Intermedin promotes breast cancer metastasis via Src/c-Myc-mediated ribosome production and protein translation

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Abstract

Purpose: Breast cancer is the most frequently diagnosed cancer and is the leading cause of cancer-associated mortality in women worldwide. Intermedin (IMD) is an endogenous peptide that belongs to the calcitonin gene-related peptide family and has been reported to play important roles in several types of cancers, including breast cancer. In this study, we sought to investigate how IMD affects the behavior of breast cancer cells, the underlying mechanism of these effects, and whether blockade of IMD has a therapeutic effect against breast cancer.

Methods: Transcriptome sequencing (RNA-Seq), cell biological experiments, Western blotting (WB), immunoprecipitation (IP), and animal tumor models were used.

Results: IMD expression was significantly increased in breast cancer samples, and the IMD level was positively correlated with lymph node metastasis and Ki67 expression. Cell biological experiments showed that IMD promoted the anchorage-independent growth, migration, and invasive ability of breast cancer cells. Inhibiting IMD activity with an anti-IMD monoclonal antibody blocked these tumor-promoting effects. In addition, blockade of IMD reduced in situ tumor growth and significantly decreased lung metastasis of 4T1 breast cancer in vivo. IMD induced Src kinase phosphorylation, which triggered the transcription of c-Myc, a major oncoprotein controlling the expression of genes that encode ribosomal components. Our data suggest that IMD is involved in breast cancer cell invasion and metastasis, potentially through increasing ribosome biogenesis and protein translation via the Src/c-Myc signaling pathway.

Conclusion: These results suggest that IMD may be a novel target for the treatment of breast cancer.

Key words: Breast Cancer, Metastasis, Intermedin (Adrenomedullin 2), Src, c-Myc, Ribosomal biogenesis

Introduction

Despite advances in the diagnosis and treatment of human malignancies, cancer remains one of the leading causes of morbidity and mortality worldwide. Breast cancer is currently the most frequently diagnosed cancer and is the leading cause of cancer-related mortality in women worldwide, accounting for 23% of all cancer cases diagnosed (1.38 million women) and 14% of all cancer-associated deaths (458,000 women) annually [1-3]. Metastasis is the primary cause of death in patients with breast cancer and [4]. In fact, the main cause of cancer-related death in patients with solid tumors is dissemination of cancer cells from a primary site to form distant metastases [5]. Thus, an improved understanding of the mechanisms underlying the metastatic process and the metastatic ability of cancer cells is urgently needed.

Intermedin (IMD), also named adrenomedullin 2 (ADM2), is a member of the calcitonin family [6]. Previous studies on IMD have mainly focused on its cardiovascular functions [7-9], but the role of IMD in tumors has recently been reported [10-15]. Morimoto first reported that the expression of IMD was elevated in malignant adrenal tumors in 2008 [12]. The level of IMD in peripheral blood was found to be elevated in breast cancer and prostate cancer patients, and high IMD levels were correlated with poor survival outcomes in those patients [10, 11]. According to the findings, we hypothesized that IMD may play a role in breast cancer occurrence or metastasis.

In this study, we evaluated the effects of IMD on the behavior of breast cancer cells, identified the mechanism underlying these effects, and determined whether blockade of IMD has a therapeutic effect on breast cancer. Herein, we reported that IMD expression was significantly increased in breast cancer samples and that the expression level of IMD was positively correlated with lymph node metastasis and Ki67 expression. IMD can recruit Src kinase to its receptor (calcitonin receptor-like receptor, CRLR) and induce subsequent Src phosphorylation that triggers the expression of c-Myc. The activation of Src-c-Myc signaling cascade initiates large-scale transcription of downstream genes, particularly genes that control ribosome biogenesis and protein translation. As a result, IMD promoted the anchorage-independent growth, migration, and invasiveness of breast cancer cells. Inhibiting IMD activity with an anti-IMD monoclonal antibody (Ab) blocked these tumor-promoting effects and significantly decreased lung metastasis in an in vivo model of 4T1 breast cancer. Our study gives novel insights into the mechanism of breast cancer metastasis and may provide a new therapeutic target for the treatment of breast cancer.

Results

IMD expression is significantly increased in breast cancer samples

We first evaluated the expression level of IMD in a tissue microarray, which contained 142 breast cancer samples and 88 adjacent nontumor tissue samples (Fig. 1A, B). The immunohistochemical (IHC) staining results showed that the breast cancer tissues exhibited significantly increased levels of IMD expression compared with the adjacent nontumor tissues (Fig. 1C). Based on the tissue microarray data, we selected 67 paired samples (that is, tumor tissue and adjacent tissue samples from the same patient) for comparison and found that the expression of IMD in the tumor tissues of most patients was significantly higher than that in the normal tissues adjacent to the cancerous tissues (Fig. 1D). In addition, stepwise binary regression analysis showed a significant association between the IMD levels and both lymph node metastasis and Ki67 expression in the breast cancer tissues (Table 1).

IMD increases the malignancy of breast cancer cells

The elevated expression of IMD in breast cancer tissues suggests that it may play a role in the growth and invasion of breast cancer cells. We investigated this hypothesis using a murine breast cancer model established with 4T1 cell, which produces a highly metastatic solid mammary cancer that can spontaneously metastasize to the lung, which closely mimics that of highly metastatic human breast cancer [16, 17]. The cell viability assay showed that treatment with an anti-IMD monoclonal antibody had an inhibitory effect on the growth of 4T1 cells (Fig. 2A). Anchorage-independent growth refers to the ability of cancer cells to grow independently on a solid surface and is considered a hallmark of cancer malignancy. The soft agar colony formation assay showed that IMD slightly increased the colony-forming ability of 4T1 cells, whereas the treatment with the anti-IMD antibody significantly decreased the number of cell colonies (Fig. 2B, C).

Cancer cell migration and invasion are highly integrated, multistep processes that play an important role in local invasion and metastasis. The wound healing assay showed that IMD promoted but the anti-IMD antibody significantly decreased the migration of 4T1 cells (Fig. 2D, E). The invasive ability of cancer cells, which indicates their ability to travel through the extracellular matrix into neighboring tissues, can be assessed by the Transwell assay. As shown in Fig. 2F-G, compared to the Vehicle-treated group, the number of cells crossing through the membrane in the IMD-treated group was higher; in contrast, treatment with the anti-IMD antibody significantly decreased the number of 4T1 cells that invaded into the lower chambers.

