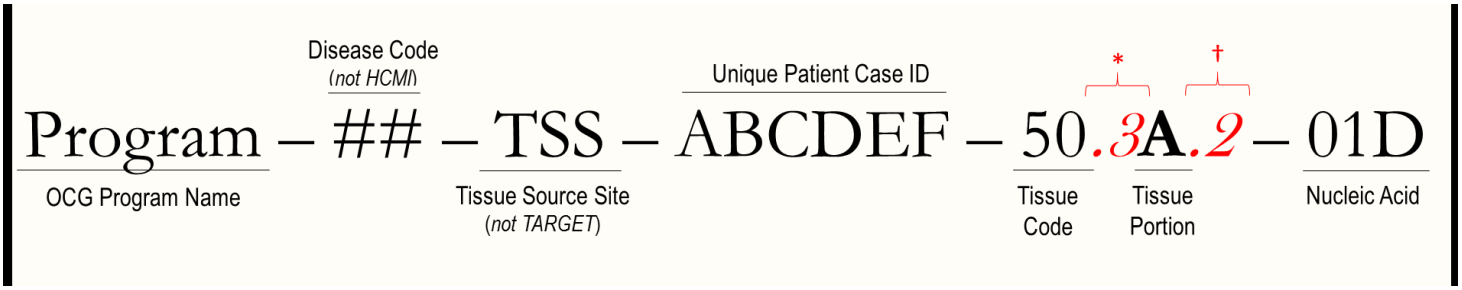
OCG Project Codes
Tissues and Samples

Date of Original: July 11, 2011

Revision date: September 29, 2011	Date applied: September 29, 2011
Revision date: October 24, 2011	Date applied: October 24, 2011
Revision date: February 17, 2012	Date applied: February 17 & 22, 2012
Revision date: June 4, 2012	Date applied: June 4, 2012
Revision date: February 27, 2013	Date applied: March 7, 2013
Revision date: June 13, 2013	Date applied: June 16, 2013
Revision date: July 5, 2013	Date applied: July 5, 2013
Revision date: June 5, 2015	Date applied: June 8, 2015
Revision date: September 1, 2015	Date applied: September 2, 2015
Revision date: January 25, 2016	Date applied: January 25, 2016
Revision date: June 13, 2016	Date applied: June 13, 2016
Revision date: September 9, 2016	Date applied: September 9, 2016
Revision date: December 12, 2016	Date applied: December 12, 2016
Revision date: February 28, 2017	Date applied: February 28, 2017
Revision date: April 19, 2017	Date applied: April 19, 2017
Revision date: May 22, 2017	Date applied: May 22, 2017
Revision date: March 13, 2018	Date applied: March 13, 2018

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 Structure:



Disease/Tumor Code:

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

Tissue Code:

Sample 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	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
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
Granulocytes	Granulocytes after a Ficoll separation	99

a. Tissue code

The 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.)*

b. 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.

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.

* *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.)”.