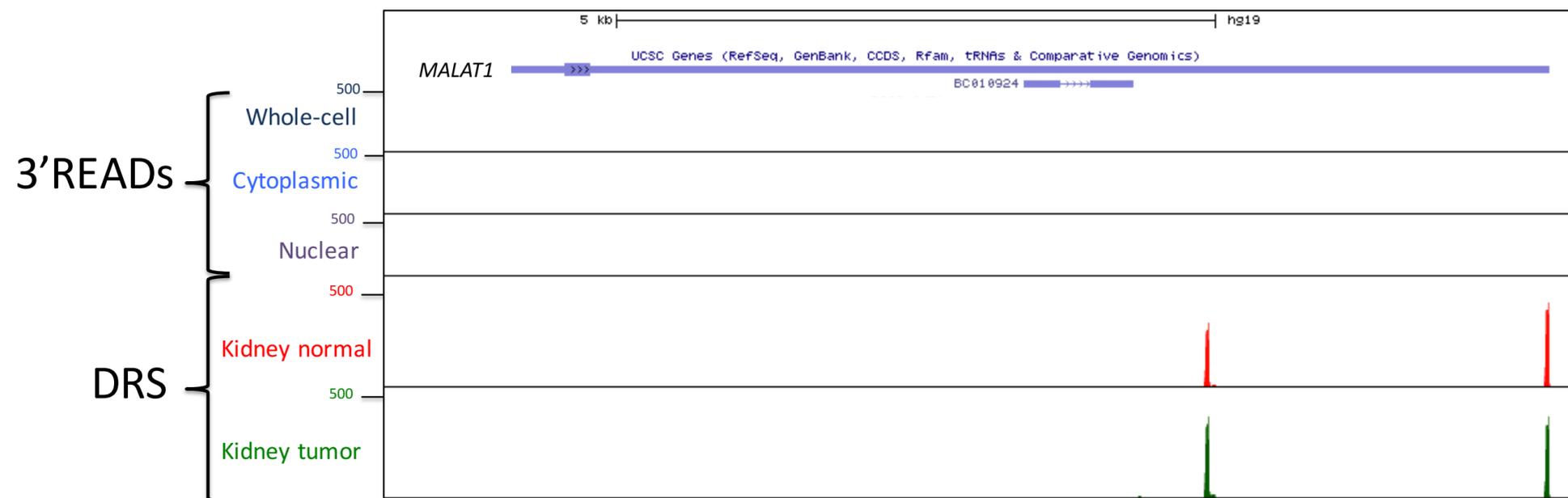
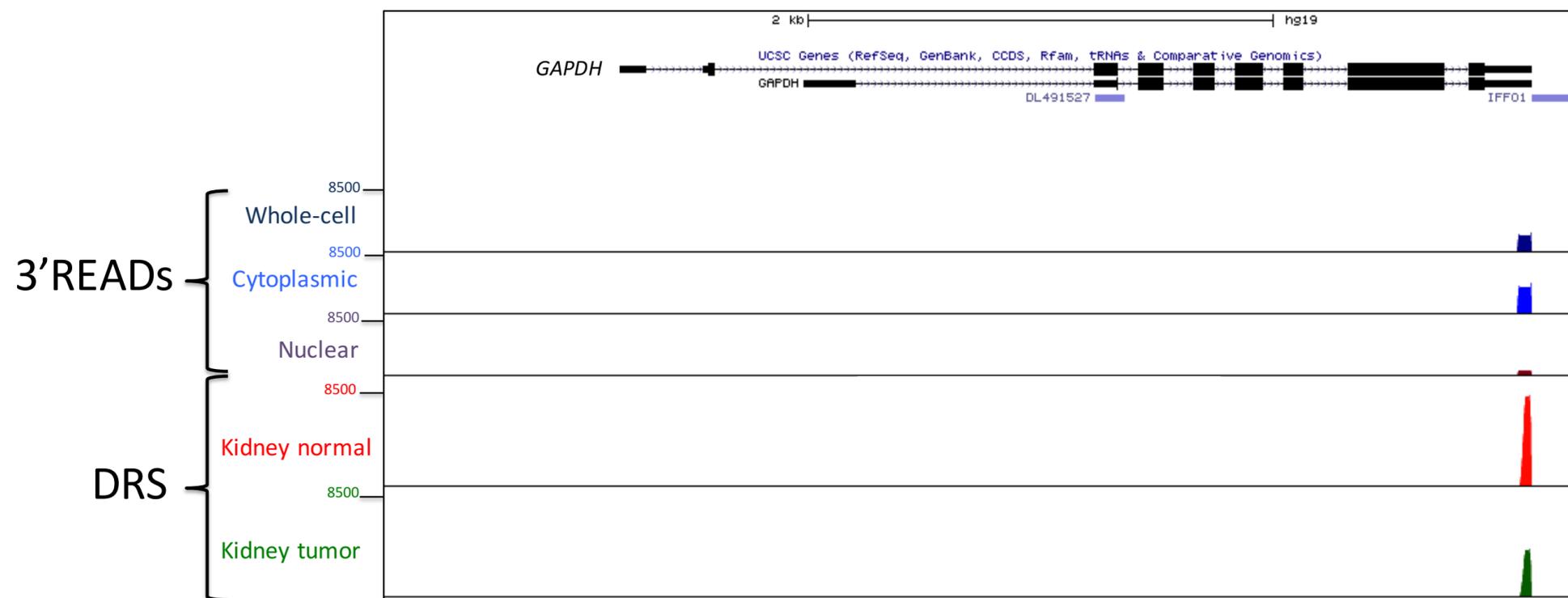


