

Supplementary Figure 1: Effect of GR α overexpression on GR chaperone expression. HUVECs (3 DEX-sensitive, and 3- DEX-resistant) were transfected with a *GR-1C* α vector to overexpress GR α , followed by starvation and DEX (1 μ M) treatment for 24 h. Total protein lysates were prepared and analyzed by immunoblotting for the expression of the GR chaperones FKBP51, BAG1 and HSP90. Representative immunoblots are shown.

GR Proximal Promoter*







-1720 -1700 -1680 -1660 -1640 -1620 CGCGCCTGAGGTTTCTAAGTGGCCCCTTTTAGAAAAAGACCCCCTGTAACCGTAATGGTT -1600 -1580 -1560 TTGTGCTGCGATTTTTACAAGTGCTAGTTTGACGTTTGGGGTTGCAGACTTGATAATTGC -1540 -1520 -1500 AACCTTGTAATACCACTTAAGACCCTCTGGCATGGTTCATTAGGGCCAATTAATGTGGCT -1480 -1460 -1440 GGGTTATTTGCAACTTAAACTGGGGGGATAATGTCGCTTGAGGGAGCGTTTTCGTTTTAGG -1420 -1400 -1380 AAATATTGTTTTGGTTTCGGGTTTGAAGGCAGCTGTCAAAAAAGCGGCATGGAAATTCAT -1360 -1340 -1320 TGGGCTCCATTCGATACCTCGTGTTTAGAGATCGTTATCGCCTCAGATAAACGGGGCAGA -1300 -1280 -1260 GAGGTGGGGAGATAAGCAGTTTACCCTCAAGATTTGTAGTGGCAAGTCCACACCCCTCTC -1220 -1240 -1200 TCTACCTTCATATTCACTTTTCAGTGAGGGCCCAGTGACATTTATGCTGCCTAACGTCATC GCATAGGAAAAGTTACCTTTTATTGGACGGGATTTGACTATAGTGTCCCAAATGCGCTTC -1100 -1120 -1080 TCCGTCTTAGCCCATCTCTTAAAACACCCCTGATTAACGATATACTAACAGTCTTACTCTC -1040 -1020 -1060 TTGAGAATAGGCTGAGAATTGGGATAGGTGAAGGTTTGGATAGGTGAAGGCAGAGAAAAT -980 -960 1 TATTTTGAACATTTTACTGGATACAGTTGTACCTGAATTTATATGAATGTGATTTTACGG -920 -940 -900 -880 -860 -840 ATGTAATAGCATTTCATATTGAGGATCTCAAGCAATGTAAACAAATGTAGCTTAATCTAG -800 -820 -780 ATGTTTTTGTGAGTTATGATAAGGGTCAGCTATATTTAAGTTATGTAAGCTAACAACGTA -760 -740 -720 1 GTGAGAAACTACTACACCTTCTCTCTGCTCTTTAAAATCTAAATTTTAGTTGGCCTATA -700 -680 -660 TAAAGTGTATCTCATTTCATATATCCAAAATTTGGAGGTAGGCACATCCAGTCAGAAGTA -640 -620 -600 1 TGGGTTAAAAAGCCTTTTCCCAGCCTGTCGGAAGATAAGCAGATCAGCATTGTTTATTTT



Supplementary Figure 2. The *GR* proximal promoter is shown with its 7 untranslated exons 1 (highlighted in yellow) followed by intron 1 and exon 2 (translational starting point highlighted in green). Analysis of the *GR* proximal promoter was performed with the aid of MattInspector (Genomatix Inc.). Putative Initiator elements (Inr) are shown in green squares and the putative downstream promoters (DPE) are shown in blue squares (dashed squares represent partial sequences instead of consensus sequences). Putative transcription factor elements with a matrix/core similarity higher than 0.9 were selected; transcription factors known to be expressed in the cardiovascular system are shown in green, and the remainder in red.



Supplementary Figure 3: Bisulfite sequencing of *GR* promoters 1D and 1F. Dex-sensitive (n=3-4) and Dex-resistant (n=3-4) HUVEC DNA was treated with bisulfite , PCR-amplified, and sequenced as described under methods. Each oval represents one CpG, black ovals represent methylated CpGs. The average \pm standard errors for the methylation percentages is shown below.

