Table S1: Number of differentially expressed genes and accessible chromatin regions detected between liver, lung, and kidney tissues at FDR ≤ 0.1

| | | | Tissue comparison | |
|-------------------|-------------------------|-----------------------------|---------------------------|----------------------------|
| | | Liver/lung | Liver/kidney | Lung/kidney |
| Genes | Up-regulated | 2,473 (20.8 ^a) | $2,123 (17.9^{a})$ | 2,246 (18.9 ^a) |
| | Down-regulated | $3,236 (27.2^{a})$ | $1,441 (12.1^{a})$ | $2,527 (21.3^{a})$ |
| | Total | $5,709 (48.0^{a})$ | $3,564 (30.0^{a})$ | $4,773 (40.2^{a})$ |
| Chromatin regions | Increased accessibility | 20,194 (19.6 ^b) | $15,252 (12.9^{b})$ | $19,202 (17.4^{\rm b})$ |
| | Decreased accessibility | $20,603 (19.7^{b})$ | $12,796 (11.4^{\rm b})$ | $12,967 (11.2^{b})$ |
| | Total | $40,797 (39.3^{b})$ | $28,048 \ (24.3^{\rm b})$ | $32,169 (28.6^{b})$ |

a Percentage of all tested genes.
b Percentage of all tested chromatin regions prior to merging adjacent genomic windows.