

1 **Figure Legends (Supplementary figures)**

2 Supplementary Figure 1: a. Age distribution of the study subjects was similar across the
3 groups (Mann-Whitney U-test) b. More than 75% of patients were younger than 60 years
4 when individual MDS patients were sorted in the increasing order of their age. c. Age
5 distribution across IPSS-R subcategories was similar (Kruskal-Wallis test). d. Age distribution
6 did not vary across MDS subtypes (Kruskal-Wallis test)

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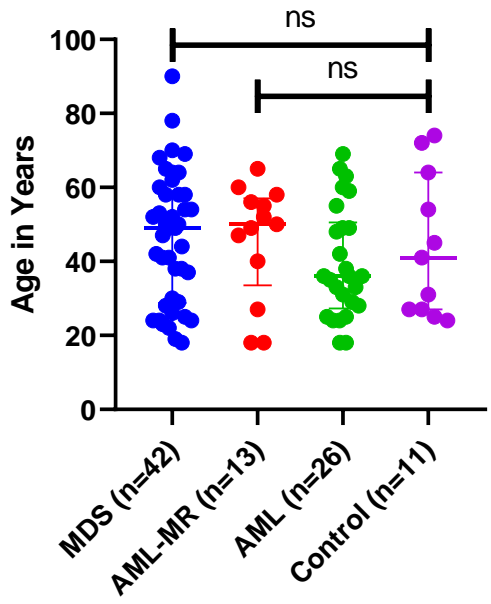
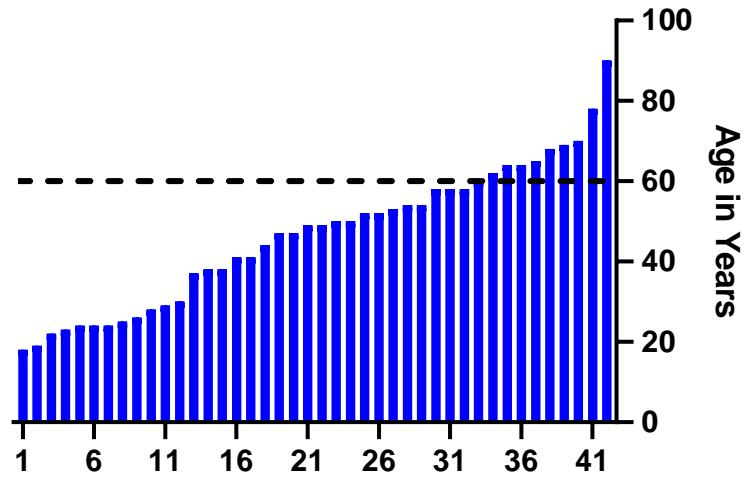
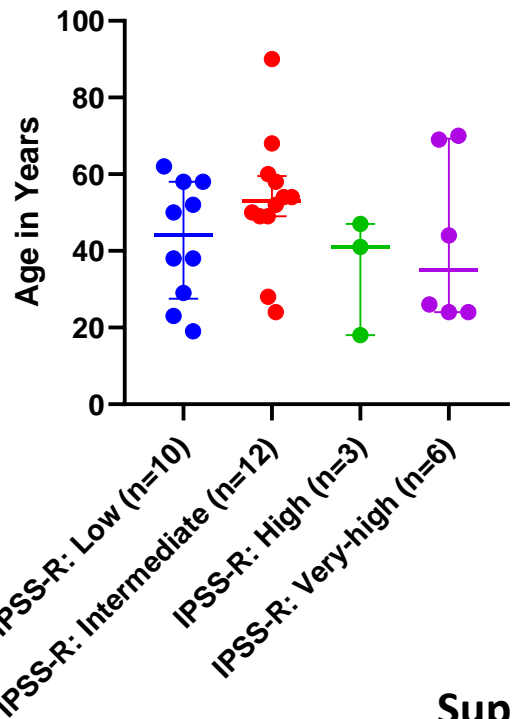
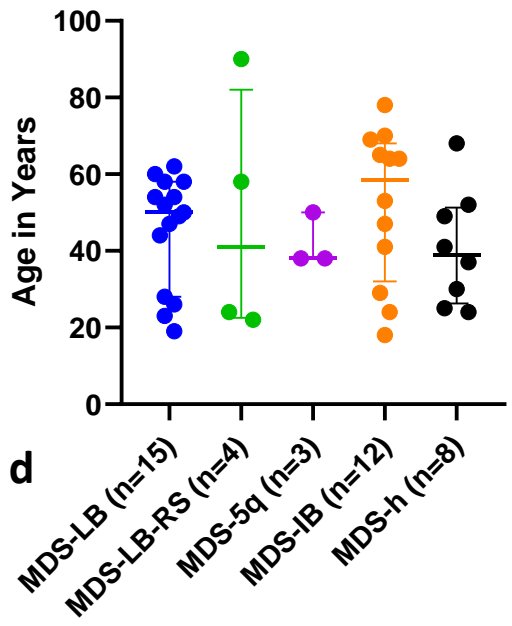
8 Supplementary Figure 2: Immunohistochemistry for 5-hmC in the study subjects' bone
9 marrow biopsy FFPE sections. The left panels (a, c, e, and g) show magnification at 10X
10 objective, and the right panels (b, d, f, and h) at 40X objective. 5-hmC positive cells show
11 brown staining. The samples are arranged IPSS-R low risk on top (a and b), followed by
12 intermediate risk (c and d), high risk (e and f), and very high risk (g and h). The percentage of
13 nuclear positivity for 5-hmC in these samples is 10%, 5-10%, < 5%, and < 5%, respectively.
14 Additional IHC images showing 5-hmC in the controls, IPSSR-Low, IPSSR-Intermediate, IPSSR-
15 High and AML-MRC samples.