Blockade of IMD significantly inhibits ribosome biogenesis and protein synthesis

To obtain a more comprehensive understanding of the influence of IMD on breast cancer cells, we analyzed the transcriptional profiles of 4T1 cells via RNA sequencing (RNA-seq) analysis. Biological replicates are necessary when performing biological experiments to ensure that the results are reliably reproducible. Herein, we analyzed two parallel samples per group (treated with vehicle, IMD, or the anti-IMD antibody). The correlation of gene expression levels between samples is an important indicator for assessing the reliability of experiments and the rationality of sample selection. The closer the correlation coefficient is to 1 indicates higher similarity of the expression patterns between samples within a group. The Encyclopedia of DNA Elements (ENCODE) Project recommends that the square of the Pearson correlation coefficient (R^2) be greater than 0.92 (under ideal sampling and experimental conditions). Quality control (QC) analysis showed that the R^2 value of each sample was greater than 0.97, indicating good reliability of the experimental results and high similarity of expression patterns between samples (Fig. 3A).

After gene expression is quantified, statistical analysis must be performed on the expression data to screen samples for genes whose expression levels are significantly different under various treatment conditions. This analysis is generally divided into three steps [18-20]: (1) normalization of the original read counts to correct for the sequencing depth; (2) calculation of the probability value (p-value) by hypothesis testing; and (3) performance of multiple hypothesis testing and calculation of the FDR (adjusted p, or p-adj) value. A volcano plot was generated to visually show the distribution of differentially expressed genes for each comparison (Fig. 3B-C). The abscissa indicates the gene expression fold change (*log2 Fold Change*) values, and the ordinate indicates the significance level of the gene expression difference (*-log10 p-adj or -log10 p-value*) between the treatment and control groups. The red dots indicate upregulated genes, and the green dots indicate downregulated genes. The volcano plot showed that IMD treatment affected gene transcriptional profiles slightly. Forty-three genes were upregulated and 41 were downregulated. The relatively small number of changed genes may be due to 4T1 cells expressing high levels of endogenous IMD; thus, supplementation with exogenous IMD may cause relatively mild effects on these cells. However, treatment with the anti-IMD antibody caused drastic changes in gene transcription; 1913 genes were significantly upregulated, and 2156 were significantly downregulated (Fig. 3C). The result suggests that inhibiting the activity of IMD may induce changes in multiple signaling pathways in breast cancer cells.

Gene Ontology (GO) analysis utilizes a comprehensive database describing gene functions that can be divided into three categories: biological processes, cellular components, and molecular functions. The most significantly enriched GO terms are displayed as scatter plots (Fig. 3D). The abscissa shows the ratio of the number of differentially expressed genes to the total number of genes in the GO term, and the ordinate shows the GO terms. The size of a dot represents the number of genes annotated to the specific GO term, and the color represents the significance of enrichment. The GO categories with significant changes (p-adj <0.05) were shown in Supplementary Table 1. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis utilizes another database for systematic analysis of biochemical pathways, metabolic pathways, and signal transduction pathways, including differentially expressed genes. The KEGG pathway enrichment results are shown in Fig. 3E, and KEGG pathways with significant changes (p-adj <0.05) are shown in Supplementary Table 2.

The terms with the most significant differences and the largest number of down-regulated genes were as follows: Ribonucleoprotein complex biogenesis, Ribosome biogenesis, rRNA processing, mRNA metabolic process et al. in GO terms; and Ribosome biogenesis in eukaryotes, Protein export, Spliceosome et al. in KEGG terms. Analysis of these two databases showed that anti-IMD antibody treatment had the greatest impact on ribosome biogenesis and protein synthesis.

Ribosomes are macromolecular machines that exist in almost all living cells and can perform mRNA translation and protein synthesis; they are categorized by their localization as either cytoplasmic or mitochondrial. Ribosomes consist of two major components: the small and large ribosomal subunits (S and L subunits). Each subunit consists of ribosomal RNA (rRNA) molecules and ribosomal proteins (RPs). After treatment with the anti-IMD antibody, among genes related to components of cytoplasmic ribosomes, 53 were downregulated and 6 were upregulated; among genes related to components of mitochondrial ribosomes, 25 were downregulated and only 3 were upregulated (Fig. 3F; the red box indicates gene upregulation, and the green box indicates gene downregulation; detailed differential gene expression (DEG) data are shown in Supplementary Table 3).

IMD upregulates the expression of ribosomal component genes by activating the Src/c-Myc signaling pathway

Cancer cells undergo uncontrolled, indefinite proliferation and persistent invasion, which requires increased production of ribosomes to support increased protein translation. The transcription of both cytoplasmic and mitochondrial ribosome components was significantly suppressed by treatment with the anti-IMD antibody, suggesting that cancer cell translation and protein production were significantly inhibited. Therefore, we sought to identify the mechanism through which IMD regulates ribosome biogenesis. KEGG pathway analysis of the "breast cancer" pathway (Fig. 4A) showed that treatment with the anti-IMD antibody suppressed the cell cycle (at the G1/S phase transition) by downregulating c-Myc and cyclin D1 (CCND1). The FPKM value from the original RNA-Seq data showed that IMD slightly affected the transcription levels of c-Myc and cyclin D1, whereas the anti-IMD antibody treatment significantly down-regulated the two genes (Fig. 4B-C).

c-Myc and cyclin D1 are two key genes that affect the cell cycle, cell growth and invasion. c-Myc is a major oncoprotein controlling the expression of almost 15% of all human genes, many of which are involved in ribosome biogenesis and protein translation [21]. As one of the most frequently studied oncoproteins that regulates ribosome biogenesis, c-Myc was reported to promote cell proliferation and invasion by enhancing ribosome biogenesis and protein translation largely via its key function in stimulating the transcription of numerous genes encoding proteins essential for ribosomal biogenesis [22]. As shown in Supplementary Table 3, the magnitude of the anti-IMD-caused reduction in the transcription of ribosome-related genes was consistent with the magnitude of the reduction in c-Myc, which may explain the extensive inhibitory effect of the anti-IMD antibody on ribosome biogenesis-related genes.

