

Table S4 Quality control of single cell sequencing upon RIF exposure

Sample	nFeature	nCount	percent.mt (%)	Clean Cell	Feature (median)
Ctrl1	200-4,500	500-15,000	15	13,172	2,389
Ctrl2	200-4,500	500-15,000	15	10,628	2,011
Ctrl3	200-4,500	500-15,000	15	13,976	2,079
RIF1	200-4,500	500-15,000	15	9,881	2,064
RIF2	200-4,500	500-15,000	15	9,589	2,183
RIF3	200-4,500	500-15,000	15	10,210	2,083

Note: Control sample group: Ctrl1, Ctrl2, Ctrl3; Treatment sample group: RIF1, RIF2, RIF3. nFeature: Range of gene numbers in the cells of each sample; nCount: Range of unique molecular identifier (UMI) counts in the cells of each sample; percent.mt: Percentage of mitochondrial content, with a cutoff of < 15% in the cells of each sample.

Table S5 qPCR primer sequences (Cyp3a11)

FP:	RP:
ACCTGGGTGCTCCTAGCAATC	AATCCCGCCGGTTTGTGAAG