

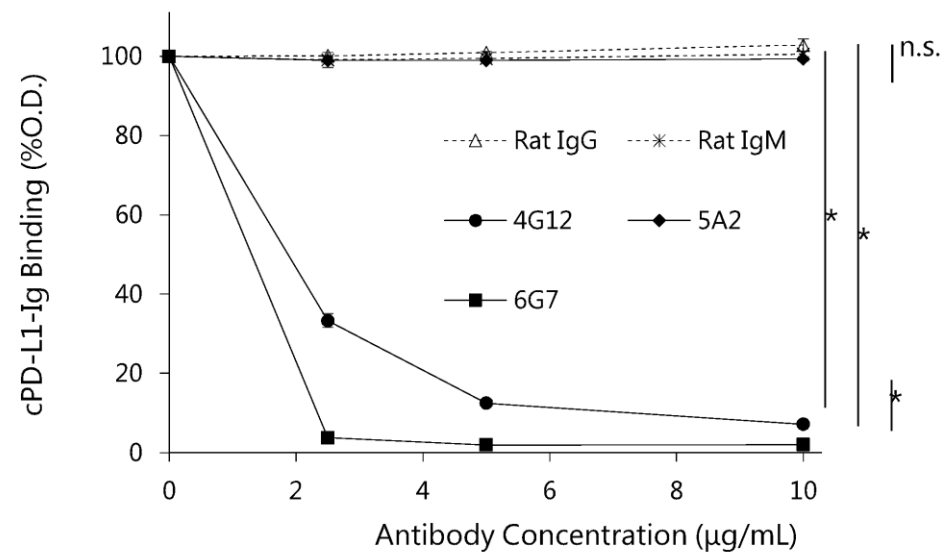
Fig. 1

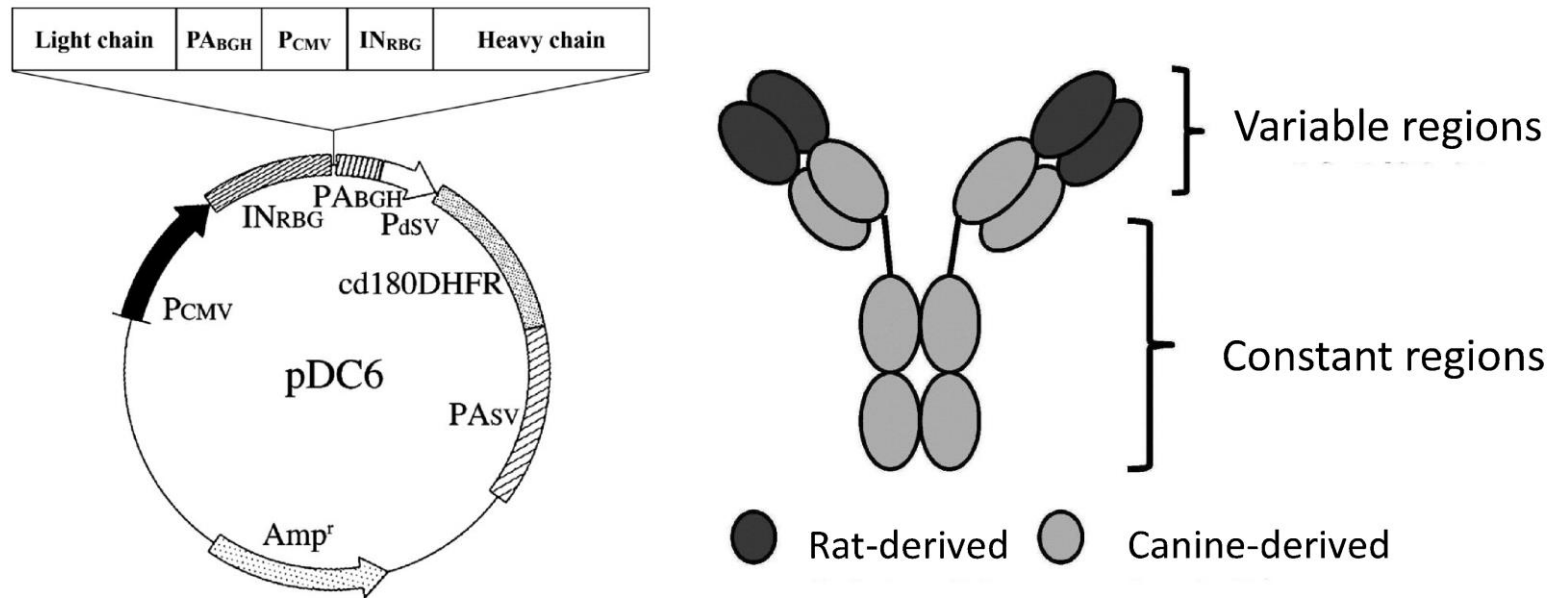
Fig. 2

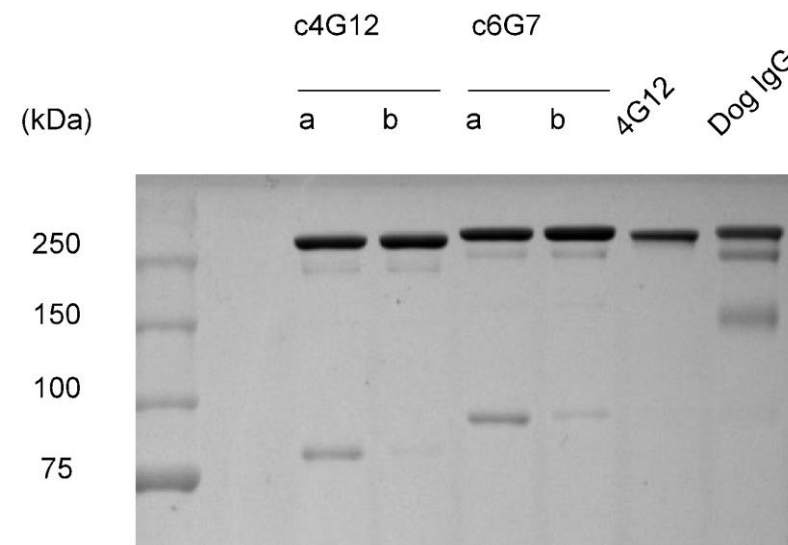
Fig. 3

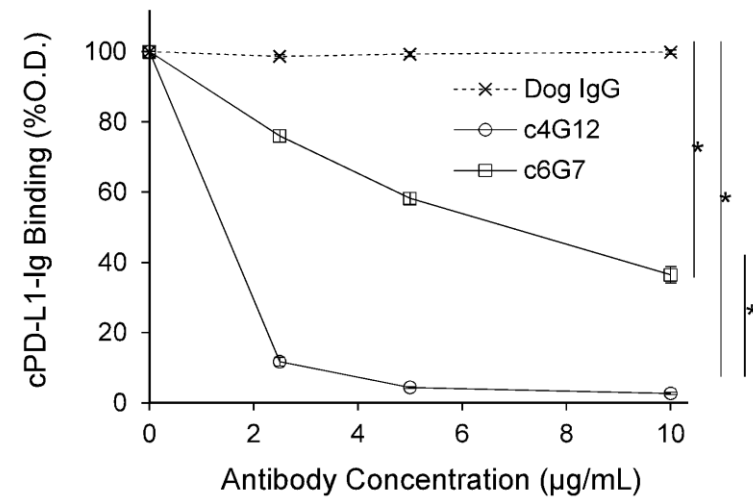
Fig. 4