	Dex-Sensitive	Dex-Resistant	Р
	(n=15)	(n=10)	
Maternal age, y	31.5 ± 2.0	30.4 ± 2.3	0.701
Pre-pregnancy BMI, kg/m ²	27.2 ± 1.1	22.0 ± 1.3	0.038*
Maternal weight gain, lb	31.8 ± 4.2	37.5 ± 3.8	0.450
Systolic blood pressure, mm Hg	115.8 ± 2.0	106.5 ± 3.1	0.025*
Diastolic blood pressure, mm Hg	72.3 ± 1.7	68.3 ± 1.4	0.173
Smoking, yes/no	3/12	0/10	0.190
Gestational age (wk)	39.8 ± 0.3	39.1 ± 0.4	0.080
Newborn sex (F/M)	6/9	4/6	0.558
Race, African American/Caucasian (%)	6/9 (40)	5/5 (50)	0.246
		2 4 0 4 1 0 4	
Birth weight (g)	3525 ± 114	3401 ± 181	0.574
Umbilical cord blood cortisol, nmol/L	441 ± 10.2	401 ± 11.1	0.061

Supplementary	Table 1.	Clinical	Characteristics	of the	Study	Subjects
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*p<0.05, Dex-sensitive vs. Dex-resistant.

Name	Sequence	Annealing Temperature (°C)	PCR product size
GR-α	5'-CAAAGAGCTAGGAAAAGCCAT-3' 5'-CAATACTCATGGTCTTATCCAA-3'	54	161
GR-β	5'-TCAGTTCCTAAGGACGGTCT-3' 5'-ACCACATAACATTTTCATGCAT-3'	50	175
GR-P	5'-TGTTTTGCTCCTGATCTGA-3' 5'-CCTTTGTTTCTAGGCCTTC-3'	50	223
1F	5'- AGAAACTCGGTGGCCCTCTTA-3' 5'- AAGCACACTGCTGGGGGTTTT-3'	57	112
1H*	5'-GGCGTTATCTGTTAGAAGTG-3' 5'-ATAGAAGTCCATCACATCTC-3'	48	149
18S	5'-CGGCTACCACATCCAAGGAA-3' 5'-GCTGGAATTACCGCGGCT-3'	60	78

Supplementary Table 2¹. SYBR green PCR primers for *GR* mRNA isoforms

¹PCR settings: 15 min hotstart activation at 94 °C, 55 cycles of 15 sec at 94 °C, 20 sec at annealing temperature, and 20 sec extension at 72 °C. Quantification was set at extension.

*Fluorescence quantification set at 76 °C, instead of 72°C.

Name*	Sequence	PCR size	Position**
1B Mlu II Bgl II	5'-AACTTGGACGCGTGCCCTGG-3' 5'-CACCGCAAGATCTGGGCGGC-3'	409	-3568/-3977
1C Kpn- Xho I	5'-GGAAGGAGGTACCGAGAAA-3' 5'-TCGGCCGCTCGAGCTGCGG-3'	568	-2646/-3214
1D Kpn I Xho I	5'-AACTGTTGGTACCTTAGGGGGC-3' 5'-TAATCCTGCTCGAGCGCTCGG-3'	672	-4443/-5115
1F Kpn I Xho I	5'-TGGTGGGGTACCTGCCGG-3' 5'-CCACCGAGTTTCTCGAGTTTCT-3'	402	-3167/-3569
1H Kpn I Xho I	5'-GCGAGCGGTACCTCTGCC-3' 5'-CGCCCAGATCTAACAGAT-3'	607	-1775/-2382

Supplementary Table 3. Primers used to clone human *GR* proximal promoters

*Name of the *GR* promoter and the restriction enzyme sites used.

**Relative to translational start codon ATG in exon 2

Name	Sequence	Annealing Temperature (°C)	Location relative to Exon 1's starting site
MeDIP	5'-CGCCCCTGCTTTCCTTAAT-3'	56	-267 to -156
Prom 1B	5'-TGTGCTCACACTCGAAGGAA-3'		
MeDIP	5'-ACCCTTTTTCCTGGGGAGTT-3'	55	-371 to -189
Prom 1C	5'-ATGCAACCTGTTGGTGACG-3'		
MeDIP	5'-GGGCAACTAGGTCAAGCAGT-3'	55	-567 to -416
Prom 1D	5'-CGCTGAGCAACTCCATGTTA-3'		
MeDIP	5-CTATCCCGTCCCTTCCCTGAA-3'	56	-305 to -187
Prom 1F	5-TGTCACTTCGAAAGGGGGCTAC-3'		
MeDIP	5'- CGGGAATCCTGGCCTCTTTT-3'	56	-172 to -50
Prom 1H	5'- CGTGCAAATATTCGGGCGAG-3'		
		10	
Bisulfite	5'- AAATTTTTTTGGTTGAGGGTTTTA -3'	40	-413 to -191
Prom ID	5 - IUUTIUITAATIUIUAAAAATAAAU -3		
Bisulfite	5'- TGTGTAATTTTGTAGTTTTTTTGA-3'	40	-218 to -42
Prom 1F	5'- AAAACTCACTCTACCCCTTAACAAC -3'		

Supplementary Table 4. Primers for MeDIP SYBR green PCR analysis and bisulfite sequencing.