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Sirius Red staining





Stroma No-PT III Injured PT III Non-injured PT 0.9% 3.5% 2.2% 34.8% 33.9% 40.3% 6.6% 15% 51.6% 56.1% 42.6% 12.8% Early Control Late



Anonymized patient number	Fibrosis estimation
1	< 10%
2	< 10%
3	5-10%
4	20%
5	10%
6	40-50%
7	40-50%
8	50%
9	75%
10	75%
11	70%
12	75%

mouse ID:	Creatinine (mg/dL)	Micro- Albumin (mg/dL)	Albumine/creatinine ratio (mg/mg)
CTL1	110.65	2.4	0.021690014
CTL2	90.03	1.3	0.014439631
CTL3	145.16	0.6	0.00413337
CTL4	113.66	0.9	0.007918353
CTL5	202.56	10.4	0.051342812
POD1	23.80	19.9	0.836134454
POD2	24.83	10.1	0.406766009
POD3	98.37	10.8	0.10978957
POD4	20.41	19.2	0.940715336
POD5	26.26	21.9	0.833968012
POD6	34.93	28.3	0.810191812
POD7	72.36	25.5	0.352404643

#### Overview of snRNAseq data integrated

Dataset	Source	GEO sample ID	Sample id	IRI	Mouse strain	
		GSM4567681	Six2_gfpNeg_Normal			
		GSM4567682	Six2_gfpPos_Normal	1		
Logovia et al Nat Mat 2020	GSE151167	GSM4567683	IRI_64h GFP positive	]		
		GSM4567684	IRI_96h GFP positive	15 min 36 5°C	C57BL6/J (Six2-TGC; Rosa26rtTA	
Legouis et al Nat.Met. 2020		GSM4567685	IRI_28d GFP positive		pTRE-H2BeGFP)	
	this paper		Sham_64h	]		
	this paper		Sham_96h	1		
	this paper		Sham_28d	1		
This paper	this paper	GSE163863	Kidney_Nuclei	none	C57BL6/J Pten pc-/-	
		GSM4131050	IRIsham1b1			
		GSM4131051	IRIsham1b2	1		
		GSM4131052	IRIsham2	]		
		GSM4131053	IRIsham3	1		
		GSM4131054	IRI4h1	1		
		GSM4131055	IRI4h2	1		
		GSM4131056	IRI4h3			
		GSM4131057	IRI12h1b1			
		GSM4131058	IRI12h1b2			
		GSM4131059	IRI12h2	1		
		GSM4131060	IRI12h3	1		
Kirita et al PNAS 2020	GSE130107	GSM4131061	IRI2d1b1	18 min 36 5 - 37 5°C	C57BL/6J	
	002100107	GSM4131062	IRI2d1b2	10 1111 00.0 - 07.0 0		
		GSM4131063	IRI2d2b1	1		
		GSM4131064	IRI2d2b2	1		
		GSM4131065	IRI2d3	1		
		GSM4131066	IRI14d1b1	1		
		GSM4131067	IRI14d1b2	1		
		GSM4131068	IRI14d2	1		
		GSM4131069	IRI14d3	]		
		GSM4131070	IRI6w1b1	1		
		GSM4131071	IRI6w1b2	]		
1		GSM4131072	IRI6w2	]		
		GSM4131073	IRI6w3			

#### Detailed composition of the integrated snRNA seq of IRI mouse model datasets. Number of nuclei per sample is reported in the table.