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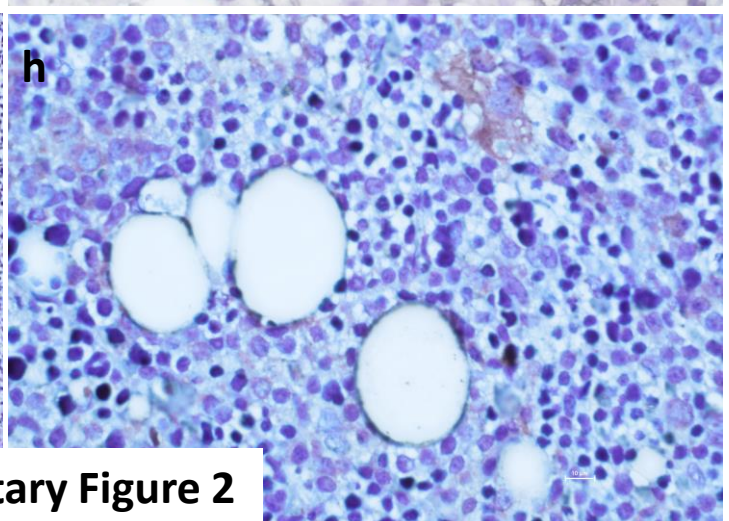
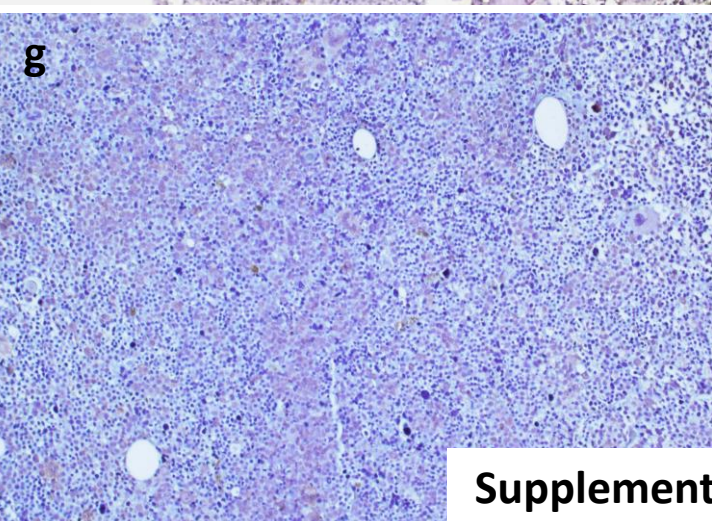
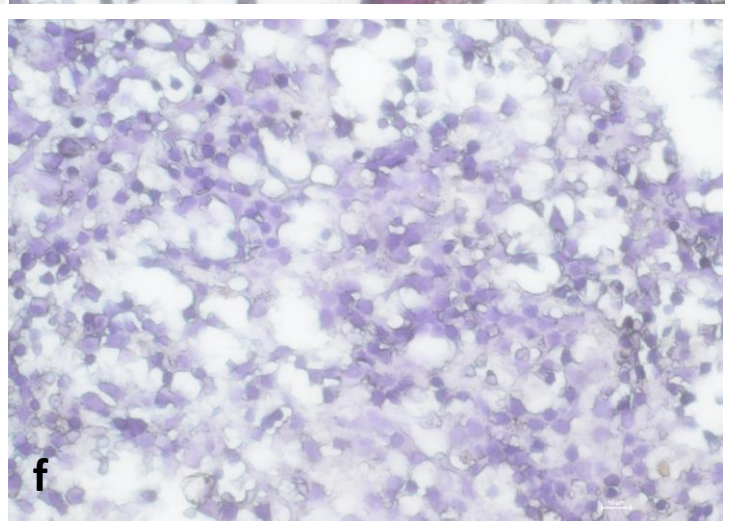
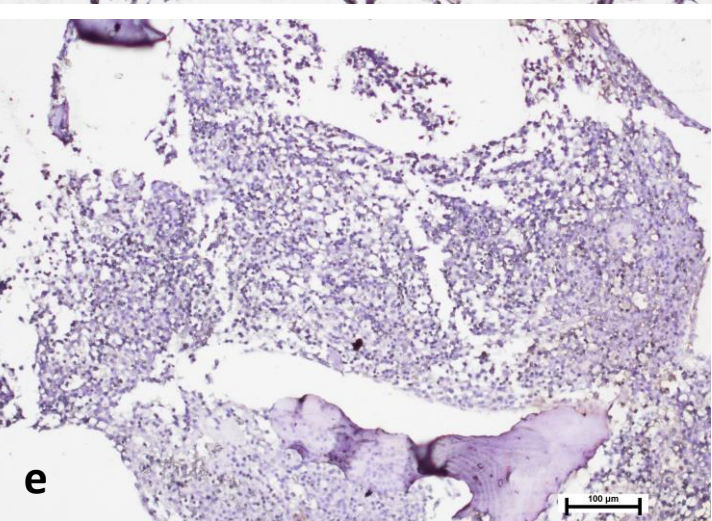
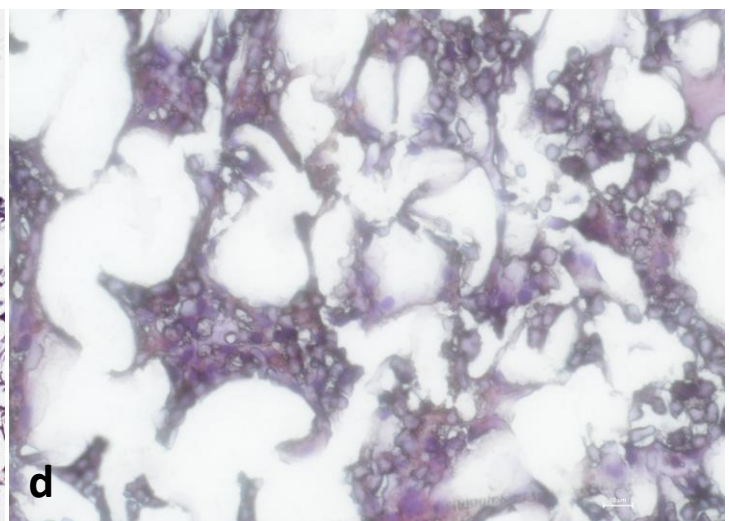
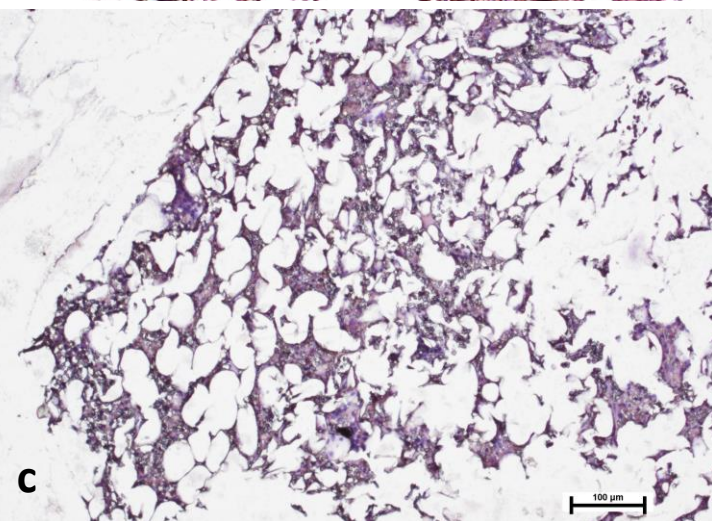
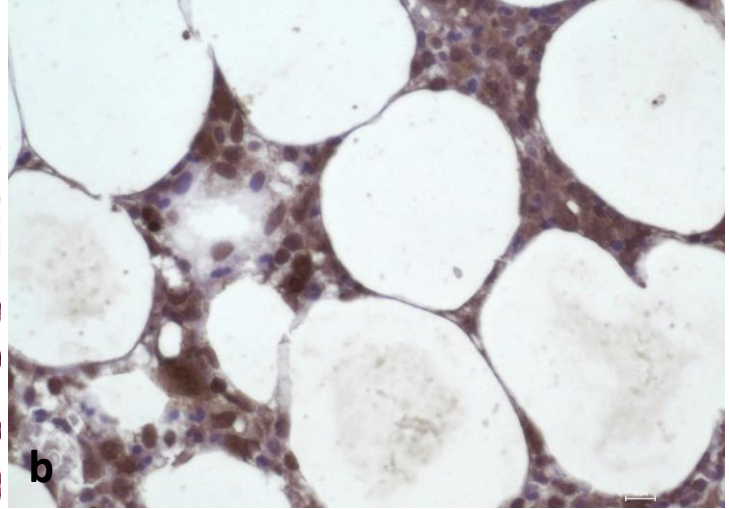
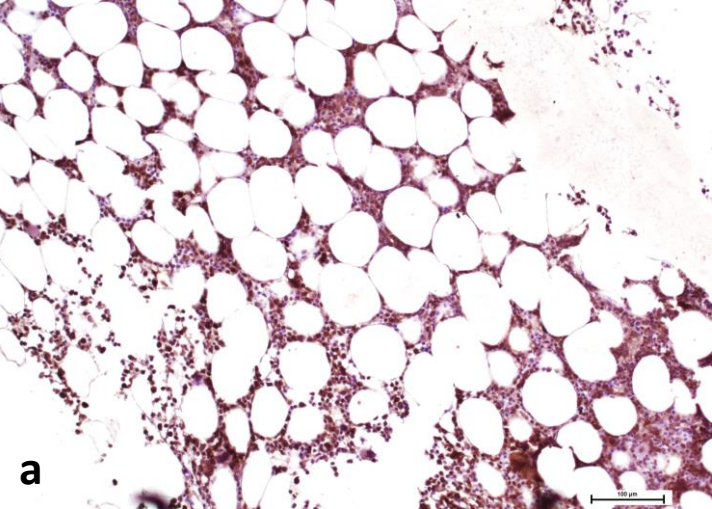
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18 Supplementary Figure 3: Deleterious effects of *TET2* p.H1778R on catalytic activity: a. *TET2*
19 variant (c.A5333G:p.H1778R) from an IPSS-R intermediate risk patient visualized in
20 Integrative Genomics Viewer showing the frequency of the pathogenic variant across all the
21 reads b. The percentage of 5-hmC of the same patient is shown using a star. c. *TET2* expression
22 in the same patient is shown using a star. d. Immunohistochemistry for 5-hmC in the patient's
23 bone marrow biopsy FFPE sections showed < 5% nuclear positivity. e. Immunohistochemistry
24 for *TET2* in the patient's bone marrow biopsy FFPE sections showed 30-35% nuclear positivity.
25 The magnification in Figures d and e are at 40X objective.

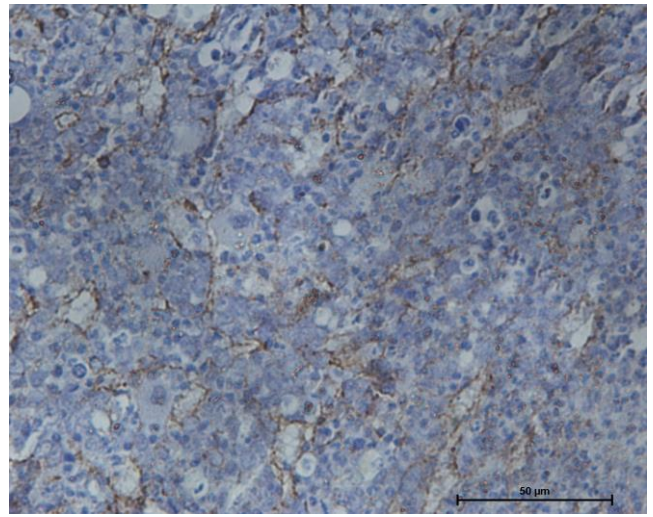
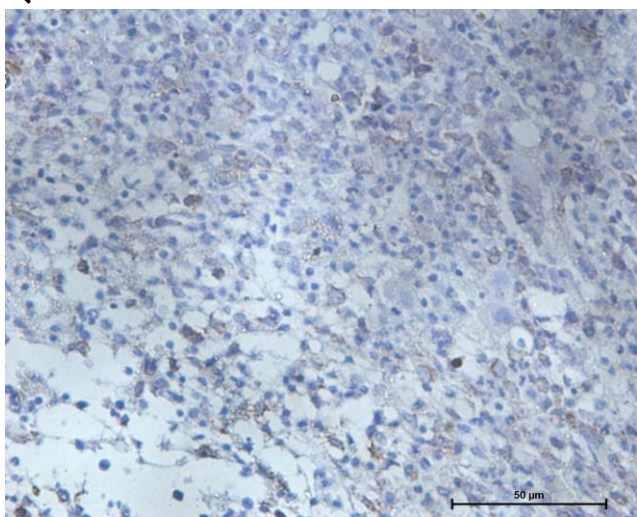
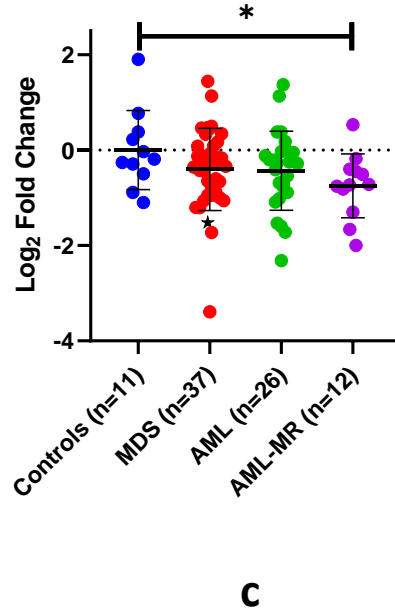
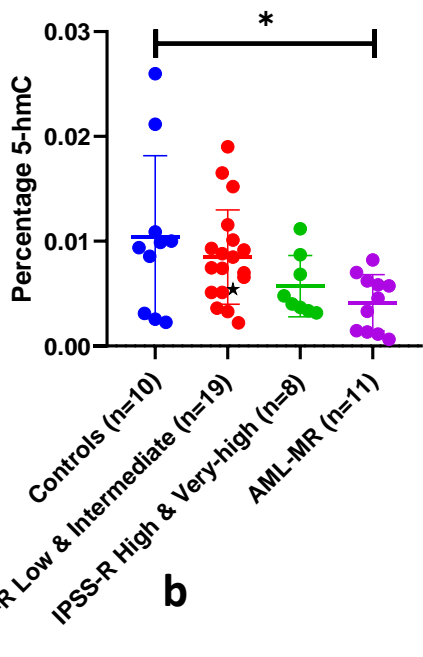
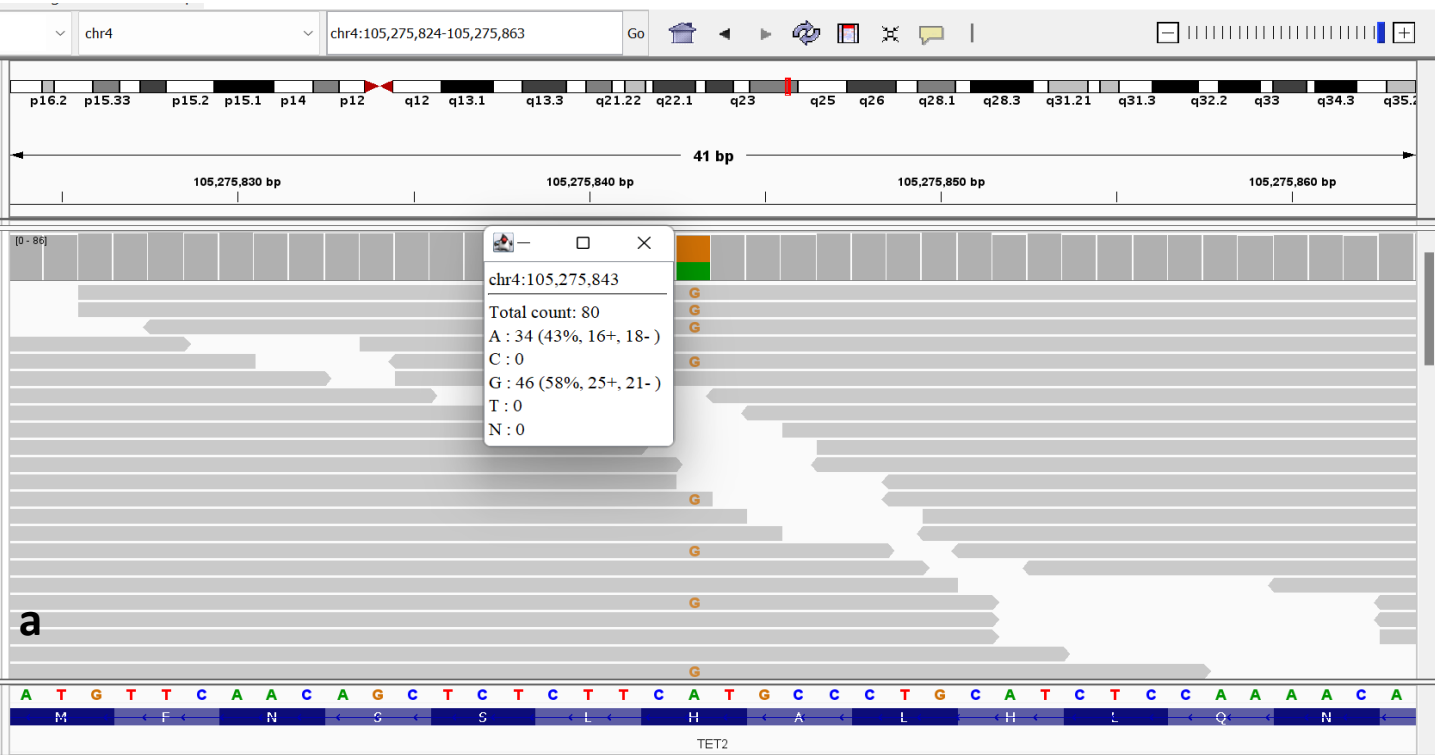
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a**b****c****d**

