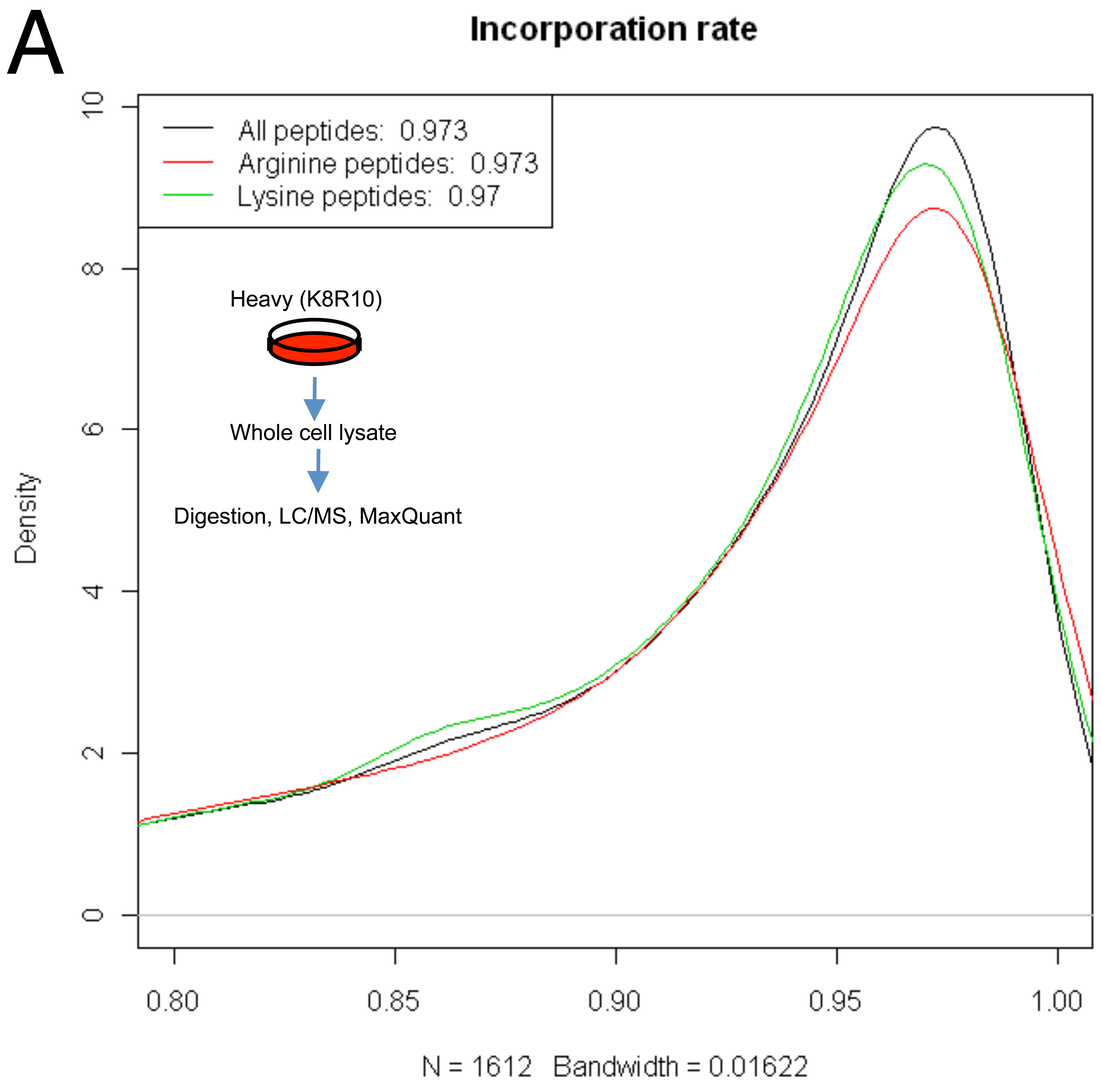
Supplementary Table 1. List of Dengue UTR-interacting proteins identified by mass spectrometry and their respective SILAC ratios with P values from independent forward and reverse experiments.

