SUPPLEMENTAL FIGURES

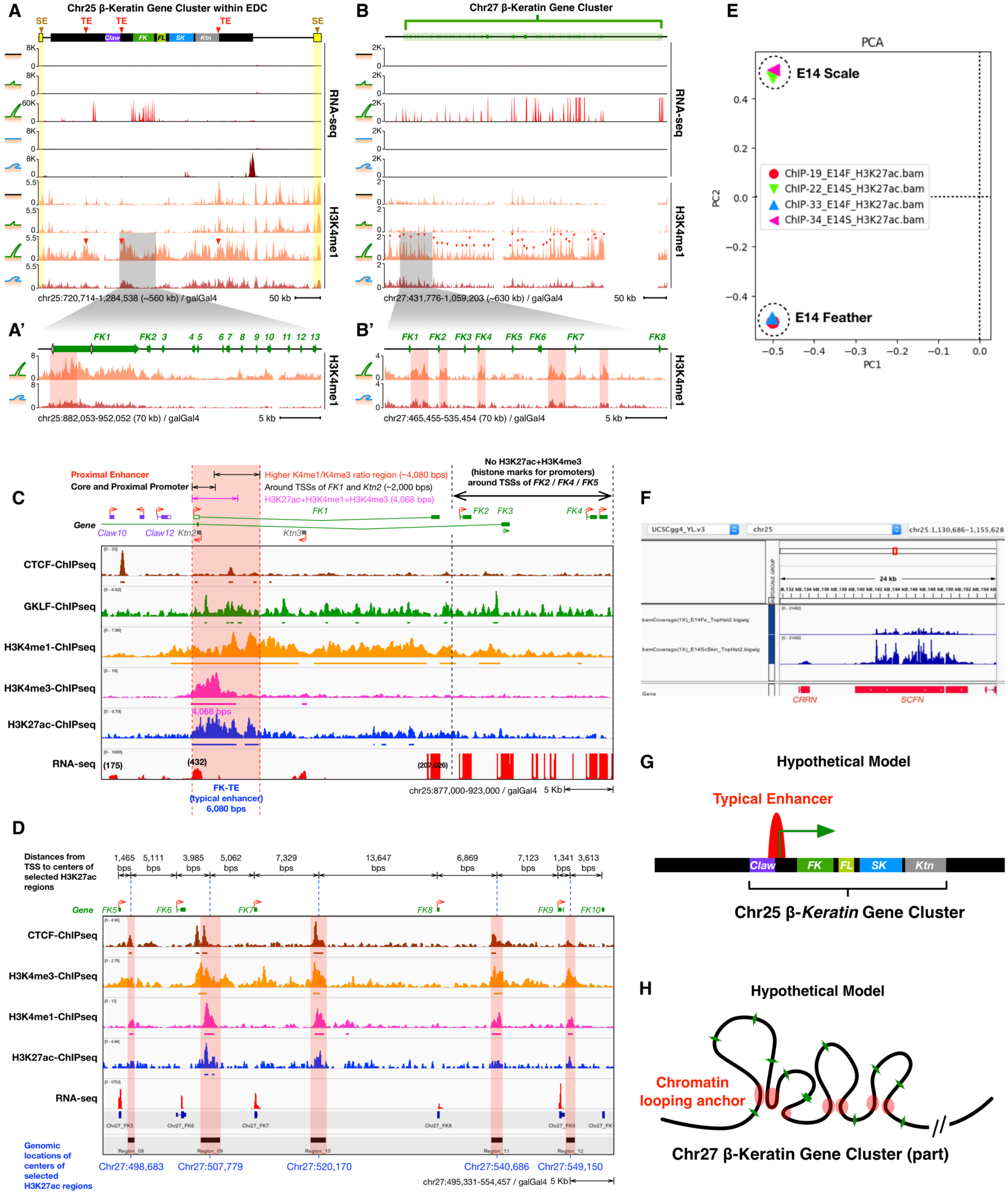
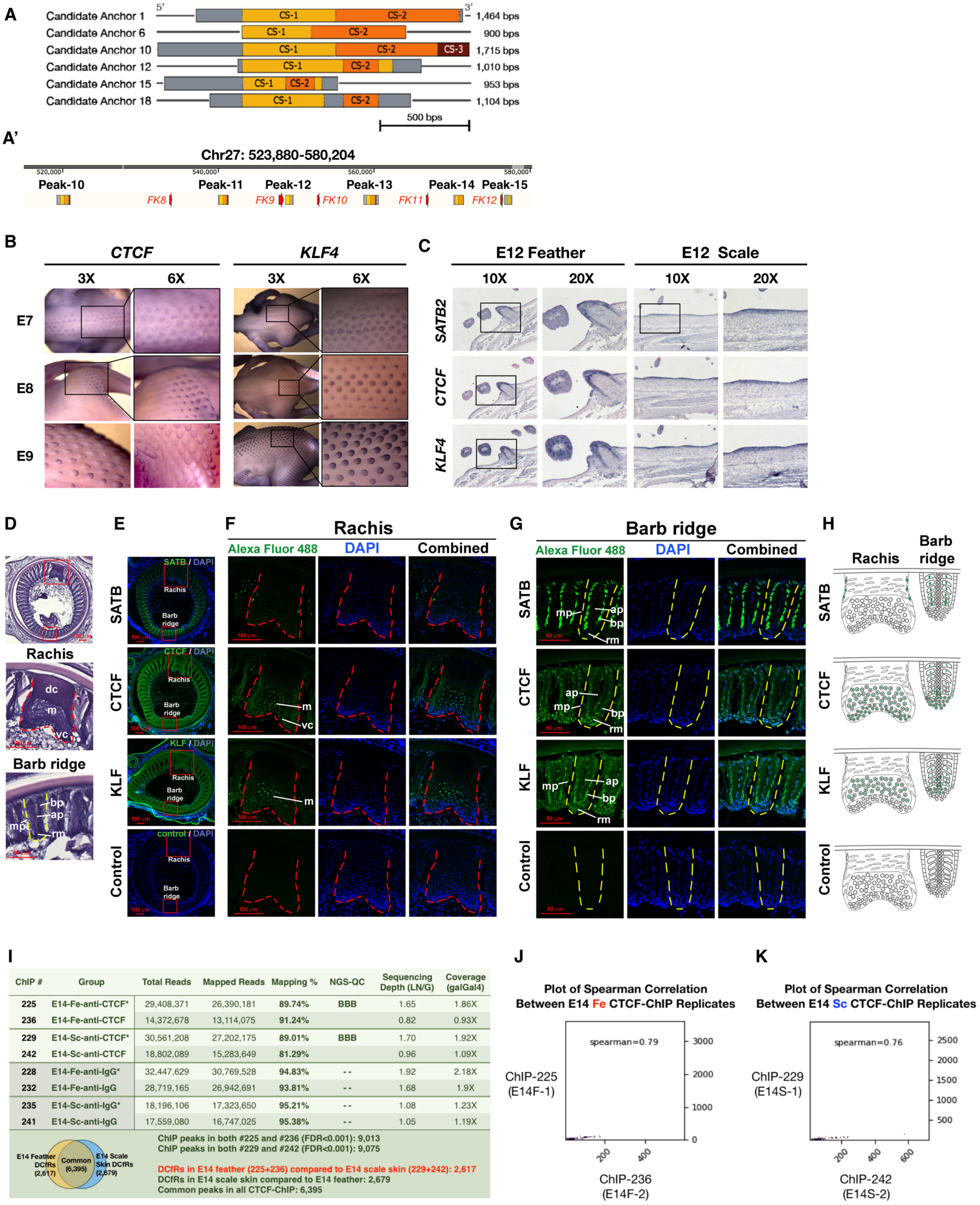


Figure S1. Epigenetic landscapes of multiplex *Keratin* gene clusters. Related to Figure 1. (**A**) Profiles of H3K4me1 on the Chr25 β-krt cluster during embryonic skin patterning. (**A'**) Enlargement of the *Feather Keratin* gene subcluster and a typical enhancer (TE; red triangles) at its 5' end. (**B**) Profiles of H3K4me1 on the Chr27 β-krt cluster during embryonic skin patterning. (**B'**) A closer look at the 5'-end of the Chr27 β-krt cluster. (**C**) Enlargement of the *Feather Keratin* gene subcluster and a typical enhancer (TE) at the 5' end of the Chr25 β-krt cluster. **(D)** Enlargement of a genomic region from the *FK5* gene to the *FK10* gene on the Chr27 β-krt cluster. (**E**) A PCA plot of H3K27ac-ChIP duplicates. (**F**) A closer look of RNA-seq signals at the black box region in Figure 1C. (**G** to **H**) Hypothetical models of two major modes of epigenetic regulation—single enhancer-driven co-expression of subclustered genes on the Chr25 β-krt cluster (**G**) and intra-cluster chromatin looping via individual H3K27ac-marked regions of the Chr27 β-krt cluster (**H**).



