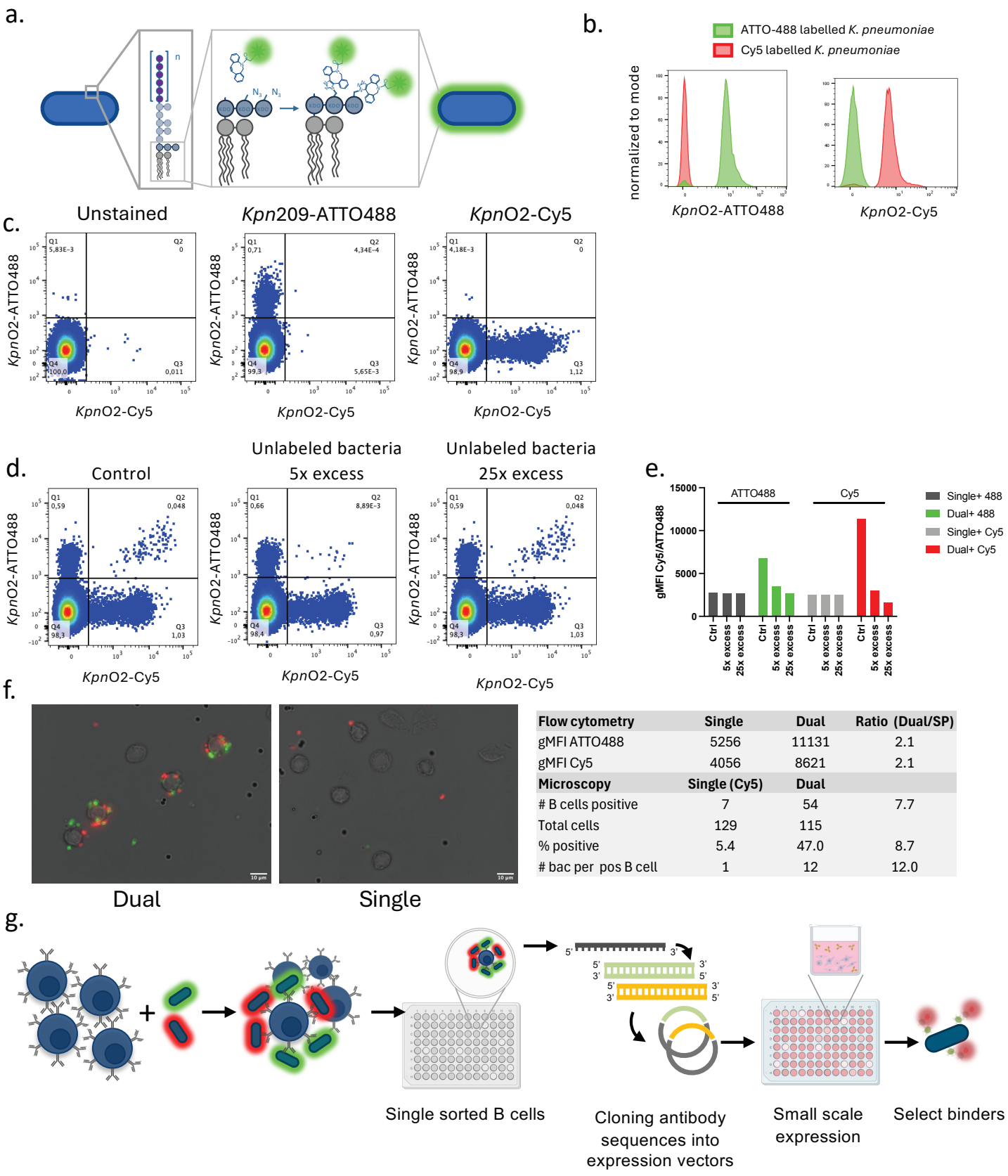

Flow cytometry	Single	Dual	Ratio (Dual/SP)
gMFI ATTO488	5256	11131	2.1
gMFI Cy5	4056	8621	2.1
Microscopy	**Single (Cy5)**	**Dual**	
# B cells positive	7	54	7.7
Total cells	129	115	
% positive	5.4	47.0	8.7
# bac per pos B cell	1	12	12.0

Figure S1 | Optimization of B cell staining with *Kpn*O2. (a) Cartoon depicting fluorescent labeling of the outer membrane of *K. pneumoniae* via click-chemistry. *K. pneumoniae* was cultured overnight in the presence of KDO-azide (2 µM), which was metabolically incorporated into the LPS core. Cyclooctyne-labelled fluorophores (50 µM) were added, which "clicked" to the azide handles. **(b)** Fluorescent labeling of *KpnO2* with Cy5 or ATTO-488 was assessed via flow cytometry and depicted as gMFI of bacterial populations. **(c)** Human B cell isolated from healthy donors were incubated with *Kpn*O2-ATTO-488 or *Kpn*O2-Cy5 (0.5 bacterium/B cell for each fluorophore). B cells ($CD19^+$) that bound *Kpn*O2-ATTO-488 or *Kpn*O2-Cy5 were detected. **(d,e)** Human B cells isolated from healthy donors were incubated with *Kpn*O2-ATTO-488 and *Kpn*O2-Cy5 (MOI of 0.5 per fluorophore) with an excess of unlabeled *Kpn*O2. B cells ($CD19^+$) that bound both *KpnO2*-ATTO-488 and *KpnO2*-Cy5 were detected. **(e)** gMFI values of single and double positive B cells with and without unlabeled bacteria. **(f)** Left, B cells that stain double positive for *Kpn*O2-A488 and *Kpn*O2-Cy5 (dual, left microscopy image) or single positive for *Kpn*O2-Cy5 (single, right microscopy image) were sorted into a chambered cover slip containing 1% PFA and analyzed by fluorescence microscopy to determine bacterial binding. Right, table with quantification of flow cytometry and microscopy data to determine the number of bacteria per cell for both single and dual stained cells. **(g)** Cartoon depicting the process of *K. pneumoniae*-specific antibody identification. B cells were stained with differently fluorescently labelled *K. pneumoniae*, and B cells double positive for both fluorescent markers were single cell sorted. The variable regions of the heavy and light chain (VH and VL, respectively) were amplified by RT-PCR and cloned into IgG1 expression vectors. Antibodies were recombinantly expressed and tested for antibody binding to *K. pneumoniae*. Figure panel g was created with BioRender.com released under a Creative Commons Attribution-NonCommercial-NoDerivs 4.0 International license.

