

1 **Supplementary information**

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3 Table S1. Samples codification and RIN number.

ADMERAID	Group code	Group	Infection	Treatment	MPI euthanization	Location	RIN
23006XR_01_02	C_P_05	4 MPI	Uninfected	Untreated	4	Posterior	7
23006XR_01_04	C_P_05	4 MPI	Uninfected	Untreated	4	Posterior	7.3
23006XR_01_06	C_P_05	4 MPI	Uninfected	Untreated	4	Posterior	7.7
23006XR_01_13	I_CP_05	4 MPI	Infected	Untreated	4	Posterior	6.5
23006XR_01_15	I_CP_05	4 MPI	Infected	Untreated	4	Posterior	7.5
23006XR_01_17	I_CP_05	4 MPI	Infected	Untreated	4	Posterior	6.8
23006XR_01_26	C_P_60	6 MPI	Uninfected	Untreated	6	Posterior	8.5
23006XR_01_28	C_P_60	6 MPI	Uninfected	Untreated	6	Posterior	7.3
23006XR_01_30	C_P_60	6 MPI	Uninfected	Untreated	6	Posterior	8.3
23006XR_01_32	C_T_P_60	6 MPI + T	Uninfected	Treated	6	Posterior	7.6
23006XR_01_34	C_T_P_60	6 MPI + T	Uninfected	Treated	6	Posterior	7.4
23006XR_01_36	C_T_P_60	6 MPI + T	Uninfected	Treated	6	Posterior	8.3
23006XR_01_37	I_CP_60	6 MPI	Infected	Untreated	6	Posterior	7
23006XR_01_41	I_CP_60	6 MPI	Infected	Untreated	6	Posterior	6.9
23006XR_01_43	I_T_CP_60	6 MPI + T	Infected	Treated	6	Posterior	6.6
23006XR_01_45	I_T_CP_60	6 MPI + T	Infected	Treated	6	Posterior	7.1
						Media	7.36
						Standard deviation	0.60

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6 Table S2. Reads before quality filtering, after quality filtering, mapping reads and count reads.

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Sample (ADMERA ID)	M Seqs	M Seqs after trimmomatic	% Seqs pass qc	M Aligned by STAR	% Aligned	M Assigned by FeatureCounts	% Assigned
23006XR_01_02	49.35	43.62	88.39	41.14	94.32	35.88	82.25
23006XR_01_04	36.25	32.85	90.62	31.37	95.49	27.34	83.24
23006XR_01_06	74.72	68.51	91.69	65.84	96.11	57.49	83.92
23006XR_01_13	36.31	33.11	91.18	31.52	95.21	27.49	83.04
23006XR_01_15	39.08	35.80	91.60	33.95	94.84	29.74	83.07
23006XR_01_17	61.72	57.33	92.89	54.36	94.82	47.61	83.05
23006XR_01_26	31.14	28.13	90.33	26.75	95.11	23.32	82.92
23006XR_01_28	44.55	41.57	93.30	39.96	96.13	35.06	84.34
23006XR_01_30	70.56	65.80	93.25	63.89	97.10	55.83	84.85
23006XR_01_32	31.90	29.05	91.07	27.94	96.15	24.23	83.38
23006XR_01_34	54.77	51.75	94.49	49.70	96.04	43.39	83.86
23006XR_01_36	38.98	35.96	92.24	34.69	96.47	30.33	84.35
23006XR_01_37	43.37	39.97	92.16	38.32	95.86	33.61	84.09
23006XR_01_41	37.74	34.30	90.88	32.13	93.66	28.01	81.65
23006XR_01_43	37.84	35.15	92.89	33.86	96.32	29.66	84.38
23006XR_01_45	37.43	34.16	91.28	32.92	96.37	28.94	84.71
Total seqs	725.71	667.04	91.92	638.33	95.70	557.93	83.64

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Table S3. Protein-protein interactions among co-expressed genes within clusters of 4 MPI, 6 MPI and 6 MPI + T.

Group	Cluster	Genes	Proteins	Interactions	Expected Interactions	Ratio (interaction/expected interaction)	P-Value
4 MPI	1	237	237	1673	359	4.66	0
	2	53	53	37	8	4.63	1.71E-13
	3	105	105	229	60	3.82	0
6 MPI	1	41	41	71	14	5.07	0
	2	52	52	144	27	5.33	0
	3	29	29	15	7	2.14	0.0033
6 MPI + T	1	567	565	2190	685	3.20	0
	2	928	928	12264	4340	2.83	0
	3	838	839	4991	2234	2.23	0

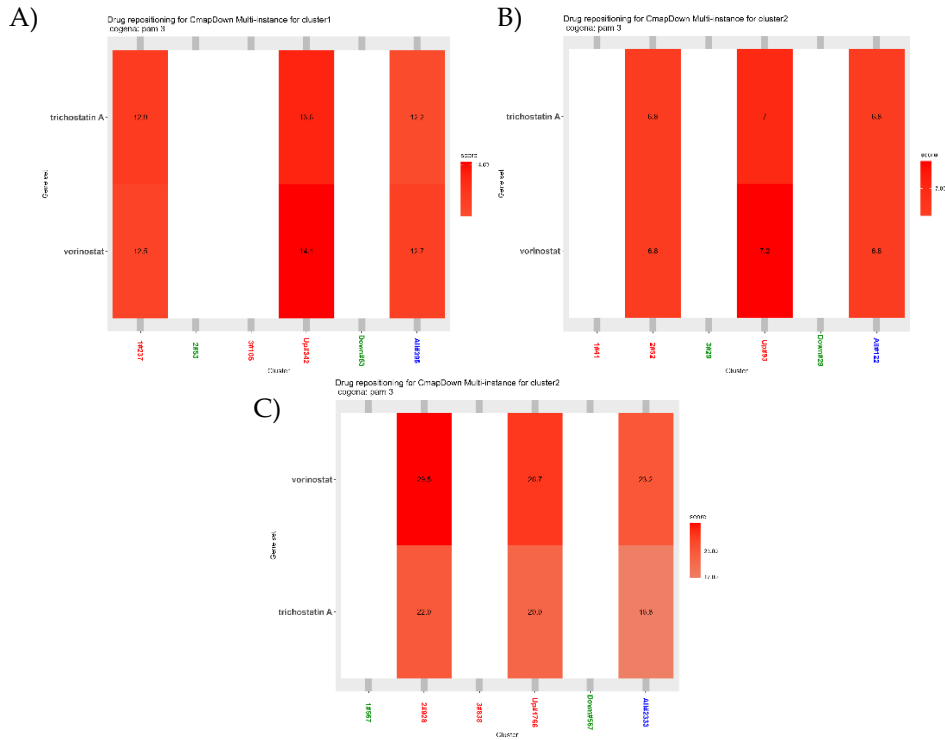


Figure S1. Drug repositioning multi-instance analysis with COGENA using CmapDn database for cluster 1, for 4 MPI (A), and cluster 2 for 6 MPI (B) and 6 MPI + T (C).