

REPORT

**Joint Consensus of the Japanese Society of Medical Oncology, Japan
Society of Clinical Oncology, and Japanese Cancer Association**

Clinical practice guidance for next-generation sequencing in cancer diagnosis and treatment (Edition 1.0)

Kuniko Sunami¹ | Hideaki Takahashi² | Katsuya Tsuchihara³ | Masayuki Takeda⁴ |
Tatsuya Suzuki⁵ | Yoichi Naito⁶ | Kazuko Sakai⁷ | Hirotohi Dosaka-Akita⁸ |
Chikashi Ishioka⁹ | Yasuhiro Koder¹⁰ | Manabu Muto¹¹ | Toshifumi Wakai¹² |
Kentarō Yamazaki¹³ | Wataru Yasui¹⁴ | Hideaki Bando¹⁵ | Yumi Fujimoto⁶ |
Shota Fukuoka¹⁵ | Kenichi Harano⁶ | Akihito Kawazoe¹⁵ | Gen Kimura² |
Shigehiro Koganemaru¹⁶ | Takahiro Kogawa⁶ | Daisuke Kotani¹⁵ | Yasutoshi Kuboki¹⁶ |
Hiroshi Matsumoto¹⁵ | Shingo Matsumoto¹⁷ | Saori Mishima¹⁵ | Yoshiaki Nakamura¹⁵ |
Kentarō Sawada¹⁵ | Sumito Shingaki¹⁶ | Kohei Shitara¹⁵ | Kumiko Umemoto² |
Shigeki Umemura¹⁷ | Kayo Yasuda¹⁵ | Takayuki Yoshino¹⁵ | Noboru Yamamoto¹⁸ |
Kazuto Nishio⁷ | Japanese Society of Medical Oncology | Japan Society of Clinical
Oncology | Japanese Cancer Association

¹Department of Pathology and Clinical Laboratories, National Cancer Center Hospital, Tokyo, Japan

²Department of Hepatobiliary and Pancreatic Oncology, National Cancer Center Hospital East, Kashiwa, Japan

³Division of Translational Informatics, Exploratory Oncology Research and Clinical Trial Center, National Cancer Center, Kashiwa, Japan

⁴Department of Medical Oncology, Kindai University, Faculty of Medicine, Osaka, Japan

⁵Department of Hematology, National Cancer Center Hospital, Tokyo, Japan

⁶Department of Breast and Medical Oncology, National Cancer Center Hospital East, Kashiwa, Japan

⁷Department of Genome Biology, Kindai University, Faculty of Medicine, Osaka, Japan

⁸Department of Medical Oncology, Hokkaido University Graduate School of Medicine, Hokkaido, Japan

⁹Department of Medical Oncology, Tohoku University Hospital, Miyagi, Japan

¹⁰Department of Gastroenterological Surgery, Nagoya University Graduate School of Medicine, Aichi, Japan

¹¹Department of Therapeutic Oncology, Graduate School of Medicine, Kyoto University, Kyoto, Japan

¹²Division of Digestive and General Surgery, Niigata University Graduate School of Medical and Dental Sciences, Niigata, Japan

¹³Division of Gastrointestinal Oncology, Shizuoka Cancer Center, Shizuoka, Japan

¹⁴Department of Molecular Pathology, Hiroshima University, Hiroshima, Japan

¹⁵Department of Gastrointestinal Oncology, National Cancer Center Hospital East, Kashiwa, Japan

¹⁶Department of Experimental Therapeutics, National Cancer Center Hospital East, Kashiwa, Japan

¹⁷Department of Thoracic Oncology, National Cancer Center Hospital East, Kashiwa, Japan

¹⁸Department of Experimental Therapeutics, National Cancer Center Hospital, Tokyo, Japan

This report is an English translation of "Clinical Practice Guidance for Next Generation Sequencing in Cancer Diagnosis and Treatment." The original version written in Japanese is available at Websites of the Japanese Society of Medical Oncology, Japan Society of Clinical Oncology, and the Japanese Cancer Association (http://www.jSCO.or.jp/jpn/user_data/upload/File/55/sequence_ver1_180109.pdf).

This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.

