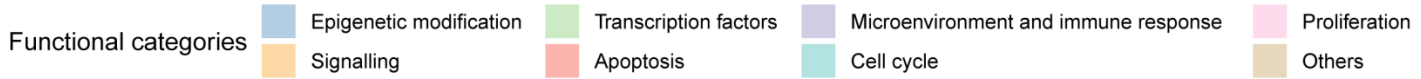
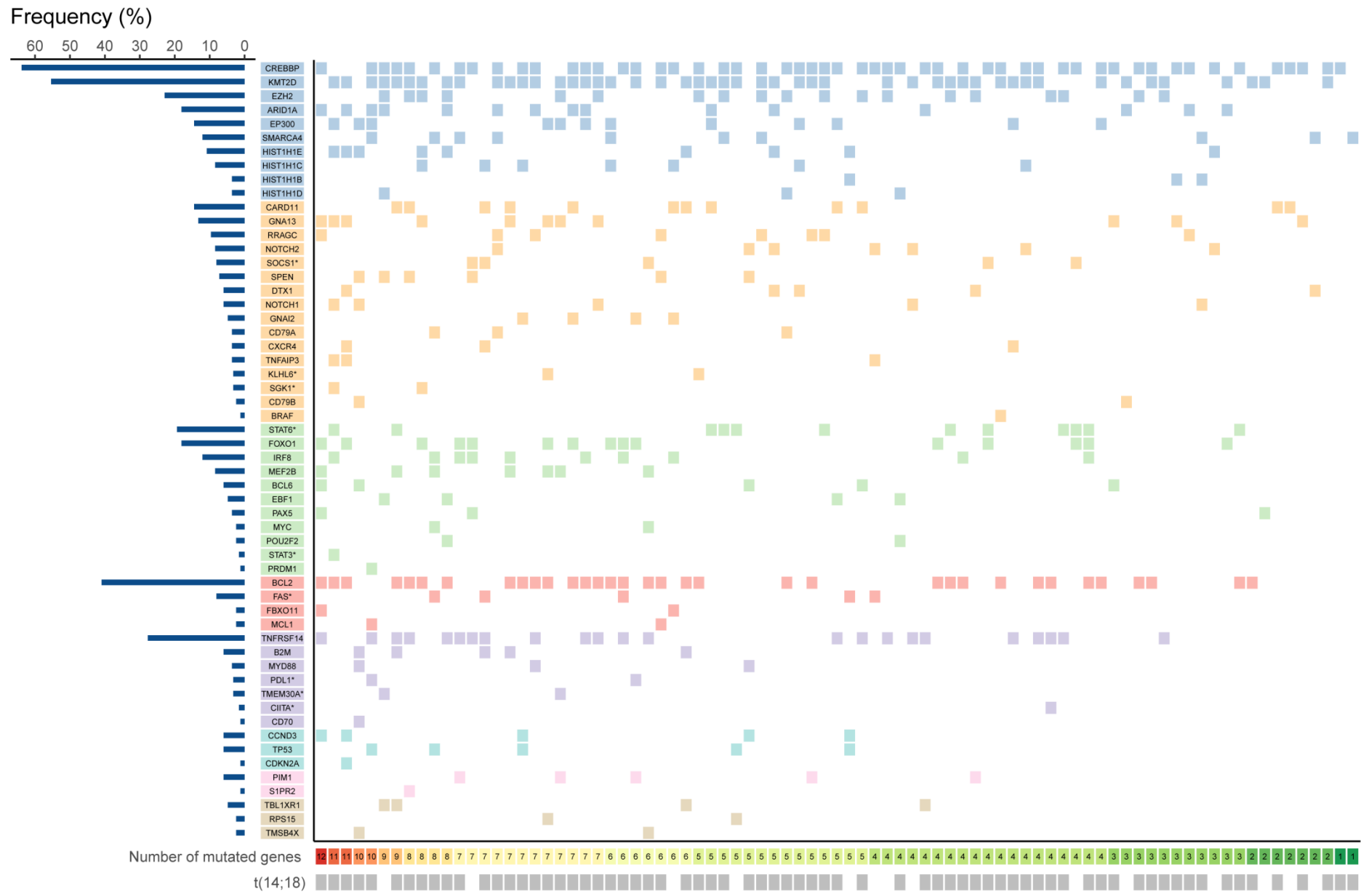
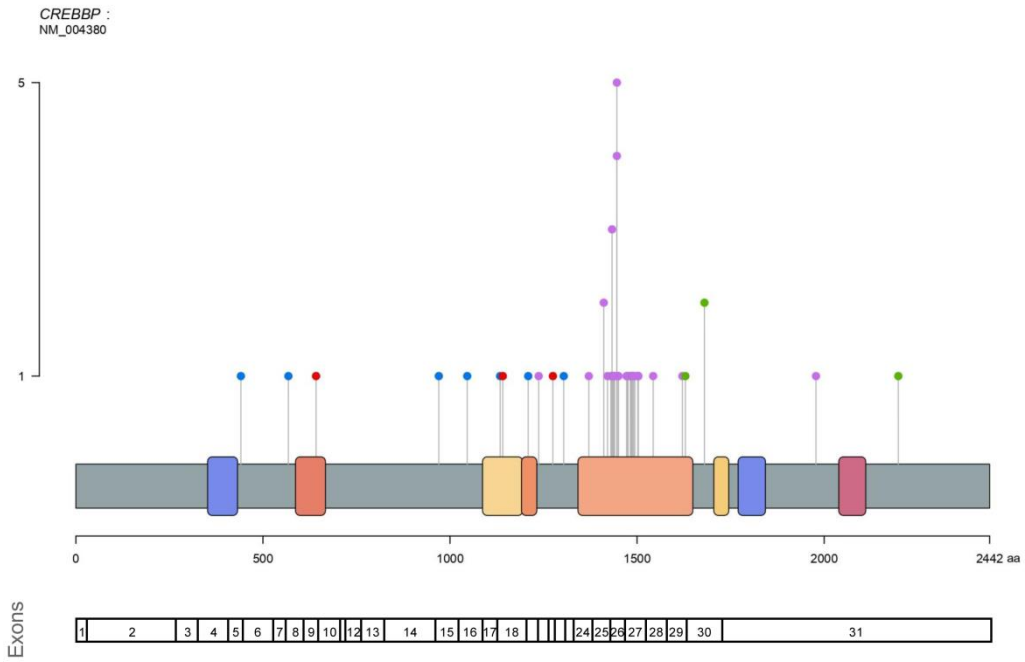


