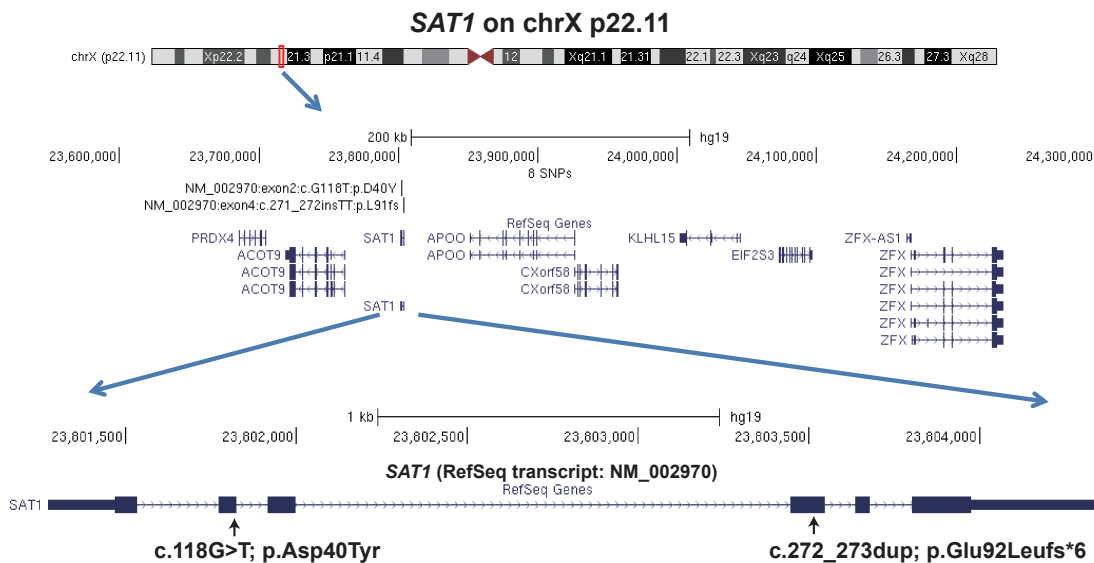
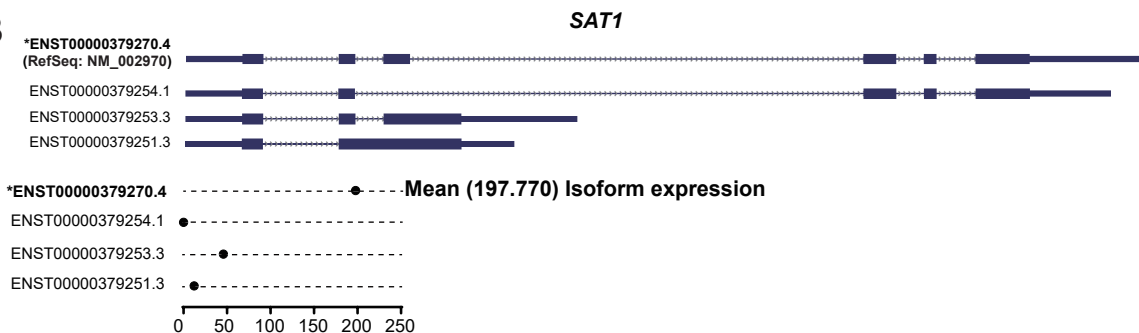