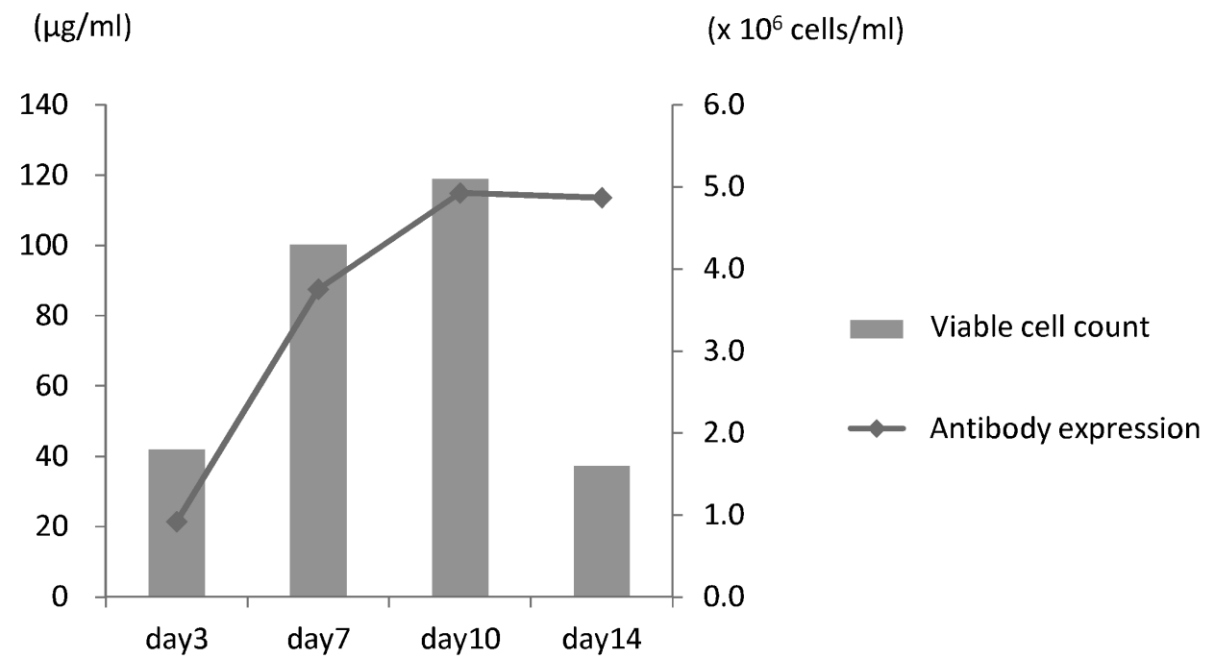
Fig. 5

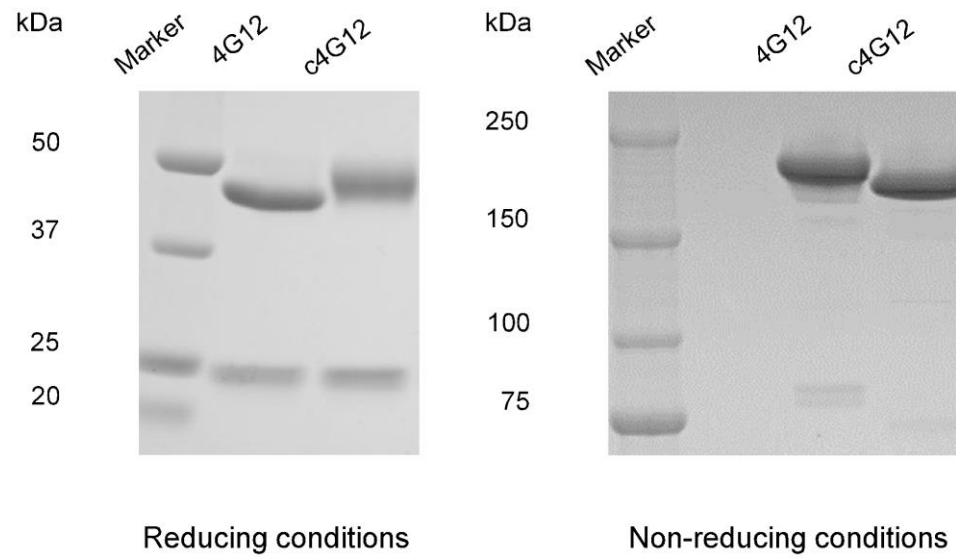
Fig. 6

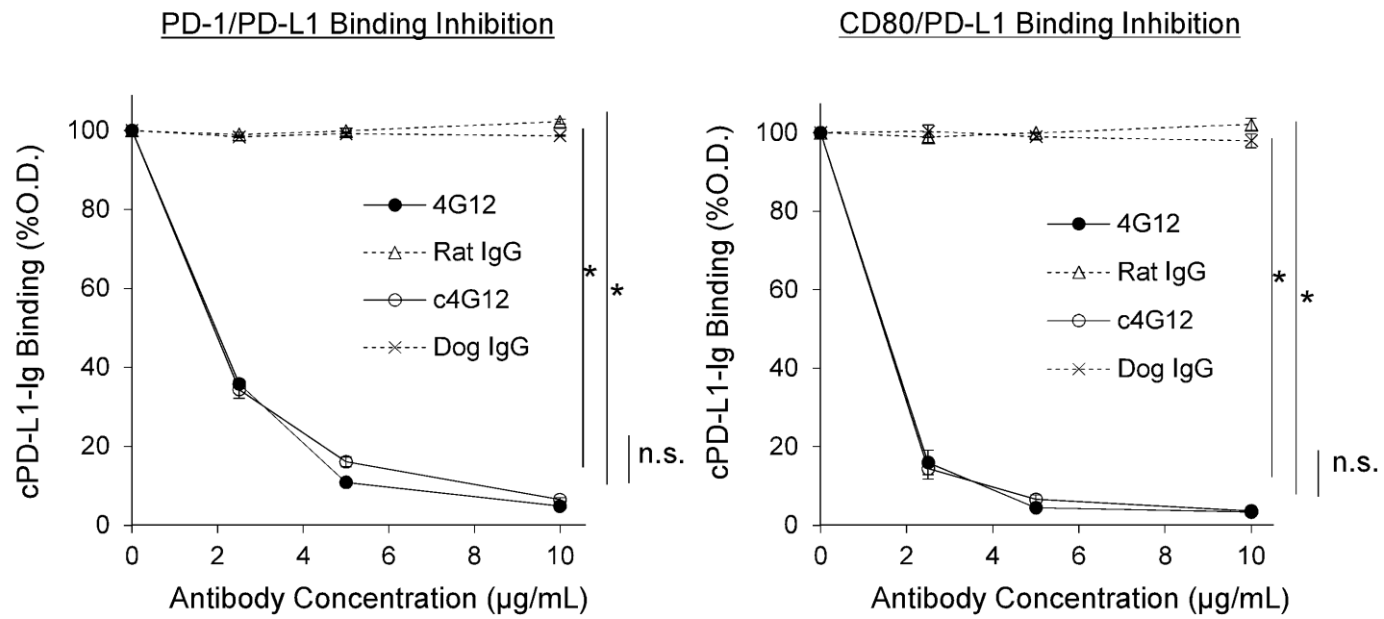
Fig. 7

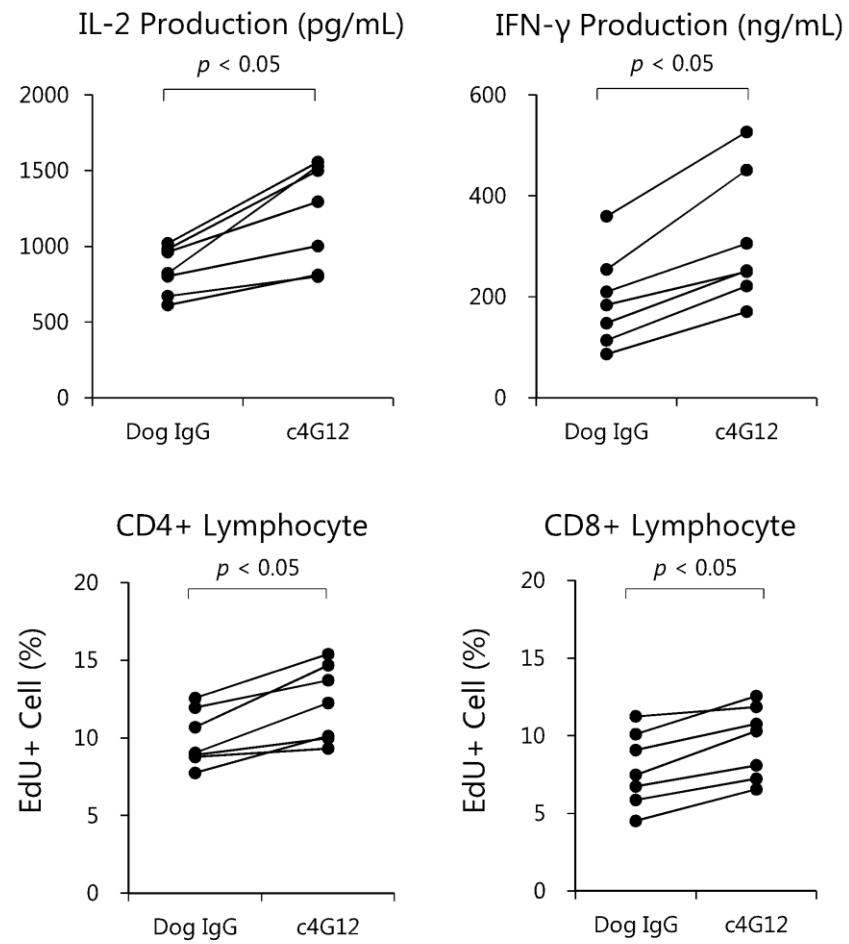
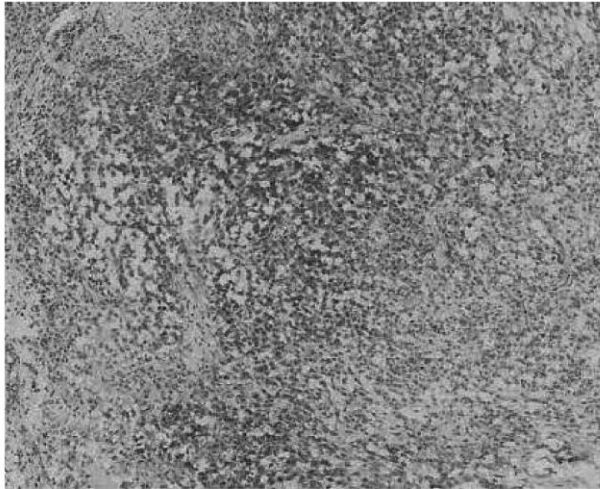
Fig. 8

