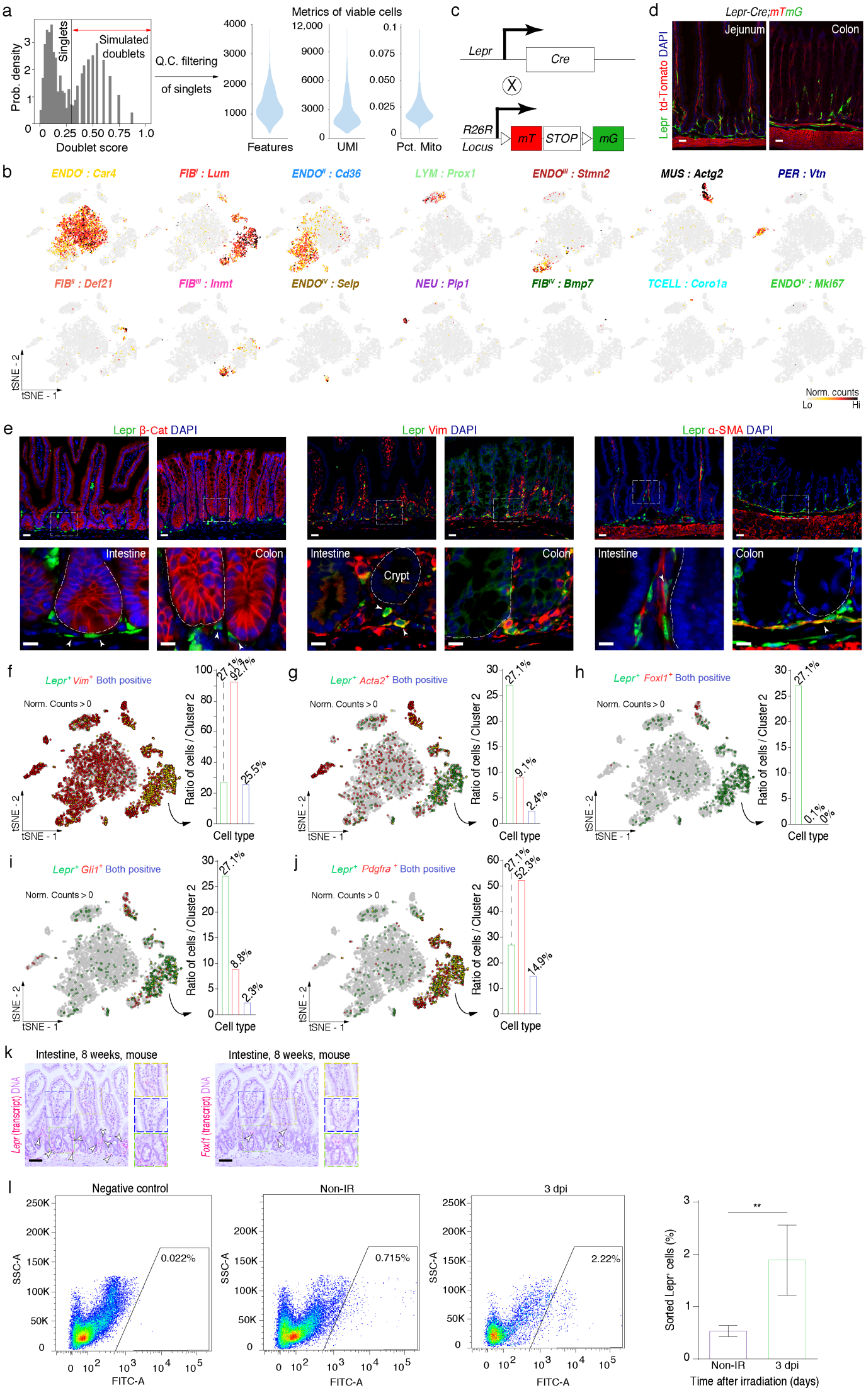
a
Prob. density
Singlets
Simulated doublets
Doublet score
Q.C. filtering of singlets
Metrics of viable cells
Features
UMI
Pct. Mito
c
Lepr
Cre
R26R Locus
mT
STOP
mG
d
Lepr-Cre;mTmG
Lepr td-Tomato DAPI
Jejunum
Colon
b
ENDOI : Car4
FIBI : Lum
ENDOII : Cd36
LYM : Prox1
ENDOIII : Stmn2
MUS : Actg2
PER : Vtn
FIBII : Def21
FIBIII : Inmt
ENDOIV : Selp
NEU : Plp1
FIBIV : Bmp7
TCELL : Coro1a
ENDOV : Mki67
tSNE - 1
tSNE - 2
Norm. counts
Lo
Hi
e
Lepr β-Cat DAPI
Lepr Vim DAPI
Lepr α-SMA DAPI
Intestine
Colon
Crypt
f
Lepr+ Vim+ Both positive
Norm. Counts > 0
Ratio of cells / Cluster 2
Cell type
27.1%
92.7%
25.5%
g
Lepr+ Acta2+ Both positive
27.1%
9.1%
2.4%
h
Lepr+ Foxl1+ Both positive
27.1%
0.1%
0%
i
Lepr+ Gli1+ Both positive
27.1%
8.8%
2.3%
j
Lepr+ Pdgfra+ Both positive
27.1%
52.3%
14.9%
k
Intestine, 8 weeks, mouse
Lepr (transcript) DNA
Foxl1 (transcript) DNA
l
Negative control
Non-IR
3 dpi
SSC-A
FITC-A
0.022%
0.715%
2.22%
Sorted Lepr+ cells (%)
**
Non-IR
3 dpi
Time after irradiation (days)

Fig. S1 Lepr$^+$ MCs surround intestinal crypts and are expanded upon irradiation. a Bimodal distribution of predicted singlet and doublet intestinal crypt MCs. Straight solid line indicates user-defined doublet score threshold. Singlets were further filtered to remove low-quality cells. Distribution of features/cell, UMI counts/cell, and percentage of mitochondrial genes/cell in valid cells post-filtering. Valid cells were used in downstream query and comparative analysis. **b** Feature plots of the identified marker genes in each cluster based on normalized counts. Expression levels for each cell are color-coded. Gray