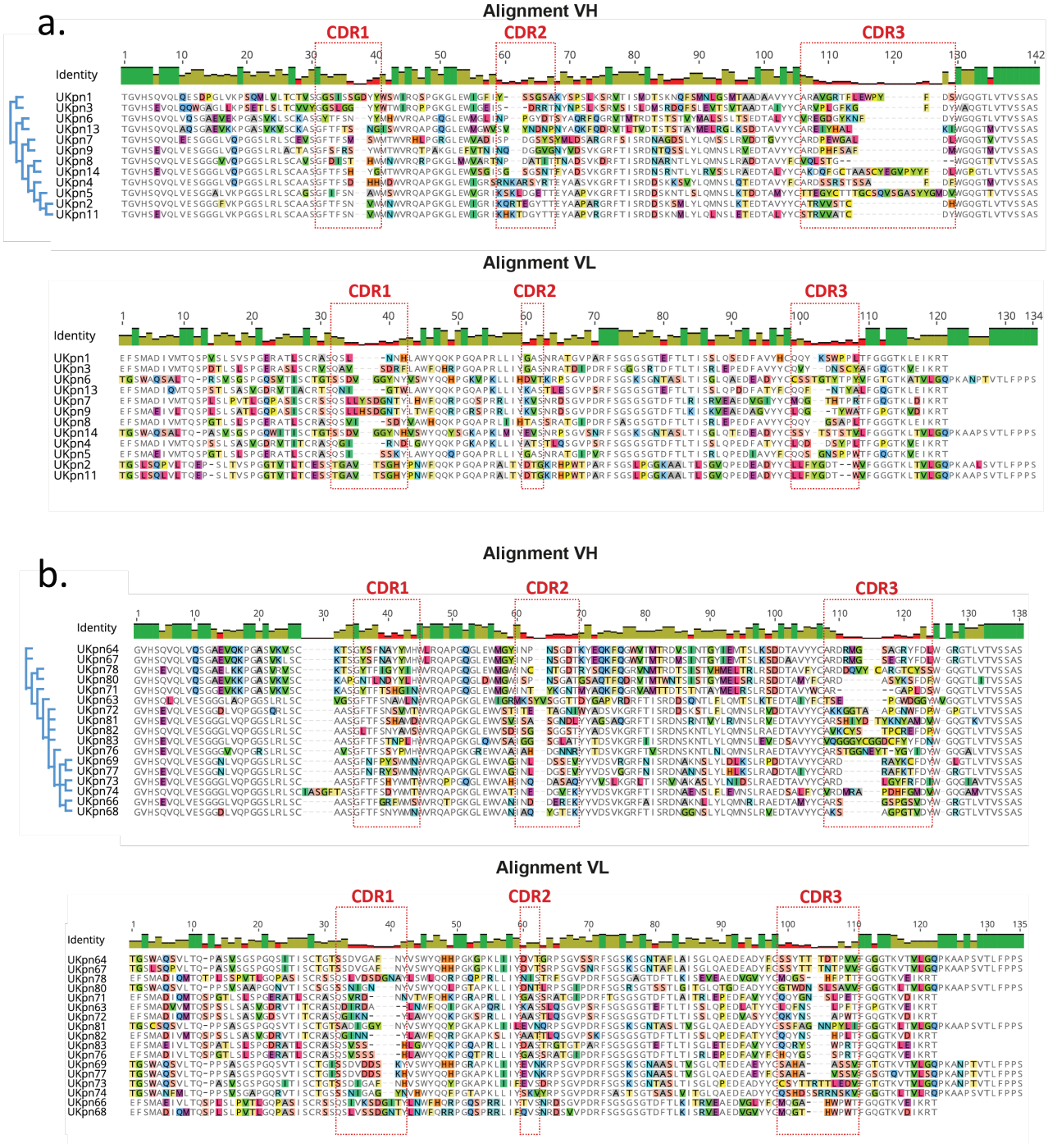

Figure S2 | VH/VL sequences of 29 anti-*Kpn* mAbs. (a&b) Alignments of the variable regions of the heavy and light chains (VH and VL, respectively) of the unique *Kpn*O2 **(a)** and *Kpn*O1 **(b)** binding antibodies. Amino acid sequence alignment was generated using Geneious R9 (v9.1.6). Location of the CDR regions determined using IgBlast web tool (Release 1.20.0)

