bioRxiv preprint doi: https://doi.org/10.1101/2023.03.13.531968; this version posted October 2, 2023. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-ND 4.0 International license.

985 Supplementary Figure 1: Δ9-THC induces ESCs proliferation for as low as 1nM.

986 **(A)** Whisker boxplot indicating the median cellular viability of ESCs exposed to the different Δ 9-THC doses 987 and associated errors. **(B)** Whisker boxplot indicating the median number of viable cells exposed to the 988 different Δ 9-THC doses indicated and associated errors. At least three independent biological repeats with

- three technical replicates (N=3, n=3). Statistical significance: *(p<0.05), ***(p<0.001), ****(p<0.0001).
- 990

991 Supplementary Figure 2: Δ9-THC induces alteration in ESCs cell cycle.

992 **(A)** Representative flow contour plots showing distribution of BrdU-stained and DAPI-stained cells, 993 exposed to the different doses of Δ 9-THC indicated. The frequency of events in each gate is indicated. **(B)** 994 The median percentage of events and associated errors for each cell cycle gate were plotted in histograms. 995 At least three independent biological repeats with three technical replicates (N=3, n=3). Statistical 996 significance: *(p<0.05), **(p<0.01).

997

998 Supplementary Figure 3: Δ9-THC exposure in male ESCs also provokes cell proliferation.

(A) Whisker boxplot indicating the median cellular viability of male ESCs (the R8 cell line, see Material and Methods section) exposed to the different Δ 9-THC doses and associated errors. (B) Whisker boxplot indicating the median number of viable cells exposed to the different Δ 9-THC doses indicated and associated errors. At least three independent biological repeats with three technical replicates (N=3, n=3). Statistical significance: *(p<0.05), **(p<0.01), ****(p<0.0001).

1004

Supplementary Figure 4: hESCs cell number decreases upon Δ9-THC exposure.

1006 **(A)** Whisker boxplot indicating the median cellular viability of human embryonic stem cells continuously 1007 exposed to 100nM Δ 9-THC doses over 6 days and associated errors. **(B)** Whisker boxplot indicating the 1008 median number of viable cells exposed to 100nM of Δ 9-THC doses indicated and associated errors. For (A 1009 and B), 6 technical repeats of 2 biological repeats (n=12) were plotted. Statistical significance: **(p<0.01).

1010

bioRxiv preprint doi: https://doi.org/10.1101/2023.03.13.531968; this version posted October 2, 2023. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-ND 4.0 International license.

1011 Supplementary Figure 5: hESCS metabolism is slightly but significantly impacted by Δ9-THC exposure.

1012 The NAD(P)+/NADPH ratio of hESCs exposed to 100nM of Δ 9-THC was normalized to the one measured in 1013 the mock-treated condition. Median and associated errors were plotted in whisker boxplots. One 1014 representative experiment out of two independent experiments was used to plot results. Statistical 1015 significance: *(p<0.05).

1016

Supplementary Figure 6: Extracellular acidification rates and oxygen consumption rates in ESCs and EpiLCs upon Δ9-THC exposure.

1019 (A and B) Traces were plotted for the extracellular acidification rate (ECAR) measurements in ESCs and 1020 EpiLCs, respectively, exposed to the different Δ 9-THC doses indicated and normalized to the protein 1021 content. The oligomycin injection time is indicated by an arrow and allows to differentiate basal glycolytic 1022 rate from maximal glycolytic rate (when mitochondria are inhibited). The datapoints used in the main 1023 figure correspond to the first timepoint in the maximal glycolytic capacity section. (C and D) Traces were 1024 plotted for the oxygen consumption rate (OCR) measurements in ESCs and EpiLCs, respectively, exposed 1025 to the different $\Delta 9$ -THC doses indicated and normalized to the protein content. The oligomycin, FCCP and 1026 AntimycinA/Rotenone injection times are indicated by arrows and allow to differentiate basal respiration 1027 from ATP-coupled respiration and maximal respiratory capacity. The datapoints used in the main figure correspond to the second timepoint in the maximal respiratory capacity section. FCCP: Carbonyl cyanide-1028 1029 p-trifluoromethoxyphenylhydrazone. Statistical significance: *(p<0.05), **(p<0.01), ****(p<0.0001).

