Experimental type	CRISPR editing and PCR-based expression quantification (CRISPR-engineered deletion to evaluate the effects of an SV on enhancer linkage)	Gene knockdown followed expression quantification (case 1)	Gene knockdown followed expression quantification (case 2)	Introducing SNVs followed by luciferase assays to measure gene expression
Provides evidence for	Modifying an extended gene neighborhood (without directly changing the coding region) can result in changes in gene expression through the introduction of enhancer-promoter interactions (in this case, elevating the expression of ERBB4 in T47D cells)	The regulatory network that we construct recapitulates intuitive biology: Genes identified as targets of MYC exhibit reduced expression upon MYC knockdown. MYC binds to the promoter of target genes to upregulate expression.	SUB1 knockdown in HepG2 cells result in significandly diminished expression of its target genes (oncogenes). SUB1 stabilizes RNA transcripts by binding to 3UTRs of targets, thereby increasing transcript lifetime in the cell.	a) We correctly prioritize SNVs (using recurrence analysis and scoring motif disruptions) that affect gene expression through a mechanism by which enhancers are changed; b) our predicted enhancers are consistent with these expression changes
Associated exhibit(s)	Figure 2 F, E	Figure 3B	Figure 3D; Table S 4-2	Figure 6C; Figure S 6-3
Associcated supp sect.	(not in original supp -- included in new version?)	Supp. sect 6.3	Supp sect. 4.3	Supp. sect. 6.2
Primary literature	---	References 4 & 5	[none in current build]	--
Associated data file IDs	---	EC-004-DBP.README.txt EC-004-DBP.MYC-KD_geneFPKM_target.txt EC-004-DBP.MYC-KD_geneFPKM_knockdown.txt	EC-002-EXT.merge.post.extendedGene.HepG2.txt EC-003-CRE.JEME_of_CASPER_HepG2.bed EC-003-NET.probNet_RBP.txt	EC-004-CRE.luciferase_raw.csv EC-004-CRE.luciferase_normalized.csv