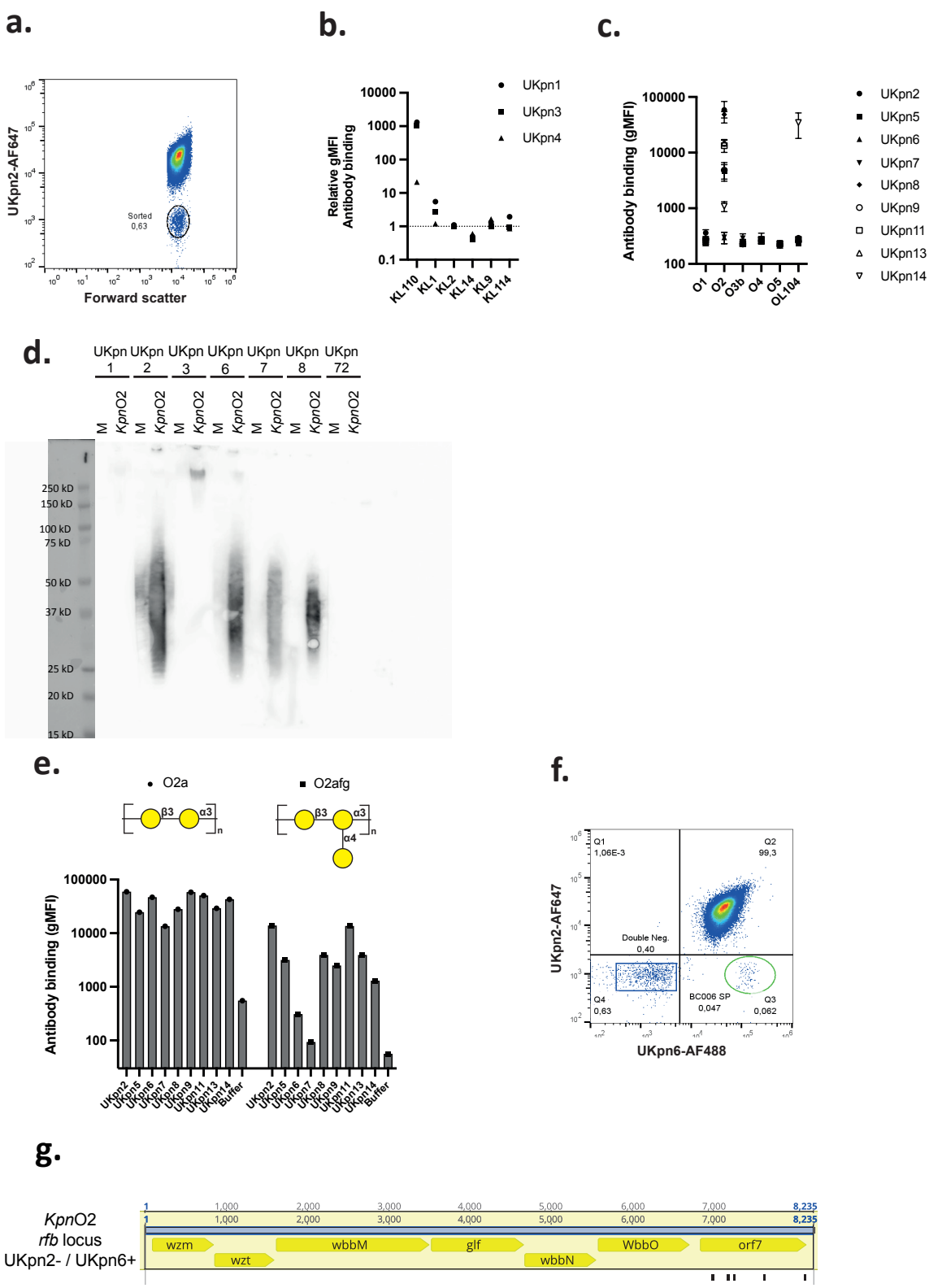

Figure S3 | Binding of anti-*Kpn*O2 mAbs to different *Kpn* isolates. (a) To identify the antigenic targets of the anti-*Kpn*O2 antibodies, a transposon library of *Kpn*O2R (isogenic variant of *Kpn*O2[34]) was incubated with fluorescently labelled UKpn2, and antibody binding was detected using flow cytometry. Bacteria that were not bound by the antibodies were single cell sorted. **(b)** Binding of UKpn1, UKpn3 and UKpn4 to clinical isolates expressing various capsule types. IgG1 binding was detected by flow cytometry using anti-hu-IgG-AF488. Flow cytometry data are represented as fold change of gMFI values of bacterial populations over the background. **(c)** Binding of UKpn2, UKpn5-9, UKpn11, UKpn13 and UKpn14 to clinical isolates expressing various O-antigen types. Data represent mean ± SD of three independent experiments. **(d)** *Kpn*O2 was lysed, and the proteins in the lysate were digested with proteinase K. Western blot was performed using different *Kpn*O2 antibodies followed by goat anti-hu-IgG-HRP. Bands were visualized using ECL. **(e)** Binding of UKpn2, UKpn5-9, UKpn11, UKpn13 and UKpn14 to clinical isolates expressing either the O2a- (UM-05-B-#1) or O2afg-antigen (MC-04166). Bacteria were incubated with 1 µg/ml IgG1, and binding was detected by flow cytometry using anti-hu-IgG-AF647. Flow cytometry data are represented by gMFI values of bacterial populations. **(f)** A transposon library of *Kpn*O2R was incubated with UKpn2-AF647 and UKpn6-AF488, and antibody binding was detected using flow cytometry. Bacteria that were bound by UKpn6-AF488 but not by UKpn2-AF647 were single cell sorted (green gate). **(g)** The barcodes of single cell sorted transposon mutants were sequenced to determine the location of the transposon inserts. Mutants that were longer bound by UKpn6-AF488 but not by UKpn2-AF647 had transposon insertions in *orf7*.

