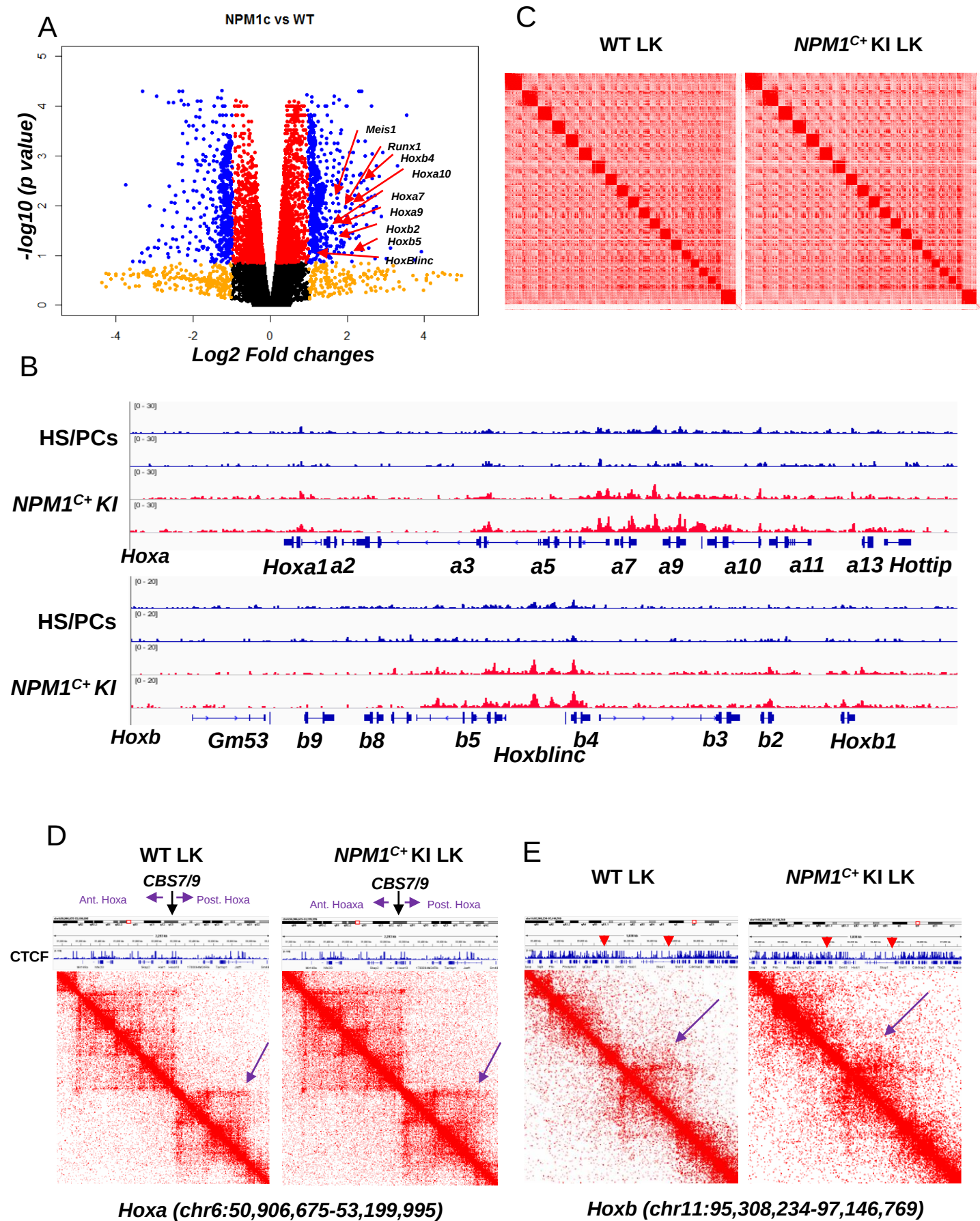
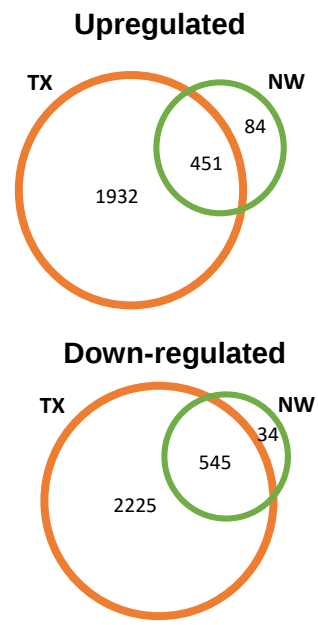
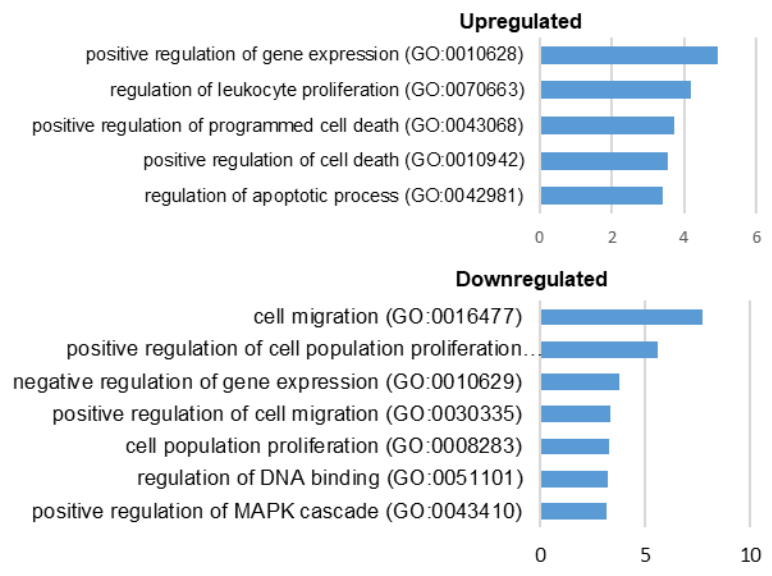




