

Supplementary information

Multi-database transcriptomic screening to identify subtype-selective cell surface targets for development of SNAP-tag based immunotherapeutics

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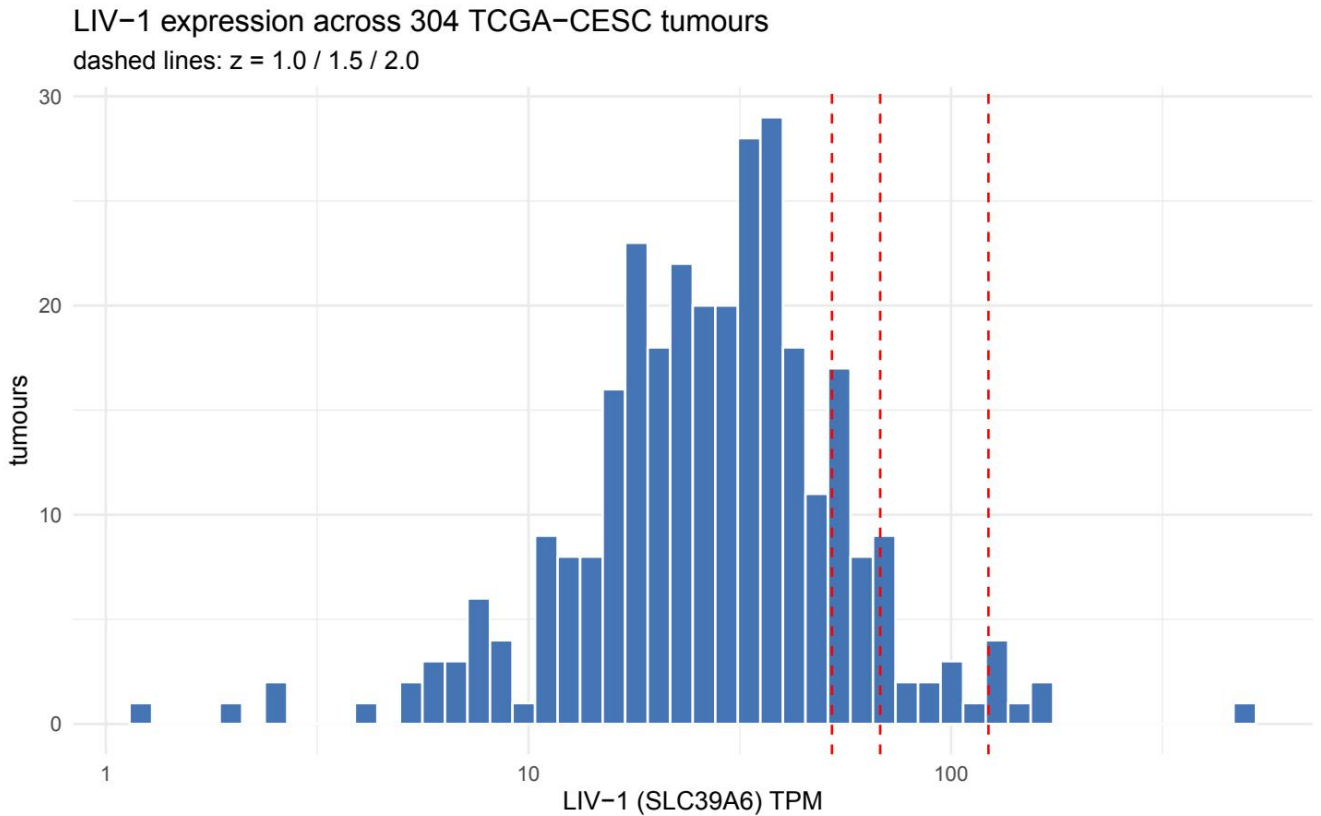


Figure S1. LIV-1 expression distribution across TCGA-CESC tumours. Histogram of LIV-1 (SLC39A6) tumour expression; dashed lines mark the $z \geq 1.0$, 1.5 and 2.0 thresholds used to define the high-expressing subgroup.

