Supplementary Table 1. Univariate and multivariate analyses of DFS and OS in patients with gene expression data (*N* = 141)

		DFS				OS			
		Univariate		Multivariate		Univariate		Multivariate	
		HR (95% CI)	*P* value	HR (95% CI)	*P* value	HR (95% CI)	*P* value	HR (95% CI)	*P* value
Arm	stCTX	1 (ref.)		1 (ref.)		1 (ref.)		1 (ref.)	
	ddCTX	0.94 (0.59–1.49)	0.790	0.78 (0.48–1.27)	0.302	0.96 (0.60–1.54)	0.857	0.80 (0.49–1.32)	0.375
Age	>43 years	1 (ref.)		1 (ref.)		1 (ref.)		1 (ref.)	
	≤43 years	**2.13 (1.20–3.78)**	**0.010**	**2.95 (1.59–5.49)**	**0.001**	**2.12 (1.17–3.82)**	**0.013**	**3.69 (1.88–7.23)**	**<0.001**
pT	1	1 (ref.)		1 (ref.)		1 (ref.)		1 (ref.)	
	2	**2.21 (1.12–4.35)**	**0.021**	**2.53 (1.25–5.12)**	**0.010**	**3.20 (1.49–6.87)**	**0.003**	**4.29 (1.90–9.72)**	**<0.001**
	3	**3.73 (1.77–7.88)**	**0.001**	**4.34 (1.91–9.88)**	**<0.001**	**4.54 (1.95–10.5)**	**<0.001**	**6.76 (2.64–17.3)**	**<0.001**
	4/X	**4.40 (1.61–12.0)**	**0.004**	**3.64 (1.21–10.9)**	**0.021**	**8.33 (2.99–23.2)**	**<0.001**	**7.82 (2.59–23.6)**	**<0.001**
Number of involved lymph nodes	4–9	1 (ref.)		1 (ref.)		**1 (ref.)**		1 (ref.)	
	>9	1.65 (0.98-2.76)	0.059	1.49 (0.85–2.63)	0.165	**1.87 (1.20–3.14)**	**0.017**	1.64 (0.94–2.85)	0.082
Hormone receptor status	Positive	1 (ref.)		1 (ref.)		1 (ref.)		1 (ref.)	
	Negative	1.06 (0.61–1.85)	0.829	1.18 (0.63–2.21)	0.609	0.88 (0.49–1.58)	0.669	1.02 (0.53–1.97)	0.943
Type of local surgery	Mastectomy	1 (ref.)		1 (ref.)		1 (ref.)		1 (ref.)	
	Breast-conserving surgery	0.66 (0.39-1.12)	0.121	0.91 (0.52–1.59)	0.734	0.94 (0.56–1.55)	0.800	1.47 (0.85–2.54)	0.173

ddCTX, dose-dense chemotherapy; ref., reference; stCTX, standard dose chemotherapy.

Statistically significant associations are shown in bold.

Supplementary Table 2. Multivariate analysis of prognostic associations for genes/signatures for DFS and OS in patients with HER2-enriched tumors (*N* = 27)

Gene/ signature	DFS				OS			
	ddCTX		stCTX		ddCTX		stCTX	
	HR (95% CI)[a]	*P* value	HR (95% CI)[a]	*P* value	HR (95% CI)[a]	*P* value	HR (95% CI)[a]	*P* value
AR	NA	NS	NA	NS	**24.5 (1.12–533)**	**0.042**	NA	NS
TIGIT	NA	NS	0.40 (0.15–1.07)	0.069	NA	NS	NA	NS
CD8+ T-cells	NA	NS	**0.27 (0.08–0.93)**	**0.039**	NA	NS	**0.09 (0.01–0.62)**	**0.015**
Cytotoxic cells	NA	NS	**0.35 (0.12–0.99)**	**0.049**	NA	NS	NA	NS
Mast cells	NA	NS	NA	NS	**11.0 (1.25–97.3)**	**0.031**	NA	NS
Treg	NA	NS	0.34 (0.09–1.32)	0.098	NA	NS	0.03 (0.0001–7.91)	0.214

AR, androgen receptor; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; HR, hazard ratio; OS, overall survival; stCTX, standard-dosed chemotherapy; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; Treg, regulatory T-cell.

Multivariate analysis was performed only for genes/signatures showing significant univariate associations. Statistically significant associations are shown in bold.

[a] Adjusted for age (<43 versus ≥43 years), pT stage (T1 versus T2 versus T3 versus T4), and number of involved nodes (4–9 versus >9).

Supplementary Table 3. Multivariate analysis of predictive associations for genes/signatures for DFS and OS in patients with HER2-enriched tumors (*N* = 27)

Gene/signature	Category	DFS			OS		
		HR (95% CI)[a]	*P* value	*P* value (interaction)	HR (95% CI)[a]	*P* value	*P* value (interaction)
Macrophages	<median	1.05 (0.17–6.67)	0.954	0.162	0.15 (0.02–1.35)	0.090	0.212
	≥median	0.94 (0.13–6.67)	0.955		0.99 (0.08–12.50)	0.995	
Inflammatory	<median	1.49 (0.13–16.67)	0.744	**0.004**	1.08 (0.10–11.11)	0.954	**0.026**
chemokines	≥median	0.46 (0.18–1.18)	0.469		0.05 (0.00–1.54)	0.085	

CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; OS, overall survival; stCTX, standard-dosed CTX.

Statistically significant associations are shown in bold.

[a] ddCTX versus stCTX, adjusted for age (<43 versus ≥43 years), pT stage (T1 versus T2 versus T3 versus T4), and number of involved nodes (4–9 versus >9). HR <1 favors ddCTX versus stCTX.

Supplementary Table 4. Multivariate analysis of prognostic associations for genes and signatures for DFS and OS in patients with basal-like tumors (*N* = 26)

Gene/ signature	DFS				OS			
	ddCTX		stCTX		ddCTX		stCTX	
	HR (95% CI)[a]	*P* value	HR (95% CI)[a]	*P* value	HR (95% CI)[a]	*P* value	HR (95% CI)[a]	*P* value
Luminal B	NA	NS	NA	NS	0.001 (1.76E-9–605)	0.310	NA	NS
TIS	0.42 (0.09–1.86)	0.255	0.08 (0.005–1.45)	0.086	0.27 (0.05–1.47)	0.130	NA	NS
ESR1	**0.01 (1.52E-4–0.90)**	**0.045**	NA	NS	NA	NS	NA	NS
IDO1	NA	NS	0.19 (0.03–1.05)	0.057	0.34 (0.10–1.11)	0.073	0.42 (0.12–1.45)	0.172
PD-L1	0.34 (0.05–2.23)	0.263	0.21 (0.03–1.59)	0.131	0.001 (7.54E-7–2.24)	0.081	NA	NS
TIGIT	NA	NS	NA	NS	0.21 (0.03–1.32)	0.098	NA	NS
CD8+ T-cells	NA	NS	NA	NS	0.11 (0.01–11.49)	0.096	NA	NS
Cytotoxic cells	NA	NS	0.31 (0.08–1.19)	0.088	0.34 (0.07–1.57)	0.166	NA	NS
Cytotoxicity	0.52 (0.12–2.27)	0.384	NA	NS	NA	NS	NA	NS
PD-1	NA	NS	0.05 (4.57E-4–5.68)	0.192	0.17 (0.02–1.09)	0.061	NA	NS

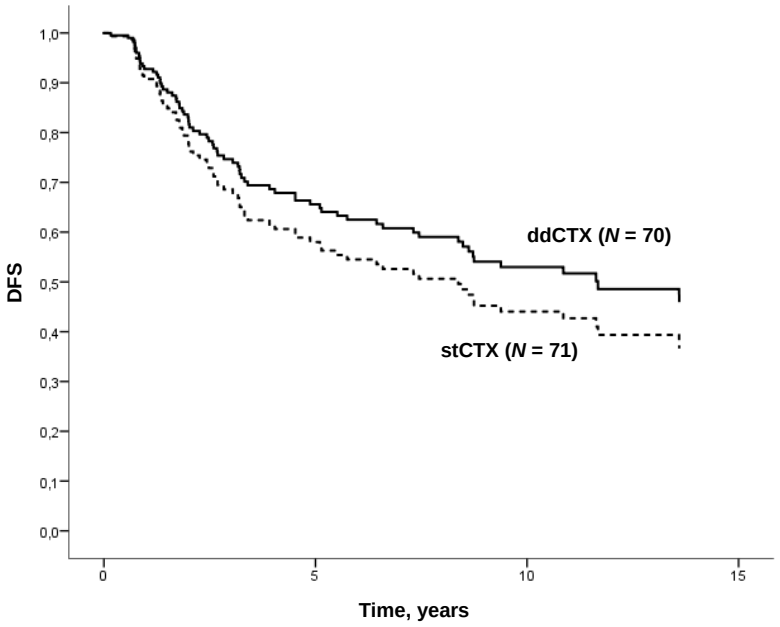
CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ESR1, oestrogen receptor-1; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; OS, overall survival; stCTX, standard-dosed chemotherapy; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature.

Multivariate analysis was performed only for genes/signatures showing significant univariate associations. Statistically significant associations are shown in bold.

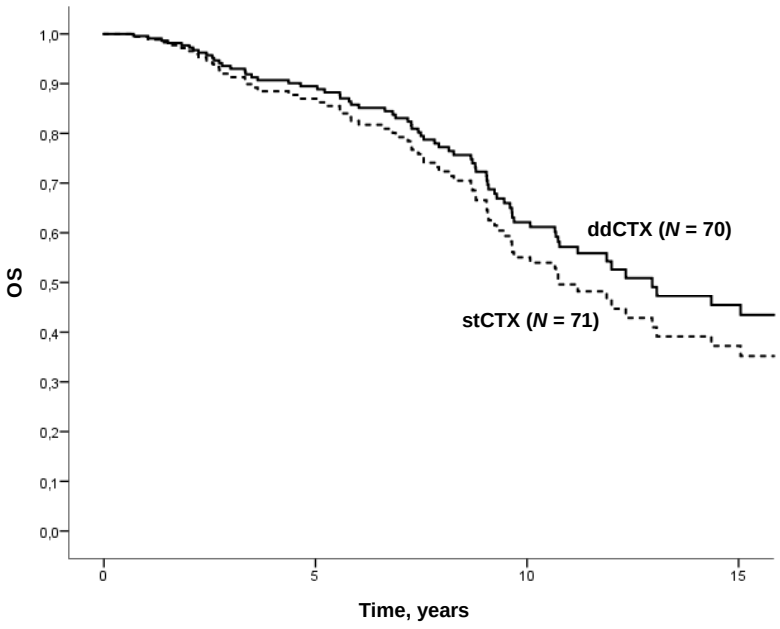
[a] Adjusted for age (<43 versus ≥43 years), pT stage (T1 versus T2 versus T3 versus T4), and number of involved nodes (4–9 versus >9).

