

Supplemental table. The 147 significant CpGs from the linear mixed model: DNA methylation in blood samples from children born to mothers with RA(FEPRA study) compared with children born to mothers from the general population(Generation R Study).

| CpG | Nearest gene (+/- bp) | Chr | Base pairs | Location | Beta | Standard error | P-value |
|------------|-----------------------|-----|------------|----------|-------------|----------------|----------|
| cg06642177 | SLC2A12(-122529) | 6 | 134496341 | - | 0.027693315 | 0.002704662 | 1.32E-24 |
| cg08867893 | ZNF365(+221) | 10 | 64134160 | - | 0.018410514 | 0.001828632 | 7.66E-24 |
| cg06778273 | TNFRSF18(+4995) | 1 | 1137117 | - | 0.022857221 | 0.002306493 | 3.77E-23 |
| cg07786668 | ZFH3(-10142) | 16 | 73092391 | - | 0.02586352 | 0.002626713 | 7.11E-23 |
| cg20116574 | NCOA5(+435) | 20 | 44718168 | Promoter | 0.018815575 | 0.002115599 | 5.91E-19 |
| cg21160472 | ATF3(+119) | 1 | 212782112 | Promoter | 0.013379402 | 0.00166464 | 9.18E-16 |
| cg09000178 | CBFB(+294) | 16 | 67063319 | - | 0.014919311 | 0.001866453 | 1.31E-15 |
| cg01067849 | WRNIP1(-102) | 6 | 2765587 | Promoter | 0.010168425 | 0.001336479 | 2.78E-14 |
| cg14119392 | DICER1(-15866) | 14 | 95623926 | Promoter | 0.009496235 | 0.001275776 | 9.81E-14 |
| cg01485645 | MLLT6(+303) | 17 | 36862199 | Promoter | - | 0.005979805 | 1.64E-13 |
| cg10196289 | NSMAF(-196) | 8 | 59572185 | - | 0.013826063 | 0.001891212 | 2.66E-13 |
| cg13018448 | ,CUTA(+600) | 6 | 33385440 | Promoter | 0.035622707 | 0.004917127 | 4.34E-13 |
| cg01402409 | FRAS1(-614) | 4 | 78978133 | - | 0.034187754 | 0.004758592 | 6.75E-13 |
| cg17492326 | ,ANXA13(-31076) | 8 | 124780746 | Promoter | 0.013530835 | 0.001894369 | 9.15E-13 |
| cg06656994 | FAM163A(+903) | 1 | 179713176 | Enhancer | 0.038178019 | 0.0053507 | 9.67E-13 |
| cg13390975 | BRIX1(+95) | 5 | 34915890 | Promoter | 0.012727324 | 0.001788634 | 1.11E-12 |
| cg17667988 | PTBP1(-73) | 19 | 797342 | Promoter | - | 0.033538136 | 1.86E-12 |
| cg14810343 | CXXC5(-127) | 5 | 139028149 | - | 0.011939828 | 0.001706185 | 2.60E-12 |
| cg17662034 | RDH10(+706) | 8 | 74207518 | - | 0.01366994 | 0.001961263 | 3.17E-12 |
| cg22247188 | H2AFY2(+1271) | 10 | 71813603 | - | 0.020553561 | 0.002959855 | 3.81E-12 |
| cg22998206 | - | 12 | 49239429 | - | 0.031783604 | 0.004590532 | 4.40E-12 |
| cg00742472 | HEATR5A(-149) | 14 | 31889912 | Promoter | - | 0.005307146 | 5.00E-12 |
| cg21423973 | TYW1B(+121) | 7 | 72298667 | Promoter | 0.034153776 | 0.004952153 | 5.32E- |

