

Table S17: Levels of let-7 miRNA in adult females and males

Tissue		C_T let-7 ± StDev	C_T 2SrRNA ± StDev	ΔC_T (ΔC_T let-7 - ΔC_T 2SrRNA) ^a	$\Delta\Delta C_T$ (ΔC_T - ΔC_T control) ^b	Average $\Delta\Delta C_T$ ± StDev	Fold Difference ^c
Female carcasses	Exp 1	25.33±0.30	6.14±0.24	19.19±0.39	0.00±0.39	0.00±0.28	1.00 (0.82 - 1.22)
	Exp 2	26.35±0.30	8.29±0.36	18.06±0.47	0.00±0.47		
Germaria	Exp 1	22.18±0.18	6.29±0.09	15.90±0.20	3.29±0.20	-2.24±0.11	4.72 (4.38 - 5.09) p=7.76x10 ^{-6***}
	Exp 2	22.35±0.05	7.72±0.11	14.63±0.12	3.43±0.12		
Male carcasses	Exp 1	22.71±0.11	7.10±0.03	15.61±0.12	3.58±0.12	-1.92±0.09	3.79 (3.57 - 4.02) p=1.55x10 ^{-6***}
	Exp 2	23.68±0.08	7.80±0.12	15.88±0.14	2.18±0.14		
Testes	Exp 1	21.14±0.26	6.56±0.03	14.58±0.26	4.61±0.26	-2.89±0.12	7.43 (6.84 - 8.07) p=7.73x10 ^{-8***}
	Exp 2	22.40±0.05	8.41±0.09	13.99±0.10	4.07±0.10		

a: ΔC_T was determined by subtracting the average 2SrRNA C_T value from the average Experimental C_T value. The standard deviation of the difference is calculated from the standard deviation of the Experimental and 2SrRNA values using the formula $s = \sqrt{(s_1^2 + s_2^2)}$ where s = standard deviation

b: $\Delta\Delta C_T$ is calculated by subtracting the ΔC_T control value (ΔC_T of female carcasses). The standard deviation is the same as for ΔC_T

c: the fold difference between the Experimental Sample and the control is calculated by: $2^{\pm\Delta\Delta C_T}$ with $\Delta\Delta C_T$ -s and $\Delta\Delta C_T$ -s where s is the standard deviation of $\Delta\Delta C_T$ value. The fold difference of the experimental values was compared to the respective control. P-value was calculated using the two tailed Students t-test. *p<0.05. **p<0.005. ***p<0.0005