The gonadotropin-induced resumption of oocyte meiosis in the preovulatory follicles is preceded by expression of epidermal growth factor (EGF)-like peptides, amphiregulin (AREG) and epiregulin (EREG), in both mural granulosa and cumulus cells. Both the gonadotropins and the EGF-like peptides possess the capacity to stimulate resumption of oocyte meiosis in vitro via activation of a broad signaling network in the cumulus cells followed by rapid and extensive changes in the cumulus cell gene expression profiles. To understand better the genomic actions of gonadotropins (FSH) and EGF-like peptides, we hybridized cumulus cells collected from cumulus-oocyte complexes to a pig oligonucleotide microarray. We have compared transcriptomes of FSH and AREG/EREG-stimulated cumulus cells with untreated control cells and vice versa and identified number of exclusively and commonly up- and down-regulated genes that were subjected to functional genomic analysis according to their molecular and cellular functions. Expression pattern of 49 selected genes with a known or potential function in ovarian development was verified by real time qRT-PCR. Both FSH and AREG/EREG up-regulated genes associated with regulation of cell proliferation, cell migration, blood coagulation and extracellular matrix remodeling. FSH exclusively induced expression of genes involved in inflammatory response and in response to reactive oxygen species. Moreover, FSH exclusively or significantly more up-regulated expression of genes closely related to some ovulatory events (AREG, ADAMTS1, HAS2, TNFAIP6, PLAUR, PLAT, PR, HSD17B7). In contrast to AREG/EREG, FSH also increased expression of genes coding for key transcription factors (CEBPB, FOS, ID1/3, NR5A2), which may contribute to the different expression profiles of FSH- and AREG/EREG-treated cumulus cells.