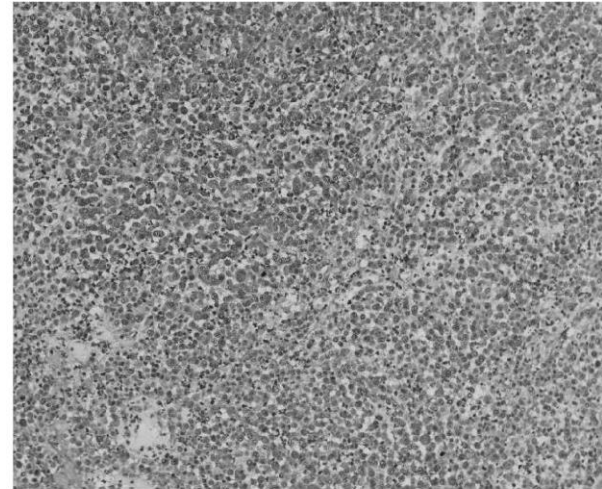
Fig. 9

A



Oral melanoma

B



Undifferentiated sarcoma

Fig. 10

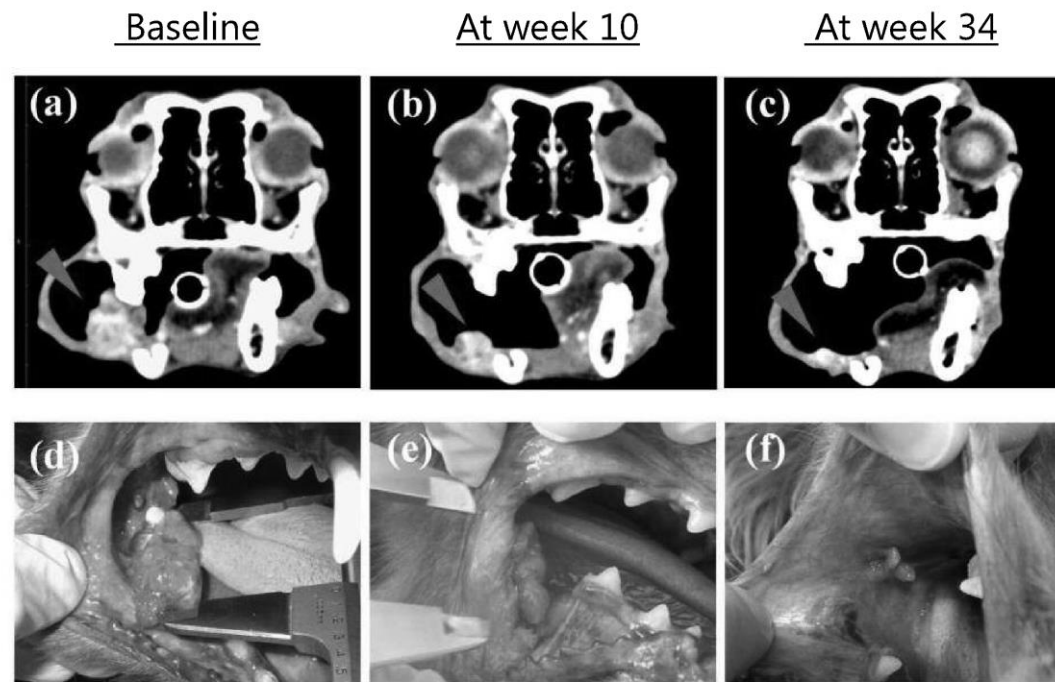


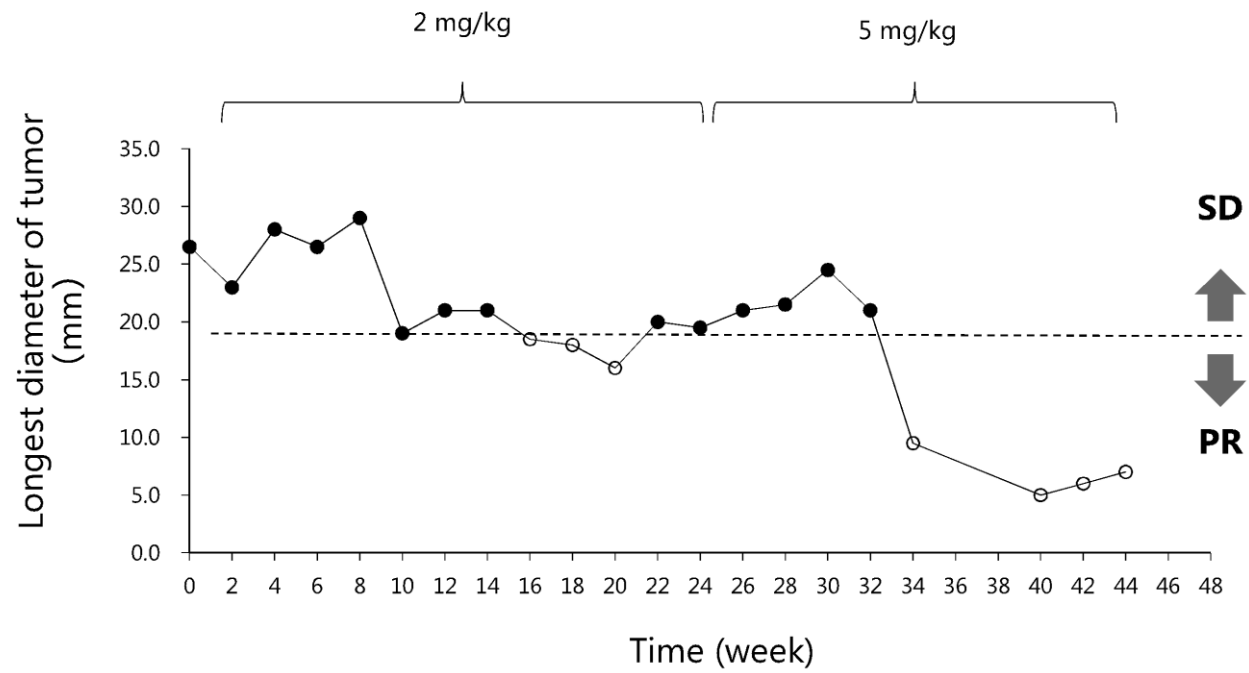
Fig. 11

Fig. 12

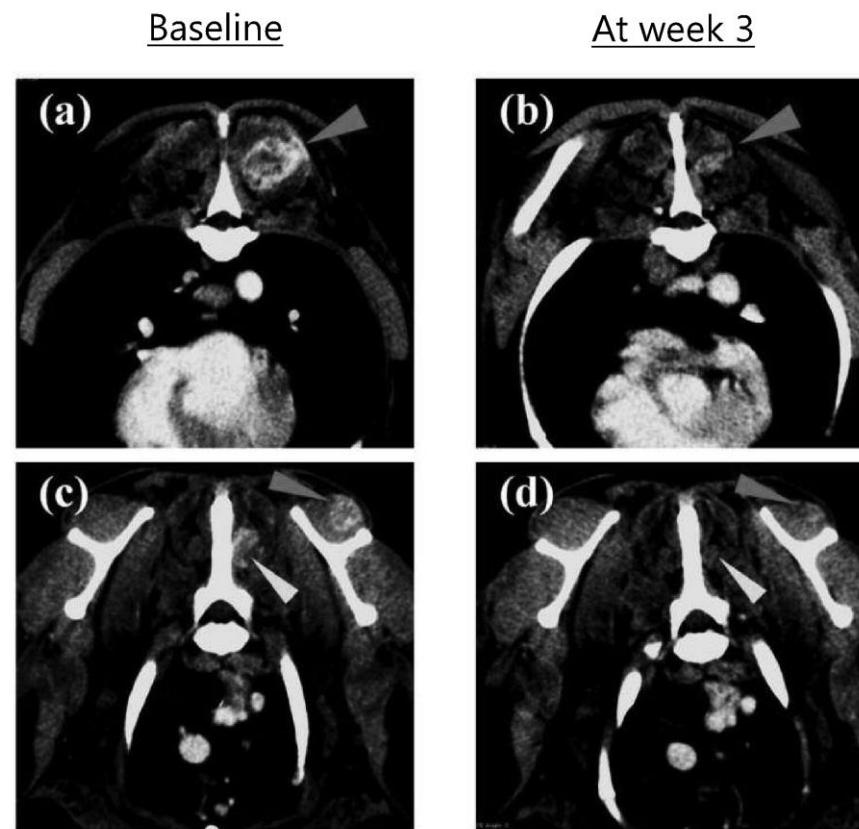


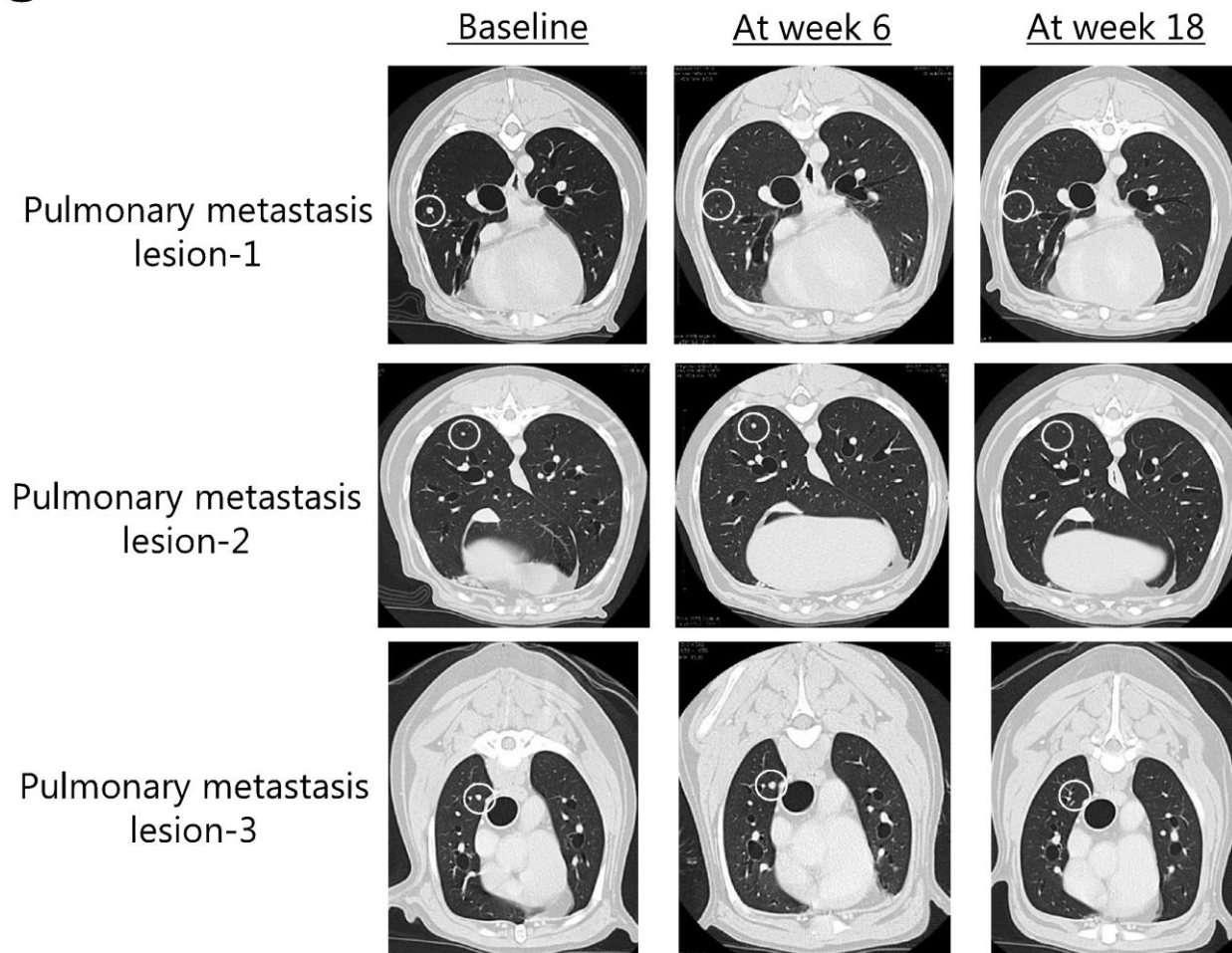
Fig. 13

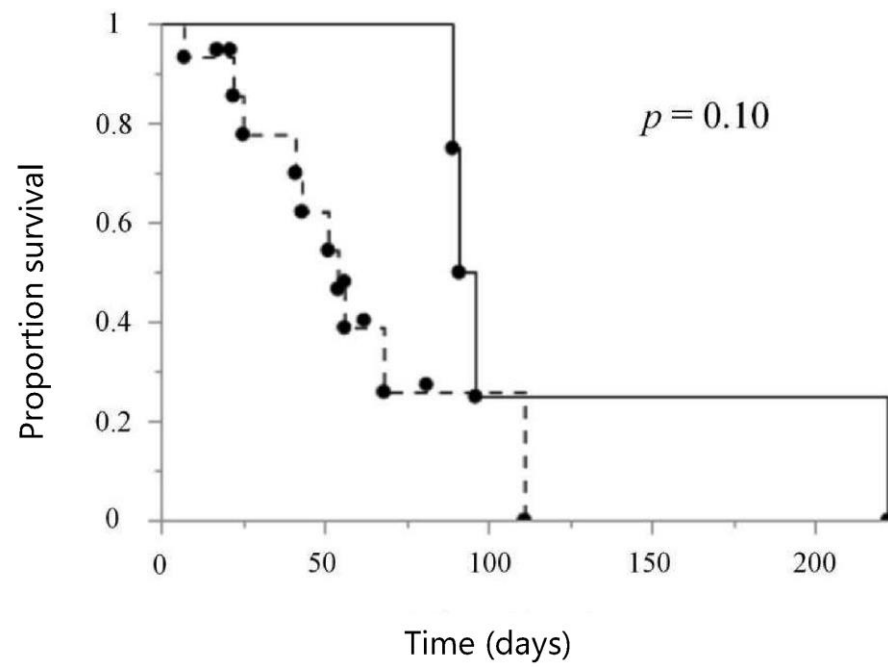
Fig. 14

