For every dataset to be displayed...

group /[dataset name]

*attribute (name='name of the experiment')*

/features

*table of features (gene, transcript, etc) ids (in our case ensembl ids),*

1: **feature\_id** (variable length string)

2: **group\_id** (variable length string)

3: **chrom** (2 character length string)

4: **location** (floating point)

5: **name** (variable length string)

6: **description** (variable length string)

*\* if genes, group\_id = feature\_id,*

*if pQTL, the group\_id will be gene\_id while the feature\_id will be protein id*

*\* location is in Mb*

/markers

*table of markers*

1: **marker\_id** (variable length string)

2: **chrom** (2 character length string)

3: **location** (floating point)

*\* location is in Mb*

/lod

/lod

*table of lod scores, features (rows) x markers (columns)*

# (COEF, EFFECT PLOT)

/coef

/strains

*table of strains (e.g. cc founders)*

1: **strain\_id** (variable length string)

2: **name** (variable length string)

3: **description** (variable length string)

/coef

*table of coef scores, features x strains x markers*

# (FACT VIEWER)

/samples

*table of samples*

1: **sample\_id** (variable length string)

2: **name** (variable length string)

3: **description** (variable length string)

/phenotypes

/factors

*table of factors (e.g. sex, diet, tissue)*

1: **factor\_id** (variable length string)

2: **name** (variable length string)

3: **description** (variable length string)

/phenotypes

*table of phenotypes samples (rows) x factors (columns)*

/genotypes

/genotypes

*table of genotypes markers (rows) x samples (columns)*

/expression

/expression

*table of expression values features (rows) x samples (columns)*