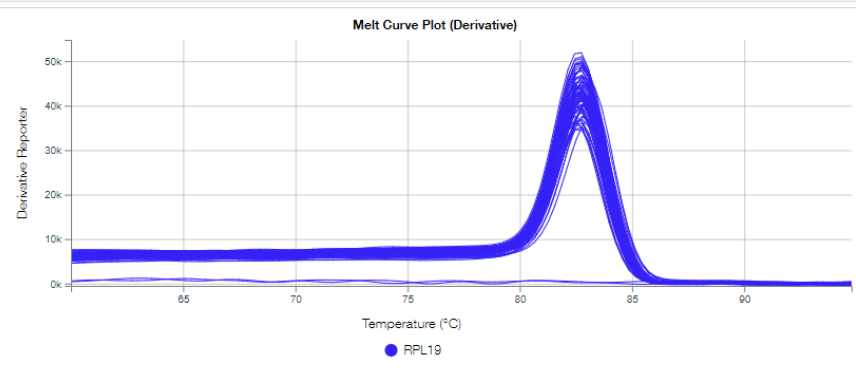
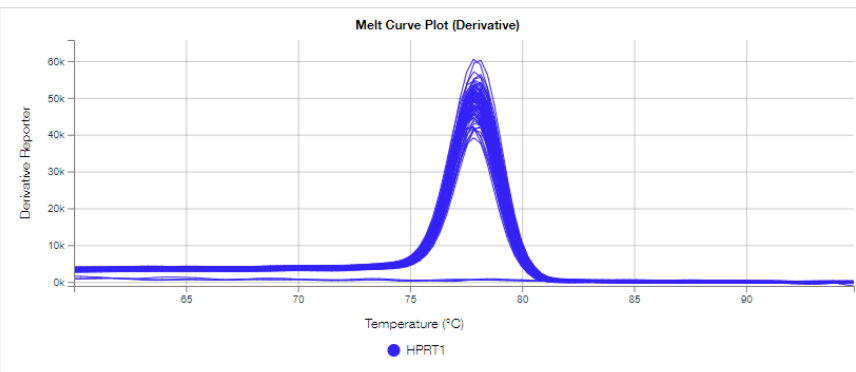
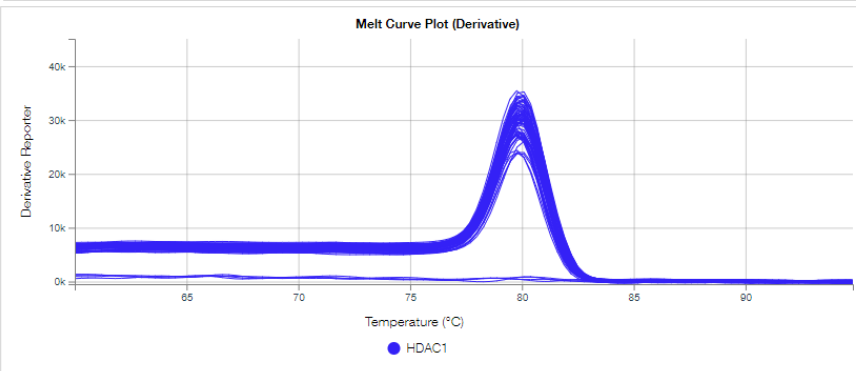
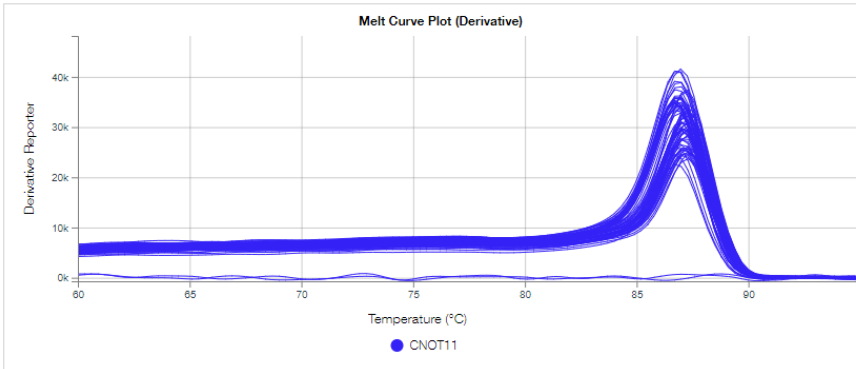
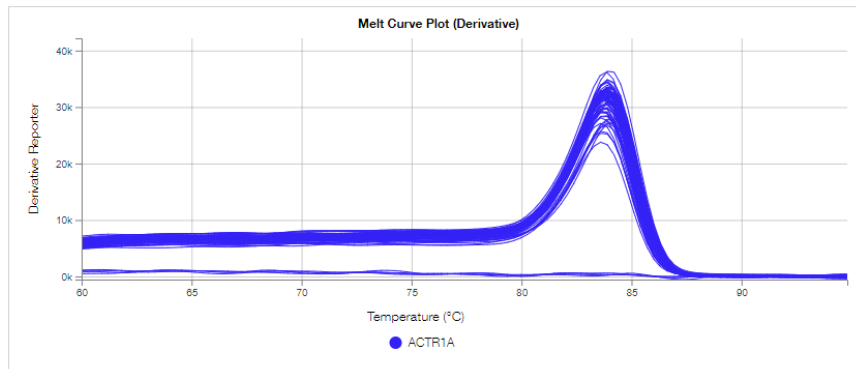