Fig. 15CDR1CDR2CDR3Light chain variable region

MESQTHVLISLLLSVSGTYGDIAITQSPSSVAVSVGETVTLSCKSSQSLLYSENQKDYL
 CDR1

GWYQQKPGQTPKPLIYWATNRHTGVPDRFTGSGSGTDFTLISSVQAEDLADYYC
 CDR2

GQYLVYPFTFGPGTKLELK
 CDR3

Heavy chain variable region

MGWSQIILFLVAAATCVHSQVQLQQSGAELVKPGSSVKISCKASGYTFTSNFMHWV
 CDR1

KQQPGNGLEWIGWIYPEYGNTKYNQKFDGKATLTADKSSSTAYMQLSSLTSEDSAV
 CDR2

YFCASEEAVISLVYWGGTTLVTVSS
 CDR3

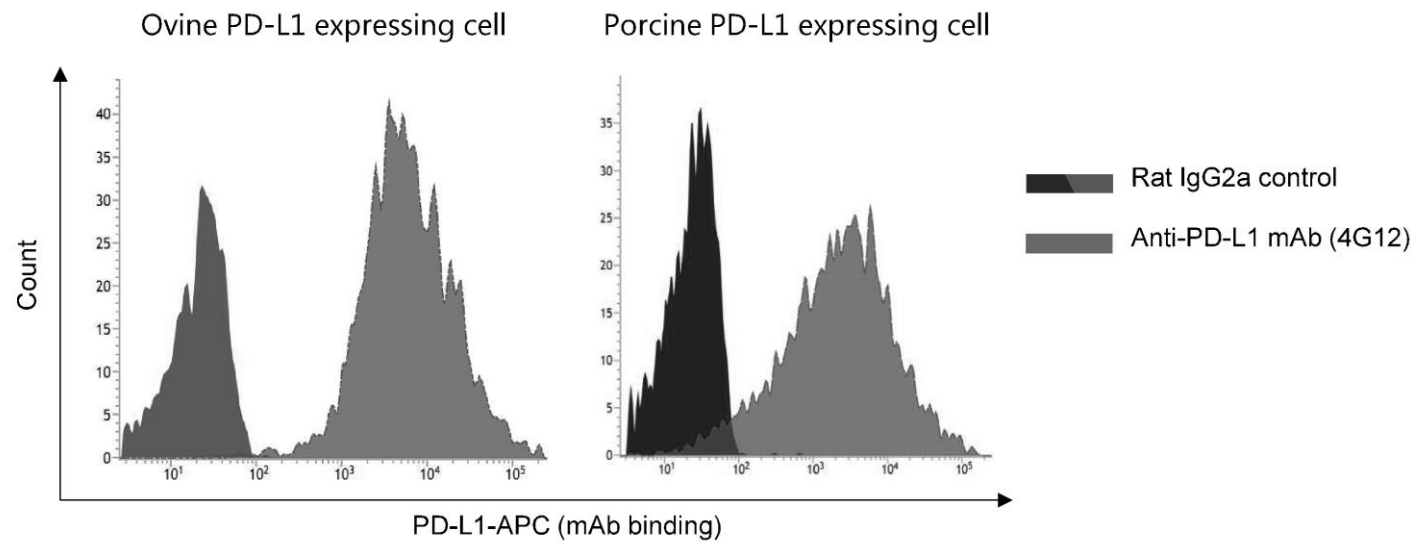
Fig. 16

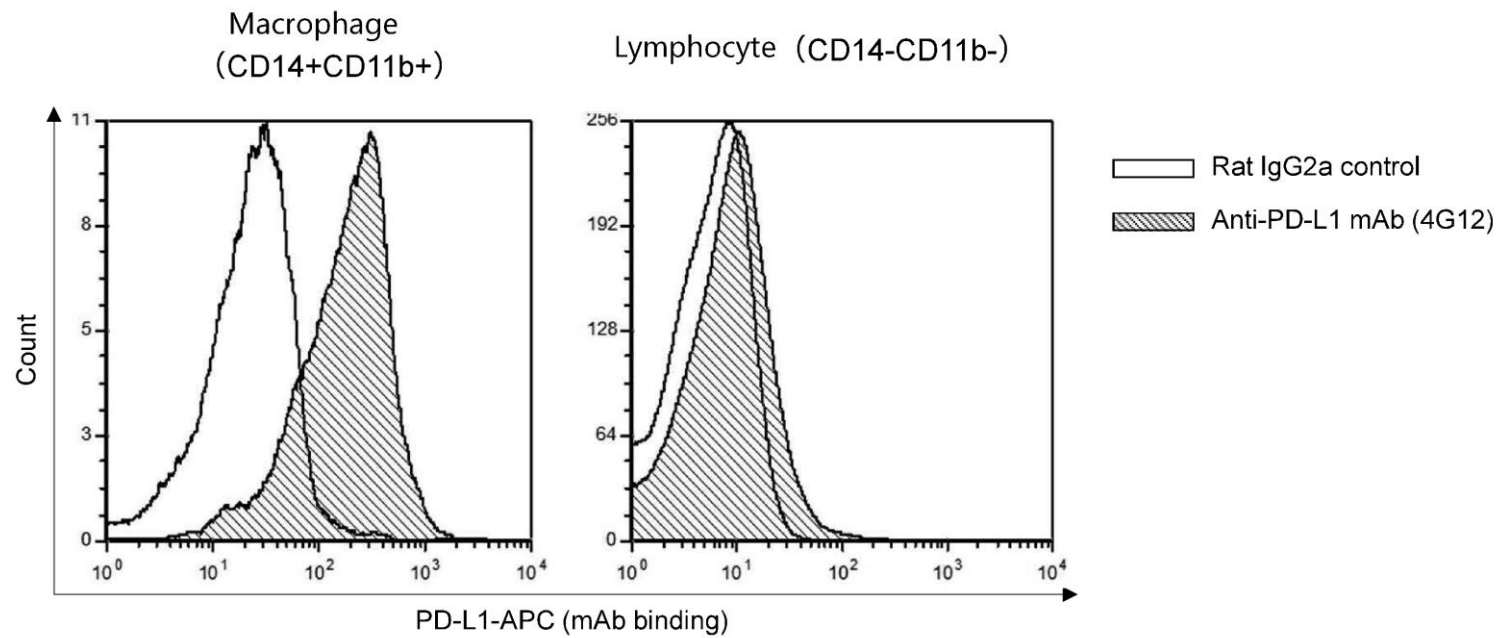
Fig. 17

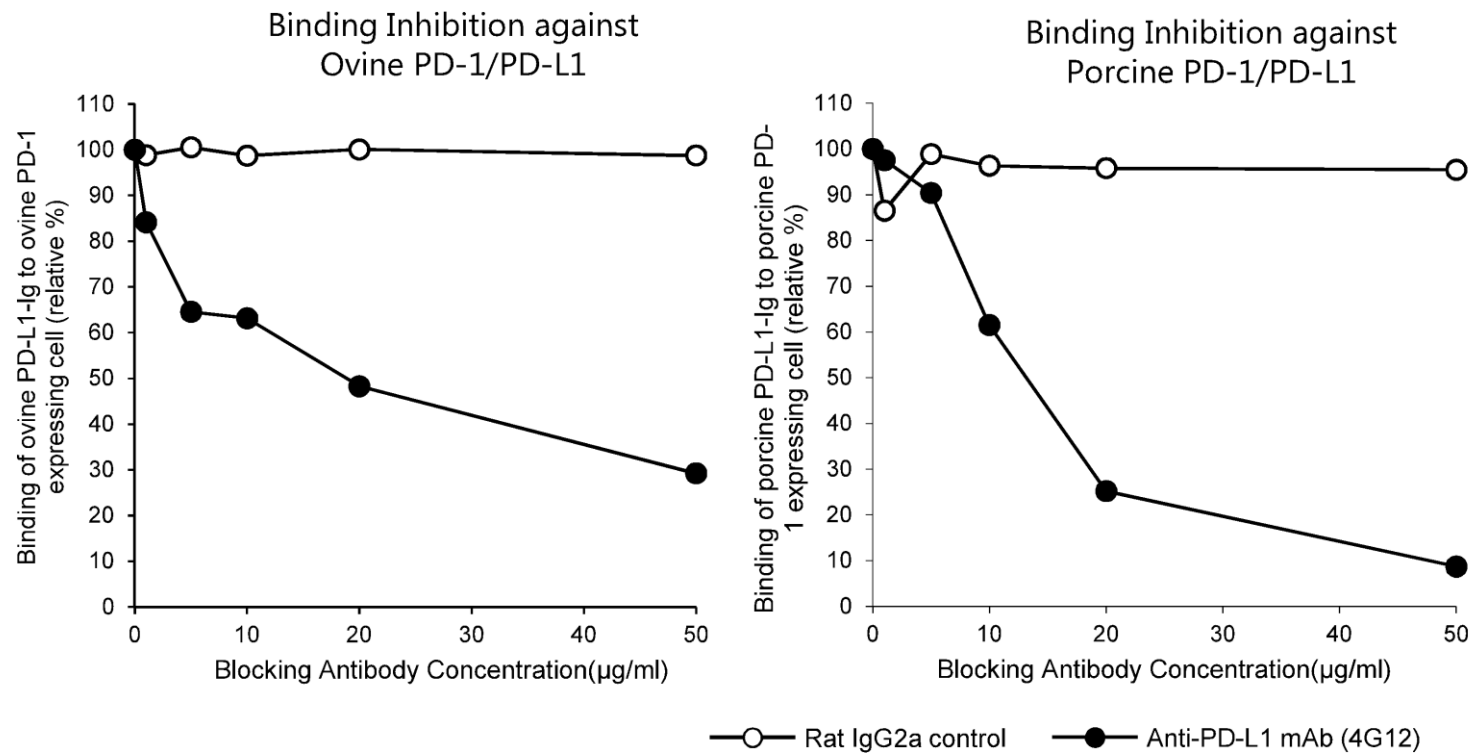
Fig. 18

Fig. 19

Light Chain

*Italicized: Variable region sequence (**Underlined boldface**: CDR1, CDR2, CDR3 in this order from NH2 terminus)*

Non-italicized: Constant region sequence (bovine Ig lambda, GenBank: X62917)