represents low expression and black represents high expression. **c** Schematic representation for generation of *Lepr-Cre*;*mTmG* mice. **d** High magnification images for GFP (Lepr$^+$ cells) and td-Tomato in jejunum and colon from *Lepr-Cre*;*mTmG* mice (n=3). Related to main **Fig. 1h**. Scale bar: 25 μm. **e** Immunofluorescence analysis for RFP (referred to Lepr$^+$ cells) and epithelial cell marker β-Catenin, MC marker Vimentin, and muscle-like MC marker α-SMA in the jejunum and colon from *Lepr-Cre*;*td-Tomato* mice. Arrowheads indicate double positive cells (appearing in yellow). n=3. The dashed line indicates the border between intestinal epithelium and mesenchyme in the crypts. Scale bar: upper panels, 25 μm; bottom panels, 10 μm. **f, g** Co-expression of *Lepr* and *Vim* (**f**) or *Acta2* (**g**) was visualized using t-SNE plot. Each dot represents an individual cell. **h - j** Co-expression of *Lepr* and *Foxl1* (**h**), *Gli1* (**i**) and *Pdgfra* (**j**) was visualized using t-SNE plot. Each dot represents an individual cell. **k** *In situ* hybridization for *Lepr* and *Foxl1* in jejunum of 8-week-old WT mice. Arrowheads point to positive signals. Insets on the right represent large magnification of selected areas (n=3). Scale bar: 50 μm. **l** Representative FACS plots for Lepr$^+$ cells physically isolated from *Lepr-Cre*;*mTmG* mice before or three days postirradiation. MCs isolated from WT mice were used as negative control. Quantification of the percentage of sorted Lepr$^+$ cells (n=3). Values in the graphs represent means ± SD. Unpaired student's t-test was used for calculating P values in **l**, $^{**}P < 0.01$.