

Figure 1

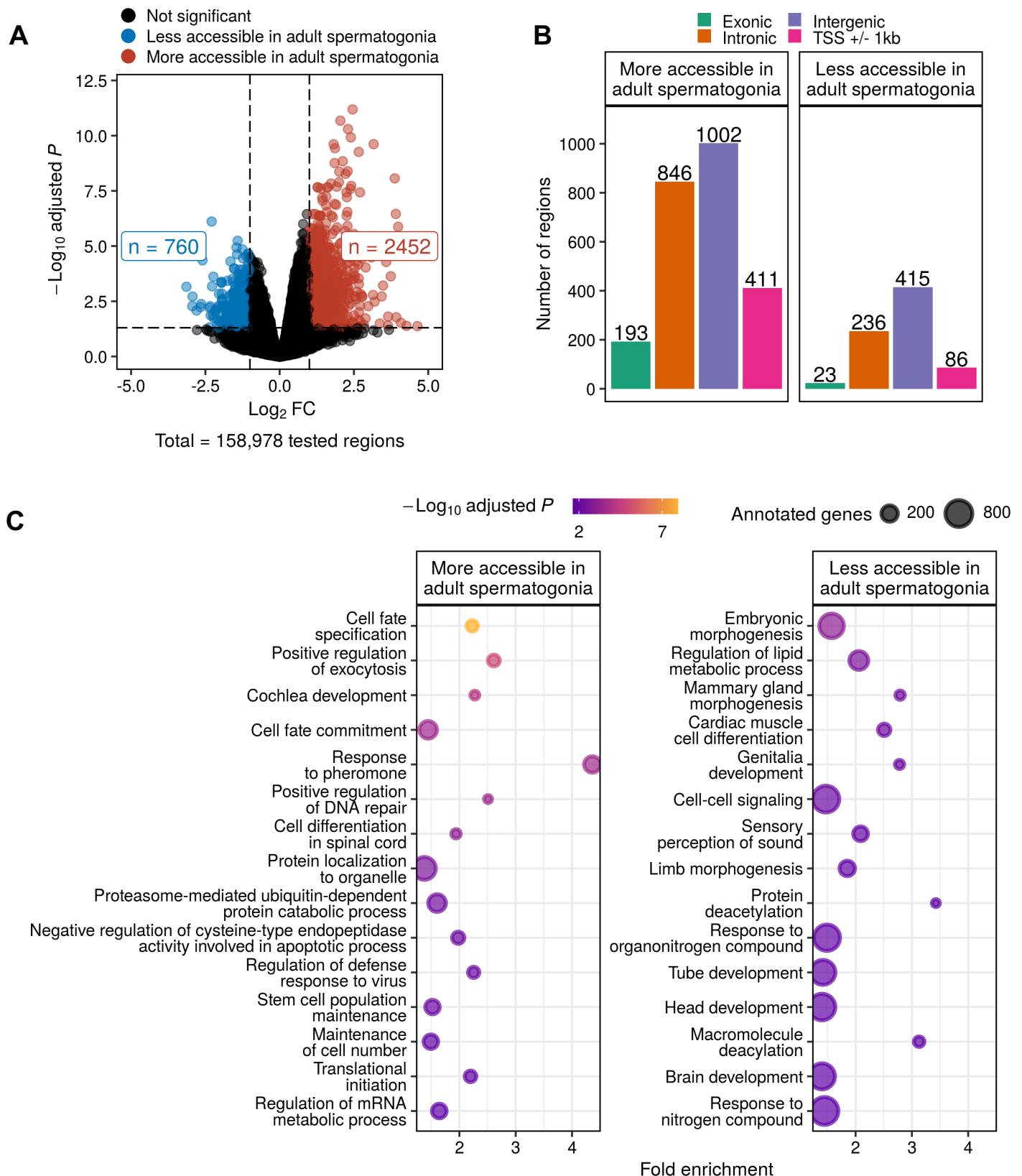


Figure 2

