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Laboratory perspective on the translational aspects of cancer genomics

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High throughput sequencing approaches developed over the past few years enable informed precision medicine approaches for cancer, in real time. Unfortunately, from huge (and not inexpensive) sequencing data analyses, only a limited set of well characterized somatic aberrations can be effectively matched with precision therapeutic options. The large bulk of somatic aberrations identified in individual patient's tumor samples typically include aberrations in hitherto non-actionable genes or uncharacterized aberrations in known, potentially actionable cancer genes- both scenarios being not immediately translatable. The latter set of findings represents a bottleneck in the translation of genomic findings in patient care, indicating a need for high throughput pre-clinical research in step with high throughput analyses.

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