A

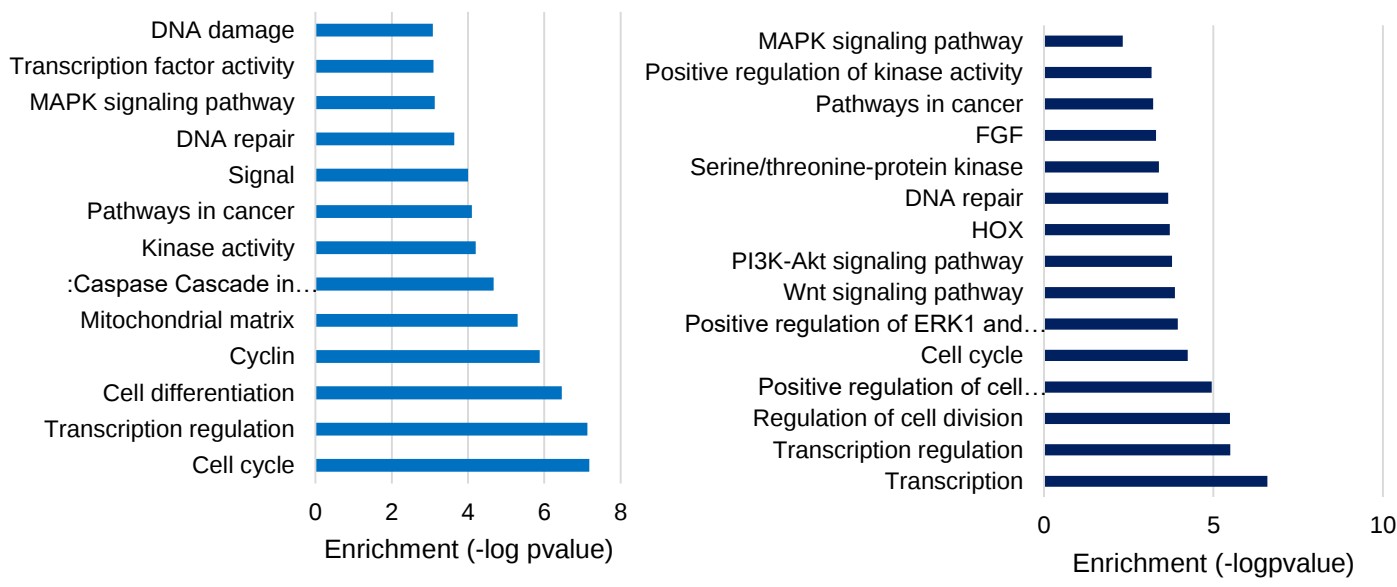


B



C

GO overlap of increased TADs and RNA-seq GO overlap of decreased TADs and RNA-seq