MALAT1



GAPDH



Top 3 hits MCF7 (Shortening)

Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. CVGCCTCC		2.6e-033	-
2. GGGAYTAC		2.1e-027	NONO
3. CAGGCTGG		1.5e-025	-

Top 3 hits HEPG2 (Shortening)

Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. GGGATTAC		3.3e-017	-
2. GAGGCKGA		1.8e-016	-
3. GTGGCTCA		4.3e-016	-

Top 3 hits K562 (Shortening)

Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. AATAAA		3.3e-019	KHDRBS1/2/3, ZFP36, PABPC1/4, RBM46
2. GCWCACRC		1.1e-012	hnRNPLL, RBMY1A1
3. TAHAAATA		2.8e-012	-

Top 3 hits HeLaS3 (Shortening)

Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. AWATAMAA		7.9e-014	-
2. TTTTAAW		3.5e-013	hnRNPC, hnRNPL1, RALY, CPEB4, TIA1, ZFP36
3. GAGGCKGA		2.4e-009	-

Top 3 hits IMR90 (Shortening)

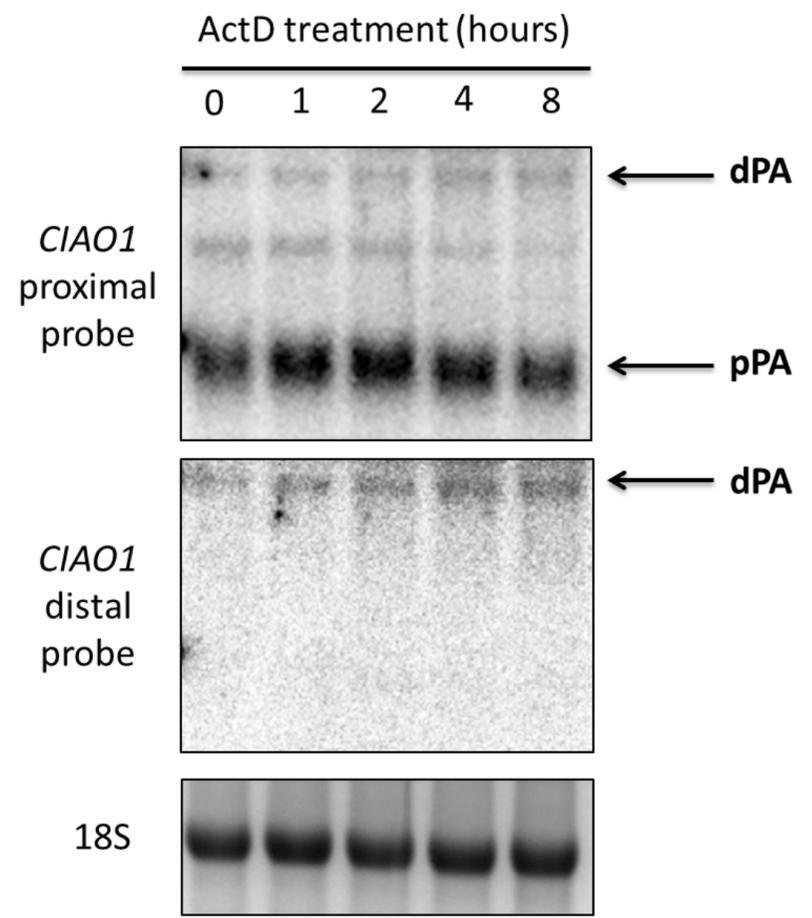
Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. DAAATAMA		3.8e-019	ZFP36, PABPC1/4
2. CWGCCTCC		2.4e-013	-
3. ATCCAGC		2.5e-012	-

Top 3 hits HUVEC (Shortening)

