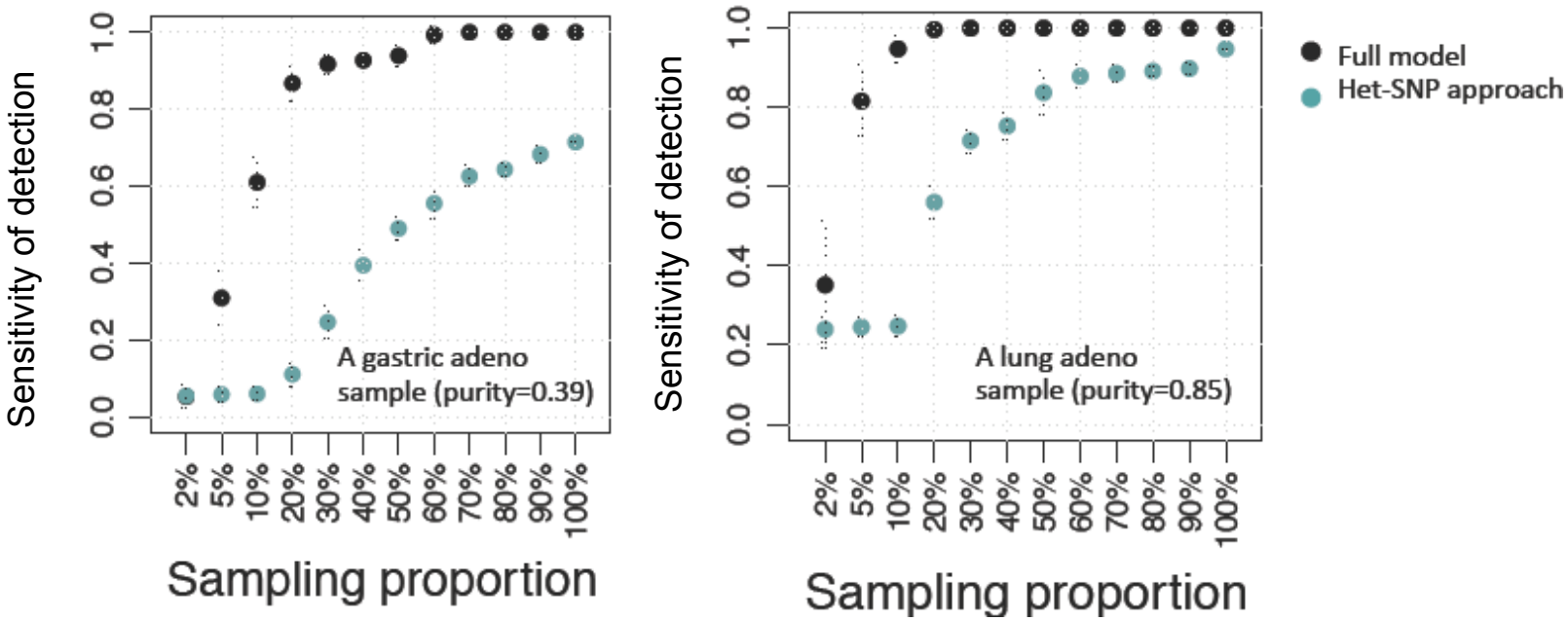
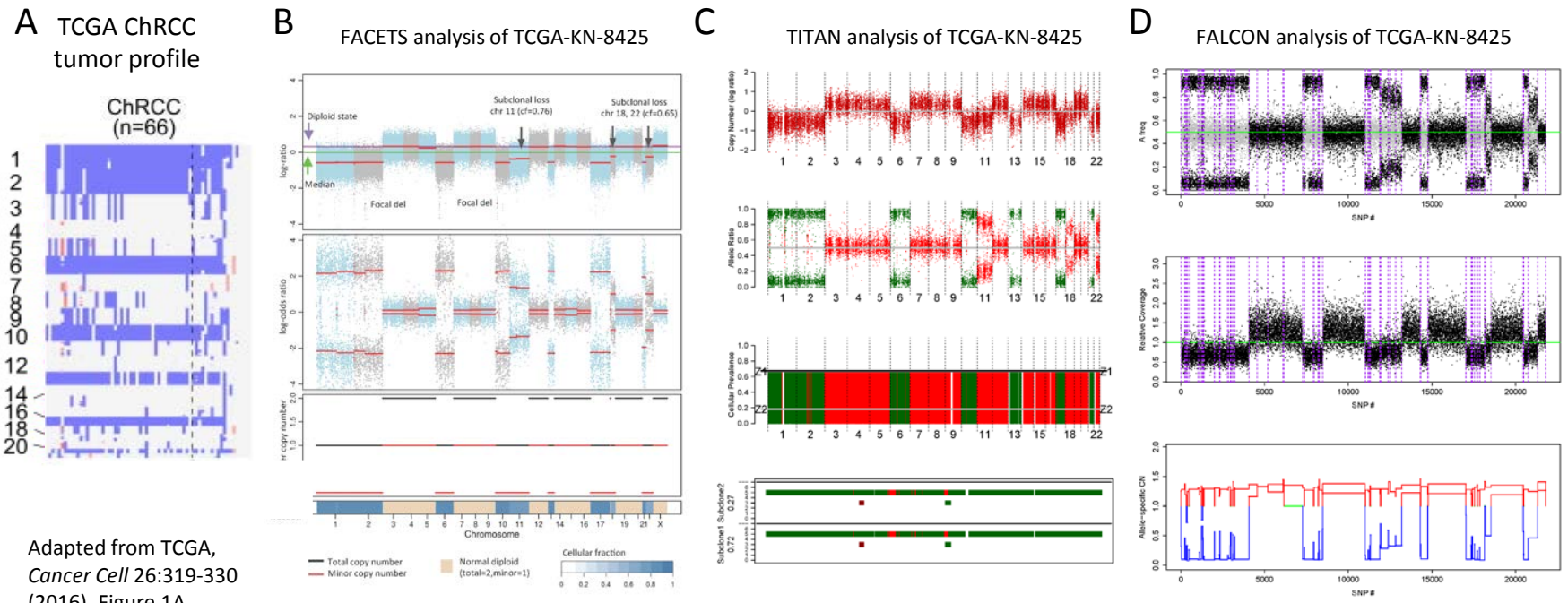
Features	FACETS	TITAN	FALCON
Input	All SNP loci	Het-SNP	Het-SNP
GC-normalization	Yes	Yes, but separate software package required.	No
Allelic imbalance	Joint tumor-normal inference based on allelic odds-ratio (logOR)	Tumor-only approach.	Joint tumor-normal inference based on bivariate binomial process
Segmentation	Bivariate Hotelling T^2	None	Binomial mixture process
Estimate and adjust for tumor purity and ploidy	Yes	Yes	N/A
Clonal heterogeneity	Clonal and subclonal classification	Need to pre-specify number of clonal clusters	N/A
Integer copy number estimates	Gaussian-Non-central X^2 model	Hidden Markov Model (HMM)	N/A. Only reports relative copy number.