MESQTHVLISLLSVSGTYGDIAITQSPSSVAHSVGETVTLSCKSSQSLLYSENQKDYL
GWYQQKPGQTPKPLIYWATNRHTGVPDRFTGSGSGTDFTLISSVQAEDLADYYCG
QYLVYPFTFGPGTKLELKQPKSPPSVTLPFPSTEELNGNKATLVCLISDFYPGSVTVV
 WKADGSTITRNVEPTRASKQSNKYAASSYLSLTSSDWKSKGSYSCEVTHEGSTVTK
 TVKPSECS*

Heavy Chain

*Italicized: Variable region sequence (**Underlined boldface**: CDR1, CDR2, CDR3 in this order from NH2 terminus)*

Non-italicized: Constant region sequence (bovine IgG1, modified from GenBank: X62916)

Doubly underlined: mutated amino acids in bovine IgG1 (CH2 domain)

(Amino acid numbers and mutations: 250 E→P, 251 L→V, 252 P→A, 253 G→deletion, 347 A→S, 348 P→S)

MGWSQIILFLVAAATCVHSQVQLQQSGAELVKPGSSVKISCKASGYTFTSNFMHWV
KQQPGNGLEWIGWIYPEYGNTKYNQKFDGKATLTADKSSSTAYMQLSSLTSEDSAV
YFCASEEAVISLVYWGQGLVTVSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYM
 PEPVTVTWNSGALKSGVHTFPAVLQSSGLYSLSSMVTVPGSTSGQTFTCNVAHPASS
 TKVDKAVDPTCKPSPDCCPPPPVAGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGH
 DPEVKFSWFVDDDEVNTATTKPREEQFNSTYRVVVSALRIHQDWTGGKEFKCKVH
 NEGLPSSIVRTISRTKGPAREPQVYVLAPPQEELSKSTVSLTCMVTSTFYPDYIAVEWQ
 RNGQPESEDKYGTTTPQLDADSSYFLYSKLRVDRNSWQEGDYYTCVVMHEALHNH
 YTQKSTSKSAGK*

