

1 **Spatial Transcriptomics Analysis of Zone-Dependent Hepatic**

2 **Ischemia-Reperfusion Injury Murine Model**

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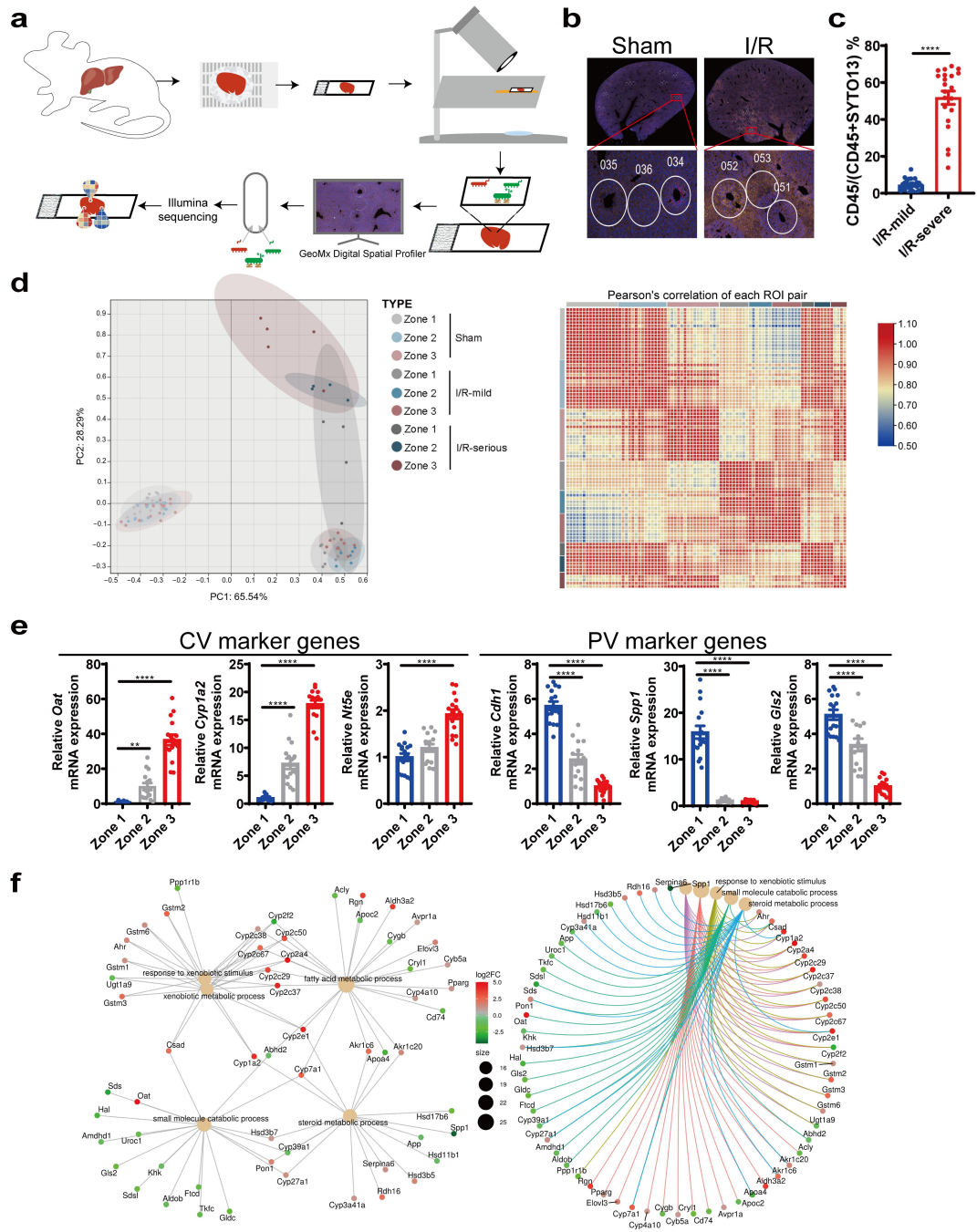
