Gene Expression Markers of Efficacy and Resistance to Cetuximab Treatment in Metastatic Colorectal Cancer: Results from CALGB 80203 (Alliance).

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Running Title: Predictive biomarkers for cetuximab in colorectal cancer

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Translational Relevance: Beyond KRAS status, there are no validated biomarkers for anti-EGFR therapy in mCRC. Expression of genes within the EGFR signaling axis has been reported to correlate with benefit, but most reports have used non-randomized data that cannot distinguish prognostic and predictive markers. This report is one of the first generated from a randomized trial to identify predictive markers of benefit from cetuximab in mCRC. Gene expression of HER3 and CD73 were identified as potential predictive markers for cetuximab. Though the current sample size is small and the conclusions should be considered preliminary they implicate both HER axis signaling and immune modulation as potential mechanisms of cetuximab action and sensitivity.

Disclosure of Potential Conflicts of Interest:

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Administrative, technical, or material support: D. Niedzwiecki

Study supervision: A.B. Nixon, H.I. Hurwitz

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ABSTRACT

Purpose: Formalin-fixed, paraffin-embedded tumor samples from CALGB 80203 were analyzed for expression of EGFR axis-related genes to identify prognostic or predictive biomarkers for cetuximab treatment.

Patients and Methods: First-line metastatic colorectal cancer (mCRC) patients (238 total) were randomized to FOLFOX or FOLFIRI chemotherapy +/- cetuximab. RT-qPCR analyses were conducted on tissues from 103 patients at baseline to measure gene expression levels of HER-related genes, including amphiregulin (AREG), betacellulin (BTC), NT5E (CD73), DUSP4, EGF, EGFR, epigen (EPGN), epiregulin (EREG), HBEGF, ERBB2 (HER2), ERBB3 (HER3), ERBB4 (HER4), PHLDA1, and TGF-A. The interactions between expression levels and treatment with respect to progression-free survival (PFS) and overall survival (OS) were modeled using multiplicative Cox proportional hazards models.

Results: High tumor mRNA levels of HER2 (HR=0.64, p=0.002) and EREG (HR=0.89, p=0.016) were prognostic markers associated with longer PFS across all patients. HER3 and CD73 expression levels were identified as potential predictive markers of benefit from cetuximab. In KRAS wild-type (WT) tumors, low HER3 expression was associated with longer OS from cetuximab treatment while high HER3 expression was associated with shorter OS from cetuximab treatment (chemo+cetuximab: HR=1.15; chemo only: HR=0.48, interaction p=0.029). High CD73 expression was associated with longer PFS from cetuximab treatment in patients with KRAS WT (chemo+cetuximab: HR=0.91; chemo only: HR=1.57, interaction p=0.026) and KRAS mutant tumors
(chemo+cetuximab: HR=0.80; chemo only: HR=1.29, p=0.025).

**Conclusions:** Gene expression of HER3 and CD73 were identified as potential predictive markers for cetuximab. These data implicate HER axis signaling and immune modulation as potential mechanisms of cetuximab action and sensitivity.
INTRODUCTION

Epidermal growth factor receptor (EGFR) targeted therapies have shown clinical benefit in the treatment of numerous cancers, including metastatic colorectal cancer (mCRC) (1). Cetuximab, a chimeric monoclonal anti-EGFR antibody, is FDA and EMA approved for use in combination with FOLFIRI chemotherapy in the first-line setting and as monotherapy or with irinotecan in late-line treatment of KRAS wild-type mCRC. Recent data also suggest the activity of cetuximab with FOLFOX-based chemotherapy (2).

EGFR is a member of the ERBB/HER family of receptor tyrosine kinases (RTKs). Ligand binding causes homo- and hetero-dimerization between EGFR and the other members of the HER family (ERBB2/HER2, ERBB4/HER4 and the kinase-inactive ERBB3/HER3) resulting in downstream activation of the RAS-RAF-MEK and PI3K-AKT pathways (3). Multiple strategies have been developed for the therapeutic inhibition of EGFR signaling pathways and significant effort has been devoted to identifying biomarkers that can predict those patients most and least likely to benefit from EGFR-targeted therapies. Currently, only RAS mutation status has been validated as a predictive marker for anti-EGFR antibodies (4, 5). Activating RAS mutations occur downstream from the receptor tyrosine kinase EGFR, providing proliferative signals independent of EGFR ligand binding and thus resistant to EGFR blockade (6, 7). The initial reports showing that mutations in KRAS conferred resistance to EGFR-targeting therapies focused on mutations in codons 12 and 13 of exon 2 (4, 8). Recent studies have identified mutations in exon 3 and 4 of KRAS and exons 2, 3 and 4 of NRAS as additional markers of resistance to anti-EGFR antibodies in colorectal cancer (9, 10).
Intriguingly, gene expression signatures of activated RAS often indicate up-regulation of several EGFR ligands and inflammatory mediators (11-13). Moreover, feedback loops involving EGFR have also been noted in the setting of RAF and MEK inhibition (14-16).

