

ZC3H12A

History

```
%%{init: { 'logLevel': 'debug', 'theme': 'dark' } }%%
timeline
  title Publication timing
    2017-10-10 : Reddy : DLBCL
```

Relevance tier by entity

Entity	Tier	Description
MCL	2	relevance in MCL not firmly established
DLBCL	1	high-confidence DLBCL gene
FL	2	relevance in FL not firmly established

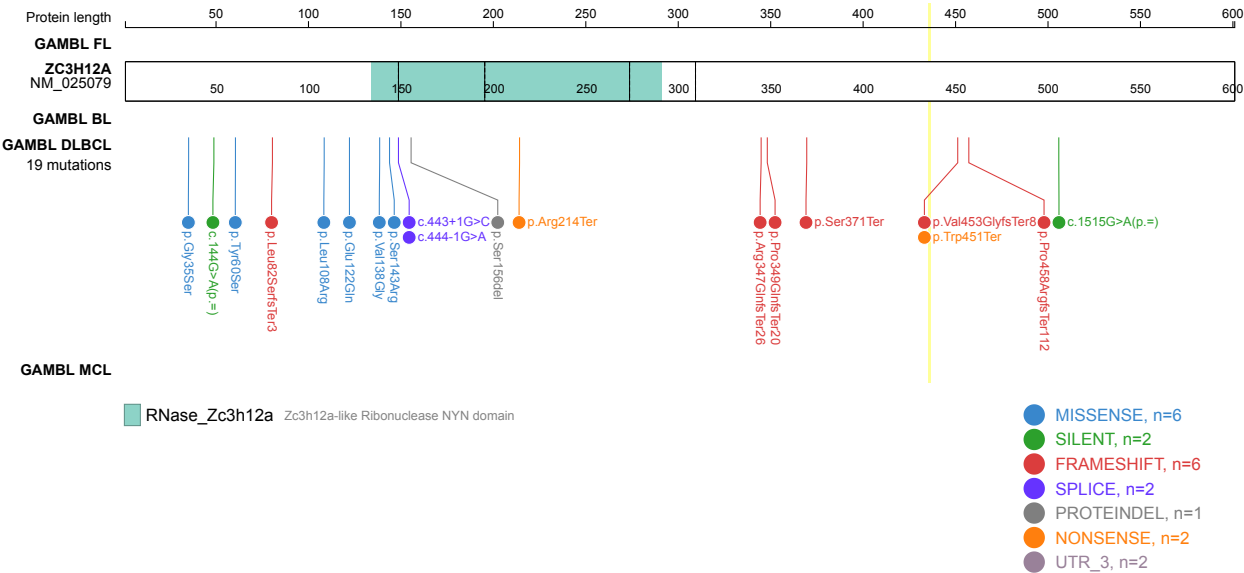
Mutation incidence in large patient cohorts (GAMBL reanalysis)

Entity	source	frequency (%)
DLBCL	GAMBL genomes	2.68
DLBCL	Schmitz cohort	5.96
DLBCL	Reddy cohort	3.10
DLBCL	Chapuy cohort	4.70
FL	GAMBL genomes	0.46

