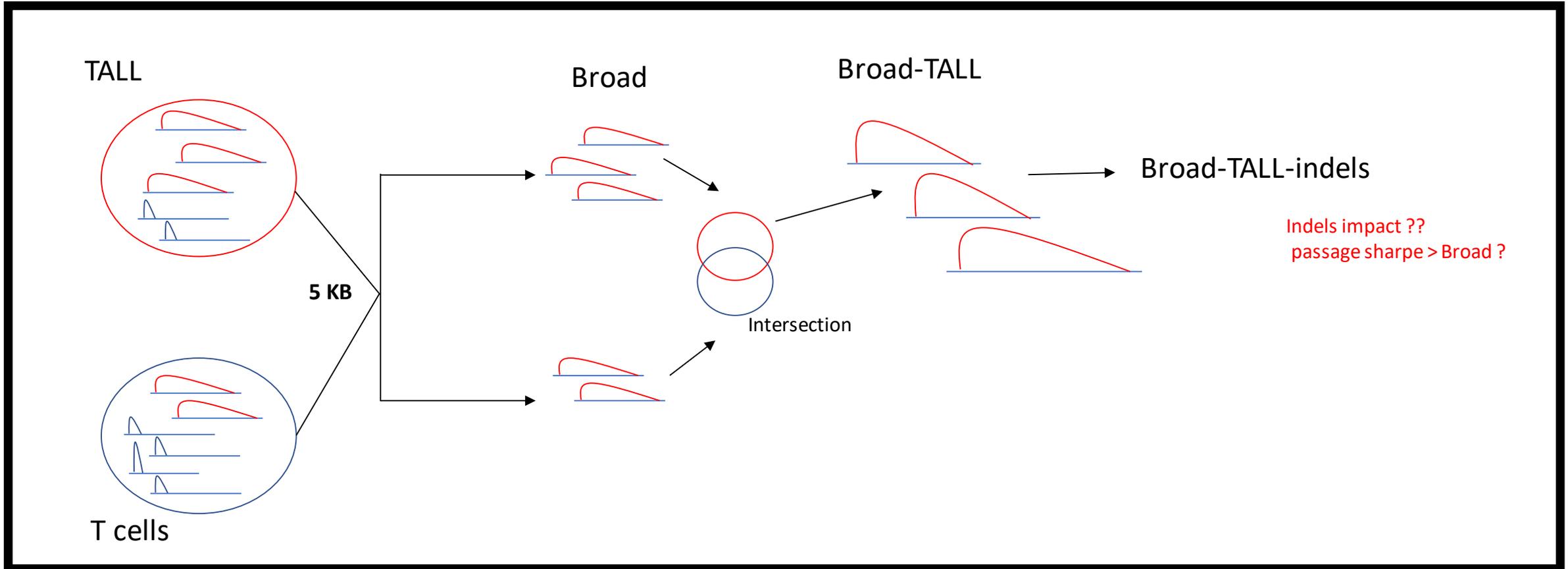
