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**Title:** Relationship between CCL5 and TGF $\beta$ 1 in breast cancer

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## Abstract

**Purpose** Investigate circulating CCL5 in breast cancer patients and healthy controls, along with gene expression levels in corresponding tumour tissue and isolated primary stromal cells. Hormonal control of CCL5, and a potential relationship with TGF $\beta$ 1, was also investigated. **Methods** Circulating levels of CCL5 and TGF $\beta$ 1 were measured in 102 breast cancer patients and 66 controls using ELISA. Gene expression levels (CCL5, CCR5, TGF $\beta$ 1, TGF $\beta$ RII) were quantified in corresponding tumour tissue (n=43), normal tissue (n=16), and isolated tumour (n=22) and normal (n=3) stromal cells using RQ-PCR. CCL5 and circulating menstrual hormones (LH, FSH, Oestradiol, Progesterone) were analysed in serum samples from healthy, premenopausal volunteers (n=60). **Results** TGF $\beta$ 1 was significantly higher in breast cancer patients (Mean(SEM) 27.4(0.9) ng/ml) compared to controls (14.9(0.9) ng/ml). CCL5 levels decreased in the transition from node negative (59.6(3.7) ng/ml) to node positive disease (40.5(6.3) ng/ml) and increased again as the number of positive lymph nodes increased ( $\geq 3$  positive 50.95(9.8) ng/ml). A significant positive correlation between circulating CCL5 and TGF $\beta$ 1 ( $r=0.423$ ,  $p<0.0001$ ) was observed, and mirrored at the gene expression level in tumour tissue from the same patients ( $r=0.44$ ,  $p<0.001$ ). CCL5, CCR5 and TGF $\beta$ 1 expression was significantly higher in tumour compared to normal breast tissue ( $p<0.001$ ). A significant negative correlation was observed between circulating CCL5, Oestradiol and Progesterone ( $r= -0.50$ ,  $r= -0.39$  respectively,  $p<0.05$ ). **Conclusion** CCL5 expression is elevated in the tumour microenvironment. The data support a role for hormonal control of circulating CCL5 and also highlight a potentially important relationship between CCL5 and TGF $\beta$ 1 in breast cancer.

## **Introduction**

A connection between inflammation and cancer was reported as early as 1863 by Virchow, who observed cancer developing in sites of chronic inflammation<sup>1</sup>. Tumours seem to seize molecular pathways seen in wound healing and as a consequence appear as “wounds that do not heal”<sup>2</sup>. However, the underlying molecular mechanisms facilitating the interconnection of inflammation and cancer remain poorly understood. CCL5(RANTES) is a chemotactic cytokine that plays an important part in inflammation through activation of T cells, monocytes, dendritic cells, natural killer cells, eosinophils and basophils<sup>3</sup>. An association between CCL5 and multiple cancer types has been reported, with the most striking findings reported in relation to breast cancer<sup>4</sup>. CCL5 binds to multiple receptors including CCR1, CCR3 and CCR4, with CCR5 recognised as its principal receptor<sup>5</sup>.

Conflicting reports exist in relation to the role of CCL5 in breast cancer progression. On a systemic level, Niwa et al found elevated plasma levels of the chemokine using ELISA in breast cancer patients compared to healthy controls, and reported a correlation with disease stage<sup>6</sup>. Another group also observed significantly elevated serum CCL5 in breast cancer patients compared to healthy controls, although no significant change was detected between patients with metastatic and non-metastatic disease<sup>7</sup>.

Using immunohistochemistry, tissue from patients with advanced breast carcinoma was reported to have elevated levels of CCL5<sup>8</sup>, with the protein rarely found in biopsies taken from healthy patients. Also joint CCL5 and CCL2 expression in the same breast tumour tissues has been correlated with more advanced disease<sup>9</sup>. In an in vivo model of breast cancer, tumours secreting lower levels of CCL5 were shown to have reduced metastatic potential<sup>10</sup>. Tumour derived CCL5 has also been implicated

in reduced T-cell response and shown to support *in vivo* growth of murine mammary carcinoma<sup>11</sup>. In contrast, Kurt et al reported that tumour-derived CCL5 on its own had no role in breast cancer progression<sup>12</sup>.

CCL5 protein expression at diagnosis has been correlated to clinical outcome in stage II patients, suggesting a potential role for the chemokine as a biomarker for the disease independent of oestrogen receptor- $\alpha$  (ER- $\alpha$ ) status<sup>13</sup>. In combination with ER status the prognostic strength of CCL5 was greatly improved in Stage II patients<sup>13</sup>. Another study also reported an interesting link between oestrogen and CCL5 in the context of atherosclerosis<sup>14</sup>, where a significant decrease in circulating CCL5 was found after three months of Estradiol replacement and raloxifene therapy<sup>14</sup>. This is interesting considering raloxifene has been shown to reduce risk of invasive breast cancer<sup>15, 16</sup>. Given the pivotal role of Oestradiol in disease progression, a potential link between circulating hormone levels and CCL5 warrants further investigation.

Transforming growth factor- $\beta$ 1(TGF $\beta$ 1) is a well-established factor in tumourigenesis<sup>17</sup>. TGF $\beta$ 1 signalling is involved in epithelial to mesenchymal transition, angiogenesis, suppression of the immune response and metastasis<sup>18</sup>. It is thought to act as a tumour suppressor in early stage disease and switch to tumour promotion in later stage breast cancer<sup>19, 20</sup>. Elevated systemic levels of TGF $\beta$ 1 were shown to drop in breast cancer patients following removal of the tumour<sup>21</sup> and a significant relationship between systemic levels prior to cancer treatment and overall survival has also been reported<sup>22</sup>.