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|------------|---------------|----|-----------|----------|-------------|-------------|----------|
| | | | | | | | 12 |
| cg24334803 | ZNF672(+281) | 1 | 249132834 | Promoter | 0.032219477 | 0.00469291 | 6.62E-12 |
| cg11014794 | CPEB3(+51162) | 10 | 93999688 | - | 0.020288544 | 0.002988909 | 1.14E-11 |
| cg15591678 | ZNF365(+216) | 10 | 64134155 | - | 0.023828478 | 0.003516927 | 1.24E-11 |
| cg08700690 | RORA(+35122) | 15 | 60884630 | Promoter | 0.009395729 | 0.001389406 | 1.36E-11 |
| cg17218495 | SMARCA4(+170) | 19 | 11071743 | Promoter | 0.010408213 | 0.001546442 | 1.69E-11 |
| cg18238491 | SKA1(+73) | 18 | 47901440 | - | 0.006920639 | 0.0010313 | 1.94E-11 |
| cg00476896 | - | 17 | 60215463 | - | 0.029335846 | 0.004389098 | 2.33E-11 |
| cg16930947 | - | 8 | 88984447 | - | 0.049809031 | 0.007505862 | 3.22E-11 |
| cg01458961 | PPP3CA(-822) | 4 | 102269425 | - | 0.022397284 | 0.003379311 | 3.41E-11 |
| cg22704520 | TYW5(+31) | 2 | 200820451 | Promoter | 0.015040524 | 0.002278848 | 4.11E-11 |
| cg25863503 | - | 6 | 27799295 | - | 0.018114832 | 0.002760384 | 5.29E-11 |
| cg23792383 | KLF5(+171) | 13 | 73633288 | Promoter | 0.009986606 | 0.001528091 | 6.35E-11 |
| cg03847293 | - | 1 | 17734508 | - | 0.032462167 | 0.004970659 | 6.54E-11 |
| cg08561325 | AKIP1(+289) | 11 | 8932965 | Promoter | 0.016285887 | 0.002494156 | 6.59E-11 |
| cg12100751 | HENMT1(+95) | 1 | 109203672 | Promoter | 0.012782918 | 0.001960274 | 6.98E-11 |
| cg18342832 | - | 7 | 99933797 | Promoter | 0.008837976 | 0.0013622 | 8.70E-11 |
| cg21384971 | COP2(+601) | 17 | 46114574 | - | 0.029200877 | 0.004508859 | 9.40E-11 |
| cg17607973 | MEPCE(+179) | 7 | 100027408 | Promoter | 0.012264221 | 0.001904559 | 1.20E-10 |
| cg22512322 | PSMD6(+47) | 3 | 64009096 | Promoter | 0.010619257 | 0.001666666 | 1.87E-10 |
| cg17255450 | EVC2(-55) | 4 | 5710372 | - | 0.016872706 | 0.002655126 | 2.09E-10 |
| cg16041611 | SRF(+785) | 6 | 43139680 | - | 0.010561056 | 0.001664015 | 2.20E-10 |
| cg11877270 | SPRED2(+1048) | 2 | 65658583 | - | 0.014862583 | 0.002349815 | 2.53E-10 |
| cg25707994 | DNAJB6(0) | 7 | 157129685 | Promoter | 0.014060725 | 0.002226484 | 2.70E-10 |

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|------------|-----------------|----|-----------|--------------------|-------------|-------------|----------|
| cg03654106 | - | 19 | 49539527 | - | 0.026109337 | 0.004139079 | 2.83E-10 |
| cg07479988 | DHX57(-281) | 2 | 39103277 | Promoter | 0.023103709 | 0.003673311 | 3.18E-10 |
| cg21538902 | ADO(+464) | 10 | 64565003 | Promoter | 0.018717869 | 0.00297763 | 3.25E-10 |
| cg19031844 | ZNF536(+347411) | 19 | 31210714 | Enhancer | 0.026178619 | 0.004168745 | 3.39E-10 |
| cg06295548 | - | 4 | 146296778 | - | 0.021299828 | 0.003393384 | 3.45E-10 |
| cg06117184 | CKAP2L(+70) | 2 | 113522207 | Promoter | 0.008425305 | 0.00134451 | 3.69E-10 |
| cg04910183 | CDC73(-75) | 1 | 193090988 | Promoter | 0.010437417 | 0.001666679 | 3.79E-10 |
| cg10181911 | RPE(-268) | 2 | 210867059 | Promoter | 0.035764362 | 0.005736336 | 4.53E-10 |
| cg17483482 | - | 1 | 117152162 | - | 0.036832852 | 0.005910728 | 4.62E-10 |
| cg02461956 | NCAPD3(+509) | 11 | 134093940 | Promoter | 0.01486645 | 0.002389714 | 4.94E-10 |
| cg19656070 | TAX1BP3(+18) | 17 | 3571978 | Promoter | 0.01069978 | 0.001727363 | 5.85E-10 |
| cg07283595 | DHX33(+400) | 17 | 5372003 | Promoter | 0.023494356 | 0.003797213 | 6.12E-10 |
| cg25757017 | OLR1(+18303) | 12 | 10306462 | Promoter, Enhancer | 0.021080747 | 0.00341288 | 6.54E-10 |
| cg02286335 | ZWINT(-11) | 10 | 58121068 | Promoter | 0.0149277 | 0.002433753 | 8.59E-10 |
| cg15248577 | ,SFMBT2(+3015) | 10 | 7450456 | Promoter | 0.013766093 | 0.002252311 | 9.84E-10 |
| cg14078059 | GNS(-21459) | 12 | 65174660 | Enhancer | 0.016388831 | 0.0026961 | 1.21E-09 |
| cg04875007 | RPS2(-21) | 16 | 2014871 | Promoter | 0.012867742 | 0.002125921 | 1.42E-09 |
| cg18764107 | LBR(+169) | 1 | 225615669 | Promoter | 0.012219992 | 0.002018668 | 1.42E-09 |
| cg04759220 | JMY(+660) | 5 | 78532560 | - | 0.014868421 | 0.002458298 | 1.46E-09 |
| cg08522087 | ANKH(0) | 5 | 14871910 | - | 0.007733637 | 0.00128734 | 1.88E-09 |
| cg13579901 | DCAF6(-280) | 1 | 167905492 | Promoter | 0.022337576 | 0.003720867 | 1.93E-09 |
| cg02750935 | PRELID2(-59) | 5 | 145214981 | Promoter, Enhancer | 0.007716834 | 0.001285997 | 1.97E-09 |
| cg05234169 | CCDC59(-78) | 12 | 82752252 | Promoter | 0.016282794 | 0.002714563 | 1.99E-09 |
| cg05884522 | NOL7(-44) | 6 | 13615538 | Promoter | 0.01307324 | 0.00218602 | 2.23E- |