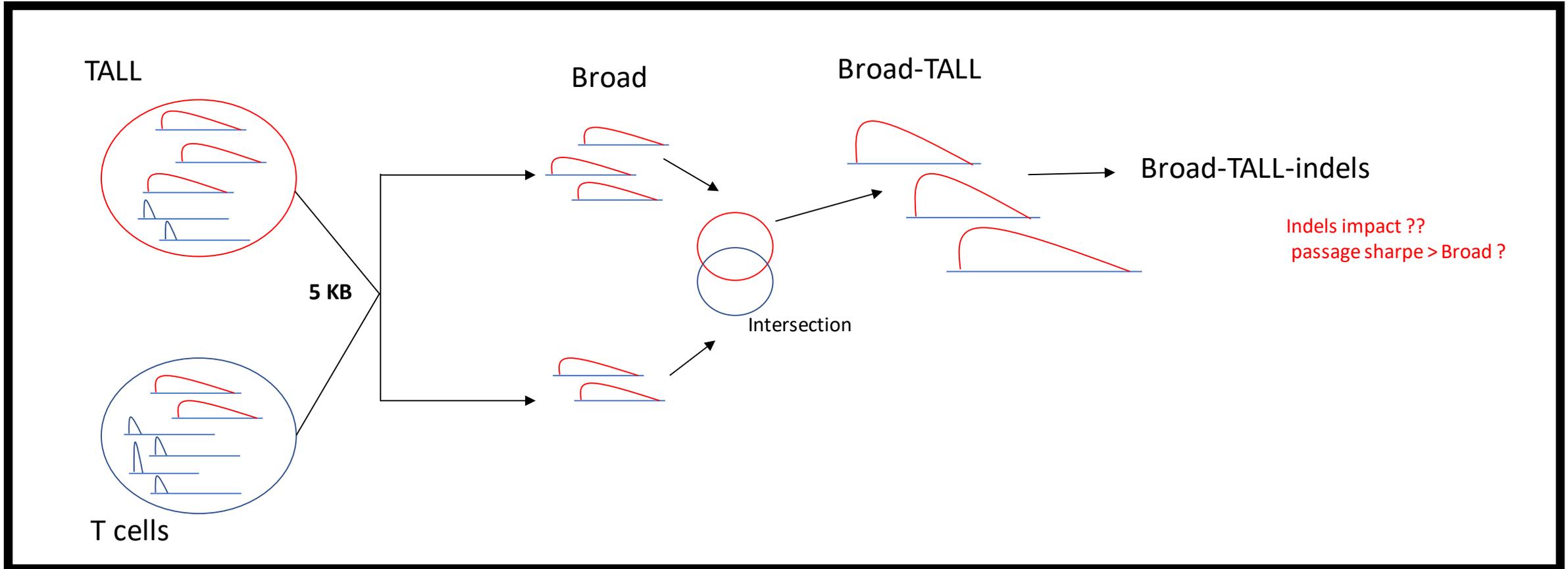


