Figure S1. Nascent RNA analysis of GR regulated genes and time dependent occupancy of GR binding in the Hepa1c1c7 cell line. GR responsive genes in the hepatocyte cell line, Hepa1c1c7, also show a time-dependent variation in the response to hormone and exhibit a similar diversity of kinetic profiles as observed in the mammary adenocarcinoma cell line (3134) and the pituitary corticotroph (AtT-20). Nascent transcript levels were determined after hormone addition for members of the rapid induction class [Sgk, Glul (Fig. S1, panels A-B)], the transiently induced class [Tgm2 (Fig. S1, panel (C)] and the continuously induced class [Sbp1 (Fig. S1, panel D)]. Transcript levels were also determined for the rapidly repressed class [Ccl2 (Fig. S1, panel E)] and the continuously repressed class [Plk2 (Fig. S1, panel F)]. Error bars show the standard deviation from the mean. q-PCR experiments represent three independent experiments (biological replicates) performed in duplicate (technical replicates).

The interaction of GR binding at hepatocyte responsive genes follows a similar complex and variable pattern during hormone treatment as observed in the 3134 and AtT-20 cell lines. GR binding can track closely with nascent transcript levels (Fig. S1, panels B, C, F) however, GR occupancy can sometimes be uncoupled from transcript levels (Fig. S1, panels A, E).

Primer sequences for q-PCR characterization of nascent RNA in Hepa1c1c7 are as follows:

Sbp1	Forward	CTGCCTGGTCTCATCTCCTC
Sbp 1	Reverse	CTCTAGTAAGACATGAGGTTAA

Primer sequences for GR ChIP in Hepa1c1c7 are as follows:

Sbp1	Forward	ATGAGCCTGTTCAACCTCCC
Sbp1	Reverse	GCTGTGTGTCCTTAGGCTTC
Tgm2	Forward	GCTCCGTGTTGCCTGTTTGC
Tgm2	Reverse	TGGTTCAGGGCACAGTCTGG

Edn1	Forward	CACTCTCCATGCTGGCTGGGAT
Edn1	Reverse	CGCAGACAGGCTAGGGAACA

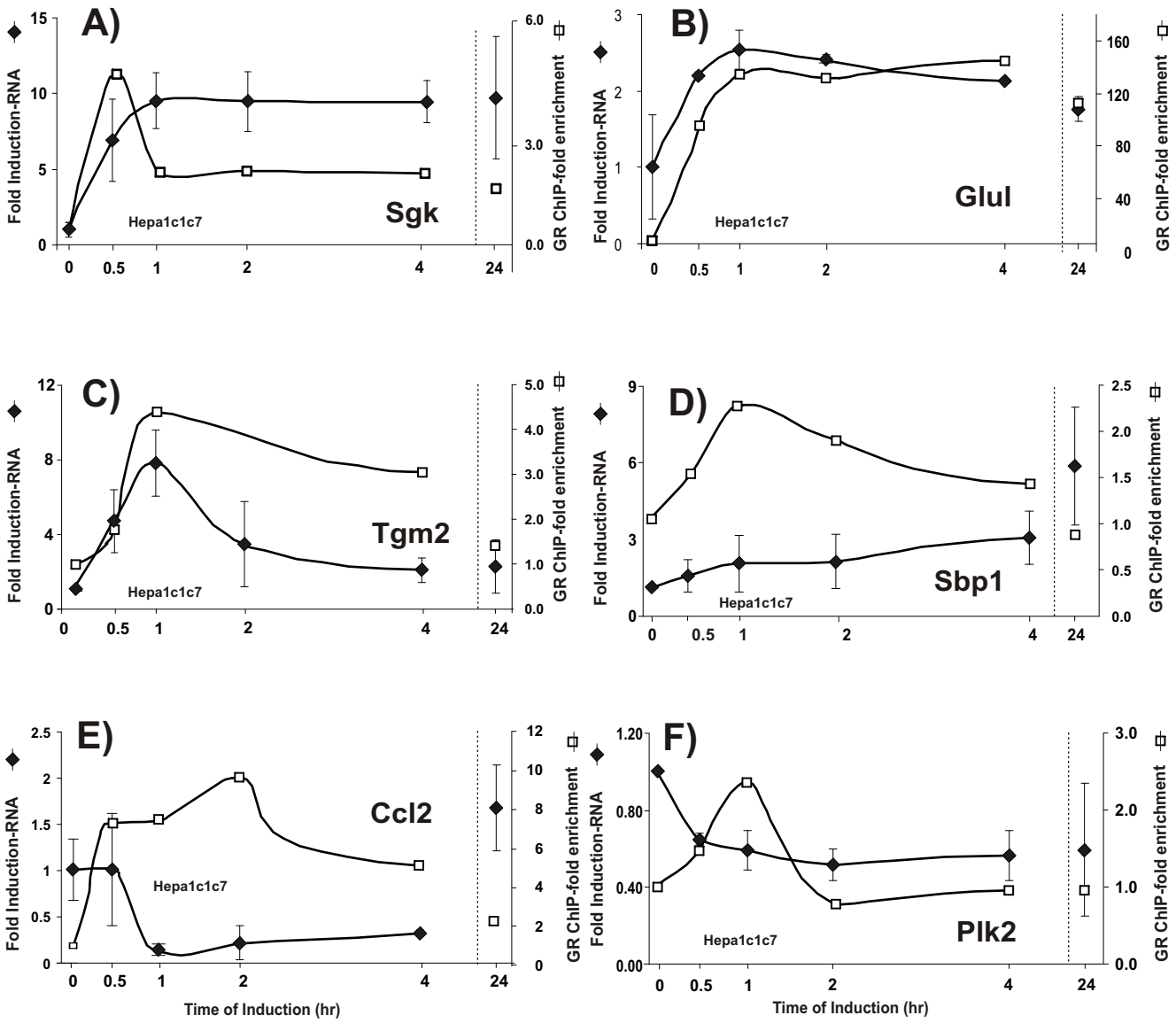
A)
Sgk
Hepa1c1c7
Fold Induction-RNA
GR ChIP-fold enrichment
B)
Glul
Hepa1c1c7
C)
Tgm2
Hepa1c1c7
D)
Sbp1
Hepa1c1c7
E)
Ccl2
Hepa1c1c7
F)
Plk2
Hepa1c1c7
Time of Induction (hr)

Fig S1