CanSeq **MD ID: _____**

Sequencing to Guide the Care of Cancer Patients

Physician Baseline Survey

Thank you for agreeing to participate in our study on the use of whole-exome sequencing in cancer care. To begin, we would appreciate it if you would complete this short questionnaire about your current use of genomic testing and about how you expect to use sequencing in your clinical practice.

Please indicate the extent to which you agree or disagree with the following statements about the return of genomic sequencing information to patients:

	Strongly disagree	Somewhat disagree	Neither agree nor disagree	Somewhat agree	Strongly agree
1. Patients should *only* be offered their genomic sequence results if evidence demonstrates that actions based on the results can change patient management decisions and improve net health outcomes.	☐	☐	☐	☐	☐
2. Patients should be offered genomic sequence results for which there is an *established relationship between genotype and phenotype* (e.g., results can be used to diagnose a disorder or to assess risk for a disease), even if the results do not alter management decisions or improve net health outcomes.	☐	☐	☐	☐	☐
3. Patients should be *offered as many of their genomic sequence results as they want*, up to and including their raw genomic sequence data.	☐	☐	☐	☐	☐

Through the use of whole-exome sequencing of **tumor DNA**, oncologists may find somatic alterations with various implications. Somatic alterations may…

- Provide **information that may be relevant to cancer treatment**. For example, somatic alterations may help to inform decisions about:
    - FDA approved targeted therapies (e.g., EGFR mutations in a patient with advanced lung cancer; KRAS mutations in a patient with advanced colorectal cancer),

      and/or

    - Clinical trials of targeted therapies (e.g., BRAF mutations in patients with advanced lung cancer, PIK3CA mutations in advanced colorectal cancer)
- Provide **information relevant to the patient's prognosis** (e.g., IDH1 mutations in glioblastoma multiforme)

(please turn page)

The questions that follow contain scenarios describing a particular type of genomic alteration derived from sequencing the patient's tumor DNA. **Assume:**

- the tumor DNA belongs to YOUR adult patient with a metastatic solid tumor
- the sequencing was performed in a clinically certified (i.e., CLIA) lab
- the patient is currently receiving a first-line standard chemotherapy regimen
- the patient has an ECOG performance status of 0 or 1
- the patient has indicated that s/he would like to be told about all clinically valid genomic results

Please check the box that reflects how likely you would be to disclose the information described in each scenario to your patient. Please read each scenario carefully.

Sequencing of tumor DNA identifies a somatic alteration that…	**In this situation, I would…**				
	Definitely disclose	**Probably disclose**	**Probably not disclose**	**Definitely not disclose**	**Unsure**
4. Is in a pathway that is *not* targeted by any FDA-approved agent. However, an agent that targets this pathway is currently being studied in a phase II clinical trial that's open at your institution. Your patient may be eligible for this trial.	☐	☐	☐	☐	☐
5. Is in a pathway that is targeted by a commercially available agent that is FDA-approved *for a different cancer*. There are no reports in the literature of agents that target this pathway being used in your patient's type of cancer.	☐	☐	☐	☐	☐
6. Is known to confer a *favorable* prognosis, compared with the average for patients with this condition. There are no available agents, either commercially or through a clinical trial, that target the relevant pathway.	☐	☐	☐	☐	☐
7. Is known to confer an *unfavorable* prognosis, compared with the average for patients with this condition. There are no available agents, either commercially or through a clinical trial, that target the relevant pathway.	☐	☐	☐	☐	☐

Whole-exome sequencing to identify somatic mutations is enhanced by sequencing patients' germline DNA in parallel. Sequencing of patients' **germline DNA** may incidentally identify information about hereditary genetic alterations with varying implications for the patient and/or the patient's family.

Below are scenarios describing types of hereditary genetic alterations that might be identified during the process of whole-exome sequencing in the patient with a metastatic solid tumor described above. *Please read each scenario carefully and think about the implications of the information for both your patient and the patient's family.*

For each scenario, please check the box that reflects how likely you would be to disclose the information described to your patient and/or family. In answering these questions, please assume your patient has biological children.