Supplementgatory figure 1

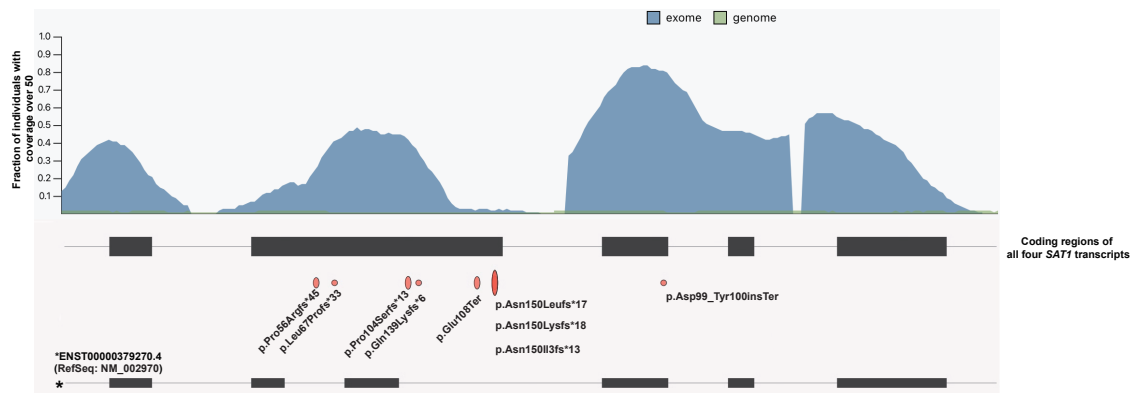
A



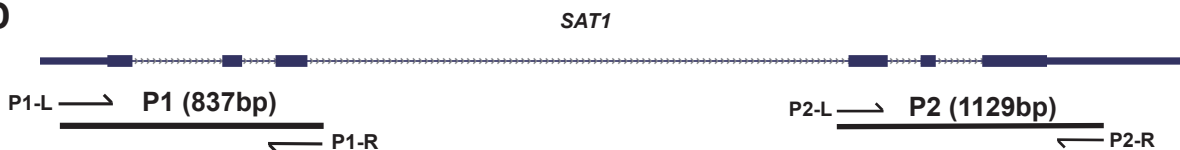
B



C



D



Supplementary figure 2

A

p.Asp40Tyr
↓

Human	M	E	E	Q	V	I	L	T	E	K	D	G	T
Rhesus	M	E	E	Q	V	I	L	T	E	K	D	G	T
Mouse	M	E	D	Q	V	I	L	T	E	K	D	G	T
Dog	R	E	G	Q	V	I	L	T	E	K	D	G	T
Elephant	M	E	E	K	V	R	L	T	E	K	D	G	T
Chicken	M	E	D	Q	V	V	L	T	E	K	D	G	T
X_tropicalis	M	E	N	Q	V	V	L	T	E	K	D	G	T
Zebrafish	M	E	D	Q	V	L	L	T	E	K	D	G	T

p.Glu92Leufs*6
↓

Human	P	W	I	G	K	L	L	Y	L	E	D	F	F
Rhesus	P	W	I	G	K	L	L	Y	L	E	D	F	F
Mouse	P	W	I	G	K	L	L	Y	L	E	D	F	F
Dog	P	W	I	G	K	L	L	Y	L	E	D	F	F
Elephant	P	W	I	G	K	L	L	Y	L	E	D	F	F
Chicken	P	W	I	G	K	L	L	Y	L	E	D	F	F
X_tropicalis	P	W	I	G	K	L	L	Y	L	E	D	F	F
Zebrafish	P	W	I	G	K	L	L	Y	L	E	D	F	F

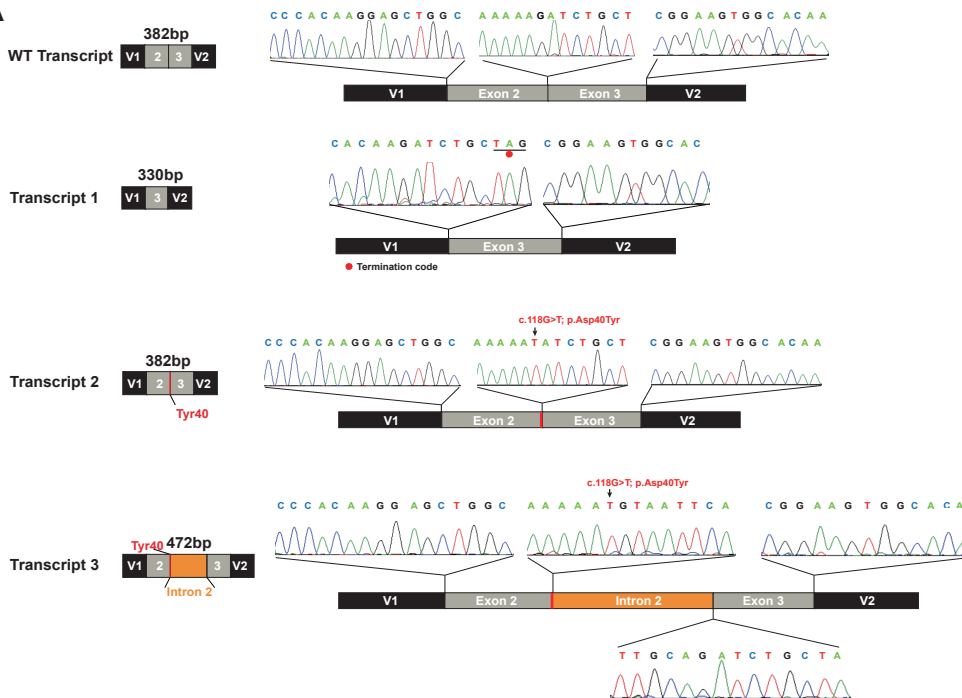
B

Computational prediction

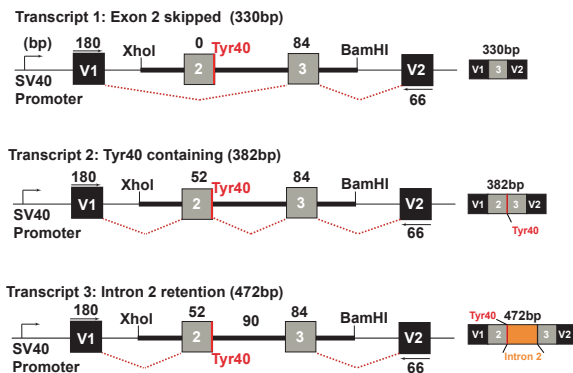
	SIFT	Polyphen2	fathmm-MKL	LRT	MutationTaster	MutationAssessor	PROVEAN	MetaSVM
p.Asp40Tyr	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious	High functional impact	Deleterious	Deleterious