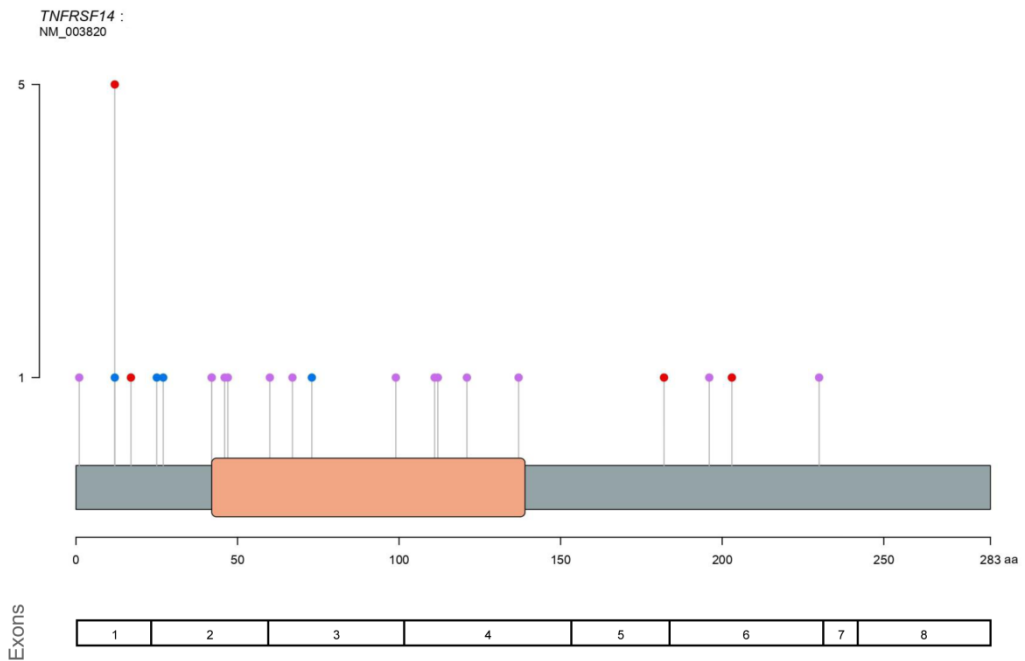
Supplementary Figure S1. Genetic landscape of FL.



Supplementary Figure S2. Mutation distribution across the genes with a mutation frequency greater than 10%.