Cyclin D1 has long been noted to play an important role in breast cancer [23]. Cyclin D1 overexpression has been reported in more than 50% of human breast cancers, and dysregulation of its expression contributes to loss of normal G1/S transition control during tumorigenesis [24]. Interestingly, Cyclin D1 was not the only cyclin-related gene affected by the anti-IMD antibody. As shown in Fig. 4D, the transcription levels of 3 genes encoding cyclin-dependent kinase inhibitors (CDKNs) were increased, whereas 5 genes encoding cyclin-dependent kinases (CDKs) and 8 genes encoding cyclins (D/E/G/L) were decreased. In general, CDKs and cyclins promote cell cycle progression from G1 to S phase, whereas CDKNs inhibit this process. The promotion of cell cycle progression is a major oncogenic mechanism of c-Myc, which not only activates the expression of cyclins and CDKs but also suppresses the expression of a set of proteins that act as cell cycle brakes [25]. These results indicate that c-Myc may be the key effector molecule in the IMD-regulated signaling cascade.

The activation of tyrosine kinase Src is believed to initiate expression of c-Myc for cell cycle progression in breast cancer cells [26-28]. IMD shares a G protein-coupled receptor (GPCR), CRLR (calcitonin receptor-like receptor), with its family members [6]. We have reported that IMD can induce the formation of a signaling complex containing CRLR and Src and promote subsequent Src phosphorylation in endothelial cells [29]. Based on these results, we hypothesized that IMD may regulate the expression of c-Myc by activating Src, thereby affecting ribosome biogenesis and the cell cycle in breast cancer cells.

We tested this hypothesis using western blot (WB) analysis and found that IMD induced a significant increase in Src phosphorylation, and this effect could be blocked by treatment with an siRNA that can specifically inhibit Src transcription (siR-Src) (Fig. 4E-G). The rescue of Src expression by transfection of Lv.Src (lentiviral vector expressing Src) restored the ability of IMD to induce Src phosphorylation (Fig. 4E-F). To determine whether the IMD-induced Src phosphorylation and c-Myc expression was causally related, we performed Real-time PCR and found that the IMD-induced c-Myc upregulation was blocked when Src was knocked down by siR-Src (Fig. 4H). On the other hand, after Src expression was rescued by transfection of Lv.Src, the c-Myc mRNA level was restored accordingly (Fig. 4H). The results suggest that IMD upregulates c-Myc expression via inducing Src phosphorylation.

We then asked how Src is activated by IMD. IMD has been reported to be a ligand of CRLR, a class B GPCR [6]. In our previous study, we have identified an IMD/CRLR/β-arrestin 1/Src signaling cascade in endothelial cells [29]. β-arrestin 1 is a scaffold protein that mediates the agonist-dependent recruitment of Src kinase to GPCRs [30, 31]. We have shown that in endothelial cells, after IMD binds to its receptor CRLR, with the help of β-arrestin 1, Src is recruited to CRLR and form a signaling protein complex. This Src/CRLR complex is subsequently internalized into cytoplasm, resulting in Src phosphorylation [29]. Herein, we sought to determine whether this signaling pathway exists in breast cancer cells.

We performed the immunoprecipitation (IP) assay to detect the protein interactions. We found that after exposure to IMD, the binding of Src to CRLR increased by more than 3 folds (Fig. 4I and 6J). This result suggested that IMD did promote the recruitment of Src to CRLR in 4T1 breast cancer cells. The siRNA that can specifically knockdown β-arrestin 1 transcription (siR-β-arr1) could inhibit the IMD-induced binding of Src and CRLR, and transfection of Lv.β-arr1 (lentiviral vector expressing β-arrestin 1) restored the ability of IMD to induce Src binding to CRLR (Fig. 4K-M). In addition, the IP-IB assay showed that the Src phosphorylation occurred on the Src/CRLR complex; β-arrestin 1 knockdown significantly inhibited the IMD-induced Src phosphorylation, and rescue of β-arrestin 1 expression restored the Src phosphorylation (Fig. 4N-O). According to these results, we may say that IMD upregulates c-Myc expression by recruiting Src to CRLR and inducing Src phosphorylation, thereby enhancing ribosome assembly and driving cell cycle progression.

Blockade of IMD reduces spontaneous lung metastasis and in situ tumor growth of breast cancer

The elevated expression of IMD in breast cancer tissue and its effect on the malignancy of breast cancer cells suggest that blockade of IMD activity may inhibit breast cancer growth and metastasis. We first tested this hypothesis in a 4T1 orthotopic breast cancer model. A total of 2.5×10^6 4T1 cells were injected under the mammary fat pads of 6-week-old female BALB/c mice. Seven days after cancer cell injection, the mice were treated with the mature IMD peptide (0.25 mg/kg/day, 2 weeks, 14 times in total, subcutaneous injection), the anti-IMD monoclonal antibody (2.5 mg/kg, twice weekly, 3 times in total, intravenous injection), or vehicle (100 μl of 0.9% saline, twice weekly, 3 times in total, intravenous injection).

The most important feature of breast cancers is not the in situ tumor growth but their spontaneous metastasis, particularly lung metastasis [16, 17]. Five weeks after inoculation of 4T1 cells, lungs from the tumor-bearing mice in the vehicle group and the anti-IMD antibody treatment group were removed for analysis (Fig. 5A-E). Statistical analysis performed by calculating the number of metastatic colonies and the metastatic area on the surface of the lungs (including the ventral and dorsal sides) showed that anti-IMD antibody treatment significantly reduced the number of lung metastases compared with the vehicle group (Fig. 5D and 5E). The analysis of H&E-stained pathologic images of the whole lungs confirmed the tumor metastasis within the lungs (Figure. S1). The results demonstrated that IMD increased, whereas the anti-IMD antibody significantly inhibited lung metastasis.

