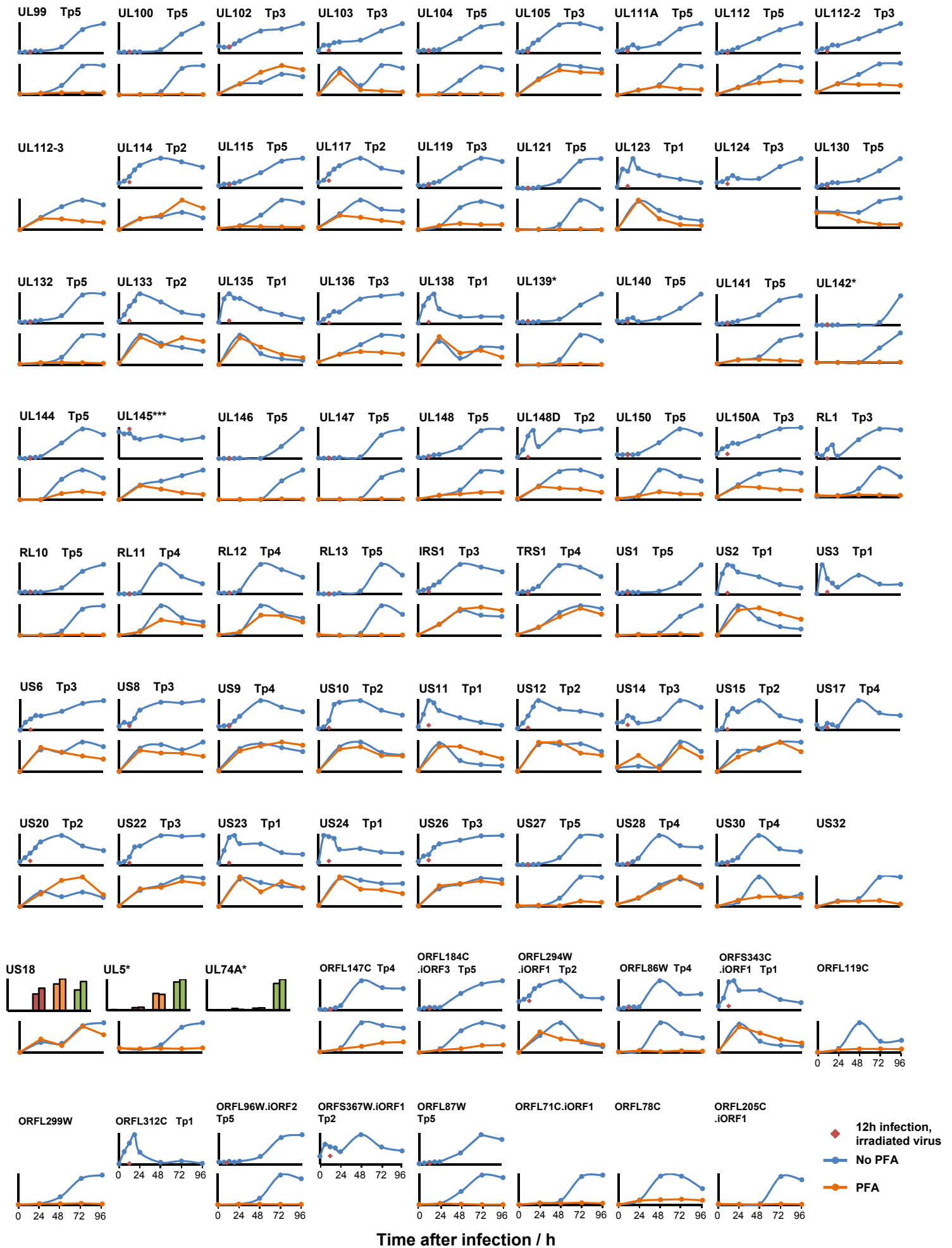
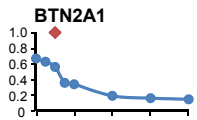