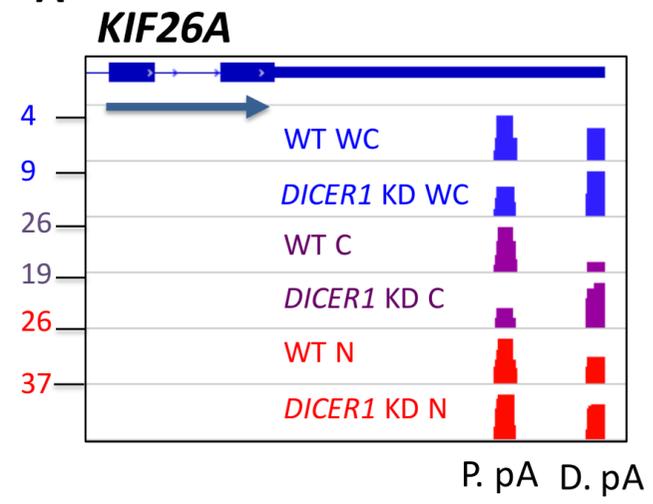
Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. AAAAWAAA		1.0e-012	ZFP36, PABPC1/3/4, SART3, PABPN1, KHDRBS2/3
2. CCAGCTAC		9.4e-012	-
3. GATTACAK		7.5e-010	-

Top 3 hits SKNSH (Shortening)

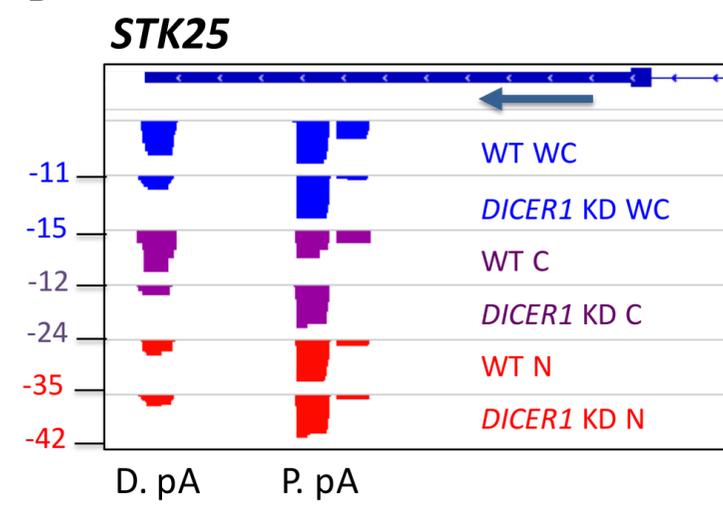
Motif ?	Logo ?	E-value ?	Hits on Target database Ray et al. 2013
1. AGGCYAG		2.0e-022	-
2. CTCCTGC		1.7e-020	-
3. CRCCTGTA		7.8e-020	Pum2 (Mus Musculus)