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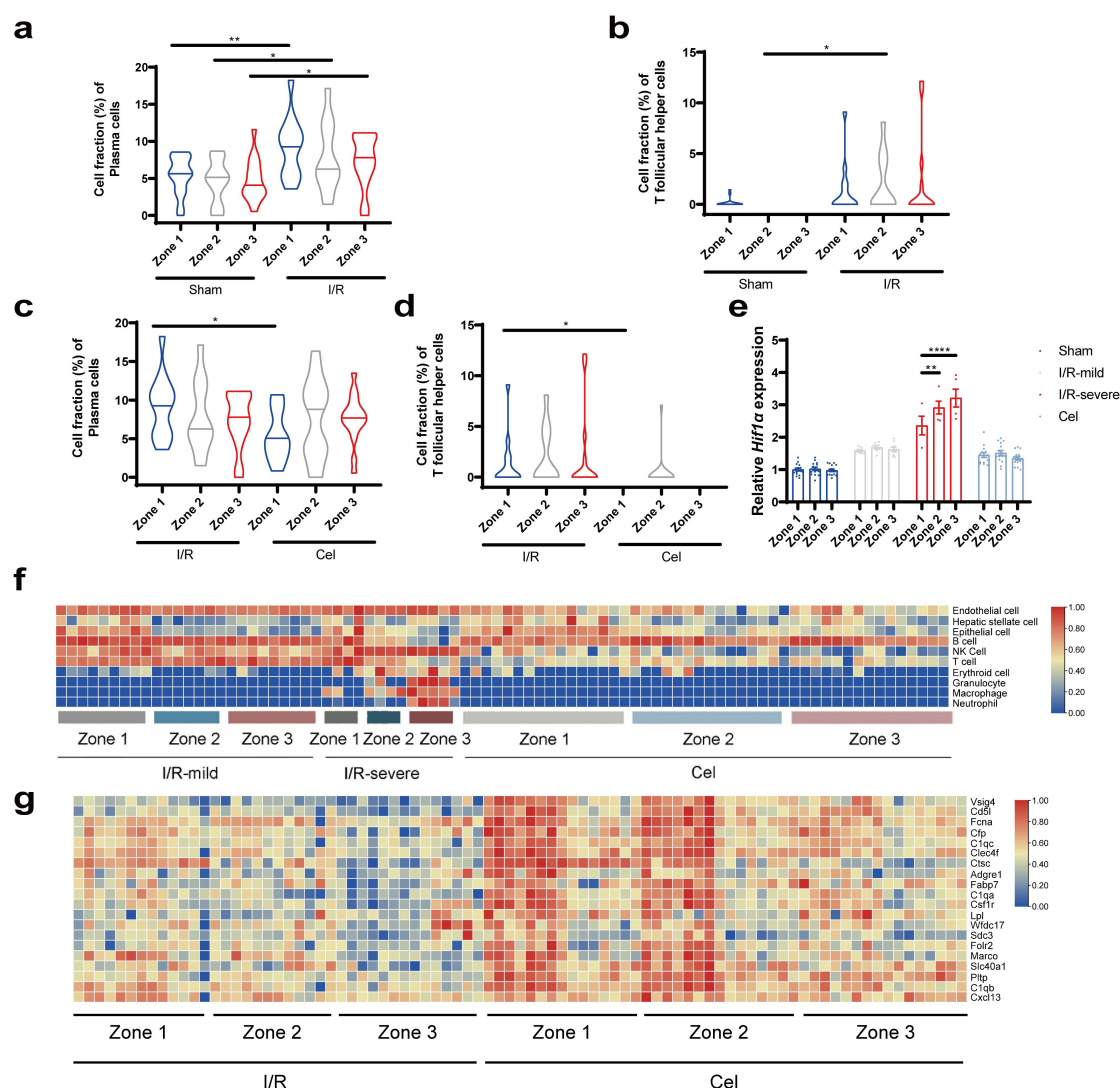
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Supplementary Fig 1. Hepatic zone-specific functional pathways and KCs abundance at the steady state.

