**Template for Reporting Results of Biomarker Testing of Specimens from Patients with Non-Small Cell Carcinoma of the Lung**

**Version:** 2.2.0.0

**Protocol Posting Date:** September 2025

This biomarker template is not required for accreditation purposes but may be used to facilitate compliance with CAP Accreditation Program Requirements.

**Version Contributors**

**Authors:** Brett W. Baskovich, MD\*, Kirtee Raparia, MD, FCAP\*

**Other Expert Contributors:** Patrick L. Fitzgibbons, MD, FCAP, George G. Birdsong, MD, Joseph D. Khoury, MD, Raja R. Seethala, MD, Frank Schneider, MD, Alexander Baras, MD, PhD

\* Denotes primary author.

For any questions or comments, contact: [cancerprotocols@cap.org.](mailto:cancerprotocols@cap.org)

**Glossary:**

**Author:** Expert who is a current member of the Cancer Committee, or an expert designated by the chair of the Cancer Committee.

**Expert Contributors:** Includes members of other CAP committees or external subject matter experts who contribute to the current version of the protocol.

**Accreditation Requirements**

Completion of the template is the responsibility of the laboratory performing the biomarker testing and/or providing the interpretation. When both testing and interpretation are performed elsewhere (eg, a reference laboratory), synoptic reporting of the results by the laboratory submitting the tissue for testing is also encouraged to ensure that all information is included in the patient’s medical record and thus readily available to the treating clinical team. This template is not required for accreditation purposes.

**Summary of Changes**

**v 2.2.0.0**

* Updates to EGFR, ALK, ROS1, RET, BRAF, NTRK, and PD-L1 sections
* Addition of NRG1 section
* Addition of optional Specify Fusion Partner question to ROS1, RET NTRK1, NTRK2, and NTRK3 Molecular Methods
* Addition of BRAF:p.V600K, BRAF:p.V600R, and BRAF:p.V600D answers to BRAF Mutational Analysis question
* Addition of specific PD-L1 markers to include PD-L1 22c3, PD-L1 228-8, PD-L1 SP142, and PD-L1 SP263

**Reporting Template**

**Protocol Posting Date:** September 2025

**Select a single response unless otherwise indicated.**

**CASE SUMMARY: (Lung Biomarker Reporting Template)**

*Completion of the template is the responsibility of the laboratory performing the biomarker testing and / or providing the interpretation. When both testing and interpretation are performed elsewhere (e.g., a reference laboratory), synoptic reporting of the results by the laboratory submitting the tissue for testing is also encouraged to ensure that all information is included in the patient’s medical record and thus readily available to the treating clinical team.*

*Gene names should follow recommendations of The Human Genome Organisation (HUGO) Nomenclature Committee (www.genenames.org; accessed September 2, 2025).*

*All reported gene sequence variations should be identified following the recommendations of the Human Genome Variation Society (www.http://varnomen.hgvs.org;accessed September 2, 2025).*

**SPECIMEN**

**+Adequacy of Sample for Testing**

\_\_\_ Adequate

**+Specify Estimated Percent of Tumor Cellularity (area used for testing): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

\_\_\_ Suboptimal (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

*Please refer to original laboratory report for explanation.*

**+Specimen Type**

\_\_\_ Untreated diagnostic specimen

\_\_\_ Relapse specimen (after treatment; specify)#: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

*# When data is available, specify treatment type. This is most relevant to targeted inhibitors associated with specific genomic changes conferring treatment resistance.*

**RESULTS**

**EGFR**

**+Mutational Analysis**

\_\_\_ No EGFR mutation detected

\_\_\_ Mutation(s) identified

*Select all that apply*

\_\_\_ EGFR:p.G719X

\_\_\_ EGFR Exon 19 deletion (specify, if known): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ EGFR Exon 20 insertion (specify, if known): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ EGFR:p.S768I

\_\_\_ EGFR:p.T790M

\_\_\_ EGFR:p.L858R

\_\_\_ EGFR:p.L861Q

\_\_\_ Other (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+EGFR L858R by Immunohistochemistry (clone 43B2)**

\_\_\_ Negative

\_\_\_ Positive

\_\_\_ Equivocal (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+EGFR Exon 19 Deletion (E746\_A750del) (clone 6B6)**

