Micro-RNAs are small, regulatory molecules approximately 21-24 nucleotides in length. They function at the post-transcriptional level by controlling the expression of more than 50% of human protein-coding genes and play an essential role in cell signaling pathways. Our goal was to explore the expression profile of oncomiRs and tumor-suppressor miRs, and to define their possible correlations in urothelial carcinoma of the bladder (BC). Seventy-seven primary BCs, along with 77 matched tumor-associated normal samples were investigated for the expression of 12 micro-RNAs using qPCR. Relationships between the expression of miR-10b, miR-19a, miR-19b, miR-21, miR-122a, miR-145_1, miR-205_1, miR-210, miR-221, miR-378-1 and miR-296-5p and the pathologic features of the tumors were also examined. The majority of the micro-RNAs exhibited down-regulation in BC vs. normal tissue (miR-10b (p=0.0007), miR-19a (p=0.012), miR-19b (p=0.0361), miR-126_1 (p=0.0021), miR-145_1 (p<0.0001), miR-221 (p=0.0001), miR-296-5p (p<0.0001), miR-378-1 (p<0.0001)), miR-21, miR-205_1 and miR-210 expression levels did not present difference between BC and normal tissue. However, we noticed a great range in the x-fold expression values of all micro-RNAs. The median x-fold expression (range) was as follows: miR-10b, 0.45 (0-12.58); miR-19a, 0.56 (0-25.63); miR-19b, 0.50 (0-18.90); miR-21, 0.36 (0-42.62); miR-145_1, 0.04 (0-56.36); miR-205_1, 1.07 (0.01-36.42); miR-210, 1.09 (0-44.43); miR-221, 0.32 (0-33.51); miR-296-5p, 0.08 (0-75.24); miR-378-1, 0.17 (0-3.66). Significant correlations among all of the studied microRNAs were scored both in BC and control tissue. Different micro-RNAs are deregulated in BC through down-regulation. A synergistic involvement of these genes in the development of BC is implied.