Supplementary figure 3

A

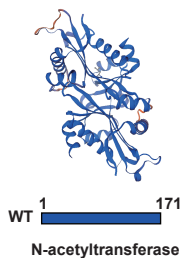


B

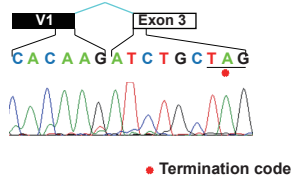


C

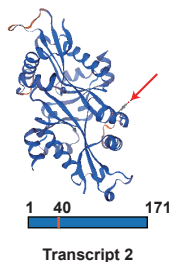
SSAT Protein Model (Homo-dimer)



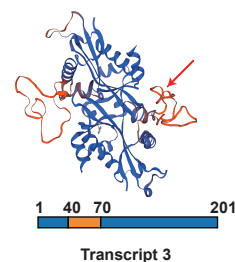
Transcript 1: Exon 2 skipped (Stop gain)



Transcript 2: Tyr40 containing

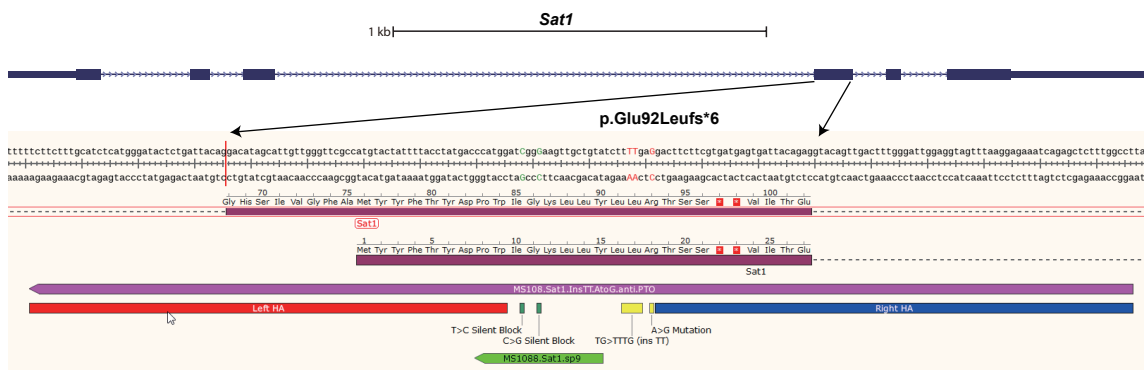


Transcript 3: Intron 2 retention



Supplementary figure 4

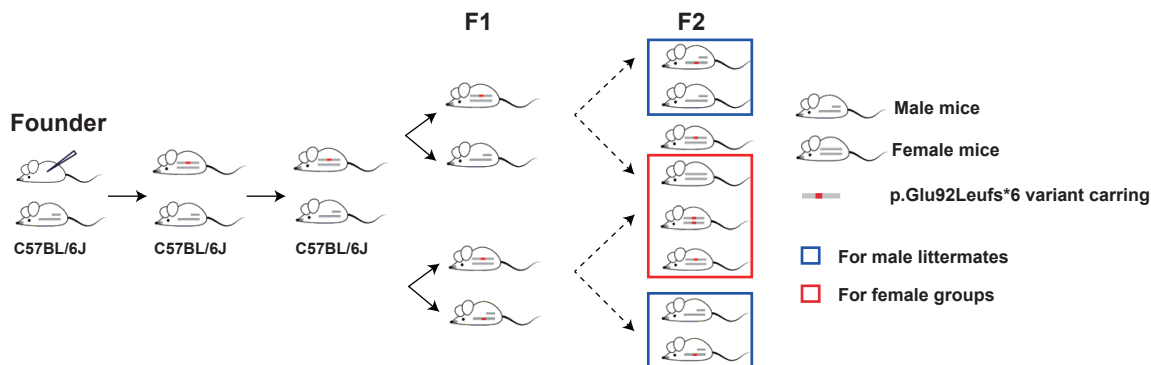
A



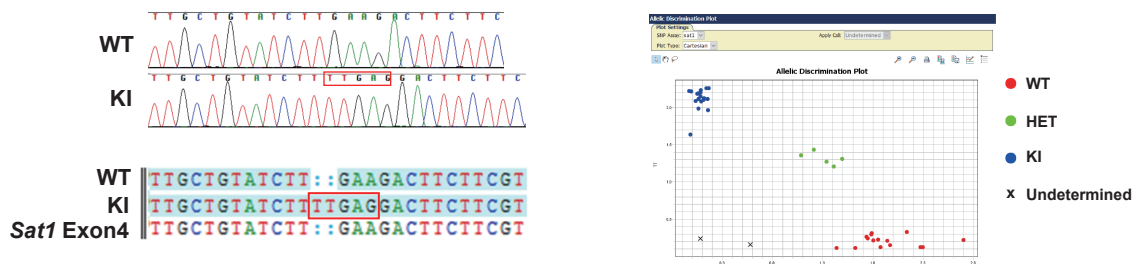
B

	Strand	Chr	Position (mm9)	Mismatch nt	Target
MS1088.Sat1.sp9	+	chrX	155214068	None	Target
MS1088.Sat1.sp9	+	chr17	16320764	5:T>C	Intergenic
MS1088.Sat1.sp9	+	chr5	29794769	5:T>C	Intergenic