Supplementary Figure 1. Adjusted survival curves for (A) DFS and (B) OS in patients with gene expression data (*N* = 141)

A



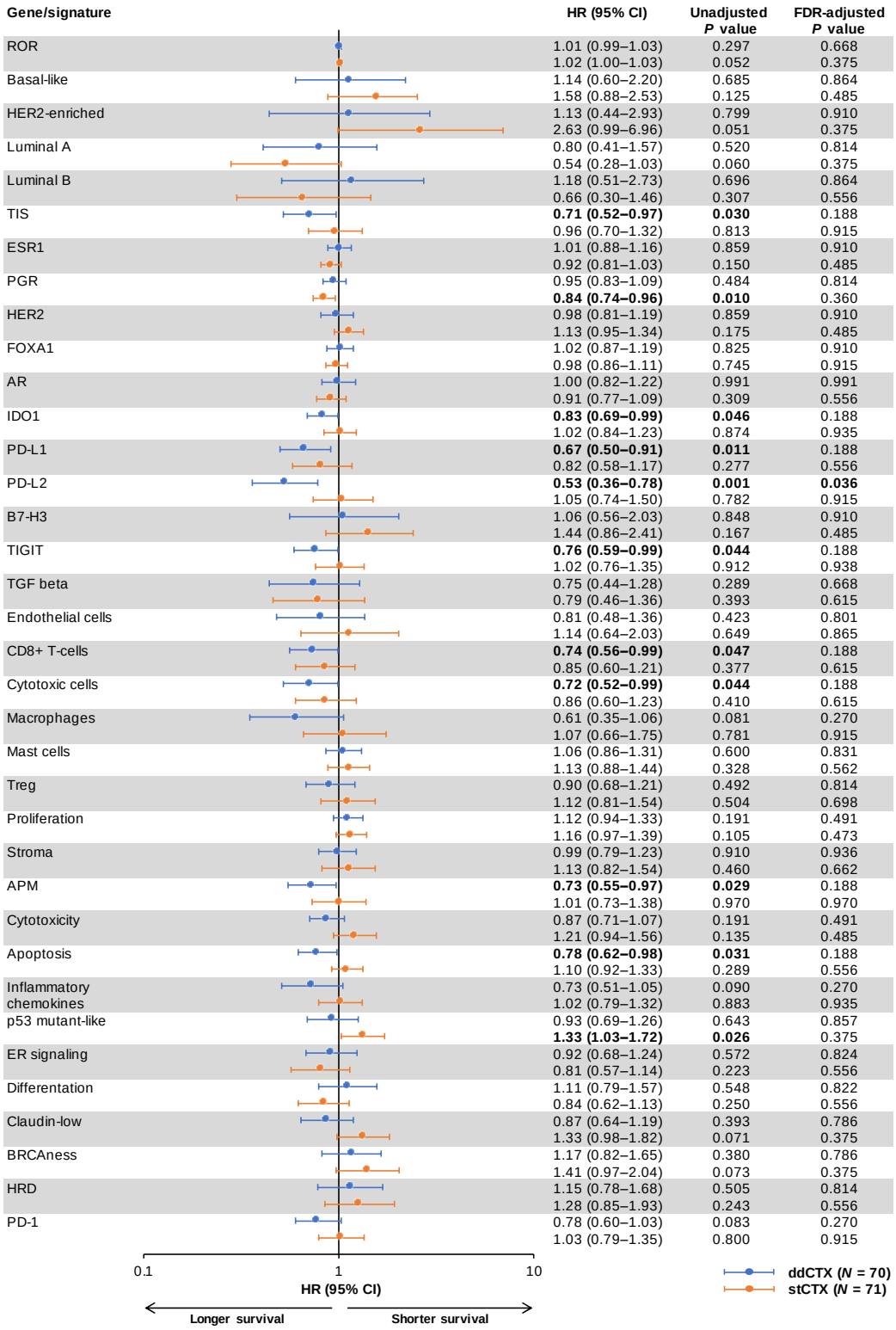
B



ddCTX, dose-dense chemotherapy; DFS, disease-free survival; OS, overall survival; stCTX, standard dose chemotherapy.

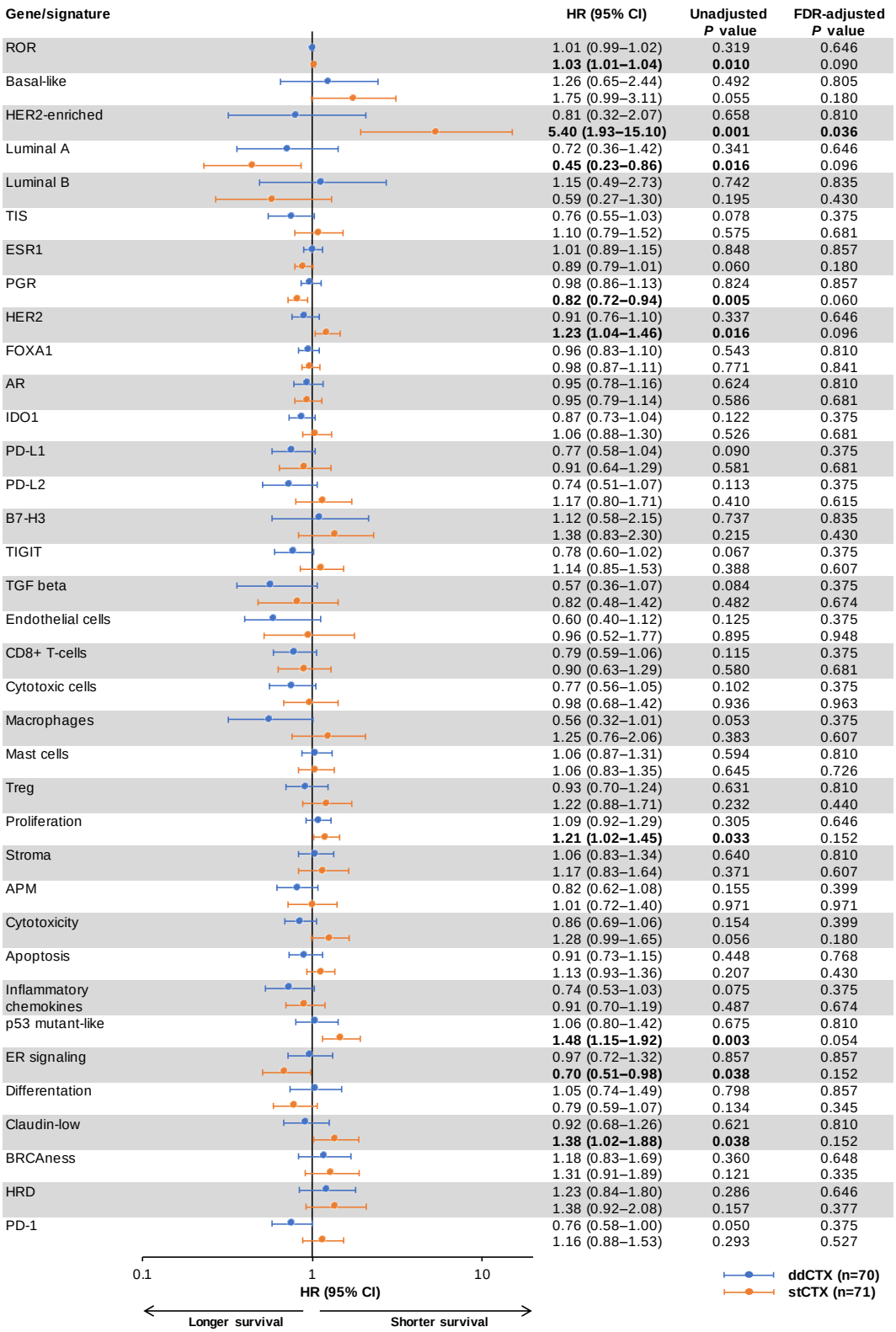
Supplementary Figure 2. Prognostic analysis of genes and signatures according to treatment arm in overall population (*N* = 141) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

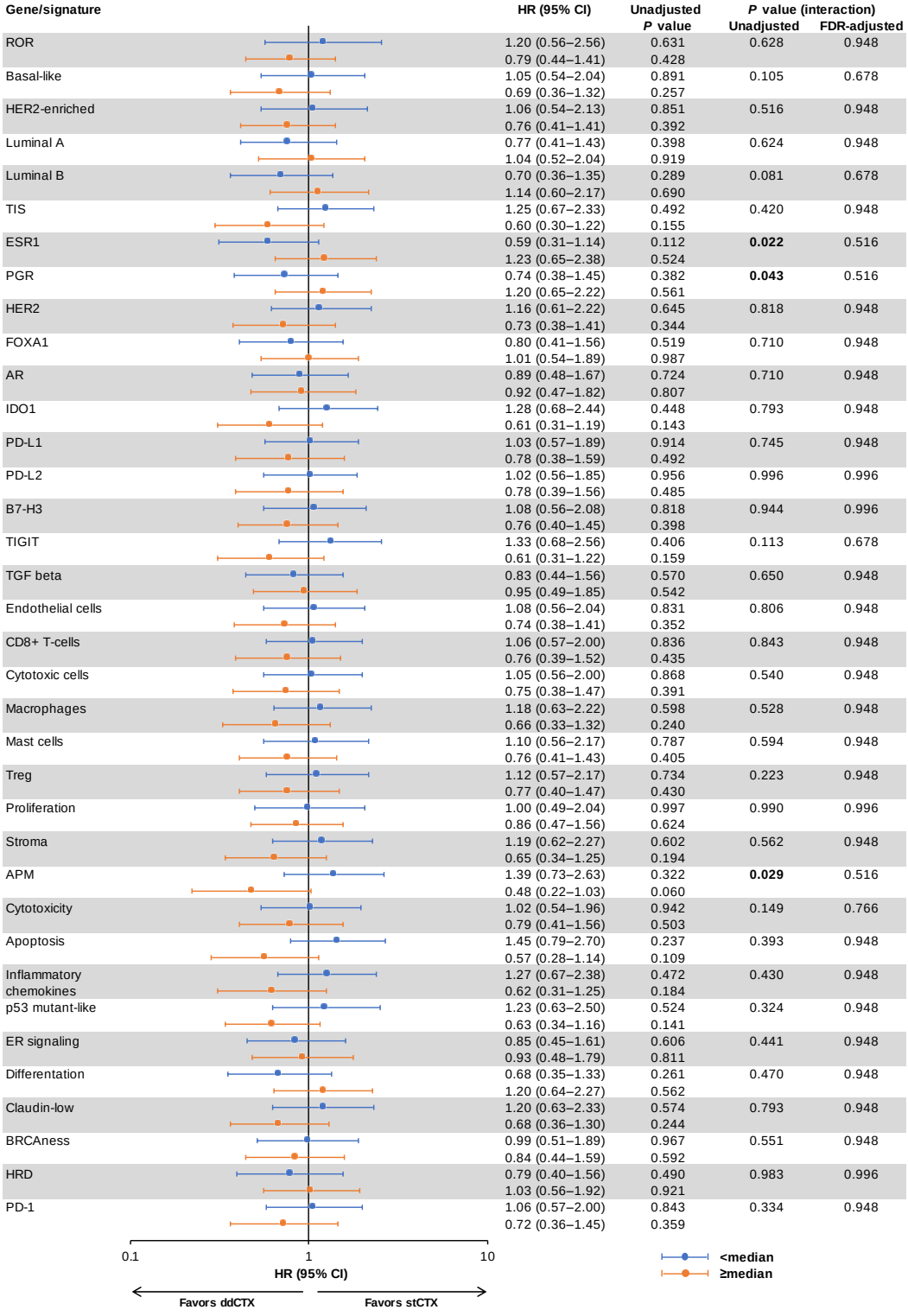
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

Supplementary Figure 3. Predictive analysis of genes and signatures in the overall population (*N* = 141) for (A) DFS and (B) OS.

