Sample Identifier Example

The sample identifier is broken down in the following format:

An example using participant identifier: **085-40990496-3**

Requisition Identifier: **997N2P4**

Primary Sample will have the identifier: **08540997N2P40201 (Barcode Number)**

**085:** Study/ Protocol Number

**40:**  Site Code; 40 for Gaborone

**997N2P4**: As above, Requisition Identifier for the sample (unique per sample)

**02**: Sample Type, 02 for whole blood

**01**: Sequence, Primary sample always 01

Aliquots/ Partitions for sample **08540997N2P40201**; analysis request is 1-hour fasting Glucose:

**08540997N2P4**: See Above

**32**: Sample Type, 32 for plasma

**02**: Sequence, second aliquot/partition generated.

The Sample Types for the Tshilo Dikotla (085) study:

1. 'Whole Blood', 'WB', '02',
2. 'Plasma', 'PL', '32',
3. 'Buffy Coat', 'BC', '16',
4. 'PBMC', 'PBMC', '31',
5. 'Serum', 'SERUM', '06'
6. UNS (RPMI) -72
7. BCG - 73
8. ESAT-6/CFP-74
9. PHA-74
10. Wba-pl-hep 77

…..

1. UNS (RPMI) – CEL 81
2. BCG - CEL 82
3. ESAT-6/CFP – CEL 83
4. PHA – CEL 84

Sample Identifier Recommended

Participant identifier: **External**

Requisition Identifier: **99AAA (5-alpha-numeric) – unique within study**

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Much better if the numeric part is at the end. An alpha-numeric code like AAA00 can generate:

 99 \* 26³ = 1.740,024 different Requistion IDs

Since the relationship between a requisition form and a Primary Sample is ~1, I'd suggest to assume the requisition ID = Primary Sample ID. Thus, I'd add the study code, as well as the sample type. E.g:

**08573AAA0102 >>08577AAA0102 wba-pl-hep uns >>08581AAA0102 wba-cel uns**

**08574AAA0103>>08578AAA0102 wba-pl-hep bcg>> 08578AAA0102 wba-cel bcg**

**08575AAA0104>>>>08579AAA0102 wba-pl-hep esat**

**08576AAA0105>>>>08580AAA0102 wba-pl-hep pha**

Where:

**085**: Study ID

**02**: Sample Type (Whole blood)

**AAA01**: (Initial) Requisition ID

**01**: Primary sample ID

Then, the system would be able to generate 1.740,024 different Sample IDs/Requisition IDs for each study+sample type intersection, and 98 different partitions for each Primary Sample (would a maximum of 8 partitions per Primary Sample would be enough?).

The ID of the first partition (of Serum Sample Type = 06) from the Sample above would look like:

**08506AAA0102**

And the ID of another partition (of Plasma = 32) from the Sample above, would look like

**08532AAA0103**

Changing both the sample type and last two digits allow us to have more than one partition with same sample type for each Primary Sample. Note that while the sample type and the last 2 digits change, the (initial) requisition ID and study ID remain untouched.

**Additional note**

You could add the site code within the study ID and the Sample Type,

**0854002AAA0101**

but I am afraid the code will be too long for the barcode to fit in small labels. In fact, we should test how many different characters can fit in the smallest label you'd like to use (the most compact barcode encoding is 3of9).

See barcode samples below ---

The previous one encoded in 3of9:



And without the Study ID:



We are assuming here that every single Sample will have only 1 Analysis Request (secondary ARs are not allowed, we use new partitions machinery instead).

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Study code: 085 (from BHP085 study code)

Sample type: 02 “whole blood” from the list of sample type codes

Aliquot number: serial

Use of R1 or R2 within Senaite??

**085997NPA0201 ---- whole blood**

**085997NPA3201 ----- Plasma ALQ 01**

**085997NPA3202 ----- Plasma ALQ 02**