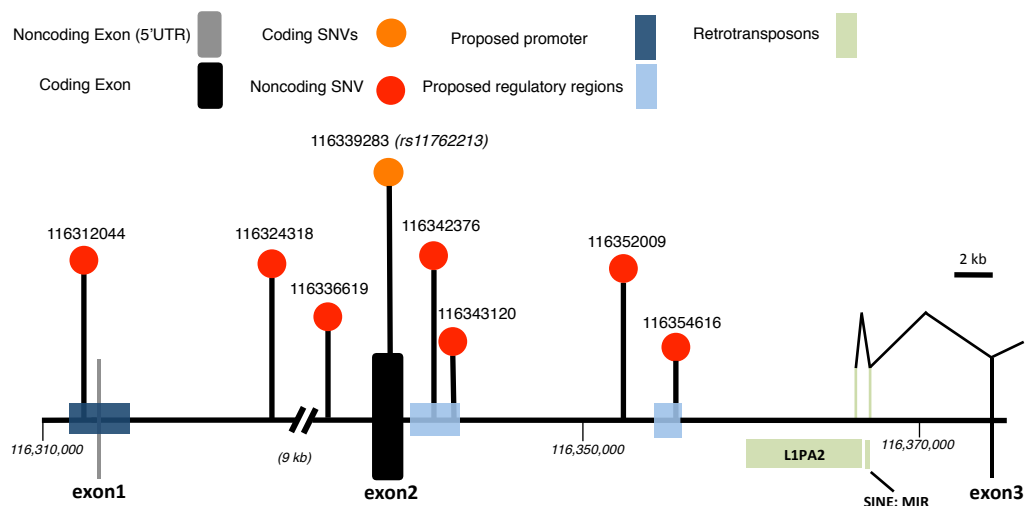
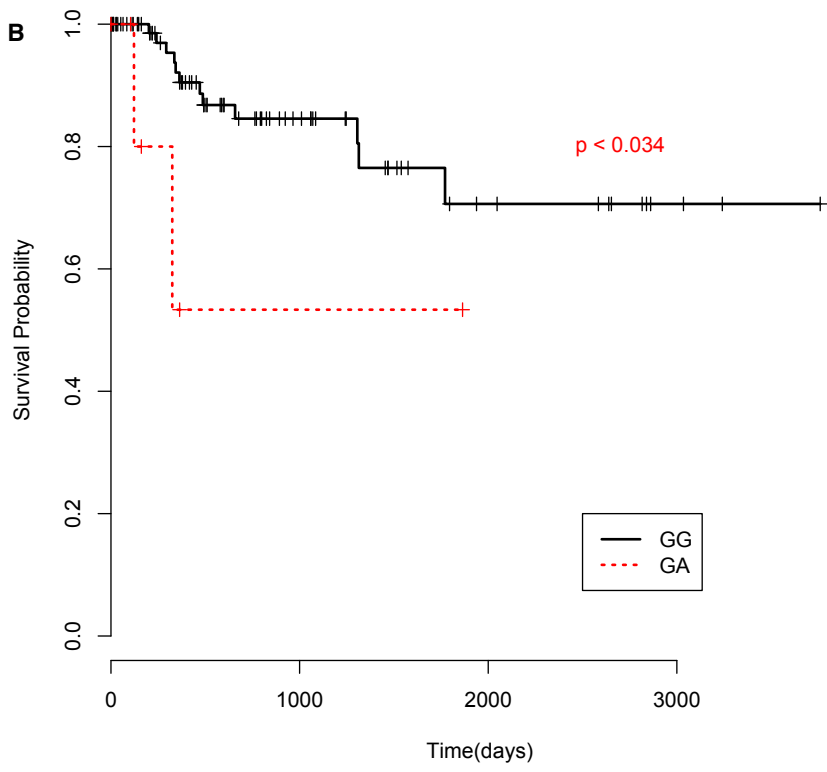