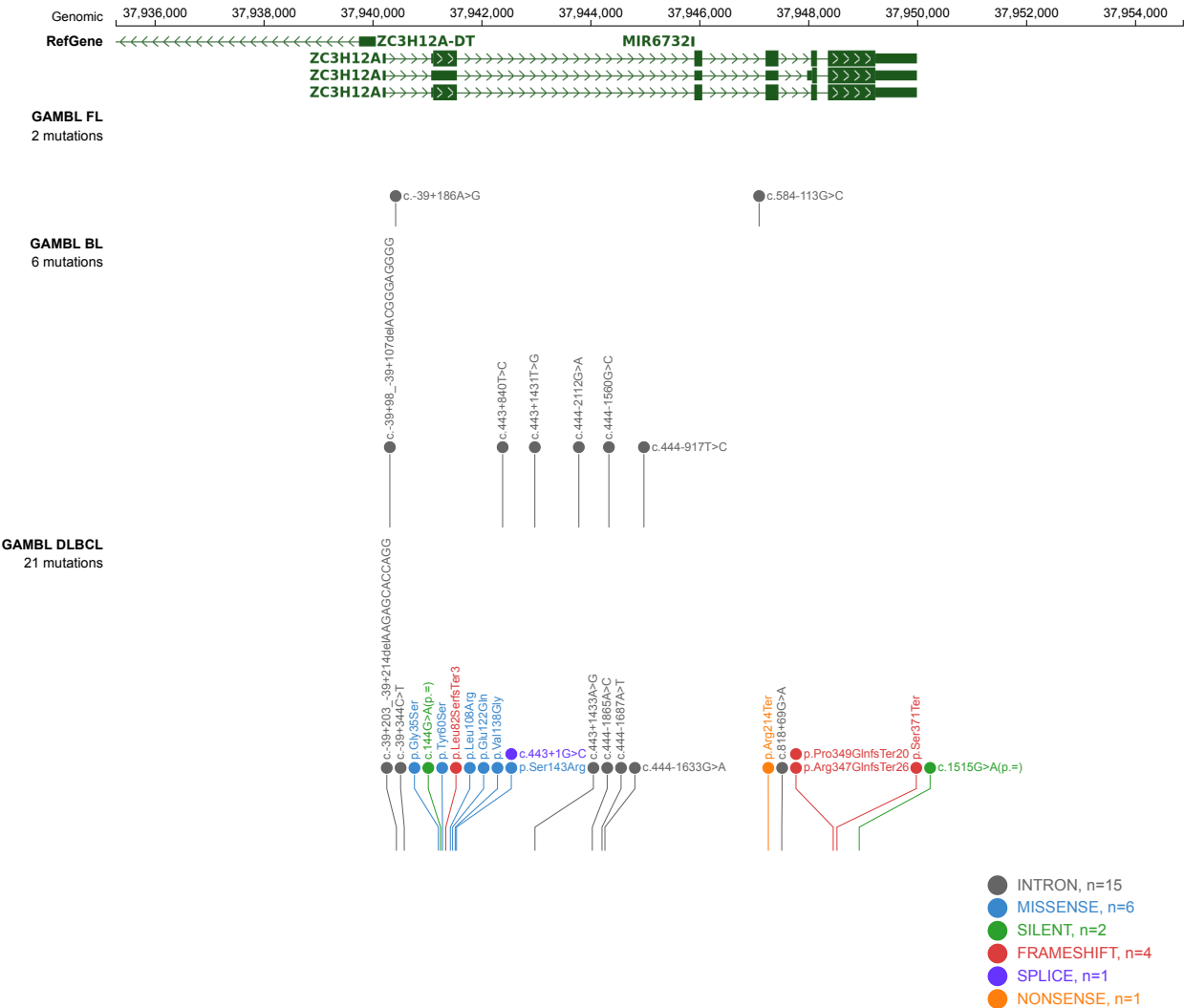
Mutation pattern and selective pressure estimates

Entity	aSHM	Significant selection	dN/dS (missense)	dN/dS (nonsense)
BL	No	No	0.000	0.000
DLBCL	No	No	2.488	18.944
FL	No	No	0.000	0.000