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| | | | | | | | 09 |
| cg06091566 | SAMD11(-523) | 1 | 860621 | - | 0.026435441 | 0.004423976 | 2.29E-09 |
| cg24079591 | MARK3(-213) | 14 | 103851511 | Promoter | 0.015991172 | 0.002680227 | 2.43E-09 |
| cg11220663 | ADD2(+7) | 2 | 70994863 | - | 0.022700901 | 0.003806692 | 2.47E-09 |
| cg12043722 | CORO2B(-38066) | 15 | 68870836 | - | 0.021346312 | 0.003589317 | 2.73E-09 |
| cg07262328 | CD44(+269) | 11 | 35160709 | Promoter | 0.013942252 | 0.00235062 | 3.01E-09 |
| cg16163324 | RAD54L(-458) | 1 | 46712932 | Promoter | 0.030437342 | 0.005137256 | 3.13E-09 |
| cg23222745 | - | 6 | 27791912 | - | 0.016727733 | 0.002826838 | 3.27E-09 |
| cg03243965 | HSH2D(+9703) | 19 | 16254516 | Promoter | 0.009874424 | 0.001670143 | 3.37E-09 |
| cg06506598 | ZFYVE16(+80028) | 5 | 79783889 | Promoter | 0.024948733 | 0.004222809 | 3.46E-09 |
| cg16370446 | FAM200B(-43) | 4 | 15683284 | Promoter | 0.010397718 | 0.001763573 | 3.73E-09 |
| cg02547025 | LBH(-97) | 2 | 30454275 | Promoter | 0.008294564 | 0.001407597 | 3.80E-09 |
| cg25335190 | - | 6 | 27791899 | - | 0.01905164 | 0.003241695 | 4.18E-09 |
| cg22270384 | ASNA1(-41) | 19 | 12848240 | Promoter | 0.02699067 | 0.004627302 | 5.45E-09 |
| cg21028463 | MFSD11(+124) | 17 | 74733682 | Promoter | 0.011167499 | 0.001916108 | 5.60E-09 |
| cg15698851 | TMEM66(+281) | 8 | 29940391 | Promoter | 0.014332978 | 0.002463582 | 5.96E-09 |
| cg15965583 | ENSA(+172) | 1 | 150601949 | Promoter | 0.025400177 | 0.004366307 | 5.98E-09 |
| cg22100652 | TRIM27(+57387) | 6 | 28834404 | Promoter | - | 0.004614584 | 6.52E-09 |
| cg08655589 | SLC6A6(+46) | 3 | 14444175 | Promoter | 0.014234875 | 0.002454671 | 6.67E-09 |
| cg17834180 | IKZF5(+94) | 10 | 124768240 | Promoter | 0.015030674 | 0.002593684 | 6.83E-09 |
| cg10101470 | LRRC8D(-870) | 1 | 90286633 | Promoter | 0.00739195 | 0.001276564 | 7.02E-09 |
| cg21597684 | HECW2(-42) | 2 | 197457400 | - | 0.015548919 | 0.002685279 | 7.02E-09 |
| cg19273746 | B3GAT2(+700) | 6 | 71666063 | Promoter | 0.023624873 | 0.004104604 | 8.63E-09 |
| cg22870667 | - | 8 | 521182 | Enhancer | - | 0.004826716 | 9.26E-09 |