© 2018 The Authors. *Cancer Science* published by John Wiley & Sons Australia, Ltd on behalf of Japanese Cancer Association.

Correspondence

Kazuto Nishio, Department of Genome Biology, Kindai University Faculty of Medicine, 377-2 Ohnohigashi, Osaka-sayama, Osaka 589-8511, Japan.
Email: knishio@med.kindai.ac.jp

Funding information

Health Labour Sciences Special Research Grant, Grant/Award Number: H30-17; Japanese Society of Medical Oncology; Japan Society of Clinical Oncology; Japanese Cancer Association

In Japan, the social (medical) health-care system is on the way to being developed to advance personalized medicine through the implementation of cancer genomic medicine, known as “cancer clinical sequencing,” which uses a next-generation sequencer. However, no Japanese guidance for cancer genomic testing exists. Gene panel testing can be carried out to help determine patient treatment, confirm diagnosis, and evaluate prognostic predictions of patients with mainly solid cancers for whom no standard treatment is available. This guidance describes how to utilize gene panel testing according to the type of cancer: childhood cancer, rare cancer, carcinoma of unknown primary, and other cancers. The level of evidence classification for unified use in Japan is also detailed. This guidance establishes the basic principles of the quality control of specimens, requirements of medical institutions, informed consent, handling of data during the postanalysis stage, and treatment options based on the evidence level. In Japan, gene panel testing for cancer treatment and diagnosis is recommended to comply with this guidance. This is a collaborative work of the Japanese Society of Medical Oncology, Japan Society of Clinical Oncology, and the Japanese Cancer Association.

KEYWORDS

evidence level, gene panel testing, guidance, next-generation sequencing, solid cancer

1 | INTRODUCTION

Progress in the field of molecular biology has facilitated the identification of multiple gene abnormalities (hereinafter referred to as “genomic mutations”) that are associated with the malignant transformation of cancer cells. Such mutations are expected to serve as tumor biomarkers that could be utilized to predict therapeutic drug efficacy, facilitate the classification and definitive diagnosis of cancer, and disease prognosis. An increase in the number of cancer-associated genomic mutations has made individual testing of target genes problematic because of a limit of sample availability and unacceptably long turnaround times of test results needed prior to treatment initiation. This guidance covers gene panel testing and the utilization of genomic mutation analysis using next-generation sequencing or comparable techniques capable of simultaneous detection of multiple genomic mutations to clarify cancer-associated genomic mutation(s) present in individual patients and facilitate the selection of the best treatment option based on an individual's profile. A typical test panel covers genes known to be useful in predicting drug response and prognosis, and definitive diagnosis. These panels can simultaneously screen a large number of transcripts and provide a wide range of data that reveal genomic alterations that include gene mutations, deletions, insertions, gene fusions, and copy number abnormalities. This guidance also describes the current clinical status of gene panel testing for patient treatment selection, definitive diagnosis, and prognostic prediction with a focus on solid

cancers for which effective treatments are not yet available. This guidance is provided on the premise that, when an approved companion diagnostic or similar gene-related test is available, as in cases of non-small-cell lung cancer and colon cancer, the established test should take priority. In instances when a portion of genes contained in the test gene panel have already been approved and are in use as a companion diagnostic, the guidelines issued by the corresponding medical governing body should be followed to determine standard therapy for the gene(s) covered by the companion diagnostic. It is also important to keep in mind that the scope covered by gene panel testing is subject to change as a result of evolving diagnostic and treatment techniques. This is a collaboration work with the Japanese Society of Medical Oncology, Japan Society of Clinical Oncology, and the Japanese Cancer Association.

2 | GENERAL OVERVIEW OF GENE PANEL TESTING

Recommendations for gene panel testing covered in this guidance focuses on mutations arising in solid cancer cells and tissues. Accordingly, germline genomic mutations are not covered in principle. Hematopoietic tumors are not covered either, due to large differences from solid cancers in terms of testing methods, target genes, applications, and other aspects. This guidance mentions hereditary tumors and hematopoietic tumors for information

purposes only and refers a guidance that is to be established separately.