- Updated Fig1, 2 and 4, re-plot most of figure 3
- New coloring scheme
- Three new supplement figures
  - 35 trees
  - SV schematic
  - NEAT1 study schematic

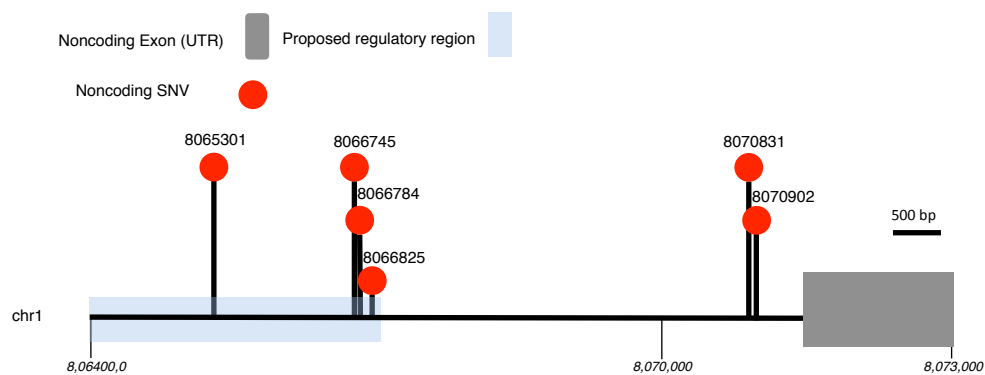
# A MET



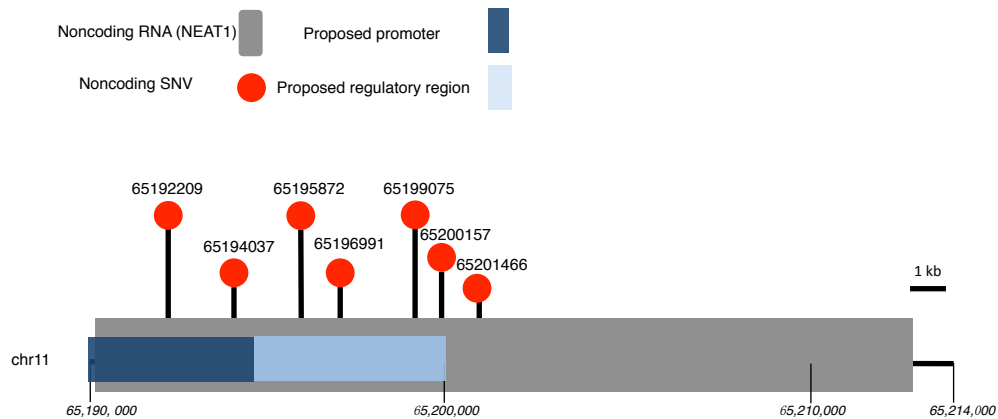
