d2rq:condition "mutations15.Mutant_AA != ('-')";

map:variation_p_description a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:variation;
d2rq:property logvd:p_description;
d2rq:propertyDefinitionLabel "variations Protein Mutation Description";
d2rq:propertyDefinitionComment "Mutation description at the protein level as recommended by HGVS." @en;

d2rq:propertyDefinitionLabel "variations Mutation rate of AA";
d2rq:propertyDefinitionComment "Mutation rate of amino-acid substitutions resulting from single nucleotide substitutions." @en;

d2rq:propertyDefinitionLabel "variations Effect";
d2rq:propertyDefinitionComment "Effect of the mutation. The terms occurring in this column are: missense (change of one amino-acid), nonsense (stop codon), FS (frameshift), silent (no change in the protein sequence), splice (mutations located in the two first and two last conserved nucleotides of the introns and are thus predicted to alter splicing, or mutations that have been shown to alter splicing experimentally), other (inframe deletions or insertions, mutations in introns)." @en;

map:variation_Polymorphism a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:variation;
d2rq:property logvd:Polymorphism;
d2rq:propertyDefinitionLabel "variations Polymorphism";
d2rq:propertyDefinitionComment "Polymorphic status of the gene variation." @en;

map:variation_Validation_type a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:variation;
d2rq:property logvd:Validation_type;
d2rq:propertyDefinitionLabel "variations Validation";
d2rq:propertyDefinitionComment "Type of validation for polymorphism, as indicated in NCBI SNP database." @en;

map:variation_dbSNP_link a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:variation;
d2rq:property logvd:dbSNP_link;
d2rq:propertyDefinitionLabel "variations dbSNP link";
d2rq:propertyDefinitionComment "Link to NCBI SNP database." @en;

d2rq:propertyDefinitionLabel "variations Residue function";
d2rq:propertyDefinitionComment 'Known function of the wild-type residue. When the function is not known but the structure is known, the solvent accessibility (SA) of the residue is indicated by the terms buried, exposed or partially exposed. "@en;

d2rq:column "mutations15.Residue_function"

d2rq:condition "mutations15.Residue_function != ('NA')"

d2rq:condition "mutations15.Residue_function != ('')"

d2rq:condition "mutations15.Residue_function != ('-')"

map:variation_Domain_function a d2rq:PropertyBridge;

d2rq:belongsToClassMap map:variation;

d2rq:property logvd:Domain_function;

d2rq:propertyDefinitionLabel "variations Domain function";

d2rq:propertyDefinitionComment 'Function of the domain in which the mutated residue is located. "@en;

d2rq:column "mutations15.Domain_function"

d2rq:condition "mutations15.Domain_function != ('NA')"

d2rq:condition "mutations15.Domain_function != ('')"

d2rq:condition "mutations15.Domain_function != ('-')"

map:variation_Structural_motif a d2rq:PropertyBridge;

d2rq:belongsToClassMap map:variation;

d2rq:property logvd:Variation_motif;

d2rq:propertyDefinitionLabel "variations Structural motif";

d2rq:propertyDefinitionComment '2D and 3D motifs where the mutation is located according to structures described in Cho et al. (1994) and May and May (1999). "@en;

d2rq:column "mutations15.Structural_motif"

d2rq:condition "mutations15.Structural_motif != ('NA')"

d2rq:condition "mutations15.Structural_motif != ('')"

d2rq:condition "mutations15.Structural_motif != ('-')"

map:variation_Grantham_variation a d2rq:PropertyBridge;

d2rq:belongsToClassMap map:variation;

d2rq:property logvd:Grantham_variation;

d2rq:propertyDefinitionLabel "variations Grantham variation";

d2rq:propertyDefinitionComment 'Grantham variation. GV is a measure of the amount of observed biochemical variation at a particular position in a multiple sequence alignment. GV was calculated with an alignment containing 9 sequences of p53 from fish to placental mammals with the A-GVGD program. "@en;

d2rq:column "mutations15.GV"

d2rq:condition "mutations15.GV != ('NA')"

d2rq:condition "mutations15.GV != ('')"

d2rq:condition "mutations15.GV != ('-')"

map:variation_Grantham_deviation a d2rq:PropertyBridge;

d2rq:belongsToClassMap map:variation;

d2rq:property logvd:Grantham_deviation;

d2rq:propertyDefinitionLabel "variations Grantham deviation";

