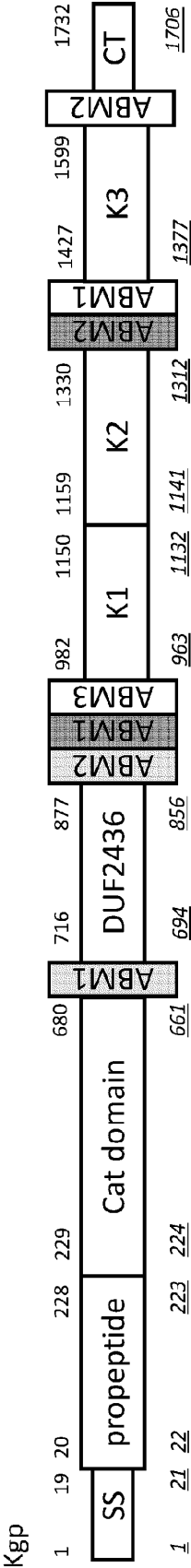


Figure 1



RgpA

Kgp

SS: 1-19
Propeptide: 20-228
Cat domain: 229-680
ABM1: 681-715
DUF: 716-877
ABM2: 878-942
ABM1: 943-966
ABM3: 967-989
K1: 982-1150
K2: 1159-1330
ABM2: 1339-1394
K3+CT: 1427-1732

RgpA

SS: 1-21
Pro-peptide: 22-223
Cat domain: 224-661
ABM1: 662-693
DUF: 694-856
ABM2: 857-921
ABM1: 922-945
ABM3: 946-971
K1: 963-1132
K2: 1141-1312
ABM2: 1321-1376
K3+CT: 1377-1706

Figure 2A

Kgp

MRKLLLLIAASLLGLVLAQSAKIKLDAPTTRTTCTNNSFKQFDASFSFNEVELTKVETKGGTFASVSIPGAFPTGEVGSPEVPAVRKLIAPVVGATPVVRVKSFTQVYSLNQYGSEKLMIPHQPSMSKSDDE
KVPFVYNAAAYARKGFVGOELTQVEMLGTMRGVRIAAALTINPVQYDVVANQLKVRNNIEIEVSFQGADEVATQRLYDASFSFPYFETAYKQLFNRRDYYTDHGDLYNTPVRLMLVAGAKFKEALKPWLTWKA
QKGFYLDVHYTDEAEVGTTNASIKAFIHKKYNDGLAASAAPVFLALVGDGTDVISGEKGKTKKVTDLVYSAVDGDFPEMYTFRMSASSPEELTNIIDKVLMEYKATMPDKSYLEKVLIIAGADYSWNSQVG
QPTIKYGMQYYNQEHGYTDVYNYLKAPYTGCSYSHLNTGVSFANYTAHGETAWADPLLTTSQKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKGAVAYIGSSPNSYWGEDYYWVSVGANAV
FGVQPTFEGTSMGSDATFLEDSTYNTVNSIMWAGNLAATHAGNIGNITHIGAHYYWEAYHVLGDGSMVPYRAMPKTNTYTLPASLPQNQASYSIQASAGSVVAISKDGVLYGTGVANASGVATVSMTK
QITENGNYDVVITRSNYLPIKIQVGEPSYQPVSNLTATTQGGKVTLKWEAPSAKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAAADNVWGDNTGYQFLDADHNTFGSVIPATGPLFTGTASS
NLYSANFEYLIPANADPVVTTQNIIVTGGQEVVIPGGVYDYCITNPEPASGKMVIAGDGGNQPARYDDFTFEAGKKYTTMRRAGMGDGTDMEVEDDSDPASVYTYTVYRDGTKIKEGLTATTFEEDGVAA
GNHEYCVVEKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLLKWDAPNGTNPNNPNPNPNTGTTLSESEFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNSNGCVVYSESGGLGGIGVLT
NYLITPALDLPNGGKLTFWVCAQDANYASEHYAVASSTGNDASNFTNALLEETITAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETTESSTHGEAPAE
WTTIDADGGDGGQWLCLSSGQLDLTAHGGSNVVSFSWNGMALNPDNYLISKDVTGATKVKYVAVNDGFGPDHYAVMISKGTNAGDFTVVFEEPTPNGINKGGARFGLSTEANGAKPQSVWJERT
VDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVVEKYTAGVSPKKCVNVTVNSTQFNPVQNLTAEQAPNSMDAILKWNAPASKRAEVLN
EDFENGIPASWKTIDADGGDGNWTTTTPPPGGSFAGHNSAICVSSASYINFEGPQNPNDNYLTPELSLPGGGTLTFWVCAQDANYASEHYAVASSTGNDASNANALLEEVLTAKTVVTAPFAIRGTRA
QGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVVITSGNAPSYYTYTYRNNNTQJASGVTEITYRDPDLATGFTYTGKVVVYPNGESALETATLNLISLADVTAQKPYTLTVVGKTTVTCQGEAMIYDM
NGRRLAAGRNTVWYTAQGGHYAVMVVVDGKSYEKLAVK

Figure 2B

RqpA[illegible]

