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| 14. ABSTRACT Multiple receptor pathways allow for redundancy in growth pathways that are dysregulated in cancer and lead to resistance to targeted therapies. EphB4 angiogenesis receptor can cooperate with HER2 growth factor signaling, and co-targeting HER2 and EphB4 could lead to significant therapeutic benefits. The goal of the full project is to assess the in vitro and in vivo growth and signaling effects of co-targeting using approved anti-HER2 agents, trastuzumab and lapatinib in combination with an agent that inhibits EphB4 signaling developed by our group, a ligand-blocking soluble albumin-stabilized EphB4 peptide termed sEphB4-HSA. The other component of this project (Partnering PI submitting this report) is to determine the presence of EphB4 and its ligand as well as other angiogenesis mediators and bypass receptors in relationship to response to HER2-targeted therapy and to assess for the enrichment of these markers in pre compared to post treatment tumor tissue. We have confirmed that trastuzumab does improve the pathological response rate in our cohort and have acquired and sectioned all the necessary blocks. We have finalized the titration and validation of all antibodies to be used. In vitro and in vivo studies (by the Submitting PI) are in progress. These studies together, if supportive of the rationale to co-target EphB4 and HER2 could be readily translated to the clinic as sEphB4-HSA is being tested in a Phase I trial at our institution. | | | | | | |
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Table of Contents

| | <u>Page</u> |
|-----------------------------------|-------------|
| Introduction..... | 4 |
| Body..... | 4 |
| Key Research Accomplishments..... | 24 |
| Reportable Outcomes..... | 25 |
| Conclusion..... | 26 |
| References..... | 27 |
| Appendices..... | 27 |

INTRODUCTION:

We hypothesize that the EphB4 angiogenesis receptor can cooperate with HER2 growth factor signaling and that co-targeting HER2 and EphB4 could lead to significant therapeutic benefits. The full project has aims to assess the in vitro and in vivo growth and signaling effects of co-targeting using approved anti-HER2 agents, trastuzumab and lapatinib in combination with an agent that inhibits EphB4 signaling developed by our group, a ligand-blocking soluble albumin-stabilized EphB4 peptide termed sEphB4-HSA. The other component cover by this project by the Partnering PI focuses on the human tissue analysis in patients who received pre-operative therapy with or without the HER2-targeted antibody trastuzumab. Markers of endothelial angiogenesis, including EphB4 and its cognate ligand EphrinB2 and downstream signaling will be analyzed for the relationship to response and to determine if enrichment of these markers occurs in non-responders from the initial biopsy to the post-treatment surgical specimen. The demonstration of these human tissue effects along with the efficacy of in vitro and in vivo co-targeting of HER2 and EphB4 will set the stage for clinical trial strategies as sEphB4-HSA is already in Phase I testing at our institution.

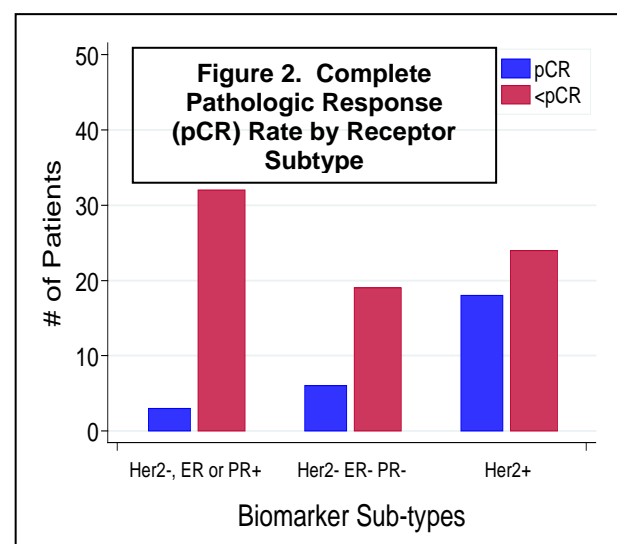
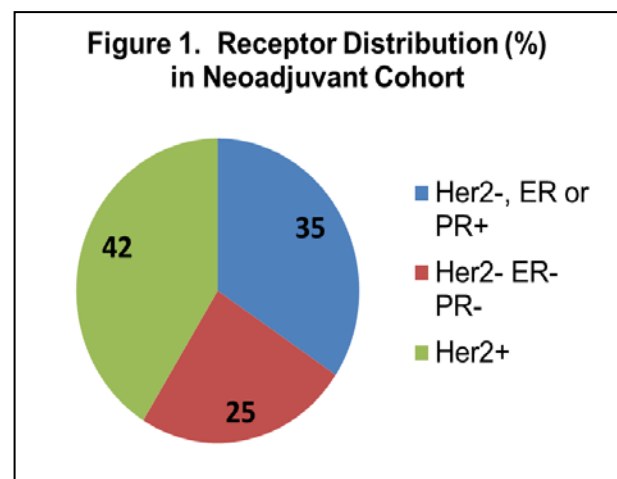
BODY:

Refer to Merged Statement of Work

Task 1: Obtain tissue and clinical data for analysis of HER2+ breast cancer treated with neoadjuvant trastuzumab-based therapy

Task 1A. We have obtained human subjects approval from USC IRB and DOD CDMRP and for consent waiver to obtain tissue blocks and clinical information (USC IRB# S10-00511).

Task 1B. We have identified consecutive patients who underwent neoadjuvant therapy and definitive surgery at our institution, a majority of such cases coming from Los Angeles County Hospital (LAC+USC). A total of 102 cases overall of neoadjuvant therapy were obtained, including 42 HER2+ cases. The breakdown of receptor subtypes in this cohort is shown in Fig 1. The ethnic breakdown of the overall cohort was representative of minority population seen at



LAC+USC, 80% Hispanic, with the HER2+ cohort being 81% Hispanic. The overall complete pathological response (pCR) rate in the cohort was 28.4%. The rates of pCR by receptor subtype are shown in Fig. 2. Within the HER2+ cohort pCR rate was 42.9%, a statistically significant difference (pCR odds ratio 15 compared to ER or PR+ and HER2-neg, $p < 0.001$ by multivariate analysis). Of the 42 HER2+ cases, 32 patients received neoadjuvant trastuzumab along with chemotherapy and exhibited a higher pCR rate (pCR 50.0 vs. 27.3%).

Task 1C. We have obtained all the blocks available on the 42 HER2+ cases, including baseline core biopsies and surgical specimens from patients who did not exhibit a pCR. A total of 24 patients did not achieve a pCR cases and 18 cases did have a pCR. A total of 63 blocks has been retrieved. For paired pre/post samples in non-pCR cases (needed for Task 3E), of the 24 non-pCR cases, 14 paired breast samples are available. The reason for this low yield in this particular group is not clear – in some cases, only nodal tissue (7 cases) was available for one of the time points in the pathology archives and in 3 cases, only pre (2 cases) or post therapy (1 case) tissue was available, potentially due to cases that were exhausted due to clinical tests needed for patient care or due to transfer of care to another facility. We have addressed this by amending our IRB protocol to allow us to extend the end date for our consent waiver to obtain additional cases. So far we have identified 30 additional HER2+ cases although given the regulatory delays in obtaining these, the analysis will not be performed in the context of this project, but will be pursued in the future with the additional of markers and increase in statistical power.

Task 2: Analysis of human HER2+ breast cancer tissue samples for angiogenic markers before and after trastuzumab-based therapy in the context of response

Task 2A. Staining for H&E for the presence of tumor cells has been done on all 63 blocks retrieved. These were scored for intensity and % positive among malignant cells by co-Investigator pathologist Debra Hawes, MD. Some of the blocks had no tumor tissue or very scant tumor as these were from core biopsies, so not all stains were performed. Some had in situ tumor only for analysis and those were read in the same fashion as invasive and scored malignant non-invasive cells (See Table 1).

Table 1. Successful Staining for Antigens Tested

| EphB4 | EphB2 | c-MET | IGF-1R | PDGFR | VEGFR1 | CXCR4 | Ki67 |
|-------|-------|-------|--------|-------|--------|-------|-------|
| 56/63 | 56/63 | 57/63 | 60/63 | 58/63 | 58/63 | 56/63 | 59/63 |

Eph B4: 6 with insufficient tumor, 1 skin and 2 in situ only; Eph B2: 6 with insufficient tumor, 1 skin and 2 in situ only; c-MET: 6 with insufficient tumor and 1 in situ only; IGF-1R: 3 with insufficient tumor and 2 in situ only; PDGFR: 4 with insufficient tumor, 1 skin; VEGFR1: 4 with insufficient tumor, 1 skin and 1 in situ only; CXCR4: 4 with insufficient tumor, 1 skin; Ki67: 4 with insufficient tumor and 1 in situ only.

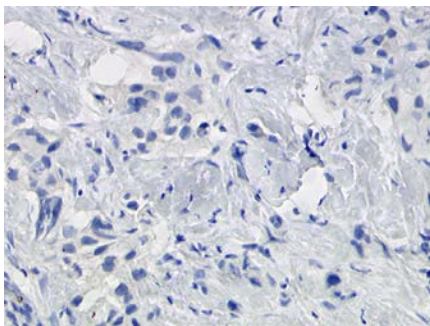
Task 2B. All cases have been reviewed for pathological response using record and pathology reports.

Task 2C. All antibodies were obtained and optimized for formalin-fixed paraffin embedded tissue analysis and scoring.

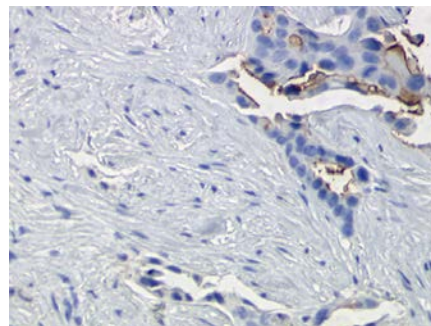
Task 2D. The planned immunohistochemical (IHC) stains - EphB4, EphB2, HGFR/c-MET, IGF-1R, PDGFR, VEGFR1 and additional stains for CXCR4 (a potential resistance markers identified in our lab) as well as Ki67 proliferation index were all optimized and then sections stained. These were scored for intensity and % positive among malignant cells by co-Investigator pathologist Debra Hawes, MD. Some of the blocks had scant tissue, so a not all stains were performed.

Representative stains for EphB4 and EphB4 are shown on Fig 3. In some cases, alternate vendors not listed in the proposal were used to obtain antibodies that work well in formalin-fixed, paraffin-embedded tissue.

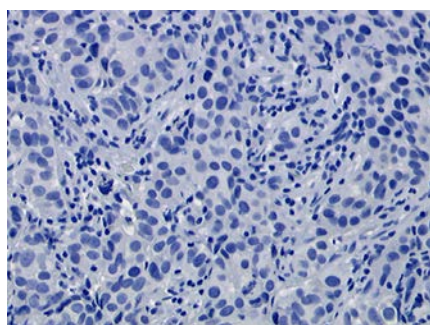
Figure 3. Representative IHC Stains for EphB4 and EphB2 on Pretreatment Cases



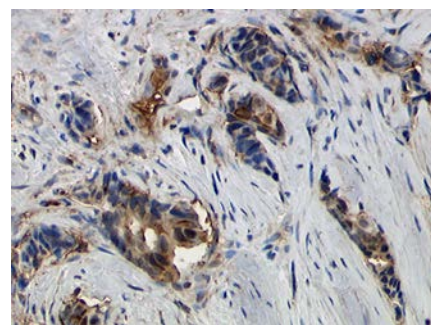
EphB4, negative – 20X



EphB4, positive – 20X



EphB2, negative – 20X



EphB2, positive – 20X

Task 2E. Statistical Analysis. Our primary objective for this aim was to identify baseline staining for the antigens of interest and their relationships to trastuzumab (Herceptin) response as measured by achievement (vs. not) of a complete pathological response (pCR), defined in the conventional fashion as the absence of invasive cancer in breast nodal tissue in the surgical specimen following trastuzumab-containing treatment and surgery. Our secondary objective was to compare markers pre and post trastuzumab-based therapy in patients who did not achieve pCR in order to assess if there was enrichment of markers suggesting that they might drive resistance. Additional objectives as to assess the same variables (pre treatment biomarkers and pCR, and changes in pre and post specimens in patients who did not achieve pCR) for all patients regardless of therapy, as some patients, particularly in earlier years, did not receive trastuzumab-based therapy and only received chemotherapy.