d2rq:propertyDefinitionComment 'Grantham deviation. GD is a measure of the deviation of the mutated residue from the different types of residues observed at that position in a multiple sequence alignment. It is derived from GV and the Grantham matrix. "@en;

d2rq:column "mutations15.GD"

d2rq:condition "mutations15.GD != ('NA')"

d2rq:condition "mutations15.GD != ('')"

d2rq:condition "mutations15.GD != ('-')"

map:variation_AGVGDClass a d2rq:PropertyBridge;

d2rq:belongsToClassMap map:variation;

d2rq:property logvd:AGVGDClass;

d2rq:propertyDefinitionLabel "variations AGVGD Class";

d2rq:propertyDefinitionComment 'Prediction of functional impact based on protein sequence conservation, taking into account GV and GD. Mutations are classified as -neutral-, -deleterious- or -unclassified-. "@en;

d2rq:column "mutations15.AGVGDClass"

d2rq:condition "mutations15.AGVGDClass != ('NA')"

d2rq:condition "mutations15.AGVGDClass != ('')"

d2rq:condition "mutations15.AGVGDClass != ('-')"

map:variation_SIFTClass a d2rq:PropertyBridge;

d2rq:belongsToClassMap map:variation;

d2rq:property logvd:SIFTClass;

d2rq:propertyDefinitionLabel "variations SIFT Class";

d2rq:propertyDefinitionComment 'Functional classification based on SIFT program using the same sequence alignment as for AGVGDclass and program default settings. Missense mutations are classified as -deleterious- or -neutral-. "@en;

d2rq:column "mutations15.SIFTClass"

d2rq:condition "mutations15.SIFTClass != ('NA')"

d2rq:condition "mutations15.SIFTClass != ('')"

d2rq:condition "mutations15.SIFTClass != ('-')"
map:variation_WAF1nWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:WAF1nWT;  
d2rq:propertyDefinitionLabel "variations WAF1nWT";  
d2rq:propertyDefinitionComment 'p21 - WAF1 promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.WAF1nWT";  
d2rq:condition "mutations15.WAF1nWT := ('NA')";  
d2rq:condition "mutations15.WAF1nWT := ('')";  
d2rq:condition "mutations15.WAF1nWT := ('-')";  

map:variation_MDM2nWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:MDM2nWT;  
d2rq:propertyDefinitionLabel "variations MDM2nWT";  
d2rq:propertyDefinitionComment 'MDM2 promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.MDM2nWT";  
d2rq:condition "mutations15.MDM2nWT := ('NA')";  
d2rq:condition "mutations15.MDM2nWT := ('')";  
d2rq:condition "mutations15.MDM2nWT := ('-')";  

map:variation_BAXnWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:BAXnWT;  
d2rq:propertyDefinitionLabel "variations BAXnWT";  
d2rq:propertyDefinitionComment 'BAX promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.BAXnWT";  
d2rq:condition "mutations15.BAXnWT := ('NA')";  
d2rq:condition "mutations15.BAXnWT := ('')";  
d2rq:condition "mutations15.BAXnWT := ('-')";  

map:variation_h1433snWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:h1433snWT;  
d2rq:propertyDefinitionLabel "variations h1433snWT";  
d2rq:propertyDefinitionComment 'h1433 promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.h1433snWT";  
d2rq:condition "mutations15.h1433snWT := ('NA')";  
d2rq:condition "mutations15.h1433snWT := ('')";  
d2rq:condition "mutations15.h1433snWT := ('-')";  

map:variation_AIP1nWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:AIP1nWT;  
d2rq:propertyDefinitionLabel "variations AIP1nWT";  
d2rq:propertyDefinitionComment 'p53AIP1 promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.AIP1nWT";  
d2rq:condition "mutations15.AIP1nWT := ('NA')";  
d2rq:condition "mutations15.AIP1nWT := ('')";  
d2rq:condition "mutations15.AIP1nWT := ('-')";  

map:variation_GADD45nWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:GADD45nWT;  
d2rq:propertyDefinitionLabel "variations GADD45nWT";  
d2rq:propertyDefinitionComment 'GADD45 promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.GADD45nWT";  
d2rq:condition "mutations15.GADD45nWT := ('NA')";  
d2rq:condition "mutations15.GADD45nWT := ('')";  
d2rq:condition "mutations15.GADD45nWT := ('-')";  

map:variation_NOXAnWT a d2rq:PropertyBridge;  
d2rq:belongsToClassMap map:variation;  
d2rq:property logvd:NOXAnWT;  
d2rq:propertyDefinitionLabel "variations NOXAnWT";  
d2rq:propertyDefinitionComment 'Noxa promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity. *\"en;  
d2rq:column "mutations15.NOXAnWT";  
d2rq:condition "mutations15.NOXAnWT := ('NA')";  
d2rq:condition "mutations15.NOXAnWT := ('')";  
d2rq:condition "mutations15.NOXAnWT := ('-')";  