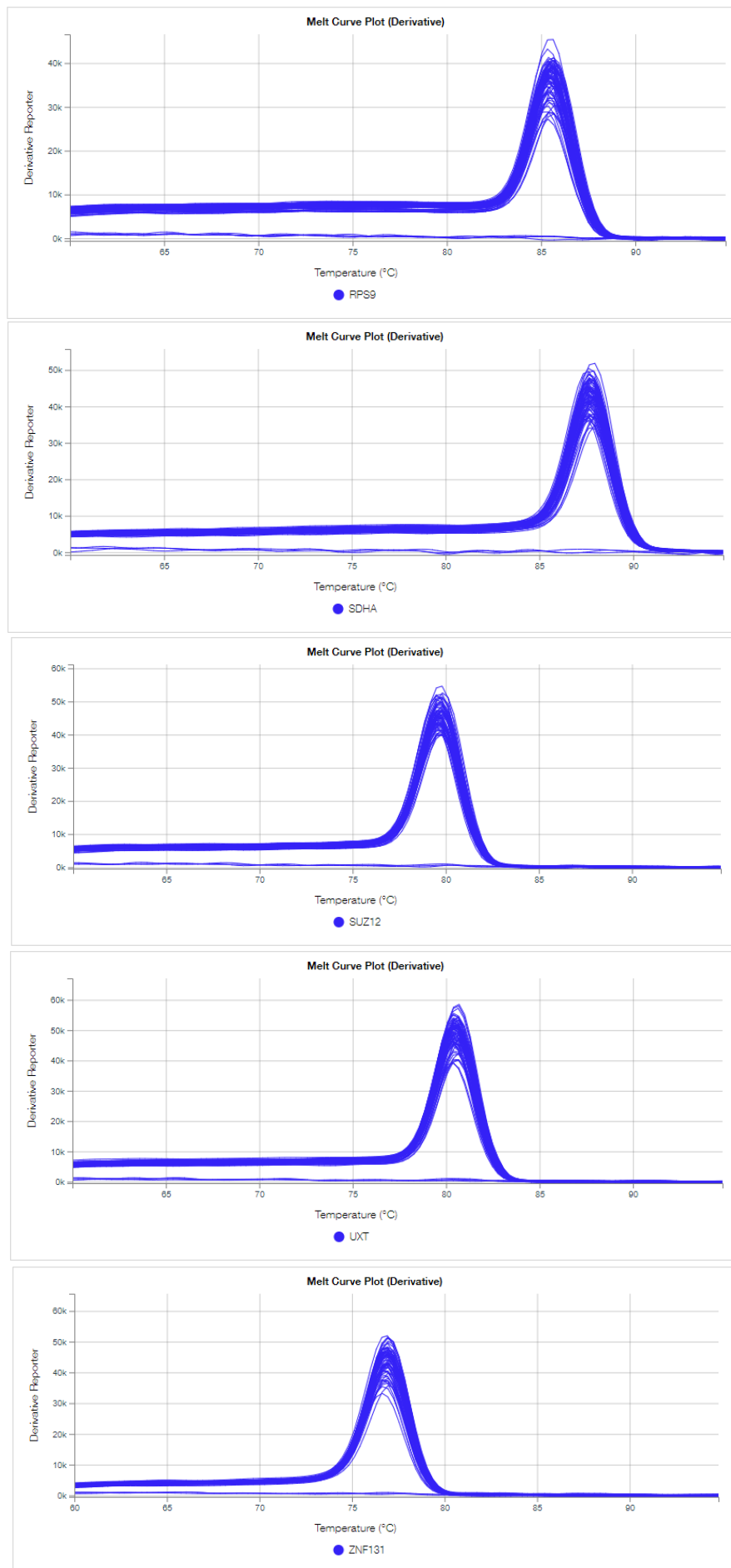


Figure S1. Dissociation curves obtained for tested reference genes. *ACTR1A* (actin-related protein 1A), *CNOT11* (CCR4-NOT transcription complex subunit 11), *HDAC1* (histone deacetylase 1), *HPRT1*

(hypoxanthine phosphoribosyltransferase 1), *RPL19* (ribosomal protein L19), *RPS9* (ribosomal protein S9), *SDHA* (succinate dehydrogenase complex flavoprotein subunit A), *SUZ12* (SUZ12 polycomb repressive complex 2 subunit), *UXT* (ubiquitously expressed prefoldin like chaperone) and *ZNF131* (zinc finger protein 131).

