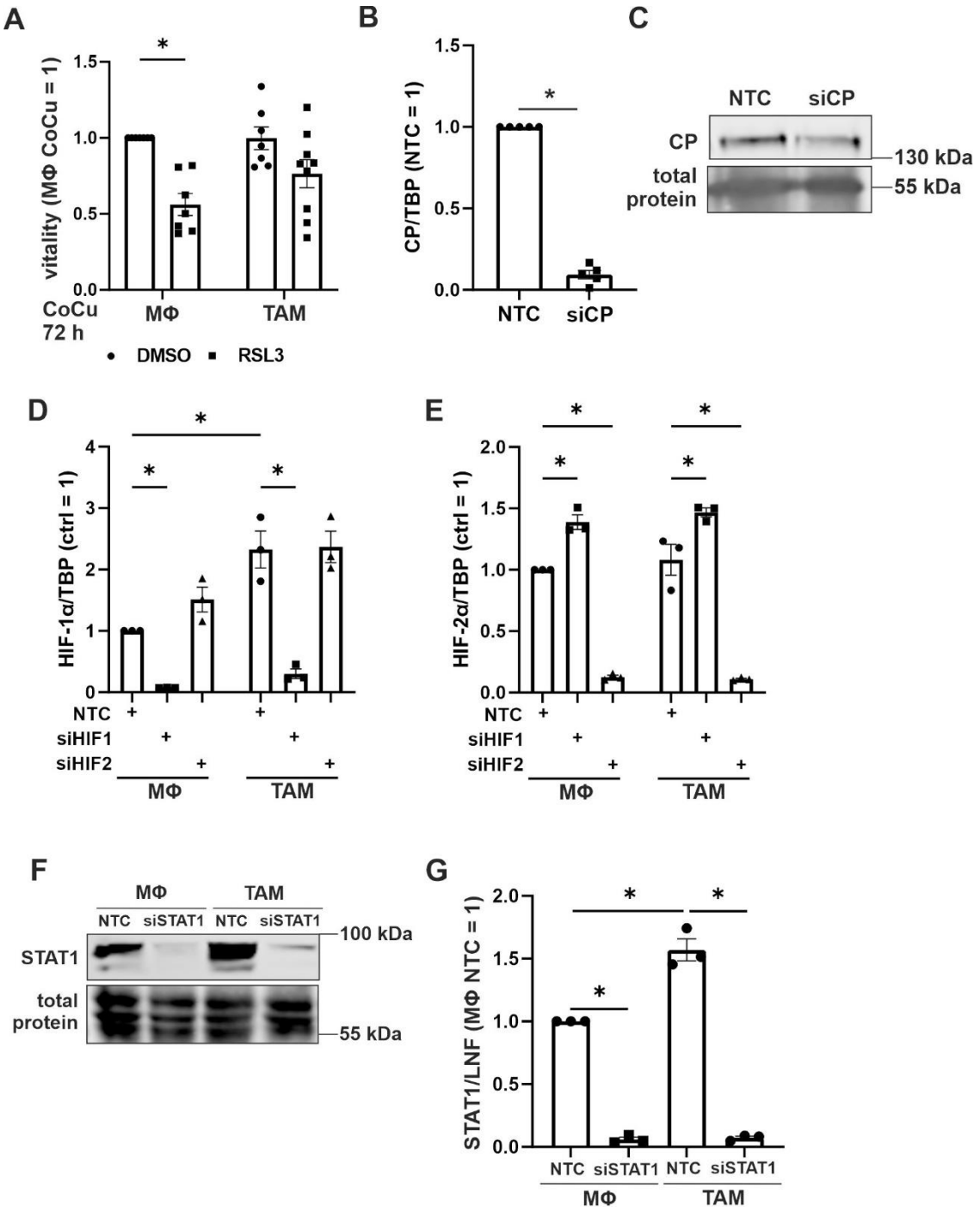



*Figure S1 Validation of siRNA experiments*

(A) HT1080 cells were co-cultured with primary human macrophages (MΦ) and tumor associated macrophages (TAM) for 72 h, treated with 1 µM RSL3 for 4 h. Vitality of HT1080 cells was measured. (B and C) Primary human macrophages were polarized to tumor associated macrophages (TAM) and transfected with siRNA against ceruloplasmin (CP) or a non-targeting control (NTC). (B) RNA of CP was measured and normalized to TATA box binding protein (TBP). (C) CP was analyzed by Western analyses. (D and E) Primary human macrophages (MΦ) and TAMs were transfected with siRNA against hypoxia inducible factor (HIF)-1α, HIF-2α, or NTC. (D) RNA of HIF-1α was measured and normalized to TBP. (E) RNA of HIF-2α was analyzed and normalized to TBP. (F and G) MΦ and TAMs were transfected with siRNA against signal transducer and activator of transcription 1 (STAT1) or NTC. (F) STAT1 protein was analyzed by Western blotting and (G) quantified and normalized to the lane normalization factor (LNF). All data are expressed as mean values ± SEM, *p ≤ 0.05.

