

Table S1: Cross-links within CSN5H138A-SCF-N8Sbp2/Cks1.								
Id	Protein1	Protein2	Residue1	Residue2	deltaS	Id-Score	FDR	distance (in Angstrom)
TFNIKNDFTEEEEQVR-RPKLNR-a5-b3	Skp1	Skp2	142	86	0.36	55.77	0	residues not modeled
SQEGRPVQVIGALIGKQEGR-MLATLFKDER-a16-b7	Csn6	Csn4	75	251	0.73	49.35	0	21
GSDKDFVIVR-GKTPPEIR-a4-b2	Skp2	Skp1	77	130	0.4	42.38	0	residues not modeled
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGK-a6-b6	Csn2	Csn1	426	418	0.16	41.71	0	13
KTFNIKNDFTEEEEQVR-RPKLNR-a6-b3	Skp1	Skp2	142	86	0.64	41.56	0	residues not modeled
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGKEFQR-a6-b6	Csn2	Csn1	426	418	0.88	41.31	0	13
KTFNIKNDFTEEEEQVR-RPKLNR-a1-b3	Skp1	Skp2	137	86	0.33	40.39	0	residues not modeled
IPPAIKSANSELGGIWSVGQR-KQPLR-a6-b1	Csn8	Csn3	65	152	0.44	39.52	0.042	15
MFQDIGVSKDLNEQFKK-LGKLYLER-a9-b3	Cul1	Csn2	552	157	0.38	39.19	0.042	16
GKTPEEIRK-RPKLNR-a2-b3	Skp1	Skp2	130	86	0.48	38.17	0.042	residues not modeled
TWELANNMQEAQSIDEIYKYDKK-VKLTGTGK-a19-b2	Csn5	Nedd8	30	6	0.41	38.15	0.042	27
INFKLTNFPPEMMNR-DLNEQFKK-a4-b7	Csn2	Cul1	81	559	0.84	37.89	0.042	12
SQNPHGLKQIGLDQIWDDLRL-RPKLNR-a8-b3	Cul1	Skp2	50	86	0.51	37.24	0.042	residues not modeled
TWELANNMQEAQSIDEIYKYDKK-VKLTGTGK-a22-b2	Csn5	Nedd8	33	6	0.52	37.1	0.042	9
GKTPEEIR-RPKLNR-a2-b3	Skp1	Skp2	130	86	0	36.98	0.042	residues not modeled
TQQQVEAEVTNIKK-KSEDKLAK-a13-b1	Csn7	Csn5	217	295	0.54	36.05	0.042	residues not modeled
RAKAMMLR-KNLQK-a3-b1	Csn1	Skp2	431	295	0.77	35.49	0.042	34
LTKTFLTLQLDMSLR-STTFEKSLLMGK-a3-b6	Csn3	Csn1	349	418	0.34	35.44	0.042	14
MFQDIGVSKDLNEQFKK-LGKLYLEREEYGGK-a9-b3	Cul1	Csn2	552	157	0.76	35.41	0.042	16
LSDPVNTLAKNSNLVR-KQPLR-a11-b1	Skp2	Csn3	228	152	0.38	35.08	0.042	89
SMGSQEDDSGNKPSSYS-TQQQVEAEVTNIKK-a12-b13	Csn3	Csn7	455	217	0	34.53	0.042	residues not modeled
DGMVSFHDNPEKYNNPAMLHNIDQEMLK-SLLMGKEFQR-a12-b6	Csn3	Csn1	403	424	0.34	34	0.042	21
TISAGKVNLGAFR-ANQYKENHNR-a6-b5	Csn5	Csn7	180	199	0.27	33.99	0.042	residues not modeled