Statistical Methods

For the participating subjects, tissues were obtained prior to treatment and post treatment (if a subject did not have a pCR). Immunohistochemically stained slides were graded for intensity staining (0, negative; 1, weak; 2, moderate; 3, strong) and percentage of cells stained (0%-100%). Histoscores were calculated as the multiplication of marker intensity score and percent of cells stained. Data on 8 markers were analyzed, including EphB4, EphB2, CXCR4, IGF1, c-MET, PDGFR, VEGFR1, and Ki67. Changes in marker histoscores post treatment vs. pre treatment were examined with paired t-test. In addition, Wilcoxon rank sum test was used to compare baseline marker histoscores between subjects who achieved a pCR vs. those who did not achieve a pCR.

Results:

Part I: Subjects who received pre-operative trastuzumab plus chemotherapy

Of the 42 subjects in the total cohort, 32 patients received trastuzumab with chemotherapy and the remainder received chemotherapy alone. Of these 32 patients, 16 had a pCR and 16 did not have a pCR.

Of the 16 patients who did not have a pCR, 12 had tissue available with evaluations of biomarkers both pre-treatment and post-treatment. For some cases, percent of staining or intensity is missing for some biomarkers. Among the 8 biomarkers examined, no significant difference was found in marker histoscores at baseline for subjects who achieved pCR vs. those who did not (Table 2). In comparing pre and post treatment values among patients not achieving a pCR, there was a significance difference in biomarker histoscores post treatment compared to pre treatment for VEGFR1 ($p=0.030$) and Ki67 ($p<0.001$) (Table 3). Distribution of biomarker histoscores pre and post treatment are shown in Figure 4. Distributions of biomarker histoscores by pCR and non pCR categories are shown in Figure 5.

Table 2. Baseline Biomarker Histoscores in Relation to Response (pCR) in Cases Treated with Trastuzumab plus Chemotherapy

| Markers | Histoscore at baseline (Median (min, max)) | | p-value ¹ |
|---------------|---|--------------|----------------------|
| | pCR | Non pCR | |
| EphB4 | 0.2 (0, 45) | 0 (0, 9) | 0.30 |
| EphB2 | 1 (0, 69) | 0.6 (0, 285) | 0.78 |
| CXCR4 | 14 (0, 200) | 0 (0, 249) | 0.41 |
| IGF-1R | 180 (57, | 178 (42, | 0.93 |
| c-MET | 24 (0, 300) | 73 (0, 200) | 0.60 |
| PDGFR | 200 (0, 300) | 194 (72, | 0.98 |
| VGEFR1 | 80 (18, 300) | 84 (9, 300) | 0.71 |
| KI67 | 95 (40, 240) | 95 (64, 189) | 0.76 |

¹ p value from Wilcoxon rank sum test.

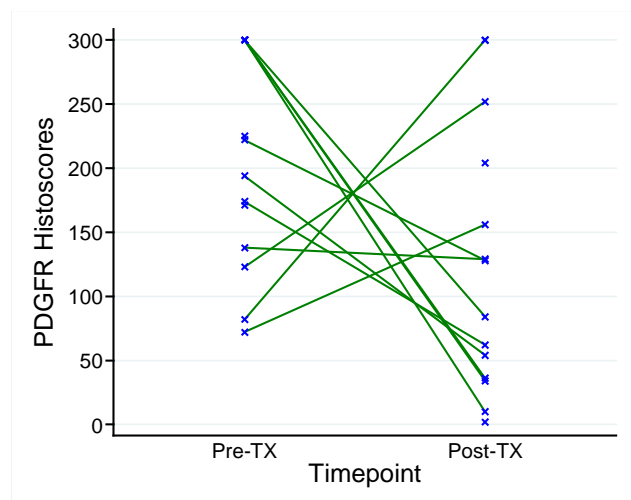
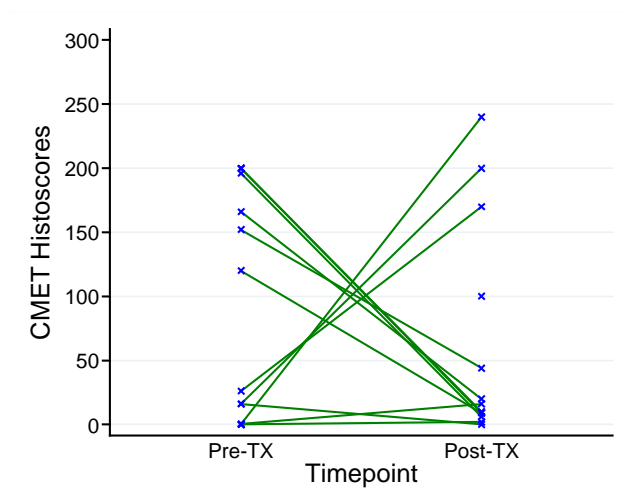
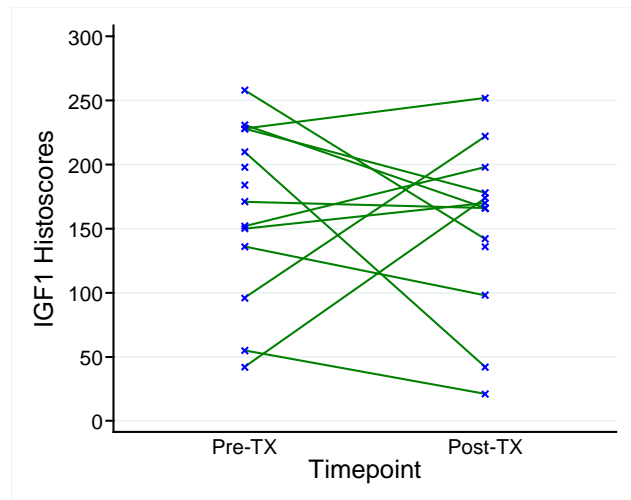
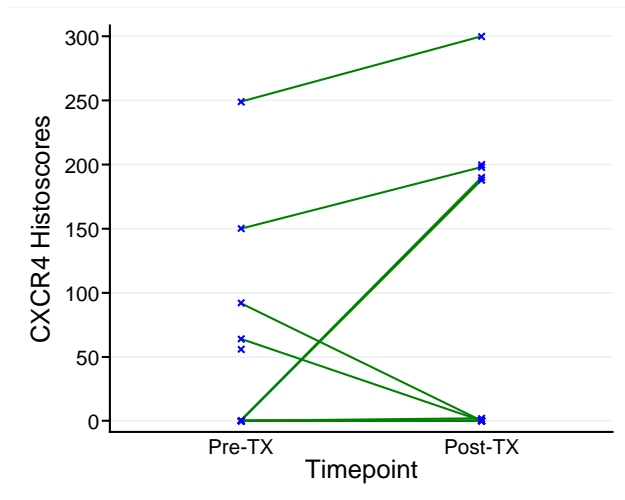
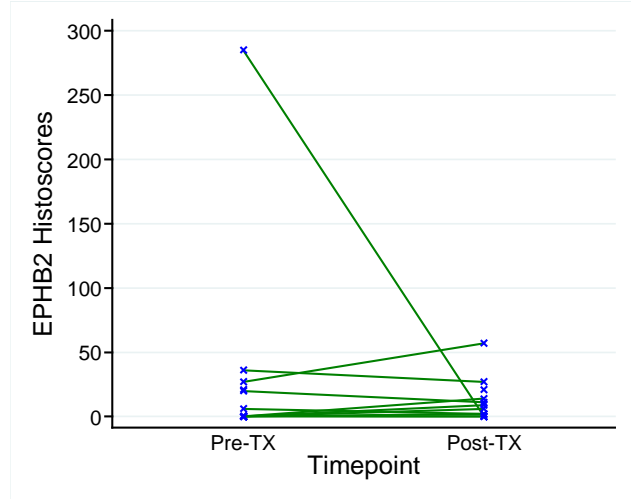
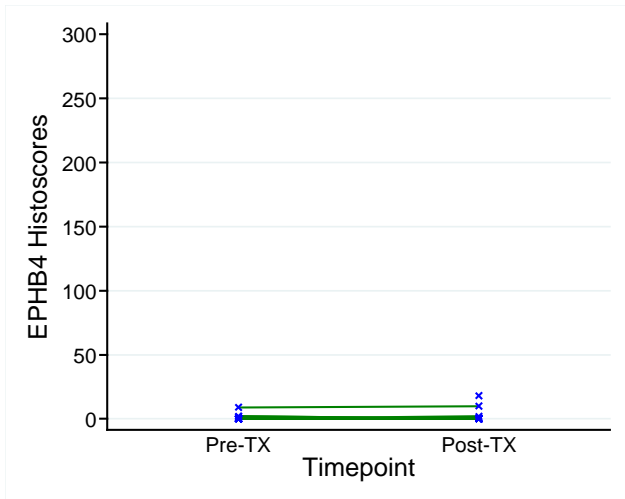
Table 3. Biomarker Histoscore Changes Pre and Post Trastuzumab plus Chemotherapy

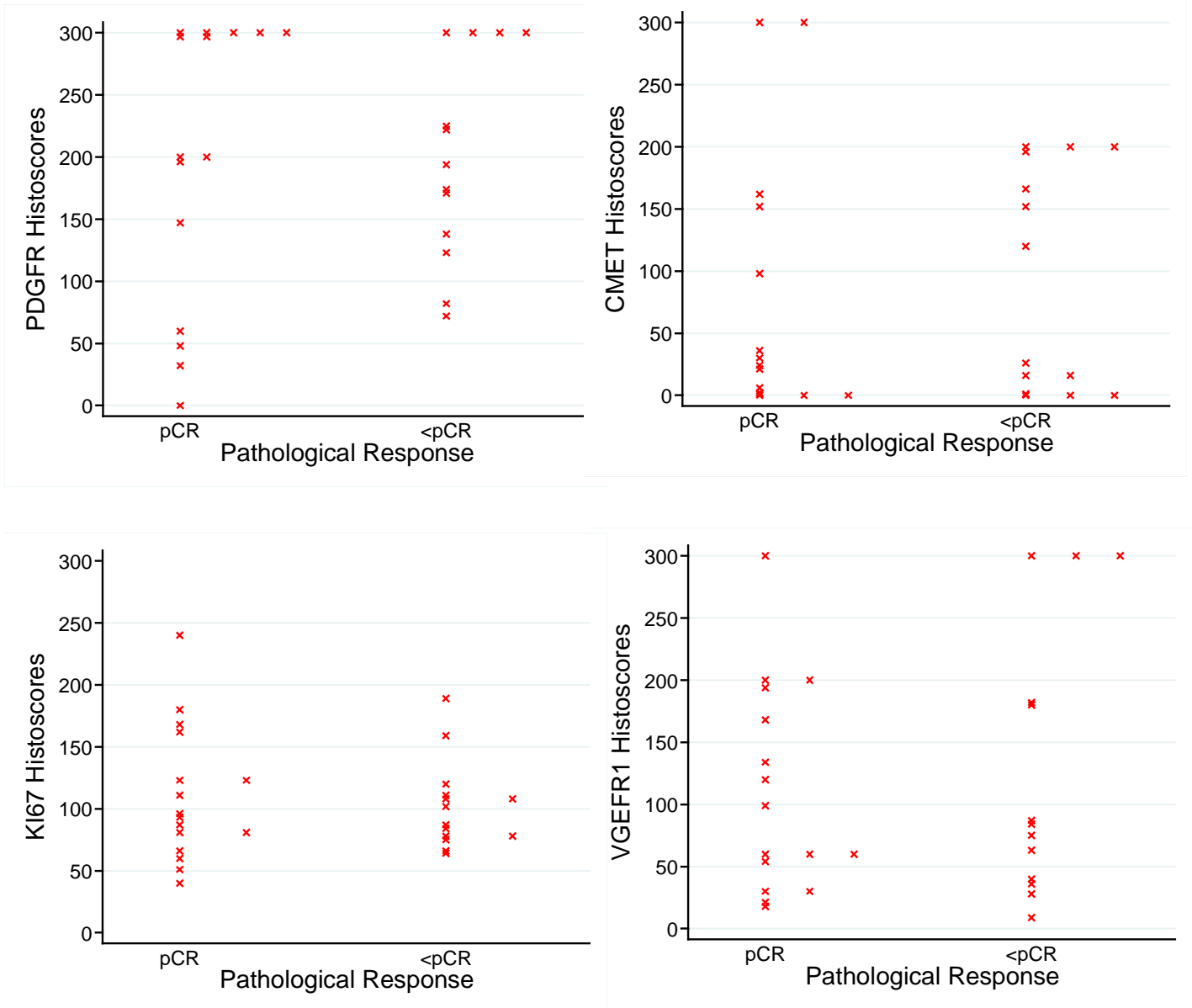
| Markers | Histoscore (Mean ± SE) | | Difference ² (Mean ± SE) | p-value ¹ |
|---------------|------------------------|----------------|--|----------------------|
| | Pre-Treatment | Post-Treatment | | |
| EphB4 | 1.2±0.82 | 1.2±0.90 | 0.001±0.34 | 0.99 |
| EphB2 | 34.1±25.4 | 11.6±5.2 | -22.4±26.5 | 0.42 |
| CXCR4 | 50.5±25.0 | 79.8±34.5 | 29.3±26.8 | 0.30 |
| IGF-1R | 163±20.6 | 152±19.7 | -10.7±25.5 | 0.68 |
| c-MET | 91.1±25.4 | 60.5±25.4 | -30.6±44.0 | 0.50 |
| PDGFR | 200±27.2 | 113±28.0 | -87.3±52.2 | 0.13 |
| VGEFR1 | 143±34.6 | 56.1±11.9 | -86.5±34.3 | 0.030 |
| Ki67 | 97.8±7.5 | 41.0±9.9 | -56.8±11.8 | <0.001 |

¹ p value from paired t-test.