# Overview

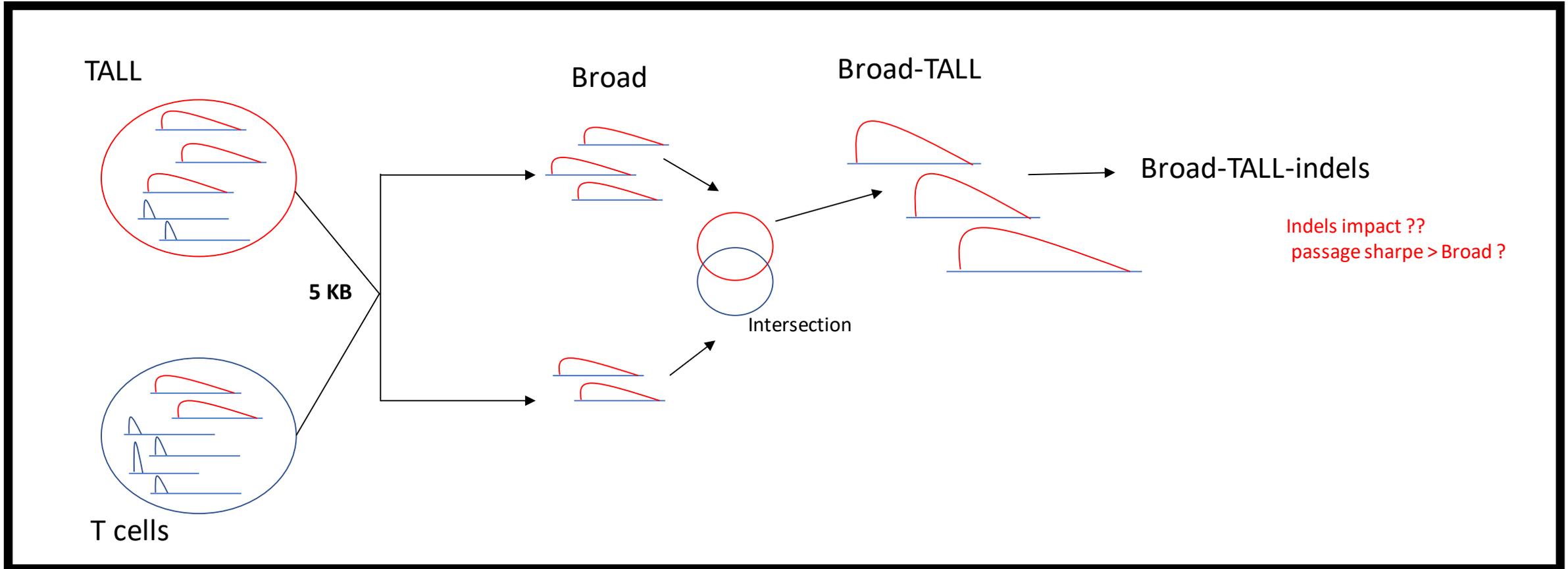


# Overview

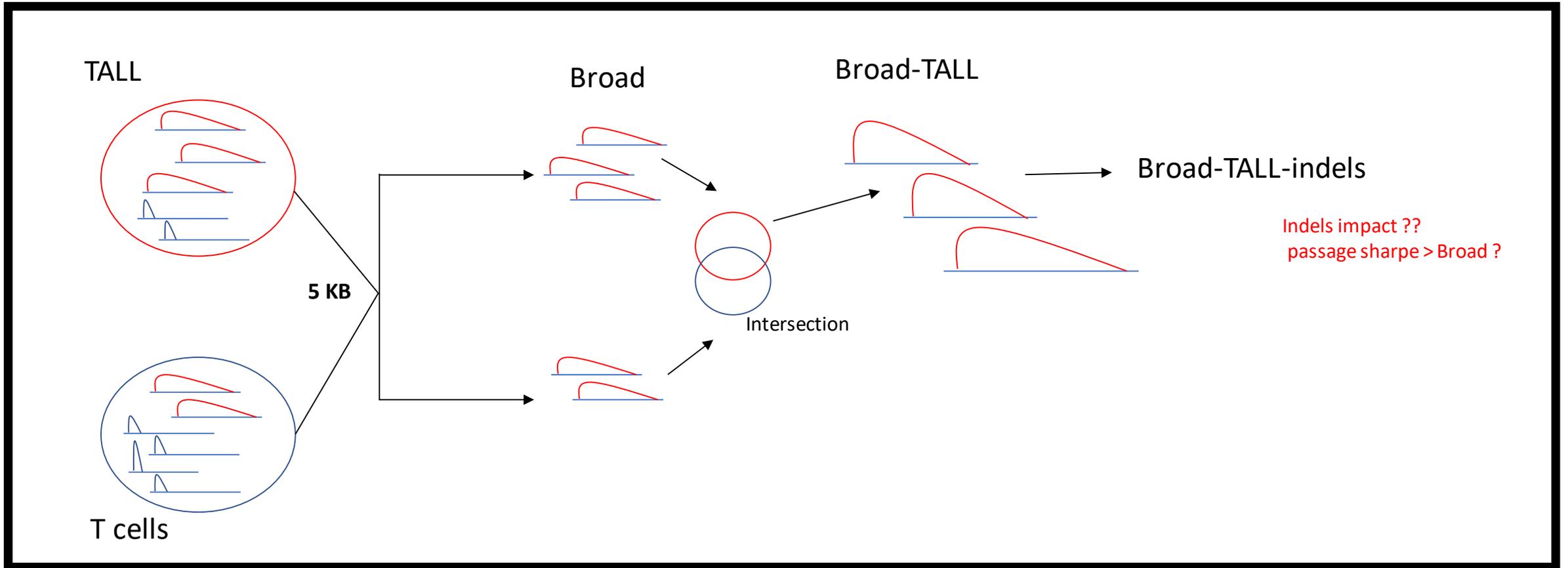


Gene x

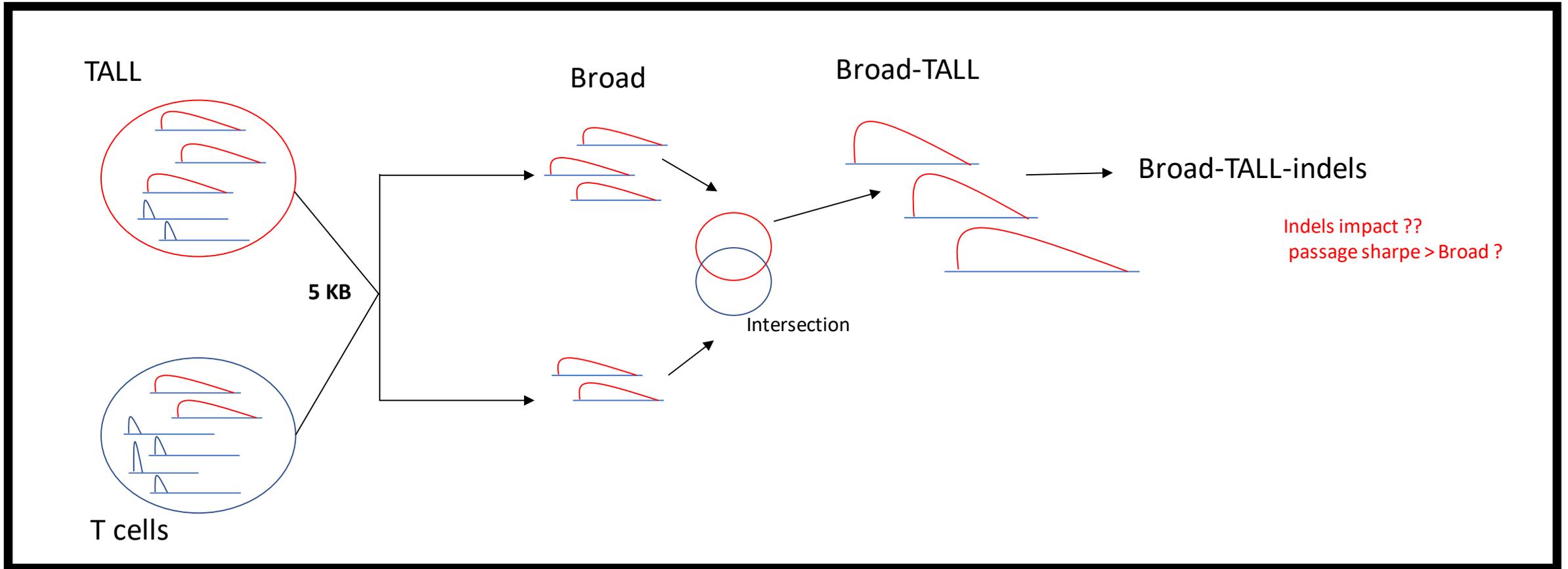
# Overview



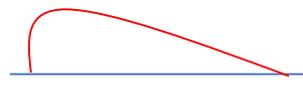
# Overview



# Overview



Gene x



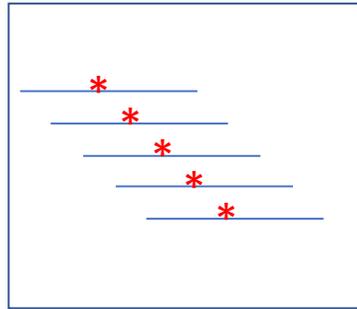
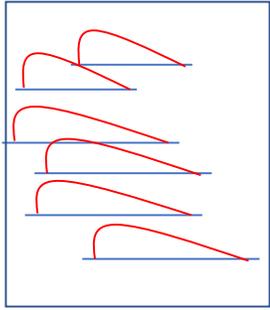
Dysfunction /  
degerulation