Supplementary Figure 1

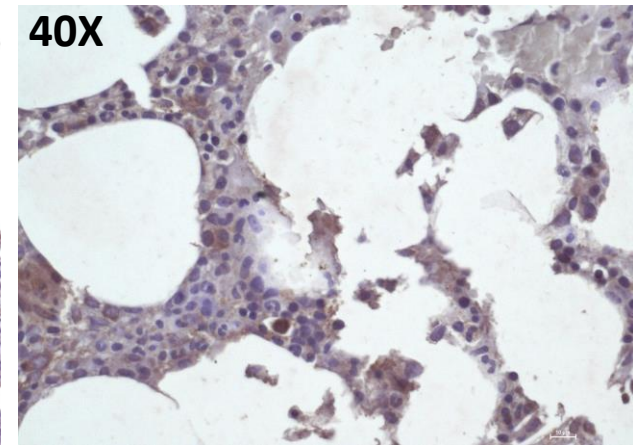
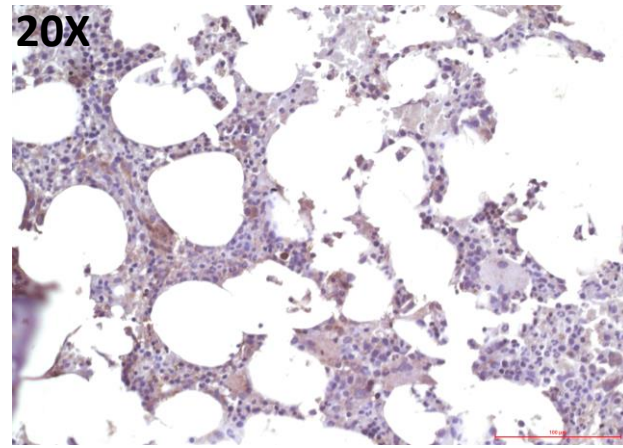
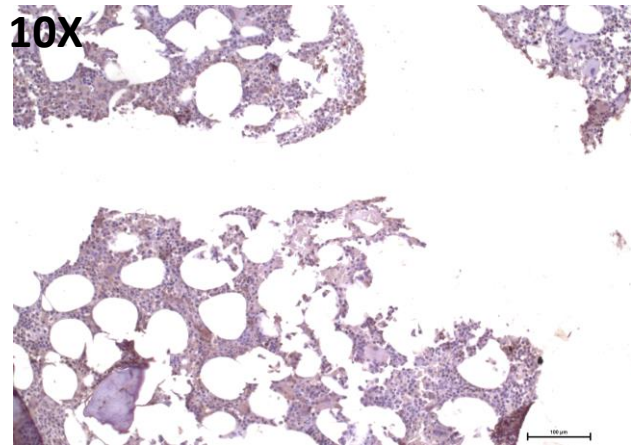
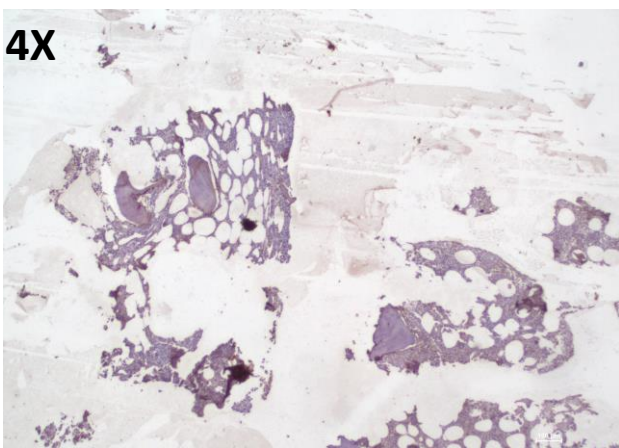


Supplementary Figure 2

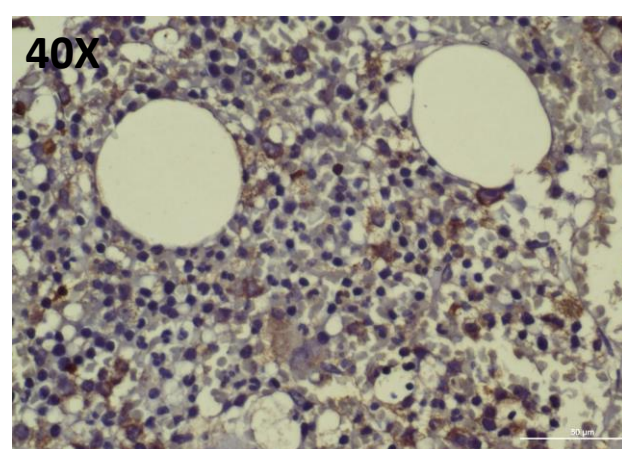
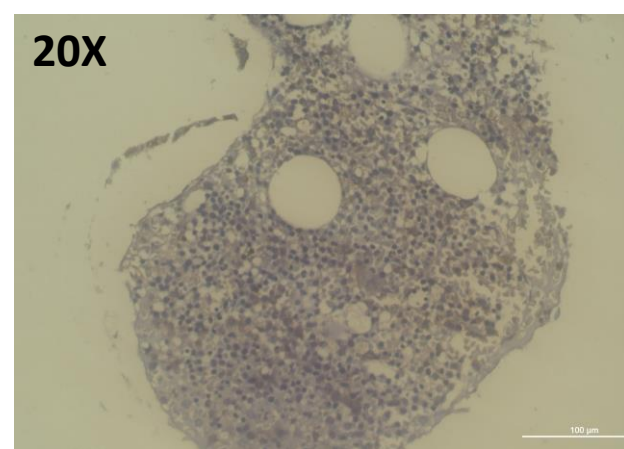
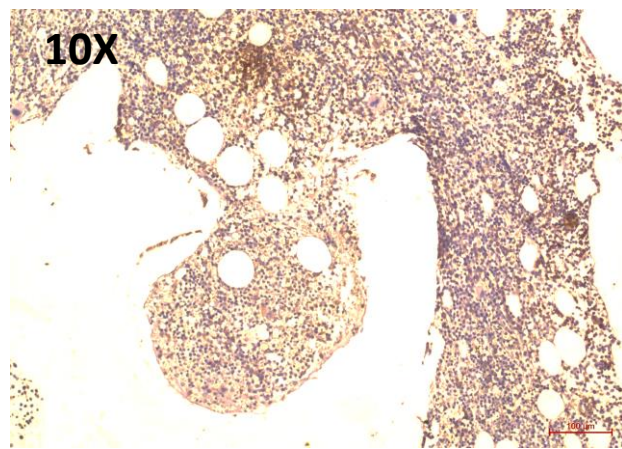
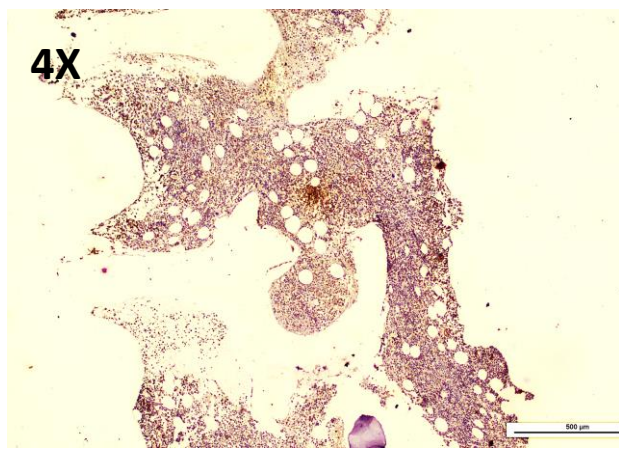