The in situ tumor growth was also measured. On the final day of the experiment, tumor growth curves were plotted (Fig. 6A). Compared with the vehicle group, IMD slightly increased, whereas the anti-IMD antibody significantly inhibited the in situ tumor growth, and the pro- or anti-tumor effects were not due to the body weight loss (Fig. 6B). We also tested it using human-derived MDA-MB-231 and MDA-MB-468 xenograft mammary cancer models. A total of 5×10^6 cells were injected under the mammary fat pads of 6-week-old female severe combined immunodeficient (SCID) mice, and treated with IMD peptide, the anti-IMD antibody, or vehicle with the same dosage and administration method. Neither 231 nor 468 mammary cancer cell lines can produce spontaneous lung metastasis. The in situ tumor growth pattern was similar to 4T1, that is, IMD slightly promoted, but anti-IMD significantly inhibited the in situ tumor growth of 231 and 468, and the effects were not due to the body weight loss (Fig. 6C-F).

Discussion

Breast cancer is the leading cause of cancer-related mortality among women worldwide and accounts for 23% of cancer diagnoses and 14% of cancer deaths annually [1-3]. Metastasis is the most important biological characteristic of all malignant tumors [32-35]. In most cases, metastasis, rather than the local growth of the primary tumor, is the primary cause of death in cancer patients [33-35]. If metastasis can be effectively controlled, the treatment efficacy for cancer patients will be significantly improved. In this study, we found that IMD, an endogenous peptide belonging to the calcitonin peptide family, can recruit and activate Src kinase to upregulate the expression of c-Myc in breast cancer cells, thereby initiating large-scale gene transcription and promoting cell cycle progression through the G1/S phase transition. Blockade of IMD inhibited the transcription of c-Myc, which decreased ribosome biogenesis and protein translation and suppressed cell cycle progression. Although the growth of primary tumors was not highly significantly inhibited, treatment with an anti-IMD antibody significantly decreased lung metastasis in an in vivo breast cancer model, suggesting that this strategy may be effective for enhancing the therapeutic effect of clinical breast cancer treatment.

Another endogenous peptide in the calcitonin peptide family in addition to IMD, adrenomedullin (*Adm*), has been reported to promote the growth and metastasis of breast cancer [36-39]. Previous studies of IMD have focused mainly on its roles in mediating various cardiovascular functions [7-9], but recent studies have suggested that IMD also plays important roles in certain types of cancers, including adrenal cancer, prostate cancer, and hepatocellular carcinoma [10, 12, 13]. Lu and colleagues had reported that preoperative plasma IMD levels are associated with poor outcomes of breast cancer patients [11]. However, whether and how IMD affects the growth and metastasis of breast cancer is unknown, and the underlying molecular mechanisms have not been studied. Herein, we analyzed 142 breast cancer samples and 88 adjacent tissue samples in a tissue microarray and found that compared with the normal tissues, the cancer tissues exhibited significantly increased expression of IMD and that high expression of IMD in cancer tissues was associated with an increased rate of lymph node metastasis. These findings provided evidences that IMD may play an important role in the malignancy of breast cancer cells.

We found that IMD significantly increased the anchorage-independent growth, migration, and invasive ability of breast cancer cells. However, inhibiting IMD activity with an anti-IMD monoclonal antibody blocked these tumor-promoting effects. The elevated expression of IMD in breast cancer and its effects on the malignancy of breast cancer cells suggest that blockade of IMD activity may inhibit breast cancer growth and metastasis. We tested this hypothesis in an orthotopic breast cancer model established with 4T1 cells, which can spontaneously metastasize to the lungs. Treatment with the anti-IMD antibody not only inhibited orthotopic tumor growth but also inhibited the lung metastasis significantly.

To provide a comprehensive understanding of gene expression profiles in breast cancer cells, we performed RNA-Seq analysis and found that the expression of both cytoplasmic and mitochondrial ribosomal components were significantly suppressed by treatment with the anti-IMD antibody. Further analysis revealed that IMD can recruit Src to its receptor CRLR and induce subsequent Src phosphorylation, triggering the expression of c-Myc, which subsequantly initiates large-scale transcription of downstream genes, particularly genes that control ribosome biogenesis and protein translation. Metastasis is a major obstacle in the treatment of breast cancers, and this process requires increased production of ribosomes to support increased protein synthesis. Thus, blockade of IMD activity with the anti-IMD antibody may be an effective strategy for inhibiting breast cancer metastasis via suppression of ribosome production and protein translation.

Taken together, our data suggest that IMD is involved in breast cancer cell metastasis by inducing increases in ribosome biogenesis and protein translation via the Src/c-Myc signaling pathway. Together with our previous finding that IMD plays a critical role in vascular remodeling and improves tumor blood perfusion [40], we may say that IMD may be a novel target for the treatment of breast cancer.

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Authors' contributions LK, LH, ZF, and YZ carried out the pathological analysis and cell studies; LK, FX, HL, and FL performed the animal studies; ML, LH, HZ, and DW participated in the RNA-Seq analysis; LK and FX performed the WB and IP assays; YX and YW analyzed the data; WZ conceived the initial concept and designed the study; WZ draft the manuscript. All authors read and approved the final manuscript.

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Declarations

Conflict of interest There is no conflict of interests among the authors.

Ethical approval The animal experiments were approved by the Animal Ethics Committee of Sichuan University and performed according to institutional and national guidelines.

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Table 1

Stepwise binary logic regression analysis(IMD score ≤5 / IMD score > 5)

		B	S.E	Wald	df	Sig.	Exp(B)
step 1[a]	Age	0.020	0.018	1.207	1	0.272	1.020
	Tumor volume	-0.001	0.004	0.058	1	0.810	0.999
	Clinical stage	0.497	0.512	0.943	1	0.332	1.644
	LNM	-2.191	1.065	4.234	1	0.040*	0.112
	ER	-0.101	0.767	0.017	1	0.895	0.904
	PR	0.271	0.831	0.106	1	0.744	1.311
	HER2	-0.245	0.730	0.112	1	0.738	0.783
	Ki67	3.202	1.222	6.871	1	0.009**	24.589
	Constant	-3.430	1.567	4.793	1	0.029*	0.032

a. variable(s) entered on step 1：Age, Tumor volume, Clinical stage, LNM, ER, PR, HER2, Ki67

IMD: intermedin; LNM: Lymph nodes metastasis; ER: estrogen receptor; PR: progesterone receptor; Her-2: Her2-receptor.