	Control			Farly				Lato	
Sample id	0	4h	12h	48h	64h	96h	14d	28d	6w
Kidney Nuclei	3429	-111	0	0	0	0	0	0	0
Six2 gfpNeg Normal	3201	ő	0	ő	ů	0	ő	ő	ő
Six2_gfpProg_Normal	3301	ő	0	ő	ů	0	ő	ő	ő
Sham 64h	4639	ő	ő	ő	ů	0	ő	ő	ő
Sham_96h	3015	ő	Ő	ő	ů	0	ő	ő	ő
Sham 28d	2543	0	0	0	0	ō	0	ō	0
IRIsham1b1	3819	0	0	0	0	ō	0	ō	0
IRIsham1b2	2989	0	0	0	0	ō	0	ō	0
IRIsham2	2317	0	0	0	0	ō	0	ō	0
IRIsham3	2272	ō	0	0	0	ō	ō	ō	ō
IRI4h1	0	1952	0	0	0	0	0	Ó	0
IRI4h2	0	1230	0	0	0	0	0	Ó	0
IRI4h3	0	2310	0	0	0	0	0	Ó	0
IRI12h1b1	0	0	929	0	0	0	0	0	0
IRI12h1b2	0	0	1119	0	0	0	0	0	0
IRI12h2	0	0	478	0	0	0	0	Ó	0
IRI12h3	0	0	841	0	0	0	0	0	0
IRI2d1b1	0	0	0	2573	0	0	0	0	0
IRI2d1b2	0	0	0	1461	0	0	0	0	0
IRI2d2b1	0	0	0	142	0	0	0	0	0
IRI2d2b2	0	0	0	131	0	0	0	0	0
IRI2d3	0	0	0	278	0	0	0	0	0
IRI_64h	0	0	0	0	2867	0	0	0	0
IRI 96h	0	0	0	0	0	2575	0	0	0
IRI14d1b1	0	0	0	0	0	0	1389	0	0
IRI14d1b2	0	0	0	0	0	0	1538	0	0
IRI14d2	0	0	0	0	0	0	736	0	0
IRI14d3	0	0	0	0	0	0	607	0	0
IRI_28d	0	0	0	0	0	0	0	3131	0
IRI6w1b1	0	0	0	0	0	0	0	0	1641
IRI6w1b2	0	0	0	0	0	0	0	0	1851
IRI6w2	0	0	0	0	0	0	0	0	1036
IRI6w3	0	0	0	0	0	0	0	0	1976
Number of nuclei per cell cluster	r across time points	3	Integrati	on of snRNAseq data of IRI n	nouse models				
	Control			Early				Late	
<b>DT</b>	0	4hrs	12hrs	48hrs	64hrs	96hrs	14d	28d	6wks
PI	19751	3186	1636	3340	2027	1967	2182	2477	3344
MD	1633	887	613	495	395	253	447	198	493
PC	1185	233	253	110	12	6	222	10	390
TAL	1401	10	0	39	40	11	259	41	452
EC	1563	119	132	22	14	1	82	20	203
DILAIL	1112	103	67	63	72	96	181	133	226
DCT	1278	17	0	62	42	9	269	39	321
CNT	917	648	458	331	154	194	221	67	356
Stroma	1097	53	58	33	17	0	96	41	163
ICB	404	110	66	24	53	21	65	25	120
	498	24	1	24	14	7	82	21	137
ICA	363	61	47	20	13	3	58	20	151
Immuné	193	9	20	15	5	4	84	27	105
FUD	130	32	16	1	а	3	22	12	43

Phase	Control
Time points	Control
N° of samples	10
Total nuclei	

Number of samples per time point

Integration of snRNAseq	data of IRI mouse models
	Early
12hrs	48hrs
4	5
	64'316

4hrs 3 6wks 4

**Late** 28d 1

14d 4

96hrs 1

64hrs 1

### 1. Readme\_FindAllMarkers output

p\_val p value was caculated based on Wilcoxon rank sum test for single cell gene expression (from Seurat package)

p\_val\_adj FDR adjusted p-value

- avg\_logFC log fold-change of the average expression between the cells from the selected cluster versus all cells
- pct.1 fraction of cells expressing the genes in the selected cells
- pct.2 fraction of cells expressing the genes in all cells

