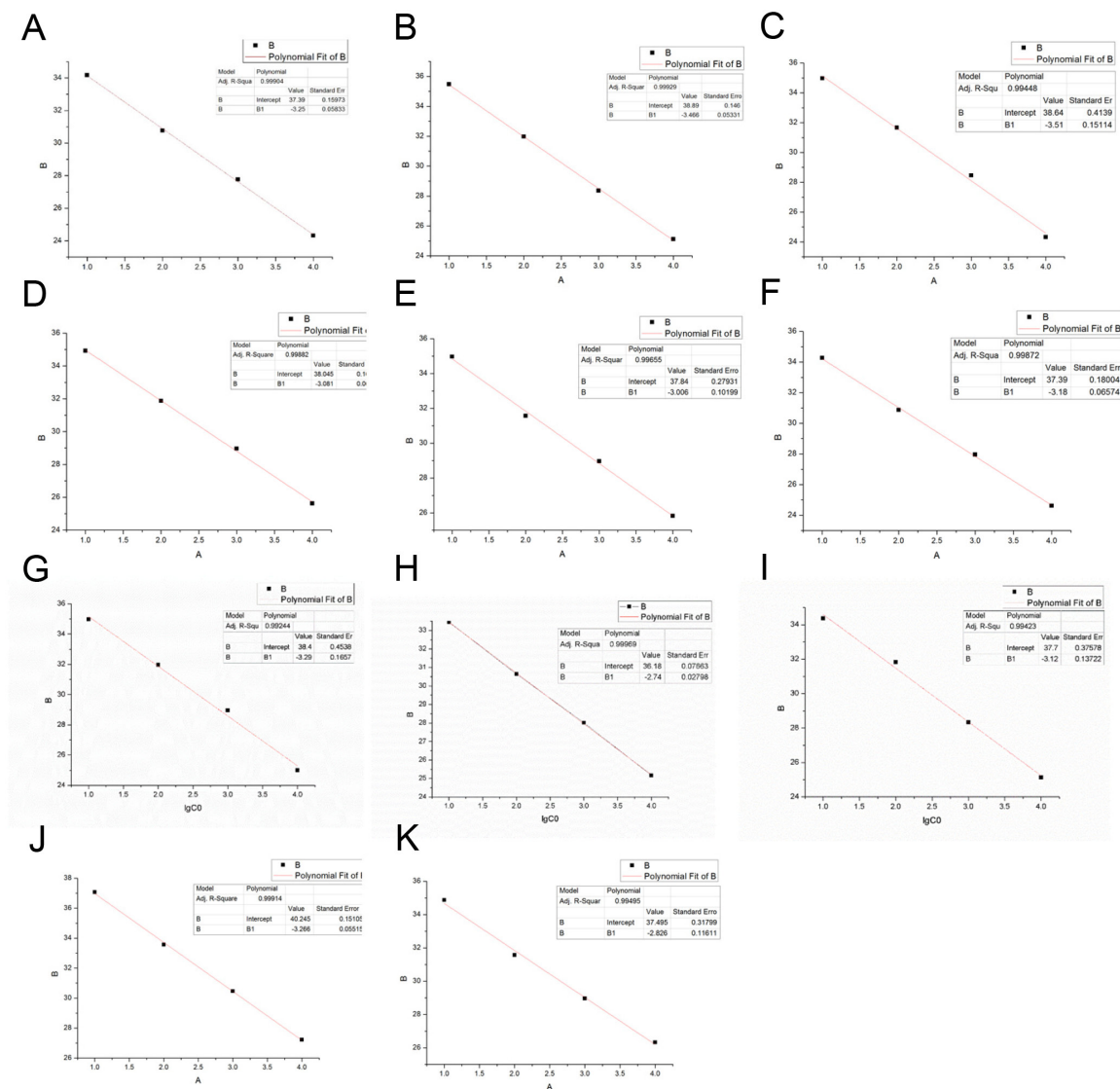
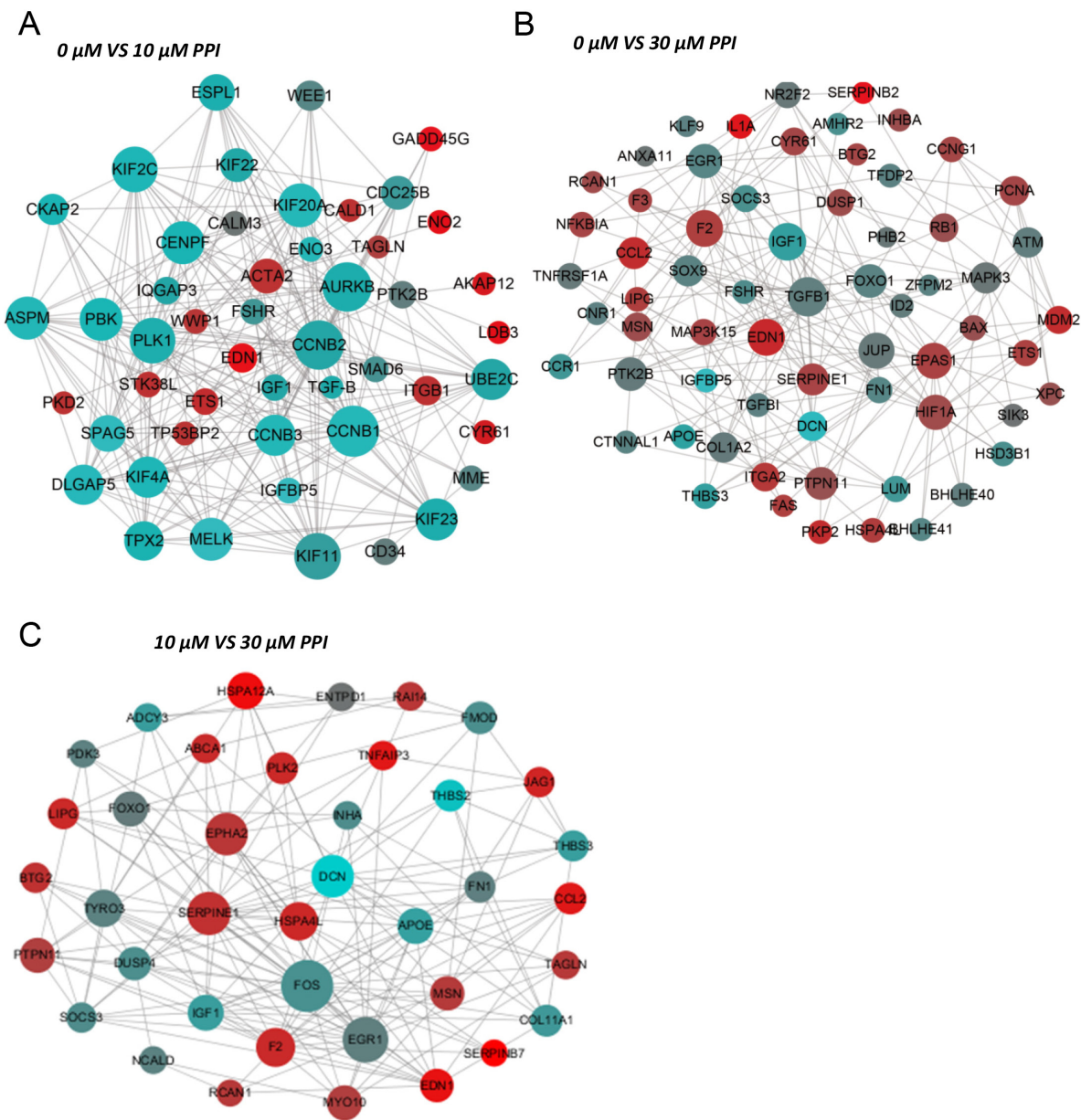


RNA-seq based gene expression analysis of ovarian granulosa