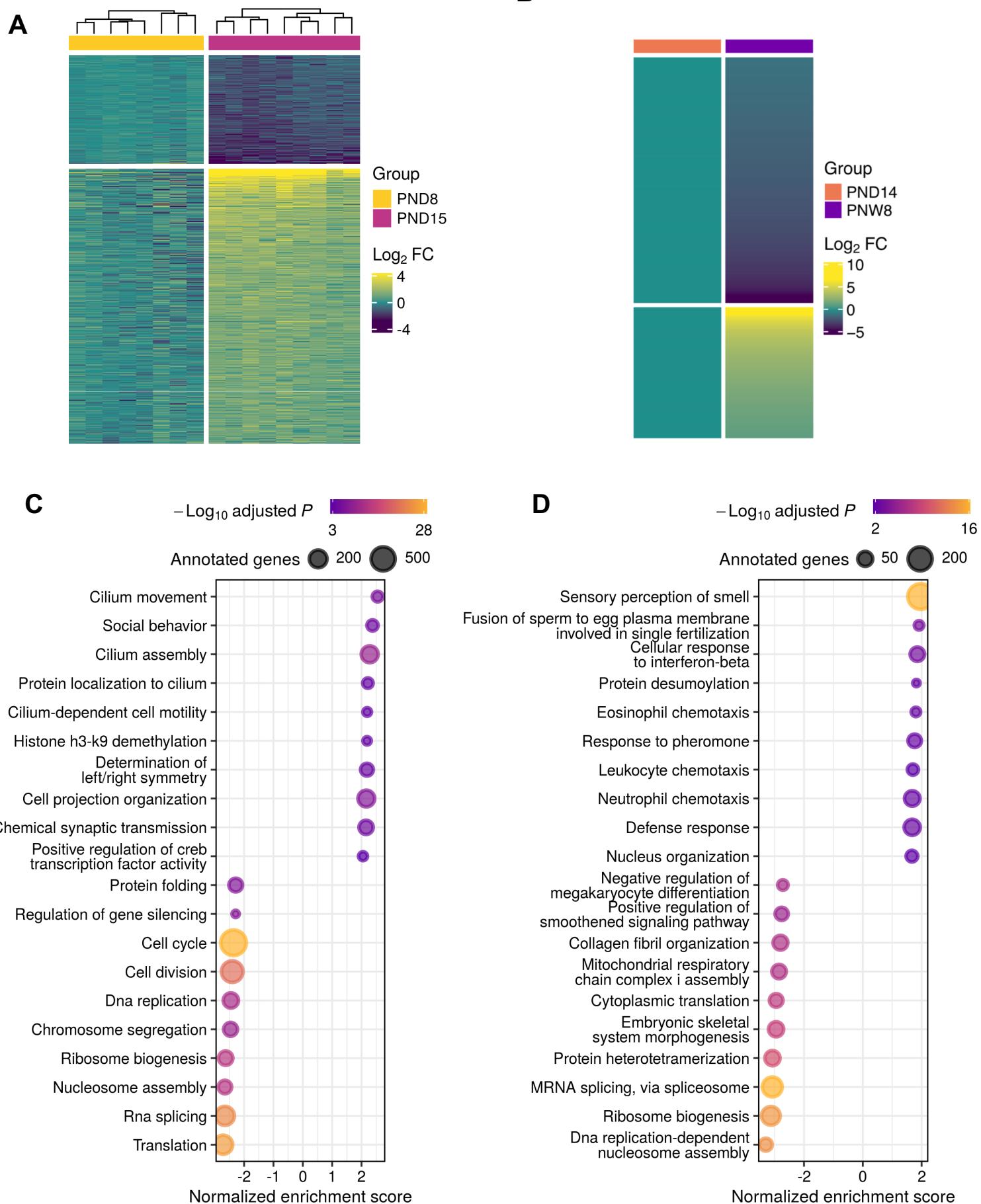


Figure 3

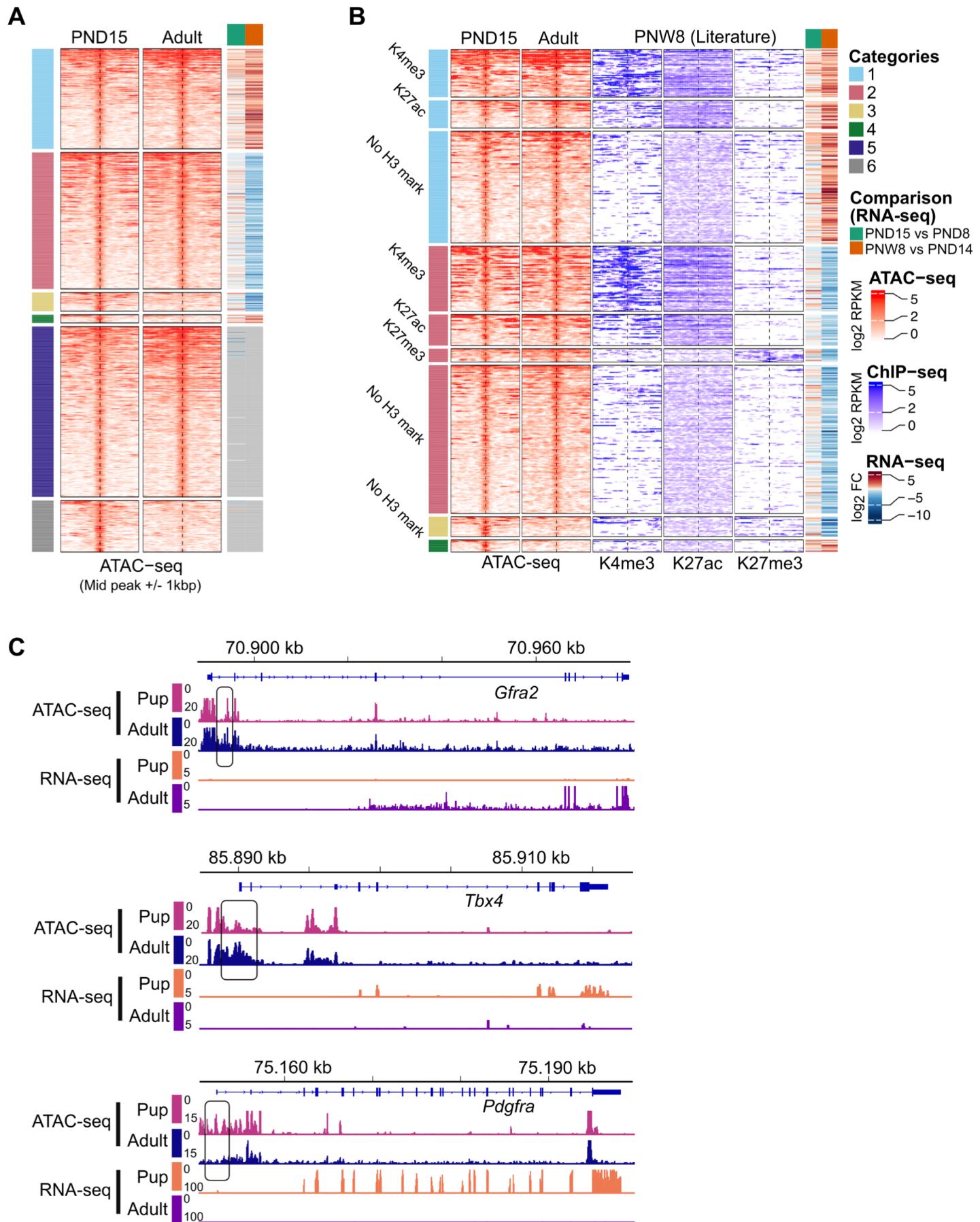