### 2. Names of the segment-specific markers used for clusterization.

Slc34a1	
Slc5a12	
Abcc2	
Ghr	
Acsm1	
Tshz1	
Rbms3	
Chn2	
Epha7	
Akap12	
Sgcz	
Slc12a1	
Mrps6	
Cacnb4	
Bckdhb	
Srgap1	
Magi2	
Thsd7a	
Robo2	
Podxl	
Erbb4	
Egf	
Slc12a1	
Enox1	
Efna5	
Slc12a3	
Klhl3	
Abca13	
Wnk1	
Trmp6	
Slc8a1	
Calb1	
Wnk1	
Slc12a3	
Klhl3	
Egfem1	
Phactr1	
Slc8a1	
Tbck	
Frmpd4	

#### 3. Top 10 Markers of the cell types in the Nephron cell subgroup.

FindAllMarkers generated the list of genes differentially expressed in each cluster compared to all other cells, within the major subgroups defined (nephron cells, collecting duct, other cells) based on the Wilcoxon rank-sum test and limiting the analysis with a cut-off for minimum log fold change difference (0.3) and minimum cells with expression (0.3). Top 10 markers selected based on average LogFC.

Ν.	p_val	avg_logFC	pct.1	pct.2	p_val_adj	cluster	gene
1	L 0	4,273323345	0,744	0,107	0	PT	Slc34a1
2	2 0	3,520709463	0,439	0,115	0	PT	Slc5a12
3	3 0	2,831755183	0,768	8 0,135	0	PT	Abcc2
4	1 O	2,650094422	0,784	0,231	0	РТ	Ghr
5	5 0	2,648894113	0,652	0,128	0	РТ	Acsm1
6	5 0	2,564790807	0,756	o,096	0	РТ	Dab2
7	7 0	2,484248173	0,73	0,112	0	РТ	Fut9
8	3 0	2,432948596	0,652	0,097	0	РТ	Keg1
9	) 0	2,382841762	0,69	0,108	0	РТ	Slc4a4
10	) 0	2,273961676	0,745	0,227	0	РТ	Bmp6
11	L 0	2,53327938	0,71	. 0,337	0	DTL-ATL	Tshz2
12	2 0	2,306096865	0,644	0,18	0	DTL-ATL	Rbms3
13	3 0	2,094355804	0,66	<b>0,288</b>	0	DTL-ATL	Chn2
14	1 O	1,96244558	0,685	0,302	0	DTL-ATL	Epha7

