

Supplementary table 1. The DEGs, GO and KEGG comparisons of four cetuximab-associated

	GSE56386	GSE5851 Khambata-Ford et al	Schütte, M. et al.	Peng et al.*
Samples	8 primary CRC samples	80 metastatic CRC biopsy samples	90 patients tumors	Cetuximab resistant/sensitive Caco-2
Top genes identified associated with cetuximab response	EGF, GNB5, GNG4, FGF2, BCL2, ACACB, KIT, ADCY4, NPY, NTS ^{&}	CD73, EREG, AREG	FYN, SORBS1, C16orf62, EREG, HOXD9, RAMP2, WARS, AHCYL2, GPD5, HEATR2, TM4SF4, STAT5B, PAAF1, TMEM70, SOX2, ZNF34	NA
No. of DEGs	1350 (FDR <0.05, log FC ≥ 2.5 or ≤ -2.5) (298 $\uparrow$, 1052 $\downarrow$)	141(FC>2, p<0.05) [#] (114 $\uparrow$, 27 $\downarrow$) 121(p<0.05) [§]	NA	306(FC>2, p<0.001) (136 $\uparrow$, 170 $\downarrow$)
Top Enriched KEGG pathways	Amoebiasis ($\uparrow$) Metabolic pathways ($\downarrow$)	Drug metabolism-cytochrome P450 PPAR signaling pathway	NA	PI3K-Akt signaling pathway PPAR signaling pathways Protein digestion and absorption
Top Enriched GO (BP/CC/MF)	Epidermis development ($\uparrow$,BP) Cornified envelop ($\uparrow$,CC) Calcium ion binding($\uparrow$, MF) Digestion ($\downarrow$,BP) Apical part of cell ($\downarrow$,CC) 3',5'-cyclic-AMP phosphodiesterase activity ($\downarrow$,MF)	Negative regulation of endopeptidase activity (BP), extracellular region (CC), serine-type endopeptidase inhibitor activity (MF)	NA	NA

studies.

[&]Hub genes identified by protein-protein interaction networks in GSE56386.

[§] Based on the results from Khambata-Ford et al.

[#] Based on the results from Peng K et al.

*No GSE expression profile of resistant/sensitive Caco-2 was available in Peng K et al.

$\uparrow$ up-regulated genes; $\downarrow$ down-regulated genes.

DEGs: differentially expressed genes; GO: gene ontologies; KEGG: Kyoto Encyclopedia of Genes and

Genomes; BP: biological processes; CC cellular components; MF: molecular functions.

Supplementary table 2. The comparison of the included studies for the prognostic values of BCL2 between Huang et al. and this manuscript.

	Yu et al.	Huang et al.
Detection methods	Microarray or RNA_seq	IHC
I-squared value	High, 68.3%	High, 59%-84.9%
Race	Europe and the USA	Europe, the USA and Asia
No. of patients	589	7658

Supplementary table 3. Inclusion and exclusion criteria of cases for univariate and multivariate analysis of BCL2 and ACACB in TCGA

Inclusion criteria	Exclusion criteria
1.Primary tumor samples or metastatic or recurrent samples;	1.Solid normal samples;
2.With complete BCL2 and ACACB expression;	2.Absent expression in BCL2 or ACACB
3.With complete OS and RFS data;	3.Absent OS or RFS results;
4.With complete and specific pathological data;	4.Incomplete or ambiguous TNM stage data;
5.Complete gender and age;	5.Absent gender or age data.

Supplementary table 4 Comparisons of the two GSE profiles.