A

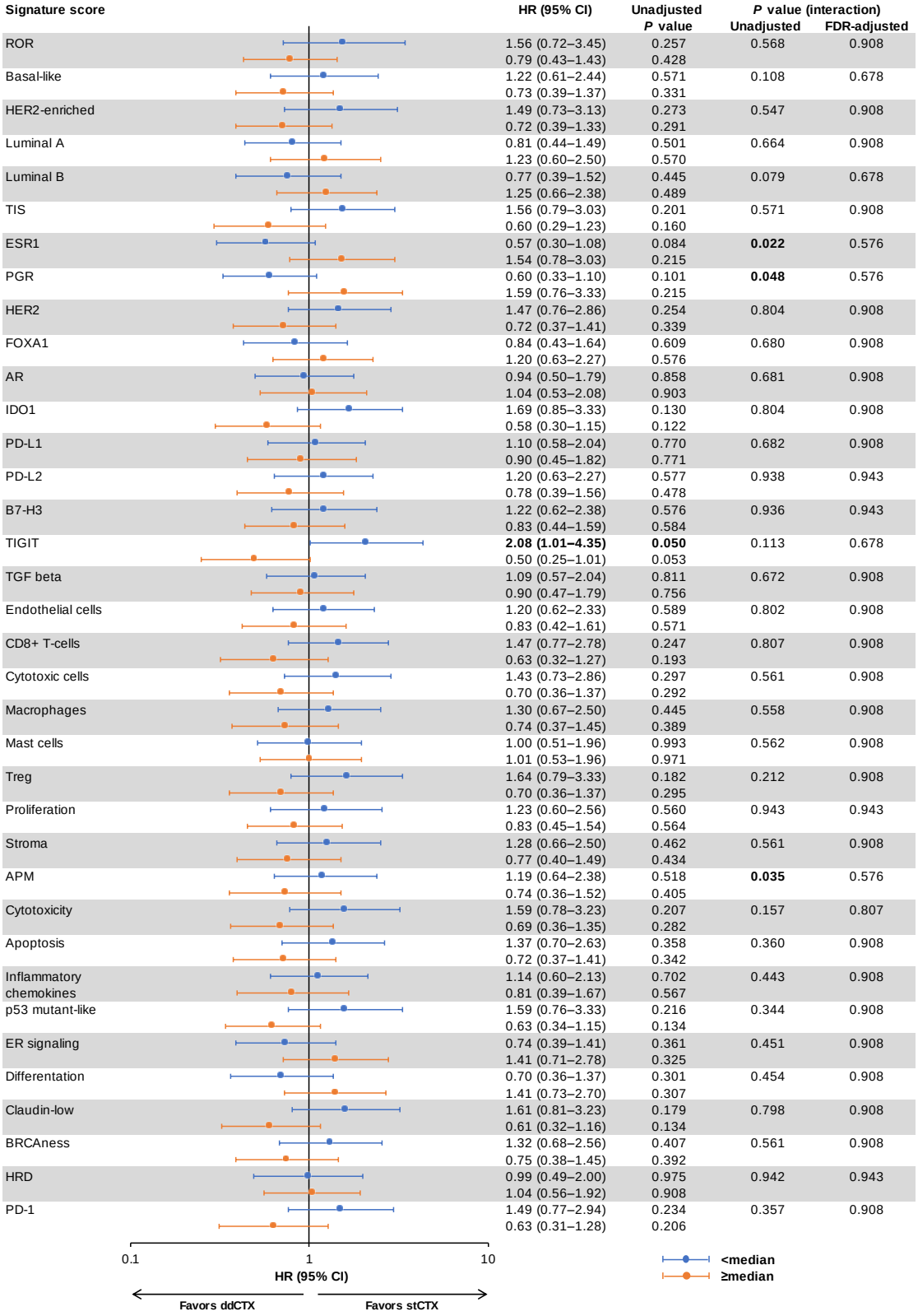


Gene/signature	HR (95% CI)	Unadjusted *P* value	*P* value (interaction) Unadjusted	FDR-adjusted
ROR	1.20 (0.56–2.56)	0.631	0.628	0.948
	0.79 (0.44–1.41)	0.428		
Basal-like	1.05 (0.54–2.04)	0.891	0.105	0.678
	0.69 (0.36–1.32)	0.257		
HER2-enriched	1.06 (0.54–2.13)	0.851	0.516	0.948
	0.76 (0.41–1.41)	0.392		
Luminal A	0.77 (0.41–1.43)	0.398	0.624	0.948
	1.04 (0.52–2.04)	0.919		
Luminal B	0.70 (0.36–1.35)	0.289	0.081	0.678
	1.14 (0.60–2.17)	0.690		
TIS	1.25 (0.67–2.33)	0.492	0.420	0.948
	0.60 (0.30–1.22)	0.155		
ESR1	0.59 (0.31–1.14)	0.112	**0.022**	0.516
	1.23 (0.65–2.38)	0.524		
PGR	0.74 (0.38–1.45)	0.382	**0.043**	0.516
	1.20 (0.65–2.22)	0.561		
HER2	1.16 (0.61–2.22)	0.645	0.818	0.948
	0.73 (0.38–1.41)	0.344		
FOXA1	0.80 (0.41–1.56)	0.519	0.710	0.948
	1.01 (0.54–1.89)	0.987		
AR	0.89 (0.48–1.67)	0.724	0.710	0.948
	0.92 (0.47–1.82)	0.807		
IDO1	1.28 (0.68–2.44)	0.448	0.793	0.948
	0.61 (0.31–1.19)	0.143		
PD-L1	1.03 (0.57–1.89)	0.914	0.745	0.948
	0.78 (0.38–1.59)	0.492		
PD-L2	1.02 (0.56–1.85)	0.956	0.996	0.996
	0.78 (0.39–1.56)	0.485		
B7-H3	1.08 (0.56–2.08)	0.818	0.944	0.996
	0.76 (0.40–1.45)	0.398		
TIGIT	1.33 (0.68–2.56)	0.406	0.113	0.678
	0.61 (0.31–1.22)	0.159		
TGF beta	0.83 (0.44–1.56)	0.570	0.650	0.948
	0.95 (0.49–1.85)	0.542		
Endothelial cells	1.08 (0.56–2.04)	0.831	0.806	0.948
	0.74 (0.38–1.41)	0.352		
CD8+ T-cells	1.06 (0.57–2.00)	0.836	0.843	0.948
	0.76 (0.39–1.52)	0.435		
Cytotoxic cells	1.05 (0.56–2.00)	0.868	0.540	0.948
	0.75 (0.38–1.47)	0.391		
Macrophages	1.18 (0.63–2.22)	0.598	0.528	0.948
	0.66 (0.33–1.32)	0.240		
Mast cells	1.10 (0.56–2.17)	0.787	0.594	0.948
	0.76 (0.41–1.43)	0.405		
Treg	1.12 (0.57–2.17)	0.734	0.223	0.948
	0.77 (0.40–1.47)	0.430		
Proliferation	1.00 (0.49–2.04)	0.997	0.990	0.996
	0.86 (0.47–1.56)	0.624		
Stroma	1.19 (0.62–2.27)	0.602	0.562	0.948
	0.65 (0.34–1.25)	0.194		
APM	1.39 (0.73–2.63)	0.322	**0.029**	0.516
	0.48 (0.22–1.03)	0.060		
Cytotoxicity	1.02 (0.54–1.96)	0.942	0.149	0.766
	0.79 (0.41–1.56)	0.503		
Apoptosis	1.45 (0.79–2.70)	0.237	0.393	0.948
	0.57 (0.28–1.14)	0.109		
Inflammatory chemokines	1.27 (0.67–2.38)	0.472	0.430	0.948
	0.62 (0.31–1.25)	0.184		
p53 mutant-like	1.23 (0.63–2.50)	0.524	0.324	0.948
	0.63 (0.34–1.16)	0.141		
ER signaling	0.85 (0.45–1.61)	0.606	0.441	0.948
	0.93 (0.48–1.79)	0.811		
Differentation	0.68 (0.35–1.33)	0.261	0.470	0.948
	1.20 (0.64–2.27)	0.562		
Claudin-low	1.20 (0.63–2.33)	0.574	0.793	0.948
	0.68 (0.36–1.30)	0.244		
BRCAness	0.99 (0.51–1.89)	0.967	0.551	0.948
	0.84 (0.44–1.59)	0.592		
HRD	0.79 (0.40–1.56)	0.490	0.983	0.996
	1.03 (0.56–1.92)	0.921		
PD-1	1.06 (0.57–2.00)	0.843	0.334	0.948
	0.72 (0.36–1.45)	0.359		

APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, ooestrogen receptor; ESR1, ooestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell

Statistically significant associations are shown in bold.

B

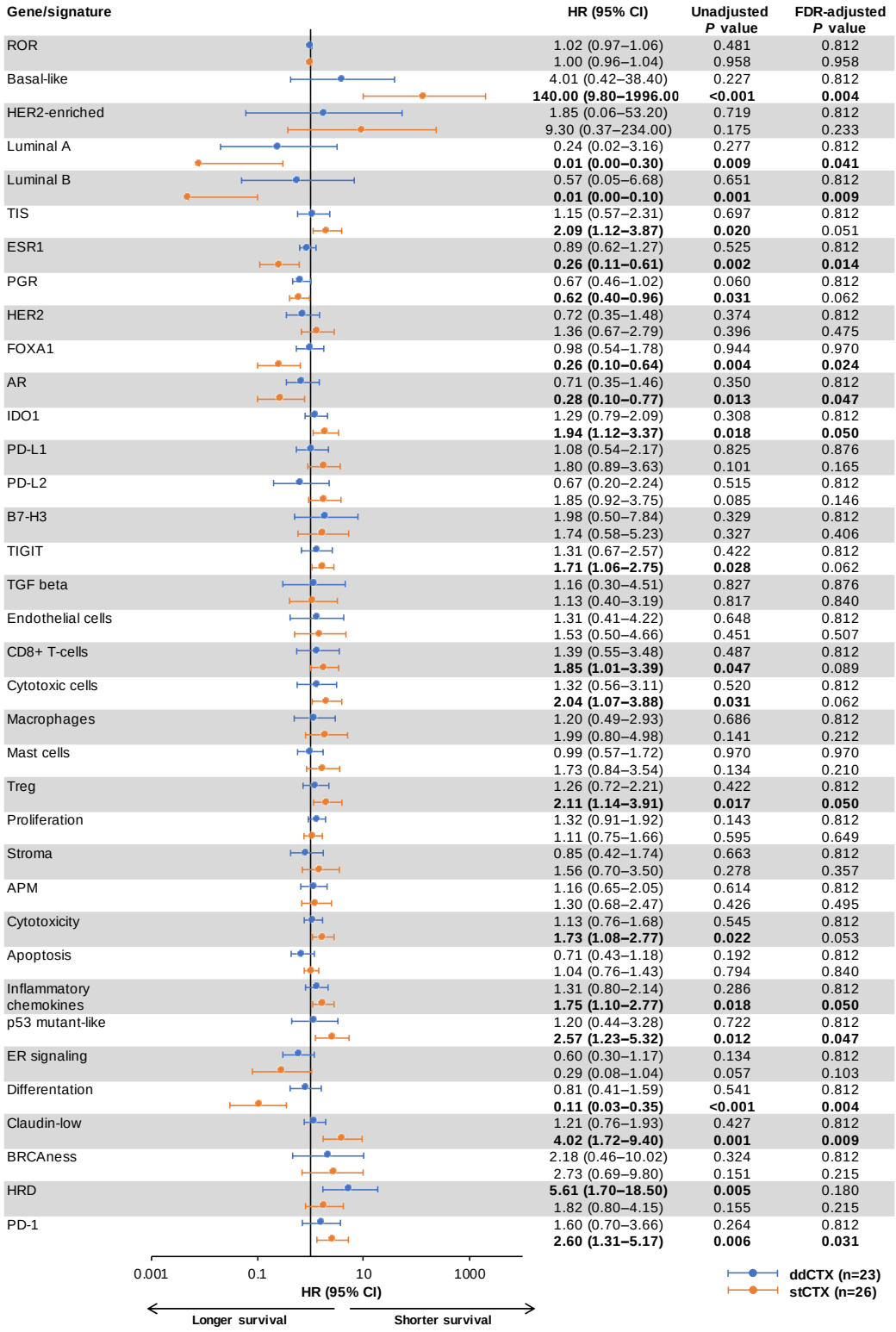


APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell

Statistically significant associations are shown in bold.