Other mutations of genes within the EGFR signaling pathway (BRAF, PI3K, loss of PTEN expression) do not consistently predict for benefit or resistance to anti-EGFR antibodies (17). Although less studied than common driver mutations, expression levels of non-mutated ligands and receptors have been reported as candidate predictors of benefit from cetuximab. High expression levels of two EGFR ligands, amphiregulin (AREG) and epiregulin (EREG), have been associated with longer progression-free survival (PFS) and higher response rates in KRAS wild-type mCRC patients treated with cetuximab (13, 18, 19). Other markers associated with treatment outcome have also been identified, including ecto 5’ nucleotidase, NT5E (CD73) (19). However, these biomarker analyses in cetuximab-treated mCRC patients were performed in non-randomized clinical studies, necessitating further investigation and validation in randomized controlled trials.

The Cancer and Leukemia Group B (CALGB, now The Alliance for Clinical Trials in Oncology) 80203 trial was originally initiated as a phase III clinical trial of FOLFOX or FOLFIRI with or without cetuximab as first-line treatment of mCRC. However, with the FDA approval of bevacizumab for mCRC in 2004, CALGB 80203 was closed and its analysis plan was formally re-designed as a 1:1 randomized phase II study. Concurrently, the cooperative group then initiated CALGB 80405 to evaluate
bevacizumab, cetuximab, and the combination of bevacizumab and cetuximab in a randomized phase III study. The clinical results for CALGB 80203 (20) and CALGB 80405 have been reported previously (2). There was no significant difference between the cetuximab and bevacizumab arms with respect to overall survival (OS), \( [HR = 0.925, 95\% CI (0.78-1.09); \text{median OS } 29.9 \text{ and } 29.0 \text{ months, respectively}] \) or progression-free survival (PFS) \( [HR = 1.04, 95\% CI (0.91-1.17); \text{median PFS } 10.4 \text{ and } 10.8 \text{ months, respectively}] \). These results again emphasize the need for further refinement of the individual patient populations and the development of new predictive biomarkers beyond \( KRAS \) status to improve patient outcomes.

To this end, we hypothesized that the gene expression of EGF-signaling related genes in colorectal tumors might be predictive for cetuximab efficacy and resistance. We evaluated tumor mRNA expression of the EGF ligands (\( AREG, \) betacellulin (\( BTC \)), epidermal growth factor (\( EGF \)), epigen (\( EPGN \)), \( EREG \), heparin binding-EGF (\( HBEGF \)), and tumor growth factor \( \alpha \) (\( TGFA \)), and their receptors (\( EGFR, HER2, HER3, \) and \( HER4 \)). In addition, \( CD73, DUSP4, \) and \( PHLDA1 \) gene expression has been correlated to cetuximab resistance in several single-arm monotherapy studies of colorectal cancer (13, 19); therefore, we also evaluated their utility as prognostic and predictive markers in this study. The closure of CALGB 80203 after partial enrollment limits the power of our retrospective analysis and we wish to emphasize that conclusions should be considered preliminary until they can be verified in larger randomized studies. While the number of patients is limited, the inclusion of \( KRAS \) mutant patients in the cetuximab arms of this study cannot be repeated in the future due to ethical concerns. Therefore,
the sample population in CALGB 80203 gives us a unique opportunity to investigate pathways relevant to cetuximab response in KRAS mutant patients. This is one of the first randomized studies to evaluate predictive gene expression markers of cetuximab efficacy and resistance in first-line treatment of mCRC (21).
PATIENTS AND METHODS

Study Design and Patients

Patients with previously untreated, metastatic adenocarcinoma of the colon or rectum were randomized to FOLFIRI, FOLFIRI+cetuximab, FOLFOX, or FOLFOX+cetuximab treatment groups. This was a multi-center trial; 238 patients were randomized to treatment. Consent for biomarker analyses was optional. The protocol was approved by the institutional review boards at each participating institution. This retrospective analysis conforms to the reporting guidelines established by the REMARK criteria.