15	0	1,938306833	0,697	0,256	0 DTL-ATL	Dnm3
16	0	1.931325248	0.685	0.398	0 DTL-ATL	Scel
		1,00102020210	0,000	0,000		
17	0	1,846540711	0,643	0,246	0 DIL-AIL	Naaladi2
18	3,51E-287	2,093103417	0,572	0,29	7,02E-284 DTL-ATL	Akap12
19	1 26F-163	1 597527489	0 522	0 337	2 52E-160 DTL-ATL	Sorcs3
20	1,202 105	1,007.027.405	0,522	0,007		DI C 4
20	1,34E-115	1,934665185	0,518	0,34	2,67E-112 DIL-AIL	RDTOX1
21	0	2,949696363	0,82	0,204	0 TAL	Sgcz
22	0	2 030330225	0 000	0 168		Slc12a1
22	0	2,550550225	0,555	0,100	0 142	5101201
23	0	2,591040981	0,986	0,332	0 TAL	Mrps6
24	0	2,397751822	0,928	0,27	0 TAL	Cacnb4
25	0	2 160310770	0.78	0 272		Bckdhh
25	0	2,100313773	0,70	0,272	0 142	Dekano
26	0	2,139403566	0,653	0,23	0 IAL	Ptger3
27	0	2,11776565	0,985	0,273	0 TAL	Erbb4
20	0	2 0727/6/9	0 5 9 2	0 154		Panhn2l
20	0	2,07374048	0,505	0,104	0 TAL	
29	0	2,010/485/8	0,736	0,312	0 IAL	Esrrb
30	0	2,004208377	0,675	0,249	0 TAL	Ppp1r1a
21	1 53F-210	3 05446807	0 012	0.16	3 06F-207 POD	\A/+1
51	1,551-210	3,03440807	0,512	0,10	5,002-207 FOD	
32	1,89E-194	3,739776069	0,978	0,381	3,78E-191 POD	Srgap1
33	3,00E-187	3,913954091	1	0,557	6,00E-184 POD	Magi2
34	1 07F-182	3 06914283	0 982	0 389	2 14F-179 POD	Pard3h
25	1,070 102	3,00314203	0,502	0,505	2,142 173 100	
35	4,37E-174	3,120203866	0,927	0,385	8,/3E-1/1 POD	Nebl
36	9,72E-174	3,475974013	0,931	0,315	1,94E-170 POD	Thsd7a
37	7 37F-165	3 100015125	0 905	0 272	1 47E-161 POD	Roho?
57	7,371-105	3,403013423	0,505	0,272	1,472-101 100	RODOZ
38	7,43E-162	3,067671121	0,887	0,293	1,49E-158 POD	Ptpro
39	4,83E-152	2,933644063	0,872	0,328	9,66E-149 POD	Synpo
40	2 525 150	2 105750020	0.961	0.280	5 04E 147 POD	Podvl
40	2,521-150	3,103730030	0,001	0,205	5,042-147 100	FUUXI
41	0	2,487024873	0,942	0,233	0 MD	Erbb4
42	0	2,384027186	0,487	0,147	0 MD	Egf
12	0	2 271671012	0 702	0 120		SIc12-1
45	0	2,271071013	0,793	0,138	0 MD	JICIZAL
44	0	2,10434847	0,446	0,282	0 MD	Enox1
45	0	1,967454833	0,734	0,394	0 MD	Efna5
16	0	1 064490612	0,617	0.254		Muc2h
40	0	1,904469013	0,017	0,234	0 MD	1019030
47	0	1,903208363	0,665	0,261	0 MD	Slit2
48	0	1,868287524	0,856	0,305	0 MD	Mrps6
10	0	1 0/55725/2	0.21	0 115		Spn1
45	0	1,045572545	0,51	0,115	0 1010	Sppi
50	0	1,786094696	0,54	0,234	0 MD	Kctd1
51	0	3,437605217	0,993	0,217	0 DCT	Slc12a3
52	0	, , 000100000	0.001	0 270		KIND
52	0	2,802183223	0,004	0,279	0 DC1	KIIIS
53	0	2,777562844	0,906	0,339	0 DCT	Abca13
54	0	2,587060385	0,985	0,339	0 DCT	Wnk1
	0	2 450457692	0.015	0.254		Trome
55	0	2,450457062	0,815	0,554	0 DC1	пріпо
56	0	2,278431434	0,737	0,416	0 DCT	Cables1
57	0	2.253490391	0.781	0.15	0 DCT	Tsc22d1
E 0	0	2 212001000	0.020	0.250		Codne?
58	0	2,212004009	0,828	0,558	0 DC1	Caupsz
59	0	1,858121344	0,971	0,32	0 DCT	Mecom
60	0	1,717089938	0,669	0,449	0 DCT	Prkd1
61	0	3 60/828121	0 00	0.338		Slc8a1
<u> </u>	0	2,00,000121	0,99	0,230		C-U 4
62	0	2,756455758	0,814	0,217	0 DCI-CNI	Calb1
63	0	2,749109333	0,99	0,353	0 DCT-CNT	Wnk1
64	0	2 460358566	0 925	0 235	0 DCT-CNT	SIc12a3
	0	2,100000000	0,525	0,200		5101205
65	0	2,362826604	0,889	0,292	0 DCI-CNI	KINI3
66	0	2,285735567	0,974	0,35	0 DCT-CNT	Phactr1
67	0	2 141187394	0 848	0 222	0 DCT-CNT	Søms2
60	0	2,1111070070	0,040	0,222		561152 T 22.14
pg	0	2,134469856	0,844	0,163	U DCI-CNI	1sc22d1
69	1,32E-302	1,942844013	0,806	0,365	2,64E-299 DCT-CNT	Trpm6
70	1 29F-294	1 844452576	0 772	0 237	2 58F-291 DCT-CNT	ĸ
74	-,,2.94	2,01770	0,772	0,237		с. ГЛ. А
/1	0	3,110496518	0,492	0,304	U CNI	Egtem1
72	0	3,108504493	0,842	0,328	0 CNT	Phactr1
73	Λ	2,553357989	0 717	0 219	0 CNT	SIc8a1
	-	4.555557565	0,717	5,215	0 0111	510001
74	0	1,555529849	0,491	0,214	U CNI	Nr3c2
75	1,23E-307	1,598896965	0,389	0,215	2,46E-304 CNT	Calb1
76	2.29F-305	1,734366383	0 32	0 157	4.58F-302 CNT	Aun3
	1.045.005	2,734300303	0,52	0,107		7.4P2
11	1,04E-267	2,016601412	0,501	0,347	2,08E-264 CN1	IDCK
78	1,59E-256	1,57291594	0,47	0,341	3,18E-253 CNT	Pde3b
79	8.97F-214	2.052595999	0.397	0.252	1.79E-210 CNT	Frmnd4
	1 425 425	1,002202222	0,007	0,202		pu+
80	1,43E-184	1,903293238	0,492	0,417	2,80E-181 CN1	irpv5