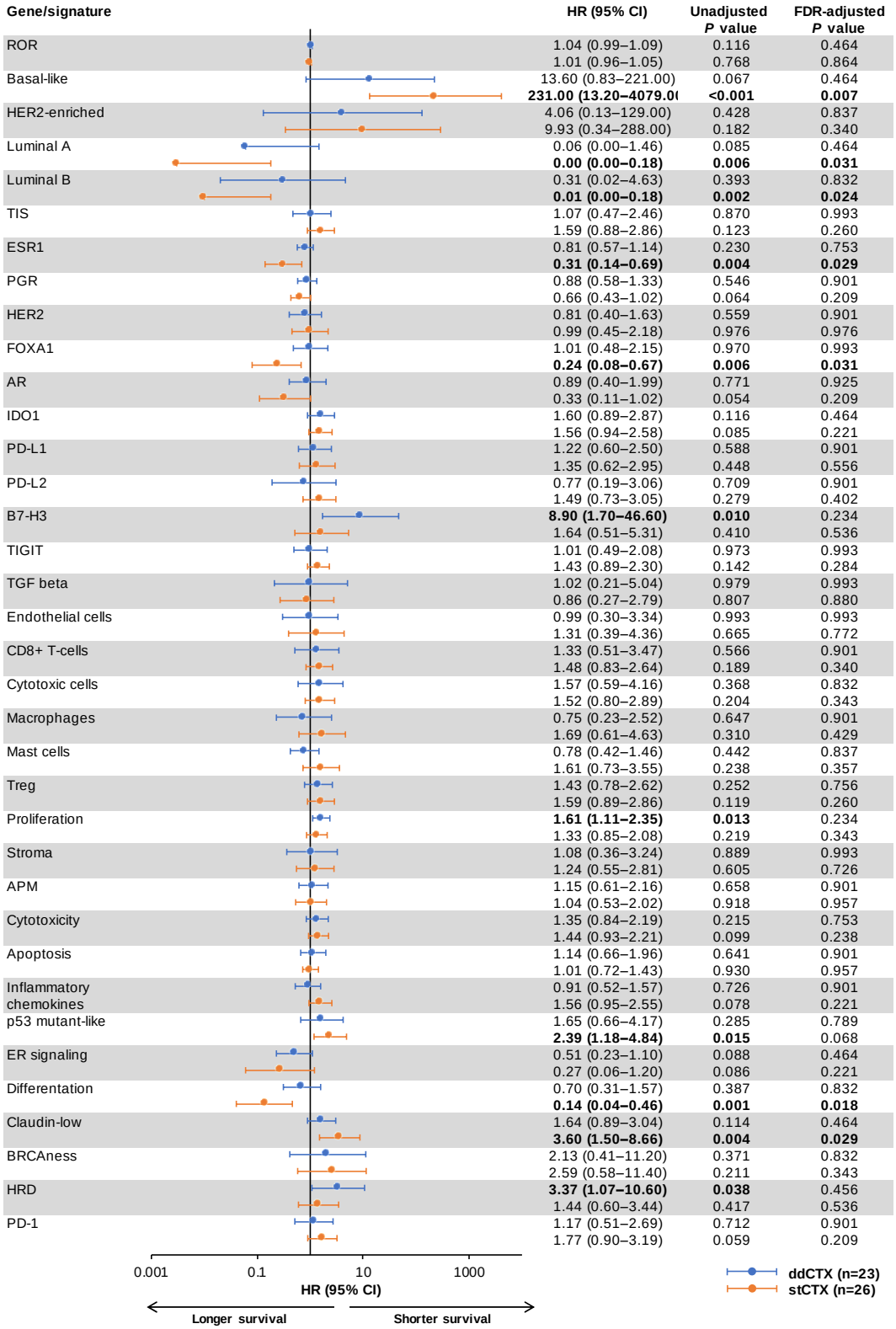
Supplementary Figure 4. Prognostic analysis of genes and signatures in patients with luminal A tumors (*N* = 49) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

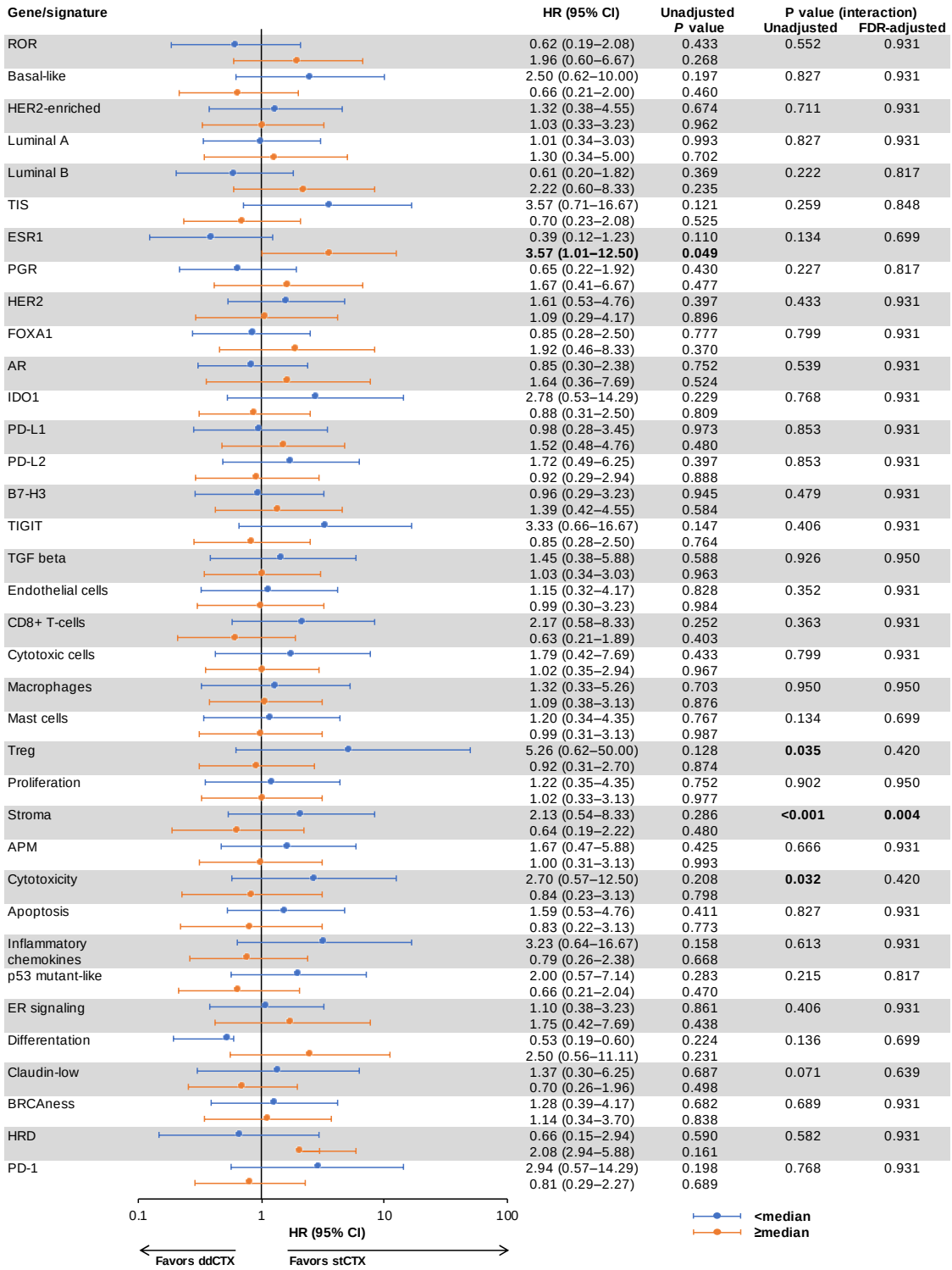
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

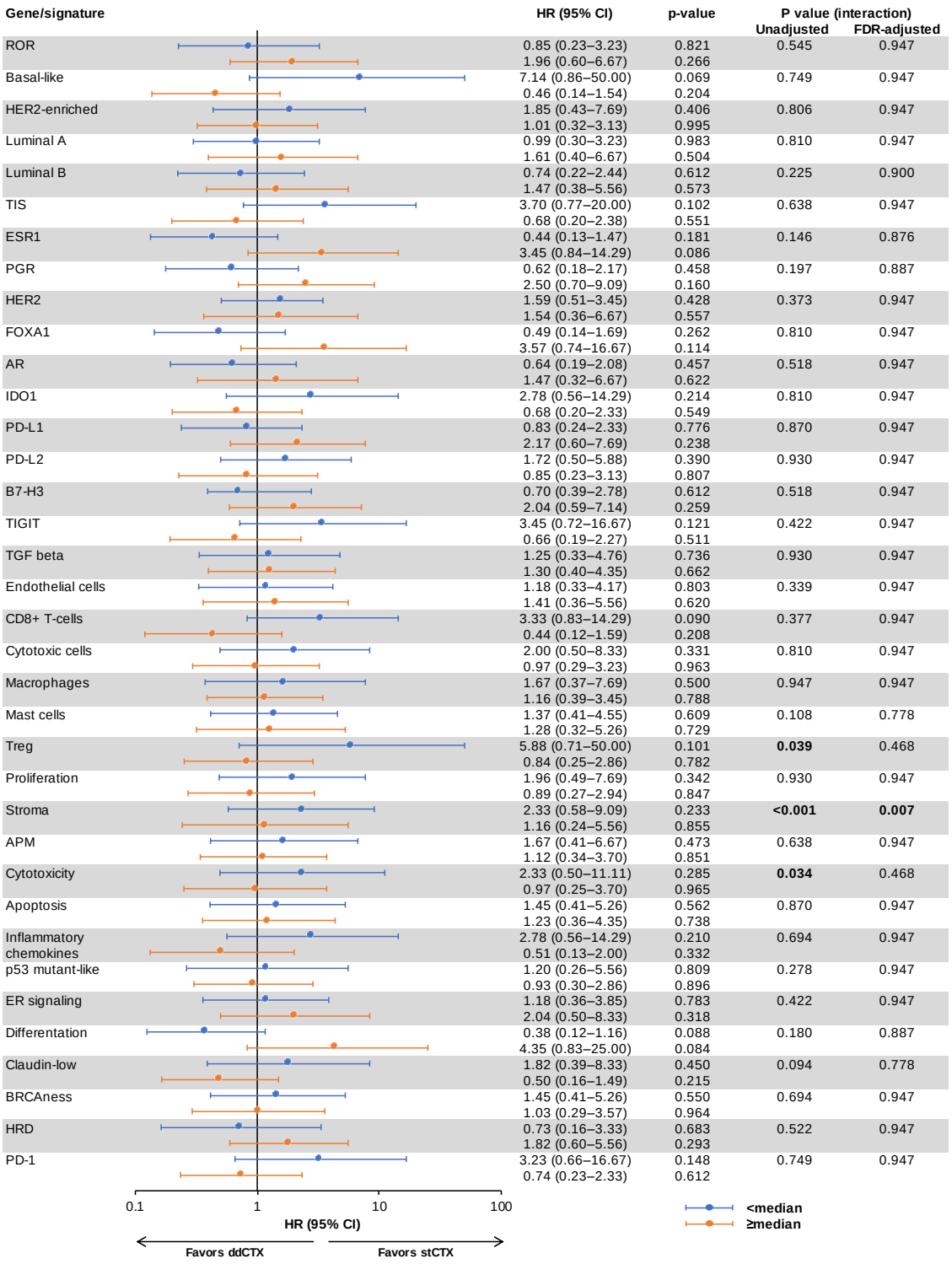
Supplementary Figure 5. Predictive analysis of genes and signatures in patients with luminal A tumors (*N* = 49) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

