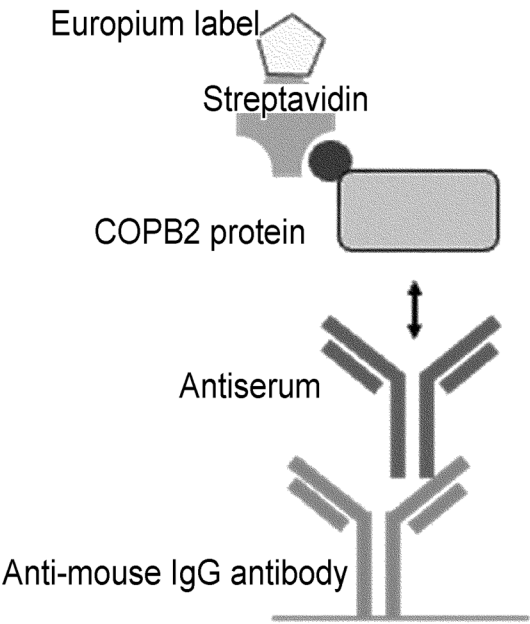
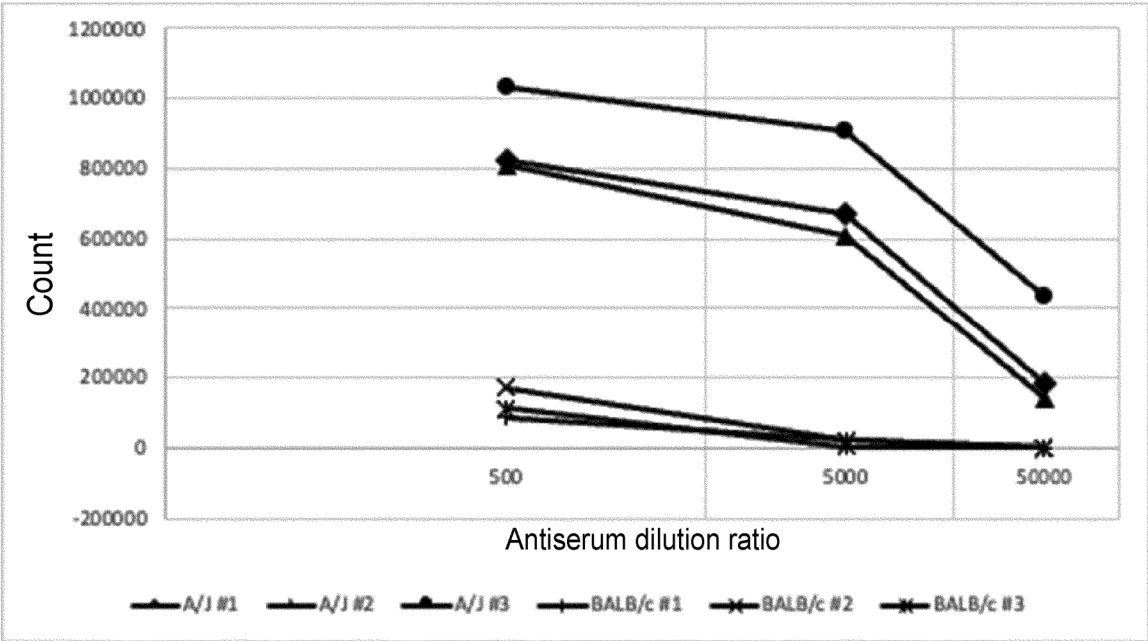


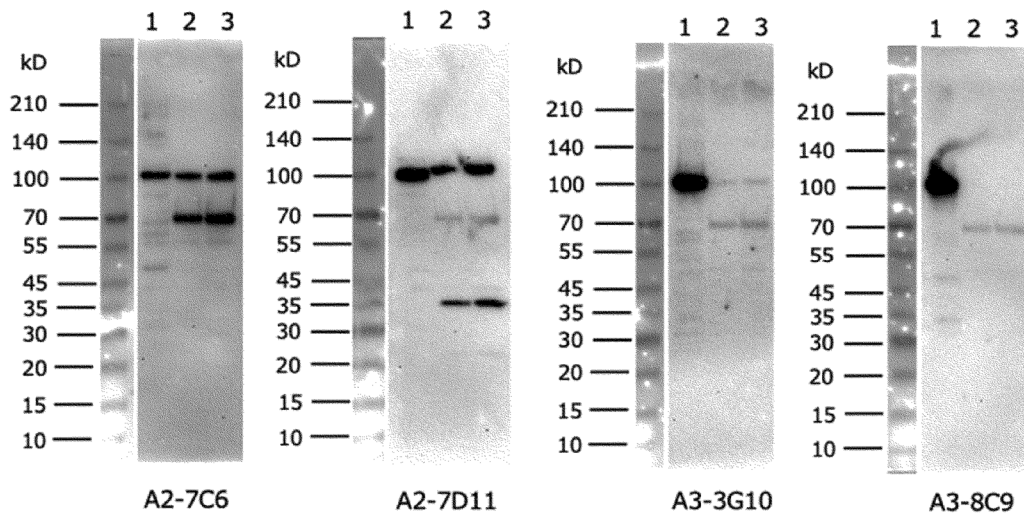
[Figure 1]



[Figure 2]