A
Adjacent non-tumor tissues
B
Breast cancer samples
C
p<0.0001
IMD staining [score]
0
2
4
6
Normal
Cancer
D
Patient 1#
Patient 2#
Patient 3#
Patient 4#
Patient 5#
Patient 6#
Patient 7#
Patient 8#
Patient 9#
Patient 10#
Patient 11#
Patient 12#
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Patient 64#
Patient 65#
Patient 66#
Patient 67#

Fig 1. IMD expression is significantly increased in breast cancer samples. A-B, IHC images of non-tumor tissues and breast cancer samples. **C**, The IMD staining scores were presented as columns with mean ± SD. Significance was assessed by *unpaired t test with Welch's correction*. **D,** The IMD staining scores of 67 one-to-one samples (a sample from a breast cancer tissue and the adjacent non-tumor tissue from the same patient).

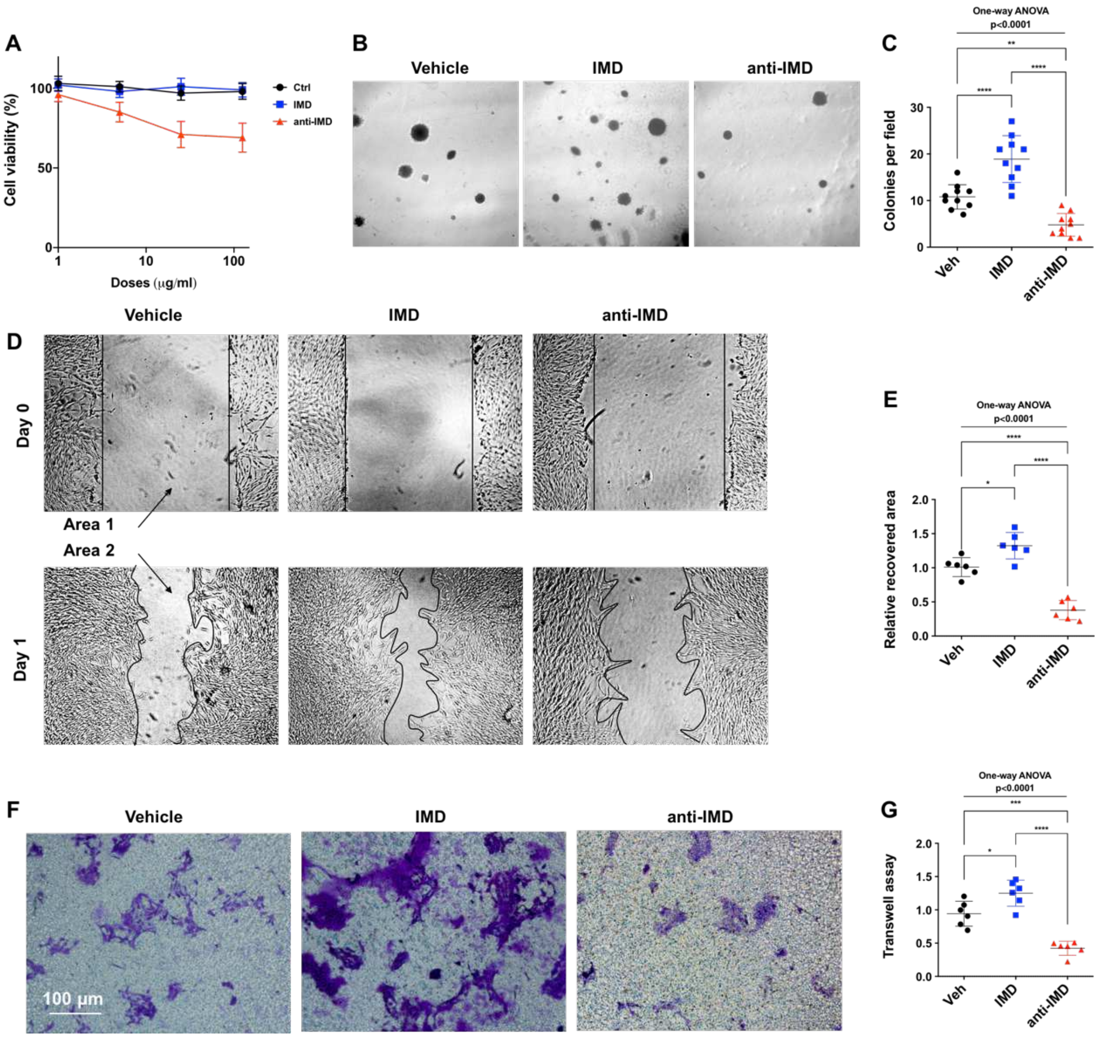


Fig 2. IMD facilitates malignancy of breast cancer cells. A, 4T1 cells were treated with IMD (2.5μg/ml), anti-IMD antibody (25μg/ml), or vehicle, and the cell viability was measured. Data were presented as scatter plots with mean ± SD (n=6). **B**, 4T1 cells treated with IMD, anti-IMD, or vehicle were subjected to Soft agar formation assay. **C**, Cell colonies were quantified using 10 randomly chosen fields. **D**, Cells were seeded on the 6-well plates. One day after cell scratching, the recovered area was measured by *Area 1* (the area that had not been covered by cells at Day 0) minus *Area 2* (the area that was not covered by cells at Day 1).” **E**: The recovered area (the mean level of the control group was set

to 1) was calculated (n=6). **F**: Cells were seeded on the upper chamber of the transwell system. Representative images demonstrated the Crystal-violet-stained cells that invaded through the membranes. **G**: The Crystal-violet-positive cells was calculated (relative to the control; the mean level in the control group was set to 1.0; n=6.). All data were presented as scatter plots with mean ± SD. Significance was assessed by *one-way ANOVA* followed by *non-parametric Dunn's post-hoc analysis*.