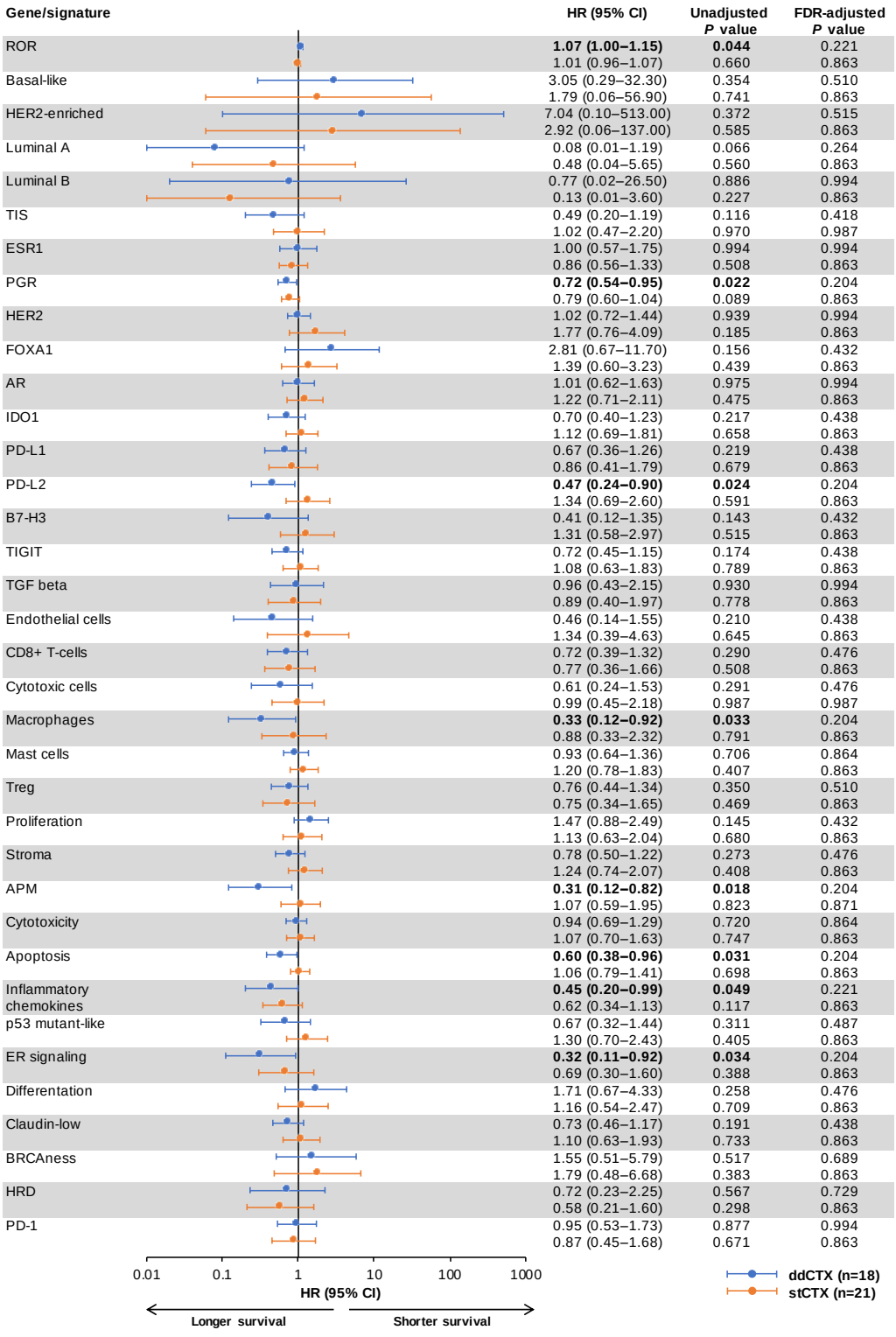
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

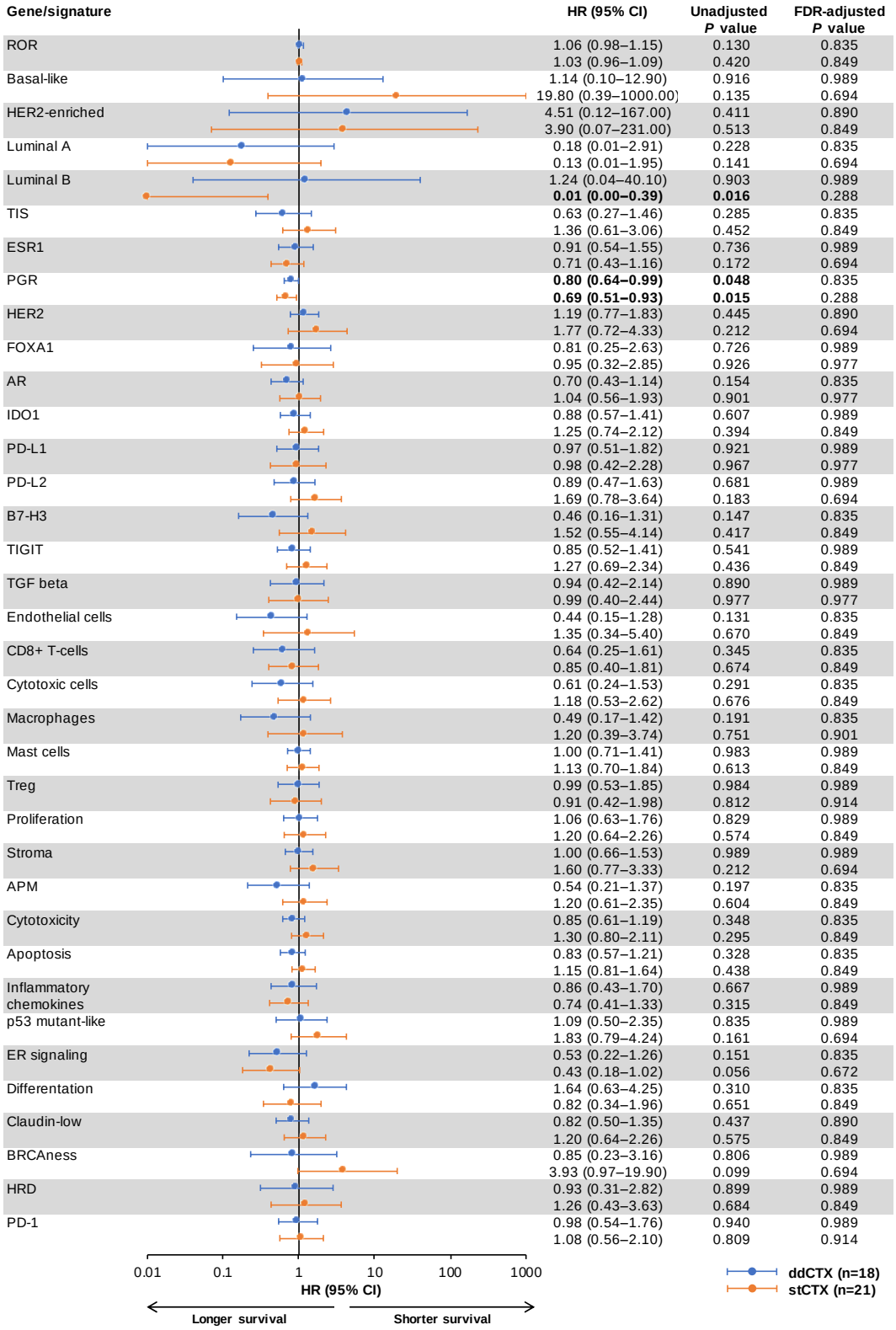
Supplementary Figure 6. Prognostic analysis of genes and signatures in patients with luminal B tumors (*N* = 39) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

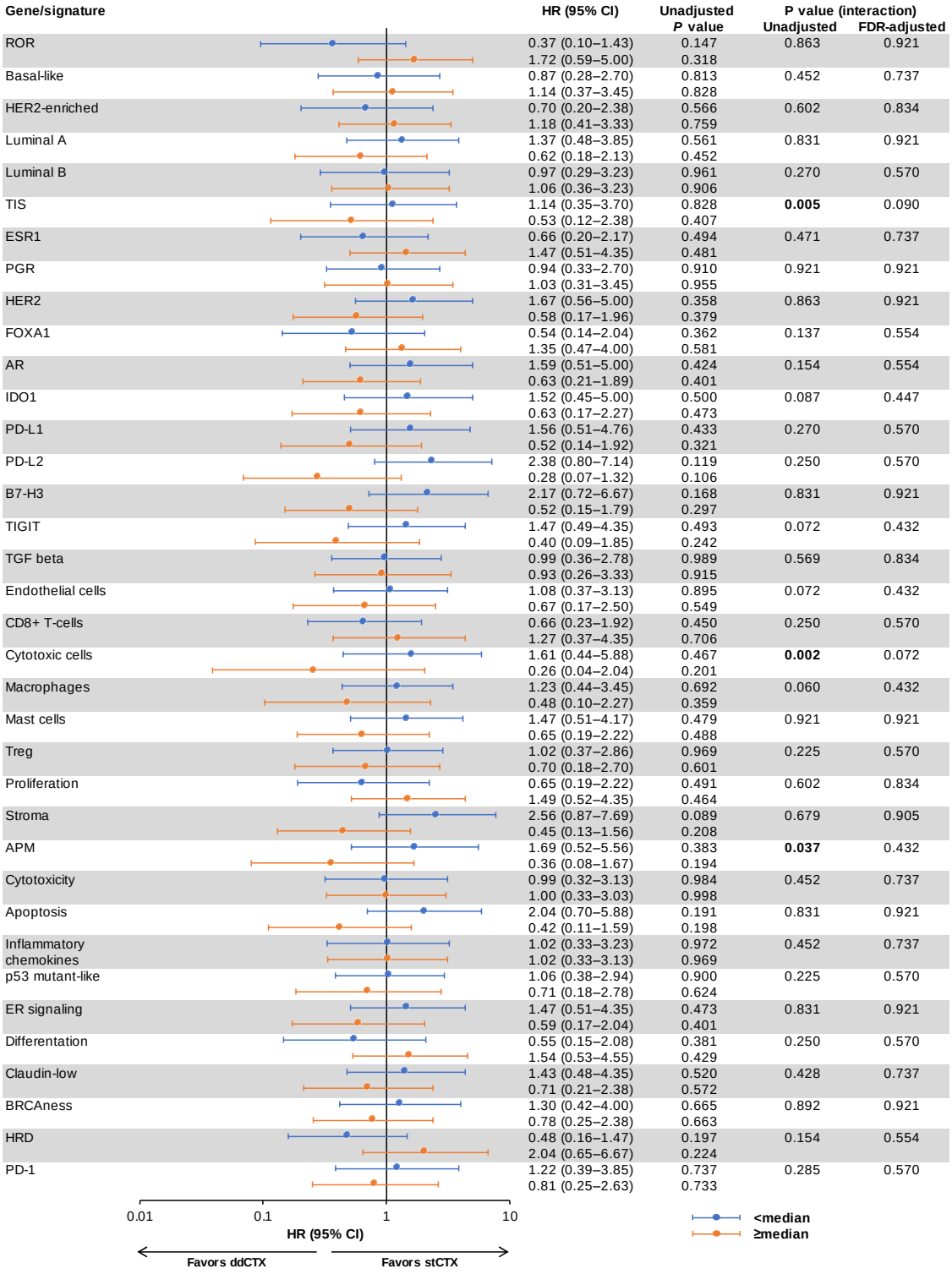
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