<table>
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<tr>
<th>Property</th>
<th>Definition</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
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<td>Variations</td>
<td>Promoter-specific transcriptional activity measured in yeast functional assays and expressed as percent of wild-type activity.</td>
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<tr>
<td>TransactivationClass</td>
<td>Variations</td>
<td>Functional classification based on the overall transcriptional activity on 8 different promoters as measured by Kato et al.</td>
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<tr>
<td>StructureFunctionClass</td>
<td>Variations</td>
<td>Functional predictions derived from a computer model that takes into account the 3D structure of WT and mutant proteins and is trained on the transactivation dataset from Kato et al. Mutations are classified as functional or non-functional.</td>
</tr>
<tr>
<td>DNEclass</td>
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<td>Dominant-negative activity over wild-type p53.</td>
</tr>
<tr>
<td>SomaticCount</td>
<td>Variations</td>
<td>The number of occurrences as somatic event for each gene variation.</td>
</tr>
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</table>

# Table somatic15

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Somatic Mutations in human cancer.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type of TP53</td>
<td>Somatic mutations dataset: Type of TP53 somatic mutations in human cancer. The dataset of Somatic Mutation contains exclusively TP53 somatic mutations that have been identified in human tissues by sequencing and published in the peer-reviewed literature. This includes mutations found in normal, pre-neoplastic and neoplastic tissues, including metastases, as well as in cell lines derived from such tissues. The database does not include (1) individual data on human tissues that are reported as negative with respect to p53 mutation, (2) mutations not precisely identified by sequencing (e.g. mutations identified only by SSCP, DGGE or restriction digestion), (3) experimentally-induced mutations in tumor cells or cell lines in vitro, (4) p53 mutations in animal tumors.</td>
</tr>
</tbody>
</table>

-
map:somatic_mutation_MUT_ID a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_mutation;
  d2rq:property logvd:hasVariation;
  d2rq:propertyDefinitionLabel "somatic MUT_ID";
  d2rq:propertyDefinitionComment "Unique identifier of each gene variation reported in
the database. This identifier is used in all datasets."@en;
  d2rq:refersToClassMap map:variation;
  d2rq:join "somatic15.MUT_ID => mutations15.MUT_ID".

map:somatic_mutation_c_description a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_mutation;
  d2rq:property logvd:c_description;
  d2rq:propertyDefinitionLabel "somatic c_description";
  d2rq:propertyDefinitionComment "Mutation nomenclature according to HGVS standards with
the coding sequence as reference."@en;
  d2rq:column "somatic15.c_description";

map:somatic_mutation_Structural_motif a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_mutation;
  d2rq:property logvd:Structural_motif;
  d2rq:propertyDefinitionLabel "somatic Structural_motif";
  d2rq:propertyDefinitionComment "2D and 3D motifs where the mutation is located
according to structures described in Cho et al. (1994) and May and May (1999)."@en;
  d2rq:column "somatic15.Structural_motif";

map:somatic_mutation_Putative_stop a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_mutation;
  d2rq:property logvd:Putative_stop;
  d2rq:propertyDefinitionLabel "somatic Putative_stop";
  d2rq:propertyDefinitionComment "Putative stop."@en;
  d2rq:column "somatic15.Putative_stop";
  d2rq:condition "somatic15.Putative_stop != ('NA')";
  d2rq:condition "somatic15.Putative_stop != ('-')";

map:somatic_mutation_Sample_ID a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_mutation;
  d2rq:property logvd:hasSample;
  d2rq:propertyDefinitionLabel "somatic Sample ref";
  d2rq:propertyDefinitionComment "Unique sample identification number. This number allows
the automatic retrieval of samples with multiple mutations."@en;
  d2rq:refersToClassMap map:sample;
  d2rq:join "somatic15.Sample_ID => somatic15.Sample_ID";

map:somatic_mutation_Ref_ID a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_mutation;
  d2rq:property logvd:hasReference;
  d2rq:propertyDefinitionLabel "somatic Pubblcation ref";
  d2rq:propertyDefinitionComment "Unique identification number for a reference."@en;
  d2rq:refersToClassMap map:somatic_ref;
  d2rq:join "somatic15.Ref_ID => SomaticRef15.Ref_ID";