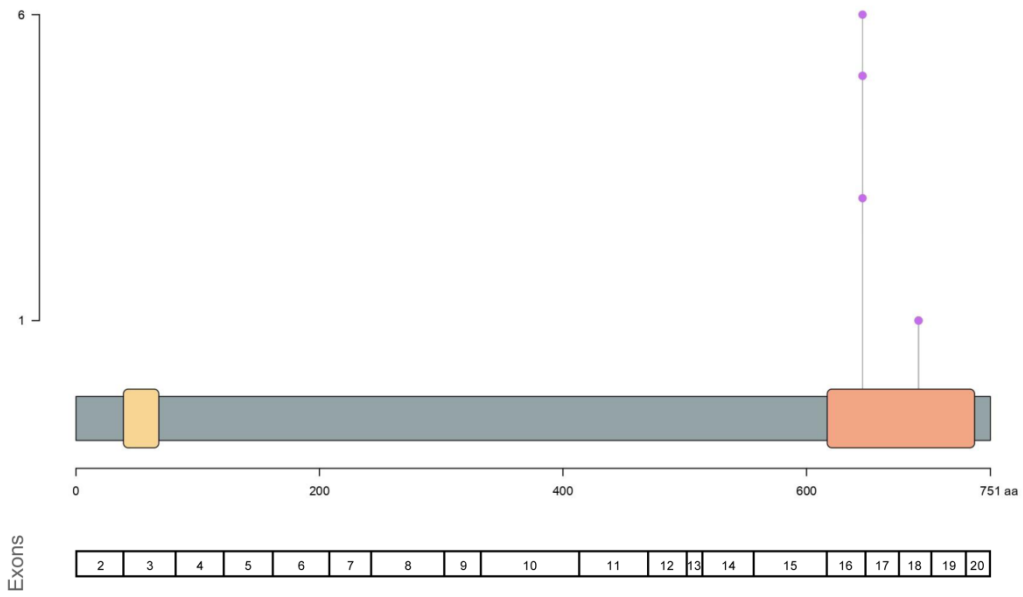


- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- KAT11
 - Bromo cbp like
 - zf-TAZ
 - KIX
 - Creb binding
 - DUF902
 - ZZ CBP



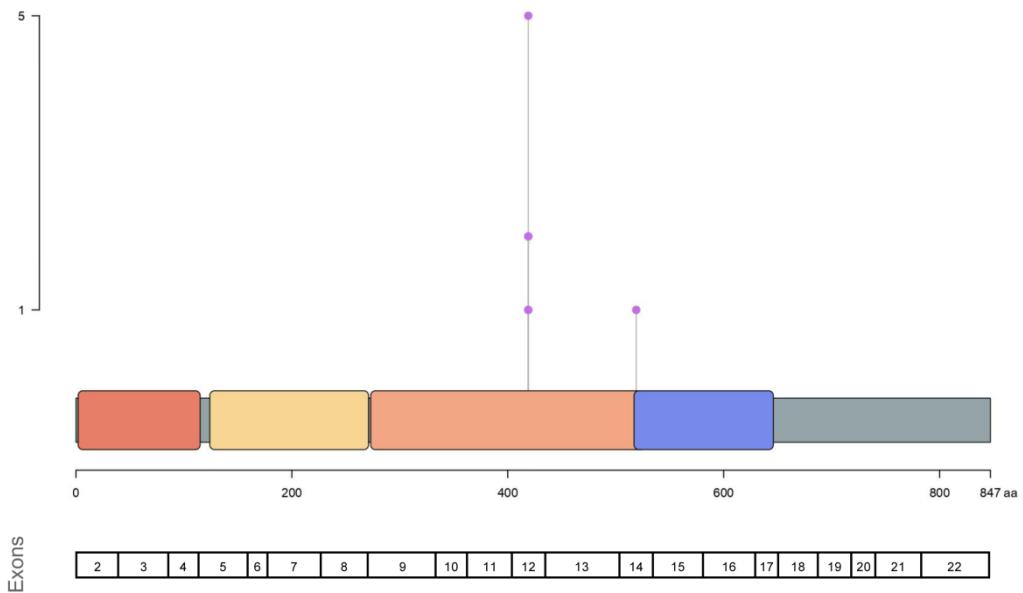
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- TNFR

EZH2 :
NM_004456



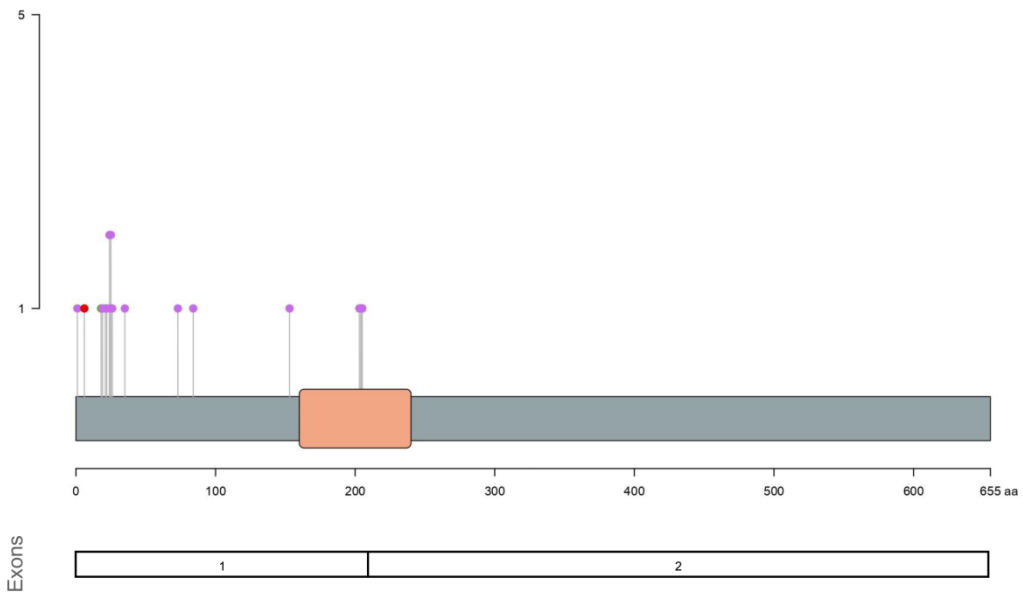
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- SET
 - EZH2 WD-Binding

