

**Supplementary Table S1. RT-qPCR Primers**

Human Genes			
Gene*	Product Size (bp)	Forward Sequence	Reverse Sequence
AITRL	158	5'-AGCCATTCAAGAACTCAAGGAG-3'	5'-GGTCCAAACTTAGCCATACAGG-3'
ANG2	73	5'-TCTTGGCCGACGCTATAAC-3'	5'-TGCTGGACCTGATATTGCTTCT-3'
APRIL	168	5'-CTCTGCTGACCCAA CA AACAG-3'	5'-TTTTCCGGATCTCTCCCAAT-3'
BAFF	79	5'-GGGAGCATCA CGCCTTAC-3'	5'-CGTGGGAGGATGGAAACACAC-3'
CCL2	152	5'-GATCTCAGTGCA GAGGCTCG-3'	5'-TGCTTGTCAGGTGGTCCAT-3'
CCL20	224	5'-TGCTGTACCAAGAGTTTGCTC-3'	5'-CGCACACAGACA ACTTTTTCTTT-3'
CSF1	228	5'-GCTCTCCCAGGATCTCATCAC-3'	5'-TCAAAGGAACGGAGTTAAAACGG-3'
CXCL1	97	5'-GAAAGCTTGCCCTCAA TCCTG-3'	5'-CTTCCTCCTCCCTTCTGGTC-3'
CXCL2	103	5'-GGGCAGAAAGCTTGCTCAA-3'	5'-GCTTCCTCCTTCTTCTGGT-3'
IL1B	100	5'-CAGCTACGAA TCTCCGACAC-3'	5'-GGCAGGAAACGACATCTTC-3'
IL4	150	5'-CCAACTGCTTCCCCCTCTG-3'	5'-TCTGTTACGGTCAACTCGGTG-3'
IL6	159	5'-AACCTGAACCTTCCAAGATGG-3'	5'-TCTGGCTTGTCTCTCACTACT-3'
IL8	194	5'-TTTTGCCAAGGAGTGCTAAA GA-3'	5'-AACCTCTGCACCCAGTTTTCT-3'
IL10	176	5'-TCAAAGCGCATGTGAACTCC-3'	5'-GATGTCAA ACTCACTCATGGCT-3'
IL13	122	5'-GAAGGCTCCGCTCTGCAAT-3'	5'-TCTGGGTCTTCTCGATGGCA-3'
TGF-β	251	5'-ACGGCGTTACAGTGTTCTG-3'	5'-ACAGTAGTTGGAAGTCTAT-3'
TNF-α	217	5'-ATGACACTGAAA GCATGATCC-3'	5'-GAGGGCTGATTAGAGAGGGTC-3'
VEGFA	117	5'-ATCACGAAGTGGTGAAGTTC-3'	5'-TGCTGTAGGAAGCTCATCTC-3'
β-actin	131	5'-TCCTCTCCCAAGTCCACA CAGG-3'	5'-GGGCAGAAAGGCTCATCATTC-3'