AMDQEITVNPQFVQKSMGSQEDDSGNKPSSYS-KNLQK-a15-b1	Csn3	Skp2	443	295	0.36	32.82	0.042	22
NLVNKHSETFTR-KNLQK-a5-b1	Csn3	Skp2	318	295	0.31	32.53	0.051	55
IDQVNQLLELDHQKR-STTFEKSLLMGK-a14-b6	Csn2	Csn1	415	418	0.63	32.43	0.051	21
NLVNKHSETFTR-RPKLNR-a5-b3	Csn3	Skp2	318	86	0.31	32.43	0.051	residues not modeled
FIKPLSNAYHELAQVYSTNNPSEL-KNLQK-a3-b1	Csn3	Skp2	291	295	0.32	32.11	0.051	39
SMGSQEDDSGNKPSSYS-KSEDKLAK-a12-b5	Csn3	Csn5	455	299	0.27	31.89	0.051	residues not modeled
AMDQEITVNPQFVQKSMGSQEDDSGNKPSSYS-NQIHVKSPPR-a15-b6	Csn3	Csn1	443	447	0.32	31.83	0.051	residues not modeled
FINNNAVTKMAQSSSK-VKLTGTGK-a9-b2	Cul1	Nedd8	447	6	0.5	31.57	0.051	62
NQIHVKSPPREGSQGELTPANSQSR-LSDPVNTLAKNSNLVR-a6-b11	Csn1	Skp2	447	228	0.79	31.53	0.051	residues not modeled
DGMVSFHDNPEKYNNPAMLHNIDQEMLK-KPVAGALDVSFNK-a12-b1	Csn3	Csn8	403	166	0.3	31.47	0.051	residues not modeled
LKAMDQEITVNPQFVQK-ANQYKENHNR-a2-b5	Csn3	Csn7	428	199	0.93	31.15	0.051	10
DGMVSFHDNPEKYNNPAMLHNIDQEMLK-STTFEKSLLMGK-a12-b6	Csn3	Csn1	403	418	0.28	30.6	0.051	17
LKAMDQEITVNPQFVQK-KSEDKLAK-a2-b1	Csn3	Csn5	428	295	0.43	30.54	0.051	residues not modeled
LSDPVNTLAKNSNLVR-NLVNKHSETFTR-a11-b5	Skp2	Csn3	228	318	0.46	30.49	0.051	69
LKAMDQEITVNPQFVQK-KSEDKLAK-a2-b5	Csn3	Csn5	428	299	0.45	30.4	0.051	residues not modeled
IDQVNQLLELDHQKR-TISAGKVNLGAFR-a14-b6	Csn2	Csn5	415	180	0.49	30.28	0.051	28

Table S2: Cross-links within CSN5H138A-SCFSkp2/Cks1.							
Id	Protein1	Protein2	Residue1	Residue2	deltaS	Id-Score	FDR
TFNIKNDFTEEEEAQVR-RPKLNR-a5-b3	Skp1	Skp2	142	86	0.35	52.26	0
SQEGRPVQVIGALIGKQEGR-MLATLFKDER-a16-b7	Csn6	Csn4	75	251	0.78	44.69	0
IPPAIKSANSELGGIWSVGQR-KQPLR-a6-b1	Csn8	Csn3	65	152	0.38	44.31	0
GKTPEEIRK-RPKLNR-a2-b3	Skp1	Skp2	130	86	0.42	40.01	0
GKTPEEIR-RPKLNR-a2-b3	Skp1	Skp2	130	86	0.47	38.28	0
KTFNIKNDFTEEEEAQVR-RPKLNR-a6-b3	Skp1	Skp2	142	86	0.34	38.13	0
KTFNIKNDFTEEEEAQVR-RPKLNR-a1-b3	Skp1	Skp2	137	86	0.45	37.71	0
LTKTFLTLSQLDMASR-STTFEKSLLMGK-a3-b6	Csn3	Csn1	349	418	0.24	37.37	0
