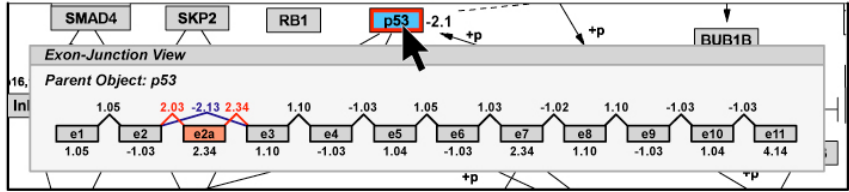
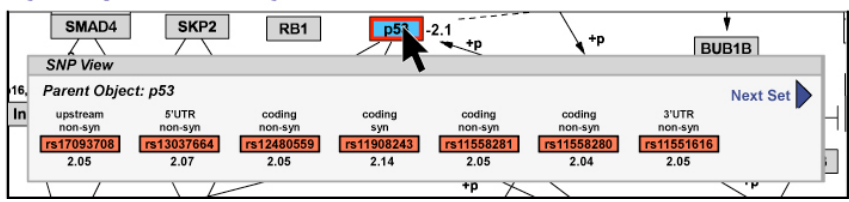


Exon and splice junction analysis



Polymorphism analysis



Pathway ColorSets

Gene/Protein Objects

- Center Box Criterion**
 - up-regulated expression
 - down-regulated expression
 - not changed
 - not present
- Rim Criterion**
 - Differential splicing
 - No differential splicing
 - Not applicable

Child Objects

- Center Box Criterion**
 - up-regulated expression
 - down-regulated expression
 - not changed
 - not present

- Rim Criterion**
 - Rare variant SNPs present
 - No rare variants detected
 - Not applicable

Figure 12. Custom Sub-Network Views. Representation of how gene information can be accessed at multiple levels of abstraction for data collected from both splicing and polymorphism microarrays. The sub-network view provides both built-in and custom coloring schemes for accessing expression, splicing, or polymorphism data from a pathway containing gene objects. In the top panel, mock data from a splicing microarray is analyzed and visualized using the built-in Dataset Manager splicing analysis method. Here, a color is assigned to the center of each gene object on a GenMAPP-CS pathway indicating the direction of transcriptional regulation (red for up, blue for down), while the rim color of the gene indicates detection of differential splicing (red for differential splicing above a given threshold or gray for no detected change). In the middle panel, selecting the Exon and Junction view and clicking on a single gene creates a new window displaying microarray data summarized at the level of exons and splice junctions (colored lines and folds) for that same gene. In the bottom panel, a similar example is shown for a theoretical polymorphism array experiment, comparing two groups. Here specific polymorphisms with differential changes between two biological groups are displayed with Ensembl gene location annotations and dbSNP coding-level annotations (synonymous or non-synonymous).