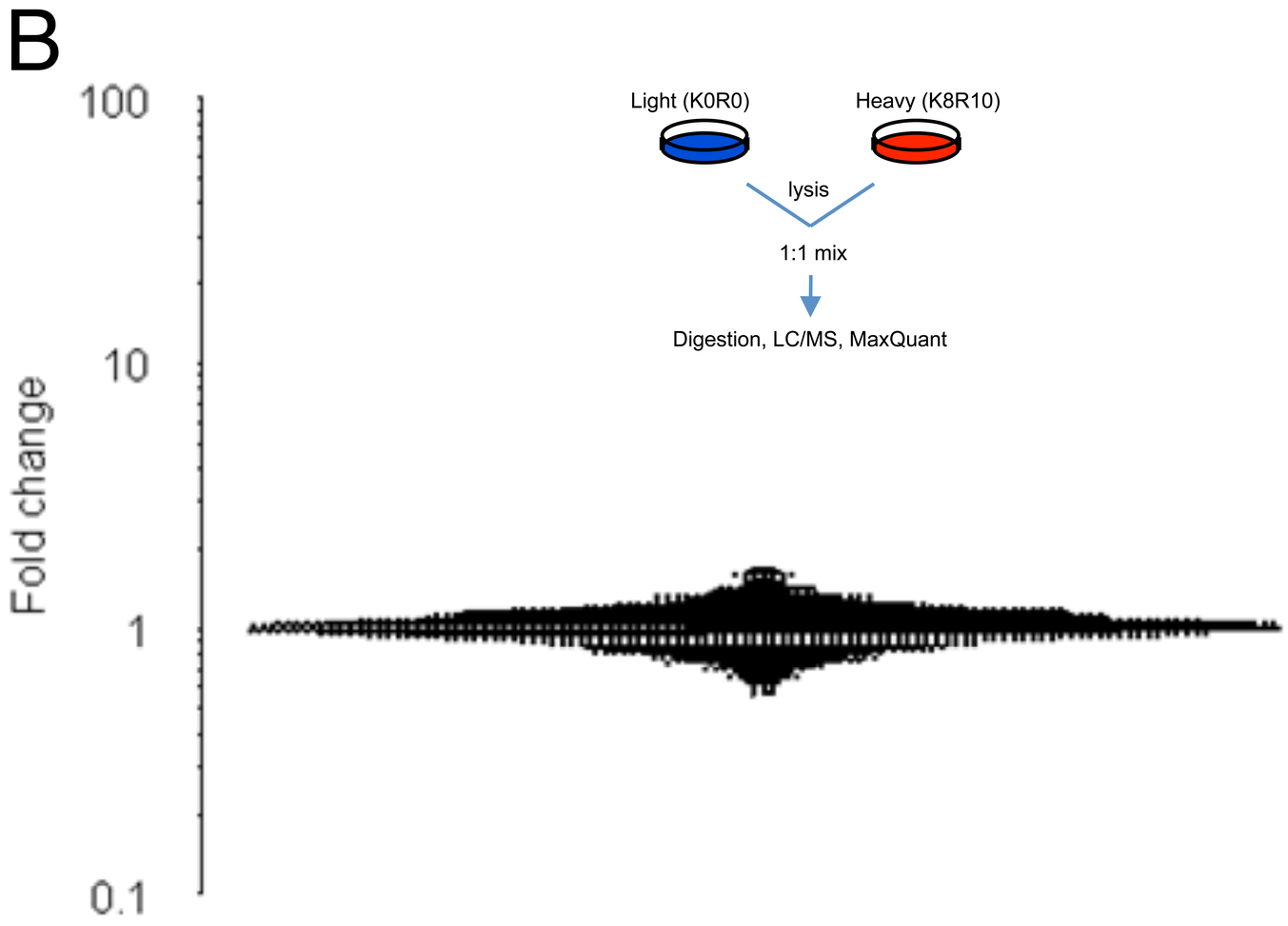
Gene Names	Ratio H/L Normalized forward	Ratio H/L Significance(B) $P^{forward}$	Ratio H/L Count forward	Ratio H/L Normalized reverse	Ratio H/L Significance(B) $P^{reverse}$	Ratio H/L Count reverse	$P^{forward}$ x $P^{reverse}$
CAPRIN1	21.72	1.29E-18	80	0.03	1.41E-13	95	1.81E-31
DDX6	14.83	9.09E-15	14	0.03	3.99E-14	42	3.63E-28
USP10	14.26	2.11E-14	22	0.07	7.22E-09	67	1.53E-22
G3BP2	16.85	5.28E-16	95	0.02	4.99E-16	178	2.64E-31
G3BP1	12.63	2.68E-13	102	0.04	2.82E-12	92	7.57E-25
LSM12	8.15	1.86E-09	6	0.04	9.89E-06	5	1.84E-14
EDC3	7.64	3.12E-09	18	0.11	0.0021238	48	6.63E-12
FMR1	7.79	3.98E-09	15	0.15	0.0073578	5	2.93E-11
NUFIP2	6.47	7.52E-08	8	0.08	0.00047617	25	3.58E-11
LSM10	7.32	1.11E-08	12	0.13	0.0051225	7	5.68E-11
RALY	4.93	3.51E-06	26	0.20	0.024443	12	8.58E-08
CNBP	4.79	3.31E-06	37	0.09	6.30E-08	29	2.08E-13
HNRNPA2B1	4.99	1.91E-06	79	0.20	0.00024171	69	4.61E-10
HNRPDL	3.61	0.00010056	131	0.12	2.03E-06	90	2.05E-10
HNRNPA1	4.99	1.90E-06	219	0.18	7.78E-05	184	1.48E-10
U2AF1	3.89	4.31E-05	25	0.17	6.11E-05	28	2.63E-09
U2AF2	3.51	0.00013623	34	0.17	4.20E-05	32	5.73E-09