4. Top 10 Markers of the cell types in the Collecting duct cell subgroup.

FindAllMarkers generated the list of genes differentially expressed in each cluster compared to all other cells, within the major subgroups defined (nephron cells, collecting duct, other cells) based on the Wilcoxon rank-sum test and limiting the analysis with a cut-off for minimum log fold change difference (0.3) and minimum cells with expression (0.3). Top 10 markers selected based on average LogFC.

N.	p.	val	avg_logFC	pct.1	pct.2	2	p_val_adj	cluster	gene
	1	1,04E-250	2,609780526		0,836	0,364	2,09E-247	ICA	Kit
	2	8,28E-182	1,965728467		0,682	0,244	1,66E-178	ICA	Adgrf5
	3	8,59E-162	1,795348976		0,648	0,198	1,72E-158	ICA	Clnk
	4	6,39E-152	1,88791788		0,674	0,256	1,28E-148	ICA	Epb41l2
	5	3,38E-147	1,599596844		0,542	0,167	6,76E-144	ICA	Dmrt2
	6	7,45E-147	1,302085084		0,814	0,413	1,49E-143	ICA	Rcan2
	7	5,18E-123	2,127384378		0,605	0,279	1,04E-119	ICA	Slc35f1
	8	7,59E-91	1,341917246		0,63	0,318	1,52E-87	ICA	Efhd1
	9	1,68E-73	1,48354411		0,5	0,203	3,37E-70	ICA	Trpm3
	10	1,21E-13	1,520773491		0,372	0,244	2,42E-10	ICA	Negr1
	11	0	3,89548694		0,941	0,18	0	ICB	Lsamp
	12	0	3,597142868		0,899	0,135	0	ICB	Slc26a4
	13	0	2,444764346		0,921	0,235	0	ICB	Nbea
	14	0	2,383591973		0,803	0,15	0	ICB	Tmem163
	15	0	2,380765523		0,899	0,296	0	ICB	Car12
	16	0	2,069609378		0,874	0,194	0	ICB	Slc4a9
	17	9,20E-239	1,7793705		0,831	0,357	1,84E-235	ICB	Pde4b
	18	5,29E-225	1,734879524		0,742	0,282	1,06E-221	ICB	Rtl4
	19	4,91E-223	1,956078774		0,64	0,136	9,82E-220	ICB	Thsd7a
	20	3,15E-206	1,785761911		0,679	0,258	6,30E-203	ICB	Rp1
	21	0	3,417144382		0,703	0,066	0	PC	Aqp2
	22	2,45E-258	1,777958397		0,758	0,326	4,90E-255	PC	Frmpd4
	23	1,96E-180	1,995346179		0,696	0,398	3,92E-177	PC	Phactr1
	24	6,13E-156	2,023502332		0,472	0,149	1,23E-152	PC	Fxyd4
	25	2,12E-126	1,934003661		0,526	0,271	4,24E-123	PC	Mgat4c
	26	2,16E-114	1,851729053		0,501	0,257	4,31E-111	PC	Рарра
	27	4,95E-100	1,756619699		0,468	0,207	9,90E-97	PC	Dnm3
	28	2,07E-96	1,904647421		0,51	0,276	4,14E-93	PC	Pde3b
	29	2,38E-72	1,816001613		0,494	0,326	4,76E-69	PC	Kcnc2
	30	9,34E-69	1,815708887		0,506	0,352	1,87E-65	PC	Gpc5