Figure 3

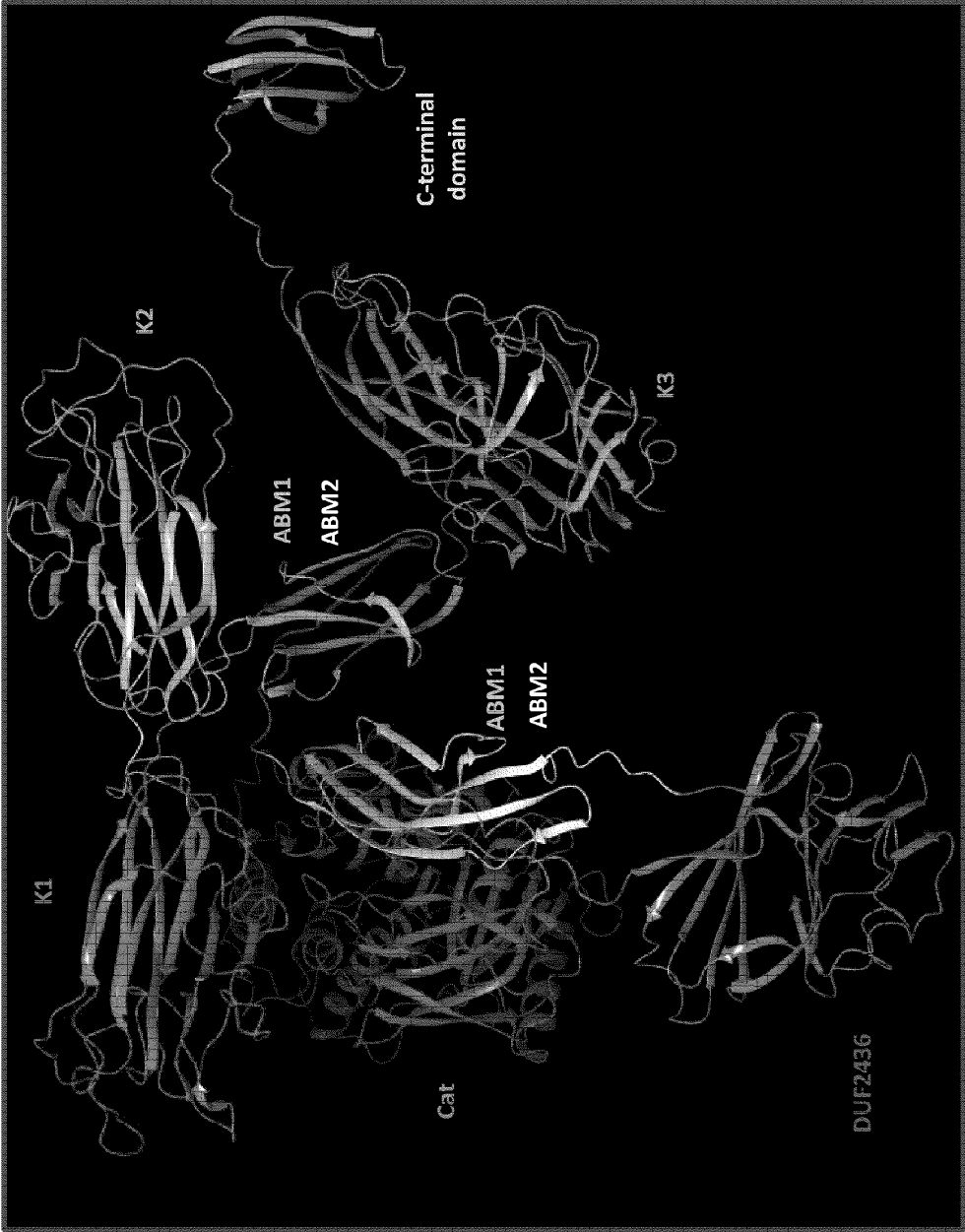


Figure 4A

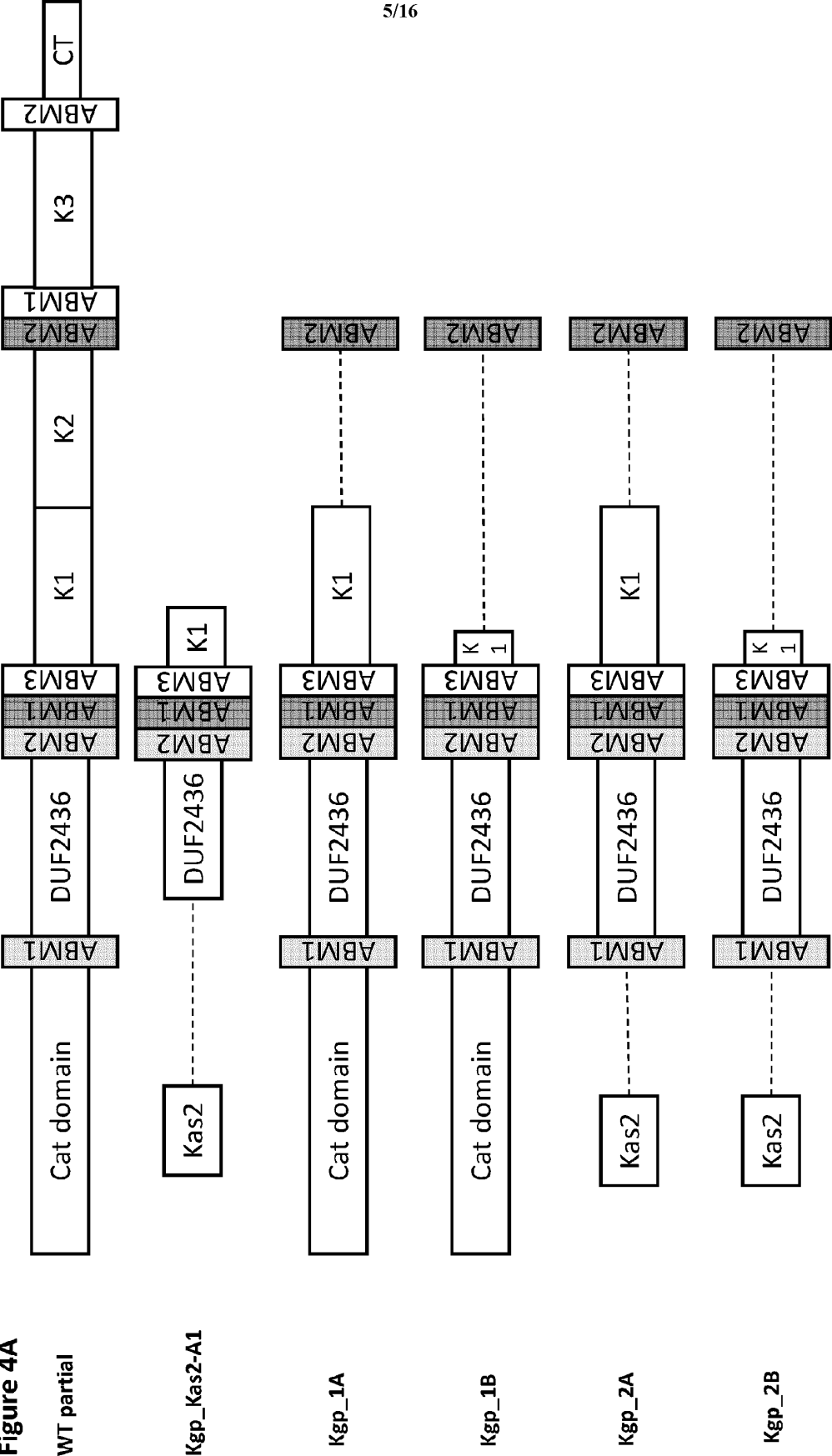


