**5-Hydroxymethylcytosine signatures in circulating cell-free DNA as predictive biomarkers for COVID-19 progression and myocardial injury**

Hang-yu Chen 1\*, Xiao-xiao Li 2b, 8\*, Chao Li 2a\*, Hai-chuan Zhu 4\*, Hong-yan Hou 5, Bo Zhang 5, Li-ming Cheng 5, Hui Hu 6, Zhong-xin Lu 6, Jia-xing Liu 4, Ze-ruo Yang 8, Lei Zhang 8, Nuo Xu 8, Long Chen 1, Chuan He 9, Chao-ran Dong 3†, Qing-gang Ge 2a†, Jian Lin 1†

**Supplementary Table 9. Coefficients for 15 DhMRs in the logistic regression model trained by the training cohort**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Coefficients | SE | Z | P>|Z| | 97.5% CI | GeneID |
| Intercept | -13.62 | 3.97 | -3.43 | 0.001 | [-21.40, -5.85] |  |
| chr6\_97578573\_97578980 | 0.66 | 0.42 | 1.57 | 0.116 | [-0.16, 1.48] | KLHL32 |
| chr19\_43866758\_43867470 | 0.08 | 0.17 | 0.46 | 0.646 | [-0.26, 0.42] | CD177 |
| chr7\_41439865\_41440450 | 0.50 | 0.36 | 1.41 | 0.159 | [-0.20, 1.20] | INHBA-AS1 |
| chr3\_152485356\_152485773 | 0.04 | 0.33 | 0.13 | 0.896 | [-0.60, 0.68] | P2RY1 |
| chr9\_21276039\_21276628 | 0.45 | 0.33 | 1.38 | 0.169 | [-0.19, 1.09] | IFNA22P |
| chr2\_98310400\_98311030 | 0.33 | 0.21 | 1.57 | 0.117 | [-0.08, 0.73] | ZAP70 |
| chr5\_59517693\_59518204 | -0.65 | 0.34 | -1.91 | 0.056 | [-1.31, 0.02] | PDE4D |
| chr1\_68715142\_68715517 | -0.24 | 0.21 | -1.15 | 0.251 | [-0.66, 0.17] | WLS |
| chr13\_72031580\_72031950 | 0.24 | 0.36 | 0.67 | 0.506 | [-0.47, 0.95] | DACH1 |
| chr1\_12769349\_12770105 | -0.39 | 0.15 | -2.58 | 0.010 | [-0.69, -0.09] | AADACL3 |
| chr10\_9628645\_9629173 | 0.27 | 0.28 | 0.96 | 0.338 | [-0.28, 0.81] | SFTA1P |
| chr5\_124121851\_124122273 | 1.63 | 0.70 | 2.33 | 0.020 | [ 0.26, 3.00] | ZNF608 |
| chr12\_4762930\_4763650 | 0.42 | 0.28 | 1.52 | 0.129 | [-0.12, 0.96] | NDUFA9 |
| chr5\_55915481\_55916120 | 0.81 | 0.42 | 1.95 | 0.052 | [-0.005, 1.63] | MAP3K1 |
| chr6\_88004302\_88004804 | -0.47 | 0.39 | -1.22 | 0.222 | [-1.23, 0.29] | SMIM8 |

**Abbreviation:** ***DhMRs***, Differentially 5hMc-enriched Regions. ***SE***, standard errors of coefficients; ***z value***, Wald z-statistic value; ***CI***, confidence interval.