AMDQEITVNPQFVQKSMGSEQEDDSGNKPSSYS-NQIHVKSPPR-a15-b6	Csn3	Csn1	443	447	0.27	37.29	0
TISAGKVNLAGFR-ANQYKENHNR-a6-b5	Csn5	Csn7	180	199	0.66	36.95	0
NLVNKHSETFTR-NQIHVKSPPR-a5-b6	Csn3	Csn1	318	447	0.61	36.94	0
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGK-a6-b6	Csn2	Csn1	426	418	0.28	36.42	0
MFQDIGVSKDLNEQFK-LGKLYLER-a9-b3	Cul1	Csn2	552	157	0.29	36.17	0
NLVNKHSETFTR-VDSHSKILYAR-a5-b6	Csn3	Csn1	318	402	0.72	35.43	0
NLVNKHSETFTR-RPKLNR-a5-b3	Csn3	Skp2	318	86	0.51	35.22	0
NLVNKHSETFTR-KLSEATR-a5-b1	Csn3	Csn1	318	81	0.57	34.91	0.043
LKAMDQEITVNPQFVQK-ANQYKENHNR-a2-b5	Csn3	Csn7	428	199	0.43	34.55	0.043
LSDPIVNTLAKNSNLVR-KQPLR-a11-b1	Skp2	Csn3	228	152	0.38	34.49	0.043
DGMVFSFHDNPEKYNNPAMLHNIDQEMLK-SLLMGKEFQR-a12-b6	Csn3	Csn1	403	424	0.21	34.4	0.043
TQQQVEAEVTNIKK-KSEDKLAK-a13-b5	Csn7	Csn5	217	299	0.56	34.07	0.043
TQQQVEAEVTNIKK-KSEDKLAK-a13-b1	Csn7	Csn5	217	295	0.56	34.06	0.043
IDQVNQLLELDHQR-WLKTR-a14-b3	Csn2	Rbx1	415	145	0.72	33.99	0.043
IDQVNQLLELDHQR-TISAGKVNLAGFR-a14-b6	Csn2	Csn5	415	180	0.73	33.95	0.043
NQIHVKSPPREGSQELTPANSQSR-SMGSEQEDDSGNKPSSYS-a6-b12	Csn1	Csn3	447	455	0.29	33.43	0.083
SQNPHGLKQIGLDQIWDDL-RPKLNR-a8-b3	Cul1	Skp2	50	86	0.57	32.68	0.12
SMGSEQEDDSGNKPSSYS-NQIHVKSPPR-a12-b6	Csn3	Csn1	455	447	0.2	31.16	0.154
IDQVNQLLELDHQR-STTFEKSLLMGK-a14-b6	Csn2	Csn1	415	418	0.64	30.33	0.185
EGIPPPQQRLIYSGKQMNDEK-QILEKAIQLSGAEQLEALK-a15-b5	Nedd8	Csn4	48	32	0.54	28.94	0.243
IDQVNQLLELDHQR-NQIHVKSPPR-a14-b6	Csn2	Csn1	415	447	0.67	28.68	0.243
TQVLIKLIKPYTR-MRKVLK-a6-b3	Csn2	Cul1,Rbx1	361	760, 3	0.74	28.38	0.243
LSDPIVNTLAKNSNLVR-NLVNKHSETFTR-a11-b5	Skp2	Csn3	228	318	0.42	27.13	0.243
GNQLQEFAAMLMPHQKATTADGSSILDR-WLKTR-a16-b3	Csn4	Rbx1	290	145	0.43	26.73	0.243
TISAGKVNLAGFR-MLATLFKDER-a6-b7	Csn5	Csn4	180	251	0.67	25.99	0.243
AMDQEITVNPQFVQKSMGSEQEDDSGNKPSSYS-KNLQK-a15-b1	Csn3	Skp2	443	295	0.26	25.57	0.243
KTLKATASSSAQEMEQLAER-MAQSSSKSPELLAR-a4-b7	Csn7	Cul1	221	454	0.57	25.06	0.263

Table S3: Cross-links within CSN-Cul1/Rbx1.							