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|------------|------------------|----|-----------|--------------------|-------------|-------------|----------|
| cg20718350 | ASCL1(+819) | 12 | 103352294 | - | 0.009430784 | 0.001644405 | 9.75E-09 |
| cg18289490 | SPATA2(+33) | 20 | 48532070 | Promoter | 0.013736303 | 0.002396973 | 1.00E-08 |
| cg20462855 | HEY2(-370) | 6 | 126070385 | - | 0.0072723 | 0.001269581 | 1.02E-08 |
| cg20297566 | TBC1D23(+267) | 3 | 99979976 | Promoter | 0.031187463 | 0.005450513 | 1.05E-08 |
| cg08709073 | RGS7BP(-243) | 5 | 63802184 | - | 0.018571888 | 0.003250119 | 1.10E-08 |
| cg19080138 | HERPUD2(+14) | 7 | 35734733 | Promoter | 0.013942223 | 0.002443189 | 1.15E-08 |
| cg26580332 | - | 8 | 143919495 | - | 0.018298842 | 0.003209963 | 1.19E-08 |
| cg03713379 | SLC12A2(+117789) | 5 | 127537295 | - | 0.016365348 | 0.002875992 | 1.27E-08 |
| cg18120578 | E2F7(-24) | 12 | 77459407 | Promoter | 0.014961422 | 0.002635655 | 1.37E-08 |
| cg02994863 | PGM1(-29613) | 1 | 64059297 | Promoter | 0.013618631 | 0.002400823 | 1.41E-08 |
| cg15408407 | RPS15(+100) | 19 | 1438438 | Promoter | 0.006751614 | 0.001191922 | 1.47E-08 |
| cg21243939 | SAMD4A(-1168) | 14 | 55033137 | - | 0.015308476 | 0.002707084 | 1.56E-08 |
| cg04041942 | INTS9(-158) | 8 | 28747613 | Promoter | 0.01474484 | 0.002608622 | 1.58E-08 |
| cg12360123 | - | 10 | 79984532 | Enhancer | - | 0.043318426 | 1.61E-08 |
| cg14229247 | ANP32B(-373) | 9 | 100745139 | Promoter | 0.005090587 | 0.000901141 | 1.61E-08 |
| cg05944369 | HMGB2(-673) | 4 | 174255616 | Promoter | 0.017054023 | 0.003024432 | 1.71E-08 |
| cg04335562 | ZNF77(-56) | 19 | 2945000 | Promoter | 0.023036961 | 0.004086777 | 1.73E-08 |
| cg15012981 | MAD2L2(+10644) | 1 | 11741009 | Promoter | 0.005040813 | 0.000896171 | 1.86E-08 |
| cg14225021 | ITGB6(-69870) | 2 | 161126482 | Promoter, Enhancer | 0.011800981 | 0.002102176 | 1.98E-08 |
| cg09572053 | C6orf1(-143622) | 6 | 34360501 | Promoter | 0.006279856 | 0.001121122 | 2.13E-08 |
| cg26646903 | TBCCD1(-92) | 3 | 186285208 | Promoter | 0.011590163 | 0.002084438 | 2.69E-08 |
| cg13841783 | - | 6 | 32293117 | - | - | 0.030474363 | 2.71E-08 |
| cg11706469 | FGF8(+420) | 10 | 103535362 | - | 0.027519708 | 0.004959609 | 2.88E-08 |
| cg13425677 | MAP3K1(+1215) | 5 | 56112090 | - | 0.014548024 | 0.0026336 | 3.31E-08 |