d **e**
 Supplementary Figure 3

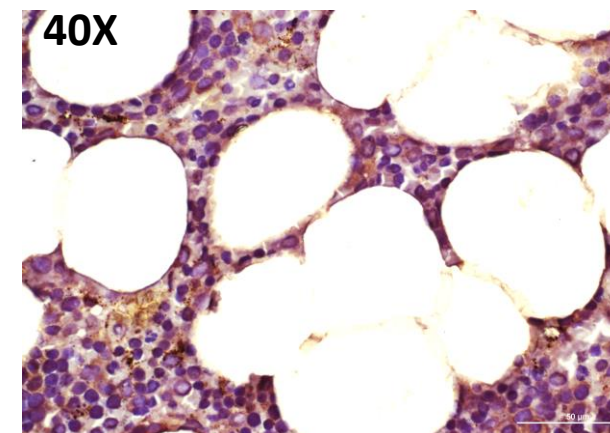
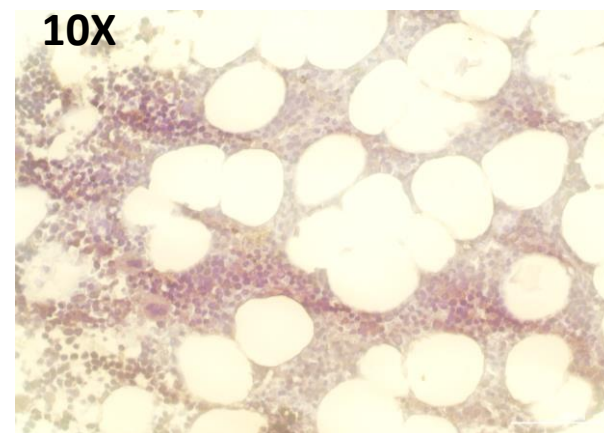
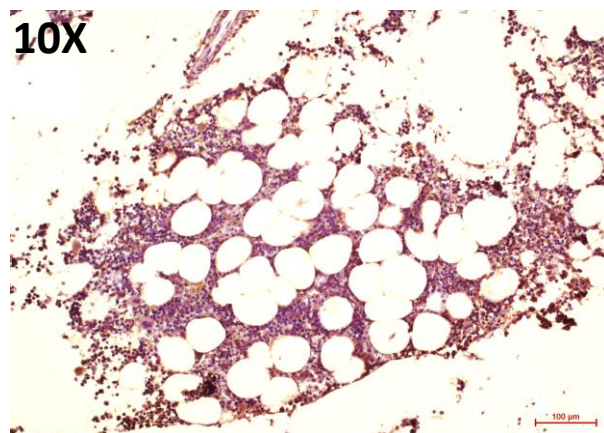
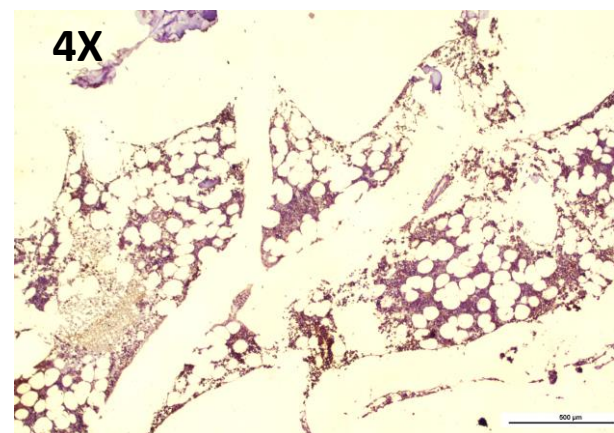
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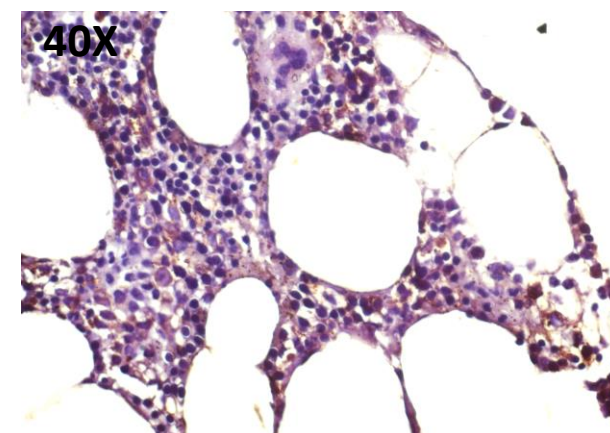
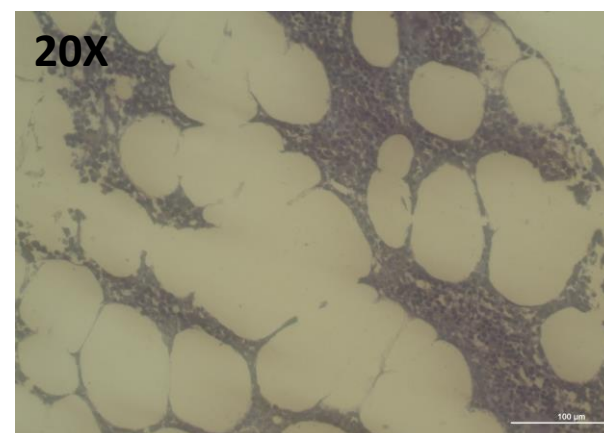
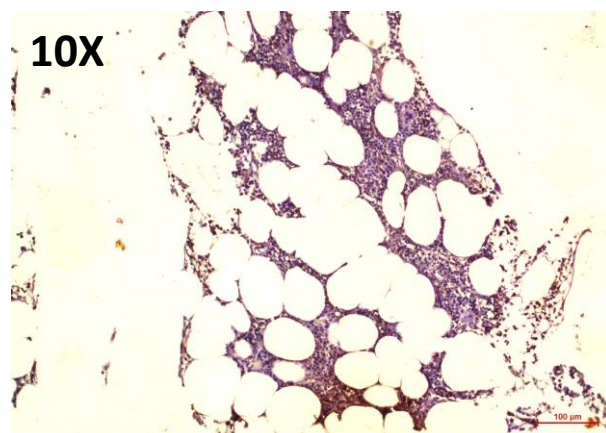
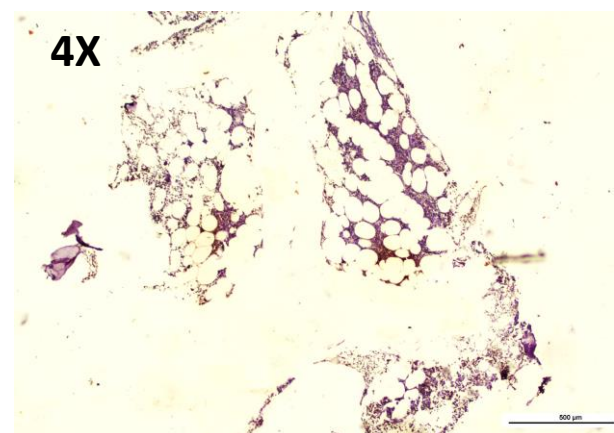
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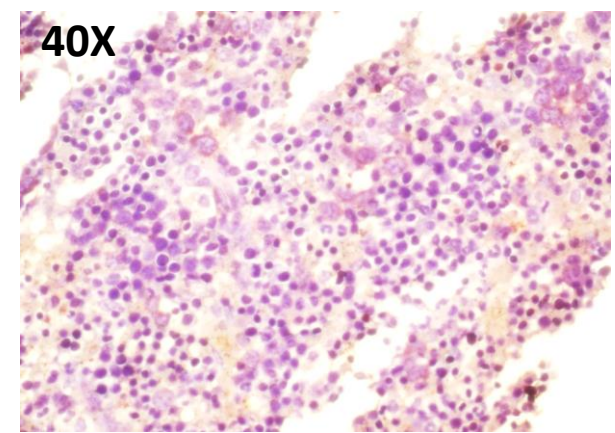
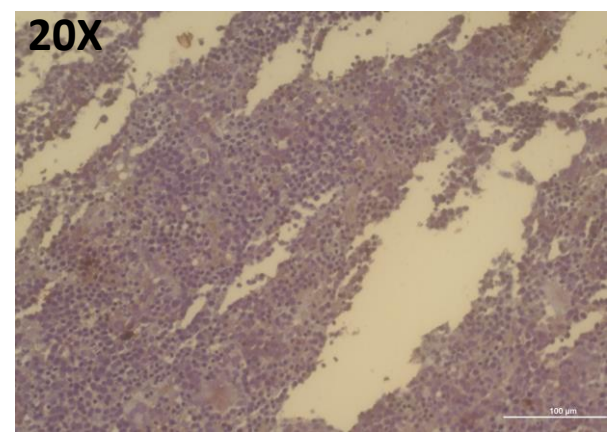
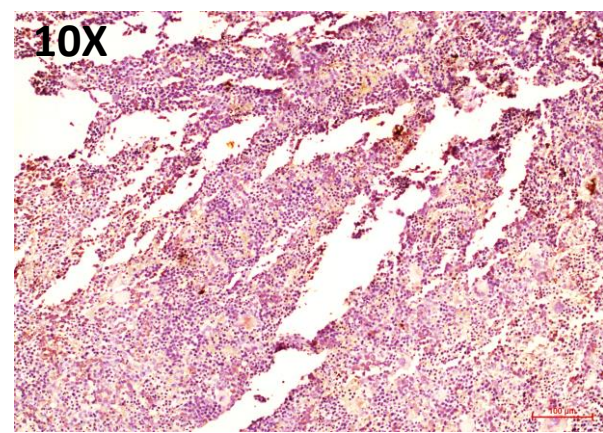
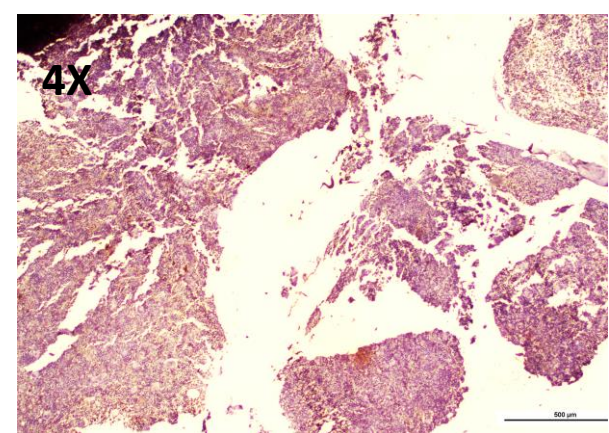
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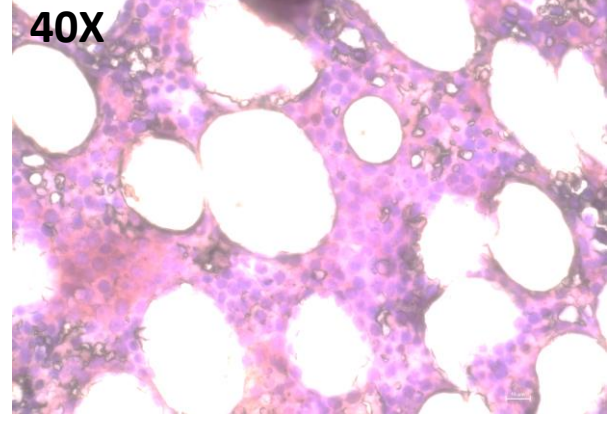
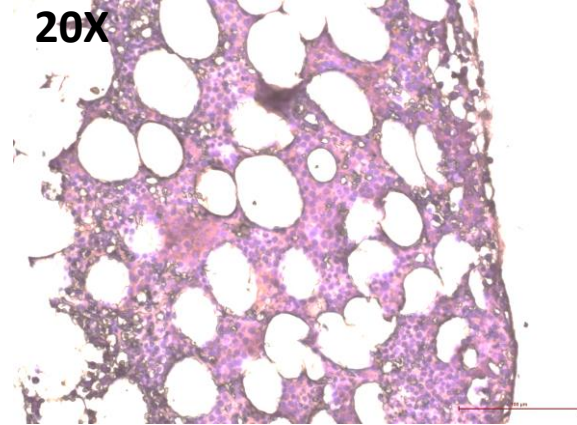
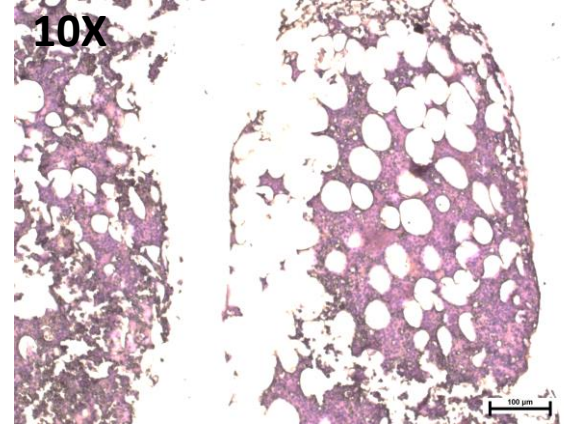
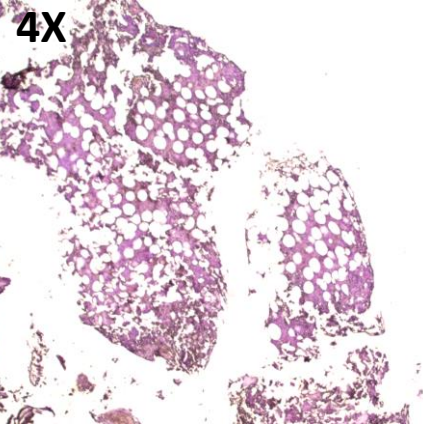
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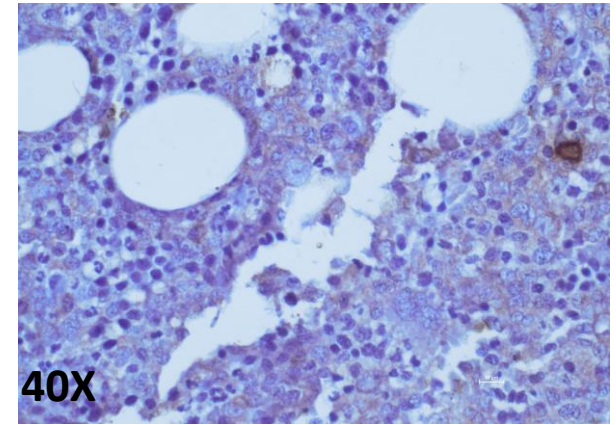
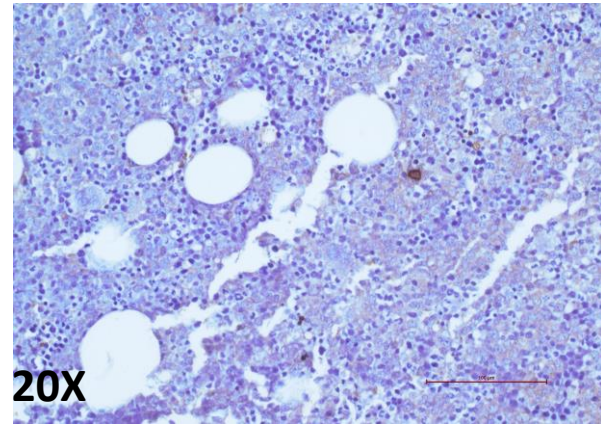
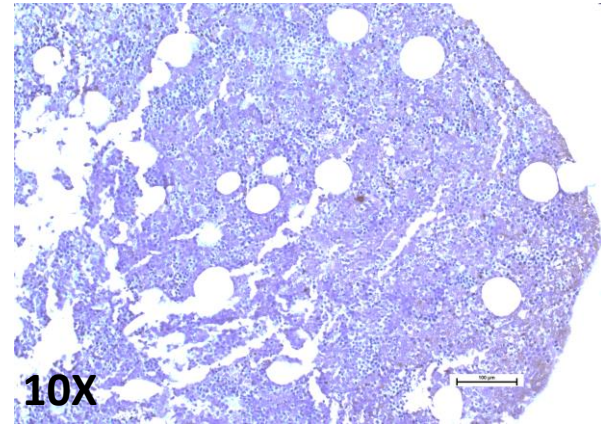
