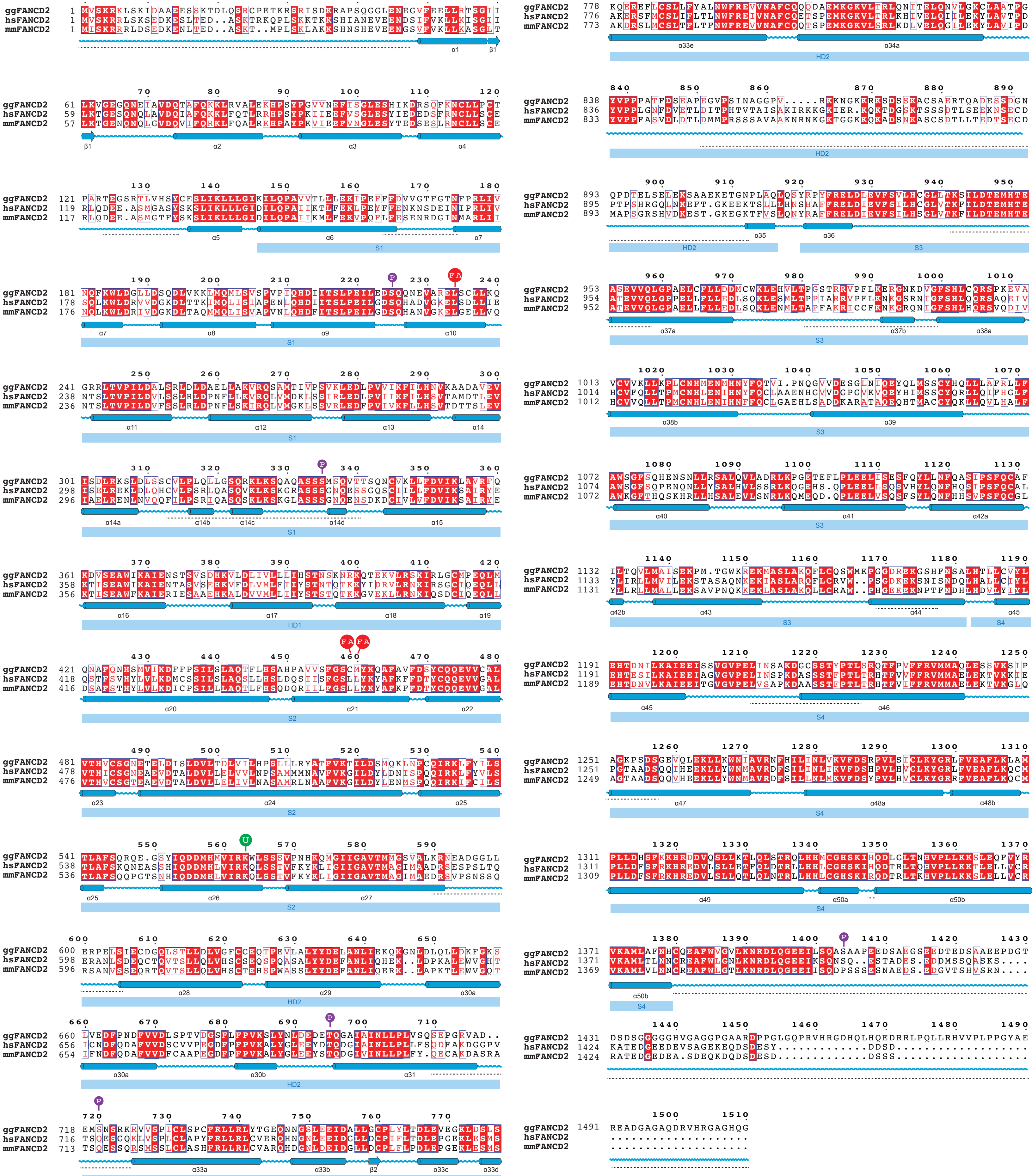
Supplementary Table 1. Comparison of *Gallus gallus* (gg) and *Mus musculus* (mm) FANCI and FANCD2 structures

	Q-score/N_{align}/RMSD* (FANCD2)	**Q-score/N_{align}/RMSD* (FANCI)**
ggD2–I vs mmD2–I	0.22/820/3.77	0.27/848/3.16
ggubD2–I vs mmD2–I	0.084/641/5.02	0.28/794/2.73
ggD2 vs mmD2–I	0.25/812/3.19	n/a
ggubD2–I vs ggD2–I	0.17/758/4.24	0.27/732/2.80
ggubD2–I vs ggD2	0.19/785/3.91	n/a