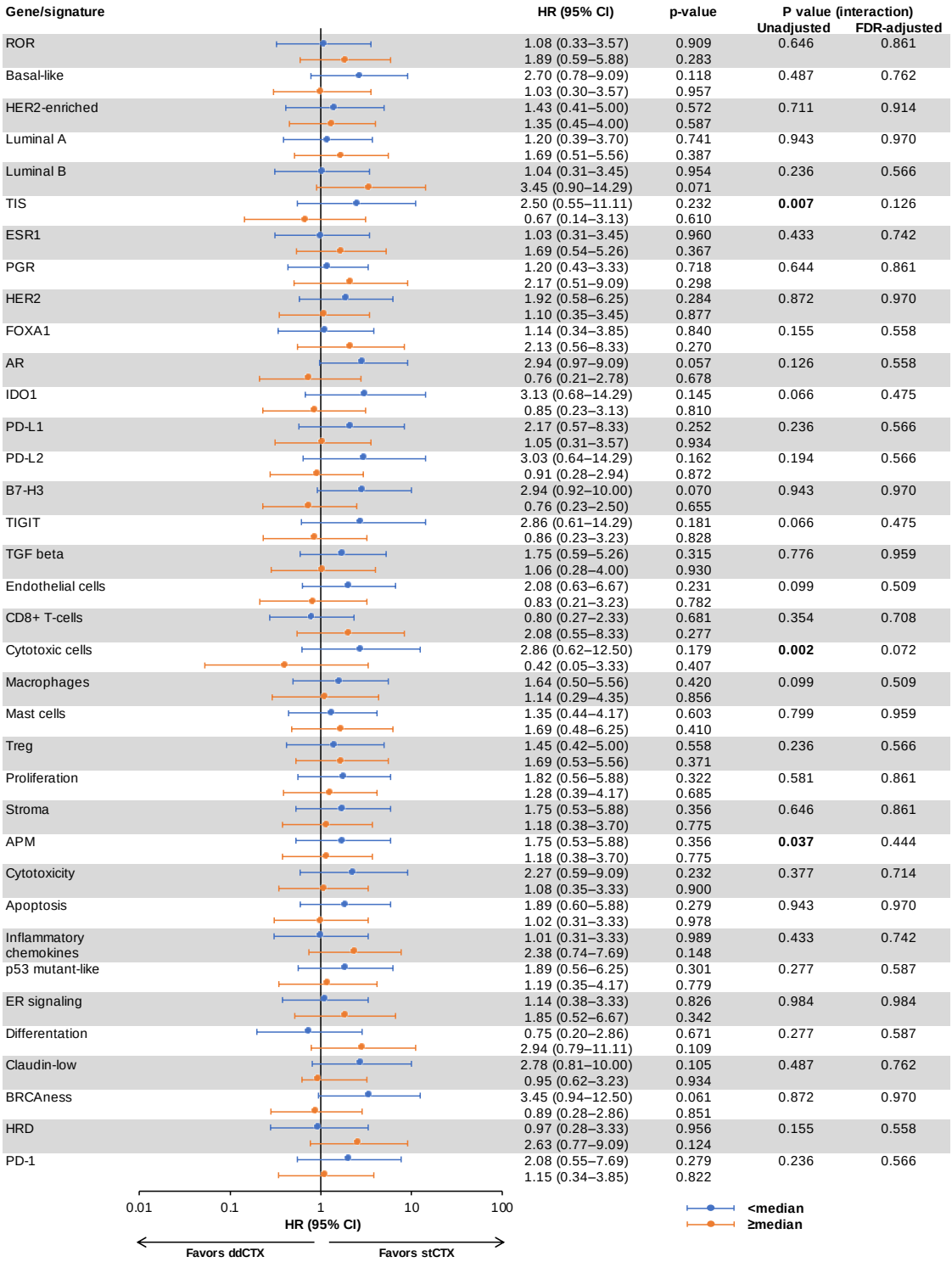
Supplementary Figure 7. Predictive analysis of genes and signatures in patients with luminal B tumors (*N* = 39) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

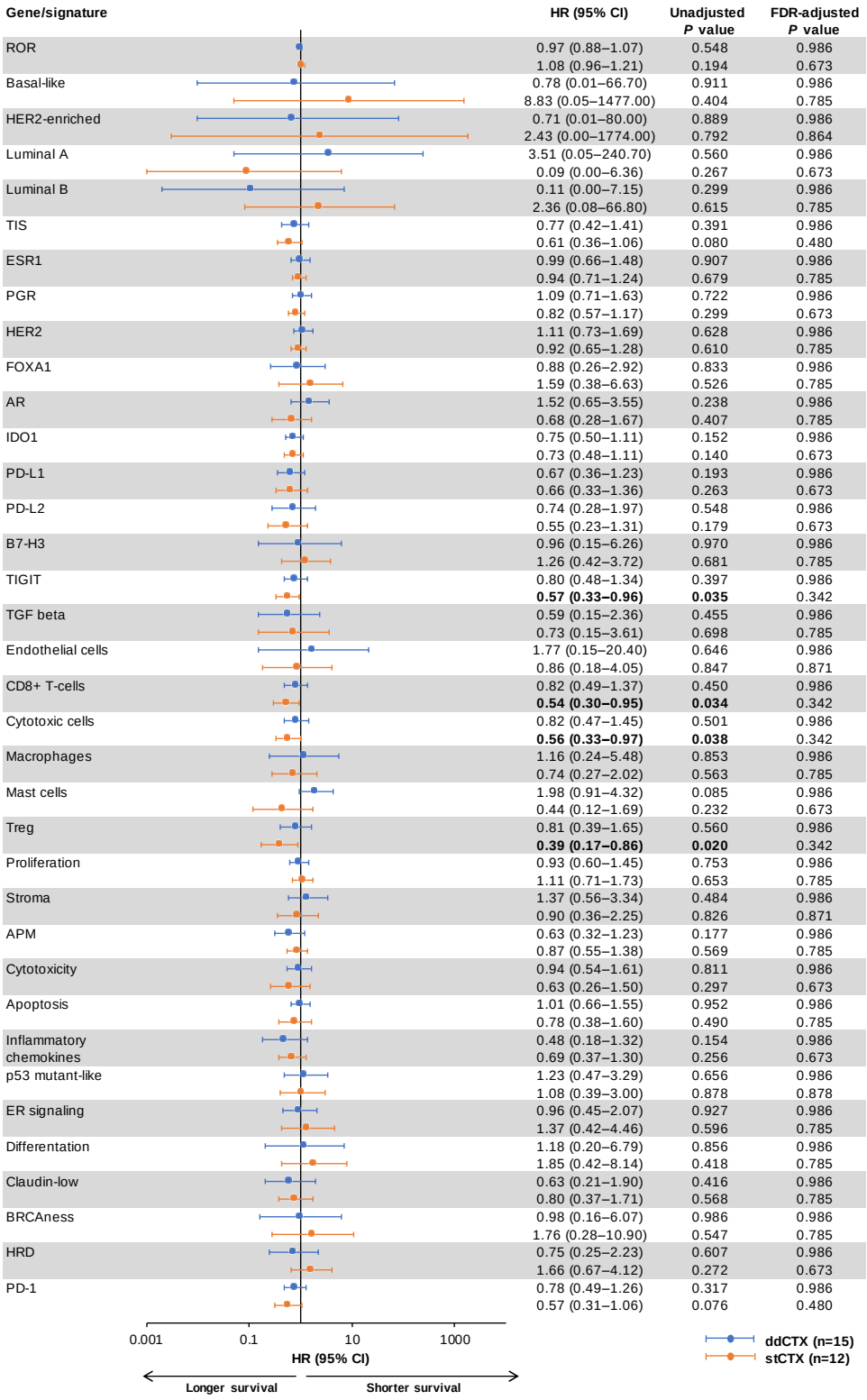
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

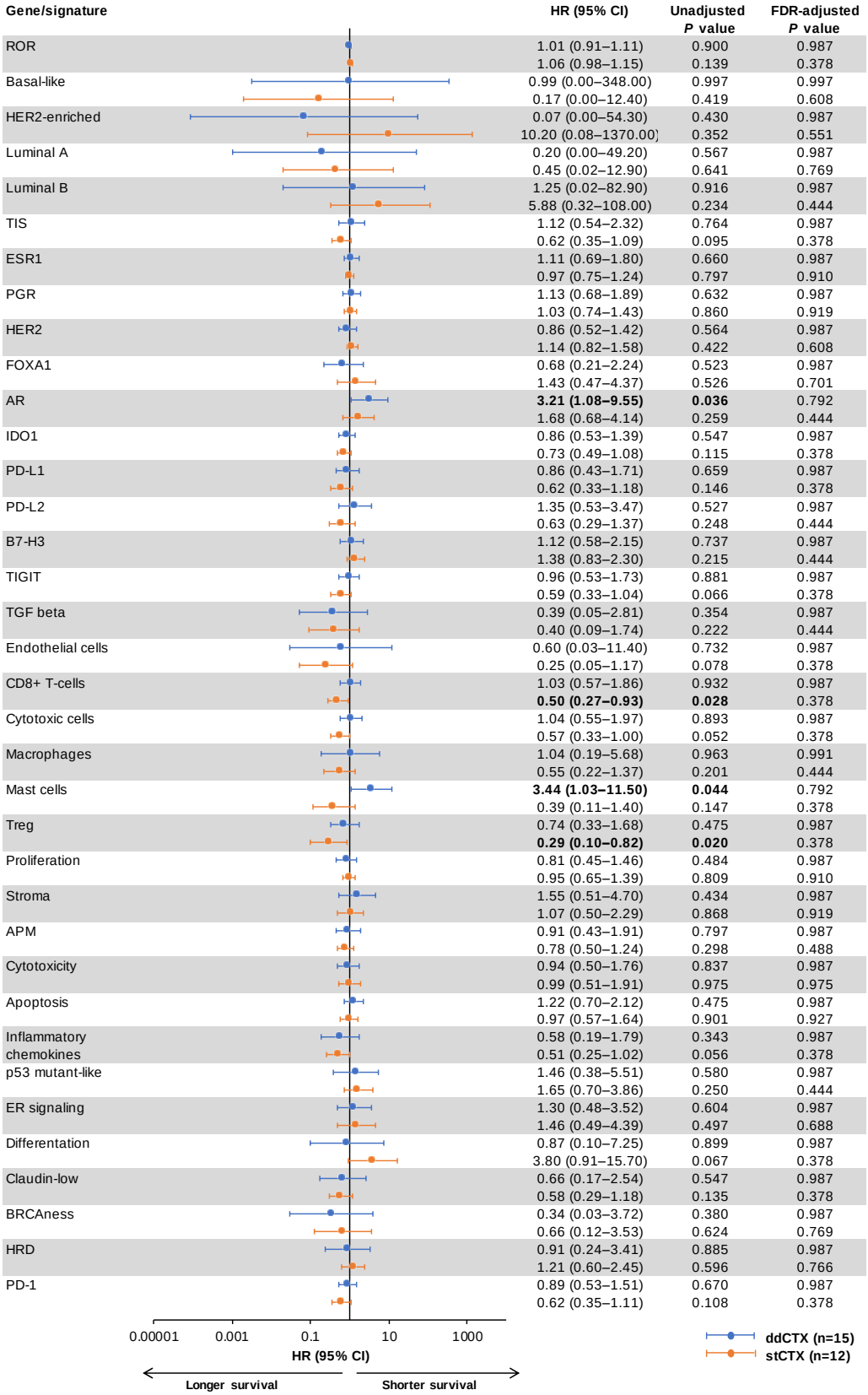
Supplementary Figure 8. Prognostic analysis of genes and signatures in patients with HER2-enriched tumors (*N* = 27) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