Japan has offered its citizens universal health insurance for more than 50 years, and the system for the whole nation covers 70%-90% of the costs for cancer treatment. Novel cancer therapies, such as immune checkpoint inhibitors and targeted therapies matching with genomic molecular alterations, have emerged as promising treatment options in a variety of cancers. Under the national public health insurance scheme, the government controls the prices of all procedures and medications, which impels the use of generic drugs and the development of next-generation sequencing-based diagnostics instead of “one companion diagnostic – one drug”; however, due to the expensive cost of next-generation sequencing, some limitations on usage are required.

Gene panel testing is primarily intended to predict the therapeutic efficacy of novel anticancer drug treatments in eligible patients who have no available options using standard therapy. In principle, testing is limited to once for each patient, but this does not apply to those patients who are able to provide new specimen(s), such as biopsy material, after failure to an anticancer drug. Also, when the gene panel contains genes used for the diagnosis and prognostic prediction, to help determine the appropriate treatment strategy, the frequency of testing is the same as that used for drug efficacy prediction.

Timing of testing is to be decided appropriately according to the type of cancer (see below). Gene panel testing is undertaken, in principle, using a DNA sequencer, sequencing sample preparation reagents, template DNA preparation reagents, and an analysis program that have been approved by the Pharmaceutical and Medical Devices Law.

3 | APPLICATION OF GENE PANEL TESTING ACCORDING TO CANCER TYPE

To consider the clinical application of gene panel testing, this guidance first reviews the general use of gene panel testing in solid cancers with regard to the timing of treatment. The subsequent section provides cancer types that should be assessed according to cancer characteristics, particularly when using gene panel testing.

3.1 | View on common test population and timing

3.1.1 | Before the start of drug therapy

Testing is carried out primarily in patients with solid cancers who are eligible for drug therapy with no standard therapy available. In principle, the primary purpose for undertaking gene panel testing prior to treatment is to obtain relevant genomic mutation data that would aid in selecting an appropriate treatment strategy. The gene panel could also contain genes useful for diagnosis and prognostic prediction. For instance, a treatment associated with a better prognosis to a known genomic mutation will be assigned to a patient with a

matching profile. Also at this point, when a portion of genes loaded on the gene panel has already been approved and is used as a companion diagnostic, the guidelines issued by the relevant medical governing body should be followed to determine standard therapy.

3.1.2 | Explore new anticancer treatments after failure of standard therapy

Approved standard therapy, as indicated by the current guidelines of each medical governing body, should be first implemented along with any companion diagnostic, as necessary. Gene panel testing is undertaken in patients who have relapsed or progressed after standard therapy, in order to identify a candidate therapeutic option. Whenever possible, the specimen used for gene panel testing should be obtained after failure to the standard therapy and may be collected by biopsy or other means. If postfailure tissue is unattainable, previously collected preserved specimens may be substituted.

3.2 | Cancer types that should be assessed according to cancer characteristics, particularly when using gene panel testing

3.2.1 | Pediatric cancers/rare cancers

Pediatric cancers and rare cancers are found in fewer patients, which makes diagnosis difficult, and standard therapy has not been established. Therefore, gene panel testing is undertaken to support diagnosis based on the findings of genomic mutations at initial diagnosis, predict prognosis, and determine treatment strategy, or to select a therapeutic drug that is likely to be effective before starting pharmacotherapy.

3.2.2 | Carcinoma of unknown primary

Carcinoma of unknown primary often requires time for diagnosis and determination of therapeutic strategy. Therefore, gene panel testing is undertaken to support diagnosis based on the findings of genomic mutations and to select a therapeutic drug that is likely to be effective.

3.2.3 | Other cancers

For handling of hematopoietic malignancies and hereditary tumors, refer to guidelines and guidance stipulated separately by the relevant medical governing bodies.

4 | QUALITY CONTROL OF SPECIMENS USED FOR GENE PANEL TESTING

Gene panel testing uses specimens that are under appropriate quality control, with reference to The Japanese Society of Pathology

Guidelines on the Handling of Pathological Tissue Samples for Genomic Medicine¹ or other relevant regulations.

