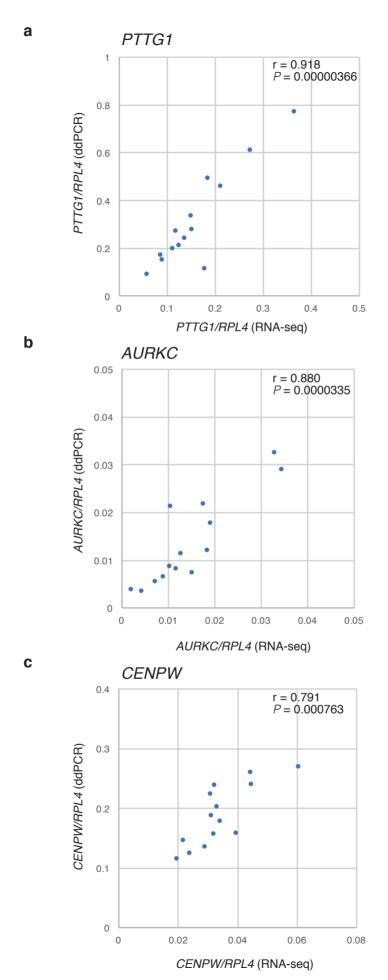
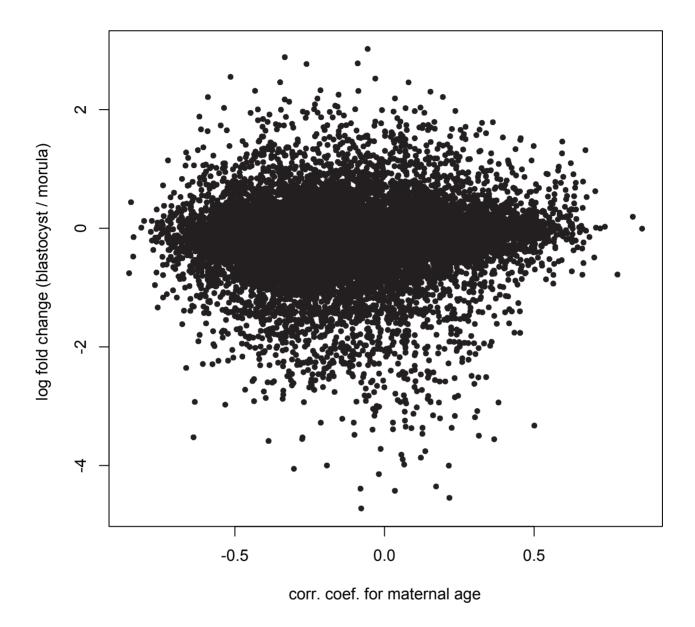
Parental age and gene expression profiles in individual human blastocysts

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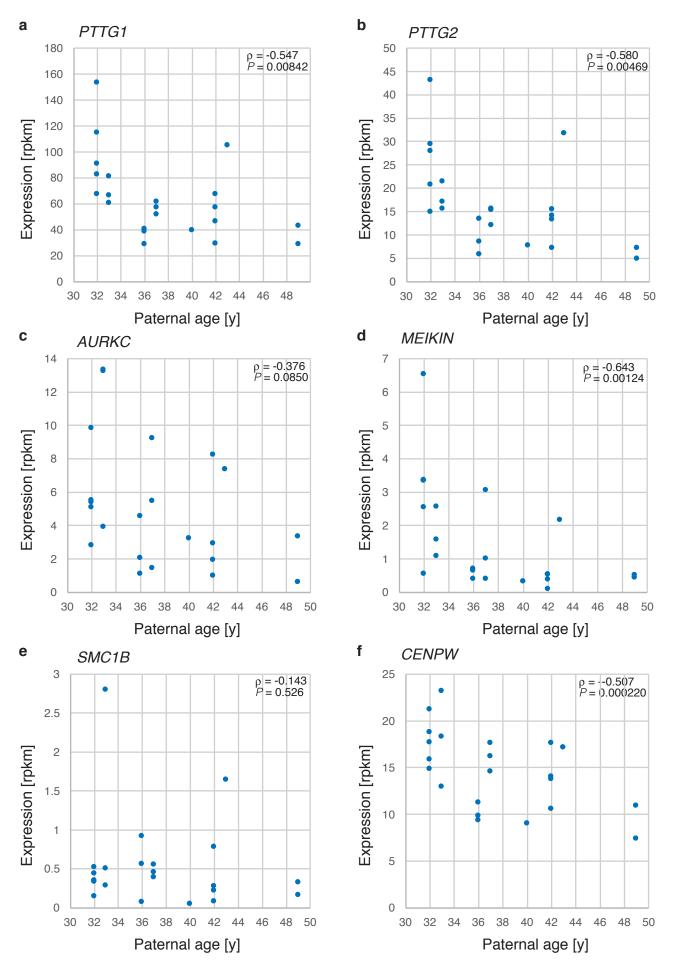


