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Erratum to: **Expression of cytochrome *P*-450 3A in HT29-MTX cells and Caco-2 clone TC7** (FEBS 14812)

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As the result of a printing error two sections of both Fig. 1 and Fig. 5 were missing in the published version of this article. Please see below for the correct complete version of both figures and their legends.

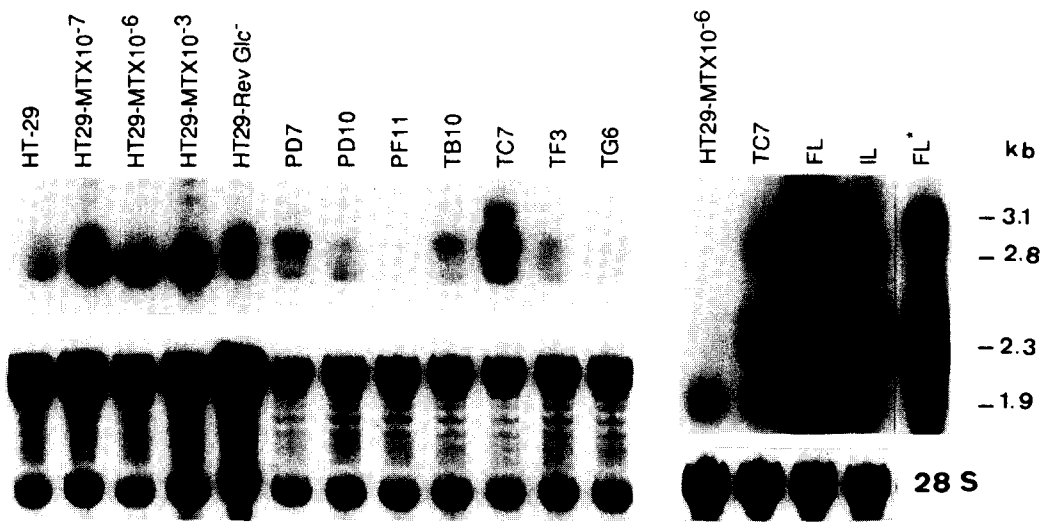

Fig. 1. Northern blot analysis of CYP3A in HT-29 subpopulations and Caco-2 clones. Left, upper panel, total RNA from post-confluent cultures (day 21) of the indicated cells (20 μg for HT-29 populations, 15 μg for Caco-2 clones) was hybridized with cDNA nf-25 (CYP3A); lower panel, Methylene blue staining of the same dehybridized membrane. Right, upper panel, the same quantity of total RNA (10 μg) from the indicated cells, fetal liver (FL) and ileum (IL) were allowed to migrate for a longer time than in left panel and hybridized with CYP3A probe; FL*, shorter exposure time in order to visualize the 1.9 kb transcript; lower panel, Methylene blue staining of 28 S from the same dehybridized membrane.

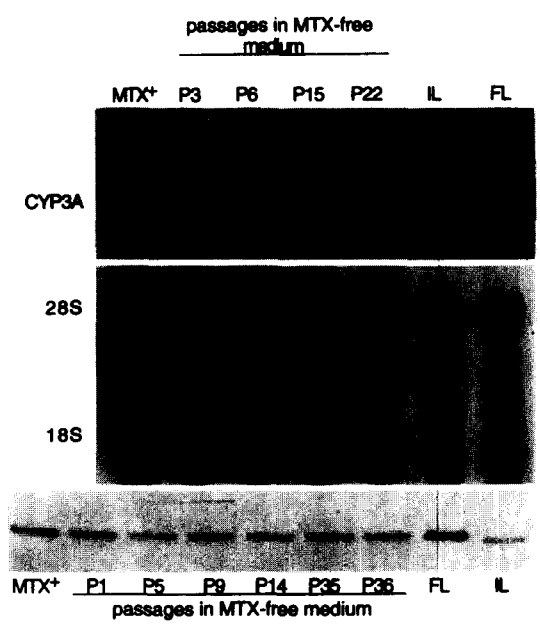

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Fig. 5. Permanence of CYP3A expression in HT29-MTX cells reversed to drug-free medium. HT29-MTX 10^{-3} cells, passage 18 (MTX^+) were subcultured for the indicated number of passages (P) in MTX free medium and analyzed at late post-confluency (day 21). Upper panel, total RNA from cells (20 μg), same IL and FL (5 mg) as in Fig. 1, hybridized with cDNA nf-25; middle panel, same membrane dehybridized and stained with Methylene blue; lower panel, Western blot analysis of microsomal fractions of the cells (40 μg) and of same preparations of FL (1 μg) and IL (5 μg) as in Fig. 3.

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