² Difference post treatment vs. pre treatment

Figure 4. Distribution of Biomarker Histoscores at Baseline and Post Trastuzumab plus Chemotherapy





Results Part II: All subjects

Among all 42 subjects in the cohort, all received chemotherapy, and 32 received trastuzumab plus chemotherapy; 18 had a pCR and 24 did not have a pCR.

Of the 24 subjects who did not have a pCR, 18 had tissue for evaluation of the biomarkers both pre-treatment and post-treatment. For some cases, percent of staining or intensity is missing for some biomarkers. No significant difference was found among the 8 biomarker histoscores at baseline for subjects who achieved pCR vs. those who did not achieve pCR (Table 4). There was a significant difference in biomarker

histoscores post treatment compared to pre treatment for PDGFR (p=0.051), VEGFR1 (p=0.007), and Ki67 (p=0.008) (Table 5). Distribution of biomarker histoscores pre and post treatment are shown in Figure 6. Distributions of biomarker histoscores by pCR and non pCR categories are shown in Figure 7.

Table 4. Baseline Biomarker Histoscores in Relation to Response (pCR) in Cases Treated with Chemotherapy with or without Trastuzumab

| Markers | Histoscore at baseline (Median (min, max)) | | p-value ¹ |
|---------|---|--------------|----------------------|
| | pCR | <pCR | |
| EphB2 | 0.9 (0, 69) | 0.6 (0, 300) | 0.83 |
| EphB4 | 0.2 (0, 45) | 0 (0, 9) | 0.15 |
| CXCR4 | 14 (0, 200) | 0 (0, 276) | 0.29 |
| IGF-1R | 156 (57, | 164 (42, | 0.89 |
| c-MET | 21 (0, 300) | 111 (0, 200) | 0.17 |
| PDGFR | 297 (0, 300) | 174 (10, | 0.24 |
| VEGFR1 | 80 (18, 300) | 69 (9, 300) | 0.86 |
| Ki67 | 90 (40, 240) | 86 (33, 189) | 0.62 |

¹ p value from Wilcoxon rank sum test.

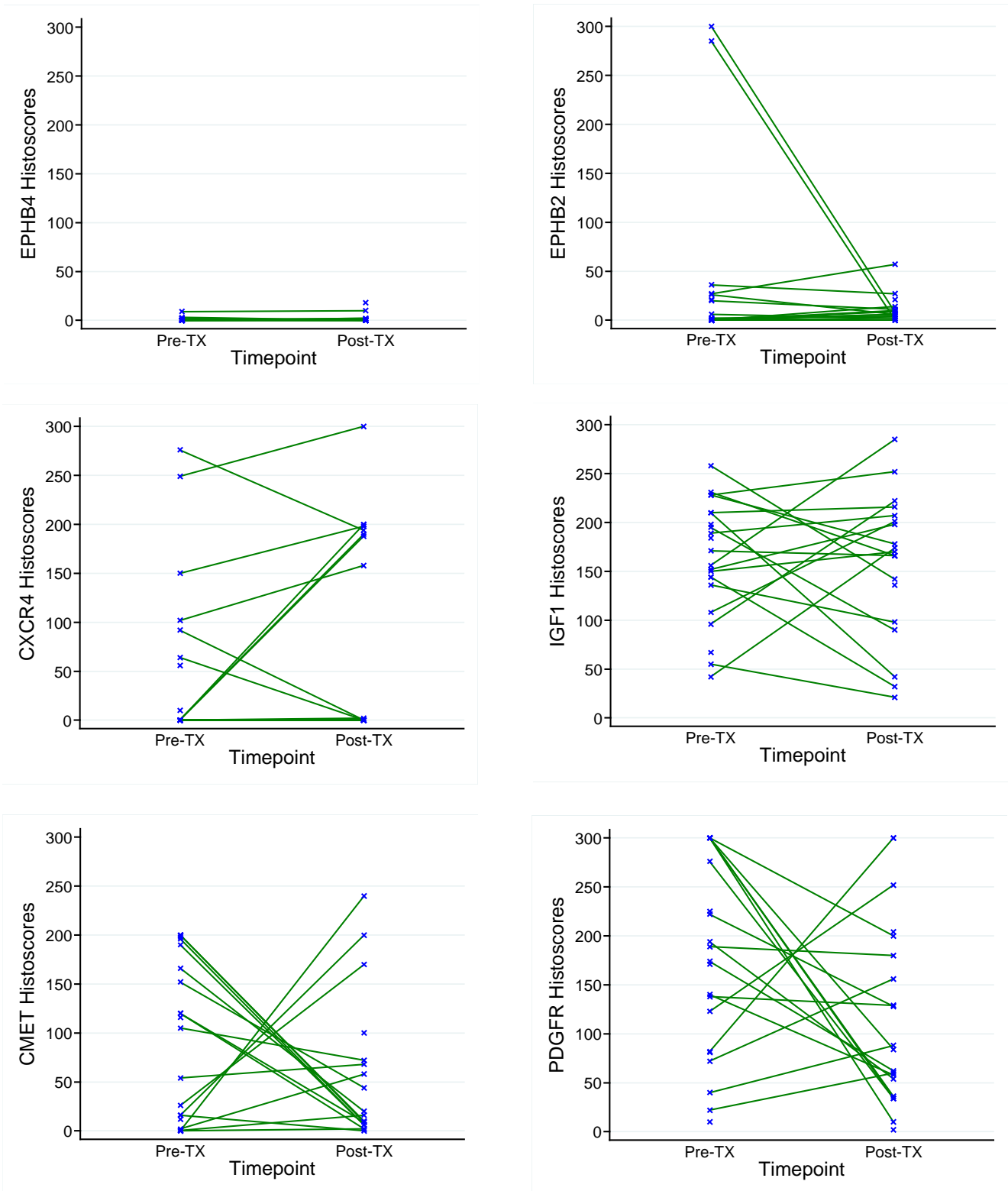
Table 5. Biomarker Histoscore Changes Pre and Post Chemotherapy with or without Trastuzumab

| Markers | Histoscore (Mean ± SE) | | Difference ² (Mean ± SE) | p-value ¹ |
|---------|------------------------|-----------|--|----------------------|
| | Pre-TX | Post-TX | | |
| EphB2 | 41.4±23.1 | 9.5±3.4 | -31.8±23.6 | 0.20 |
| EphB4 | 0.99±0.55 | 0.92±0.59 | -0.07±0.31 | 0.82 |
| CXCR4 | 54.9±22.1 | 84.1±25.9 | 29.2±21.4 | 0.19 |
| IGF-1R | 164±14.4 | 159±17.7 | -5.5±21.1 | 0.80 |
| c-MET | 92.0±19.7 | 54.8±18.3 | -37.2±33.0 | 0.28 |
| PDGFR | 187±23.9 | 110±20.2 | -76.9±36.5 | 0.051 |
| VEGFR1 | 119±25.1 | 45.4±8.6 | -73.7±23.8 | 0.007 |
| Ki67 | 98.2±6.9 | 60.7±14.6 | -37.5±12.4 | 0.008 |

¹ p value from paired t-test.

² Difference post treatment vs. pre treatment

Figure 6. Distribution of Biomarker Histoscores at Baseline and Post Chemotherapy with or without Trastuzumab