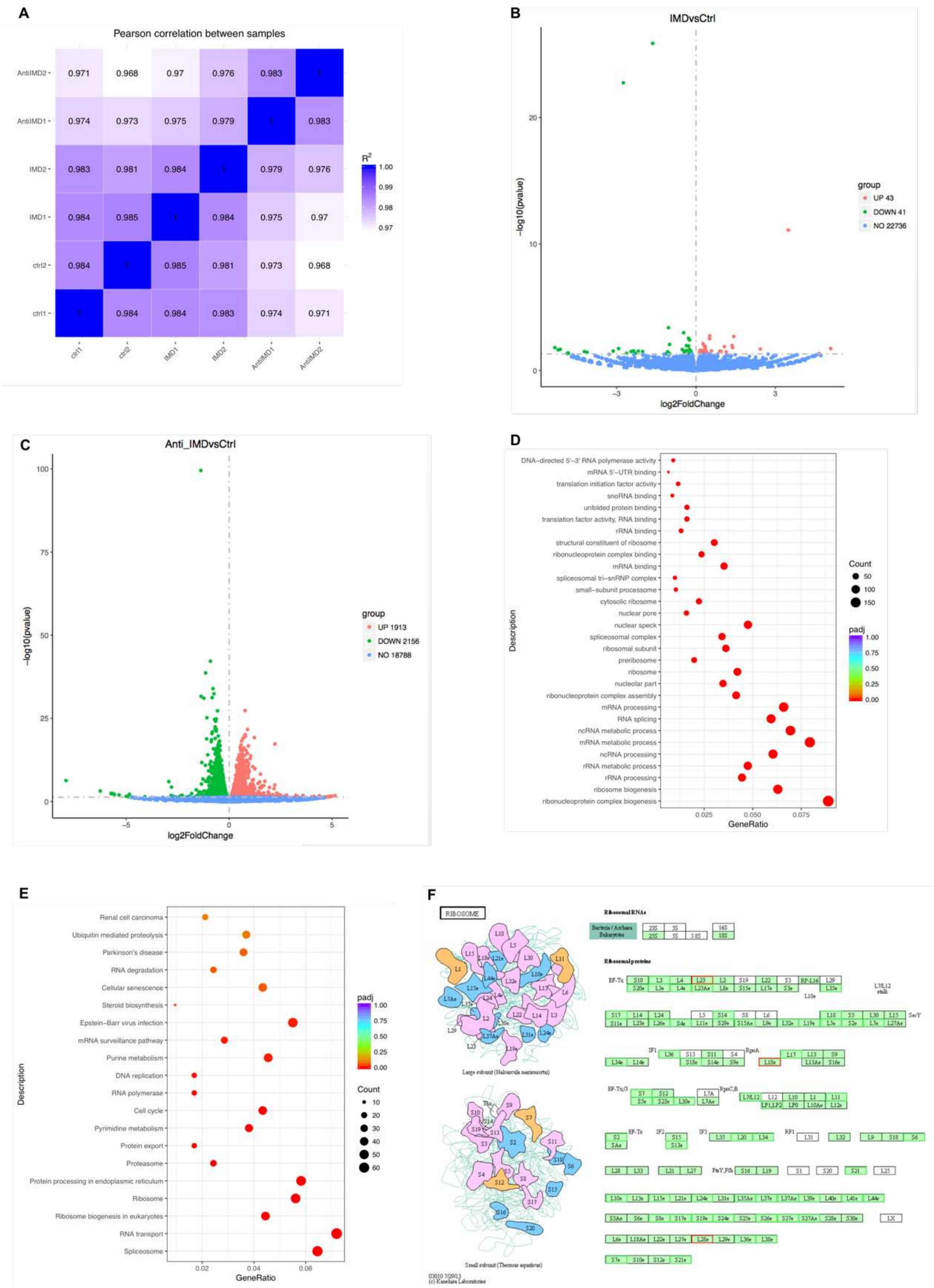


Fig 3. Blockade of IMD significantly inhibited ribosomal biogenesis and protein synthesis. A, The square of Pearson correlation coefficient (R2) of the RNA-Seq analysis. R2 > 0.92 indicates good reliability. **B-C**, Volcano graphs showed the distribution of differentially expressed genes for IMD vs. Ctrl and anti-IMD vs. Ctrl comparisons. **D-E**, GO and KEGG analysis showed that the anti-IMD antibody treatment had the greatest impact on ribosomal biogenesis and protein synthesis. **F**, The KEGG

graphic analysis (KEGG term: *Ribosome*) showed that the anti-IMD antibody significantly reduced the transcription of the large and small subunits of ribosomes. The down-regulated genes were marked with green borders, and the upregulated genes were marked with red borders.