	GSE56386	GSE65021
No. of Samples	8	40
Colorectal	8	0
Liver	0	0
Others	0	40 ^{&}
Sample sources	Primary tumors tested in ex vivo platform for response to cetuximab	Formalin-fixed, paraffin-embedded tumor specimens either from recurrence or primary position
Exposure to cetuximab	Yes	NA [#]
Gene expression profiles type	Microarray	Microarray
Sample date	2014	2015
Platform	GPL13607	GPL14951
Equipment	Agilent DNA Microarray Scanner	Illumina HumanHT-12 WG-DASL
Country	India	Italy
Samples subtypes	NA	Basal (BA); classical (CL); inflamed/mesenchymal (IMS)
Top genes identified	EGF, GNB5, GNG4, FGF2, BCL2, ACACB, KIT, ADCY4, NPY, NTS ^{&}	NA
No. of DEGs	1350 (FDR <0.05, log FC ≥ 2.5 or ≤ -2.5) (298↑, 1052↓)	509 (FDR<0.15) (336↑ in long-PFS; 173 ↑ in short-PFS)
Top Enriched KEGG pathways	Amoebiasis (↑)	NA
Top Enriched GO (BP/CC/MF)	Metabolic pathways (↓) Epidermis development (↑,BP) Cornified envelop (↑,CC) Calcium ion binding(↑, MF) Digestion (↓,BP)	NA

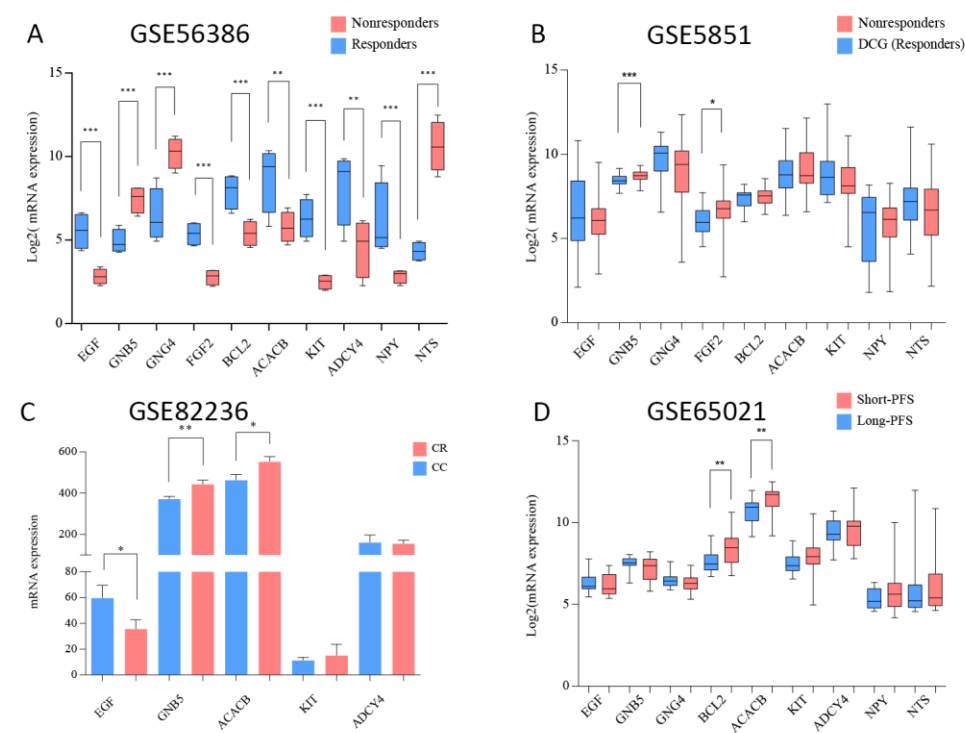
Apical part of cell (↓,CC) 3',5'-cyclic-AMP phosphodiesterase activity (↓,MF)		
GSEA	NA	Ectoderm/Epidermis, defense response, EGFR signaling pathway in long-PFS Muscle, Cation-trasport in short-PFS

& Head and neck squamous cell cancer

#No information of tumor samples prior or post to cetuximab treatment.

Supplementary figure 1

The hub genes expression in four genomic profiles. (A) Genes expression in responders and nonresponders in GSE56386; (B) genes expression in responders and nonresponders in GSE5851; (C) genes expression in cetuximab-resistant (CR) and control (CC) in GSE82236; (D) genes expression in short-PFS and long-PFS in GSE65021.



Supplementary figure 2

The pairwise correlations of hub genes in GSE65021.



Supplementary figure 3

The progression-free survival of BCL2 and ACACB in GSE5851.