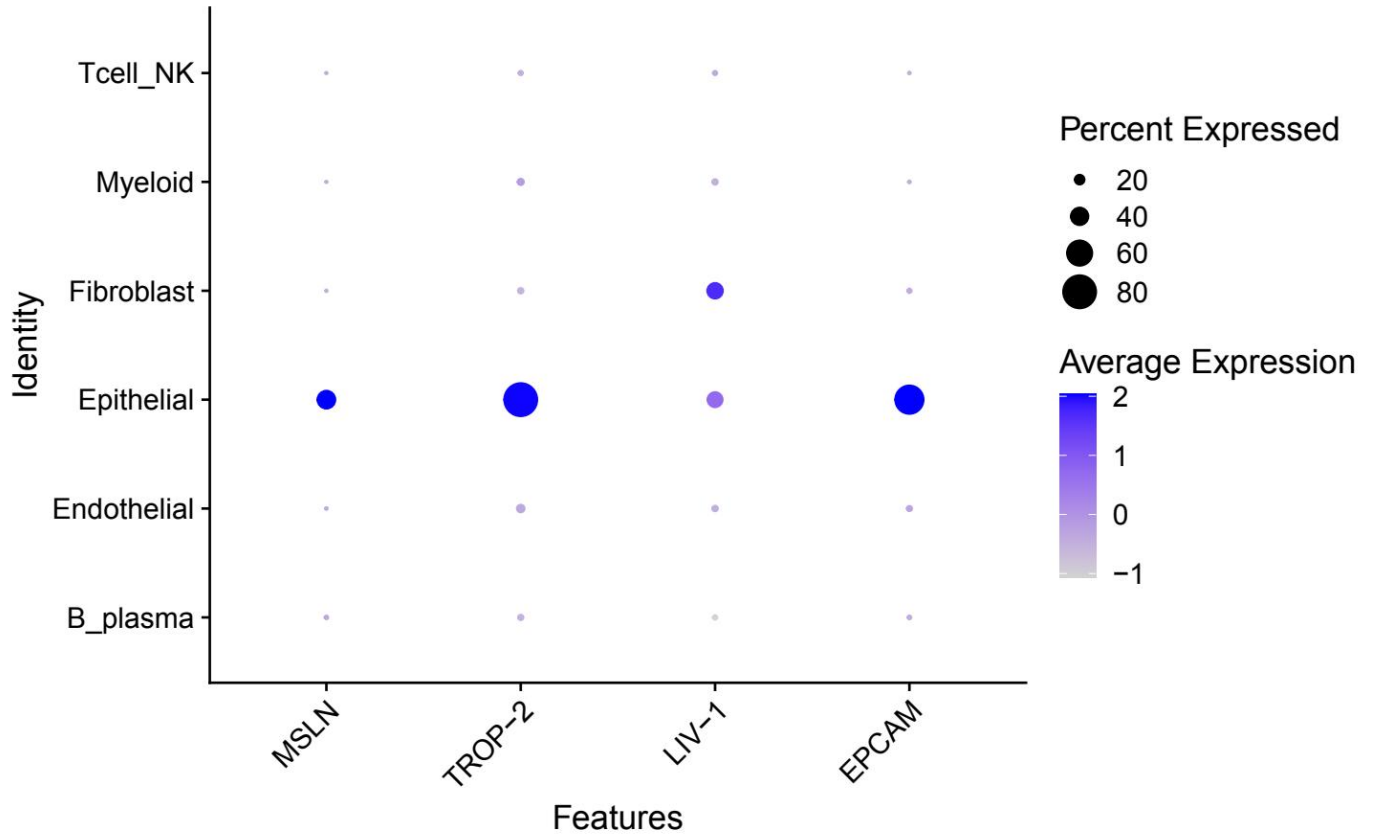


Figure S2. Single-cell expression dot-plot of the validated targets. Mean expression and percent of cells positive for each target across annotated cell types in cervical scRNA-seq (GSE208653).

Table S1. Global overexpression screen: top 30 surface targets in TCGA-CESC. The 30 cell-surface genes passing the global discovery filters, ranked by tumour-vs-normal fold-change (304 TCGA-CESC tumours vs 7,597 GTEx samples across 52 tissues). Non-validated candidates shown by anonymised identifier.

