Table S9.1. Expression concordance analysis of RNA-seq datasets from untreated, Matrigel-grown, 1,6-hexanediol-treated, and cells subjected to heats shock after exclusion of silent genes (TPM = 0.0).

HEK293T	TAD database	z_e	$p(z_e)$	$p(z_e)_{adj}$	z_c	$p(z_c)$	$p(z_c)_{adj}$	C
Untreated	TADMap	-1.126	0.26028	NA	-0.986	0.16217	NA	NS
Matrigel	TADMap	-2.366	0.01798	NA	-1.515	0.06483	NA	NS
HS 2.5h	TADMap	-3.218	0.00128	0.00171	-2.031	0.02113	0.02817	0.074
HS 4h	TADMap	-5.549	2.86e-08	5.72e-08	-2.043	0.02052	0.02817	0.077
HS 6h	TADMap	-2.340	0.01928	0.01928	-1.415	0.07851	0.07851	NS
HS 24h	TADMap	-6.251	4.06e-10	1.62e-09	-2.269	0.01163	0.02817	0.216
1,6-HD	TADMap	-4.332	0.00002	NA	**-2.676**	**0.00373**	NA	**0.495**
Untreated	TAD_Maxima	-1.079	0.28059	NA	-0.453	0.32541	NA	NS
Matrigel	TAD_Maxima	-3.192	0.00141	NA	-1.950	0.02559	NA	NS
HS 2.5h	TAD_Maxima	**-4.120**	**0.00004**	**0.00005**	**-2.781**	**0.00271**	**0.00632**	**0.536**
HS 4h	TAD_Maxima	**-5.639**	**1.71e-08**	**3.42e-08**	**-2.594**	**0.00474**	**0.00632**	**0.454**
HS 6h	TAD_Maxima	-3.173	0.00151	0.00151	-1.792	0.03656	0.03656	NS
HS 24h	TAD_Maxima	**-5.742**	**9.36e-09**	**3.42e-08**	**-2.671**	**0.00378**	**0.00632**	**0.493**
1,6-HD	TAD_Maxima	**-4.852**	**1.22e-06**	NA	**-3.453**	**0.00028**	NA	**0.698**
Untreated	onTADs.10kb	-1.225	0.22058	NA	-0.897	0.18481	NA	NS
Matrigel	onTADs.10kb	-2.658	0.00786	NA	-1.815	0.03478	NA	NS
HS 2.5h	onTADs.10kb	**-3.854**	**0.00012**	**0.00016**	**-2.558**	**0.00526**	**0.00792**	**0.434**
HS 4h	onTADs.10kb	**-6.154**	**7.56e-10**	**1.51e-09**	**-2.516**	**0.00594**	**0.00792**	**0.408**
HS 6h	onTADs.10kb	-2.686	0.00723	0.00723	-1.670	0.04744	0.04744	NS
HS 24h	onTADs.10kb	**-6.430**	**1.28e-10**	**5.12e-10**	**-2.650**	**0.00403**	**0.00792**	**0.422**
1,6-HD	onTADs.10kb	**-4.672**	**2.98e-06**	NA	**-3.207**	**0.00067**	NA	**0.649**

Matrigel – HEK293T grown on Matrigel matrix; HS – HEK293T after heatshock; 1,6-HD – HEK293T treated for 10 min with 5% 1,6-hexanediol; for all datasets presented, H=0.5 was assigned by the fallback procedure, so the reported concordance estimates C were obtained using the corresponding calibration; NS – non-significant; bold marks the statistically significant results; TAD databases: TADMap, TAD_Maxima, onTAD (see Methods 4.1). Concordance tests for Untreated, Matrigel-grown and treated with 1,6-HD cells address separate biological questions; therefore, no multiple-testing correction was applied for these conditions. Results highlighted in orange should be interpreted with caution because the unadjusted and BH-adjusted p-values yield conflicting conclusions. Results highlighted in green can be considered statistically robust because both the unadjusted and BH-adjusted p-values fall below the left-tailed significance threshold (p = 0.025).