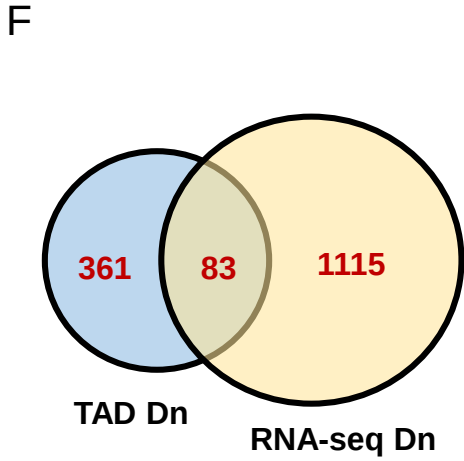
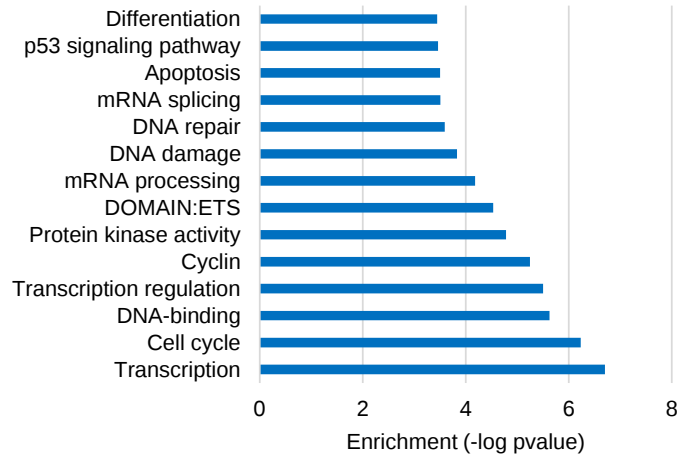
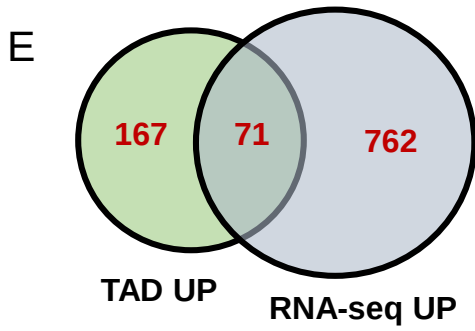


D

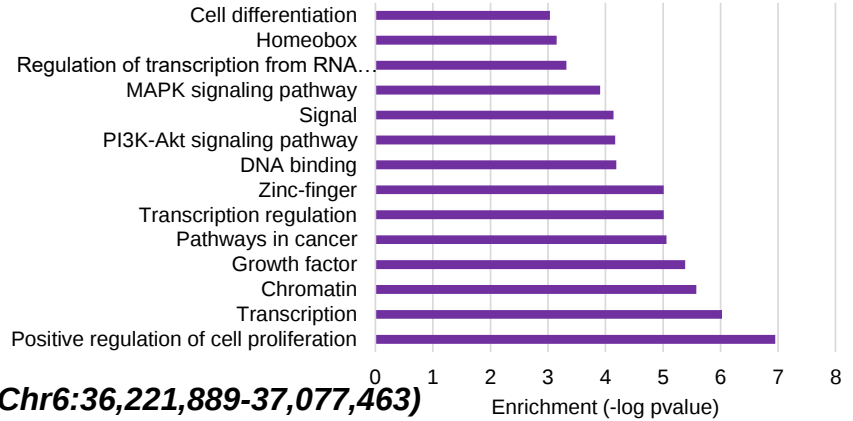
Top 10 downregulated TADs upon *NPM1*^{OE}

Top 10 TADs	Chromosome loci	Genes
TAD1	Chr15:28,908,000-30,411,998	TJP1 FAM189A1 APBA2 NR135221 GOLGA
TAD2	Chr4:19,951,026-21,964,971	SLIT2 PACRGL KCNIP4
TAD3	Chr9:138,910,026-139,281,971	LHX3 QSOX2 TMEM250 NACC2 GPSM1
TAD4	Chr18:5,371,400-7,016,598	L3MBTL4 TMEM200C EPB41L3 ARHGAP2B LAMA1
TAD5	Chr15:30,884,000-32,543,998	KLF13 OTUD7A TRPM1 FAN1 CHRNA7 LINC02352
TAD6	Chr17:46,440,109-46,866,473	HOXB1 B2 B3 B4 B5 B6 B8 B9 SKAP1 PRAC1
TAD7	Chr2:85,087,715-85,728,283	KCMF1 LINC01964 TCF7L1 TGOLN2 ELMOD3 SH2D6
TAD8	Chr13:72,618,603-75,045,395	KLF5 PIBF1 MZT1 KLF12 LINC00392
TAD9	Chr1:63,082,983-65,709,015	JAK1 CACHD1 ROR1 UBE2U ALG6 EFCAB7
TAD10	Chr19:47,823,937-48,134,429	MEIS3 SLC8A2 DHX34 KPTN NAPA

