**Supplemental Table 1.** Primer sequences used in real-time qPCR.

<table>
<thead>
<tr>
<th>Primer name</th>
<th>DNA sequence (5' --&gt; 3')</th>
<th>product size (bp)</th>
<th>Tm (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNORD27 - Forward</td>
<td>actccatgatgaacacaaatgac</td>
<td>72</td>
<td>60</td>
</tr>
<tr>
<td>SNORD27 - Reverse</td>
<td>actttctcagtagtagtagagcactc</td>
<td></td>
<td></td>
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<tr>
<td>SNORD28 - Forward</td>
<td>gtcagatgattgaattgataagcgtg</td>
<td>75</td>
<td>60</td>
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<tr>
<td>SNORD28 - Reverse</td>
<td>tgccatcagaactctaactgc</td>
<td></td>
<td></td>
</tr>
<tr>
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<td>tgcattaataatggeggatctc</td>
<td>150</td>
<td>59</td>
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<tr>
<td>SNORD44 - Reverse</td>
<td>cccccagtccaaactaacaatg</td>
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<td>tatcgtgtgtgatcttattccga</td>
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<td>SNORD50A - Reverse</td>
<td>atctcagaagccagatccgtaaaa</td>
<td></td>
<td></td>
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<td>tgctgatgatgactttcttagaca</td>
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<td>SNORD58A - Reverse</td>
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<td>ggtatcagacctatcgaccaag</td>
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<td>SNORD59B - Reverse</td>
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<td>SNORD82 - Forward</td>
<td>ccaacagaaagcactctgaag</td>
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<td>SNORD82 - Reverse</td>
<td>cagcacatcagcaactacatg</td>
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<tr>
<td>SNORD116-21 - Forward</td>
<td>atttgccaggacaaataactgtgc</td>
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<td>SNORD116-21 - Reverse</td>
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<tr>
<td>SNORD117 - Forward</td>
<td>tggatgaatgtgataagagttta</td>
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<tr>
<td>SNORD117 - Reverse</td>
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**Supplemental Table 2.** Primer sequences used in bisulfite sequencing.

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<th>Primer name</th>
<th>DNA sequence (5' --&gt; 3')</th>
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<td>SNORD44bisR</td>
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<tr>
<td>SNORD59bisF</td>
<td>gaatgggatatattagaggtttt</td>
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<td>SNORD59bisR</td>
<td>aaccaatctaattccctacctttac</td>
</tr>
<tr>
<td>SNORD82bisF</td>
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</tr>
<tr>
<td>SNORD82bisR</td>
<td>caataaccacaaacacttaataacct</td>
</tr>
<tr>
<td>SNORD116-21bisF</td>
<td>tttatggttagttaagtttttttttttt</td>
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<tr>
<td>SNORD116-21bisR</td>
<td>ttatatccaaaaactctcaatatc</td>
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</tbody>
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**Supplemental Table 3.** Primer sequences used in ChIP assay.

<table>
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<th>Primer name</th>
<th>DNA sequence (5' --&gt; 3')</th>
<th>product size (bp)</th>
<th>Tm (C)</th>
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<tr>
<td>SNORD27ChIP-R</td>
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<tr>
<td>SNORD28ChIP-F</td>
<td>agggatgtgtgctgacccctactc</td>
<td>141</td>
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<tr>
<td>SNORD28ChIP-R</td>
<td>tgaagctttattcataaaacaacaactgc</td>
<td>150</td>
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<tr>
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</tr>
<tr>
<td>SNORD44ChIP-R</td>
<td>cccctgccaaaaactaacaatg</td>
<td>143</td>
<td>57</td>
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<tr>
<td>SNORD50AChIP-F</td>
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<td>164</td>
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<tr>
<td>SNORD50AChIP-R</td>
<td>tgtcctttataaggtctctcagt</td>
<td>164</td>
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<tr>
<td>SNORD58AChIP-F</td>
<td>ctagttgtgtacaaccagttcctc</td>
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<tr>
<td>SNORD58AChIP-R</td>
<td>tcacaacagctacattcttacacc</td>
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<td>SNORD59AChIP-F</td>
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<td>SNORD59AChIP-R</td>
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<td>SNORD59BChIP-F</td>
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<td>SNORD59BChIP-R</td>
<td>aaaaagtaattgcctcttctcactc</td>
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<td>caaacaaggagcagctctgaag</td>
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<td>gcataataaagaccaaccagggac</td>
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</tr>
</tbody>
</table>
Supplemental Figure 1

Heatmap of sample correlations. Columns and rows are samples. The value in the cell of the heatmap is the Pearson’s correlation coefficient between the samples in the corresponding column and row. The Pearson’s correlation coefficient was calculated based on all probes on the array. For each probe set, data with the highest correlation are in yellow and those with the lowest correlation in orange red. Data were generated from BPA-treated (7-day) PPrEC prostaspheres from three individual Caucasian donors. Inter- and intra-donor and treatment variation were compared. PPrEC prostaspheres were treated with vehicle (ctrl) or with 0.1 nM E₂, 10nM BPA (B10), 200 nM BPA (B200), and 1000 nM BPA (B1000). In summary, the samples from same donors showed the highest correlation coefficient and clustered together regardless of the treatment.
Supplemental Figure 2

SNORD expression is not regulated by methylation. PPrEC prostaspheres either untreated (control) or treated with 10 nM BPA (B10) were used for bisulfite sequencing to determine the methylation status at the promoter region upstream of (A) SNORD44, (B) SNORD59A, (C) SNORD82, and (D) SNORD116-21. Sequencing results of different independent clones from three individuals are shown. Open circles indicate unmethylated CpG nucleotides and closed circles indicate methylated CpG nucleotides.
Supplemental Figure 3

Expression of TFF1 is not associated with the histone modifications observed with SNORD. ChIP assay was performed on NPrEC prostatespheres treated with conditions as in Supplemental Figure S1. ChIP assay was performed on active marks H3K4me3 and H3K27me3, and repress mark H3K9me3. The amount of DNA sample loaded for the ChIP assay was denoted as Input.