\_\_\_ Negative

\_\_\_ Positive

\_\_\_ Equivocal (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ An EGFR mutation is present that is associated with response to EGFR tyrosine kinase inhibitors

\_\_\_ An EGFR mutation is present that is associated with resistance to EGFR tyrosine kinase inhibitors

\_\_\_ Two EGFR mutations are present, one of which is associated with resistance to EGFR tyrosine

kinase inhibitors

\_\_\_ EGFR L858R immunohistochemical staining is positive, which is associated with response to

EGFR tyrosine kinase inhibitors

\_\_\_ EGFR E746\_A750del immunohistochemical staining is positive, which is associated with response

to EGFR tyrosine kinase inhibitors

**ALK**

**+Rearrangement by Molecular Methods**

\_\_\_ No ALK rearrangement detected

\_\_\_ Rearrangement identified

\_\_\_ EML4::ALK (specify variant type, if known): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ KIF5B::ALK

\_\_\_ KLC1::ALK

\_\_\_ Other ALK rearrangement (specify, if known): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+ALK Immunohistochemistry**

\_\_\_ Negative

\_\_\_ Positive

\_\_\_ Equivocal (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ An ALK fusion is identified that is associated with response to ALK tyrosine kinase inhibitors

\_\_\_ ALK immunohistochemical staining is positive which is associated with response to ALK tyrosine

kinase inhibitors

**ROS1**

**+Rearrangement by Molecular Methods**

\_\_\_ No ROS1 rearrangement detected

\_\_\_ ROS1 rearrangement identified

**+Specify Fusion Partner: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+ROS1 by Immunohistochemistry**

\_\_\_ Negative

\_\_\_ Positive

\_\_\_ Equivocal (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ A ROS1 fusion is present, which is associated with response to ROS tyrosine kinase inhibitors

\_\_\_ ROS1 immunohistochemical staining is positive, which is associated with response to ROS1

tyrosine kinase inhibitors

**RET**

**+Rearrangement by Molecular Methods**

\_\_\_ No RET rearrangement detected

\_\_\_ RET rearrangement identified

**+Specify Fusion Partner: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation**

\_\_\_ A RET fusion is present which is associated with response to RET tyrosine kinase inhibitors

\_\_\_ No RET fusions are detected

**KRAS**

**+Mutational Analysis**

\_\_\_ No KRAS mutation detected

\_\_\_ Mutation(s) identified

*Select all that apply*

\_\_\_ KRAS:p.G12C

\_\_\_ KRAS:p.G12D

\_\_\_ KRAS:p.G12V

\_\_\_ KRAS:p.G12S

\_\_\_ KRAS:p.G12A

\_\_\_ KRAS:p.G12R

\_\_\_ KRAS:p.G13D

\_\_\_ KRAS:p.G13C

\_\_\_ KRAS:p.Q61L

\_\_\_ Other (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ A KRAS mutation is identified which is associated with resistance to tyrosine kinase inhibitor

therapy

\_\_\_ A KRAS mutation is identified which is associated with response to specific inhibitors

**BRAF**

**+Mutational Analysis**

\_\_\_ No BRAF mutations detected

\_\_\_ Mutation(s) identified

*Select all that apply*

\_\_\_ BRAF:p.V600E

\_\_\_ BRAF:p.V600K

\_\_\_ BRAF:p.V600R

\_\_\_ BRAF:p.V600D

\_\_\_ Other (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation**

\_\_\_ A BRAF mutation is present which is associated with response to BRAF inhibitors

\_\_\_ No BRAF mutations are detected

**ERBB2**

**+Mutational Analysis**

\_\_\_ No ERBB2 mutations detected

\_\_\_ Mutation(s) identified

*Select all that apply*

\_\_\_ ERBB2:p.S310F

\_\_\_ ERBB2:p.L755S

\_\_\_ ERBB2:p.Y772\_A775dup insertion

\_\_\_ Other (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Copy Number Analysis**

\_\_\_ No ERBB2 (HER2) amplification detected

\_\_\_ ERBB2 (HER2) amplification identified

*Select all that apply*

\_\_\_ Specify Copy Number: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Specify Ratio to Centromere 17: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+HER2 Immunohistochemistry**

\_\_\_ Negative (0-1)

\_\_\_ Equivocal (2+)

\_\_\_ Positive (3+)