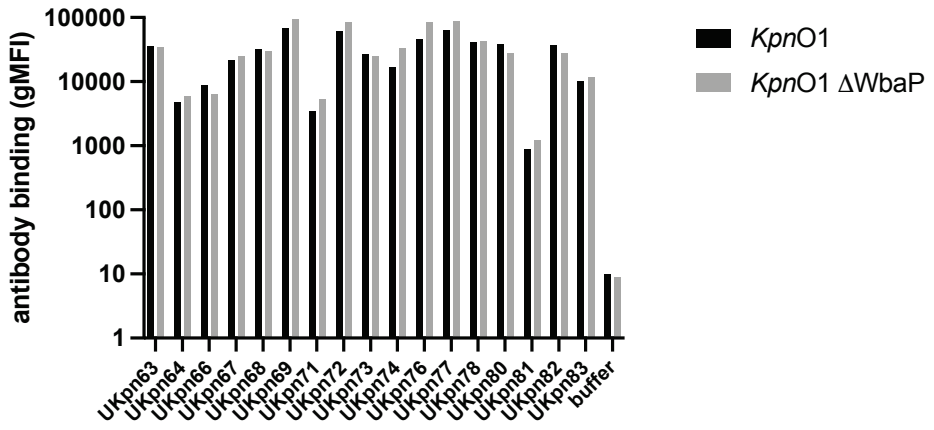

Figure S4 | mAbs directed against *Kpn*O1 do not target the capsule. Anti-*Kpn*O1 IgG1 binding to the capsule deletion mutant of *Kpn*O1 (Δ*wbaP*). Bacteria were incubated with 1 µg/ml IgG1, and binding was detected by flow cytometry using anti-hu-IgG-AF647. Data represent gMFI values of bacterial populations.

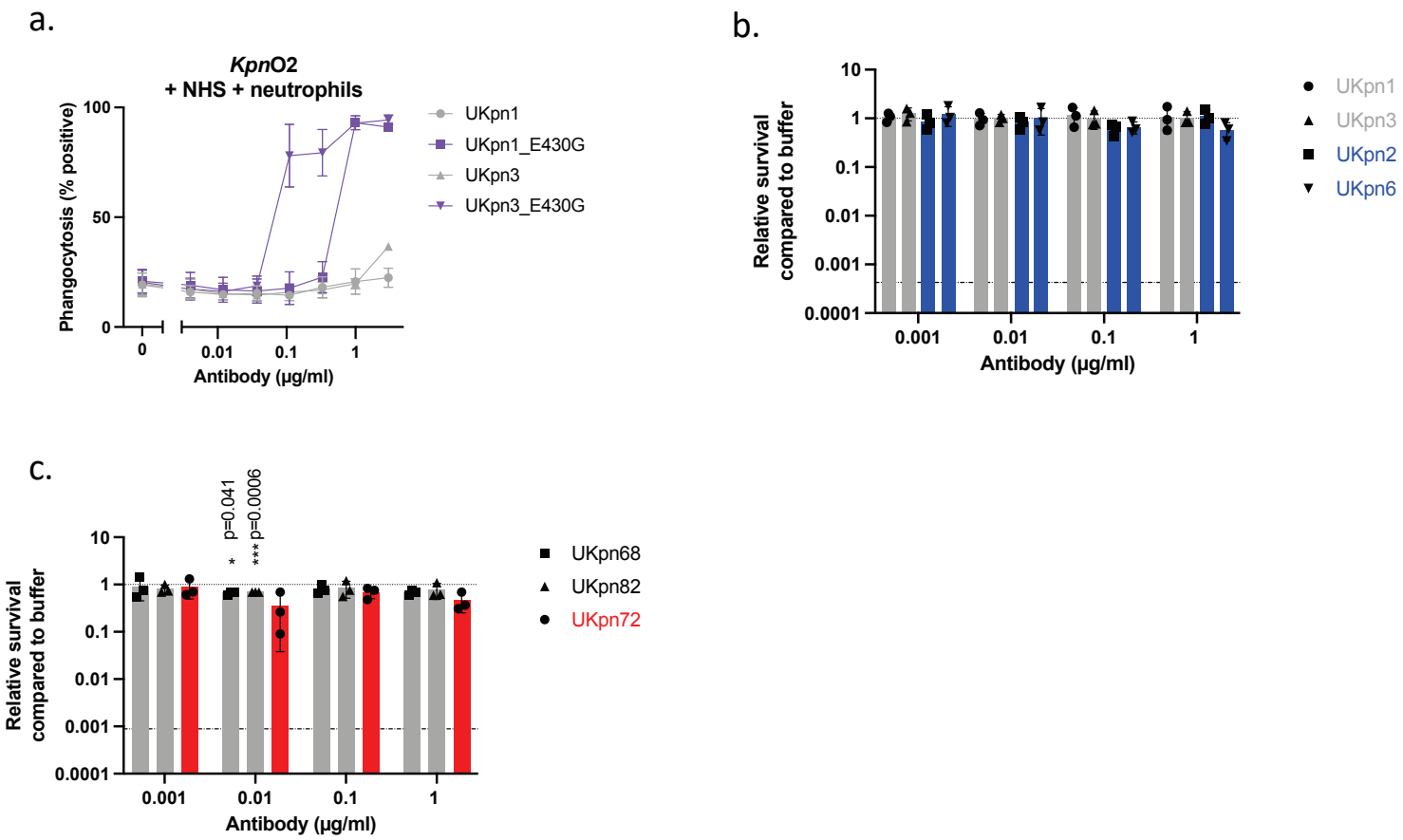

Figure S5 | Antibodies targeting Klebsiella induce phagocytosis and killing by neutrophils. (a) Antibody-dependent phagocytosis of *K. pneumoniae Kpn*O2. GFP expressing bacteria were incubated in the presence of antibody and 3% ΔNHS (*Kpn*O2) as a source of complement for 15 minutes at 37°C. Isolated human neutrophils were allowed to phagocytose opsonized bacteria for 15 minutes at 37°C. Afterwards, the percentage of GFP-positive neutrophils was determined by flow cytometry. **(b,c)** *K. pneumoniae Kpn*O2 **(b)** or *Kpn*O1 **(c)** at 2 x 10^5 bacteria/ml were incubated with antibodies and 8% ΔNHS (*Kpn*O2) or 1% ΔNHS (*Kpn*O1) for 3 hours at 37°C. The number of CFU/ml was calculated and shown as relative survival by dividing by the no antibody control. **(a-c)** Data represent mean ± SD of three independent experiments. **(a,b)** Data were analyzed by one-way ANOVA with Dunnett multiple comparison analysis compared to without mAb control. Significant differences are indicated, * p<0.05, ** p<0.01 and ***p<0.001.

