**Supplemental Text S1**

**Real time RT-PCR**

**Primers and PCR consumables :** Primers for the *TBP* and *GPR126* genes were chosen with the assistance of the computer programs Oligo 4.0 (National Biosciences, Plymouth, MN). We conducted BLASTN searches against dbEST, htgs and nr (the nonredundant set of the GenBank, EMBL and DDBJ database sequences) to confirm the total gene specificity of the nucleotide sequences chosen for the primers and the absence of DNA polymorphisms. To avoid amplification of contaminating genomic DNA, 1 of the 2 primers was placed in a different exon. For example, the upper primer of *TBP* were placed at the junction between exons 5 and 6, whereas the lower primer was placed in exon 6.

**RNA extraction :** Total RNA was extracted from bladder specimens by using the acid-phenol guanidium method. The quality of the RNA samples was determined by electrophoresis through agarose gels and staining with ethidium bromide, and the 18S and 28S RNA bands were visualized under ultraviolet light.

**cDNA synthesis :** RNA was reverse transcribed in a final volume of 20µLl containing 1X RT buffer (500 mM each dNTP, 3 mM MgCl2 , 75 mM Kcl and 50 mM Tris-HCl pH 8.3), 10 units of RNasin™ Ribonuclease inhibitor (Promega, Madison, WI), 10 mM dithiothreitol, 50 units of Superscript II RNase H- reverse transcriptase (Gibco BRL, Gaithersburg, MD), 1.5 mM random hexamers (Pharmacia, Uppsala, Sweden) and 1 µg of total RNA. The samples were incubated at 20°C for 10 min and 42°C for 30 min, and reverse transcriptase was inactivated by heating at 99°C for 5 min and cooling at 5°C for 5 min.

**PCR amplification :** All PCR reactions were performed using a ABI Prism 7700 Sequence Detection System (Perkin-Elmer Applied Biosystems, Oak Brook, IL). PCR was performed using the SYBR Green PCR Core Reagents kit (Perkin-Elmer Applied Biosystems). The thermal cycling conditions comprised an initial denaturation step at 95°C for 10 min and 50 cycles at 95°C for 15 sec and 65°C for 1 min