cells exposed to zearalenone *in vitro*: significance to steroidogenesis

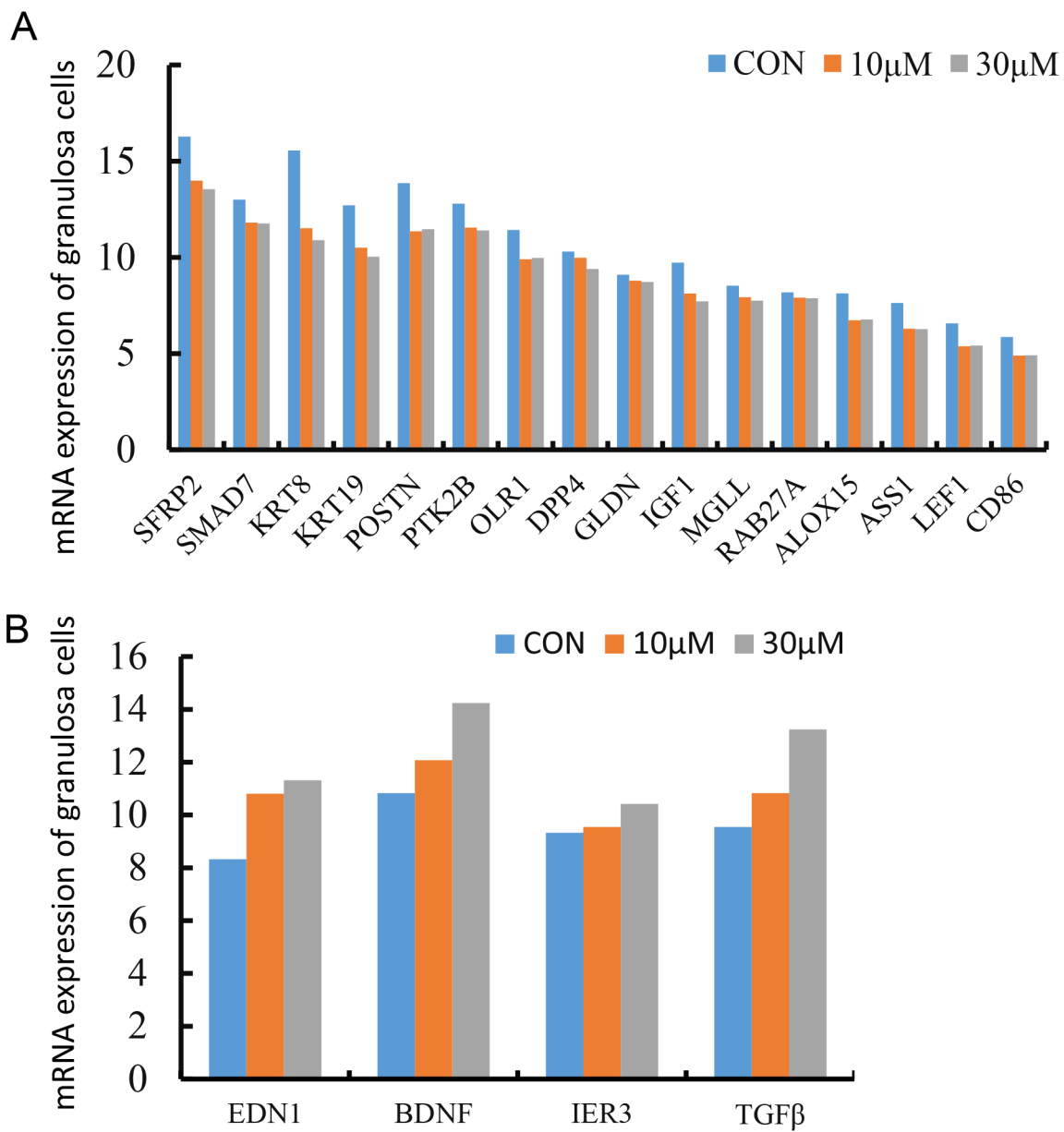
SUPPLEMENTARY MATERIALS