Figure 4B

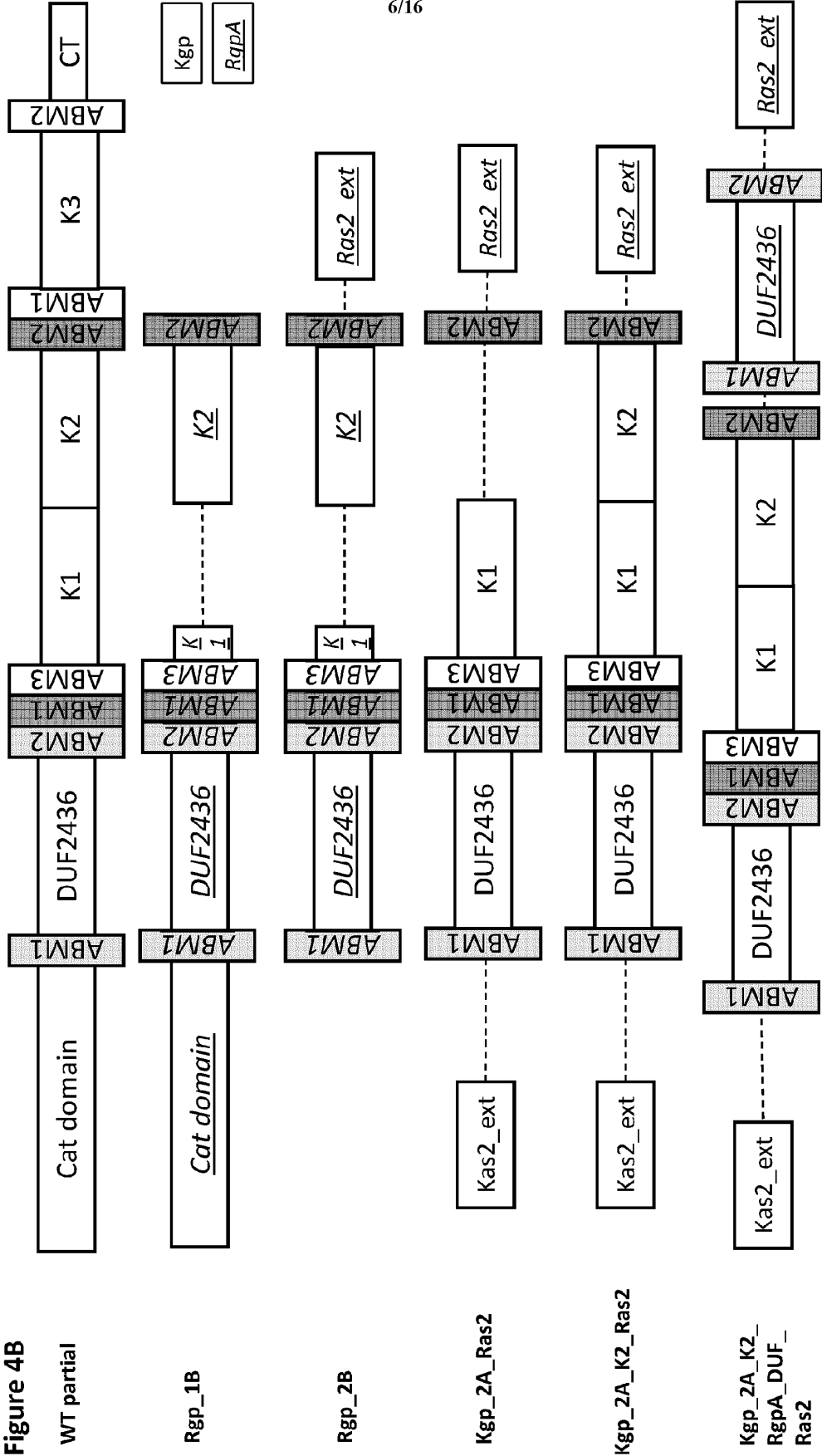


Figure 4C