5 | REQUIREMENTS FOR MEDICAL INSTITUTIONS/LABORATORIES CARRYING OUT GENE PANEL TESTING

Medical institutions/laboratories carrying out gene panel testing must meet several requirements and must be capable of: (i) ensuring the quality of the testing process; (ii) objective and valid interpretation of test results; and (iii) providing treatment based on test results and in the framework of appropriate systems, such as clinical studies, including clinical trials, or off-label use of unapproved drugs available concomitantly with health insurance services such as advanced medicine (*senshin-iryō* in Japanese). For specific requirements for medical institutions, refer to requirements for the designation of Cancer Genome Medicine Core Hospitals to be discussed at the Ministry of Health, Labour and Welfare in response to a report by the meeting of Cancer Genomic Medicine Promotion Consortium.²

6 | INFORMED CONSENT FOR GENE PANEL TESTING

Use of gene panel testing that covers a wide variety of genes will increase the chance of detecting “incidental and/or secondary findings.” Furthermore, one should be aware that gene panel testing might not always lead to presentation of therapeutic options and that therapeutic options will be restricted when based on genomic mutations with a low evidence level. Thus, before undertaking gene panel testing, each patient and/or legal representative should be provided with explanations on the usefulness of testing, limitations of testing, and restrictions on the use of test results for therapeutic strategy, as well as the possible discovery of incidental and/or secondary findings, such as germline gene mutations, in cooperation with a genetics counselor, as appropriate, followed by the consent of the patient or his/her legal representative.

In making a decision on the therapeutic strategy based on the results of gene panel testing, one should give consideration to the assurance of “right to know and right not to know” in the process of returning results, and disclosure of the results to the patient's family under disapproval of the patient. Please refer to “Study on the Establishment of Genomic Medicine Implementation System and Development of Human Resources at Medical Genome Centers, etc.” (Principal Investigator: Hitoshi Nakagama from National Cancer Center Japan) Sub-Theme 2 Separate Report “Review and Recommendations on the Actions for Accidental and/or Secondary Findings” (Sub-Investigator: Kazuto Katoh from Osaka University, Graduate School of Medicine) within the 2016 Annual Program for Promoting Practical Applications of Genomic Medicine, Japan Agency for Medical Research and Development.³

7 | HANDLING OF GENE PANEL TESTING AT THE POSTANALYSIS STAGE

The Act on Partial Revision of the Act on the Protection of Personal Information and the Act on the Use of Numbers to Identify a Specific Individual in Administration Procedure (revision in September 2016; complete enforcement on May 30, 2017) clearly defines what personal information is. According to Guidelines on the Act on the Protection of Personal Information (General Notices) (partial revision in March 2017), genomic data that make it possible to identify an individual based on genotype information, such as whole-genome sequencing data, whole-exome sequencing data, whole-genome single nucleotide polymorphism data, sequencing data comprised of 40 or more mutually independent single nucleotide polymorphisms, and short tandem repeats with 4 bases repeated at 9 or more loci, are regarded as an “individual identification code.” Medically annotated genomic data that provide “genomic information” are regarded as “special care-required personal information.” Attention should be given to handling of these data.

Gene panel testing reports are prepared by an expert panel capable of providing medical interpretation for the gene panel testing results. Contents and details to be summarized in the report are listed below.

7.1 | Report contents

A gene panel testing report should contain the following information whenever possible: specimen and data quality (assurance), biological significance and evidence levels of genomic mutations detected, presence or absence of secondary findings and their related evidence levels, recommendation of subsequent actions to take and the expected risks, approval status of therapeutic drugs, and presence or absence of clinical trial information of related therapeutic drugs.

7.2 | Evidence level-based classification

The definition of evidence level for individual genomic mutations acquired by gene panel testing should not differ greatly from the definitions standardized in the USA and EU.⁴ The definitions adopted in this guidance (Table S1) have been developed to be suitable for the medical system in Japan, while paying attention to maintaining consistency with those published in the USA and EU. Table S1 also provides actionable examples for evidence levels that are relevant to specific levels of therapeutic efficacy. Actionable examples based on the evidence level of genes that are related to “diagnosis” or “prognosis” may be further amended at a later date to reflect new or accumulated findings. Information acquired by gene panel testing is described in a standardized manner based on the evidence level defined in this guidance, whenever possible, using the evidence levels listed in Table S2 as well as cancer genome knowledge databases (Table S3). This guidance covers experimental gene panels comprised of cancer-related genes that are under development or in

preparation for development in Japan, when requested by the deadline, and are assigned individual evidence levels based on the evidence classification adopted in this guidance. Following external review, the genes and their evidence levels are summarized in Table S2, with the exception of genes for which the evidence level is difficult to assign. Also added are hereditary tumor-related genes listed in the recommendation by the American College of Medical Genetics and Genomics⁵ and the guidelines of the National Comprehensive Cancer Network.⁶ Therefore, Table S2 will be continuously updated.