Sample Collection

Formalin-fixed, paraffin-embedded (FFPE) baseline tumor samples were collected during study enrollment. A total of 110 consenting patients (48%) had at least one paraffin block of primary colon or rectum tumor available for analysis. Seven samples were further excluded from this analysis due to quality and quantity issues related to the RNA isolation (Figure 1).

KRAS mutational analysis

KRAS mutation status was determined by Real Time PCR using the TheraScreen: KRAS Mutation Test Kit from Qiagen-DxS Diagnostic Innovations, which is able to detect the seven common mutations of the KRAS gene at codons 12 and 13 (G12A, G12D, G12R, G12C, G12S, G12V, and G13D). Analysis was performed in the Alliance molecular reference laboratory of Dr. Greg Tsongalis at Dartmouth Medical School.
RNA Isolation and RT-qPCR Analysis

An H&E stained image of the tumor sample was reviewed by a pathologist to ensure the presence of >70% tumor tissue within the sample and quality of the tumor. If samples were <70% tumor, macro-dissection was performed manually. FFPE tumor biopsies were cut at the CALGB (Alliance) pathology coordinating office and shipped overnight to the Alliance molecular reference laboratory at Duke University. RNA was isolated from six 10-µm sections using the Ambion RecoverAll Total Nucleic Isolation kit according to manufacturer’s protocol (Ambion-Life Technologies, Austin, TX, USA). RNA (200 ng) from each sample was reverse transcribed using the High Capacity cDNA Reverse Transcription kit (Applied Biosystems-Life Technologies, Foster City, CA, USA).

Taqman quantitative PCR was performed for EGF-related gene expression (primer-probe sets described in Supplementary Table 1), using the ABI 7900HT Real Time PCR System (Applied Biosystems-Life Technologies, Foster City, CA, USA). The log transformed relative amounts of mRNA expression were normalized to β-actin mRNA and expressed as \[ \log_2(\text{Cycle}_{X} - \text{Cycle}_{\beta\text{-actin}}) = -(\text{Cycle}_{X} - \text{Cycle}_{\beta\text{-actin}}), \] where CT is the threshold cycle. Taqman gene expression assays were chosen for each gene to span exon-exon junctions and have small amplicons < 100 base pairs to allow for specific and sensitive detection of degraded RNA. Life Technologies Taqman Gene Expression Assays have amplification efficiencies of ~100% (+/-10%). The β-actin endogenous control was used in this analysis. We observed uniform expression of β-actin across the mCRC tumor samples in this study. The mean CT value was 23.6 cycles with a standard deviation of 1.9 cycles across the CALGB 80203 sample population. Duplicate
samples with $C_T$ standard deviation greater than 0.5 cycles were re-run for improved qPCR reproducibility.

**Statistical Analysis**

Expression levels were normalized relative to $\beta$-actin, as described above, and analyzed as continuous measures. A Kendall tau analysis was performed to identify co-regulated genes. Univariate Cox (22) regression was used to identify markers prognostic of clinical outcomes (OS and PFS), and the resulting p-values, hazard ratios, and 95% confidence intervals are reported. To identify predictive markers, expression level was correlated with clinical outcomes (OS and PFS) using multiplicative Cox proportional hazards models to test for interaction between genetic expression and treatment (chemo vs. chemo+cetuximab). Visualizations of the resulting effect sizes are provided in the form of forest plots. The forest plots illustrate the hazard ratios of the expression levels (and the corresponding 95% confidence interval) within each treatment group, and the p-values for the tests of interaction are provided. Kaplan-Meier plots of OS and PFS were generated as additional visualizations of selected predictive markers, with separate curves for each combination of treatment group and expression level (where expression level is dichotomized at the median as “high” or “low”). Analyses were conducted using all patients, as well as separately within KRAS wild-type (WT) and KRAS mutant (Mut) subgroups, due to known differential responses to cetuximab across these populations. The reported p-values have not been adjusted for multiple testing. Due to the small sample size, uncorrected p-values, and retrospective nature of this study, results should be considered exploratory and hypothesis-
generating in nature. Further validation of predictive markers in other data sets will be necessary before they can be applied prospectively. Data collection and statistical analyses were conducted by the Alliance Statistics and Data Center. All clinical data was locked on March 5, 2012. Statistical analyses and figures were generated using the R software environment for statistical computing and graphics (23) with the *survival* (22) package.