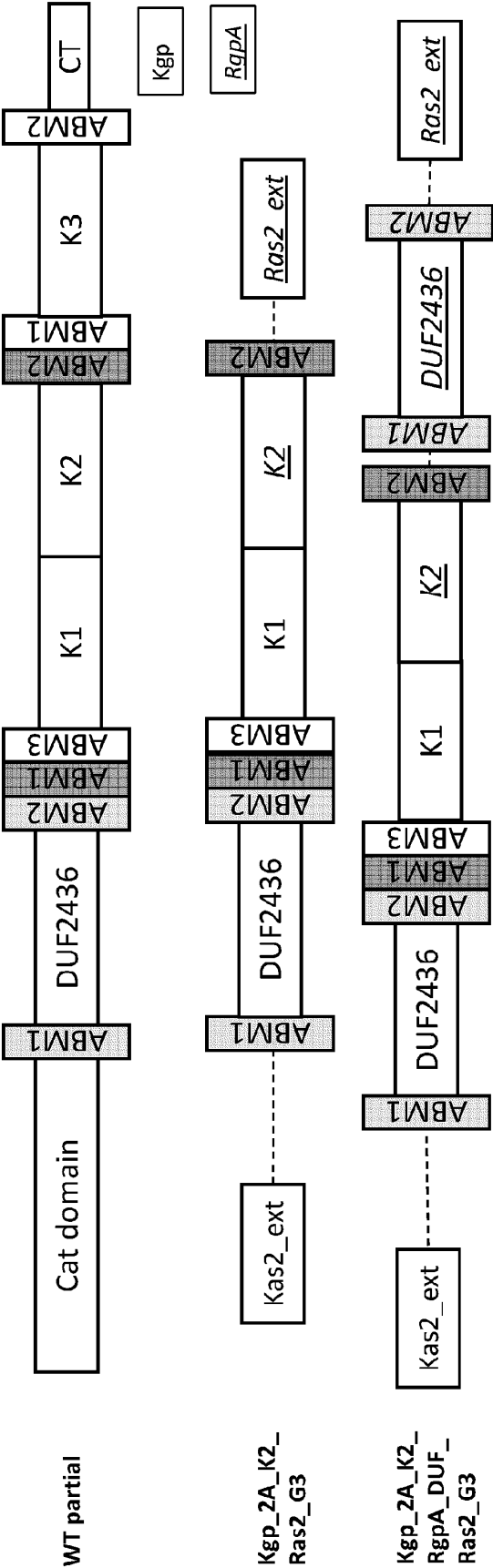


Figure 5

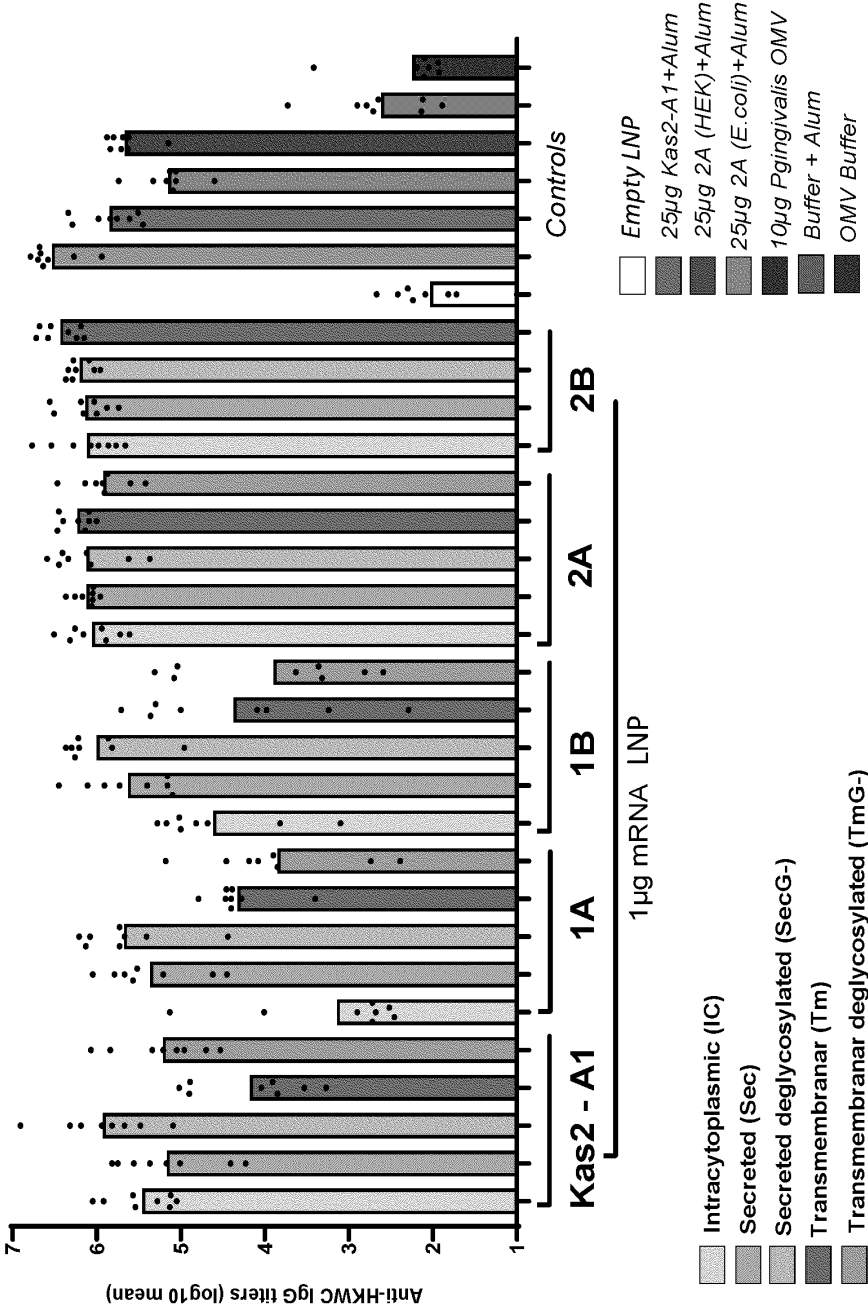


Figure 6

