

Figure S1.

(A-B) Western blots of Neuro 2A (N2A) cell lysates showing low levels of endogenous GR and MR.
(A) Untransfected N2A cells, N2As + GR (wild-type), N2As + EGFP-tagged GR
(B) Untransfected N2A cells, N2As + MR (wild-type), N2As + mCherry-tagged MR.
Primary antibodies used were rabbit anti-GR (M-20) and mouse anti-MR (1D5) at 1:5000 and 1:4000.

(C) CORT induces MMTV-luciferase reporter expression from MR, mCherry-MR and EGFP-GR transfected cells. COS1 cells (with no endogenous GR/MR) were transiently transfected with MR/GR expression vectors (1 μ g), pFC31-luc MMTV-luciferase reporter (1.98 μ g) and pRL-CMV control (0.02 μ g) plasmids. Cells were harvested after 24 hrs CORT 100 nM treatment and assayed with Dual-Luciferase® Reporter Assay System (Promega). Data was normalised to Renilla luciferase expression and are represented as means, \pm SEM, $n = 3$.

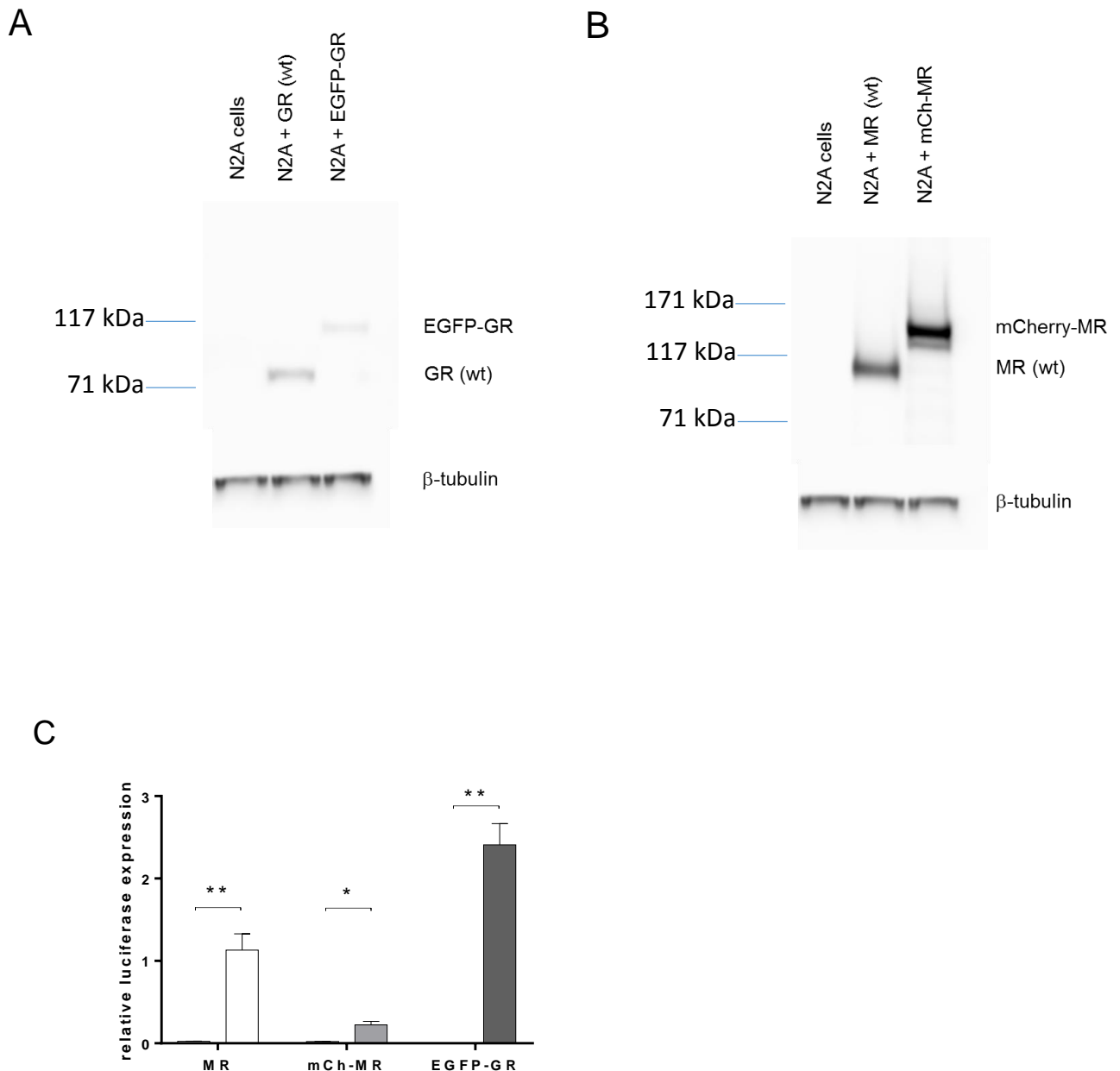


Figure S2.

Motif probability matrices of known motifs used to calculate motif frequency for GRE, GATA3 and AP-1 motif mapping.

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>VAGRACAKWCTGTTC GRE(NR),IR3/RAW264.7-GRE-ChIP-Seq(Unpublished)/Homer 7.809859 -4041.196255 0
T:1437.0(71.35%),B:1197.7(2.63%),P:1e-1755 Tpos:101.8,Tstd:27.3,Bpos:98.0,Bstd:69.4,StrandBias:-0.0,Multiplicity:1.13
0.232 0.373 0.231 0.163
0.619 0.006 0.262 0.113
0.058 0.005 0.924 0.013
0.433 0.120 0.287 0.160
0.957 0.008 0.015 0.020
0.002 0.963 0.008 0.027
0.767 0.019 0.135 0.079
0.123 0.231 0.249 0.397
0.259 0.179 0.165 0.397
0.210 0.403 0.228 0.160
0.101 0.044 0.009 0.846
0.006 0.015 0.972 0.007
0.021 0.026 0.018 0.935
0.179 0.288 0.131 0.401
0.041 0.865 0.014 0.080
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>AGATAASR GATA3(Zf)/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer 5.938282 -2390.596730 0
T:3368.0(49.21%),B:5753.5(14.09%),P:1e-1038 Tpos:100.1,Tstd:42.5,Bpos:100.6,Bstd:63.6,StrandBias:-0.0,Multiplicity:1.21
0.662 0.066 0.006 0.266
0.001 0.007 0.991 0.001
0.989 0.004 0.001 0.006
0.002 0.023 0.001 0.974
0.825 0.061 0.011 0.103
0.778 0.048 0.129 0.045
0.184 0.401 0.348 0.067
0.433 0.167 0.359 0.041
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>GATGACTCATCN Jun-AP1(bZIP)/K562-cJun-ChIP-Seq(GSE31477)/Homer 8.486263 -3.459607e+04 0
74838.0,37419.0,20963.2,20135.0,0.00e+00
0.244 0.149 0.396 0.211
0.473 0.218 0.268 0.041
0.001 0.001 0.001 0.997
0.001 0.001 0.991 0.007
0.997 0.001 0.001 0.001
0.051 0.462 0.440 0.047
0.021 0.001 0.001 0.977
0.024 0.974 0.001 0.001
0.997 0.001 0.001 0.001
0.050 0.258 0.227 0.465
0.210 0.394 0.153 0.243
0.241 0.319 0.211 0.229
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Figure S3.

Distribution of sizes of identified MACE regions from CHIP-nexus samples, treatments ii and iii, for MR, GR and background datasets.

