**>>Sequence variations  ----**

1. Reference Sequence

* ​ I think that the limitations and temporary status of the IWGSC-Survey Sequence should be emphasised, encouraging contributors to be up-to-date with the latest releases.
* It should be mentioned that there is the possibility of successively replacing individual CSS chromosomes in the reference with the bac-by-bac equivalents as they become available.

2. Format

* ​​The warning about exome capture VCFs is somewhat cryptic and should be explain (Perhaps something could be distilled from  <https://www.broadinstitute.org/gatk/guide/best-practices>)

3. Tools

         Should VarScan2  be included in the list of SNP Calling Tools ?

•           *Question posed:*  (in the cookbook it says:)

            **Name    Description**

**RUN NAME**    Name of the sequencing run that produced the data we are interested in.

In VCF Specfications 4.1 & 4.2, RUN NAME etc.. do not appear to be available as meta-information lines. Is the plan to ask the developers of the specification to incorporate these lines?

**>> Germplasm**

The FAO/BIOVERSITY MULTI-CROP PASSPORT DESCRIPTORS V.2 document mentions a “Global unique identifier” which could be used to enable linkage across different information systems. This sounds like a good idea but it is not mentioned on the web page. Is it under consideration as part of the adoption of the MCPD vocabulary ?

**>> Gene expression ----**

         For microarray analysis: Please add links to MIAME and MAQC

         Also note that there was a special issue  [**Special Issue of *Nature Collections*in *Nature Biotechnology:* 2014**](http://www.nature.com/nbt/collections/seqc/index.html)which introduced MACIII (<http://www.fda.gov/ScienceResearch/BioinformaticsTools/MicroarrayQualityControlProject/#MAQC-IIIalsoknownasSEQC>) which is aimed at NGS benchmarks and reproducibility of results. This information could also be added.

         Should there be information on the reference genes provided?

         **qPCR:** How about including guidelines for qPCR experiment as well   - this point was mentioned by two people. Perhaps we need to address the point and say why it is not part of the cookbook

**>> Genetic & Physical Maps ----**

For genetic maps, consider adopting  HapMap format for molecular marker data  exchange / storage . Why ?

         It is the output format generated from the Tassel GBS pipeline

         Possible to convert between HapMap-to - VCF  and vice versa using Tassel or GATK

         Input format for latest GWAS packages e.g. GAPIT

         R package (snpmatrix) available for converting hapmap-formatted genotype data into a matrix

         PERL script (<http://bioinf.wehi.edu.au/software/linkdatagen/>) can convert genotyping data from Illumina or Affy chips into various formats e.g. PLINK. Possibly adaptable to HapMap ?