RBMX	3.30	0.00026195	24	0.24	0.04124	49	1.08E-05
HNRNPA3	4.39	1.03E-05	52	0.18	7.55E-05	40	7.75E-10
PRNPIP	2.37	0.0055835	55	0.24	0.00090717	23	5.07E-06
HNRNPU	2.35	0.0058362	308	0.35	0.0097164	396	5.67E-05
PABPN1	2.74	0.001599	55	0.26	0.0015433	33	2.47E-06
CHD3	2.09	0.014387	72	0.29	0.0033661	157	4.84E-05
SFRS2	2.20	0.0097681	110	0.13	5.27E-06	86	5.14E-08
HSPB1	3.51	0.00019846	19	0.93	0.41001	8	8.14E-05
PTRF	2.79	0.0018939	14	0.36	0.11711	22	2.22E-04
BAT2D1	2.40	0.0066458	13	0.30	0.073605	4	4.89E-04
PLOD1	2.32	0.006597	37	0.45	0.037784	106	2.49E-04
SRBD1	2.12	0.012729	65	0.38	0.016941	82	2.16E-04
STRAP	1.90	0.027723	33	0.41	0.024371	27	6.76E-04
TFAM	2.16	0.0112	84	0.40	0.02135	51	2.39E-04
POLR1A	2.02	0.023232	22	0.49	0.22842	6	5.31E-03
POLR1B	1.65	0.077192	4	0.55	0.27241	4	2.10E-02
FAM120A	2.02	0.018259	57	0.40	0.021054	87	3.84E-04
MYO1E	1.62	0.083055	9	0.52	0.25074	27	2.08E-02
WDR12	1.91	0.026042	27	0.54	0.083576	23	2.18E-03
IFIT5	1.93	0.024268	86	0.33	0.007859	61	1.91E-04
MKRN2	1.91	0.032673	13	0.29	0.070989	6	2.32E-03
HNRPR	1.66	0.074527	5	0.57	0.29235	3	2.18E-02
CSDE1	2.25	0.010959	23	0.40	0.15045	34	1.65E-03