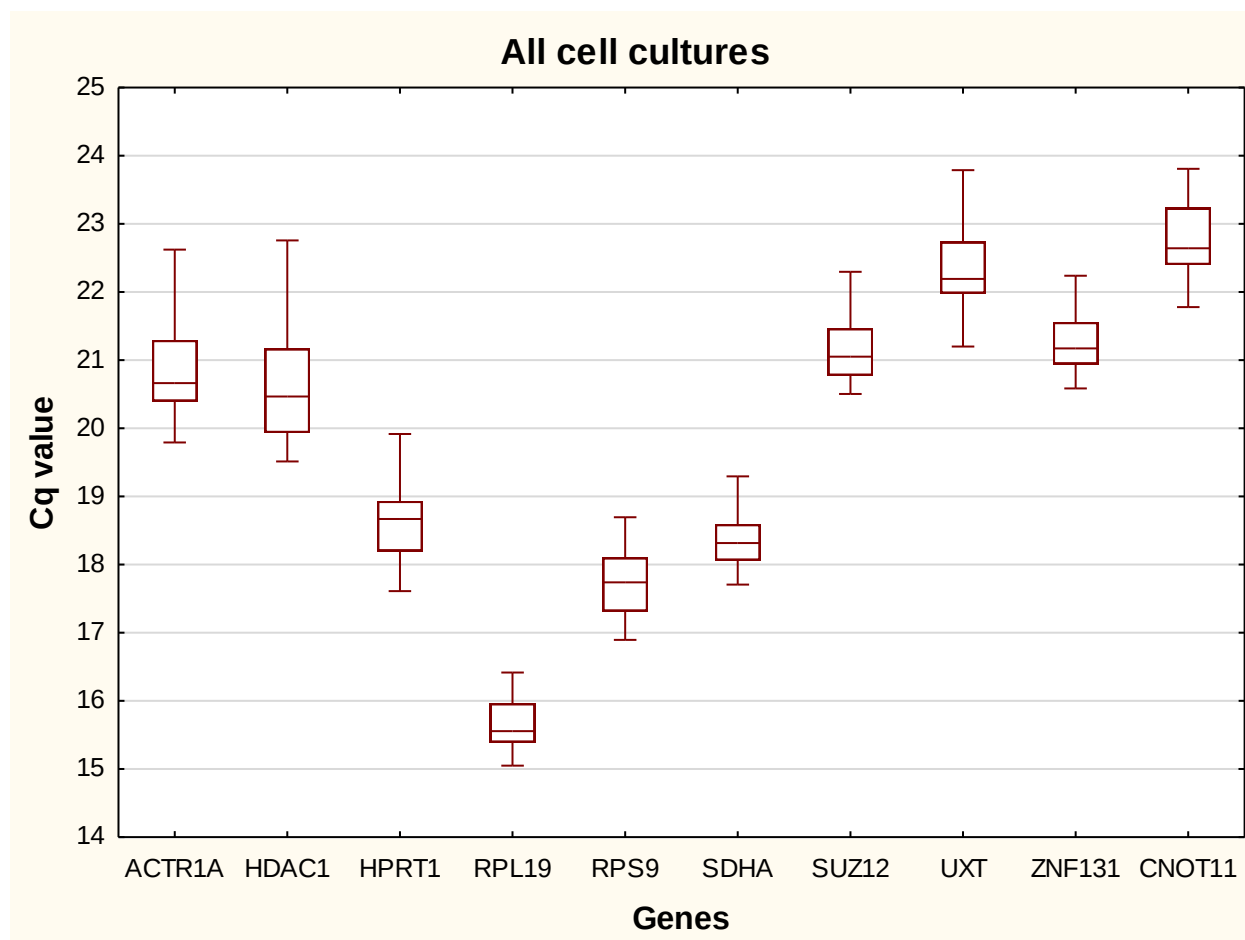


Figure S2. The quantification cycle values (Cq) for all examined genes. Data are shown in the box plots including the minimum and the maximum value (whiskers), the sample median (line in the middle), and the first and third quartiles (frame).