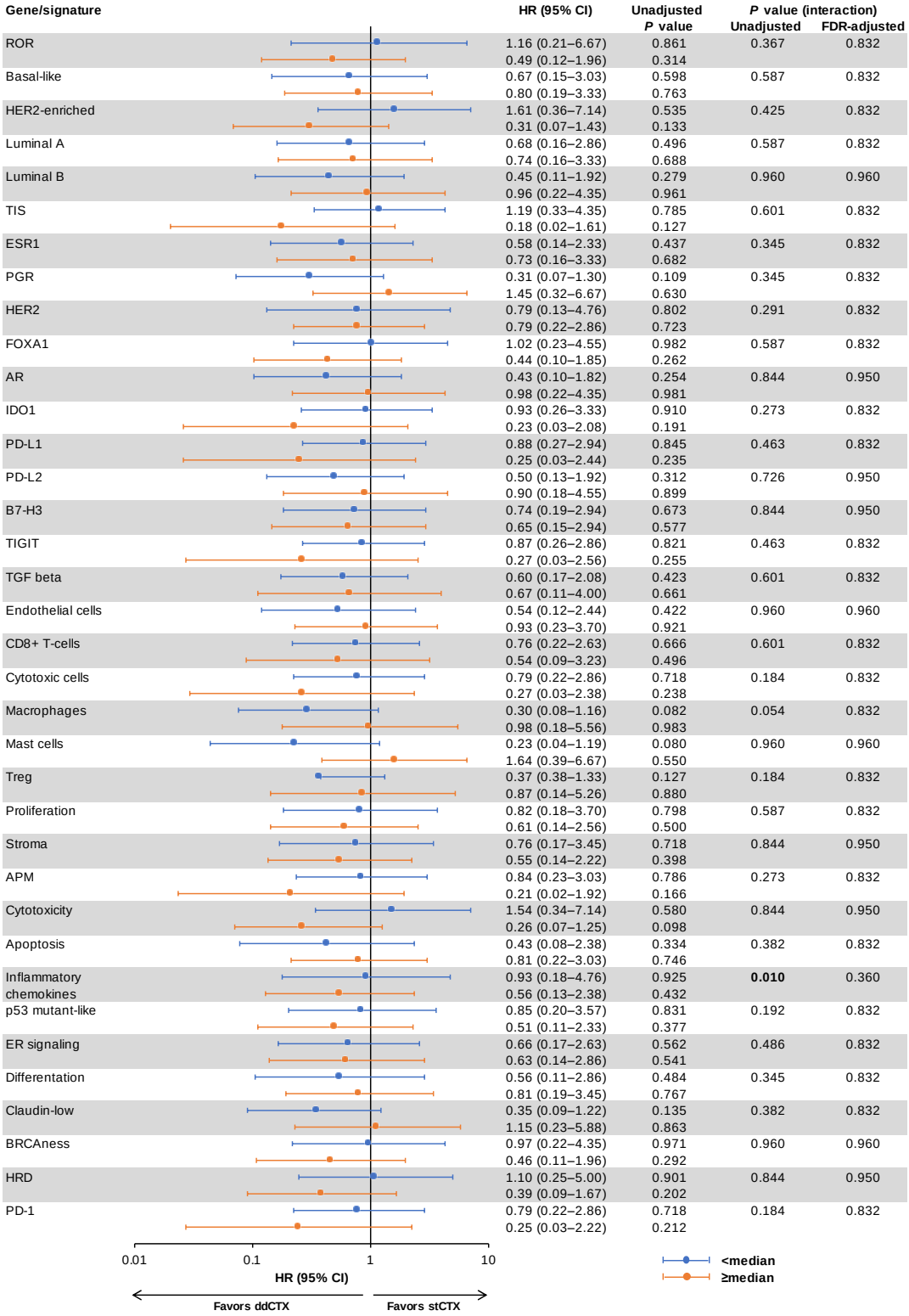
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

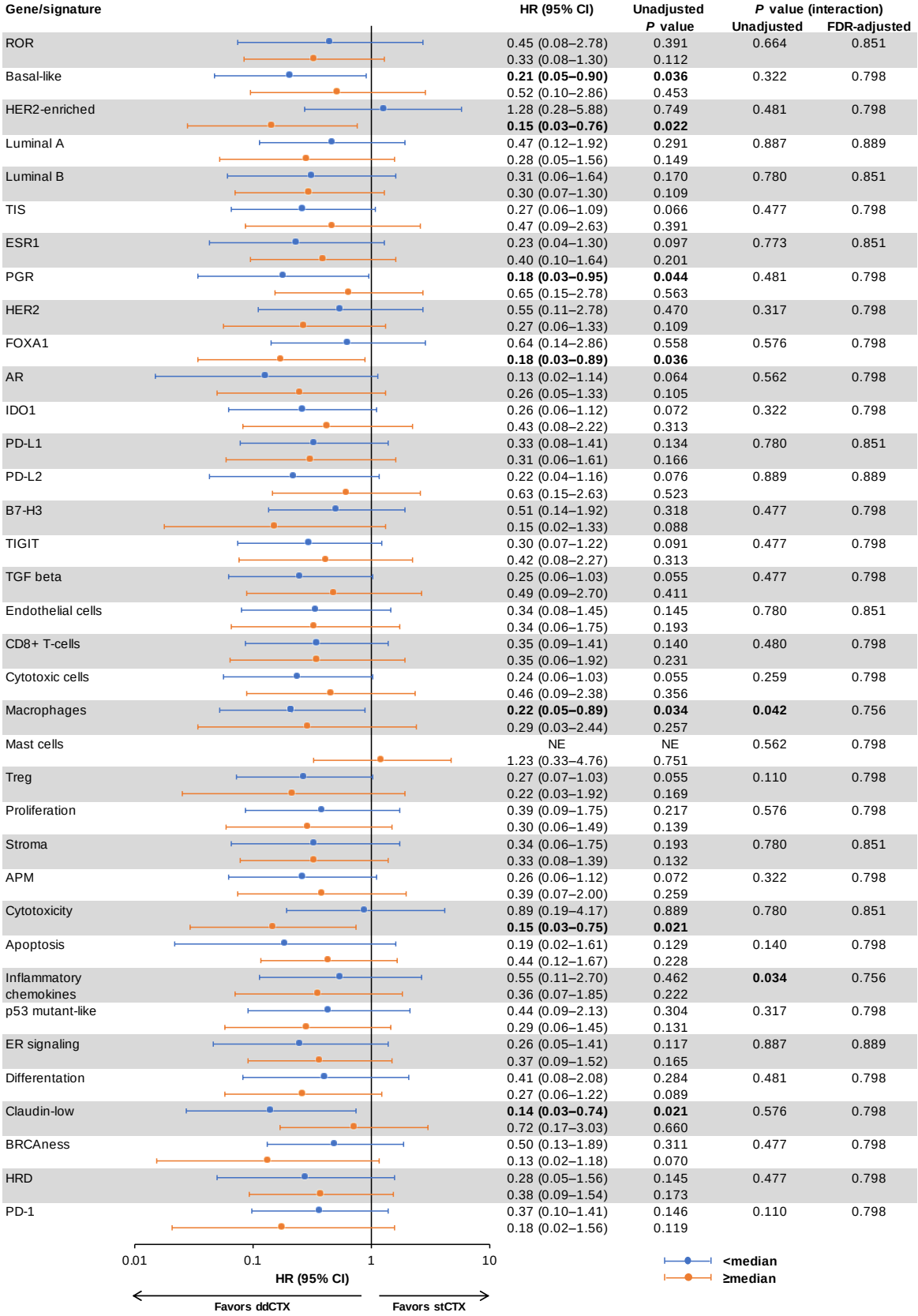
Supplementary Figure 9. Predictive analysis of genes and signatures in patients with HER2-enriched tumors (*N* = 27) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

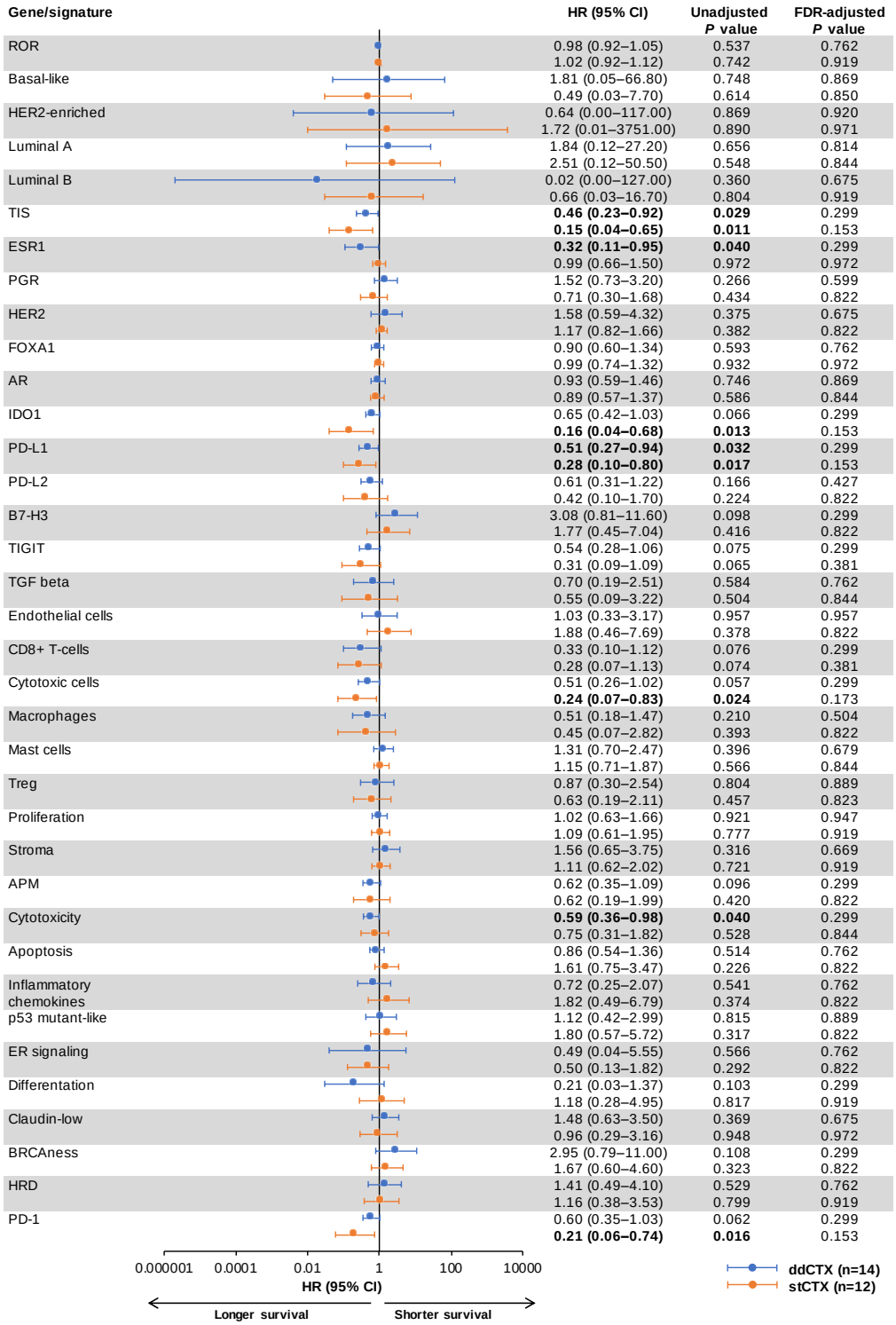
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