# B



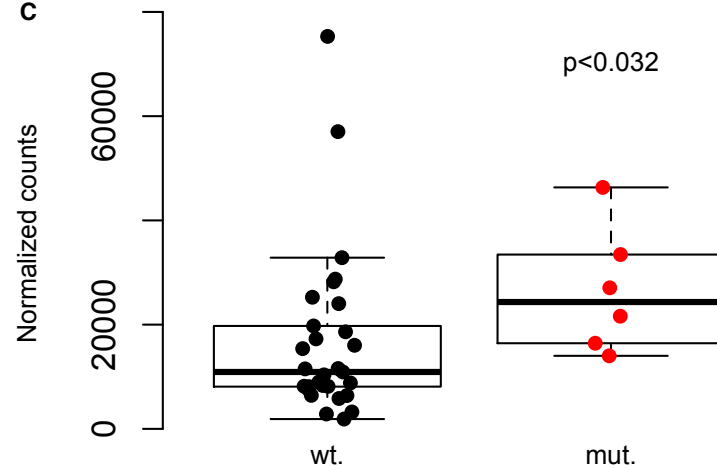
### A ERRFI1



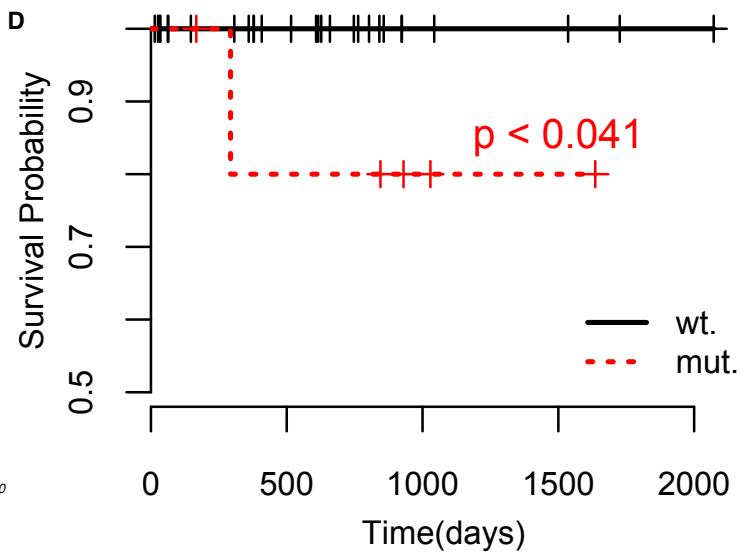
### B NEAT1

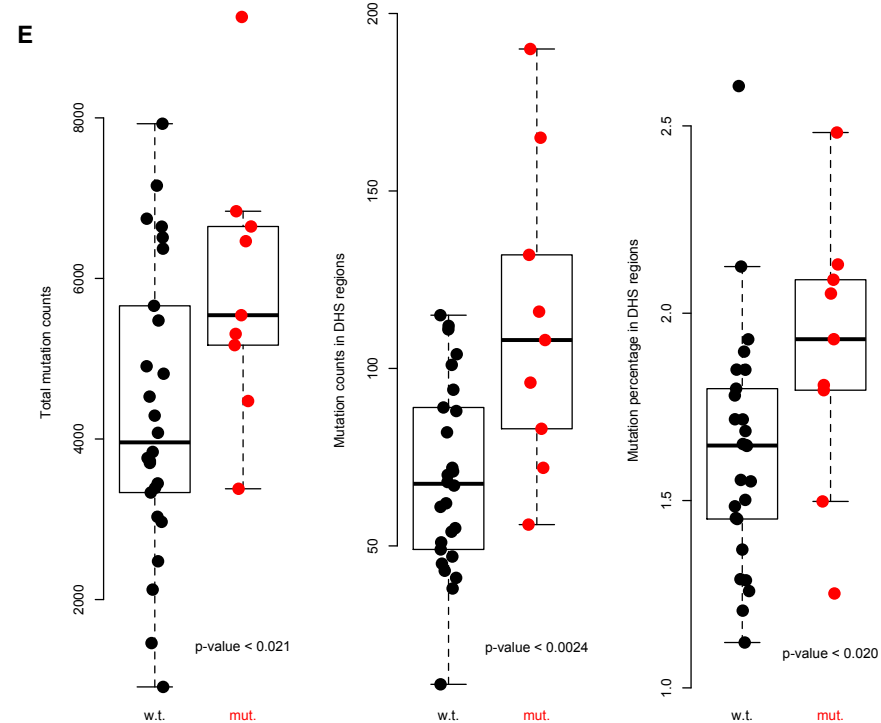
