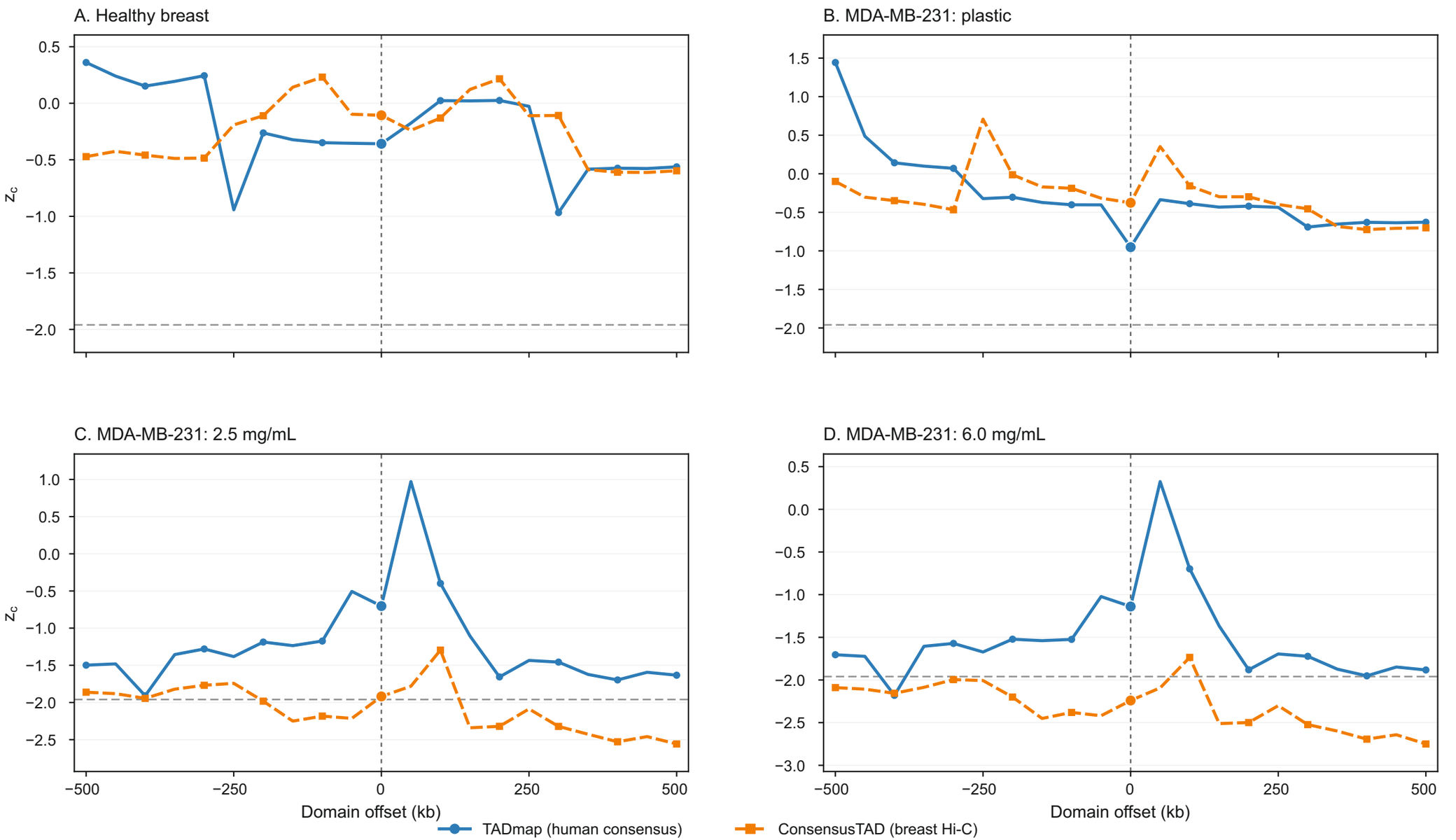
