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Title: Philips' Cross-Check Results for CE2 of MPEG-G Part 6
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1 Introduction

This document describes the cross-check results for MPEG-G, Part 6, CE2, according to the cross check procedure described in section 4.8 of N19312.

2 Cross-check procedure

According to the cross-check procedure, Genomsys has provided:

- A SW tool accepting as input the sanitized input file and generating descriptors/attribute streams.
- A SW tool that accepts as input a set of descriptor/attribute streams and reconstruct the sanitized input file.

Genomsys has further provided descriptor/attribute streams produced by the encoding SW tool.

3 Results

Philips has run bot the encoding and decoding SW tools on the following sub-set of input test items, encoding both in “binary mode” and “string mode”, and has verified that the decoding of the produced descriptors/attribute streams perfectly reproduces the sanitized input file:

```
1.3.1/homo_sapiens-chr1.vcf.gz
1.3.2/homo_sapiens_somatic.vcf.gz
1.3.3/homo_sapiens_structural_variations.vcf.gz
1.3.5/Selected.integrated_phase1_v3.20101123.snps_indels_svs.genotypes.vcf.gz
1.3.6/nstd112.GRCh37.variant_call.vcf.gz
1.3.6/nstd112.GRCh37.variant_region.vcf.gz
1.6.x/Variant/10xGenomics_HG001.GATK38.liftover.b37.indel.vcf.gz
1.6.x/Variant/10xGenomics_HG001.GATK38.liftover.b37.snp.vcf.gz
1.6.x/Variant/NovaSeqS2_HG001_Rep1to3_100x.GATK38.b37.indel.vcf.gz
1.6.x/Variant/NovaSeqS2_HG001_Rep1to3_100x.GATK38.b37.snp.vcf.gz
1.6.x/Variant/clinvar_20200224.vcf.gz
1.1.6/Homo_sapiens.GRCh38.95.chr_patch_hapl_scaff.gtf.gz
```

Philips has furthermore run the decoding SW tool on the following sub-set of test item descriptor/attribute streams provided by Genomsys and has verified that the decoding perfectly reproduces the sanitized input file:

1.1.6_Homo_sapiens.GRCh38.95.chr_patch_hapl_scaff.gtf.gz
1.3.1_homo_sapiens-chr1.vcf.gz
1.3.2_homo_sapiens_somatic.vcf.gz
1.3.3_homo_sapiens_structural_variations.vcf.gz
1.3.5_Selected.integrated_phase1_v3.20101123.snps_indels_svs.genotypes.vcf.gz
1.3.6_nstd112.GRCh37.variant_call.vcf.gz
1.3.6_nstd112.GRCh37.variant_region.vcf.gz
1.3.7_nstd152.GRCh37.variant_call.vcf.gz
1.3.7_nstd152.GRCh37.variant_region.vcf.gz
1.4.15_raw_peak_bc_matrix.gz
1.4.15_raw_peak_bc_matrix.gz_features.bed.gz
1.4.15_raw_peak_bc_matrix.gz_samples.tsv.gz
1.5.15_test.tsv.gz
1.5.16_test1.tsv.gz_values.gz
1.6.x_10xGenomics_HG001.GATK38.liftover.b37.indel.vcf.gz
1.6.x_10xGenomics_HG001.GATK38.liftover.b37.snp.vcf.gz
1.6.x_ALL.chrX.phase1_release_v3.20101123.snps_indels_svs.genotypes.vcf.gz
1.6.x_ALL.chrY.snps_indels_complex_STRs_svs.genotype_likelihoods.vcf.gz
1.6.x_HG00104.bw.bed.gz
1.6.x_NA07357.bw.bed.gz
1.6.x_NovaSeqS2_HG001_Rep1to3_100x.GATK38.b37.indel.vcf.gz
1.6.x_NovaSeqS2_HG001_Rep1to3_100x.GATK38.b37.snp.vcf.gz
1.6.x_clinvar_20200224.vcf.gz
1.6.x_dbSNP-common_all_20180423.vcf.gz
1.6.x_dbVar-GRCh37.variant_call.all.vcf.gz
1.6.x_ExprMatrices.gz_eff_len.gz
1.6.x_ExprMatrices.gz_est_counts.gz
1.6.x_ExprMatrices.gz_tpm.gz

Other test item descriptor/attribute streams could not be verified to produce perfect reconstruction of the sanitized input file.