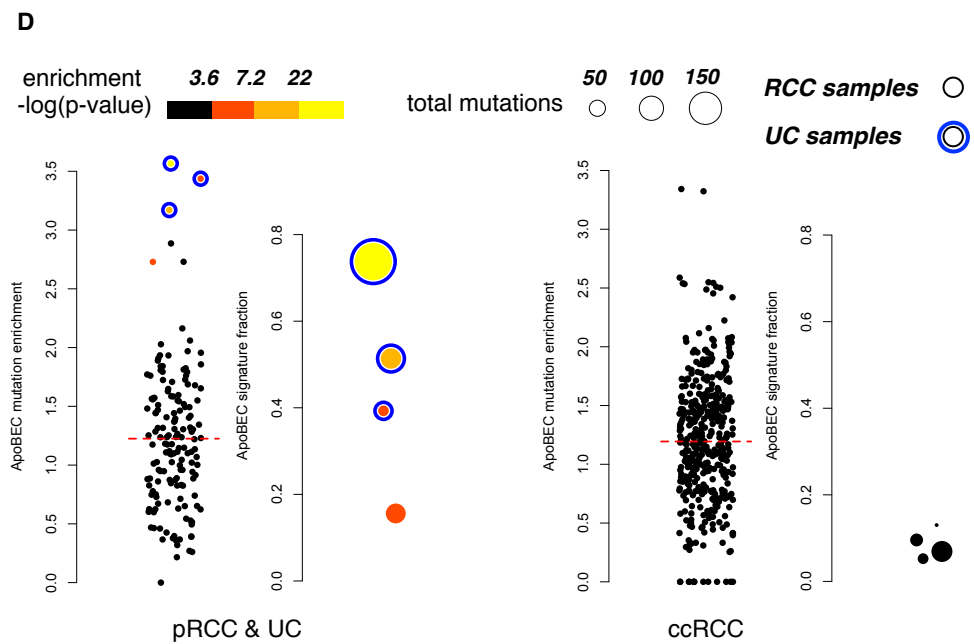
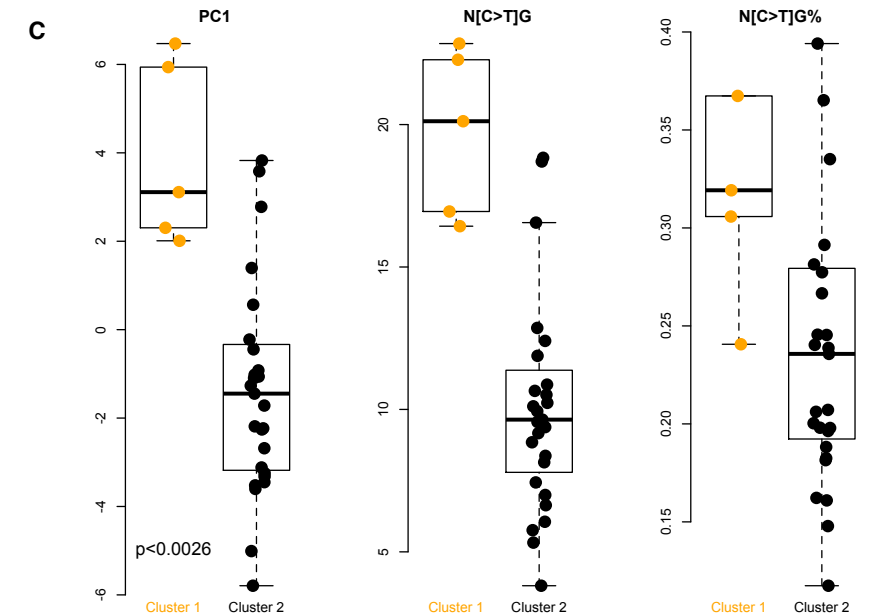
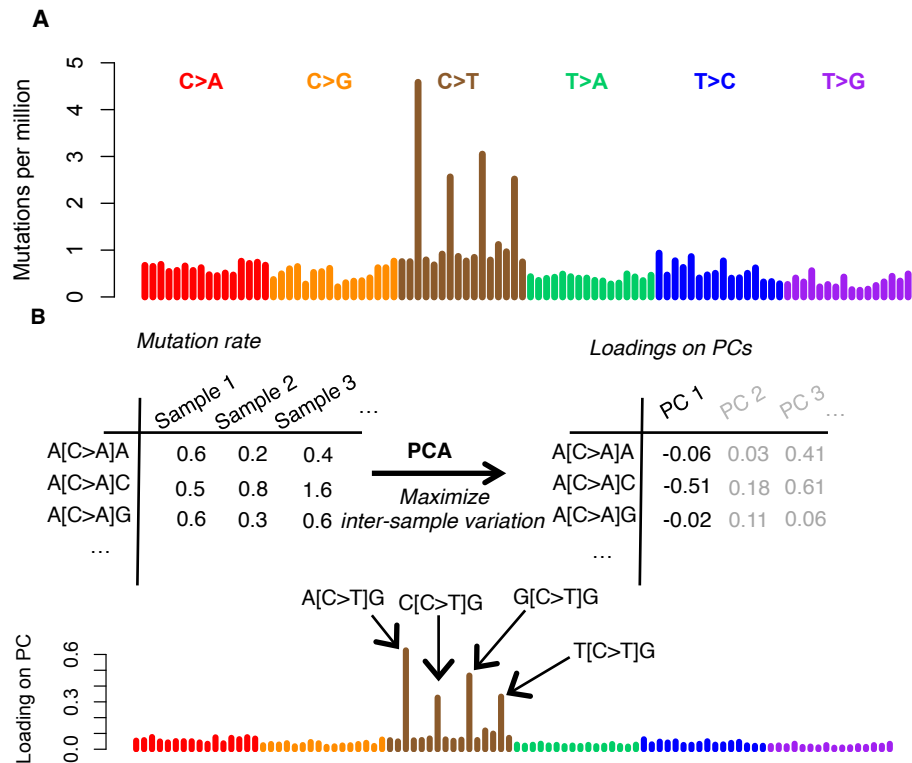


