | 251 | 152.45 | + | 1.65 | 7.31E-16 | 7.30E-13 |
| anatomical structure morphogenesis (GO:0009653) | 2181 | 170 | 88.8 | + | 1.91 | 1.23E-15 | 1.16E-12 |
| cellular developmental process (GO:0048869) | 3798 | 252 | 154.64 | + | 1.63 | 2.17E-15 | 1.92E-12 |
| regulation of localization (GO:0032879) | 2838 | 202 | 115.56 | + | 1.75 | 6.47E-15 | 5.44E-12 |
| regulation of biological process (GO:0050789) | 11825 | 592 | 481.48 | + | 1.23 | 2.70E-14 | 2.15E-11 |
| regulation of biological quality (GO:0065008) | 4134 | 264 | 168.33 | + | 1.57 | 3.14E-14 | 2.38E-11 |
| regulation of developmental process (GO:0050793) | 2651 | 188 | 107.94 | + | 1.74 | 1.39E-13 | 1.01E-10 |
| regulation of cellular process (GO:0050794) | 11288 | 567 | 459.62 | + | 1.23 | 2.60E-13 | 1.80E-10 |
| animal organ morphogenesis (GO:0009887) | 973 | 93 | 39.62 | + | 2.35 | 2.99E-13 | 1.99E-10 |
| signaling (GO:0023052) | 5504 | 323 | 224.11 | + | 1.44 | 4.78E-13 | 3.05E-10 |
| regulation of multicellular organismal development (GO:2000026) | 2082 | 155 | 84.77 | + | 1.83 | 1.18E-12 | 7.23E-10 |
| cell communication (GO:0007154) | 5610 | 324 | 228.43 | + | 1.42 | 2.83E-12 | 1.67E-09 |
| cellular response to stimulus (GO:0051716) | 6801 | 374 | 276.92 | + | 1.35 | 1.05E-11 | 5.99E-09 |
| regulation of cell differentiation (GO:0045595) | 1857 | 139 | 75.61 | + | 1.84 | 1.55E-11 | 8.52E-09 |
| response to stimulus (GO:0050896) | 8572 | 449 | 349.03 | + | 1.29 | 1.57E-11 | 8.35E-09 |
| regulation of cell development (GO:0060284) | 966 | 88 | 39.33 | + | 2.24 | 1.62E-11 | 8.37E-09 |
| cellular response to organic substance (GO:0071310) | 2400 | 167 | 97.72 | + | 1.71 | 1.79E-11 | 8.94E-09 |
| response to endogenous stimulus (GO:0009719) | 1512 | 119 | 61.56 | + | 1.93 | 2.74E-11 | 1.32E-08 |
| behavior (GO:0007610) | 600 | 64 | 24.43 | + | 2.62 | 3.18E-11 | 1.49E-08 |
| regulation of neurogenesis (GO:0050767) | 840 | 79 | 34.2 | + | 2.31 | 4.67E-11 | 2.13E-08 |
| positive regulation of multicellular organismal process (GO:0051240) | 1783 | 133 | 72.6 | + | 1.83 | 5.58E-11 | 2.48E-08 |
| neuron development (GO:0048666) | 828 | 78 | 33.71 | + | 2.31 | 6.03E-11 | 2.60E-08 |
| negative regulation of multicellular organismal process (GO:0051241) | 1224 | 102 | 49.84 | + | 2.05 | 6.18E-11 | 2.59E-08 |
| regulation of cell communication (GO:0010646) | 3646 | 227 | 148.46 | + | 1.53 | 6.44E-11 | 2.63E-08 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| regulation of signaling (GO:0023051) | 3686 | 228 | 150.08 | + | 1.52 | 1.05E-10 | 4.20E-08 |
| regulation of nervous system development (GO:0051960) | 952 | 85 | 38.76 | + | 2.19 | 1.10E-10 | 4.27E-08 |
| positive regulation of biological process (GO:0048518) | 6278 | 346 | 255.62 | + | 1.35 | 1.14E-10 | 4.31E-08 |
| signal transduction (GO:0007165) | 5146 | 295 | 209.53 | + | 1.41 | 1.46E-10 | 5.40E-08 |
| positive regulation of cellular process (GO:0048522) | 5725 | 321 | 233.11 | + | 1.38 | 1.63E-10 | 5.90E-08 |
| cell development (GO:0048468) | 1632 | 123 | 66.45 | + | 1.85 | 1.91E-10 | 6.78E-08 |
| central nervous system development (GO:0007417) | 1001 | 87 | 40.76 | + | 2.13 | 1.97E-10 | 6.82E-08 |
| positive regulation of developmental process (GO:0051094) | 1401 | 110 | 57.05 | + | 1.93 | 2.23E-10 | 7.57E-08 |
| regulation of transport (GO:0051049) | 1906 | 137 | 77.61 | + | 1.77 | 3.01E-10 | 1.00E-07 |
| neuron projection development (GO:0031175) | 683 | 67 | 27.81 | + | 2.41 | 3.03E-10 | 9.88E-08 |
| response to organic substance (GO:0010033) | 3033 | 194 | 123.5 | + | 1.57 | 3.19E-10 | 1.02E-07 |
| cellular response to endogenous stimulus (GO:0071495) | 1224 | 99 | 49.84 | + | 1.99 | 4.47E-10 | 1.40E-07 |
| localization (GO:0051179) | 5802 | 321 | 236.24 | + | 1.36 | 6.92E-10 | 2.12E-07 |
| cellular response to chemical stimulus (GO:0070887) | 2961 | 189 | 120.56 | + | 1.57 | 7.59E-10 | 2.29E-07 |
| negative regulation of biological process (GO:0048519) | 5541 | 308 | 225.62 | + | 1.37 | 1.36E-09 | 4.03E-07 |
| regulation of cell population proliferation (GO:0042127) | 1656 | 121 | 67.43 | + | 1.79 | 1.39E-09 | 4.03E-07 |
| negative regulation of developmental process (GO:0051093) | 972 | 83 | 39.58 | + | 2.1 | 1.44E-09 | 4.11E-07 |
| locomotion (GO:0040011) | 1314 | 102 | 53.5 | + | 1.91 | 1.73E-09 | 4.85E-07 |
| positive regulation of cell differentiation (GO:0045597) | 1001 | 83 | 40.76 | + | 2.04 | 4.35E-09 | 1.20E-06 |
| regulation of response to stimulus (GO:0048583) | 4403 | 254 | 179.28 | + | 1.42 | 4.41E-09 | 1.19E-06 |
| tissue development (GO:0009888) | 1789 | 126 | 72.84 | + | 1.73 | 5.00E-09 | 1.33E-06 |
| detection of chemical stimulus involved in sensory perception (GO:0050907) | 483 | 0 | 19.67 | - | < 0.01 | 6.92E-09 | 1.81E-06 |
| cell fate commitment (GO:0045165) | 252 | 34 | 10.26 | + | 3.31 | 8.81E-09 | 2.27E-06 |
| embryonic organ development (GO:0048568) | 447 | 48 | 18.2 | + | 2.64 | 9.85E-09 | 2.49E-06 |
| cell migration (GO:0016477) | 957 | 79 | 38.97 | + | 2.03 | 1.42E-08 | 3.53E-06 |
| negative regulation of neurogenesis (GO:0050768) | 292 | 36 | 11.89 | + | 3.03 | 2.66E-08 | 6.53E-06 |
| neuron projection morphogenesis (GO:0048812) | 494 | 50 | 20.11 | + | 2.49 | 2.84E-08 | 6.87E-06 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| negative regulation of cell development (GO:0010721) | 335 | 39 | 13.64 | + | 2.86 | 2.88E-08 | 6.85E-06 |
| detection of chemical stimulus involved in sensory perception of smell (GO:0050911) | 439 | 0 | 17.87 | - | < 0.01 | 3.28E-08 | 7.71E-06 |
| plasma membrane bounded cell projection morphogenesis (GO:0120039) | 498 | 50 | 20.28 | + | 2.47 | 3.32E-08 | 7.68E-06 |
| central nervous system neuron differentiation (GO:0021953) | 190 | 28 | 7.74 | + | 3.62 | 3.42E-08 | 7.80E-06 |
| cellular response to oxygen-containing compound (GO:1901701) | 1080 | 85 | 43.97 | + | 1.93 | 3.58E-08 | 8.04E-06 |
| cell projection morphogenesis (GO:0048858) | 502 | 50 | 20.44 | + | 2.45 | 3.95E-08 | 8.76E-06 |
| negative regulation of cell differentiation (GO:0045596) | 715 | 63 | 29.11 | + | 2.16 | 4.74E-08 | 1.04E-05 |
| regulation of signal transduction (GO:0009966) | 3160 | 190 | 128.67 | + | 1.48 | 5.07E-08 | 1.09E-05 |
| negative regulation of cellular process (GO:0048523) | 4888 | 270 | 199.03 | + | 1.36 | 5.21E-08 | 1.11E-05 |
| negative regulation of nervous system development (GO:0051961) | 315 | 37 | 12.83 | + | 2.88 | 5.30E-08 | 1.11E-05 |
| regulation of cellular component movement (GO:0051270) | 1027 | 81 | 41.82 | + | 1.94 | 6.58E-08 | 1.36E-05 |
| cell part morphogenesis (GO:0032990) | 524 | 51 | 21.34 | + | 2.39 | 7.44E-08 | 1.52E-05 |
| tube development (GO:0035295) | 859 | 71 | 34.98 | + | 2.03 | 8.40E-08 | 1.70E-05 |
| response to organonitrogen compound (GO:0010243) | 1014 | 80 | 41.29 | + | 1.94 | 8.65E-08 | 1.73E-05 |
| embryo development (GO:0009790) | 1016 | 80 | 41.37 | + | 1.93 | 8.86E-08 | 1.75E-05 |
| regulation of neuron differentiation (GO:0045664) | 672 | 60 | 27.36 | + | 2.19 | 8.97E-08 | 1.75E-05 |
| embryonic morphogenesis (GO:0048598) | 581 | 54 | 23.66 | + | 2.28 | 1.04E-07 | 2.01E-05 |
| cell-cell signaling (GO:0007267) | 1175 | 88 | 47.84 | + | 1.84 | 1.25E-07 | 2.37E-05 |
| movement of cell or subcellular component (GO:0006928) | 1570 | 109 | 63.93 | + | 1.71 | 1.31E-07 | 2.46E-05 |
| cell morphogenesis involved in neuron differentiation (GO:0048667) | 445 | 45 | 18.12 | + | 2.48 | 1.68E-07 | 3.13E-05 |
| regulation of anatomical structure morphogenesis (GO:0022603) | 1107 | 84 | 45.07 | + | 1.86 | 1.87E-07 | 3.44E-05 |
| sensory organ development (GO:0007423) | 560 | 52 | 22.8 | + | 2.28 | 1.99E-07 | 3.61E-05 |
| embryonic organ morphogenesis (GO:0048562) | 305 | 35 | 12.42 | + | 2.82 | 2.02E-07 | 3.62E-05 |
| localization of cell (GO:0051674) | 1078 | 82 | 43.89 | + | 1.87 | 2.04E-07 | 3.62E-05 |
| cell motility (GO:0048870) | 1078 | 82 | 43.89 | + | 1.87 | 2.04E-07 | 3.58E-05 |
| positive regulation of cell development (GO:0010720) | 564 | 52 | 22.96 | + | 2.26 | 2.25E-07 | 3.90E-05 |