The aim of this study was to further investigate a potential relationship between CCL5 and breast cancer, both at the systemic and tumour tissue level. Serum CCL5 levels were observed to decrease in the switch from node negative to node positive disease, and increase again as the number of positive lymph nodes increased. This pattern has

previously been described for TGF $\beta$ 1<sup>19</sup>, and led to further investigations into a potential relationship between the two factors. Investigation of a relationship between CCL5 and circulating menstrual hormones was also performed.

## **Materials and Methods**

### **Study cohort**

The study was approved by the institutional ethical committee. Preoperative blood samples were obtained with informed consent from 102 breast cancer patients (Table 1). Blood samples from healthy female volunteers (n=66) with no past or present history of malignant or inflammatory conditions were collected in an outpatient facility.

To investigate a relationship with circulating hormones, serum samples were obtained from 15 healthy premenopausal volunteers every week for four consecutive weeks (n=60) to investigate the relationship between CCL5 and circulating menstrual hormones.

All blood samples were collected in Vacutainer Serum Separator Tubes II (Becton Dickinson), allowed to clot for 30 min and centrifuged at 2,000 rpm @ 4°C for 10 min. Serum was then stored at -80°C until required.

### **Chemokine detection**

Circulating levels of CCL5 and TGF $\beta$ 1 were measured in 168 samples (102 breast cancer, 66 healthy controls) using Quantikine® Enzyme Linked Immunosorbent Assay (ELISA) kits (R&D Systems).

### **Analysis of circulating menstrual hormones**

Leutinsing Hormone (LH), Follicular Stimulating Hormone (FSH), Oestradiol and Progesterone were measured in serum samples (n=60) by direct chemiluminescence, using Siemens ADVIA® Centaur™ Immunoassay System. The mid-cycle phase was determined by an LH peak, and the mid-luteal phase established by a peak in Progesterone.

### **Analysis of gene expression**

Corresponding tissue specimens (n=43) were available on a subset of the breast cancer patients from whom serum samples had been obtained. Breast tissue obtained from breast reduction mammoplasty (n=16) served as normal controls. At the time of harvest breast tissue was snap frozen in liquid nitrogen and homogenized in 1 ml QIAzol reagent (Qiagen Ltd.). Total RNA was then isolated using RNeasy® tissue mini kit (Qiagen Ltd) according to manufacturer's instructions, including an on-column DNase treatment step.

RNA was reverse transcribed using SuperScript III reverse transcriptase enzyme (Invitrogen). Real-time quantitative PCR (RQ-PCR) was carried out using an ABI Prism 7000 (Applied Biosystems) targeting CCL5, CCR5, TGFβ1 and TGFβRII. Results were normalized to endogenous control genes MRPL19 and PPIA<sup>23</sup> and expression levels of the respective genes in tumour tissues compared to normal tissues.

### **Culture of primary stromal cells**

To investigate gene expression on a cellular level, fresh breast tissue specimens were harvested from patients undergoing surgery with prior informed consent. Breast tissues obtained from reduction mammoplasty served as normal controls. All tissue

specimens were washed twice in phosphate buffered saline (PBS), supplemented with 200U penicillin/200µg/ml streptomycin. They were minced finely using crossed scalpels and digested for 12-18 hrs in 0.1% Collagenase Type III (Biochem Corp) at 37°C in Dulbecco's Modified Eagle's Medium (DMEM) supplemented with 10% heat inactivated FBS. Following differential centrifugation of digested tissue, the stromal fraction was cultured in stromal medium selective for fibroblast growth as described previously<sup>24</sup>. Cells were confirmed to be positive for the stromal marker CD 90 and negative for epithelial pancytokeratin (MNF116, Dako).

### **Statistical analysis**

Continuous variables of interest are summarised numerically by Mean(SEM), and graphically using boxplots and scatterplots. Two sample t-test, one way ANOVA and repeated measures ANOVA were used to compare mean responses as appropriate. The degree of relationship between pairs of response variables was assessed using the Pearson or Spearman correlation coefficient as appropriate. Scatterplot smoothers were employed to indicate the likely relationship between variables in a population. All analyses were performed using Minitab 15.

## **Results**

### **Systemic CCL5 and TGFβ1 levels**

Patient demographics and clinicopathological details are shown in Table 1. There was no significant difference detected in CCL5 serum levels of breast cancer patients (Mean(SEM) 46.1 ng/ml(4.0) ng/ml) compared to healthy controls (45.4(3.4) ng/ml, Figure 1A). When divided on the basis of lymph node status CCL5 levels were found to decrease in the transition from node negative (59.6(3.7) ng/ml) to node positive



disease ( $\leq 2$  lymph nodes positive 40.5(6.3) ng/ml) and increase again as the number of positive lymph nodes increased ( $\geq 3$  lymph nodes positive 50.95(9.8) ng/ml, Figure 1B). When correlated with other clinicopathological characteristics including menopausal status, tumour epithelial subtype, tumour stage or tumour grade, no significant relationships were identified.

Serum TGF $\beta$ 1 levels were found to be significantly higher in the breast cancer cohort (27.4(1.5) ng/ml) compared to healthy controls (14.9(0.9) ng/ml, Figure 1C). When grouped on the basis of nodal status, TGF $\beta$ 1 levels, similar to the pattern observed in CCL5, were found to decrease from node negative (27.3(2.2) ng/ml) to node positive disease ( $\leq 2$  lymph nodes positive 22.0(2.7) ng/ml), and then increase again as the number of nodes positive increased ( $\geq 3$  lymph nodes positive 30.7(3.5) ng/ml, Figure 1D).

Further investigation revealed a significant positive correlation between systemic CCL5 and TGF $\beta$ 1 across all serum samples examined ( $r=0.42$ ,  $p<0.0001$ , Figure 2).