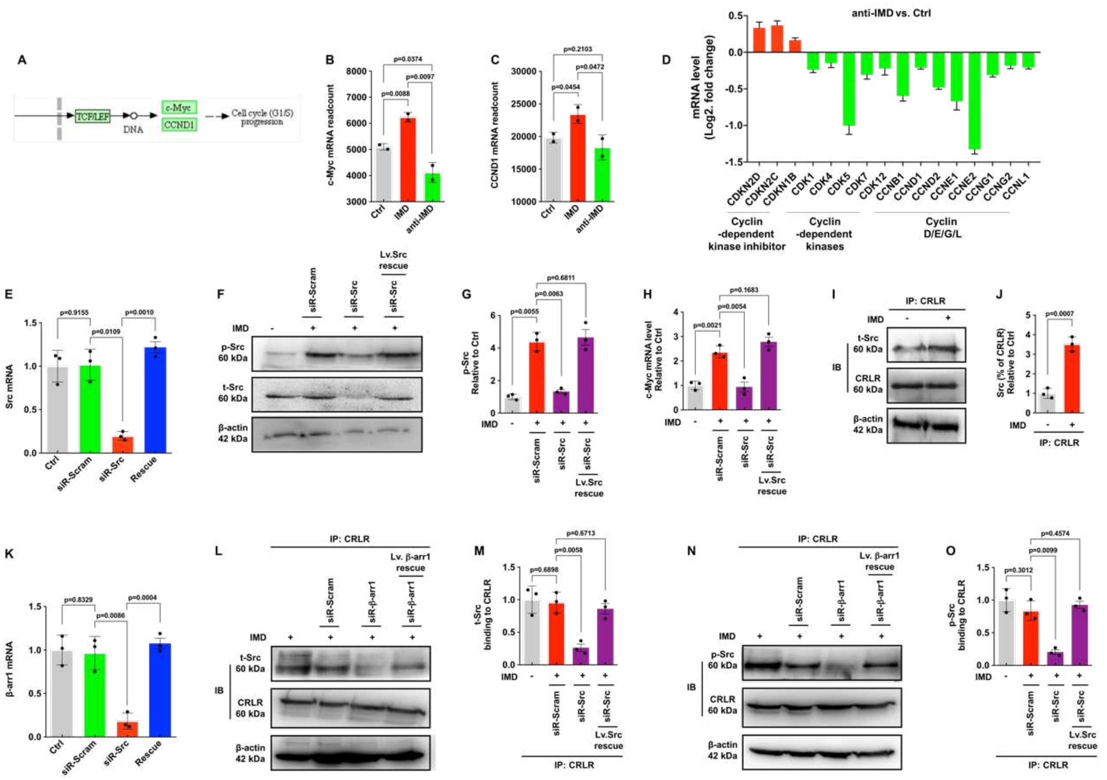
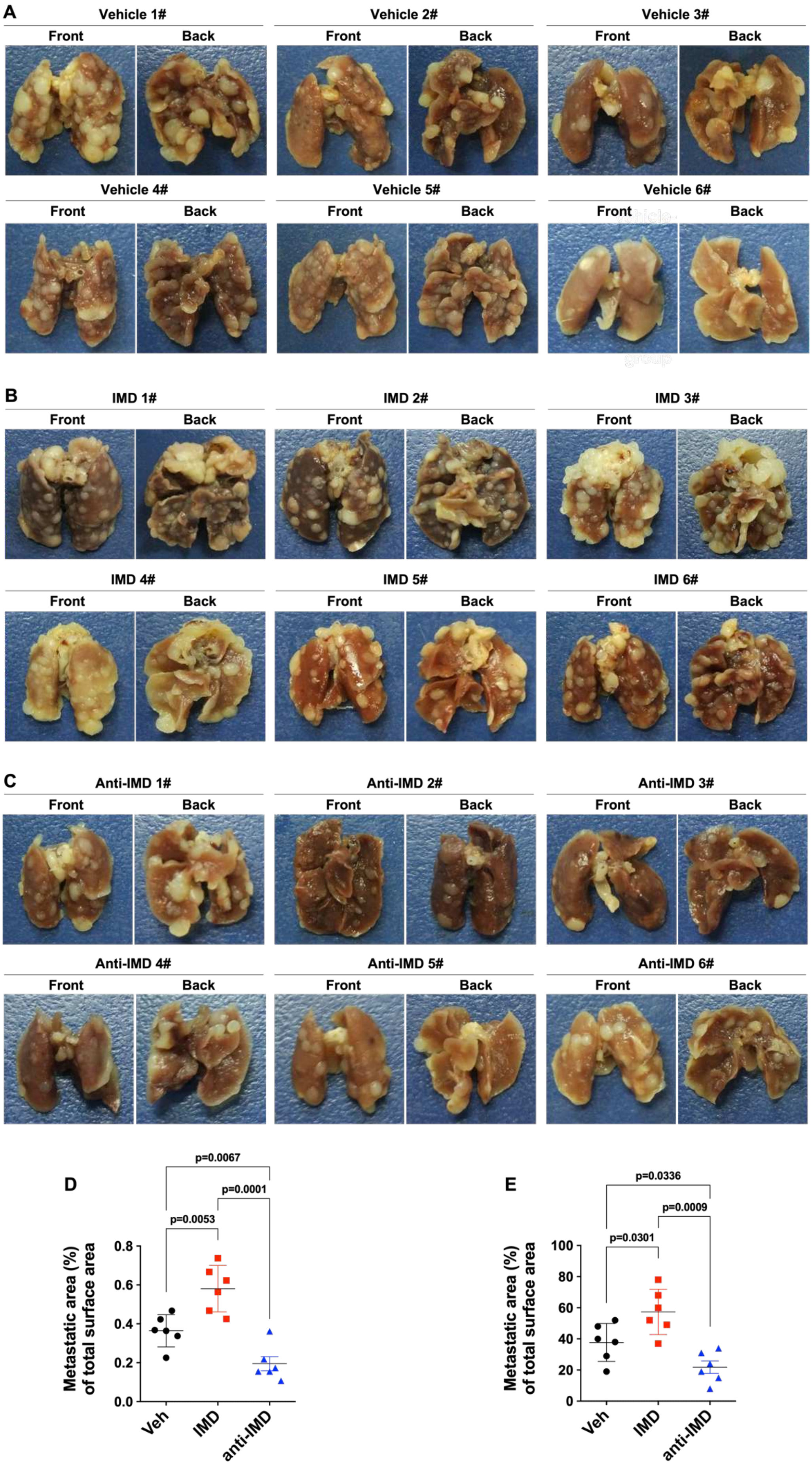


Fig 4. IMD activated a Src/c-Myc signaling pathway. A, The KEGG pathway analysis (KEGG term: *Breast cancer*) showed that treatment with the anti-IMD antibody suppressed the cell cycle (at the G1/S phase) by downregulating c-Myc and cyclin D1 (CCND1). Green borders marked the down-regulated c-Myc and CCND1. **B-C**: The RNA-Seq read counts of c-Myc and CCND1 genes from 4T1 cells treated with vehicle (PBS), IMD (2.5μg/ml), or the anti-IMD antibody (25μg/ml). **D**, The mRNA level changes (Log2. fold change) of cyclins, cyclin-dependent kinases, or cyclin-dependent kinase inhibitors after treatment of the anti-IMD antibody. Green bars indicate the down-regulated genes, and red bars indicate the upregulated genes. **E**, The mRNA level of Src in cell transfected with siR-Scram, siR-Src (or rescued by Lv.Src transfection). The mean value of control Src mRNA was set to 1.0, n=3. **F**, 4T1 cells transfected with siR-Scram, siR-Src (or rescued by Lv.Src transfection) were subjected to WB assay to detect Src phosphorylation. **G**, The density of the band for p-Src (referred to β-actin) is presented relative to that of the control. The mean level in the control group was set to 1.0; n=3. **H**, Level of c-Myc mRNA (relative to control) was calculated (n=3). **I**, 4T1 Cells were treated with IMD or vehicle for 10 min. Cell

lysates were immunoprecipitated for CRLR and probed for total-Src and CRLR (as a reference). **J**, Density of the bands for co-precipitated proteins (relative to CRLR) were presented relative to that of the control, n=3. **K**, The mRNA level of β-arr1 in cell transfected with siR-Scram, siR-β-arr1 (or rescued by Lv.β-arr1 transfection), n=3. **L and N**, 4T1 Cells transfected with siR-Scram, siR-β-arr1 (or rescued by Lv.β-arr1 transfection) with the presence of IMD were immunoprecipitated for CRLR and probed for total-Src or phospho-Src and CRLR (as a reference). **M and O**, Density of the bands for co-precipitated proteins (relative to CRLR) were presented relative to that of the control; The mean level in the control group was set to 1.0; n=3. Data were presented with presented as scatter plots with mean ± SD. Significance was assessed by *unpaired t test with Welch's correction*.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D
p=0.0067
p=0.0001
p=0.0053
Metastatic area (%) of total surface area
0.8
0.6
0.4
0.2
0.0
Veh
IMD
anti-IMD
E
p=0.0336
p=0.0009
p=0.0301
Metastatic area (%) of total surface area
100
80
60
40
20
0
Veh
IMD
anti-IMD