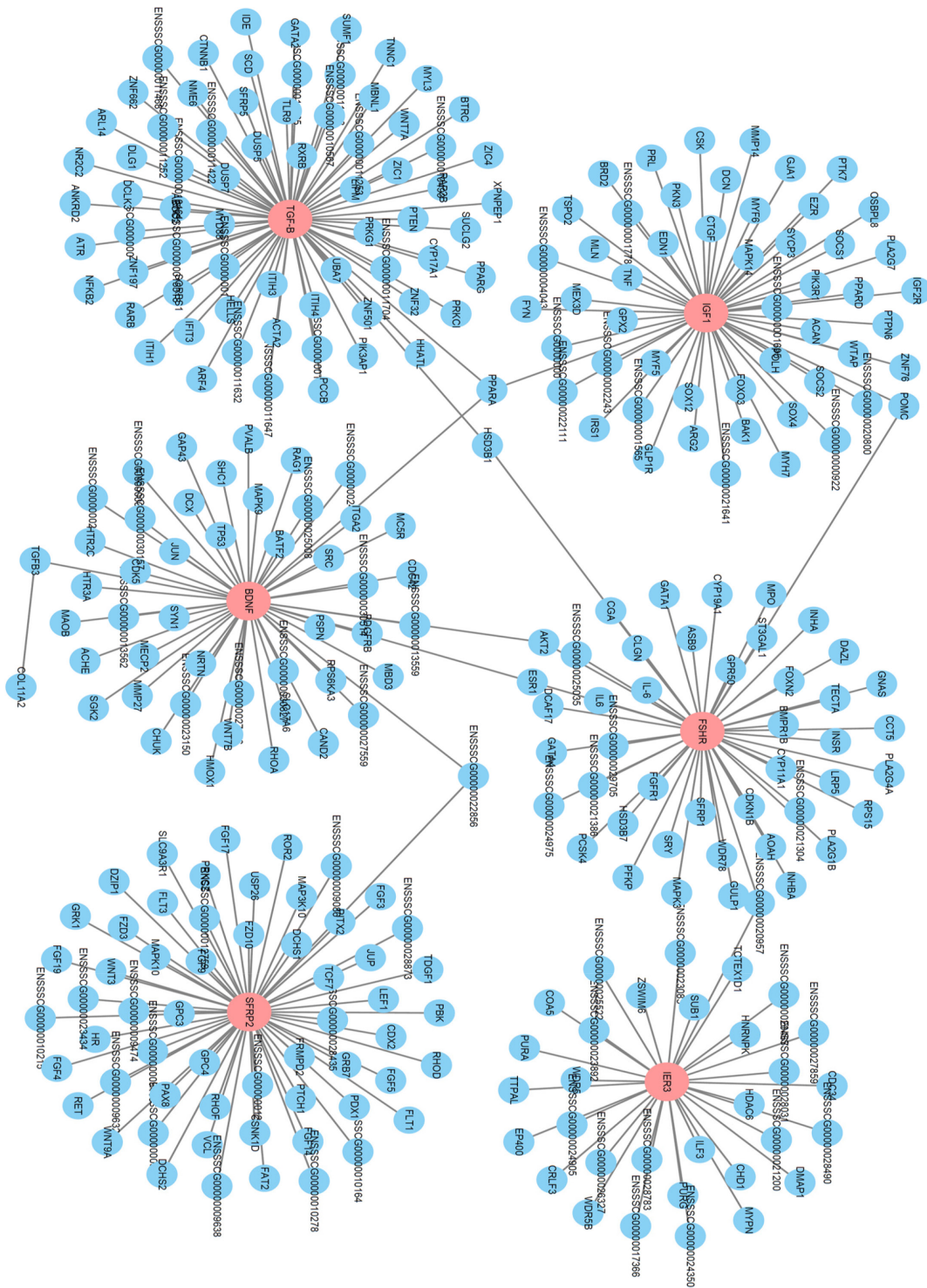
Supplementary Figure 1: The standard curve and primer efficiency of all the Q-PCR primers. (A-K) represent the standard curve and primer efficiency of *TGF-β*, *BDNF*, *IER-3*, *EDN-1*, *IGF-1*, *SFRP-2*, *CYP19A1*, *FSHR*, *HSD17β*, *Bax* and *Bcl-2* genes.