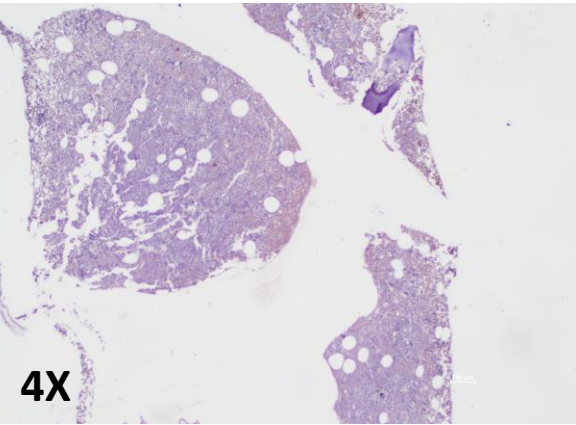
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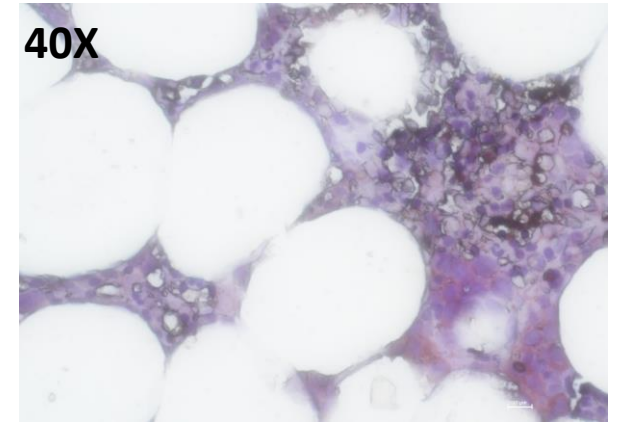
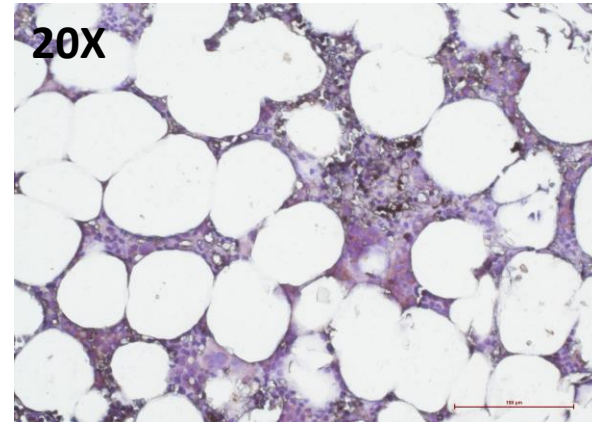
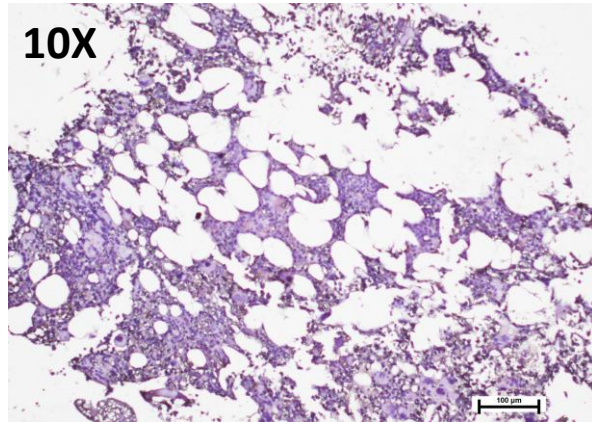
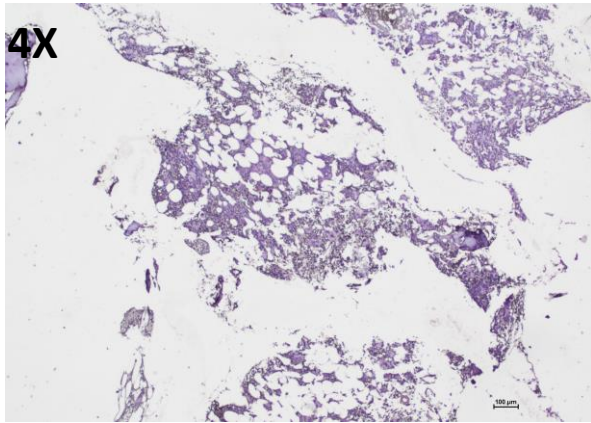
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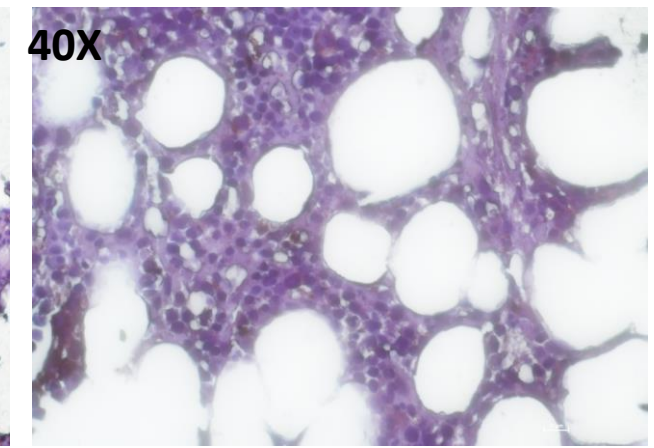
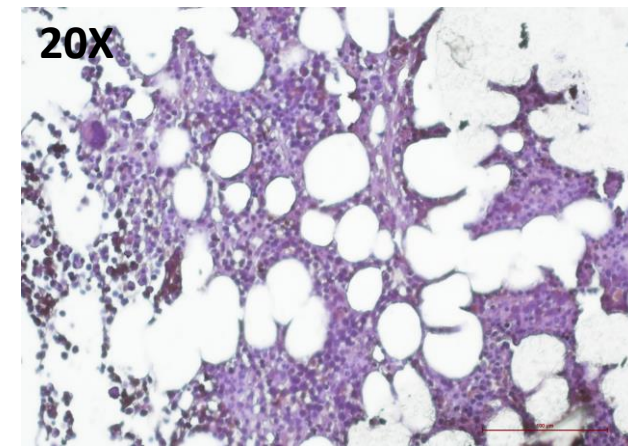
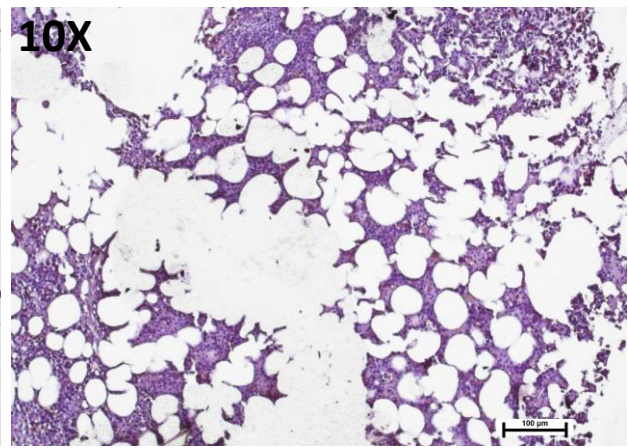
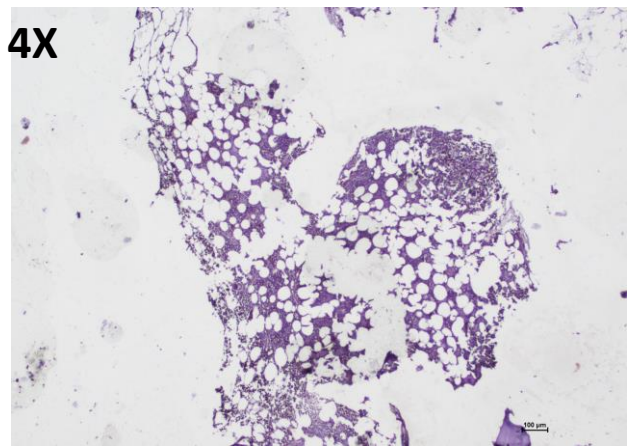
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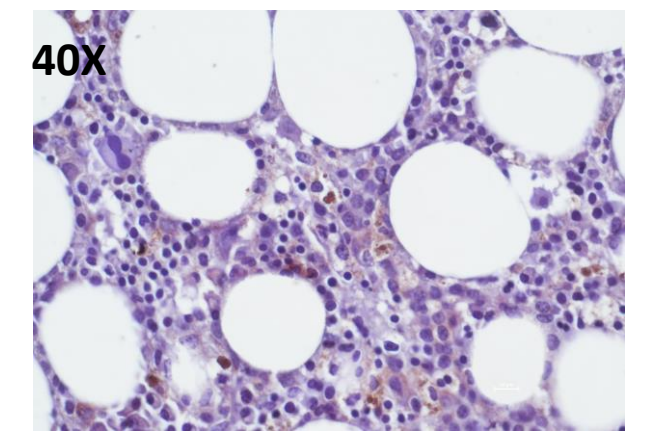
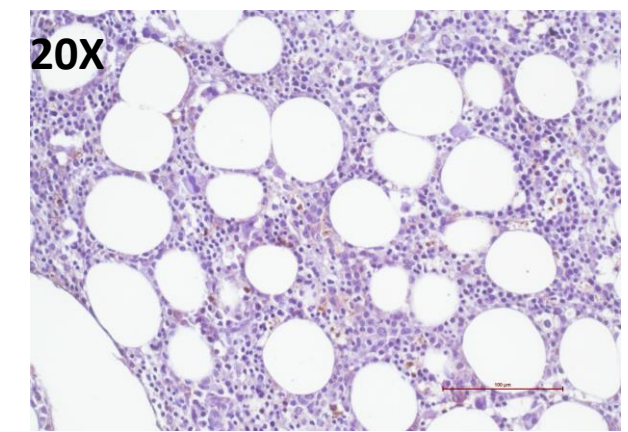
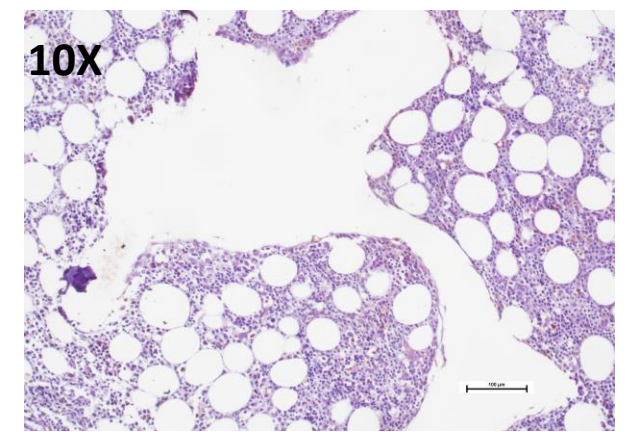
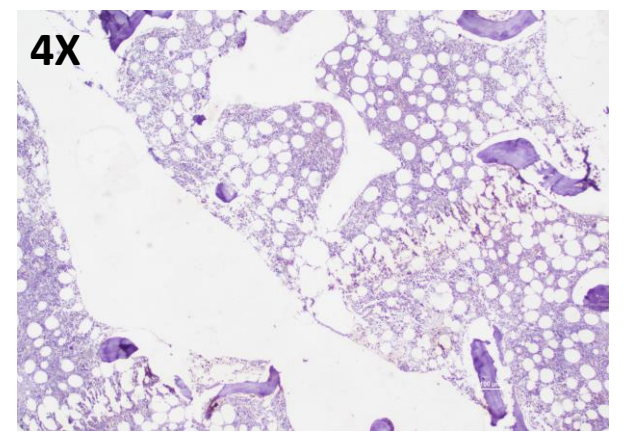
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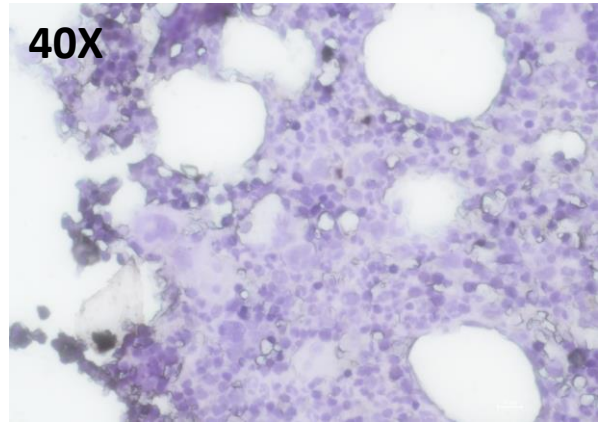
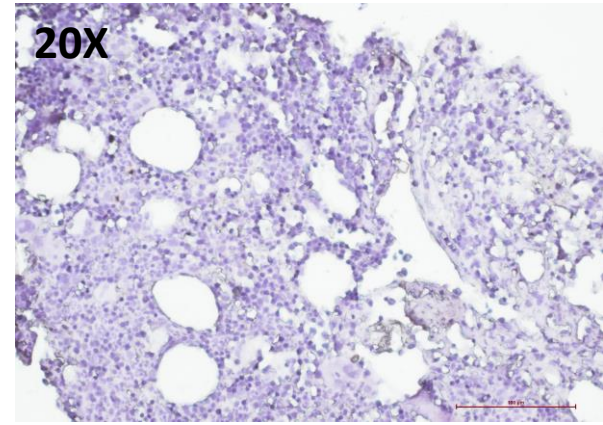
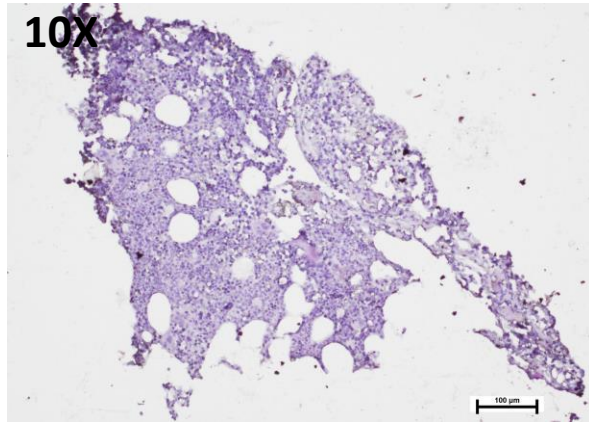
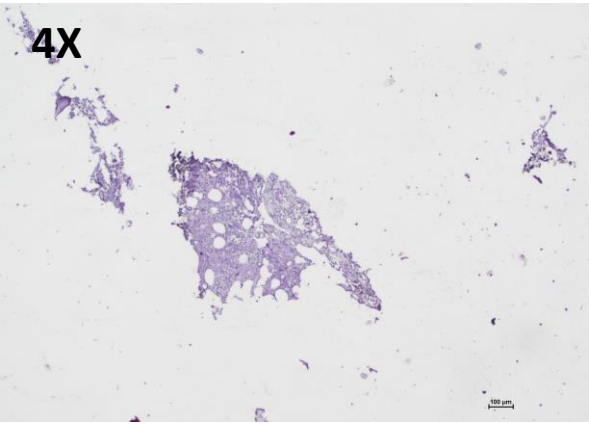
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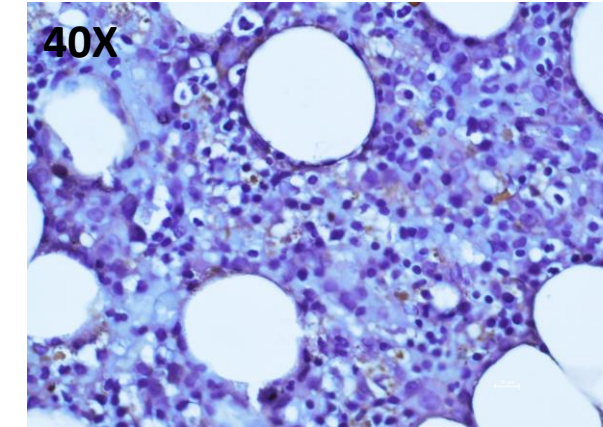