[Figure 3]



[Figure 4A]

Clone name	CDR name	Amino acid sequence	SEQ ID NO
A2-7C6	Heavy chain CDR1	EFTFSRNG	SEQ ID NO:1
	Heavy chain CDR2	ISSGGVST	SEQ ID NO:2
	Heavy chain CDR3	CARHEGSRFAYW	SEQ ID NO:3
	Light chain CDR1	QDINSY	SEQ ID NO:4
	Light chain CDR2	LVN	SEQ ID NO:5
	Light chain CDR3	CLQYDEFPLTF	SEQ ID NO:6

[Figure 4B]

Clone name	Sequence name	Amino acid sequence	SEQ ID NO
A2-7C6	Heavy chain variable region	MSTEHGPLTMNFGLSLIFLVILKGVQCEVQLVESG GGLVKPGGSLKLSCAASEFTFSRNGMSWVRQTPA KRLEWVATISSGGVSTYYPD TVKGRFTISRDN AKNT LYLQMSSLRSEDTAMYYCARHEGSRFAYWGQGT LVTVSA	SEQ ID NO:19
	Light chain variable region	MQLESSGVLPGLSMDMRTPAQFLGILLWFPGIK CDIKMTQSPSSMYTSLGERVTITCKASQDINSYLSW FQQKPGNSPKTLIYLVNRLVDGVPSRFSGSGSQD YSLTIGSLEFEDVGIYYCLQYDEFPLTFGAGTKLELK	SEQ ID NO:20

[Figure 5A]

Clone name	CDR name	Amino acid sequence	SEQ ID NO
A2-7D11	Heavy chain CDR1	GFTFNNSA	SEQ ID NO:7
	Heavy chain CDR2	ISNGGVT	SEQ ID NO:8
	Heavy chain CDR3	CARGHYPYFFDYW	SEQ ID NO:9
	Light chain CDR1	QDINNY	SEQ ID NO:10
	Light chain CDR2	RAN	SEQ ID NO:11
	Light chain CDR3	CLQYDEFPLTF	SEQ ID NO:12

[Figure 5B]

Clone name	Sequence name	Amino acid sequence	SEQ ID NO
A2-7D11	Heavy chain variable region	MSTEHRHLMNFGSLIFLVVLKGVQCEVKLVES GGGLVKPGGSLKLSVASGFTFNNSAMSWVRQTP EKRLWVSSISNGGVTFYPDNVKGRTISRDDARDI LYLQMSSLKSEDTAMYYCARGHYPYFFDYWGQGT TLTVSS	SEQ ID NO:21
	Light chain variable region	MDMRTPAQFLGILLWFPGIKCDIKMTQSPSSMYA SLGERVTITCKASQDINNYSWFQQKPGKSPKTLIY RANRLVDGVPSRFSGSGSGRDYSLTISSEYEDIGIY YCLQYDEFPLTFGAGTKLELK	SEQ ID NO:22

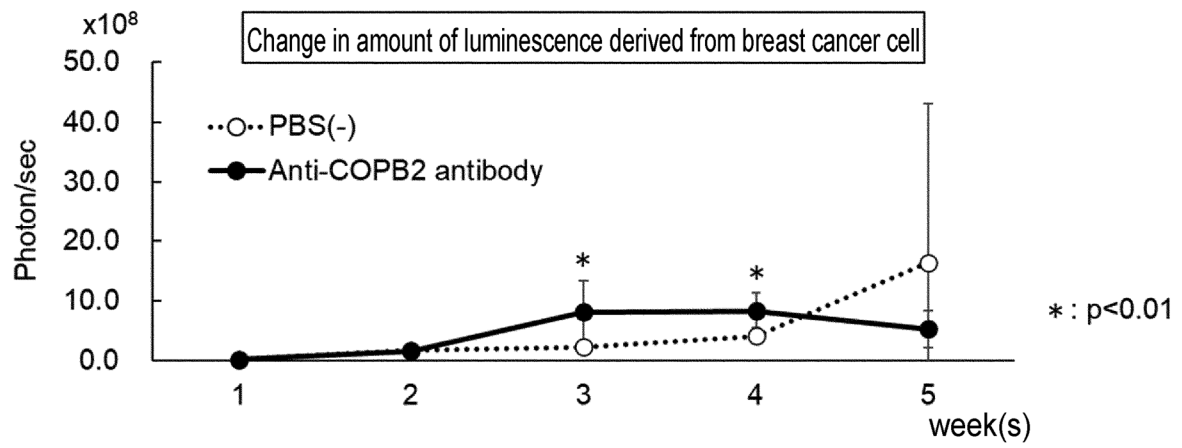
[Figure 6A]

Clone name	CDR name	Amino acid sequence	SEQ ID NO
A3-8C9	Heavy chain CDR1	GYTFTNYG	SEQ ID NO:13
	Heavy chain CDR2	INTYSGVA	SEQ ID NO:14
	Heavy chain CDR3	CARADLFAYW	SEQ ID NO:15
	Light chain CDR1	QSLVHSNGNTY	SEQ ID NO:16
	Light chain CDR2	KVS	SEQ ID NO:17
	Light chain CDR3	CSQSTHVPRTF	SEQ ID NO:18

[Figure 6B]