ChIP #	Group	Total Reads	Mapped Reads	Mapping %	NGS-QC	Sequencing Depth (LN/G)	Coverage (galGal4)
225	E14-Fe-anti-CTCF*	29,408,371	26,390,181	89.74%	BBB	1.65	1.86X
236	E14-Fe-anti-CTCF	14,372,678	13,114,075	91.24%		0.82	0.93X
229	E14-Sc-anti-CTCF*	30,561,208	27,202,175	89.01%	BBB	1.70	1.92X
242	E14-Sc-anti-CTCF	18,802,089	15,283,649	81.29%		0.96	1.09X
228	E14-Fe-anti-IgG*	32,447,629	30,769,528	94.83%	- -	1.92	2.18X
232	E14-Fe-anti-IgG	28,719,165	26,942,691	93.81%	- -	1.68	1.9X
235	E14-Sc-anti-IgG*	18,196,106	17,323,650	95.21%	- -	1.08	1.23X
241	E14-Sc-anti-IgG	17,559,080	16,747,025	95.38%	- -	1.05	1.19X

ChIP peaks in both #225 and #236 (FDR<0.001): 9,013
ChIP peaks in both #229 and #242 (FDR<0.001): 9,075

DCfRs in E14 feather (225+236) compared to E14 scale skin (229+242): 2,617
DCfRs in E14 scale skin compared to E14 feather: 2,679
Common peaks in all CTCF-ChIP: 6,395

Figure S2. Discovery of consensus sequences from H3K27ac regions of the Chr27 β-keratin gene cluster and expression patterns of CTCF, KLF4, and SATB2 during avian skin development. Related to Figure 2. (**A**) Alignment of SnapGene features of candidate looping anchors on the Chr27 β-krt cluster. (**A'**) Relative locations of consensus regions in the candidate looping anchors (Peak-10 to Peak-15). (**B**) *ISH* of CTCF and KLF4 in embryonic chicken skin. (**C**) *ISH* of CTCF, KLF4, and SATB2 at chick embryonic stage E12. (**D-H**) IM of SATBs, CTCF, and KLFs in developing feather follicles. (**D**) H&E staining of a flight feather follicle from E21. Middle and lower panels are rachis and barb ridge with higher magnification, respectively. Note the enlarged barb ridge image has been rotated 180 degrees. The developing rachis is composed of the dorsal cortex (dc), medulla (m) and ventral cortex (vc). A barb ridge includes a barbule plate (bp), axial plate (ap), marginal plate (mp) and a ramus zone (rm). Only the ramus zone and barbule plate will form the final feather structure. Other cell types will go through apoptosis and disappear when the mature feather opens. (**E**) IM of SATBs (first row), CTCF (second row), KLFs (third row) and control without primary antibody (fourth row). (**F-G**) IM of rachis and barb ridge, respectively. Left column, shows fluorescent IM signals. Middle column, DAPI staining. Right column, combined channels. In panels G and J, dotted red lines outline the rachis, whereas dotted yellow lines outline a single barb ridge. (**H**) Schematic drawing summarizing the strong expression patterns of these factors. (**I**) Quality control of CTCF-ChIP. (**J-K**) Spearman correlation of CTCF-ChIP duplicates.

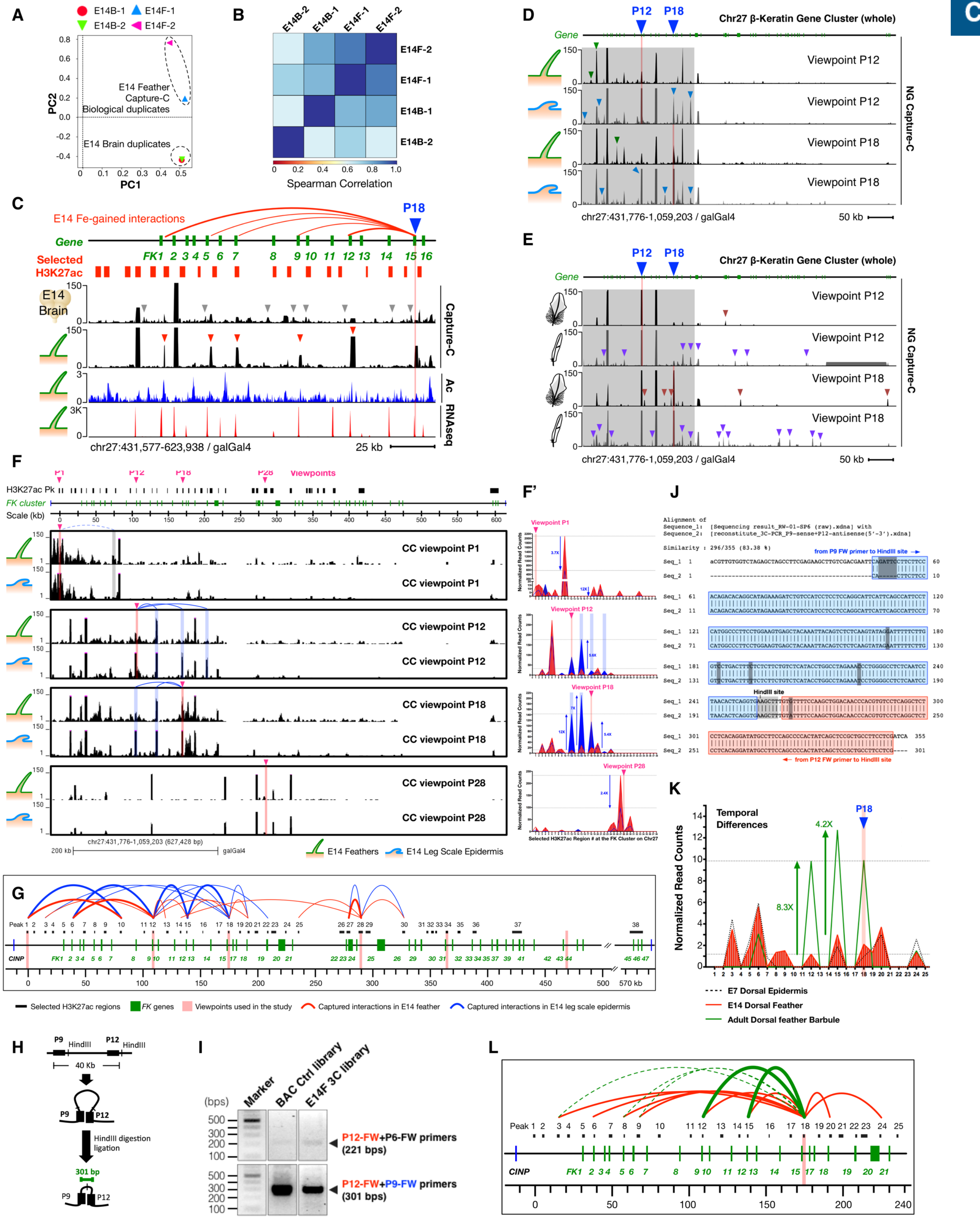


Figure S3. Validation of chromatin interactions at the *Keratin* gene clusters by NG Capture-C and 3C-PCR. Related to Figure 3. (**A**) A PCA plot of NG Capture-C duplicates. E14B-1/-2, embryonic stage Day 14 whole brain tissue, replicate 1/2; E14F-1/-2, embryonic stage Day 14 feather filament base, replicate 1/2. (**B**) Spearman correlation of NG Capture-C duplicates. (**C**) A whole cluster view of NG Capture-C interactions of different skin regions (feather filaments and scale epidermis) from the same aged chicks (E14). (**E**) A whole cluster view of NG Capture-C interactions of different feather types (dorsal contour feather barbs and flight feather barbs) from the same aged adult chickens. (**F**) NG Capture-C interactions of different skin regions (feather filaments and scale epidermis) from the same aged chicks (E14) using viewpoints P1/P12/P28. (**F'**) Normalized read counts of panel S3F. (**G**) Illustration of region-specific chromatin interactions of the feather- and scale-bearing skin at E14. (H) Schematic of the 3C-PCR primer design. (**I**) DNA agarose gel results of the P12-P9 interacting band. (**J**) TA-cloning of the P12-P9 interacting band and its sequencing result. (**K**) Normalized read counts of captured chromatin interactions from panel 3E. (**L**) Schematic of dynamic intra-cluster chromatin looping of Chr27 β-krt cluster during feather skin development.