Id	Protein1	Protein2	Residue1	Residue2	deltaS	Id-Score	FDR
SQEGRPVQVIGALIGKQEGR-MLATLFKDER-a16-b7	Csn6	Csn4	75	251	0.76	42.99	0
IPPAIKSANSELGGIWSVGQR-KQPLR-a6-b1	Csn8	Csn3	65	152	0.37	42.99	0
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGK-a6-b6	Csn2	Csn1	426	418	0.1	42.93	0
TISAGKVNLGAFR-ANQYKENHNR-a6-b5	Csn5	Csn7	180	199	0.68	38.81	0
NLVNKHSETFTR-KLSEATR-a5-b1	Csn3	Csn1	318	81	0.34	38.52	0
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGKEFQR-a6-b6	Csn2	Csn1	426	418	0.91	38.29	0
TISAGKVNLGAFR-MLATLFKDER-a6-b7	Csn5	Csn4	180	251	0.63	36.72	0
LTKTFLTSLQDMASR-STTFEKSLLMGK-a3-b6	Csn3	Csn1	349	418	0.21	36.67	0
LKAMDQEITVNPQFVQK-ANQYKENHNR-a2-b5	Csn3	Csn7	428	199	0.91	36.53	0
NLVNKHSETFTR-NQIHVKSPPR-a5-b6	Csn3	Csn1	318	447	0.52	35.96	0
TQQQVEAEVTNIKK-KSEDKLAK-a13-b5	Csn7	Csn5	217	299	0.64	35.88	0
IDQVNQLELDHQKR-TISAGKVNLGAFR-a14-b6	Csn2	Csn5	415	180	0.6	35.55	0
AMDQEITVNPQFVQKSMGSEQEDDSGNKPSSYS-DKLFNQINIS-a15-b2	Csn3	Csn5	443	326	0.9	34.64	0
TQQQVEAEVTNIKK-KSEDKLAK-a13-b1	Csn7	Csn5	217	295	0.56	34.53	0
VDSHSKILYAR-ANQYKENHNR-a6-b5	Csn1	Csn7	402	199	0.53	33.64	0
NQIHVKSPPREGSQGELTPANSQSR-SMGSEQEDDSGNKPSSYS-a6-b12	Csn1	Csn3	447	455	0.55	33.34	0.048
SMGSEQEDDSGNKPSSYS-NQIHVKSPPR-a12-b6	Csn3	Csn1	455	447	0.22	33.07	0.048
IDQVNQLELDHQKR-NQIHVKSPPR-a14-b6	Csn2	Csn1	415	447	0.59	33.04	0.048
IDQVNQLELDHQKR-WLKTR-a14-b3	Csn2	Rbx1	415	145	0.71	31.99	0.048
IDQVNQLELDHQKR-STTFEKSLLMGK-a14-b6	Csn2	Csn1	415	418	0.6	31.51	0.048
SMGSEQEDDSGNKPSSYS-TQQQVEAEVTNIKK-a12-b13	Csn3	Csn7	455	217	0	31.24	0.048
LTWLQYLSKGELVTNCFKNR-QILEKAIQLSGAEQLEALK-a18-b5	Cul1	Csn4	633	32	0.32	30.34	0.087
DGMVSFHDNPEKYNNPAMLHNIDQEMLK-SLLMGKEFQR-a12-b6	Csn3	Csn1	403	424	0.34	30.19	0.087
KTLKATASSSAQEMEQLAER-MAQSSKSPELLAR-a4-b7	Csn7	Cul1	221	454	0.54	26.27	0.216
NLVNKHSETFTR-ANQYKENHNR-a5-b5	Csn3	Csn7	318	199	0.37	26.17	0.216
DGMVSFHDNPEKYNNPAMLHNIDQEMLK-IDQVNQLELDHQKR-a12-b14	Csn3	Csn2	403	415	0.42	26.09	0.216
SMGSEQEDDSGNKPSSYS-KSEDKLAK-a12-b5	Csn3	Csn5	455	299	0	26.05	0.216
AMDQEITVNPQFVQKSMGSEQEDDSGNKPSSYS-NQIHVKSPPREGSQGELTPAN	Csn3	Csn1	443	447	0.27	25.01	0.216

Table S4: Cross-links within CSN5H138A-SCF-N8Fbw7FL.							
