Is Next Generation Sequencing ready for being used in daily practice?

1. Yes
2. No
3. Don’t know

Is Next Generation Sequencing ready for being tested in clinical trials?

1. Yes
2. No
3. Don’t know

Is Next Generation Sequencing a technology for the whole or could it generate unequal care delivery?

1. Yes
2. No
3. Don’t know

Whole-genome DNA sequencing currently represents the most comprehensive strategy for variant detection, hence I would like to implement it in my hospital

1. Yes
2. No
3. Don’t know

Whole-exome sequencing (entire set of exons in the genome) can provide a list of the majority of mutations in coding regions, hence provides an appropriate solution for mid-sized clinical centers

1. Yes
2. No
3. Don’t know

Sequencing a set of approximately 100 genes/mutations frequently occurring in cancer is sufficient for my clinical decision-making process

1. Yes
2. No
3. Don't know

In the next 5-10 years, a comprehensive list of all mutations occurring in a tumor will not significantly affect selection of treatment modalities

1. Yes
2. No
3. Don't know

Intra-tumor variation of mutations (heterogeneity) preempts the utility of NGS data

1. Yes
2. No
3. Don’t know

The landscape of tumor genomics, as revealed by deep-sequencing, is not sufficient for tailored cancer therapy

1. Yes
2. No
3. Don’t know