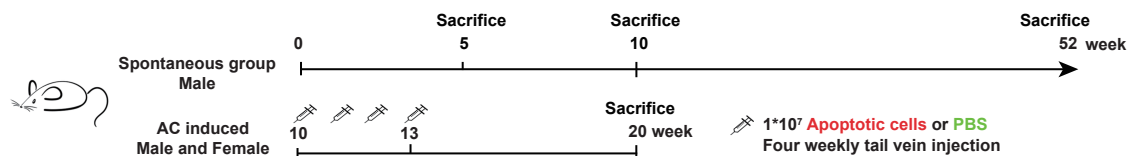
C



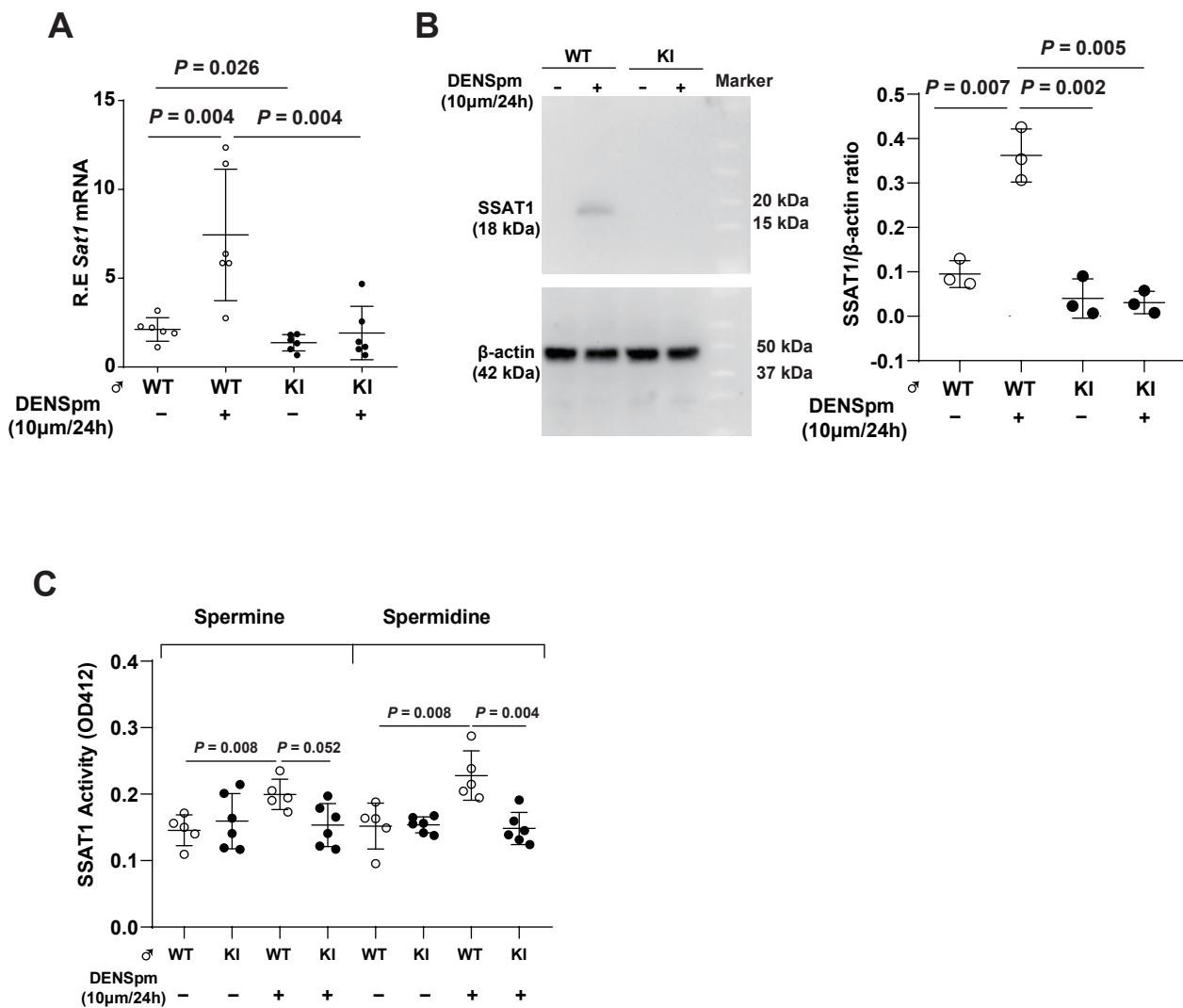
D



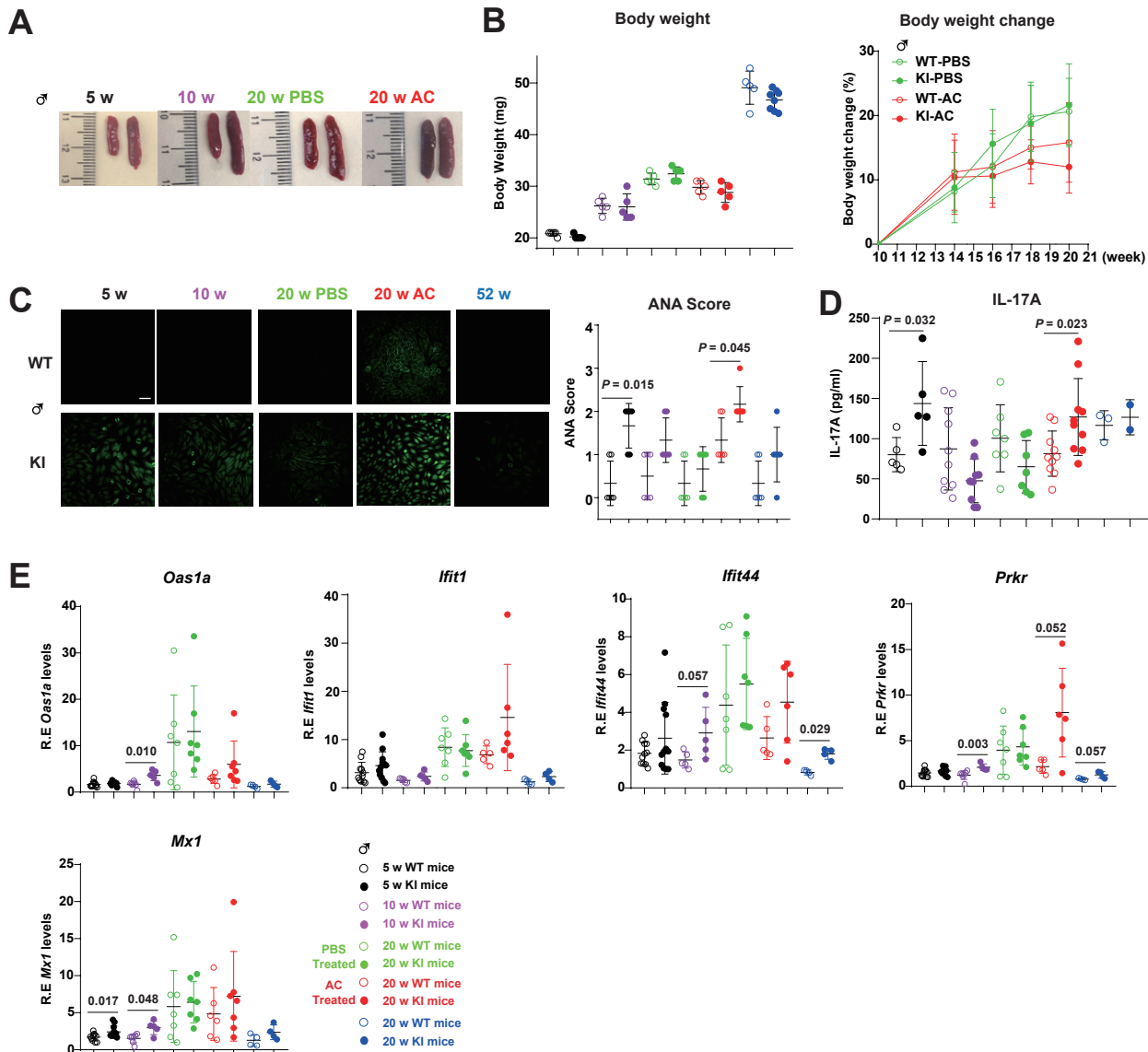