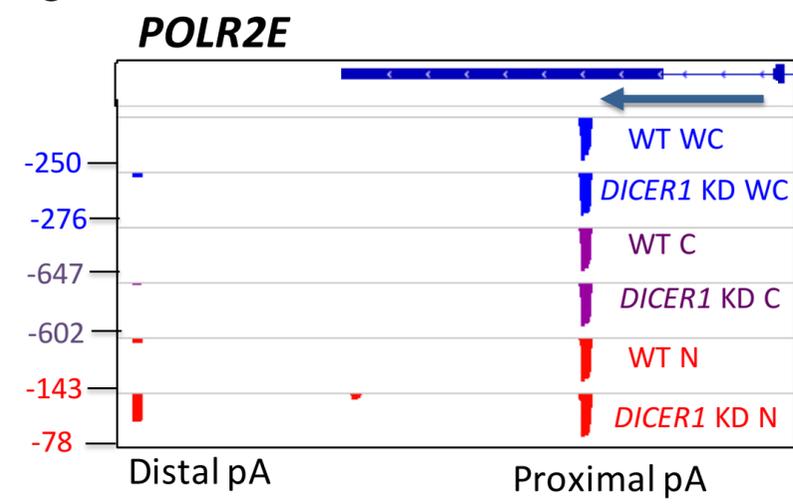
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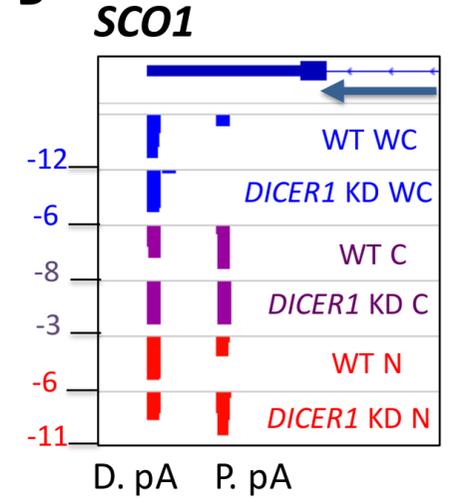
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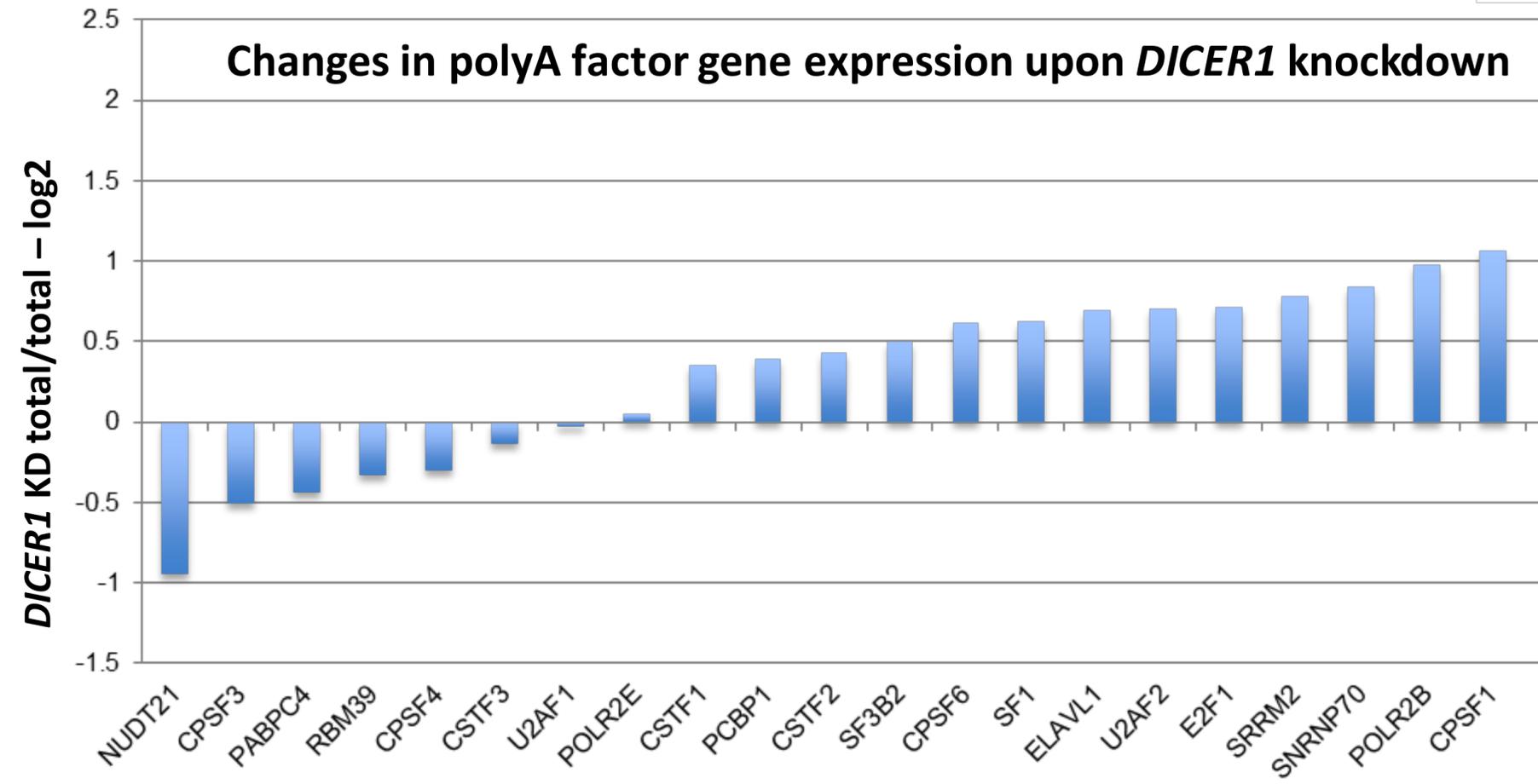


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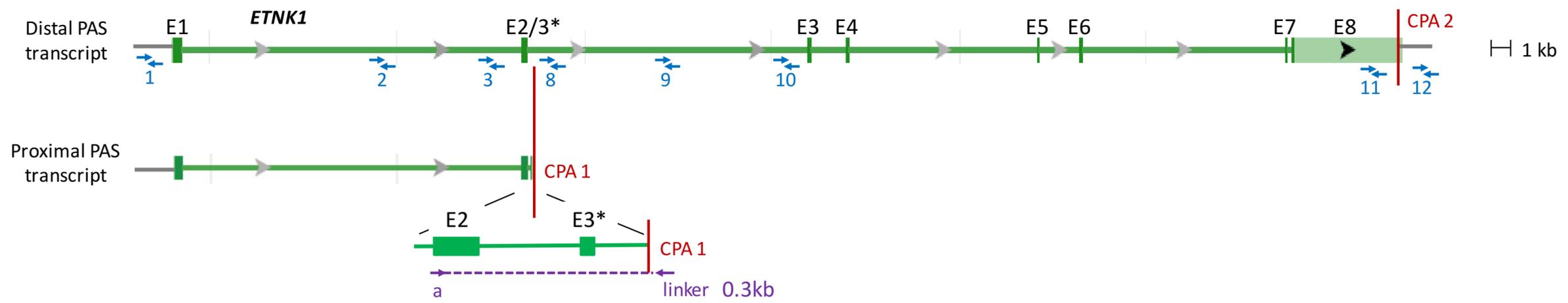