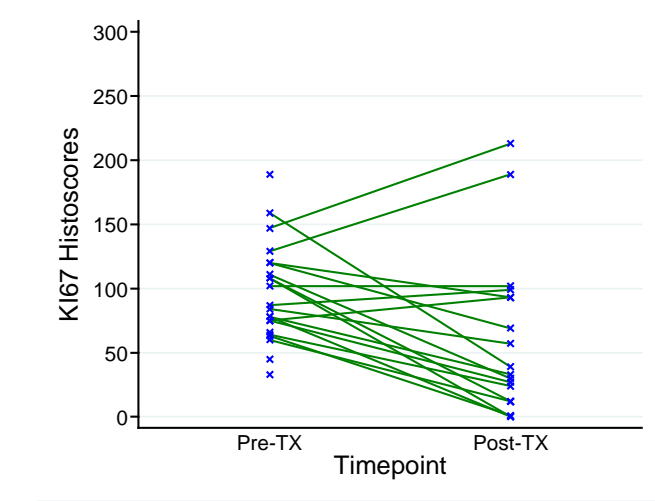
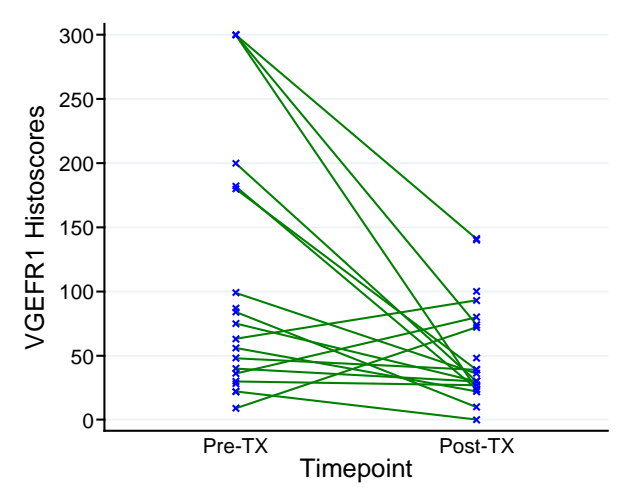
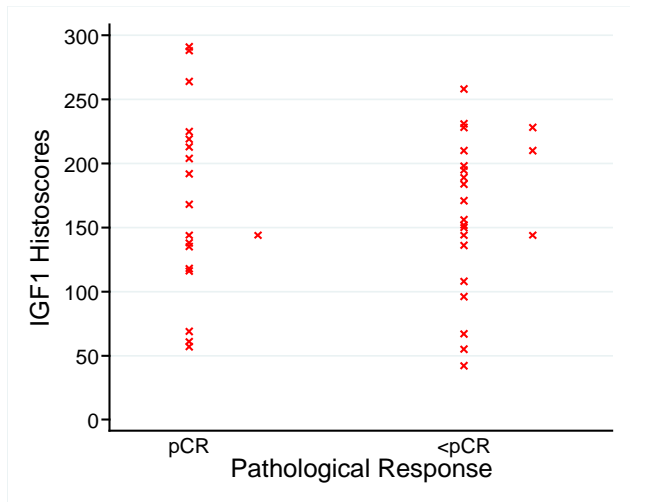
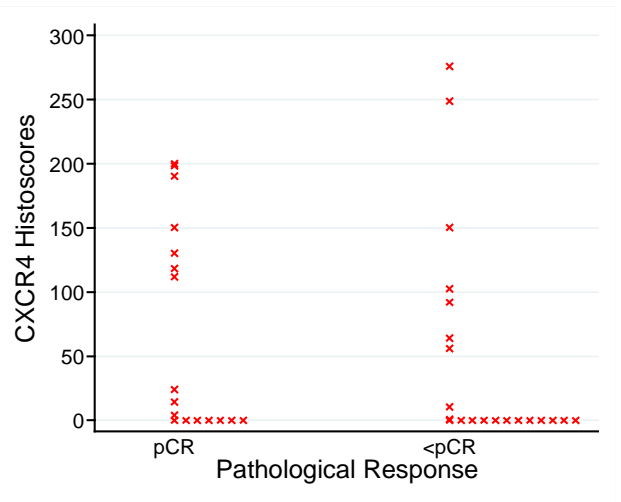
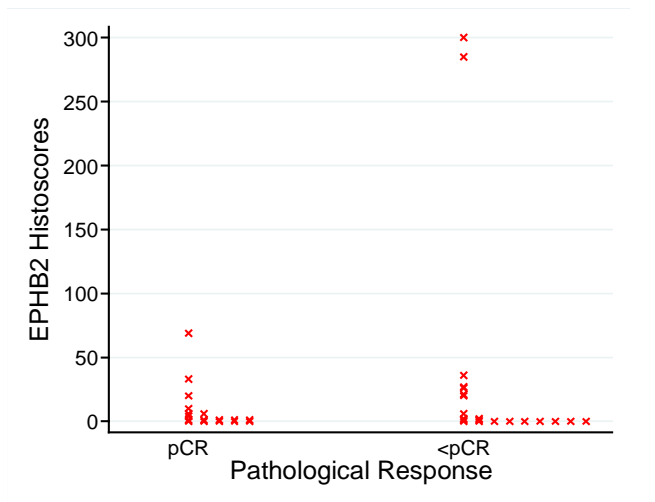
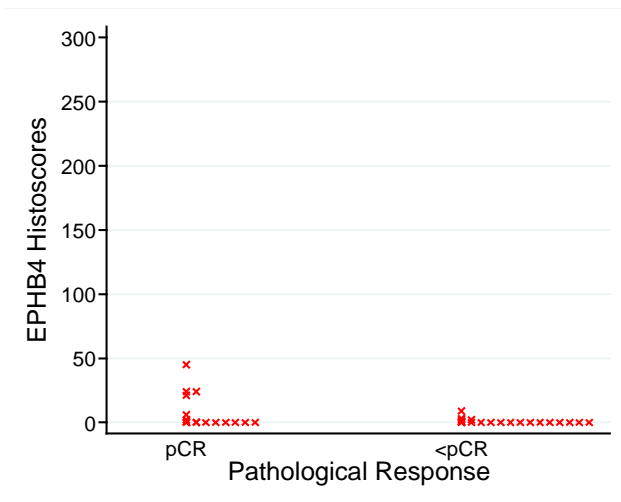
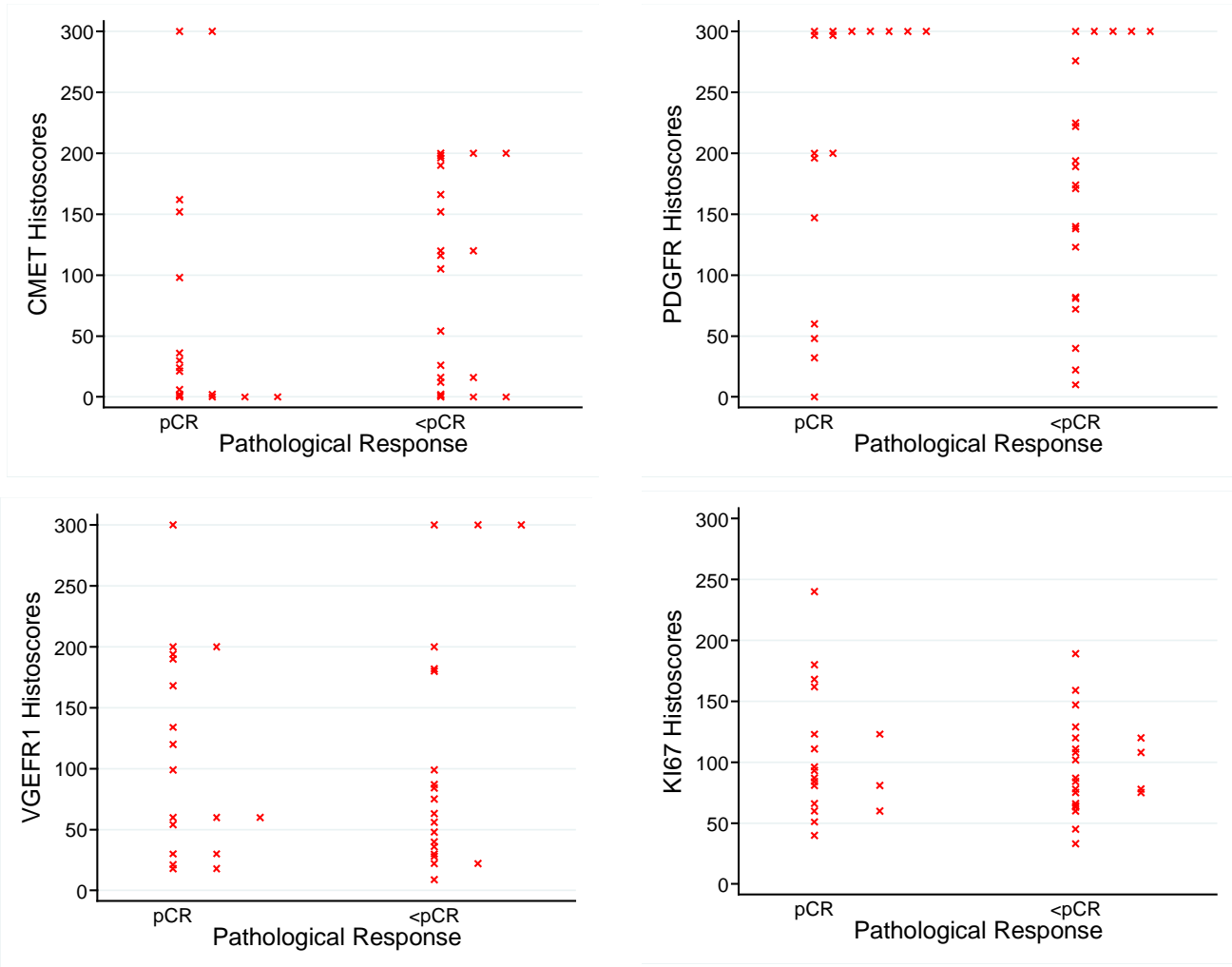


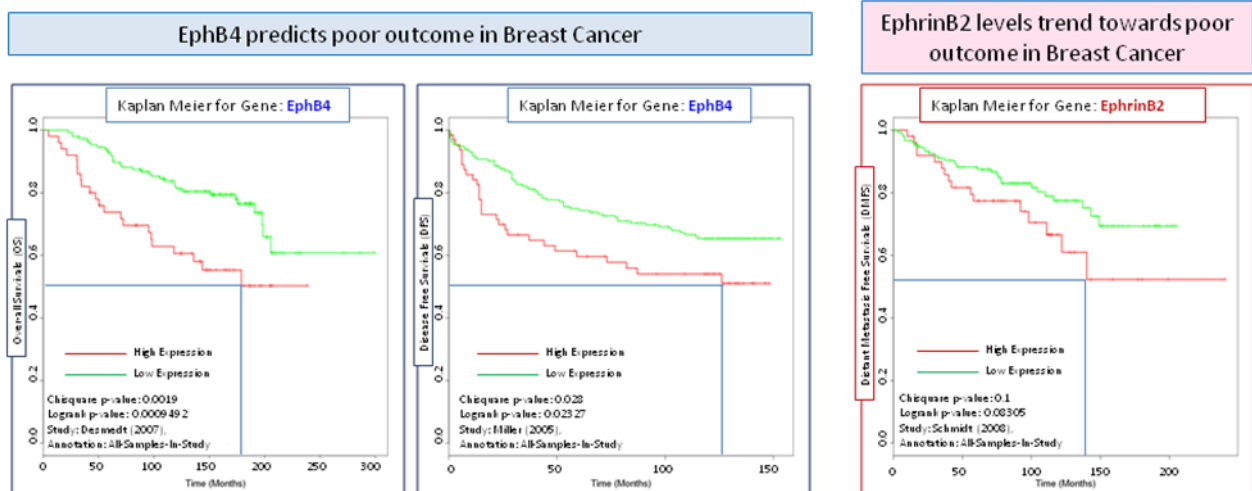
Figure 7. Distribution of Biomarker Histoscores by Response to Chemotherapy with or without Trastuzumab



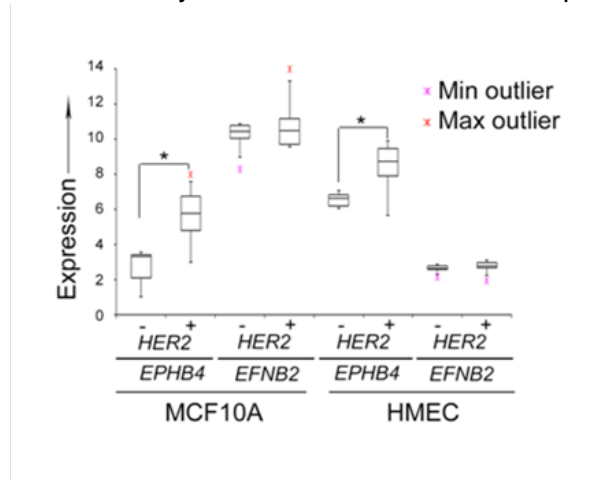


Task 3: Assess efficacy of EphrinB2-targeted therapy in HER2-driven transgenic mice

Task 3A. In a publicly available human breast cancer database, the expression of EphB4 and EphrinB2 and correlated with survival. Three different datasets were analyzed, and in each, the expression of EphB4 and EphrinB2 correlated with decreased survival.

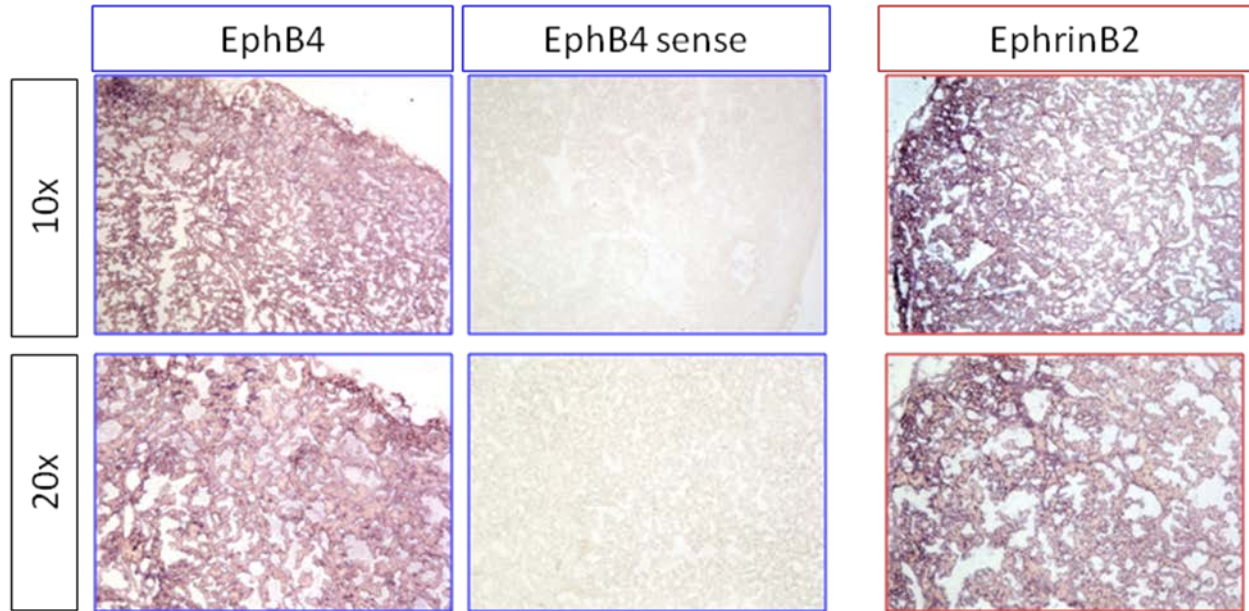


Task 3B. We next determined if HER2 specifically induces the expression of EphB4 and EphrinB2. Isogenic cell lines with stable expression of HER2 or empty vector were studied for eh gene expression with focus on EphB4 and EphrinB2. HER2 expressing cell line had higher expression of EphB4 and EphrinB2 compared to empty vector. Furthermore, the induction of EphB4 and EphrinB2 correlated directly. Thus HER2 induces both EphB4 and EphrinB2.