<i>Gene</i>	<i>Tumour log₂</i>	<i>Tumour TPM</i>	<i>Normal log₂</i>	<i>FC (log₂)</i>	<i>% Tumours</i>	<i>Wilcoxon FDR</i>
<i>CSR-FB97DA</i>	5.75	53.7	-3.67	9.42	75.3	1.2e-98
<i>TROP-2</i>	9.01	515.5	0.08	8.93	100.0	7.0e-148
<i>CSR-2E068C</i>	6.76	108.2	-0.22	6.97	100.0	1.8e-149
<i>MSLN</i>	5.49	45.0	-1.44	6.93	86.8	1.1e-123
<i>CSR-6C3866</i>	7.29	156.2	0.56	6.73	100.0	2.7e-177
<i>CSR-606EBC</i>	6.1	68.7	0.03	6.07	97.7	8.2e-168
<i>CSR-25666B</i>	3.61	12.2	-1.77	5.38	94.1	1.4e-151
<i>CSR-A661D0</i>	5.16	35.9	-0.08	5.24	99.0	2.1e-137
<i>EpCAM</i>	6.45	87.3	1.32	5.13	100.0	1.5e-122
<i>CSR-6C64FC</i>	6.04	65.6	0.95	5.09	99.3	8.0e-126
<i>CSR-B9FBE2</i>	4.66	25.3	0.03	4.64	99.3	3.2e-137
<i>CSR-27F664</i>	5.21	36.9	0.58	4.62	99.7	1.4e-155
<i>CSR-E3CEA0</i>	5.48	44.5	1.53	3.95	98.4	7.7e-93
<i>CSR-CA255C</i>	3.08	8.4	-0.62	3.69	95.7	1.2e-112
<i>CSR-AA62BC</i>	7.9	239.5	4.35	3.55	100.0	1.2e-139
<i>CSR-A80B71</i>	6.0	64.0	2.76	3.24	100.0	3.5e-132
<i>CSR-78F76F</i>	4.26	19.2	1.05	3.21	100.0	4.5e-147
<i>CSR-613CFC</i>	4.65	25.2	1.62	3.03	99.7	1.2e-84
<i>CSR-0508C7</i>	5.48	44.7	2.59	2.89	100.0	1.5e-109
<i>CSR-559564</i>	5.86	58.2	3.02	2.84	100.0	2.2e-125
<i>CSR-4DD813</i>	3.27	9.6	0.44	2.83	88.8	1.8e-48
<i>CSR-2DBC31</i>	3.05	8.3	0.37	2.68	97.0	1.9e-104
<i>CSR-7CBD2E</i>	3.85	14.4	1.26	2.59	98.7	4.0e-114
<i>CSR-A22AA4</i>	3.18	9.0	0.67	2.51	97.0	1.5e-67
<i>CSR-D025D8</i>	5.63	49.4	3.25	2.38	100.0	1.2e-86
<i>CSR-6A5781</i>	2.72	6.6	0.51	2.22	91.1	5.7e-89
<i>CSR-3FA3D7</i>	3.37	10.3	1.17	2.2	95.7	1.2e-52
<i>CSR-7E8AA6</i>	5.28	38.8	3.13	2.14	100.0	1.3e-125
<i>CSR-8A7DB4</i>	5.56	47.0	3.49	2.06	100.0	5.7e-83
<i>CSR-DBF43D</i>	2.33	5.0	0.29	2.04	91.1	2.5e-62

Table S2. Tissue-of-origin fold-change for the top candidates (GTEx v10 cervix references). Fold-change of each top candidate (whole TCGA-CESC cohort) against normal ectocervix and normal endocervix (GTEx v10; ectocervix n = 24, endocervix n = 23); 95% CIs by bootstrap. Subtype-stratified fold-changes are given in Supplementary Table S3.