### 5. Top 10 Markers of the cell types in the Other cell subgroup.

FindAllMarkers generated the list of genes differentially expressed in each cluster compared to all other cells, within the major subgroups defined (nephron cells, collecting duct, other cells) based on the Wilcoxon rank-sum test and limiting the analysis with a cut-off for minimum log fold change difference (0.3) and minimum cells with expression (0.3). Top 10 markers selected based on average LogFC.

N.	p_\	val	avg_logFC	pct.1		pct.2		p_val_adj	cluster	gene
	1	0	2,830437209		0,793		0,422	0	EC	Ptprb
	2	0	2,606827352		0,87		0,302	0	EC	Plpp1
	3	2,47E-280	2,138443575		0,74		0,31	4,95E-277	EC	Heg1
	4	6,35E-255	2,479003314		0,754		0,528	1,27E-251	EC	Shank3
	5	1,26E-243	2,688769393		0,77		0,533	2,53E-240	EC	Flt1
	6	2,74E-212	2,096500483		0,714		0,482	5,47E-209	EC	Dysf
	7	4,98E-147	2,232007301		0,622		0,38	9,96E-144	EC	Cyyr1
	8	1,09E-110	2,132158913		0,607		0,41	2,17E-107	EC	Tek
	9	9,91E-109	2,191392873		0,632		0,482	1,98E-105	EC	Adgrl4
	10	8,44E-77	2,195237567		0,543		0,376	1,69E-73	EC	D5Ertd615e
	11	0	2,841511535		0,836		0,476	0	Stroma	Lhfp
	12	5,64E-306	2,088451419		0,786		0,245	1,13E-302	Stroma	Rbms3
	13	4,44E-266	2,688808479		0,738		0,298	8,88E-263	Stroma	Gpc6
	14	2,31E-236	2,141519372		0,74		0,355	4,61E-233	Stroma	Sox5
	15	1,27E-186	2,324955266		0,678		0,341	2,55E-183	Stroma	4930578G10Rik
	16	8,16E-186	2,18527447		0,646		0,346	1,63E-182	Stroma	6530403H02Rik
	17	2,09E-181	2,23912503		0,655		0,176	4,18E-178	Stroma	Lama2
	18	2,87E-181	2,046204714		0,713		0,421	5,73E-178	Stroma	Gucy1a2
	19	2,49E-174	2,139259489		0,709		0,41	4,99E-171	Stroma	Cfh
	20	6,79E-39	2,733591245		0,549		0,387	1,36E-35	Stroma	Csmd1
	21	5,62E-94	2,824477523		0,595		0,289	1,12E-90	Immune	Camk1d
	22	3,14E-74	2,410623524		0,693		0,51	6,27E-71	Immune	Pid1
	23	6,07E-42	2,435645999		0,545		0,436	1,21E-38	Immune	Fyb
	24	2,82E-30	1,878168487		0,519		0,416	5,65E-27	Immune	Arhgap15
	25	2,71E-26	2,105055484		0,539		0,526	5,41E-23	Immune	Epsti1
	26	3,81E-24	1,953440633		0,524		0,508	7,61E-21	Immune	Ctsc

