

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau

(43) International Publication Date
23 July 2020 (23.07.2020)



(10) International Publication Number
WO 2020/150705 A1

(51) International Patent Classification:

C12Q 1/6876 (2018.01) C12Q 1/6811 (2018.01)
C12Q 1/6874 (2018.01)

(21) International Application Number:

PCT/US2020/014251

(22) International Filing Date:

20 January 2020 (20.01.2020)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/794,364 18 January 2019 (18.01.2019) US

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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP,

(54) Title: DNA METHYLATION MEASUREMENT FOR MAMMALS BASED ON CONSERVED LOCI

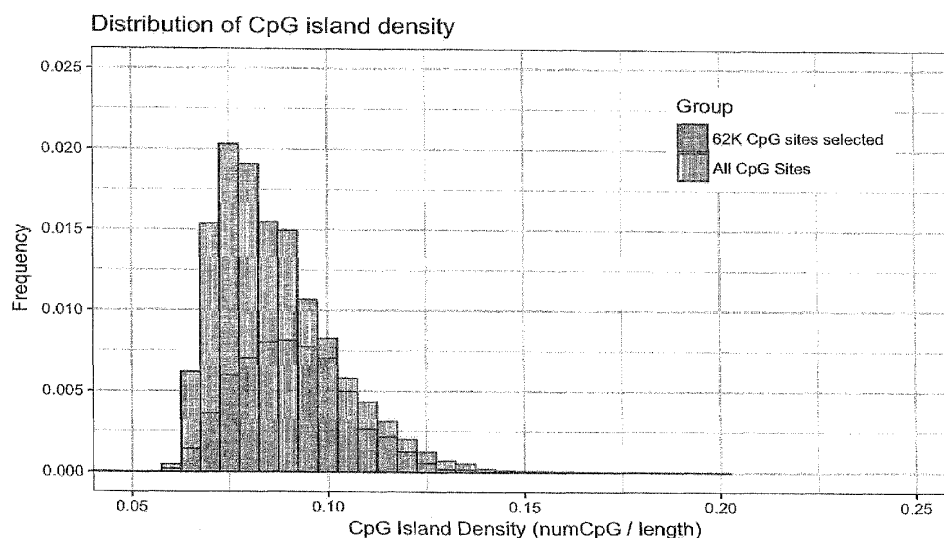


FIGURE 1

(57) Abstract: While methylation chips have been widely used in human studies over the last ten years, methylation chips for non-human species have not, perhaps due to lack of sufficient demand and/or because species specific methylation chips may be suboptimal for cross-species comparisons. To address challenges in this technology, we developed an algorithm, Conserved Methylation Array Probe Selector (CMAPS), 10 which repurposes the degenerate base technology used to tolerate within-human variation to tolerate cross-species mutations. CMAPS performs a greedy search to obtain a maximal number of species that can be targeted using a probe for any CpG in the human genome, based on a multiple sequence alignment. CMAPS then ranks all the probes and chooses a final set so that arrays can be made that can query a large 15 number of mammalian species and varied genomic positions based on external annotations of exons, CpG islands and hyper versus hypo methylated regions.

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KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME,
MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ,
OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA,
SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR,
TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *of inventorship (Rule 4.17(iv))*

Published:

— *with international search report (Art. 21(3))*