# Table SomaticRef15
map:somatic_ref a d2rq:ClassMap;
  d2rq:dataStorage map:database;
  d2rq:urlPattern "somatic_ref/@@SomaticRef15.Ref_ID@@";
  d2rq:class logvd:somatic_ref;
  d2rq:classDefinitionLabel "Somatic mutations References";
  d2rq:classDefinitionComment "TP53SomaticRefR15 dataset that includes the references in
which are described the mutations."@en;

map:somatic_ref__label a d2rq:PropertyBridge;
  d2rq:belongsToClassMap map:somatic_ref;
  d2rq:property rdfs:label;
  d2rq:pattern "somatic_ref/@@SomaticRef15.Ref_ID@@";
d2rq:additionalClassDefinitionProperty map:somatic_ref_PubMedEquivalence;
map:somatic_ref_PubMedEquivalence a d2rq:AdditionalProperty;
d2rq:belongsToClassMap map:somatic_ref;
d2rq:property rdfs:seeAlso;
d2rq:propertyDefinitionLabel "SomaticRef ncbi PubMed";
d2rq:propertyDefinitionComment "PubMed Id ref."@en;

map:somatic_ref_Comment a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:somatic_ref;
d2rq:property rdfs:seeAlso;
d2rq:propertyDefinitionLabel "SomaticRef Comment";
d2rq:propertyDefinitionComment "Any relevant information."@en;
d2rq:column "SomaticRef15.Comment";
d2rq:condition "SomaticRef15.Comment != ('NA')";
d2rq:condition "SomaticRef15.Comment != ('')";
d2rq:condition "SomaticRef15.Comment != ('-')";

map:somatic_ref_Exclude_analysis a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:somatic_ref;
d2rq:property logvd:Exclude_analysis;
d2rq:propertyDefinitionLabel "SomaticRef Exclude_analysis";
d2rq:propertyDefinitionComment "Papers that we recommend to exclude from any analysis because of poor data quality."@en;

# From Table somatic15 to patients demographic details
map:individual a d2rq:ClassMap;
d2rq:dataStorage map:database;
d2rq:uriPattern "individual/@@somatic15.Individual_ID@@";
d2rq:class logvd:individual;
d2rq:classDefinitionLabel "Demographic information of patient-individual.";
d2rq:classDefinitionComment "Patients demographic details and description of the patient origin and life-style. This dataset contains heterogeneous notes, usually comments emphasized by authors reporting the mutations."@en;

map:individual__label a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property rdfs:label;
d2rq:pattern 'individual/@@somatic15.Individual_ID@@';

map:individual_Sex a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Sex_or_Gender;
d2rq:propertyDefinitionLabel "individual Sex";
d2rq:propertyDefinitionComment "Sex of the patient."@en;

map:individual_Age a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Age;
d2rq:propertyDefinitionLabel "individual Age";

map:individual_Ethnicity a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Ethnicity;

from_table somatic15 to patients demographic details
d2rq:column "somatic15.Ethnicity";
d2rq:condition "somatic15.Ethnicity != ('NA')";
d2rq:condition "somatic15.Ethnicity != ('')";
d2rq:condition "somatic15.Ethnicity != ('-')";
map:individual_Population a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Population_Group;
d2rq:propertyDefinitionLabel "individual Population";
d2rq:column "somatic15.Population";
d2rq:condition "somatic15.Population != ('NA')";
d2rq:condition "somatic15.Population != ('')";
d2rq:condition "somatic15.Population != ('-')";

map:individual_Country a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Country;
d2rq:propertyDefinitionLabel "individual Country";
d2rq:condition "somatic15.Country != ('NA')";
d2rq:condition "somatic15.Country != ('')";
d2rq:condition "somatic15.Country != ('-')";