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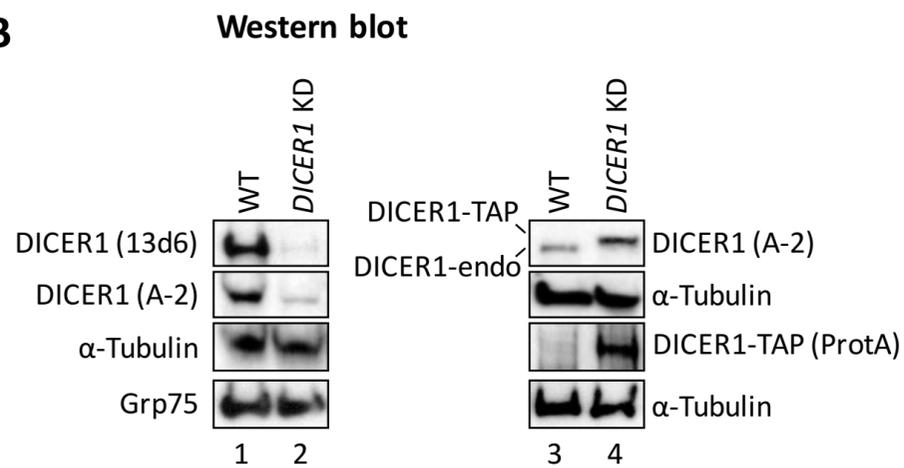