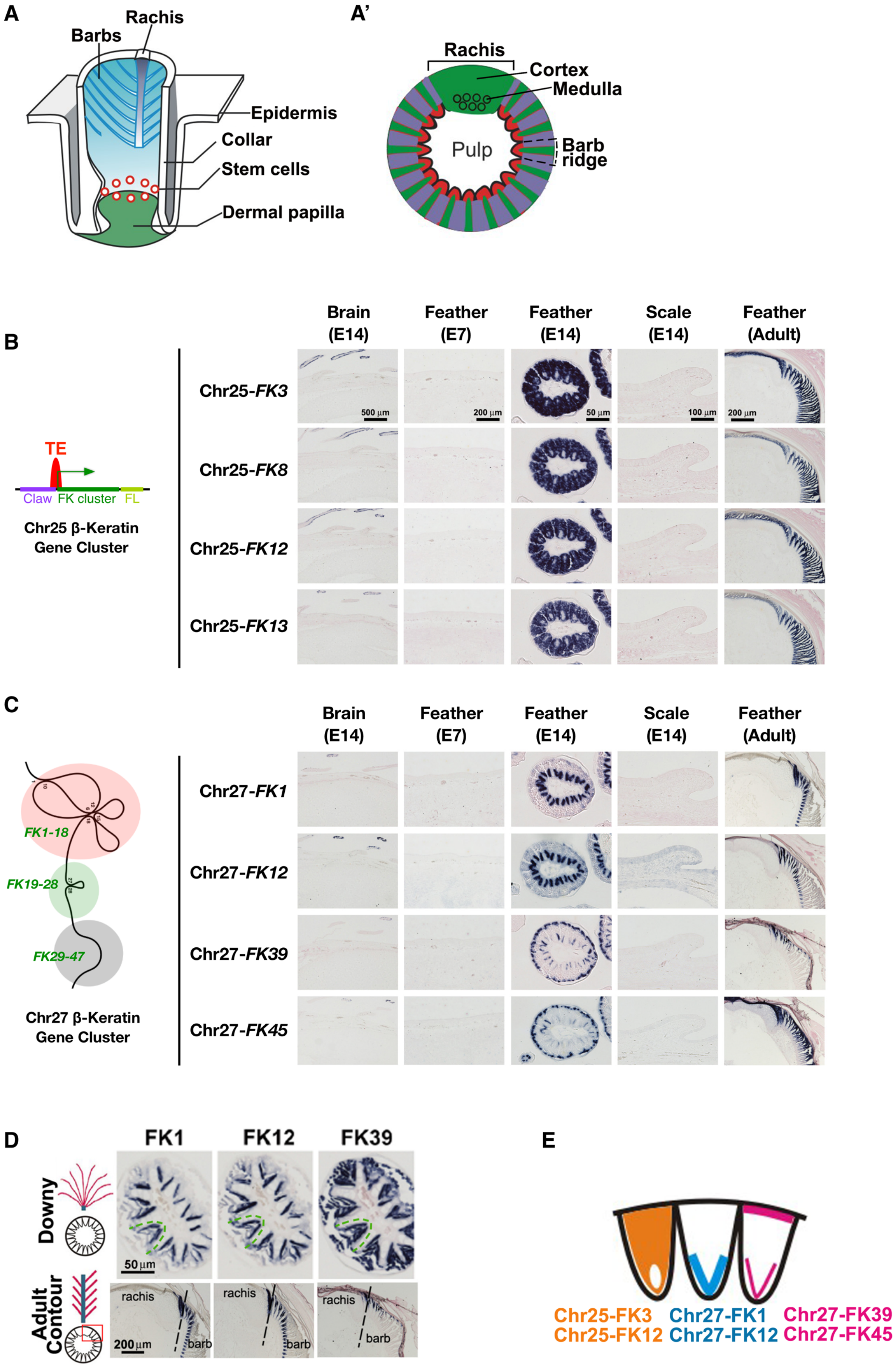


Figure S4. Expression of β-keratin genes in different skin regions during development. Related to Figure 4. (**A** to **A'**) Schematic drawing (**A)** and cross-section (**A'**) of a feather follicle. (**B**-**D**) A full panel of *ISH* results of *FK* genes in different skin regions and the brain (control). (**E**) Schematic of a feather cross-section, showing expression patterns of indicated keratins in a barb ridge.

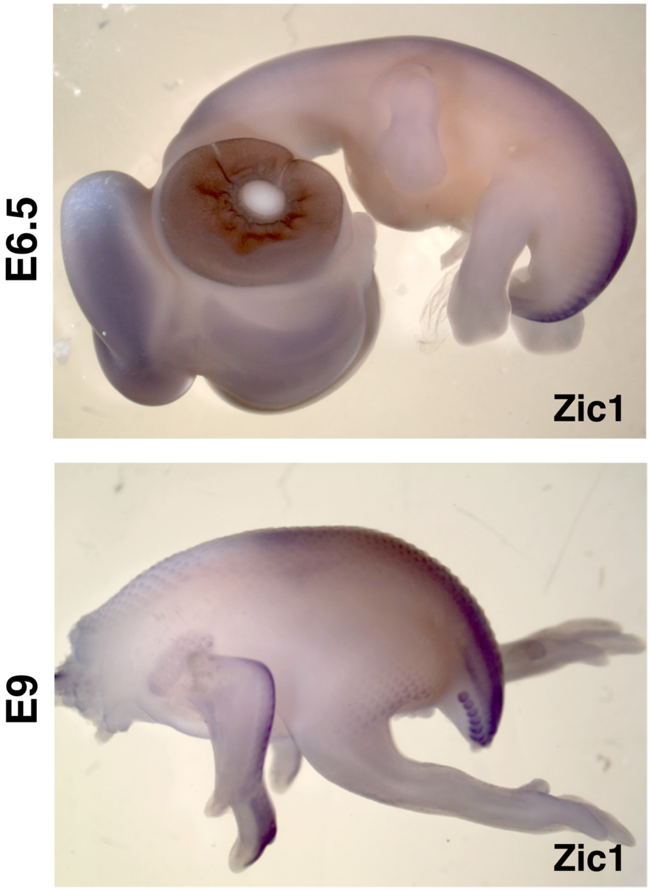


Figure S5. ***In-situ* hybridization of Zic1 during chicken embryonic development. Related to Figure 5.**

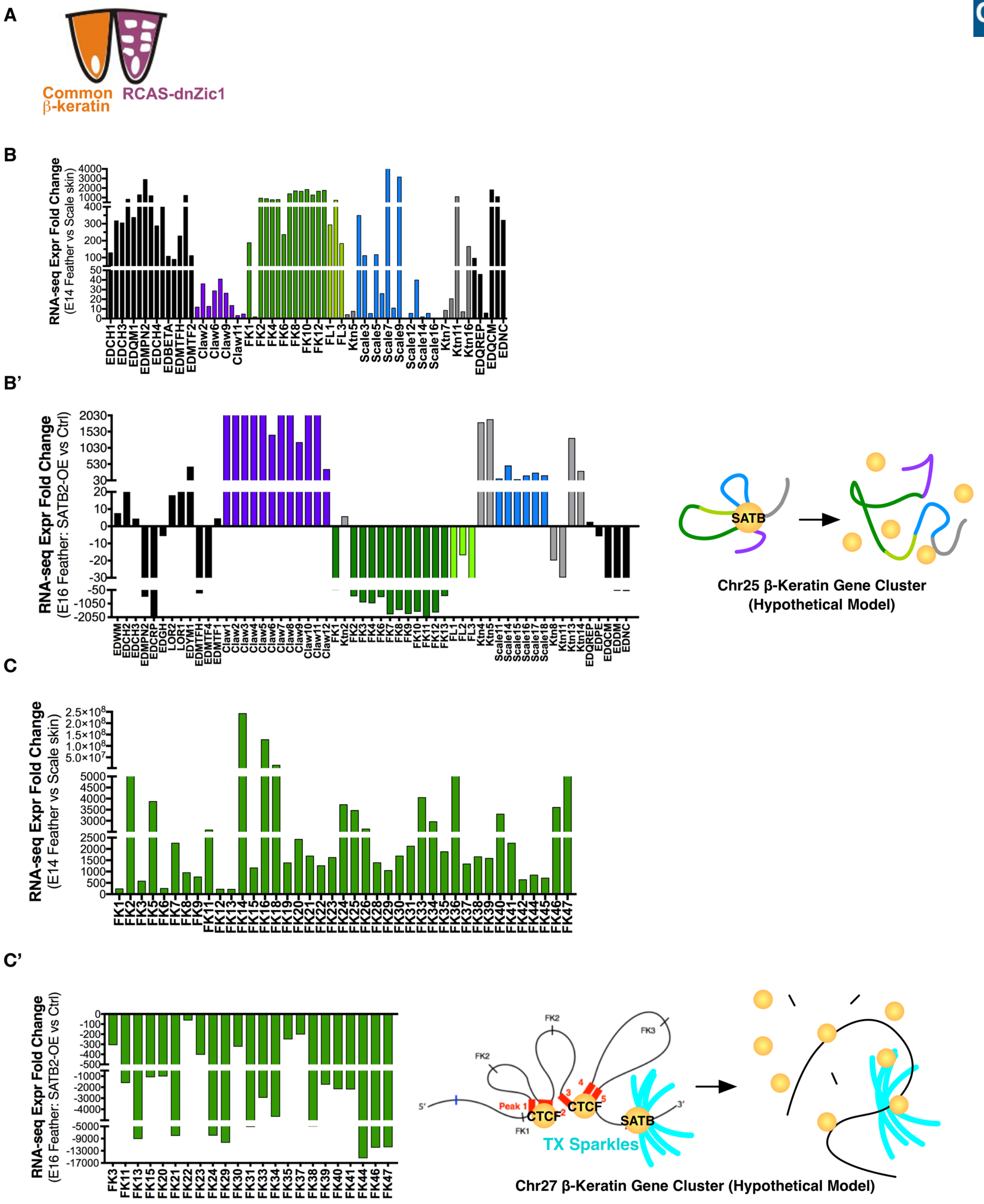


Figure S6. Misexpression of feather specifier *Zic1* and chromatin regulator *SATB2* disrupts expression profiles of β-keratin genes. Related to Figure 6. (**A**) Schematic of a feather cross-section from Figure 6C, showing expression patterns of β-krt genes in a barb ridge when over-expression of dnZic. (**B**) RNA-seq expression fold changes of Chr25 β-krt genes using normal E14 feather compared to scale skins. (**C**) RNA-seq expression fold changes of Chr27 β-krt genes using normal E14 feather compared to scale skins. (**C'**) RNA-seq expression fold changes of Chr27 β-krt genes using E16 RCAS-SATB2-infected feather skins compared to un-infected skins. The right panel shows a hypothetical model of how misexpression of SATB2 disrupts expression of *FK* genes on the Chr27 β-krt cluster.

