

Table S1: Reactome pathways and corresponding categories

Reactome category significantly enriched in primary infection			1*		2°	
			*NES	**FDR <0.05	NES	FDR >0.05
Disease (Infection)	No / Pathways					
	1	Export of viral ribonucleoproteins from nucleus	-2.03	0.0013	-1.34	0.4211
	2	HCMV early events	-1.88	0.0003	-1.05	0.6668
Cellular responses to stimuli						
	3	DNA damage telomere stress induced senescence	-2.07	0.0002	-1.44	0.2190
	4	Cellular senescence	-1.69	0.0030	1.42	0.1113
Vesicle-mediated transport						
	5	Vesicle mediated transport	-1.39	0.0049	-1.08	0.5653
	6	Intra golgi and retrograde golgi to ER traffic	-1.72	0.0007	-1.31	0.2311
	7	Membrane trafficking	-1.47	0.0007	-1.15	0.4150
Chromatin organization						
	8	Chromatin modifying enzymes	-1.75	0.0001	-1.29	0.2003
	9	PKMTS methylate histone lysines	-2.26	2.28e-05	-1.39	0.3097
	10	HATS acetylate histones	-1.93	0.0001	-1.22	0.4435
	11	RMTS methylate histone arginines	-1.93	0.0020	-1.18	0.5358
Immune System						
	12	Antigen processing ubiquitination proteasome degradation	-1.57	0.0023	-1.39	0.0716
	13	IL6 type cytokine receptor ligand interactions	2.03	0.0049	1.79	0.0905
Gene Expression						
	14	Nuclear receptor transcription pathway	2.24	8.62e-05	1.64	0.1307
Signal transduction						
	15	GPCR (G-protein coupled receptor) ligand binding	1.55	0.0020	1.36	0.1137
	16	Class A1 rhodopsin like receptors (largest group of GPCRs)	1.72	0.0006	1.3	0.2223
	17	Peptide ligand binding receptors (subset of the Class A/1 family, peptide ligands which include the chemokines)	1.90	0.0002	1.34	0.1881
	18	Chemokine receptors bind chemokines	2.33	3.01e-05	1.54	0.2190

Reactome category significantly enriched in secondary infection			1°		2°	
			NES	FDR >0.05	NES	FDR <0.05
Signal transduction	No / Pathways					
	19	Signaling by nuclear receptors	1.21	0.2829	1.60	0.0048
	20	Negative regulation of MAPK pathway	1.65	0.0663	2.07	0.0048
Metabolism proteins						
	21	Activation of the mRNA upon binding of the cap binding complex and EIFS and subsequent binding to 43S	1.17	0.5814	2.29	5.47e-05
	22	Translation	0.8	1	1.85	7.15e-06
	23	Metabolism of amino acids and derivatives	1.07	0.5994	1.80	3.41e-05
	24	Eukaryotic translation initiation	1.54	0.0521	2.63	5.429e-11
Disease (infection)						
	25	Infectious disease	0.98	0.8427	1.54	5.47e-05
	26	Influenza infection	1.22	0.3767	2.1	6.89e-06
Cellular responses to stimuli						
	27	Cellular response to external stimuli	-1.07	0.5782	1.72	3.94e-07

Reactome category common to both infection			1°		2°	
			NES	FDR <0.05	NES	FDR <0.05
Signal transduction	No / Pathways					
	28	Rho GTPase cycle	-1.61	0.0002	-1.53	0.0022
	29	Signaling by Rho GTPases miro GTPases and RhoBTB3	-1.84	1.91e-10	-1.47	0.0010
Programmed cell death						
	30	Apoptotic execution phase	-1.97	0.0027	-1.92	0.0078
	31	Apoptosis induced DNA fragmentation	-2.1	0.0007	-2.02	0.0011
DNA repair						
	32	DNA repair	-2.27	2.21e-13	-1.76	3.51e-05
	33	HDR through homologous recombination (HRR)	-2.18	8.63e-05	-1.78	0.0228
	34	Homology directed repair (HDR)	-2.32	5.33e-08	-1.66	0.0228
	35	Homologous DNA pairing and strand exchange	-2.34	1.72e-05	-1.88	0.0134
	36	Resolution of Dloop structures through synthesis dependent strand annealing (SDSA)	-2.21	0.0002	-2.04	0.0075
	37	DNA double strand break repair	-2.28	9.02e-09	-1.66	0.0056
	38	Resolution of D loop structures	-2.17	0.0002	-2.05	0.0022
Gene Expression						
	39	RNA polymerase II transcription	-1.95	2.72e-21	-1.67	8.18e-11
	40	FOXO mediated transcription	2.03	0.0006	2.14	0.0003
Cellular responses to stimuli						
	41	Response of EIF2AK4 GCN2 to amino acid deficiency	1.87	0.0013	2.74	6.73e-12
	42	Cellular response to starvation	1.55	0.0344	2.32	3.22e-08
Immune system						
	43	Signaling by Interleukins	1.85	1.05e-06	1.83	4.62e-06
	44	Interleukin 4 and Interleukin 13 signaling	2.30	1.01e-06	2.21	2.21e-05
	45	Interleukin 10 signaling	2.20	0.0005	2.32	0.0003
	46	Cytokine signaling in immune system	1.60	6.65e-05	1.54	0.0003
	47	Toll like receptor TLR1 TLR2 cascade	1.66	0.0160	1.88	0.0040

*NES: Normalized enrichment score **FDR: False discovery rate