

Publicly available genotyping and microarray expression data for 52 endometrial carcinoma samples were downloaded from NCBI GEO 14860

mRNA expression data for 8,543 genes remained after elimination of the bottom 50% by variance

Genotype calling by crlmm algorithm yielded genotype information for over 100,000 SNPs

8,543 genes were assigned to 282 clusters based on similar expression profiles using a genome-wide implementation of the geneRecommender gene clustering algorithm

eQTL analysis by ANOVA with inclusion of SVA-identified covariates  
**(Table 4; Additional File 4)**

Filtering by quality control and deviations from Hardy-Weinberg equilibrium yielded 68,523 SNPs for creQTL analysis

Association of gene coregulation with genotype using the  $Z^2_{E(j)}$  statistic identified significant creQTLs  
**(Table 1; Table 2; Figure 3; Additional File 1)**

Gene Ontology analysis for creQTLs  
**(Table 3; Additional File 3)**