SUPPLEMENTAL TABLES

Table S2. Genomic locations of selected candidate looping anchors. Related to Figure 3.

Candidate Looping Anchor #	Relative Position	Position (galGal4)	Size (bps)
Peak 1	before *FK1*	chr27:441,776-443,239	1,464
Peak 2	before *FK1*	chr27:446,178-447,746	1,569
Peak 3	before *FK1*	chr27:458,467-460,144	1,678
Peak 4	before *FK1*	chr27:463,986-465,668	1,683
Peak 5	between *FK1* and *FK2*	chr27:472,466-474,122	1,657
Peak 6	between *FK2* and *FK3*	chr27:479,712-480,611	900
Peak 7	right after *FK4*	chr27:488,381-490,636	2,256
Peak 8	after *FK5*	chr27:498,294-499,070	777
Peak 9	between *FK6* and *FK7*	chr27:506,688-508,869	2,182
Peak 10	between *FK7* and *FK8*	chr27:519,312-521,026	1,715
Peak 11	between *FK8* and *FK9*	chr27:540,047-541,324	1,278
Peak 12	after *FK9*	chr27:548,645-549,654	1,010
Peak 13	between *FK10* and *FK11*	chr27:558,703-560,605	1,903
Peak 14	between *FK11* and *FK12*	chr27:570,286-571,512	1,227
Peak 15	After *FK12*	chr27:576,797-577,749	953
Peak 16	between *FK13* and *FK14*	chr27:591,601-592,145	545
Peak 17	between *FK14* and *FK15*	chr27:604,262-605,772	1,511
Peak 18	between *FK15* and *FK16*	chr27:612,634-613,737	1,104
Peak 19	right after *FK17*	chr27:620,337-621,819	1,483
Peak 20	after *FK18*	chr27:629,204-630,889	1,686
Peak 21	in the middle of *FK18* & *FK19*	chr27:637,488-640,511	3,024
Peak 22	KF19	chr27:646,616-647,721	1,106
Peak 23	a H3K27ac region located in *FK19-FK20*	chr27:650,076-654,175	4,100
Peak 24	right after *FK20*	chr27:661,675-662,983	1,309
Peak 25	after *FK21*	chr27:671,645-672,953	1,180
Peak 26	before *FK22*, no H3K4me3 signal	chr27:708,448-712,053	3,406
Peak 27	right before *FK23*	chr27:714,204-717,402	3,199
Peak 28	after *FK24*	chr27:725,484-729,205	3,622
Peak 29	between *FK24* and *FK25*	chr27:733,507-738,158	4,217
Peak 30	right before *FK26*	chr27:760,833-763,507	2,575
Peak 31	the first peak after *FK29*	chr27:783,391-785,135	1,645
Peak 32	the second H3K27ac peak after *FK29*	chr27:787,227-789,785	2,126
Peak 33	the third H3K27ac peak after *FK29*	chr27:790,366-792,110	1,536
Peak 34	*FK30*	chr27:798,389-800,366	1,978
Peak 35	after *FK31*	chr27:806,761-809,203	2,443
Peak 36	*FK32*	chr27:820,366-823,738	3,373
Peak 37	cross *FK38-FK39* (no peak between FK39-FK44)	chr27:855,715-863,971	8,157
Peak 38	cross *FK45-FK47*	chr27:1,037,343-1,049,203	11,139

Table S3. Sequences of NG Capture-C probes and 3C-PCR primers. Related to Figure 3.

Usage	Oligo Name	Oligo Sequence (5' -- 3')	Modification
NG Capture-C	Capture_Peak-1_right	GATCAGCAGGTCAACATCCTCTTCCATATGGGAAGCATTCGCAGTTCGAAGCAACCCCGAGAGACGCCGGTGCAGGGCGGAGCCCCGGGGCGGAGCCGGCGGCTGCGGCGTGGAGGAGGC	5' Biotin
NG Capture-C	Capture_Peak-18_right	GTTCCTCGAGTTCCCTTTCTCACTCTTTTCTTGCTACGAGTGCCATCCTTCAACTGACATGACCCGAGAGACGACAGAGCTACATCACGGTGACATTACGCTATCAAACGCCATTGGATC	5' Biotin
NG Capture-C	Capture_25_FK-TE_left	GCTGAATGCCGCACATGATGGGCCCCATGTGGGGGTTCGCCACCAACGGTCACCAGCCCCACACCCCGAGGCCCATCCCCACCTCCACTGTGCTGCACCAGGAAAATGCGTATGGAGAGA	5' Biotin
NG Capture-C	Capture_Peak-28_left	GATCTGCGACAGCGCCGGGCACAGTGGGGGAACAGGATTCGGCCACGTCGCGCTCCCCGACCATTCCCGTCCCGTCTGTACCCCTCTCGCTGGGGACACTCCAGGAGGGCATCTGCTTTG	5' Biotin
NG Capture-C	Capture_Peak12_right	AGTTCCTCGAGTTCCCTTTCTCACTCTTTCCTTGCTACGAGTGCCATCCTTCAACTGACATGACCCGAGAGACAACAGAGCTACATTGCGGTGACATTACGCTATCAAACGCAATTGGATC	5' Biotin
digestion efficiency	CapSequm_Peak12_R_RV(2)_99	GTAAAAGTCTAACATAATGAATGC	
digestion efficiency	DpnII-P12-FW-100	GAAAGGAGAAATGTTTTAGTTTTAGTACTGG	
digestion efficiency	DpnII-P12-RV-50	GTGTACTGTACAGGAAAACATTTGC	
digestion efficiency	DpnII-P19-FW-41	CATAGAGTCATAGAATCACTCAGGTTGGAATAG	
digestion efficiency	DpnII-P19-RV-80	GGATGTGATGCTCAGGGGCATG	
digestion efficiency	DpnII-P29-FW-40	CAGAACCTGTAATGAAAAGCAGAGCGTTATGG	
digestion efficiency	DpnII-P29-RV-29	GAGCATTGGGACAGGAACTTGATAG	
digestion efficiency	DpnII-P30-FW-34	CCATCAGCTCTTACCCTGCAGAACAGCGTTG	
digestion efficiency	DpnII-P30-RV-110	GCACAATGGGCACTTTCTGCCA	
digestion efficiency	DpnII-P33-FW-50	TCTGCTTTGTAACCACGTGAGCCTGAAGTCC	
digestion efficiency	DpnII-P33-RV-82	GTGGAAAGTCTGGCCAGATGCAAC	
digestion efficiency	DpnII-P34-FW-36	CATCAGTCCCTGCCTTGACGTGCTTCTCCTTAC	
digestion efficiency	DpnII-P34-RV-101	GAGTTCTGGCTCCCCTGGGCCTTC	
digestion efficiency	DpnII-P35-FW-69	CGAAATTGAAATGCAGAGTAAACCAATGTAC	
digestion efficiency	DpnII-P35-RV-39	CCAGGGGCATCACTTCTAGC	
digestion efficiency	DpnII-P36-FW-37	CTACAACCTCTTTTAAGGTACTTGTGGAGAAC	
digestion efficiency	DpnII-P36-RV-87	CTGGTAACGTATCTGGAACACAAG	
digestion efficiency	DpnII-P37-FW-47	GATGTATCTGGTATGCACTCTTTACACATC	
digestion efficiency	DpnII-P37-RV-29	GTAACTGTGGGAAGGTACTAGTAC	
digestion efficiency	DpnII-P38-FW-41	CTGTCCCTAATGCTTTCTGCACCAGAGCC	
digestion efficiency	DpnII-P38-RV-63	GGATAACACAGAGGCAAAGGCTG	
digestion efficiency	DpnII-GTSF1-FW-42	CTGCCAGGAGCAGTGATGCTTTACTAG	
digestion efficiency	DpnII-GTSF1-RV-49	GGAAATCAACTTTCCATGTGGC	
digestion efficiency	DpnII-CINP-FW-74	GAGCCAGAAAACAAATAAGGGTTCTCACATG	
digestion efficiency	DpnII-CINP-RV-75	CTGGTGTATCTGCCATTCCTCACAG	
digestion efficiency	DpnII-P2-FW-75	CCCTGAGTGGTGTTCCTGGCATCCTGTGGGC	
digestion efficiency	DpnII-P2-RV-74	GGCTGTCCCTCTTTTCAGACTCCTCC	
digestion efficiency	DpnII-P3-FW-204	CTGTGCCTGGGGAAGGCCCAGGGGAGCCAGAGCT	
digestion efficiency	DpnII-P3-RV-58	GAGGGAAGACTTACCCCATCACAGTCCAACC	
digestion efficiency	DpnII-P4-FW-79	GTCCAGCCTATCTGCCTTGGAATCTGAACAC	
digestion efficiency	DpnII-P4-RV-101	CTGGGCCAGGAATGAGTTAGTGATGGCAG	
digestion efficiency	DpnII-P5-FW-64	CTCCAGTTCTGGGAACAATGGTAGCTCTCTAC	
digestion efficiency	DpnII-P5-RV-50	GATGGGAATGTCCTCTCCTTTGTCAGTGCGGG	
digestion efficiency	DpnII-P6-FW-74	GTGACTCATGCCCCAAAATTCACAGCTTCTC	
digestion efficiency	DpnII-P6-RV-99	CACACTCTCAGTGCCATTTCCCAC	
digestion efficiency	DpnII-P8-FW-80	CCTTTAAAACTCACTGACCATGTCTTCTTCCTACAG	
digestion efficiency	DpnII-P8-RV-54	GACATGCCATTTCAGAAGAGACACAGACCC	

