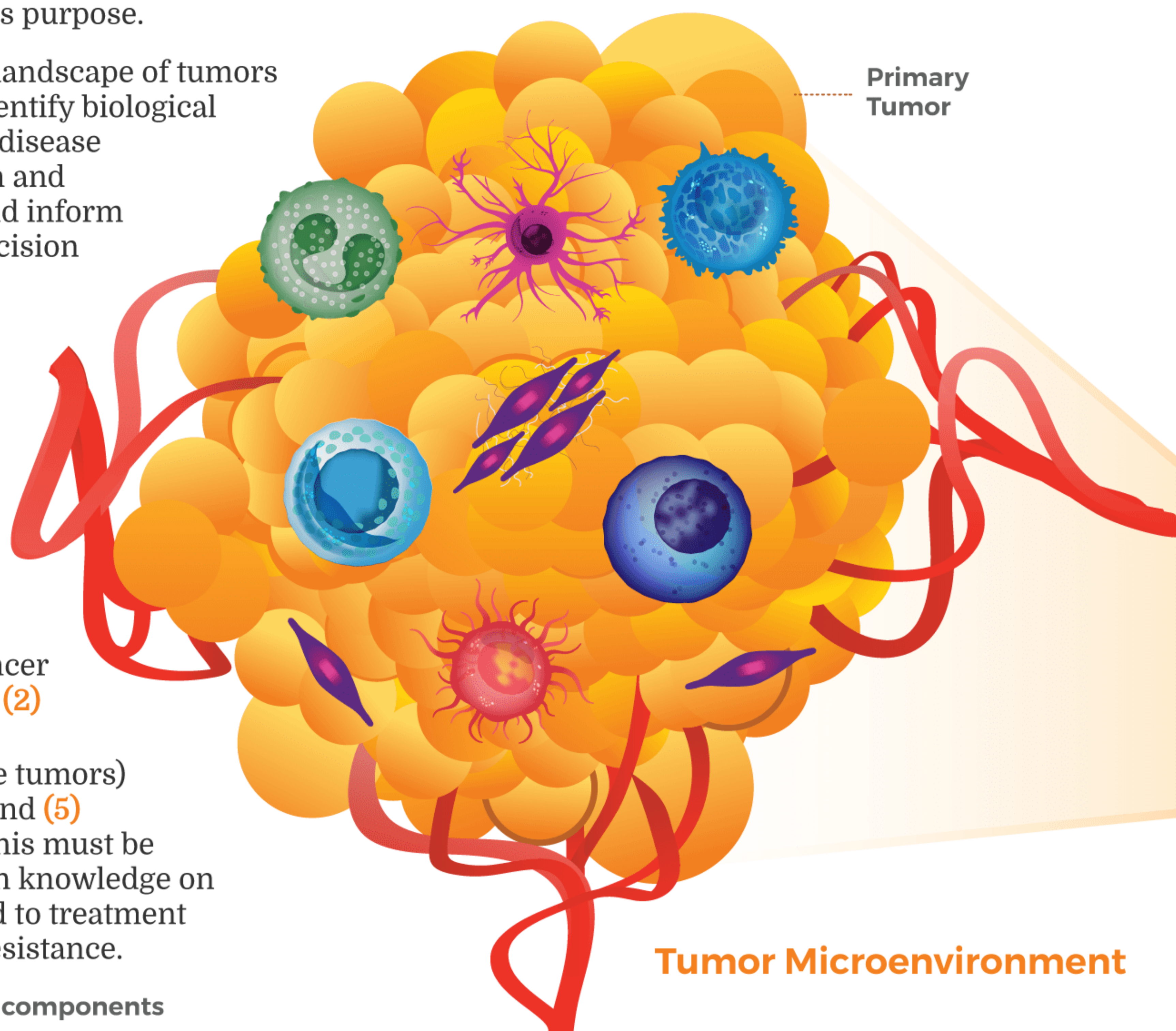


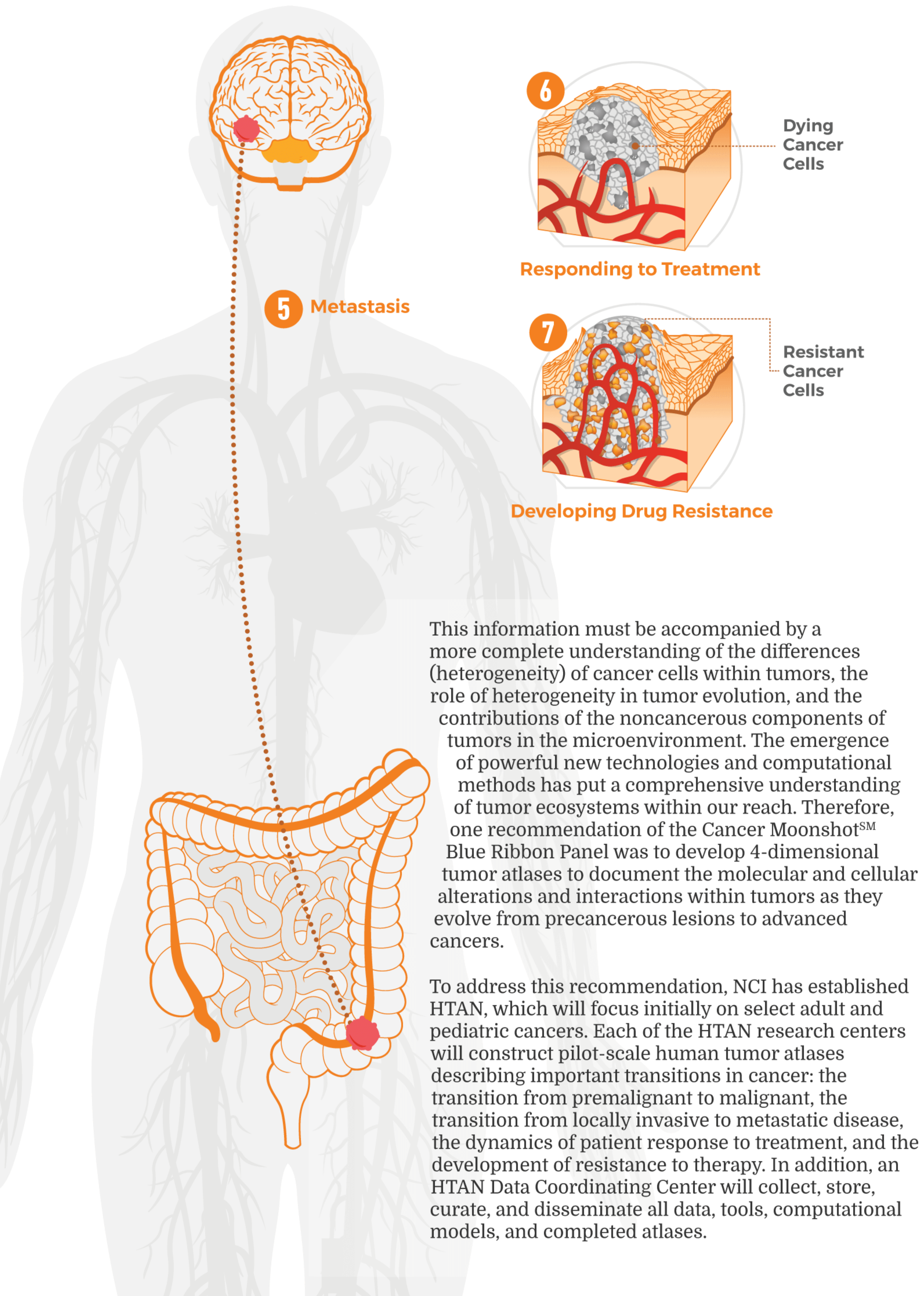