map:individual_Geo_area a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Geographic_Area;
d2rq:propertyDefinitionLabel "individual Geo_area";
d2rq:condition "somatic15.Geo_area != ('NA')";
d2rq:condition "somatic15.Geo_area != ('')";
d2rq:condition "somatic15.Geo_area != ('-')";

map:individual_TP53polymorphism a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property logvd:TP53polymorphism;
d2rq:propertyDefinitionLabel "somatic TP53polymorphism";
d2rq:condition "somatic15.TP53polymorphism != ('NA')";
d2rq:condition "somatic15.TP53polymorphism != ('')";
d2rq:condition "somatic15.TP53polymorphism != ('-')";

map:individual_germline_mutation a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property logvd:germline_mutation;
d2rq:propertyDefinitionLabel "somatic germline mutation";
d2rq:propertyDefinitionComment " Presence of a germline mutation in TP53 or any other gene. "@en;
d2rq:column "somatic15.Germline_mutation";
d2rq:condition "somatic15.Germline_mutation != ('NA')";
d2rq:condition "somatic15.Germline_mutation != ('')";
d2rq:condition "somatic15.Germline_mutation != ('-')";

map:individual_Family_history a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property logvd:Family_history;
d2rq:propertyDefinitionLabel "individual Family_history";
d2rq:propertyDefinitionComment " Information on the presence or absence of cancers in the family of the patient. "@en;
d2rq:column "somatic15.Family_history";
d2rq:condition "somatic15.Family_history != ('NA')";
d2rq:condition "somatic15.Family_history != ('')";
d2rq:condition "somatic15.Family_history != ('-')";

map:individual_Tobacco a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Tobacco_Use;
d2rq:propertyDefinitionLabel "individual Tobacco";
d2rq:propertyDefinitionComment " Information on the smoking status of the patient. "@en;
d2rq:column "somatic15.Tobacco";
d2rq:condition "somatic15.Tobacco != ('NA')";
d2rq:condition "somatic15.Tobacco != ('')";
d2rq:condition "somatic15.Tobacco != ('-')";

map:individual_Alcohol a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property NCIT:Alcohol_Consumption;
d2rq:propertyDefinitionLabel "individual Alcohol";
d2rq:propertyDefinitionComment 'Information on the drinking status of the patient.
"@en;

d2rq:column 'somatic15.Alcohol';
d2rq:condition "somatic15.Alcohol != ('NA')";
d2rq:condition "somatic15.Alcohol != ('')";
d2rq:condition "somatic15.Alcohol != ('-')";

map:individual_Exposure a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property logvd:Exposure;
d2rq:propertyDefinitionLabel "individual Exposure";
d2rq:propertyDefinitionComment 'Risk factors to which the patient has been exposed, such as aflatoxins, radon, thorotrast, etc."@en;

d2rq:column 'somatic15.Exposure';
d2rq:condition "somatic15.Exposure != ('NA')";
d2rq:condition "somatic15.Exposure != ('')";
d2rq:condition "somatic15.Exposure != ('-')";

map:individual_Infectious_agent a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:individual;
d2rq:property logvd:Infectious_agent;
d2rq:propertyDefinitionLabel "individual Infectious_agent";
d2rq:propertyDefinitionComment 'Pathogen (virus or bacteria) detected in the patient.
"@en;

d2rq:column 'somatic15.Infectious_agent';
d2rq:condition "somatic15.Infectious_agent != ('NA')";
d2rq:condition "somatic15.Infectious_agent != ('')";
d2rq:condition "somatic15.Infectious_agent != ('-')";

# From Table somatic15 to sample details
map:sample a d2rq:ClassMap;
d2rq:dataStorage map:database;
d2rq:uriPattern "sample/@@somatic15.Sample_ID@@";
d2rq:class logvd:sample;
d2rq:classDefinitionLabel 'sample details';
d2rq:classDefinitionComment 'Tumor site, type and origin. Tumor samples are classified according to standards of the International Classification of Diseases for Oncology (ICD-O 3rd Edition, World Health Organization, Geneva, 2000) and SNOMED."@en;

map:sample__label a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property rdfs:label;
d2rq:pattern "sample/@@somatic15.Sample_Name@@";

map:sample_Sample_Name a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Name;
d2rq:propertyDefinitionLabel "sample Sample Name";
d2rq:propertyDefinitionComment 'Name or number given by the authors to the tumor sample or cell line. If the name is not distinctive, e.g., if the publication refers to samples as tumors 1,2,3, etc, we have arbitrarily assigned a name, usually the first letters of the first author's name, followed by the numbers in the series. The same name or number can occur several times as in some samples more than one mutation has been reported."@en;