### **CCL5 and circulating menstrual hormones**

A potential relationship between circulating hormones and CCL5 was examined in serum samples from healthy premenopausal volunteers ( $n=15 \times 4$  weekly samples, total  $n=60$ ). CCL5 levels were stratified based on phase of the menstrual cycle (Figure 3A). A significant drop in CCL5 levels in the transition from late luteal/early follicular to mid follicular phase of the menstrual cycle was observed ( $p<0.05$ ). This corresponds with an increase in Oestradiol levels in the first two phases of the menstrual cycle. Further investigation revealed a significant negative correlation between Oestradiol (Figure 3B), Progesterone (Figure 3C) and circulating CCL5, with

the strongest correlation detected with Oestradiol (n=60,  $r_s = -0.502$ ,  $p < 0.0001$ ). No relationship between circulating LH or FSH and CCL5 was detected.

### **Analysis of Tissue Gene Expression**

Gene expression analysis was carried out on corresponding tissue from breast cancer patients (n=43), on whom circulating levels had been measured, and compared to normal tissue obtained at reduction mammoplasty (n=16). Results were normalised to endogenous control genes and expressed as Relative Quantity ( $\text{Log}_{10}$ )<sup>23</sup>. Expression of CCL5 and CCR5 was significantly elevated in tissue from breast cancer patients compared to controls ( $p < 0.001$ , Figure 4A). A significant positive correlation between expression of the CCL5 ligand and its principle receptor CCR5 was detected (n=43,  $r = 0.562$ ,  $p < 0.0001$ ). TGF $\beta$ 1 expression was significantly increased in tumour compared to normal breast tissue ( $p < 0.0001$ ) while expression of TGF $\beta$ R2 remained unchanged (Figure 4B). A significant positive correlation between CCL5 and TGF $\beta$ 1 gene expression was observed across all tissue samples (n=59,  $r = 0.435$ ,  $p < 0.001$ , Figure 4C).

### **Analysis of primary breast tumour stromal cells**

Gene expression analysis was carried out on primary tumour stromal cells isolated from tumour (n=22) and normal breast tissue (n=3) harvested at reduction mammoplasty. Results were normalised using the endogenous control gene PPIA and expressed relative to normal stromal cell gene expression. CCL5 expression was increased (Mean(SEM) 0.8(0.2)  $\text{Log}_{10}$  Relative Quantity(RQ)), and TGF $\beta$ 1 expression decreased (-0.12(0.05)  $\text{Log}_{10}$  RQ) in tumour stromal cells compared to normal stromal cells (Figure 5). CCR5 was not detected in any of the stromal populations

examined (Figure 5). A significant negative correlation was found between CCL5 and TGF $\beta$ 1 gene expression in primary stromal cells (n=32, r= -0.38, p<0.05).

## **Discussion**

In contrast to previous studies<sup>6, 7</sup>, the results presented show no significant difference between circulating CCL5 levels in breast cancer patients and healthy controls. The contradicting findings may be as a result of the fact that this study contains the largest cohort of breast cancer patients (n=102) to date. Niwa et al compared plasma samples from breast cancer patients (n=43) to healthy controls (n=12), while Eissa et al<sup>7</sup> detected elevation of CCL5 in serum samples from 60 breast cancer patients and 30 healthy controls. At initial stages of the current study, CCL5 levels were also found to be elevated in breast cancer patients, however when the number of samples was increased, this pattern was lost. The control group in the current study also contained an equal proportion of pre- and post-menopausal subjects as the breast cancer group, which may impact the outcome, particularly considering the observed relationship between CCL5 and circulating hormones.

Previous studies have shown that Estradiol replacement therapy decreases serum CCL5<sup>15</sup>. The significant negative correlation between serum CCL5, oestradiol and progesterone observed in this study in healthy premenopausal volunteers provides direct evidence of a cyclical variation of the chemokine. A previous study reported cyclical variation of vascular endothelial growth factor (VEGF), and its importance in terms of choosing the optimal time point of surgery in the menstrual cycle of premenopausal breast cancer patients<sup>25</sup>. The results presented here may warrant consideration in determining the optimal time point in the menstrual cycle for surgical intervention in premenopausal breast cancer patients.

Previous evidence suggests that circulating CCL5 is elevated in late stage breast cancer<sup>6, 8</sup>. In this study, a trend towards increased CCL5 levels was observed as the number of positive lymph nodes increased. This pattern has previously been associated with TGF $\beta$ 1<sup>19</sup>, and further investigation revealed a significant positive correlation between circulating CCL5 and TGF $\beta$ 1. Further investigation of expression of CCL5 and TGF $\beta$ 1 in tumour tissue from a subset of the same patients also revealed a correlation between the two factors, adding further significance to this finding.

Although no difference in circulating CCL5 levels was observed, in agreement with previous reports based on immunohistochemistry<sup>6</sup>, a significant increase in CCL5 expression in tumour tissue compared to normal tissue was detected. Also, expression of CCL5 and its principle receptor CCR5, displayed a significant positive correlation, indicating a strong affinity between the ligand and receptor. TGF $\beta$ 1 gene expression was also significantly higher in tumour tissue compared to normal tissue, while expression of TGF $\beta$ II remained unchanged.

While a positive correlation between CCL5 and TGF $\beta$ 1 was observed at the systemic level, and also in whole tumour tissues, upon isolation of primary tumour stromal cells, an inverse relationship between the two factors was observed. CCL5 was found to be significantly elevated in tumour, compared to normal stromal cells, while TGF $\beta$ 1 was decreased. Interestingly, previous studies have shown that reduced TGF $\beta$  signalling in tumour stroma supports breast cancer metastasis<sup>26</sup>, whereas increased CCL5 secretion from adjacent stromal cells has been shown to stimulate metastasis of breast cancer cells<sup>27</sup>. Cheng et al<sup>26</sup> reported that TGF $\beta$ RII deletion in an in vivo model led to blockage of the stromal autocrine TGF $\beta$  loop and increased proliferation in fibroblasts. This group also found that TGF $\beta$ RII deletion in stromal cells altered the paracrine stromal-epithelial crosstalk and led to increased proliferation of the

mammary epithelium<sup>26</sup>. Forrester et al<sup>28</sup> also showed in an in vivo model of breast tumorigenesis, that loss of TGF $\beta$ RII in tumour cells lead to increased pulmonary metastases and decreased time to tumour formation.