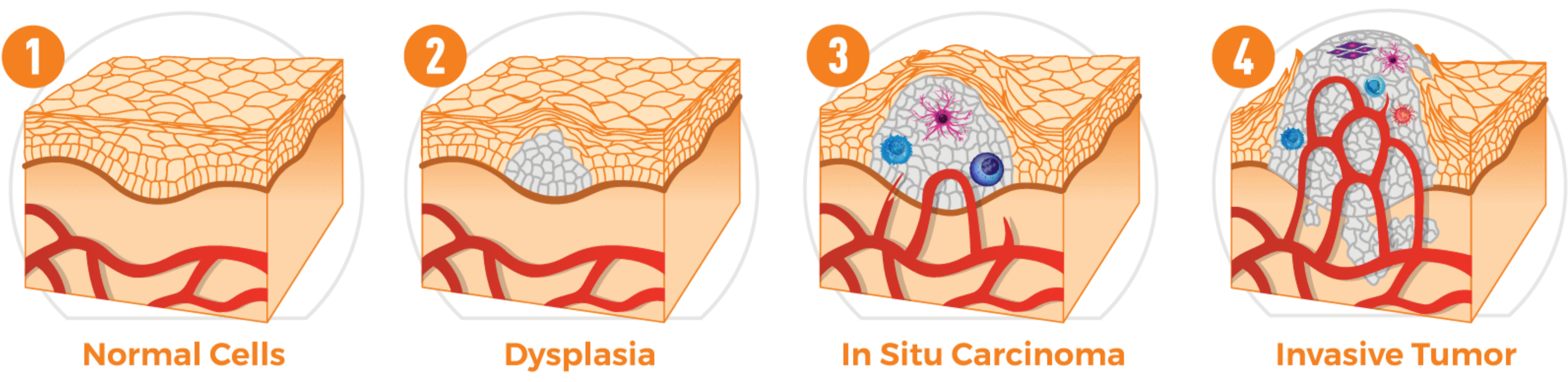
Cancer and the Human Tumor Atlas Network