<i>Gene</i>	<i>FC vs. ectocervix</i>	<i>95% CI</i>	<i>FC vs. endocervix</i>	<i>95% CI</i>
<i>CSR-FB97DA</i>	0.03	[-1.36, 7.72]	9.72	[9.32, 10.53]
<i>CSR-A661D0</i>	-0.99	[-1.80, 7.00]	6.94	[6.08, 7.53]
<i>TROP-2</i>	0.04	[-1.26, 5.66]	6.11	[4.49, 6.93]
<i>MSLN</i>	5.72	[4.35, 6.38]	6.04	[2.57, 6.94]
<i>CSR-2E068C</i>	0.79	[-0.07, 5.13]	5.23	[4.46, 6.98]
<i>CSR-25666B</i>	2.65	[1.81, 4.54]	5.11	[4.44, 5.72]
<i>CSR-27F664</i>	3.43	[2.87, 5.78]	5.72	[4.28, 6.50]
<i>CSR-606EBC</i>	4.12	[3.21, 5.30]	5.35	[4.79, 6.09]
<i>EpCAM</i>	4.51	[3.64, 5.47]	4.29	[2.77, 7.33]
<i>CSR-78F76F</i>	0.99	[-0.23, 3.83]	4.11	[2.90, 5.85]
<i>CSR-3FA3D7</i>	3.94	[3.49, 4.48]	3.28	[2.41, 4.04]
<i>CSR-6C3866</i>	3.09	[2.97, 3.62]	3.35	[3.20, 3.89]
<i>CSR-D025D8</i>	1.62	[0.86, 3.27]	3.41	[2.77, 3.88]
<i>CSR-6C64FC</i>	-0.07	[-0.86, 2.36]	3.03	[2.23, 3.57]
<i>CSR-2DBC31</i>	1.65	[1.28, 2.42]	2.02	[1.59, 2.24]
<i>CSR-B9FBE2</i>	1.03	[0.45, 2.25]	2.67	[1.66, 2.94]
<i>CSR-613CFC</i>	1.22	[0.83, 1.89]	1.63	[1.38, 2.09]
<i>CSR-AA62BC</i>	1.74	[1.29, 2.15]	2.38	[1.93, 2.80]
<i>CSR-6A5781</i>	2.84	[1.61, 3.33]	1.66	[1.28, 2.05]
<i>CSR-559564</i>	2.21	[1.84, 2.50]	2.03	[1.73, 2.37]
<i>CSR-7E8AA6</i>	0.8	[0.49, 1.53]	1.27	[0.64, 1.42]
<i>CSR-A22AA4</i>	1.76	[1.36, 2.49]	2.17	[1.86, 2.31]
<i>CSR-E3CEA0</i>	0.88	[0.38, 1.29]	2.07	[1.40, 2.61]
<i>CSR-CA255C</i>	0.71	[-0.42, 1.36]	1.2	[0.21, 1.57]
<i>CSR-7CBD2E</i>	1.01	[0.90, 1.34]	1.32	[1.11, 1.49]
<i>CSR-0508C7</i>	-0.72	[-1.78, 0.44]	0.9	[0.42, 1.09]
<i>CSR-DBF43D</i>	0.79	[0.34, 1.12]	0.86	[0.59, 1.28]
<i>CSR-8A7DB4</i>	-0.29	[-0.45, -0.07]	-0.43	[-0.65, -0.23]
<i>CSR-4DD813</i>	-0.48	[-0.96, -0.28]	-0.01	[-0.71, 0.17]
<i>CSR-A80B71</i>	0.18	[-0.17, 0.33]	-0.4	[-0.59, -0.28]

Table S3. Histology-stratified overexpression for all candidate surface genes. Subtype-resolved fold-change for every candidate that passed the global screen. TCGA-CESC tumours stratified by histology, each subtype compared to its cell of origin (SCC vs ectocervix; adenocarcinoma vs endocervix; GTEx v10). Non-validated candidates shown by anonymised identifier.

