**Supplementary Table 2:** Genetic and Environmental Category Definitions and Examples Used for Data Abstraction

**Genetic Categories**

* **Germline:** Variation in the DNA sequence, often in the form of single nucleotide polymorphism (SNPs) and structural variations (e.g. copy number variation, insertions/deletions). These typically remain constant during an individual’s lifetime. Germline DNA is the source of DNA for all other cells in the body.
* **Somatic:** Somatic genetic variation, usually described as somatic mutations, occur during mitotic divisions within an individual. Somatic mutations are most commonly studied in the context of tumor cells, or genetic alterations in tumor tissue.
* **GWAS (or genome-wide association study):** Agnostic studies of germline genetic variation that use an array technology (e.g. GWAS array, Oncoarray, Illumina chip, Affymetrix chip) to survey genetic variation across the entire genome.For the purposes of this portfolio analysis, to be categorized as GWAS, the grant must be using a GWAS-based approach in the GxE analysis (or a genome-wide GxE analysis).
* **Candidate Gene:** The candidate gene approach to conducting genetic association studies or studies of somatic alterations in tumors focuses on associations between genetic variation within pre-specified genes of interest and cancer.
* **Whole Exome/Genome Sequencing:** Both of these approaches are using next generation sequencing technology and are largely agnostic approaches.
  + Whole Genome sequencing (also known as WGS, full genome sequencing, complete genome sequencing, or entire genome sequencing) is the process of determining the complete DNA sequence of an organism's genome at a single time.
  + Exome sequencing, also known as whole exome sequencing (WES), is a genomic technique for sequencing the protein-coding genes (i.e., exons) in a genome (known as the exome).
* **Targeted Sequencing:** In contrast to whole exome or whole genome sequencing approaches, specific candidate genes or specified regions of the genome are sequenced using next generation sequencing technology.
* **Epigenetic:** Functional changes to the genome that are not due to changes in the DNA sequence. DNA methylation is an example of an epigenetic change where methyl groups are added to DNA which can influence gene activity and expression. Epigenetic modifications can result from exposure and aging.

**Environmental Exposure Categories and Terms**

* **Infection and Inflammation:** infection, bacteria, virus, allergy, inflammatory bowel disease, autoimmune diseases, such as rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
* **Drugs/Treatment:** drugs, medication, radiation therapy, nonsteroidal anti-inflammatory drugs (NSAIDs)
* **Reproductive Factors:** parity, age of menarche, age of menopause, age of first full-term pregnancy
* **Exogenous Hormones:** hormone replacement therapy (HRT), oral contraceptives (OC)
* **Chemical Environment:** carcinogens, chemicals, solvents, dioxins, pesticides, metals, vinyl chloride, benzidine, diesel exhaust particles, polycyclic aromatic hydrocarbons (PAH), phthalates, polychlorinated biphenyl (PCB), phenols, bisphenol A (BPA), perfluorinated compounds, perfluorooctanoic acid (PFOA), enterolactone (ENL), genistein, cotinine, polybrominated diphenyl ether (PBDE), organochlorine pesticides
* **Physical Environment:** electromagnetic field (EMF), ionizing radiation (could include cell phone use), ultraviolet (UV) exposure (could also be lifestyle depending on focus of application)
* **Lifestyle:** Behaviors, smoking, tobacco use, alcohol use
* **Energy Balance:** Diet (e.g. nutrients, phytoestrogens, vitamin D), physical activity, physical inactivity, weight, obesity (Note: although these factors contribute to energy balance, the grants were not necessarily specifically assessing the balance of intake/output of energy.)
* **Metabolomics:** metabolites, often assessed using mass spectrometry technology
* **Microbiome:** sequencingof microbial species in thegut or oral cavity
* **Social:** social environment (cultural, political, neighborhoods), social determinants
* **General:** Applications that did not specify a specific environmental exposure and indicated they will examine GxE interactions. Most of the funded applications that were coded in this category were methods grants examining GxE.

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