7.3 | Description of therapeutic options

Efforts should be made to provide therapeutic options based on genomic mutation-specific cancer type indications and evidence levels to date as well as other information, such as cancer genome knowledge databases operated in and outside Japan. In principle, when the evidence level is 2 or greater, the patient should be treated according to the patient's condition and other circumstances based on sufficient explanation and consent. Therefore, the patient should be provided with documented therapeutic options in document along with information based on appropriate systems, such as clinical studies, including clinical trials, or off-label use of unapproved drugs available concomitantly with health insurance services, such as advanced medicine (*senshin-iryō* in Japanese).

ACKNOWLEDGMENTS

This work was supported by the Japanese Society of Medical Oncology (JSMO), the Japan Society of Clinical Oncology (JSCO), and the Japanese Cancer Association (JCA). The JSMO and JSCO, and JCA Guideline Committee members reviewed the guidance. This project was supported by Health Labour Sciences Special Research Grant (H30-17).

CONFLICT OF INTEREST

HT received research funding from Bayer Yakuhin, Ltd., Bristol-Myers Squibb Company. KT received honoraria for lectures from Takeda Pharmaceutical Co., Ltd. YN received honoraria for lectures from Novartis Pharma K.K. and Chugai Pharmaceutical Co., Ltd., and received research funding from AstraZeneca K.K.; Eli Lilly Japan K.K.; Nippon Kayaku Co., Ltd.; and Merck Serono Co., Ltd.; HA received research funding from AstraZeneca K.K.; Eisai Co., Ltd.; Ono Pharmaceutical Co., Ltd.; Taiho Pharmaceutical Co., Ltd.; Eli Lilly Japan K.K. CI received research funding from The Tokyo cooperative Oncology Group; Ono Pharmaceutical Co., Ltd.; Taiho Pharmaceutical Co., Ltd.; Daiichi Sankyo Co., Ltd.; Novartis Pharma K.K.; Bristol-Myers Squibb Company, Eisai Co., Ltd.; Takeda Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Merck Serono Co., Ltd.; Mochida Pharmaceutical Co., Ltd.; Yakult Honsha Co., Ltd.; YK received honoraria for lectures from Taiho Pharmaceutical Co., Ltd.; and Chugai Pharmaceutical Co., Ltd., and received