<i>Candidate</i>	<i>SCC TPM</i>	<i>Adeno TPM</i>	<i>% SCC+</i>	<i>% Adeno+</i>	<i>log₂FC SCC/ecto</i>	<i>95% CI SCC</i>	<i>log₂FC adeno/endo</i>	<i>95% CI adeno</i>	<i>log₂FC SCC/adeno</i>	<i>p (SCC vs adeno)</i>
<i>MSLN</i>	33.1	248.8	85.6	95.7	5.28	[3.81, 5.94]	8.51	[4.12, 9.27]	-2.91	6.1e-07
<i>CSR- 3FA3D7</i>	12.5	4.0	97.5	87.0	4.22	[3.77, 4.90]	1.91	[0.97, 2.77]	1.64	7.5e-07
<i>EpCAM</i>	70.9	529.6	100.0	100.0	4.21	[3.39, 5.41]	6.9	[5.37, 10.18]	-2.9	6.4e-23
<i>CSR- 606EBC</i>	72.6	58.4	99.6	89.1	4.2	[3.29, 5.38]	5.12	[4.56, 5.87]	0.31	2.5e-03
<i>CSR- 27F664</i>	37.7	33.9	100.0	100.0	3.46	[2.93, 5.81]	5.6	[4.32, 6.47]	0.15	3.5e-01
<i>CSR- 6C3866</i>	178.3	44.6	100.0	100.0	3.28	[3.13, 3.92]	1.54	[1.39, 2.08]	2.0	1.1e-15
<i>CSR- 6A5781</i>	6.9	6.6	90.5	95.7	2.91	[1.68, 3.40]	1.67	[1.29, 2.06]	0.06	5.9e-01
<i>CSR- 25666B</i>	14.3	4.5	95.5	87.0	2.87	[2.03, 4.76]	3.68	[3.00, 4.07]	1.65	1.2e-09
<i>CSR- 559564</i>	60.4	50.5	100.0	100.0	2.26	[1.90, 2.55]	1.83	[1.53, 2.15]	0.26	6.3e-01
<i>CSR- A22AA4</i>	10.2	5.0	97.5	95.7	1.93	[1.53, 2.66]	1.33	[1.02, 1.58]	1.01	1.7e-05
<i>CSR- AA62BC</i>	261.9	178.5	100.0	100.0	1.87	[1.42, 2.24]	1.96	[1.51, 2.38]	0.55	5.2e-03
<i>CSR- 2DBC31</i>	9.0	5.8	97.9	95.7	1.78	[1.36, 2.54]	1.51	[1.08, 1.73]	0.64	9.5e-03
<i>CSR- D025D8</i>	52.3	34.8	100.0	100.0	1.7	[0.94, 3.36]	2.9	[1.89, 3.37]	0.59	9.3e-04
<i>CSR- 613CFC</i>	27.9	16.6	100.0	100.0	1.37	[0.98, 1.91]	1.03	[0.77, 1.48]	0.75	8.8e-03
<i>CSR- B9FBE2</i>	25.5	24.9	99.2	100.0	1.04	[0.46, 2.26]	2.64	[1.84, 3.02]	0.04	9.8e-01
<i>CSR- 78F76F</i>	19.0	20.4	100.0	100.0	0.98	[-0.24, 3.84]	4.21	[2.99, 5.96]	-0.11	5.4e-01
<i>CSR- 7CBD2E</i>	14.1	17.8	98.4	100.0	0.98	[0.87, 1.22]	1.62	[1.41, 1.79]	-0.33	1.5e-01
<i>CSR- CA255C</i>	9.5	5.5	96.3	95.7	0.88	[-0.17, 1.53]	0.6	[-0.32, 0.96]	0.78	3.8e-04
<i>CSR- 7E8AA6</i>	39.2	39.3	100.0	100.0	0.81	[0.50, 1.50]	1.29	[0.66, 1.34]	0.0	7.0e-01
<i>CSR- 2E068C</i>	108.1	108.6	100.0	100.0	0.79	[-0.05, 5.48]	5.23	[4.46, 6.98]	-0.01	8.9e-01
<i>CSR- DBF43D</i>	4.8	5.5	92.6	89.1	0.72	[0.27, 1.08]	1.0	[0.72, 1.38]	-0.2	7.6e-01
<i>CSR- FB97DA</i>	83.6	0.1	89.7	4.3	0.67	[-0.72, 8.36]	0.43	[0.06, 1.25]	9.93	3.4e-24
<i>CSR- E3CEA0</i>	38.3	93.3	98.8	97.8	0.66	[0.16, 1.18]	3.13	[2.63, 3.45]	-1.29	2.8e-05