d2rq:column 'somatic15.Sample_Name';
d2rq:condition "somatic15.Sample_Name != ('NA')";
d2rq:condition "somatic15.Sample_Name != ('')";
d2rq:condition "somatic15.Sample_Name != ('-')";

map:sample_Sample_source a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Sample_source;
d2rq:propertyDefinitionLabel "sample Sample source";
d2rq:propertyDefinitionComment 'Nature of the sample from which the mutation has been identified: cell-line, surgery (surgical or autopsy specimen, including fresh samples and archival pathology specimen), biopsy, xenograft, body fluid (blood, saliva, urine...)."@en;

d2rq:column 'somatic15.Sample_source';
d2rq:condition "somatic15.Sample_source != ('NA')";
d2rq:condition "somatic15.Sample_source != ('')";


d2rq:condition "somatic15.Sample_source != ('-')";

map:sample_Tumor_origin a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Tumor_origin;
d2rq:propertyDefinitionLabel "sample Tumor origin";
d2rq:propertyDefinitionComment "Origin of the tumor sample. Terms occurring in this column are: primary, secondary (second primary tumor in the same patient), metastasis (with the localisation of the metastasis in brackets), recurrent (tumor recurrence)." @en;
d2rq:column "somatic15.Tumor_origin";
d2rq:condition "somatic15.Tumor_origin != ('NA')";
d2rq:condition "somatic15.Tumor_origin != ('')";
d2rq:condition "somatic15.Tumor_origin != ('-')";

map:sample_Topography a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property NCIT:Topography;
d2rq:propertyDefinitionLabel "sample Topography";
d2rq:propertyDefinitionComment "Site of the tumor defined by organ or group of organs, according to the ICD-O nomenclature." @en;
d2rq:column "somatic15.Topography";
d2rq:condition "somatic15.Topography != ('NA')";
d2rq:condition "somatic15.Topography != ('')";
d2rq:condition "somatic15.Topography != ('-')";

map:sample_Top_code a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Topo_code;
d2rq:propertyDefinitionLabel "sample Topology code";
d2rq:propertyDefinitionComment "ICD-O code for topography." @en;
d2rq:column "somatic15.Topo_code";
d2rq:condition "somatic15.Topo_code != ('NA')";
d2rq:condition "somatic15.Topo_code != ('')";
d2rq:condition "somatic15.Topo_code != ('-')";

map:sample_Sub_topography a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Sub_topography;
d2rq:propertyDefinitionLabel "sample Sub topography";
d2rq:propertyDefinitionComment "Precise identification of anatomic site, organ or tissue. The description given in the publication is translated to ICD-O nomenclature." @en;
d2rq:column "somatic15.Sub_topography";
d2rq:condition "somatic15.Sub_topography != ('NA')";
d2rq:condition "somatic15.Sub_topography != ('')";
d2rq:condition "somatic15.Sub_topography != ('-')";

map:sample_Morphology a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property NCIT:Neoplasm_by_Morphology;
d2rq:propertyDefinitionLabel "sample Morphology";
d2rq:propertyDefinitionComment "Tumor type, including morphology and/or histologic type. The terminology used is based on ICD-O (2nd and 3rd editions) and SNOMED classifications. Terms have been added, such as normal-tissue or na." @en;
d2rq:column "somatic15.Morphology";
d2rq:condition "somatic15.Morphology != ('NA')";
d2rq:condition "somatic15.Morphology != ('')";
d2rq:condition "somatic15.Morphology != ('-')";

map:sample_Morpho_code a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Morpho_code;
d2rq:propertyDefinitionLabel "sample Morphology code";
d2rq:propertyDefinitionComment "ICD-O or SNOMED codes for morphology." @en;
d2rq:column "somatic15.Morpho_code";
d2rq:condition "somatic15.Morpho_code != ('NA')";
d2rq:condition "somatic15.Morpho_code != ('')";
d2rq:condition "somatic15.Morpho_code != ('-')";

