

Supplemental Materials

Molecular Biology of the Cell

Pashkova et al.

Supplemental Figure 1. PRE effects on ^{15}N Ubiquitin.

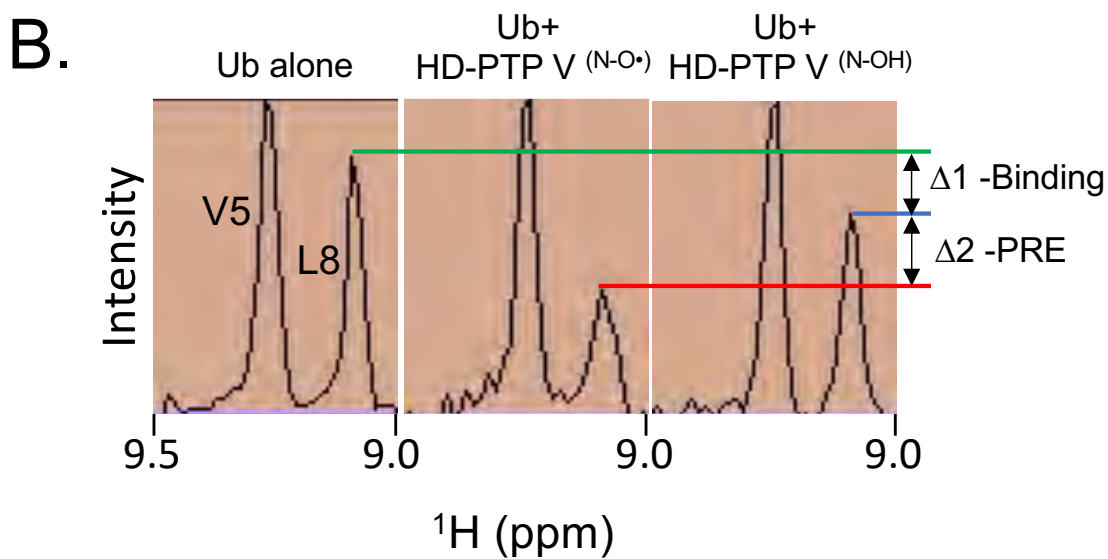
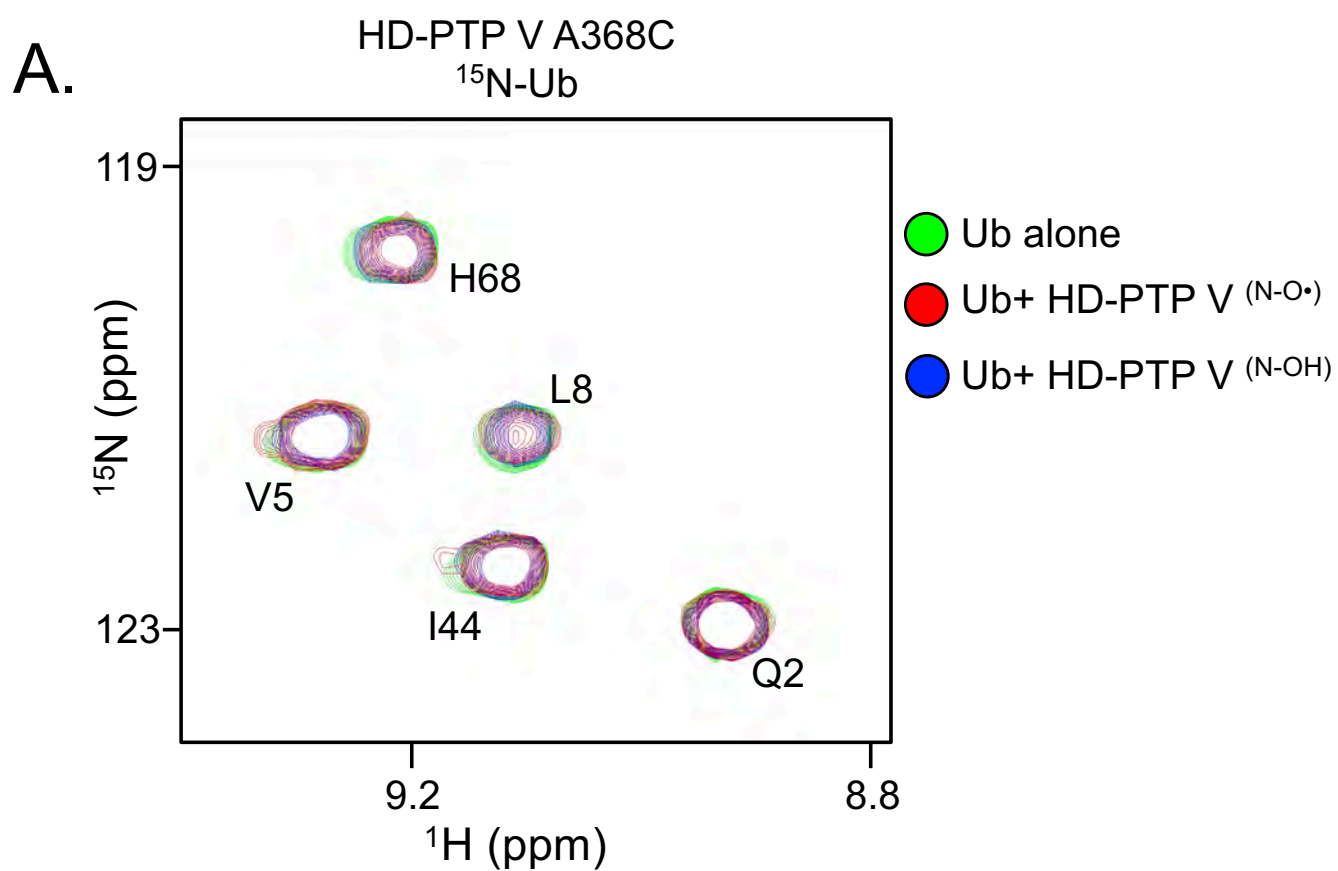
Top shows portion of HSQC of $30\mu\text{M}$ ^{15}N Ub alone or in the presence $30\mu\text{M}$ VHDPTP spin-labelled at position 368 under oxidizing conditions or reduced in the presence of 2mM ascorbate. The backbone amide for L8 has a low peak height in the presence of spin-label that is partially restored in the presence of ascorbate. Binding of reduced V^{HDPTP} also reduces peak heights, which can also be observed in the slice view below. The extent of binding is reflected in decrease peak height in the presence of ascorbate ($\Delta 1$) and the PRE effect is reflected in the difference in peak height in the presence of V^{HDPTP} under oxidized and reduced conditions ($\Delta 2$).

