Genomic Visualization

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Discussion with PIs

PI	Existing Visualization	Study	Goal
Daniel Kim (Kim Lab)	RasVis	- noncoding RNA in stem cells and cancer	- Trying to understand different pathways between proteins and RNA sequences, and how these contribute to cancer
Angela Brooks (Brooks Lab)		- somatic mutations that cause changes to the transcriptome	- Develop computational techniques to analyze genome and transcriptome sequencing data

Evip data (From Brook's Lab)

id	RNF43_WT_4	RNF43_WT_3	RNF43_WT_2	RNF43_WT_1	GFP_4	GFP_3	GFP_2	GFP_1	RNF43_659fs_4	RNF43_659fs_3	RNF43_659fs_2	RNF43_659fs_1	RNF43_117fs_4	RNF43_117fs_3	RNF43_117fs_2	RNF43_117fs_1
ENSG00000198242.13	0.3024	0.1094	-0.1280	0.9370	-1.0952	-0.1731	-0.4922	-0.1250	-0.0241	0.6749	0.5268	0.5824	1.8746	-2.2823	-1.4579	0.7703
ENSG00000134108.12	-0.6278	0.0309	-0.7000	0.2914	1.5018	1.3131	1.5731	1.1274	-1.3516	-0.8480	-1.4773	-0.7508	0.7395	-0.3860	0.1154	-0.5510
ENSG00000276644.4	0.1284	0.1917	-0.7127	-0.3272	0.8217	0.6441	0.6924	0.6964	-0.1575	0.6385	-0.2218	0.0816	-2.9864	-0.6416	-0.3711	1.5234
ENSG00000182141.9	0.6693	0.8966	0.7770	0.0328	-0.0337	1.1870	1.6086	-0.2424	-1.6091	0.1856	-0.6233	0.8666	-1.9700	-0.9853	-0.0768	-0.6828
ENSG00000167578.17	0.0239	0.0782	-0.4171	-0.3919	0.7666	1.1346	0.1677	1.2442	0.3945	-0.0669	0.2587	-2.8328	1.3020	-0.1215	-0.5883	-0.9522
ENSG00000236830.6	0.1872	-1.2277	-1.5023	-0.7278	2.2592	-0.8537	0.3215	0.4669	0.3723	-0.0548	0.2122	-1.7337	0.4447	0.5792	0.6017	0.6551
ENSG00000197557.6	-0.5834	0.2394	-0.6555	0.0845	0.7152	0.9320	0.6840	0.9811	-1.6818	-1.1047	-1.7513	-0.9075	-0.1384	1.1062	1.1052	0.9752
ENSG00000278616.1	-0.5913	-0.4719	-0.9343	-1.0241	1.6230	0.9415	1.1917	0.6486	0.7307	-0.1839	-0.3941	-0.0359	1.7004	-1.3294	-0.8607	-1.0102
ENSG00000146083.11	-1.1762	-0.3973	-0.5637	-1.2513	0.5952	0.4836	-0.8358	0.9851	-0.3585	-0.0222	0.1311	0.0518	2.9726	-0.4025	0.1661	-0.3780
ENSG00000070087.13	0.5583	0.4926	0.6907	0.9418	0.7055	0.6186	0.5121	0.7888	-0.1122	-0.3974	-0.0269	-0.4356	-3.1614	-0.9351	-0.2903	0.0504
ENSG00000204946.9	0.4682	0.1514	-0.0235	0.3067	-1.3004	0.0918	-1.5685	0.5789	-0.9662	-1.3218	-0.3165	-0.2194	2.2107	-0.2060	1.3524	0.7621
ENSG00000153561.12	-0.8895	-0.1961	0.1207	-1.3216	0.7698	0.3322	0.9056	-0.1234	0.4035	0.7861	0.0699	0.2696	-2.8987	1.0116	0.7660	-0.0056
ENSG00000179262.9	0.2951	0.0560	-0.5053	-1.3211	-0.2743	-1.4607	-0.0573	-0.9790	-0.0754	-0.4887	-0.0454	0.3629	2.8866	0.5242	0.8305	0.2520
ENSG00000104833.10	0.3988	-0.9136	0.3576	-0.9307	0.3046	-1.0677	-0.0185	0.3693	-0.4647	1.4283	-0.5650	-0.8339	2.8339	-0.3161	-0.4801	-0.1024