research funding from Novartis Pharma K.K., Eli Lilly Japan K.K., Ono Pharmaceutical Co., Ltd.; Taiho Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Merck Serono Co., Ltd.; Eisai Co., Ltd.; Otsuka Pharmaceutical Co., Ltd.; KCI KK.; CSL Behring K.K.; Shionogi & Co., Ltd.; Johnson & Johnson K.K.; Daiichi Sankyo Co., Ltd.; Mitsubishi Tanabe Pharma Corporation, Toyama Chemical Co., Ltd.; Pfizer Inc., Bristol-Myers Squibb Company; Yakult Honsha Co., Ltd. MM received honoraria for lectures from Meiji Seika Pharma Co., Ltd., and received research funding from Olympus Corporation; Taiho Pharmaceutical Co., Ltd.; and Mitsui Knowledge Industry Co. Ltd.; Ono Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Yakult Honsha Co., Ltd. TW received remuneration from Denka Company Limited and received research funding from Denka Company Limited, Eisai Co., Ltd.; Taisho Toyama Pharmaceutical Co., Ltd.; Taiho Pharmaceutical Co., Ltd.; Sumitomo Dainippon Pharma Co., Ltd.; Takeda Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Eli Lilly Japan K.K.; Yakult Honsha Co., Ltd. KY received honoraria for lectures from Takeda Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; and Bayer Yakuhin, Ltd., and received research funding from Otsuka Pharmaceutical Co., Ltd.; Nippon Boehringer Ingelheim Co., Ltd. WY received research funding from Hiroshima City Medical Association Clinical laboratory. HB received research funding from Sysmex Corporation and AstraZeneca K.K. TK received research funding from Daiichi Sankyo Co., Ltd. YK received research funding from Takeda Pharmaceutical Co., Ltd. SM received research funding from Chugai Pharmaceutical Co., Ltd., Pfizer Inc., Novartis Pharma K.K., Merck Serono Co., Ltd. KS received research funding from Daiichi Sankyo Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Taiho Pharmaceutical Co., Ltd.; Sumitomo Dainippon Pharma Co., Ltd.; MSD K.K.; Eli Lilly Japan K.K.; SU received research funding from MSD K.K. TY received honoraria for lectures from Takeda Pharmaceutical Co., Ltd.; Taiho Pharmaceutical Co., Ltd.; Bayer Yakuhin, Ltd.; Chugai Pharmaceutical Co., Ltd.; and Eli Lilly Japan K.K. and received research funding from Non-Profit Organization Japan Clinical Research Support Unit., Sumitomo Dainippon Pharma Co., Ltd.; PPD-SNBL K.K.; GlaxoSmithKline K.K.; Nippon Boehringer Ingelheim Co., Ltd.; MSD K.K. NY received honoraria for lectures from AstraZeneca K.K.; Eli Lilly Japan K.K.; Ono Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Pfizer Inc., Bristol-Myers Squibb Company; and USACO Corporation and received research funding from Astellas Pharma Inc., Eisai Co., Ltd.; Ono Pharmaceutical Co., Ltd.; Kyowa Hakko Kirin Co., Ltd.; IQVIA Services Japan K.K.; Taiho Pharmaceutical Co., Ltd.; Daiichi Sankyo Co., Ltd.; Takeda Pharmaceutical Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Novartis Pharma K.K.; Pfizer Inc.; Bayer Yakuhin, Ltd.; Bristol-Myers Squibb Company; Nippon Boehringer Ingelheim Co., Ltd. KN received honoraria for lectures from Sumitomo Bakelite Co., Ltd.; Daiichi Sankyo Co., Ltd.; Chugai Pharmaceutical Co., Ltd.; Nippon Boehringer Ingelheim Co., Ltd.; and Eisai Co., Ltd., and received research funding from Korea Otsuka Pharmaceutical Co., Ltd.; and Nippon Boehringer Ingelheim Co., Ltd. All remaining authors have no conflict of interest to declare.

REFERENCES

1. Japanese Society of Pathology. Guidelines on the handling of pathological tissue samples for medical practice. http://pathology.or.jp/genome_med/. Accessed January 10, 2017.
2. Cancer Genomic Medicine Promoting Consortium Meeting Report. <http://www.mhlw.go.jp/stf/shingi2/0000169238.html> Accessed January 10, 2017.
3. "Study on the Establishment of Genomic Medicine Implementation System and Development of Human Resources at Medical Genome Centers, etc." (Principal Investigator: Hitoshi Nakagama from National Cancer Center Japan) Sub-Theme 2 Separate Report "Review and Recommendations on the Actions for Accidental and/or Secondary Findings". <http://http://www.biobank.amed.go.jp/elsi/finding/index.html> Accessed January 10, 2017.
4. Li MM, Datto M, Duncavage EJ, et al. Standards and guidelines for the interpretation and reporting of sequence variants in cancer: a joint consensus recommendation of the association for molecular pathology, American society of clinical oncology, and college of American pathologists. *J Mol Diagn*. 2017;19:4-23.
5. Kalia SS, Adelman K, Bale SJ, et al. Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2016 update (ACMG SF v2.0): a policy statement of the American College of Medical Genetics and Genomics. *Genet Med*. 2017;19:249-255.
6. NCCN Guidelines. https://www.nccn.org/professionals/physician_gls/default.aspx. Accessed January 10, 2017.

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

How to cite this article: Sunami K, Takahashi H, Tsuchihara K, et al. Clinical practice guidance for next-generation sequencing in cancer diagnosis and treatment (Edition 1.0). *Cancer Sci*. 2018;109:2980–2985. <https://doi.org/10.1111/cas.13730>