Supplementary table 1: Genes in blue and turquoise modules

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| Module | Genes |
| blue | DSG3, HOMER1, CMYA5, CD2, PKP1, MNDA, KRT6B, CACNA1D, IL15, PSMB8-AS1, ITGAL, PLEK, SNX20, STAT4, SLAMF8, CXorf65, CD28, XCL1, CTSS, CD84, PRF1, HCP5, ZC3H12D, PRRG4, PATL2, CCR2, SLA, TRAT1, RASSF4, CD163, CD3D, TLR1, MAP4K1, LCK, GBP4, TRBC1, TSPOAP1-AS1, PIK3R5, CDS1, CLUAP1, KLHDC7B, CD96, FOLR2, FLT3LG, APBB1IP, NRBF2, LY9, NLRC3, APOBEC3G, FLNB, CLIC6, CRTAM, KIF21B, APBB2, TFEC, CHRM3, COL4A4, SLC6A16, CTSB, CST7, MS4A6A, TLE1, CBLN3, FLJ32255, TRAF3IP3, HEG1, MS4A4A, LILRB2, RGS22, GALNT16, PLA2G4C, CLEC5A, CLECL1, LGALS2, CD1E, ITGB2-AS1, IL21R, CARHSP1, LAIR1, DDIT4L, CST3, ESRRG, ANP32A, TIMP3, CD82, YME1L1, CILP, ANTXR2 |
| turquoise | HOXC13, PPP1R1C, KRTAP4-11, CHAC1, KRTAP1-3, GPRC5D, PIRT, KRTAP8-1, FAM83A, KRTAP5-8, KRTAP4-2, KRT33A, MLLT11, KRT83, KRTAP2-4, LY6G6F, KRTAP4-8, LYPD6, KRTAP4-4, PSORS1C2, KRTAP9-9, S100A3, KRT81, PARM1, KRTAP4-3, KRTAP9-3, KRTAP9-4, KRT16, KRTAP2-1, KRT34, MGC24103, FGF18, KRTAP4-5, KRTAP10-12, KRTAP4-12, LOC101928881, SLC16A9, PLEKHG1, KRTAP19-1, KRTAP10-11, DSC2, LYG2, KRTAP4-6, KRT33B, KRT31, FLRT3, KRTAP4-1, KRTAP9-8, CHST2, KRT75, DSG4, VSNL1, JMY, KRTAP7-1, KRTAP1-5, SERPINA3, KRTAP3-2, TENM2, KRTAP1-1, KRTAP2-3, KRTAP4-7, SLC39A10, KRTAP19-3, KRT82, KRTAP1-3, KRTAP17-1, KRTAP3-1, KRT32, KRT86, SLC27A6, CTNND2, KRTAP11-1, LYPD6, TNIK, CAPN12, SULF2, CST1, GJA3, LOC105376379, UBE2H, OXCT2, RIMS2, KRTAP9-2, BNC1, SLC7A8, FZD3, ATP8A2, COMP, ATP8A2, SHISA2, CD109, RMND5A, ANGPTL7, LOC100505782, FAM49A, KRTAP4-9, BMP2, KRT40, C1orf168, FGF5, DNAJC6, TRPM6, RNF182, PDZRN3, PPP1R2, ABCA4, SERPINB13, KRTAP3-3, EHD3, HSPA2, TCP11L2, SERPINA1, KRT85, LRRC15, PADI3, ATG10, GCC2, BNC2, TM4SF1, FETUB, CBLN2, MREG, LINGO1-AS2, UBE2D1, LGR5, OVOL1, ODC1, SAMD5, KRT35, SRD5A3, CCBE1, KRTAP5-9, TRIM9, CREB5, USP38, CYFIP2, CNTNAP2, CST4, ARL15, WNK4, HSPA14, EIF5, PRKCB, CD8A, ZAR1, SMTNL2, SLC40A1, SLC1A6, SLC7A11, SESN3, KRT36, NELL2, SYTL5, CCL13, HHIP, RC3H1, SLN, KRT73, PPP2R1B, GMCL1, KRTAP13-1, SLC6A14, EFNA5, APOL6, THBS1, KLK12, BAMBI, ALDOB, LEF1, LINC00504, CAPN14, FOXE1, NCS1, SIGLEC1, CYP24A1, CYP1B1-AS1, RHCG, KRT72, DACH1, MSX2, MUM1L1, PRSS53, KALRN, AIF1, SP6, DLX3, DMBT1, TMOD3, KRT73, SLC5A9, FLG-AS1, KRT27, KRT74, GOLGA7B, CAPN8, KRT84, DACH1, MYCN, CELF2, TMEM163, CYP1B1, ATP12A, PCDH8, F5, CRNN, SIGLEC10, LINC00302, DLX2, IL1F10, LOC101928100, CNTN4, LCN2, SYN2, SHH, CEACAM5, NHLH2, SPINK7, TRIM10, NOV, PADI1 |

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| Gene | GO term | Description |
| CD28 | GO:0046649  | lymphocyte activation |
|  | GO:0002250  | adaptive immune response |
|  | GO:0050900  | leukocyte migration |
|  | GO:0002274  | myeloid leukocyte activation |
|  | GO:0002697  | regulation of immune effector |
|  | GO:0050851  | antigen receptor-mediated sign |
|  | GO:0009615  | response to virus |
|  | GO:0031349  | positive regulation of defense |
|  | GO:0050777  | negative regulation of immune |
|  | GO:0032743  | positive regulation of interle |
| HOXC13 | GO:0031424 | keratinization |
|  | GO:0042303 | molting cycle |
|  | GO:0035878  | nail development |
|  | GO:0042475 | odontogenesis of dentin-contai |
|  | GO:0007423  | sensory organ development |
| KRTAP1-3 | GO:0031424 | keratinization |
| GPRC5D | NA | NA |

Supplementary table 2: The GO functional annotation of key genes

Abbreviations: NA: not available.



Supplementary Fig. 1: Heatmap of DEGs among samples from normal, AAP.T/AAP, and AU/AT tissues. DEGs: differentially expressed genes.