digestion efficiency	DpnII-P9-FW-79	GTGGCCCATCATCCCAGTAGAAAGTGACTGTG	
digestion efficiency	DpnII-P9-RV-101	CCATCTCAGGTGTCACAAGGTCCTG	
digestion efficiency	DpnII-P13-FW-112	GGAGGTGCCGGTCTCCTCTCCCTGTTATCTG	
digestion efficiency	DpnII-P13-RV-144	GCTCCTCGAAGGATGCCCTG	
digestion efficiency	DpnII-P15-FW-35	CAACAGGAGCCAAGACTTTGCCCTGGCAGCC	
digestion efficiency	DpnII-P15-RV-226	CACGTGTCCTCAGGCTCTCCTCACTGGATATG	
digestion efficiency	DpnII-P16-FW-43	CTCTTCCTACAATAAAAAGGTTTGACTTCAG	
digestion efficiency	DpnII-P16-RV-56	CAGACATGCCGTTTCAGAGGAGAC	
digestion efficiency	DpnII-P17-FW-40	CAGAACCTATGATGAAAAGCAGGGTATTATGG	
digestion efficiency	DpnII-P17-RV-84	GACGCCGAAAGTAGCACTGTCC	
digestion efficiency	DpnII-P18-FW-68	GAAAAACATCAGCACAGGAAACCAACACACTGTC	
digestion efficiency	DpnII-P18-RV-74	GCTGGCTTTTATAATGGCCCCAAG	
digestion efficiency	DpnII-P20-FW-102	CCATCAGTCCCTGCCTTGATGTATTTCTCCT	
digestion efficiency	DpnII-P20-RV-27	CTTTGCTGGGCTTCCCCCG	
digestion efficiency	DpnII-P21-FW-100	CCTCCTTAAAAGGATGAAGATTCACACAAGC	
digestion efficiency	DpnII-P21-RV-30	CAGTAATGGACAAAGTCCCTTTAC	
digestion efficiency	DpnII-P22-FW-100	CCTACCAAAAATGAGGTCTCCCCTTTAAAAC	
digestion efficiency	DpnII-P22-RV-29	GCCTCTTGGATATTGGGGAGAAAG	
digestion efficiency	DpnII-P24-FW-72	CTTCCTGAGGAGCCTAAAATGTGCTCTTTTG	
digestion efficiency	DpnII-P24-RV-28	GCAGTGACCATGAACCTGTGCATC	
digestion efficiency	DpnII-P27-FW-105	CTGGTCTTCCTTCTCTGGTATCTGATGACAG	
digestion efficiency	DpnII-P27-RV-137	GATGGATGGCCTGGGGTTTG	
3C-PCR	Hind3-CINP-FW-68	GCAGCACCCATCACTTGCC	
digestion efficiency	Hind3-CINP-RV-73	CATTGTCAAACAGGACTGGAC	
3C-PCR	Hind3-GTSF1-FW-104	CCAACCCAAGCCATTCTATAATTCTAGAG	
digestion efficiency	Hind3-GTSF1-RV-52	GGGTCACTATAAGTGCTGAAAATCAAAG	
3C-PCR	Hind3-K42-FW-53	GATCAGAAGGTAATGTGGGAGGAAATAC	
digestion efficiency	Hind3-K42-RV-51	GCTTTTGAGTGGATGCAAGGGC	
3C-PCR	Hind3-P2-FW-53	GGTGAGGCACAAGCAAAAGCC	
digestion efficiency	Hind3-P2-RV-82	GGTCCCCTGGGAGACTTGG	
3C-PCR	Hind3-P4+25-RV(2)-90+93	GTCCAACTGCCATGCTGAAGC	
3C-PCR	Hind3-P4-FW-27	GCAGAGCACTGGAACCAGC	
3C-PCR	Hind3-P6-FW-123	GTGCACATCAGCTTATATTCATAACTTACG	
digestion efficiency	Hind3-P6-RV(3)-129	GTCCAAACATCTGTCAACACTGACACGC	
digestion efficiency	Hind3-P7+19-RV(2)-70	GGATGACACCAAGTTTAGTGGTGC	
3C-PCR	Hind3-P7-FW-36	GTTGAACCTCATTAGGTTCATAACGG	
3C-PCR	Hind3-P8-FW-23	GGTTGCCCAGCTTGGAGAAC	
digestion efficiency	Hind3-P8-RV-56	CCTCCCTCTGTTCTCTCCCTC	
3C-PCR	Hind3-P9-FW(2)-203	CACTTCTTCCACAGACACAGGC	
digestion efficiency	Hind3-P9-RV(2)-62	GGCTGTTTCCACTTACACAGCC	
3C-PCR	Hind3-P11+17-RV(3)-47	CTGCTTTCCCTGCACAGGAC	
3C-PCR	Hind3-P11-FW-23	GGTTGCCCAGCTTGGAGAAG	
3C-PCR	Hind3-P12-FW-153-92	CGAGGAAGGCAGCGGAGC	
digestion efficiency	Hind3-P12-RV-55	CTCCCTCTCTTCTTTCCCTGCAC	
3C-PCR	Hind3-P13-FW-26	CAGGGCATCCTTCGAGGAGC	
digestion efficiency	Hind3-P13-RV-83	CTCTAGGAAACCTGTTCCACTG	
3C-PCR	Hind3-P15-FW-57	GGCATATCCAGTGAGGAGAGCC	
digestion efficiency	Hind3-P15-RV-26	GTTGTAGAGAGCAAAGAGGTGCC	
3C-PCR	Hind3-P17-FW-24	GGGTTGCCCAGCTTGGAGAG	
digestion efficiency	Hind3-P18+20-RV(2)-56	CCTCCCTCTCTTCTTTCCCTCC	
3C-PCR	Hind3-P18-FW(2)-27	CGTGGGTTGTCCAGCTTGG	
3C-PCR	Hind3-P19-FW-45	CTTGGCCTTGTTGAACCTCATTTG	
3C-PCR	Hind3-P20-FW-24	GGGTTGTCCAGCTTGAAAAGC	
3C-PCR	Hind3-P21-FW-99	CTTACGTTACATATGCAAACACTCATG	
3C-PCR	Hind3-P24-FW-43	GTTTTCTAAACAAATTCCAGGGCATCC	
digestion efficiency	Hind3-P24-RV-112	CACTGACACACATGGGTCATCAC	
3C-PCR	Hind3-P25-FW-51	CATCTTCAGTGTGAGTGTGAAAGAGC	
digestion efficiency	Hind3-P27+21-RV(5)-67+67	CCACTGTTTGACCACCTTCATATTCAAC	