Table S9.2. Expression concordance analysis of RNA-seq datasets from untreated, Matrigel-grown, 1,6-hexanediol-treated, and cells subjected to heats shock after exclusion of low-expression genes (TPM < 0.5).

HEK293T	TAD database	z_e	$p(z_e)$	$p(z_e)_{adj}$	z_c	$p(z_c)$	$p(z_c)_{adj}$	C
Untreated	TADMap	-1.211	0.22596	NA	-1.018	0.15431	NA	NS
Matrigel	TADMap	-2.054	0.03998	NA	-1.465	0.07152	NA	NS
HS 2.5h	TADMap	-2.974	0.00294	0.00392	-2.018	0.02181	0.02909	0.071
HS 4h	TADMap	-5.000	5.72e-07	1.14e-06	-2.038	0.02075	0.02909	0.076
HS 6h	TADMap	-2.197	0.02804	0.02804	-1.376	0.08437	0.08437	NS
HS 24h	TADMap	-5.486	4.12e-08	1.65e-07	-2.202	0.01383	0.02909	0.145
1,6-HD	TADMap	-3.656	0.00026	NA	**-2.431**	**0.00754**	NA	0.354
Untreated	TAD_Maxima	-0.992	0.32120	NA	-0.461	0.32233	NA	NS
Matrigel	TAD_Maxima	-2.895	0.00378	NA	-1.885	0.02974	NA	NS
HS 2.5h	TAD_Maxima	**-3.899**	**0.00010**	**0.00013**	**-2.707**	**0.00339**	**0.01358**	**0.508**
HS 4h	TAD_Maxima	**-4.320**	**1.56e-05**	**0.00003**	**-2.166**	**0.01515**	**0.02020**	**0.111**
HS 6h	TAD_Maxima	-3.016	0.00256	0.00256	-1.708	0.04381	0.04381	NS
HS 24h	TAD_Maxima	**-4.527**	**5.96e-06**	**0.00002**	**-2.376**	**0.00876**	**0.01751**	**0.315**
1,6-HD	TAD_Maxima	-4.238	0.00002	NA	**-3.290**	**0.00050**	NA	**0.667**
Untreated	onTADs.10kb	-1.294	0.19566	NA	-0.988	0.16165	NA	NS
Matrigel	onTADs.10kb	-2.250	0.02442	NA	-1.845	0.03255	NA	NS
HS 2.5h	onTADs.10kb	**-3.544**	**0.00039**	**0.00052**	**-2.590**	**0.00480**	**0.01317**	**0.452**
HS 4h	onTADs.10kb	**-4.999**	**5.76E-07**	**1.15e-06**	**-2.331**	**0.00988**	**0.01317**	**0.277**
HS 6h	onTADs.10kb	-2.633	0.00846	0.00846	-1.762	0.03908	0.03908	NS
HS 24h	onTADs.10kb	**-5.273**	**1.34E-07**	**5.36e-07**	**-2.472**	**0.00671**	**0.01317**	**0.326**
1,6-HD	onTADs.10kb	**-4.005**	**0.00006**	NA	**-3.096**	**0.00098**	NA	**0.624**

Matrigel – HEK293T grown on Matrigel matrix; HS – HEK293T after heatshock; 1,6-HD – HEK293T treated for 10 min with 5% 1,6-hexanediol; for all datasets presented, H=0.5 was assigned by the fallback procedure, so the reported concordance estimates C were obtained using the corresponding calibration; NS – non-significant; bold marks the statistically significant results; TAD databases: TADMap, TAD_Maxima, onTAD (see Methods 4.1). Concordance tests for Untreated, Matrigel-grown and treated with 1,6-HD cells address separate biological questions; therefore, no multiple-testing correction was applied for these conditions. Results highlighted in orange should be interpreted with caution because the unadjusted and BH-adjusted p-values yield conflicting conclusions. Results highlighted in green can be considered statistically robust because both the unadjusted and BH-adjusted p-values fall below the left-tailed significance threshold (p = 0.025)