### C



### D







		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35		
Coding	Histological type	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Green	Green	Green	Green	Green	Green	Green	Green	Green	
	COCA	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	NA	Orange	Orange	Orange	Orange	Orange	Teal	Teal	Teal	Teal	NA	NA	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	
	MET copy number gain	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey
	MET somatic mut.												Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	
	MET splicing event	Grey	Grey														NA											NA	NA			Grey						
	MET germline mut.																						Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey
	BAP1/PBRM1/SETD2 somatic mut.																																					
Noncoding	CDKN2A copy number loss			Grey																																		
	MET promoter mut.			Grey																																		
	MET 1-2 intronic mut.					Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey	Grey
	NEAT1 somatic mut.																																					
Mut. Processes	ERRF1 promoter mut.																																					
	Whole genome mut. rate	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue	
	Mut. rate DHS	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Orange
	Evolution tree topology	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green	

**Affected**  **Not affected**

**Histological type**

Type 1  Type 2

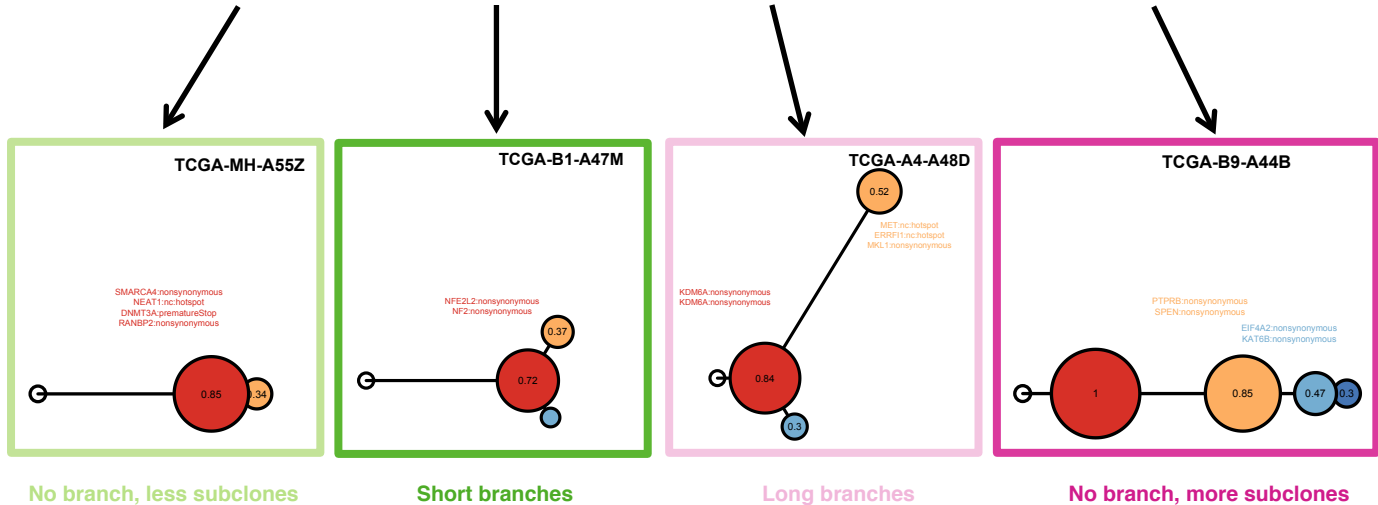
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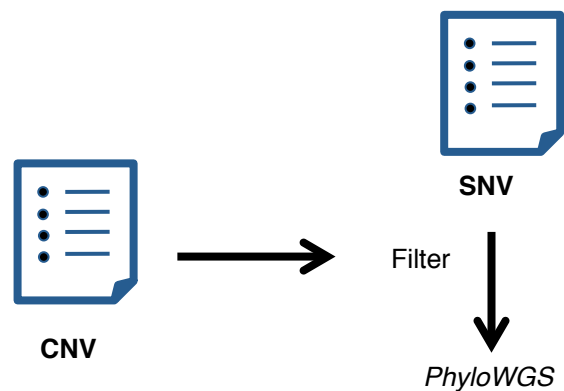
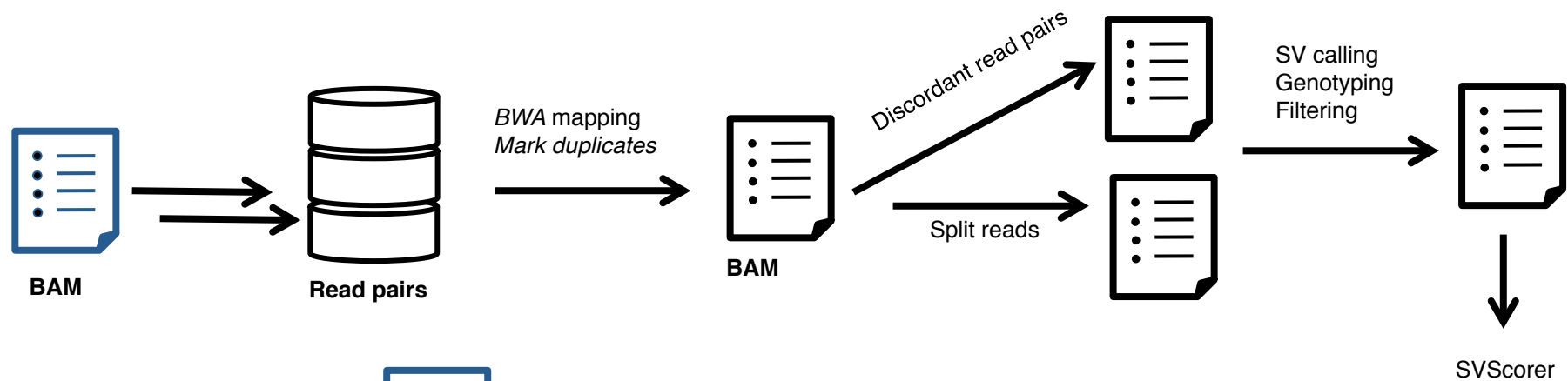
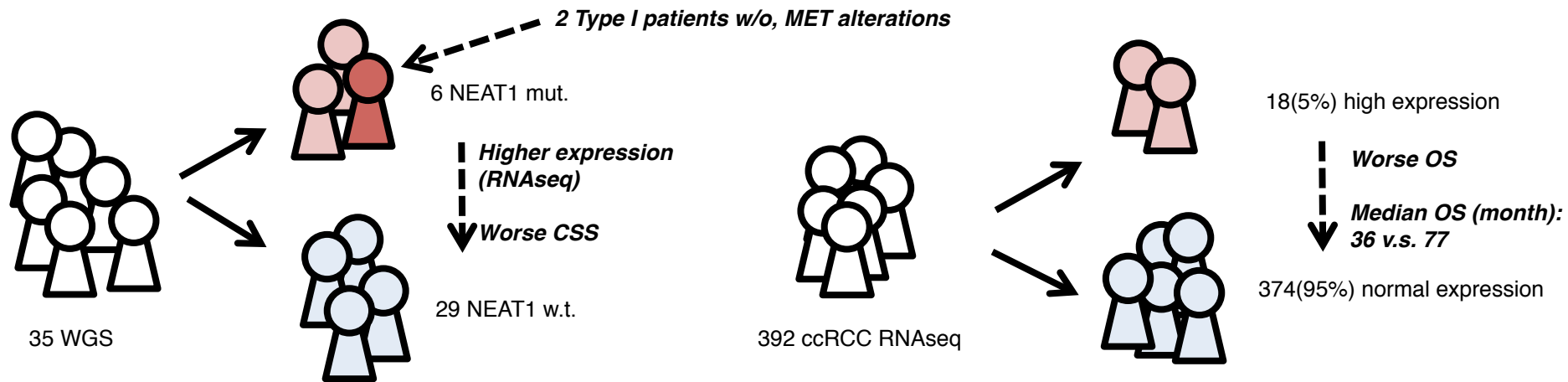
**COCA**