Fig 5. Blockade of IMD reduced spontaneous lung metastasis. A-C, 2.5×10^6 4T1 cells were injected into the mammary fat pad of mice. Seven days after tumor inoculation, the mature IMD peptide (0.25 mg/kg/day, 2 weeks, 14 times in total, subcutaneous injection), or the anti-IMD monoclonal antibody (2.5 mg/kg, twice weekly, 3 times in total, intravenous injection), or vehicle (100 µl of 0.9% saline, twice weekly, 3 times in total, intravenous injection) were administrated. Five weeks after cancer cell inoculation, lungs from the tumor-bearing mice were removed. Pictures of the lungs (front side and back side) from the tumor-bearing mice were shown. **D and E**, Number of metastatic colonies and the metastatic area (%) of total surface area of the lungs were calculated. Data were presented as scatter plots with mean ± SD. Significance was assessed by *unpaired t test with Welch's correction* (n=6).

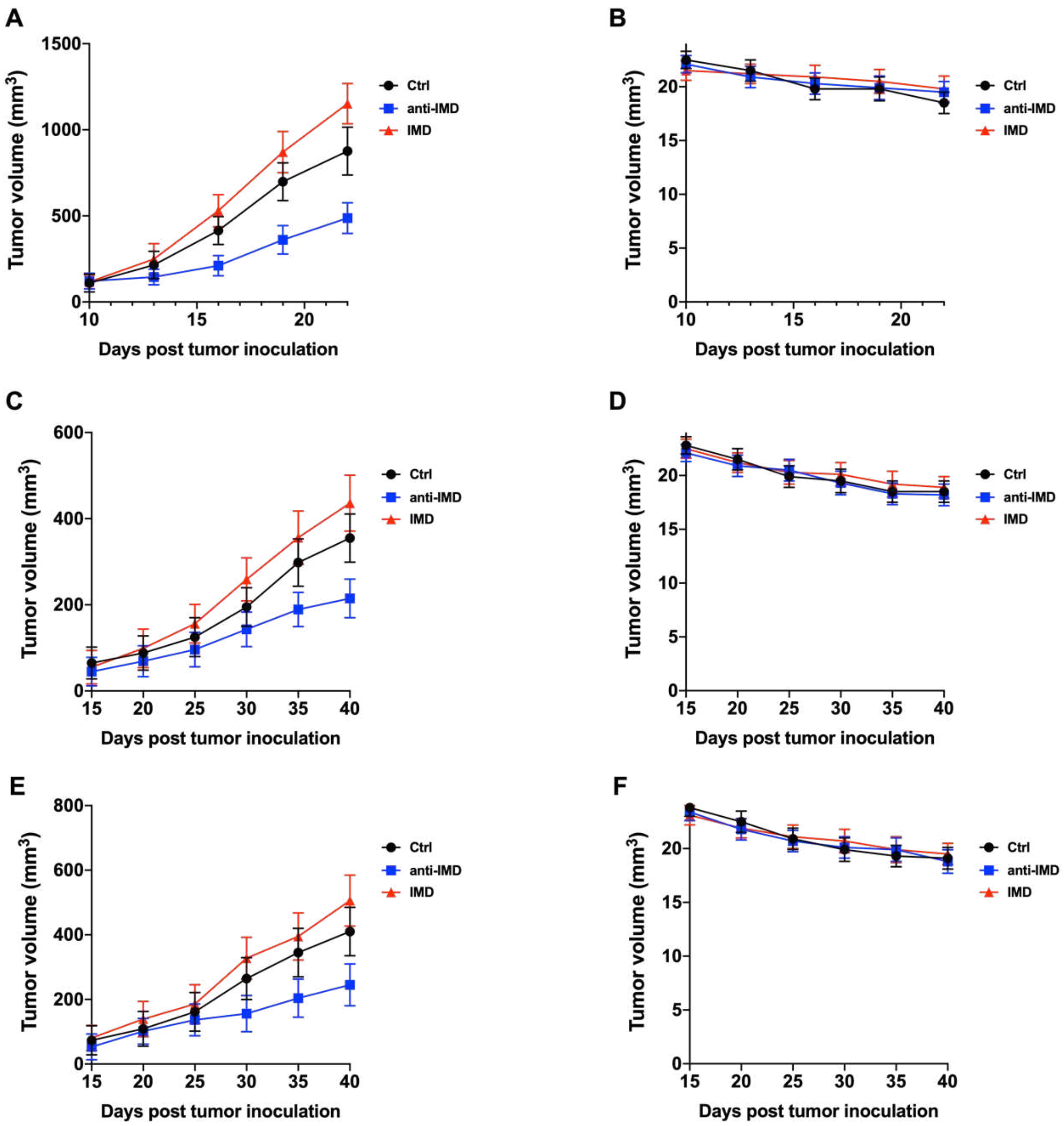

Fig 6. Blockade of IMD reduced the in situ tumor growth. A, C, E 2.5×10^6 4T1 cells, 5×10^6 MDA-MB-231 cells, and 5×10^6 MDA-MB-468 cells were injected into the mammary fat pad of Balb/c or SCID mice. The tumor volumes were measured every 3 days (for 4T1) or 5 days (for 231 and 468). **B, D, E** Body weight of the tumor-bearing mice were measured every 3 days (for 4T1) or 5 days (for 231 and 468). Data were presented as growth curve with plots (mean ± SD). Significance was assessed using the final tumor size by *unpaired t test with Welch's correction* (n=6).