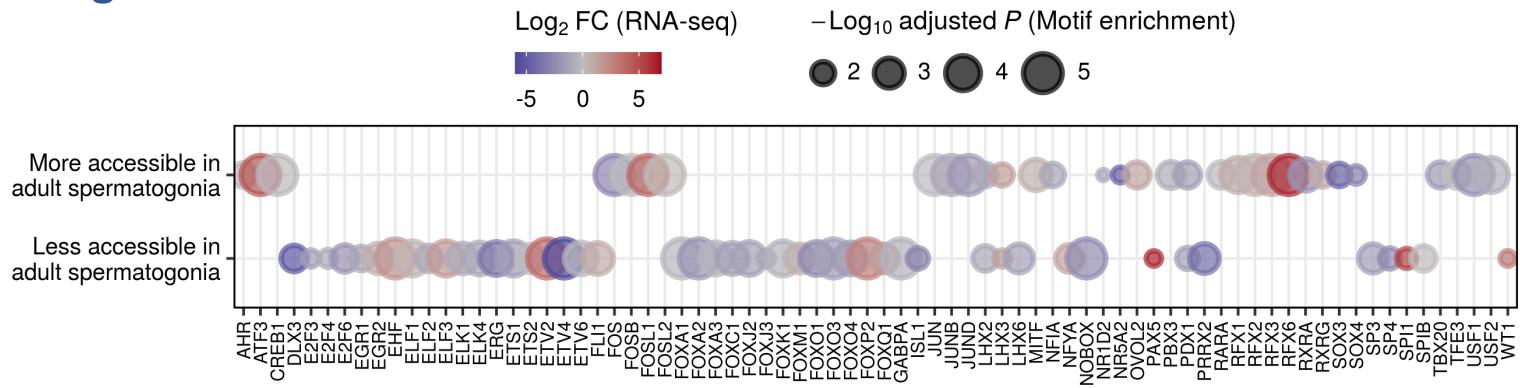
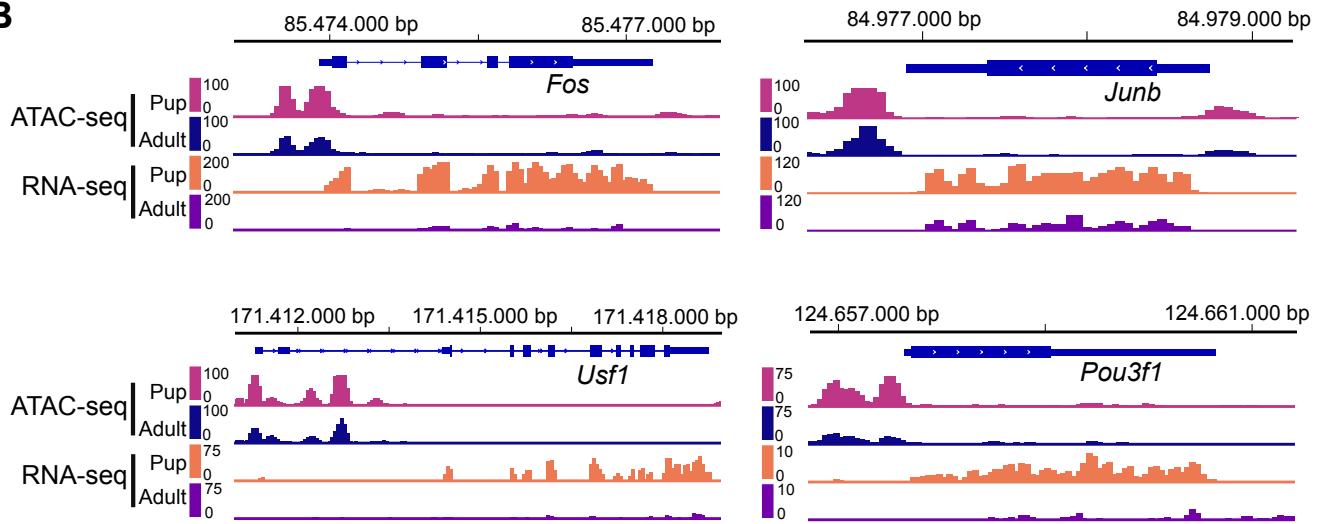