map:sample_Grade a d2rq:PropertyBridge;
d2rq:belongsToClassMap map:sample;
d2rq:property logvd:Grade;
d2rq:propertyDefinitionLabel "sample tumor grade";
d2rq:propertyDefinitionComment "Information on tumor grade, as given in the cited publication." @en;
d2rq:column "somatic15.Grade";
d2rq:condition "somatic15.Grade != ('NA')";
d2rq:condition "somatic15.Grade != ('')";
d2rq:condition "somatic15.Grade != ('-')";
```
map:sample_Stage a d2rq:PropertyBridge;
    d2rq:belongsToClassMap map:sample;
    d2rq:property NCIT:Stage;
    d2rq:propertyDefinitionLabel "sample tumor stage";
    d2rq:propertyDefinitionComment "Information on tumor stage, as given in the cited publication.";
    d2rq:column "somatic15.Stage";
    d2rq:condition "somatic15.Stage != ('NA')";
    d2rq:condition "somatic15.Stage != ('')";
    d2rq:condition "somatic15.Stage != ('-')";

d2rq:condition "somatic15.Grade != ('-')";
```
```
\texttt{d2rq:propertyDefinitionComment} "The typology of the IARC TP53 Somatic Mutation database: Locus Specific DataBase";\texttt{d2rq:column} "iarc.type"; \\
\texttt{map:DB_source_target_gene a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:DB_source;}
\texttt{d2rq:property logvd:hastarget_gene;}
\texttt{d2rq:propertyDefinitionLabel} "IARC database target gene";
\texttt{d2rq:propertyDefinitionComment} "The gene whose information are collected at the IARC TP53 Somatic Mutation database";
\texttt{d2rq:pattern} "gene/TP53"; \\
\texttt{map:DB_source_URL a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:DB_source;}
\texttt{d2rq:property logvd:IARC_URL;}
\texttt{d2rq:propertyDefinitionLabel} "IARC web address";
\texttt{d2rq:propertyDefinitionComment} "Web address of the IARC database";
\texttt{d2rq:uriPattern} "http://www-p53.iarc.fr/"; \\
\texttt{map:DB_source_view_coding-seq a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:DB_source;}
\texttt{d2rq:property logvd:IARC_TP53_coding-seq;}
\texttt{d2rq:propertyDefinitionLabel} "IARC coding sequence";
\texttt{d2rq:propertyDefinitionComment} "View coding sequence with residue numbers, amino-acids, highlighted CpG sites and exon-intron boundaries.";
\texttt{d2rq:uriPattern} "http://www-p53.iarc.fr/p53Sequence.html"; \\
\texttt{map:DB_source_view_refseq a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:DB_source;}
\texttt{d2rq:property logvd:IARC_TP53_refseq;}
\texttt{d2rq:propertyDefinitionLabel} "IARC reference sequence";
\texttt{d2rq:propertyDefinitionComment} "View NC_000017.9 gene sequence (new reference sequence used from R13 version) with exon-intron boundaries and highlighted polymorphic sites.";
\texttt{map:DB_source_somatic_mutation a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:DB_source;}
\texttt{d2rq:property logvd:TP53_somatic_mutation;}
\texttt{d2rq:propertyDefinitionLabel} "TP53 somatic mutations";
\texttt{d2rq:propertyDefinitionComment} "IARC TP53 somatic mutations reported in the database.";
\texttt{d2rq:uriPattern} "somatic_mutation/@@somatic15.Mutation_ID@@"; \\

# IARC-TP53 the database

\texttt{map:gene a d2rq:ClassMap;}
\texttt{d2rq:belongsToClassMap map:database;}
\texttt{d2rq:pattern} "gene/TP53";
\texttt{d2rq:class logvd:gene;}
\texttt{d2rq:classDefinitionLabel} "Genes";
\texttt{d2rq:classDefinitionComment} "Genes";

\texttt{map:gene__label a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:gene;}
\texttt{d2rq:property rdfs:label;}
\texttt{d2rq:pattern} "gene/TP53";

\texttt{map:gene_ENSEMBL_ID a d2rq:PropertyBridge;}
\texttt{d2rq:belongsToClassMap map:gene;}
\texttt{d2rq:property rdfs:seeAlso;}
\texttt{d2rq:propertyDefinitionLabel} "TP53 ENSEMBL gene view";
\texttt{d2rq:propertyDefinitionComment} "TP53 gene view at the ENSEMBL database.";
\texttt{d2rq:uriPattern} "http://www.ensembl.org/Homo_sapiens/geneview?db=&gene=ENSG00000141510";