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|------------|-----------------|----|-----------|----------|-------------|-------------|----------|
| | | | | | | | 08 |
| cg15642758 | HDGFRP3(-268) | 15 | 83876612 | Promoter | 0.013003375 | 0.002354288 | 3.33E-08 |
| cg06812693 | RBPJ(+794) | 4 | 26323246 | - | 0.020035197 | 0.003629075 | 3.38E-08 |
| cg11336323 | - | 19 | 41946040 | Promoter | -0.03675832 | 0.00666397 | 3.47E-08 |
| cg18913103 | FBXW7(-1391) | 4 | 153457599 | Promoter | 0.016671965 | 0.003022876 | 3.48E-08 |
| cg10393416 | PLK4(+86) | 4 | 128802077 | Promoter | 0.011204472 | 0.002035668 | 3.71E-08 |
| cg20692684 | EPC1(-99070) | 10 | 32735158 | Promoter | 0.013607155 | 0.002480731 | 4.13E-08 |
| cg04551440 | KATNAL1(-8) | 13 | 30881194 | Promoter | 0.017295098 | 0.003153543 | 4.15E-08 |
| cg04738301 | NTN4(-21) | 12 | 96184580 | - | 0.006624531 | 0.001210765 | 4.47E-08 |
| cg01374398 | SCAP(+493) | 3 | 47516975 | Promoter | 0.02248462 | 0.004109964 | 4.48E-08 |
| cg05740879 | CDKN1C(+185152) | 11 | 2721866 | - | 0.027389961 | 0.005036612 | 5.38E-08 |
| cg09636406 | RECQL5(+110) | 17 | 73663134 | Promoter | 0.013516309 | 0.002488052 | 5.56E-08 |
| cg10391895 | ARL2(+112) | 11 | 64781672 | Promoter | 0.016185438 | 0.002980622 | 5.63E-08 |
| cg07361491 | GATA6(+96) | 18 | 19749535 | - | 0.011950742 | 0.002201116 | 5.65E-08 |
| cg23055081 | TRIM26(-21) | 6 | 30181315 | Promoter | 0.019228906 | 0.003543944 | 5.77E-08 |
| cg15040188 | - | 19 | 621137 | - | 0.025437993 | 0.004696691 | 6.09E-08 |
| cg07226281 | MAPK8IP3(+378) | 16 | 1756622 | Promoter | 0.009645234 | 0.001783131 | 6.33E-08 |
| cg17364044 | PELI1(+378) | 2 | 64371202 | Promoter | 0.012546186 | 0.00232473 | 6.78E-08 |
| cg12260146 | PDCD6IP(+196) | 3 | 33840237 | Promoter | 0.030045517 | 0.005570297 | 6.90E-08 |
| cg24906202 | NEO1(+412) | 15 | 73345212 | - | 0.013867409 | 0.002573678 | 7.12E-08 |
| cg06803925 | CENPL(+167) | 1 | 173793126 | Promoter | 0.009030316 | 0.001677537 | 7.32E-08 |
| cg16485682 | GATA6(+101) | 18 | 19749540 | - | 0.006185935 | 0.001149349 | 7.36E-08 |
| cg23681311 | MAPK1(+67) | 22 | 22221878 | Promoter | 0.008424076 | 0.001567243 | 7.65E-08 |
| cg23243902 | SIDT2(-113) | 11 | 117049849 | - | 0.022369089 | 0.004171023 | 8.19E-08 |

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| cg19906131 | PANX1(+447) | 11 | 93862516 | - | 0.011899087 | 0.002224471 | 8.84E-08 |
| cg25668236 | ST8SIA4(+2169) | 5 | 100236841 | - | 0.010861389 | 0.002033066 | 9.17E-08 |
| cg21475747 | HNRNPAB(-58) | 5 | 177631425 | Promoter | 0.012719026 | 0.00238298 | 9.43E-08 |
| cg26021273 | MNX1(-10742) | 7 | 156814112 | - | 0.020861613 | 0.003918929 | 1.02E-07 |
| cg05300158 | SETD7(-127) | 4 | 140477727 | - | 0.008149892 | 0.00153159 | 1.03E-07 |
| cg02613964 | - | 3 | 44690321 | Promoter | 0.019188607 | 0.003608882 | 1.05E-07 |
| cg04678743 | COPG2(+106) | 7 | 130353515 | Promoter | 0.011250205 | 0.00211627 | 1.06E-07 |

bp=base pair; Chr= chromosome; SE= standard error

[§] Beta represents the difference in DNA methylation at the given CpG site in children born to mothers with RA(FEPRA study) as compared with children born to mothers from the general population(Generation R Study)

[#] Location in promoter, enhancer or unknown(-)