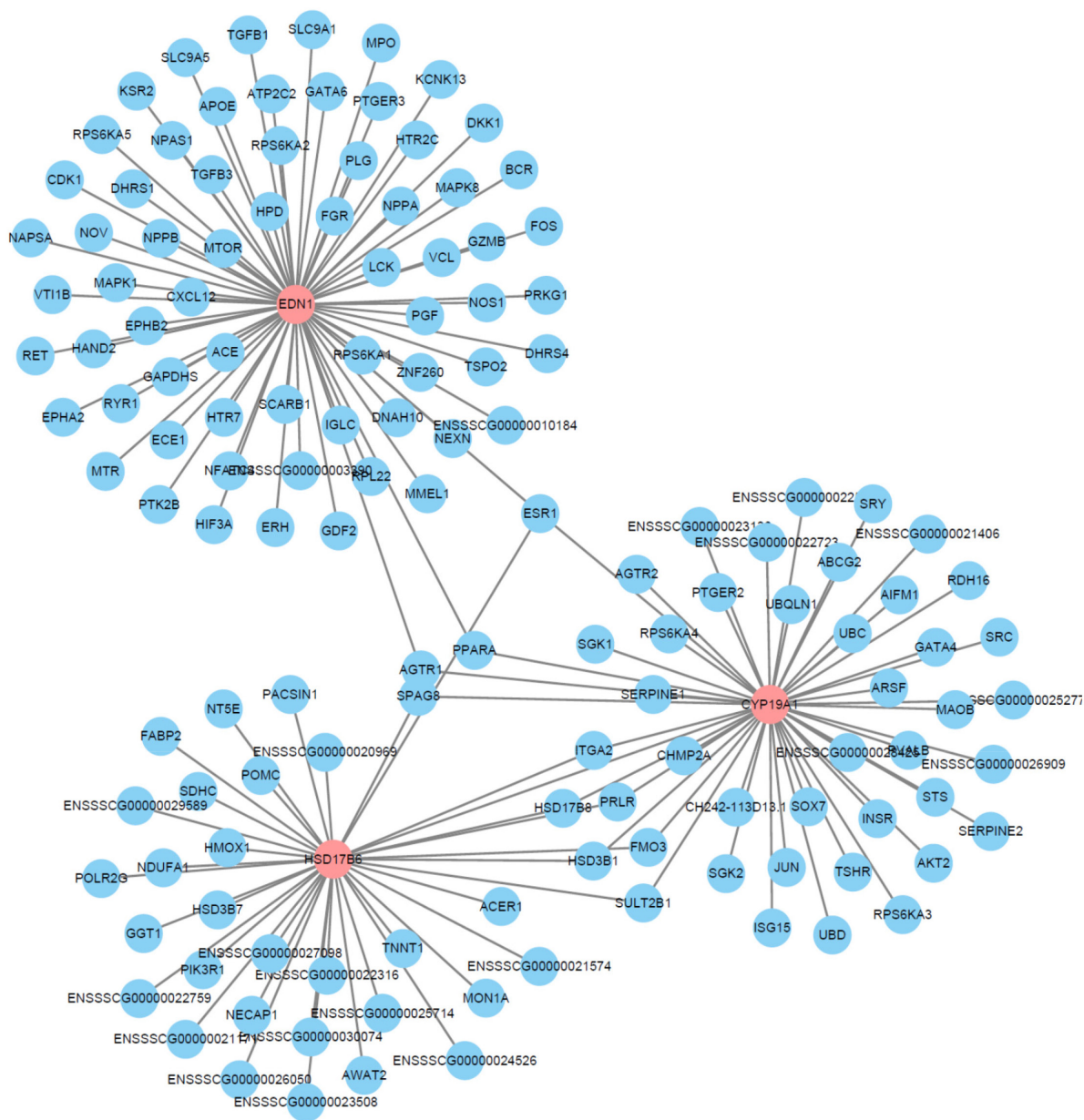
Supplementary Figure 2: Protein-protein interaction (PPI) network based on the Search Tool for the Retrieval of Interacting Genes (STRING) database to annotate functional interactions between different expression genes in ZEA-treatment and control groups. The 120 genes in 10 μM and 30 μM ZEA treatment group and node degree ≥ 20 was selected as the threshold. Red points represent genes up-regulated and blue points represent genes down-regulated in every two groups.