# pipeline

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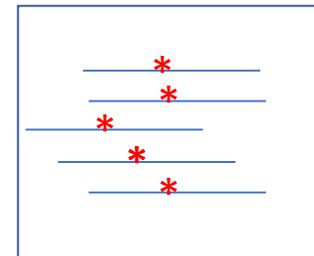
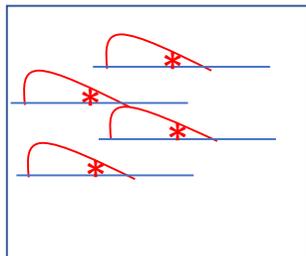
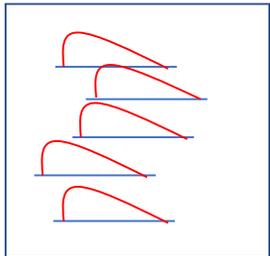
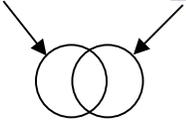
Borad-TALL

Indel



1883

480

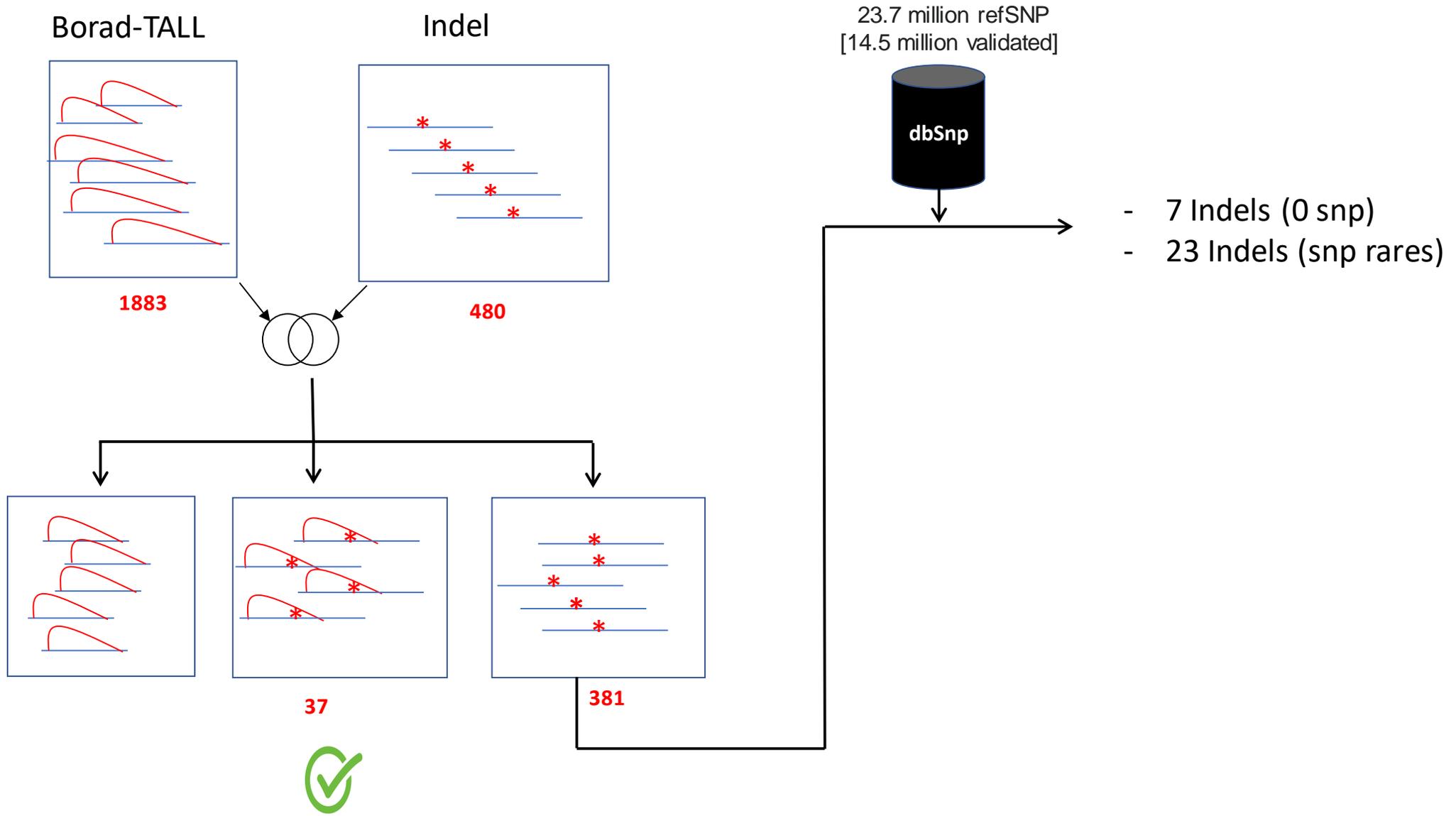


37

381



# pipeline



## Possible somatic mutations

indel_start	Indel_end	gene	IEM	REM	REF	ALT	sample
32980376	32980377	ENSG00000116514 RNF19B		4	3 A	AGTGCCGCCGGCCGGCTGTCAAGCAG	939
32342872	32342873	ENSG00000206127 GOLGA80		6	3 C	CG	532
87456660	87456661	ENSG00000280721 LINC01943		13	6 GG	GGCTGGTGGATCTCG	939
87456660	87456661	ENSG00000280721 LINC01943		23	11 GG	GGCTGGTGGATCTCG	856
186104557	186104558	ENSG00000164342 TLR3		9	5 TCC	TCCAAGAGGGCTGGCCCTGGGGGGCCCC	1118
39792522	39792523	ENSG00000146122 DAAM2		10	8 TCTC	TCTCTACCTCCCAGCTCACCTGTCCCACCTGCCCGCGGATCCTCACCTCTC	924