**RESULTS**

**Patient Characteristics**

Patients (238) with previously untreated mCRC were enrolled and randomly assigned to one of four treatment groups: FOLFOX, FOLFOX+cetuximab, FOLFIRI, or FOLFIRI+cetuximab. The FOLFOX and FOLFIRI treatment groups showed similar response rates, PFS and OS (20). Due to the small size of this study and similar outcomes across the FOLFOX and FOLFIRI treatment groups, these groups were combined into chemotherapy (chemo) only and chemo+cetuximab cohorts for this analysis. Patient characteristics of the biomarker population were similar to those of the overall population (Table 1). While most studies have indicated that *KRAS* exon 2 mutations comprise approximately 40% of the CRC patient population, the biomarker population in this study had a slightly higher proportion of *KRAS* Mut patients (Table 1). Within the biomarker population, the chemo+cetuximab cohort showed longer median PFS and OS times with higher response rates compared to the chemo only cohort, but these differences were not statistically significant.
FFPE tissue blocks from the primary tumor site (colon or rectum) were processed from 110 patients, however seven RNA samples were excluded due to RNA quality and quantity issues, leaving 103 patients (43%) to be included in this RNA biomarker analysis (Figure 1). These patients were evenly distributed within the chemo only and chemo+cetuximab treatment groups (52 vs. 51 patients). The median follow-up time for all 103 patients included in the biomarker cohort was 69.2 months.

**Gene Expression in Primary Tumors**

Expression of 14 genes related to the EGF-signaling pathway (AREG, BTC, CD73, DUSP4, EGF, EGFR, EPGN, EREG, HBEGF, HER2, HER3, HER4, PHLDA1, and TGFA) was analyzed using Taqman RT-qPCR from the primary tumors. Most genes were expressed at detectable levels in >90% patients (Supplementary Table 1). Gene expression was most strongly correlated between EREG and AREG (τ=0.553), with HER2 and HER3 also showing strong co-expression (τ=0.475) (Supplementary Table 2). EPGN was co-expressed with both HER4 (τ=0.500) and EGF (τ=0.571), but the low expression levels of these genes may affect interpretation of these results. (Supplementary Table 1).

**Prognostic Gene Expression Biomarkers**
The baseline gene expression levels were tested for association with OS and PFS using Cox proportional hazards regression modeling. Prognostic univariate Cox regression analyses were conducted across all patients, and within KRAS WT and KRAS Mut subgroups. For OS across all patients, none of the assayed genes were identified as statistically significant prognostic markers for OS across all patients (Table 2), but favorable prognostic trends were noted for HER2 (HR=0.78, CI 0.60-1.02, p=0.071) and EGF (HR=0.84, CI 0.68-1.03, p=0.093). For OS, EREG expression was favorably prognostic for OS in the KRAS WT group (HR=0.87, CI 0.77-0.98, p=0.017). For PFS, HER2 (HR=0.64, CI 0.49-0.85, p=0.002) and EREG (HR=0.89, CI 0.80-0.98, p=0.016) were favorable prognostic markers across all patients. This effect seems to be driven by the KRAS WT subgroup. Both HER2 (HR=0.66, CI 0.47-0.92, p=0.013) and EREG (HR=0.84, CI 0.74-0.96, p=0.008) were significant prognostic markers in the KRAS WT group, but failed to show significance in the KRAS Mut group (HER2 p=0.123, EREG p=0.526). The prognostic associations of each assayed gene with OS and PFS are included in Supplementary Figures 1 and 2.

**Predictive Gene Expression Biomarkers**

Cox proportional hazards models of OS and PFS were used to test for interaction between treatment and continuous tissue gene expression, and identified expression of HER3 and CD73 as potential predictive markers for benefit or lack of benefit from cetuximab. Forest plots of the hazard ratio of gene expression by treatment group are presented for OS and PFS outcomes. Markers with an interaction p-value ≤ 0.2 are
shown in Figures 2 and 3, while a complete analysis showing all markers is included in the supplementary data (Supplementary Figures 3 and 4).

