Genetic Pathology Report Format

- **Specimen (compulsory)**
  - *Specimen Type must be stated: This could be any of blood, cells, fluids [state type], and could include tissue, frozen sample, formalin fixed paraffin Embedded sample. etc*
  - *Note the complication that a sample from a fetus may contain DNA from both the fetus AND the mother*
- **Request**
  - Genetic disease / condition assessed
    - *"A coded disease (recommend SNOMED) which is known to be caused by or identified by genomic DNA Markers. eg SCT 190905008 | Cystic fibrosis |*
  - Clinical question
    - *Freeform text entered by requester to further annotate the coded Reason for Study associated with an ordered test.*
    - *Note: Although "Clinical Question" is shown as freeform text in this version, it is anticipated that a future "structured request framework" will be developed*
- **Test**
  - Genetic Test
    - Genomic Source class
    - Genetic Level
      - *Whole Genome*
      - *Chromosome*
      - *Intergenic*
      - *Gene*
    - Gene Name or Locus
      - Coding System
      - Code (actual code for the genetic test)
      - Additional information
  - Genetic Test Method
    - Category
      - Mutational analysis
        - *The intention is to expand each of the following by one sublevel analogous to Chromosomal conditions so as to hold more detailed information relevant to each Type of Mutational Analysis. (Next level of detail for these Mutational Analysis tests has not yet been shown)*
        - Tests for multiple mutations ...
        - Test for selected mutations only ...
        - Assay for size of triplet repeat only ...
      - Chromosome microarray (CMA)
        - Microarray platform
        - Microarray platform version number
        - Base pair start coordinate
        - Base pair end coordinate
        - Flanking normal region before start
      - Analysis by Chromosome Banding
        - ISCN band level [#]
        - Chromosome band involved start
        - Chromosome band involved end
        - Chromosome banding method
        - Cells analysed [#]
        - Cells counted [#]
        - Cells karyotyped.total [#]
        - Colonies counted [#]
        - Mosaicism detected
      - Analysis by in situ hybridisation
        - Cell phase
        - Probe gene name
        - Probe locus
        - Probe vendor
        - Cells analysed
      - Functional analysis
        - DNA methylation
        - DNA transcription
    - Other
      - Linkage studies
      - *Details of test method not already specified (e.g. MLPA or direct DNA sequencing or list mutations searched for)*
  - Genetic Test Result
    - Cytogenetics
      - Karyotype analysis result in ISCN expression
        - *47,XY,+2*
        - *46,XY,-18,+der(13q18q),t(13;18)(13q18q;13p18p)pat*
      - Microarray analysis result in ISCN expression
        - *arr 16p13.11(14,817,706-16,649,713)x3 dn*
        - *arr 1p36.22p31.3(9,240,258-67,037,576)x2 hmz*
    - Molecular Genetics
      - DNA sequence variation type
        - *"Codified type for associated DNA Marker. DNA Marker's use the HGVS notation which implies the DNA Marker Type, but the concurrent use of this code will allow a standard and explicit type for technical and display convenience.*
        - *1 Wild type - LA6658-1 2 Deletion - LA6692-3 3 Duplication - LA6686-5 4 Insertion - LA6687-3 5 Insertion/Deletion - LA6688-1 6 Inversion - LA6689-9 7 Substitution - LA6690-7*
      - HGVS DNA Sequence Variation
        - *Human Genome Variation Society (HGVS) nomenclature for a single DNA marker. The use of the nomenclature must be extended to describe non-variations (aka. wild types) see samples for wild type examples.*
          - *e.g. c.3869A>C heterozygote*
        - *"Massively Parallel Sequencing [NGS/WGS] is anticipated to go here, but we have postponed specific inclusion pending the outcome of the MPS Working Party recommendations*
      - DNA region name
        - *"A human readable name for the region of interest. Typically Exon #, Intron # or other. NOTE: This is not standardized and is mainly for convenience and display purposes.*
      - RNA
        - *This section is anticipated to hold the results of RNA-specific changes, such as RNA Editing, Transcriptomic results, etc*
      - Amino acid change
        - *"Human Genome Variation Society (HGVS) nomenclature for an amino acid sequence. This value is derivable from the DNA Marker value if available. It is provided for convenience. The use of the nomenclature must be extended to describe non-variations (aka. wild types) see samples for wild type examples.*
      - Genomic RefSeq String
        - *"Definition: Carries the literal string that represents the DNA sequence that is the basis for deciding what is a different (a variation) in the study subject The same information can also be reported more compactly by reference (see LOINC code 48013-7) if the reference sequence has been catalogued by a registration authority such as RefSeq at NCBI a. Reference sequences can be quite long*
        - *Example answer: 241 GGAGTAATCA GCAACTCAGG GGGACCTGTA CGAGTCTATA GCCTACCTGG TCGAGAAAAC 301 TATTTCCTCAG TAGATGCCAA TGGCATCCAG TCTCAAATGC TTTCTAGATG GTCTGCTTCT 361 TTCACAGTAA CTA"*
      - Amino acid change type
      - Allelic State
        - *"Includes Copy Number Variation [CNV], Loss of Heterozygosity [LOH], Quantitative gene dosage"*
    - Result modifier
      - RNA/Protein consequences
      - Reports
      - Co-occurrence with deleterious mutations
      - Species conservation
      - Biochemical
        - *This modifier can be used to correlate genetic findings with (e.g.) pharmacogenomic or biochemical results*
      - Biophysical change
      - In-silico analyses
      - RNA Studies
      - Functional studies
      - Control data
      - Segregation data
      - Loss of normal allele in cancer
  - Genetic Test Interpretation
    - Limitations and Disclaimers (compulsory)
      - *This section would describe the status of the result. Has it been validated? Is it research-use only? Are there known weaknesses? Is this study partial, in progress, complete, etc*
    - Result Interpretation (compulsory)
      - *This section summarises the laboratory findings. What were the results of testing? What are the biological and genetic implications of this result?*
      - Genetic Screen findings (optional)
      - Carrier status summary (optional)
        - *"Carrier identification interpretation of all identified DNA Markers and/or Individual Alleles along with any known clinical information for the benefit of aiding clinicians in understanding the results overall. "*
      - Sequence variation summary (optional)
    - Clinical Interpretation (Compulsory):
      - *This section summarises the clinical significance (if any) of the laboratory findings. It can take into account Family History or Clinical History.*
      - Genotype clinical interpretation (optional)
      - Phenotype clinical interpretation (optional)
    - Conclusion (optional)
      - *This is the final "tie it all together" field, if not already done so above.*
    - Interpretation modifier
      - *As for Result modifier, see above*