In a study incorporating an admix of Mesenchymal Stem Cells and epithelial breast cancer cells, MSC-secreted CCL5 was shown to exert its action in a paracrine manner and stimulate increased breast cancer metastasis in vivo<sup>27</sup>. Pinilla et al<sup>29</sup> found that co-culture with tissue resident stem cells stimulated increased invasion of breast cancer cell lines, an effect which was blocked in the presence of an antibody to CCL5. The adipose-derived stem cells were identified as the source of CCL5 secretion, which was found to be induced through the influence of tumour derived humoral factors.

It is worth noting that CCR5 expression was not detected in any of the tumour stromal cells examined in the current study, supporting paracrine action of the chemokine in the tumour microenvironment. This may also have impacted a previous report showing that CCL5 on its own has little or no effect in breast cancer growth and metastasis<sup>12</sup>. The investigation employed a mouse model of breast cancer established using epithelial cells alone. The current study, along with previous reports, suggests that in vivo models using mixed stromal-epithelial xenografts may be more appropriate to elucidate the true role of CCL5 in breast cancer.

Although unchanged at a systemic level, CCL5 expression in the tumour microenvironment is significantly increased compared to healthy tissue, with the stromal compartment partly responsible for this. The cyclical variation in CCL5 detected supports a role for hormonal control of the chemokine. It appears that CCL5 may play an important role in the primary tumour microenvironment, most likely through paracrine effects on tumour epithelial cells. This study has also identified a

potentially important relationship between CCL5 and TGF $\beta$ 1 in breast cancer which warrants further investigation.

**Conflict of interest statement**

None declared

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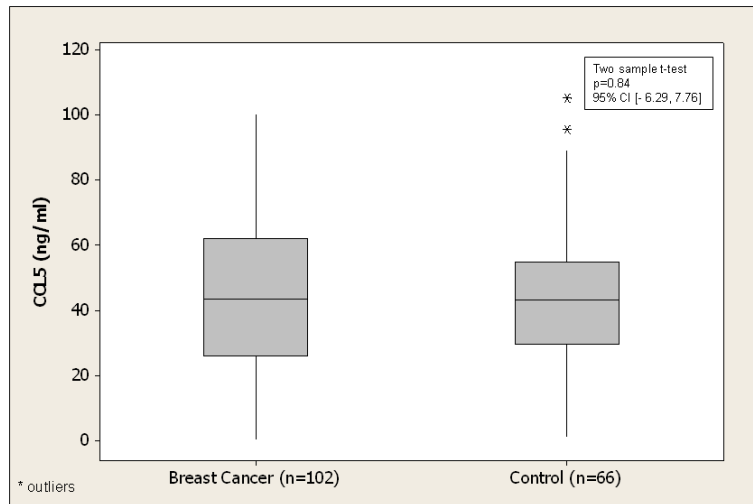
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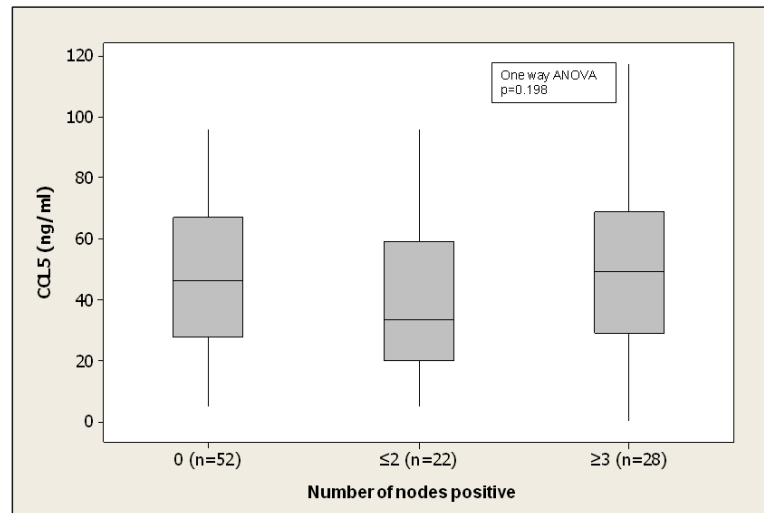
	Breast cancer patients	Control group
<i>Number of Patients</i>	<b>n (%)</b>	<b>n(%)</b>
<i>Total</i>	102	66
premenopausal	40 (39.2)	26 (39.4)
postmenopausal	62(60.8)	40 (60.6)
<i>Tumour Characteristics</i>	<b>n (%)</b>	
<i>Histology</i>		
Ductal	66 (64.7)	
Lobular	15 (14.7)	
Other	10 (9.8)	
Unknown	11 (10.8)	
<i>Epithelial subtype</i>		
Luminal A	68 (66.7)	
Luminal B	9 (8.8)	
Her-2/neu	6 (5.9)	
Basal	8 (7.8)	
Unknown	11 (10.8)	
<i>Grade</i>		
I	10 (9.8)	
II	36 (35.3)	
III	37 (36.3)	
Unknown	19 (18.6)	