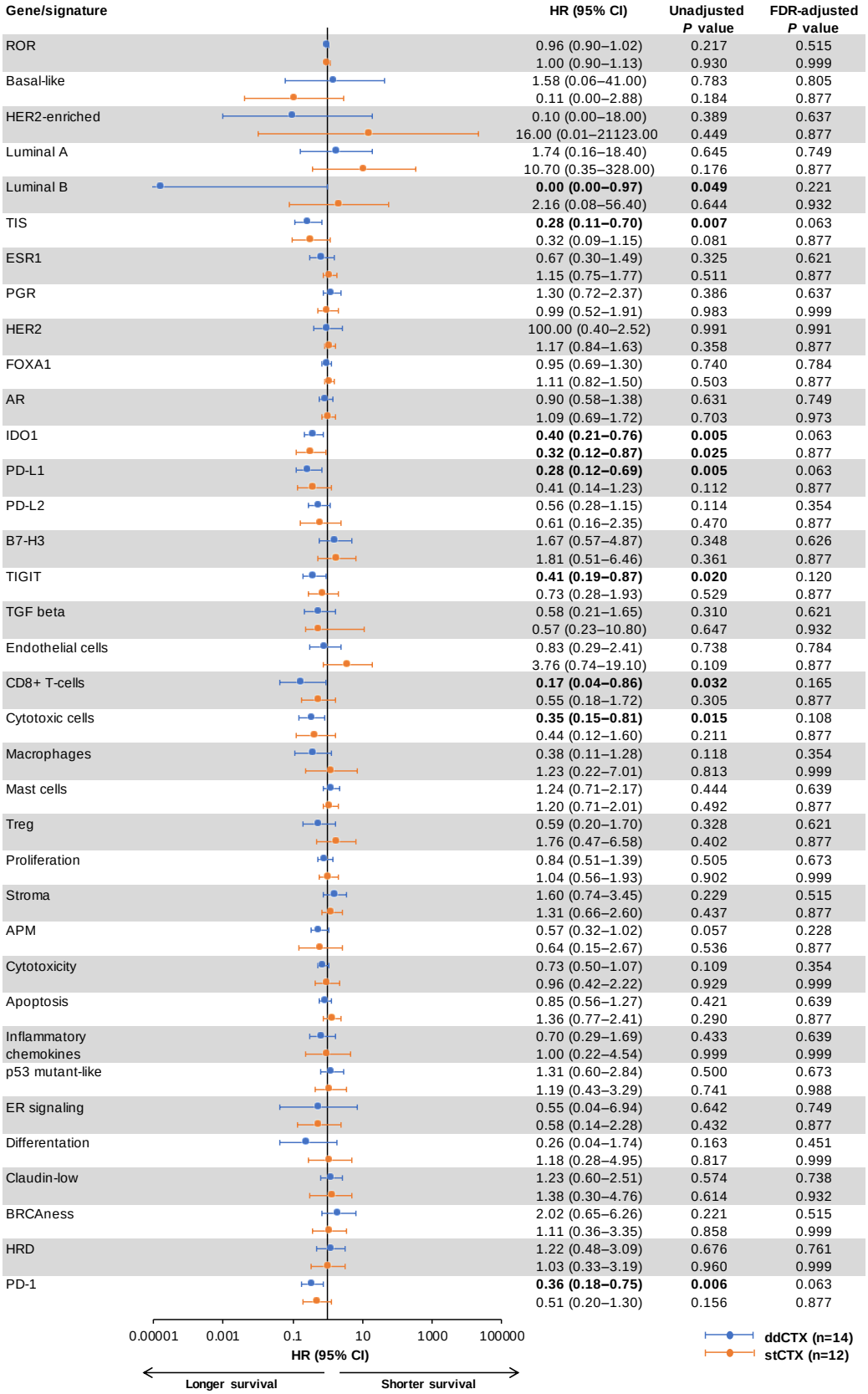
Supplementary Figure 10. Prognostic analysis of genes and signatures according to treatment arm in patients with basal-like tumors (*N* = 26) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

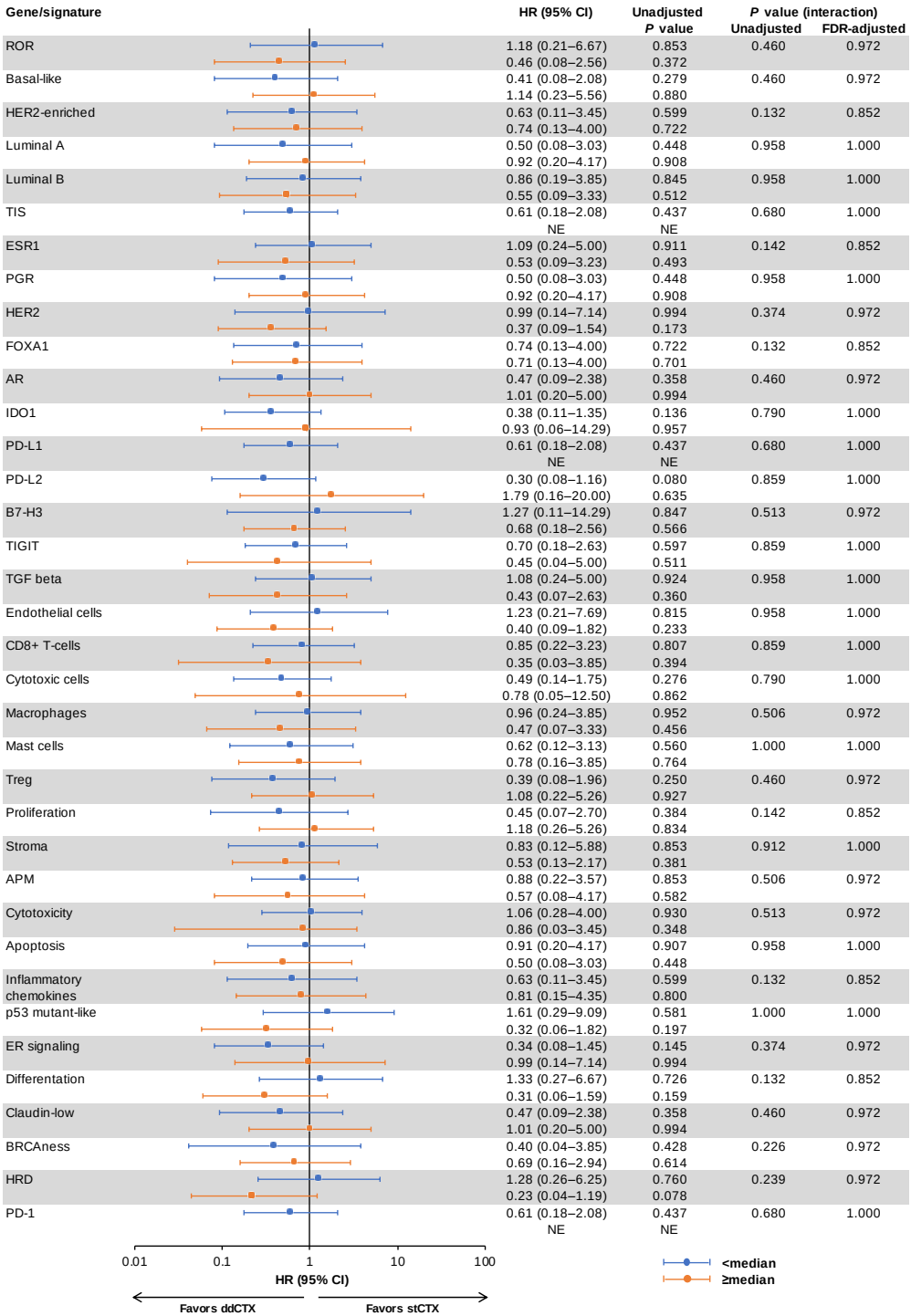
B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

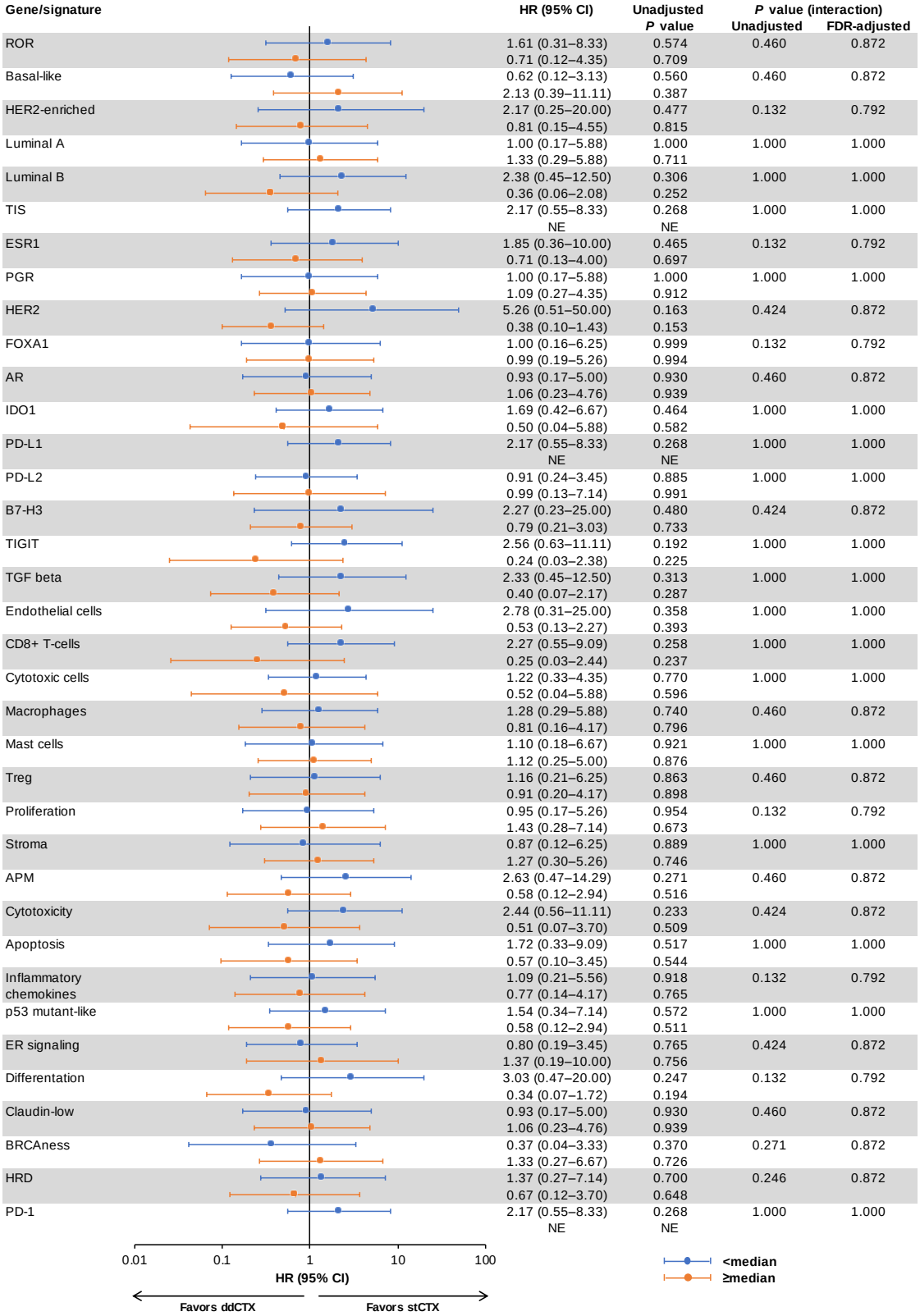
Supplementary Figure 11. Predictive analysis of genes and signatures according to treatment arm in patients with basal-like tumors (*N* = 26) for (A) DFS and (B) OS.

A



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.

B



APM, antigen processing machinery; AR, androgen receptor; BRCA, breast cancer susceptibility gene; CI, confidence interval; ddCTX, dose-dense chemotherapy; DFS, disease-free survival; ER, oestrogen receptor; ESR1, oestrogen receptor-1; FDR, false-discovery rate; FOXA1, forkhead box A1; HER2, human epidermal growth factor receptor-2; HR, hazard ratio; IDO1, indoleamine 2,3-dioxygenase-1; HRD, homologous recombination deficiency; IDO1, indoleamine 2,3-dioxygenase-1; OS, overall survival; PD-1, programmed death-1; PD-L1, programmed death-ligand-1; PD-L2, programmed death-ligand-2; PGR, progesterone receptor; ROR, risk of recurrence; stCTX, standard-dosed chemotherapy; TGF, transforming growth factor; TIGIT, T-cell immunoreceptor with immunoglobulin and immunoreceptor tyrosine-based inhibition motif domains; TIS, tumor inflammation signature; Treg, regulatory T-cell
Statistically significant associations are shown in bold.