3C-PCR	Hind3-P27-FW-45	CTGTTTTCTAAACAAACCCCAGGCC	
3C-PCR	Hind3-P29-FW(2)-118	GGTGTCCAGGGTGCTTAATAGC	
digestion efficiency	Hind3-P29-RV-49	CTCTGCTTTCTCTCCGCAGG	
3C-PCR	Hind3-P32-FW-30	CTGAGGCCTCTTAATCCTAACACTC	
digestion efficiency	Hind3-P32-RV(2)-51	CTTACACGGCCTTGCCATTTTC	
3C-PCR	Hind3-P34-FW-50	CCTGTGAGGAGAGCTTGAGG	
digestion efficiency	Hind3-P34-RV-52	CCTCTGTGCTTTCCCTCTTTGG	
3C-PCR	Hind3-P35-FW-27	CATTAGGTTCTCATGGGCCCC	
digestion efficiency	Hind3-P35-RV-51	GGTGCATGGAATGCAACAGAAG	
3C-PCR	Hind3-P36-FW-50	GAGAGCTGAAGTCTCTCCTCTGTC	
digestion efficiency	Hind3-P36-RV-70	GTTAACTAGCATTAAGACAGTGGTAATGG	
3C-PCR	Hind3-P37-FW-50	GGCCTGACGTCAATAGACGTC	
digestion efficiency	Hind3-P37-RV-50	CTCCAGGCTAAATCTTCTGCCC	
3C-PCR	Hind3-P38-FW-50	CTCATCATGGGACAAATAAGCCTAACG	
digestion efficiency	Hind3-P38-RV-50	GAAAAATTGGAGCTTTCAGTATGTCCC	
ChIP-qPCR	CTCF Peak flanks FK-TE-FW	GAGACAAGCAGTGCATGGATAG	
ChIP-qPCR	CTCF Peak flanks FK-TE-RV	GAATGGTGCCTCCCTTATCC	
ChIP-qPCR	FK-TE-FW	CATATATCCGTCACTGAAGTCCTC	
ChIP-qPCR	FK-TE-RV	CAGGTAAGCGGAGGAACAG	
ChIP-qPCR	Site-1-FW	CTTGGAAAGCAACCGCTAAAG	
ChIP-qPCR	Site-2_RV	CAGGTGCTGGAAGACTTTTACC	
ChIP-qPCR	Site-5-FW	CCCTGCCAGGTTCGGTAC	
ChIP-qPCR	Site-5_RV	CAGCGAGGGCATCTACTG	
ChIP-qPCR	Site-7-FW	GTCCTTGAGACCGGGCCG	
ChIP-qPCR	Site-7_RV	CAGACTCCACGGAGGTGC	
ChIP-qPCR	Site-9-FW	GTTGCACCTGGGCTTTGC	
ChIP-qPCR	Site-9_RV	GCATCACTCTCCGTTCTGCATG	
ChIP-qPCR	Site-13-FW	CTGGAACGCATTACTCCGG	
ChIP-qPCR	Site-13_RV	CAGGGGGCGCTGCTGCTC	
ChIP-qPCR	Site-21-FW	CATGTCAGCAGTATCAGCTCGGGCG	
ChIP-qPCR	Site-21_RV	CTTTGGGCGGGGCGGTGG	
ChIP-qPCR	Site-24-FW	CTCAGTGAATCACTACTGCGTATGC	
ChIP-qPCR	Site-24_RV	CGGGGGTACAGTGCCGTC	

Table S4. Quality control of omic data, including RNA-seq, ChIP-seq, and NG Capture-C. Related to Figures 1-3.

Table S4.1. Quality control of RNA-seq. Related to Figures 1 and 2.

Sample ID	Group	Stage	Total Reads	Mapping %	Sequencing Depth (LN/G)
Chuong-1	dorsal back skin	E7	22,078,251	90.99%	1.38
Chuong-13	dorsal back skin	E7	27,106,148	91.10%	1.69
Chuong-29	dorsal feather epidermis	E9	33,555,295	90.67%	2.1
Chuong-33	dorsal feather epidermis	E9	27,243,786	90.95%	1.7
Chuong-86	dorsal feather filament base	E14	30,907,669	92.95%	1.93
Chuong-187	dorsal feather filament base	E14	29,565,041	93.82%	1.85
Chuong-386	dorsal feather filament base	E14	35,514,832	89.76%	2.22
Chuong-387	dorsal feather filament base	E14	39,771,479	89.71%	2.49
Chuong-31	leg scale epidermis	E9	31,129,252	90.93%	1.95
Chuong-87	leg scale epidermis	E14	33,027,593	91.83%	2.06
Chuong-188	leg scale epidermis	E14	32,013,585	92.87%	2

Table S4.2. Quality control of ChIP-seq. Related to Figures 1 and 2.

Sample ID	Stage	Regions	Antibody	Total Reads	Mapping %	Sequencing Depth (LN/G)
ChIP-31	E7	dorsal back skin	gDNA	24,646,232	97.86%	1.7
ChIP-25	E7	dorsal back skin	anti-H3K27ac	21,278,193	91.29%	1.37
ChIP-51	E7	dorsal back skin	anti-H3K27ac	21,193,480	97.15%	1.45
ChIP-15	E9	feather skin	gDNA	21,457,662	97.84%	1.48
ChIP-1	E9	feather skin	anti-H3K27ac	30,296,497	93.50%	1.99
ChIP-11	E9	feather skin	anti-H3K27ac	20,573,865	94.66%	1.37
ChIP-32	E9	scale skin	gDNA	18,095,139	97.89%	1.25
ChIP-26	E9	scale skin	anti-H3K27ac	21,583,440	90.85%	1.38
ChIP-52	E9	scale skin	anti-H3K27ac	21,259,710	96.49%	1.44
ChIP-21	E14	feather skin	gDNA	26,190,250	97.30%	1.79
ChIP-19	E14	feather skin	anti-H3K27ac	22,367,997	76.47%	1.2
ChIP-33	E14	feather skin	anti-H3K27ac	18,295,996	93.62%	1.21
ChIP-20	E14	scale skin	gDNA	21,680,839	96.37%	1.47
ChIP-34	E14	scale skin	anti-H3K27ac	22,638,290	93.19%	1.49
ChIP-22	E14	scale skin	anti-H3K27ac	18,747,984	81.88%	1.08
ChIP-223	E14	feather skin	gDNA	49,667,530	98.25%	3.05
ChIP-228	E14	feather skin	anti-IgG	32,447,629	94.83%	2.17
ChIP-232	E14	feather skin	anti-IgG	28,719,165	93.81%	1.9
ChIP-225	E14	feather skin	anti-CTCF	29,408,371	89.74%	1.86
ChIP-236	E14	feather skin	anti-CTCF	14,372,678	91.24%	0.92
ChIP-234	E14	scale skin	gDNA	43,540,970	96.07%	2.61
ChIP-235	E14	scale skin	anti-IgG	18,196,106	95.21%	1.22
ChIP-241	E14	scale skin	anti-IgG	17,559,080	95.38%	1.18
ChIP-229	E14	scale skin	anti-CTCF	30,561,208	89.01%	1.91
ChIP-242	E14	scale skin	anti-CTCF	18,802,089	81.29%	1.08
ChIP-226	E14	feather skin	anti-KLF4	29,700,399	85.51%	1.79
ChIP-237	E14	feather skin	anti-KLF4	13,819,214	79.91%	0.78
ChIP-230	E14	scale skin	anti-KLF4	32,066,777	83.07%	1.96
ChIP-243	E14	scale skin	anti-KLF4	16,079,004	81.74%	0.93
ChIP-227	E14	feather skin	anti-H3K4me1	57,175,979	91.49%	3.68
ChIP-238	E14	feather skin	anti-H3K4me1	152,404,558	88.44%	9.49
ChIP-231	E14	scale skin	anti-H3K4me1	55,875,862	91.48%	3.6
ChIP-244	E14	scale skin	anti-H3K4me1	111,488,400	87.62%	6.87
ChIP-73	E14	feather skin	anti-H3K4me3	20,067,127	77.35%	1.09
ChIP-74	E14	scale skin	anti-H3K4me3	22,762,971	76.83%	1.23

Table S4.3. Quality control of NG Capture-C. Related to Figure 3.

Sample ID	Stage-Region	Total number of reads entering the analysis	Capture-containing reads entering the analysis	Actual reported fragments	Paired-end
dCAP1	E14 non-keratinized feather filament	79,105,609	25,709,833	92,496	40-PE
dCAP-2-1	E7 whole brain	44,781,641	4,023,584	55,716	75-PE
dCAP-2-2	E7 whole brain	50,505,262	4,348,962	56,494	75-PE
dCAP-2-3	E7 dorsal back skin epidermis	30,160,644	2,327,254	37,668	75-PE
dCAP-2-4	E7 dorsal back skin epidermis	45,350,463	4,126,177	40,321	75-PE
dCAP-2-5	E14 whole brain	52,019,460	4,420,350	58,199	75-PE
dCAP-2-6	E14 whole brain	50,669,020	4,261,090	56,426	75-PE
dCAP-2-7	E14 non-keratinized feather filament	46,521,279	4,227,767	82,890	75-PE
dCAP-2-8	E14 non-keratinized feather filament	40,611,452	2,888,175	40,227	75-PE
dCAP-2-9	E14 leg scale skin epidermis	47,013,349	4,700,417	33,862	75-PE
dCAP-2-10	E14 leg scale skin epidermis	36,038,572	3,600,577	19,511	75-PE
dCAP-2-11	adult wing feather barb branch	38,350,547	3,616,525	27,793	75-PE
dCAP-2-12	adult wing feather barb branch	38,559,293	3,767,165	26,709	75-PE
dCAP-2-13	adult dorsal feather barb branch	33,161,297	2,566,443	10,364	75-PE
dCAP-2-14	adult dorsal feather barb branch	29,729,411	2,635,274	9,126	75-PE

Table S5. Summary of NG Capture-C interactions. Related to Figure 3. P#-P#, selected H3K27ac bait Peak # interacts target Peak #.