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|---|---|---|---|---|---|---|---|
| mesenchymal cell development (GO:0014031) | 81 | 17 | 3.3 | + | 5.15 | 2.35E-07 | 4.03E-05 |
| cellular response to drug (GO:0035690) | 411 | 42 | 16.73 | + | 2.51 | 2.44E-07 | 4.14E-05 |
| response to oxygen-containing compound (GO:1901700) | 1609 | 110 | 65.51 | + | 1.68 | 2.51E-07 | 4.21E-05 |
| response to drug (GO:0042493) | 1030 | 79 | 41.94 | + | 1.88 | 2.62E-07 | 4.35E-05 |
| sensory organ morphogenesis (GO:0090596) | 268 | 32 | 10.91 | + | 2.93 | 3.01E-07 | 4.95E-05 |
| regulation of ion transport (GO:0043269) | 705 | 60 | 28.71 | + | 2.09 | 3.18E-07 | 5.18E-05 |
| cell junction organization (GO:0034330) | 490 | 47 | 19.95 | + | 2.36 | 3.49E-07 | 5.63E-05 |
| response to organic cyclic compound (GO:0014070) | 930 | 73 | 37.87 | + | 1.93 | 3.97E-07 | 6.33E-05 |
| anatomical structure formation involved in morphogenesis (GO:0048646) | 898 | 71 | 36.56 | + | 1.94 | 3.99E-07 | 6.31E-05 |
| negative regulation of cellular component movement (GO:0051271) | 315 | 35 | 12.83 | + | 2.73 | 4.04E-07 | 6.33E-05 |
| cellular component morphogenesis (GO:0032989) | 613 | 54 | 24.96 | + | 2.16 | 4.44E-07 | 6.87E-05 |
| cell morphogenesis (GO:0000902) | 729 | 61 | 29.68 | + | 2.06 | 4.75E-07 | 7.28E-05 |
| neural crest cell differentiation (GO:0014033) | 86 | 17 | 3.5 | + | 4.85 | 4.91E-07 | 7.47E-05 |
| axon development (GO:0061564) | 416 | 42 | 16.94 | + | 2.48 | 5.02E-07 | 7.56E-05 |
| regulation of locomotion (GO:0040012) | 982 | 75 | 39.98 | + | 1.88 | 5.54E-07 | 8.26E-05 |
| response to growth factor (GO:0070848) | 531 | 49 | 21.62 | + | 2.27 | 5.67E-07 | 8.38E-05 |
| positive regulation of cell population proliferation (GO:0008284) | 925 | 72 | 37.66 | + | 1.91 | 5.81E-07 | 8.50E-05 |
| neural crest cell development (GO:0014032) | 77 | 16 | 3.14 | + | 5.1 | 5.94E-07 | 8.62E-05 |
| cellular component organization (GO:0016043) | 5536 | 293 | 225.41 | + | 1.3 | 6.04E-07 | 8.68E-05 |
| ossification (GO:0001503) | 264 | 31 | 10.75 | + | 2.88 | 6.37E-07 | 9.08E-05 |
| response to nitrogen compound (GO:1901698) | 1098 | 81 | 44.71 | + | 1.81 | 8.74E-07 | 1.23E-04 |
| pattern specification process (GO:0007389) | 432 | 42 | 17.59 | + | 2.39 | 8.82E-07 | 1.23E-04 |
| respiratory system development (GO:0060541) | 200 | 26 | 8.14 | + | 3.19 | 9.22E-07 | 1.28E-04 |
| stem cell development (GO:0048864) | 81 | 16 | 3.3 | + | 4.85 | 1.07E-06 | 1.47E-04 |
| response to chemical (GO:0042221) | 4520 | 246 | 184.04 | + | 1.34 | 1.08E-06 | 1.47E-04 |
| neural crest cell migration (GO:0001755) | 52 | 13 | 2.12 | + | 6.14 | 1.15E-06 | 1.55E-04 |
| circulatory system development (GO:0072359) | 876 | 68 | 35.67 | + | 1.91 | 1.18E-06 | 1.59E-04 |
| response to alcohol (GO:0097305) | 245 | 29 | 9.98 | + | 2.91 | 1.26E-06 | 1.67E-04 |
| forebrain development (GO:0030900) | 404 | 40 | 16.45 | + | 2.43 | 1.26E-06 | 1.67E-04 |
| positive regulation of neurogenesis (GO:0050769) | 488 | 45 | 19.87 | + | 2.26 | 1.32E-06 | 1.72E-04 |
| brain development (GO:0007420) | 757 | 61 | 30.82 | + | 1.98 | 1.34E-06 | 1.74E-04 |

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|---|---|---|---|---|---|---|---|
| chemical synaptic transmission (GO:0007268) | 426 | 41 | 17.35 | + | 2.36 | 1.47E-06 | 1.89E-04 |
| anterograde trans-synaptic signaling (GO:0098916) | 426 | 41 | 17.35 | + | 2.36 | 1.47E-06 | 1.87E-04 |
| cellular response to growth factor stimulus (GO:0071363) | 502 | 46 | 20.44 | + | 2.25 | 1.61E-06 | 2.04E-04 |
| negative regulation of response to stimulus (GO:0048585) | 1836 | 118 | 74.76 | + | 1.58 | 1.66E-06 | 2.08E-04 |
| synapse organization (GO:0050808) | 293 | 32 | 11.93 | + | 2.68 | 1.76E-06 | 2.20E-04 |
| modulation of chemical synaptic transmission (GO:0050804) | 459 | 43 | 18.69 | + | 2.3 | 1.79E-06 | 2.22E-04 |
| positive regulation of nervous system development (GO:0051962) | 556 | 49 | 22.64 | + | 2.16 | 1.80E-06 | 2.21E-04 |
| G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (GO:0007187) | 250 | 29 | 10.18 | + | 2.85 | 1.82E-06 | 2.21E-04 |
| regulation of cell motility (GO:2000145) | 942 | 71 | 38.36 | + | 1.85 | 1.82E-06 | 2.20E-04 |
| plasma membrane bounded cell projection organization (GO:0120036) | 1126 | 81 | 45.85 | + | 1.77 | 1.84E-06 | 2.21E-04 |
| regulation of trans-synaptic signaling (GO:0099177) | 460 | 43 | 18.73 | + | 2.3 | 1.86E-06 | 2.21E-04 |
| regionalization (GO:0003002) | 336 | 35 | 13.68 | + | 2.56 | 1.90E-06 | 2.25E-04 |
| muscle system process (GO:0003012) | 295 | 32 | 12.01 | + | 2.66 | 2.01E-06 | 2.36E-04 |
| negative regulation of cell population proliferation (GO:0008285) | 698 | 57 | 28.42 | + | 2.01 | 2.12E-06 | 2.47E-04 |
| positive regulation of cell communication (GO:0010647) | 1943 | 123 | 79.11 | + | 1.55 | 2.17E-06 | 2.51E-04 |
| regulation of system process (GO:0044057) | 592 | 51 | 24.1 | + | 2.12 | 2.19E-06 | 2.52E-04 |
| regulation of ossification (GO:0030278) | 197 | 25 | 8.02 | + | 3.12 | 2.20E-06 | 2.51E-04 |
| trans-synaptic signaling (GO:0099537) | 445 | 42 | 18.12 | + | 2.32 | 2.23E-06 | 2.52E-04 |
| negative regulation of developmental growth (GO:0048640) | 109 | 18 | 4.44 | + | 4.06 | 2.28E-06 | 2.56E-04 |
| axonogenesis (GO:0007409) | 380 | 38 | 15.47 | + | 2.46 | 2.29E-06 | 2.56E-04 |
| cell junction assembly (GO:0034329) | 268 | 30 | 10.91 | + | 2.75 | 2.35E-06 | 2.60E-04 |
| circulatory system process (GO:0003013) | 402 | 39 | 16.37 | + | 2.38 | 2.38E-06 | 2.62E-04 |
| regulation of hormone levels (GO:0010817) | 546 | 48 | 22.23 | + | 2.16 | 2.50E-06 | 2.74E-04 |
| chemotaxis (GO:0006935) | 547 | 48 | 22.27 | + | 2.16 | 2.57E-06 | 2.79E-04 |
| diencephalon development (GO:0021536) | 77 | 15 | 3.14 | + | 4.78 | 2.68E-06 | 2.89E-04 |
| cell projection organization (GO:0030030) | 1171 | 83 | 47.68 | + | 1.74 | 2.69E-06 | 2.88E-04 |
| taxis (GO:0042330) | 549 | 48 | 22.35 | + | 2.15 | 2.71E-06 | 2.89E-04 |

