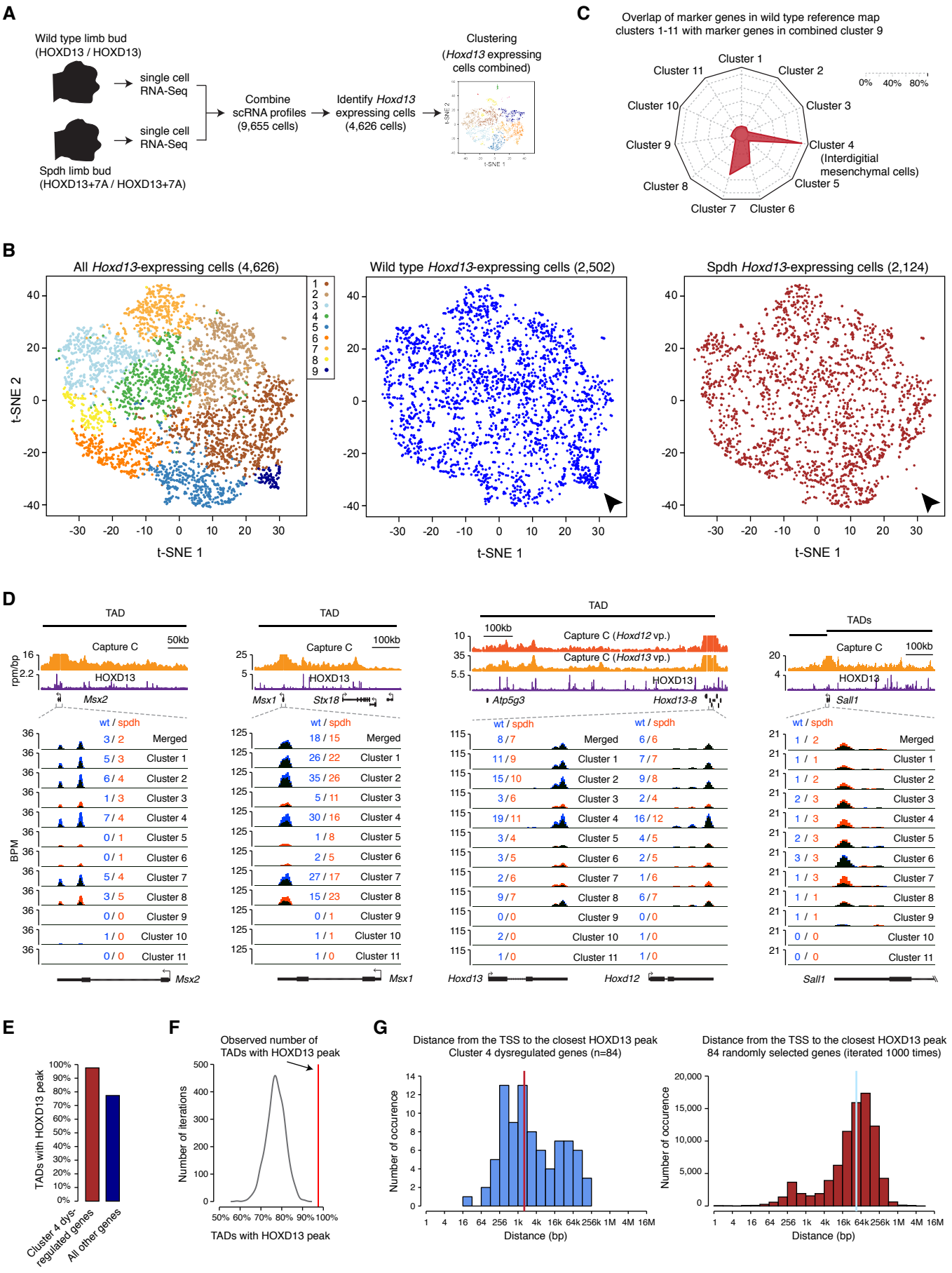
## Figure S5


A
Wild type limb bud
(HOXD13 / HOXD13)
single cell
RNA-Seq
single cell
RNA-Seq
Spdh limb bud
(HOXD13+7A / HOXD13+7A)
Combine
scRNA profiles
(9,655 cells)
Identify Hoxd13
expressing cells
(4,626 cells)
Clustering
(Hoxd13 expressing
cells combined)
C
Overlap of marker genes in wild type reference map
clusters 1-11 with marker genes in combined cluster 9
Cluster 1
Cluster 2
Cluster 3
Cluster 4
(Interdigitial
mesenchymal cells)
Cluster 5
Cluster 6
Cluster 7
Cluster 8
Cluster 9
Cluster 10
Cluster 11
0%
40%
80%
B
All Hoxd13-expressing cells (4,626)
Wild type Hoxd13-expressing cells (2,502)
Spdh Hoxd13-expressing cells (2,124)
t-SNE 2
t-SNE 1
D
TAD
Capture C
50kb
100kb
HOXD13
rpm/bp
Msx2
Msx1
Stx18
Atp5g3
Hoxd13-8
Sall1
Capture C (Hoxd12 vp.)
Capture C (Hoxd13 vp.)
TADs
wt / spdh
BPM
Merged
Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 7
Cluster 8
Cluster 9
Cluster 10
Cluster 11
Hoxd13
Hoxd12
E
TADs with HOXD13 peak
Cluster 4 dys-
regulated genes
All other genes
F
Observed number of
TADs with HOXD13 peak
Number of iterations
TADs with HOXD13 peak
G
Distance from the TSS to the closest HOXD13 peak
Cluster 4 dysregulated genes (n=84)
Distance from the TSS to the closest HOXD13 peak
84 randomly selected genes (iterated 1000 times)
Number of occurence
Distance (bp)