STAT6 :
NM_003153



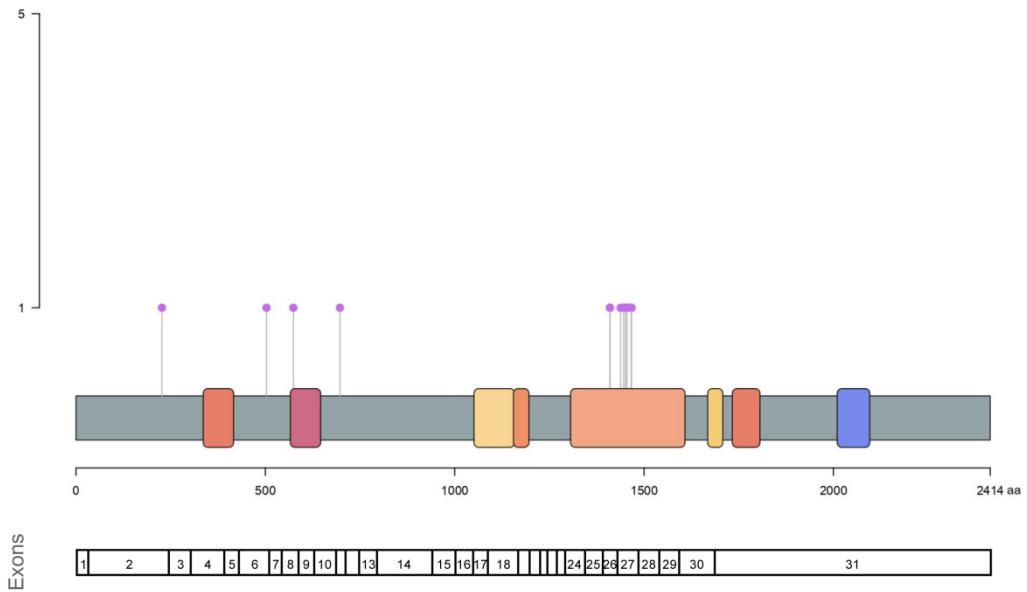
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- STAT bind
 - STAT alpha
 - SH2 STAT6
 - STAT int

FOXO1 :
NM_002015



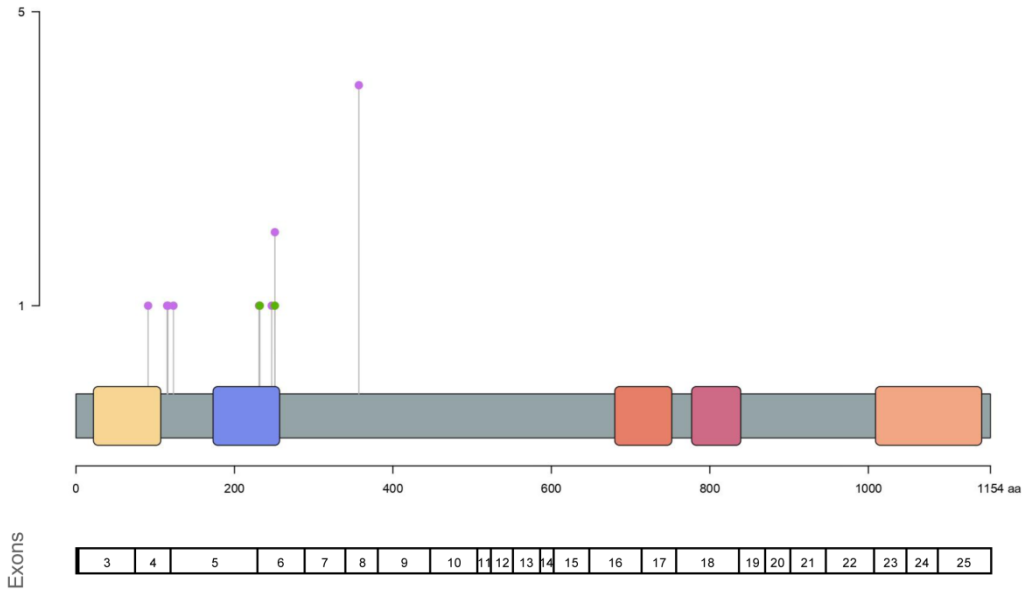
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- FH