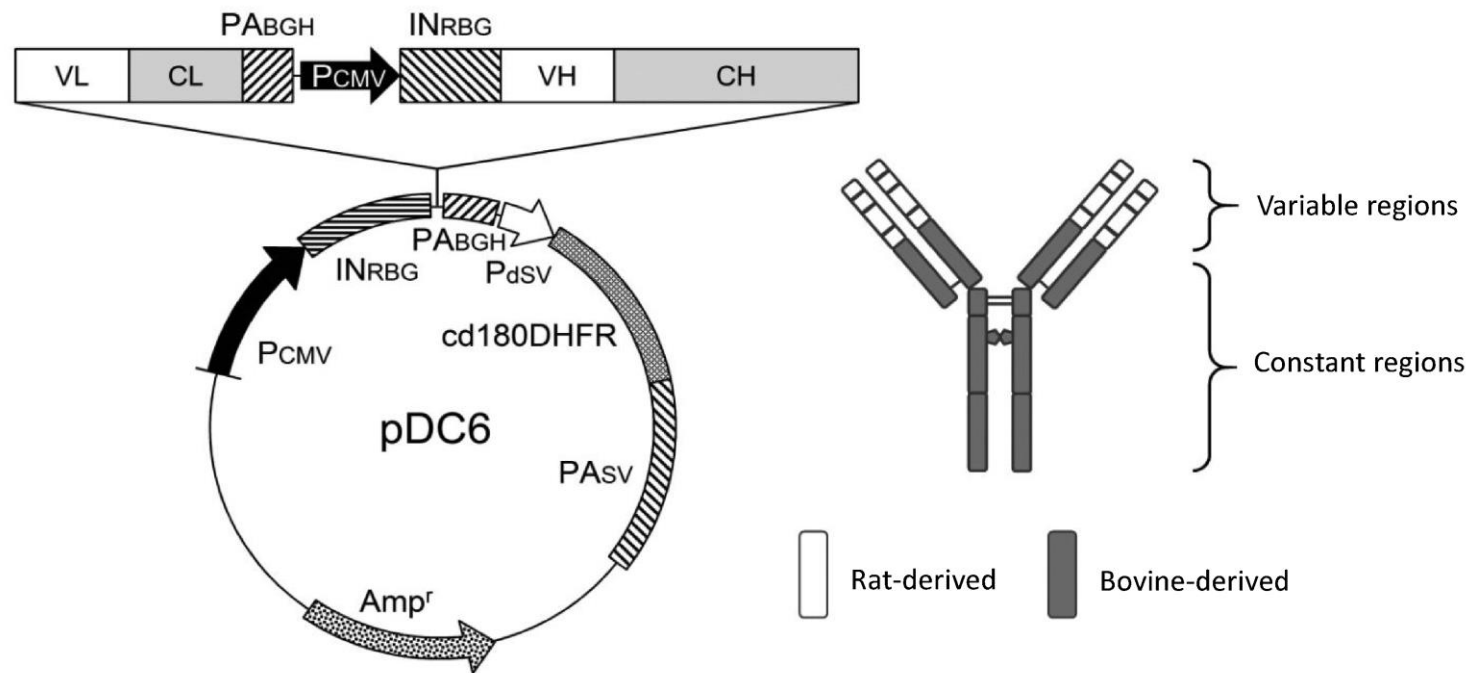
Fig. 20

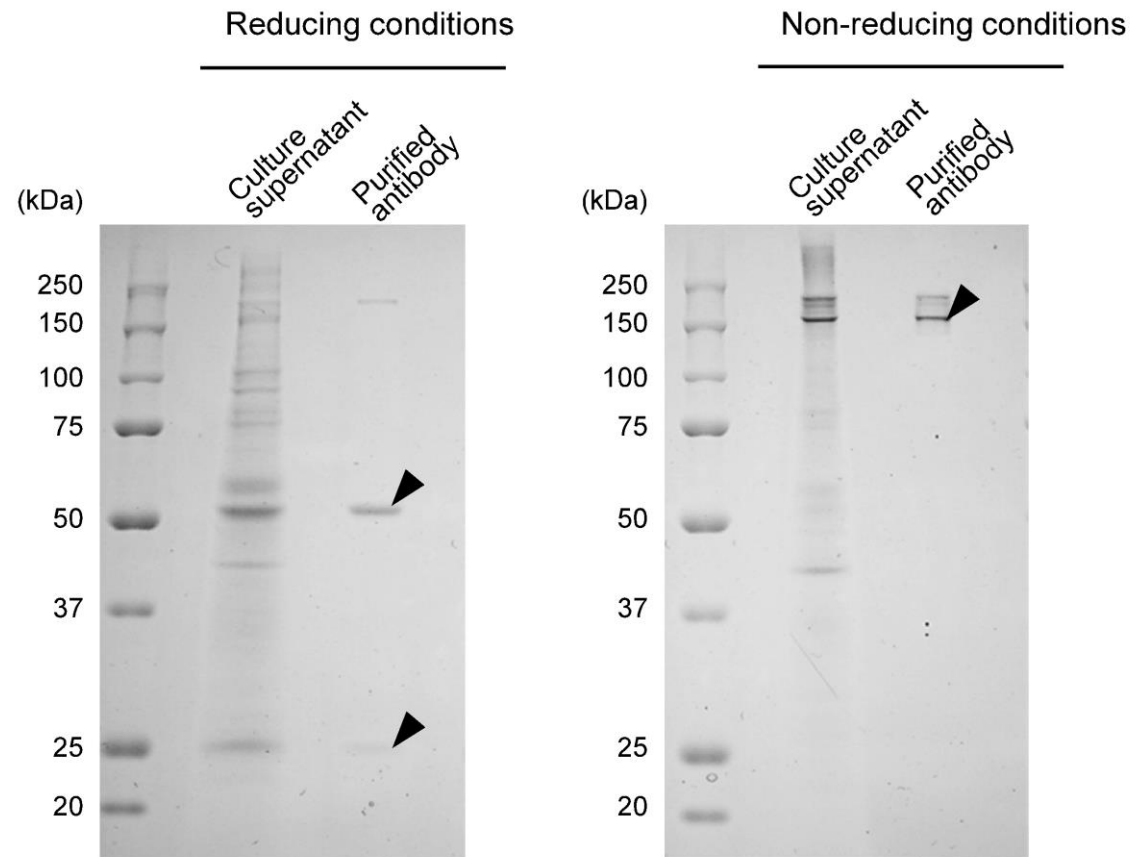
Fig. 21

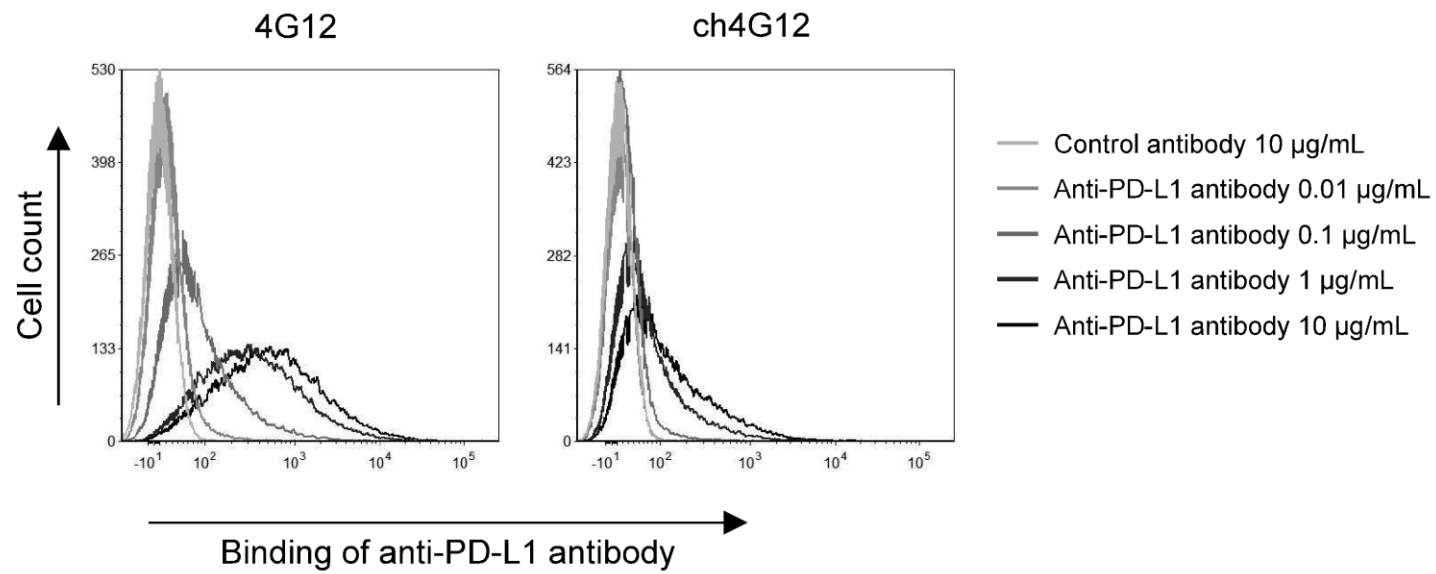
Fig. 22

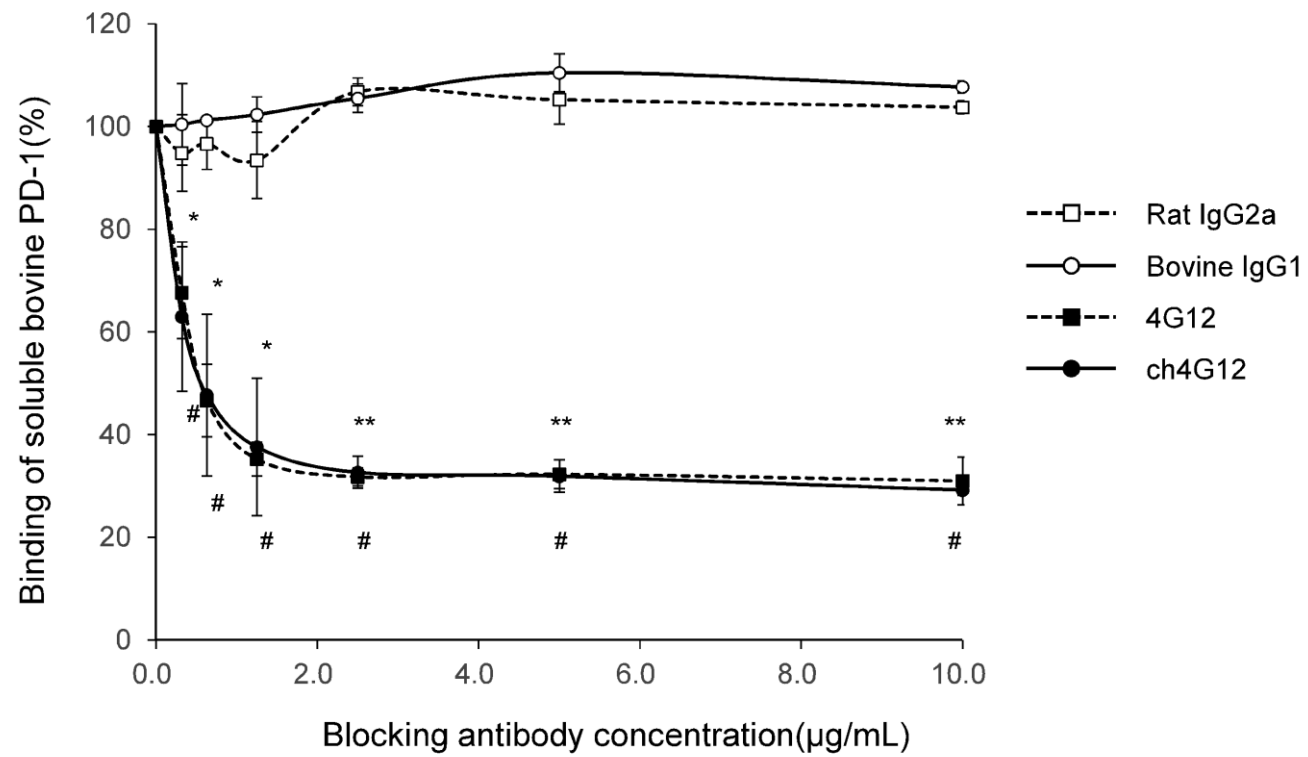
Fig. 23