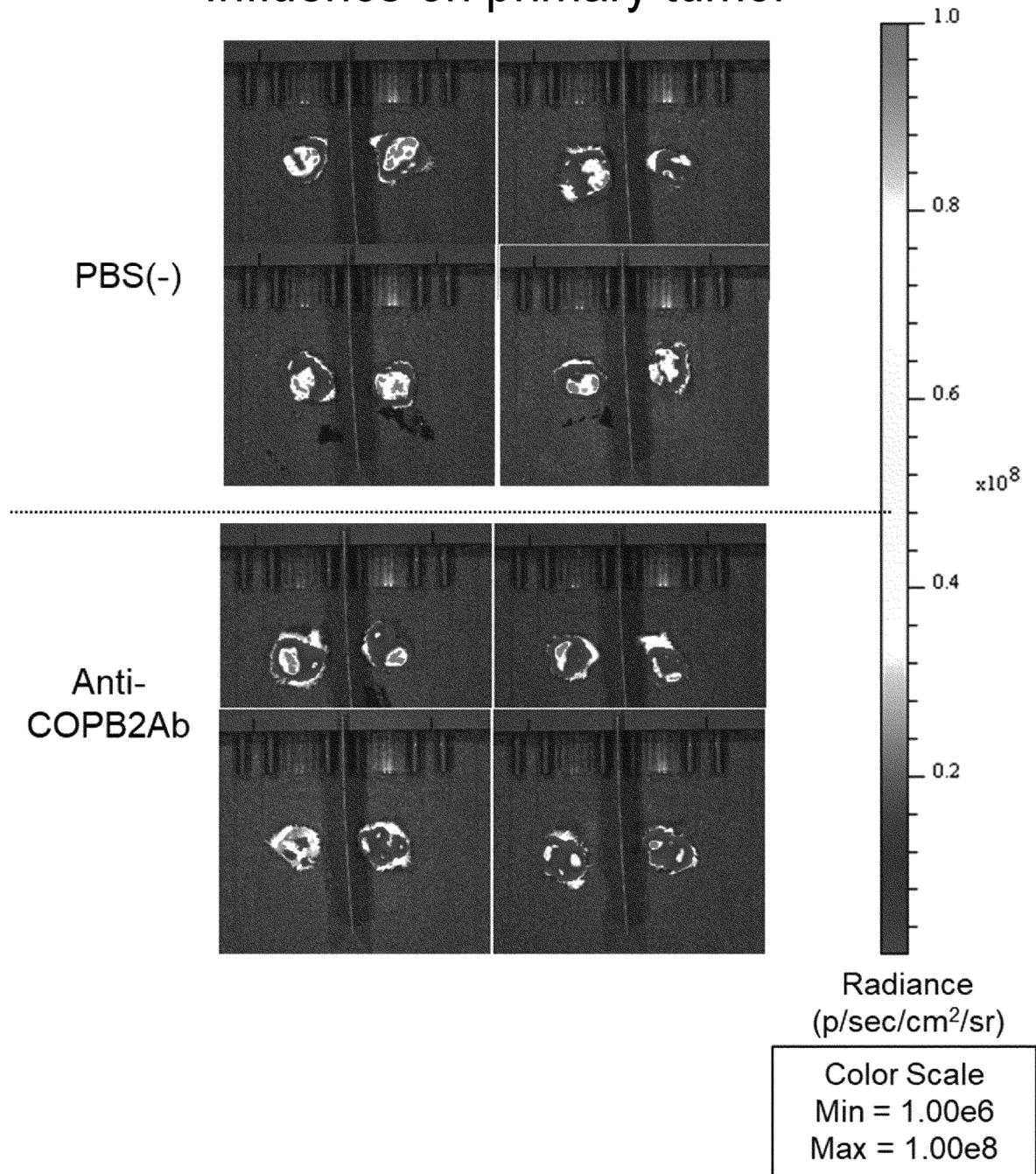
Clone name	Sequence name	Amino acid sequence	SEQ ID NO
A3-8C9	Heavy chain variable region	MDWVWNLLFLMAAAQSIQAQIQLVQSGPELKKP GETVKISCKASGYTFTNYGMNWKQAPGKGLK WMAWINTYSGVATHADDFKGRFDFSLETSASTA YLQINNLLKNETATYFCARADLFAYWGQGTLLVT VSA	SEQ ID NO:23
	Light chain variable region	MKLPVRLLVLMFWIPASSSDVVMQTPLSLPVS LGDQASISCRSSQSLVHSNGNTYLHWYLVKPGQ SPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISR VEAEDLGVFCSQSTHVPRTFGGGTKLEIK	SEQ ID NO:24

[Figure 7]