1030

1031 Supplementary Figure 7: Metabolite profiling in ESCs and EpiLCs upon Δ9-THC exposure.

1032 **(A and B)** Heatmaps showing the log2 of the amount of each metabolite upregulated in ESCs and EpiLCs 1033 upon exposure to 100nM of Δ 9-THC. The relative amounts of metabolites were normalized to the mean 1034 value across all samples for one same condition and to the number of viable cells harvested in parallel on 1035 a control plate. **(C)** Histograms showing the ratio of reduced to oxidized glutathione (GSH/GSSG) based on 1036 the amounts measured in the metabolomics profiling.

1037

Supplementary Figure 8: Extracellular acidification rates and oxygen consumption rates in ESCs upon Δ9-THC and 2-DG exposure.

1040 (A) Traces were plotted for the extracellular acidification rate (ECAR) measurements in ESCs exposed to 1041 100nM of Δ 9-THC and 10mM of 2-DG, as indicated, and normalized to the protein content. The oligomycin 1042 injection time is indicated by an arrow and allows to differentiate basal glycolytic rate from maximal glycolytic rate (when mitochondria are inhibited). (B) Traces were plotted for the oxygen consumption 1043 1044 rate (OCR) measurements in ESCs exposed to 100nM of Δ 9-THC and 10mM of 2-DG, as indicated, and 1045 normalized to the protein content. The oligomycin, FCCP and AntimycinA/Rotenone injection times are 1046 indicated by arrows and allow to differentiate basal respiration from ATP-coupled respiration and maximal 1047 respiratory capacity. FCCP: Carbonyl cyanide-p-trifluoromethoxyphenylhydrazone. Statistical significance: *(p<0.05), **(p<0.01). 1048

Supplementary Figure 9: Δ9-THC exposure does not alter markers of pluripotency.

1050 Gene expression profiles of markers for the inner cell mass (ICM) and epiblast. Histograms show the

1051 median and associated errors of normalized gene counts in each condition, as indicated.

bioRxiv preprint doi: https://doi.org/10.1101/2023.03.13.531968; this version posted October 2, 2023. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-ND 4.0 International license.

1052

Supplementary Figure 10: Δ9-THC exposure alter the expression of some epigenetic modifiers.

Histograms show the median and associated errors of normalized gene counts in each condition, as
indicated. Only genes with |(log2(FC)|>0.25 and p-value<0.01 from Supplementary Table 1 were plotted.
Statistical significance: **(p<0.01), ***(p<0.001), ****(p<0.0001).

1057

1058 Supplementary Figure 11: PGCLCs gating and sorting strategy.

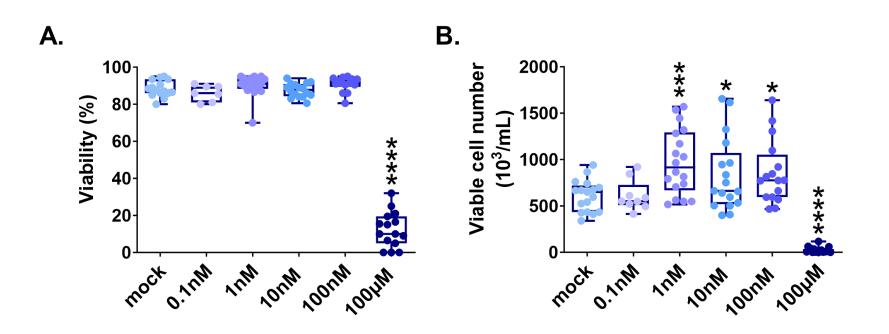
(A) Representative flow contour plots showing distribution of events and gating based on embryoid bodies dissociation. (B and C) Representative flow contour plots to isolate singlets based on width to height ratios on the side scatter and front scatter, respectively. (D) Gating strategy for Stella:CFP versus Blimp1:mVenus on the negative control, corresponding to embryoid bodies obtained in an induction medium without cytokines and BMPs (GK15 only). (E) Gating strategy for Stella:CFP versus Blimp1:mVenus on mock-treated cells, corresponding to embryoid bodies obtained in an induction medium cytokines and BMPs. DN: double negative, SP: single positive, DP: double positive subpopulations.