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|---|---|---|---|---|---|---|---|
| synaptic signaling (GO:0099536) | 470 | 43 | 19.14 | + | 2.25 | 2.74E-06 | 2.89E-04 |
| locomotory behavior (GO:0007626) | 200 | 25 | 8.14 | + | 3.07 | 2.81E-06 | 2.95E-04 |
| regulation of cell migration (GO:0030334) | 879 | 67 | 35.79 | + | 1.87 | 2.82E-06 | 2.94E-04 |
| cellular component organization or biogenesis (GO:0071840) | 5754 | 298 | 234.29 | + | 1.27 | 3.22E-06 | 3.34E-04 |
| cellular response to organonitrogen compound (GO:0071417) | 606 | 51 | 24.67 | + | 2.07 | 3.23E-06 | 3.33E-04 |
| blood circulation (GO:0008015) | 392 | 38 | 15.96 | + | 2.38 | 3.33E-06 | 3.41E-04 |
| negative regulation of locomotion (GO:0040013) | 313 | 33 | 12.74 | + | 2.59 | 3.36E-06 | 3.41E-04 |
| system process (GO:0003008) | 1989 | 124 | 80.99 | + | 1.53 | 3.77E-06 | 3.80E-04 |
| head development (GO:0060322) | 802 | 62 | 32.66 | + | 1.9 | 4.01E-06 | 4.02E-04 |
| positive regulation of signaling (GO:0023056) | 1951 | 122 | 79.44 | + | 1.54 | 4.10E-06 | 4.09E-04 |
| positive regulation of gene expression (GO:0010628) | 2038 | 126 | 82.98 | + | 1.52 | 4.73E-06 | 4.69E-04 |
| positive regulation of transcription, DNA-templated (GO:0045893) | 1560 | 102 | 63.52 | + | 1.61 | 4.95E-06 | 4.88E-04 |
| negative regulation of transport (GO:0051051) | 500 | 44 | 20.36 | + | 2.16 | 5.43E-06 | 5.31E-04 |
| detection of stimulus involved in sensory perception (GO:0050906) | 546 | 4 | 22.23 | - | 0.18 | 5.79E-06 | 5.64E-04 |
| regulation of molecular function (GO:0065009) | 3073 | 175 | 125.12 | + | 1.4 | 6.02E-06 | 5.82E-04 |
| cell morphogenesis involved in differentiation (GO:0000904) | 565 | 48 | 23.01 | + | 2.09 | 6.21E-06 | 5.97E-04 |
| positive regulation of signal transduction (GO:0009967) | 1709 | 109 | 69.59 | + | 1.57 | 6.54E-06 | 6.25E-04 |
| positive regulation of molecular function (GO:0044093) | 1832 | 115 | 74.59 | + | 1.54 | 7.05E-06 | 6.70E-04 |
| response to toxic substance (GO:0009636) | 520 | 45 | 21.17 | + | 2.13 | 7.41E-06 | 7.00E-04 |
| regulation of anatomical structure size (GO:0090066) | 521 | 45 | 21.21 | + | 2.12 | 7.61E-06 | 7.14E-04 |
| chemical homeostasis (GO:0048878) | 1131 | 79 | 46.05 | + | 1.72 | 8.11E-06 | 7.57E-04 |
| RNA processing (GO:0006396) | 911 | 13 | 37.09 | - | 0.35 | 8.20E-06 | 7.61E-04 |
| regulation of neurotransmitter levels (GO:0001505) | 359 | 35 | 14.62 | + | 2.39 | 8.29E-06 | 7.65E-04 |
| cellular response to nitrogen compound (GO:1901699) | 663 | 53 | 27 | + | 1.96 | 8.41E-06 | 7.72E-04 |
| ion homeostasis (GO:0050801) | 798 | 61 | 32.49 | + | 1.88 | 8.41E-06 | 7.67E-04 |
| lung development (GO:0030324) | 173 | 22 | 7.04 | + | 3.12 | 8.56E-06 | 7.76E-04 |
| growth (GO:0040007) | 405 | 38 | 16.49 | + | 2.3 | 8.86E-06 | 7.99E-04 |
| regulation of secretion (GO:0051046) | 837 | 63 | 34.08 | + | 1.85 | 8.95E-06 | 8.02E-04 |

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|---|---|---|---|---|---|---|---|
| ameboidal-type cell migration (GO:0001667) | 174 | 22 | 7.08 | + | 3.11 | 9.29E-06 | 8.29E-04 |
| regulation of cellular localization (GO:0060341) | 1026 | 73 | 41.78 | + | 1.75 | 9.56E-06 | 8.48E-04 |
| adult behavior (GO:0030534) | 148 | 20 | 6.03 | + | 3.32 | 9.76E-06 | 8.61E-04 |
| regulation of response to external stimulus (GO:0032101) | 1196 | 82 | 48.7 | + | 1.68 | 9.89E-06 | 8.68E-04 |
| ear development (GO:0043583) | 231 | 26 | 9.41 | + | 2.76 | 9.97E-06 | 8.70E-04 |
| camera-type eye morphogenesis (GO:0048593) | 124 | 18 | 5.05 | + | 3.57 | 1.13E-05 | 9.80E-04 |
| regulation of blood vessel diameter (GO:0097746) | 137 | 19 | 5.58 | + | 3.41 | 1.16E-05 | 1.00E-03 |
| regulation of tube diameter (GO:0035296) | 137 | 19 | 5.58 | + | 3.41 | 1.16E-05 | 9.99E-04 |
| mesenchyme development (GO:0060485) | 219 | 25 | 8.92 | + | 2.8 | 1.18E-05 | 1.01E-03 |
| respiratory tube development (GO:0030323) | 177 | 22 | 7.21 | + | 3.05 | 1.18E-05 | 1.01E-03 |
| homeostatic process (GO:0042592) | 1668 | 106 | 67.92 | + | 1.56 | 1.24E-05 | 1.05E-03 |
| cellular response to alcohol (GO:0097306) | 89 | 15 | 3.62 | + | 4.14 | 1.26E-05 | 1.06E-03 |
| regulation of tube size (GO:0035150) | 138 | 19 | 5.62 | + | 3.38 | 1.28E-05 | 1.07E-03 |
| neuromuscular process (GO:0050905) | 113 | 17 | 4.6 | + | 3.69 | 1.30E-05 | 1.08E-03 |
| synapse assembly (GO:0007416) | 101 | 16 | 4.11 | + | 3.89 | 1.31E-05 | 1.08E-03 |
| response to lipid (GO:0033993) | 869 | 64 | 35.38 | + | 1.81 | 1.32E-05 | 1.08E-03 |
| cellular response to organic cyclic compound (GO:0071407) | 550 | 46 | 22.39 | + | 2.05 | 1.32E-05 | 1.08E-03 |
| heart morphogenesis (GO:0003007) | 250 | 27 | 10.18 | + | 2.65 | 1.34E-05 | 1.09E-03 |
| negative regulation of growth (GO:0045926) | 250 | 27 | 10.18 | + | 2.65 | 1.34E-05 | 1.08E-03 |
| developmental growth (GO:0048589) | 399 | 37 | 16.25 | + | 2.28 | 1.36E-05 | 1.10E-03 |
| positive regulation of macromolecule metabolic process (GO:0010604) | 3417 | 189 | 139.13 | + | 1.36 | 1.43E-05 | 1.15E-03 |
| mesenchymal cell differentiation (GO:0048762) | 153 | 20 | 6.23 | + | 3.21 | 1.51E-05 | 1.21E-03 |
| response to hormone (GO:0009725) | 924 | 67 | 37.62 | + | 1.78 | 1.56E-05 | 1.24E-03 |
| detection of chemical stimulus (GO:0009593) | 519 | 4 | 21.13 | - | 0.19 | 1.69E-05 | 1.33E-03 |
| limb development (GO:0060173) | 182 | 22 | 7.41 | + | 2.97 | 1.75E-05 | 1.38E-03 |
| appendage development (GO:0048736) | 182 | 22 | 7.41 | + | 2.97 | 1.75E-05 | 1.37E-03 |
| sensory perception of smell (GO:0007608) | 468 | 3 | 19.06 | - | 0.16 | 1.77E-05 | 1.38E-03 |
| negative regulation of neuron differentiation (GO:0045665) | 225 | 25 | 9.16 | + | 2.73 | 1.79E-05 | 1.39E-03 |
| tube morphogenesis (GO:0035239) | 659 | 52 | 26.83 | + | 1.94 | 1.80E-05 | 1.39E-03 |
| positive regulation of nitrogen compound metabolic process (GO:0051173) | 3239 | 180 | 131.88 | + | 1.36 | 1.81E-05 | 1.39E-03 |

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|---|---|---|---|---|---|---|---|
| vascular process in circulatory system (GO:0003018) | 169 | 21 | 6.88 | + | 3.05 | 1.86E-05 | 1.42E-03 |
| negative regulation of cell communication (GO:0010648) | 1428 | 93 | 58.14 | + | 1.6 | 1.88E-05 | 1.43E-03 |
| negative regulation of signaling (GO:0023057) | 1432 | 93 | 58.31 | + | 1.59 | 1.94E-05 | 1.46E-03 |
| RNA metabolic process (GO:0016070) | 1702 | 37 | 69.3 | - | 0.53 | 1.94E-05 | 1.46E-03 |
| regulation of ion transmembrane transport (GO:0034765) | 490 | 42 | 19.95 | + | 2.11 | 1.97E-05 | 1.47E-03 |
| regulation of transcription by RNA polymerase II (GO:0006357) | 2264 | 134 | 92.18 | + | 1.45 | 2.04E-05 | 1.52E-03 |
| positive regulation of nucleic acid-templated transcription (GO:1903508) | 1658 | 104 | 67.51 | + | 1.54 | 2.16E-05 | 1.60E-03 |
| positive regulation of RNA biosynthetic process (GO:1902680) | 1659 | 104 | 67.55 | + | 1.54 | 2.18E-05 | 1.61E-03 |
| stem cell differentiation (GO:0048863) | 158 | 20 | 6.43 | + | 3.11 | 2.30E-05 | 1.69E-03 |
| striated muscle tissue development (GO:0014706) | 287 | 29 | 11.69 | + | 2.48 | 2.35E-05 | 1.72E-03 |
| adenylate cyclase-modulating G protein-coupled receptor signaling pathway (GO:0007188) | 215 | 24 | 8.75 | + | 2.74 | 2.45E-05 | 1.78E-03 |
| cyclic-nucleotide-mediated signaling (GO:0019935) | 173 | 21 | 7.04 | + | 2.98 | 2.56E-05 | 1.85E-03 |
| cardiovascular system development (GO:0072358) | 532 | 44 | 21.66 | + | 2.03 | 2.62E-05 | 1.89E-03 |
| regulation of cell death (GO:0010941) | 1706 | 106 | 69.46 | + | 1.53 | 2.72E-05 | 1.95E-03 |
| skeletal system development (GO:0001501) | 502 | 42 | 20.44 | + | 2.05 | 2.76E-05 | 1.98E-03 |
| regulation of cellular component organization (GO:0051128) | 2428 | 141 | 98.86 | + | 1.43 | 2.83E-05 | 2.01E-03 |
| epithelium development (GO:0060429) | 1121 | 76 | 45.64 | + | 1.67 | 3.07E-05 | 2.18E-03 |
| inner ear development (GO:0048839) | 204 | 23 | 8.31 | + | 2.77 | 3.11E-05 | 2.20E-03 |
| positive regulation of cellular metabolic process (GO:0031325) | 3405 | 186 | 138.64 | + | 1.34 | 3.28E-05 | 2.31E-03 |
| regulation of axon guidance (GO:1902667) | 43 | 10 | 1.75 | + | 5.71 | 3.37E-05 | 2.36E-03 |
| regulation of axonogenesis (GO:0050770) | 191 | 22 | 7.78 | + | 2.83 | 3.43E-05 | 2.39E-03 |
| regulation of peptide hormone secretion (GO:0090276) | 220 | 24 | 8.96 | + | 2.68 | 3.43E-05 | 2.38E-03 |
| regulation of transmembrane transport (GO:0034762) | 575 | 46 | 23.41 | + | 1.96 | 3.44E-05 | 2.38E-03 |
| positive regulation of transcription by RNA polymerase II (GO:0045944) | 1224 | 81 | 49.84 | + | 1.63 | 3.45E-05 | 2.37E-03 |
| regulation of developmental growth (GO:0048638) | 342 | 32 | 13.93 | + | 2.3 | 3.64E-05 | 2.49E-03 |
| regulation of gliogenesis (GO:0014013) | 124 | 17 | 5.05 | + | 3.37 | 3.78E-05 | 2.58E-03 |
| ion transport (GO:0006811) | 1342 | 87 | 54.64 | + | 1.59 | 3.84E-05 | 2.61E-03 |