Tissue	Captured Read >1000	Captured Read >100	Captured Read >20
E7 brain dCAP2-1 + dCAP2-2	P1-P10 P12-P6 P28-P27	P1-P2 P12-P3 P12-P20 P18-P3 P18-P5 P18-P6 P18-P15 P18-P20 P28-P4 P28-P14 P28-P25 P28-P30	P1-P1 P1-P3 P1-P5 P1-P7 P1-P17 P1-P19 P1-P20 P1-P21 P1-P27 P1-P33 P12-P5 P12-P11 P12-P12 P12-P15 P12-P19 P12-P24 P18-P8 P18-P9 P18-P11 P18-P12 P18-P18 P18-P19 P18-P24 P18-P31 P28-P1 P28-P3 P28-P29
E7 epidermis dCAP2-3 + dCAP2-4	P1-P10 P12-P6	P1-P2 P12-P3 P18-P3 P18-P6 P28-P27 P28-P30	P1-P1 P1-P3 P1-P4 P1-P7 P1-P12 P1-P19 P1-P21 P12-P5 P12-P15 P12-P19 P12-P20 P12-P24 P18-P5 P18-P7 P18-P15 P18-P18 P18-P19 P18-P20 P18-P24 P28-P1 P28-P4 P28-P14 P28-P25 chr25-FK-TE-chr25Ktn
E14 feather dCAP2-7 + dCAP2-8	P1-P10 P12-P6 P28-P27	P1-P2 P12-P3 P12-P15 P12-P20 P18-P3 P18-P6 P18-P15 P18-P20 P28-P14 P28-P25 P28-P30	P1-P1 P1-P3 P1-P5 P1-P7 P1-P19 P1-P21 P1-P33 P12-P5 P12-P12 P12-P19 P12-P24 P18-P5 P18-P8 P18-P9 P18-P12 P18-P18 P18-P19 P18-P24 P28-P1 P28-P4 P28-P9 P28-P29
E14 scale epidermis dCAP2-9 + dCAP2-10	P1-P10 P12-P6 P12-P15 P18-P15	P12-P12 P12-P18 P12-P22 P18-P3 P18-P6 P18-P12 P18-P18 P18-P20 P28-P27 P28-P30 P34-P34	P1-P1 P1-P2 P1-P4 P1-P21 P12-P3 P12-P9 P12-P19 P12-P20 P12-P24 P18-P8 P18-P22 P18-P24 P28-P1 P28-P14 P28-P25 P28-P29
Adult wing feather branch dCAP2-11 + dCAP2-12	P1-P10 P12-P6	P1-P2 P12-P12 P12-P15 P18-P6 P18-P12 P18-P15 P18-P18 P28-P27 P34-P34	P1-P1 P1-P21 P12-P20 P12-P22 P12-P24 P18-P3 P18-P5 P18-P20 P18-P24 P28-P14 P28-P25 P28-P29 P28-P30

Continued

Tissue	Captured Read >1000	Captured Read >100	Captured Read >20
E14 brain dCAP2-5 + dCAP2-6	P1-P10 P12-P6 P28-P27	P1-P1 P1-P2 P12-P20 P18-P6 P18-P20 P28-P4 P28-P14 P28-P25 P28-P30	P1-P4 P1-P5 P1-P7 P1-P11 P1-P19 P1-P21 P1-P27 P1-P33 P12-P3 P12-P5 P12-P12 P12-P24 P18-P3 P18-P5 P18-P11 P18-P18 P18-P19 P18-P24 P28-P1 P28-P3 P28-P9 P28-P29

Tissue	Captured Read >1000	Captured Read >100	Captured Read >20
Adult dorsal feather branch dCAP2-13 + dCAP2-14	P1-P10	P12-P6 P12-P12 P12-P15 P18-P12 P18-P15 P18-P18 P28-P27 P34-P34	P18-P6 P18-P24 P28-P30

Table S7. Bioinformatic analysis pipelines including software for manuscript preparation. Related to the STAR Methods, Bioinformatic Analysis.

Table S7.1. General analysis.

Process	Tool ID	Version	Tool Parameter (only shows custom options used in this work)
QC	FastQC	Galaxy Version 0.72	
	Qualimap	Version 2	
Calculation of correlation between replicates	multiBigwigSummary	Galaxy Version 3.1.2.0.0	—outRawCounts Yes
	plotCorrelation	Galaxy Version 3.1.2.0.0	--whatToPlot Heatmap Save the matrix of values underlying the heatmap

Table S7.2. RNA-seq analysis.

Process	Tool ID	Version	Tool Parameter (only shows custom options used in this work)	Order
Manipulation	fastq_groomer	Galaxy Version 1.1.1	default	1
	fastq_trimmer_by_quality	Galaxy Version 1.1.1	Window size 3; min score >= 20	2
Mapping	tophat2	Galaxy Version 2.1.1	Genome: UCSC galGal4	3
Quantification	Cufflinks	Galaxy Version 2.2.1.2	default	4
	Cuffmerge	Galaxy Version 2.2.1.1	default	5
	Cuffquant	Galaxy Version 2.2.1.1	default	6
Differentially expressed gene analysis	Cuffdiff	Galaxy Version 2.2.1.3	default	7
	deeptools_bam_coverage	Galaxy Version 3.1.2.0.0	default	A8-1
Convert Formats	wig_to_bigWig	Galaxy Version 1.1.1	default	A9
Graph/Display Data	pyGenomeTracks	2.0	$ make_tracks_file --trackFiles input.bigwig -o config.ini $ pyGenomeTracks --tracks config.ini --region displayed-ex-chr27:chr27:4500721-4700799 --outFileName figure.pdf	A10
Enriched pathway analysis	IPA	01-12		B8-2
	PGS	6.6		B8-3

Table S7.3. Manuscript preparation.

Process	Tool ID	Version	Tool Parameter (only shows custom options used in this work)	Price
Visualization	UCSC Genome Browser			free

	pyGenomeTracks	2.0	Commands (example):
			$ make_tracks_file --trackFiles input.bigwig -o config.ini
			$ pyGenomeTracks --tracks config.ini —region chr27:chr27:4500721-4700799 --outFileName output.pdf
				free

	IGV	2.4.15		free
	GraphPad Prism	version 7.0a for Mac OS X	Generate charts and plots	$$$
Figure Arrangement	OmniGraffle	7.8.2	1) arrange each figure containing multiple panels in a canvas 2) export each figure into a high quality TIFF file (600 dpi)	$$
Compile PDF (Generate a high-resolution but small-size PDF file for submission)	Microsoft Word for Mac	15.13.4	1) import each figure TIFF file on one page 2) File > Reduce File Size > select Print (220 ppi) and check Delete cropped areas of pictures > OK 3) File > Save As > select File Format as PDF	$$$
	Preview (Mac default software)		Merge figure PDF with main text PDF and Save	free
	PDF Expert (the best!)	Version 2.4.22 (611)	It can direct reduce file size of OmniGraffle output PDF with good resolution.	$

Table S7.4. ChIP-seq analysis. Related to the STAR Methods, Bioinformatic Analysis.

Process	Tool ID	Version	Tool Parameter (only shows custom options used in this work)	Order
Manipulation	fastq_groomer	Galaxy Ver 1.1.1	default	1
	fastq_quality_filter	Galaxy Ver 1.0.2	default	2
	fastq_trimmer_by_quality	Galaxy Ver 1.1.1	Window size 3; min score >= 20	3
Mapping	bowtie2	Galaxy Ver 2.3.4.2	Genome: UCSC galGal4 --very-sensitive Save the bowtie2 mapping statistics to the history Yes	4
Filtering	samtool_filter2	Galaxy Ver 1.8	-q 1	5
	samtools_sort	Galaxy Ver 2.0.1	default	6
	samtools_rmdup	Galaxy Ver 1.0.1	BAM is single-end	7
Peak-calling and normalization	macs2	Galaxy Ver 2.1.1.20160309.4	**# for H3K27ac-ChIP** --gsize 1065365425 --nomodel --extsize 147 Additional Outputs --bdg Advanced Options --broad --broad-cutoff 0.1 **# for CTCF-/KLF4-/SATB-ChIP** --gsize 1065365425 --nomodel --extsize (value obtained from macs2 predictd tool: CTCF=205; KLF=160; SATB=257) Additional Outputs --bdg Advance options (only for SATB) --broad --broad-cutoff 0.1	A8
	macs2_bdgcmp	Galaxy Ver 2.1.1.20160309.0	Two executions for one comparison: 1) -m FE 2) -m logLR -p 0.00001	A9
Convert Formats	wig_to_bigWig	Galaxy Ver 1.1.1	default	A10
Graph/Display Data	pyGenomeTracks	2.0	$ make_tracks_file --trackFiles input.bigwig -o config.ini $ pyGenomeTracks --tracks config.ini --region displayed-ex-chr27:chr27:4500721-4700799 --outFileName figure.pdf	A11-1
	IGV	2.4.15	For CTCF-ChIP and KLF-ChIP	A11-2
Identification of differentially enriched peaks	PGS	6.6		B8
Identification of typical- and super-enhancers	findPeak.pl	HOMER Ver 4.10	-style super -typical TE	B9-1
Discovery of transcription factor-binding motifs	findMotifsGenome.pl	HOMER Ver 4.10		B9-2
	TRANSFACT			B9-3

Table S9. Complete enriched motifs found on differential transposase accessible regions of RCAS-Sox2/Grem1/Spry2/beta-catenin-infected skin. Related to Figure 6.