EP300 :
NM_001429



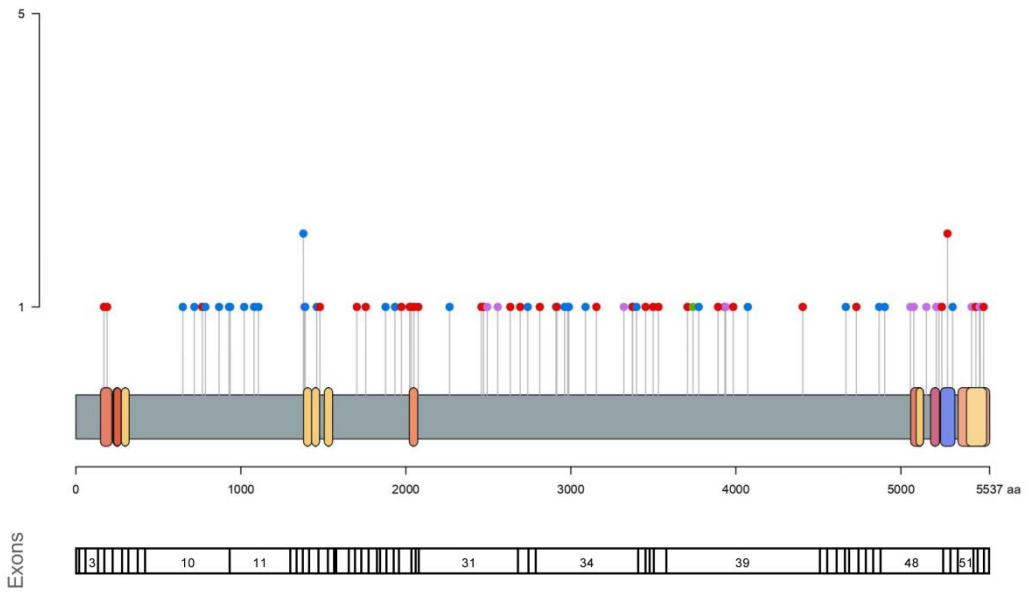
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- KAT11
 - Bromo cbp like
 - Creb binding
 - zf-TAZ
 - KIX
 - DUF902
 - ZZ CBP

CARD11 :
NM_032415



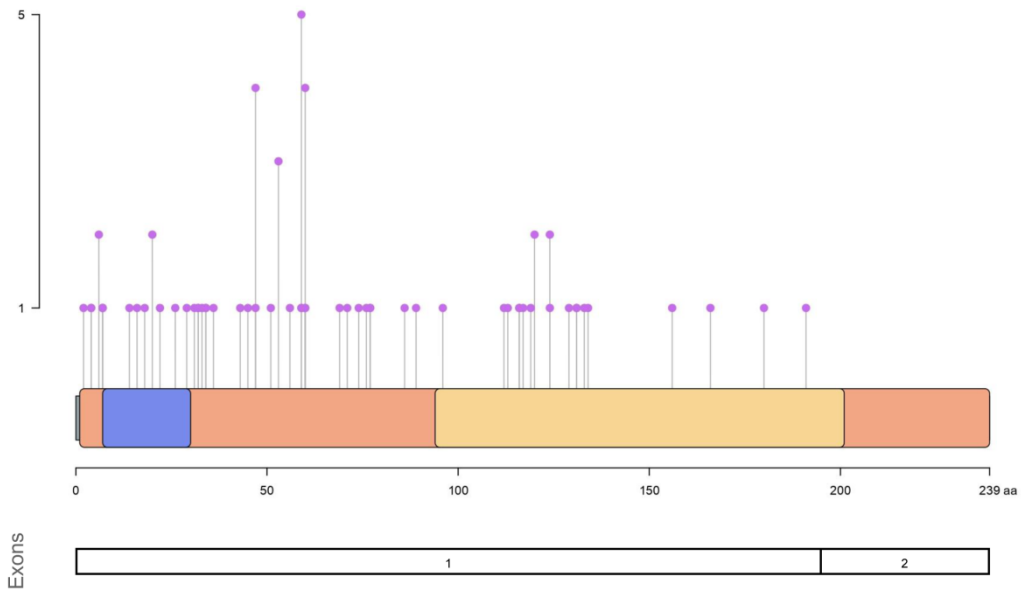
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- P-loop NTPase
 - CARD CARD11 CARMA1
 - BAR
 - PDZ signaling
 - SH3

KMT2D :
NM_003482



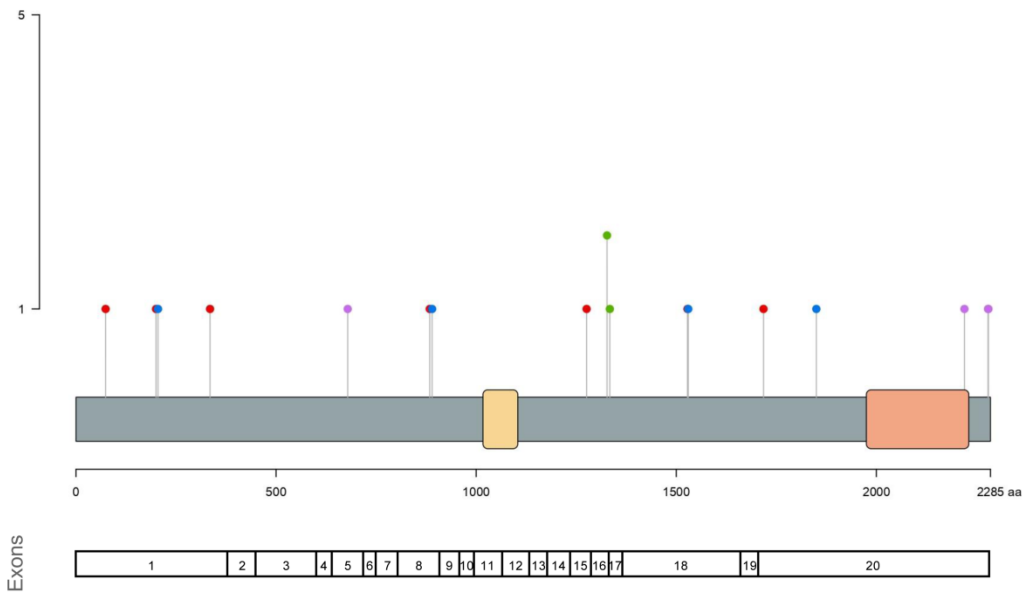
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- COG2940
 - SET
 - FYRC
 - zf-HC5HC2H
 - FYRN
 - HMG-box
 - PHD
 - zf-C3HC4 2
 - RING