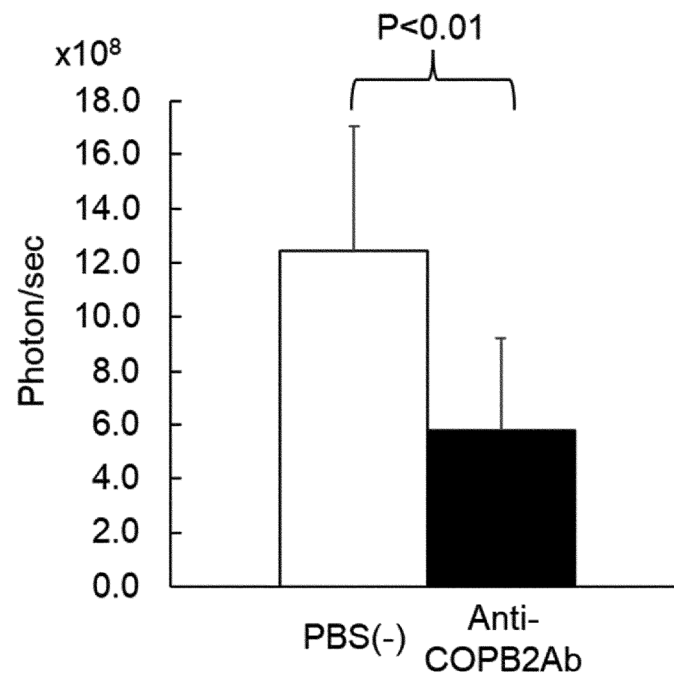
[Figure 8]

- Influence on primary tumor -



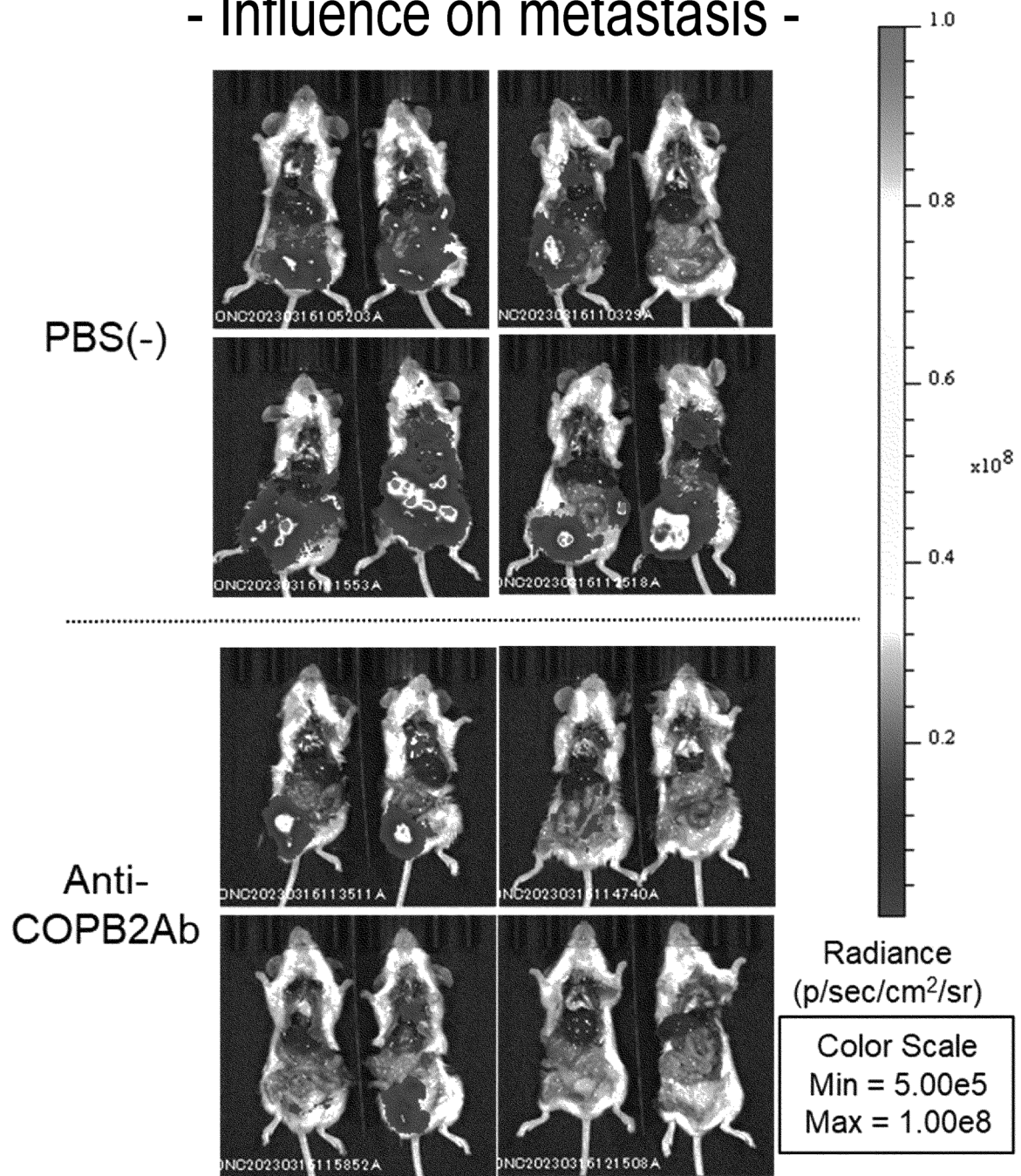
[Figure 9]

