



**Fig.1** Extending analysis of next generation sequencing studies to large numbers of individuals or conditions in the context of a MOD. MOD genome browsers are able to display many tracks of data from e.g. transcription factor, histone mark and ChIP studies. However the number of tracks available is growing rapidly and often is too large to browse effectively. There is a need to extract data from regions of interest, for specified experiments, so that e.g. possible correlations can be examined.