Figure S1. **Daily mean realized temperatures (A) for the cold treatment (blue) and the warm treatment (red) and the difference in daily mean expected temperatures between the cold and warm treatment (B) shown from 1 January (January day = 1) until 6 August (January day = 218).** The cold and warm treatments reflect daily mean realized temperatures from an extremely cold (2013) and warm (2014) spring respectively, in The Netherlands. Differences increase nearing the breeding season, but decrease again during and after (right panel). From 10 July (January day 191) onwards, birds in both temperature environments received the same temperatures, indicated by the overlapping circles and flattening line, because they were transitioned to and entered the period with short days and low temperatures at 14 July (January day 195).
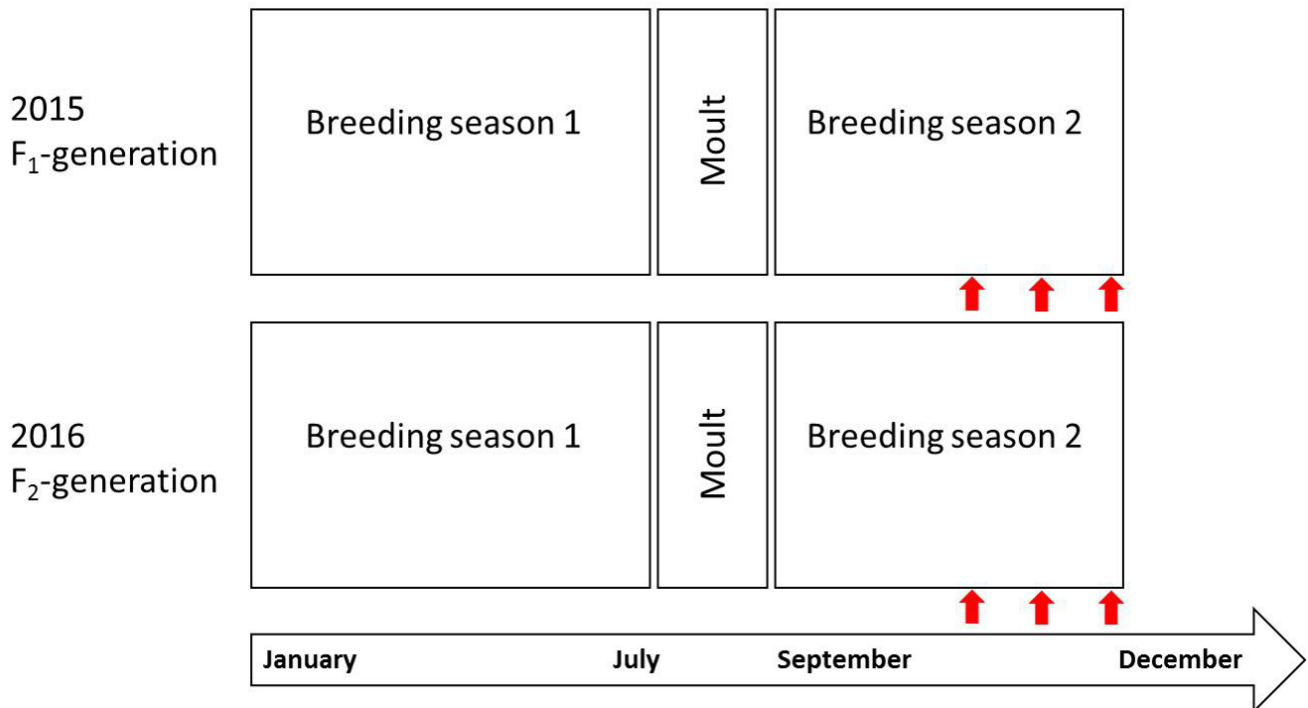
Figure S2. **Representation of the two breeding seasons within one year, which are identical for the F_1-generation in 2015 and their offspring, the F_2-generation, in 2016.** The red arrows indicate the three time points at which birds were sampled.