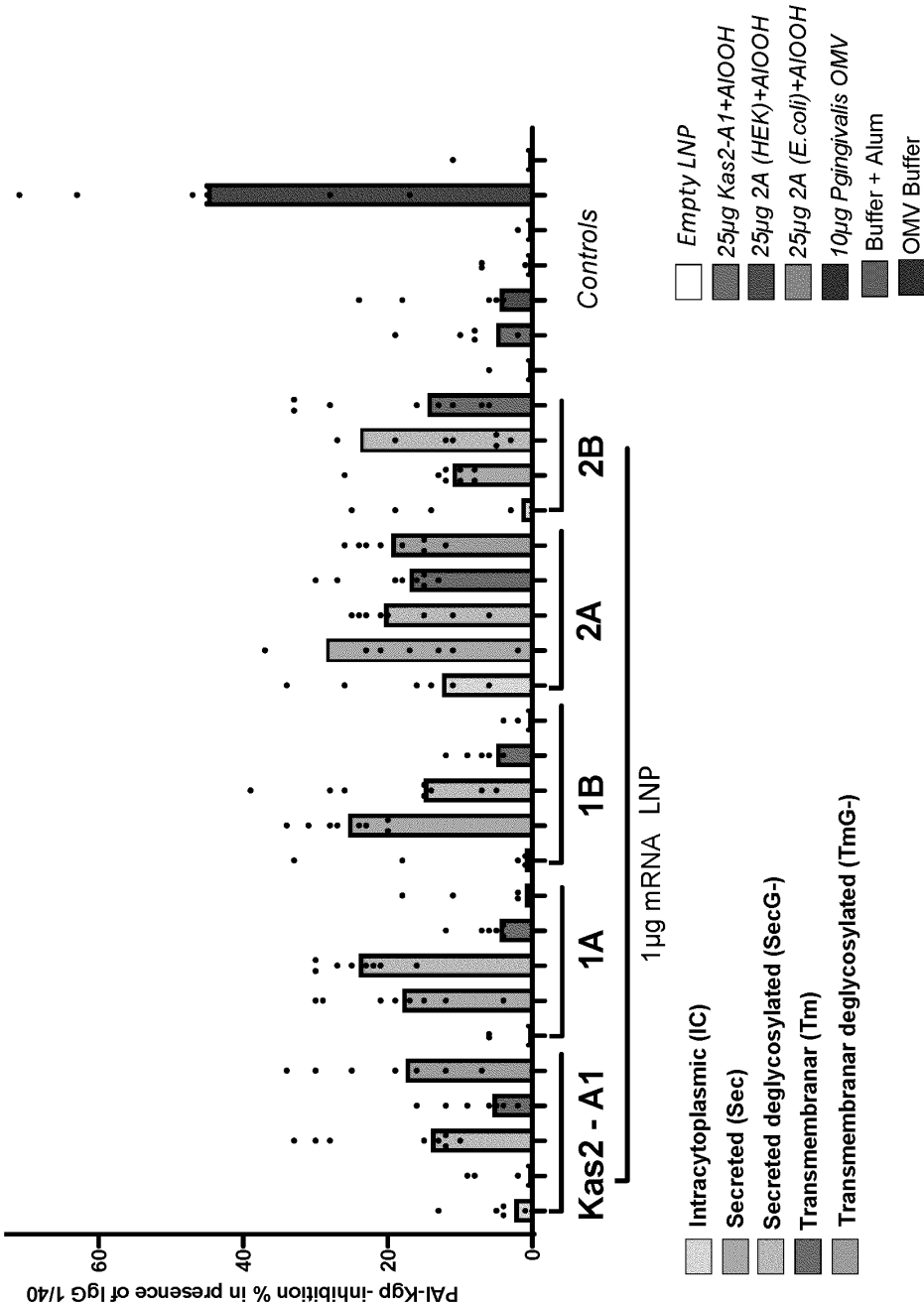


Figure 7

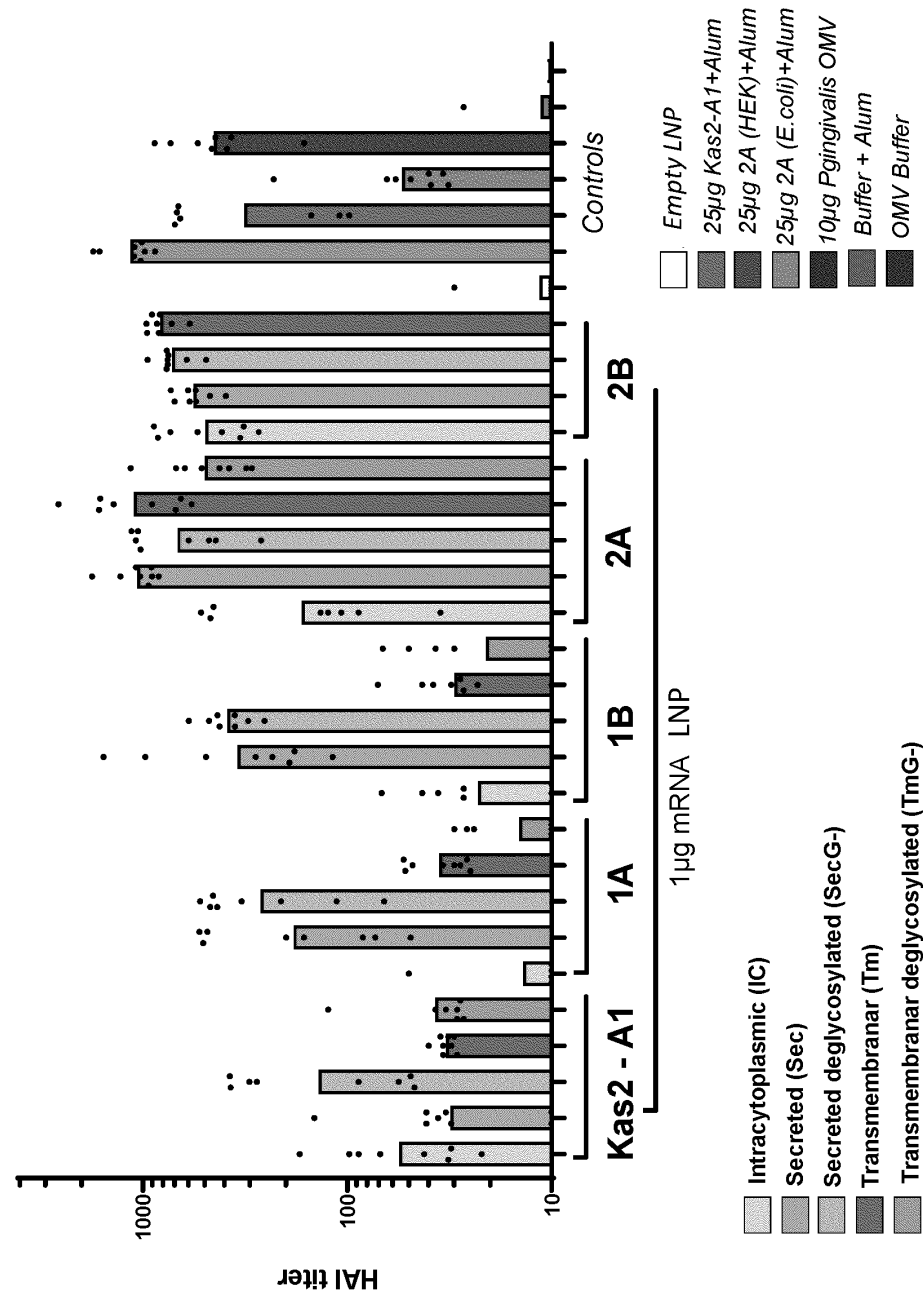