Supplemental Figure 2. DEEPN Yeast 2-Hybrid analysis of WT and ΔUb V^{HDPTP} .

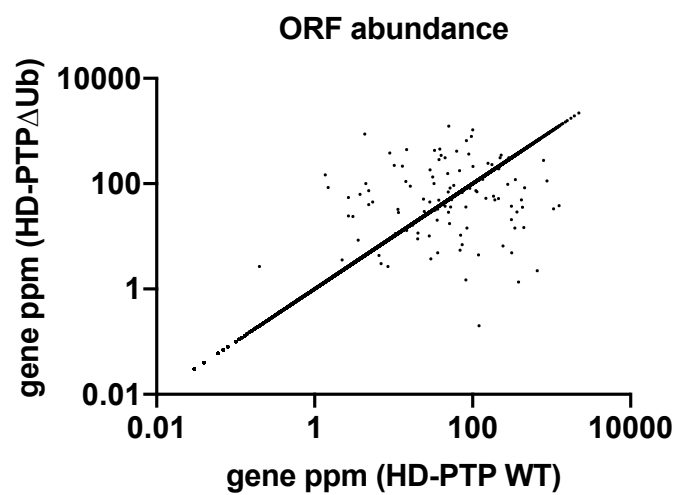
- A. Abundance of reads for each potential interacting 'prey' gene in rank order for diploids carrying the Y2H pan-mouse cDNA library grown under permissive (His+) non-Y2H-selective conditions that contain the WT V^{HDPTP} as prey (x axis) vs the corresponding abundance of reads for those same genes for the population carrying the ΔUb V^{HDPTP} (Y-axis). These data demonstrate the variance in distribution of library plasmids between the two populations that carry different V^{HDPTP} baits with an overall dispersion of 0.2.
- B. Summary of in-frame open-reading frame fragments that enriched with high confidence (blue) when selected for interaction with WT or ΔUb V^{HDPTP} .
- C. Data on each Y2H interactor in B. Shown is a plot of the nucleotide positions for each indicated cDNA sequence with the start and stop codon indicated. The left Y axis shows the read-depth for a 20 bp window along the cDNA sequence. The right Y axis shows the position and number of reads that bridge the 3' end of the Gal4-DNA binding domain and the 5' end of the interacting gene in blue. All fusion points were determined to be in-frame with the Gal4-DNA binding domain. Paired summary sequence data is shown for WT and ΔUb V^{HDPTP} on the right and left, respectively.