- Influence on primary tumor -



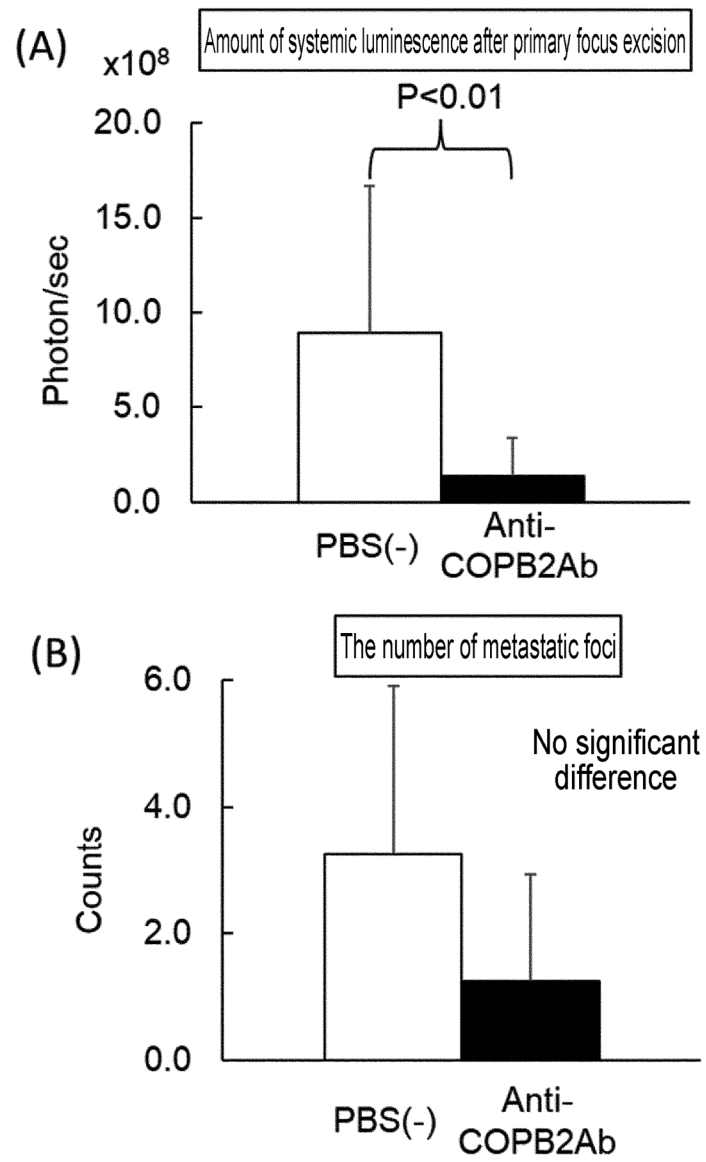
[Figure 10]

- Influence on metastasis -



[Figure 11]

- Influence on metastasis -



[Figure 12]

Sequence name	Amino acid sequence	SEQ ID NO
Full-length amino acid sequence of human COPB2	MPLRLDIKRKL TARSDRVKSVDLHPTPEWMLASLYNGSVCVWNHETQTLVKTFEVCDDL PVRAAKFVA RKNWVVTGADDMQIRVFNYNTLERVHMFEAHSDYIRCIADVHPTQPFIL TSSDDMLIKLWDWDKKWSC SQVFEHGHYVMQIVINPKDNNQFASASLDRITIKVWQLGSSSPNFTLEGHEKGVNCIDYYSGGDKPYL ISGADDRLVKIWDYQNKTCVQTLEGHAQNVSCASFHPELPIITGSEDGTVRIWHSSTYRLESTLNYGM ERVWCVASLRGSNNVALGYDEGSIVKLGREEPAMSMMDANGKIWAKHSEVQQANLKAMGDAEIKDG ERLPLAVKDMGSCIEYPQTIQHNPNGRFVVVCGDGEYIYTAMALRNKSFGSAQEFAWAHDSSSEYAIR ESNSIVKIFKNFKEKKSFKPDFGAESYGGFLLGVRSVNGLA FYDWDNTELRIRRIEIQPKHIFWSDSGELV CIA TEESFFILKYLSEKVLAAQETHEGVTEGIEDAFEVLGEIQEIVKTGLWVGDCFIYTSSVNRLNYYVG GEIVTIAHLDRMTMYLLGYIPKDNRLYLGDKELNIISYLLSVLEYQTAVMRRDFSMADKVLPTIPKEQR TRVAHFLEKQGFQQAL TVSTDPEHRFELALQLGELKIAYQLAVEASEQKWQLAELAIKCCQFGLA QECLHHAQDYGGLLLLLATASGNANMNVNKLAEGAERDGKNNVAFMSYFLQGVKVDACLELLIRTGRLP EAAFLARTYLP SQVSRVVKLWRENLSKVNQKAAESLADPT EYENLFPGLKEAFVVEEWVKETHADLW PAKQYPLVTPNEERNVMEEGKDFQPSRSTAQQELDGKPSPTPVIVASHTANKEEKSLELEVDLDNL ELEDIDTTDINLDEIDDD	SEQ ID NO:31

[Figure 13A]

Clone name	CDR name	Amino acid sequence	SEQ ID NO
TA201C003a	Heavy chain CDR1	GYTFTSY	SEQ ID NO:32
TA201C003a	Heavy chain CDR2	INPSTGST	SEQ ID NO:33
TA201C003a	Heavy chain CDR3	TRGGITMVRGVSPHYGMDV	SEQ ID NO:34
TA201C003a	Light chain CDR1	QSVLYTSNNKNY	SEQ ID NO:35
TA201C003a	Light chain CDR2	WAS	SEQ ID NO:36
TA201C003a	Light chain CDR3	QQYYRTPT	SEQ ID NO:37