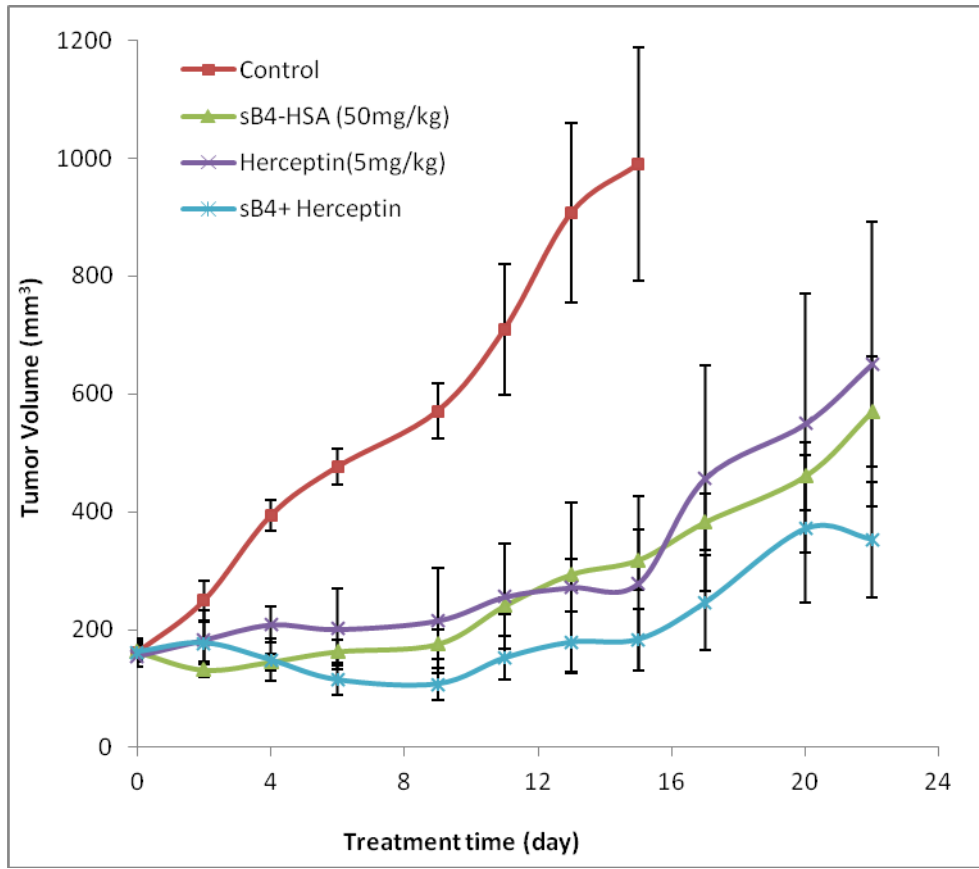
Box Whisker plot with 95% confidence intervals indicating the level of expression of indicated genes in MCF10A and HMEC breast tissue cell lines. Box whisker plots indicate median expression of gene in various cell lines (line in the box). The whiskers present an entire range of expression levels of gene and the ends of the whisker are set at $1.5 \times \text{IQR}$ (interquartile range) above the third quartile (Q3) and $1.5 \times \text{IQR}$ below the first quartile (Q1). If the Minimum or Maximum values are outside this range, then they are shown as outliers as detailed previously (Punj et al. 2009; Blood 113(22); 5660-5668). The expression of EPHB4 and ENFB2 in MCF10A and HMEC cells was significantly increased in Her2 knock-in cells while these genes are not statistically up-regulated in either cell lines.

Task 3C: EphB4 and EphrinB2 expression is induced in HER2 transgene expression in mouse mammary tissue: Transgenic mouse expressing HER2 under the MMTV promoter induced preferentially in mammary tissue leads to mammary tumor. Tumor samples were harvested and analyzed for the mRNA expression of EphB4 and EphrinB2 using in situ hybridization. Marked induction of EphB4 and EphrinB2 was observed. Control mRNA probe as expected had no background signal. Thus inclusion from the studies in task 3A,B,C show that HER2 induces EphB4 and EphrinB2 in vitro, in murine model and in human tumor tissue analysis.

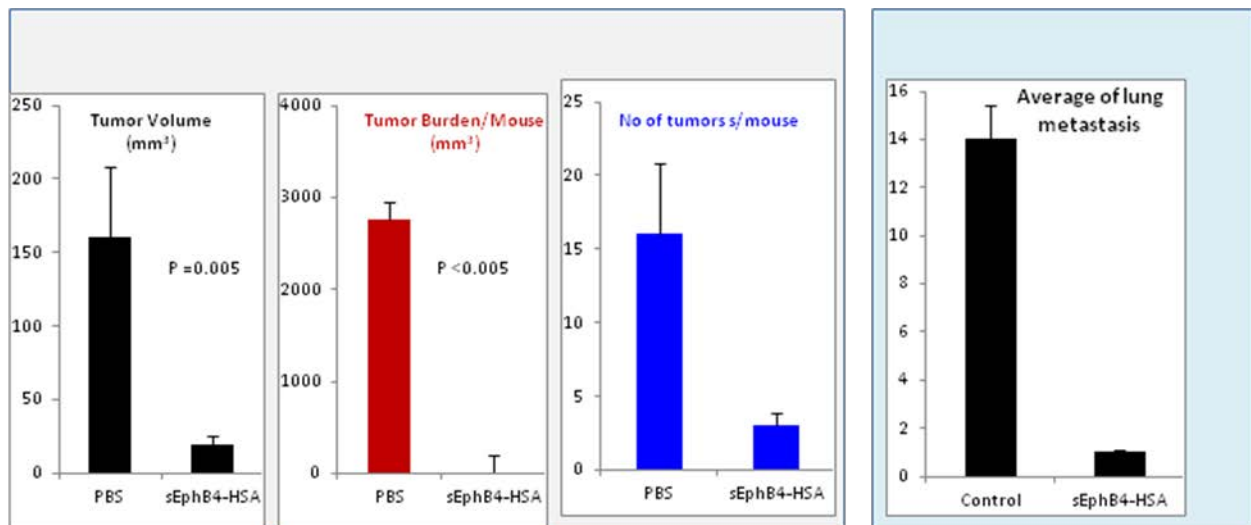


Task 3D. Does induction of EphB4 and EphrinB2 regulate HER2 positive breast cancer cell line proliferation and viability? HER2 positive breast cancer cell lines were seeded in vitro in multi-well plates and treated with the soluble form of EphB4 receptor that blocks EphB4-EphrinB2 interaction and thus functions as an antagonist of bidirectional signaling. Cell viability was measured on day 3. A dose dependent decrease in cell viability was observed in HER2-positive breast tumor cell lines indicating that EphB4-EphrinB2 provides survival or proliferative function. Data for Task3 thus far supported the investigation of sEphB4 in vivo

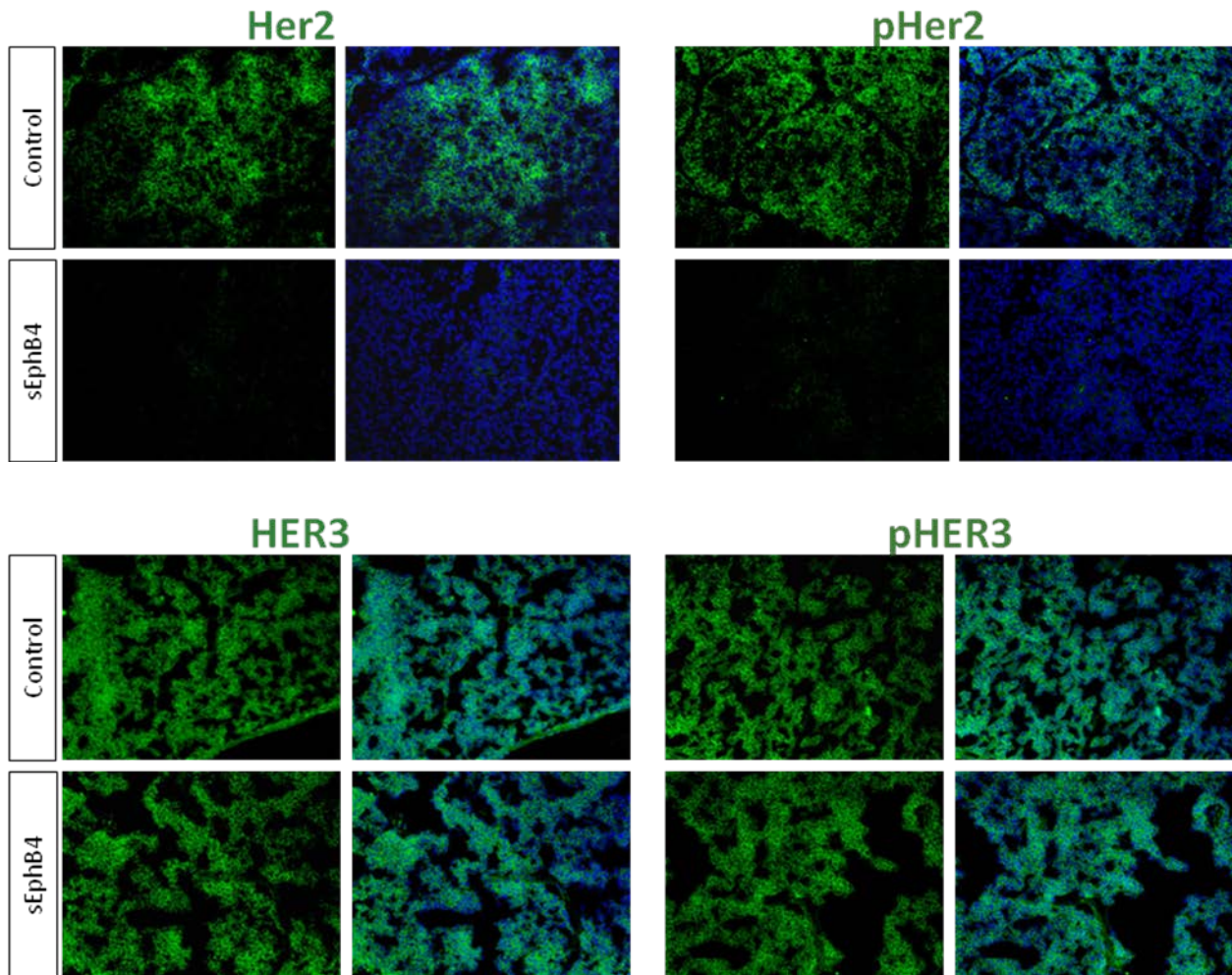
Task 3E: HER2 positive human breast cancer cell line shows tumor growth inhibition in vivo. H1419 tumor cell line was implanted in athymic mouse and allowed to establish. Mice were then randomly assigned to receive either sEphB4, trastuzumab or a combination of both. Tumor growth was measured twice or three times a week for the duration of the study. sEphB4 and trastuzumab both showed tumor growth inhibition and they were comparable to each other. Combination of both further reduced the rate of tumor growth. Thus sEphB4 has a direct anti-tumor effect in HER2-positive tumors.



Task 3F: Study EphB4 antagonist in HER2-positive spontaneous tumors in mouse. HER2 transgenic mouse were monitored until the development of mammary tumor. Mice were then treated with either sEphB4 or PBS. Tumors were measured over time for the total number of tumors, tumor size, cumulative tumor burden and the tumor metastasis. Tumor number, size, cumulative tumor burden and the tumor metastasis to the lungs were markedly reduced in the sEphB4 treatment group compared to the controls.



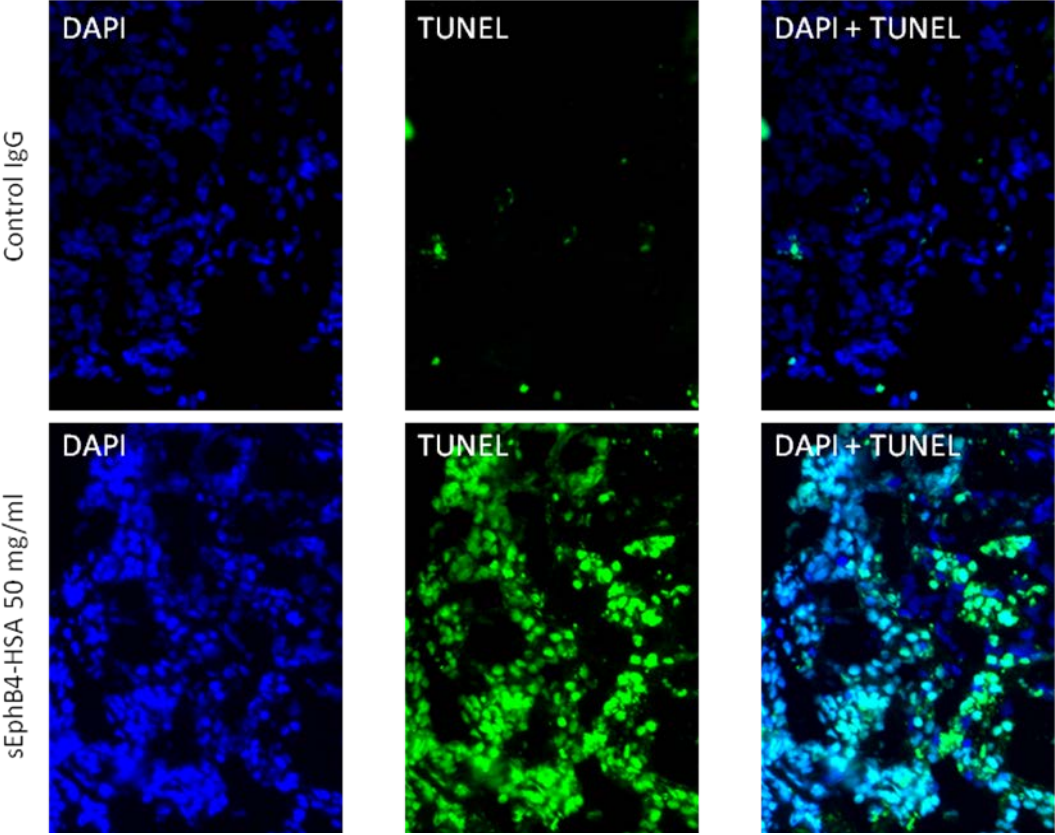
Task 3F: EphB4-EphrinB2 targeting with sEphB4 antagonist blocks the HER2 receptor activation: In order to study the mechanism of action of EphB4 in the efficacy in HER2-induced mammary tumor, we studied the status of HER2, EGFR1 and HER3 phosphorylation. sEphB4 markedly inhibited the phosphorylation of HER2 as well as EGFR1 but not HER3. Thus the effect is specific and directed to the HER2 oncogene. Inaction of the driver oncogene provides the strong rational to apply EphB4 targeted therapy. sEphB4 may thus be particularly effective when combined with HER2-targeted therapy or even more likely to be effective if HER2 is mutated and non-responsive to the tyrosine kinase inhibitor. These approaches will need to be studied in human trials.



