

Table 1. Genotypes and phenotypes of CMV *pol* mutants

BAC ¹	Virus ²	Genotype ³		Cyclopropavir phenotype				EC50 ratio (fold change) ⁸		
		UL97	<i>pol</i>	EC50, μM ⁴	SD ⁵	EC50 ratio ⁶ (fold change)	N ⁷	GCV	FOS	CDV
Control strains										
	T2211	(baseline)	(baseline)	0.24	0.05		55			
BA29	T3261	(baseline)	(baseline)	0.21	0.06		24			
BA31	T3265	(baseline)	(baseline)	0.24	0.06		41			
BA27	T3259	C592G		0.65	0.15	3.1	26	3.0		
Exonuclease mutants										
	T2293		N408K	0.14	0.06	0.6	15	4.2	0.7	21
BA35	T3267		F412L	0.11	0.04	0.5	11	4.6	1.1	9.4
	T3005		P522A	0.12	0.05	0.5	7	3.0	1.0	4.1
BA96	T3400		L545W	0.14	0.05	0.6	14	4.9	1.3	6.3
Amino terminal catalytic domain mutants										
BA112	T3426		Q578H	1.51	0.16	6.3	7	3.3	4.5	2.3
BA103	T3408		D588N	0.41	0.09	1.7	14	2.0	2.8	1.3
Catalytic (palm1) domain mutants										
BA143	T3525		P744T	0.23	0.07	1.0	11	0.9	1.1	1.1
BA189	T3658		E756D	0.74	0.11	3.1	10	1.1	2.7	1.1
BA116	T3430		E756K	0.66	0.10	2.8	8	1.9	3.5	1.7
Catalytic (finger) domain mutants (regions VI, III)										
BA108	T3417		V781I	0.69	0.20	2.9	9	2.4	3.9	1.5
	T2417		A809V	0.70	0.15	2.9	10	2.4	3.3	1.9
	T2784	C592G	A809V	1.58	0.52	6.6	8	5.6	3.3	2.1
	T2542		T813S	1.89	0.59	7.9	9	2.5	4.9	2.7
	T2798	C592G	T813S	3.09	0.55	13	9	6.0	5.0	1.7
Catalytic (palm2) domain mutants (region III)										
	T2291		A834P	1.35	0.48	5.6	16	5.4	6.4	3.0
	T2311		N408K, A834P	0.61	0.25	2.5	13	23	7.2	19
	T2420		G841A	3.16	0.59	13	8	3.2	4.3	2.6
	T2817	C592G	G841A	6.07	1.74	25	11	7.6	5.2	3.0
	T2483		M844T	0.98	0.30	4.1	14	1.4	2.5	1.3
	T2785	C592G	M844T	2.03	0.48	8.5	16	2.5	2.0	1.2
BA187	T3652		M844V	1.06	0.15	4.4	10	2.3	2.2	1.6
Catalytic (thumb) domain mutants (region V)										
	T2222		981-2del	0.33	0.08	1.4	8	4.8	3.5	4.1
	T2261	C592G	981-2del	0.65	0.19	2.7	16	17	4.1	5.7
BA115	T3429		A987G	0.12	0.04	0.5	7	6.2	0.9	5.3

Table footnotes:

1. Bacterial artificial chromosome name
2. Recombinant virus strain
3. Amino acid change in recombinant virus
4. By SEAP yield reduction assay, mean value of the number of assays shown
5. Standard deviation of the number of assays shown
6. Ratio of mean EC50 value to that of matching control with baseline genotype
Items shown in **bold** have CPV EC50 ratio >1.9
7. Number of assays (replicates performed over at least 4 independent assay setups)
8. EC50 ratios for recombinant viruses containing the same mutation(s)
Values are previously published except for data from Table 2.
Items shown in **bold** have FOS EC50 ratio >1.9