E



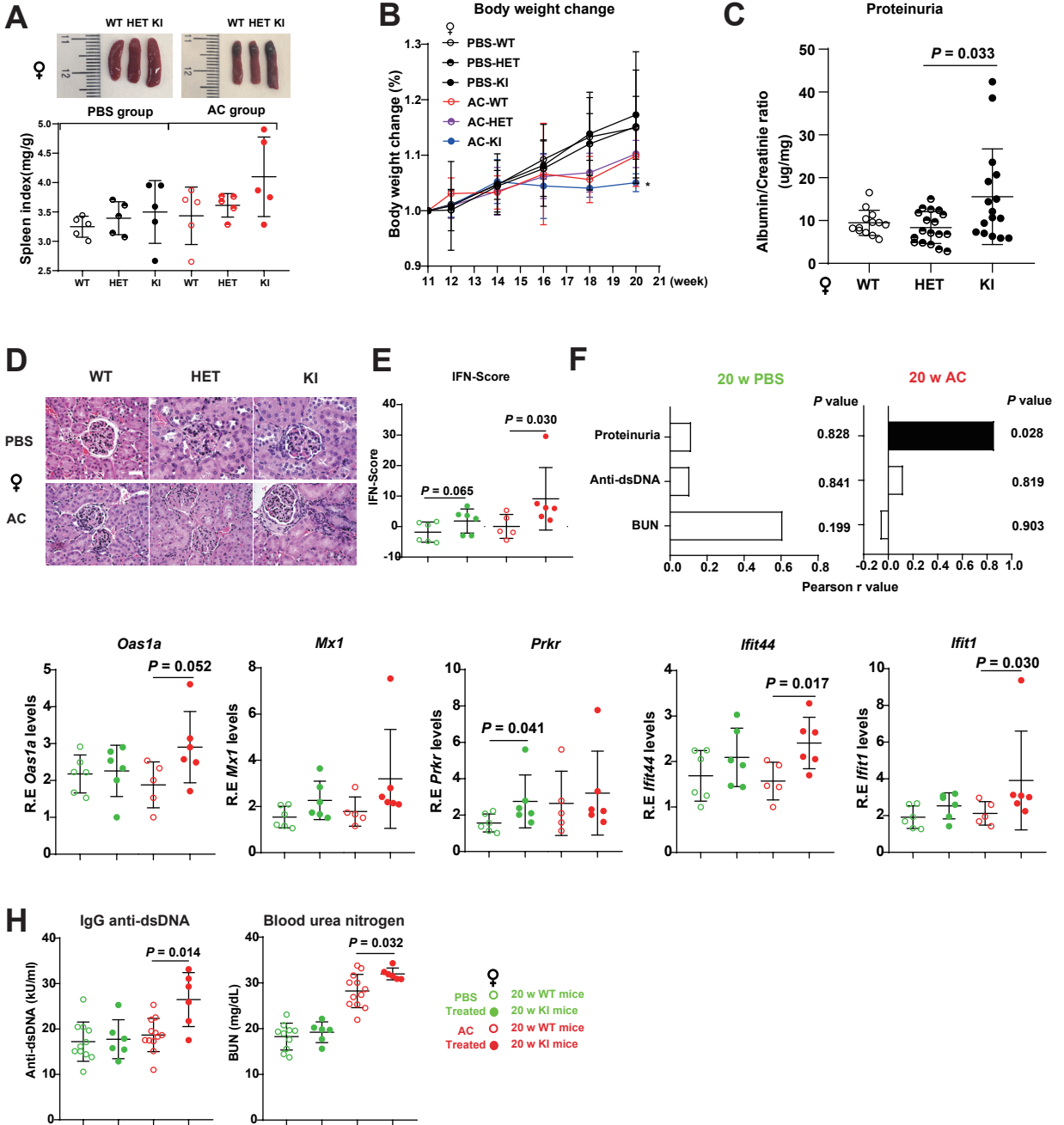
Supplementary figure 5



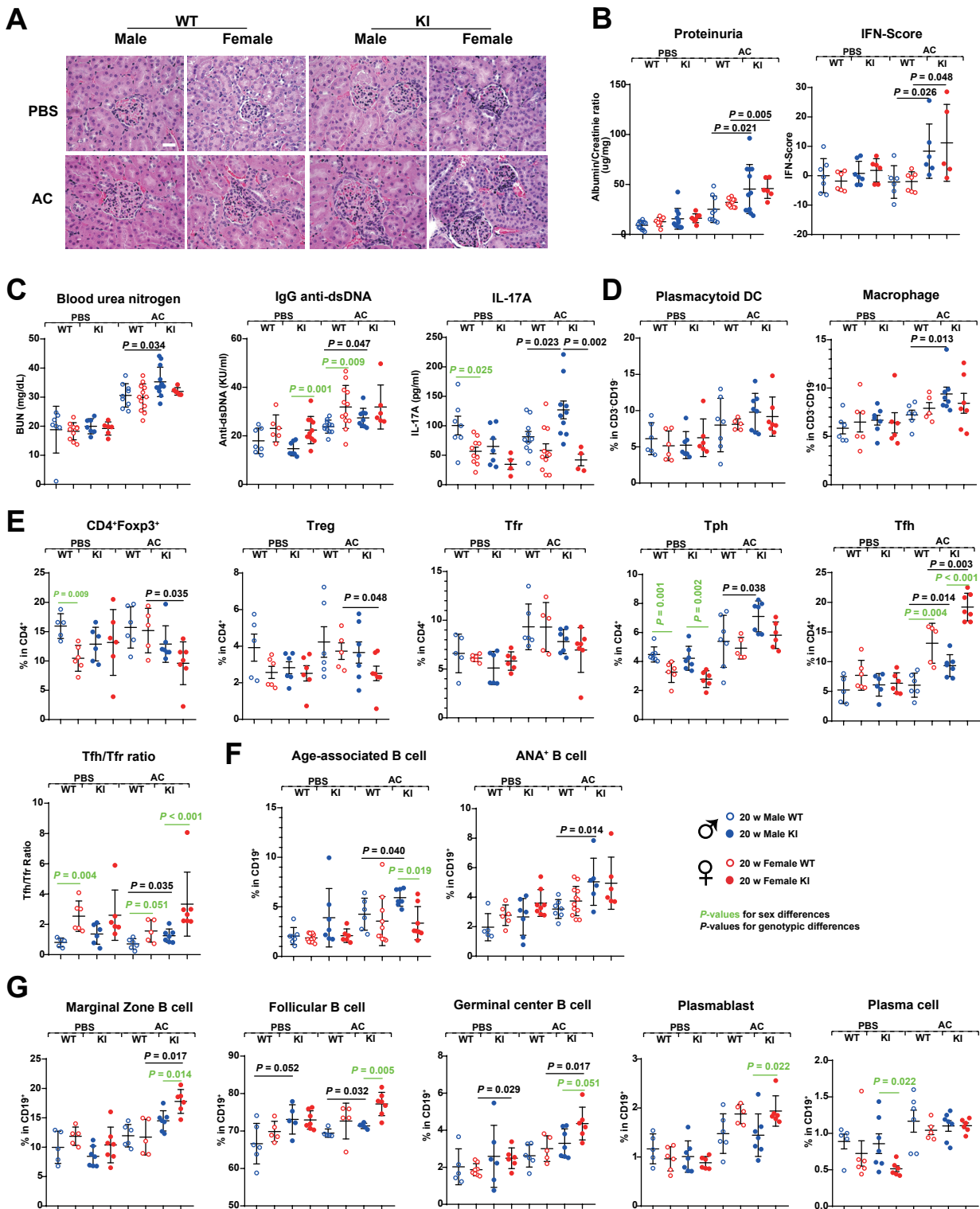
