

Supplementary Materials: Assessment of Zearalenone-Induced Cell Survival and of Global Gene Regulation in Mouse TM4 Sertoli Cells

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Table S4. Comparison of fold-change in mRNA levels (ZEA treated vs non-treated cell) for selected genes, as determined by RNAseq and RT-qPCR.

Gene	RT-qPCR fold-change	RNAseq fold-change	Average reads in ZEA treated cells	Average reads in control cells
<i>Btg2</i>	2,45	2,23	446.6 ± 13.8	199.4 ± 7.3
<i>Car8</i>	-5,08	-6,93	9.4 ± 1.1	65.29 ± 3.4
<i>Ctgf</i>	2,25	2,03	26508 ± 538.3	13050 ± 497.5
<i>Fst</i>	-3,87	-3,77	462.6 ± 12.21	1745 ± 50.9
<i>Igf1</i>	1,48	5,58	149.8 ± 26.5	14.51 ± 3.9
<i>Pgr</i>	5,14	4,34	216.9 ± 3.9	49.53 ± 3.8
<i>Sox9</i>	-4,11	-3.56	29.1 ± 3.1	103 ± 6.7
<i>Spp1</i>	-4,15	-4,43	1738 ± 53.0	7691 ± 395.4
<i>Thbs2</i>	11,22	8,03	44913 ± 1986	5505 ± 584.6

Table S5. Quantitative RT-PCR primer sequences.

Gene	Forward	Reverse
<i>Btg2</i>	GTGGGTTTCCTCTCCAGTCTC	CCAGTGGTGTTTGTAAATGATCGGT
<i>Car8</i>	GATGTCCGCCTGTCTCCAAA	TGGTCCTCCTGACAAGACTGA
<i>Ctgf</i>	GAGGAAAACATTAAGAAGGGCAAAA	CCGCAGAACTTAGCCCTGTA
<i>Fst</i>	CAAAGTCCTGTGAAGATATCCAGT	TAGGAAAGTTGTAGTCCTGGTCT
<i>Igf1</i>	AAGGCAGTTTACCCAGGCTC	TCTTTATTGCAGGTGCGGTCA
<i>Pgr</i>	TCCAGGTGACCCATGAGGAA	TTGCCTTGATCAATTCGCGG
<i>Rpl19</i>	CTGAAGGTCAAAGGGAATGTG	GGACAGAGTCTTGATGATCTC
<i>Sox9</i>	TGCTGCTTCGACATCCACACGTG	GACGTGCAAGCTGGCAAAGTTGA
<i>Spp1</i>	CCTTGCTTGGGTTTGCAGTC	TGGTCGTAGTTAGTCCCTCAGA
<i>Thbs2</i>	TGGCATCGCTGTAGGTTTCG	TGCCACTGAAGTCCACAGAC