



PUBLICLY AVAILABLE ACC BIOINFORMATIC DATASETS – DECEMBER 2022

(listed in reverse chronological order)

DNA- Copy number array, CGH and WES/WGS

- [Karpinets et al.](#), Whole-genome sequencing of common salivary gland carcinomas: subtypes and shared genetic alterations. Clin Cancer Res. 2021 May 19; 4071.2020. DOI: [10.1158/1078-0432.CCR-20-4071](https://doi.org/10.1158/1078-0432.CCR-20-4071)
 - WGS on 20 ACCs
- [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](https://doi.org/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
- [Yang et al.](#), Immunogenic neoantigens derived from gene fusions stimulate T cell response. Nat Med. 2019 May; 25(5):767-775. DOI: [10.1038/s41591-019-0434-2](https://doi.org/10.1038/s41591-019-0434-2)
 - RNA sequencing of 8 ACC samples and WGS of 2 ACC samples;
<https://www.ncbi.nlm.nih.gov/sra/?term=PRJNA527992>
- [CSER: Exploring Precision Cancer Medicine for Sarcoma and Rare Cancers](#) (U of Michigan, unpublished but deposited into SRA); Study accession number: [SRP048907](https://www.ncbi.nlm.nih.gov/sra/PRJNA527992) (includes data for many other cancers), can access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
 - SRX1910099
 - SRX1909669
 - SRX1909426
 - SRX1909214
 - SRX1909162
- [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)
 - WGS via Illumina of 4 ACC breast samples;
<https://www.ncbi.nlm.nih.gov/sra/?term=SRP108137>
 - MSK-IMPACT targeted NGS panel on 2 ACC breast samples;
<https://www.ncbi.nlm.nih.gov/sra/?term=SRP108155>
- [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)
 - Affymetrix oncoscan of multiple tumor sections from 2 ACC breast cases;
<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE79052> and
<https://www.ncbi.nlm.nih.gov/sra?term=SRP068515>
- [Rettig et al.](#), Whole-Genome Sequencing of Salivary Gland Adenoid Cystic Carcinoma. Cancer Prev Res (Phila). 2016 Apr;9(4):265-74. DOI:[10.1158/1940-6207.CAPR-15-0316](https://doi.org/10.1158/1940-6207.CAPR-15-0316)
 - WGS of 25 ACC samples <https://www.ebi.ac.uk/ega/studies/EGAS00001002812>
- [Martelotto et al.](#), Genomic landscape of ACC of the breast. J Pathol. 2015 Oct;237(2):179-80. DOI: [10.1002/path.4573](https://doi.org/10.1002/path.4573)
 - Exome sequencing via Illumina of 12 ACC breast samples;
<https://www.ncbi.nlm.nih.gov/sra/?term=SRP053134>
- [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>
 - Capillary sequencing of SPEN and FGFR2 in 48 ACC samples; <https://ega-archive.org/datasets/EGAD00001000175>



- Expression profiling via Illumina array of 21 ACC samples;
<https://www.ebi.ac.uk/ega/studies/EGAS00001000193>
- [Persson et al.](#), Clinically significant copy number alterations and complex rearrangements of MYB and NFIB in head and neck adenoid cystic carcinoma. *Genes Chromosomes Cancer* 2012 Aug;51(8):805-17. DOI:[10.1002/gcc.21965](https://doi.org/10.1002/gcc.21965)
 - High-resolution acGH on fresh frozen tissue from 40 ACC 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)
 - Array-based CGH in 10 ACC samples;
<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22328>

RNA- Gene expression array, RNA sequencing, miRNA

- [Viragova et al.](#), bioRxiv preprint, Phenotypic dissection of epithelial lineages and therapeutic manipulation of differentiation programs in human Adenoid Cystic Carcinomas (ACCs). doi: <https://doi.org/10.1101/2022.01.19.476843>
 - PDX RNAseq data deposited in dbGAP (accession number: [phs002764.v1.p1](#))
- [Parikh et al.](#), Single-cell RNA sequencing identifies a paracrine interaction that may drive oncogenic notch signaling in human adenoid cystic carcinoma. *Cell Rep.*, 2022 Nov 29; 41(9):111743. DOI: [10.1016/j.celrep.2022.111743](https://doi.org/10.1016/j.celrep.2022.111743)
 - Processed scRNA-seq data from 7 primary tumors and 1 matched local recurrence deposited at GEO: [GSE210171](#); raw data deposited at dbGAP: phs003070.v1; contact [Dr. Sid Puram](#) for any additional information needed for reanalysis of data.
- [Lin et al.](#), Single-cell transcriptomic analysis of the tumor ecosystem of adenoid cystic carcinoma. *Front Oncol.*, 2022 Nov 17; 12:1063477. DOI: [10.3389/fonc.2022.1063477](https://doi.org/10.3389/fonc.2022.1063477).
 - scRNA-seq data from 3 primary tumors and 1 matched recurrence are deposited in the CNCB-NGDC (National Genomics Data Center, China National Center for Bioinformatics, <https://ngdc.cncb.ac.cn/gsa-human/s/j2QOEb3S>), accession number is PRJCA012307.
- [Dou et al.](#), The Immune Landscape of Chinese Head and Neck Adenoid Cystic Carcinoma and Clinical Implication. *Front. Immunol.*, 2021 Sept 6. PMID: [34552580](#); PMCID: [PMC8450584](#); DOI: [10.3389/fimmu.2021.618367](https://doi.org/10.3389/fimmu.2021.618367)
 - WES and RNAseq on 75 ACC specimens can be found in supplementary info (filtered/processed):
<https://www.frontiersin.org/articles/10.3389/fimmu.2021.618367/full#supplementary-material>