[Figure 13B]

Clone name	Sequence name	Amino acid sequence	SEQ ID NO
TA201C003a	Heavy chain variable region	MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASG YTFTSYLHWVRQAPGQGLEWMGIINPSTGSTMYAQLQGSVTMTR DTSTSTVYMELSSLRSEDVAVYYCTRGGITMVRGVSPHYGMDVWG QGTTTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHNKPSNTKVDKKVEPKSCDKHTCTPPCPAPELLGGPSVFLFP	SEQ ID NO:44
TA201C003a	Light chain variable region	MVLQTQVFISLLWISGAYGDIVMTQSPDSLAVSQGERATINCKSSQS VLYTSNNKNYLGWYQQKPGQPPKLLIYWASTRESGVPRFSGSGSG TDFTLTISSLQAEDVAVYYCQQYYRTPTFGGGTKVEIKRTVAAPSVFIF PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDS	SEQ ID NO:45

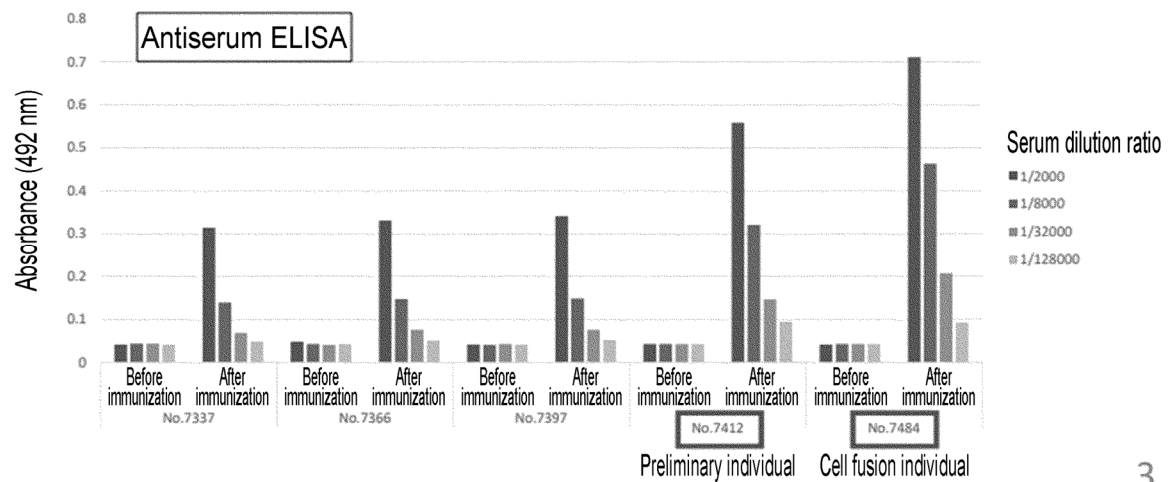
[Figure 14A]

Clone name	CDR name	Amino acid sequence	SEQ ID NO
TA201B010a	Heavy chain CDR1	GFTFSSYS	SEQ ID NO:38
TA201B010a	Heavy chain CDR2	ISSSGSYI	SEQ ID NO:39
TA201B010a	Heavy chain CDR3	ARDHGSYYGSGSYCWFD	SEQ ID NO:40
TA201B010a	Light chain CDR1	QGISIW	SEQ ID NO:41
TA201B010a	Light chain CDR2	AAS	SEQ ID NO:42
TA201B010a	Light chain CDR3	QQADSFPLT	SEQ ID NO:43

[Figure 14B]

Clone name	Sequence name	Amino acid sequence	SEQ ID NO
TA201B010a	Heavy chain variable region	MELGLRWVFLVAILEGVQCEVQLVESGGGLVKPGGSLRLSCAASGFT FSSYSMHWVRQAPGKGLEWVSSISSGSYIFYADSVRGRFTISRDN KNSLFLQMNSLRAEDTAVYYCARDHGSYYGSGSYCWFDWPWGQGT LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKHTHTCPPCPAPELLGGPSVFLFP	SEQ ID NO:46
TA201B010a	Light chain variable region	MDMRVPAQLLGLLLWFPGSRCDIQTQSPSSVSASVGDRVTITCR ASQGISIWLAWYQKPKGAPKLLIYAASSLQSGVPSRFGSGSGTDFT LTISSLQPEDFATYYCQQADSFPPLTFGGGTKVEIKRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDS	SEQ ID NO:47

[Figure 15]