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|---|---|---|---|---|---|---|---|
| heart development (GO:0007507) | 526 | 43 | 21.42 | + | 2.01 | 3.97E-05 | 2.69E-03 |
| positive regulation of metabolic process (GO:0009893) | 3716 | 200 | 151.31 | + | 1.32 | 4.01E-05 | 2.70E-03 |
| axon guidance (GO:0007411) | 265 | 27 | 10.79 | + | 2.5 | 4.22E-05 | 2.83E-03 |
| eye morphogenesis (GO:0048592) | 152 | 19 | 6.19 | + | 3.07 | 4.27E-05 | 2.85E-03 |
| mRNA metabolic process (GO:0016071) | 696 | 9 | 28.34 | - | 0.32 | 4.36E-05 | 2.90E-03 |
| regulation of muscle organ development (GO:0048634) | 139 | 18 | 5.66 | + | 3.18 | 4.45E-05 | 2.95E-03 |
| ear morphogenesis (GO:0042471) | 126 | 17 | 5.13 | + | 3.31 | 4.53E-05 | 2.99E-03 |
| neuron projection guidance (GO:0097485) | 268 | 27 | 10.91 | + | 2.47 | 4.80E-05 | 3.15E-03 |
| negative regulation of axon guidance (GO:1902668) | 27 | 8 | 1.1 | + | 7.28 | 4.88E-05 | 3.19E-03 |
| response to auditory stimulus (GO:0010996) | 27 | 8 | 1.1 | + | 7.28 | 4.88E-05 | 3.18E-03 |
| positive regulation of response to stimulus (GO:0048584) | 2458 | 141 | 100.08 | + | 1.41 | 4.98E-05 | 3.23E-03 |
| cardiac chamber morphogenesis (GO:0003206) | 128 | 17 | 5.21 | + | 3.26 | 5.41E-05 | 3.50E-03 |
| regulation of neuron projection development (GO:0010975) | 516 | 42 | 21.01 | + | 2 | 5.42E-05 | 3.49E-03 |
| response to estradiol (GO:0032355) | 143 | 18 | 5.82 | + | 3.09 | 6.21E-05 | 3.98E-03 |
| intracellular signal transduction (GO:0035556) | 1705 | 104 | 69.42 | + | 1.5 | 6.27E-05 | 4.00E-03 |
| negative regulation of ion transport (GO:0043271) | 157 | 19 | 6.39 | + | 2.97 | 6.34E-05 | 4.03E-03 |
| adenylate cyclase-activating G protein-coupled receptor signaling pathway (GO:0007189) | 130 | 17 | 5.29 | + | 3.21 | 6.44E-05 | 4.08E-03 |
| anterior/posterior pattern specification (GO:0009952) | 216 | 23 | 8.79 | + | 2.62 | 6.95E-05 | 4.38E-03 |
| muscle tissue development (GO:0060537) | 301 | 29 | 12.26 | + | 2.37 | 7.05E-05 | 4.43E-03 |
| regulation of nitrogen compound metabolic process (GO:0051171) | 5891 | 294 | 239.87 | + | 1.23 | 7.47E-05 | 4.68E-03 |
| regulation of cation channel activity (GO:2001257) | 188 | 21 | 7.65 | + | 2.74 | 7.65E-05 | 4.77E-03 |
| inner ear morphogenesis (GO:0042472) | 106 | 15 | 4.32 | + | 3.48 | 7.73E-05 | 4.80E-03 |
| muscle contraction (GO:0006936) | 246 | 25 | 10.02 | + | 2.5 | 8.72E-05 | 5.40E-03 |
| multicellular organismal response to stress (GO:0033555) | 71 | 12 | 2.89 | + | 4.15 | 8.96E-05 | 5.52E-03 |
| vasculature development (GO:0001944) | 522 | 42 | 21.25 | + | 1.98 | 9.25E-05 | 5.68E-03 |
| regulation of membrane potential (GO:0042391) | 441 | 37 | 17.96 | + | 2.06 | 1.01E-04 | 6.20E-03 |
| regulation of cell morphogenesis involved in differentiation (GO:0010769) | 313 | 29 | 12.74 | + | 2.28 | 1.02E-04 | 6.20E-03 |
| regulation of primary metabolic process (GO:0080090) | 6077 | 301 | 247.44 | + | 1.22 | 1.02E-04 | 6.18E-03 |

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|---|---|---|---|---|---|---|---|
| response to external stimulus (GO:0009605) | 2477 | 140 | 100.86 | + | 1.39 | 1.04E-04 | 6.29E-03 |
| cell surface receptor signaling pathway (GO:0007166) | 2493 | 141 | 101.51 | + | 1.39 | 1.08E-04 | 6.50E-03 |
| blood vessel development (GO:0001568) | 499 | 40 | 20.32 | + | 1.97 | 1.09E-04 | 6.54E-03 |
| negative regulation of response to external stimulus (GO:0032102) | 565 | 44 | 23.01 | + | 1.91 | 1.10E-04 | 6.55E-03 |
| tissue morphogenesis (GO:0048729) | 568 | 44 | 23.13 | + | 1.9 | 1.15E-04 | 6.87E-03 |
| regulation of secretion by cell (GO:1903530) | 783 | 56 | 31.88 | + | 1.76 | 1.17E-04 | 6.97E-03 |
| protein complex oligomerization (GO:0051259) | 235 | 24 | 9.57 | + | 2.51 | 1.19E-04 | 7.04E-03 |
| sensory perception of chemical stimulus (GO:0007606) | 540 | 6 | 21.99 | - | 0.27 | 1.21E-04 | 7.11E-03 |
| positive regulation of blood circulation (GO:1903524) | 74 | 12 | 3.01 | + | 3.98 | 1.27E-04 | 7.46E-03 |
| regulation of ion transmembrane transporter activity (GO:0032412) | 272 | 26 | 11.08 | + | 2.35 | 1.30E-04 | 7.61E-03 |
| endocrine system development (GO:0035270) | 125 | 16 | 5.09 | + | 3.14 | 1.31E-04 | 7.64E-03 |
| positive regulation of cellular biosynthetic process (GO:0031328) | 2027 | 118 | 82.53 | + | 1.43 | 1.31E-04 | 7.63E-03 |
| spinal cord development (GO:0021510) | 112 | 15 | 4.56 | + | 3.29 | 1.34E-04 | 7.78E-03 |
| regulation of cellular metabolic process (GO:0031323) | 6284 | 309 | 255.87 | + | 1.21 | 1.38E-04 | 7.95E-03 |
| regulation of apoptotic process (GO:0042981) | 1557 | 95 | 63.4 | + | 1.5 | 1.57E-04 | 8.99E-03 |
| regulation of metabolic process (GO:0019222) | 6772 | 329 | 275.74 | + | 1.19 | 1.62E-04 | 9.28E-03 |
| positive regulation of RNA metabolic process (GO:0051254) | 1748 | 104 | 71.17 | + | 1.46 | 1.63E-04 | 9.28E-03 |
| negative regulation of gliogenesis (GO:0014014) | 43 | 9 | 1.75 | + | 5.14 | 1.67E-04 | 9.48E-03 |
| pituitary gland development (GO:0021983) | 43 | 9 | 1.75 | + | 5.14 | 1.67E-04 | 9.45E-03 |
| positive regulation of locomotion (GO:0040017) | 562 | 43 | 22.88 | + | 1.88 | 1.68E-04 | 9.50E-03 |
| skeletal system morphogenesis (GO:0048705) | 244 | 24 | 9.94 | + | 2.42 | 1.71E-04 | 9.62E-03 |
| tissue regeneration (GO:0042246) | 65 | 11 | 2.65 | + | 4.16 | 1.73E-04 | 9.68E-03 |
| cardiac chamber development (GO:0003205) | 171 | 19 | 6.96 | + | 2.73 | 1.76E-04 | 9.81E-03 |
| cell-cell adhesion (GO:0098609) | 505 | 40 | 20.56 | + | 1.95 | 1.79E-04 | 9.95E-03 |
| regulation of blood circulation (GO:1903522) | 290 | 27 | 11.81 | + | 2.29 | 1.79E-04 | 9.93E-03 |
| regulation of insulin secretion (GO:0050796) | 186 | 20 | 7.57 | + | 2.64 | 1.79E-04 | 9.90E-03 |
| positive regulation of biosynthetic process (GO:0009891) | 2059 | 119 | 83.84 | + | 1.42 | 1.83E-04 | 1.01E-02 |
| regulation of cell morphogenesis (GO:0022604) | 512 | 40 | 20.85 | + | 1.92 | 2.01E-04 | 1.10E-02 |