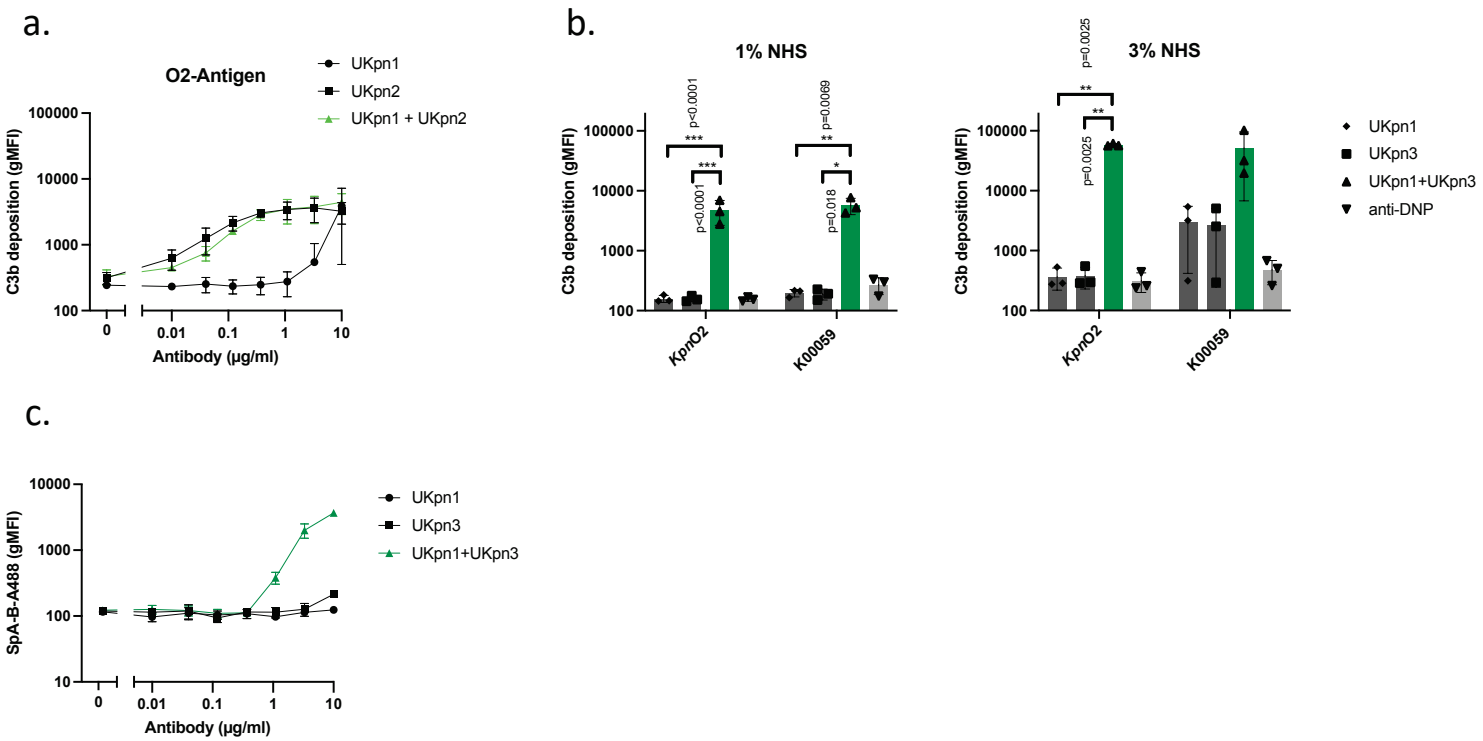

Figure S6 | Combining capsule targeting antibodies improves complement activation on *Kpn*O2. (a) Antibody-dependent C3b deposition on *Kpn*O2 pre-incubated with UKpn1, UKpn2 or a combination of both. After antibody binding, bacteria were incubated in 3% normal human serum (NHS) as a complement source. C3b-deposition was detected using anti-hu-C3b-AF647 by flow cytometry. **(b)** Same setup as in (a) with strains *Kpn*O2 and K00059 at a fixed antibody concentration of 1 µg/ml with 1% NHS (left panel) and 3% NHS (right panel). As a control antibody anti-DNP was used. Data represent the gMFI of anti-hu-C3b-A647 of bacterial populations. **(c)** *Kpn*O2 was incubated with UKpn1, UKpn3 or a combination thereof. To this mixture 10 µg/ml SpA-B was added and incubated for 30 minutes at 4°C. SpA-B binding was measured by flow cytometry and depicted as gMFI of the bacterial population. **(a-c)** When antibodies were combined, both antibodies were added in the same concentration. The total antibody concentration in the assay is the same for single or combination of antibodies. Data represent mean ± SD of three independent experiments. **(c)** Data were analyzed by one-way ANOVA with Tukey multiple comparison analysis. Significant differences are indicated, * p<0.05, ** p<0.01 and ***p<0.001.