Supplemental Figure 3. HSQC of ^{15}N -labelled Vps4 MIT domain bound to V domains.

HSQC spectra of $35\mu\text{M}$ ^{15}N -MIT domain from yeast Vps4 in the absence (green) and presence (red) of V^{Bro1} , V^{HDPTP} , and V^{Rim20} at the indicated ratios under the conditions described in Figure 8A



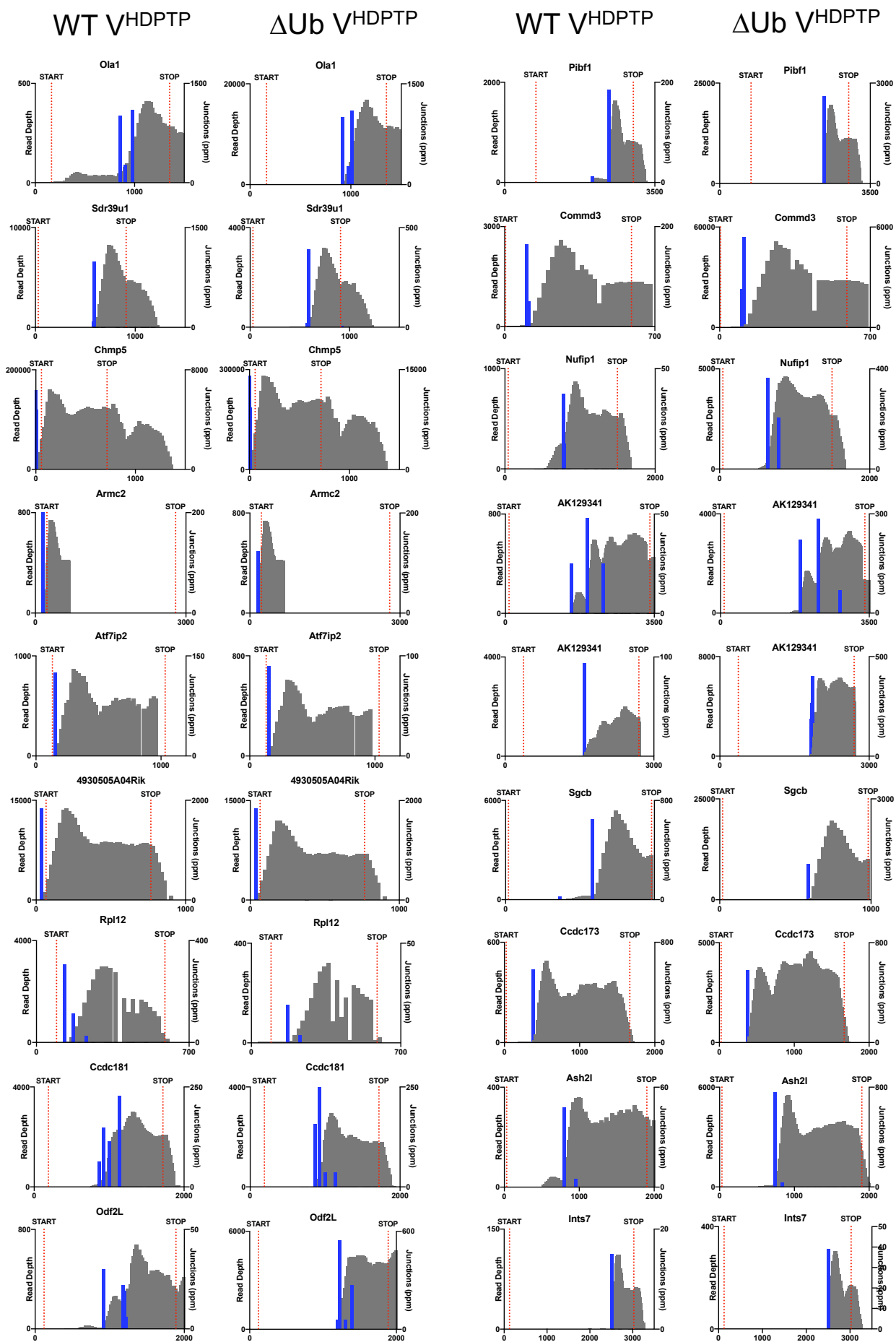
A.