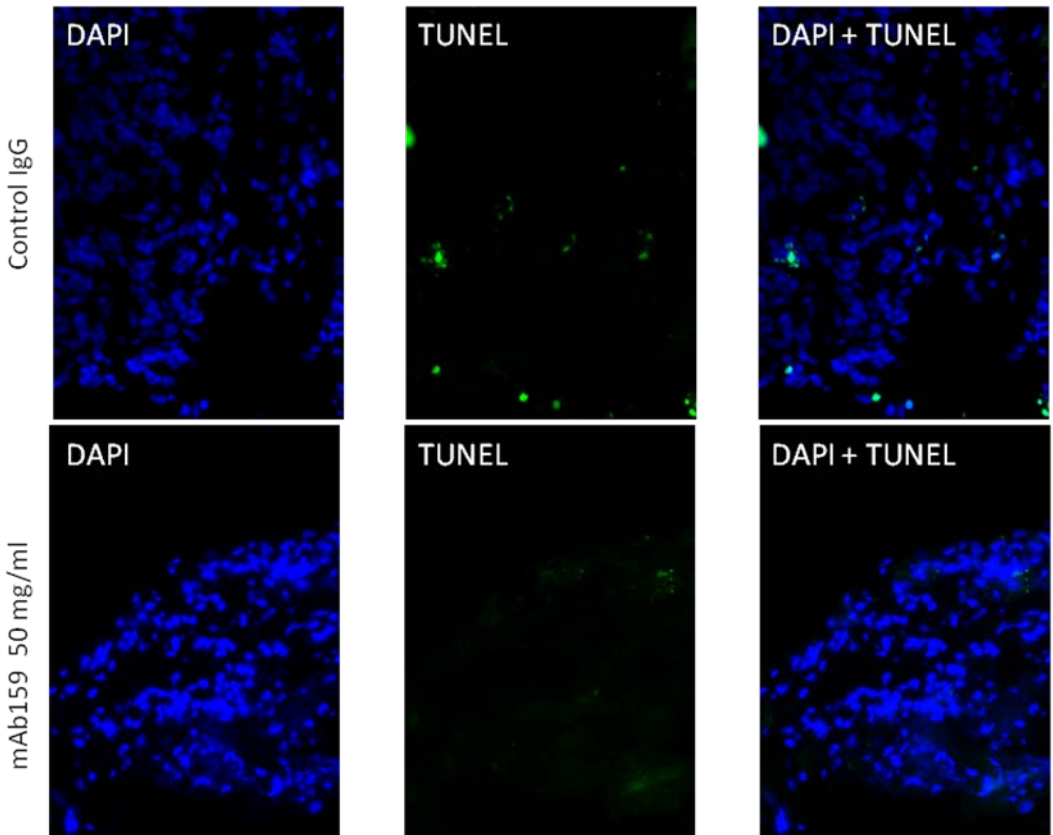
Task 3G: sEphB4 has direct antitumor activity in HER2 positive human tumor. In order to further document the potential utility of EphB4 targeted therapy in HER2 positive tumor, we studied freshly collected human tumor tissue and conducted ex-vivo efficacy study. sEphB4 or other test compounds were incubated with the tumor and 24 hr after treatment the tissue was harvested,

processed and studied for apoptosis using TUNEL assay. HER2-positive tumor showed marked apoptosis after sEphB4 treatment, while there was no apoptosis in control (MAb159) treated tumor. These results demonstrate the direct tumor specific effect of sEphB4 in HER2-positive tumors.

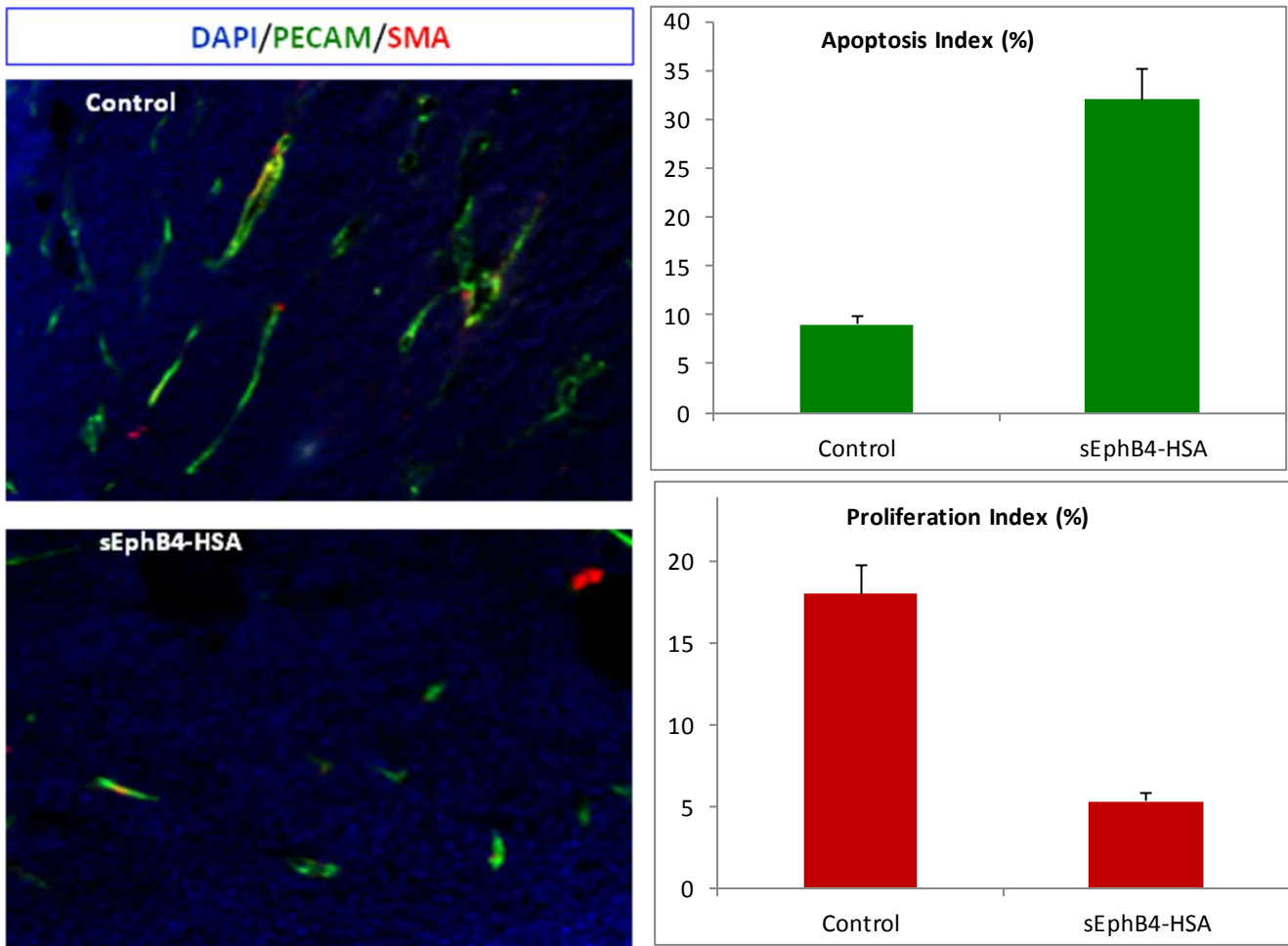
sEphB4-HSA induces apoptosis of human breast cancer 5789 tissue sections in 3-D histoculture



**mAb159 does not induce apoptosis of human breast cancer 5789
tissue sections in 3-D histoculture**

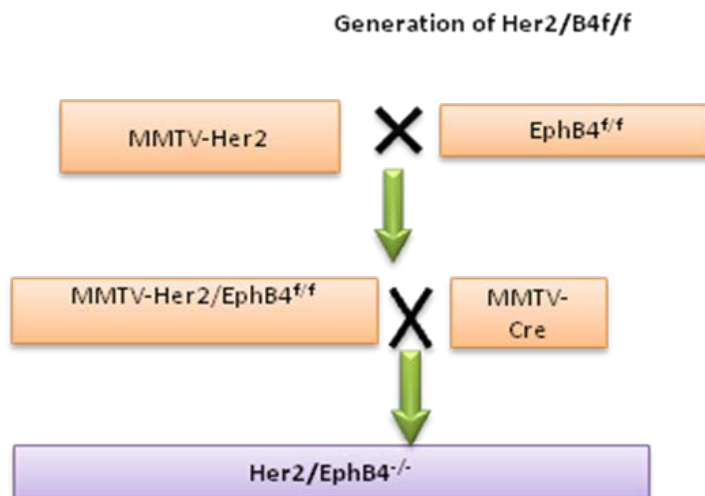


Task 3H: Analysis of tumor and normal tissue from above studies for activated HER2/HER family receptors, angiogenic markers, vessel density, signal transduction (PI3K, Akt, mTOR, S6), proliferation (Ki-67) and apoptosis (TUNEL) Tumor samples from the control and treated tumor samples were studied for various markers. sEphB4 markedly inhibited PI3K pathway including pAkt, pS6, Ki-67 and induced cell death by apoptosis.



Task 4: Generate and study mammary tissue-specific EphrinB2 and EphB4 knock-out mice using MMTV-Cre system

Task 4.A: Generate and study mammary tissue-specific EphrinB2 and EphB4 knock-out mice using MMTV-Cre system: The schema for the generation of HER2 transgenic mouse and concurrent deletion of EphB4 in the mammary gland is outlined below. Similar approach is applied to the development of EphrinB2 knock out in the mammary gland and crossed with HER2 overexpression to produce mammary tumor.



Task 4 B: Deletion of EphB4 and mammary gland: Deletion of Ephb4 in mammary gland did not alter the development of mammary gland.

Task 4 C. Determine the impact of EphB4 knock out on the time to tumor development, and rate of growth and risk of lung metastasis when mice from above task are crossed with NDL HER2 transgenic mice. Preliminary data reveals marked decrease in the development of tumor to less than 50% compared to 100% of controls, tumor lesions 36% of control. Survival is increased and a median has not yet been reached. (See table on next page)

| Genotype | Survival (preliminary data) | |
|--|-----------------------------|------------------------|
| | Number | Median survival (days) |
| MMTV-HER2; | 12 | 175 |
| MMTV-HER2;MMTV-Cre; EphB4 ^{-/-} | 19 | 236 + |

Task 5: Formulation of next steps to bring co-targeting of EphB4 and HER2 in HER2+ breast cancer

Significant progress has been made toward the clinic. An IND has been obtained for sEphbB4-HSA, an albumin stabilized soluble EphB4 decoy receptor that efficiently blocks EphB4/EphB2 signaling. A phase I study for solid tumors using this agent given intravenously is now open and accruing patients, with one head and neck tumor response seen.