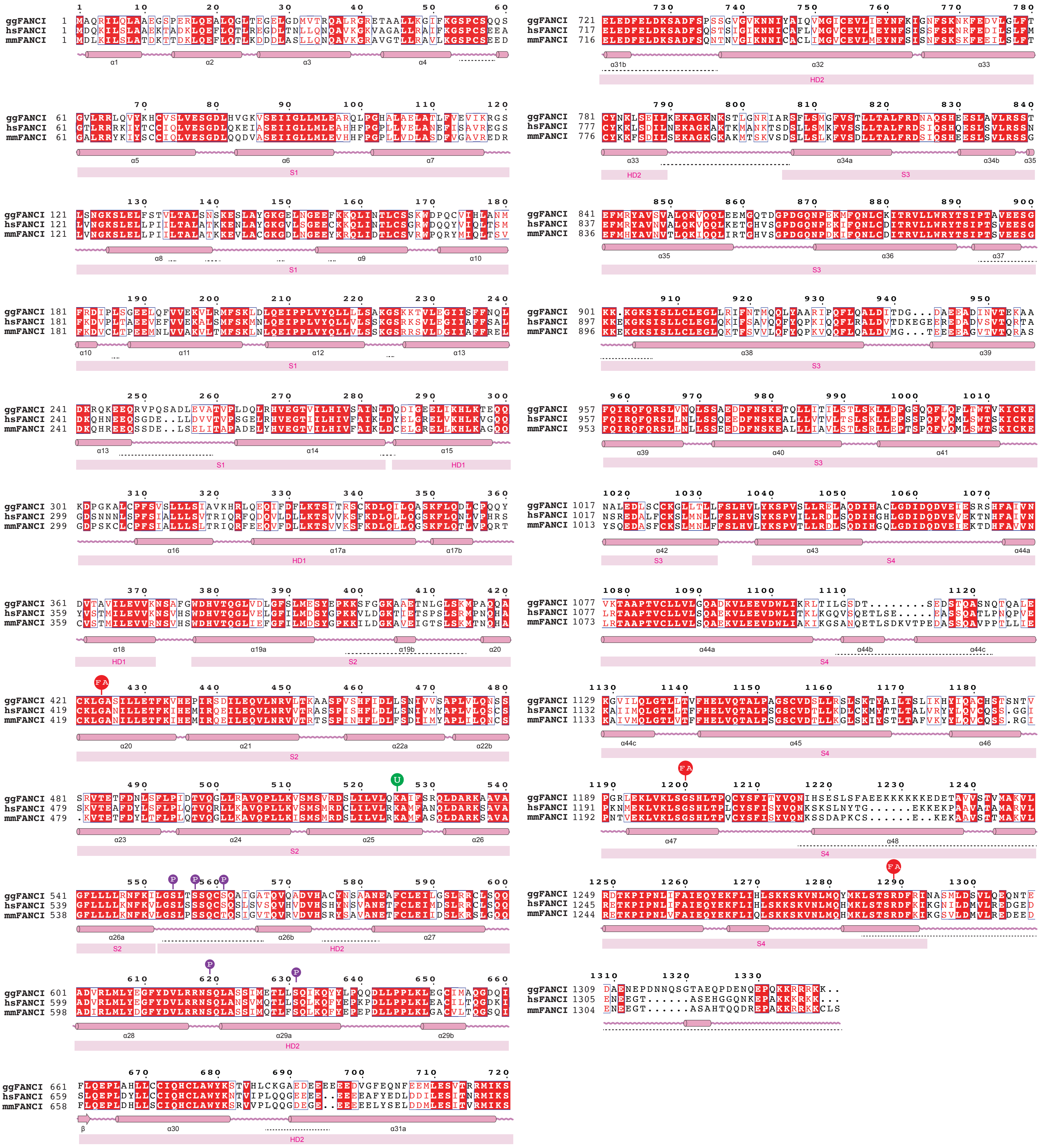
*Calculations were performed using PDBeFOLD (http://www.ebi.ac.uk/msd-srv/ssm/). Q-score represents the quality function of Cα-alignment, maximized by the SSM alignment algorithm. Quality of alignment takes both the alignment length and root-mean squared deviation (RMSD) into account, reaching a value of 1 only for identical structures. N_{align} is the number of matched residues, calculated from the best 3D superposition of query and target structures. The residues are aligned in 3D on the basis of their spatial closeness. The orientation of the structures is optimized such as to minimize RMSD and to maximize the number of aligned residues. Note that when there are substantial conformational changes, N_{align} decreases (e.g. ggubD2–I vs mmD2–I).