Skin Region	Gene	Best Match Motif of DNA-binding Factor from HOMER De Novo Motif Discovery (motif rank #, % of analyzed sequences w/ motif)	
E12.5 Feather Epidermis RCAS-infected	**RACS-Sox2**	(1, 32.68%) KLF3, KLF4, KLF5, KLF6, SP1 (2, 10.33%) NFY8, NFY4 (3, 7.13%) Gabpa, ELK4, ELF1, ELK3, ETV3 (4, 9.5%) YY1 (5, 10.11%) NRF, RBFox2, RBFox1 (6, 8.41%) CTCF, NeuroD1, AtMYB15 (MYB), (7, 24.06%) GRHL1, TFCP2, RBFox2 (8, 10.74%) TP73, TP63 (9, 8.01%) TFAP2B, TFAP2A (11, 9.81%) CREB1, Atf1 (bZIP) (12, 10.55%) RFX5, RFX6 (13, 2.39%) ZBTB33, ZBED1 (14, 10.92%) IRF4, TBX20)	(15, 4.64%) HoxA9, HoxC9, Pdx1, HoxA2, HoxB4, PBx1 (18, 0.39%) E2F1, E2F3, E2F2, HNRNPK (19, 1.39%) TEAD1, TEAD4, TEAD3 (20, 0.46%) BTD (21, 11.59%) TCF7L2, TCF3, TCF4, TCF7, LEF1 (23, 0.48%) XBP1 (24, 0.60%) EGR1, BTD, SP2, PCBP2 (25, 10.36%) MEIS2 (26, 0.65%) CDX4 (27, 3.36%) SMAD3, SP4, MYB (28, 0.47%) Sox9, Olig2 (29, 0.21%) CEBPG, CEBPB
E12.5 Feather Epidermis RCAS-infected	**RCAS-Spry2**	(1, 40%) KLF3, KLF4, KLF5, KLF6, KLF7, SP5 (2, 9.21%) Gabpa, ELF1, ELK3, ELK4, ETV4, ETV6 (3, 18.58%) LHX8, ISX, NKX1-1, NFYB (4, 10.52%) CTCF, NeuroD1, YY1 (5, 10.51%) NRF1, RBFox2, RBFox1 (6, 15.91%) CREB1, SREBF2, SREBF1, MLX, Atf1(bZIP) (7, 4.93%) NFYB, NFYA (11, 5.26%) RFX2, RFX3, RFX4, RFX5, XBP1 (12, 12,54%) MBNL1, NR2E3, ZFX, SP4, ABI3, RBFox2 (13, 0.40%) SAMD4A, E2F6 (14, 0.63%) RUNX1, RUNX2, Olig2 (15, 1.84%) ZIC1, ZIC3, ZNF143, ACE2	(16, 3.05%) RFX3, RFX4, RFX5, RFX6 (17, 0.30%) Six1, Six2, SDX5 (18, 0.39%) IRF4, IRF5, IRF6 (19, 0.88%) CDX4 (20, 3.93%) TBP, KHDRBS1 (22, 0.22%) HBP1, Sox2, Sox9 (23, 0.21%) YY1, MATR3 (24, 0.38%) E2F3, BTD, ZNF740, SP1, SP5, E2F4, EGR1 (25, 2.09%) TEAD1, TEAD3, TEAD4, CNOT4 (26, 0.18%) Osr2 (27, 45.29%) RBMS3, TBP (28, 2.65%) HuR (ELAV1), PABPC4, SRF
E12.5 Feather Epidermis RCAS-infected	**RCAS-B-cat**	(1, 44.67%) KLF3, KLF4, KLF5, KLF6, KLF7, GC-Box, SP1, SP5 (2, 19.25%) NFYB (3, 16.77%) ELK3, ELK4, Gabpa, ELF1, ETV3 (4, 13.48%) NRF1, RBFox1, RBFox2 (5, 13.96%) Gata2, Gata3, Gata4, Gata5 (7, 13.50%) YY1, MATR3, CTCF, E2F2, E2F3 (8, 15.63%) CREB1, Atf1, CREM (9, 15.19%) CDX4, TRB2, CDX2 (10, 4.57%) THAP, MSI, SFPQ (11, 14.35%) RBM45, E2F1	(12, 4.02%) CTCF (13, 2.39%) ZBTB33, ZBED1 (14, 1.84%) KHDRBS1 (15, 2.11%) ABI3, ZNF143, RBFox2, RBFox1, Zic1, Zic3 (16, 7.31%) RFX2, RFX3, RFX4, RFX5, X-box (17, 11.11%) RBM5, E2F6, HNRNPA2B1, SRSF1 (18, 6.29%) Hoxc11, Hoxc12, CDX4, Hoxd11, Hoxd12, Hoxa11 (19, 1.75%) c-Jun-Cre, Atf1, Atf2, Atf7, THR6, JDP2 (20, 1.59%) HuR (ELAV1), PABPC4 (21, 0.60%) MYB (23, 0.11%) Nkx2-1, Nkx2-5
E12.5 Feather Epidermis RCAS-infected	**RCAS-Grem1**	(1, 34.97%) KLF5 (2, 8.79%) CTCF (3, 9.66%) NFY (4, 15.55%) Elk1 (5, 11.82%) FUS3 (6, 9.77%) AP-2gamma (7, 9.66%) YY1 (8, 2.98%) p73(p53) (9, 7.97%) Atf1(bZIP) (10, 4.01%) GFY (11, 19.98%) Adf1 (12, 10.12%) STP3 (13, 3.01%) GFX (14, 9.45%) Six1 (15, 0.71%) HNRNPK (15, 3.37%) E2F1	(16, 20.41%) Rfx1 (17, 20.41%) MafA(bZIP) (18, 7.59%) prd, grh (19, 12.42%) Olig2 (19, 3.16%) twi (20, 3.16%) Cbf1, Usf2, USF1 (21, 2.61%) GAGA-repeat, RF8, SRSF10, PTBP1, IRF1, Tb_0220, RAV1 (22, 1.74%) E2F3(E2F), hkb, btd (23, 7.93%) A1CF, Rbm42, PUM (24, 2.42%) Ot_0263 (26, 0.63%) caudal, cad (28, 2.29%) CAMTA1 (29, 0.41%) Su(H), ovo (30, 0.38%) DPL-1 (31, 0.27%) Gfi1b
E12.5 Feather Epidermis RA-treated	**RA**	(1, 41.9%) KLF3, KLF5, Sp5(Zf), KLF6(Zf) (2, 18.31%) ETS, Elk1, ELF1, Elk4 (3, 15.28%) NFY (4, 13.8%) YY1, MATR3, NeuroD1, CTCF (5; 11.3%) NRF, NRF1, EIF-2ALPHA, RBFox2, RBFOX1, FOX-1 (6; 7.95%) Atf1, TGA5, TGA6, FEA4, TGA1 (7; 7.9%) CTCF, BORIS(Zf) (8; 27.64%) CRF4 (9; 6.33%) MSI1, ZBTB12(Zf) (10; 3.42%) GFY, Rbm42, bZIP910 (11; 11.96%) Rfx5, Rfx6 (12; 4.02%) GFX, ZBTB33 (13; 18.78%) RBM5, SF2, SRSF1, B52, E2F6	(14, 10.65%) ZC3H10, Sf3b4 (15, 1.55%) TATA-Box, bap, Isl1, Tup (16, 1.03%) AT2G15740(C2H2) (17, 2.55%) Rfx1, X-box, Rfx2, RFX (18, 56.52%) VRN1, SXL, HuR, PABPC4 (20, 1.09%) RUNX2, cad, RUNX (22, 1.59%) REB1, ftz, Nkx6.1 (23, 1.27%) MYB (24, 0.28%) Rfx5, IRF4, kni (25, 1.33%) ovo, MYB (26; 0.80%) brk (27, 0.23%) E2F3, Egr2, DEL1 (28, 0.20%) FUS3 (29, 10.30%) cad, SRSF10, TIA1, IRF2, RALY