Relative Abundance

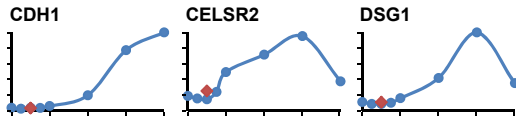


Supplemental plots B: profiles of proteins from Table S5A

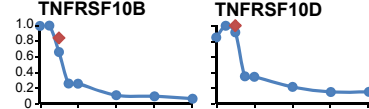
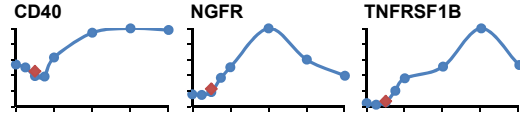
Butyrophylins



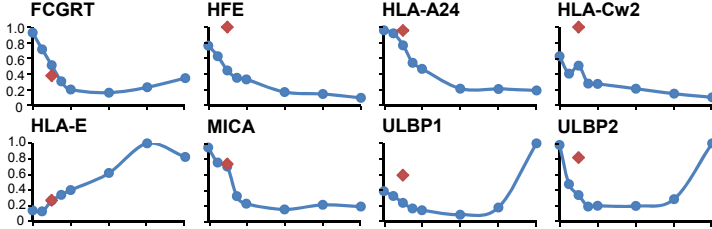
Cadherins



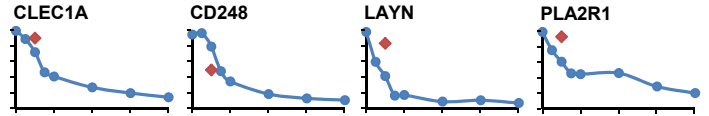
TNF-related molecules



MHC-related molecules

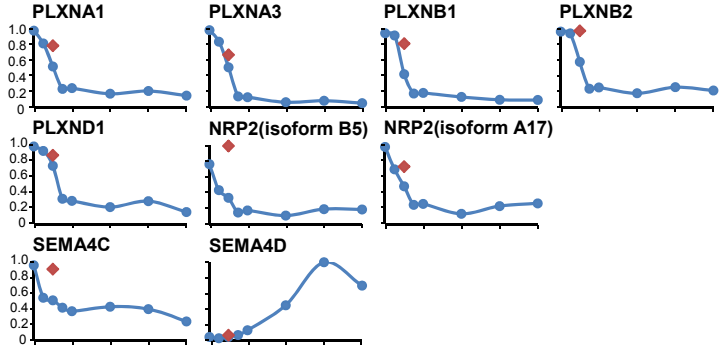


C-type lectins

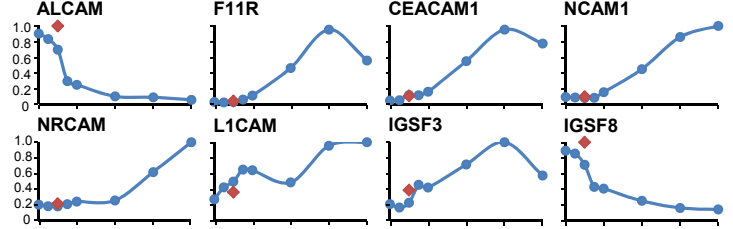


Immunoglobulin domain containing

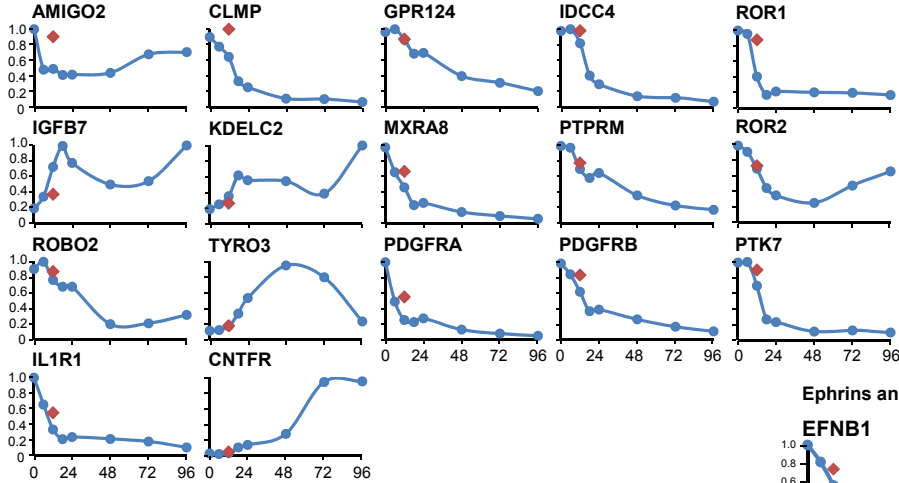
Plexin / Neuropilin / Semaphorin



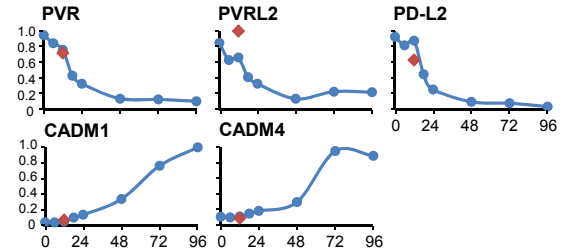
Adhesion molecules



Other

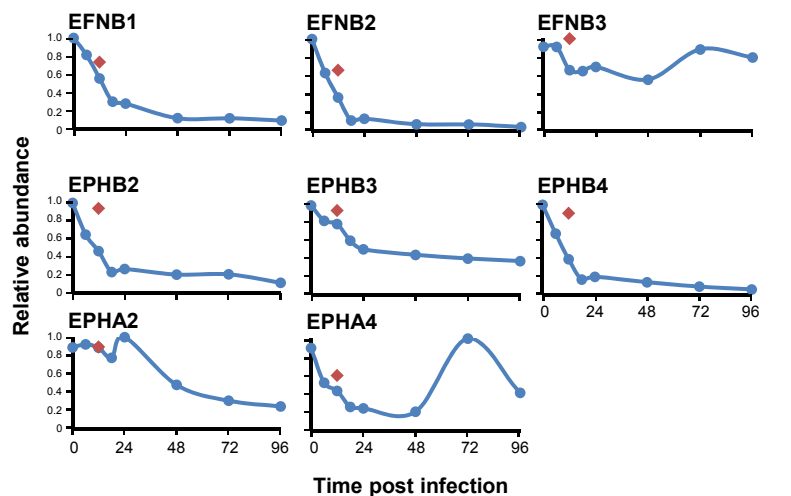


Known or putative NK or T-cell ligands



Time post infection / h

Ephrins and Ephrin receptors



Relative abundance

Time post infection

Supplemental plots A

Temporal profiles of HCMV canonical proteins and new ORFs, related to Figure 5. All 139 quantified canonical HCMV proteins and 14 new ORFs are shown. Top sets of panels - data from experiment WCL2.

*data is shown from experiment PM2, as the protein was not quantified in WCL2. Data for US18 is shown from experiment WCL1, and data for UL5 and UL74A are shown from experiment PM1 as these proteins were not quantified in experiment 2.

