SOCIAL GENOMIC MECHANISMS OF HEALTH DISPARITIES AMONG ADOLESCENT AND YOUNG ADULT (AYA) CANCER SURVIVORS (ECOG-ACRIN TRIAL EAQ211) Funded in part by the National Cancer Institute, National Institutes of Health Division of Cancer Control and Population Sciences (DCCPS), Grant Number: 1R01CA61752-01; and ECOG-ACRIN

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Specific Aims

#1: To identify the genome-wide transcriptional impact of **SOCIAL-ENVIRONMENTAL RISK factors** and define the relationships of those genomic profiles to AYA lymphoma survivor OUTCOMES (i.e., morbidity, mortality, QOL).

#2: To identify the genome-wide transcriptional impact of **INDIVIDUAL RESILIENCE factors** and define the relationships of those genomic profiles to AYA lymphoma survivor health **OUTCOMES** (i.e., morbidity, mortality, QOL).

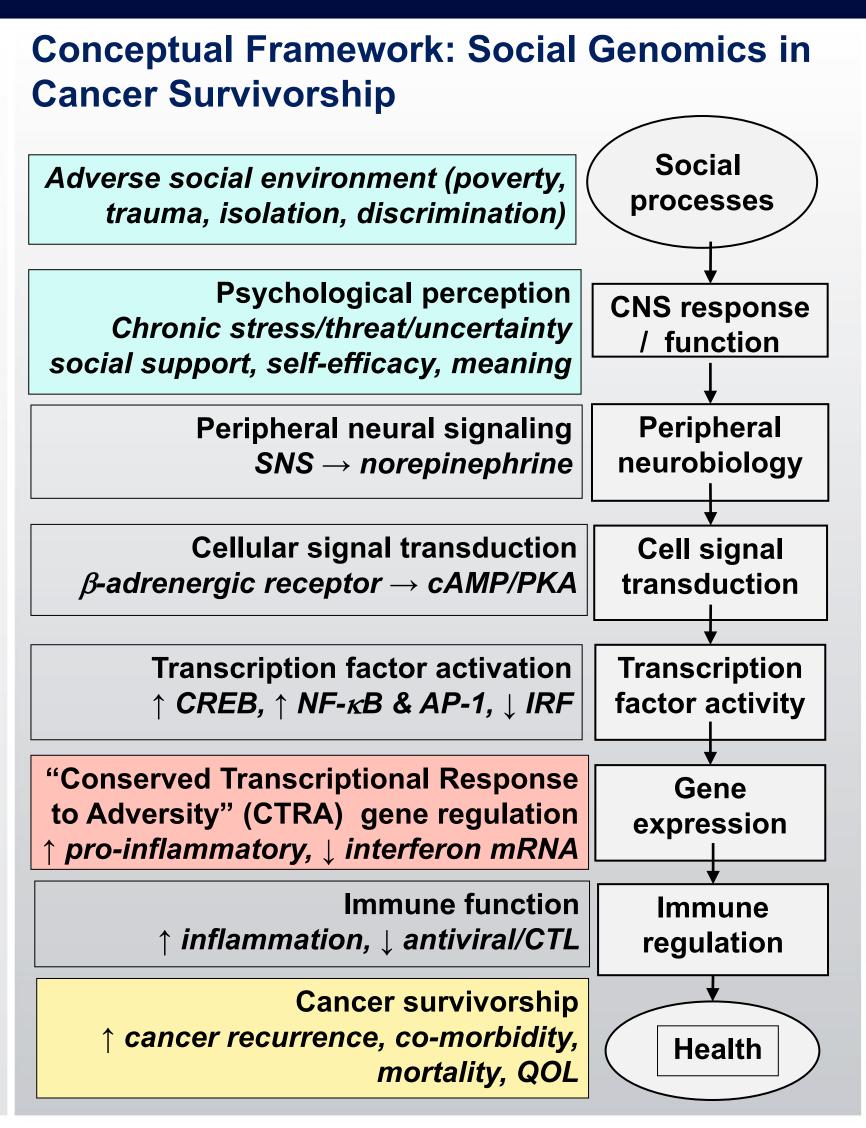
#3: To examine disparities in these mechanisms as a function of race/ethnicity, sexual orientation and gender identification, and geography (urban/rural).

Method

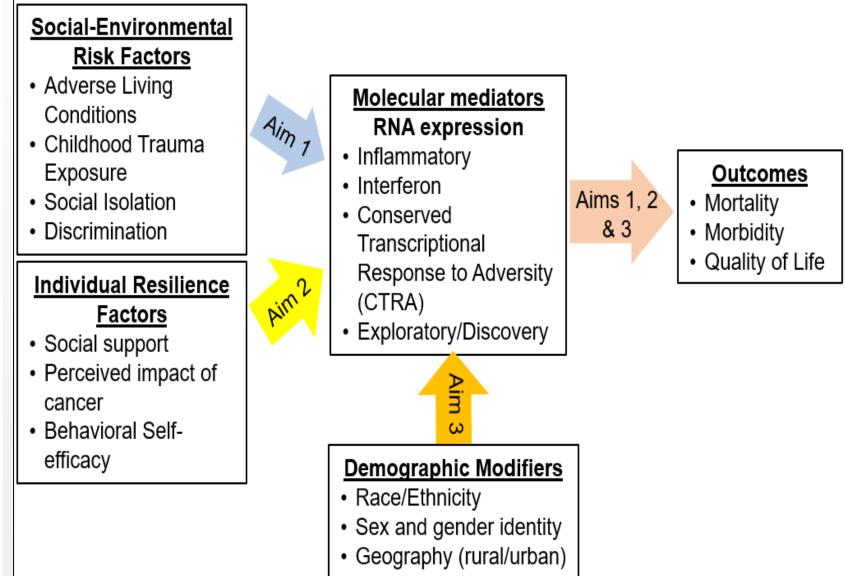
Study Design: Longitudinal prospective single cohort of AYAs recruited from community oncology settings, with repeated measures of two years

Study Participants: 2000 patients diagnosed with Hodgkin or Non-Hodgkin Lymphoma, recruited at completion of therapy – Recruitment through the ECOG-ACRIN Cancer Research Base and NCI Community Oncology Research Program (NCORP)

Data Collection: Patient-Reported Outcome (PRO) measures administered via survey; blood samples at baseline, 6-, 12-, 18-, and 24-month follow-up.



Data Analytic Framework



Investigative Team

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AYA Stakeholder Organizations: TeenCancerAmerica; Cactus Cancer; Leukemia and Lymphoma Society; Cervivor

<u>Disclosures</u>: Cole: BlueNote Therapeutics; Wagner: Johnson & Johnson, Lilly, Gilead Sciences, Celgene, Athenex; Parsons: Seattle Genetics; Prasad: Vertex; Dinner: Kite, Pfizer, Novartis





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