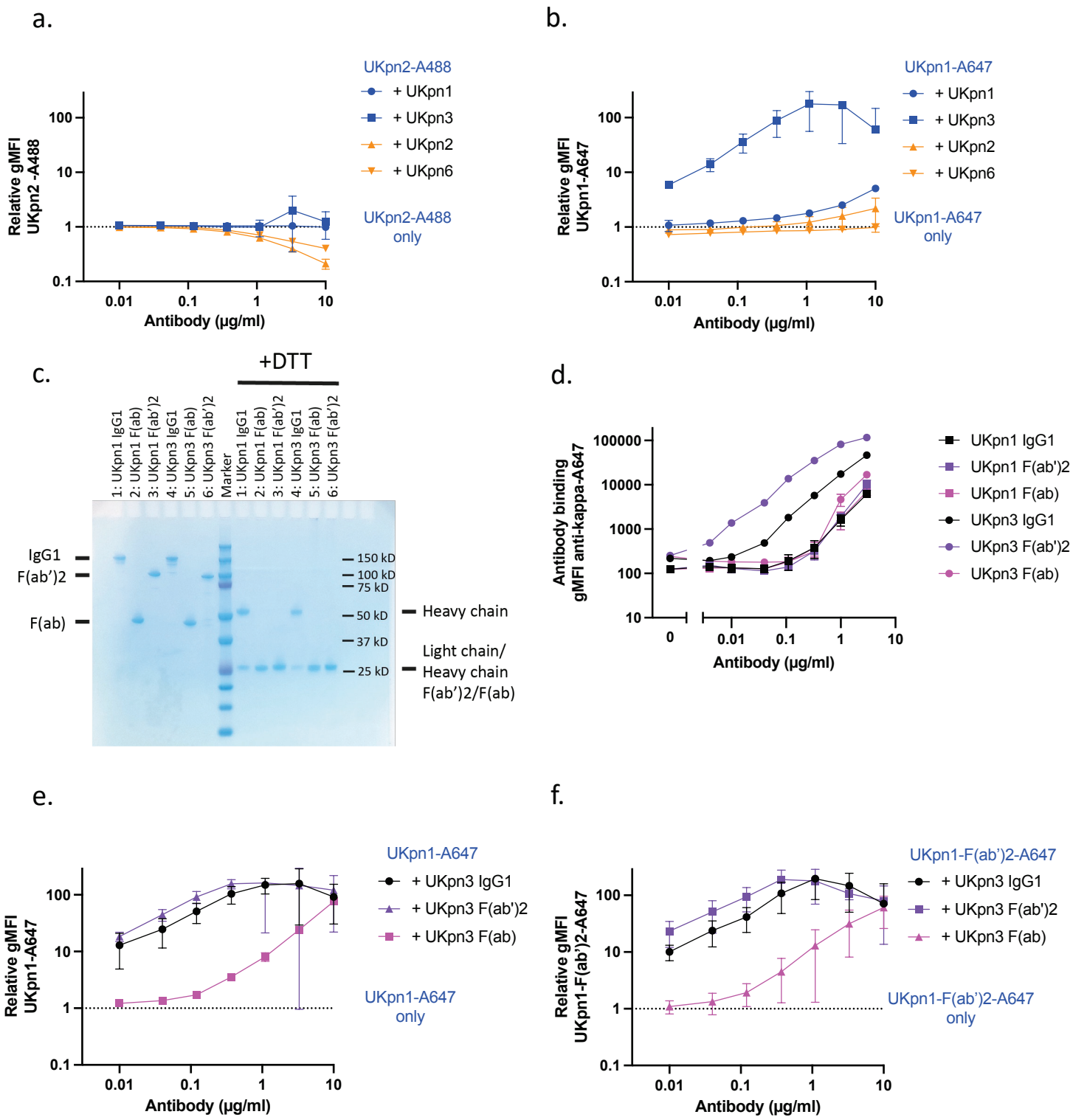

Figure S7 | Anti-capsular antibodies strengthen each other's binding. (a,b) *Kpn*O2 was incubated with **(a)** 0.1 µg/ml directly labeled anti-O2-antigen UKpn2-AF488 or **(b)** 1 µg/ml anti-capsule UKpn1-AF647. A concentration range of antibodies UKpn1, UKpn2, UKpn3 or UKpn6 was added to the labeled antibodies. UKpn2-AF488 and UKpn1-AF647 binding was detected by flow cytometry. **(c)** The IgG1, F(ab')2 and F(ab) of UKpn1 and UKpn3 all at 150 µg/ml were analyzed by SDS-PAGE and Instant blue staining in the absence (left) or presence (right) of DTT. **(d)** IgG1, F(ab')2 and F(ab) of UKpn1 and UKpn3 were incubated with *Kpn*O2, followed by detection with anti-kappa-A647 using flow cytometry. **(e-f)** *Kpn*O2 was incubated with 1 µg/ml **(e)** UKpn1-A647 or **(f)** UKpn1-F(ab')2-A647 together with various concentrations of UKpn3 variants (IgG1, F(ab')2 or F(ab)). The level of antibody binding was measured by detection of A647 using flow cytometry. **(a,b,e,f)** The relative antibody binding was calculated by dividing gMFI by fluorescent antibody only condition. Data represent mean ± SD of three independent experiments. **(c,d)** Data represent data obtained from a single experiment.

