

For every dataset to be displayed...

group /[dataset name]  
attribute (name='name of the experiment')

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/features	<i>table of features (gene, transcript, etc) ids (in our case ensembl ids),</i>  1: <b>feature_id</b> (variable length string) 2: <b>group_id</b> (variable length string) 3: <b>chrom</b> (2 character length string) 4: <b>location</b> (floating point) 5: <b>name</b> (variable length string) 6: <b>description</b> (variable length string)  <i>* if genes, group_id = feature_id, if pQTL, the group_id will be gene_id while the feature_id will be protein id</i>  <i>* location is in Mb</i>
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/markers	<i>table of markers</i>  1: <b>marker_id</b> (variable length string) 2: <b>chrom</b> (2 character length string) 3: <b>location</b> (floating point)  <i>* location is in Mb</i>
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/lod	/lod <i>table of lod scores, features (rows) x markers (columns)</i>
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# (COEF, EFFECT PLOT)	
/coef	<i>table of coef scores, features x strains x markers</i>
/strains	<i>table of strains (e.g. cc founders)</i>  1: <b>strain_id</b> (variable length string) 2: <b>name</b> (variable length string) 3: <b>description</b> (variable length string)

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# (FACT VIEWER)	
/samples	<i>table of samples</i>  1: <b>sample_id</b> (variable length string) 2: <b>name</b> (variable length string) 3: <b>description</b> (variable length string)

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/phenotypes	<i>table of phenotypes samples (rows) x factors (columns)</i>
/factors	<i>table of factors (e.g. sex, diet, tissue)</i>  1: <b>factor_id</b> (variable length string) 2: <b>name</b> (variable length string) 3: <b>description</b> (variable length string)

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/genotypes	<i>table of genotypes markers (rows) x samples (columns)</i>
/genotypes	

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/expression	<i>table of expression values features (rows) x samples (columns)</i>
/expression	

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