BCL2 :
NM_000633



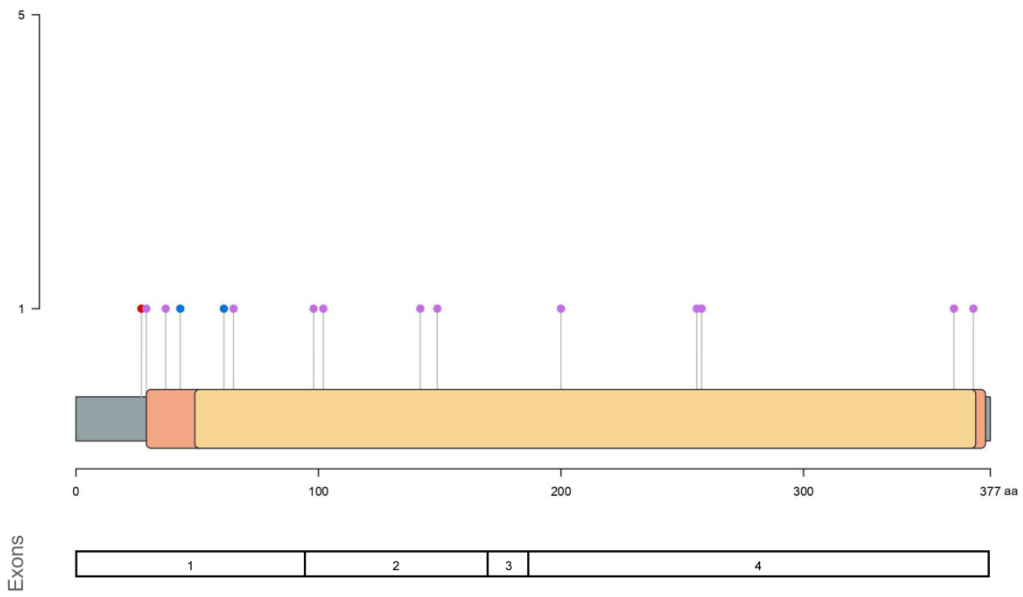
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- bcl-2
 - Bcl-2 like
 - BH4

ARID1A :
NM_006015



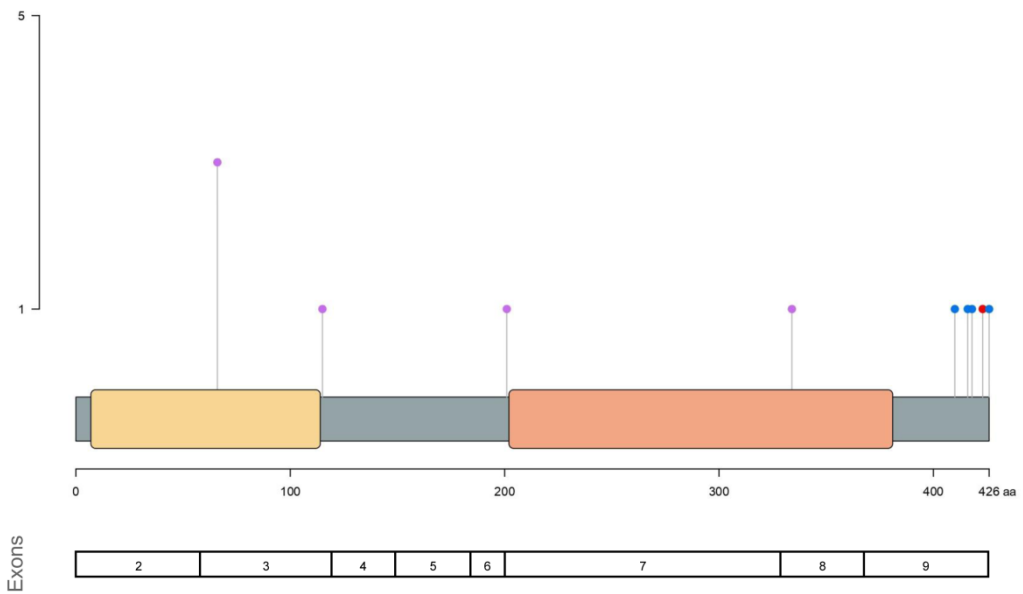
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- DUF3518
 - ARID