39792522	39792523	ENSG00000235033 DAAM2-AS1		10	8 TCTC	TCTCTACCTCCCAGCTCACCTGTCCCACCTGCCCGCGGATCCTCACCTCTC	924

5 indels

## Possible somatic mutations

indel_start	Indel_end	gene	IEM	REM	REF	ALT	sample
32980376	32980377	ENSG00000116514 RNF19B		4	3 A	AGTGCCGCCGCCGGCTGTCAAGCAG	939
32342872	32342873	ENSG00000206127 GOLGA8O		6	3 C	CG	532
87456660	87456661	ENSG00000280721 LINC01943		13	6 GG	GGCTGGTGGATCTCG	939
87456660	87456661	ENSG00000280721 LINC01943		23	11 GG	GGCTGGTGGATCTCG	856
186104557	186104558	ENSG00000164342 TLR3		9	5 TCC	TCCAAGAGGGCTGGCCCTGGGGGGCCCC	1118
39792522	39792523	ENSG00000146122 DAAM2		10	8 TCTC	TCTCTACCTCCCAGCTCACCTGTCCCACCTGCCCGCGGATCCTCACCTCTC	924
39792522	39792523	ENSG00000235033 DAAM2-AS1		10	8 TCTC	TCTCTACCTCCCAGCTCACCTGTCCCACCTGCCCGCGGATCCTCACCTCTC	924