Supplementary Table 1. Comparison of ASCN analysis methods for sequencing data. FACETS provides a more comprehensive and integrated analysis pipeline that includes GC-normalization, total and allele-specific joint segmentation analysis, estimation of tumor purity, ploidy, integer copy number, clonal and subclonal classification of the alterations.



Supplementary Figure 1 . Sensitivity analysis of reducing genome coverage from down-sampling whole-exomes on detection rates for copy number alterations (F,G).



Adapted from TCGA, *Cancer Cell* 26:319-330 (2016), Figure 1A

Monosomies of chr 1,2,6,10,13,17,20

Adapted from Figure 2
Ploidy=1.6, Puirty=0.89
Monosomies of chr 1,2,6,10,13,17,20 at clonal level
Monosomies of chr 11, 18, and 22 at subclonal level

Ploidy=5.3, Puirty=0.68

N/A

Supplementary Figure 2. Comparison of ASCN analysis of TCGA whole-exome sequencing of chromophobe renal cell carcinoma (ChRCC). A. The TCGA ChRCC tumor copy number profile from SNP array data analysis using ABSOLUTE showing classic profile of monosomies of chromosomes 1, 2, 6, 10, 13 and 20. B. FACETS analysis of whole-exome sequencing of one of the TCGA chRCC patient sample (TCGA-KN-8425) showing monosomies of chromosomes 1, 2, 6, 10, 13 and 20 at a clonal level with additional subclonal changes detected in this sample. Two other ASCN analysis methods including TITAN (panel C) and FALCON (panel D) are also included using default parameter setting. The output is less interpretable.