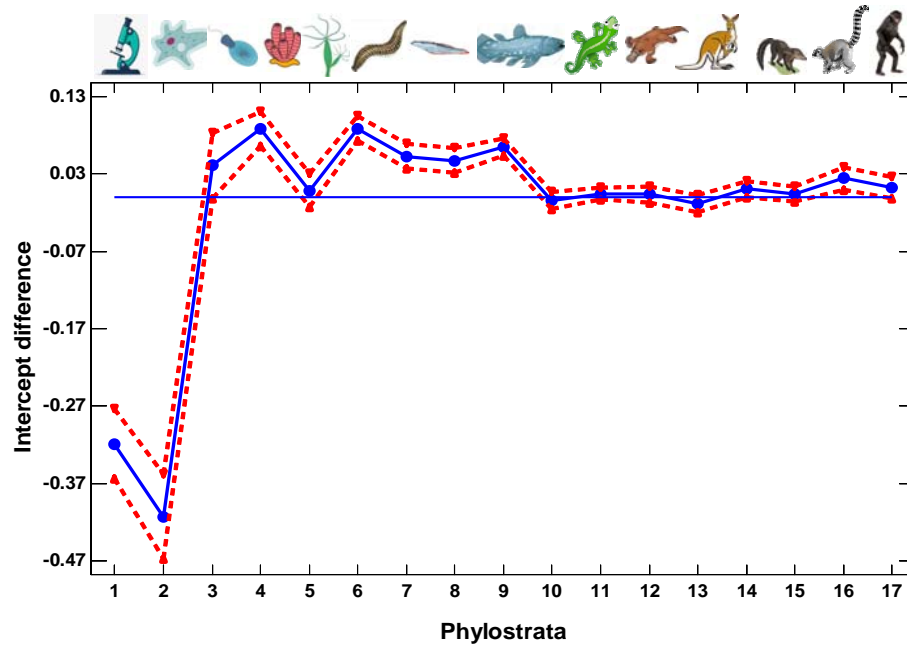
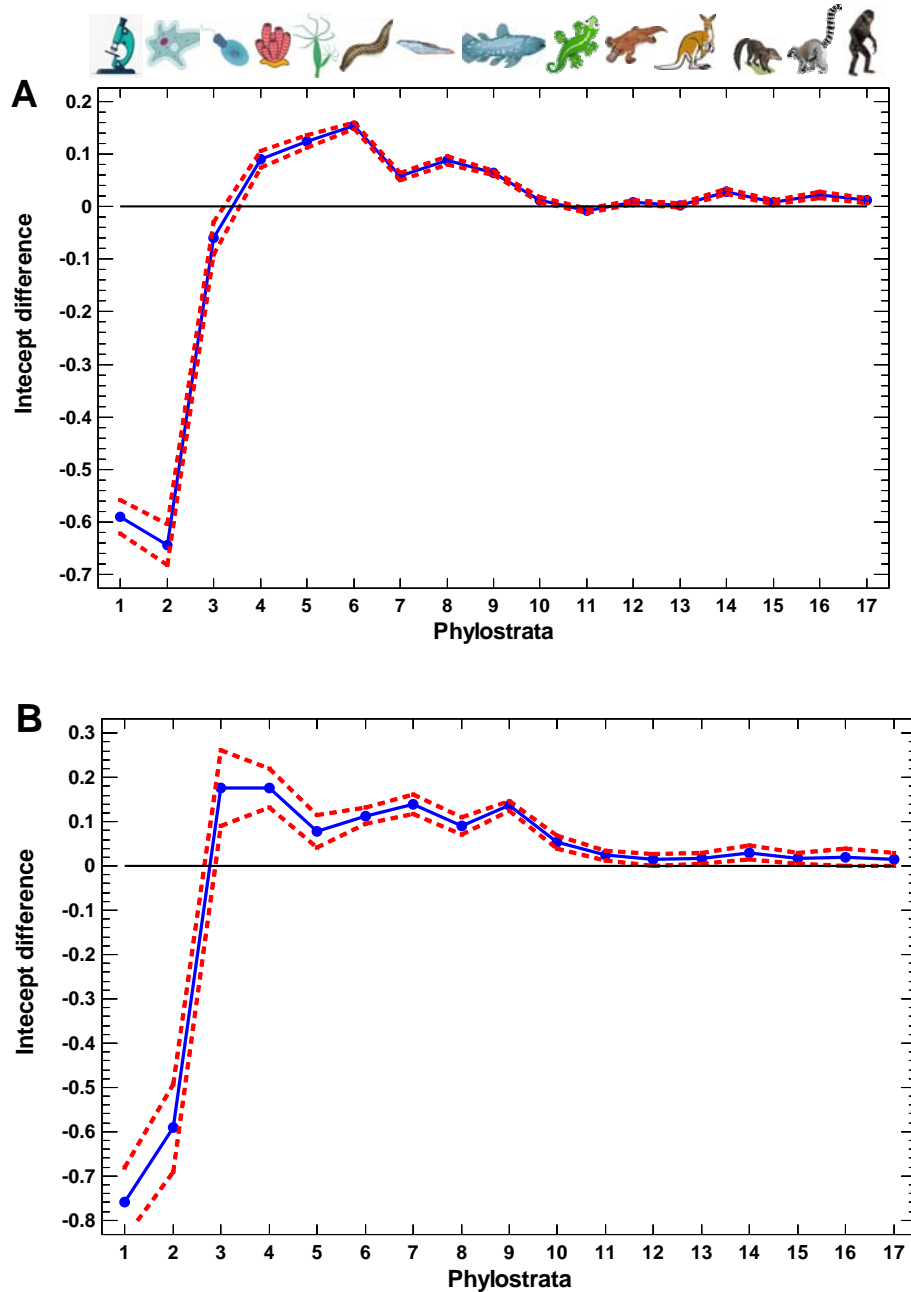