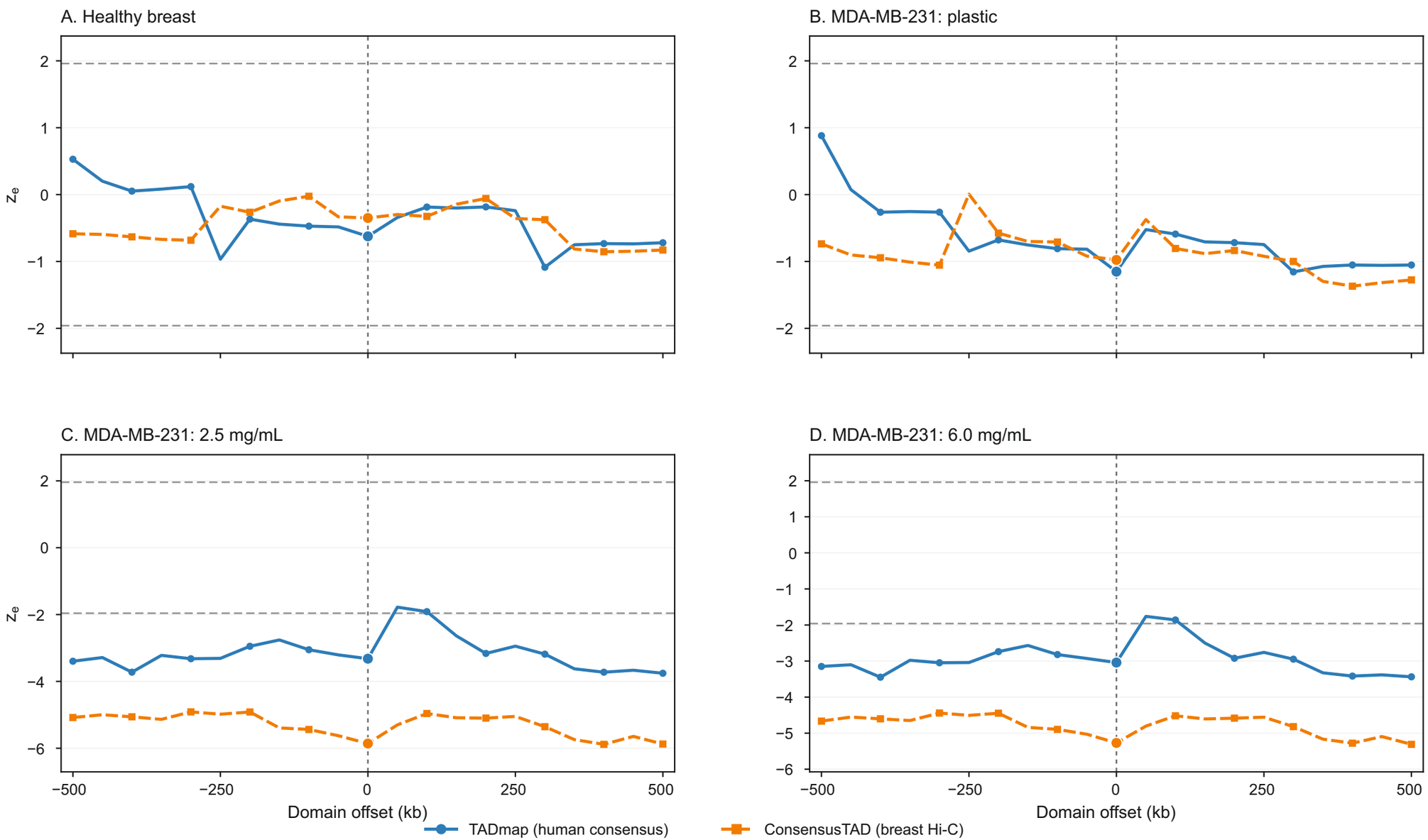