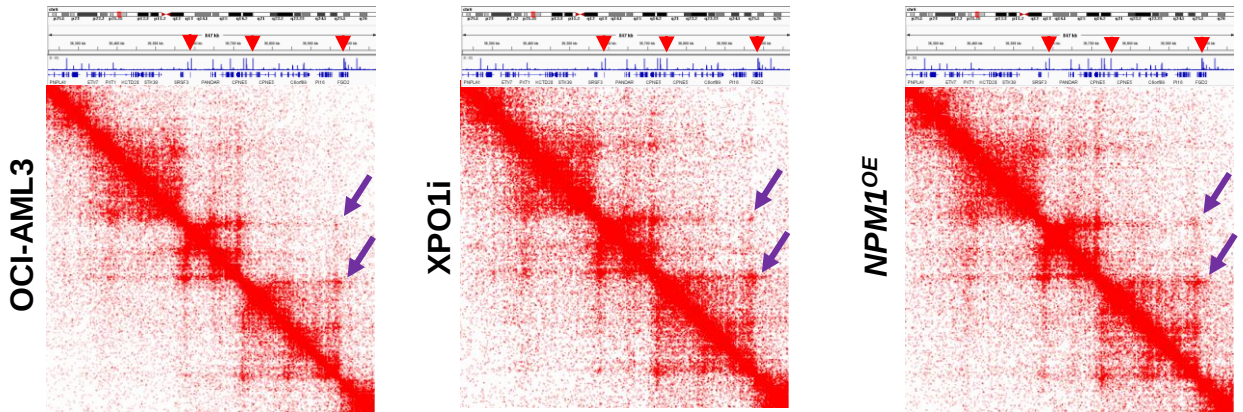
GO overlap of increased TADs and RNA-seq



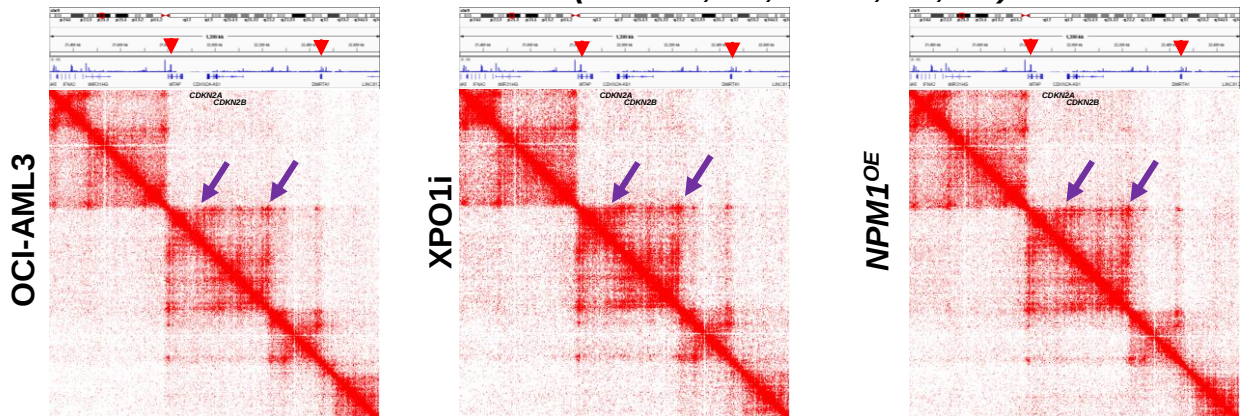
GO overlap of decreased TADs and RNA-seq



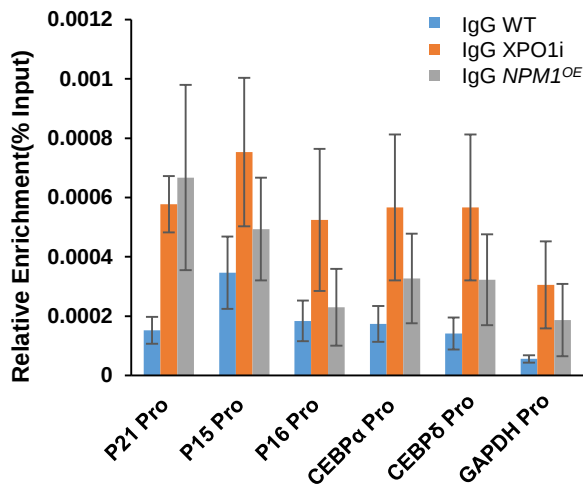
G *CDKN1A* (Chr6:36,221,889-37,077,463)