KEY RESEARCH ACCOMPLISHMENTS:

- Characterization of demographic, ethnic, clinical, treatment, genetic predisposition variables in patients with HER2+ breast cancer receiving neoadjuvant therapy, determination of response rate and clinical predictors of response to therapy (see reportable outcomes).
- Optimization of antibodies and conditions to stain for several antigens on very small amounts of core biopsy tissue
- Development of a neoadjuvant tissue repository, currently with 102 total cases and 42 HER2+ cases, and now to 72+ HER2+ cases identified. This resource is unique in that pre and post treatment tissue is available with highly annotated immunohistochemical data. Also, a database with the demographic, clinical, treatment and pathological information is linked to the tissue repository.

- Establishment of EphB4 and EphB2 as adverse prognostic factors in human breast cancer and confirmation of a causal effect of HER2 expression driving EphB4 and EphrinB2 in human breast cell line and in mammary tissue in a transgenic mouse model.
- Demonstration that the targeting of EphB4-EphrinB2 using a soluble EphB4 blocking peptide in human HER2+ cells lead to decreased cell viability in vitro and in a mouse model. This effect is further potentiated with HER2 blockade using the approved humanized HER2 antibody trastuzumab (Herceptin). Furthermore, it is shown that EphB4 blockade inhibits HER2 and EGFR1 activation (phosphorylation), but not HER3. The effect of EphB4 blockade was extended to freshly collected human tumor tissue and conducted ex-vivo, showing decrease in proliferation, induction of apoptosis and inhibition of signal transduction (inhibition of PI3K, assessed by pAkt and pS6)
- Creation of a mammary tissue-specific EphrinB2 and EphB4 knock-out mice and demonstration that EphB4 knockout does not alter mammary gland development, but when crossed with HER2 transgenic mouse, decreases HER2-drive mammary tumor development
- Movement of EphB4 targeted soluble peptide (sEphB4-HSA) to the clinic with initiation of Phase I trial in solid tumors as a single agent.

REPORTABLE OUTCOMES:

1. Abstract presentation of the clinicopathological aspects of our neoadjuvant cohort that is supporting the tissue based studies :

Tripathy D, Ahmed S, Bahl P, Wang Y, Ji L, Ricker C, Weng Grumley J, Liu SV, Sener SF, Klipfel N, Kaur C. Neoadjuvant therapy response, subtype and BRCA status in an underserved population. 34th Annual San Antonio Breast Cancer Symposium (Abstr P3-14-21), 2011.

2. We have successfully applied for a proposal that is related to this strategy to co-target EphB4 and the Notch receptor, using an in-house developed antibody to the tumor-specific Notch ligands DLL-1 and DLL-4. (California Breast Cancer Research Program Project entitled "Co-Targeting the Notch and EphB4 Receptor in Breast Cancer" (CBCRP 18IB-0048). This project received the highest scientific score of all review submissions. Work on this project is now proceeding with cell line data being generated

on the combination EphB4 and DLL-1, 4 targeting with and without chemotherapy and animal studies initiated.

3. Phase I trial with soluble EphB4 is now ongoing at USC in multiple solid tumor types and showing safety tolerability and evidence of clinical activity at preliminary analysis.

CONCLUSION: Patients in our population (primarily Hispanic) exhibit the same patterns of response to neoadjuvant chemotherapy for breast cancer, with higher pathological complete response (pCR) rates seen in triple negative and HER2+ breast cancer, and with higher pCR rates with the use of trastuzumab when added to chemotherapy for HER2+ breast cancer. In the trastuzumab treated cohort, there were no biomarkers that predicted pathological response, but VEGFR1 did change significantly from pre to post treatment in the nonresponders, as did (as expected) Ki67. In the overall cohort treated with chemotherapy with or without trastuzumab, again no biomarker predicted response, but VEGFR1 and PDGFR as well as Ki67 decreased following therapy. This suggests that downstream markers of EphB4 are modulated downward by therapy, although it is not clear that this effect is clearly mediated via EphB4/EphB2.

Human breast cancer expression databases confirm earlier findings that both EphB4 and EphrinB2 are adverse prognostic factors. Both in vivo and in vitro models demonstrate that EphB4/EphrinB2 blockade using a soluble EphB4 construct can lead to growth inhibition of HER2-positive breast cancer in vitro and in vivo. The effect is accentuated with co-targeting with the HER2 antibody trastuzumab. EphB4 blockade also inhibits growth, promotes apoptosis and inhibits downstream signaling (pAkt, pS6) in human primary tumor explants. EphB4 mammary gland-targeted knockout does not affect gland development, but when crossed into a HER2 transgenic model, markedly reduces spontaneous mammary tumor formation.

Together, these form a solid foundation for the co-targeting of HER2 and EphB4. These studies will lay the foundation for clinical trials co-targeting EphB4 and HER2. EphB4-targeted therapy is now here with a Phase I trial approved our institution with our in-house developed inhibitor, a ligand-blocking soluble albumin-stabilized EphB4 peptide termed sEphB4-HSA, so we are well positioned to transition this strategy of combined EphB4 and HER2 blockade, or co-targeting to the clinic.

REFERENCES:

1. Tripathy D, Ahmed S, Bahl P, Wang Y, Ji L, Ricker C, Weng Grumley J, Liu SV, Sener SF, Klipfel N, Kaur C. Neoadjuvant therapy response, subtype and BRCA status in an underserved population. 34th Annual San Antonio Breast Cancer Symposium (Abstr P3-14-21), 2011.

APPENDICES:

Appendix 1: Statement of Work

Appendix 2: Poster of above referenced abstract.

Statement of Work

Title:

Co-Targeting HER2 and EphB4 Pathways

Study Site Information:

University of Southern California

Initiating Principal Investigator:

Parkash Gill, MD

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Partnering Principal Investigator:

Debasish Tripathy, MD

University of Southern California

Department of Medicine, Division of Hematology

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Project Tasks:

Task 1: Obtain tissue and clinical data for analysis of HER2+ breast cancer treated with neoadjuvant trastuzumab-based therapy (Months 1-20):

- Obtain human subjects DOD CDMRP and USC IRB approval for consent waiver to obtain tissue blocks and clinical information (Months 1-8). Tripathy
- Identify screening patients, then identify eligible patients and enter clinical data into database (Months 9-18). Tripathy
- Obtain tissue blocks of pretreatment core biopsies and post treatment surgical specimens (Months 10-20) Tripathy

Task 2: Analysis of human HER2+ breast cancer tissue samples for angiogenic markers before and after trastuzumab-based therapy in the context of response (Months 1-20):

- Section and stain tissue for H&E and immunohistochemical (IHC) analysis with appropriate antibodies (Months 10-20). Tripathy
- Perform pathological analysis for assessment of response (Months 11-20). Tripathy
- Order antibodies, standardize IHC protocols, perform staining on tissue sections (Months 1-6). Gill

- Perform IHC staining (EphrinB, EphB1/2/3/4/6, MVD, VEGF, VEGFR-1, 2, 3, PDGFR, cMET, IGF-1R) (Months 11-20). Gill
- Perform statistical analysis of baseline markers in relations to response and pre/post marker level change upon therapeutic exposure (Months 12-22). Tripathy

Task 3: Assess efficacy of EphrinB2-targeted therapy in HER2-driven transgenic mice: (Months 3-20)

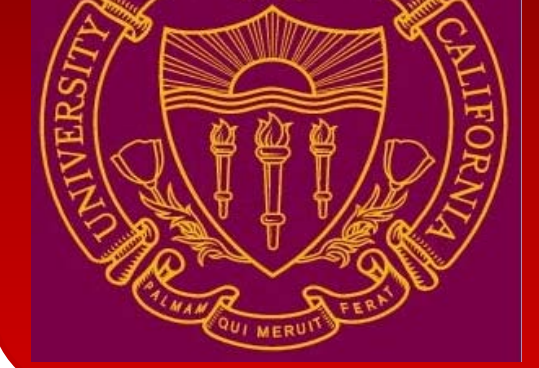
- Prevention and efficacy studies in vivo of soluble EphB4 fused to albumin (sEphB4HSA) in HER2-driven transgenic mice (Months 3-12). Gill
- Analysis of tumor and normal tissue from above studies for activated HER2/HER family receptors, angiogenic markers (EphrinB2, EphB1,2,3,4,6, VEGF, VEGFR-1, 2, 3 and PDGFR), vessel density, signal transduction (PI3K, Akt, mTOR, S6), proliferation (Ki-67) and apoptosis (TUNEL) (Months 12-20). Gill
- Assessment of the effects of sEphB4HSA on the same markers along with cell viability and DNA incorporation in breast cancer cell lines and mammosphere preps (Months 12-18). Gill

Task 4: Generate and study mammary tissue-specific EphrinB2 and EphB4 knock-out mice using MMTV-Cre system: (Months 3-22)

- Generate tissue-specific knock out mice for EphrinB2 and EphB4 (Months 3-12). Gill
- Determine the impact of EphrinB2 and EphB4 knock out on the time to tumor development, and rate of growth and risk of lung metastasis when mice from above task are crossed with NDL HER2 transgenic mice (Months 12-22). Gill

Task 5: Synthesize data across clinical tissue and preclinical platforms for presentation and toward the formulation of a dual human tissue and in vivo/in vitro-modeled and informed clinical protocol

- Review and analyze clinical tissue and laboratory data jointly (Months 22-24). Gill and Tripathy
- Formulate a clinical strategy with detailed treatment protocol and eligibility criteria that are informed by dual platform results (Months 22-24). Gill and Tripathy



Abstract

Preoperative (neoadjuvant) chemotherapy is typically used for larger operable breast cancer cases, and the degree of pathological response correlates with long term outcome. Therapeutic response also depends on biological and molecular subtype and is increasingly studied in the research setting to identify prognostic biomarkers and potential therapeutic targets. Little is known about the interactions of neoadjuvant response with biomarker subtypes and genetic predisposition in underserved and minority populations.

Methods

IRB approval was obtained to capture demographic, clinico-pathological and genetic testing data on patients diagnosed with invasive breast cancer and treated with preoperative chemotherapy and definitive surgery between 2005 and 2010 at Los Angeles County Medical Center, which serves a primarily Hispanic and indigent population. Treatment followed NCCN guidelines with the exception that not all patients with HER2+ disease received trastuzumab. Genetic counseling and testing has been available at this center since 2007. Pathological complete response (pCR) was defined as no residual invasive disease in breast or axillary nodes.

Statistical Methods: Pearson's Chi-square test was used to examine whether the distribution of patient and disease characteristics were similar among the patients from different biomarker sub-types ("HER2 -, ER or PR + [HR+]", "HER2 -, ER - and PR - [HR-]" and "HER2 + [FISH ratio ≥2.0 or IHC 3+]". When the number of patients was limited in any sub-group, Fisher's Exact test was used instead. Similarly, Chi-square test or Fisher's Exact test were also used to examine whether there was an association between different patient and disease characteristics and the achievement of pCR. Logistic regression analyses were performed to assess the individual contribution of each variable of interest on the achievement of pCR, with or without adjusting for the biomarker sub-types. Backward selection method was used to select a final multivariate logistic regression model, with the variables having a p value of >0.15 successively dropped from the models.