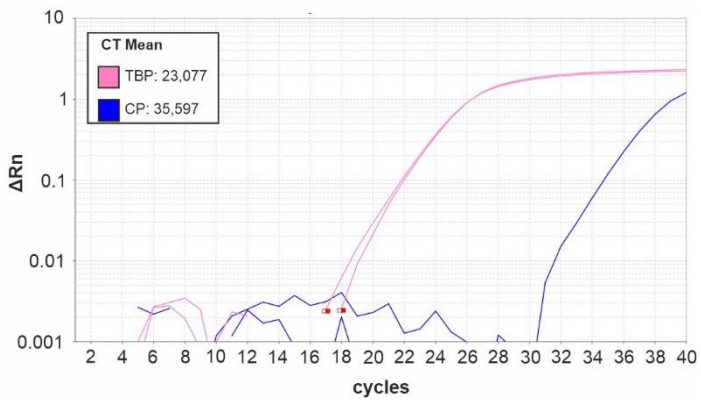



*Figure S2*
Basal CT values of ceruloplasmin mRNA compared to TATA-box binding protein in HT1080 cells. All data are expressed as mean values ± SEM, *p ≤ 0.05.

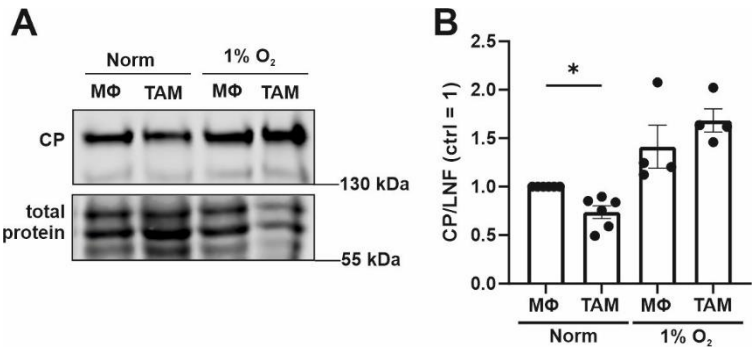
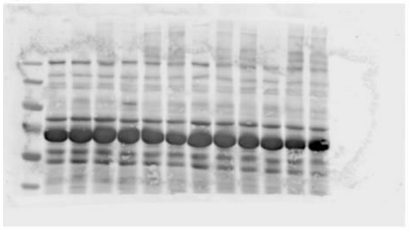


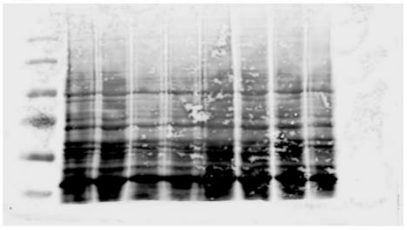

*Figure S3*
(A) Primary human macrophages (MΦ) and tumor associated macrophages (TAM) were incubated under hypoxia (1% $O_2$) for 24 h and ceruloplasmin (CP) was measured by Western analyses. (B) Quantification of (A). Data were normalized to the lane normalization factor (LNF). All data are expressed as mean values ± SEM, *p ≤ 0.05.

## Figure 3

A



C



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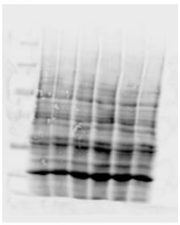
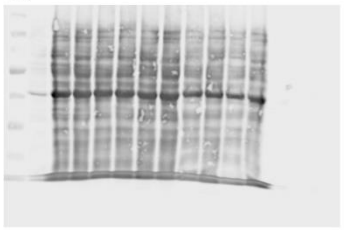
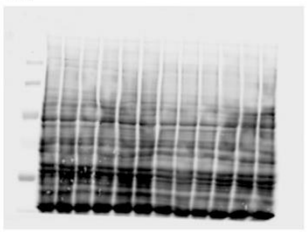


## Figure 4

B

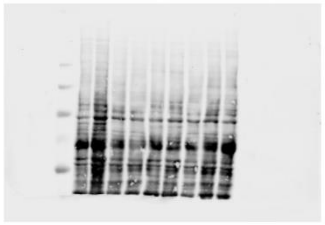


H



## Figure 5

C



## Figure 6

B

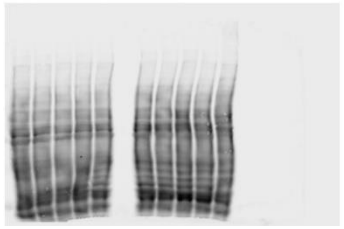


*Figure S4 Total protein stains*
Complete total protein stain for Western blots shown in indicated figures. Membranes were stained with Revert total protein stain and scanned on an Odyssey CFx scanner.