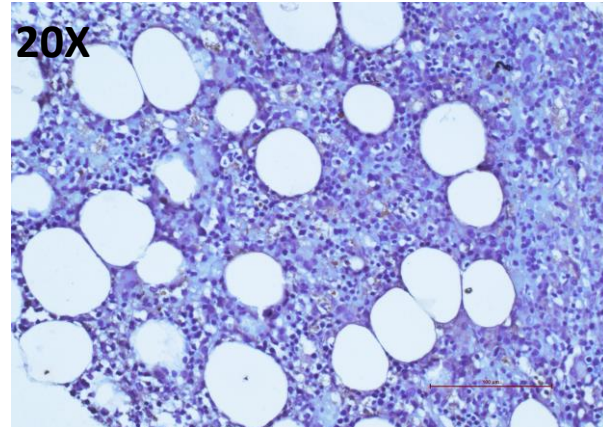
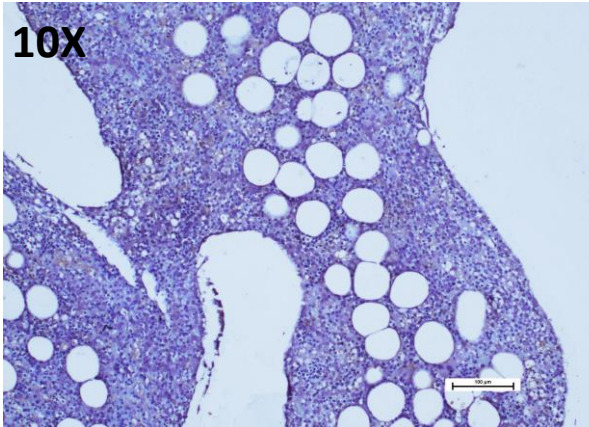
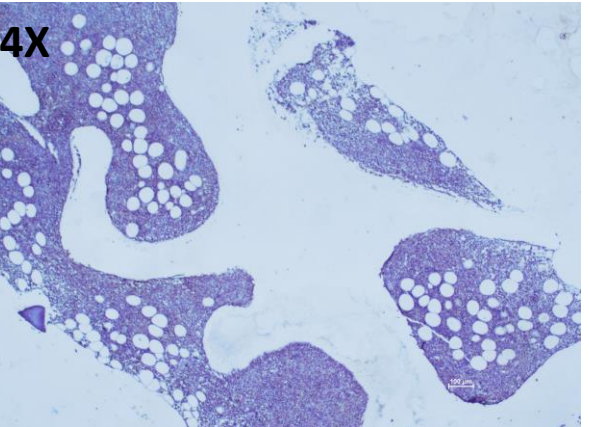
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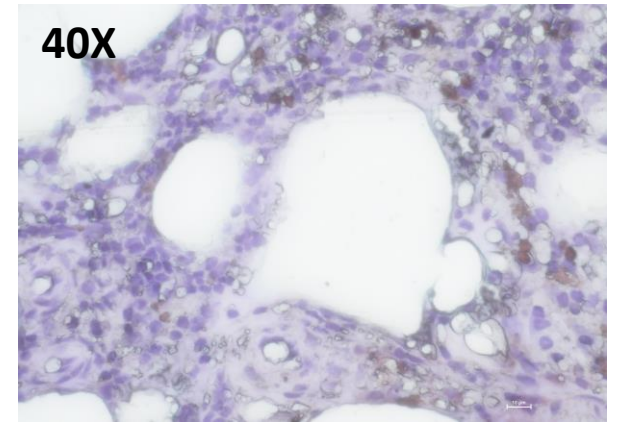
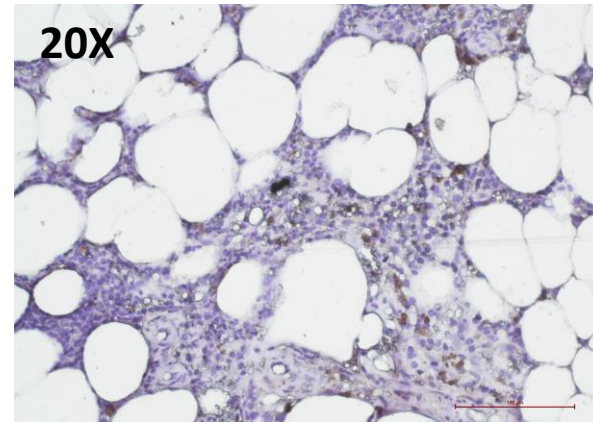
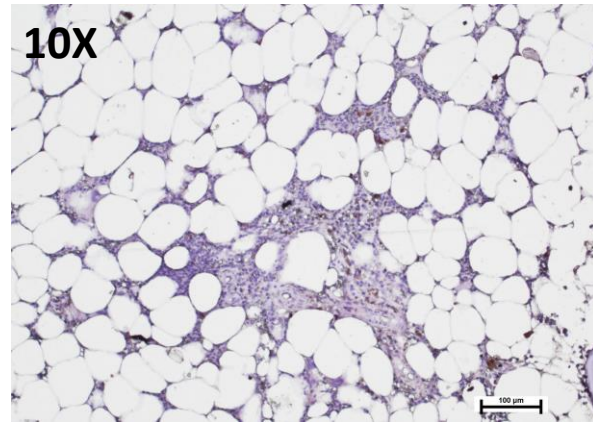
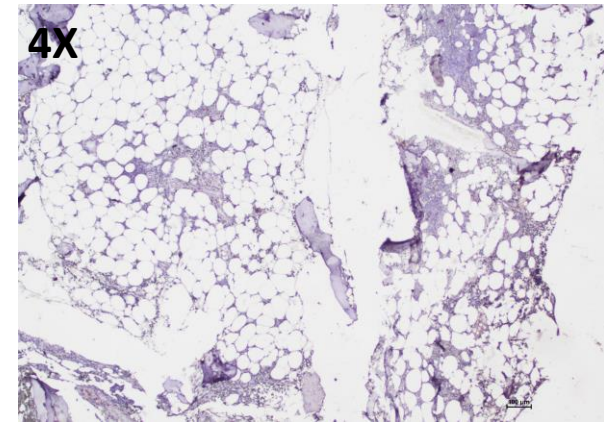
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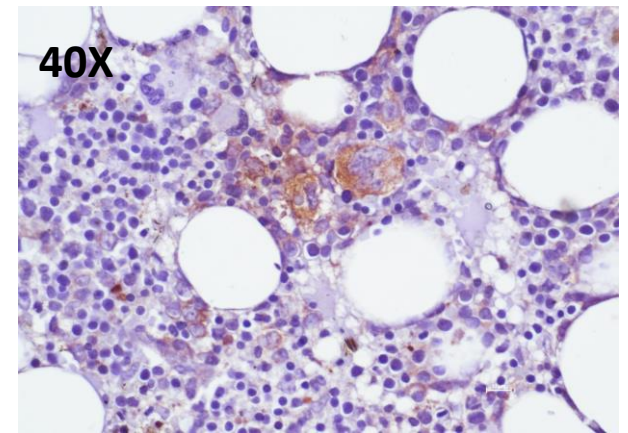
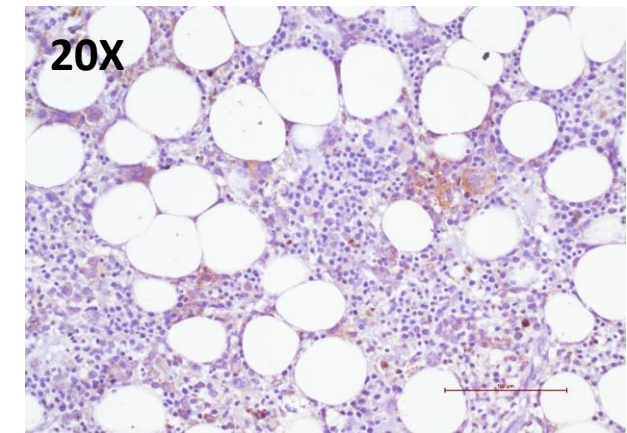
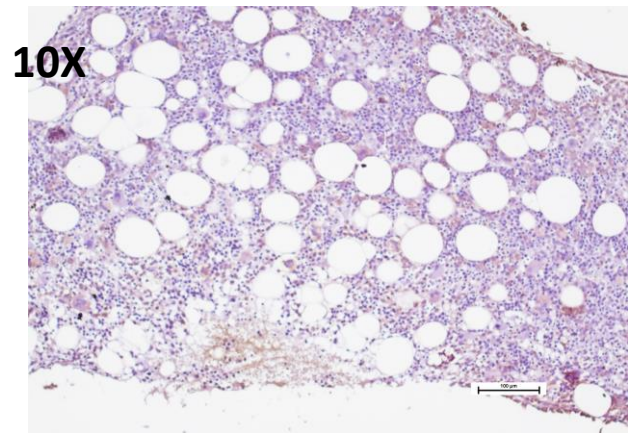
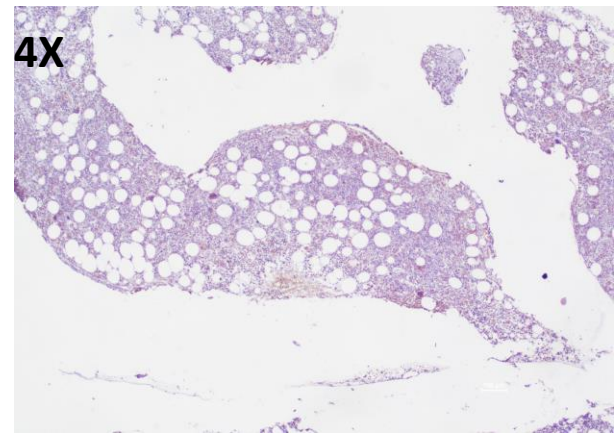
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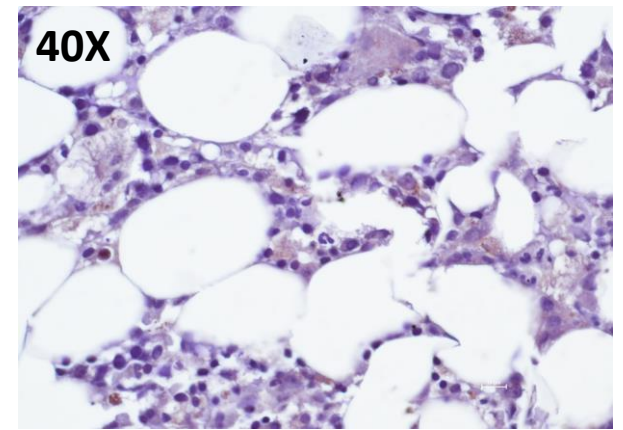
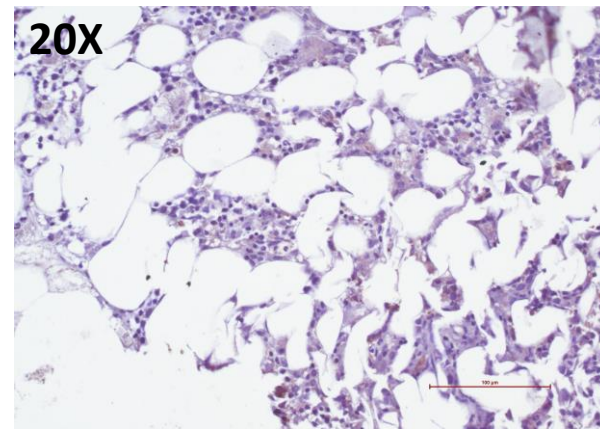
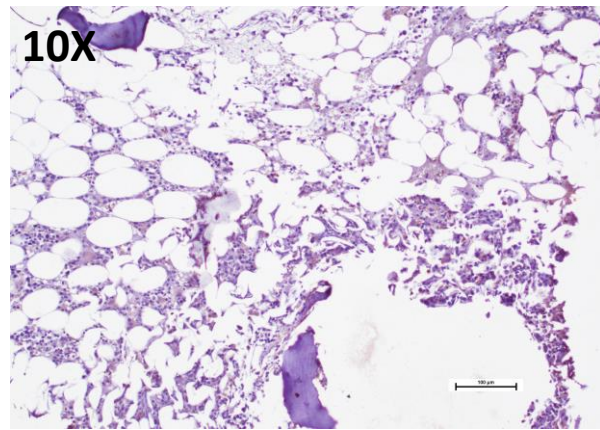
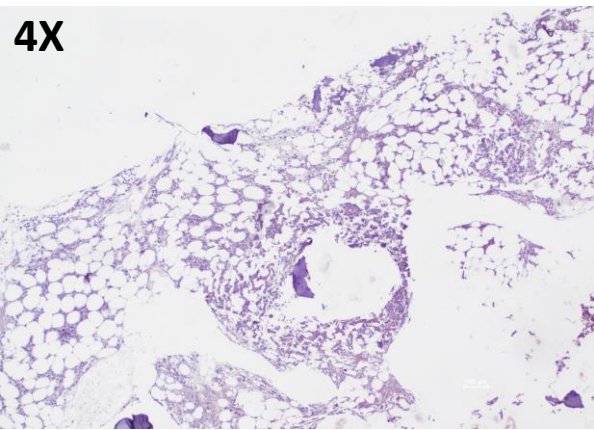
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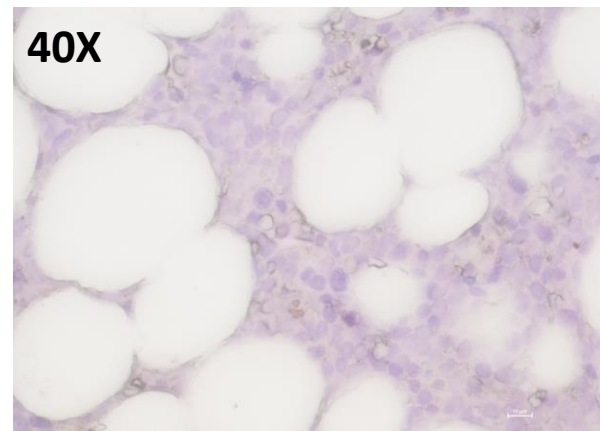
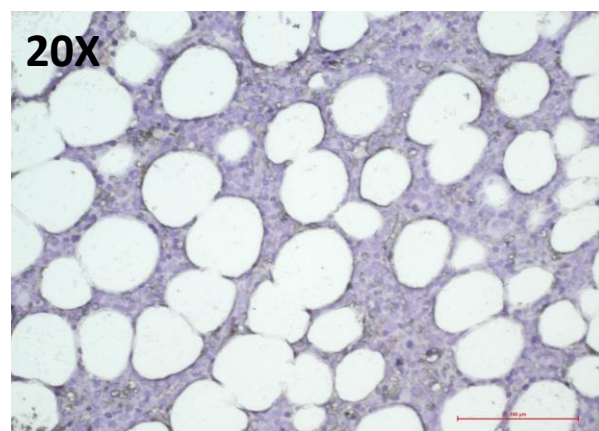
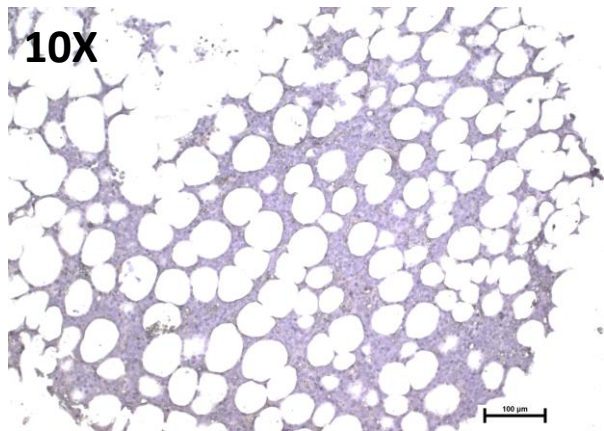
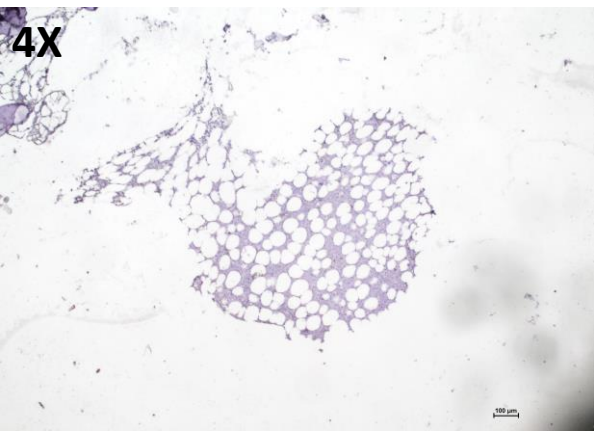
IPSS-R High