Higher levels of HER3 expression showed evidence of being predictive for lack of benefit from cetuximab, an effect that appeared restricted to the KRAS WT group. For OS in the KRAS WT group, the HR for chemo+cetuximab was 1.15 (CI 0.81-1.62) and the HR in the chemo only group was 0.48 (CI 0.27-0.87; interaction p=0.029) (Figure 2A). However, in the KRAS Mut population, HER3 was not predictive of either OS or PFS benefit from cetuximab (Figures 2B and 3B).

Gene expression of CD73 showed a similar trend toward predicting for OS benefit from cetuximab in the KRAS WT (interaction p=0.14) and KRAS Mut (interaction p=0.092) groups. Higher levels of CD73 expression predict for PFS benefit from cetuximab, an effect that appeared to be consistent in both KRAS WT and KRAS Mut groups. For PFS in the KRAS WT group, the HR was 0.91 (CI 0.70-1.18) for the chemo+cetuximab group and 1.57 (CI 1.11-2.23) for the chemo only group (interaction p= 0.026). For PFS in the KRAS Mut group, the HR was 0.80 (CI 0.60-1.07) for the chemo+cetuximab and 1.29 (CI 0.91-1.83) for the chemo only group (interaction p=0.025). Kaplan-Meier plots of high and low expression of HER3 and CD73 (dichotomized at the median) are also shown (Figure 4).

**DISCUSSION**
To date, the search for predictive markers for anti-EGFR therapies has focused largely on driver mutations, such as KRAS, NRAS, RAF, and PI3K. However, the importance of non-mutated factors in the HER axis is supported by several pre-clinical and clinical reports (18, 21, 24). For these reasons, we undertook an analysis of gene expression of all HER axis ligands and receptors, as well as other top candidates that had been previously identified (19).

Our analysis of CALGB 80203 is one the largest analyses of gene expression in a first-line mCRC study to date and focused exclusively on defined candidates previously reported in the literature with known biological relevance to the EGFR axis. A key advantage of CALGB 80203 for biomarker analyses is its use of randomization between chemotherapy with and without cetuximab. Without randomization, the prognostic and predictive roles of candidate markers cannot be distinguished and their roles may be confounded or obscured. Nevertheless, our results should be considered exploratory due to the limited sample size of the study, the number of markers analyzed, and the potential for higher order interactions between markers, between markers and KRAS status, and with FOLFOX vs FOLFIRI treatment.

Despite these limitations, our findings suggest both the HER axis and inflammatory pathways in mediating resistance to cetuximab. High HER3 levels were associated with both resistance and lack of benefit from cetuximab. This effect was most prominent in patients whose tumors were KRAS WT. Expression of other markers in the HER axis showed a trend for predicting benefit from cetuximab. Her3 is kinase-deficient, but it
heterodimerizes with Her2 to generate a potent signaling module. Her3 contains SH2 domains that, when phosphorylated by co-receptors, can activate the downstream PI3K pathway (25). Her2 and Her3 are also activated by EGF and BTC providing additional means for these ligands to support cell signaling and growth (26). Although signaling through Her3 has been shown to confer resistance to anti-EGFR agents in pre-clinical models (27, 28), evidence for this effect in CRC patients treated with cetuximab has been retrospective and lacked the randomization of the current study (29, 30). The co-expression of AREG and EREG has been shown to play a role in the physiological response to cetuximab treatment (18). The co-expression of HER2 and HER3 has also been shown previously (31) and is of particular interest as Her3 is capable of activating downstream pathways even within the context of Her2 inhibition (27). Our data provide additional clinical rationale for the evaluation of strategies that co-target EGFR and Her3 in patients with mCRC.

We also identified tissue CD73 expression as a potential predictive marker for benefit from cetuximab. CD73 was among the top markers that correlated with outcome in the report by Baker et al. (19). Intriguingly, our results were consistent in both KRAS WT and KRAS Mut populations. CD73 is known to play a central role in regulating multiple inflammatory responses, primarily by controlling levels of extracellular adenosine (32). CD73 is regulated by multiple factors, including RAS, STAT, HIF, and TGFβ (33, 34). The biology of CD73 and adenosine signaling has been extensively reviewed (35-37). CD73 acts with CD39 to convert inflammatory extra-cellular ATP to anti-inflammatory adenosine. CD73 is expressed on endothelial cells and Treg and its overexpression may
impair the ability of the immune system to respond to growing malignancies (35-37).

