OCG Project Codes
Tissues and Samples

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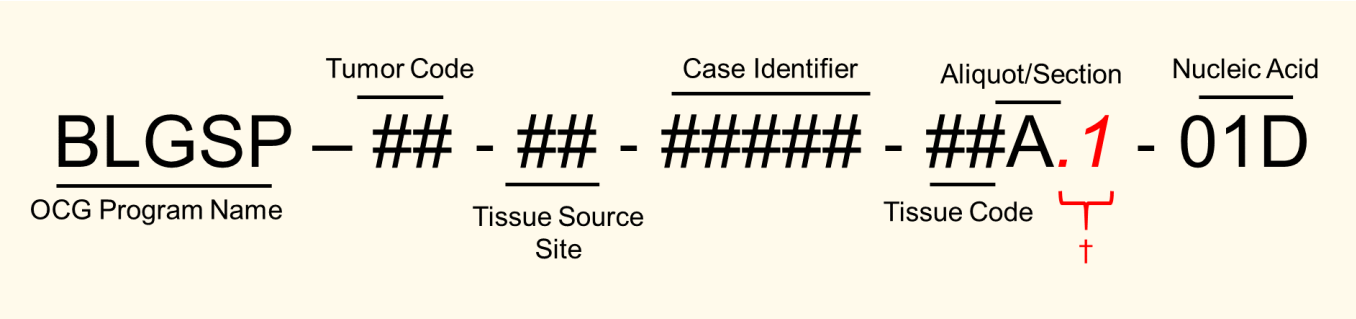
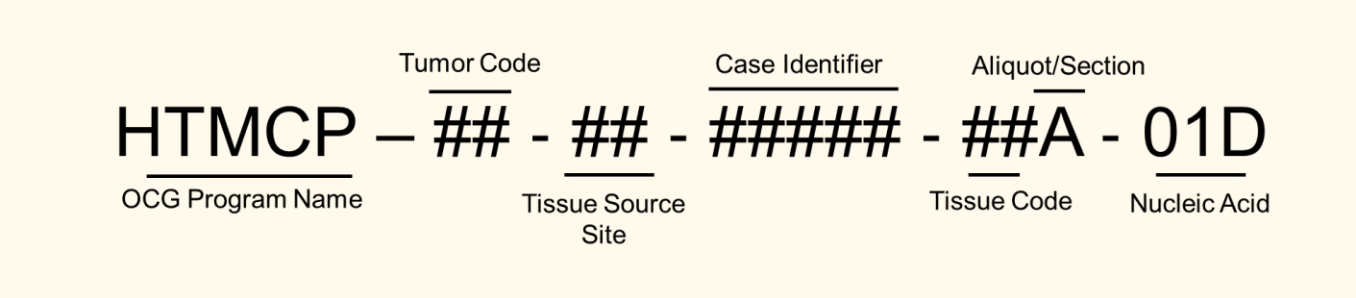
The ID of each sample will have a specific identifier that depends on the specific project. However, the codes used in each are the same throughout OCG projects.

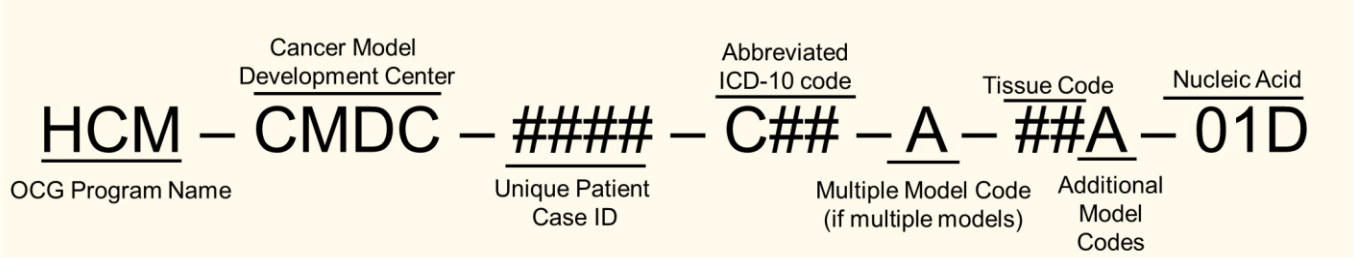
Nomenclature:

CGCI Nomenclature Structure:

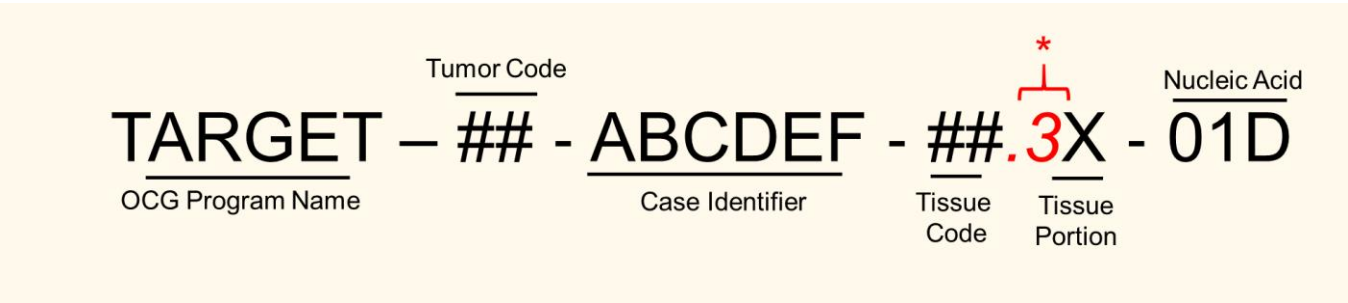




HCMI Nomenclature Structure:



TARGET Nomenclature Structure:



Tumor Code:

Tumor Code	Description
00	Non-cancerous tissue
01	Diffuse large b-cell lymphoma (DLBCL)
02	Lung cancer (all types)
03	Cervical cancer (all types)
04	Anal cancer (all types)
10	Acute lymphoblastic leukemia (ALL)
15	Acute leukemia of ambiguous lineage (ALAL)
20	Acute myeloid leukemia (AML)
21	Induction failure AML (AML-IF)
30	Neuroblastoma (NBL)
40	Osteosarcoma (OS)
41	Ewing sarcoma
50	Wilms tumor (WT)
51	Clear cell sarcoma of the kidney (CCSK)
52	Rhabdoid tumor (kidney) (RT)
60	CNS, ependymoma
61	CNS, glioblastoma (GBM)
62	CNS, rhabdoid tumor
63	CNS, low grade glioma (LGG)
64	CNS, medulloblastoma
65	CNS, other
70	NHL, anaplastic large cell lymphoma
71	NHL, Burkitt lymphoma (BL)
80	Rhabdomyosarcoma
81	Soft tissue sarcoma, non-rhabdomyosarcoma

Tissue Code:

Tissue code	Description	Code
Primary tumor	Primary solid tumor	01
Recurrent tumor	Recurrent solid tumor	02
Primary blood cancer	Primary blood derived cancer – peripheral blood	03
Recurrent blood cancer	Recurrent blood derived cancer – bone marrow	04
Additional - new primary	Additional – new primary	05
Metastatic	Metastatic	06
Additional metastatic	Additional metastatic	07
Post neo-adjuvant therapy	Tissue disease-specific post-adjuvant therapy	08
Primary blood cancer BM	Primary blood derived cancer – bone marrow	09
Blood derived normal	Blood derived normal	10
Solid tissue normal	Solid tissue normal	11
Buccal cell normal	Buccal cell normal (including saliva)	12
EBV normal	Epstein-Barr virus (EBV) immortalized normal	13
BM normal	Bone marrow normal	14
Fibroblast normal	Fibroblasts from bone marrow normal	15
Mononuclear cell normal	Mononuclear cells from bone marrow normal	16
Lymphoid normal	Lymphatic tissue normal (including centroblasts)	17
Tumor adjacent normal – post neo-adjuvant therapy	Solid tissue "normal" near tumor, post-adjuvant therapy	18
Cell line control	Cell line control (control analyte)	20
Premalignant tissue	Neoplasms of uncertain and unknown behavior	31
Recurrent blood cancer	Recurrent blood derived cancer – peripheral blood	40
Post treatment blood cancer bone marrow	Blood derived cancer- bone marrow, post-treatment	41
Post treatment blood cancer blood	Blood derived cancer- peripheral blood, post-treatment	42
Cancer cell line	Cell line from patient tumor	50
Xenograft, primary	Xenograft from patient not grown as intermediate on plastic tissue culture dish	60
Xenograft, cell-line derived	Xenograft grown in mice from established cell lines	61
Next generation cancer model	Cancer models developed with next generation methods	85
Expanded next generation cancer model	Cancer models developed with next generation methods and expanded for distribution	86
Next generation cancer model expanded under non-conforming conditions	Next generation cancer models expanded differently than how they were developed	87
Granulocytes	Granulocytes after a Ficoll separation	99

