

## Supplementary Figure Legends

**Supplementary Figure 1.** Unsupervised hierarchical clustering of all 85 tissue samples by use of all expression data for the 13,158 gene. Pearson's correlation distance is shown to the left. NT = nontumor tissue; Str = stroma; T = tumor; T.str = tumor-stroma tissue; SE = selenium; VE = vitamin E; PL = placebo; p.ex: PL.T.109 means "placebo-treated tumor from patient 109."

**Supplementary Figure 2.** Gene ontology categories of differentially expressed genes in tumor, normal and stromal cells, in treatment (selenium, vitamin E or combination) versus placebo. Gene ontology descriptions of biological function were assigned on the basis of information retrieved from the software's literature database, with a *P* value calculated with Fisher exact test (Ingenuity Pathways Analysis software, Ingenuity Systems, Redwood City, CA). Gene ontology groups with a *P* of less than .009 (Fisher exact test) are shown for stromal, tumor, and normal epithelial prostate cells from patients in each treatment group (selenium, vitamin E, both, or placebo). Red arrows = higher expression of the gene indicated than with placebo treatment; green arrows = lower expression of the gene indicated than with placebo treatment. All statistical tests were two-sided.

**Supplementary Figure 3.** Gene expression network in normal tissue samples treated with either selenium or the combination of selenium and vitamin E. This network was generated by Ingenuity Pathways Analysis (Ingenuity Systems, Redwood City, CA) from differentially expressed genes in normal prostate tissue between treatment groups and the placebo group. The differentially expressed genes in this network are those found in normal tissue samples from both

selenium-treated and combination-treated patients. Genes are represented as nodes (geometrical shapes whose description is given in Supplementary Figure 9). The intensity of the node color indicates the degree of increased (red) or decreased (green) gene expression in the treated group compared with the placebo group.

**Supplementary Figure 4.** Gene expression network in normal tissue samples treated with either vitamin E or the combination of selenium and vitamin E. This network was generated by Ingenuity Pathways Analysis (Ingenuity Systems, Redwood City, CA) from differentially expressed genes in normal prostate tissue between treatment groups and the placebo group. The differentially expressed genes in this network are those found in normal tissue samples from both vitamin E-treated and combination-treated patients. Genes are represented as nodes (geometrical shapes whose description is given in Supplementary Figure 9). The intensity of the node color indicates the degree of increased (red) or decreased (green) gene expression in the treated group compared with the placebo group.

**Supplementary Figure 5.** Gene expression networks in stromal tissue samples treated with either selenium or the combination of selenium and vitamin E. These networks were generated by Ingenuity Pathways Analysis (Ingenuity Systems, Redwood City, CA) from differentially expressed genes in stromal prostate tissue between treatment groups and the placebo group. The differentially expressed genes in these networks were those found in stromal tissue samples from both selenium-treated and combination-treated patients. Genes are represented as nodes (geometrical shapes whose description is given in Supplementary Figure 9). The intensity of the

node color indicates the degree of increased (red) or decreased (green) gene expression in the treated group compared with the placebo group.

**Supplementary Figure 6.** Gene expression networks in stromal tissue samples treated with either vitamin E or the combination of selenium and vitamin E. These networks were generated by Ingenuity Pathways Analysis (Ingenuity Systems, Redwood City, CA) from differentially expressed genes in stromal prostate tissue between treatment groups and the placebo group. The differentially expressed genes in these networks were those found in stromal tissue samples from both vitamin E-treated and combination-treated patients. Genes are represented as nodes (geometrical shapes whose description is given in Supplementary Figure 9). The intensity of the node color indicates the degree of increased (red) or decreased (green) gene expression in the treated group compared with the placebo group.

**Supplementary Figure 7.** Gene expression networks in tumor tissue samples treated with either selenium or the combination of selenium and vitamin E. These networks were generated by Ingenuity Pathways Analysis (Ingenuity Systems, Redwood City, CA) from differentially expressed genes in prostate tumor tissue between treatment groups and the placebo group. The differentially expressed genes in these networks were those found in tumor tissue samples from both selenium-treated and combination-treated patients. Genes are represented as nodes (geometrical shapes whose description is given in Supplementary Figure 9). The intensity of the node color indicates the degree of increased (red) or decreased (green) gene expression in the treated group compared with the placebo group.

**Supplementary Figure 8.** Gene expression networks in tumor tissue samples treated with either vitamin E or the combination of selenium and vitamin E. These networks were generated by Ingenuity Pathways Analysis (Ingenuity Systems, Redwood City, CA) from differentially expressed genes in prostate tumor tissue between treatment groups and the placebo group. The differentially expressed genes in these networks were those found in tumor tissue samples from both vitamin E-treated and combination-treated patients. Genes are represented as nodes (geometrical shapes whose description is given in Supplementary Figure 9). The intensity of the node color indicates the degree of increased (red) or decreased (green) gene expression in the treated group compared with the placebo group.

**Supplementary Figure 9.** Geometrical shapes (nodes) denoting types of interactions in the gene networks of Supplementary Figures 3–8.