- [Ferrarotto et al.](#), Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. Clin Cancer Res., 2020 Nov 10. DOI: [10.1158/1078-0432.CCR-20-1192](https://doi.org/10.1158/1078-0432.CCR-20-1192)
 - RNA/DNA sequencing of 54 flash-frozen salivary ACCs and reverse phase protein array (RPPA) in 38 specimens. DOI: 10.17632/6sbv7bpj5n.1; (filtered/processed) data deposited on Mendeley Data at: <https://data.mendeley.com/datasets/6sbv7bpj5n/1>
- [Linxweiler et al.](#), The Immune Microenvironment and Neoantigen Landscape of Aggressive Salivary Gland Carcinomas Differ by Subtype. Clin Cancer Res. 2020 Jun 15; 26(12):2859-2870. DOI: [10.1158/1078-0432.CCR-19-3758](https://doi.org/10.1158/1078-0432.CCR-19-3758)
 - 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. Data deposited in NCBI Sequence Read Archive (SRA) under accession numbers SRP109264, SRP096726, and PRJNA601423.
- [Mandelbaum et al.](#), Zebrafish blastomere screen identifies retinoic acid suppression of MYB in ACC. J Exp Med. 2018 Oct 1;215(10):2673-2685. DOI:[10.1084/jem.20180939](https://doi.org/10.1084/jem.20180939)
 - RNAseq of the ACCX9 PDX model treated with ATRA or vehicle (3 replicates); <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE98007>
- [Andreasen et al.](#), MicroRNA dysregulation in adenoid cystic carcinoma of the salivary gland in relation to prognosis and gene fusion status: a cohort study. Virchows Arch. 2018 Sep; 472(3):329-340. DOI:[10.1007/s00428-018-2423-0](https://doi.org/10.1007/s00428-018-2423-0)
 - 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
- [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](https://doi.org/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](https://doi.org/10.18632/oncotarget.23641)
 - RNAseq of 94 ACC and 4 normal salivary gland FFPE samples; <https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA287156>.



- [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](#)
 - Expression array of 13 ACC, 2 ACC xenograft and 7 normal salivary gland samples; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE88804>
 - Expression array after MYB or IGF1R inhibition; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE76094>
- [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](#)
 - RNA seq on 20 epithelial-dominant ACC samples, 22 myoepithelial-dominant ACC samples and 5 normal salivary tissue samples; <https://www.ncbi.nlm.nih.gov/sra/?term=SRP067524>
- [Gao et al.](#), A unifying gene signature for adenoid cystic cancer identifies parallel MYB-dependent and MYB-independent therapeutic targets. Oncotarget. 2014 Dec 30;5(24):12528-42. DOI:[10.18632/oncotarget.2985](#)
 - mRNA Affymetrix arrays for 12 ACC samples with matched normal; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE59701>
 - miRNA chip Affymetrix arrays for 12 ACC samples with matched normal; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE59700>
- [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>
- [Moskaluk et al.](#), Development and characterization of xenograft model systems for adenoid cystic carcinoma. Lab Invest. 2011 Oct;9(10):1480-90. DOI:[10.1038/labinvest.2011.105](#)
 - Expression profiling via Affymetrix Array of 11 ACC PDX and 3 normal salivary gland samples; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36820>
 - Expression profiling via Affymetrix Array of 12 ACC PDX and 10 ACC samples; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE28996>
- [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](#)
 - Expression profiling via Affymetrix Array of normal salivary gland cells treated plus or minus 5—Aza/TSA; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE25746>



ChIP seq

- [Mandelbaum et al.](#), Zebrafish blastomere screen identifies retinoic acid suppression of MYB in ACC. J Exp Med. 2018 Oct 1;215(10):2673-2685. DOI:[10.1084/jem.20180939](#)
 - ChIP seq data for: H3K27ac, RAR and MYB on ACCX9 PDX samples treated with ATRA or vehicle; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE98006>
- [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>

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>. Gene expression data may be downloaded from here:

- [Gene expression – Array Express \(2012\)](#)
- [Gene expression – GEO \(2012\)](#)
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- [Gene expression – GEO \(2011\)](#)