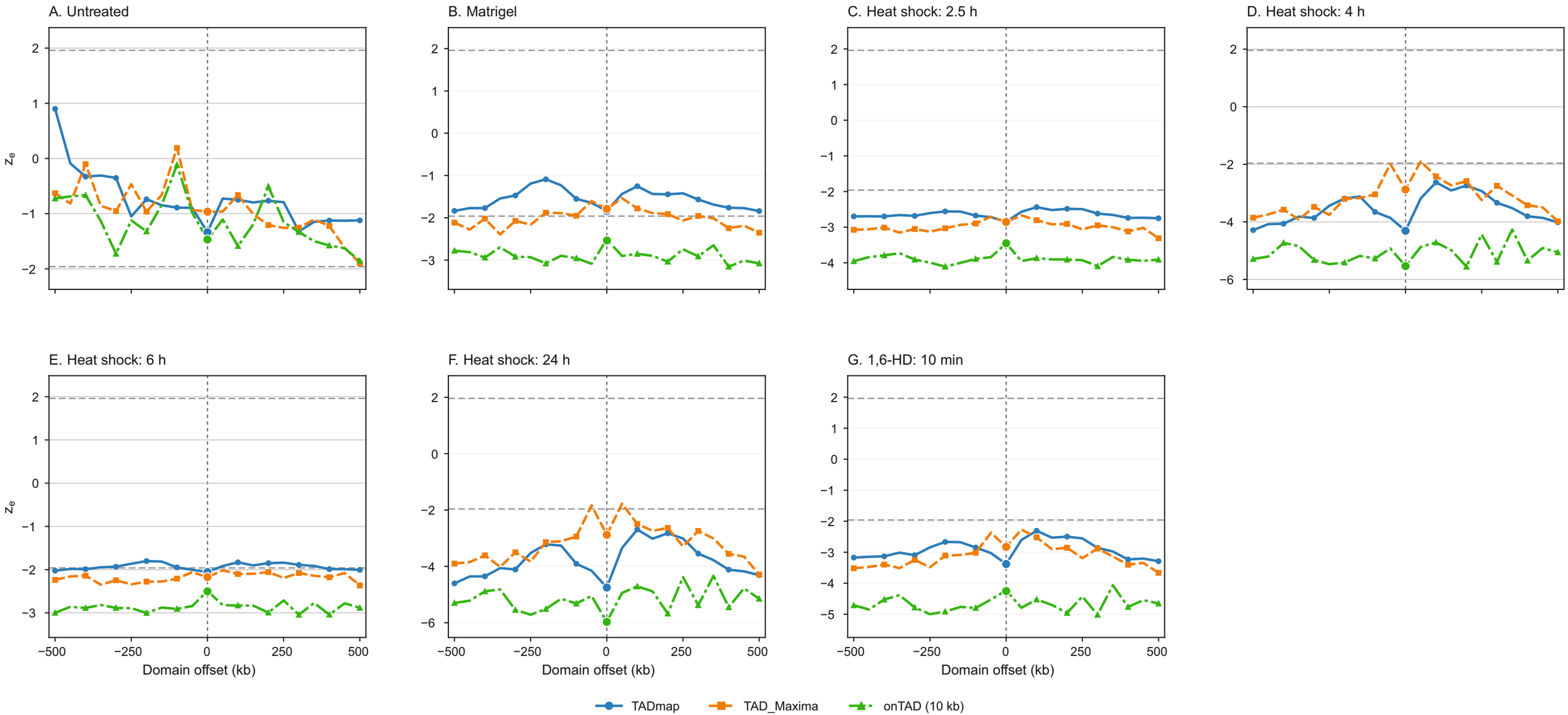
Dashed horizontal line: $z_c = -1.96$ (nominal one-sided p= 0.025). Dotted vertical line: 0 kb; enlarged markers: unshifted retained-map values. Offset-wise p values are unadjusted; offsets are not independent replicates. Panel y-axis scales differ.