NCL	1.71	0.052451	1066	0.54	0.083372	946	4.37E-03
COPB2	1.91	0.033238	12	0.21	0.026633	36	8.85E-04
DDX50	1.99	0.024972	19	0.56	0.28159	46	7.03E-03
SART3	1.97	0.021253	163	0.27	0.0022013	284	4.68E-05
HNRNPF	1.78	0.041531	69	0.61	0.13629	50	5.66E-03
HNRNPD	1.65	0.063242	106	0.35	0.010315	62	6.52E-04
COPA	1.99	0.020078	85	0.19	0.00015661	100	3.14E-06
MSI2	1.59	0.076487	70	0.39	0.019698	45	1.51E-03
TSR1	1.70	0.054095	42	0.33	0.0076666	117	4.15E-04
RBM39	1.56	0.084253	22	0.41	0.025475	97	2.15E-03
RAN	1.57	0.081096	38	1.96	0.020676	5	1.68E-03
C17orf42	1.57	0.08342	52	0.49	0.058806	31	4.91E-03
HNRNPAB	1.50	0.10444	140	0.46	0.042108	100	4.40E-03
TSN	2.20	0.012845	6	0.29	0.067521	3	8.67E-04
ZBTB7A	2.15	0.014769	7	0.20	0.021437	8	3.17E-04
PRPF19	1.76	0.043284	64	0.53	0.076309	34	3.30E-03
RG9MTD2	2.02	0.022693	3	0.27	0.05868	8	1.33E-03
PURB	1.77	0.042641	81	0.47	0.04826	79	2.06E-03
GTF3C1	1.70	0.053075	134	0.38	0.016585	181	8.80E-04
LSM1	2.02	0.023303	8	0.18	0.015441	8	3.60E-04
COPE	1.59	0.092343	12	0.24	0.038887	7	3.59E-03
DAXX	2.00	0.024568	3	0.31	0.083048	7	2.04E-03

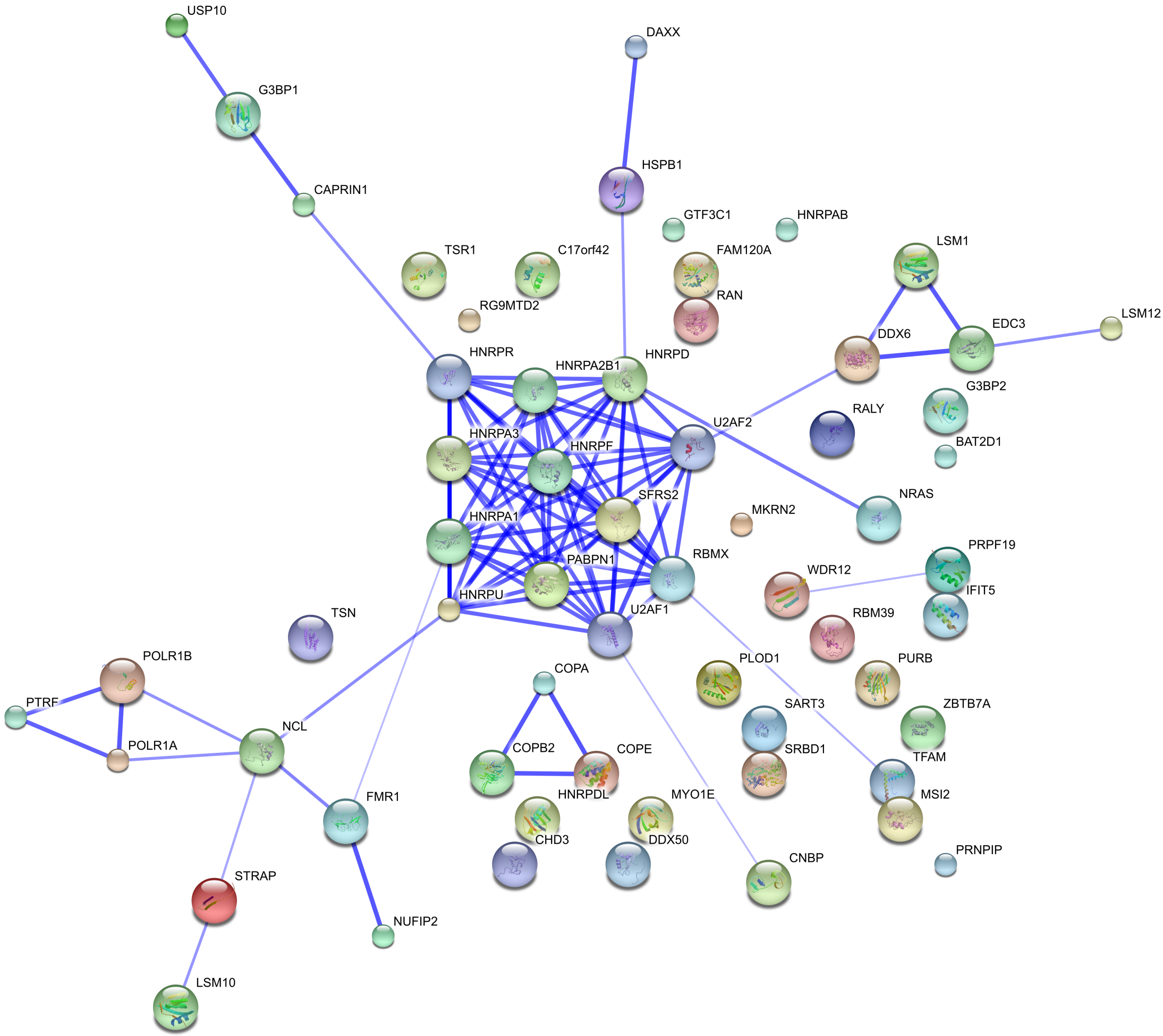