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ An ERBB2 (HER2) mutation is present which is associated with response to anti-HER2 therapy

\_\_\_ ERBB2 (HER2) amplification is present which is associated with response to anti-HER2 therapy

\_\_\_ HER2 is positive by immunohistochemistry (3+) which is associated with response to anti-HER2

therapy

**MET**

**+Mutational Analysis**

\_\_\_ No MET mutation detected

\_\_\_ Mutation(s) identified

*Select all that apply*

\_\_\_ MET:p.D963\_splice mutation

\_\_\_ MET:p.D1010N

\_\_\_ MET:p.D1010\_splice mutation

\_\_\_ MET exon 14 deletion

\_\_\_ Other (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Copy Number Analysis**

\_\_\_ No MET amplification detected

\_\_\_ MET amplification identified

*Select all that apply*

\_\_\_ Specify Copy Number: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Specify Ratio to Centromere 7: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ A MET alteration is present which is associated with response to MET tyrosine kinase inhibitors

\_\_\_ MET amplification is present which is associated with response to MET tyrosine kinase inhibitors

**NTRK**

**+NTRK1 by Molecular Methods**

\_\_\_ No NTRK1 rearrangement detected

\_\_\_ NTRK1 rearrangement identified

**+Specify Fusion Partner: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+NTRK2 by Molecular Methods**

\_\_\_ No NTRK2 rearrangement detected

\_\_\_ NTRK2 rearrangement identified

**+Specify Fusion Partner: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+NTRK3 by Molecular Methods**

\_\_\_ No NTRK3 rearrangement detected

\_\_\_ NTRK3 rearrangement identified

**+Specify Fusion Partner: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+NTRK by immunohistochemistry**

\_\_\_ Negative

\_\_\_ Positive

\_\_\_ Equivocal

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ An NTRK fusion is present which is associated with response to NTRK inhibitors

\_\_\_ NTRK immunohistochemical staining is present. Fusion testing by NGS or FISH will be performed

\_\_\_ NTRK immunohistochemical staining is present but fusion testing is negative. This is not

associated with response to NTRK inhibitors

\_\_\_ Other (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**NRG1**

**+Rearrangement by Molecular Methods**

\_\_\_ No NRG1 rearrangement detected

\_\_\_ NRG1 rearrangement identified

**+Specify Fusion Partner: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation**

\_\_\_ An NRG1 fusion is present which is associated with response to NRG1 inhibitors

\_\_\_ No NRG1 fusions are detected

**Mismatch Repair**

**+Immunohistochemistry (IHC) Testing for Mismatch Repair (MMR) Proteins (select all that**

**apply)**

\_\_\_ MLH1

**MLH1 Result**

\_\_\_ Intact nuclear expression

\_\_\_ Loss of nuclear expression

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ MSH2

**MSH2 Result**

\_\_\_ Intact nuclear expression

\_\_\_ Loss of nuclear expression

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ MSH6

**MSH6 Result**

\_\_\_ Intact nuclear expression

\_\_\_ Loss of nuclear expression

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ PMS2

**PMS2 Result**

\_\_\_ Intact nuclear expression

\_\_\_ Loss of nuclear expression

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Background non-neoplastic tissue / internal control with intact nuclear expression

**+Microsatellite Instability (MSI)**

\_\_\_ MSI-Stable (MSS)

\_\_\_ MSI-Low (MSI-L)

\_\_\_ MSI-High (MSI-H)

\_\_\_ Cannot be determined: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation (select all that apply)**

\_\_\_ The case is MSI-H which is associated with response to immune checkpoint inhibitors

\_\_\_ The case is mismatch repair deficient which is associated with response to immune checkpoint

inhibitors

**Tumor Mutational Burden**

**+Specify Tumor Mutational Burden: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**+Tumor Mutational Burden Level**

\_\_\_ Low

\_\_\_ High

\_\_\_ Equivocal

\_\_\_ Cannot be determined (explain): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**+Interpretation**

\_\_\_ The case is TMB-high which is associated with response to immune checkpoint inhibitors

\_\_\_ The case is TMB-low which is not associated with response to immune checkpoint inhibitors

**PD-L1 IHC**

**+PD-L1 22c3 IHC Interpretation**

\_\_\_ Positive

\_\_\_ Negative

\_\_\_ Cannot be determined

**+Specify Percentage of Tumor Cells with Staining (TPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**+Specify Combined Number of Tumor and Immune Cells with Staining per 100 Tumor Cells**