Proportional gene-to-domain assignment; 21 displacements from -500 to +500 kb in 50-kb increments.



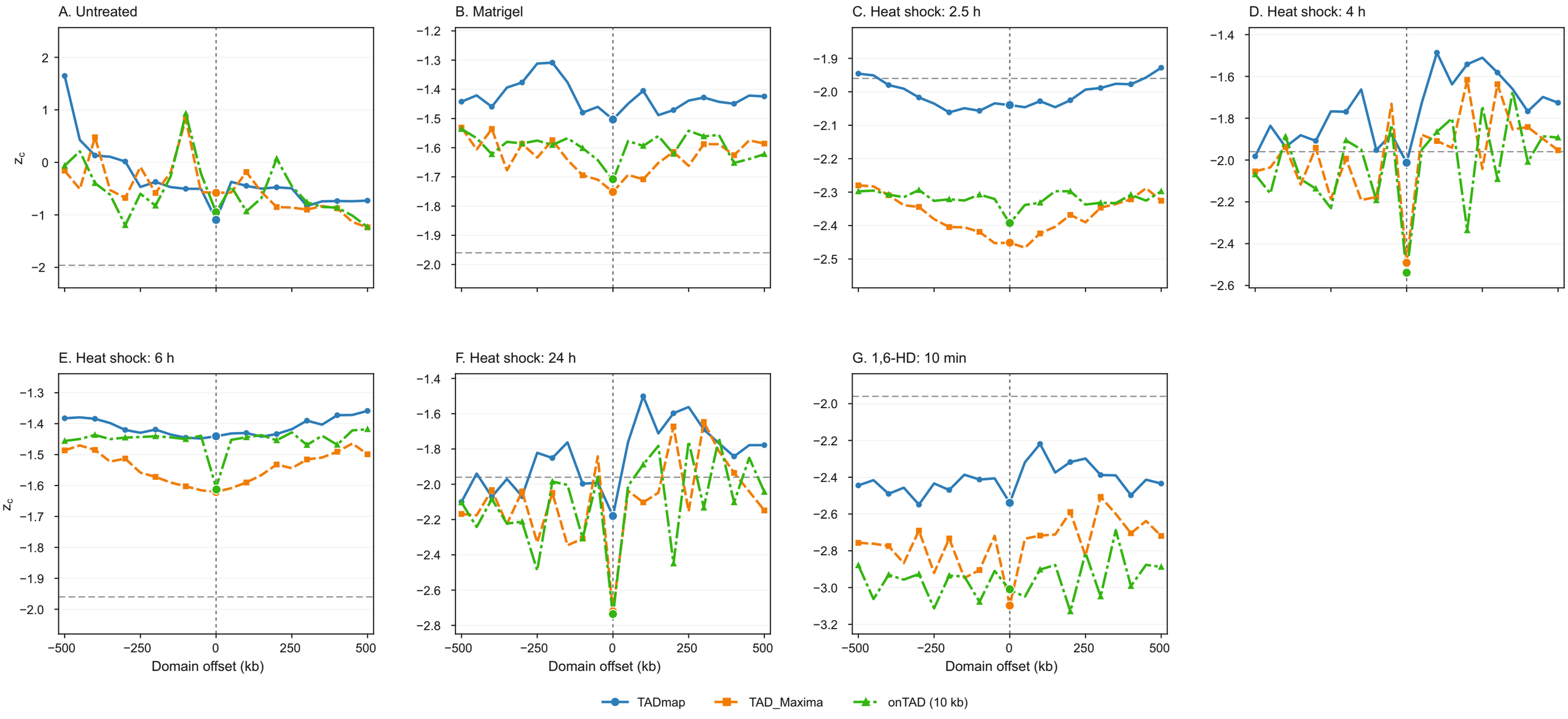
Dashed horizontal lines: z_e = ±1.96 (nominal two-sided p= 0.05). Dotted vertical line: 0 kb; enlarged markers: unshifted retained-map values. The statistic compares domain-averaged expression against its cyclic-shift reference; panel y-axis scales differ.

Proportional gene-to-domain assignment; 21 displacements from -500 to +500 kb in 50-kb increments.



Dashed horizontal lines: $z_e = \pm 1.96$ (nominal two-sided $p = 0.05$). Dotted vertical line: 0 kb; enlarged markers: unshifted retained-map values. The statistic compares domain-averaged expression against its cyclic-shift reference; panel y-axis scales differ.

Proportional gene-to-domain assignment; 21 displacements from -500 to +500 kb in 50-kb increments.


HEK293T — displacement sensitivity: Expression concordance z_c
A. Untreated
B. Matrigel
C. Heat shock: 2.5 h
D. Heat shock: 4 h
E. Heat shock: 6 h
F. Heat shock: 24 h
G. 1,6-HD: 10 min
z_c
Domain offset (kb)
TADmap
TAD_Maxima
onTAD (10 kb)
Dashed horizontal line: z_c = −1.96 (nominal one-sided p= 0.025). Dotted vertical line: 0 kb; enlarged markers: unshifted retained-map values. Offset-wise p values are unadjusted; offsets are not independent replicates. Panel y-axis scales differ.
Proportional gene-to-domain assignment; 21 displacements from -500 to +500 kb in 50-kb increments.

ConGEE supplementary summary: breast / MDA-MB-231 TAD-displacement sensitivity

All analyses used proportional gene assignment. Each profile was evaluated at 21 offsets (-500 to +500 kb, 50-kb steps). Significant-offset counts use nominal one-sided p < 0.025, without adjustment for the number of offsets.