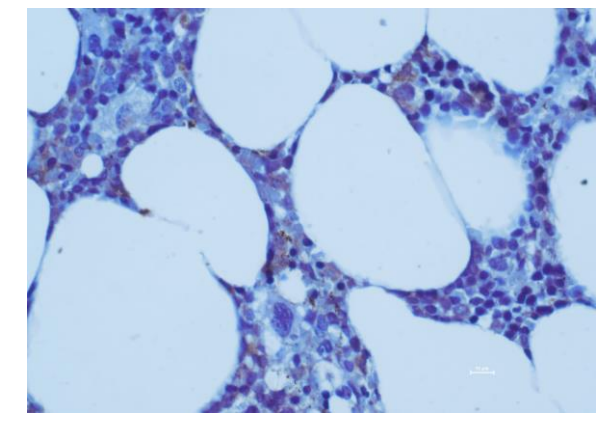
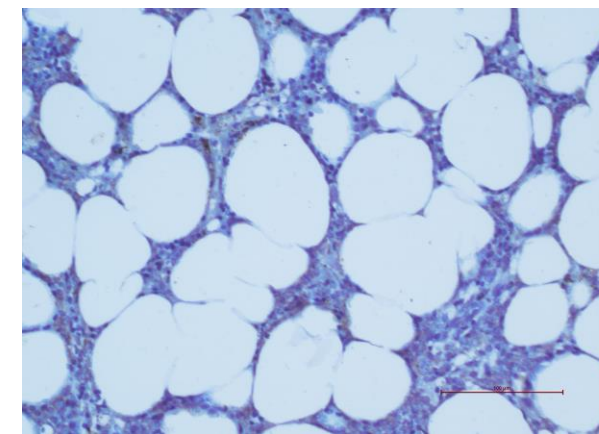
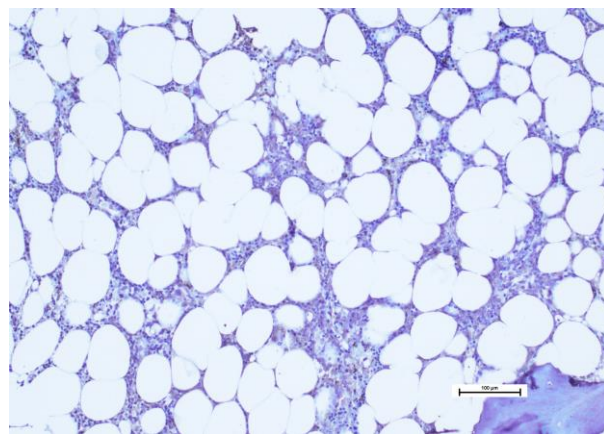
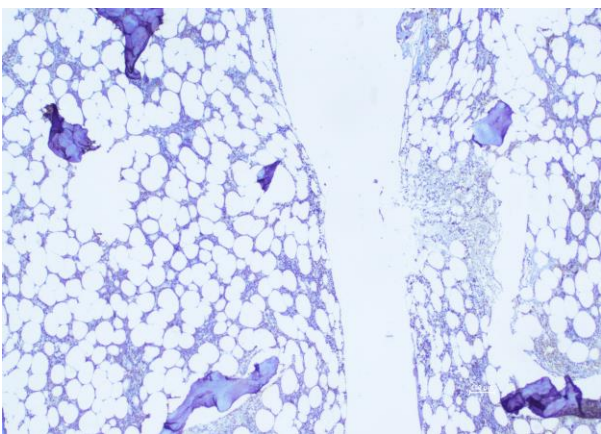
IPSS-R Very High