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|---|---|---|---|---|---|---|---|
| regulation of cytosolic calcium ion concentration (GO:0051480) | 342 | 30 | 13.93 | + | 2.15 | 2.02E-04 | 1.10E-02 |
| response to wounding (GO:0009611) | 579 | 44 | 23.58 | + | 1.87 | 2.03E-04 | 1.10E-02 |
| regulation of synaptic vesicle cycle (GO:0098693) | 118 | 15 | 4.8 | + | 3.12 | 2.25E-04 | 1.22E-02 |
| regulation of programmed cell death (GO:0043067) | 1579 | 95 | 64.29 | + | 1.48 | 2.28E-04 | 1.23E-02 |
| rhythmic behavior (GO:0007622) | 26 | 7 | 1.06 | + | 6.61 | 2.40E-04 | 1.29E-02 |
| regulation of macromolecule metabolic process (GO:0060255) | 6215 | 304 | 253.06 | + | 1.2 | 2.42E-04 | 1.30E-02 |
| regulation of cell projection organization (GO:0031344) | 700 | 50 | 28.5 | + | 1.75 | 2.43E-04 | 1.30E-02 |
| positive regulation of macromolecule biosynthetic process (GO:0010557) | 1934 | 112 | 78.75 | + | 1.42 | 2.48E-04 | 1.32E-02 |
| regulation of retinal ganglion cell axon guidance (GO:0090259) | 5 | 4 | 0.2 | + | 19.65 | 2.50E-04 | 1.33E-02 |
| epoxide metabolic process (GO:0097176) | 5 | 4 | 0.2 | + | 19.65 | 2.50E-04 | 1.33E-02 |
| regulation of transcription, DNA-templated (GO:0006355) | 3469 | 183 | 141.25 | + | 1.3 | 2.58E-04 | 1.36E-02 |
| regulation of transmembrane transporter activity (GO:0022898) | 281 | 26 | 11.44 | + | 2.27 | 2.59E-04 | 1.36E-02 |
| negative regulation of chemotaxis (GO:0050922) | 57 | 10 | 2.32 | + | 4.31 | 2.62E-04 | 1.37E-02 |
| negative regulation of cell motility (GO:2000146) | 282 | 26 | 11.48 | + | 2.26 | 2.67E-04 | 1.40E-02 |
| positive regulation of neuron differentiation (GO:0045666) | 382 | 32 | 15.55 | + | 2.06 | 2.69E-04 | 1.40E-02 |
| response to abiotic stimulus (GO:0009628) | 1165 | 74 | 47.44 | + | 1.56 | 2.76E-04 | 1.43E-02 |
| regulation of nucleic acid-templated transcription (GO:1903506) | 3536 | 186 | 143.98 | + | 1.29 | 2.84E-04 | 1.47E-02 |
| cAMP-mediated signaling (GO:0019933) | 149 | 17 | 6.07 | + | 2.8 | 2.86E-04 | 1.48E-02 |
| regulation of RNA biosynthetic process (GO:2001141) | 3541 | 186 | 144.18 | + | 1.29 | 2.88E-04 | 1.48E-02 |
| positive regulation of nucleobase-containing compound metabolic process (GO:0045935) | 1914 | 111 | 77.93 | + | 1.42 | 2.90E-04 | 1.49E-02 |
| regulation of striated muscle tissue development (GO:0016202) | 135 | 16 | 5.5 | + | 2.91 | 2.90E-04 | 1.49E-02 |
| cellular chemical homeostasis (GO:0055082) | 762 | 53 | 31.03 | + | 1.71 | 2.99E-04 | 1.52E-02 |
| inorganic ion homeostasis (GO:0098771) | 726 | 51 | 29.56 | + | 1.73 | 3.11E-04 | 1.58E-02 |
| ncRNA metabolic process (GO:0034660) | 515 | 6 | 20.97 | - | 0.29 | 3.24E-04 | 1.64E-02 |
| regulation of plasma membrane bounded cell projection organization (GO:0120035) | 691 | 49 | 28.14 | + | 1.74 | 3.26E-04 | 1.65E-02 |
| negative regulation of cell migration (GO:0030336) | 267 | 25 | 10.87 | + | 2.3 | 3.27E-04 | 1.65E-02 |

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|---|---|---|---|---|---|---|---|
| central nervous system neuron development (GO:0021954) | 83 | 12 | 3.38 | + | 3.55 | 3.30E-04 | 1.66E-02 |
| wound healing (GO:0042060) | 485 | 38 | 19.75 | + | 1.92 | 3.31E-04 | 1.66E-02 |
| export from cell (GO:0140352) | 1049 | 68 | 42.71 | + | 1.59 | 3.33E-04 | 1.66E-02 |
| negative regulation of axonogenesis (GO:0050771) | 71 | 11 | 2.89 | + | 3.8 | 3.42E-04 | 1.70E-02 |
| second-messenger-mediated signaling (GO:0019932) | 339 | 29 | 13.8 | + | 2.1 | 3.49E-04 | 1.73E-02 |
| negative regulation of neuron projection development (GO:0010977) | 152 | 17 | 6.19 | + | 2.75 | 3.53E-04 | 1.74E-02 |
| regulation of muscle tissue development (GO:1901861) | 138 | 16 | 5.62 | + | 2.85 | 3.63E-04 | 1.79E-02 |
| dendrite morphogenesis (GO:0048813) | 60 | 10 | 2.44 | + | 4.09 | 3.77E-04 | 1.85E-02 |
| negative regulation of multicellular organism growth (GO:0040015) | 12 | 5 | 0.49 | + | 10.23 | 3.78E-04 | 1.85E-02 |
| cellular homeostasis (GO:0019725) | 924 | 61 | 37.62 | + | 1.62 | 3.86E-04 | 1.88E-02 |
| cellular response to lipid (GO:0071396) | 529 | 40 | 21.54 | + | 1.86 | 3.88E-04 | 1.89E-02 |
| cation homeostasis (GO:0055080) | 714 | 50 | 29.07 | + | 1.72 | 3.96E-04 | 1.92E-02 |
| regulation of hormone secretion (GO:0046883) | 274 | 25 | 11.16 | + | 2.24 | 3.99E-04 | 1.93E-02 |
| regulation of transporter activity (GO:0032409) | 293 | 26 | 11.93 | + | 2.18 | 4.00E-04 | 1.93E-02 |
| positive regulation of catalytic activity (GO:0043085) | 1477 | 89 | 60.14 | + | 1.48 | 4.09E-04 | 1.97E-02 |
| outflow tract morphogenesis (GO:0003151) | 73 | 11 | 2.97 | + | 3.7 | 4.23E-04 | 2.03E-02 |
| morphogenesis of an epithelium (GO:0002009) | 440 | 35 | 17.92 | + | 1.95 | 4.25E-04 | 2.03E-02 |
| blood vessel morphogenesis (GO:0048514) | 410 | 33 | 16.69 | + | 1.98 | 4.36E-04 | 2.08E-02 |
| gliogenesis (GO:0042063) | 230 | 22 | 9.37 | + | 2.35 | 4.36E-04 | 2.07E-02 |
| negative regulation of cell morphogenesis involved in differentiation (GO:0010771) | 99 | 13 | 4.03 | + | 3.22 | 4.38E-04 | 2.07E-02 |
| rhythmic process (GO:0048511) | 277 | 25 | 11.28 | + | 2.22 | 4.42E-04 | 2.09E-02 |
| bone mineralization (GO:0030282) | 50 | 9 | 2.04 | + | 4.42 | 4.47E-04 | 2.10E-02 |
| regulation of growth (GO:0040008) | 684 | 48 | 27.85 | + | 1.72 | 4.52E-04 | 2.12E-02 |
| cardiac septum morphogenesis (GO:0060411) | 74 | 11 | 3.01 | + | 3.65 | 4.68E-04 | 2.19E-02 |
| response to steroid hormone (GO:0048545) | 329 | 28 | 13.4 | + | 2.09 | 4.80E-04 | 2.24E-02 |
| cognition (GO:0050890) | 307 | 27 | 12.5 | + | 2.16 | 4.81E-04 | 2.24E-02 |
| small molecule metabolic process (GO:0044281) | 1718 | 100 | 69.95 | + | 1.43 | 4.91E-04 | 2.28E-02 |
| cellular ion homeostasis (GO:0006873) | 660 | 47 | 26.87 | + | 1.75 | 4.91E-04 | 2.27E-02 |
| regulation of nucleobase-containing compound metabolic process (GO:0019219) | 4065 | 208 | 165.52 | + | 1.26 | 4.95E-04 | 2.28E-02 |

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|---|---|---|---|---|---|---|---|
| embryonic limb morphogenesis (GO:0030326) | 128 | 15 | 5.21 | + | 2.88 | 4.95E-04 | 2.28E-02 |
| embryonic appendage morphogenesis (GO:0035113) | 128 | 15 | 5.21 | + | 2.88 | 4.95E-04 | 2.27E-02 |
| regulation of animal organ morphogenesis (GO:2000027) | 260 | 24 | 10.59 | + | 2.27 | 4.97E-04 | 2.27E-02 |
| activation of adenylate cyclase activity (GO:0007190) | 40 | 8 | 1.63 | + | 4.91 | 5.00E-04 | 2.28E-02 |
| negative regulation of signal transduction (GO:0009968) | 1284 | 79 | 52.28 | + | 1.51 | 5.00E-04 | 2.27E-02 |
| porphyrin-containing compound metabolic process (GO:0006778) | 51 | 9 | 2.08 | + | 4.33 | 5.08E-04 | 2.30E-02 |
| intermediate filament-based process (GO:0045103) | 51 | 9 | 2.08 | + | 4.33 | 5.08E-04 | 2.29E-02 |
| epithelial tube morphogenesis (GO:0060562) | 311 | 27 | 12.66 | + | 2.13 | 5.26E-04 | 2.37E-02 |
| transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0007178) | 198 | 20 | 8.06 | + | 2.48 | 5.38E-04 | 2.42E-02 |
| gene expression (GO:0010467) | 2043 | 54 | 83.19 | - | 0.65 | 5.72E-04 | 2.56E-02 |
| regulation of bone mineralization (GO:0030500) | 76 | 11 | 3.09 | + | 3.55 | 5.73E-04 | 2.56E-02 |
| metal ion homeostasis (GO:0055065) | 634 | 45 | 25.81 | + | 1.74 | 5.73E-04 | 2.55E-02 |
| skeletal muscle tissue development (GO:0007519) | 130 | 15 | 5.29 | + | 2.83 | 5.73E-04 | 2.55E-02 |
| smooth muscle contraction (GO:0006939) | 52 | 9 | 2.12 | + | 4.25 | 5.75E-04 | 2.55E-02 |
| feeding behavior (GO:0007631) | 89 | 12 | 3.62 | + | 3.31 | 5.81E-04 | 2.57E-02 |
| response to ketone (GO:1901654) | 201 | 20 | 8.18 | + | 2.44 | 5.93E-04 | 2.62E-02 |
| response to pain (GO:0048265) | 31 | 7 | 1.26 | + | 5.55 | 5.98E-04 | 2.63E-02 |
| positive regulation of cellular component movement (GO:0051272) | 563 | 41 | 22.92 | + | 1.79 | 6.05E-04 | 2.65E-02 |
| cellular response to toxic substance (GO:0097237) | 220 | 21 | 8.96 | + | 2.34 | 6.08E-04 | 2.66E-02 |
| enzyme linked receptor protein signaling pathway (GO:0007167) | 726 | 50 | 29.56 | + | 1.69 | 6.19E-04 | 2.70E-02 |
| camera-type eye development (GO:0043010) | 317 | 27 | 12.91 | + | 2.09 | 6.21E-04 | 2.70E-02 |
| regulation of mitochondrial depolarization (GO:0051900) | 22 | 6 | 0.9 | + | 6.7 | 6.34E-04 | 2.75E-02 |
| positive regulation of hydrolase activity (GO:0051345) | 770 | 52 | 31.35 | + | 1.66 | 6.47E-04 | 2.80E-02 |
| skeletal muscle cell differentiation (GO:0035914) | 53 | 9 | 2.16 | + | 4.17 | 6.50E-04 | 2.80E-02 |
| regeneration (GO:0031099) | 162 | 17 | 6.6 | + | 2.58 | 6.85E-04 | 2.95E-02 |
| regulation of RNA metabolic process (GO:0051252) | 3807 | 195 | 155.01 | + | 1.26 | 7.01E-04 | 3.01E-02 |

