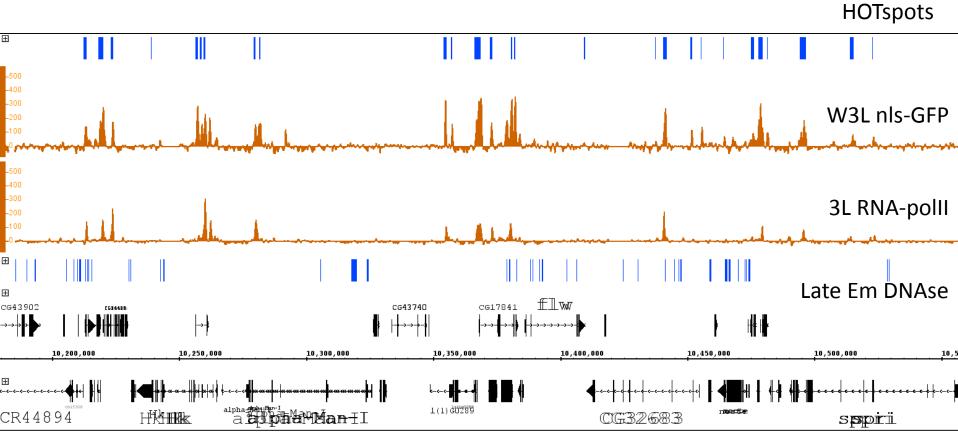
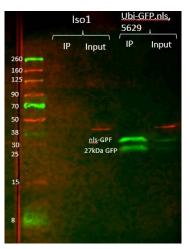
nls-GFP

- 86.3% peaks are hotspots, p<1e⁻⁵
- 45% Embryonic DNasel, p<1e⁻⁵
- Looks closer to RNA-Polli. 70% overlap, p<1e⁻⁵

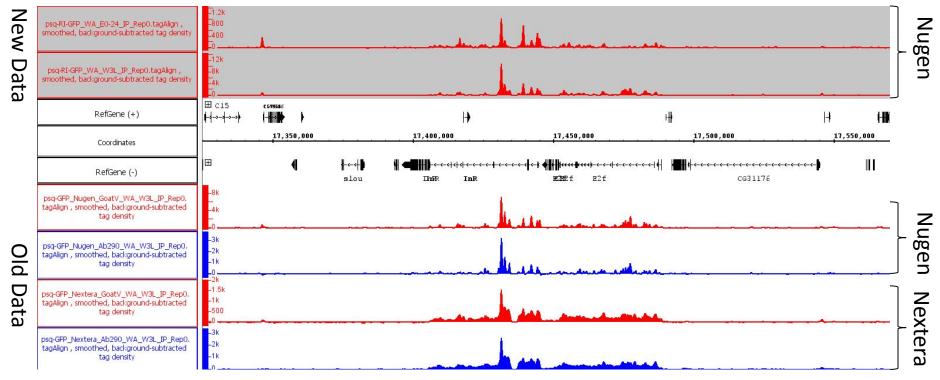


Old Data vs New

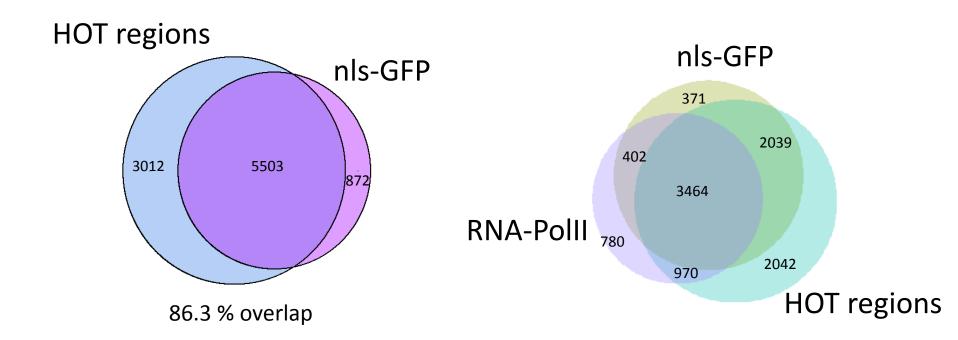
- Ab290 (blue tracks) show similar traces to GoatV (red tracks)
- Nugen libraries have better defined peaks than Nextera