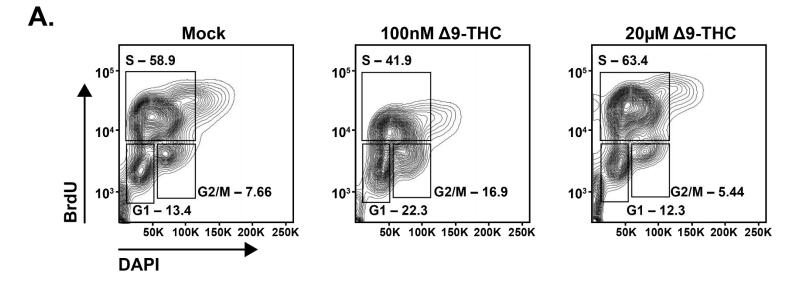
Supplementary Figure 12: Male PGCLCs deriving from ESCs and EpiLCs exposed to 100nM of Δ9-THC proliferate.

(A) Diagram illustrating Δ 9-THC exposure scheme and experimental strategy. (B) Representative flow 1068 contour plots showing distribution of live-gated events, gating strategy for Stella:CFP versus 1069 1070 Blimp1:mVenus and percentages of cells in each subpopulations for ESCs and EpiLCs exposed to 100nM of 1071 Δ 9-THC. DN: double negative, SP: single positive, DP: double positive subpopulations. (C) The percentage 1072 of events in the gates associated to each subpopulation was normalized to the one measured in the mocktreated condition. Median and associated errors were plotted in whisker boxplots independently for each 1073 1074 subpopulation. At least three independent biological repeats with three technical replicates (N=3, n=3). Statistical significance: *(p<0.05). 1075 1076

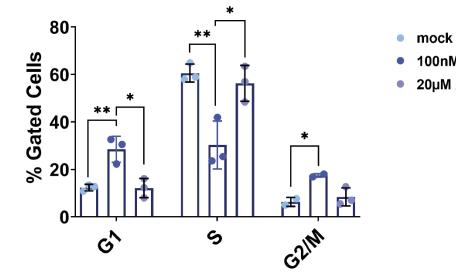
1077 Supplementary Figure 13: No residual Δ9-THC is detected in day 5 embryoid bodies.

- 1078 Intracellular levels of Δ9-THC were quantified by mass spectrometry in EpiLCs on the day of aggregate
 1079 formation and in day 5 embryoid bodies (referred as to "EpiLCs" and "PGCLCs"). Histograms show the
- 1080 median and associated errors of two independent quantifications. Statistical significance:
- 1081 ****(p<0.0001).
- 1082

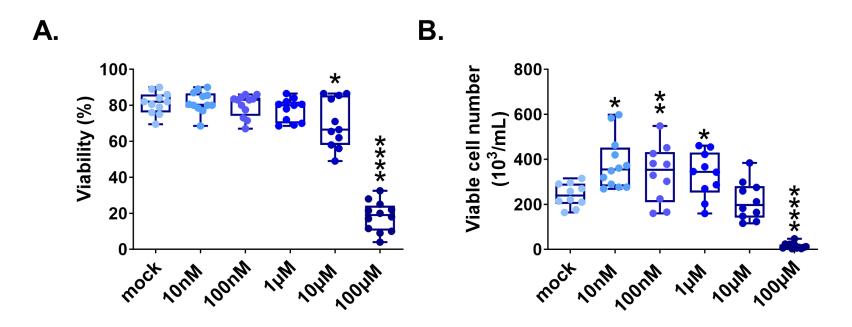


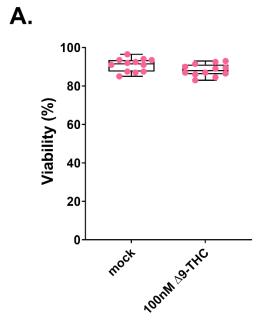


Β.