**Table 1:** Clinicopathological details of breast cancer cohort

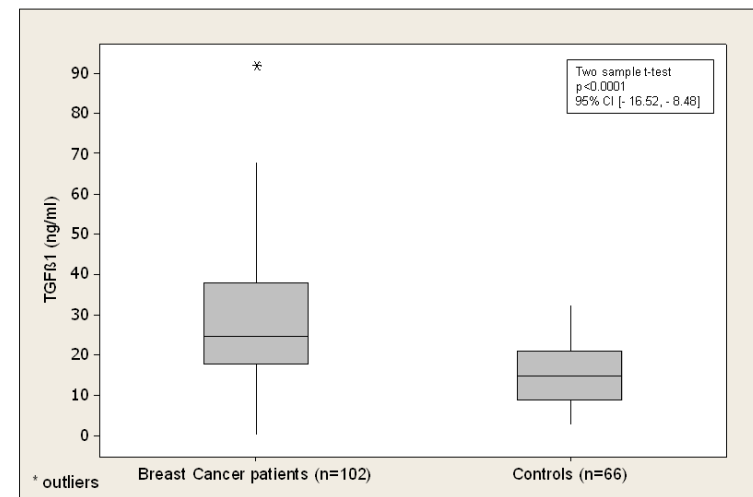
(a) Circulating CCL5 levels in breast cancer patients compared to controls



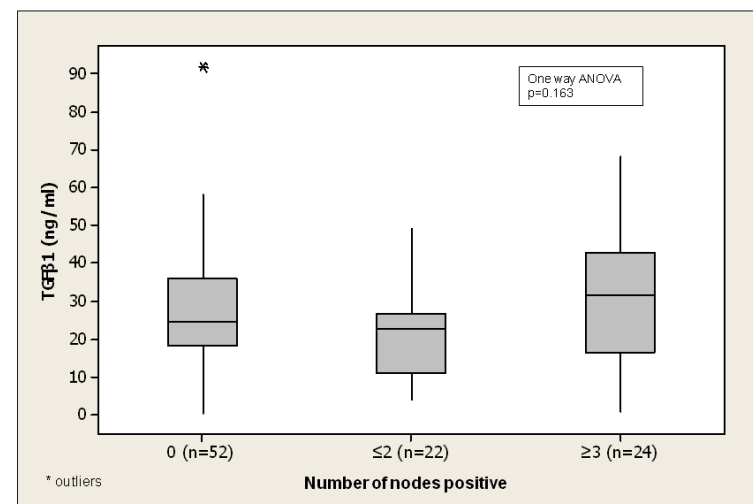
(b) Circulating CCL5 and lymph node status



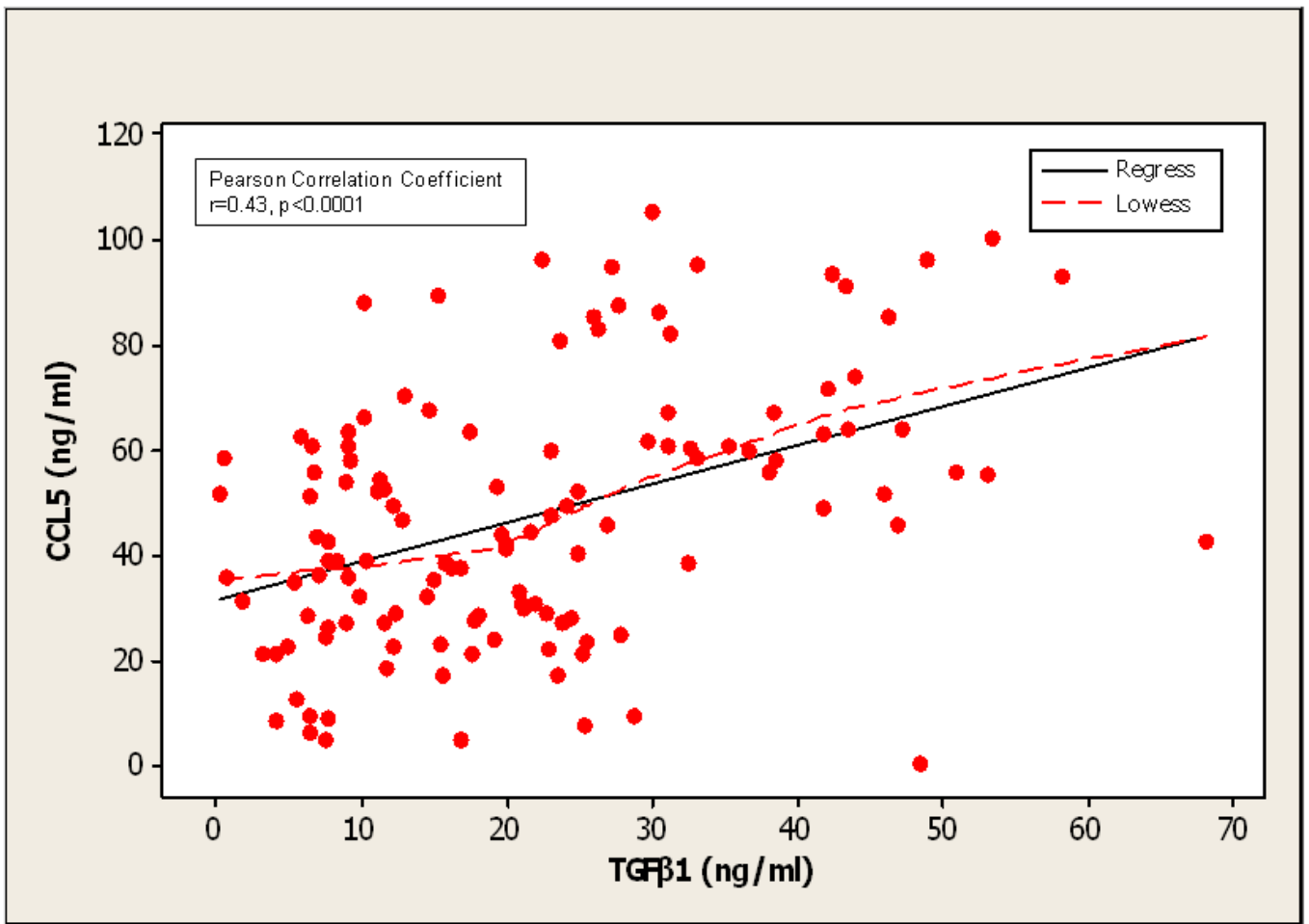
(c) Circulating TGFβ1 levels in breast cancer patients compared to controls



