

S3 Table: Characteristics of proteins found differentially represented between virions of TB40/E wild type and the respective pp65 deletion mutant

DeCyder analysis		Mr / pI	Mr / pI	mass spectrometric analysis			accession	protein
wt/mut	t-test	predicted	in gel	seq cov	peptides	mascot		
6.59	0.00025	25.1 / 6.1	25.1 / 5.9	15.20	4	125.0	gi 47496673	Grb2
5.05	0.005	73.0 / 7.2	73.0 / 6.7	3.20	2	67.8	gi 2580556	DDX3Y
3.70	0.042	25.1 / 6.1	25.1 / 5.6	32.71	9	471.2	gi 47496673	Grb2
3.50	0.004	21.1 / 9.1	20.0 / 8.0	24.46	6	273.7	gi 29423456	UL26 (HCMV)
3.07	0.022	73.2 / 6.8	73.0 / 6.8	25.52	18	768.6	gi 87196351	DDX3X
2.96	0.021	23.9 / 9.5	28.0 / 8.6	18.77	6	338.8	gi 62896867	CHMP2B
2.96	0.021	27.0 / 7.9	28.0 / 8.6	15.57	6	213.6	gi 6166390	CYB5R2
2.24	0.032	20.9 / 9.0	27.3 / 6.0	22.10	5	229.9	gi 39842106	UL99 (HCMV)
2.20	0.0078	21.8 / 9.9	27.5 / 8.0	8.16	2	73.7	gi 39644911	CHMP1.5
2.20	0.0078	26.2 / 9.0	27.5 / 8.0	10.52	3	129.4	gi 41350397	CACYBP
2.19	0.044	20.9 / 9.0	27.5 / 6.2	10.00	2	43.5	gi 39842106	UL99 (HCMV)
2.06	0.022	20.9 / 9.0	27.0 / 6.4	10.00	2	46.6	gi 39842106	UL99 (HCMV)
1.95	0.07	20.9 / 9.0	28.5 / 5.5	14.21	3	110.0	gi 39842106	UL99 (HCMV)
1.92	0.044	20.9 / 9.0	27.5 / 5.8	22.10	5	178.3	gi 39842106	UL99 (HCMV)
1.89	0.030	37.5 / 5.9	38.0 / 5.9	3.05	1	48.3	gi 54696354	PP1
1.88	0.041	45.7 / 4.9	52.0 / 4.9	12.46	4	127.6	gi 28373252	UL71 (HCMV)
1.73	0.019	21.7 / 6.3	23.0 / 6.4	24.48	5	226.2	gi 20531765	CLDD6. hypothetical protein
1.67	0.027	16.8 / 4.9	17.0 / 5.2	6.52	2	46.5	gi 12653915	eIF-5A
1.60	0.047	21.6 / 6.2	25.1 / 6.1	21.69	5	223.5	gi 55962165	RHOC
1.55	0.015	68.4 / 5.0	76.0 / 5.3	20.80	13	770.1	gi 81097637	cytoplasmic dynein intermediate
-1.78	0.00027	47.2 / 4.8	49.0 / 4.9	14.50	6	305.4	gi 12803811	ENO2. Enolase 2
-1.92	0.044	38.6 / 8.5	37.0 / 5.3	17.40	6	225.0	gi 18645167	Annexin A2
-2.33	0.0016	29.9 / 4.6	27.0 / 5.5	27.92	9	477.5	gi 49119653	YWHAZ
-2.65	0.0023	29.4 / 5.4	29.5 / 5.4	19.01	5	271.2	gi 40226101	Actin beta
-2.69	0.00005	29.8 / 5.5	28.0 / 5.5	19.11	12	493.3	gi 49456373	PHB. prohibitin
-2.75	0.0027	41.0 / 5.5	40.0 / 5.8	23.36	17	697.6	gi 14250401	Actin beta
-2.99	0.02	36.0 / 9.3	37.0 / 8.8	6.56	2	49.0	gi 31645	GAPDH
-3.35	0.00048	13.8 / 8.9	12.5 / 8.9	31.50	4	148.7	gi 825616	124 aa fragment of beta actin
-3.44	0.0015	41.0 / 5.5	40.0 / 5.7	7.75	2	64.8	gi 14250401	Actin beta
-4.26	0.042	15.1 / 9.7	11.5 / 6.8	25.53	3	90.1	gi 1335076	Alpha-2-globin (cleavage product)
-4.57	0.0031	41.0 / 5.5	40.0 / 5.6	22.00	12	441.6	gi 14250401	Actin beta
-7.57	0.018	15.1 / 9.7	11.5 / 8.2	11.34	2	73.1	gi 1335076	Alpha-2-globin (cleavage product)

wt/mut = ratio of protein amount between wild type virions and mutant virions

Mr = relative molecular mass

pI = isoelectric point

Seq cov = sequence coverage [%]

Peptide = number of unique peptides

Mascot = mascot score

(HCMV) = viral protein