**Supplementary Table 10. Coefficients for 10 DhMRs in the logistic regression model trained by the training cohort.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Coefficients | SE | Z | P>|Z| | 97.5% CI | GeneID |
| Intercept | 4.10 | 1.05 | 3.89 | 0.000 | [2.03, 6.16] |  |
| chr2\_98310458\_98310908 | -0.41 | 0.20 | -2.04 | 0.041 | [-0.80，-0.02] | ZAP70 |
| chr3\_108275906\_108276361 | 0.15 | 0.21 | 0.72 | 0.470 | [-0.27, 0.57] | CIP2A |
| chr3\_114931868\_114932289 | 0.17 | 0.24 | 0.72 | 0.474 | [-0.30, 0.65] | ZBTB20 |
| chr4\_16664143\_16664615 | -0.008 | 0.17 | -0.05 | 0.964 | [-0.34, 0.32] | LDB2 |
| chr5\_58634218\_58634729 | -0.10 | 0.18 | -0.55 | 0.582 | [-0.46, 0.26] | PDE4D |
| chr7\_156842323\_156843081 | 0.15 | 0.17 | 0.84 | 0.401 | [-0.19, 0.49] | MNX1-AS1 |
| chr8\_122427723\_122428315 | 0.11 | 0.20 | 0.54 | 0.591 | [-0.29, 0.50] | HAS2-AS1 |
| chr11\_128451949\_128452270 | -0.18 | 0.14 | -1.28 | 0.201 | [-0.46, 0.10] | ETS1 |
| chr16\_84387122\_84387490 | -0.18 | 0.14 | -1.31 | 0.191 | [-0.44, 0.09] | ATP2C2 |
| chr20\_48218885\_48219411 | 0.17 | 0.16 | 1.04 | 0.297 | [-0.15, 0.48] | PTGIS |

**Abbreviation:** ***DhMRs***, Differentially 5hMc-enriched Regions. ***SE***, standard errors of coefficients; ***z value***, Wald z-statistic value; ***CI***, confidence interval.

**Supplementary Table 11. Coefficients for 12 DhMRs in the logistic regression model trained by the training cohort.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Coefficients | SE | Z | P>|Z| | 97.5% CI | GeneID |
| Intercept | 2.15 | 3.25 | -0.06 | 0.007 | [-5.68, 4.53] |  |
| chr19\_44509716\_44510190 | -0.24 | 0.25 | -0.95 | 0.34 | [-0.73, 0.25] | ZNF230 |
| chr14\_34575454\_34575921 | 0.57 | 0.30 | 1.89 | 0.059 | [-0.02, 1.17] | EGLN3 |
| chr22\_30457270\_30458221 | 0.002 | 0.11 | 0.02 | 0.985 | [-0.22, 0.22] | HORMAD2 |
| chr7\_9403511\_9404396 | 0.26 | 0.26 | 0.98 | 0.327 | [-0.26, 0.78] | PER4 |
| chr7\_41354441\_41355196 | -0.11 | 0.14 | -0.82 | 0.411 | [-0.39, 0.16] | INHBA-AS1 |
| chr3\_187971220\_187971826 | 0.23 | 0.22 | 1.03 | 0.302 | [-0.21, 0.67] | LPP |
| chr5\_59049866\_59050599 | 0.13 | 0.10 | 0.22 | 0.043 | [-0.16, 0.35] | PDE4D |
| chr11\_16985087\_16985664 | -0.08 | 0.17 | -0.48 | 0.629 | [-0.40, 0.24] | PLEKHA7 |
| chr20\_60562515\_60562912 | -0.08 | 0.17 | -0.45 | 0.653 | [-0.41, 0.26] | MIR1257 |
| Chr6\_152238602\_152239181 | 0.09 | 0.08 | -0.21 | 0.036 | [0.11, 0.33] | ESR1 |
| chr6\_88476279\_88476842 | -0.19 | 0.22 | -0.86 | 0.388 | [-0.61, 0.24] | AKIRIN2 |
| chr2\_102278044\_102278804 | -0.04 | 0.22 | -0.16 | 0.870 | [-0.47, 0.39] | MAP4K4 |

**Abbreviation:** ***DhMRs***, Differentially 5hMc-enriched Regions. ***SE***, standard errors of coefficients; ***z value***, Wald z-statistic value; ***CI***, confidence interval.