Figure 8

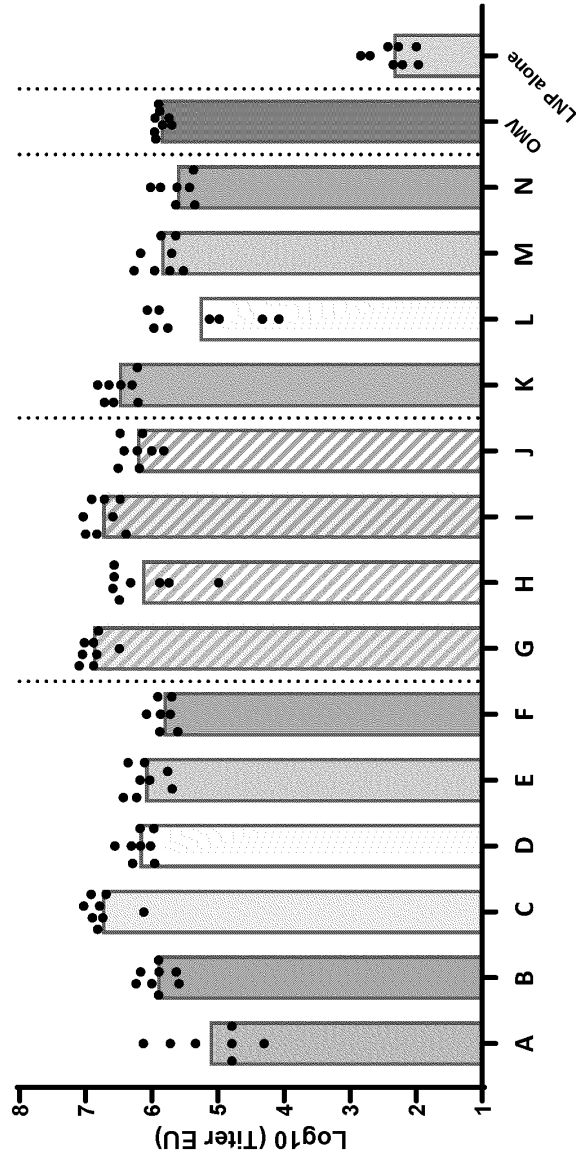


Figure 9

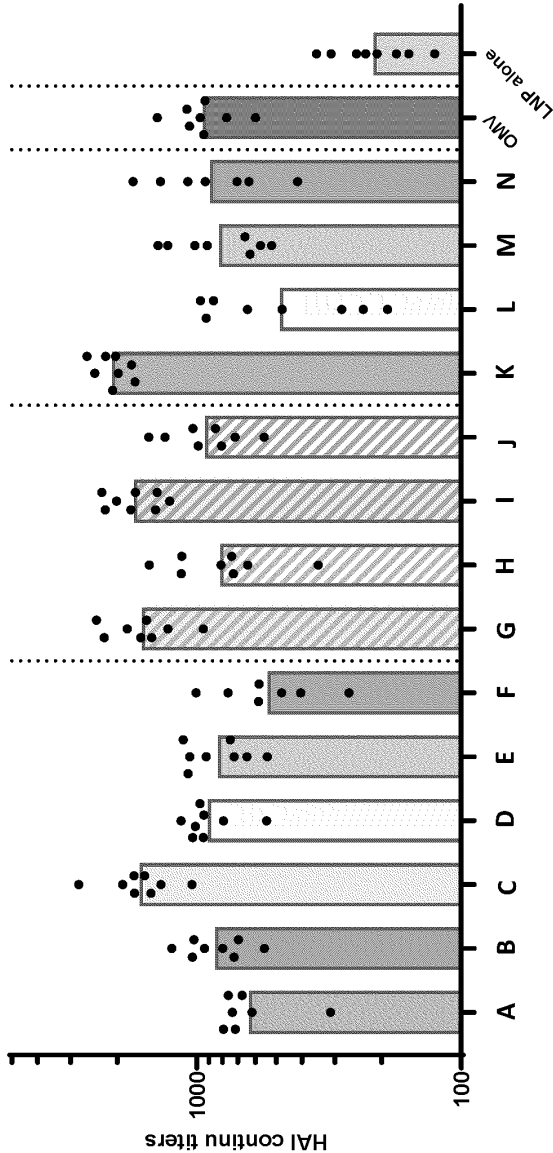


