PUBLICLY AVAILABLE ACC BIOINFORMATIC DATASETS - NOVEMBER 2019
(listed in reverse chronological order)

DNA- Copy number array, CGH and WES/WGS

- Ho et al., Genetic hallmarks of recurrent/metastatic adenoid cystic carcinoma. J Clin Invest. 2019 Oct 1; 129(10):4276-4289. DOI: 10.1172/JCI128227
  - Combination of WES, WGS or targeted NGS panel for 1045 ACC cases (177 primary tumors in patients with localized disease and 868 cases with R/M disease)
    https://www.cbioportal.org/study/summary?id=acc_2019

  - RNA sequencing of 8 ACC samples and WGS of 2 ACC samples;

- CSER: Exploring Precision Cancer Medicine for Sarcoma and Rare Cancers (U of Michigan, unpublished but deposited into SRA); Study accession number: SRP048907 (includes data for many other cancers), can access here as well.
  - RNA-seq experiment accession numbers for ACC samples:
    SRX1910423
    SRX1910422
    SRX1910162
    SRX1910161
    SRX1910115
    SRX1910114
    SRX1910100
    SRX1909671
    SRX1909670
    SRX1909428
    SRX1909216
    SRX1909215
    SRX1909164
    SRX1909163
  - WES experiment accession numbers for ACC samples:
    SRX1910421
    SRX1910160
    SRX1910113
• **Kim et al.**, MYBL1 rearrangements and MYB amplification in breast adenoid cystic carcinomas lacking the MYB-NFIB fusion gene. J Pathol. 2018 Feb; 244(2); 143-150. DOI: [10.1002/path.5006](https://doi.org/10.1002/path.5006)

• **Fusco et al.**, Genetic events in the progression of adenoid cystic carcinoma of the breast to high-grade triple-negative breast cancer. Mod Pathol 2016 Nov;29(11):1292-1305. DOI: [10.1038/modpathol.2016.134](https://doi.org/10.1038/modpathol.2016.134)

  - WGS of 25 ACC samples [https://www.ebi.ac.uk/ega/studies/EGAS00001002812](https://www.ebi.ac.uk/ega/studies/EGAS00001002812)


• **Stephens et al.**, Whole exome sequencing of adenoid cystic carcinoma. J Clin Invest. 2013 Jul;123(7):2965-8. DOI: [10.1172/JCI67201](https://doi.org/10.1172/JCI67201)
  - Exome sequencing via Illumina in 125 ACC samples; [https://ega-archive.org/datasets/EGAD00001000101](https://ega-archive.org/datasets/EGAD00001000101)
  - Capillary sequencing of SPEN and FGFR2 in 48 ACC samples; [https://ega-archive.org/datasets/EGAD00001000175](https://ega-archive.org/datasets/EGAD00001000175)
  - Expression profiling via Illumina array of 21 ACC samples; [https://www.ebi.ac.uk/ega/studies/EGAS00001000193](https://www.ebi.ac.uk/ega/studies/EGAS00001000193)
  o High-resolution acGH on fresh frozen tissue from 40 ACC samples; [https://www.ebi.ac.uk/arrayexpress/experiments/E-GEOD-34816/samples/](https://www.ebi.ac.uk/arrayexpress/experiments/E-GEOD-34816/samples/)

• **Oga et al.**, Loss of 6q or 8p23 is associated with the total number of DNA copy number aberrations in adenoid cystic carcinoma. Oncol Rep. 2011 Dec;26(6):1393-8. DOI: [10.3892/or.2011.1446](https://doi.org/10.3892/or.2011.1446)

**RNA- Gene expression array, RNA sequencing, miRNA**

  o RNA/DNA sequencing of 54 flash-frozen salivary ACCs and reverse phase protein array (RPPA) in 38 specimens.

  o RNAseq in salivary gland tumors, including ACC, and bioinformatic analysis related to immune markers, mutation- and fusion-derived neoantigens and correlations with immune infiltration. Matched whole exome sequencing also available.


  o miRNA profile via Affymetrix array for 64 ACC samples and 10 normal samples; [https://static-content.springer.com/esm/art%3A10.1007%2Fs00428-018-2423-0/MediaObjects/428_2018_2423_MOESM2_ESM.xlsx](https://static-content.springer.com/esm/art%3A10.1007%2Fs00428-018-2423-0/MediaObjects/428_2018_2423_MOESM2_ESM.xlsx)
• **Andreasen et al.**, Adenoid cystic carcinomas of the salivary gland, lacrimal gland, and breast are morphologically and genetically similar but have distinct microRNA expression profiles. Mod Pathol. 2018 Aug;31(8):1211-1225. DOI:10.1038/s41379-018-0005-y
  - miRNA profile via Affymetrix array for 64 salivary ACC and 10 adjacent normal salivary gland samples, 9 lacrimal ACC and 6 adjacent normal lacrimal gland samples, 11 breast ACC and 7 adjacent normal breast samples; link TBD.

• **Frerich et al.** Transcriptomes define distinct subgroups of salivary acc with different driver mutations and outcomes. Oncotarget. 2017 Dec 23;9(7):7341-7358. DOI:10.18632/oncotarget.23641

• **Andersson et al.**, Targeting the Oncogenic Transcriptional Regulator MYB in Adenoid Cystic Carcinoma by Inhibition of IGF1R/AKT Signaling. J Natl Cancer Inst 2017 Sep 1;109(9). DOI:10.1093/jnci/djx017

• **Bell et al.**, In-depth characterization of the salivary adenoid cystic carcinoma transcriptome with emphasis on dominant cell type. Cancer. 2016 May 15;122(10):1513-22. DOI:10.1002/cncr.29959


• **Stephens et al.**, Whole exome sequencing of adenoid cystic carcinoma. J Clin Invest. 2013 Jul;123(7):2965-8. DOI:10.1172/JCI67201
  - Expression profiling of 21 human ACC samples from the head and neck; RNA analyzed by Illumina array; [https://www.ebi.ac.uk/ega/studies/EGAS00001000193](https://www.ebi.ac.uk/ega/studies/EGAS00001000193)

• **Shao et al.,** Integrated, genome-wide screening for hypomethylated oncogenes in salivary gland ACC, Clin Cancer Res. 2011 Jul 1;17(13):4320-30. DOI:10.1158/1078-0432.CCR-10-2992

**ChIP seq**


• **Drier et al.,** An oncogenic MYB feedback loop drives alternate cell fates in adenoid cystic carcinoma. Nat Genet 2016 Mar;48(3):265-72. DOI:10.1038/ng.3502
  - ChIP seq data for: MYB (4 ACC PDX samples), BRD4 (2 ACC PDX samples), TP63 (1 ACC PDX sample), H3K4me1 (3 ACC PDX samples), H3K4me3 (8 ACC PDX samples) and H3K27ac (8 ACC PDX samples and 5 ACC tumor samples); [https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE76465](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE76465)

We have done WES/WGS and RNA sequencing on a number of ACC PDX models. These datasets have not yet been published/deposited into a public database, but can be shared. Mutations were called for some of the DNA sequencing data and can be downloaded here: [http://www.accrf.org/wp-content/uploads/ACC-PDX-WES-WGS-Mutations-2015.xls](http://www.accrf.org/wp-content/uploads/ACC-PDX-WES-WGS-Mutations-2015.xls). Gene expression data may be downloaded from here:

• Gene expression – Array Express (2012)
• Gene expression – GEO (2012)
• Gene expression – Array Express (2011)
• Gene expression – GEO (2011)