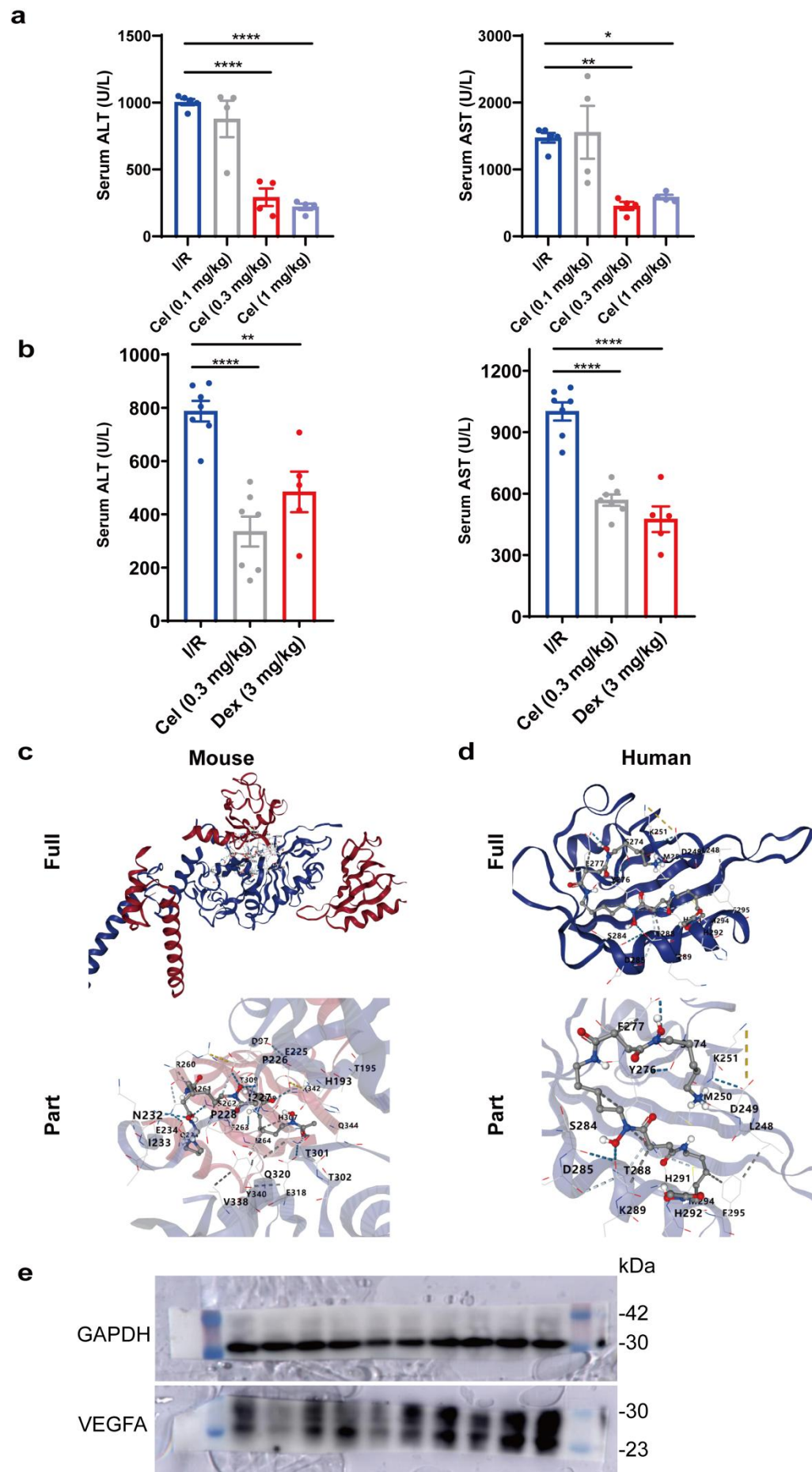
a Workflow of spatial transcriptomics. **b** Representative ROIs images of sham and I/R group. **c** CD45 positive rates calculated as $CD45/(CD45+SYTO13)$ by ImageJ software (Student's t test, $n=21-26$, **** $p < 0.0001$). **d** PCA and ROI correlation heatmap of each ROI pair. **e** Expression of representative CV and PV marker genes (One-way ANOVA, $n=15-16$, ** $p < 0.01$, **** $p < 0.0001$). **f**

