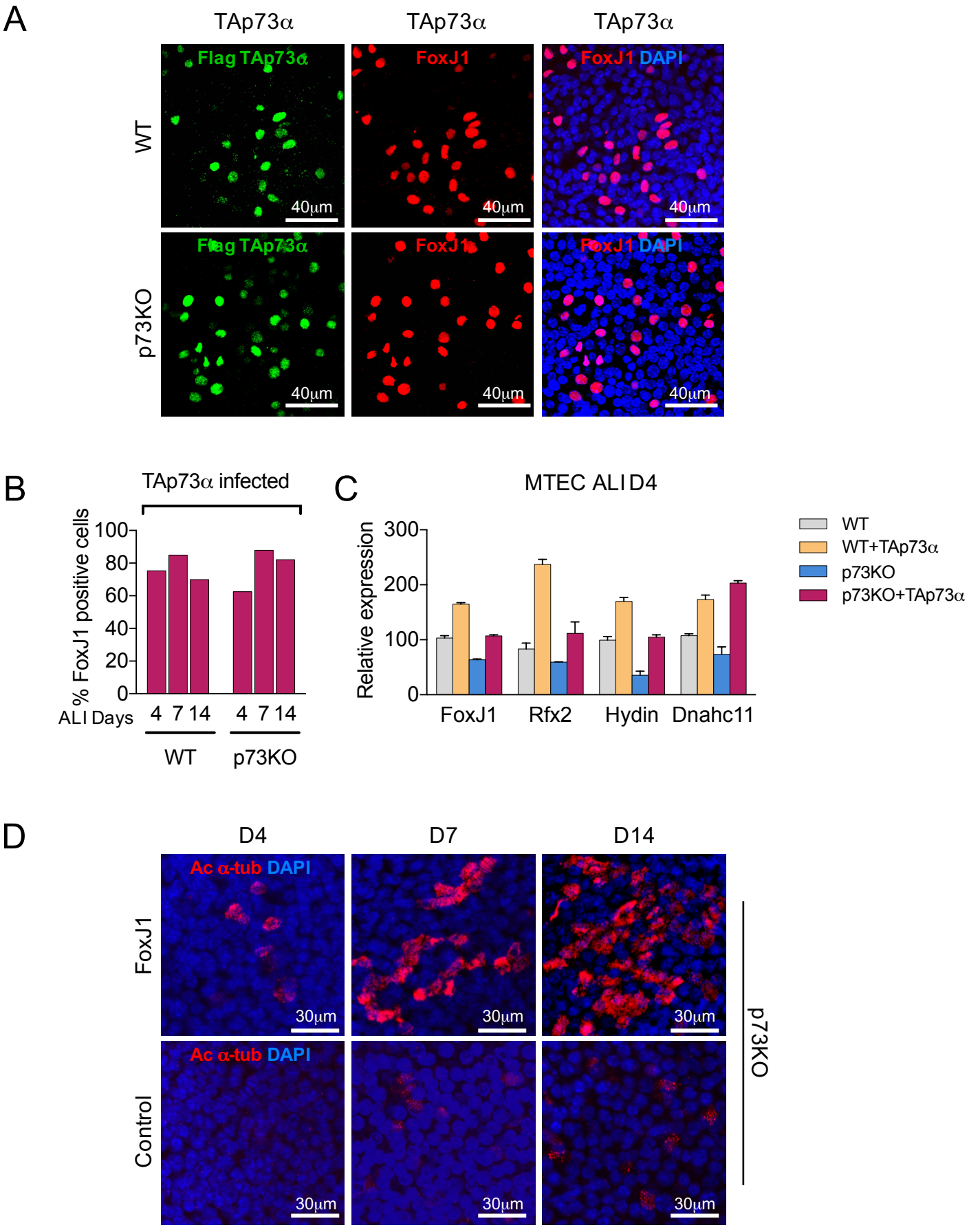
A
TAp73α
TAp73α
TAp73α
WT
p73KO
Flag TAp73α
FoxJ1
FoxJ1 DAPI
40μm
B
TAp73α infected
% FoxJ1 positive cells
100
80
60
40
20
0
ALI Days
4 7 14
4 7 14
WT
p73KO
C
MTEC ALI D4
Relative expression
300
200
100
0
FoxJ1
Rfx2
Hydin
Dnahc11
WT
WT+TAp73α
p73KO
p73KO+TAp73α
D
D4
D7
D14
FoxJ1
Control
Ac α-tub DAPI
30μm
p73KO

Supplemental Figure S8 (related to Fig. 6)**. FoxJ1 functions downstream of TAp73α in the transcriptional network to drive motile multiciliogenesis. Functional rescue.**

(**A-C**) Reintroduction of TAp73α (Flag-tagged) induces expression of FoxJ1 in p73KO MTEC cultures to WT levels.

(**A**) WT and p73KO MTECs, infected at seeding with lentivirus targeting mouse TAp73α expression to MCC-fated cells. Representative confocal images on ALI D14 stained for FlagTAp73α and FoxJ1.

(**B**) Quantitation of FoxJ1-positive cells from (**A**) in all TAp73α-expressing at ALI D4, D7 and D14. Data derived from five WT and five p73KO mice.

(**C**) Reintroduction of TAp73α induces expression of FoxJ1, Rfx2, Hydin and Dnahc11 in p73KO MTEC cultures. qRT-PCR assay of WT and p73KO MTEC cultures, infected and uninfected at ALI D4.

(**D**) p73KO MCCs are 100% rescued by FoxJ1 to undergo motile multiciliogenesis. Representative confocal images of the epistasis experiment from Fig. 6E-G. Immunofluorescence for Ac-α-tub with DAPI counterstain.