Supplementary figure 6



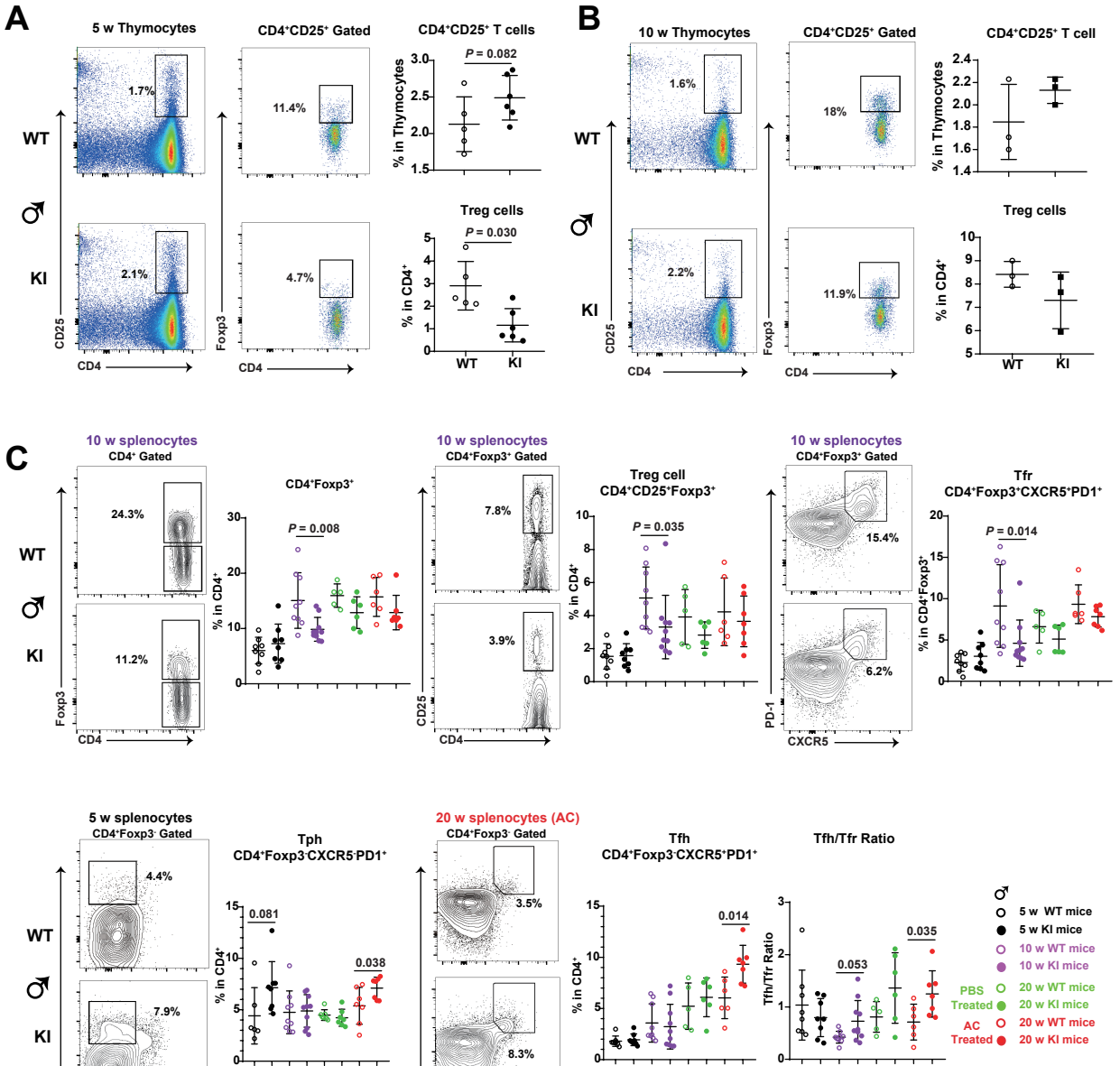
Supplementary figure 7



Supplementary figure 8