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|---|---|---|---|---|---|---|---|
| porphyrin-containing compound biosynthetic process (GO:0006779) | 32 | 7 | 1.3 | + | 5.37 | 7.04E-04 | 3.01E-02 |
| transport (GO:0006810) | 4550 | 228 | 185.26 | + | 1.23 | 7.13E-04 | 3.04E-02 |
| cellular response to BMP stimulus (GO:0071773) | 105 | 13 | 4.28 | + | 3.04 | 7.24E-04 | 3.08E-02 |
| response to BMP (GO:0071772) | 105 | 13 | 4.28 | + | 3.04 | 7.24E-04 | 3.07E-02 |
| positive regulation of cell motility (GO:2000147) | 547 | 40 | 22.27 | + | 1.8 | 7.24E-04 | 3.07E-02 |
| developmental growth involved in morphogenesis (GO:0060560) | 119 | 14 | 4.85 | + | 2.89 | 7.27E-04 | 3.07E-02 |
| regulation of muscle contraction (GO:0006937) | 163 | 17 | 6.64 | + | 2.56 | 7.30E-04 | 3.07E-02 |
| biological adhesion (GO:0022610) | 930 | 60 | 37.87 | + | 1.58 | 7.52E-04 | 3.16E-02 |
| regulation of voltage-gated calcium channel activity (GO:1901385) | 43 | 8 | 1.75 | + | 4.57 | 7.60E-04 | 3.19E-02 |
| connective tissue development (GO:0061448) | 225 | 21 | 9.16 | + | 2.29 | 7.63E-04 | 3.19E-02 |
| cellular response to prostaglandin stimulus (GO:0071379) | 23 | 6 | 0.94 | + | 6.41 | 7.73E-04 | 3.22E-02 |
| response to stress (GO:0006950) | 3635 | 187 | 148.01 | + | 1.26 | 7.83E-04 | 3.25E-02 |
| mRNA processing (GO:0006397) | 477 | 6 | 19.42 | - | 0.31 | 7.91E-04 | 3.28E-02 |
| regulation of gene expression (GO:0010468) | 4494 | 225 | 182.98 | + | 1.23 | 7.91E-04 | 3.27E-02 |
| gland development (GO:0048732) | 421 | 33 | 17.14 | + | 1.93 | 8.01E-04 | 3.30E-02 |
| cellular response to nutrient (GO:0031670) | 67 | 10 | 2.73 | + | 3.67 | 8.15E-04 | 3.35E-02 |
| response to ethanol (GO:0045471) | 135 | 15 | 5.5 | + | 2.73 | 8.17E-04 | 3.35E-02 |
| tetrapyrrole biosynthetic process (GO:0033014) | 33 | 7 | 1.34 | + | 5.21 | 8.25E-04 | 3.38E-02 |
| response to prostaglandin (GO:0034694) | 33 | 7 | 1.34 | + | 5.21 | 8.25E-04 | 3.37E-02 |
| postsynapse organization (GO:0099173) | 93 | 12 | 3.79 | + | 3.17 | 8.26E-04 | 3.36E-02 |
| regulation of integrin activation (GO:0033623) | 15 | 5 | 0.61 | + | 8.19 | 8.60E-04 | 3.49E-02 |
| negative regulation of glial cell proliferation (GO:0060253) | 15 | 5 | 0.61 | + | 8.19 | 8.60E-04 | 3.48E-02 |
| mechanosensory behavior (GO:0007638) | 15 | 5 | 0.61 | + | 8.19 | 8.60E-04 | 3.48E-02 |
| regulation of cardiac muscle cell proliferation (GO:0060043) | 44 | 8 | 1.79 | + | 4.47 | 8.68E-04 | 3.50E-02 |
| limb morphogenesis (GO:0035108) | 151 | 16 | 6.15 | + | 2.6 | 8.86E-04 | 3.56E-02 |
| appendage morphogenesis (GO:0035107) | 151 | 16 | 6.15 | + | 2.6 | 8.86E-04 | 3.55E-02 |
| neuron fate commitment (GO:0048663) | 68 | 10 | 2.77 | + | 3.61 | 9.03E-04 | 3.61E-02 |
| nucleic acid metabolic process (GO:0090304) | 2303 | 64 | 93.77 | - | 0.68 | 9.05E-04 | 3.61E-02 |
| cellular metal ion homeostasis (GO:0006875) | 570 | 41 | 23.21 | + | 1.77 | 9.15E-04 | 3.64E-02 |
| response to catecholamine (GO:0071869) | 108 | 13 | 4.4 | + | 2.96 | 9.17E-04 | 3.64E-02 |

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|---|---|---|---|---|---|---|---|
| response to monoamine (GO:0071867) | 108 | 13 | 4.4 | + | 2.96 | 9.17E-04 | 3.63E-02 |
| trabecula formation (GO:0060343) | 24 | 6 | 0.98 | + | 6.14 | 9.35E-04 | 3.69E-02 |
| phosphorus metabolic process (GO:0006793) | 2177 | 120 | 88.64 | + | 1.35 | 9.43E-04 | 3.71E-02 |
| neuron fate specification (GO:0048665) | 34 | 7 | 1.38 | + | 5.06 | 9.62E-04 | 3.78E-02 |
| regulation of inflammatory response (GO:0050727) | 537 | 39 | 21.87 | + | 1.78 | 9.63E-04 | 3.78E-02 |
| segmentation (GO:0035282) | 95 | 12 | 3.87 | + | 3.1 | 9.77E-04 | 3.82E-02 |
| response to nutrient levels (GO:0031667) | 538 | 39 | 21.91 | + | 1.78 | 9.78E-04 | 3.82E-02 |
| reproductive structure development (GO:0048608) | 432 | 33 | 17.59 | + | 1.88 | 9.81E-04 | 3.82E-02 |
| regulation of epithelial cell proliferation (GO:0050678) | 343 | 28 | 13.97 | + | 2 | 9.85E-04 | 3.83E-02 |
| lung morphogenesis (GO:0060425) | 45 | 8 | 1.83 | + | 4.37 | 9.88E-04 | 3.83E-02 |
| regulation of monooxygenase activity (GO:0032768) | 57 | 9 | 2.32 | + | 3.88 | 1.03E-03 | 3.99E-02 |
| positive regulation of blood vessel diameter (GO:0097755) | 57 | 9 | 2.32 | + | 3.88 | 1.03E-03 | 3.98E-02 |
| neuron migration (GO:0001764) | 124 | 14 | 5.05 | + | 2.77 | 1.05E-03 | 4.02E-02 |
| regulation of neurotransmitter secretion (GO:0046928) | 110 | 13 | 4.48 | + | 2.9 | 1.07E-03 | 4.10E-02 |
| skeletal muscle organ development (GO:0060538) | 139 | 15 | 5.66 | + | 2.65 | 1.07E-03 | 4.10E-02 |
| establishment of localization (GO:0051234) | 4680 | 232 | 190.56 | + | 1.22 | 1.09E-03 | 4.16E-02 |
| cardiac muscle tissue regeneration (GO:0061026) | 3 | 3 | 0.12 | + | 24.56 | 1.09E-03 | 4.16E-02 |
| neuromuscular process controlling posture (GO:0050884) | 16 | 5 | 0.65 | + | 7.67 | 1.09E-03 | 4.15E-02 |
| coronary vasculature morphogenesis (GO:0060977) | 16 | 5 | 0.65 | + | 7.67 | 1.09E-03 | 4.14E-02 |
| response to ATP (GO:0033198) | 35 | 7 | 1.43 | + | 4.91 | 1.12E-03 | 4.22E-02 |
| response to progesterone (GO:0032570) | 46 | 8 | 1.87 | + | 4.27 | 1.12E-03 | 4.23E-02 |
| coronary vasculature development (GO:0060976) | 46 | 8 | 1.87 | + | 4.27 | 1.12E-03 | 4.22E-02 |
| negative regulation of amine transport (GO:0051953) | 25 | 6 | 1.02 | + | 5.89 | 1.12E-03 | 4.21E-02 |
| negative regulation of axon extension involved in axon guidance (GO:0048843) | 25 | 6 | 1.02 | + | 5.89 | 1.12E-03 | 4.20E-02 |
| circadian behavior (GO:0048512) | 25 | 6 | 1.02 | + | 5.89 | 1.12E-03 | 4.19E-02 |
| response to prostaglandin E (GO:0034695) | 25 | 6 | 1.02 | + | 5.89 | 1.12E-03 | 4.18E-02 |
| glial cell differentiation (GO:0010001) | 179 | 18 | 7.29 | + | 2.47 | 1.13E-03 | 4.22E-02 |
| learning or memory (GO:0007611) | 265 | 23 | 10.79 | + | 2.13 | 1.14E-03 | 4.22E-02 |