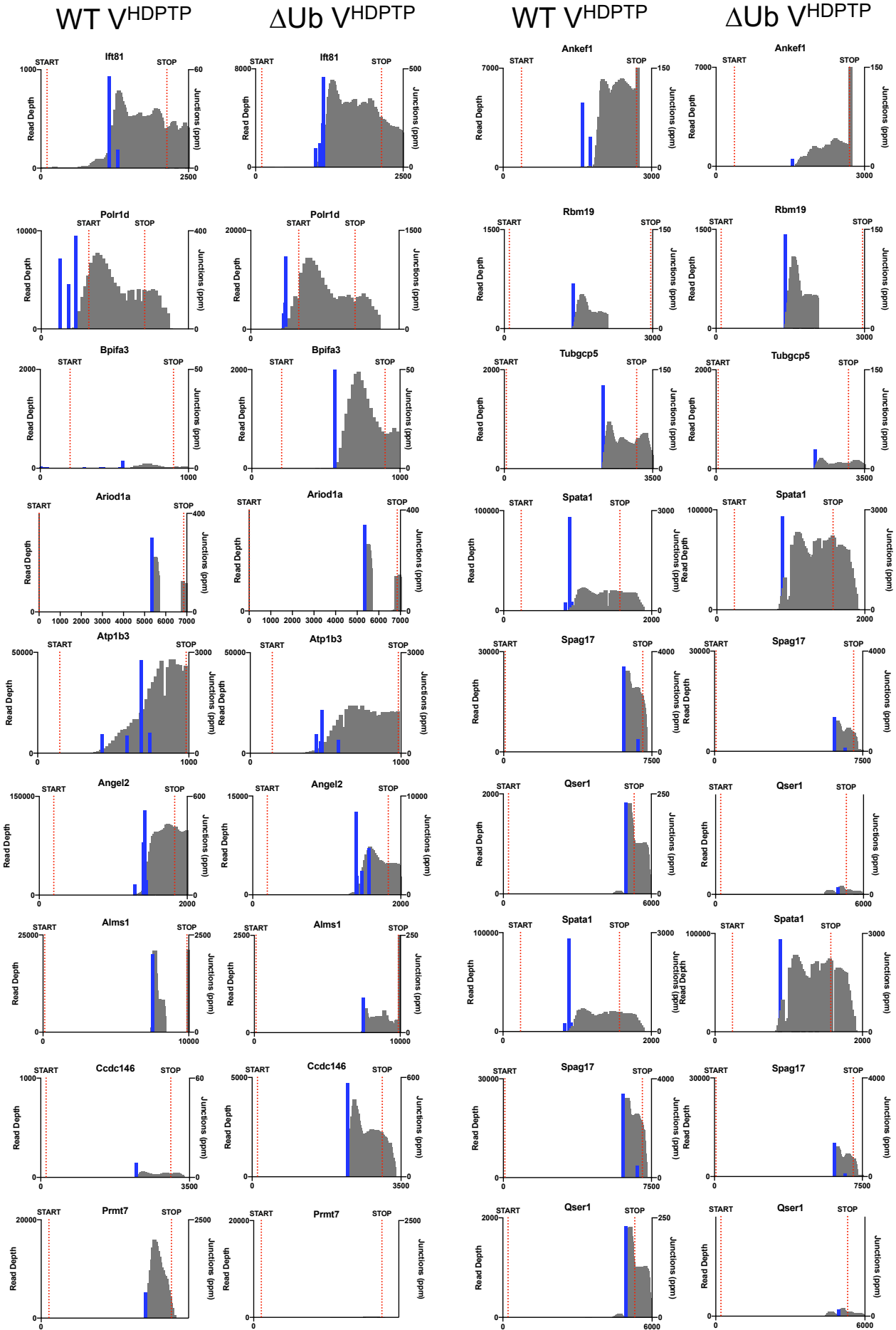
B.