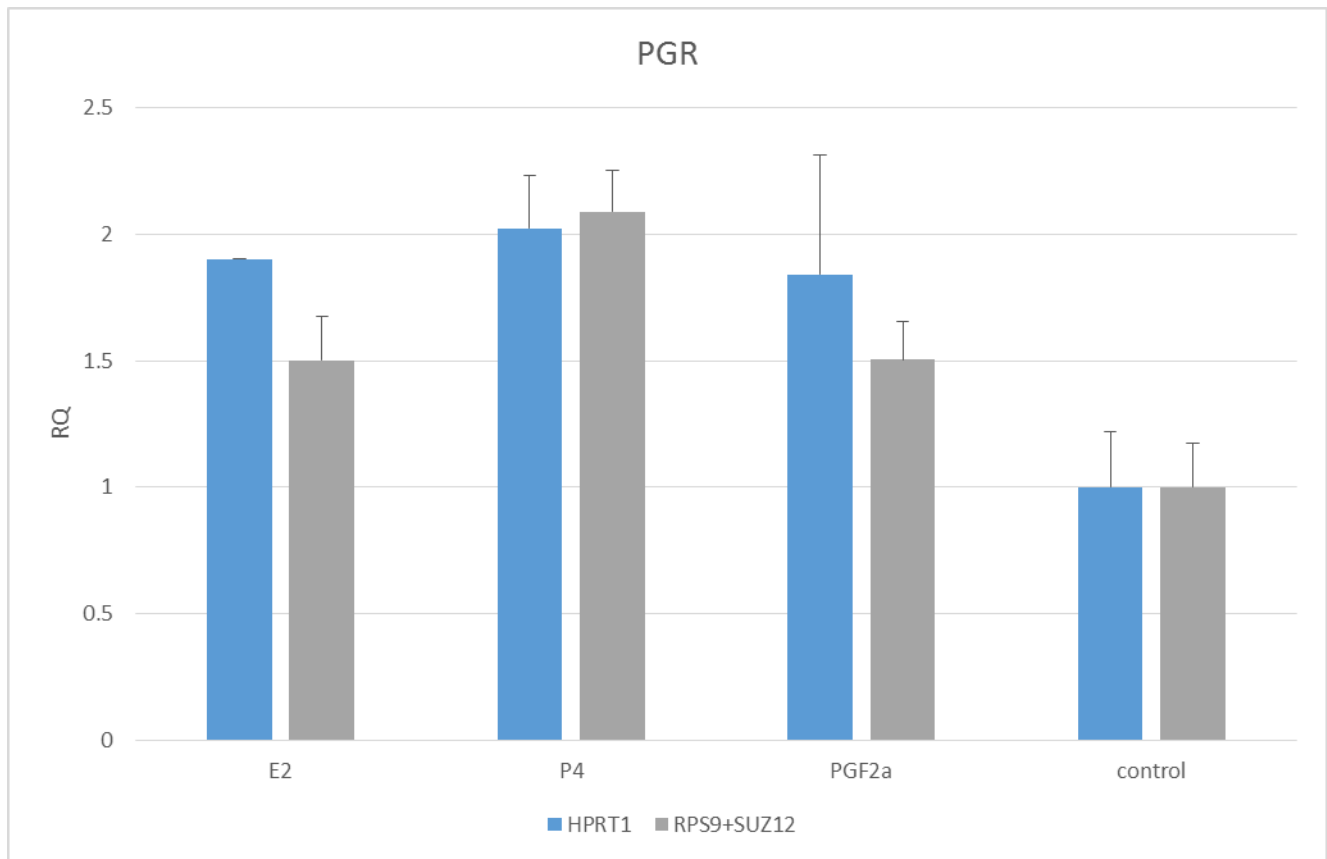


Figure S3. Relative expression of the *PGR* gene in the cell line obtained from the 4th month of pregnancy. Analysis was performed with normalization against two best performing RGs (*RPS9*+*SUZ12*) and the least stable RG, *HPRT1*. Data is shown as mean $\pm$ SD.

Table S1. Parameters derived from RT-qPCR analysis - slope, regression coefficient (R^2), amplification efficiency and melting temperature of the amplicon (T_m).

Gene	Slope	R^2	Efficiency (%)	T_m (°C)
<i>ACTR1A</i>	-3.19	0.998	105.663	84
<i>CNOT11</i>	-3.20	0.999	105.223	87
<i>HDAC1</i>	-3.29	0.998	101.384	80
<i>HPRT1</i>	-3.49	0.993	93.288	78
<i>RPL19</i>	-3.40	0.991	96.999	83
<i>RPS9</i>	-3.16	0.998	107.060	86
<i>SDHA</i>	-3.43	0.992	95.576	88
<i>SUZ12</i>	-3.56	0.990	91.042	79
<i>UXT</i>	-3.22	0.996	104.319	81
<i>ZNF131</i>	-3.57	0.994	90.647	77
<i>PGR</i>	-3.29	0.994	101.303	81