**Supplementary Methods**

***The selection of SNPs:***

Many SNPs in *CYP17*, *CYP19A1*, *ERα* and *COMT* have been found, but only some of them have been extensively studied. Functional evidence of specific SNPs were the major consideration when we selected SNPs for individual genes and each selected SNP has been widely studied in the development of cancer susceptibility. For example, the SNPs of *CYP17* rs743573, *CYP19A1* $(TTTA)_n$, and *ERα* rs2234693 are known to result in change of gene expression. The nonsynonymous substitution (valine to methionine) of *COMT* rs4680 may decrease enzymatic activity of COMT. Furthermore, SNPs with interethnic difference in allele frequencies are also consideration, such as *COMT* rs4680 and *CYP19A1* $(TTTA)_n$, Therefore, *CYP17* rs743572, *CYP19A1* $(TTTA)_n$, *ERα* rs2234693, and *COMT* rs4680 were chosen as representative polymorphisms of these genes.

***Genotyping***

TaqMan assays were used for genotyping of the *CYP17*, *ERα*, and *COMT* .The thermal cycling condition was 50 °C for 2 minutes, 95°C for 10 minutes, followed by 40 cycles of 95°C for 15 seconds, and 60°C for 60 seconds. The PCR reaction was performed in the total reaction volume of 5 uL containing 10 ng genomic DNA, 2.5 uL of the 2X TaqMan® Universal PCR Master Mix (Applied Biosystems) and 0.125 uL of the 40X primers/ probes mixing in the 384-well plate format on ABI7900HT. The genotyping was designed as Assay-by-Design method (Applied Biosystems), the primer and probe sequences were described in Supplementary Table 1.

The TTTA tetra-nucleotide repeats of the *CYP19A1* were determined by polymerase chain reaction using primers as described in Supplementary Table 1. The PCR mixture consisted of 30 uL reaction volume with 10 ng genomic DNA, 2.5mM

dNTPs, 1.5 mM $MgCl_2$, and 1 U of Fast-Start Taq DNA polymerase (Roche, Germany). The PCR condition included an initial denaturation step at 94°C for 4 minutes, followed by 35 cycles of denaturation at 94°C for 40 seconds, annealing at 55°C for 30 seconds, extension at 72°C for 40 seconds, and a final extension at 72°C for 10 minutes. Two uL of 10 X diluted PCR products were mixed in a running mixture consisting of 8 uL formamide and 0.5 uL ET400-R (Rox) fluorescent size standard (Amersham Bioscience, USA), subsequently denatured and subjected to electrophoresis in the ABI PRISM 3130XL. Allelic bands were identified by GeneMapper.

**Supplementary Table 1.** Sequences of primers and Taqman probes for genotyping:

| Gene | dbSNP ID | Primer / probe sequences | |
|---|---|---|---|
| CYP17 | rs743572 | Forward primer: | CCTCCTTGTGCCCTAGAGTTG |
| | | Reverse primer: | CACGAGCTCCCACATGGT |
| | | Probe 1 (Vic): | AGATAGACAGCGGTGGAG |
| | | Probe 2 (Fam) | AAGATAGACAGCAGTGGAG |
| ERα | rs2234693 | Forward primer: | TCTGTGTTGTCCATCAGTTCATCTG |
| | | Reverse primer: | CTCAGGGTCTCTGGGAAACAG |
| | | Probe 1 (Vic): | CTCAGGGTCTCTGGGAAACAG |
| | | Probe 2 (Fam): | CAAAGCATAAAACGGCTG |
| COMT | rs4680 | Forward primer: | CCCAGCGGATGGTGGAT |
| | | Reverse primer: | CAGGCATGCACACCTTGTC |
| | | Probe 1 (Vic): | TTCGCTGGCATGAAG |
| | | Probe 2 (Fam): | TCGCTGGCGTGAAG |
| CYP19A1 | rs5921193 | Forward primer: | (Hex)GCAGGTACTTAGTTAGCTAC |
| | | Reverse primer: | TTACAGTGAGCCAAGGTCGT |