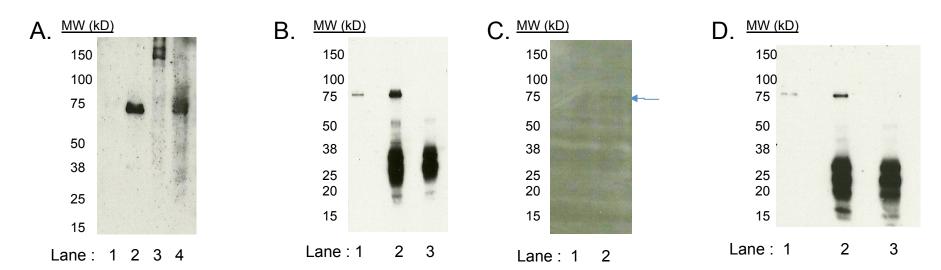
ENCODE DCC Antibody Validation Document

Date of Submission			
Name: Email:			
Lab			
Lab			
Antibody Name: Target:			
Company/			
Source:			
Catalog Number, database ID, laboratory Lot Number			
Antibody			
Description:			
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Validation Method #1 Validation Method #2			
Purification Polyclonal/			
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Validation #1 Analysis					
Insert Validation Image (click here)					

ARID3A (NB100-279) & (sc-8821) Immunoblot / Immunoprecipitation



A. Western Blot using NB100-279 on nuclear lysates from cell lines GM12878 (Lane1), K562 (Lane2), HeLaS3 (Lane3), and HepG2 (Lane4). **B**. Immunoprecipitation was performed on nuclear lysates from K562 cells using antibody NB100-279. Lane1: Nuclear lysate. Lane 3: Bound material from control immunoprecipitation with rabbit IgG. . Lane 2: Bound material from immunoprecipitation with NB100-279. **C**. Western Blot using sc-8821 on nuclear lysates from cell lines GM12878 (Lane1), K562 (Lane2). **D**. Immunoprecipitation was performed on nuclear lysates from K562 cells using antibody sc-8821 and immunoblot with NB100-279. Lane1: Nuclear lysate. Lane 2: Bound material from immunoprecipitation with sc-8821. Lane 3: Bound material from control immunoprecipitation with Goat IgG. Arrow indicates band of expected size (~80kD) that is highly enriched in the specifically immunoprecipitated fraction.

Validation #2 Analysis					
Insert Validation I	mage (Click here)				
Insert Validation Image (Click here)					

Validation 2: ChIPseq with alternate antibodies to the same factor

	ARID3A NB100-279	ARID3A sc-8821
Total peaks	122875	48018
% Peak overlap	86.8	86.5

Antibodies/Immunogens:

NB100-279: Immunogen: A synthetic peptide, which represented a portion of human Dead Ringer-Like 1 encoded

within exon 8

sc-8821: epitope mapping at the N-terminus of ARID3A of human origin

Comparison: K562 cells were used for ChIP-seq with antibody sc-8821 or antibody NB100-279. Peaks were called from replicate experiments using PeakSeq with a .01 q-value cut-off. Comparisons between experiments were made using these peaks according to standard ENCODE replicate comparison parameters (

http://genome.ucsc.edu/ENCODE/protocols/dataStandards/ChIP_DNase_FAIRE_DNAme_v2_2011.pdf; reported is the fraction of the top 40% of peaks in one list that are found in the full list of peaks obtained with the other antibody.