(d) Circulating TGFβ1 and lymph node status

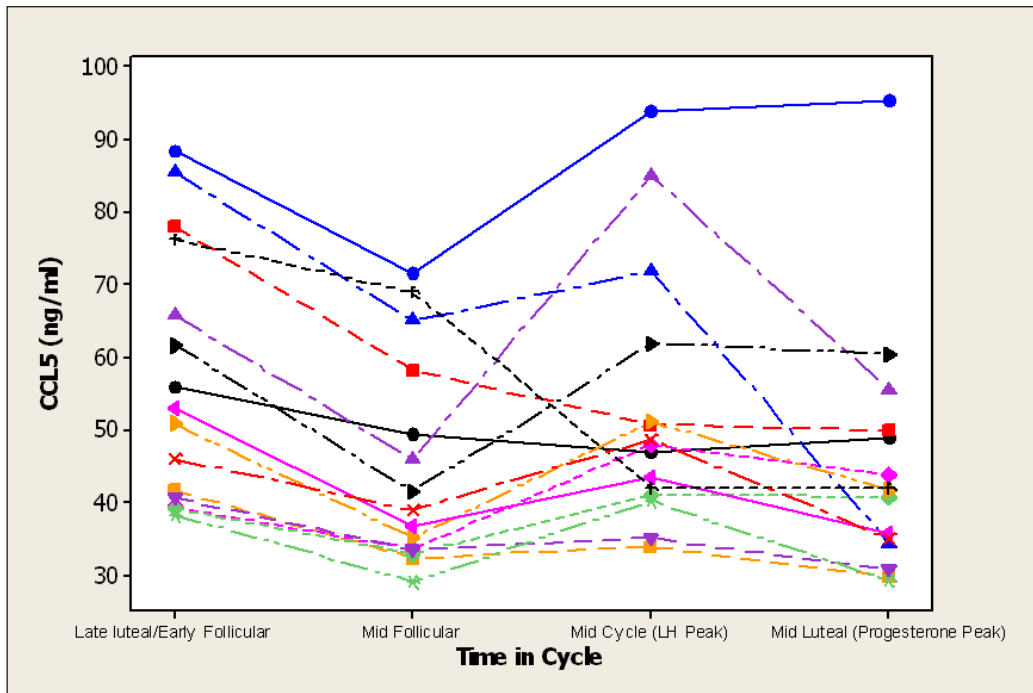


**Fig. 1** (a) Circulating levels of CCL5 in breast cancer patients (n=102) and age matched controls (n=66). Data is presented as boxplots showing the range of circulating CCL5 in ng/ml. The interquartile range box represents CCL5 levels from the 25<sup>th</sup> percentile to the 75<sup>th</sup> percentile, with the line representing the median. There was no significant difference detected in serum levels of CCL5 in breast cancer patients compared to controls (\* represents outliers). (b) Circulating serum CCL5 levels based on lymph node status. Graph depicts drop in CCL5 serum levels from node negative (59.6 (3.7) ng/ml) to node positive disease (≤2 lymph nodes positive 40.5 (6.3) ng/ml). CCL5 serum levels increased again as number of positive lymph nodes increased (≥3 positive lymph nodes 50.95 (6.2) ng/ml). Data is presented as boxplots. (c) Circulating serum levels of TGFβ1 in breast cancer patients (n=102) and age matched controls (n=66). Significantly higher levels of TGFβ1 were detected in breast cancer patients compared to normal controls (p<0.0001). (d) TGFβ1 serum Mean (SD) levels stratified based on lymph node status.

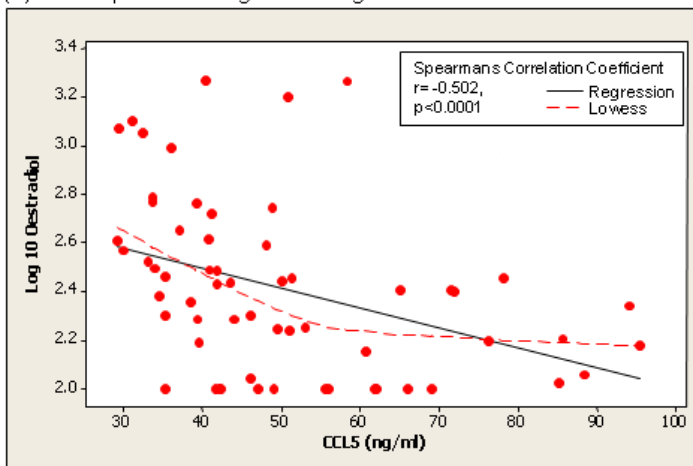


**Fig. 2** Scatterplot depicting significant positive correlation between serum CCL5 and TGFβ1 (n=127, r=0.43, p<0.0001).

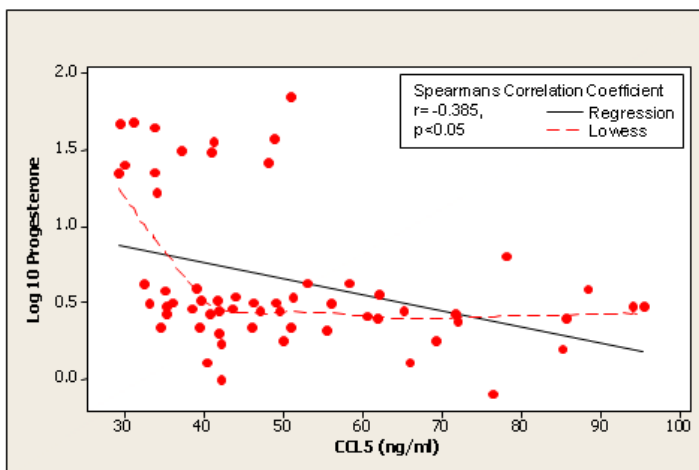
(a) Variation of systemic CCL5 across phases of menstrual cycle



