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This paradigm has led to the development of many agents that have modest or no benefit in the vast majority of patients. Agents with profound activity in only a small number of patients, on the other hand, were deemed inactive and abandoned.

Our laboratory is collaborating with cancer researchers from Weill Cornell Medical Center and the New York Genome Center to perform integrated next-generation sequencing analyses of responding patients enrolled in phase I/II clinical trials or treated with standard systemic agents at Memorial Sloan Kettering and Weill Cornell Medical Center. The primary goal will be to ensure that the development of agents with profound, life-altering activity in only a minority of patients is not prematurely halted but rather redirected to the subset of patients most likely to benefit.

As solid tumors defined by site of origin in fact represent genetically heterogeneous collections of distinct diseases, such efforts will accelerate the shift toward individually tailored, genetically based treatment approaches. This work is supported by STARR Award I7-A771 (PI: David Solit, Co-PIs Mark Rubin and Robert Darnell).

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