The recent success of immune-activating agents targeting PD-1/PD-L1 are an interesting analogy showing the potential benefit of up-regulating the immune system to aid tumor inhibition. Several pre-clinical studies have provided support for targeting CD73 as a therapeutic mechanism. In Figure 4B, patients in the high CD73 group who received chemotherapy only seemed to have the shortest OS indicating that larger studies may potentially identify a negative prognostic effect of high CD73 expression.

Multiple pre-clinical models have shown that inflammatory factors, including IL6, IL8, STAT3, and TGFβ, may mediate resistance to anti-EGFR therapies. Intriguingly, cetuximab induces an acneiform rash, which is predominantly neutrophillic and responds to anti-inflammatory agents, such as minocycline and steroids (38, 39). Whether similar infiltrates are also induced in the tumor microenvironment in patients is not known but is highly plausible. In this context, our CD73 data suggest potentially important roles for inflammation and immunity as mechanisms of sensitivity and resistance to cetuximab treatment. The predictive role for CD73 in patients whose tumors are KRAS Mut suggests that inflammation could be an additional mechanism of RAS mediated resistance to cetuximab. Many immune sub-populations, particularly those mediating inflammation, can exert a negative effect on anti-tumor immunity, including cell types regulated by CD73 such as neutrophils, Tie2 expressing macrophages, and Treg (40-45). Macrodissection enriched the tumor content for each sample, but this still represents a complex mixture of both tumor and the surrounding stroma. The expression patterns we have observed may not be intrinsic to the tumor...
only. In fact, these samples represent a baseline snapshot of expression that may reflect complex signaling between the tumor and its environment. Further studies are required to evaluate changes in mRNA expression associated with either cetuximab treatment or the progression of the disease.

Our results serve to extend and refine many of the findings initially reported by Baker et al. (19). However, our results also differ somewhat from the results of those studies. These differences may relate to numerous factors, including potential differences in study populations, pre-analytic considerations, which analytes were measured, and whether the studies were or were not randomized. A major strength of the current analysis is the randomization used in the parent study. In a recent report from the randomized CO.17 study of cetuximab vs best supportive care in patients with refractory colorectal cancer, the combination of KRAS status plus EREG was found to be a significant predictor of benefit from cetuximab, although EREG alone was of only borderline significance (21). Other candidate markers beyond EREG were not reported in that analysis.

In conclusion, using samples from the randomized CALGB 80203 study in first-line mCRC we identified two strong potential candidate predictors of benefit from cetuximab, HER3 and CD73. These data implicate specific and targetable factors in the HER axis and inflammation as key mediators of resistance to cetuximab.
References


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Tables

Table 1: Patient characteristics

<table>
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<th></th>
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<th>Overall biomarker population</th>
<th>Chemo only (biomarker population)</th>
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<td>26.4</td>
<td>22.8</td>
<td>27.6</td>
</tr>
<tr>
<td>Median PFS (95%CI)</td>
<td>(20.6-26.1)</td>
<td>(22.6-32)</td>
<td>(16.7 – 33)</td>
<td>(23.4-38.0)</td>
</tr>
<tr>
<td>Response Rate (CR/PR)</td>
<td>104</td>
<td>43.7</td>
<td>42</td>
<td>40.8</td>
</tr>
<tr>
<td></td>
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<td>20</td>
<td>38.5</td>
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</table>

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Table 2: Prognostic analyses of all markers for association with OS and PFS.

