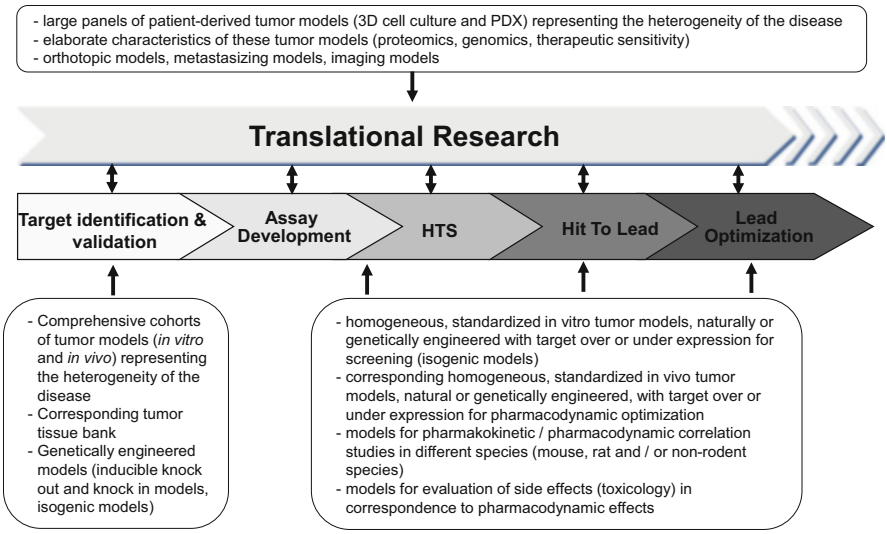

Fig. 1 Oncology drug development requires well-characterized panels of in vitro and in vivo tumor models, standardized analytical methods, as well as experimental settings to transfer bench-side targets into drugs for the clinic

of specific drugs is now seen as a prerequisite for the development of molecular-targeted therapies. Slamon and colleagues were the first using a cancer cell line panel to validate overexpression of Her2 as a predictive marker in breast cancer for the efficacy of Herceptin (Slamon and Pegram 2001). The lack of such studies in large cell culture panels in other indications has hindered the development of further epidermal growth factor receptor (EGFR) targeting drugs, i.e., gefitinib, cetuximab, or panitumumab. Initially, some unstratified studies failed, and only a posteriori genotype-dependent stratification of patient cohorts allowed predicting efficacy and further development of targeted therapeutics like cetuximab or panitumumab (Lièvre et al. 2006; Amado et al. 2008).

The requirements on new models for target identification and validation (TIV) include among others:

- Availability of large panels of tumor models (in vitro and in vivo) representing the heterogeneity of the disease
- Extensive data about the characteristics of these tumor models (gene and protein expression, gene amplifications, mutations, epigenetics, miRNA expression, histology, reference drug sensitivity)
- Corresponding databases containing all these information and tools allowing bioinformatic analyses
- Tumor tissue banks (frozen and paraffin-embedded tissue, tissue microarrays)
- Technology to generate genetically engineered models (inducible knockout and knock-in models, isogenic models)