### Supplementary Table 1.

| Gene             | Sequences                        |
|------------------|----------------------------------|
| nmnat1 Forward Primer | TGGCTCTTTTAACCCCATCAC         |
| nmnat1 Reverse Primer  | TCTTCTTGTACGCCATCACCCA         |
| nmnat3 Forward Primer   | ATCACGAATATGCACCTGGCG         |
| nmnat3 Reverse Primer   | ATTGACGGGTGAGATGATGCC         |
| gapdh Forward Primer    | AGGTCGGTGTGAACGGATTTG         |
| gapdh Reverse Primer    | TGTAGACCATGTAGTTGAGGCTCA      |

**Supplementary Table 1.** Primer sequences for quantitative real-time PCR.
**Supplementary Table 3.**

| KEGG terms                              | ProEGCG: Fold Enrichment | ProEGCG: P value | ProEGCG: Count | EGCG: Fold Enrichment | EGCG: P value | EGCG: Count |
|------------------------------------------|---------------------------|------------------|----------------|------------------------|----------------|-------------|
| Prostate cancer                          | 4.522257701               | 0.00001          | 14             | 5.255156608            | 2.47604E-06   | 15          |
| Metabolism of xenobiotics by cytochrome P450 | 4.993689971               | 0.00000829       | 13             | 4.687031569            | 3.94965E-05   | 12          |
| Adherens junction                        | 5.204690956               | 0.00000531       | 13             | 5.69925435             | 6.81546E-06   | 14          |
| Progestogen-mediated oocyte maturation   | 4.247506412               | 0.0000447        | 13             | 4.651115619            | 7.34864E-06   | 14          |
| Epithelial cell signaling in Helicobacter pylori infection | 5.091155791               | 0.0000176        | 12             | 4.745327982            | 8.59112E-05   | 11          |
| PPAR signaling pathway                   | 5.091155791               | 0.0000176        | 12             | 4.745327982            | 8.59112E-05   | 11          |
| Melanoma                                 | 4.804330113               | 0.000031         | 12             | 4.47798556             | 0.000141754   | 11          |
| Colorectal cancer                        | 4.584777393               | 0.000274         | 10             | 4.195649227            | 0.001193955   | 9           |
| Glycolysis / Gluconeogenesis             | 4.242629826               | 0.000496         | 10             | 4.313934529            | 0.000438899   | 10          |
| Steroid hormone biosynthesis             | 4.410872043               | 0.00085          | 9              | 4.485004347            | 0.00076191    | 9           |
| Non-small cell lung cancer               | 4.566403188               | 0.000669         | 9              | 5.161314526            | 0.000108128   | 10          |
| VEGF signaling pathway                   | 4.19394391                | 0.001193499      | 9              | 4.738255958            | 0.000213044   | 10          |
| Drug metabolism - other enzymes          | 4.943586058               | 0.000988         | 8              | 4.398337596            | 0.004632482   | 7           |
| Cysteine and methionine metabolism       | 5.236298391               | 0.001869921      | 7              | 4.563688633            | 0.0092286     | 6           |
| Bladder cancer                           | 4.853154606               | 0.002790321      | 7              | 7.049600328            | 7.85009E-06   | 10          |

*Supplementary table 3. Top 15 enriched common KEGG pathways of EGCG and ProEGCG, along with Fold enrichment values, P values and genes count.*
### Supplementary Table 4

| FB    | Gene symbol | Target name                                             | PMA expression in endometrium | Protein expression in endometrium | Protein expression in endometrial epithelial cells | Protein expression in endometrial stromal cells | Endometriosis status | Affinity energy (kcal/mol) |
|-------|-------------|---------------------------------------------------------|--------------------------------|-----------------------------------|--------------------------------------------------|------------------------------------------------|---------------------|--------------------------|
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | high                          | high                              | low                                              | low                                            | Transcribed         | -10                      |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 317L1 | MBPAT2      | Veryleucine monooxygenase beta subunit 3               | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 62Q2 | MMETF1      | Acrylamide monooxygenase beta subunit 1                | 10.1                           | medium                            | low                                              | low                                            | Transcribed         | -3.7                     |
| 11R1 | MMETK2      | Methionyl-adenylate pyruvate kinase 6                 | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |
| 723L1 | MPRK        | RNA synthase G protein complex                       | 15.3                           | high                              | high                                             | high                                           | Transcribed         | -3.7                     |

Supplementary Table 4: Profile of genes that are involved in the KEGG pathway of ProEGCG with top 10 highest enrichment values. Data are sorted in descending order of affinity energies. Only proteins with gene expressions in endometrium, protein expressions in endometrial epithelial cells and are transcribed in endometriosis patients were proceed for molecular docking. After that, proteins with the most negative affinity energy were selected as final potential protein targets for further chemical binding and functional analysis. PDB is 4 characters identification code for each molecular model.