**Figure S18.** Differences in the intercepts between the regression lines of expression of UC genes (1-2 phylostrata) on cell-cycle signature in the single-cell transcriptomes of ESC cultured for 12-96 h (GSE75748, 'time course' dataset), with confidence intervals ( $p=0.05$ ). The intercept for ESC cultured for 12 h is taken for zero. The step-wise downregulation of UC genes with the increase of culturing time can be seen (with the plateau at 36-72 h).



**Figure S19.** Evolutionary profiles: the differences in intercepts between the regression lines of expression of genes belonging to different phylostrata on cell-cycle signature in the single-cell transcriptomes of ESC cultured for 96 h vs. 12 h (GSE75748, 'time course' dataset), with confidence intervals ( $p=0.05$ ).

Phylostrata: 1—cellular organisms (Prokaryota); 2—Eukaryota; 3—Opisthokonta; 4—Metazoa; 5—Eumetazoa; 6—Bilateria; 7—Chordata; 8—Vertebrata; 9—Euteleostomi; 10—Tetrapoda; 11—Amniota; 12—Mammalia; 13—Theria; 14—Eutheria; 15—Boreoeutheria; 16—Primates; 17—Hominidae.

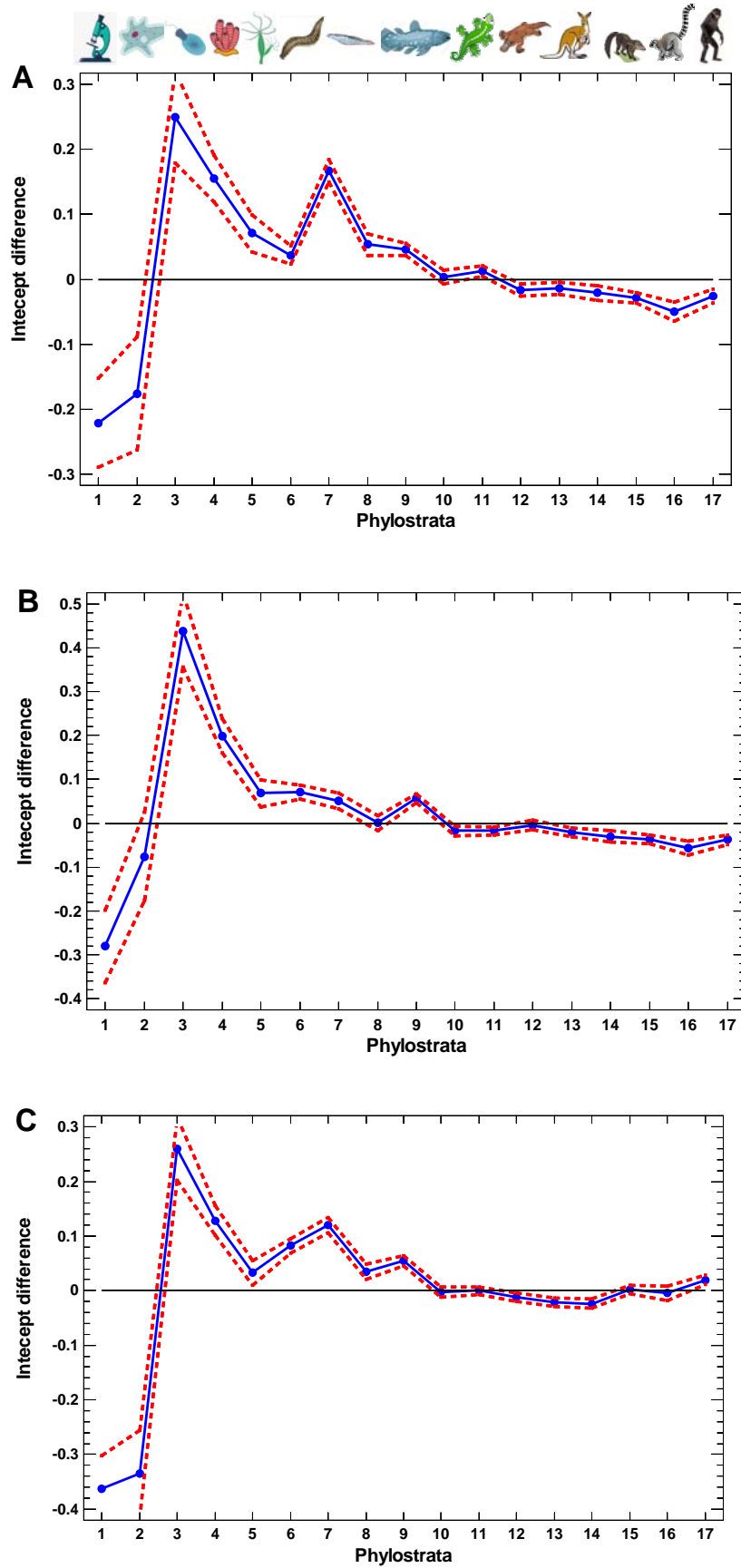


**Figure S20.** Evolutionary profiles: the differences in intercepts between the regression lines of expression of genes belonging to different phylostrata on cell-cycle signature in the single-cell transcriptomes for different cell types (with confidence intervals,  $p=0.05$ ).

**A** -- neural progenitors (NPC) vs. ESC (GSE75748, 'cell type' dataset).

**B** -- endothelial cells, mesoderm derivatives (EC) vs. ESC (GSE75748, 'cell type' dataset).

Phylostrata: 1—cellular organisms (Prokaryota); 2—Eukaryota; 3—Opisthokonta; 4—Metazoa; 5—Eumetazoa; 6—Bilateria; 7—Chordata; 8—Vertebrata; 9—Euteleostomi; 10—Tetrapoda; 11—Amniota; 12—Mammalia; 13—Theria; 14—Eutheria; 15—Boreoeutheria; 16—Primates; 17—Hominidae.