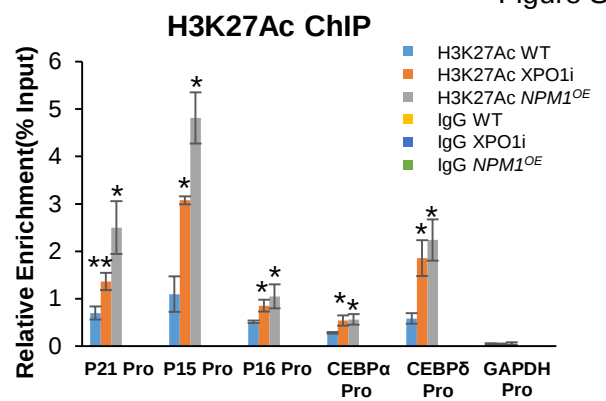
H *CDKN2A/CDKN2B* (Chr9:21,300,040-22,712,173)



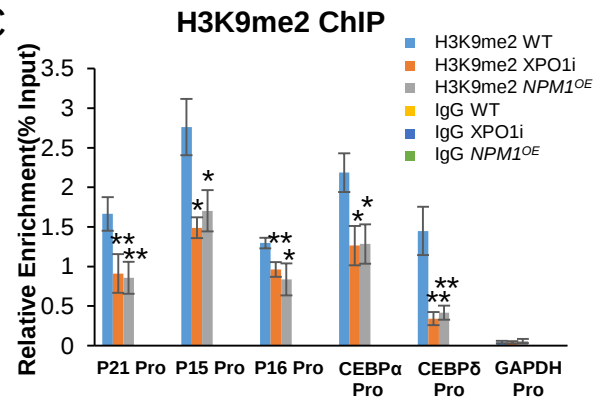
A



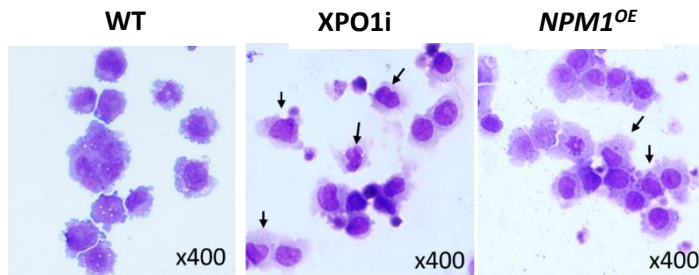
B



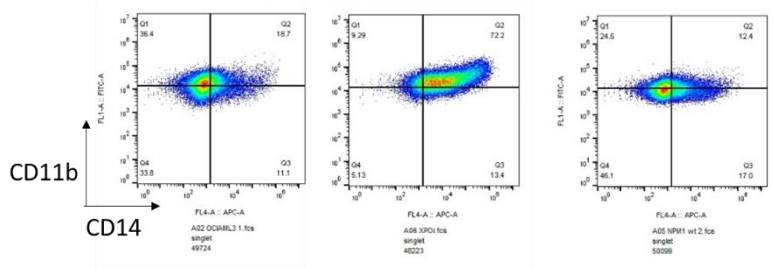
C



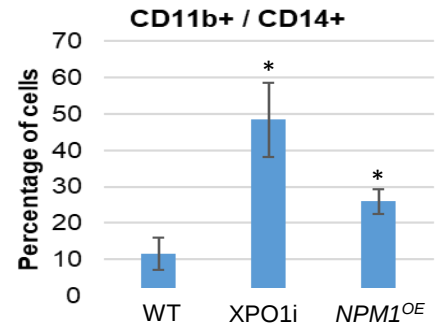
D



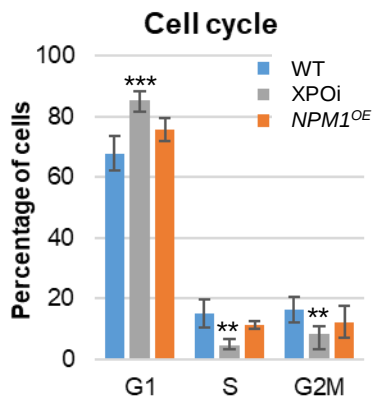
E



F



G



H