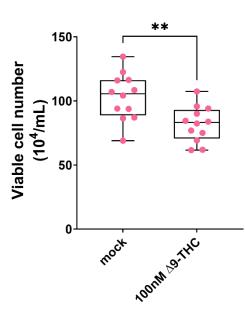


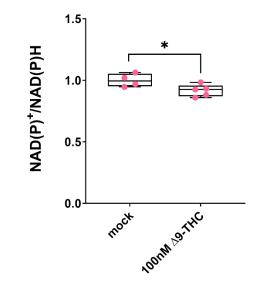
- 100nM ∆9-THC
- $\textbf{20}\mu\textbf{M} \ \Delta\textbf{9-THC}$

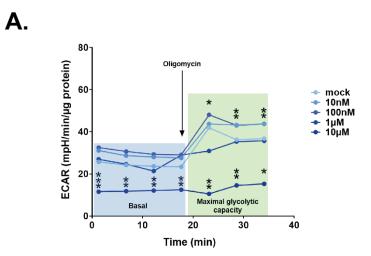


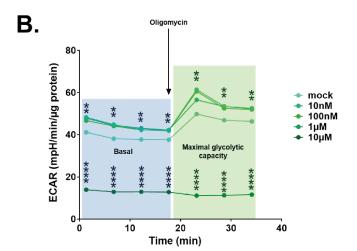


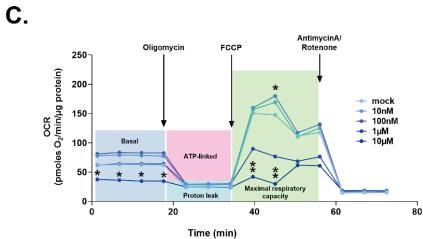


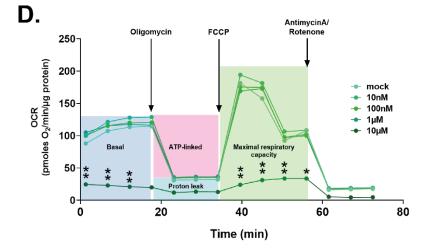


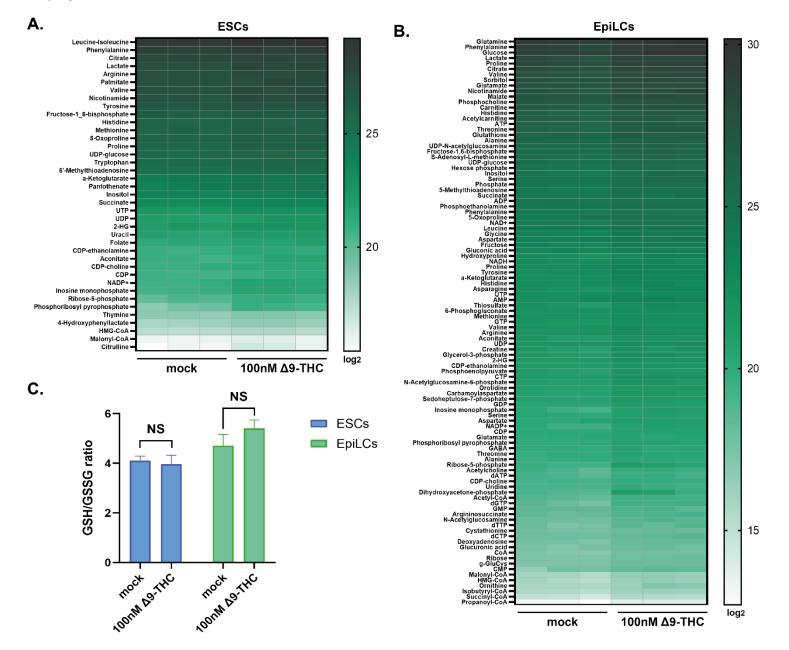