5 indels

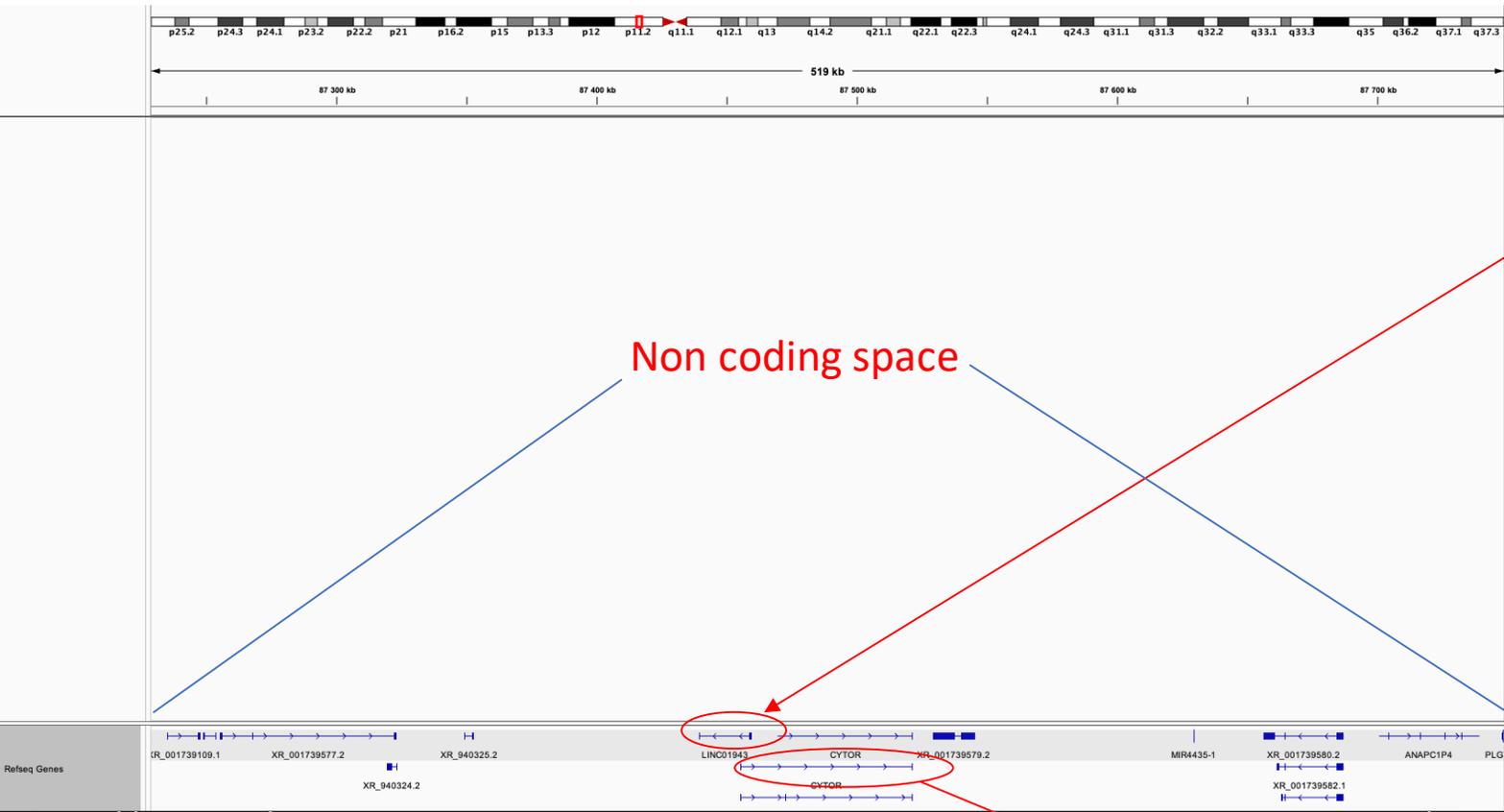
## Indels intersected with rare snps

chr	start	end	gene	biotype	IEM	REM	REF	ALT	Sample	chip	chr	sttstart	end	rs_id	REF	ALT	Frequency	ALT less freq ??
13	27826517	27826518	ENSG00000247381 PLUT	coding		4	0 GATAAAATA	GATAAA	565 H3K4me3		13	27826517	27826518	rs376498190	G	A	0.9998/0.0001997	
13	27826517	27826518	ENSG00000247381 PLUT	coding		4	0 GATAAAATA	GATAAA	920 H3K4me3		13	27826517	27826518	rs376498190	G	A	0.9998/0.0001997	
13	27961697	27961698	ENSG00000247381 PLUT	coding		6	0 tAAAAAAAAA	tAAAAAAAA	527 H3K4me3		13	27961697	27961698	rs553278211	T	A	0.9996/0.0003994	yes
19	54593812	54593813	ENSG00000104970 KIR3DX1	pseudogenes		5	4 TGG	TGGG	920 H3K4me3		19	54593812	54593813	rs560897371	T	C	0.9998/0.0001997	yes
19	54593812	54593813	ENSG00000239998 LILRA2	coding		5	4 TGG	TGGG	920 H3K4me3		19	54593812	54593813	rs560897371	T	C	0.9998/0.0001997	yes
20	46308589	46308590	ENSG00000273828 AL133227.1	antisense RNA		4	0 AGC	AGCGC	939 H3K4me3		20	46308589	46308590	rs11472606	A	AGC	0.0001997/0.9998	No
20	46308589	46308590	ENSG00000273828 AL133227.1	antisense RNA		4	0 AGC	AGCGC	939 H3K4me3		20	46308589	46308590	rs138496328	A	AGC,AGG	0.0001997/0.9998/.	No
5	148230300	148230301	ENSG00000133710 SPINK5	coding		8	0 TAGACAG	TAG	533 H3K4me3		5	148230300	148230301	rs367959714	T	C	0.9998/0.0001997	yes
5	148230300	148230301	ENSG00000247199 AC011346.1	coding		8	0 TAGACAG	TAG	533 H3K4me3		5	148230300	148230301	rs367959714	T	C	0.9998/0.0001997	yes