<table>
<thead>
<tr>
<th>Gene</th>
<th>OS</th>
<th>All Patients</th>
<th>KRAS WT</th>
<th>KRAS Mut</th>
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<tbody>
<tr>
<td></td>
<td>HR 95% CI p-value</td>
<td>HR 95% CI</td>
<td>HR 95% CI p-value</td>
<td>HR 95% CI p-value</td>
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<tr>
<td>-------</td>
<td>----------------------------</td>
<td>--------------</td>
<td>---------</td>
<td>----------</td>
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<tr>
<td>AREG</td>
<td>1.01 (0.88-1.15) 0.923</td>
<td>0.97 (0.82-1.16) 0.760</td>
<td>1.07 (0.89-1.30) 0.475</td>
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<tr>
<td>BTC</td>
<td>1.01 (0.85-1.21) 0.903</td>
<td>1.05 (0.83-1.34) 0.678</td>
<td>1.01 (0.75-1.35) 0.963</td>
<td></td>
</tr>
<tr>
<td>CD73</td>
<td>1.05 (0.91-1.21) 0.495</td>
<td>1.06 (0.88-1.27) 0.536</td>
<td>1.04 (0.83-1.30) 0.751</td>
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<tr>
<td>DUSP4</td>
<td>0.99 (0.86-1.13) 0.884</td>
<td>1.04 (0.89-1.23) 0.599</td>
<td>0.91 (0.70-1.18) 0.473</td>
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</tr>
<tr>
<td>EGF</td>
<td>0.84 (0.68-1.03) 0.093</td>
<td>0.81 (0.63-1.04) 0.098</td>
<td>0.84 (0.61-1.76) 0.890</td>
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<tr>
<td>EGFR</td>
<td>1.09 (0.91-1.30) 0.372</td>
<td>1.04 (0.81-1.34) 0.748</td>
<td>1.18 (0.88-1.59) 0.272</td>
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<tr>
<td>EPGN</td>
<td>0.86 (0.60-1.23) 0.399</td>
<td>0.96 (0.58-1.59) 0.871</td>
<td>1.00 (0.59-1.68) 0.988</td>
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<tr>
<td>EREG</td>
<td>0.94 (0.86-1.03) 0.212</td>
<td>0.87 (0.77-0.98) 0.017</td>
<td>1.07 (0.91-1.25) 0.405</td>
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<tr>
<td>HBEGF</td>
<td>0.87 (0.73-1.04) 0.121</td>
<td>0.86 (0.66-1.12) 0.261</td>
<td>0.87 (0.68-1.11) 0.250</td>
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<tr>
<td>HER2</td>
<td>0.78 (0.60-1.02) 0.071</td>
<td>0.83 (0.61-1.14) 0.246</td>
<td>0.72 (0.41-1.28) 0.264</td>
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<tr>
<td>HER3</td>
<td>0.98 (0.81-1.18) 0.831</td>
<td>1.03 (0.81-1.31) 0.795</td>
<td>0.90 (0.64-1.28) 0.565</td>
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<tr>
<td>HER4</td>
<td>0.88 (0.70-1.11) 0.283</td>
<td>0.87 (0.64-1.19) 0.391</td>
<td>0.84 (0.53-1.31) 0.414</td>
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<tr>
<td>PHLDA1</td>
<td>1.06 (0.87-1.29) 0.567</td>
<td>1.06 (0.81-1.38) 0.679</td>
<td>1.21 (0.85-1.72) 0.299</td>
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<tr>
<td>TGFA</td>
<td>1.01 (0.83-1.22) 0.952</td>
<td>1.06 (0.85-1.32) 0.621</td>
<td>0.84 (0.54-1.29) 0.422</td>
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<table>
<thead>
<tr>
<th>Gene</th>
<th>PFS</th>
<th>All Patients</th>
<th>KRAS WT</th>
<th>KRAS Mut</th>
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<tr>
<td></td>
<td>HR 95% CI p-value</td>
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</tr>
<tr>
<td>-------</td>
<td>----------------------------</td>
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<td>---------</td>
<td>----------</td>
</tr>
<tr>
<td>AREG</td>
<td>0.91 (0.80-1.03) 0.144</td>
<td>0.90 (0.77-1.06) 0.220</td>
<td>0.93 (0.77-1.13) 0.461</td>
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<tr>
<td>BTC</td>
<td>0.89 (0.76-1.05) 0.172</td>
<td>0.94 (0.75-1.17) 0.578</td>
<td>0.84 (0.63-1.12) 0.234</td>
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<tr>
<td>CD73</td>
<td>0.99 (0.86-1.14) 0.910</td>
<td>1.02 (0.85-1.22) 0.866</td>
<td>0.97 (0.78-1.21) 0.799</td>
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<tr>
<td>DUSP4</td>
<td>0.95 (0.83-1.08) 0.412</td>
<td>0.98 (0.84-1.15) 0.799</td>
<td>0.89 (0.69-1.14) 0.360</td>
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<tr>
<td>EGF</td>
<td>0.89 (0.74-1.07) 0.223</td>
<td>0.86 (0.68-1.09) 0.202</td>
<td>1.16 (0.75-1.80) 0.492</td>
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<tr>
<td>EGFR</td>
<td>0.89 (0.73-1.07) 0.220</td>
<td>0.80 (0.58-1.09) 0.168</td>
<td>0.95 (0.73-1.23) 0.696</td>
<td></td>
</tr>
<tr>
<td>EPGN</td>
<td>0.96 (0.67-1.36) 0.815</td>
<td>1.04 (0.62-1.75) 0.890</td>
<td>1.01 (0.60-1.71) 0.963</td>
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<tr>
<td>EREG</td>
<td>0.89 (0.80-0.98) 0.016</td>
<td>0.84 (0.74-0.96) 0.008</td>
<td>0.95 (0.82-1.11) 0.526</td>
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<tr>
<td>HBEGF</td>
<td>0.87 (0.73-1.03) 0.117</td>
<td>0.92 (0.71-1.19) 0.507</td>
<td>0.83 (0.66-1.04) 0.103</td>
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<tr>
<td>HER2</td>
<td>0.64 (0.49-0.85) 0.002</td>
<td>0.66 (0.47-0.92) 0.013</td>
<td>0.65 (0.38-1.12) 0.123</td>
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<tr>
<td>HER3</td>
<td>0.87 (0.74-1.04) 0.127</td>
<td>0.91 (0.73-1.14) 0.425</td>
<td>0.80 (0.59-1.10) 0.174</td>
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<tr>
<td>HER4</td>
<td>0.80 (0.62-1.02) 0.067</td>
<td>0.79 (0.56-1.12) 0.180</td>
<td>0.77 (0.50-1.17) 0.180</td>
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</tr>
<tr>
<td>PHLDA1</td>
<td>0.95 (0.79-1.15) 0.618</td>
<td>0.97 (0.76-1.24) 0.827</td>
<td>1.00 (0.71-1.39) 0.976</td>
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</tr>
<tr>
<td>TGFA</td>
<td>0.90 (0.73-1.12) 0.359</td>
<td>0.95 (0.74-1.23) 0.704</td>
<td>0.81 (0.53-1.22) 0.306</td>
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</table>
**Figure Legends**

