**# Proposed beacon v2 schema changes discussed today and maybe a couple other suggestions**

Note: whatever is in automatic/black font is kept the same as in current version, things in blue font means additions or changes. Things marked with gray boxes (A) are things currently available in viral beacon data so far

**Variant basic** A

refAssemblyId

startPos

endPos

ref

alt

variantType Variant classification e.g SNV, indel, CNV, structural variant

**Organism** A

taxonId categorical value (ontology ID). Taxon ID of species from where variants come from, for example, the SARSCoV 2 taxon id and not human’s in the case of viral beacons)

**Individual**

individualId A

datasetId

taxon\_id alphanumeric ID (reference taxon ID for this individual human, animal or plant)

sex A

ethnicity

geographicOrigin A

phenotypicFeature list of

phenotype categorical value (ontology ID) Phenotypic feature observed (not disease)

level/severity categorical value (ontology ID) Level/severity when and as applicable to phenotype observed e.g “mild”, “severe”

diseases list of A

diseaseId A

dateOfOnset

ageOfOnset

age alphanumeric value (ISO8601 duration format)

ageGroup categorical value (ontology ID)

stage categorical value (ontology ID) A

outcome categorical value (ontology ID) Outcome of disease e.g fatal (death) or non-fatal A

level/severity categorical value (ontology ID Level/severity when and as applicable to disease observed e.g “mild”, “severe”

familyHistory

treatment

id categorical value (ontology ID) eg. chemotherapy

dateAtOnset alphanumeric value (ISO8601 duration format)

ageOfOnset

age alphanumeric value (ISO8601 duration format)

dose numerical value

units categorical value (ontology ID)

schedule free text for now eg. 3/week

duration alphanumeric value (ISO8601 duration format)

intervention

id categorical value (ontology ID) eg. Vasectomy

date alphanumeric value (ISO8601 duration format)

ageAtIntervention alphanumeric value (ISO8601 duration format)

pedigrees list of

pedigreeID

disease disease format

pedigreeRole

numberOfIndividualsTested

info

**Biosample**

biosampleId A

individualId A

description

biosampleStatus

collectionDate alphanumeric value (ISO8601 duration format). Date at which sample is collected.

IndividualAgeAtCollection A

sampleOriginType categorical value (ontology ID) Category of sample origin e.g “organism primary tissue”, “organism xenograft”, “organism-derived fluid”, “cell culture”, “environmental sample” A

sampleOriginDetail categorical value (ontology ID) Specific instance of sample origin matching e.g “HEK293T”, “nasopharyngeal swab” A

obtentionProcedure categorical value (ontology ID)

cancerFeatures list of

tumorProgression

tumorGrade

info

**Variant Annotation**

variantId A

genomicHGVSId

transcriptHGVSId alphanumeric ID (HGVSId descriptor at transcript level)

proteinHGVSId

genomicRegionClass A categorical value (ontology ID) eg protein coding, intergenic, untranslated region

featureID A list of categorical value(s) List of IDs of genes, genomic regions, subgenomic regions, transcripts, other RNA species and proteins that are affected by the variant names or genomic region ref seq accessions (NC, NM, YP )

annotationToolVersion A alphanumeric value. Tool used for annotation and prediction of variant effects e.g “SnpEffVersion=4.3t (build 2017-11-24 1018)”

molecularEffect A categorical value (ontology ID) Predicted effect at nucleotide level eg “STOP\_GAINED” as opposed to the description at protein level for protein affecting variants eg. “Nonsense” that goes into molecularConsequence

molecularConsequence A

aminoacidChange A string. Change at aminoacid level for for protein affecting variants eg. V304\*

phenotypicEffect categorical value (ontology ID) Annotated effect on any phenotypic feature other than a disease

phenotypeId Phenotype associated

phenotypeEffect categorical value (ontology ID). Phenotypic effect classification

references list of PMIDs

clinicalRelevance list of

disieaseId

clinicalEffect previously variantClassification

references

allelleOrigin list of

info

**Run**

runId A alphanumeric ID (external accession) e.g "SRR10903401"

librarySource A categorical value e.g “Metagenomic”, “Viral RNA”

libraryStrategy A categorical value e.g “WGS”

librarySelection A categorical value e.g “RANDOM”, “RT-PCR”

libraryLayout A categorical value e.g “PAIRED” “SINGLE”

platform A categorical value Sequencing platform group e.g “Illumina”, “Nanopore”

platformModel A categorical value Sequencing platform model e.g “Illumina MiSeq” , ”GridION"

info (or handover maybe)

experiment\_info A

experimentId alphanumeric ID External experiment accession e.g "SRX7571571"

experimentTitle string e.g ”Total RNA sequencing of BALF (human reads removed)”

study\_info

studyId alphanumeric ID External study reference/accession e.g "SRP242226"

studyRef list of PMIDs

**Variant in Sample**

variantId A alphanumeric ID

runId A alphanumeric ID

variantCaller A categorical value e.g GATK vxx

biosampleId alphanumeric ID

individualId categorical value (ontology ID)

variantFrequency A numeric value

zygosity

alleleOrigin

clinicalRelevance list of

disieaseId categorical value (ontology ID)

clinicalEffect categorical value (ontology ID)

info

**Encounter**

encounterID alphanumeric ID

encounterDate alphanumeric value (ISO8601 duration format) Date of encounter/medical visit

ageAtEncounter

age alphanumeric value (ISO8601 duration format)

ageGroup categorical value (ontology ID)

clinicalFindings Non quantifiable or not quantified clinical findings

finding categorical value (ontology ID) eg: arrithmia

level/severity categorical value (ontology ID) e.g mild

measurements (list of) measurements taken during encounter

id categorical value (ontology ID)

value numerical value

units categorical value (ontology ID)

info