Results

Table 1. Patient / Disease Characteristics, pCR Rates and Odds Ratios (OR) of pCR

| Variable | N | pCR (%) | Univariate OR (95% CI) | p-value | OR Adjusted for Subtype | p-value | Multivariate OR | p-value |
|-----------------|-----|---------|------------------------|---------|-------------------------|---------|------------------|---------|
| All Pts | 102 | 28.4 | | | | | | |
| Age <50 years | 60 | 20.0 | Reference | | Reference | | Reference | |
| Age ≥50 | 42 | 35.7% | 2.2 (0.91, 5.4) | 0.079 | 2.5 (0.95, 6.5) | 0.064 | 2.4 (0.83, 6.8) | 0.10 |
| BRCA Normal | 36 | 27.8% | Reference | | | | Not In Model | |
| BRCA Mutated* | 9 | 11.1% | 0.33 (0.036, 2.9) | 0.32 | 0.34 (0.034, 3.4) | 0.36 | | |
| BRCA Untested | 57 | 28.1% | 1.01 (0.40, 2.6) | 0.97 | 0.76 (0.28, 2.1) | 0.59 | | |
| Hispanic | 80 | 26.3% | Reference | | Reference | | Not In Model | |
| Non-Hispanic | 22 | 27.3% | 1.1 (0.36, 3.0) | 0.92 | 1.2 (0.40, 3.9) | 0.71 | | |
| cT1, cT2 | 24 | 37.5% | Reference | | Reference | | Reference | |
| Other | 78 | 23.1% | 0.50 (0.19, 1.3) | 0.17 | 0.41 (0.14, 1.2) | 0.10 | 0.37 (0.11, 1.3) | 0.12 |
| cN0 | 25 | 40.0% | Reference | | Reference | | Not In Model | |
| cN1-3 | 77 | 22.1% | 0.43 (0.16, 1.1) | 0.082 | 0.41 (0.14, 1.2) | 0.099 | | |
| Grade I/II | 29 | 24.1% | Reference | | Reference | | Not In Model | |
| Grade III | 73 | 27.4% | 1.2 (0.44, 3.2) | 0.74 | 0.49 (0.15, 1.7) | 0.26 | | |
| Mastectomy | 87 | 20.7% | Reference | | Reference | | Reference | |
| Lumpectomy | 15 | 60.0% | 5.8 (1.8, 18) | 0.003 | 8.5 (2.2, 33) | 0.002 | 9.5 (2.2, 44) | 0.002 |
| HER2 -, HR+ | 35 | 8.6% | Reference | | | | Ref | 0.001 |
| Triple Negative | 25 | 24.0% | 3.4 (0.75, 15) | 0.11 | | | 4.5 (0.87, 23) | 0.073 |
| HER2 + | 42 | 42.9% | 8.0 (2.1, 30) | 0.002 | | | 15 (2.9, 74) | 0.001 |
| HER2 - | 60 | 15.0% | | | | | | |
| HER2+ | 42 | 42.9% | | | | | | |
| HR+ | 56 | 17.9% | | | | | | |
| HR - | 46 | 37.0% | | | | | | |

* 7 BRCA1 and 2 BRCA2 mutations

Figure 1: Distribution of Ethnicity

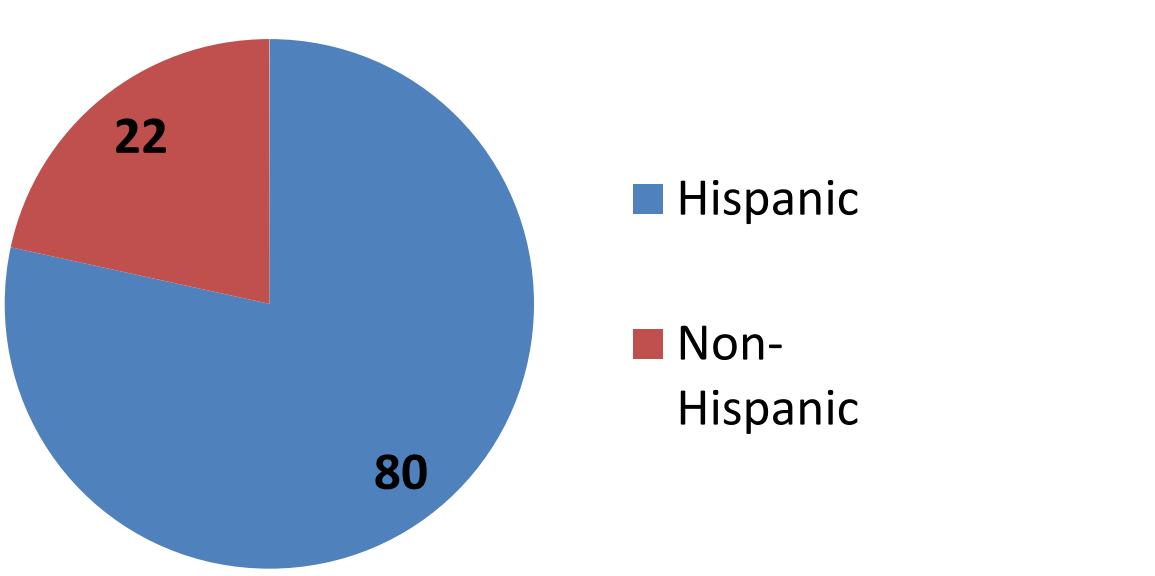


Figure 2: Distribution of Biomarker Subtype

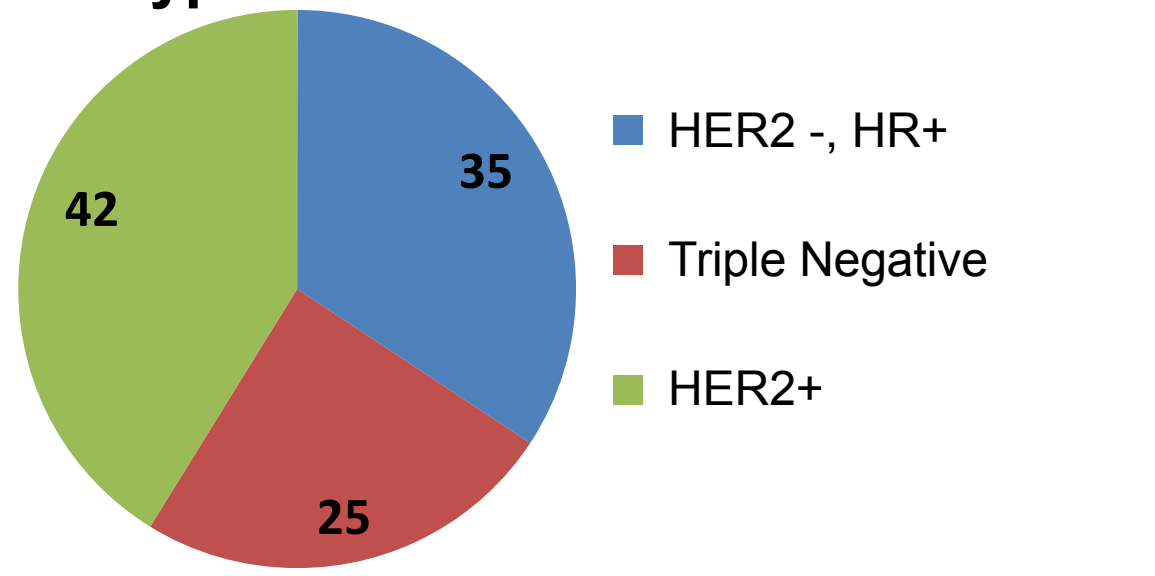


Figure 3: pCR by Age

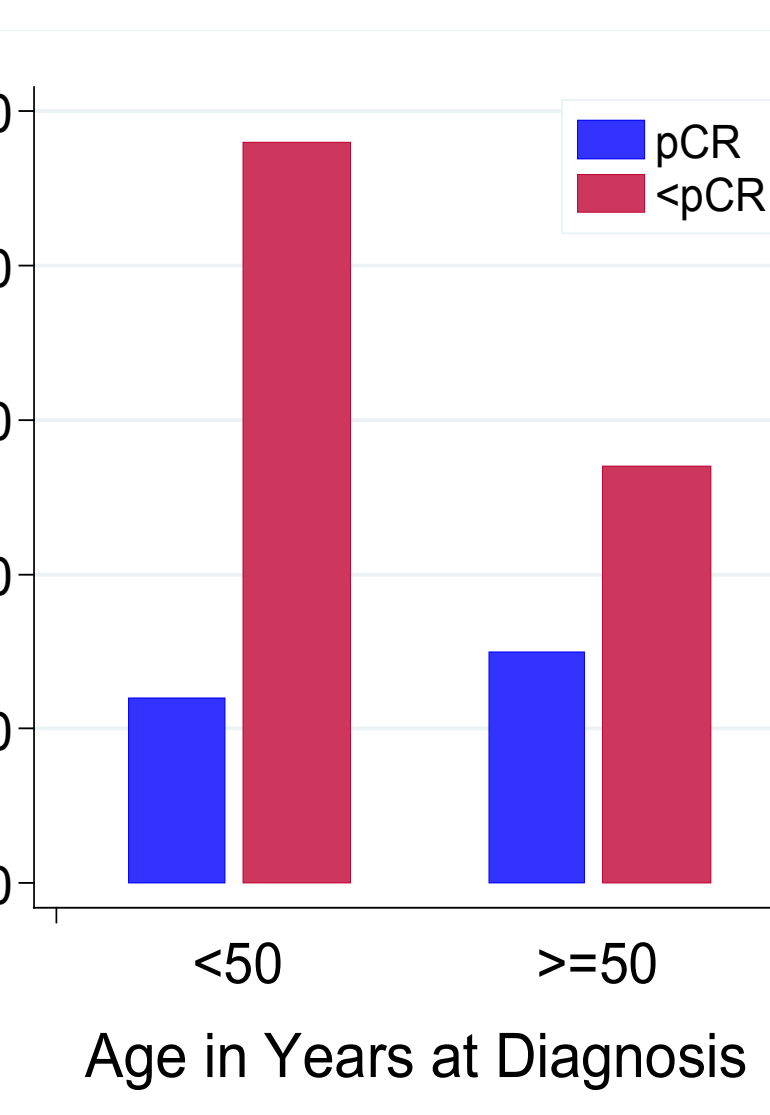
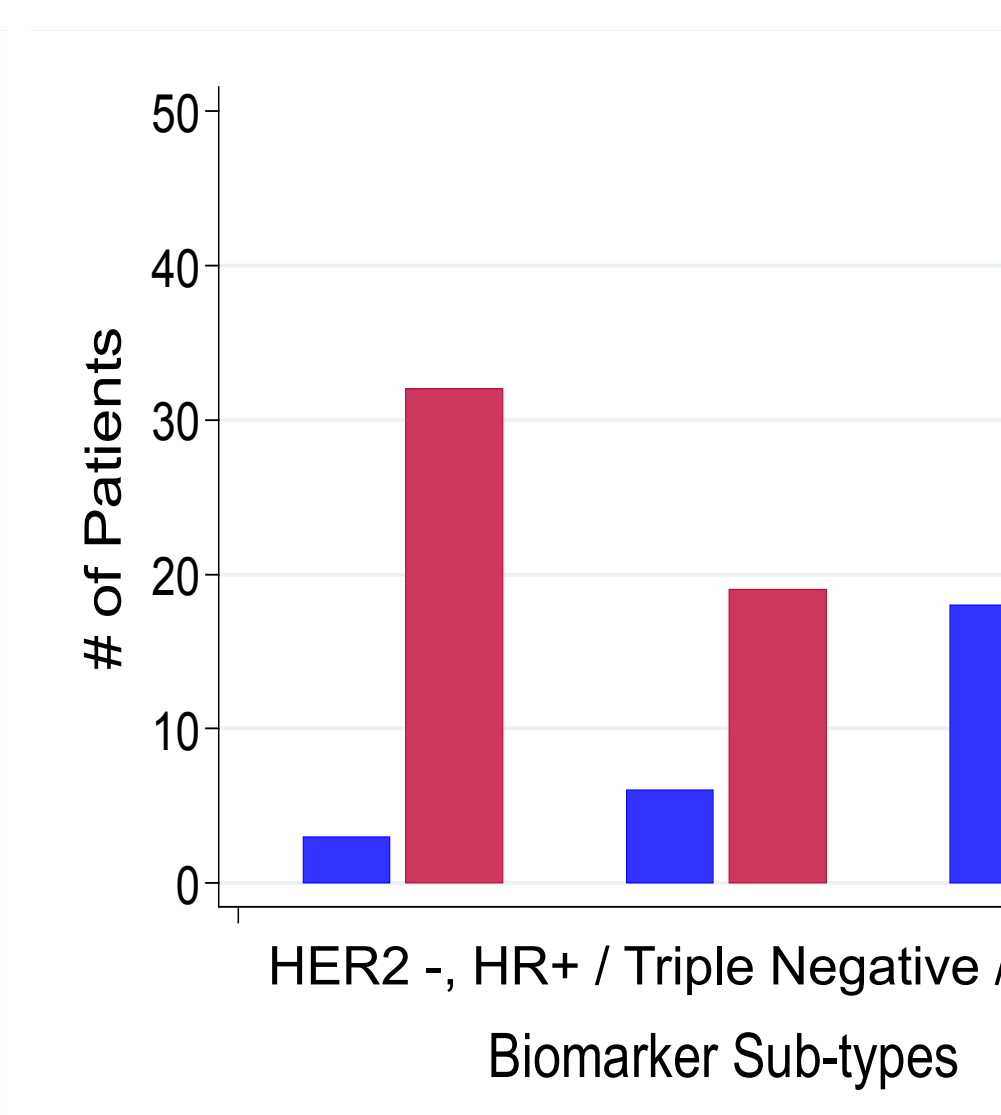


Figure 4: pCR by Biomarker



Conclusions

In this underserved cohort, with 44% undergoing genetic testing, significantly higher pCR rates were seen in HER2+ and triple negative and lumpectomy cases, with a trend seen in older patients and smaller tumors. There was an unexpected trend of lower pCR rate seen in BRCA mutation carriers (pCR OR 0.33), albeit with small numbers. No differences were seen in pCR rates in Hispanic cases compared to other ethnicities. Further tissue analyses are planned to examine established and novel markers and to define exploratory markers that could be used for decision-making and target discovery in larger datasets within this population.