IPed with GoatV
Blotted with Roche antiGFP

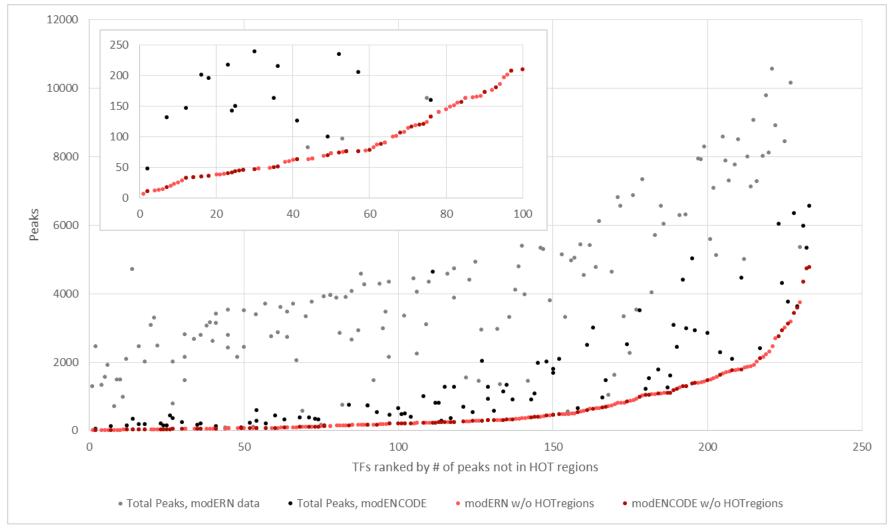


Overlap



Average overlap with HOT regions: 75.8% (SD:23.1%)

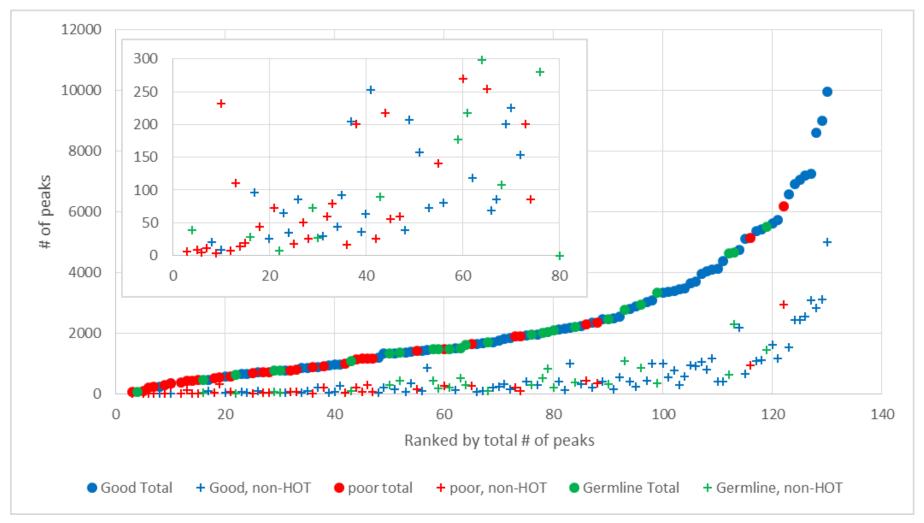
New Ab/lib kit more peaks, more HOT regions



Average # cold peaks: 674.9

Median: 254

Worm data with and without HOT regions



Average # cold peaks: 539.4

Median=247