27	9,66E-24	1,988167523	0,502	0,5	1,93E-20 Immune	Cadm1
28	3,49E-12	1,750391992	0,303	0,553	6,97E-09 Immune	lkzf1
29	0,00022378	1,999778189	0,461	0,528	0,447560102 Immune	Runx1
30	0,007920797	1,805374029	0,396	0,47	1 Immune	Slc9a9

### **Perfusion solution**

Prismasol 4 (Baxter)	
Calcium	1.75
Magnesium	0.5
Sodium	140
Chloride	113.5
Lactate	3
Bicarbonates	32
Potassium	4
Glucose	6.1
Glutamine	1 mM
Pyruvate	0.1 mM
Cernevit	200 mg/L
D2glucose	1 :100
Human erythrocytes	10%
Addaven 1 :70	
chrome	2.86 nM
cuivre	0.09 μΜ
manganese	14.29 μM
fluorure	0.71 μΜ
selenium	0.01 μΜ
zinc	1.1 μΜ
molybdene	2.86 nM
Cernevit	200 mg/L
VitA	52.15 mg/L
VitD3	1.56 μg/L
VitE	2.92 mg/L
VitC	32.6 mg/L
VitB1	0.92 mg/L
VitB2	1.07 mg/L
VitB6	1.18 mg/L
VitB12	1.56 μg/L
VitB9	0.11 mg/L

VitB5	4.17 mg/L
VitB8	0.02 mg/L
VitPP	12 mg/L

Control pH and adjust if necessary

Theoretical osmolarity: 301 mOsm/L

RESOURCE	SOURCE	IDENTIFIER	
Antibodies			
Anti-FBP1 polyclonal rabbit antibody for mouse/human	Abcom	Ab109020RRID:	
	Abcam	AB_10865049	
Anti DCK1 polyclopol robbit optibody for mouse	Abcom	Ab70358	
	Abcam	RRID: AB_1925305	
Secondary anti IaG Pabbit HPP	BD Biosciences	554021	
		RRID: AB_395213	

Chemicals		
Albumin Fraction V	Calbiochem	126579
LPS	Calbiochem	437625
TGFb	Peprotech	100-21
EGF	Sigma aldrich	E4127
Acid lactic	Sigma aldrich	L1750
DMEM	Gibco	11966025
F12	Gibco	11765054
FITC-Sinistrin	Fresenius-Kebi	
Prismasol 4	Baxter	112565
TGFb inhibitor (SB431542)	Sigma aldrich	S4317
Dimerizer	Clontech Laboratories, Inc	AP20187
ECL (WesternBright Quantum)	Advansta	K-12024-D20
Neo-Clear (Xylene substitute)	Merck Millipore	1098435000
Trizol reagent	Invitrogen	15596026
qScript cDNA supermix	Quanta-bio	95048-100
PowerUP SYBR Green master mix	Applied Biosystems	A25741

Commercial Assays		
FBP1 enzymatic activity kit	Biovision	K590-100
PCK1 enzymatic activity kit	Biovision	K359-100