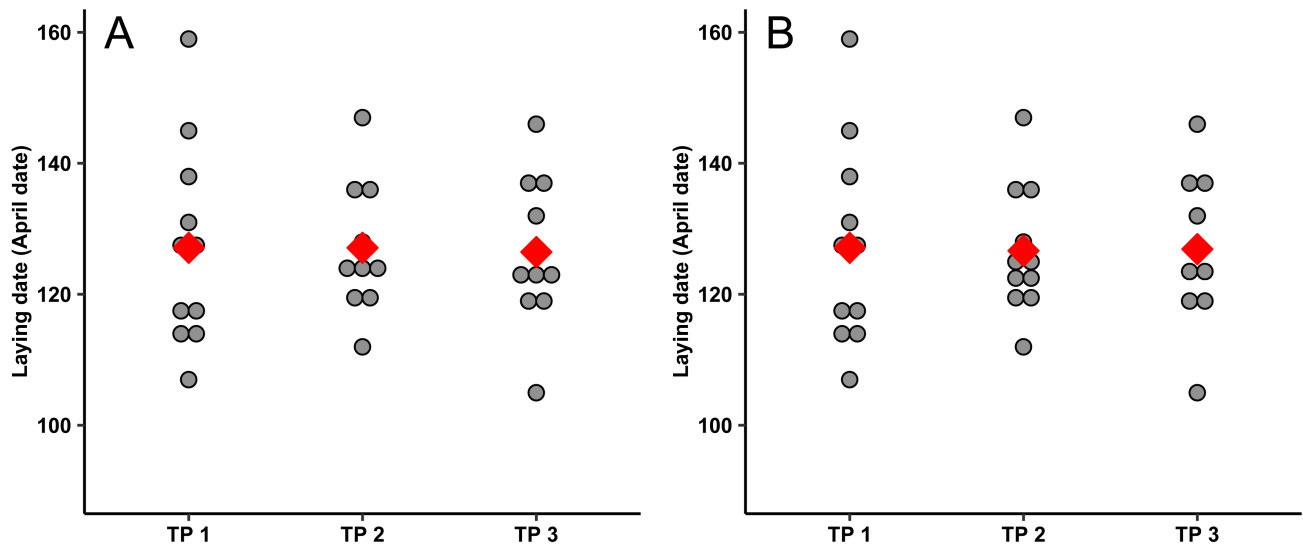
Figure S3. **Distributions (grey dots) and means (red diamonds) of laying dates (y-axis) in the groups for the three time points (x-axis) for 2015 (A) and 2016 (B)**. Laying dates are shown as January dates (1 = 1 January, 100 = 10 April etc.). Means between groups within a year were not significantly different (2015; $p > 0.730$ for all t-tests, 2016; $p > 0.930$ for all t-tests).
