Supplementary information, Figure S7

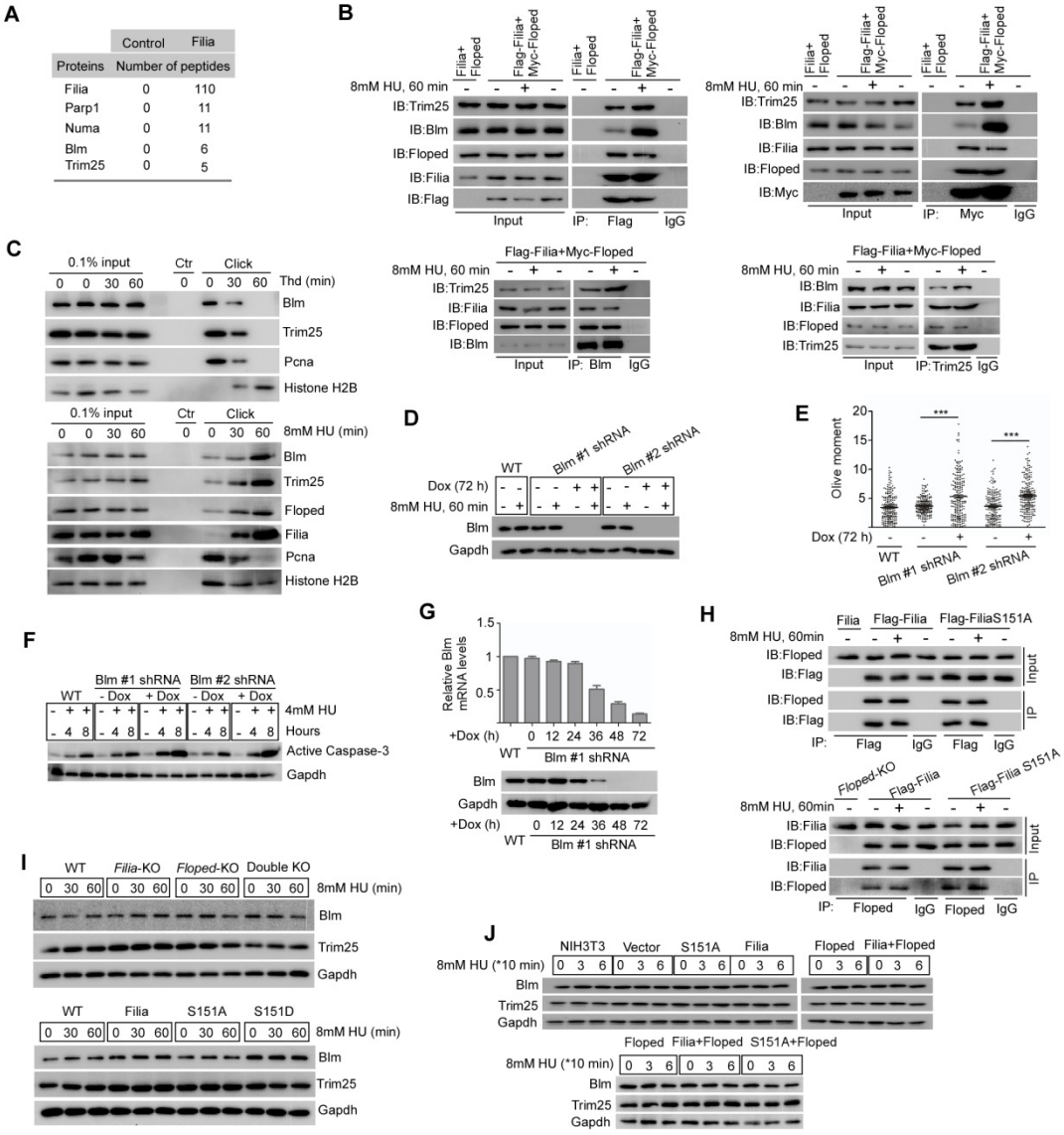

Figure S7 Filia-Floped associates with Blm and promotes its recruitment to replication forks. (**A**) Mass spectrometry analysis identified potential interaction proteins of Filia in Flag-Filia complemented ESCs. Several detected proteins were shown as examples. (**B**) Immunoprecipitation (IP) combined with immunoblotting (IB) confirmed the physical associations of Filia, Floped, Blm and Trim25 in NIH3T3 cells

co-expressing Flag-Filia and Myc-Floped. (**C**) iPOND confirmed the localization of Blm and Trim25 at replication forks under the normal culture condition (upper panel) and their increased recruitment upon HU treatment (lower panel) in NIH3T3 cells co-expressing both Filia and Floped. (**D**) Efficient knockdown of *Blm* by two individual Dox-inducible shRNAs in mESCs. (**E**) The increased level of DNA double strand breaks in *Blm*-knockdown ESCs under normal culture condition. (**F**) Depletion of Blm in ESCs led to increased apoptosis after HU treatment. (**G**) Measurement of the doxycycline (Dox)-induced *Blm* knockdown by q-PCR (upper panel) and immunoblotting (lower panel) at various time-points. (**H**) FiliaS151A mutant proteins were able to interact with Floped normally. (**I**) The total protein levels of Blm and Trim25 were comparable in WT, *Filia*-knockout (KO), *Floped*-KO and double KO ESCs (upper panel). The protein levels of Blm and Trim25 were also similar among the WT ESCs, WT Filia-, FiliaS151A-, and FiliaS151D-rescued ESCs (lower panel). (**J**) The total protein levels of Trim25 and Blm were comparable in NIH3T3 cells and NIH3T3 cells expressing Filia, Floped, FiliaS151A and Filia plus Floped (upper panel). The protein levels of Blm and Trim25 were also similar among NIH3T3 cells expressing Floped, Filia plus Floped, and FiliaS151A plus Floped. Data are represented as mean ± SEM. ***$P < 0.001$.