**(CPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ cells**

**+Specify Percentage of Tumor-associated Immune Cells with Staining: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**%**

**+Specify Percentage of Tumor Area Occupied by Tumor-associated Immune Cells:**

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**PD-L1 22c3 IHC Methods**

**+Controls (select all that apply)**

\_\_\_ Internal control cells present; expected immunoreactivity

\_\_\_ Internal control cells present; no immunoreactivity of either tumor cells or internal controls

\_\_\_ External controls available; expected immunoreactivity

\_\_\_ External controls available; no immunoreactivity in expected cells

**+Assay Information**

\_\_\_ Food and Drug Administration (FDA) cleared test / vendor (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Laboratory-developed test

**+Specify Quantitative Imaging Analytics Performed: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**+PD-L1 28-8 IHC Interpretation**

\_\_\_ Positive

\_\_\_ Negative

\_\_\_ Cannot be determined

**+Specify Percentage of Tumor Cells with Staining (TPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**+Specify Combined Number of Tumor and Immune Cells with Staining per 100 Tumor Cells**

**(CPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ cells**

**+Specify Percentage of Tumor-associated Immune Cells with Staining: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**%**

**+Specify Percentage of Tumor Area Occupied by Tumor-associated Immune Cells:**

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**PD-L1 28-8 IHC Methods**

**+Controls (select all that apply)**

\_\_\_ Internal control cells present; expected immunoreactivity

\_\_\_ Internal control cells present; no immunoreactivity of either tumor cells or internal controls

\_\_\_ External controls available; expected immunoreactivity

\_\_\_ External controls available; no immunoreactivity in expected cells

**+Assay Information**

\_\_\_ Food and Drug Administration (FDA) cleared test / vendor (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Laboratory-developed test

**+Specify Quantitative Imaging Analytics Performed: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**+PD-L1 SP142 IHC Interpretation**

\_\_\_ Positive

\_\_\_ Negative

\_\_\_ Cannot be determined

**+Specify Percentage of Tumor Cells with Staining (TPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**+Specify Combined Number of Tumor and Immune Cells with Staining per 100 Tumor Cells**

**(CPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ cells**

**+Specify Percentage of Tumor-associated Immune Cells with Staining: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**%**

**+Specify Percentage of Tumor Area Occupied by Tumor-associated Immune Cells:**

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**PD-L1 SP142 IHC Methods**

**+Controls (select all that apply)**

\_\_\_ Internal control cells present; expected immunoreactivity

\_\_\_ Internal control cells present; no immunoreactivity of either tumor cells or internal controls

\_\_\_ External controls available; expected immunoreactivity

\_\_\_ External controls available; no immunoreactivity in expected cells

**+Assay Information**

\_\_\_ Food and Drug Administration (FDA) cleared test / vendor (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Laboratory-developed test

**+Specify Quantitative Imaging Analytics Performed: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**+PD-L1 SP263 IHC Interpretation**

\_\_\_ Positive

\_\_\_ Negative

\_\_\_ Cannot be determined

**+Specify Percentage of Tumor Cells with Staining (TPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**+Specify Combined Number of Tumor and Immune Cells with Staining per 100 Tumor Cells**

**(CPS): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ cells**

**+Specify Percentage of Tumor-associated Immune Cells with Staining: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**%**

**+Specify Percentage of Tumor Area Occupied by Tumor-associated Immune Cells:**

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ %**

**PD-L1 SP263 IHC Methods**

**+Controls (select all that apply)**

\_\_\_ Internal control cells present; expected immunoreactivity

\_\_\_ Internal control cells present; no immunoreactivity of either tumor cells or internal controls

\_\_\_ External controls available; expected immunoreactivity

\_\_\_ External controls available; no immunoreactivity in expected cells

**+Assay Information**

\_\_\_ Food and Drug Administration (FDA) cleared test / vendor (specify): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_ Laboratory-developed test

**+Specify Quantitative Imaging Analytics Performed: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Variants with Potential Pathologic Relevance**

**+Specify Marker and Results (repeat up to 20 times): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Other Variants of Unknown Significance (VUS)**

**+Specify Marker and Results (repeat up to 20 times): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**COMMENTS**

**Comment(s): \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**