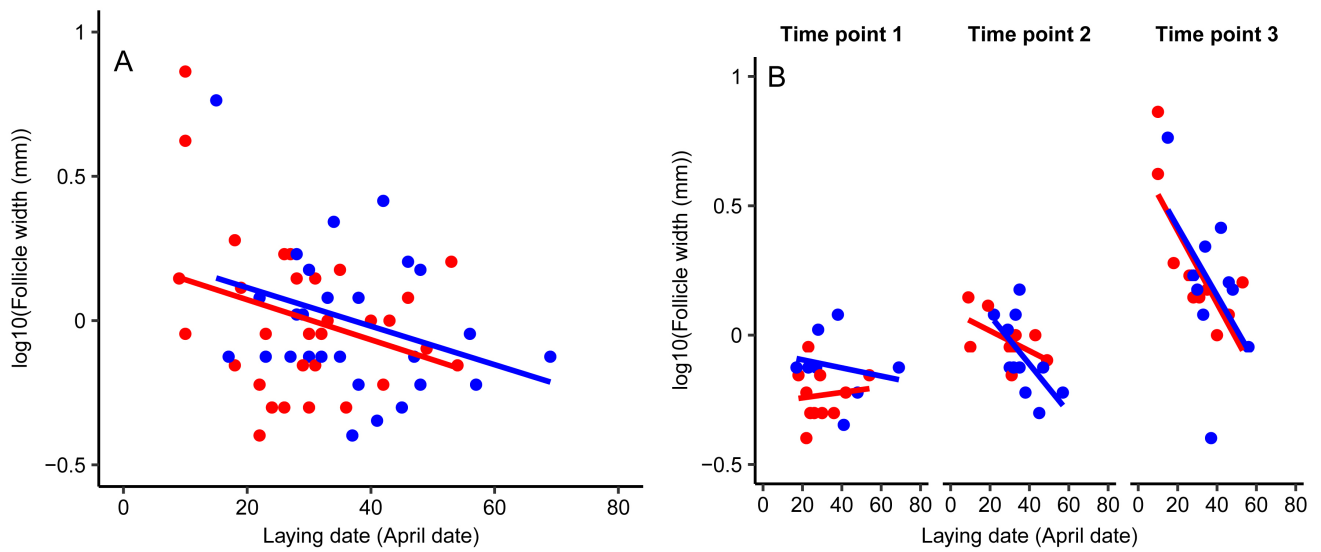
Figure S4. **Relationships between laying dates (x-axis) and log10 transformed widths of the largest follicle measured (y-axis) for all females (A), shown per generation (F_1 = red, F_2 = blue) and per time point, shown per generation (B)**. Every dot represents an individual female.
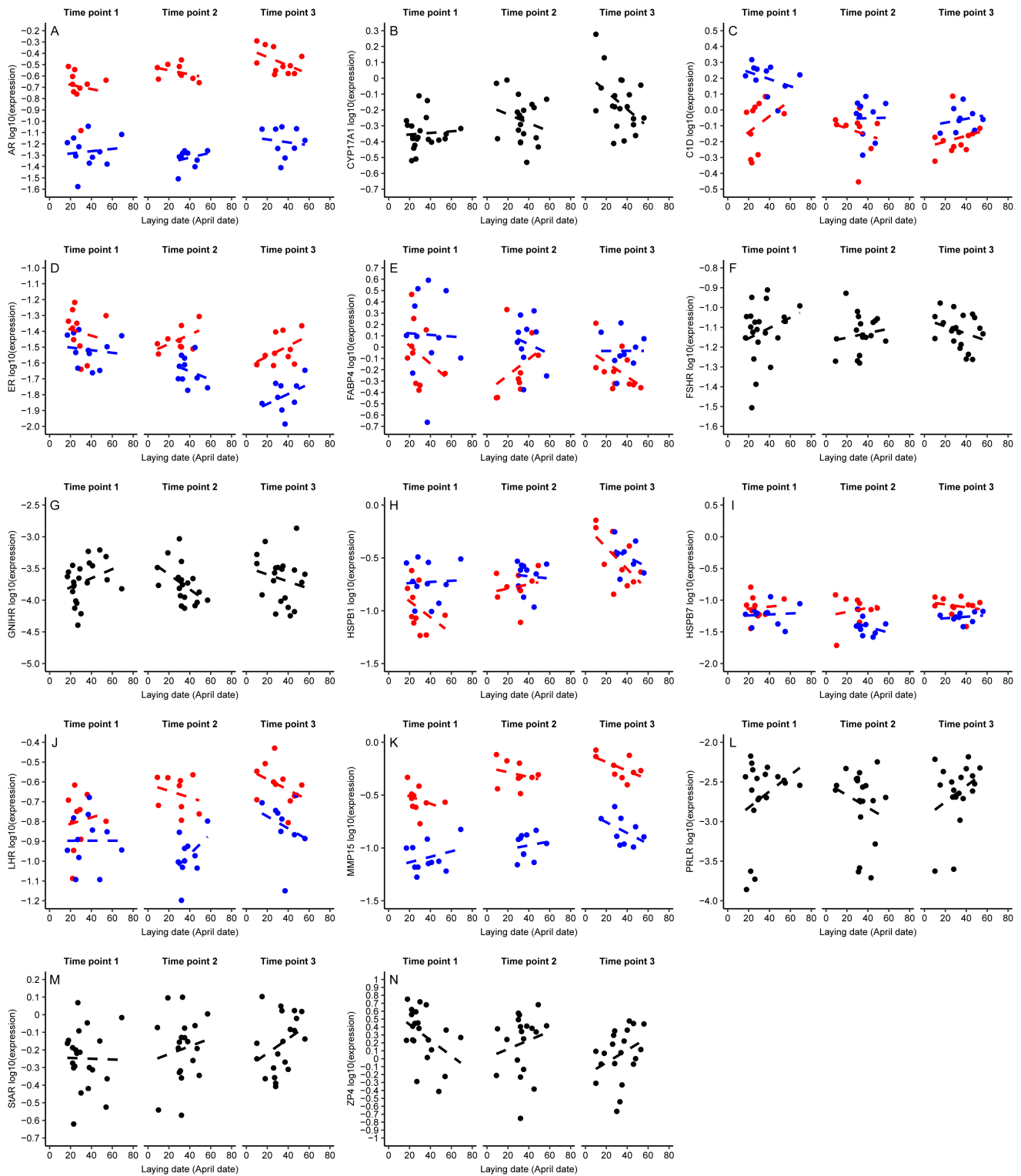
Figure S5. **Normalized and subsequently Log10 transformed mRNA levels of candidate genes in the three time points in *ovary*.** The expression of these genes did not explain variation in laying dates, but main effects of generation (F_1 = red, F_2 = blue) were found. When no generation