Supplementary Table 3. DNA oligonucleotides used in this study.

Name	Sequence (5’ to 3’)	nt
44-P1/36-FAM/	ATCGATGTCTCTAGACAGCTGCTCAGGATTGATCTGTAATGGCC/36-FAM/	44
39-P1/36-FAM/	ATCGATGTCTCTAGACAGCTGCTCAGGATTGATCTGTAA/36-FAM/	39
34-P1/36-FAM/	ATCGATGTCTCTAGACAGCTGCTCAGGATTGATC/36-FAM/	34
29-P1/36-FAM/	ATCGATGTCTCTAGACAGCTGCTCAGGAT/36-FAM/	29
24-P1/36-FAM/	ATCGATGTCTCTAGACAGCTGCTC/36-FAM/	24
19-P1/36-FAM/	ATCGATGTCTCTAGACAGC/36-FAM/	19
14-P1/36-FAM/	ATCGATGTCTCTAG/36-FAM/	14
10-P1/36-FAM/	ATCGATGTCT/36-FAM/	10
44-P1	ATCGATGTCTCTAGACAGCTGCTCAGGATTGATCTGTAATGGCC	44
44-P7	GGCCATTACAGATCAATCCTGAGCAGCTGTCTAGAGACATCGAT	44
39-P1	ATCGATGTCTCTAGACAGCTGCTCAGGATTGATCTGTAA	39
39-P7	TTACAGATCAATCCTGAGCAGCTGTCTAGAGACATCGAT	39
34-P1	ATCGATGTCTCTAGACAGCTGCTCAGGATTGATC	34
34-P7	GATCAATCCTGAGCAGCTGTCTAGAGACATCGAT	34
29-P1	ATCGATGTCTCTAGACAGCTGCTCAGGAT	29
29-P7	ATCCTGAGCAGCTGTCTAGAGACATCGAT	29
24-P1	ATCGATGTCTCTAGACAGCTGCTC	24
24-P7	GAGCAGCTGTCTAGAGACATCGAT	24
19-P1	ATCGATGTCTCTAGACAGC	19
19-P7	GCTGTCTAGAGACATCGAT	19
14-P1	ATCGATGTCTCTAG	14
14-P7	CTAGAGACATCGAT	14
10-P1	ATCGATGTCT	10
10-P7	AGACATCGAT	10
X1	GCGCACCAAGAGATACGCGGTCGAATGCCGAGTAGCCATCAGCG	44
X2	ACCATGCAGCTACTCGGCATTCGACCGCGTATCTGGCGACTACG	44
X3	TATCTCTTGGTGCGC	15
X4	CGCTGATGGCTACTC	15
X5	CGTAGTCGCCAGATA	15
X6	GAGTAGCTGCATGGT	15



Supplementary Note 1. Sequence alignment of FANCD2. Sequences from *Gallus gallus* (gg), *Homo sapiens* (hs) and *Mus musculus* (mm) are shown. Under the sequence alignment, the secondary structure of ggFANCD2 is represented in blue: tubes for α-helices and arrows for β-strands. For comparison, the helices have been labelled according to their equivalent nomenclature in the murine structure of unmodified D2–I (PDB 3S4W), and the solenoid (S) and helical domain (HD) numbers are indicated in light blue boxes. Red signs ("FA") indicate mutations characterized in FA patients, purple signs ("P") indicate phosphorylation sites and the monoubiquitination site K563 is marked in green ("U"). Disordered regions are marked with dashed lines. Sequence identities with ggFANCD2 are 56.6% for hsFANCD2 and 51.5% for mmFANCD2.



Supplementary Note 2. Sequence alignment of FANCI. Sequences from *Gallus gallus* (gg), *Homo sapiens* (hs) and *Mus musculus* (mm) are shown. Under the sequence alignment, the secondary structure of ggFANCI is represented in red: tubes for α-helices and arrows for β-strands. For comparison, the helices have been labelled according to their equivalent nomenclature in the murine structure of unmodified D2–I (PDB 3S4W), and the solenoid (S) and helical domain (HD) numbers are indicated in light red boxes. Red signs ("FA") indicate mutations characterized in FA patients, purple signs ("P") indicate phosphorylation sites and the monoubiquitination site K525 is marked in green ("U"). Disordered regions are marked with dashed lines. Sequence identities with ggFANCI are 66.4% for hsFANCI and 63.1% for mmFANCI.