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|---|---|---|---|---|---|---|---|
| cell differentiation in spinal cord (GO:0021515) | 58 | 9 | 2.36 | + | 3.81 | 1.15E-03 | 4.26E-02 |
| cardiac septum development (GO:0003279) | 111 | 13 | 4.52 | + | 2.88 | 1.15E-03 | 4.26E-02 |
| secretion (GO:0046903) | 1119 | 69 | 45.56 | + | 1.51 | 1.16E-03 | 4.27E-02 |
| muscle structure development (GO:0061061) | 483 | 36 | 19.67 | + | 1.83 | 1.16E-03 | 4.28E-02 |
| negative regulation of cell projection organization (GO:0031345) | 181 | 18 | 7.37 | + | 2.44 | 1.20E-03 | 4.41E-02 |
| regulation of synaptic transmission, glutamatergic (GO:0051966) | 71 | 10 | 2.89 | + | 3.46 | 1.21E-03 | 4.44E-02 |
| cell adhesion (GO:0007155) | 924 | 59 | 37.62 | + | 1.57 | 1.29E-03 | 4.70E-02 |
| response to purine-containing compound (GO:0014074) | 157 | 16 | 6.39 | + | 2.5 | 1.29E-03 | 4.70E-02 |
| regulation of cellular biosynthetic process (GO:0031326) | 4217 | 211 | 171.71 | + | 1.23 | 1.30E-03 | 4.71E-02 |
| response to organophosphorus (GO:0046683) | 142 | 15 | 5.78 | + | 2.59 | 1.30E-03 | 4.72E-02 |
| regulation of cytokine production (GO:0001817) | 734 | 49 | 29.89 | + | 1.64 | 1.31E-03 | 4.73E-02 |
| phosphate-containing compound metabolic process (GO:0006796) | 2150 | 118 | 87.54 | + | 1.35 | 1.31E-03 | 4.75E-02 |
| regulation of sprouting angiogenesis (GO:1903670) | 72 | 10 | 2.93 | + | 3.41 | 1.33E-03 | 4.81E-02 |
| adenylate cyclase-activating adrenergic receptor signaling pathway (GO:0071880) | 26 | 6 | 1.06 | + | 5.67 | 1.34E-03 | 4.80E-02 |
| cellular response to prostaglandin E stimulus (GO:0071380) | 17 | 5 | 0.69 | + | 7.22 | 1.37E-03 | 4.91E-02 |
| Analysis Type: | PANTHER Overrepresentation Test (Released 20200407) | | | | | | |
| Annotation Version and Release Date: | GO Ontology database DOI: 10.5281/zenodo.3727280 Released 2020-03-23 | | | | | | |
| Analyzed List: | DeepMage_genes (Homo sapiens) | | | | | | |
| Reference List: | Homo sapiens (all genes in database) | | | | | | |
| Test Type: | FISHER | | | | | | |
| Correction: | FDR | | | | | | |

**Supplementary Table 4.** DeepMAge outperformed both the 71 CpG and the 89 CpG clocks published by Hannum et al. in 2013. The baseline is defined as the mean age assignment.

| GEO | MAE, years | | | | RMSE, years | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Accession | 71 CpG | 89 CpG | DeepMAge | Baseline | 71 CpG | 89 CpG | DeepMAge | Baseline | N |
| GSE102177 | 3.87 | 7.59 | 1.98 | 2.22 | 4.56 | 8.03 | 2.23 | 2.63 | 36 |
| GSE103911 | 16.31 | 31.25 | 7.43 | 8.24 | 20.44 | 33.99 | 9.16 | 10.66 | 65 |
| GSE105123 | 4.4 | 16.53 | 2.32 | 1.14 | 5.78 | 17.1 | 2.87 | 1.34 | 107 |
| GSE107459 | 5.7 | 19.46 | 2.23 | 3.63 | 7.09 | 20.51 | 2.79 | 4.38 | 127 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| GSE107737 | 8.19 | 15.9 | 3.87 | 2.88 | 9.99 | 17.12 | 4.96 | 3.32 | 24 |
| GSE112696 | 6.89 | 14.64 | 4.42 | 2.33 | 7.23 | 15.14 | 5.17 | 2.94 | 12 |
| GSE34639 | 0.98 | 1 | 1.79 | 0.5 | 1.1 | 1.12 | 2.06 | 0.5 | 48 |
| GSE59065 | 8.31 | 19.49 | 5.93 | 23.46 | 10.26 | 21.11 | 8.14 | 23.63 | 295 |
| GSE61496 | 18.14 | 22.85 | 2.77 | 15.07 | 22.01 | 27.23 | 3.7 | 15.42 | 310 |
| GSE87582 | 7.63 | 17.16 | 5.4 | 4.53 | 9.46 | 19.41 | 6.04 | 5.67 | 21 |
| GSE87640 | 14.12 | 19.35 | 4.53 | 9.78 | 17.85 | 23.52 | 6.54 | 11.9 | 240 |
| GSE98876 | 10.45 | 21.13 | 3.49 | 7.99 | 14.13 | 24.48 | 4.64 | 9.98 | 71 |
| GSE99624 | 8.89 | 19.71 | 4.12 | 8.74 | 11.41 | 22.05 | 5.43 | 9.81 | 48 |
| Total | 11.05 | 19.54 | 3.97 | 18.62 | 15.12 | 22.96 | 5.75 | 21.35 | 1404 |

GEO = Gene Expression Omnibus; N = Number of samples in the corresponding GEO project; MAE = Mean absolute error; RMSE = Root mean square error.

**Supplementary Table 5.** Linear regression coefficients for the model produced by replicating Horvath's training protocol. Ranks are based on absolute coefficient value (higher importance features come first).

| Rank | CpG_site | coefficient | Rank | CpG_site | coefficient | Rank | CpG_site | coefficient | Rank | CpG_site | coefficient |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | cg21801378 | 0.983653 | 31 | cg19885761 | 0.355402 | 61 | cg05675373 | 0.237629 | 91 | cg07845392 | 0.176361 |
| 2 | cg02479575 | 0.939384 | 32 | cg04836038 | 0.354184 | 62 | cg16168311 | -0.233731 | 92 | cg19759064 | -0.175474 |
| 3 | cg00059225 | 0.816305 | 33 | cg27015931 | -0.348080 | 63 | cg14918082 | 0.233498 | 93 | cg05724065 | -0.175079 |
| 4 | cg22736354 | 0.793852 | 34 | cg00630583 | -0.342940 | 64 | cg11017269 | -0.232564 | 94 | cg08668790 | 0.172569 |
| 5 | cg01580888 | 0.681322 | 35 | cg17861230 | 0.340669 | 65 | cg04587910 | -0.231216 | 95 | cg23320649 | -0.172294 |
| 6 | cg06493994 | 0.582153 | 36 | cg17471102 | -0.337370 | 66 | cg02840794 | -0.229842 | 96 | cg25713185 | 0.170709 |
| 7 | cg19761273 | -0.568068 | 37 | cg09118625 | 0.332719 | 67 | cg06836772 | -0.223745 | 97 | cg17706173 | 0.169717 |
| 8 | cg27225570 | -0.566827 | 38 | cg13663218 | -0.329015 | 68 | cg20392764 | 0.220477 | 98 | cg15957394 | 0.169437 |
| 9 | (Intercept) | -0.549722 | 39 | cg11299964 | -0.328907 | 69 | cg19357849 | -0.216828 | 99 | cg15804973 | -0.168001 |
| 10 | cg09809672 | -0.532471 | 40 | cg22580512 | -0.326412 | 70 | cg15297650 | -0.216779 | 100 | cg12422450 | 0.167622 |
| 11 | cg00343092 | -0.500909 | 41 | cg13921352 | 0.320154 | 71 | cg11296937 | -0.215436 | 101 | cg07158339 | -0.166068 |
| 12 | cg04474832 | -0.463950 | 42 | cg18328933 | -0.318381 | 72 | cg04564646 | -0.210781 | 102 | cg12340144 | -0.165421 |
| 13 | cg14915263 | -0.461811 | 43 | cg07850604 | 0.309722 | 73 | cg12261786 | -0.210380 | 103 | cg02654291 | 0.160027 |
| 14 | cg00503840 | 0.455829 | 44 | cg23124451 | -0.309382 | 74 | cg18055007 | 0.208290 | 104 | cg01459453 | -0.157035 |
| 15 | cg04528819 | 0.446599 | 45 | cg21256649 | -0.308976 | 75 | cg07388493 | -0.206733 | 105 | cg05492845 | -0.152588 |
| 16 | cg25256723 | -0.440934 | 46 | cg08468689 | -0.307241 | 76 | cg00168942 | -0.205629 | 106 | cg04983977 | 0.151666 |
| 17 | cg16785344 | -0.422005 | 47 | cg21296230 | 0.299826 | 77 | cg22947000 | -0.203777 | 107 | cg18440048 | 0.150148 |
| 18 | cg26005082 | 0.418708 | 48 | cg20125091 | 0.291461 | 78 | cg20692569 | 0.200028 | 108 | cg11554937 | 0.146277 |
| 19 | cg24170090 | -0.409602 | 49 | cg13975369 | 0.289659 | 79 | cg06615861 | -0.199849 | 109 | cg01919208 | 0.145546 |
| 20 | cg08888956 | -0.408093 | 50 | cg13494498 | 0.280318 | 80 | cg12437239 | 0.197764 | 110 | cg11007423 | 0.143615 |
| 21 | cg08209133 | 0.406863 | 51 | cg18815943 | 0.277910 | 81 | cg18008766 | 0.189601 | 111 | cg00451635 | -0.131398 |
| 22 | cg02228185 | -0.406239 | 52 | cg06885782 | -0.276366 | 82 | cg11465372 | 0.188791 | 112 | cg18628483 | -0.130806 |
| 23 | cg27320127 | 0.404825 | 53 | cg14754581 | 0.275500 | 83 | cg25148589 | 0.187226 | 113 | cg24127874 | 0.130118 |
| 24 | cg13500819 | 0.390582 | 54 | cg11668844 | 0.264290 | 84 | cg12467090 | 0.185320 | 114 | cg26842024 | 0.128317 |
| 25 | cg01511567 | -0.390299 | 55 | cg19945840 | 0.260856 | 85 | cg15798153 | 0.184923 | 115 | cg10822172 | -0.128046 |
| 26 | cg19722847 | -0.387929 | 56 | cg27544190 | -0.258460 | 86 | cg15836394 | -0.183558 | 116 | cg19046959 | -0.125864 |
| 27 | cg22809047 | 0.371073 | 57 | cg14732136 | -0.254872 | 87 | cg17291001 | 0.182513 | 117 | cg03330058 | -0.125722 |
| 28 | cg07408456 | -0.362516 | 58 | cg26614073 | -0.253922 | 88 | cg13899108 | 0.181476 | 118 | cg26847866 | -0.124492 |