The tissue codes in the table above denote the source of tissue collected for study. A patient may undergo multiple tissue collections and/or resected tissue can be separated into smaller portions of material for research, and those smaller sections may even be preserved using different methods (i.e. some flash frozen vs some with FFPE). Cell lines and xenografts may also be grown up at different times. Therefore, a letter identifier is added to the tissue code number to track separate aliquots/tissue sections from the same patient. For example:

1. **A** – first aliquot, growth or section of tissue reviewed to meet clinical quality criteria
2. **B** – second aliquot, growth or section of tissue reviewed to meet clinical quality criteria

*Note: When characterizing multiple tissues from the same case, the sample codes must distinguish between these two types of tissue by using a separate portion designation (i.e. the tissue codes used could be "01**A**" and "01**B**", etc.)*

Nucleic Acid Codes:

- 01D = DNA, unamplified, from the first isolation of a tissue (fresh/frozen)
- 01E = DNA, unamplified, from the first isolation of a tissue embedded in FFPE
- 01W = DNA, whole genome amplified by Qiagen (one independent reaction)
- 01X = DNA, whole genome amplified by Qiagen (a second, separate independent reaction)
- 01Y = DNA, whole genome amplified by Qiagen (pool of "W" and "X" aliquots)
- 01R = RNA, from the first isolation of a tissue (fresh/frozen)
- 01S = RNA, from the first isolation of a tissue embedded in FFPE

Note: If additional isolations are needed from the same tissue aliquot, the # would change to 02D, etc.

BLGSP: Additional tissue code sample identifiers (when a single tissue yields multiple sample subtypes)

† *Pre-Extraction Manipulation of Tissue Samples (including Cell Sorting)*:
Some analyses of patient tissues require certain tissue manipulation prior to nucleic acid extraction. For example, some OCG tissue samples have undergone a specialized form of handling using flow cytometry called Fluorescence-activated Cell Sorting (FACS) to separate a heterogeneous mixture of biological cells into two or more subpopulations, one cell at a time, based upon the specific light scattering and fluorescent characteristics of each cell type. Therefore, multiple cell types may be available for certain cases. Sorted samples can originate from and/or result in tumor or normal tissues and will contain an extension of the tissue code following the letter "tissue portion" identifier (i.e. BLGSP-XX-(USI)-03A**.1**-01(D, R, etc.)). From the extension, it is not possible to determine specific modifications or cell markers used to sort a subpopulation; users must use the metadata files to ascertain specific details regarding the pre-extraction, post-pathology review handling of tissue. Tissue extension codes use sequential numbers to denote only that a given sample is unique; the numbers themselves do not provide any additional information on specifics of the sample.

Here is an example of two subpopulations from a FACS sort of the same tissue sample:

OCG Sorted Tissue Samples	**OCG Sample ID** *(multiple samples per case)*
Mixed Phenotype ALL, FACS sorted (would need metadata for details)	TARGET-15-(USI)-03A**.1**-01(D, R, etc.)
Mixed Phenotype ALL, FACS sorted (a separate sorted cohort from the same case; need metadata for details)	TARGET-15-(USI)-03A**.2**-01(D, R, etc.)

Note: Specific antibodies used for and sorted sample populations can be found in the associated OCG project metadata. Additionally, small "c" before the antigen marker indicates the location is intracellular rather than cell surface.

HCMI ICD-10 Codes:

An abbreviated ICD-10 code is used to denote the anatomic site of the diagnostic tumor origin.