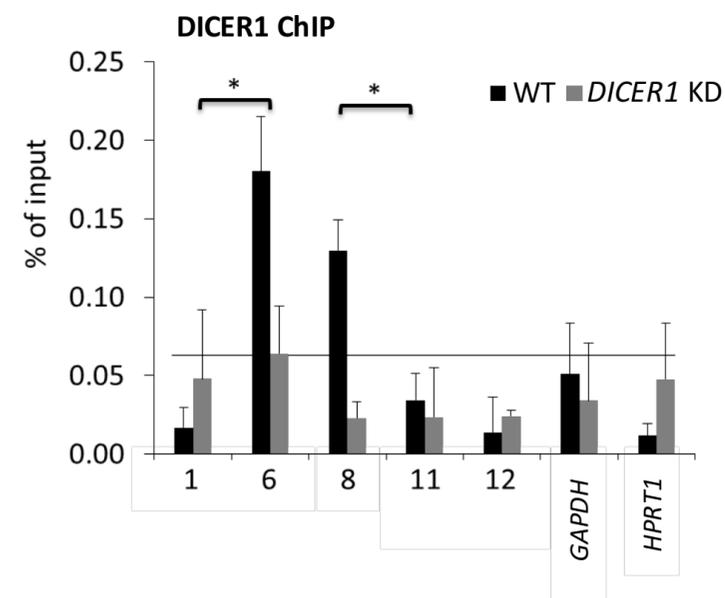
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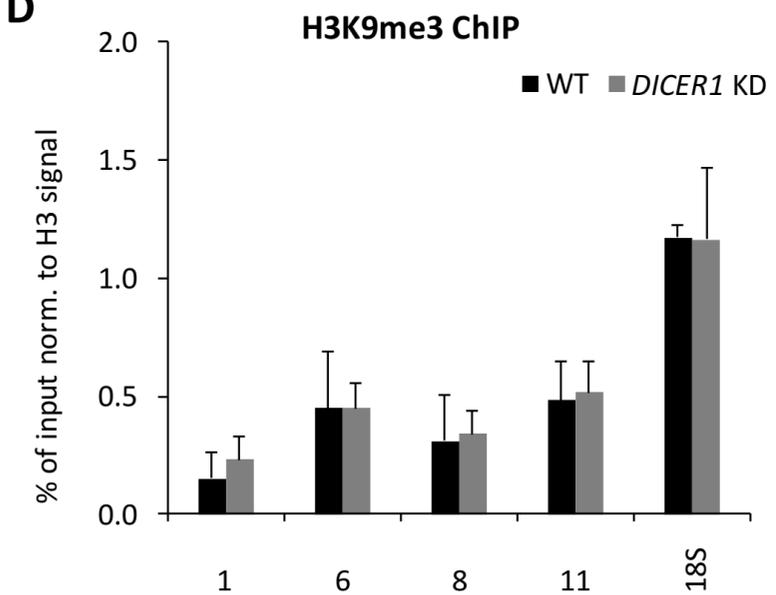
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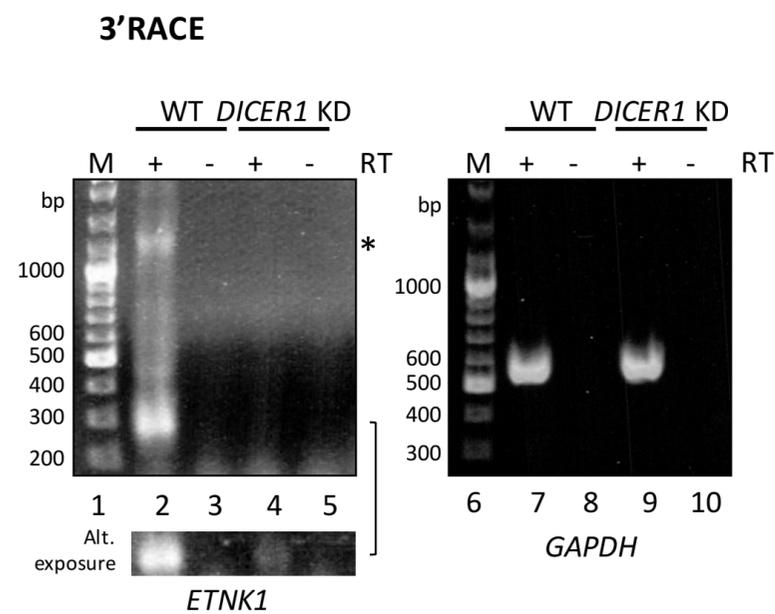
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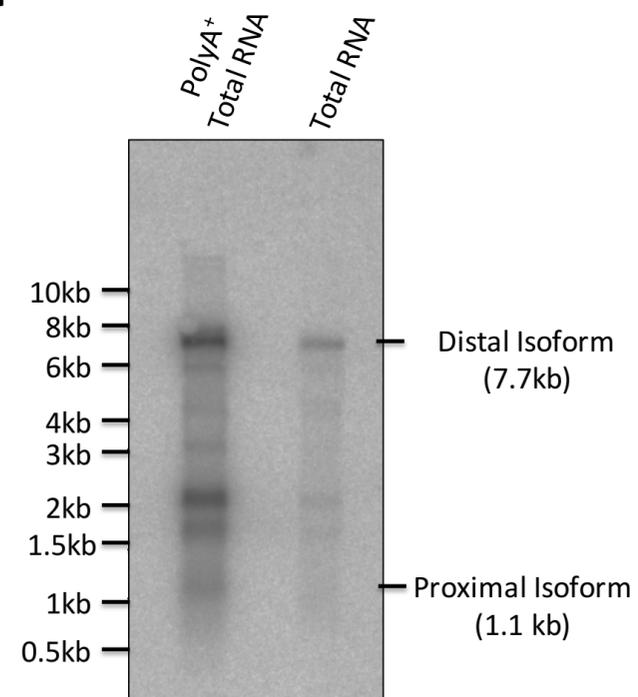