# SUPPLEMENTARY DATA

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 29 | cg20295671 | -0.361302 | 59 | cg01007201 | 0.246585 | 89 | cg10523019 | 0.179182 | 119 | cg19560758 | 0.124417 |
| 30 | cg01820374 | -0.355981 | 60 | cg18236477 | 0.244505 | 90 | cg21232015 | 0.178062 | 120 | cg09706243 | -0.124360 |
| **Rank** | **CpG_site** | **coefficient** | **Rank** | **CpG_site** | **coefficient** | **Rank** | **CpG_site** | **coefficient** | **Rank** | **CpG_site** | **coefficient** |
| 121 | cg13460409 | 0.120700 | 151 | cg20761322 | 0.098329 | 181 | cg24231716 | 0.073321 | 211 | cg15410903 | -0.052966 |
| 122 | cg16363586 | -0.119329 | 152 | cg23749046 | 0.096361 | 182 | cg02085507 | 0.072851 | 212 | cg19904653 | 0.052474 |
| 123 | cg17465304 | 0.118849 | 153 | cg20240860 | -0.094244 | 183 | cg27210390 | -0.072419 | 213 | cg16714091 | 0.052409 |
| 124 | cg02142461 | 0.118652 | 154 | cg18691434 | 0.093386 | 184 | cg20732137 | 0.072384 | 214 | cg20419410 | -0.052102 |
| 125 | cg05671018 | 0.116750 | 155 | cg25771195 | 0.092643 | 185 | cg11051139 | -0.070007 | 215 | cg06288351 | -0.052079 |
| 126 | cg00433406 | 0.116722 | 156 | cg27491887 | 0.092029 | 186 | cg20143092 | -0.066992 | 216 | cg10648908 | -0.051900 |
| 127 | cg12024906 | 0.116126 | 157 | cg23674788 | 0.089757 | 187 | cg02196655 | 0.066945 | 217 | cg23968383 | 0.051490 |
| 128 | cg11896923 | -0.115847 | 158 | cg09238598 | -0.089702 | 188 | cg04425624 | -0.065455 | 218 | cg00563932 | -0.050910 |
| 129 | cg09667582 | 0.115700 | 159 | cg00528967 | -0.088380 | 189 | cg16034652 | 0.064228 | 219 | cg10681065 | 0.050569 |
| 130 | cg14360917 | 0.115690 | 160 | cg13697378 | 0.087401 | 190 | cg08072716 | 0.064033 | 220 | cg21432842 | -0.050569 |
| 131 | cg25762706 | 0.113164 | 161 | cg15201877 | 0.086424 | 191 | cg25020850 | 0.063756 | 221 | cg05436231 | 0.050171 |
| 132 | cg15538427 | -0.112250 | 162 | cg26203861 | -0.085473 | 192 | cg22971191 | 0.063552 | 222 | cg15792367 | -0.049766 |
| 133 | cg17628717 | 0.111783 | 163 | cg08317263 | -0.085192 | 193 | cg06238491 | -0.063003 | 223 | cg16529592 | 0.048889 |
| 134 | cg15095327 | 0.111534 | 164 | cg00689340 | -0.083082 | 194 | cg11618577 | 0.062549 | 224 | cg02828104 | -0.048105 |
| 135 | cg16547529 | 0.111106 | 165 | cg12782180 | 0.082635 | 195 | cg26372517 | 0.062243 | 225 | cg16330965 | 0.047424 |
| 136 | cg09462576 | -0.109677 | 166 | cg15156836 | -0.082545 | 196 | cg18081258 | -0.061605 | 226 | cg17191178 | 0.047321 |
| 137 | cg15013019 | -0.108504 | 167 | cg26673195 | -0.082272 | 197 | cg15563382 | 0.060942 | 227 | cg11879514 | 0.046374 |
| 138 | cg00240880 | 0.106645 | 168 | cg02844545 | 0.081288 | 198 | cg00187380 | -0.060720 | 228 | cg10322876 | 0.046245 |
| 139 | cg16744741 | -0.106124 | 169 | cg23894058 | 0.080975 | 199 | cg08032971 | 0.059374 | 229 | cg25372195 | 0.045917 |
| 140 | cg25459323 | -0.105747 | 170 | cg17655614 | 0.079729 | 200 | cg02310296 | 0.058791 | 230 | cg20969242 | 0.045905 |
| 141 | cg19724470 | -0.104476 | 171 | cg22909609 | -0.079372 | 201 | cg23887396 | -0.057687 | 231 | cg13493001 | 0.045881 |
| 142 | cg18303397 | -0.103026 | 172 | cg11393848 | -0.078721 | 202 | cg01600189 | -0.056979 | 232 | cg12830694 | 0.045029 |
| 143 | cg26083396 | -0.102282 | 173 | cg10989517 | 0.077383 | 203 | cg14709524 | 0.056268 | 233 | cg03991512 | -0.044471 |
| 144 | cg12167564 | 0.102049 | 174 | cg23303074 | -0.076855 | 204 | cg21426387 | -0.056218 | 234 | cg26845300 | 0.043818 |
| 145 | cg07211259 | -0.100932 | 175 | cg11126134 | 0.076425 | 205 | cg26394940 | -0.055434 | 235 | cg22472290 | 0.042385 |
| 146 | cg00757070 | -0.100919 | 176 | cg21600563 | -0.076349 | 206 | cg20582779 | 0.055430 | 236 | cg05358404 | 0.042356 |
| 147 | cg19850406 | 0.100517 | 177 | cg27016307 | -0.075887 | 207 | cg12289045 | 0.055241 | 237 | cg08965235 | -0.041639 |
| 148 | cg24081819 | -0.100099 | 178 | cg13813391 | 0.075797 | 208 | cg11819637 | 0.054954 | 238 | cg10674793 | 0.041490 |
| 149 | cg05749577 | -0.099570 | 179 | cg24847163 | -0.075789 | 209 | cg02489552 | 0.053384 | 239 | cg10676060 | 0.041424 |
| 150 | cg16913124 | 0.099268 | 180 | cg09307279 | -0.075082 | 210 | cg19777783 | 0.053383 | 240 | cg03019000 | -0.041335 |
| **Rank** | **CpG_site** | **coefficient** | **Rank** | **CpG_site** | **coefficient** | **Rank** | **CpG_site** | **coefficient** | **Rank** | **CpG_site** | **coefficient** |
| 241 | cg03929796 | -0.041099 | 271 | cg04304130 | 0.025783 | 301 | cg19356189 | -0.013159 | 331 | cg03805684 | 0.004344 |
| 242 | cg14166009 | 0.040661 | 272 | cg23854009 | 0.025638 | 302 | cg09195271 | 0.012800 | 332 | cg26376809 | -0.004212 |
| 243 | cg22022041 | 0.040321 | 273 | cg06736444 | 0.025217 | 303 | cg02829654 | 0.012382 | 333 | cg20436912 | 0.003965 |
| 244 | cg06458239 | 0.039813 | 274 | cg23881601 | -0.025032 | 304 | cg05294243 | 0.012290 | 334 | cg06144905 | 0.003305 |
| 245 | cg21289015 | 0.039448 | 275 | cg20648149 | 0.024993 | 305 | cg27169020 | 0.012111 | 335 | cg21098323 | 0.002805 |
| 246 | cg08090640 | -0.038989 | 276 | cg03943081 | 0.024911 | 306 | cg18847227 | 0.011814 | 336 | cg20775254 | 0.002624 |
| 247 | cg15408407 | -0.038133 | 277 | cg12774845 | -0.024566 | 307 | cg22335340 | -0.011134 | 337 | cg07895149 | -0.002459 |
| 248 | cg18017908 | -0.037211 | 278 | cg13269407 | -0.024451 | 308 | cg21301148 | -0.010720 | 338 | cg05507459 | -0.002235 |
| 249 | cg11219178 | -0.036830 | 279 | cg15537850 | -0.024411 | 309 | cg26057752 | 0.010613 | 339 | cg20747455 | 0.002161 |
| 250 | cg06896207 | 0.036030 | 280 | cg22799321 | 0.023824 | 310 | cg21448423 | -0.010174 | 340 | cg09554443 | 0.002072 |

# SUPPLEMENTARY DATA

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 251 | cg20492912 | 0.036028 | 281 | cg25282410 | 0.023754 | 311 | cg12426141 | -0.010024 | 341 | cg10281002 | 0.001749 |
| 252 | cg22941086 | 0.035732 | 282 | cg08558340 | 0.023500 | 312 | cg20387706 | 0.009523 | 342 | cg16519742 | 0.001362 |
| 253 | cg06268694 | 0.035268 | 283 | cg04123409 | -0.022247 | 313 | cg03224418 | -0.008908 | 343 | cg21652958 | 0.001228 |
| 254 | cg25004981 | 0.033099 | 284 | cg11976790 | 0.020600 | 314 | cg18279742 | 0.008791 | 344 | cg08723608 | 0.000896 |
| 255 | cg10919204 | 0.032924 | 285 | cg19109050 | 0.019781 | 315 | cg08861115 | 0.008731 | 345 | cg11377136 | 0.000827 |
| 256 | cg26538442 | 0.032287 | 286 | cg16858125 | 0.018828 | 316 | cg10249734 | 0.008316 | 346 | cg00208830 | 0.000789 |
| 257 | cg15780361 | 0.031666 | 287 | cg01560871 | -0.016904 | 317 | cg10917602 | -0.008023 | 347 | cg08124399 | 0.000608 |
| 258 | cg06630241 | 0.031412 | 288 | cg12717203 | -0.016663 | 318 | cg10362475 | 0.007987 | 348 | cg07549715 | 0.000344 |
| 259 | cg08331960 | -0.030947 | 289 | cg08022502 | -0.016501 | 319 | cg14972143 | 0.007970 | | | |
| 260 | cg21057046 | -0.030385 | 290 | cg16254309 | 0.016370 | 320 | cg05113558 | 0.007859 | | | |
| 261 | cg25221254 | 0.029982 | 291 | cg04633513 | 0.016306 | 321 | cg18902090 | 0.007801 | | | |
| 262 | cg04765422 | 0.029879 | 292 | cg25809905 | -0.015482 | 322 | cg00308665 | -0.007369 | | | |
| 263 | cg06971096 | 0.029082 | 293 | cg24341129 | 0.015423 | 323 | cg15379633 | 0.007226 | | | |
| 264 | cg18678185 | -0.028961 | 294 | cg21663431 | -0.015366 | 324 | cg05420896 | 0.006647 | | | |
| 265 | cg26976437 | 0.028689 | 295 | cg25564800 | -0.014755 | 325 | cg13726191 | -0.006321 | | | |
| 266 | cg22215728 | 0.028028 | 296 | cg01656853 | 0.014466 | 326 | cg00565075 | 0.005736 | | | |
| 267 | cg22805308 | 0.027331 | 297 | cg13302154 | -0.014253 | 327 | cg19595170 | -0.005258 | | | |
| 268 | cg26297688 | 0.027140 | 298 | cg01400401 | 0.014041 | 328 | cg14576824 | 0.005170 | | | |
| 269 | cg08822227 | -0.027097 | 299 | cg22511947 | 0.013973 | 329 | cg01753375 | -0.004934 | | | |
| 270 | cg17832674 | -0.026777 | 300 | cg17453778 | 0.013909 | 330 | cg09150232 | -0.004447 | | | |