



**Figure S1.** Enrichment for wide/bimodal (i.e., “Switching”) phenotype. WT clones were isolated by FACS using three different sorting methods: 1) cells sorted from the entire infected population; 2) cells sorted from the mid-GFP region of the infected population; and 3) cells sorted from the activating fraction after one round of selection. Switching fraction was estimated as described in Text S2. Error bars indicate 95% CIs, estimated by a bootstrap method.