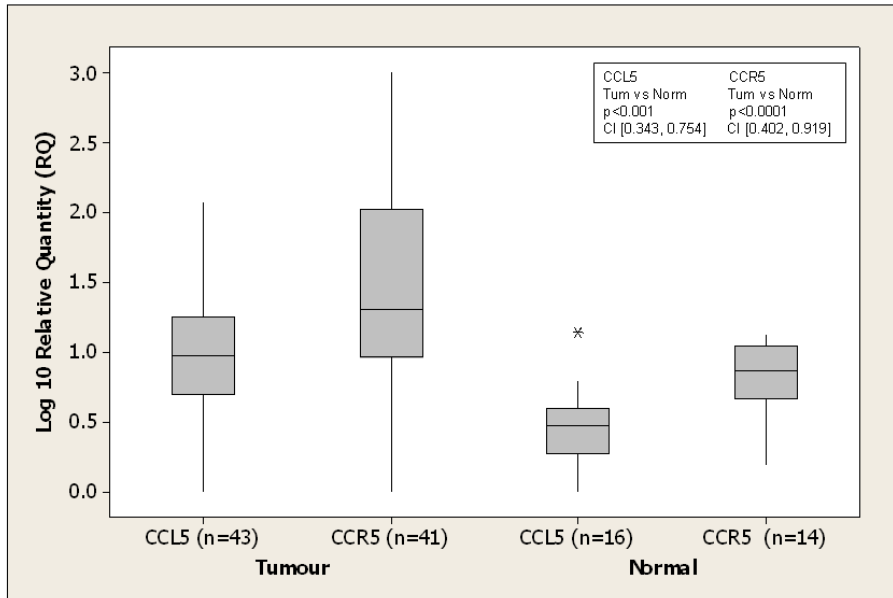
(b) Scatterplot showing circulating Oestradiol and CCL5



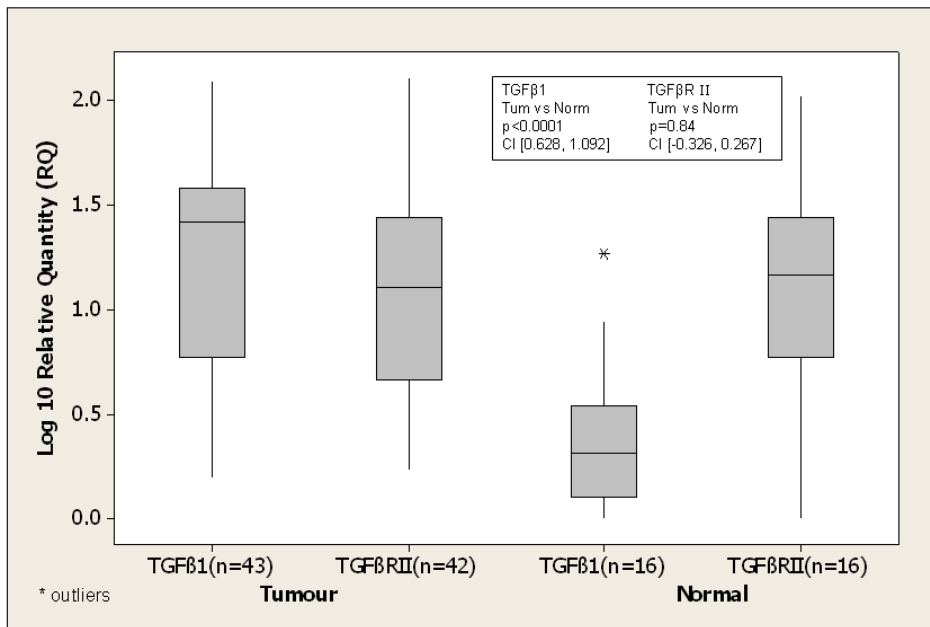
(c) Scatterplot showing circulating Progesterone and CCL5



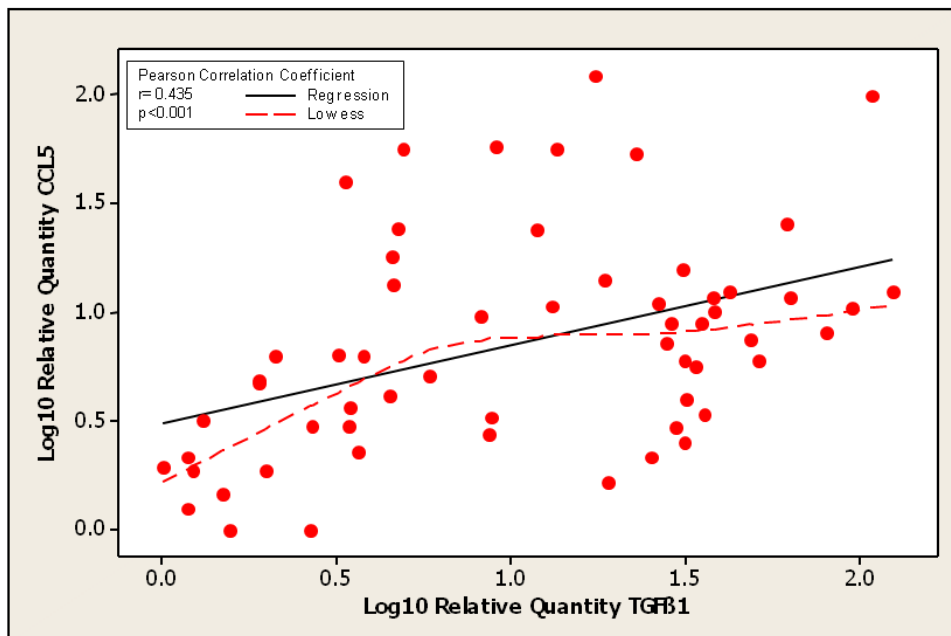
**Fig. 3 (a)** Variation of systemic CCL5 across phases of menstrual cycle (n=15 samples over four consecutive weeks, total n=60). The levels of CCL5 were significantly decreased in the transition from late luteal/early follicular to mid follicular phase ( $p < 0.05$ ). **(b)** Scatterplot depicting significant negative correlation between CCL5 and Oestradiol (n=60,  $r = -0.502$ ,  $p < 0.0001$ ). **(c)** Scatterplot showing significant negative correlation between CCL5 and Progesterone (n=60,  $r = -0.385$ ,  $p < 0.05$ ).