Supplemental Table 2. Pseudoknot sequences for wildtype and mutant DB2 and DB1 structures from Fig. 6.

Pseudoknot structure	DENV-2 NGC nts	Sequence
pk2' wildtype	10475-10479	GCUGU
pk2' mutant	10475-10480	CGACA
pk1' wildtype	10563-10567	GCUGU
pk1' mutant	10563-10568	CGACA
pk2 wildtype	10531-10535	GCAGC
pk2 mutant	10531-10536	UGUCG
pk1 wildtype	10618-10622	ACAGC
pk1 mutant	10618-10623	UGUCG

©2011 Landes Bioscience.
Do not distribute.


A
Incorporation rate
All peptides: 0.973
Arginine peptides: 0.973
Lysine peptides: 0.97
Heavy (K8R10)
Whole cell lysate
Digestion, LC/MS, MaxQuant
Density
0
2
4
6
8
10
0.80
0.85
0.90
0.95
1.00
N = 1612 Bandwidth = 0.01622


B
Light (K0R0)
Heavy (K8R10)
lysis
1:1 mix
Digestion, LC/MS, MaxQuant
Fold change
100
10
1
0.1


USP10
G3BP1
CAPRIN1
DAXX
HSPB1
GTF3C1
HNRPAB
TSR1
C17orf42
FAM120A
RAN
RG9MTD2
LSM1
LSM12
EDC3
DDX6
G3BP2
BAT2D1
RALY
HNRPR
HNRPA2B1
HNRPD
U2AF2
HNRPA3
HNRPF
SFRS2
HNRPA1
MKRN2
NRAS
PABPN1
RBMX
HNRPU
U2AF1
WDR12
PRPF19
IFIT5
RBM39
TSN
POLR1B
PTRF
POLR1A
NCL
COPA
PLOD1
PURB
SART3
ZBTB7A
SRBD1
TFAM
COPB2
COPE
HNRPDL
MYO1E
MSI2
FMR1
CHD3
DDX50
CNBP
PRNPIP
STRAP
NUFIP2
LSM10