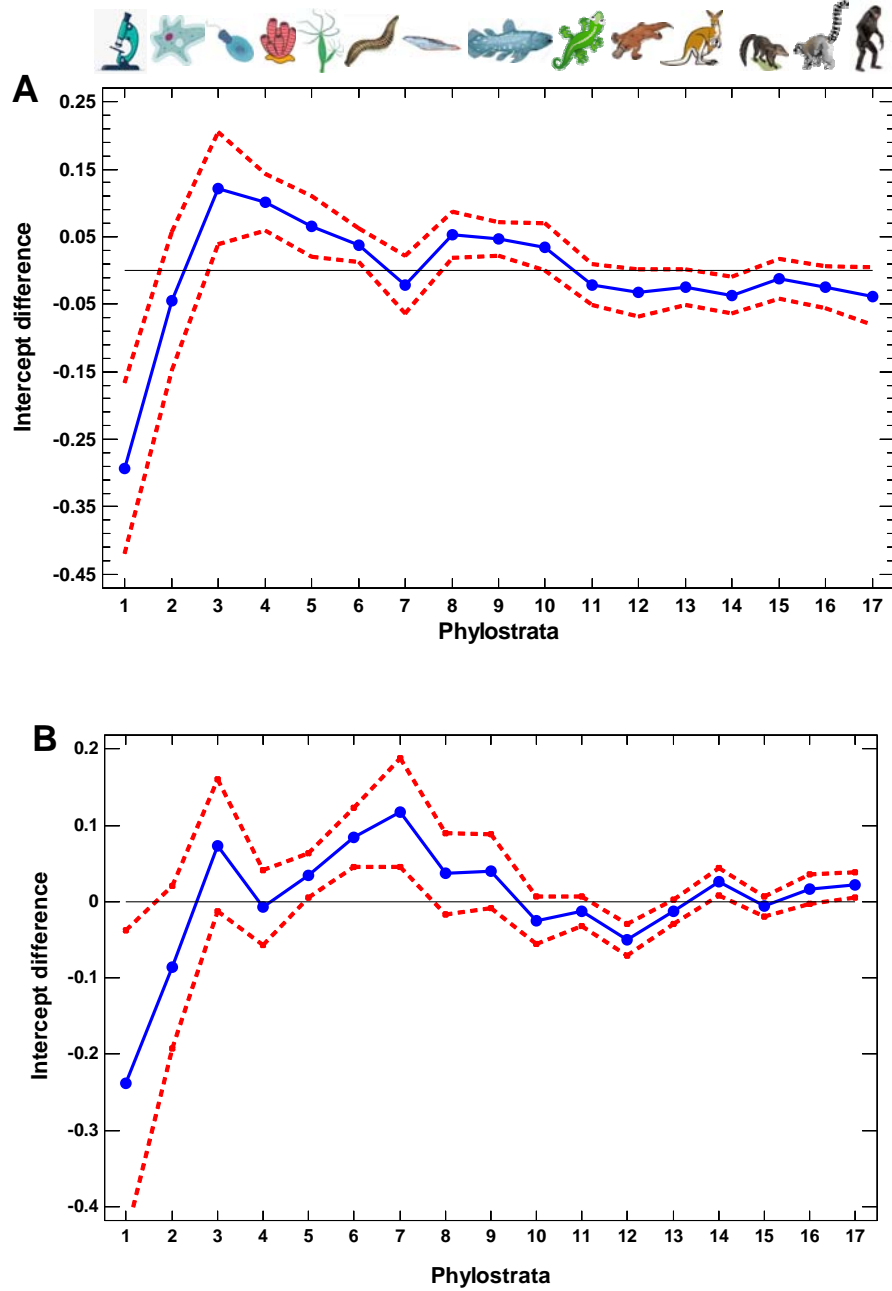
**Figure S21.** Evolutionary profiles: the differences in intercepts between the regression lines of expression of genes belonging to different phylostrata on cell-cycle signature in the single-cell transcriptomes for different cell types (with confidence intervals,  $p=0.05$ ).

**A** -- foreskin fibroblasts (HFF) compared with ESC (GSE75748, 'cell type' dataset).

**B** -- trophoblast-like cells, extraembryonic derivatives (TB) compared with ESC (GSE75748, 'cell type' dataset).

**C** -- endoderm derivatives (DEC) compared with ESC (GSE75748, 'cell type' dataset).

Phylostrata: 1—cellular organisms (Prokaryota); 2—Eukaryota; 3—Opisthokonta; 4—Metazoa; 5—Eumetazoa; 6—Bilateria; 7—Chordata; 8—Vertebrata; 9—Euteleostomi; 10—Tetrapoda; 11—Amniota; 12—Mammalia; 13—Theria; 14—Eutheria; 15—Boreoeutheria; 16—Primates; 17—Hominidae.



**Figure S22.** Evolutionary profiles: the differences in intercepts between the regression lines of expression of genes belonging to different phylostrata on cell-cycle signature in the single-cell transcriptomes for different cell types (with confidence intervals,  $p=0.05$ ).

**A** -- mature hepatocytes compared with iPSC (GSE81252).

**B** -- white adipocytes compared with iPSC (GSE90749).

Phylostrata: 1—cellular organisms (Prokaryota); 2—Eukaryota; 3—Opisthokonta; 4—Metazoa; 5—Eumetazoa; 6—Bilateria; 7—Chordata; 8—Vertebrata; 9—Euteleostomi; 10—Tetrapoda; 11—Amniota; 12—Mammalia; 13—Theria; 14—Eutheria; 15—Boreoeutheria; 16—Primates; 17—Hominidae.