Supplementary Figure 1. Validation of RNA-seq expression data by ddPCR. Normalized gene expression level for *PTTG1* (a), *AUKRC* (b) and *CENPW* (c) calculated from RT-ddPCR (y-axis) was plotted against that estimated from RNA-seq data (x-axis). Pearson's correlation coefficients r and P values are also shown in each panel. *RPL4* expression level was used as a control for normalization.

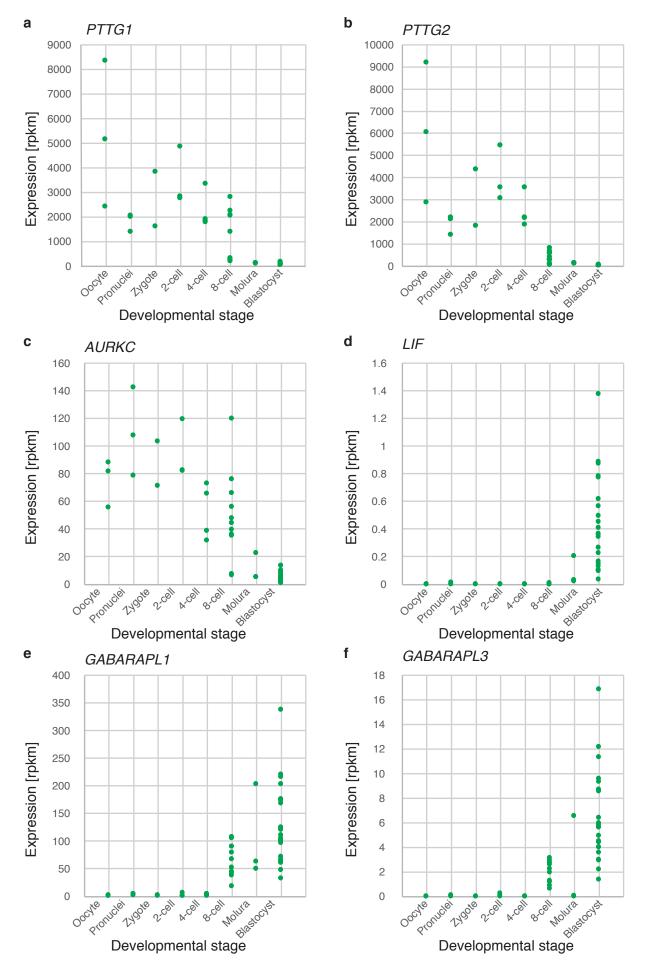


Supplementary Figure 2. Gene expression changes between morulae and blastocysts compared to gene expression of blastocyst-stage embryo correlation coefficients with maternal age.

The x-axis represents the correlation coefficient between each rpkm value of this study and maternal age. The y-axis represents the log fold change between the mean rpkm value of morulae and blastocysts for the data reported by Hendrickson *et al*.

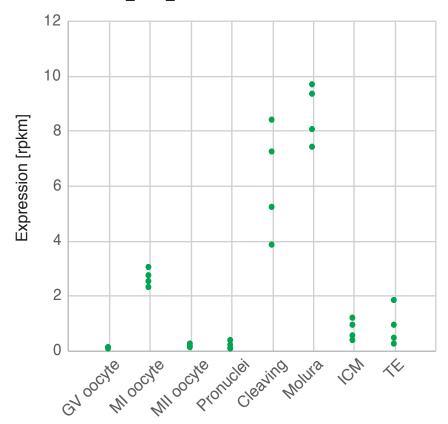


Supplementary Figure 3. Genes down-regulated with increased maternal age. Expression levels in rpkm were plotted against the paternal age for *PTTG1* (a), *PTTG2* (b), *AUKRC* (c), *CENPW* (d), *MEIKIN* (e) and *SMC1B* (f). Spearman's rank order correlation coefficients and *P* values are also shown in each panel.



Supplementary Figure 4. Gene expression patterns at the pre-implantation stage for the genes down-regulated with increased parental age. Expression levels, in rpkm, were plotted during development from the oocyte to the blastocyst stage by Xue *et al.* for *PTTG1* (a), *PTTG2* (b), *AUKRC* (c), *LIF* (d), *GABARAPL1* (e) and *GABARAPL3* (f).

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Developmental stage