Brooks Lab Visualization

eVIP Z-Score Visualization
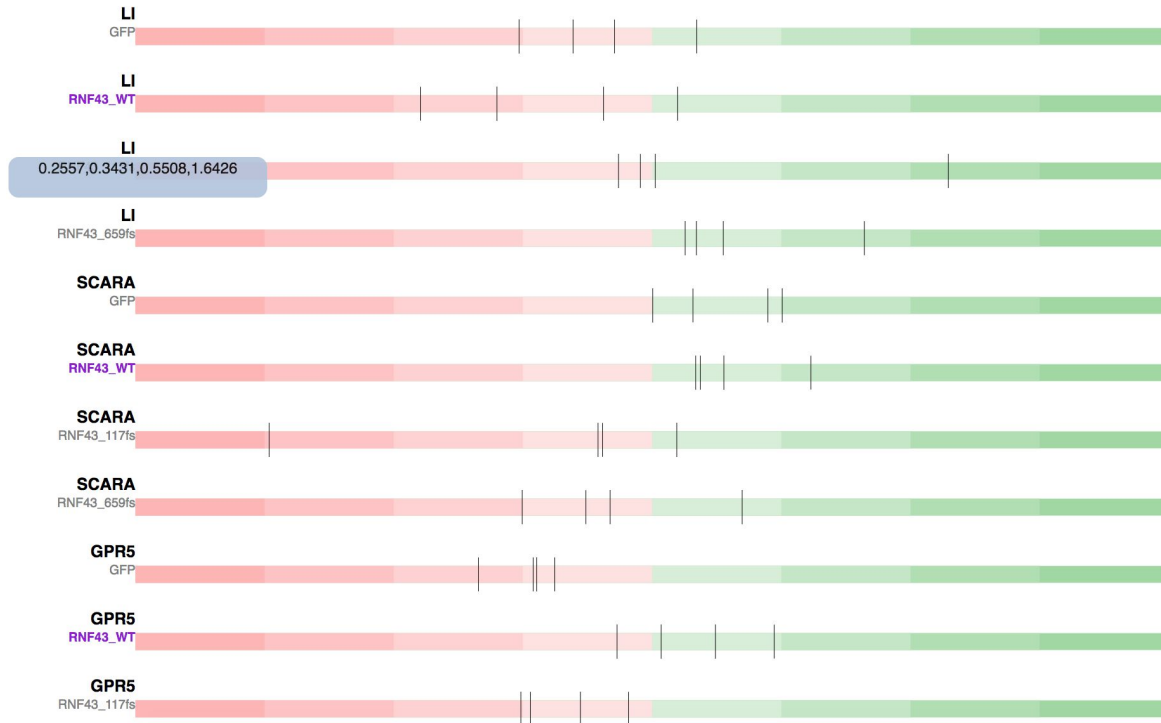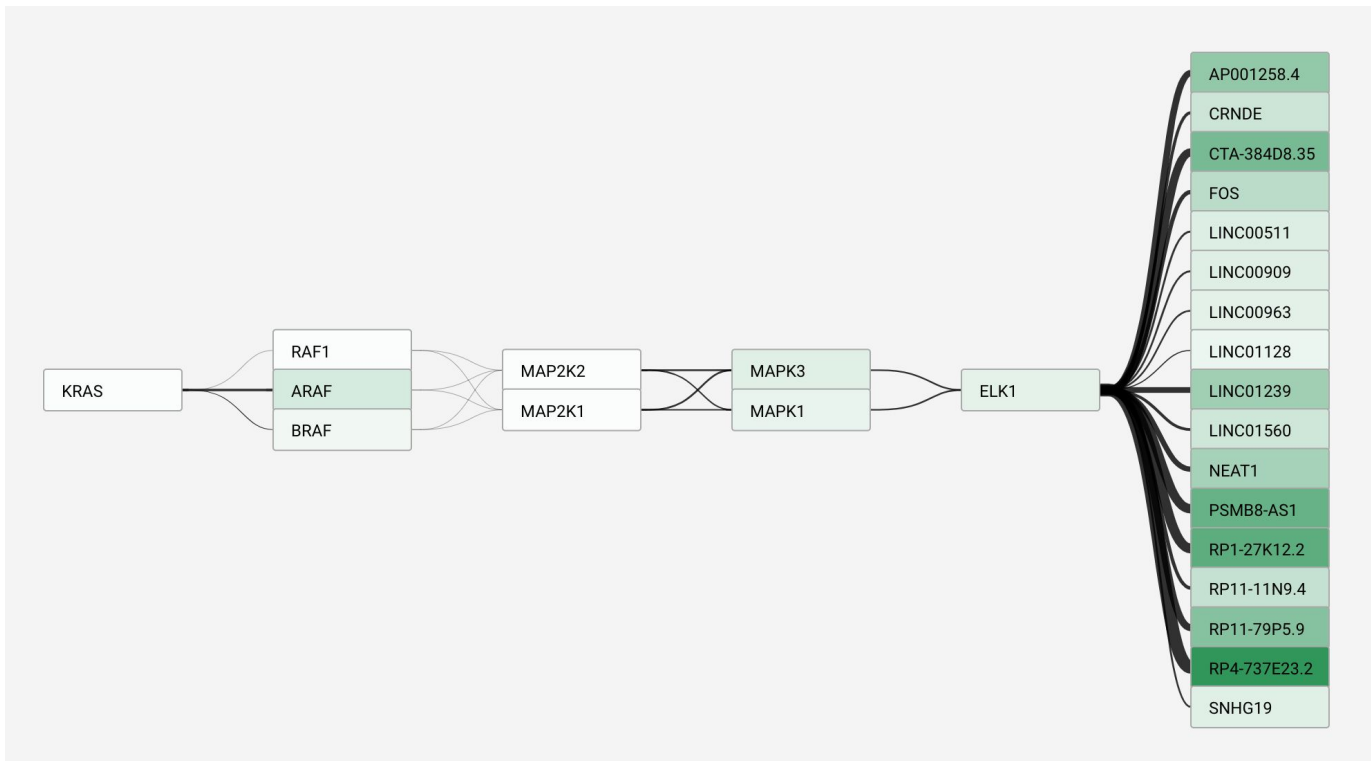
Design Choices

Visualization

- Color and shading to indicate number line scale
- Z-score values on hover over title for all 4 replicates
- Checkbox system for removing and re-adding a gene
- Highlight wild type gene

Pre-processing Data

- Parser uses provided txt files to construct a suitable json for D3
- Gene name used for clarity instead of ensemble ID

RasVis

In Progress

- Pseudo-universal parser for automatic generation of network visualization for any pathway data
- Replication of Adobe Illustrator changes (color outlines, dynamic readjustment) in D3 visualization
- Interactivity for real-time modifications

Questions?

Thank you!