Supplemental Digital Content

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NGSHM-A-2017 Result Form Questions used in Manuscript

1. Using the NGS Platform Master List on the kit instructions, indicate which platform is used in your laboratory for somatic variant detection for this assay?
    a. Applied Biosystems SOLiD
    b. Illumina HiSeq 2000
    c. Illumina HiSeq 2500
    d. Illumina HiSeq 3000/4000
    e. Illumina HiSeq X Five/Ten
    f. Illumina MiSeq
    g. Illumina MiSeqDx
    h. Illumina NextSeq 500
    i. Ion Torrent PGM
    j. Ion Torrent Proton
    k. Ion Torrent S5/S5 XL
    l. Pacific Biosciences (PacBio) RS/RS II
    m. Roche 454 GS Junior/Junior+/FLX+
    n. Other, specify

2. Which categories of somatic variants are detected by the assay described in Question #1? (Select all that apply.)
    a. Single nucleotide variants
    b. Small insertions and deletions (eg, < 50 bp)

3. For each variant category selected in Question #2, what is the lower limit of detection for your assay in terms of somatic allele percentage? If the limit of detection varies depending on the gene and region, please indicate the highest allele percentage.

4. Is a sensitivity control at or near the lower limit of detection of the assay included in each run?
    a. Yes
    b. No

5. Which sequencing strategies are used by your laboratory for somatic variant detection in hematologic malignancies for the single assay being described in this Survey? (Select all that apply.)
    a. Exome sequencing
    b. Genome sequencing
    c. RNA sequencing
    d. Targeted sequencing of cancer genes or mutation hotspots, such as custom or commercial targeted amplicon or hybrid capture panels
    e. Other(s), specify

6. If your laboratory performs targeted sequencing of cancer genes or mutation hotspots in hematologic malignancies, which selection method is used for this assay?
    a. Not applicable; our laboratory performs exome or genome sequencing for somatic variant detection
    b. Agilent ClearSeq AML
    c. Fluidigm Access Array
    d. Illumina TruSight Myeloid Sequencing Panel

e. Ion AmpliSeq Cancer Hotspot Panel
f. Ion AmpliSeq Comprehensive Cancer Panel
g. RainDance ThunderBolts Myeloid Panel
h. Roche NimbleGen Comprehensive Cancer Design
i. Custom Enrichment Approach
j. Custom designed captured- or amplicon-based enrichment approach
k. Other, specify

7. If Custom Enrichment Approach was selected in Question #6, specify:
    a. Agilent Custom SureSelect
    b. Agilent HaloPlex Custom Kit
    c. Illumina TruSeq Custom Amplicon
    d. Ion AmpliSeq Custom DNA Panel
    e. Nextera Rapid Capture Custom Enrichment Kit
    f. RainDance Custom Gene Panel
    g. Roche NimbleGen SeqCap EZ Designs
    h. Other, specify

8. What is the read configuration used by your laboratory for this assay used for somatic variant detection in hematologic malignancies?
    a. Single-end reads
    b. Paired-end reads
    c. Other, specify

9. What is the read length in base pairs for this assay used for somatic variant detection in hematologic malignancies?
    a. 25 bp
    b. 36 bp
    c. 50 bp
    d. 75 bp
    e. 100 bp
    f. 125 bp
    g. 150 bp
    h. 200 bp
    i. 250 bp
    j. 300 bp
    k. 400 bp
    l. Other, specify

10. What is the average number of reads that covers the targeted bases in your laboratory's assay?
    a. 0 – 50X
    b. 51 – 150X
    c. 151 – 250X
    d. 251 – 350X
    e. 351 – 500X
    f. 501 – 750X
    g. 751 – 1,000X
    h. 1,001 – 1,500X
    i. 1,501 – 2,500X
    j. > 2,500X
    k. We have not established this metric

11. What is the minimum number of reads that your laboratory requires for each targeted base in the assay?
    a. 0 – 25 reads

b. 26 – 50 reads
c. 51 – 150 reads
d. 151 – 250 reads
e. 251 – 350 reads
f. 351 – 500 reads
g. 501 – 750 reads
h. 751 – 1,000 reads
i. 1,001 – 1,500 reads
j. 1,501 – 2,500 reads
k. > 2,500 reads
l. We do not have a minimum read requirement

12. Does your laboratory perform sequencing on tumor-normal paired specimens as part of routine tumor testing?
    a. Yes, our laboratory sequences tumor-normal paired specimens
    b. No, our laboratory only sequences tumor specimens

13. If you answered Yes to Question #12, what control tissue(s) does your laboratory use? (Select all that apply.)
    a. Buccal swabs
    b. Fixed "normal" tissue
    c. Fresh "normal" tissue (eg, skin biopsy)
    d. Peripheral blood
    e. Other, specify

14. If you answered Yes to Question #12, does your laboratory report constitutional variants?
    a. Yes
    b. No

15. Which specimen types does your laboratory test for somatic variant detection for the single assay being described? (Select all that apply.)
    a. FFPE cell blocks
    b. FFPE tissues
    c. Fine-needle aspirates
    d. Frozen tissues
    e. Fresh bone marrow
    f. Fresh peripheral blood
    g. Fresh tissue
    h. Other, specify

16. Which quantity of purified genomic DNA does your laboratory require to perform this assay?
    a. 0 – 100 ng
    b. 101 – 200 ng
    c. 201 – 500 ng
    d. 501 – 1,000 ng
    e. 1,001 – 2,000 ng
    f. > 2,000 ng

17. If your laboratory performs confirmatory testing on any somatic variants for this assay, what methods are used? (Select all that apply.)
    a. Not applicable; somatic variants are reported without confirmations
    b. Fragment analysis
    c. Sanger sequencing
    d. Pyrosequencing
    e. Sequenom

f. Other targeted mutation testing (eg, allele-specific PCR or real-time PCR)
g. Other NGS-based platform, specify
h. Other, specify

18. In your laboratory's clinical reports, does your laboratory list the variant allele fraction?
    a. Yes, for all reported variants
    b. Yes, when allele fraction and tumor content suggest subclonality
    c. No

19. In your laboratory's clinical reports, does your laboratory report total coverage depth (variant and reference reads) at the variant position?
    a. Yes
    b. No

20. What types of interpretation does your laboratory routinely provide? (Select all that apply.)
    a. No interpretation provided beyond listing the mutations detected
    b. Categorization of variants into classes of medical significance
    c. Biological function, known
    d. Biological function, speculative
    e. Clinical implications, known
    f. Clinical implications, speculative
    g. Specific treatment recommendations, standard of care
    h. Specific treatment recommendations, investigational therapies
    i. Listing of clinically significant mutations that were not detected, general
    j. Listing of clinically significant mutations that were not detected, disease-specific
    k. Listing of undercovered/underperforming regions that were not detected, general
    l. Listing of undercovered/underperforming regions that were not detected, disease-specific

21. Does your laboratory report variants using a tiered approach (ie, tier 1: variants known to be associated with the disease in question; tier 2: variants known to be associated disease, but in a different disease type…tier x: variant with unknown disease association)?
    a. Yes
    b. No