Figure 10

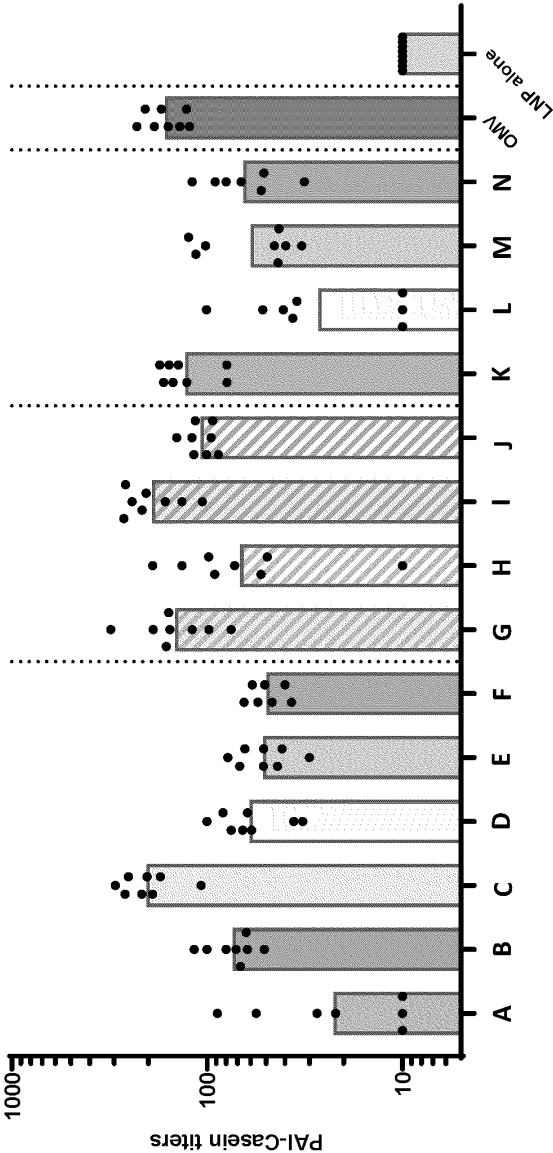


Figure 11