Figure 4



B



C

More accessible regions in adult spermatogonia		
TF	Enriched motif	% of target sequences
JUND		24.35%
FOS		23.98%
ATF3		25.94%
RFX2		30.71%
USF1		23.00%
POU3F1		9.01%

Less accessible regions in adult spermatogonia		
TF	Enriched motif	% of target sequences
EHF		37.63%
FOXO3		36.71%
FOXA1		27.63%
FOXL2		35.53%
GABPA		45.13%
ETV4		38.55%

D

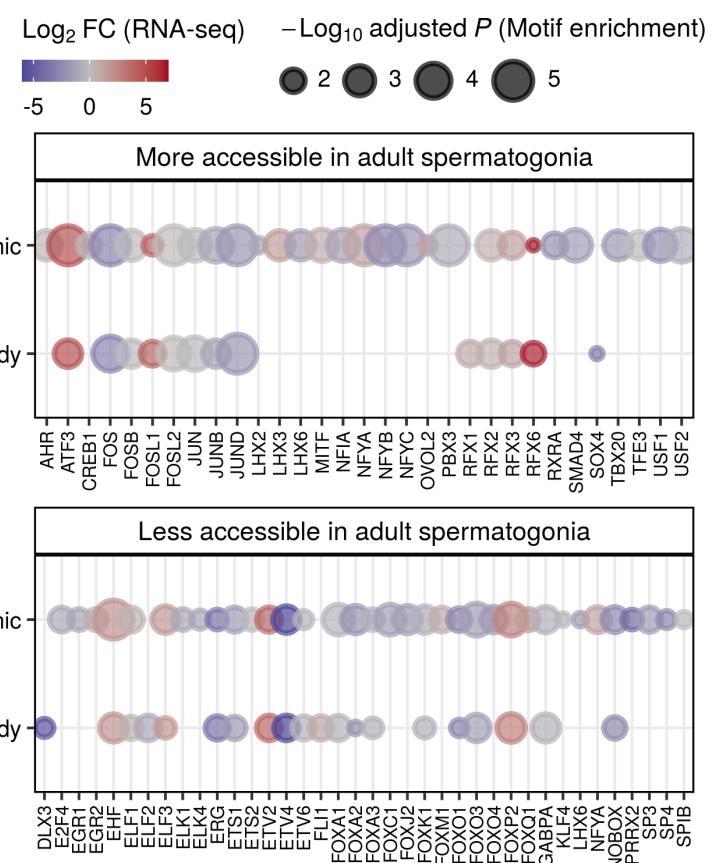


Figure 5

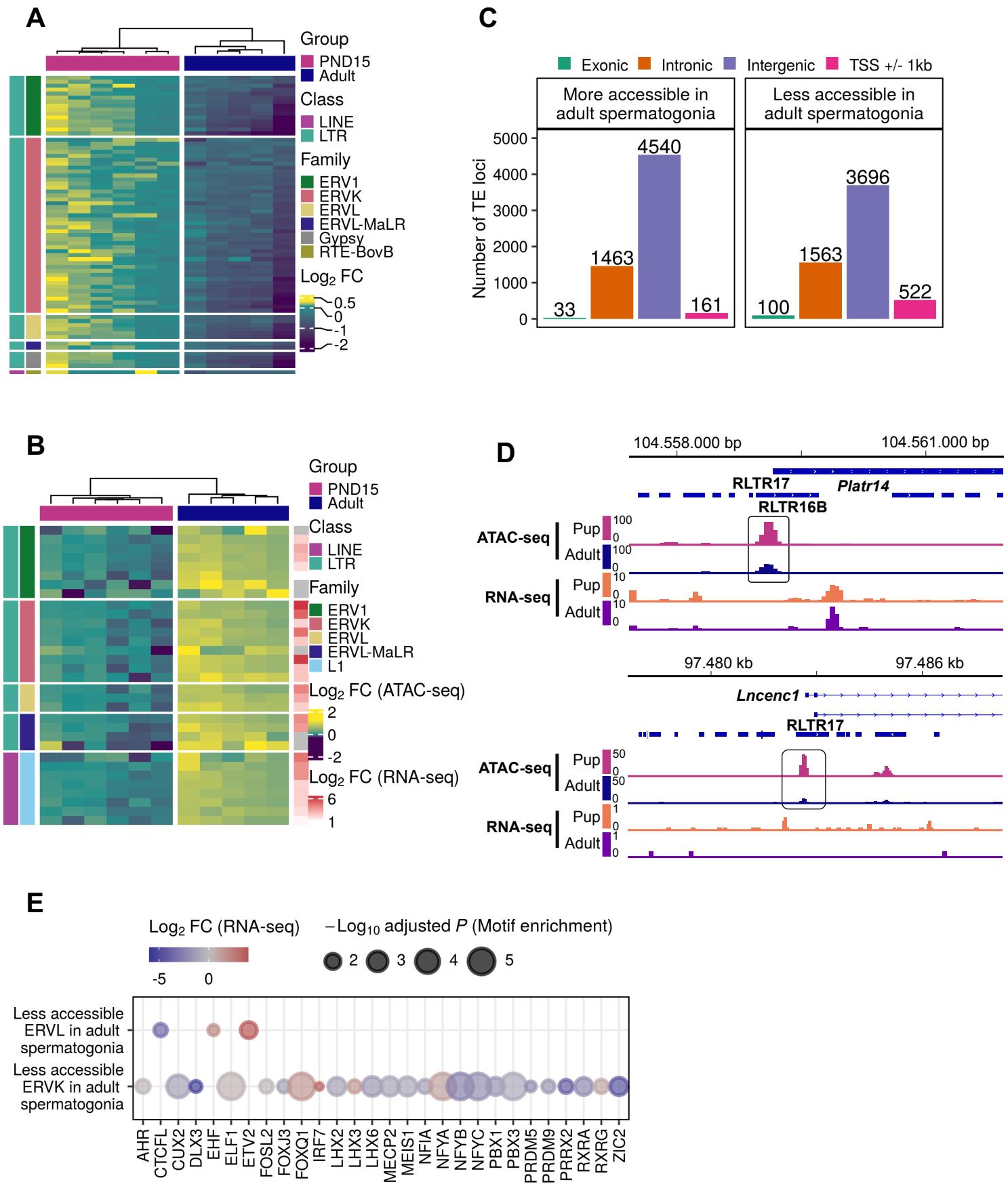
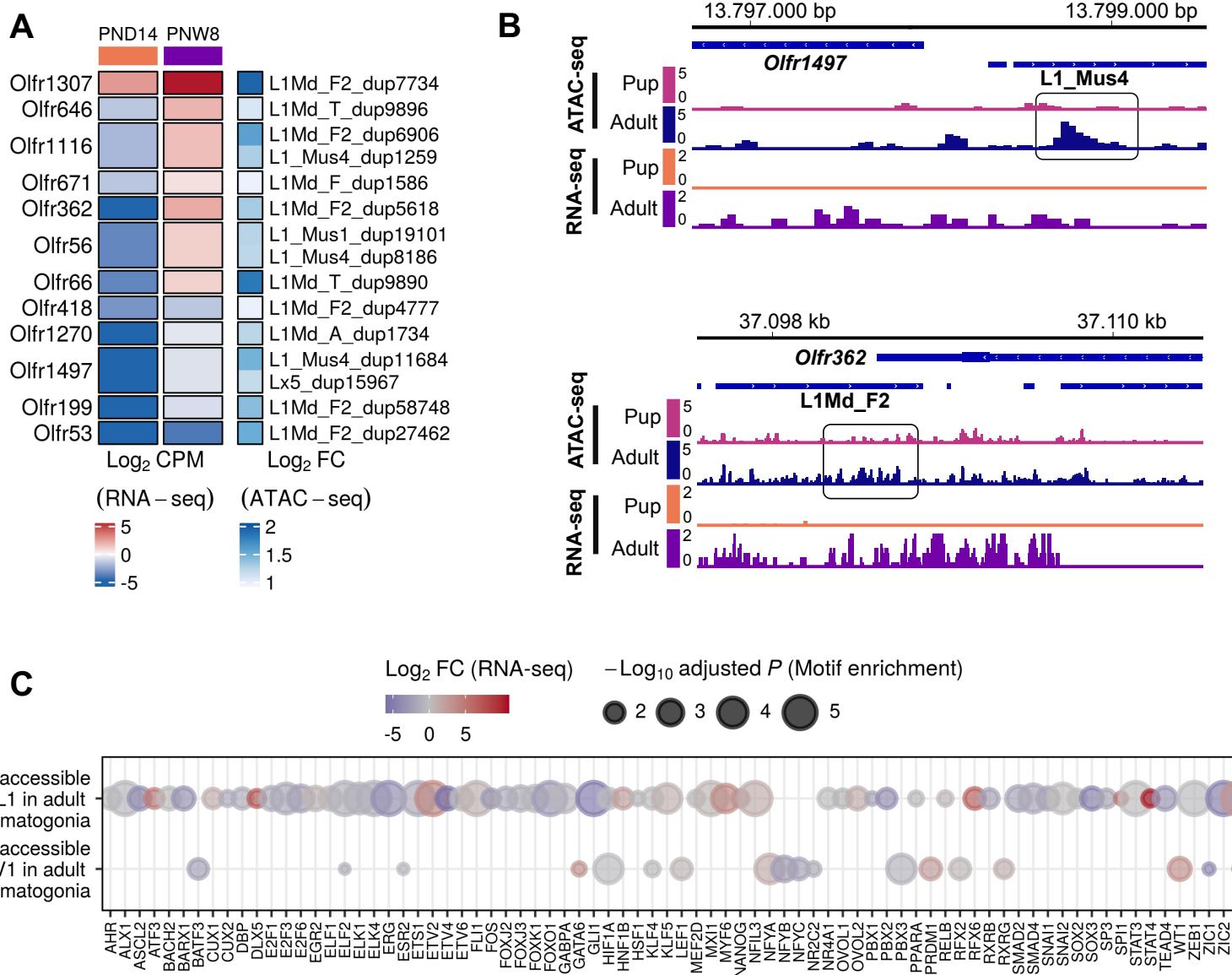
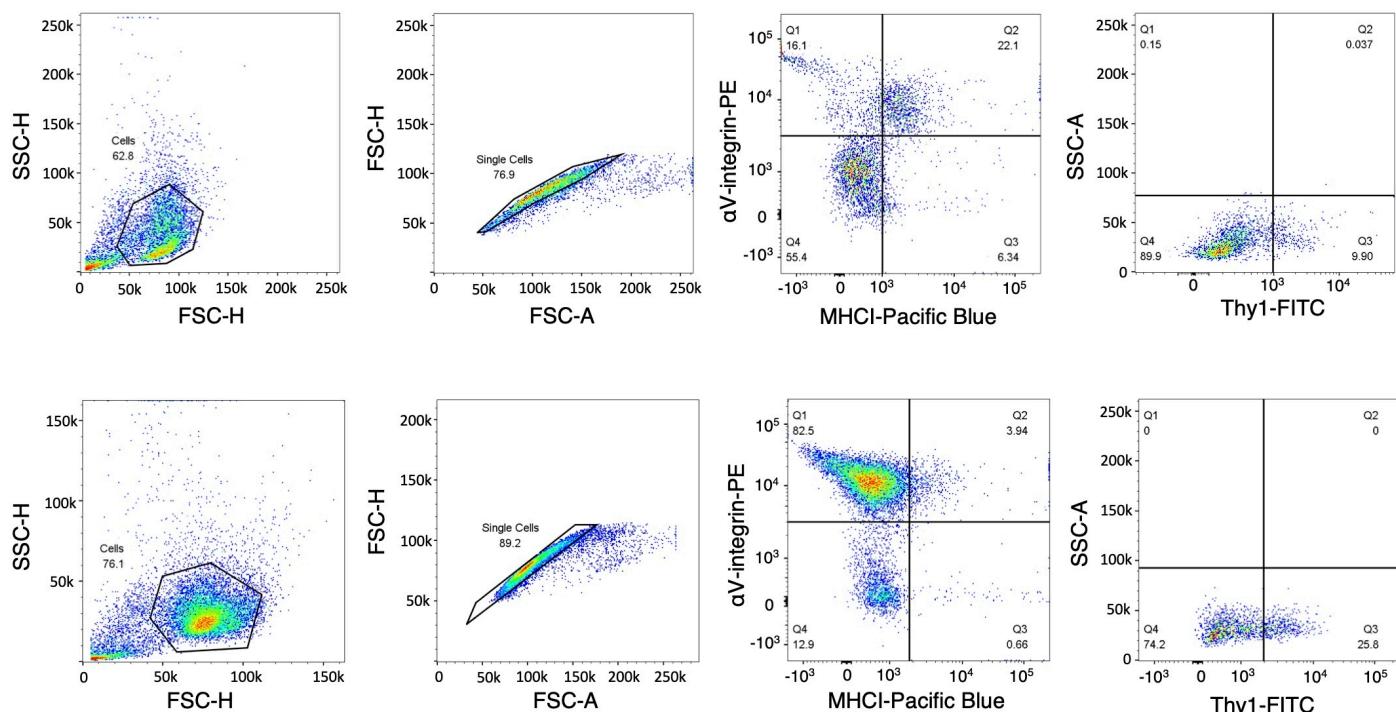


