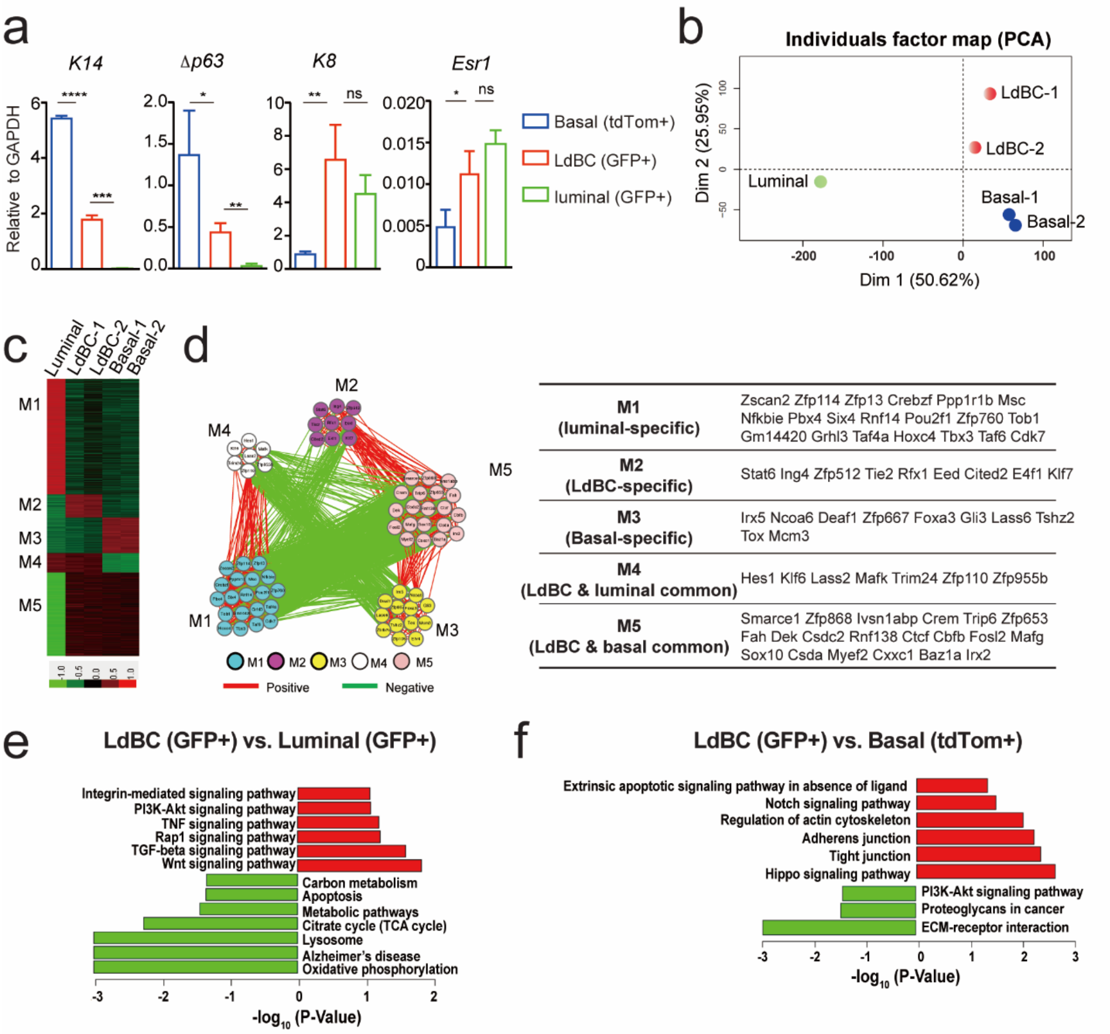

M1 (luminal-specific)	Zscan2 Zfp114 Zfp13 Crebzf Ppp1r1b Msc Nfkbie Pbx4 Six4 Rnf14 Pou2f1 Zfp760 Tob1 Gm14420 Grhl3 Taf4a Hoxc4 Tbx3 Taf6 Cdk7
M2 (LdBC-specific)	Stat6 Ing4 Zfp512 Tie2 Rfx1 Eed Cited2 E4f1 Klf7
M3 (Basal-specific)	Irx5 Ncoa6 Deaf1 Zfp667 Foxa3 Gli3 Lass6 Tshz2 Tox Mcm3
M4 (LdBC & luminal common)	Hes1 Klf6 Lass2 Mafk Trim24 Zfp110 Zfp955b
M5 (LdBC & basal common)	Smarce1 Zfp868 Ivsn1abp Crem Trip6 Zfp653 Fah Dek Csdc2 Rnf138 Ctcf Cbfb Fosl2 Mafg Sox10 Csda Myef2 Cxxc1 Baz1a Irx2

Supplementary information, Figure S6. Transcriptome analyses of LdBCs in hormonal stimulated mammary glands

(**a**) qPCR analysis indicating that LdBCs isolated from hormone-treated mammary gland express both basal (*K14 and Δp63*) and luminal (*K8*) markers, as well as *Esr1*. **** p<0.0001, *** p<0.001, ** p<0.01, * p<0.05, ns p>0.1.

(**b**) PCA analysis of basal cell (Lin$^-$, CD24$^+$, CD29^{hi}, tdTomato$^+$), luminal cell (Lin$^-$, CD24$^+$, CD29^{low}, GFP$^+$) and LdBC (Lin$^-$, CD24$^+$, CD29^{hi}, GFP$^+$) transcriptome indicating a closer relationship of LdBC with basal population than that with luminal population.

(**c**) Heat map and GBA analysis of three populations illustrating the common and distinct features of basal cells, luminal cells and LdBCs.

(**d**) Clustering analysis of transcription factors indicating LdBCs (M2) share similarity with and have positive connection (red lines) with basal cells (M5), while LdBCs (M2) have negative connection (green lines) with luminal cells (M1). Transcription factors featured in each module are listed on the right.

(**e-f**) KEGG analyses reveal upregulation of Wnt and TGF-β signaling pathways in LdBCs compared to luminal cells (**e**), and upregulation of Notch signaling in LdBCs compared to basal cells (**f**).