Fig. 1b

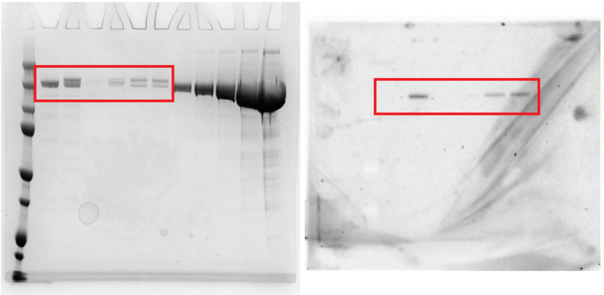


Fig. 4

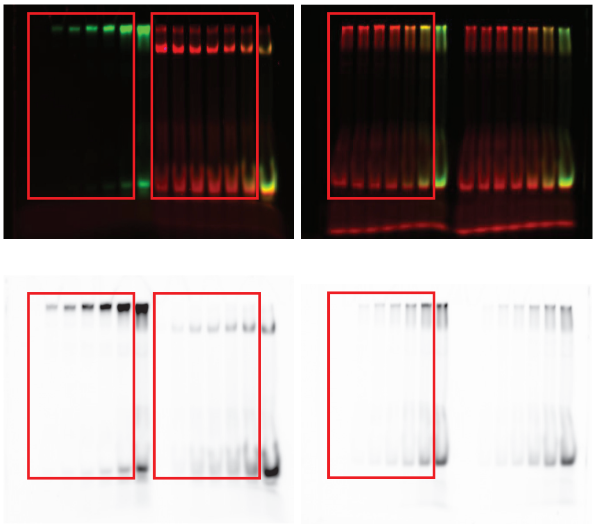
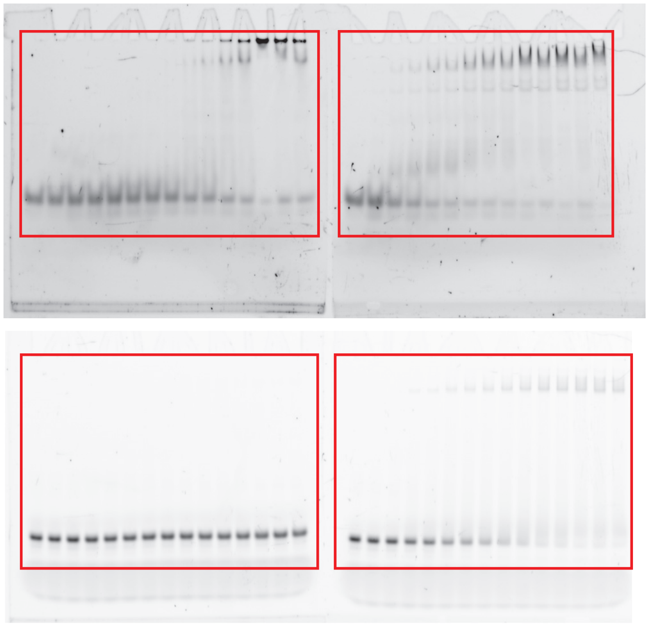
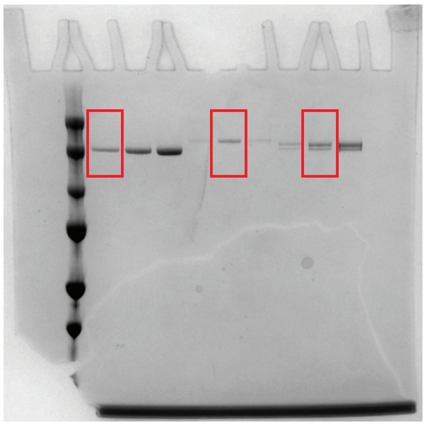