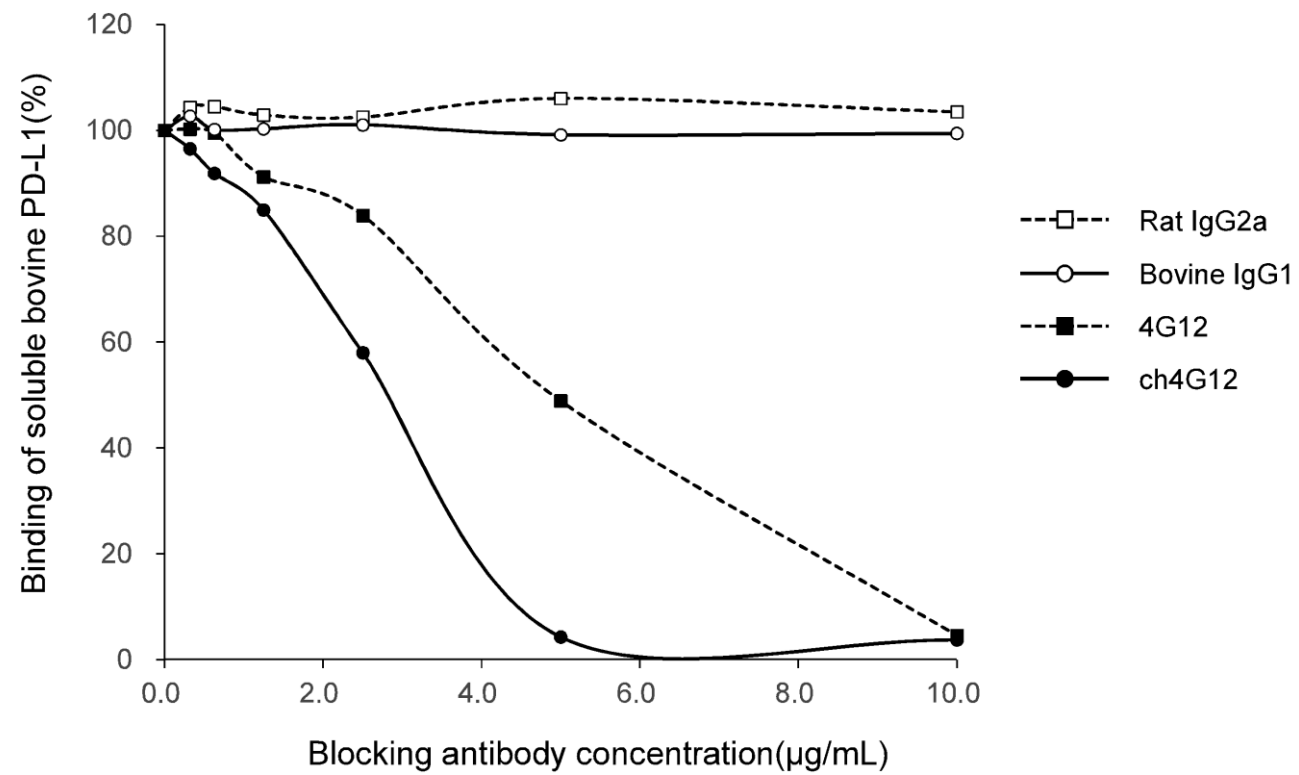
Fig. 24

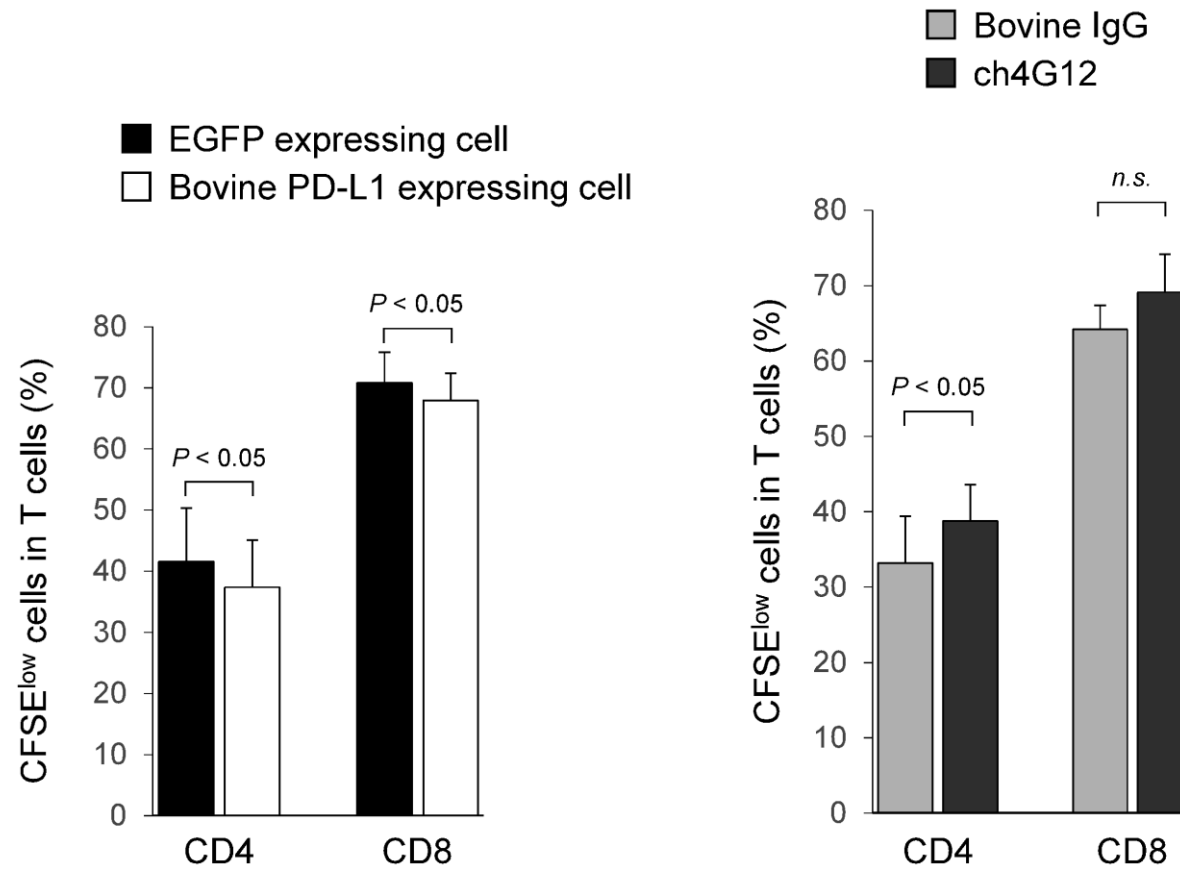
Fig. 25

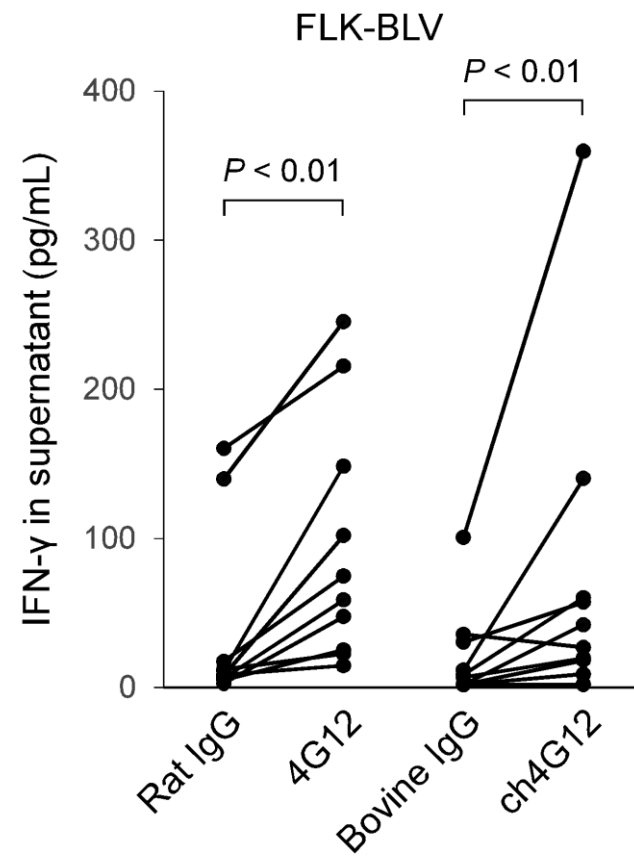
Fig. 26

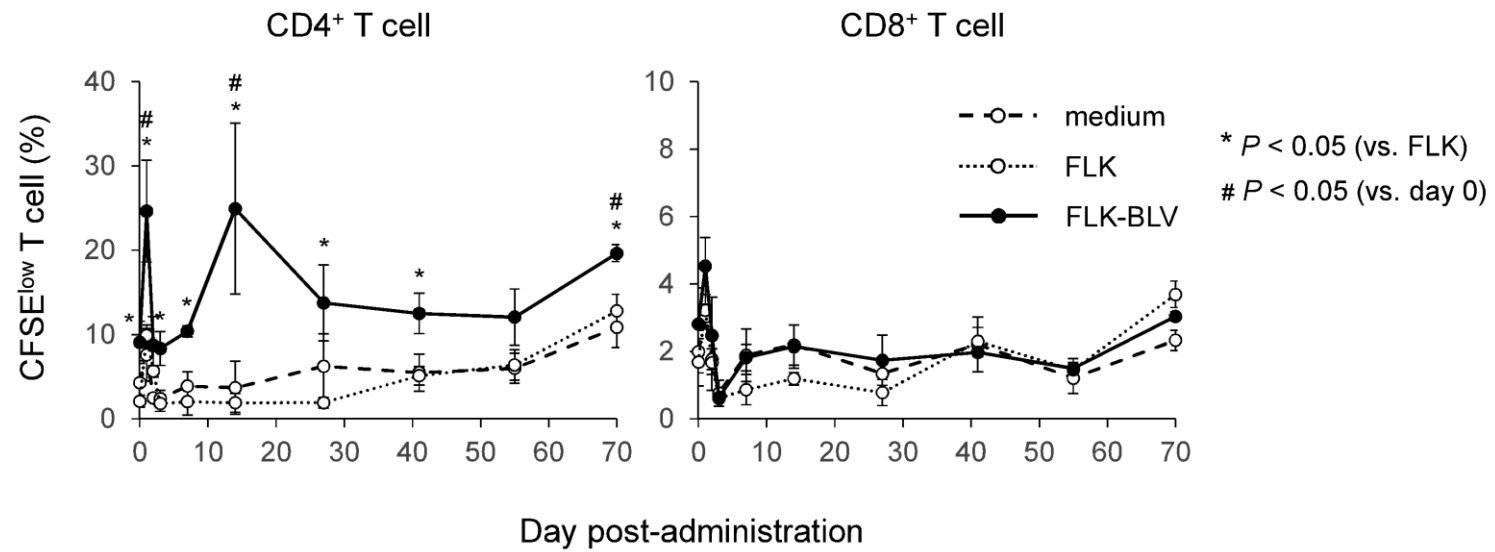
Fig. 27

Fig. 28