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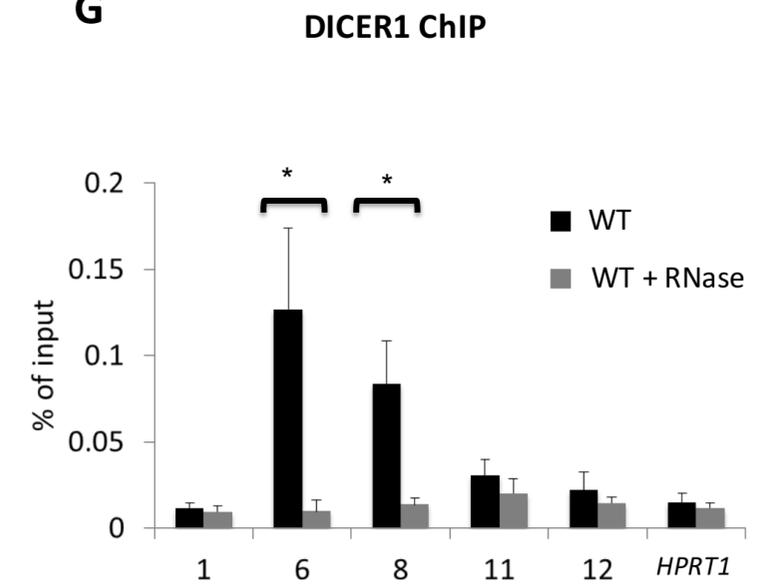
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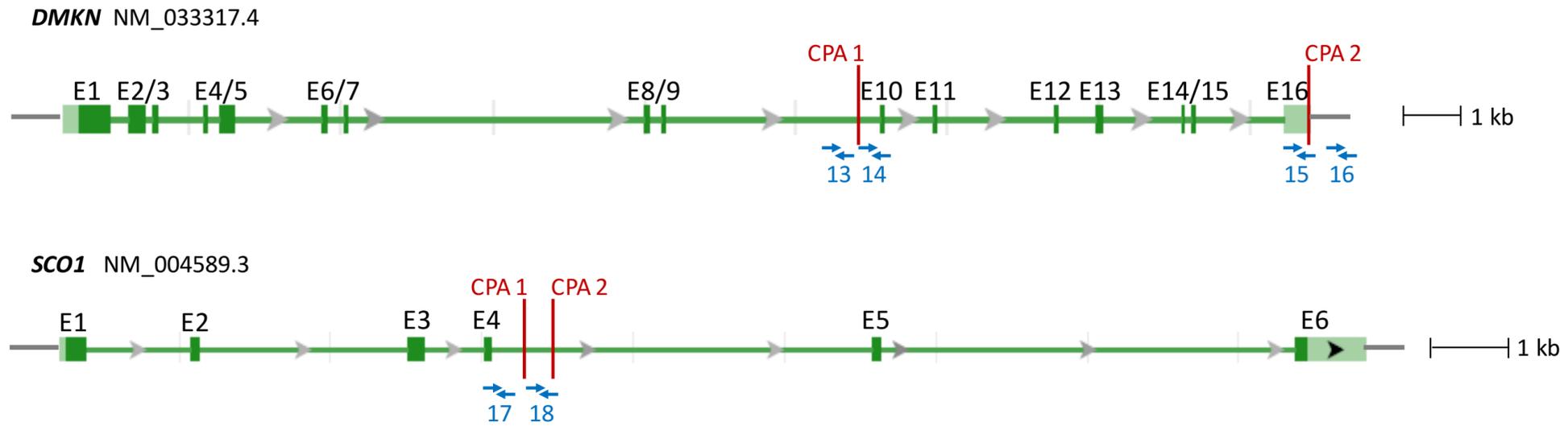
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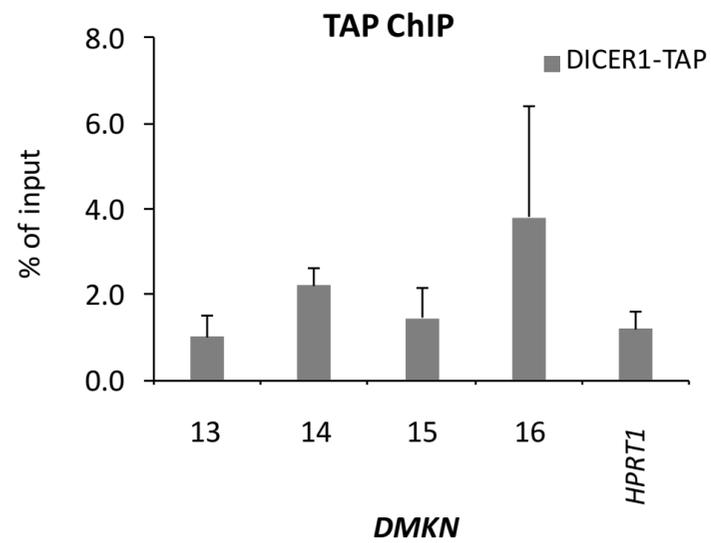
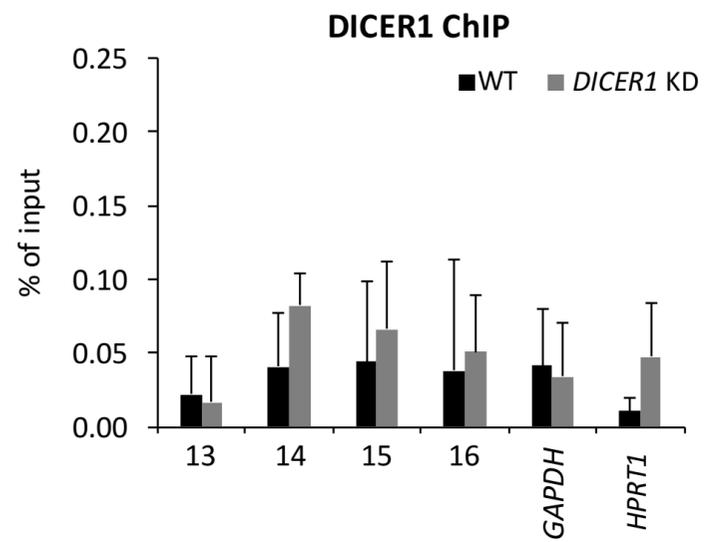
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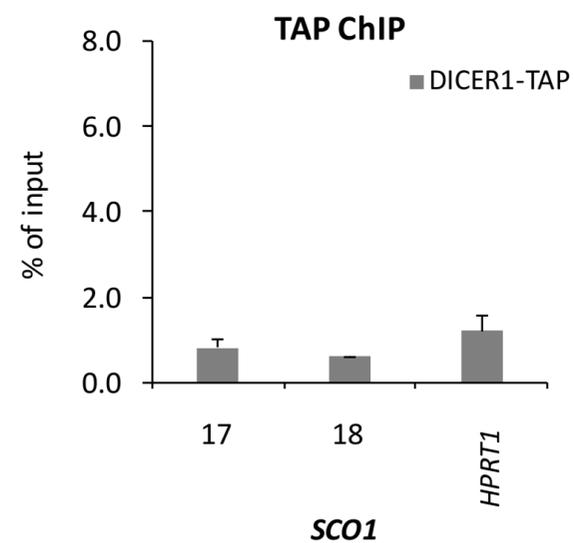