Mouse Genes			
Gene*	Product Size (bp)	Forward Sequence	Reverse Sequence
AITRL	131	5'-ATGTCTTTCTAACCTTGATC-3'	5'-AGAGTTTGGAGGATTAAGG-3'
Ang 2	68	5'-TGGTACTACTGGAA GGGGTCCG-3'	5'-GAAATCTGCTGGCCGGATCA-3'
APRIL	109	5'-AGTCCTGCATCTTGTTCCAG-3'	5'-TGTCTTCCCAGATACACAC-3'
BAFF	129	5'-TGGGTCA TGTCATCCAGAGG-3'	5'-CATCTCCTTCTTCCAGCCTC-3'
CCL2	91	5'-CCA CTCACTGCTGCTA CTC-3'	5'-GGTTCGGATCCAGGTTTTTA-3'
CCL20	179	5'-AGGCAGAA GCAAGCAACTAC-3'	5'-TTTTACCCAGTTCTGCTTT-3'
CSF1	149	5'-ACAGAGGACCAAAA GCCAGT-3'	5'-ACGGGGTGGCTGAGTTGCT-3'
CXCL1	168	5'-GCTGGGATTACCTCAAGAA-3'	5'-TGGGGACACCTTTTAGCATC-3'
CXCL2	175	5'-AGGCTACA GGGGCTGTTGT-3'	5'-TTCA GGGTCAAGGCAAACTT-3'
IL1B	89	5'-CAGCTACGAA TCTCCGACAC-3'	5'-GGCAGGAA CCA GCATCTTC-3'
IL4	169	5'-AGTTGTCA TCCTGCTTCT-3'	5'-CTGTGGTGTCTTCTGTTGCT-3'
IL6	76	5'-TAGTCCTTCC TACCCCAATTCC-3'	5'-TTGGTCTTAGCCACTCCTTC-3'
IL10	149	5'-TGCA GTGTGTA TTGAGTCTG-3'	5'-GCTCAGTGAATAAA TAGAAT-3'
IL13	179	5'-GTCTCTCCCTCTGACCCCTA-3'	5'-CTCTGGGTCTGTAGATGGC-3'
TGF-β	133	5'-CTCCCGTGGCTTCTAGTGC-3'	5'-GCCTTAGTTGGACAGGATCTG-3'
TNF-α	61	5'-CCCTCACACTCAGATCATCTTCT-3'	5'-GCTACGACGTGGGCTACAG-3'
VEGFA	105	GCACATAGAGAGAATGAGCTTCC	5'-CTCCGCTGTAAACAAGGCT-3'
β-actin	153	5'-GGCTGTATTCCCCTCCATCG-3'	5'-CCAGTTGGTAA CAATGCCATGT-3'

\*Primers were designed based on human or mouse CDS of targets found in NCBI database. All primers were validated using human and mouse universal cDNA. Primers were confirmed to exclusively detect species-specific cDNA.

**Supplementary Table S2.** Effect of TLR4 on incidence and metastatic burden in nab-PXL treated and untreated mice

Organ	TLR4 Status	Treatment <sup>a</sup>	Incidence	Burden <sup>b</sup>	Fold Change <sup>c</sup>	P-Value	
						TLR4- vs. TLR4+	Untreated vs. Treated
<b>MDA-MB-231 Model</b>							
Lymph Nodes	TLR4+	---	100	344.7 ± 92.6	--	---	---
Lungs	TLR4+	nab-PXL	100	139.1 ± 96.3	2.5↓	---	NS <sup>d</sup>
	TLR4+	---	100	23.5 ± 11.3	--	---	---
Lungs	TLR4+	nab-PXL	100	11.3 ± 3.8	2.1↓	---	NS
	TLR4-	---	100	222.8 ± 100.6	--	NS	---
Lungs	TLR4-	nab-PXL	20	50.0 <sup>e</sup>	4.4↓	NS	---
	TLR4-	---	80	2.7 ± 0.9	--	0.03	---
Lungs	TLR4-	nab-PXL	20	0.6	4.5↓	0.003	0.04
	<b>HCC1806 Model</b>						
Lymph Nodes	TLR4-	---	50	19.5 ± 11.4	--	---	---
	TLR4-	nab-PXL	20	2.1 ± 1.7	9.3↓	---	NS
Lungs	TLR4-	---	10	0.2	--	---	---
	TLR4-	nab-PXL	30	1.1 ± 1.0	<b>5.5↑</b>	---	NS
Lymph Nodes	TLR4+	---	50	5.4 ± 2.4	--	NS	---
	TLR4+	nab-PXL	90	1325.5 ± 649.3	<b>245.3↑</b>	0.008	0.002
Lungs	TLR4+	---	40	0.1 ± 0.08	--	NS	---
	TLR4+	nab-PXL	90	1.2 ± 0.3	<b>12.0↑</b>	0.01	0.004

<sup>a</sup>Mice were treated with nab-PXL at the dose of 10 mg/kg for 10 days

<sup>b</sup>Expressed as RLU/mg of total protein × 10<sup>4</sup> ± SEM

<sup>c</sup>Fold decrease (↓) or increase (↑) as compared with untreated controls; increases are bolded

<sup>d</sup>NS, non-significant

<sup>e</sup>The values without SEM indicate a single positive animal per group