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Name	O-type	K-type	Sequence type	Isolation	Selection marker	Reference
KpnO2 (Kp209)	O2a	KL110	11	Urine		Janssen et al., 2020[43]
KpnO2 ΔwbbO	-	KL110	11		Gentamicin	This study
KpnO2 ΔwbaP	O2a	-	11		Gentamicin	This study
KpnO2 pULTRA-gfp	O2a	KL110	11		Kanamycin	This study
KpnO2 pULTRA-lux			11		Gentamicin	This study
KpnO2R (Kp209_CSTR) transposon library	O2a	KL110	11		Kanamycin	Van der Lans et al., 2023[34]
KpnO1 (UM-05-A#1)	O1	KL114	219	Fecal		Verschuren et al., unpublished
KpnO1 ΔwbbO	-	KL114	219		Gentamicin	This study
KpnO1 ΔwbbY	O2a	KL114	219		Gentamicin	This study
KpnO1 ΔwbaP	O1	-	219		Gentamicin	This study
KpnO1 pULTRA-gfp	O1	KL114	219		Kanamycin	This study
KpnO1 pULTRA-lux	O1	KL114	219		Gentamicin	This study
UM-2A#3.1	O1	KL20	20			Verschuren et al., unpublished
UM13B#1	O1	KL9	29			Verschuren et al., unpublished
MB-17667	O1	KL30-D1	391			Van den Bunt et al., 2020[53]
JS367*	O2afg	KL9	560			This study
MA-25932	O3b	KL60	2459			Van den Bunt et al., 2020 [53]
MA-49950	O4	KL17	211			Van den Bunt et al., 2020 [53]
MA-44575	O5	KL10	187			Van den Bunt et al., 2020 [53]
MA-18898	OL104	KL14	513			Van den Bunt et al., 2020 [53]
K00059	O3a	KL110	483			Van den Bunt et al., 2020 [53]
UM-05-B-#1	O2a	KL114	219			Verschuren et al., unpublished
MC-04166	O2afg	KL136				Van den Bunt et al., 2020 [53]
N0008	O3a	KL1				This study
MB-16059	O3b	KL2	628			Van den Bunt et al., 2020 [53]

Table S1| Strains used in this study

RT-PCR	
Heavy IgG	Sequence
H1_For_VH1	ACAGGTGCCCACTCCCAGGTGCAG
H1_For_VH3	AAGGTGTCCAGTGTGARGTGCAG
H1_For_VH4/6	CCCAGATGGGTCCTGTCCCAGGTGCAG
H1_For_VH5	CAAGGAGTCTGTTCCGAGGTGCAG
H1_Rev_int_CH1	GTTCGGGGAAGTAGTCCTTGAC
Kappa	
K1_For_Vκ1/2	ATGAGGSTCCCYGCTCAGCTGCTGG
K1_For_Vκ3	CTCTTCCTCCTGCTACTCTGGCTCCCAG
K1_For_Vκ4	ATTTCTCTGTTGCTCTGGATCTCTG
K1_For_Pan_Vκ	ATGACCCAGWCTCCABYCWCCCTG
K1_Rev_Cκ543	GTTTCTCGTAGTCTGCTTTGCTCA
K1_Rev_Cκ494	GTGCTGTCCTTGCTGTCCTGCT
Lambda	
λ1_For_Vλ1	GGTCCTGGGCCCAGTCTGTGCTG
λ1_For_Vλ2	GGTCCTGGGCCCAGTCTGCCCTG
λ1_For_Vλ3	GCTCTGTGACCTCCTATGAGCTG
λ1_For_Vλ4/5	GGTCTCTCTCSCAGCYTGTGCTG
λ1_For_Vλ6	GTTCTTGGGCCAATTTTATGCTG
λ1_For_Vλ7	GGTCCAATTCYCAGGCTGTGGTG
λ1_For_Vλ8	GAGTGGATTCTCAGACTGTGGTG
λ1_Rev_Cλ	CACCAGTGTGGCCTTGTTGGCTTG
2nd PCR	
Heavy IgG	
H2_For_AgeIC_VH1/5	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCGAGGTGCAGCTGGTGCAG
H2_For_AgeIC_VH3	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCTGAGGTGCAGCTGGTGGAG
H2_For_AgeIC_VH3–23	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCTGAGGTGCAGCTGTTGGAG
H2_For_AgeIC_VH4	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCCAGGTGCAGCTGCAGGAG
H2_For_AgeIC_VH4–34	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCCAGGTGCAGCTACAGCAGTG
H2_For_AgeIC_VH1–18	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCCAGGTTCAGCTGGTGCAG
H2_For_AgeIC_VH1–24	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCCAGGTCCAGCTGGTACAG
H2_For_AgeIC_VH3–33	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCTCAGGTGCAGCTGGTGGAG
H2_For_AgeIC_VH3–9	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCTGAAGTGCAGCTGGTGGAG
H2_For_AgeIC_VH4–39	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCCAGCTGCAGCTGCAGGAG
H2_For_AgeIC_VH6–1	GTTTCTGGTGGCTACTGCAACCGGTGTACATTCCCAGGTACAGCTGCAGCAG
H2_Rev_JH1/2/4/5	GATGGGCCCTTGGTGCTAGCTGAGGAGACGGTGACCAG
H2_Rev_JH3	GATGGGCCCTTGGTGCTAGCTGAAGAGACGGTGACCATTG
H2_Rev_JH6	GATGGGCCCTTGGTGCTAGCTGAGGAGACGGTGACCGTG
Kappa	
K2_For_Vκ1–5	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGACATCCAGATGACCCAGTC
K2_For_Vκ1–9	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGACATCCAGTTGACCCAGTCT
K2_For_Vκ1D–43	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGCCATCCGGATGACCCAGTC
K2_For_Vκ2–24	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGATATTGTGATGACCCAGAC
K2_For_Vκ2–28	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGATATTGTGATGACTCAGTC
K2_For_Vκ2–30	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGATGTTGTGATGACTCAGTC
K2_For_Vκ3–11	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGAAATTGTGTTGACACAGTC
K2_For_Vκ3–15	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGAAATAGTGATGACGCAGTC
K2_For_Vκ3–20	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGAAATTGTGTTGACGCAGTCT
K2_For_Vκ4–1	GTAATCAGCACTTGCCTGGAATTCTCTATGGCTGACATCGTGATGACCCAGTC
K2_Rev_Jκ1/4	GATGGTGCAGCCACCGTACGTTTGATYTCCACCTTGGTC
K2_Rev_Jκ2	GATGGTGCAGCCACCGTACGTTTGATCTCCAGCTTGGTC
K2_Rev_Jκ3	GATGGTGCAGCCACCGTACGTTTGATATCCACTTTGGTC
K2_Rev_Jκ5	GATGGTGCAGCCACCGTACGTTTAATCTCCAGTCGTGTC
Lambda	
λ2_For_Vλ1	GTTTCTGGTGGCTACTGCTACCGGTTCCTGGGCCCAGTCTGTGCTGACKCAG
λ2_For_Vλ2	GTTTCTGGTGGCTACTGCTACCGGTTCCTGGGCCCAGTCTGCCCTGACTCAG
λ2_For_Vλ3	GTTTCTGGTGGCTACTGCTACCGGTTCTGTGACCTCCTATGAGCTGACWCAG
λ2_For_Vλ4/5	GTTTCTGGTGGCTACTGCTACCGGTTCTCTCTCSCAGCYTGTGCTGACTCA
λ2_For_Vλ6	GTTTCTGGTGGCTACTGCTACCGGTTCTTGGGCCAATTTTATGCTGACTCAG
λ2_For_Vλ7/8	GTTTCTGGTGGCTACTGCTACCGGTTCCAATTCYCAGRCTGTGGTGACYCAG
λ2_Rev_Cλ	GTTGGCTTGAAGCTCCTCACTCGAGGGYGGGAACAGAGTG