	(WT)	(Δ Ub)
4930505A04Rik		
6820408C15Rik		
AK129341		
Alms1		
Angel2		
Ankef1		
Arid1a		
Armc2		
Ash2l		
Atf7ip2		
Atp1b3		
Bpifa3		
Bsg		
Cacybp		
Ccdc146		
Ccdc173		
Ccdc181		
Ccdc79		
Chmp5		
Cinp		
Clca1		
Commd3		
Cspp1		
Fcho2		
Gpsm2		
Hpcal1		
Ift81		
Ikzf5		
Ints7		
Lancl1		
Mien1		
Ndufaf1		
Nufip1		
Odf2l		
Ola1		
Parp2		
Parpbbp		
Pibf1		
Polr1d		
Prmt7		
Qser1		
Rbm19		
Rpl12		
Sdr39u1		
Sgcb		
Spag17		
Spata1		
Thrap3		
Toporsl		
Tubgcp5		
Tulp4		

C-1



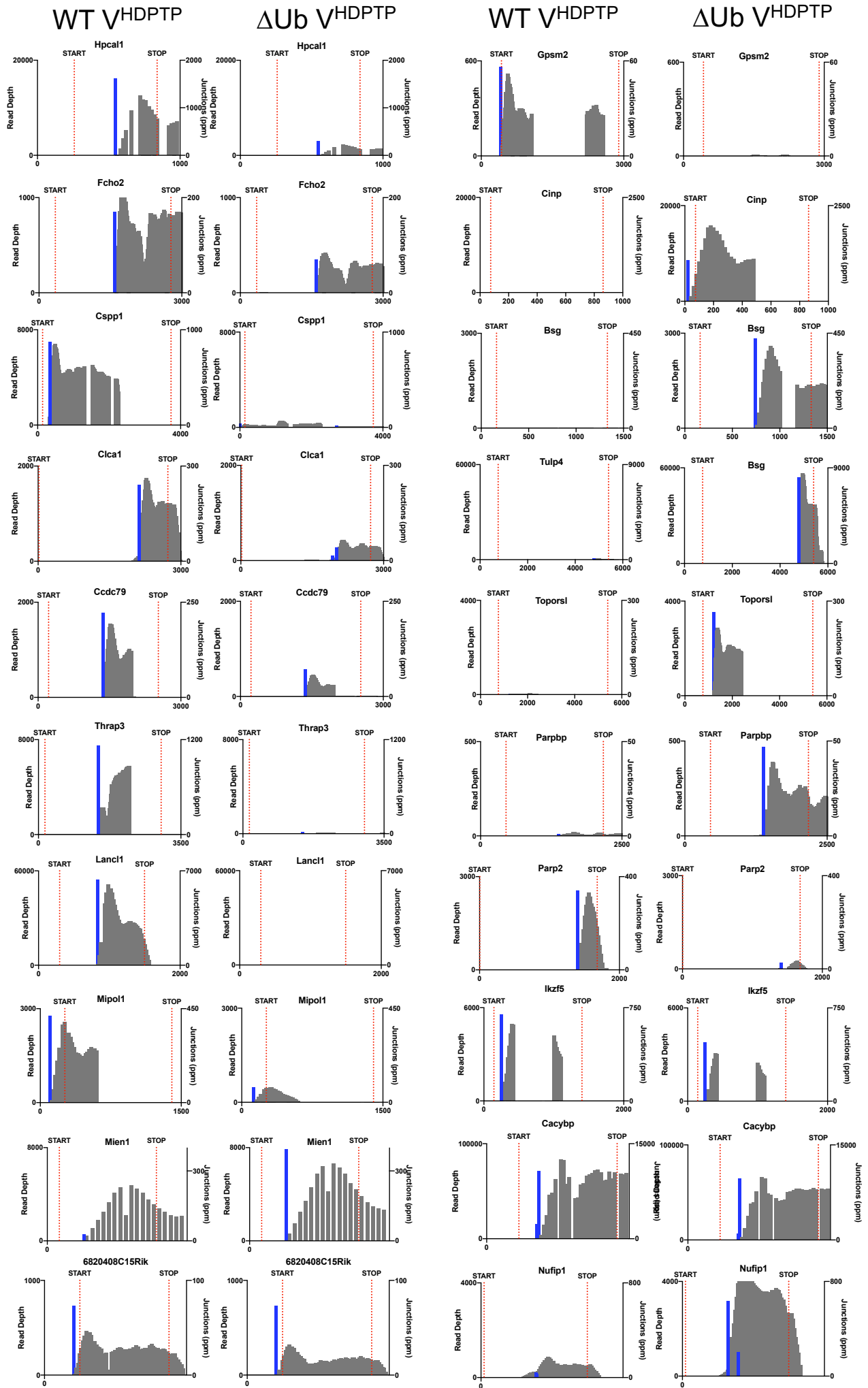
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Supplemental Figure 2. Pashkova et al. 2021

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