Id	Protein1	Protein2	Residue1	Residue2	deltaS	Id-Score	FDR
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGK-a6-b6	Csn2	Csn1	426	418	0.2	39.12	0
IPPAIKSANSELGGIWSVGQR-KQPLR-a6-b1	Csn8	Csn3	65	152	0.43	36.68	0
NLVNKHSETFTR-KLDHGSEVR-a5-b1	Csn3	Fbw7fl	318	208	0.67	33.36	0
TISAGKVNLGAFR-ANQYKENHNR-a6-b5	Csn5	Csn7	180	199	0.47	30.42	0
FINNNAVTKMAQSSSK-VKTLTGK-a9-b2	Cul1	Nedd8	447	6	0.54	30.4	0
TQQQVEAEVTNIKK-KSEDKLAK-a13-b1	Csn7	Csn5	217	295	0.6	29.4	0
MAGEQKPSSNLEQFILLAK-SFSLGKKPCK-a6-b7	Csn7	Fbw7fl	6	223	0.51	29.22	0
YTALDKWTNQLNSLNQAVVSK-KAEARLLEEQR-a6-b1	Csn2	Cul1	426	300	0.27	29.15	0
VEEKEGIPPPQQR-EEYGKLQKILR-a4-b5	Nedd8	Csn2	33	167	0.94	28.92	0
LTKTFLTLQLDMASR-STTFEKSLLMGK-a3-b6	Csn3	Csn1	349	418	0.46	28.62	0

Table S5: Cross-links within CSN5H138A-SCF-N8Fbw7trunc							
Id	Protein1	Protein2	Residue1	Residue2	deltaS	Id-Score	FDR
SQEGRPVQVIGALIGKQEGR-MLATLFKDER-a16-b7	Csn6	Csn4	75	251	0.72	44	0
IPPAIKSANSELGGIWSVGQR-KQPLR-a6-b1	Csn8	Csn3	65	152	0.52	40.55	0
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGK-a6-b6	Csn2	Csn1	426	418	0.18	38.91	0
MFQDIGVSKDLNEQFK-LGKLYLER-a9-b3	Cul1	Csn2	552	157	0.27	38.66	0
IDQVNQLLELDHQKR-STTFEKSLLMGK-a14-b6	Csn2	Csn1	415	418	0.56	36.03	0

Table S6: Cross-links within CSN-Cul3/Rbx1							
Id	Protein1	Protein2	Residue1	Residue2	deltaS	Id-Score	FDR
FYLAKHSGR-LGKLYLER-a5-b3	Cul3	Csn2	579	157	0.76	45.11	0
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGK-a6-b6	Csn2	Csn1	426	418	0.27	44.01	0
YTALDKWTNQLNSLNQAVVSK-STTFEKSLLMGKEFQR-a6-b6	Csn2	Csn1	426	418	0.83	41.73	0
NLVNKHSETFTR-KGEVVDR-a5-b1	Csn3	Cul3	318	211	0.37	41.42	0
IPPAIKSANSELGGIWSVGQR-KQPLR-a6-b1	Csn8	Csn3	65	152	0.88	40.9	0
SQEGRPVQVIGALIGKQEGR-MLATLFKDER-a16-b7	Csn6	Csn4	75	251	0.72	40.88	0
LGKLYLEREEYGK-FYLAKHSGR-a3-b5	Csn2	Cul3	157	579	0.56	40.03	0
TISAGKVNLGAFR-ANQYKENHNR-a6-b5	Csn5	Csn7	180	199	0.26	38.74	0
MQHNVLVAEVTQQLKAR-WLKTR-a15-b3	Cul3	Rbx1	768	145	0.31	38.51	0
RFYLAKHSGR-LGKLYLER-a6-b3	Cul3	Csn2	579	157	0.8	37.22	0
AMDQEITVNPQFVQKSMGSQEDDSGNKPSSYS-NQIHVKSPPR-a15-b6	Csn3	Csn1	443	447	0.3	35.74	0