C1  C2a  C2b

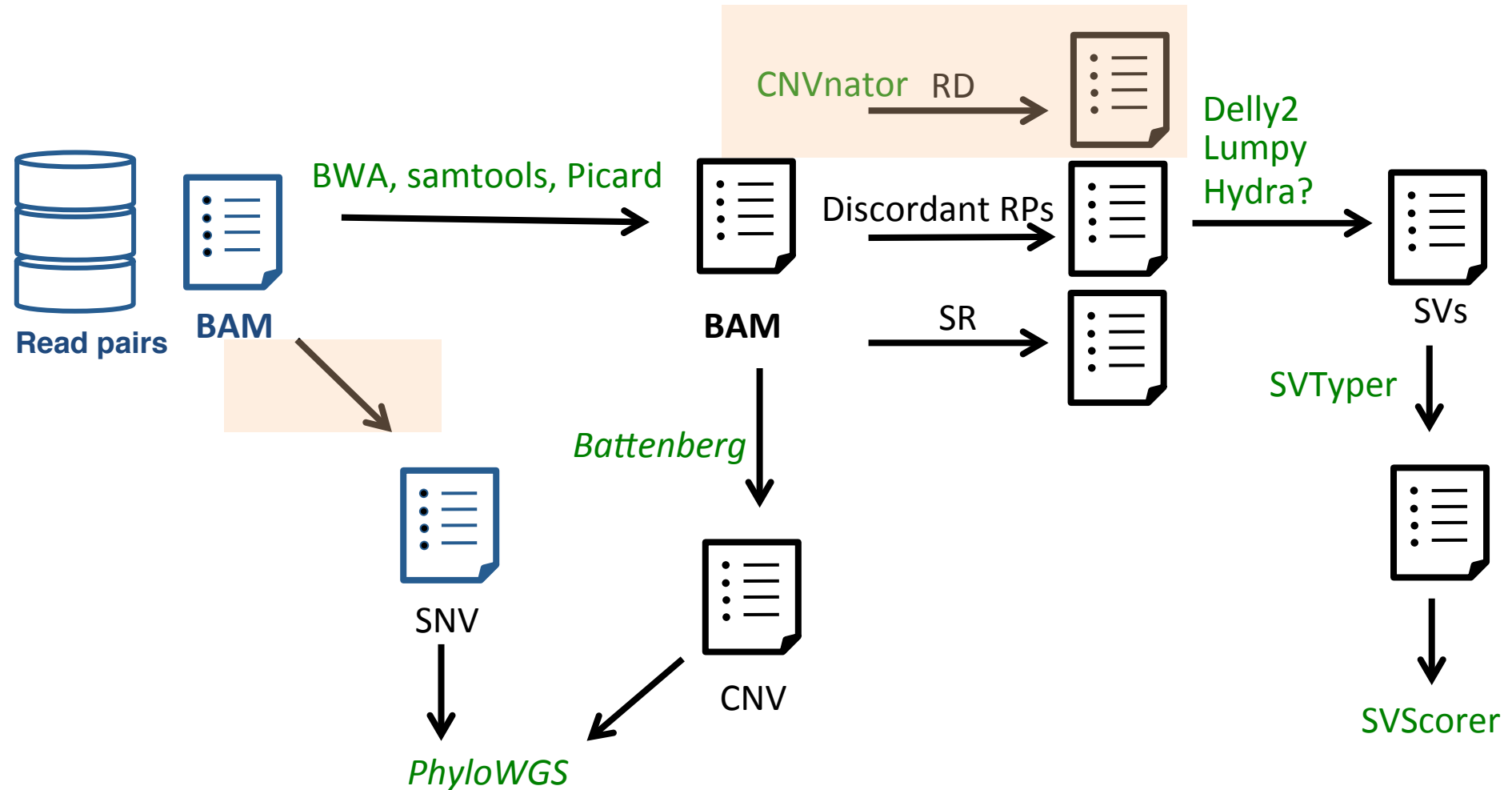
**Mutation rate/percentage**

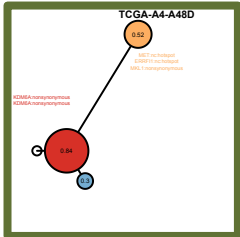
High  Medium  Low





# 1. SV pipeline



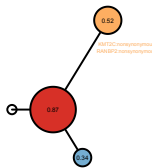


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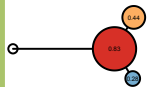
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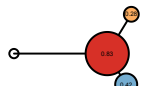
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TCGA-AL-3468



TCGA-B1-A47O



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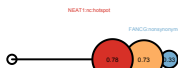
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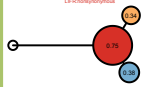
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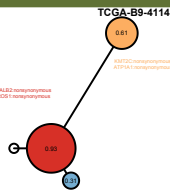
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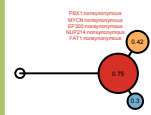
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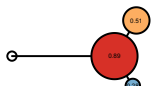
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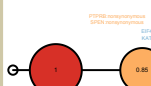
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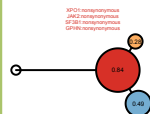
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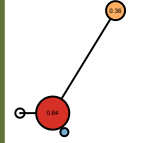
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TCGA-GL-A59R



TCGA-HE-A5NF



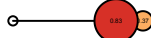
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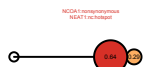
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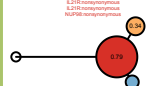
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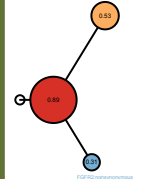
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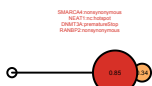
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TCGA-MH-A560



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TCGA-MH-A562

