In a future release, the file attachments guidance below, will be changed to utilize upcoming FHIR R5 updates to the DiagnosticReport.media backbone element. The attribute will refer to DocumentReference instead of Media, and this guidance will then be updated. This approach to file attachments needs to be carefully reviewed and considered. There are many potential issues and the Work Group welcomes feedback.

There are use cases in genomics where a deeper level of data than that provided by the variant profile is warranted, thus, specifications such as VCF, BAM, CRAM, and MAF have been developed. Best practices in exchanging these files along with the metadata necessary to make use of them through a FHIR API remains a complicated and open issue. See [operations](http://build.fhir.org/ig/HL7/genomics-reporting/branches/kp-file-attachments/operations.html) for a description of an experimental alternative workflow.

While in future versions of FHIR other resources or options might be preferred, currently, DocumentReference is a good candidate as a means to provide access to genomic data formats (AH QUESTION: We call them data formats here and specifications in paragraph above – which should we use?) such as VCF, BAM, CRAM and MAF. As opposed to the files just mentioned: attachments which are individually useful (such as clinical notes) would likely be sent in FHIR using the DocumentReference resource, which allows the file and its captured metadata (e.g. within the DocumentReference.context element) to be discovered via search queries.

(AH NOTE: - This was originally the key point of this section, but is now a bit lost – and I can’t harmonize the earlier draft with this current draft. It DEFINITELY needs work however, as I can’t easily make sense of it …. To many references to “objects” without enough clear text providing the context) The Genomics File extension can be used to transmit the contents of, or links to, files that were produced as part of the testing process The [Genomics File](http://build.fhir.org/ig/HL7/genomics-reporting/branches/kp-file-attachments/StructureDefinition-genomics-file.html) extension can be used to reference files from the GenomicsReport. Also provided is the [Genomics Document Reference](http://build.fhir.org/ig/HL7/genomics-reporting/branches/kp-file-attachments/StructureDefinition-genomics-document-reference.html) profile which provides guidance for the genomic file itself.

When sending genomic files there are many considerations. For example, it is not unusual for files to be gigabytes in size. The DocumentReference resource has different options to evaluate for your use case. If embedded directly using using DocumentReference.content.attachment.data, servers receiving the files may have size constraints per resource or per transaction which may limit your options. Instead of sending a large data file, the file can be referenced by a URL and title using the using DocumentReference.content.attachment.url element. This can point to an online resource that hosts the file or from where the file can be accessed. For genomic files, the host is likely not the FHIR server providing the DocumentReference data instance. Be aware that use of DocumentReference to provide access to files through URLs introduces authorization requirements that are out of scope of this Implementation Guide.

For receivers to make use of these files, many facets of the generation of the genomic files will be needed, such as what pipelines, tools, and settings were used. The intended downstream use case must be carefully evaluated to ensure appropriate file preparation. The DocumentReference.description might be helpful for a sending system to provide guidance on how the file was generated. A fully computable approach for this issue has yet to be defined.

It should be noted that the Genomic File extension is *not* an appropriate way to send a copy of the report (e.g., PDF or other document containing the written report). Instead, use DiagnosticReport.presentedForm. Also note the Genomic File extension is different than the [Genomics Artifact](http://build.fhir.org/ig/HL7/genomics-reporting/branches/kp-file-attachments/StructureDefinition-genomics-artifact.html) extension, which is used to reference citations, evidence and other supporting documentation for the observation or report. In this release, another approach to avoid for attaching files is the DiagnosticReport.media attribute. Its definition focuses on "Key images associated with this report" which does not align well with this use case. However, as noted in the STU note above, this will be changing in a future release.

A full, detailed implementation discussion, is outside the scope of this IG. In a future release, this IG may include other profiles or artifacts along with more specific guidance.