Zone 3-specific top GO and DEGs network. The node color represents log₂ fold change in gene expressions of zone 3 versus zone 1. Data were expressed as mean ± SEM.



Supplementary Fig 2. The abundance of hepatic NPCs after I/R injury and celastrol treatment.

a-d Cell fractions of plasma cells and Tfh cells were calculated by Cibersort algorithm (Center lines indicate median value. Student's t test, $n=11-16$, $*p < 0.05$, $**p < 0.01$). **e** Relative HIF1 α expression in each zone of different groups (Two-way ANOVA, $n=15-16$ for Sham and Cel group, and $n=7-9$ for I/R mild regions and $n=4-5$ for I/R severe regions, $**p < 0.01$, $***p < 0.0001$, data were expressed as mean $\pm$ SEM). **f** The scaled proportion of NPCs in I/R and celastrol group. **g** The scaled Kupffer cells marker genes expression in I/R and celastrol group.



Supplementary Fig 3. Celastrol reduced I/R injury and activated the hypoxia pathway.

a, b Effect of one-week pre-treatment of celastrol or dexamethasone sodium phosphate on Serum transaminase levels after I/R injury (One-way ANOVA, $n=4-7$, $*p < 0.05$, $**p < 0.01$, $***p < 0.0001$, data were expressed as mean $\pm$ SEM). **c, d** *In silico* molecular docking results of deferoxamine-mesylate with mouse HIF1 α protein in **c** and human HIF1 α protein in **d**. **e** Unprocessed gels of Fig. 7h.

68 **Supplementary Table 1: qPCR primer sequences**

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
<i>Il-6</i>	TACCACTTCACAAGTCGGAGGC	CTGCAAGTGCATCATCGTTGTTC
<i>Il-1β</i>	TTGACGGACCCCAAAGATG	AGGACAGCCCAGGTCAAAG
<i>Mcp-1</i>	ACTCACCTGCTGCTACTCATTAC	GTATGTCTGGACCCATTCCTTCTT
<i>Gapdh</i>	AACTTTGGCATTGTGGAAGG	ACACATTGGGGGTAGGAACA
<i>Vegf</i>	GGCCTCCGAAACCATGAACT	CTGGGACCACTTGGCATGG
<i>Hif1α</i>	CCCATTCCATCCGTCAAATA	CCTGTGGTGACTTGTCTTTAG

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Supplementary Table 2: Antibody information

Antibody	Company	Cat No.
Anti-VEGF	Bioss	Bs-1313R
Anti-GAPDH	Proteintech	10494-1-AP
Anti-iNOS	Servicebio	GB11119
Anti-CD163	Servicebio	GB113751
Anti-F4/80	Servicebio	GB113373
Anti-Rabbit IgG	Proteintech	SA00001-2

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**Supplementary Table 3: Putative docking sites between
celastrol/deferroxamine-mesylate and HIF1 α**

Ligand	Protein	Binding	Cavity	Center			Size		
		Energy	Size	x	y	z	x	y	z
		(kcal/mol)	(Å ³)						
Celastrol	Mouse	-9.6	512	-124	-49	6	23	23	23
	HIF1 α	-9.4	548	-112	-61	-31	23	23	23
		-8.8	3811	-114	-44	1	23	23	23
		-8.3	497	-106	-58	-15	23	23	23
		-7.4	1595	-95	-34	14	23	23	23
	Human	-7.3	44	19	-17	-35	23	23	23
	HIF1 α	-6.7	33	12	-13	-21	23	23	23
		-6.6	30	16	7	-28	23	23	23
		-6.4	31	16	1	-17	23	23	23
		-6.1	36	24	3	-23	23	23	23
Deferoxamine-mesylate	Mouse	-6.6	3811	-114	-44	1	38	38	38
	HIF1 α	-6.4	512	-124	-49	6	38	38	38
		-6.3	1595	-95	-34	14	38	38	38
		-6	548	-112	-61	-31	38	38	38
		-5.5	497	-106	-58	-15	38	38	38
	Human	-4.7	30	16	7	-28	38	38	38
	HIF1 α	-4.6	33	12	-13	-21	38	38	38
		-4.5	44	19	-17	-35	38	38	38
		-4.3	36	24	3	-23	38	38	38
		-4.3	31	16	1	-17	38	38	38