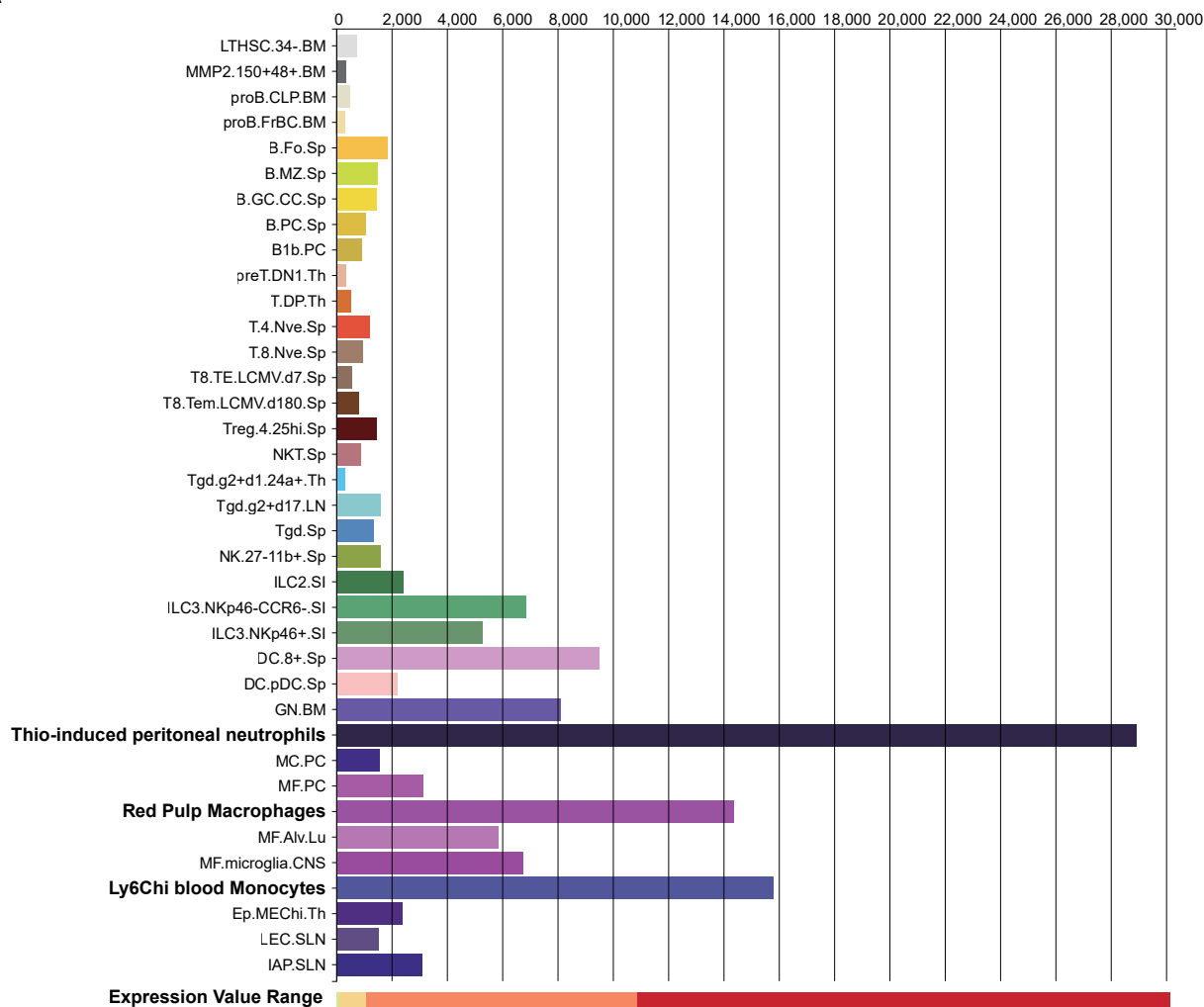
Supplementary figure 9



Supplementary figure 10

A

Gene: **Sat1 (C57BL/6J)**



B

Consensus dataset¹

RNA cell type specificity: Cell type enhanced (neutrophil)

Lineage Expression Alphabetical