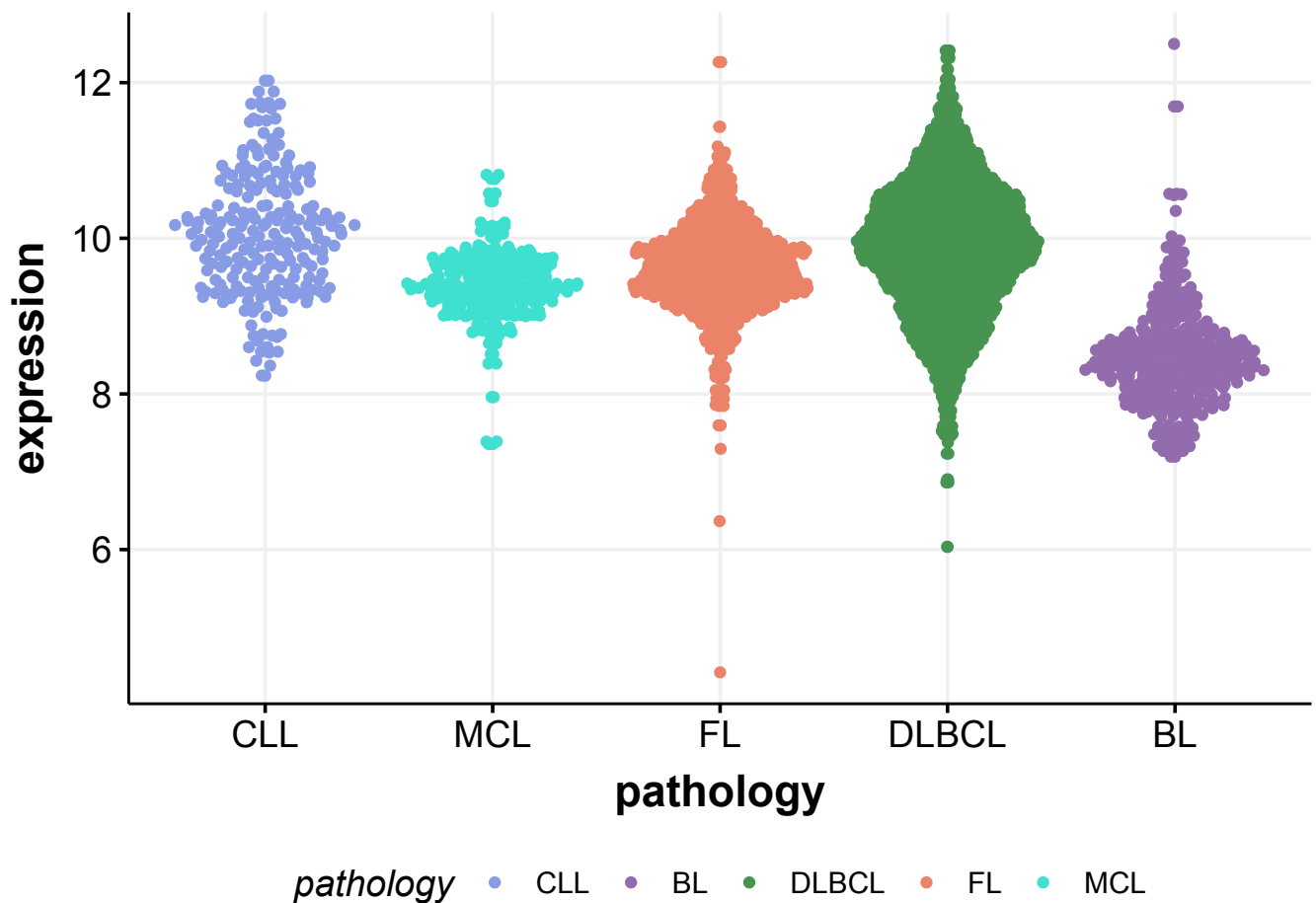
View coding variants in ProteinPaint [hg19](#) or [hg38](#)



View all variants in GenomePaint [hg19](#) or [hg38](#)



ZC3H12A Expression



References

1. Zhang J, Jima D, Moffitt AB, Liu Q, Czader M, Hsi ED, Fedoriw Y, Dunphy CH, Richards KL, Gill JI, Sun Z, Love C, Scotland P, Lock E, Levy S, Hsu DS, Dunson D, Dave SS. The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. *Blood*. 2014 May 8;123(19):2988–2996.
2. Arthur SE, Jiang A, Grande BM, Alcaide M, Cojocaru R, Rushton CK, Mottok A, Hilton LK, Lat PK, Zhao EY, Culibrk L, Ennishi D, Jessa S, Chong L, Thomas N, Pararajalingam P, Meissner B, Boyle M, Davidson J, Bushell KR, Lai D, Farinha P, Slack GW, Morin GB, Shah S, Sen D, Jones SJM, Mungall AJ, Gascoyne RD, Audas TE, Unrau P, Marra MA, Connors JM, Steidl C, Scott DW, Morin RD. Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. *Nat Commun*. 2018 Oct 1;9(1):4001. PMID: PMC6167379