Expression dataset	Reference TAD annotation	zc(0 kb)	p(0 kb)	Lowest zc	Offset of lowest zc (kb)	Offsets with p < 0.025
Healthy breast	TADmap (human consensus)	-0.358	0.3601	-0.967	300	0/21
Healthy breast	ConsensusTAD (breast Hi-C)	-0.107	0.4576	-0.612	450	0/21
MDA-MB-231: plastic	TADmap (human consensus)	-0.952	0.1704	-0.952	0	0/21
MDA-MB-231: plastic	ConsensusTAD (breast Hi-C)	-0.377	0.3532	-0.724	400	0/21
MDA-MB-231: 2.5 mg/mL	TADmap (human consensus)	-0.703	0.2409	-1.909	-400	0/21
MDA-MB-231: 2.5 mg/mL	ConsensusTAD (breast Hi-C)	-1.919	0.0275	-2.558	500	12/21
MDA-MB-231: 6.0 mg/mL	TADmap (human consensus)	-1.139	0.1274	-2.180	-400	1/21
MDA-MB-231: 6.0 mg/mL	ConsensusTAD (breast Hi-C)	-2.241	0.0125	-2.750	500	20/21

Note. The offset of the lowest observed zc is the minimum on the tested grid, not an inferred or statistically tested optimum. Displaced annotations may retain overlapping gene memberships. The zero-offset runs use the map subset retained for this sweep and may not reproduce the full-map statistics in the main manuscript tables. The maps were not inferred from these expression profiles.

ConGEE supplementary summary: HEK293T TAD-displacement sensitivity

All analyses used proportional gene assignment. Each profile was evaluated at 21 offsets (-500 to +500 kb, 50-kb steps). Significant-offset counts use nominal one-sided p < 0.025, without adjustment for the number of offsets.

Expression dataset	Reference TAD annotation	zc(0 kb)	p(0 kb)	Lowest zc	Offset of lowest zc (kb)	Offsets with p < 0.025
Untreated	TADmap	-1.095	0.1367	-1.095	0	0/21
Untreated	TAD_Maxima	-0.580	0.2810	-1.238	500	0/21
Untreated	onTAD (10 kb)	-0.93	0.1762	-1.231	500	0/21
Matrigel	TADmap	-1.503	0.0664	-1.503	0	0/21
Matrigel	TAD_Maxima	-1.752	0.0399	-1.752	0	0/21
Matrigel	onTAD (10 kb)	-1.704	0.0442	-1.704	0	0/21
Heat shock: 2.5 h	TADmap	-2.040	0.0207	-2.062	-200	17/21
Heat shock: 2.5 h	TAD_Maxima	-2.451	0.0071	-2.466	50	21/21
Heat shock: 2.5 h	onTAD (10 kb)	-2.392	0.0084	-2.392	0	21/21
Heat shock: 4 h	TADmap	-2.013	0.0221	-2.013	0	2/21
Heat shock: 4 h	TAD_Maxima	-2.491	0.0064	-2.491	0	9/21
Heat shock: 4 h	onTAD (10 kb)	-2.539	0.0056	-2.539	0	10/21
Heat shock: 6 h	TADmap	-1.441	0.0748	-1.448	-50	0/21
Heat shock: 6 h	TAD_Maxima	-1.621	0.0525	-1.621	0	0/21
Heat shock: 6 h	onTAD (10 kb)	-1.608	0.0539	-1.608	0	0/21
Heat shock: 24 h	TADmap	-2.180	0.0146	-2.180	0	7/21
Heat shock: 24 h	TAD_Maxima	-2.721	0.0033	-2.721	0	16/21
Heat shock: 24 h	onTAD (10 kb)	-2.724	0.0032	-2.724	0	15/21
1,6-HD: 10 min	TADmap	-2.539	0.0056	-2.549	-300	21/21
1,6-HD: 10 min	TAD_Maxima	-3.098	0.0010	-3.098	0	21/21
1,6-HD: 10 min	onTAD (10 kb)	-3.010	0.0013	-3.130	200	21/21

Note. The offset of the lowest observed zc is the minimum on the tested grid, not an inferred or statistically tested optimum. Displaced annotations may retain overlapping gene memberships. The zero-offset runs use the map subset retained for this sweep and may not reproduce the full-map statistics in the main manuscript tables. The maps were not inferred from these expression profiles.