GNA13 :
NM_006572



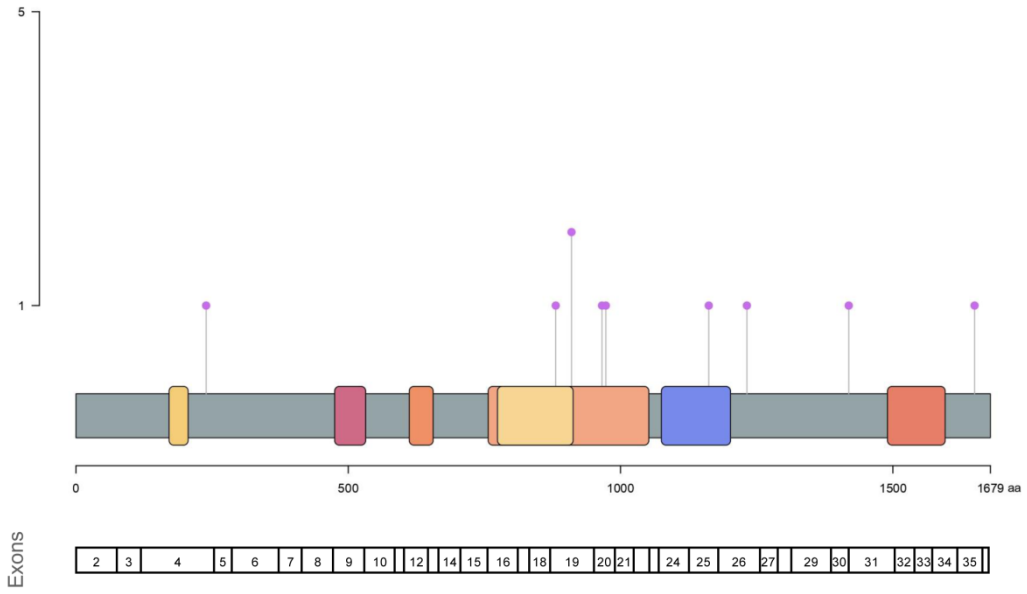
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- G alpha
 - G-alpha

IRF8 :
NM_002163



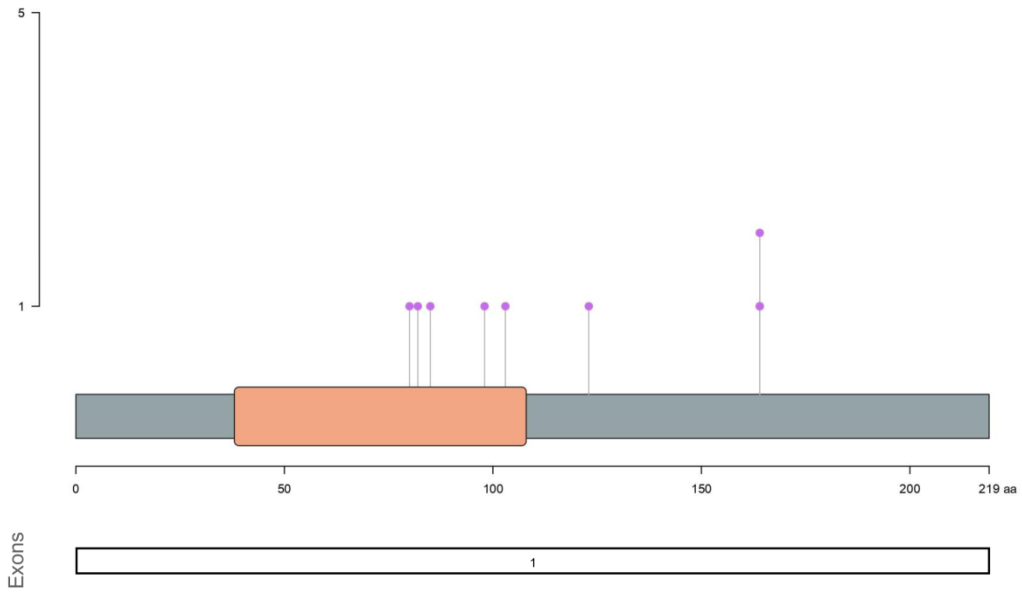
- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- IRF-3
 - IRF

SMARCA4 :
NM_001128849



- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- SNF2 N
 - DEXDc
 - HELICc
 - Bromo SNF2L2
 - HSA
 - BRK
 - QLQ