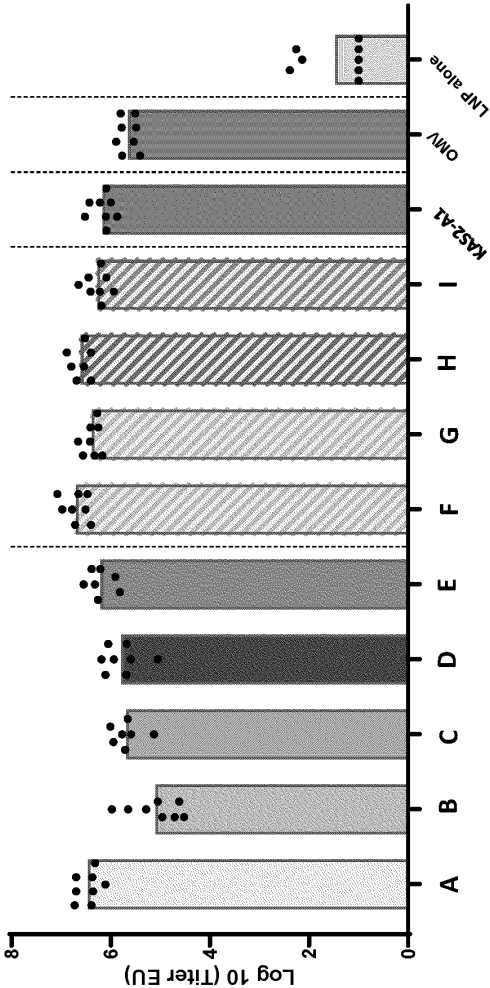


Figure 12

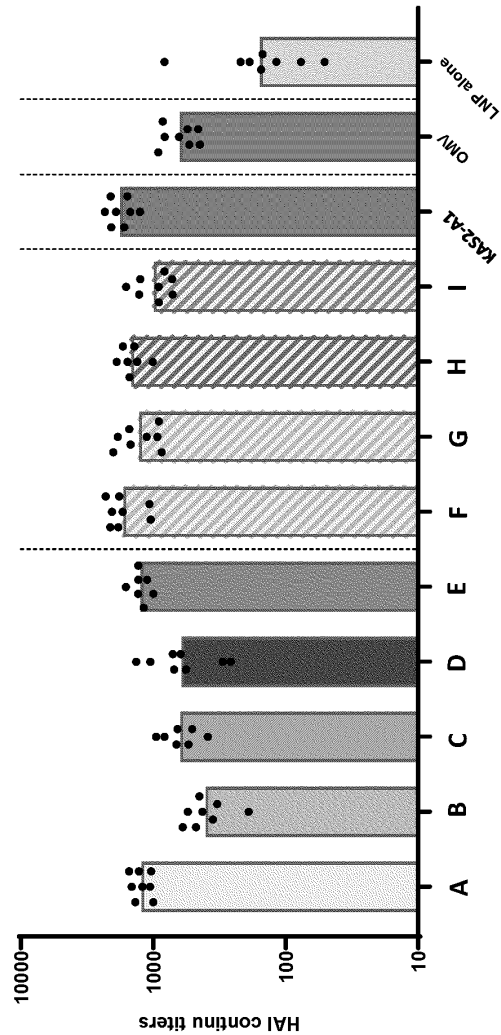


Figure 13