Oligonucleotides		
	5' AAT CTC CAG AGG CAC CAT TG 3'	Microsynth
Rpipu	3' GTT CAG CAT GTT CAG CAG TG 5'	NM_007475.5
<b>D</b> .	5' GAG CTT ATC CCG AAC ATC CC 3'	Microsynth
Pcx	3' TCC ATA CCA TTC TCT TTG GCC 5'	NM_001162946.1
<b>F</b> ()	5' GTG TCA ACT GCT TCA TGC TG 3'	Microsynth
Гор 1	3' GAG ATA CTC ATT GAT GGC AGG G 5'	NM_019395.3
Dalid	5' CCA TCC CAA CTC GAG ATT CTG 3'	Microsynth
РСК1	3' CTG AGG GCT TCA TAG ACA AGG 5'	NM_011044.3
00	5' AAA AAG CCA ACG TAT GGA TTC CG 3'	Microsynth
Сорс	3' CAG CAA GGT AGA TCC GGG A 5'	NM_008061.4
111-4	5' CGT GCC GAC AAT CCA AAA TAG 3'	Microsynth
НКТ	3' AAT GTT AGC GTC ATA GTC CCC 5'	NM_001146100.1
Dim	5' GGT GTT TGC ATC TTT CAT CCG 3'	Microsynth
PKIII	3' CTG GCC TCC AAG ATC TCA TC 5'	NM_001378870.1
0.010	5' GTT GGC TCA GCC AGA TGC 3'	Microsynth
Ccl2	3' AGC CTA CTC ATT GGG ATC 5'	NM_011333.3
Lloverd	5' ACT AAG GGC TTC TAT GTT GGC 3'	Microsynth
Haveri	3' AGC TTC AAT CTT AGA GAC ACG G 5'	NM_134248.2
5' ACG ACA AGA GGC GGA CAC 3'		Microsynth
Мус	3' GCT GCG CTT CAG CTC GTT 5'	NM_010849.4
En1	5' TGC CTT CAA CTT CTC CTG TG 3'	Microsynth
	3' CAC TAA CCA CGT ACT CCA CAG 5'	NM_010233.2
Ecve1	5' TCT ACG AGT GGA TGG TGA AGA 3'	Microsynth
FOXOT	5' TGC TGT GAA GGG ACA GAT TG 3'	NM_019739.3
Forro	5'-GCC ACT CTC TGT GAC CTT T-3	Microsynth
Esita	5'-CAC TTC CAT CCA CAC ACT CT-3'	NM_007953.2
Unfdo	5'-CAG ATC ACC TCT CCC ATC TCT-3'	Microsynth
п/II4a	5'-GCT CCT TCA TAG ACT CAC ACA C-3'	NM_008261.3
Dearo	5'-TGC AAA CTT GGA CTT GAA CG-3'	Microsynth
rpara	5'-GAT CAG CAT CCC GTC TTT GT-3'	NM_001113418.1
Taih	5' CGG AGA GCC CTG GAT ACC A 3'	Microsynth
rgib	3' GCC GCA CAC AGC AGT TCT T 5'	NM_011577.2

Softwaree
Softwares

	10X Genomics	
	https://support.10xgen	
	omics.com/	
Cell Ranger (3.1.0)	single-cell-gene-	
	expression/software/	RRID: SCR_017344
	pipelines/latest/what-	
	is-cell-ranger	
D.: 400	https://www.r-	N/A
R V4.0.2	project.org/	RRID: SCR_001905
	https://satijalab.org/se	
R package Seurat V3.2.0	urat/	RRID: SCR_016341
	https://github.com/alex	
STAR V.2.5.10	dobin/STAR	RRID: 5CR_015899
	https://ccb.jhu.edu/soft	
TopHat 2.0.13	ware/tophat/index.sht	RRID: SCR_013035
	ml	
	https://htseq.readthed	0.6.1
	ocs.io/en/master/	0.0.1
Edge P v3 30 3		3.30.3
		RRID: SCR_012802
Disc	GraphPad software	8.4.0
Prism	Inc	RRID: SCR_002798
MP&D lab	Mannheim Pharma & Diagnostics	1.0
	Zeiss	3.0
Zen (blue edition)		RRID: SCR_013672
	Definiens Inc	2.7
Definiens Developer XD <sup>™</sup>		RRID: SCR_014283
Opath	QuPath developers,	0.2.2
	Edinburgh	0.2.2
		1.52a
ImageJ	magej.nin.gov	RRID: SCR_003070

Instruments measure		
Glucometer (Contour next USB)	Bayer	7414
Lactatemeter (Stat Strip Xpress)	Nova biomedical	47487