**Figure 1:** Consort diagram showing patient enrollment numbers and groups.

**Figure 2:** Forest plots showing the associations of gene expression and treatment group with OS in KRAS WT (A) and KRAS Mut (B) patients. Only genes with an interaction p-value ≤ 0.2 are shown. The length of the line indicates the 95% confidence interval and the diameter of the median dot is inversely proportional to the standard deviation.

**Figure 3:** Forest plots showing the associations of gene expression and treatment group with PFS in KRAS WT (A) and KRAS Mut (B) patients. Only genes with an interaction p-value ≤ 0.2 are shown. The length of the line indicates the 95% confidence interval and the diameter of the median dot is inversely proportional to the standard deviation.

**Figure 4:** Kaplan-Meier plots of tumor gene expression levels significantly associated with outcome. (A) OS by HER3 expression in KRAS WT pts (B) PFS by CD73 expression in KRAS WT pts (C) PFS by CD73 expression in KRAS Mut pts (all groups dichotomized at the median). Interaction p-values are shown.
Patients randomly assigned (n=238)

Excluded (n=135; 56.7%)
- Did not consent for the use of tumor sample (n=37; 15.5%)
- No tissue block available (n=51; 21.4%)
- No primary (colon or rectum) tumor available (n=39; 16.4%)
- Poor RNA QA/QC (n=7; 3%)

Total RNA samples available (n=103; 43.3%)

Allocated to Chemo only & Analyzed (n=52; 50.5%)
KRAS WT (n=29; 55.8%)
KRAS MUT (n=23; 44.2%)

Allocated to Chemo + Cetux & Analyzed (n=51; 49.5%)
KRAS WT (n=26; 51.0%)
KRAS MUT (n=25; 49.0%)
Figure 4

A

B

C

p=0.029

p=0.026

p=0.025
Clinical Cancer Research

Gene Expression Markers of Efficacy and Resistance to Cetuximab Treatment in Metastatic Colorectal Cancer: Results from CALGB 80203 (Alliance).

Stephanie Cushman, Chen Jiang, Ace Hatch, et al.

Clin Cancer Res Published OnlineFirst December 17, 2014.

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