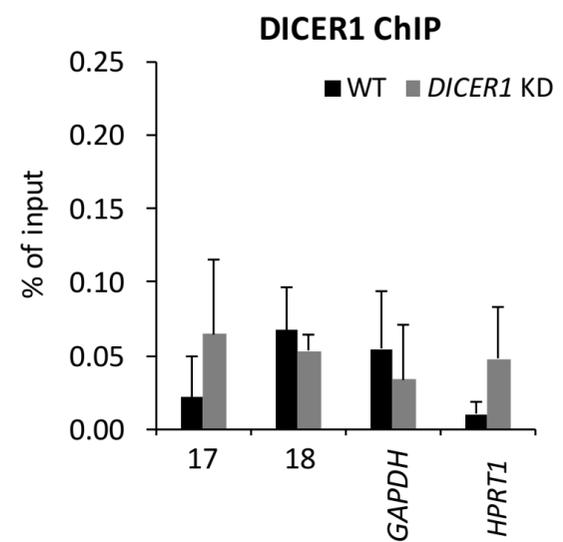
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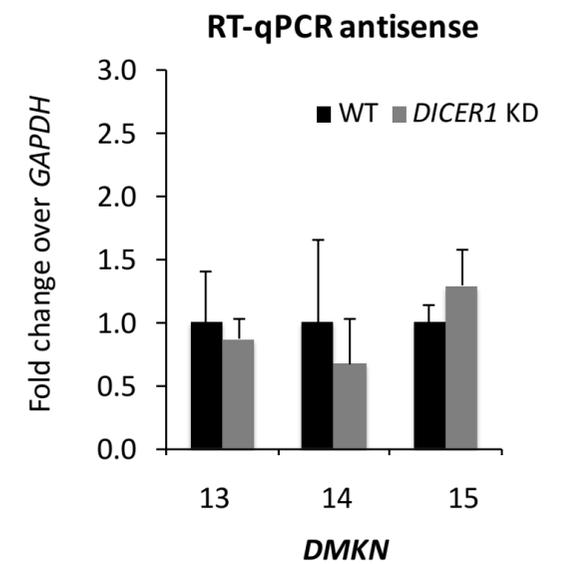
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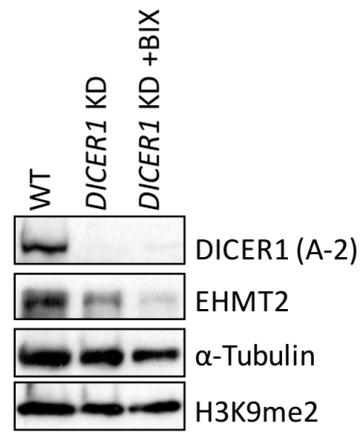
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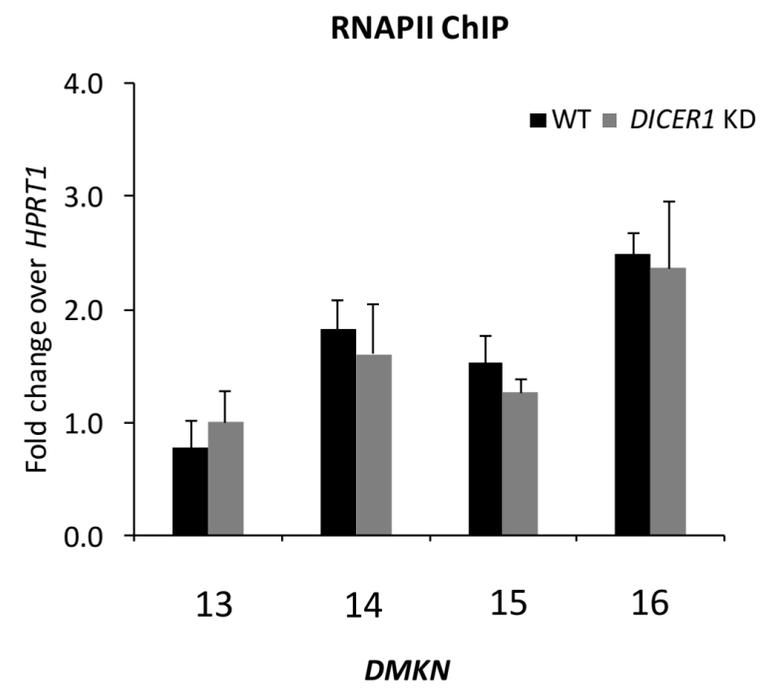


D



Western Blot



A**B**