

**A subset of gastric cancers with EGFR amplification and overexpression
respond to cetuximab therapy**

Authors

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Supplement:

Supplementary Table 1. Clinicopathological parameters of GC patients and the pathology confirmation of corresponding PDX models.

ID	Sex	Tumor Size	Depth of Wall	Lymph Node	Distant	TNM stages	Histology	Differentiation
		(cm)	Invasion	Metastasis	Metastasis		(patients and PDX)	
GA0006	M	>5.0	T4a	N1	M0	IIIa	adenocarcinoma	moderately-poorly
GA0022	M	≤5.0	T4a	N2	M0	IIIb	adenocarcinoma	moderately-poorly
GA0023	F	≤5.0	T4a	N2	M0	IIIb	adenocarcinoma	poorly
GA0025	F	≤5.0	T4a	N1	M0	IIIa	signet-ring cell carcinoma	poorly
GA0033	M	>5.0	T4a	N0	M0	IIb	adenocarcinoma	poorly
GA0037	M	≤5.0	T4a	N0	M0	IIb	adenocarcinoma	poorly
GA0044	M	lesion from liver	n/a	n/a	M1	IV	adenocarcinoma	moderately-poorly
GA0046	M	>5.0	T4a	N2	M0	IIIb	adenocarcinoma	poorly
GA0055	F	≤5.0	T4a	N3b	M0	IIIc	adenocarcinoma	moderately
GA0060	M	≤5.0	T4a	N3a	M0	IIIc	adenocarcinoma	moderately-poorly
GA0075	F	>5.0	T4a	N1	M0	IIIa	adenocarcinoma	moderately-poorly
GA0080	M	>5.0	T4a	N2	M0	IIIb	adenocarcinoma	moderately-poorly
GA0098	M	≤5.0	T4a	N0	M0	IIb	adenocarcinoma	moderately
GA0114	F	>5.0	T4a	N1	M0	IIIa	adenocarcinoma	moderately-poorly
GA0119	M	>5.0	T4a	N3b	M0	IIIc	adenocarcinoma	poorly
GA0138	M	>5.0	T2	N1	M0	IIa	adenocarcinoma	poorly
GA0139	M	>5.0	T4a	N0	M0	IIb	adenocarcinoma	well
GA0151	F	>5.0	T4a	N1	M0	IIIa	adenocarcinoma	moderately-poorly
GA0152	F	>5.0	T4a	N0	M0	IIb	adenocarcinoma	poorly
GA2140	M	>5.0	T4a	N0	M0	IIb	adenocarcinoma	moderately-poorly

* Stage of GC was classified according to 7th edition tumor-node-metastasis (TNM) classification recommended by the International Union Against Cancer.

Supplementary Table 2. Panel of primers used for mutation analyses.

Mutation	Primers
EGFR	
Exon 18	Forward 5'-CATGGTGAGGGCTGAGGTGA-3' Reverse 5'-CCCCACCCAGACCATGAGAGG-3'
Exon 19	Forward 5'-GTGCATCGCTGGTAACATCCA-3' Reverse 5'-GGAGATGAGCAGGGTAGAGCA-3'
Exon 20	Forward 5'-CGCATTCATGCGTCTTCACC-3' Reverse 5'-CTATCCCAGGAGCGCAGACC-3'
Exon 21	Forward 5'-TGGCATGAACATGACCCTGAA-3' Reverse 5'-CAGCCTGGTCCCTGGTGTGTC-3'
KRAS	
Exon 2	Forward 5'-TTATGTGTGACATGTTCTAAT-3' Reverse 5'-AGAATGGTCCTGCACCAAGTAA-3'
Exon 3	Forward 5'-TCAAGTCCTTGCCCATTTC-3' Reverse 5'-TGCATGGCATTAGCAAAGAC-3'
Exon 4	Forward 5'-TTGTGGACAGGTTTGAAAGA-3' Reverse 5'-AGAACATGCCCTCTCAAG-3'
BRAF	
Exon 15	Forward 5'-CTCTTCATAATGCTTGCTC-3' Reverse 5'-GTGAATACTGGAACTATG-3'
c-MET	
Exon 14	Forward 5'-TGGGCACTGGGTCAAAGTCTC-3' Reverse 5'-AACAAATGTCACAACCCACTGAGGTA-3'
Exon 16	Forward 5'-ATTAAATGTTACGCAGTGCTAAC-3' Reverse 5'-GGTTGCAAACCACAAAAGTAT-3'
Exon 17	Forward 5'-GTATTCACTGTTCCATAATGAAGT-3' Reverse 5'-GATGGCTGGCTTACAGCTAGTT-3'
Exon 18	Forward 5'-AACAGTAGATGCTTAGTTATGCT-3' Reverse 5'-AACAGATTCCCTCTGTCACTT-3'
Exon 19	Forward 5'-TTCTATTTCAGCCACGGGTAAT-3' Reverse 5'-ATGAAAGTAAAGAGGGAGAAACTC-3'
Exon 21	Forward 5'-CACCTAAAGCCGAAATGCG-3' Reverse 5'-CAAGGAGCAAAGAATATCGATGGC-3'
PI3KCA	
Exon 1	Forward 5'-CTCCACGACCATCATCAGG-3' Reverse 5'-GATTACGAAGGTATTGGTTAGACAG-3'
Exon 9	Forward 5'-GATTGGTTCTTCCTGTCTCTG-3' Reverse 5'-CCACAAATATCAATTACAACCATTG-3'
Exon 20	Forward 5'-TGGGGTAAAGGGAATCAAAAG-3' Reverse 5'-CCTATGCAATCGGTCTTGC-3'