Table S2| RT-PCR primers

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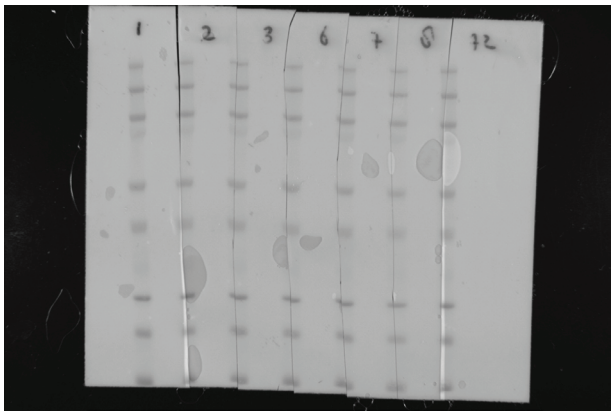

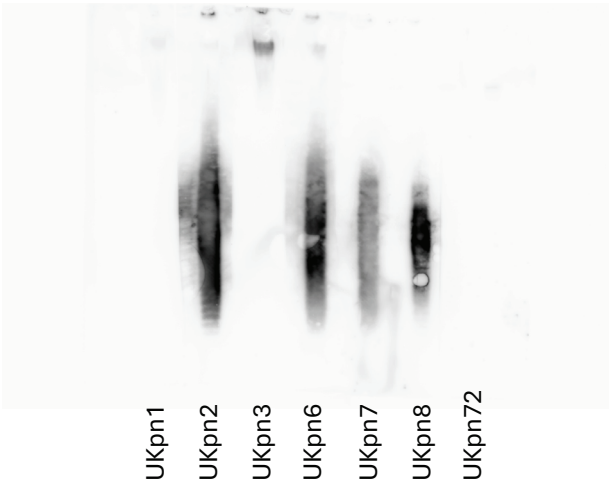

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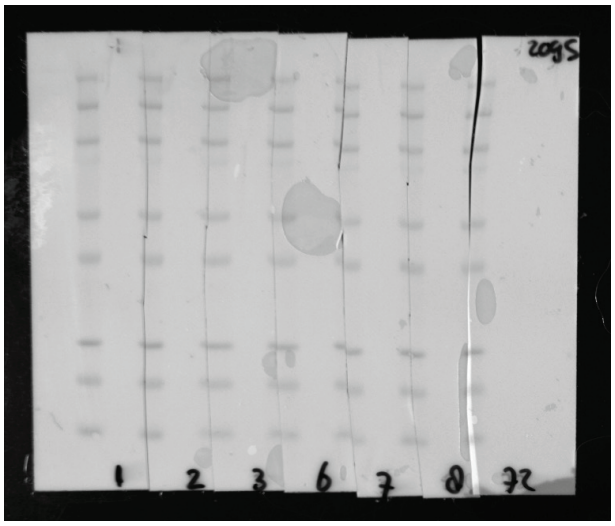

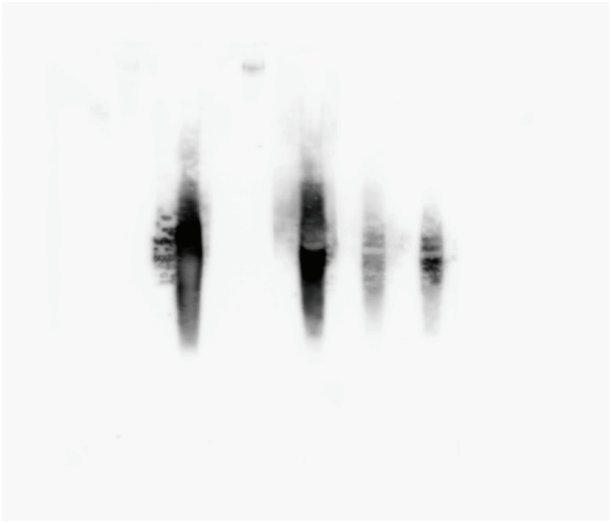

Source data supplementary fig S3d
Uncropped scan of blots from Sfig 3d