Figure 6

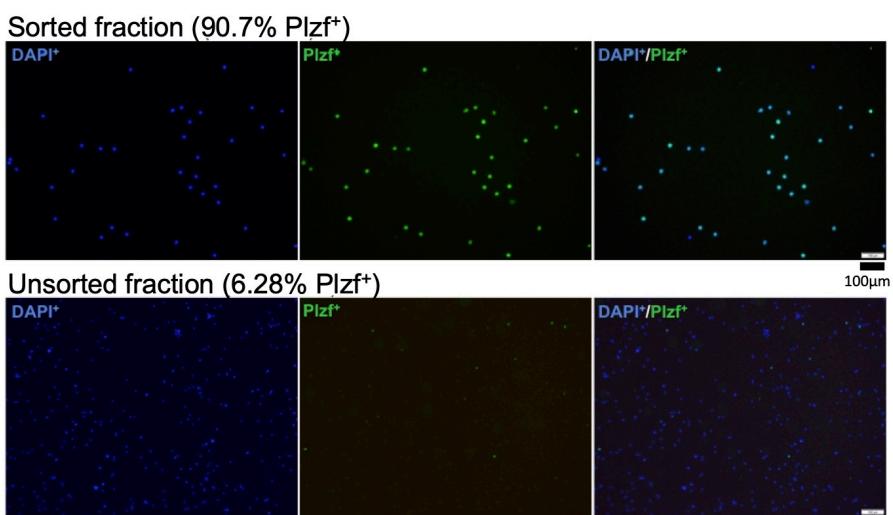


Supplementary figure 1

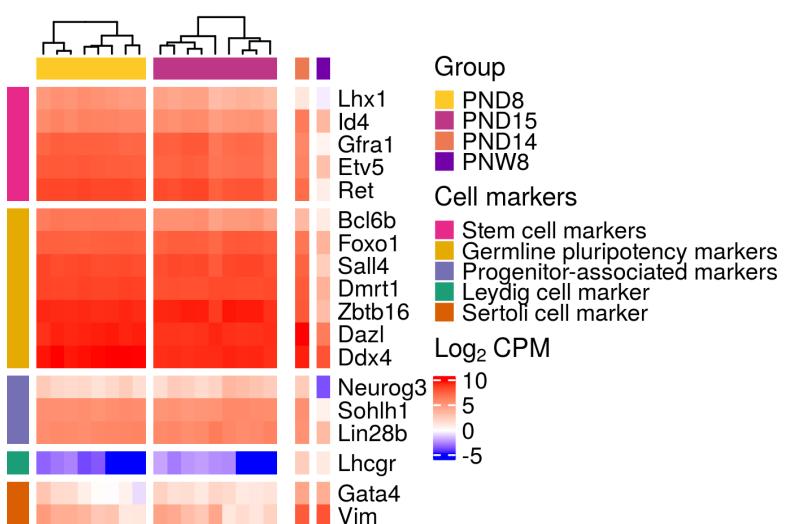
A



B

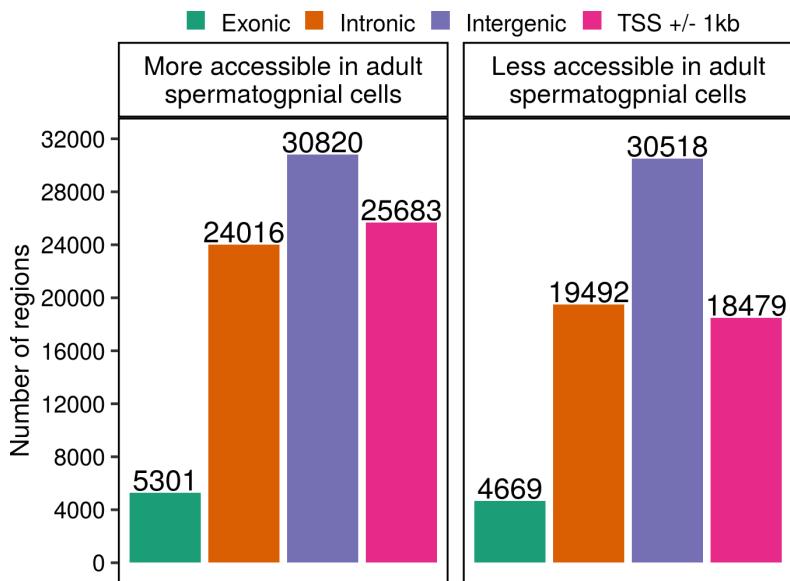


C

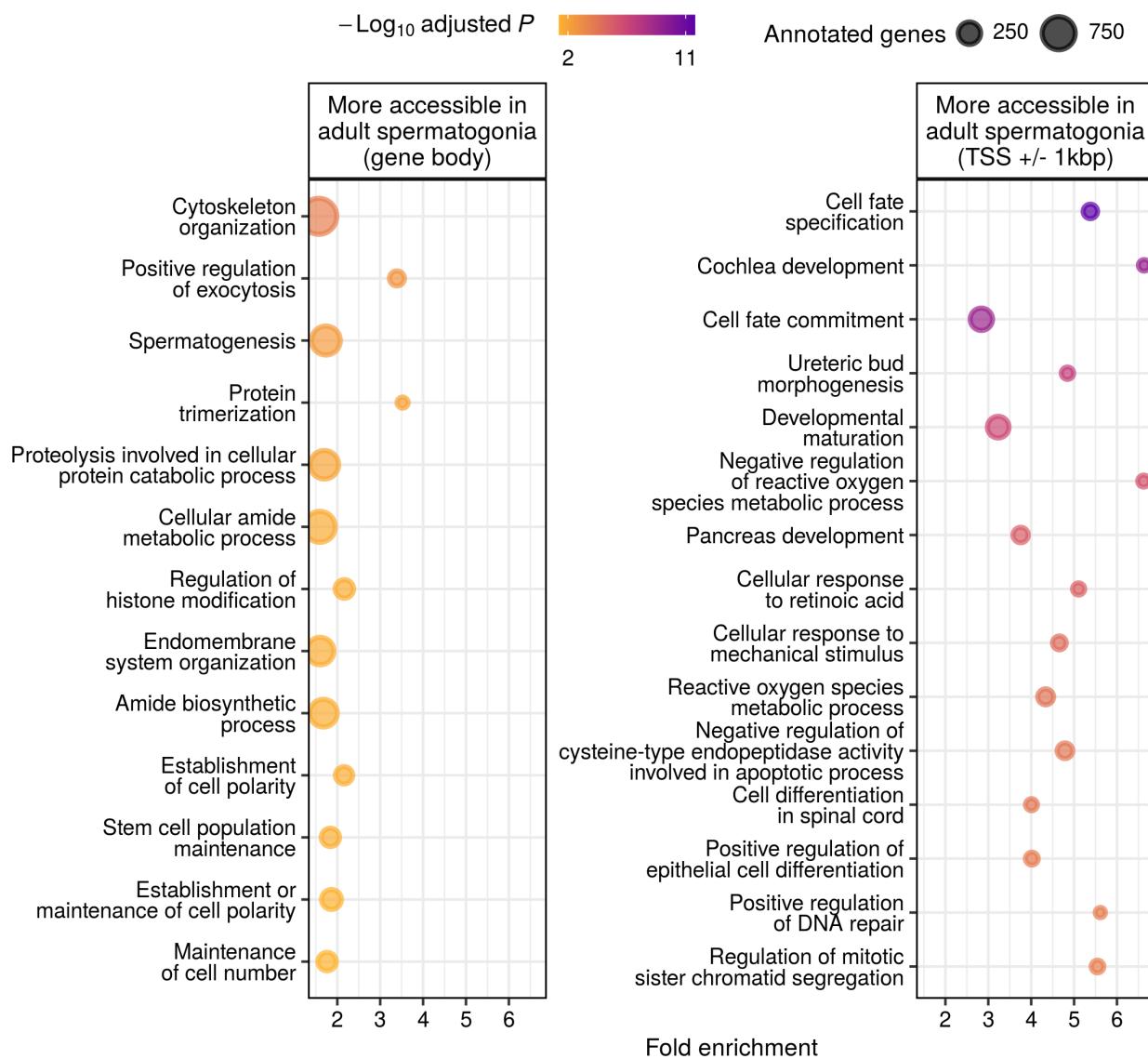


Supplementary figure 2

A

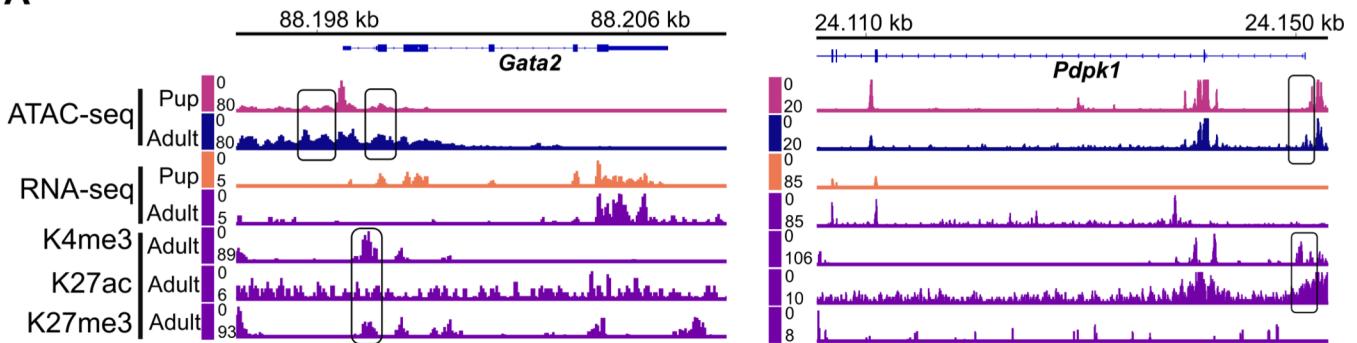


B

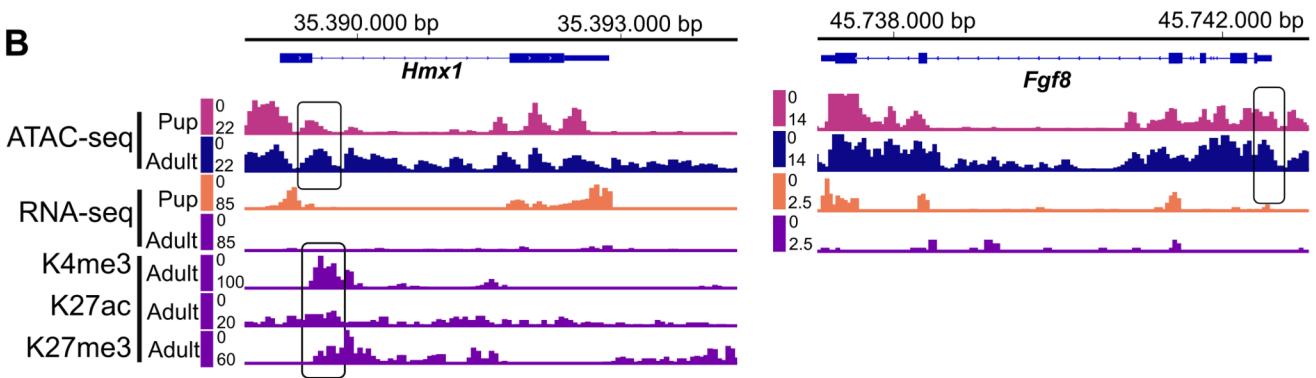


Supplementary figure 3

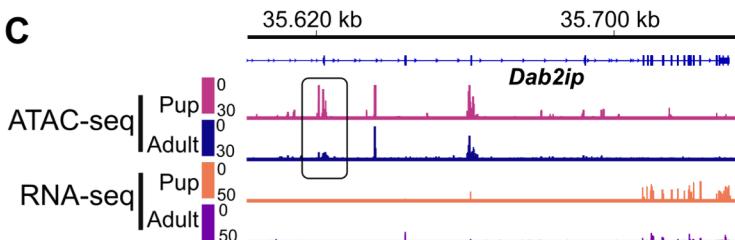
A