effect was found, we did not distinguish between generations (data shown in black). Regression lines are dashed, as not to imply significant interactions. Note that the scale on the y-axis differs per panel.
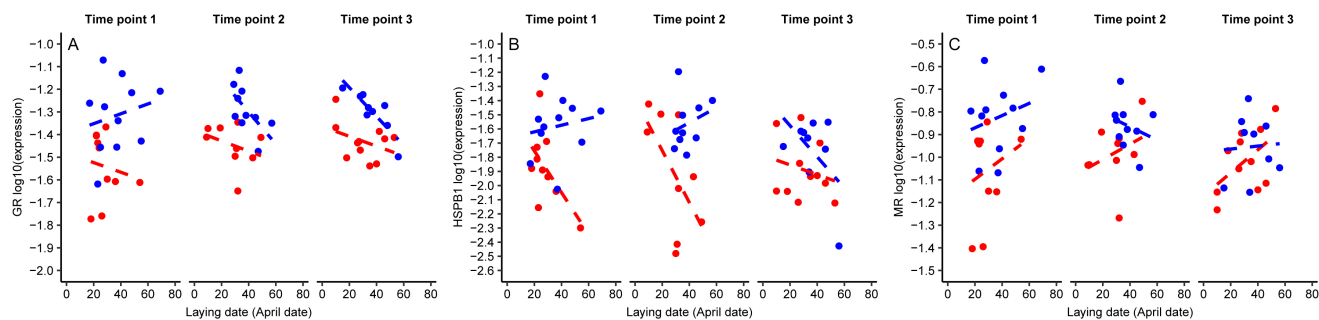
Figure S6. **Normalized and subsequently log10 transformed mRNA levels of candidate genes in the three time points in *liver*.** The expression of these genes (over time) did not explain variation in laying dates, but main effects of generation (F_1 = red, F_2 = blue) were found. Note that the scale on the y-axis differs per panel.

Tables S1-S10

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