Structural Basis for Cooperative Binding of EBNA1 to the Epstein-Barr Virus Dyad Symmetry Minimal Origin of Replication

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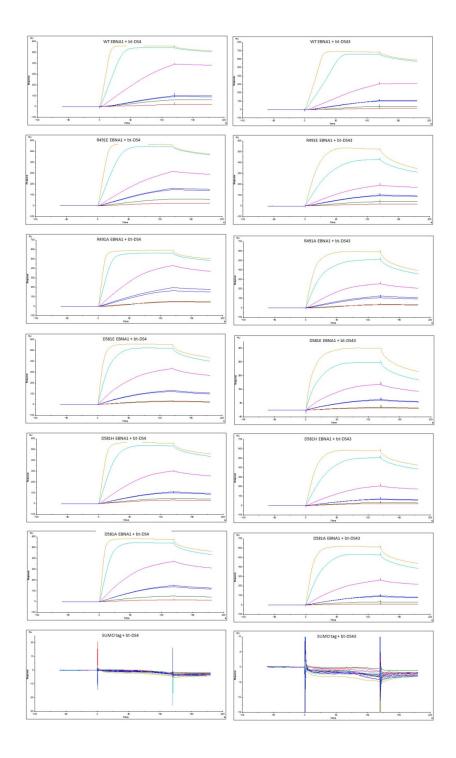
Supplemental Figures and Tables Legends

Supplemental Figure 1. Biacore sensorgrams for all EBNA1 WT, mutants. Left, representative sensorgrams for EBNA1 + biotinylated DS4 as indicated. Right, representative sensorgrams for EBNA1 + biotinylated DS34 as indicated.

Supplemental Table 1. Root mean square deviations for all published EBNA1 dimers. RMSDs were calculated by PyMOL using the CA alpha alignment script.

Supplemental Figure 1

Supplemental Table 1

	DimerDimer 1b	DimerDimer 2a	DimerDimer 2b	1VHI	1B3T	5T7X	Hexamer 1	Hexamer 2	Hexamer 3
DimerDimer_1a	0.261	0.242	0.240	0.674	0.379	0.423	0.602	0.576	0.574
DimerDimer_1b		0.259	0.227	0.672	0.416	0.419	0.542	0.552	0.535
DimerDimer_2a			0.237	0.664	0.410	0.433	0.555	0.571	0.574
DimerDimer_2b				0.683	0.429	0.465	0.585	0.574	0.561
1VHI					0.579	0.572	0.292	0.454	0.450
1B3T						0.252	0.447	0.436	0.445
5T7X							0.415	0.449	0.412
Hexamer_1								0.247	0.169
Hexamer_2									0.276