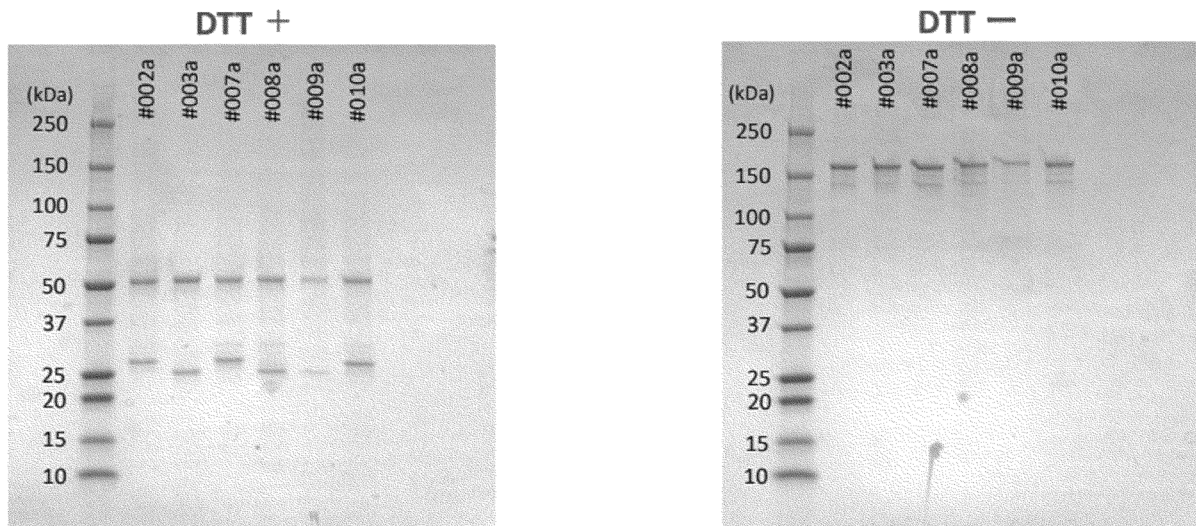


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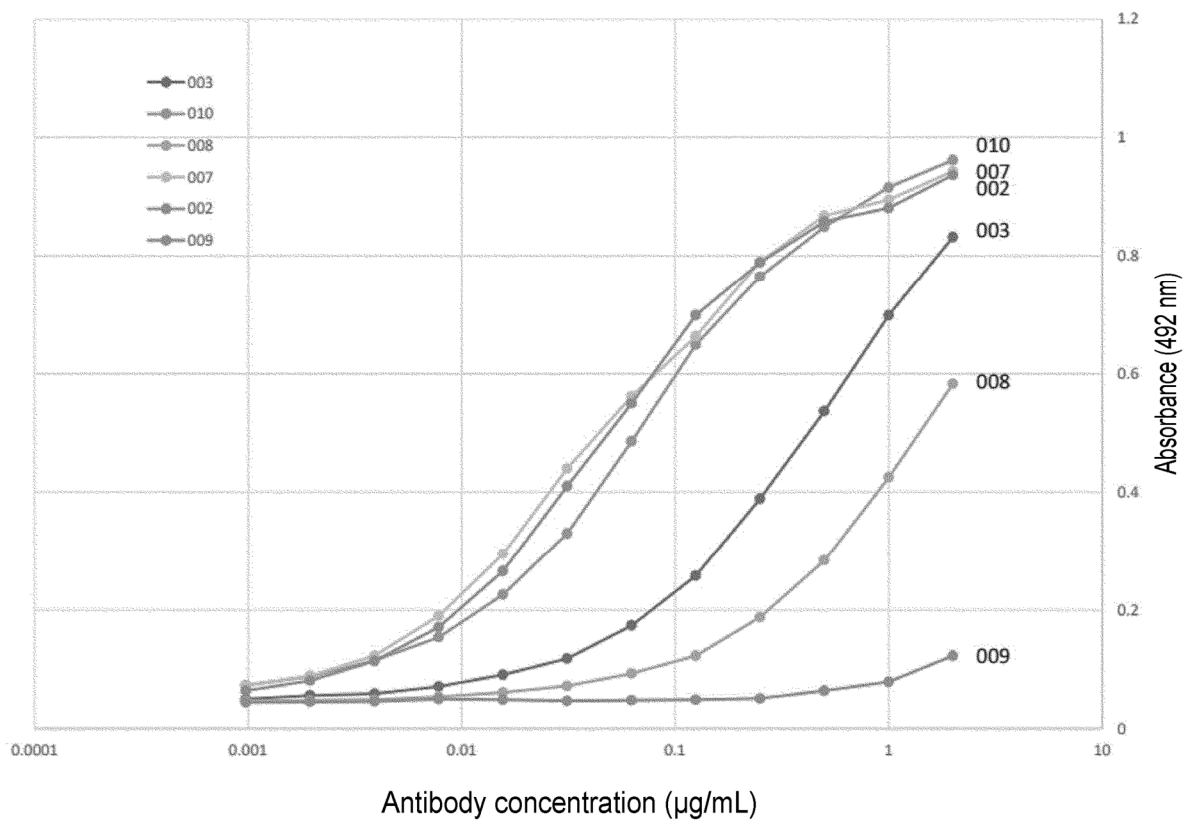
[Figure 16]

Clone No	#001	#002	#003	#004	#005	#006	#007	#008	#009	#010
<i>E. coli</i> -derived antigen	0.758	0.775	0.812	0.722	0.723	0.727	0.743	0.818	0.813	0.866
Animal-derived antigen	0.715	0.772	0.729	0.648	0.634	0.726	0.751	0.719	0.689	0.71