ICD-10	**Anatomic Site**
C00-C14	Head and neck
C15	Esophageal
C16	Stomach
C17	Small intestine
C17	Duodenal gastrinoma
C18	Colon; Cecum
C19	Rectosigmoid junction
C20	Rectum
C22	Liver or intrahepatic bile duct
C23	Gallbladder
C24	Ampulla of Vater or extrahepatic bile duct

C25	Pancreas
C30	Olfactory neuroblastoma
C30-C32	Head and neck
C34	Bronchus and lung
C40-C41	Ewing Sarcoma or osteosarcoma
C41	Chordoma
C43	Skin/Melanoma
C45	Mesothelioma
C49	Rhabdomyosarcoma
C50	Breast
C54	Endometrium
C56	Ovary
C57	Other female reproductive organs
C61	Prostate
C64	Wilms Tumor
C67	Bladder
C71	Brain and glioblastoma
C73	Thyroid
C74	Neuroblastoma

HCMI: Multiple Model Codes:

Some cases may have multiple models derived from independent tumors (primary, recurrent, metastatic, etc.). To distinguish between the unique models, each will be identified using a letter identifier following the ID3's ICD-10 code to. For example:

1. **A** – first cancer model
2. **B** – second cancer model

Note: For cases in which multiple models per subject are known at the time of ID3 assignment, the first model will have suffix "A", the second model suffix "B", etc. While it would be useful if suffix A would be associated with primary tumor, and the other suffix letters with pre-malignant, recurrence, or metastasis, this may not be always true. For example, if a model that is successfully generated and already gone through the CMDC pipeline (CDC-approved, shipped to BPC and ATCC), and in the future, a model is generated from another tumor, the second model will receive the "B" suffix. The ID3 of the first model will not be changed to include the "A" suffix.

HCMI Additional Model Codes:

If models from independent tumors from the same patient are generated, the samples will be identified by using the following letter identifiers:

1. **M** – metastatic tumor model
2. **N** – second metastatic tumor model, from alternative location
3. **R** – recurrent tumor model
4. **S** – second recurrent tumor model, from a later date than R
5. **P** – premalignant model

TARGET: Additional tissue portion code sample identifier

**Cancer Models: Cell Lines/Xenografts:*

Some tissues are propagated as cell lines or xenografts. Multiple cell lines or xenografts may be available for certain cases, which are derived from the tumor either at the time of surgery, at relapse, or during monitoring of therapeutic response. Various NCI projects have decided to keep the codes for cell lines and xenografts "simple", and OCG attempts to comply so that users can translate codes easily.
To address the issue of multiple *in vitro* cancer models per case, OCG projects will use the extension of ".1, .2, .3, etc." following the tumor tissue code within the sample name to differentiate the cell lines and xenografts; this extension is prior to the letter identifier (unlike sorted cells). As with pre-extraction tissue

manipulations, it is not possible to determine at which time point the original tumor was obtained from the extension. It simply denotes a difference in samples, and users must refer to the appropriate metadata for details.

If xenografts or cell lines were established either from 2 separate aliquots/tissue sections (either in the same lab or another), then the letter in the tissue code will reflect it.

Here are some examples:

Laboratory name	**OCG Sample ID** *(multiple models per case)*
SMS-KCN - Dx (pre-therapy) cell line	OCG-30-(USI)-50**.1**A-01(D, R, etc.)
SMS-KCNR - Progressive disease (post-therapy) cell line	OCG-30-(USI)-50**.2**A-01(D, R, etc.)
SMS-KCNR - Progressive disease (post-therapy) cell line	OCG-30-(USI)-50**.2**B-01(D, R, etc.)

Note that the .1, .2, etc. does not indicate any additional information except that there are multiple cell lines from this patient. In the above example ".1" does not indicate that this cell line was established from a tumor obtained pre-therapy, nor ".2" post-therapy. The number just indicates that they are separate isolates from a single case. In addition, any case with only a single cell line or xenograft will not include the extension. The extension will only be used in the few cases where multiple samples are available.

In the example above, "OCG-30-(USI)-50**.2**B-01(D, R, etc.)" was generated either in another laboratory or from a different tissue aliquot than "OCG-30-(USI)-50**.2**A-01(D, R, etc.)".