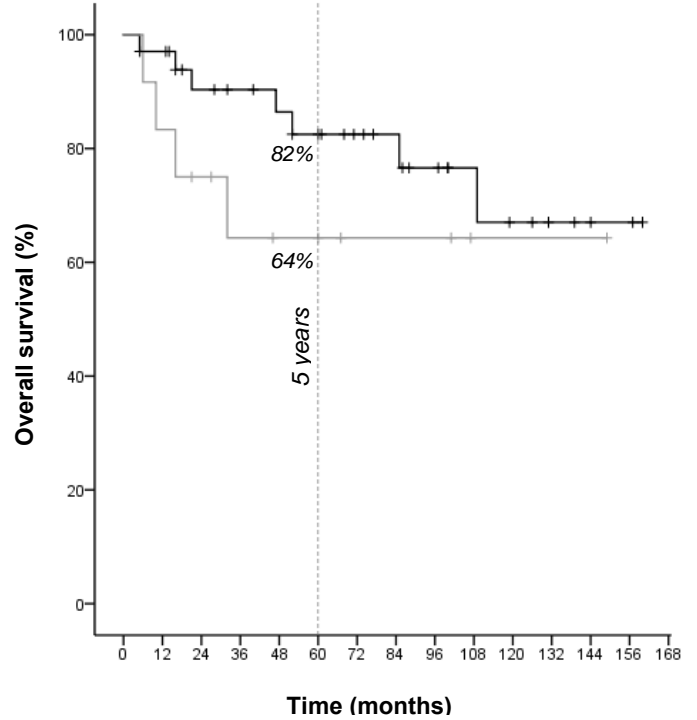
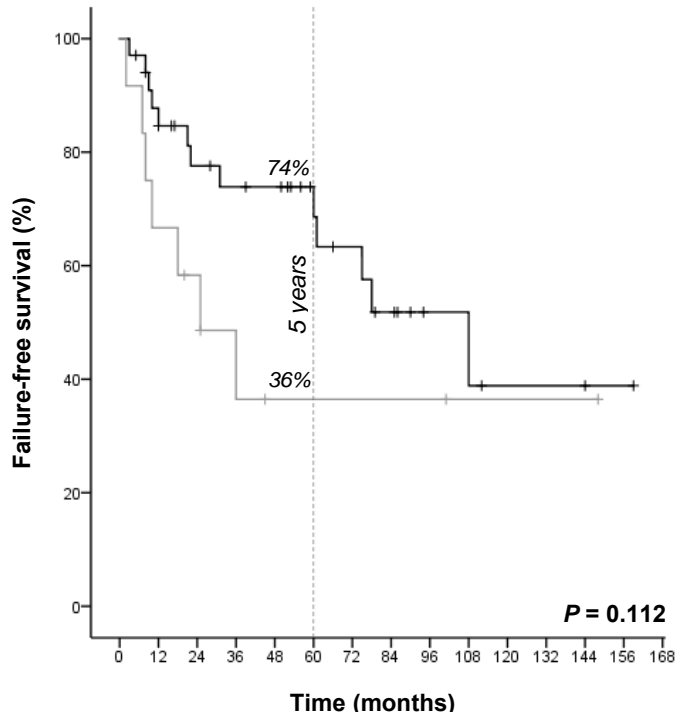
HIST1H1E :
NM_005321



- Nonsense mutations
 - Missense mutations
 - Frameshift indels
 - Inframe indels
- Domains
- H15

Supplementary Figure S3. Kaplan-Meier analysis of (A) failure-free survival and overall survival by m7-FLIPI model, and (B) overall survival by FLIPI index in FL patients treated with R-ICT (n=47). The vertical dashed line indicates 5-year follow-up.

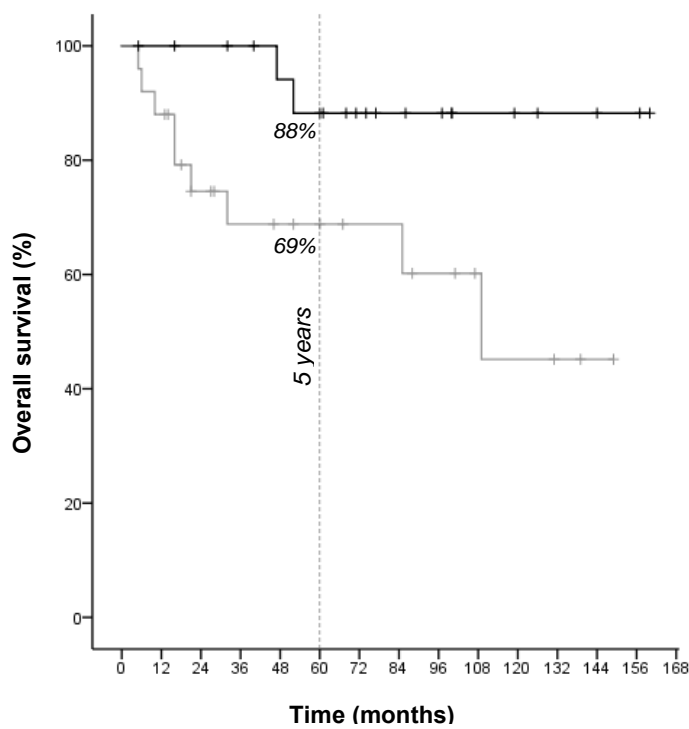
A. m7-FLIPI



— Low-risk m7-FLIPI (n=34) — High-risk m7-FLIPI (n=12)

— Low-risk m7-FLIPI (n=34) — High-risk m7-FLIPI (n=12)

B. FLIPI



— Low/Intermediate-risk FLIPI (n=21) — High-risk FLIPI (n=25)