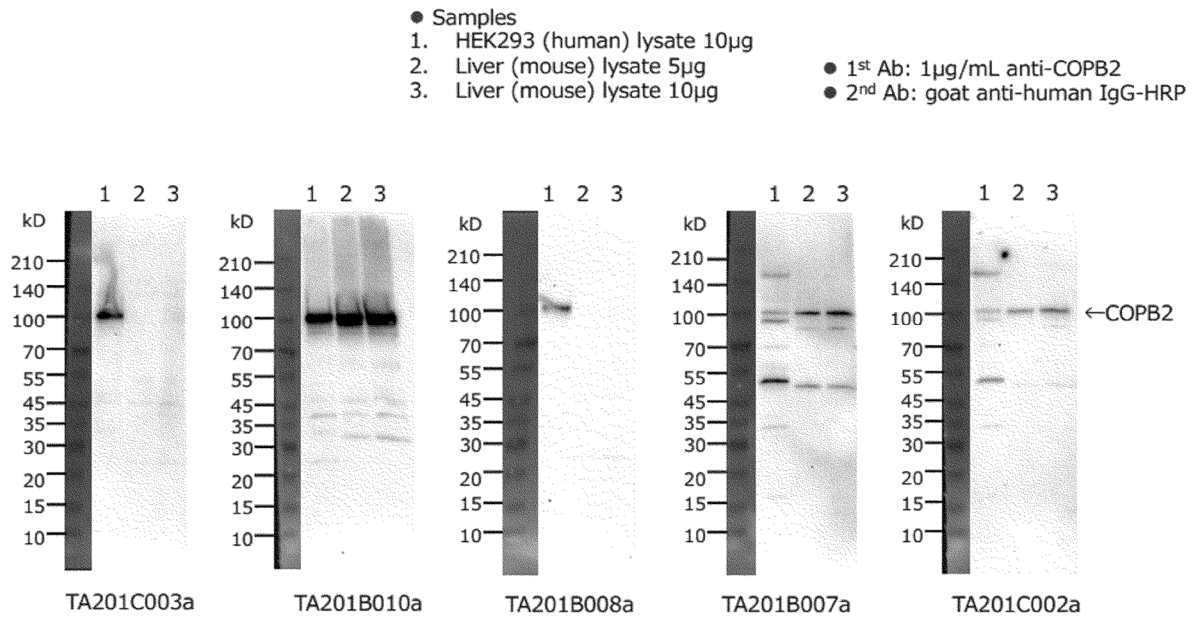
[Figure 17]



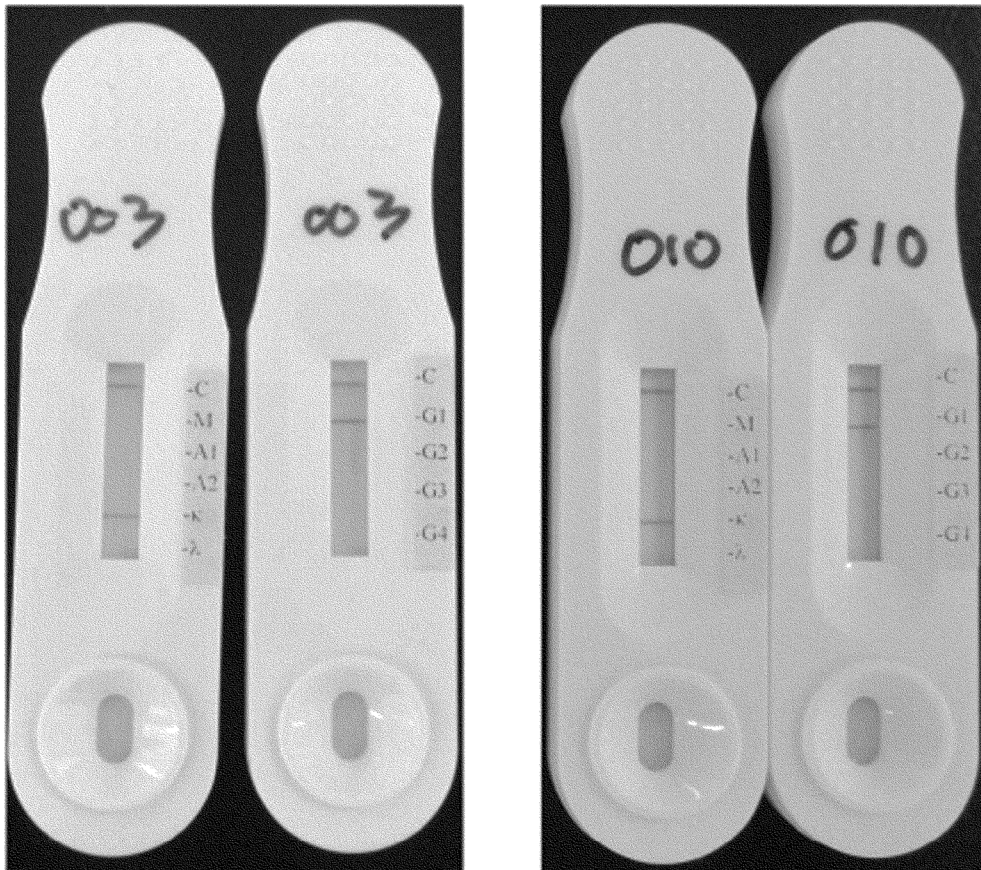
[Figure 18]



[Figure 19]



[Figure 20]



Both #003 and #010 were confirmed to have IgG1/kappa subclass

[Figure 21]

