**Supplemental Methods:**

* Hierarchical Bayesian Multiple Logistic Regression Model:
  + : Binary outcome (case = 1, control = 0) for individual *i*;
  + : Probability of the outcome for individual *i*;
  + : Sample size;
  + : Vector of covariates specific to individual *i* (age, education, alcohol use);
  + : Vector of regression parameters for the covariates;
  + : Exposure to compound *j* specific to individual *i*;
  + : Risk parameter describing the association between compound *j* and thyroid cancer risk.
* Prior Distributions:
* Hyperprior Distributions:
* Posterior Sampling:
  + We used rjags (Plummer, 2016) within R statistical software (R Core Team, 2018) to fit the model. We collected 100,000 posterior samples from all model parameters after removing the first 10,000 during a burn in period. We then thinned the 100,000 posterior samples by 100, leaving us with 1,000 nearly independent posterior samples with which to make statistical inference. Visual inspection of each individual parameter trace plot and calculation of the Geweke convergence diagnostic (Geweke, 1991) for each parameter suggested no obvious signs of convergence failure in the primary analysis with the full set of cases/controls. Effective sample size was used to ensure we collected enough posterior samples to make accurate statistical inference. Quantile-based 95% credible intervals and posterior means are used to summarize posterior distributions.

**References:**

Geweke, J. (1991). Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments (Vol. 196). Minneapolis, MN, USA: Federal Reserve Bank of Minneapolis, Research Department.

Martyn Plummer (2016). rjags: Bayesian Graphical Models using MCMC. R package version 4-6. https://CRAN.R-project.org/package=rjags

R Core Team (2018). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.