AML-MRC



AML-MRC



Supplementary Tables:

Alterations of the expression of *TET2* and DNA 5-hmC predict poor prognosis in Myelodysplastic Neoplasms: An observational study from India

Supplementary Table 1: List of primers used in this study

Gene	Primer	Annealing Temperature	Purpose
<i>TET1</i>	F: ACCTGCAGCTGTCTTGATCG	60°C	qPCR
	R: CACCCATGAGAGCTTTCCCT		
<i>TET2</i>	F: AGGACTGAGCTGCTGAATTC	60°C	qPCR
	R: GGGCTTCCATTCTGGAGCTT		
<i>GAPDH</i>	F: ACGGATTTGGTCGTATTGGG	60°C	qPCR
	R: CGCTCCTGGAAGATGGTGAT		
<i>TET2-Exon 11</i>	F: AATGGAAACCTATCAGTGGACAAC	60°C	PCR for Sanger sequencing
	R: TATATATCTGTTGTAAGGCCCTGTGA		
<i>TET2-Exon 11</i>	F: AATGGAAACCTATCAGTGGACAAC	60°C	Sanger sequencing
<i>TET2-Exon 11</i>	R: TATATATCTGTTGTAAGGCCCTGTGA	60°C	Sanger sequencing

Supplementary Table 2: Pathogenic variants of TET2 in patient samples

Sample	Start: chr4	Ref	Alt	Type	Change: NM_001127208:			
A2	105234042	C	T	SNV	exon3:c.C100T:p.L34F			
	105275570	AG	-	frameshift del	exon11:c.5060_5061del:p.Q1687fsX3			
	105275843	A	G	SNV	exon11:c.A5333G:p.H1778R			
	105276132	GT	-	frameshift del	exon11:c.5622_5623del:p.E1874fsX2			
A3	105235006	G	A	SNV	exon3:c.G1064A:p.G355D			
V2	105234028	C	G	SNV	exon3:c.C86G:p.P29R			
H3	105276348	-	A	frameshift ins	exon11:c.5839dupA:p.G1946fsX2			
I1	105275843	A	G	SNV	exon11:c.A5333G:p.H1778R			
I3	105234028	C	G	SNV	exon3:c.C86G:p.P29R			
L1	105234028	C	G	SNV	exon3:c.C86G:p.P29R			
<i>Continued...</i>								
Sample	AA Change	ExAC_ All	1000g_ All	gnomAD_All		SIFT	Polyphen2 _HDIV	CADD_ phred
				Exome	Genome			
A2	p.L34F	0.02	0.01	0.02	0.01	D	B	23
	p.Q1687fsX 3
	p.H1778R	0.05	0.08	.	.	D	D	23.5
	p.E1874fsX2
A3	p.G355D	0.03	0.02	0.03	0.03	D	P	24.9
V2	p.P29R	0.06	0.09	0.06	0.04	T	D	24.2
H3	p.G1946fsX 3
I1	p.H1778R	0.05	0.08	.	.	D	D	23.5
I3	p.P29R	0.06	0.09	0.06	0.04	T	D	24.2
L1	p.P29R	0.06	0.09	.	.	T	D	24.2
<i>Legend: A: AML-MR, V: IPSS-R very high, H: IPSS-R high, I: IPSS-R intermediate, L: IPSS-R low</i>								