Supplementary Figure 3: (A) Part of declined expression genes between control and ZEA-treatment groups. (B) The increased expression genes in ZEA-treatment groups. Node degree ≥ 20 was selected as the threshold.



Supplementary Figure 4: PPI network based on the STRING database to annotate functional interactions between apoptosis-related genes in ZEA-treatment groups. We obtained 6 core differentially expression genes between control and ZEA-treated groups. Node degree ≥ 20 was selected as the threshold.



Supplementary Figure 5: PPI network based on the STRING database to annotate functional interactions between steroidogenesis-related genes in ZEA-treatment groups. We obtained 3 core differentially expression genes between control and ZEA-treated groups. Node degree ≥ 20 was selected as the threshold.

Supplementary Table 1: Primers used for quantitative-PCR

Genes	Sequences of primers	Production(bp)	Genbank
<i>CYP19A1</i>	F:5'- GATGCTGCATTGTCACTGCT -3' R:5'-GGGAAGGTGTCACTCAAGGA-3'	238	KF_314685
<i>FSHR</i>	F:5'- CGCTGGAAAGATGGCATAACC-3' R:5'- GCTCACCTTCATGTAGCTGC -3'	155	GU_990798
<i>HSD17β</i>	F:5'- TGATGGACTTCACCTGTGCT -3' R:5'- GGCATGATCCCAGCATTCAG -3'	207	NM_001185137
<i>TGF-β</i>	F:5'-AGGAAACCCATAATGCCCCA-3' R:5'- TGGGCCCTATGGATAGCTG-3'	208	NM_214015.2
<i>EDN-1</i>	F:5'- CTCCTTTGCGGTGATGATGG-3' R:5'- GGTGTGGACTTGGGTGTTTC-3'	174	NM_213882.1
<i>IGF-1</i>	F:5'- TCCTGGAGTTGGTAGATTGCT-3' R:5'- ACGAATGTCTCTAGCAGCCA-3'	224	NM_214256.1
<i>SFRP-2</i>	F:5'- GGCCTCAGGAATGGATAGCT-3' R:5'- CCCCAAACATCACACCCAAG-3'	165	NM_001244395.1
<i>IER-3</i>	F:5'- AGATCGAAGGCCAAGGACAA-3' R:5'- AGGGATGGAGAAAACCTCGGG-3'	154	XM_001927551.3
<i>BDNF</i>	F:5'-CCTGGATGCTGCAAACATGT-3' R:5'-CCCTCCTTTGTGTACCCCAT-3'	226	NM_214259.2
<i>Bax</i>	F:5'-ATGCGTCCAAGGAAGACTGAG-3' R:5'-CCCCAGTTGAAGTTGCCATCAG-3'	198	XM_003127290.4
<i>Bcl-2</i>	F:5'-GCAGAGATGTCCAGTCAG-3' R:5'-CACCGAACTCAAAGAAGG-3'	166	XM_003121700.4
<i>GAPDH</i>	F:5'-CCCCTTCATTGACCTCCACT-3' R:5'-CCATTTGATGTTGGCGGGAT-3'	157	NM_001206359.1