Supplementary Table 1

		ChIP-qPCR data				ChIP-ddPCR data		
		CT values				Copies/uL		
Sample	IP	*Tat* promoter	Negative region	deltaCT (*Tat* - Negative)	Fold change (*Tat*/negative)*	*Tat* promoter	Negative region	Fold change (*Tat*/negative)
Control replicate 1	IgG	34.3	32.9	1.4	0.4	0.9	3.6	0.3
	GR	27.5	33.4	-6.0	62.2	52.3	3.1	16.9
	H3K27ac	22.2	27.8	-5.7	51.6	789	21.3	37.0
Control replicate 2	IgG	35.3	34.6	0.7	0.6	0.77	1.5	0.5
	GR	27.2	32.6	-5.4	42.2	79	2.5	31.6
	H3K27ac	23.3	27.3	-4.1	16.6	468	34.8	13.4
Dexamethasone replicate 1	IgG	33.8	33.6	0.2	0.9	3	1.8	1.7
	GR	27.5	33.6	-6.1	70.0	49.7	1.2	41.4
	H3K27ac	23.2	26.4	-3.1	8.8	511	62.1	8.2
Dexamethasone replicate 2	IgG	33.0	32.7	0.3	0.8	3.1	2.6	1.2
	GR	26.3	32.0	-5.7	52.0	158	5.4	29.3
	H3K27ac	22.7	26.8	-4.0	16.2	675	64.4	10.5

*calculated as $2^{-deltaCT}$

Legend: Table showing the raw ChIP-qPCR data (CT values) and raw ChIP-ddPCR data (copies/µl) for mouse liver chromatin samples (as indicated in the first column) immunoprecipitated with IgG, or antibodies to GR or H3K27ac (as indicated in the second column). For ChIP-qPCR data, the fold-change of positive signal (Tat promoter) over negative signal was calculated by subtracting the CT values as indicated, then calculating fold-change as $2^{-deltaCT}$. For ChIP-ddPCR data, the fold-change was calculated as the Tat promoter signal divided by the negative control signal.