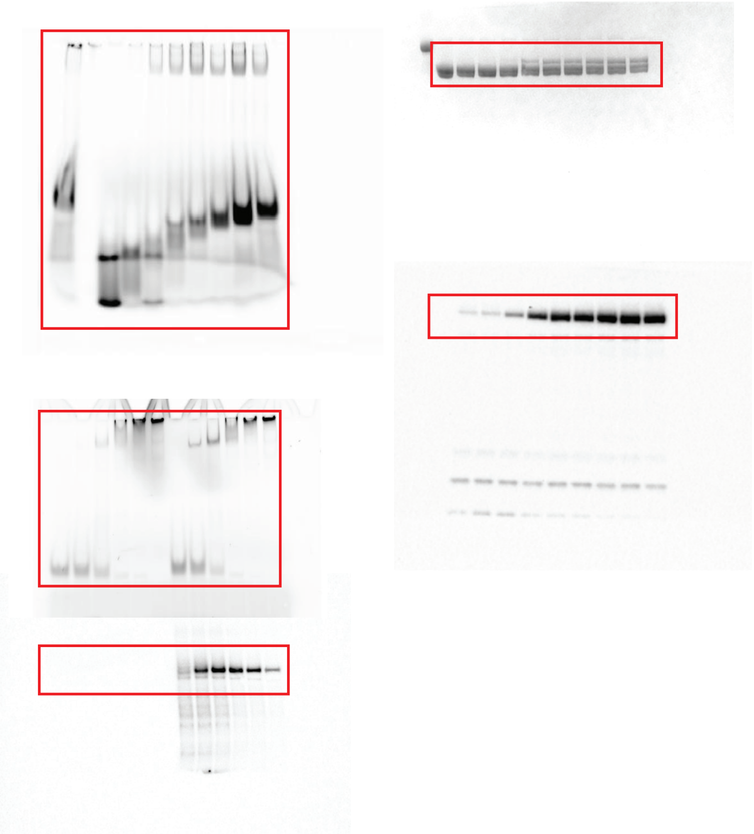
Fig. 5a and Extended Data Fig. 4b



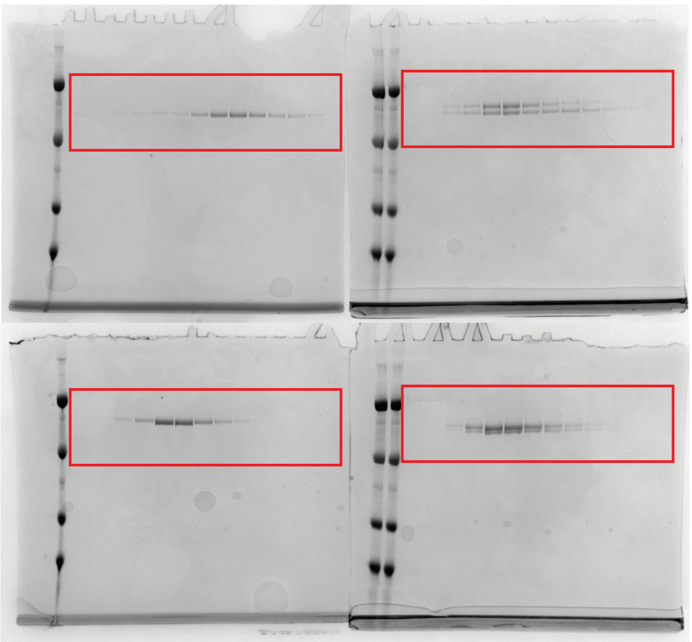
Extended Data Fig. 1a



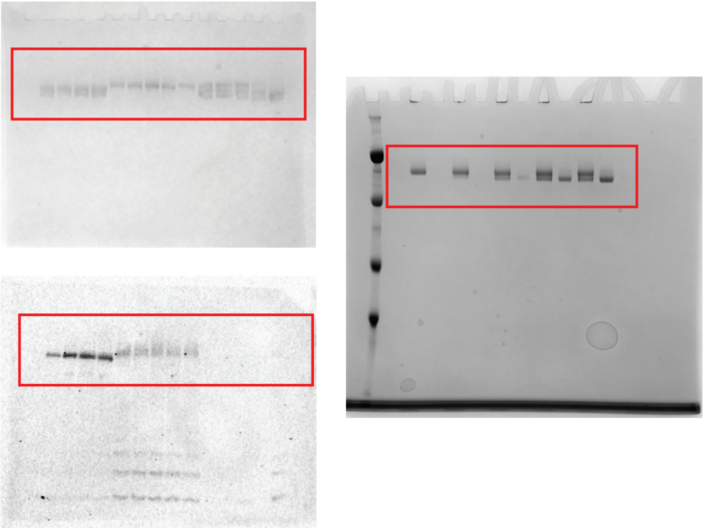
Extended Data Fig. 3



Extended Data Fig. 4a



Extended Data Fig. 5



Supplementary Figure 1. Uncropped gels and blots