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# **Supplemental Material**

Linking Prenatal Environmental Exposures to Lifetime Health with Epigenome-Wide Association Studies: State-of-the-Science Review and Future Recommendations

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Prenatal environmental epigenome-wide association studies (EWAS) were identified through Pubmed, Web of Science, and Embase searches with the following terms.

### **PubMed**

### Web of Science All Databases

### **Embase**

**Figure S1.** Inclusion and exclusion of studies for consideration in systemic review. Using the search terms described in the Supplementary Methods, we conducted a systemic review of epigenome-wide association studies. We excluded studies which were not epigenome-wide association studies (n=199) and studies which evaluated non-external exposures (n=27). We review in depth only studies that either performed replication in an independent sample or conducted a meta-analysis. We retained only EWAS of external exposures (n=134), excluding studies with only global or candidate methylation positions or examining non-exogenous exposures. We included studies using array or sequencing-based methods to measure methylation; 128 of the 134 exogenous exposure EWAS used the Illumina450K or EPIC arrays.

**Table S1.** Summary statistics on sample sizes of epigenome wide association studies.

**Table S2.** Complete data used to create Figure 2 from 134 epigenome wide association studies of external exposures. Please note not all rows included as data points in all facets of Figure 2, Figure 2 footnote explains exclusions.