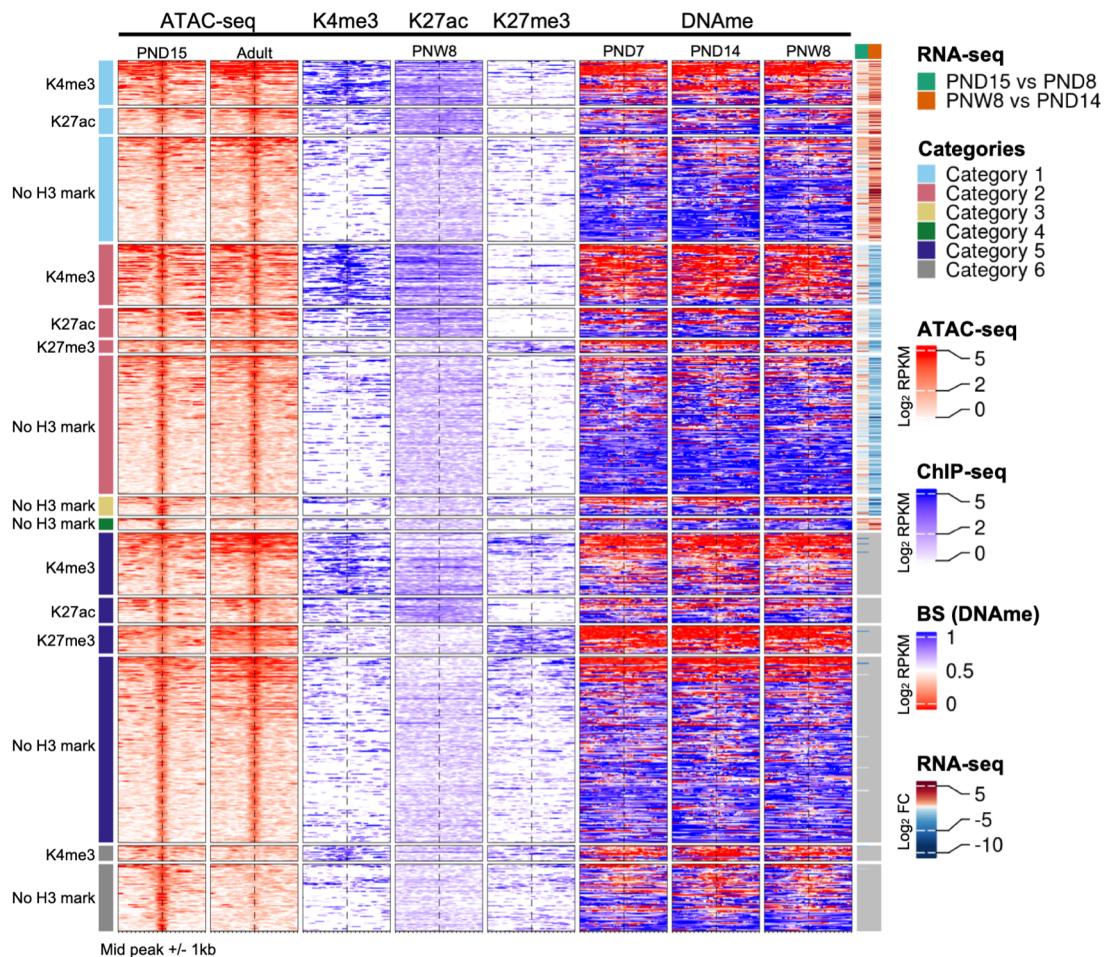
B



C

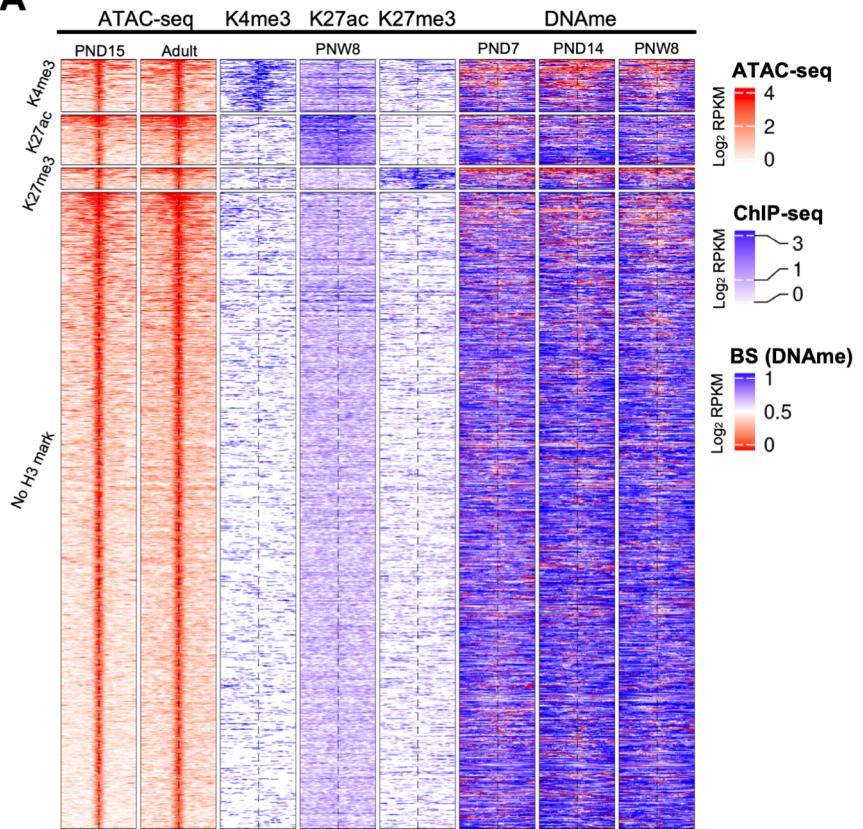


Supplementary figure 4

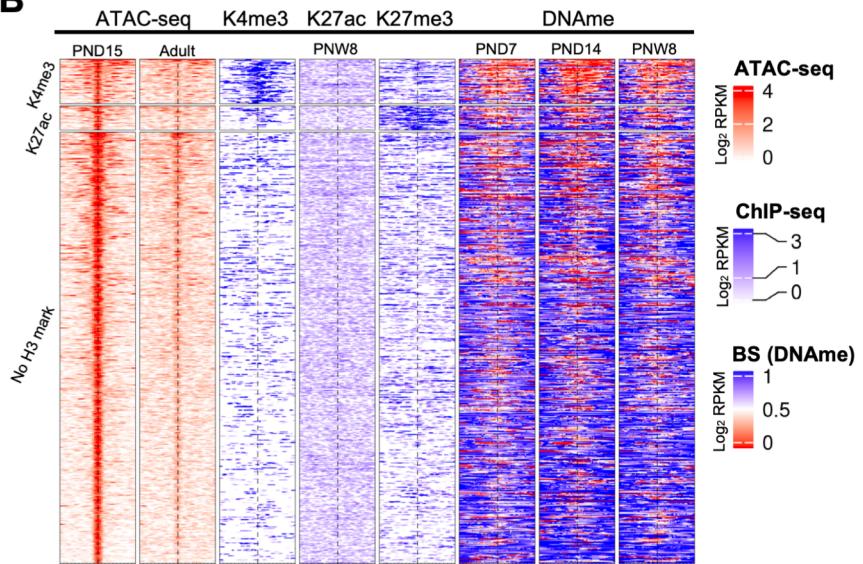


Supplementary figure 5

A



B



Supplementary figure 6

A

Enriched TF motifs in less accessible ERVKs in adult spermatogonia			Enriched TF motifs in less accessible LINE L1s in adult spermatogonia		
TF	Enriched motif	% of target sequences	TF	Enriched motif	% of target sequences
PBX3	CTC TGATTGGCTGG AAGCCCGAACTT	24.15%	FOXO1	CCC TGTTCAC CGG TGGCTTG	15.02%
THAP11	GACATCTGGAGTTGAGTC TCACTGTTGTTA	22.25%	ZEB1	GACAGGTGAG CCATGGAACT	14.7%
ZNF143	GACATCTGGAGATGTAGTC TCACTGTTGTTA	27.21%	E2F3	GGCCGGGAAGG ACCTGGGAACT	13.79%
FOXL1	CTC TGATTGGTTCC AAGCGCTT	24.53%	KLF5	GGGGCAGGGT AAACGTCGGGC	12.67%
NF-YA	TCAGGCCAATCAGAA CTGACCCGACG	25.88%	ZBTB17	GGGGGTGGGGGACGGG CCGGCGGCGAAC	12.74%

B