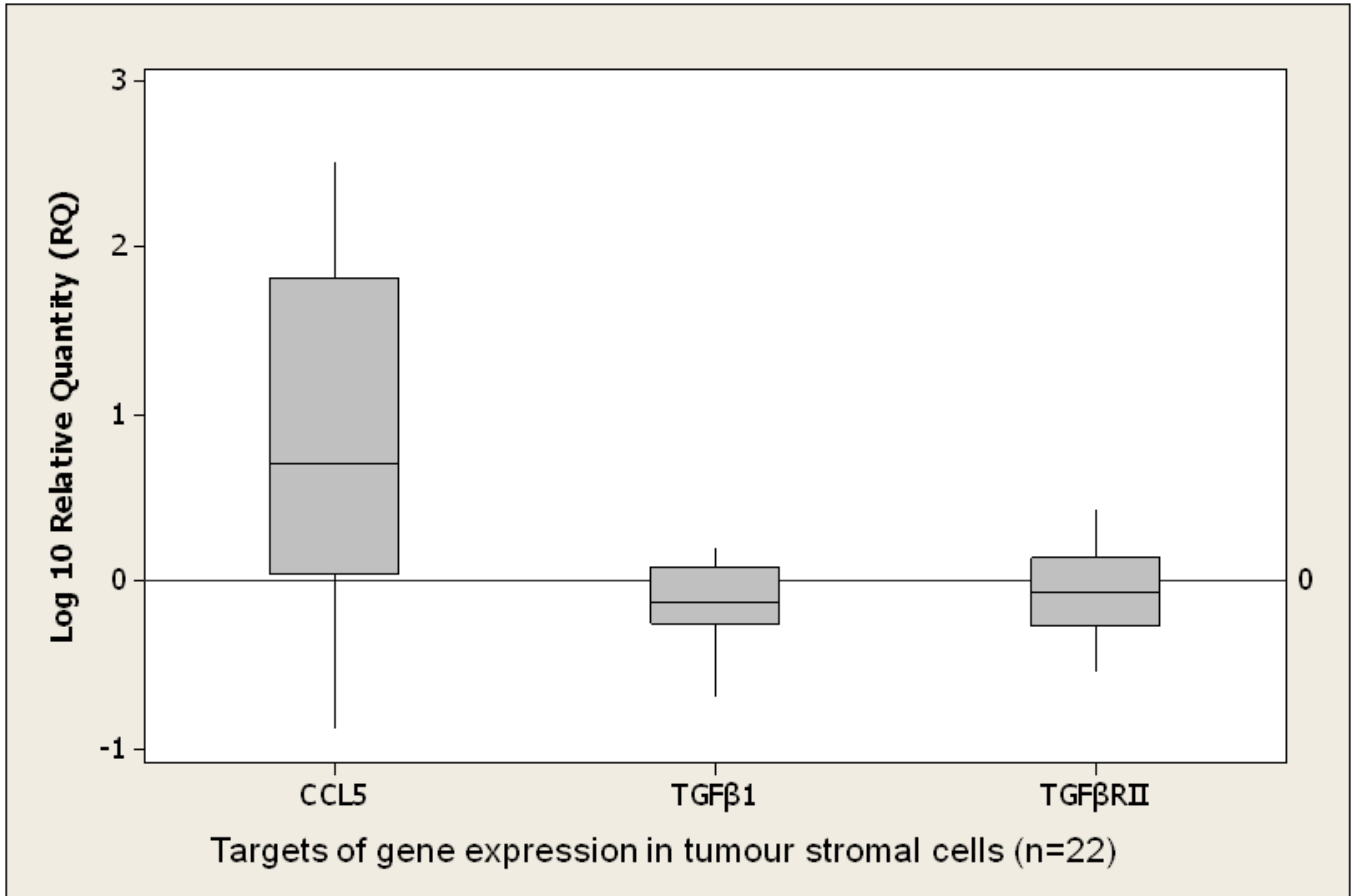
(b) RQ PCR targeting TGFβ1 and TGFβRII, tumour compared to normal tissue



(c) Scatterplot showing CCL5 and TGFβ1 gene expression in tissue samples



**Fig. 4 (a)** Gene expression analysis targeting CCL5 and CCR5 in breast cancer tissue (n=43) compared to normal tissue (n=16). Significantly higher expression of CCL5 and CCR5 was found in tumour compared to normal breast tissue ( $p<0.0001$ ). The data is presented as a boxplots showing the range of Log<sub>10</sub> Relative Quantity gene expression of CCL5 and CCR5. **(b)** Gene expression analysis targeting TGFβ1 and TGFβRII in tumor and normal breast tissue. A significant increase in TGFβ1 expression was found in breast cancer tissue compared to normal controls ( $p<0.0001$ ) whereas no significant difference in gene expression of its receptor TGFβRII was found. **(c)** Pearson correlation between CCL5 and TGFβ1 gene expression in all breast tissue samples examined (n=59,  $r=0.44$ ,  $p<0.001$ ).



**Fig. 5** Boxplots depicting CCL5, TGFβ1 and TGFβRII expression in primary tumour stromal compared to normal stromal cells harvested at reduction mammoplasty (n=3). Normal stromal cell expression is represented by the reference line.