**UL44 has three transcription start sites utilized either from early infection onwards (sites 1, 3) or at late times only (middle start site). The same UL44 ORF is transcribed from each site, and accumulates to high levels late in infection (Leach and Mocarski, 1989). Our analysis correspondingly classified UL44 as Tp5.

***UL145 was quantified in experiment WCL2 by two peptides, one of which followed the pattern expected for a Tp3 protein, the other a likely misidentification.

Bottom sets of panels – data from experiment WCL3. The effect of the viral DNA replication inhibitor PFA can be understood by comparing protein abundance throughout infection with mock infection (where viral protein abundance relates to noise). Expression of 48/55 Tp5-class proteins was completely or almost-completely inhibited by PFA. Three UL112 isoforms were quantified: UL112, and isoforms p50 (UL112-2) and p43 (UL112-3) (Table S2). RL13 was quantified by a single peptide in both experiments WCL2 and WCL3, which was close to the N-terminus of the protein. The RL13 gene is truncated in HCMV Merlin, hence the expression kinetics we measure may not reflect the full ORF.

Supplemental plots B

Profiles are shown of all proteins from Table S5A that are not already represented in Figure 4. We quantified 3/3 ephrin B ligands, of which ephrins B1 and B2 were heavily downregulated. We quantified 3/6 Ephrin B receptors, all of which were downregulated. Ephrin receptors A2 and A4 exhibited different patterns of regulation, which were independently confirmed in experiment PM1 (Table S2).

Red diamonds – 12h after infection with irradiated HCMV. y-axes represent relative abundance.