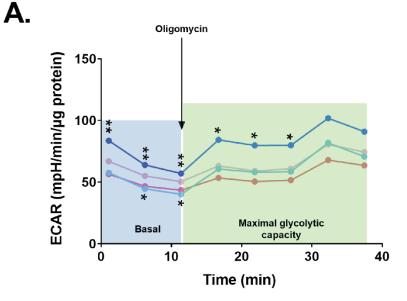








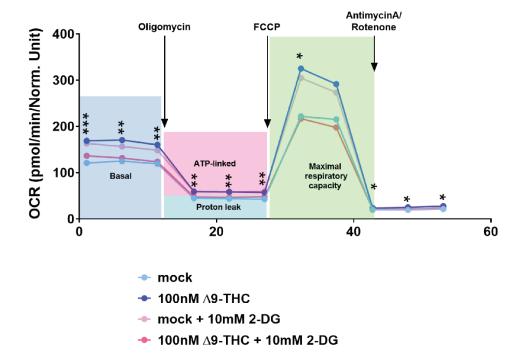
1100

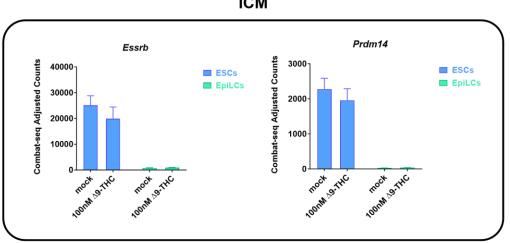




- 100nM ∆9-THC
- mock + 10mM 2-DG
- ◆ 100nM △9-THC + 10mM 2-DG

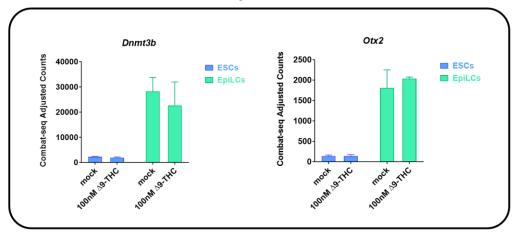


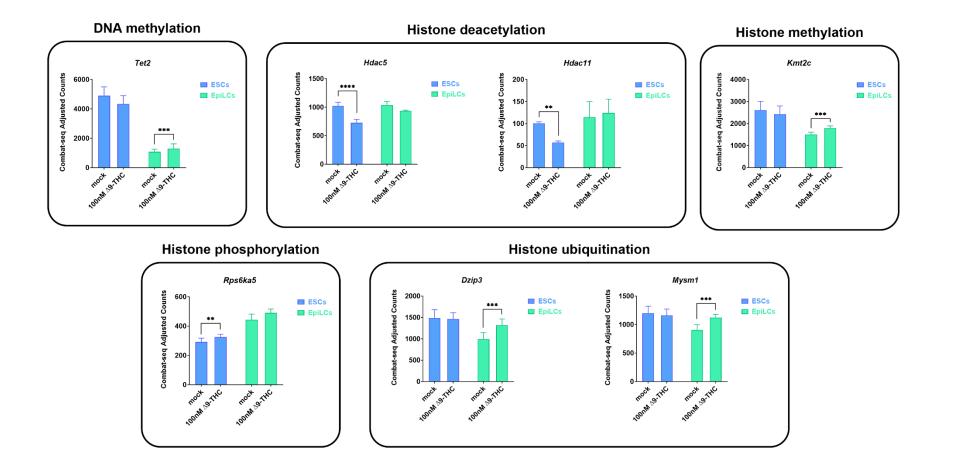


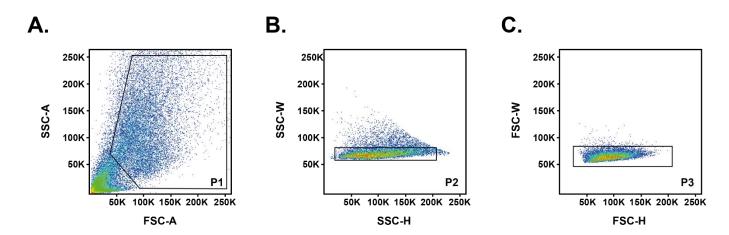
















Ε.