The construction of human tumor atlases will provide a more comprehensive understanding of the ecosystems of tumors at the macro- and the micro-level. NCI has established the Human Tumor Atlas Network (HTAN) for this purpose.

Mapping the landscape of tumors will help identify biological markers of disease progression and treatment resistance and inform the development of precision risk-stratification, prevention, screening, diagnostic, and treatment strategies. To accomplish this, a better understanding of the molecular-, cellular-, and tissue-level communication networks that drive the major transitions in cancer from (1) normal cells to (2) dysplasia to (3) *in situ* carcinoma (noninvasive tumors) to (4) invasive disease and (5) metastasis is needed. This must be integrated with in-depth knowledge on how tumors (6) respond to treatment and (7) develop drug resistance.



Tumor Microenvironment components



This information must be accompanied by a more complete understanding of the differences (heterogeneity) of cancer cells within tumors, the role of heterogeneity in tumor evolution, and the contributions of the noncancerous components of tumors in the microenvironment. The emergence of powerful new technologies and computational methods has put a comprehensive understanding of tumor ecosystems within our reach. Therefore, one recommendation of the Cancer MoonshotSM Blue Ribbon Panel was to develop 4-dimensional tumor atlases to document the molecular and cellular alterations and interactions within tumors as they evolve from precancerous lesions to advanced cancers.

To address this recommendation, NCI has established HTAN, which will focus initially on select adult and pediatric cancers. Each of the HTAN research centers will construct pilot-scale human tumor atlases describing important transitions in cancer: the transition from premalignant to malignant, the transition from locally invasive to metastatic disease, the dynamics of patient response to treatment, and the development of resistance to therapy. In addition, an HTAN Data Coordinating Center will collect, store, curate, and disseminate all data, tools, computational models, and completed atlases.

Multilevel Network Analyses & Data Integration

Human tumor atlases will show the tissue, tumor, cell, and molecular level interactions of cancer. Computer modeling and data integration of this multilevel information will allow for the creation of dynamic visual resources of tumor evolution.



Tumor cells communicate with other cells, both locally and distantly. The organ- and tissue-level communication networks that support tumor growth, and metastasis can be mapped and analyzed with analyses at multiple levels.



Molecular networks are systems of interacting molecules (i.e., genes, proteins, etc.) that underlie specific biological functions. These intracellular networks can be mapped in all cells in the tumor microenvironment for integration into an atlas.



Cancer development, progression, and metastasis require complex interactions within the local tumor microenvironment that are mediated by many factors. These interactions can be mapped spatially and temporally in a tumor atlas.



Cancer cells have genetic and epigenetic alterations that influence the organization and expression of genes. These alterations and their effects on cancer cells can be mapped and integrated with other-level analyses in a tumor atlas.