

## Indel analysis results

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# Indels summary

Subj-Z (Z):750238

Snyderome (S):742362

NA12878 (NA):834149

	promoter	Enh	DHS	TFP	MotifG	motifB	Intron	Total	Rare
Z	9276	56870	69636	82385	2682	26820	307048	750238	407690
S	8328	56511	68530	80828	2424	26443	306645	742362	402194
NA	10056	60568	73694	88148	3125	27314	341219	834149	481632

Rare indel:  $MAF \leq 0.5\%$  or Not occurred in 1000genome indel set.

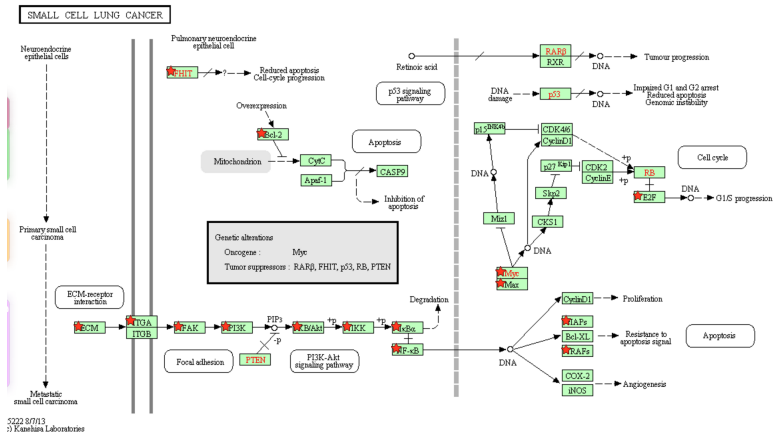
# Deleterious indel filtering and functional annotation

- ▶ Has motif gain/break event, and
- ▶ Occurs in one of the following regions: HOT, Sensitive, conserv region, and
- ▶ Has a HUB target gene, and be in one of categories: Cancer related, distal regulatory target, promoter/intron/UTR target.

1037 indels are identified, which are associated with 1254 genes (multi-to-multi relation). Function annotation and enrichment analysis:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">cytoskeletal protein binding</a>	RT		69	5.7	6.4E-8	7.1E-5
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">cytoskeleton organization</a>	RT		63	5.2	6.9E-8	2.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of cell death</a>	RT		99	8.2	7.3E-8	1.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of programmed cell death</a>	RT		98	8.1	1.2E-7	1.4E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">regulation of apoptosis</a>	RT		96	8.0	2.6E-7	2.3E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">actin cytoskeleton organization</a>	RT		39	3.2	4.0E-7	2.8E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">actin filament-based process</a>	RT		40	3.3	7.7E-7	4.5E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">anchoring junction</a>	RT		31	2.6	9.5E-7	5.3E-4
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">identical protein binding</a>	RT		78	6.5	9.9E-7	5.5E-4
<input type="checkbox"/>	GOTERM_MF_FAT	<a href="#">actin binding</a>	RT		48	4.0	1.1E-6	4.2E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">basolateral plasma membrane</a>	RT		34	2.8	1.4E-6	4.0E-4
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">adherens junction</a>	RT		28	2.3	3.4E-6	6.3E-4
<input checked="" type="checkbox"/>	KEGG_PATHWAY	<a href="#">Small cell lung cancer</a>	RT		21	1.7	6.2E-6	1.1E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cytosol</a>	RT		129	10.7	7.4E-6	1.0E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">actin cytoskeleton</a>	RT		39	3.2	7.8E-6	8.7E-4
<input type="checkbox"/>	GOTERM_BP_FAT	<a href="#">macromolecular complex subunit organization</a>	RT		82	6.8	8.3E-6	4.2E-3
<input type="checkbox"/>	GOTERM_CC_FAT	<a href="#">cellular homeostasis</a>	RT		73	6.1	1.0E-5	6.6E-4

# Target genes enrich in Small Cell Lung Cancer Pathway



**Star:** affected genes (ECM, ITGA, FAK, PI3K, FHIT, AKT, IKK, NF- $\kappa$ B, Myc, Max, RAFs, cIAPs, E2F).