Sequencing of germline DNA identifies…	**In this situation, I would…**				
	Definitely disclose	**Probably disclose**	**Probably not disclose**	**Definitely not disclose**	**Unsure**
8. An alteration in a cancer risk gene for which risk reduction strategies *are* available.	☐	☐	☐	☐	☐
9. An alteration in a cancer risk gene for which risk reduction strategies *are not* available.	☐	☐	☐	☐	☐
10. A pharmacogenetic polymorphism that impacts the metabolism of *anti-cancer medications* that may be relevant to your patient's care.	☐	☐	☐	☐	☐
11. A pharmacogenetic polymorphism that impacts the metabolism of *non-cancer-related medications* that may be relevant to your patient's care.	☐	☐	☐	☐	☐
12. An alteration that confers an increased risk of developing a condition, other than cancer, for which risk reduction strategies *are* available.	☐	☐	☐	☐	☐
13. An alteration that confers an increased risk of developing a condition, other than cancer, for which risk reduction strategies *are not* available.	☐	☐	☐	☐	☐
14. An alteration that identifies your patient as a carrier of a non-cancer-related condition that might be passed on to a child.	☐	☐	☐	☐	☐

The next set of questions is about you and your experience with genomic information.

Please indicate how confident you are in your ability to do the following things.

	Very confident	Moderately confident	A little confident	Not confident at all
15. Ability to interpret somatic (tumor) genomic results in your disease area.	☐	☐	☐	☐
16. Ability to explain somatic genomic concepts to patients.	☐	☐	☐	☐
17. Ability to make treatment recommendations based on somatic genomic information.	☐	☐	☐	☐
18. Ability to identify consultants who have special expertise in integrating somatic genomic information into patients' care.	☐	☐	☐	☐
19. Ability to provide psychosocial support related to coping with a somatic alteration that has adverse prognostic implications.	☐	☐	☐	☐

Please indicate how confident you are in your ability to carry out each of the following tasks related to germline genetic conditions.

	Very confident	Moderately confident	A little confident	Not confident at all
20. Take a family history.	☐	☐	☐	☐
21. Identify a family history of a potentially inherited condition.	☐	☐	☐	☐
22. Identify an autosomal dominant family pattern.	☐	☐	☐	☐
23. Explain an autosomal dominant family pattern to a patient.	☐	☐	☐	☐
24. Counsel an individual with a family history of an inherited cancer risk syndrome to decide whether or not to have presymptomatic genetic testing.	☐	☐	☐	☐
25. Provide psychosocial support related to coping with a genetic test result that confirms the presence of an inherited cancer risk syndrome.	☐	☐	☐	☐
26. Identify specialist genetic services in your local area.	☐	☐	☐	☐
27. Obtain informed consent before taking blood for DNA testing to evaluate for an inherited cancer risk syndrome.	☐	☐	☐	☐

The next set of questions is about your use of genomics in practice.

On average, how many times a year do you order or interpret the following types of genetic or genomic tests in your clinical practice?

Include both cases in which you order the test yourself and cases in which you use or interpret the results of tests ordered by others.

	Approximate Number of Times Per Year
28. Somatic tests to evaluate for alterations in tumor DNA.	___
29. Germline tests to evaluate for inherited cancer predisposition syndromes.	___
30. Germline tests to evaluate for pharmacogenetic polymorphisms (i.e., that affect drug metabolism or toxicity) related to *cancer drugs*.	___
31. Germline tests to evaluate for pharmacogenetic polymorphisms related to *non-cancer drugs*.	___
32. Germline tests to evaluate for inherited conditions *unrelated to cancer.*	___
33. Germline tests to evaluate whether a patient is a carrier of a non-cancer-related condition that might be passed on to a child.	___

The final set of questions is about you.

34. Do you consider yourself Hispanic or Latino/a?

- ☐ Yes, Hispanic or Latino/a
- ☐ No

35. What is your race? *Please check all that apply.*

- ☐ American Indian or Alaska Native
- ☐ Asian
- ☐ Black or African American
- ☐ Native Hawaiian or other Pacific Islander
- ☐ White

36. In what year did you complete fellowship training?

_____ (year)

37. What is your gender?

- ☐ Male
- ☐ Female

38. On average, how many unique patients do you see for treatment or evaluation each month? Please include both new and established patients. *Your best estimate is fine*.

_____ number

39. Are you a principal investigator for research in any of in the following areas? *Please c**heck all that apply.*

- ☐ Clinical trials research
- ☐ Translational science research
- ☐ Basic science research
- ☐ Outcomes or health services research
- ☐ Other research (please specify):

_____

_____

40. During a typical month, approximately what percent of your professional time do you spend in the following activities?
    a. Providing patient care: _____percent of time
    b. Research: _____percent of time
    c. Teaching: _____percent of time
    d. Administration: _____percent of time

Do you have any additional thoughts that you wish to share about the issues raised in this survey? Please feel free to write in the space below as we welcome your feedback.

Thank you very much for completing this survey! Your participation is greatly appreciated.

Survey and Data Management core
qualitative and quantitative research