**Collection of raw data**

We studied the interaction of the processed viral DNA LTR32 by each of the three inhibitors (RAL, EVG and DTG) at three different temperatures (5, 15 and 25C), respectively.

For that, we conducted the titration of LTR32 by increased concentrations of the inhibitor at one temperature, using a Jobin-Yvon Fluoromax II instrument. We collected the corresponding anisotropy value, doing several trials for every titration point. For each anisotropy measurement, the parallel and the perpendicular intensities of the background solution (i.e. buffer and drug contributions) were automatically subtracted from the sample value, calculating the G-value correction each time.

The excel sheets contain respectively:

1st column: sample name (content)

2nd column: number of trials per titration point

3rd column: Anisotropy Value (A)

4th column: Standard error (for A) (%)

5th column: Total intensity of the fluorophore (i.e. VM of fluorescein)

6th column: Standard error (for VM) (%)

For every titration point, we determine the anisotropy value by doing the average of all the replications (with 5 trials each). We register VM in order to control the anisotropy values as well as the standard errors. The more the increase in Anisotropy is, the more the decrease in VM should be, since with the increase of the hydrodynamic volume of the DNA, particularly fluorescein, anisotropy increases and the signal intensity decreases.

We repeated every experiment (titration) at least 3 times. The titration curves in annex represent average anisotropy values over at least triplicates for every experiment. For every obtained titration curve (here in annex), we analyzed the collected anisotropy values using Graph Pad Prism Software. We determined Kd for every experiment using the least square method.

Please find in attachment one replicate of the titration of LTR32 by each inhibitor at 3 different temperatures, respectively.