6	73389056	73389057	ENSG00000203907 O0EP	coding		9	0 GC	GCC	933 H3K4me3		6	73389056	73389057	rs11390423	G	GC	0.0003994/0.9996	No
6	73389056	73389057	ENSG00000203907 O0EP	coding		9	0 GC	GCC	933 H3K4me3		6	73389056	73389057	rs397788669	G	GC	0.0003994/0.9996	No
6	73389056	73389057	ENSG00000224221 RPS6P8	pseudogenes		9	0 GC	GCC	933 H3K4me3		6	73389056	73389057	rs11390423	G	GC	0.0003994/0.9996	No
6	73389056	73389057	ENSG00000224221 RPS6P8	pseudogenes		9	0 GC	GCC	933 H3K4me3		6	73389056	73389057	rs397788669	G	GC	0.0003994/0.9996	No
X	102155850	102155851	ENSG00000184515 BEX5	coding		12	0 GCC	GCCC	375 H3K4me3	X		102155850	102155851	rs11451071	G	GC	0.0002649/0.9997	No
X	102155850	102155851	ENSG00000184515 BEX5	coding		12	0 GCC	GCCC	375 H3K4me3	X		102155850	102155851	rs5903198	G	GC	0.0002649/0.9997	No
X	102155850	102155851	ENSG00000184515 BEX5	coding		12	0 GCC	GCCC	375 H3K4me3	X		102155850	102155851	rs869131083	G	GC	0.0002649/0.9997	No

9 indels

# Unknown function !!!

87456660	87456661	ENSG00000280721 LINC01943	13	6 GG	GGCTGGTGGATCTCG
87456660	87456661	ENSG00000280721 LINC01943	23	11 GG	GGCTGGTGGATCTCG



Non coding space

CYTOR gene produces a long non-coding RNA that is overexpressed in cancer cells and promotes cell proliferation and epithelial-mesenchymal transition. This RNA may bind enhancer of zeste homolog 2 and participate in the transcriptional silencing of tumor suppressor genes. It may act as a sponge for microRNAs. Alternatively spliced variants have been observed. [provided by RefSeq, Dec 2017]