<i>TROP-2</i>	596.8	218.3	100.0	100.0	0.25	[-0.99, 5.12]	4.88	[3.25, 5.70]	1.45	8.0e-11
<i>CSR-A80B71</i>	64.0	62.2	100.0	100.0	0.18	[-0.17, 0.33]	-0.44	[-0.63, -0.32]	0.04	4.2e-01
<i>CSR-6C64FC</i>	76.1	33.8	99.6	97.8	0.14	[-0.65, 2.48]	2.08	[1.70, 2.62]	1.17	3.6e-08
<i>CSR-8A7DB4</i>	51.8	25.7	100.0	100.0	-0.15	[-0.31, 0.05]	-1.3	[-1.52, -1.11]	1.01	3.6e-08
<i>CSR-4DD813</i>	11.3	1.1	96.3	54.3	-0.25	[-0.74, 0.02]	-3.15	[-3.41, -2.98]	3.38	8.7e-14
<i>CSR-0508C7</i>	52.4	19.7	100.0	100.0	-0.49	[-1.55, 0.67]	-0.28	[-0.76, -0.09]	1.41	9.9e-08
<i>CSR-A661D0</i>	45.2	12.4	99.6	97.8	-0.65	[-1.47, 7.05]	5.41	[4.55, 5.97]	1.87	1.4e-12

Table S4. LIV-1 high-subgroup sensitivity to the z-score threshold. The LIV-1-high subgroup fold-change recomputed across z-score thresholds from 0.5 to 2.5. $z \geq 1.5$ used for primary reporting. Permutation p from 10,000 random draws matched to subgroup size (seed 42); $z \geq 2.5$ yielded a single tumour and no stable estimate.

<i>z threshold</i>	<i>n high-expressing</i>	<i>% cohort</i>	<i>Subgroup median TPM</i>	<i>log₂FC vs normal</i>	<i>95% CI</i>	<i>Permutation p</i>
0.5	85	28.0	55.2	1.92	[1.76, 1.98]	0.0
1.0	41	13.5	69.0	2.24	[2.13, 2.44]	0.0
1.5	14	4.6	122.7	3.07	[2.81, 3.29]	0.0
2.0	8	2.6	137.9	3.24	[3.07, 3.48]	0.0
2.5	1	nan	nan	nan	nan	nan

Table S5. Human Protein Atlas immunohistochemistry for the validated targets. Protein-level staining intensity in normal cervical epithelium and the distribution of staining intensities across cervical-cancer patients (HPA v25.1). H/M/L/N = patients staining High/Medium/Low/Not detected.

<i>Target</i>	<i>Normal ectocervix (squamous)</i>	<i>Normal endocervix (glandular)</i>	<i>Cervical cancer staining (H/M/L/N)</i>	<i>% cancers Medium/High</i>
<i>MSLN</i>	Low	Low	H0/M3/L4/N5	25
<i>TROP-2</i>	Medium	Not detected	H0/M5/L2/N4	45
<i>EpCAM</i>	Not detected	Low	H2/M2/L4/N3	36
<i>LIV-1</i>	Low	Low	H0/M0/L5/N7	0

Table S6. Single-cell expression across cell types and epithelial compartments (GSE208653). Mean expression (percent positive) of each target by major cell type (upper panel) and in malignant, HSIL, normal epithelial and non-epithelial compartments (lower panel). Cervical scRNA-seq (4 normal, 2 HSIL, 2 SCC, 1 adenocarcinoma; 10x Genomics), Seurat v5.

<i>Target</i>	<i>B_plasma</i>	<i>Endothelial</i>	<i>Epithelial</i>	<i>Fibroblast</i>	<i>Myeloid</i>	<i>Tcell_NK</i>
<i>MSLN</i>	0.03 (4%)	0.02 (2%)	0.56 (41%)	0.01 (1%)	0.01 (1%)	0.02 (1%)
<i>TROP-2</i>	0.08 (9%)	0.15 (15%)	1.60 (80%)	0.08 (9%)	0.16 (11%)	0.09 (6%)
<i>LIV-1</i>	0.05 (7%)	0.09 (9%)	0.22 (34%)	0.30 (35%)	0.07 (9%)	0.08 (6%)
<i>EpCAM</i>	0.04 (5%)	0.08 (8%)	1.02 (68%)	0.06 (6%)	0.03 (3%)	0.03 (2%)

<i>Target</i>	<i>Malignant epithelial</i>	<i>HSIL epithelial</i>	<i>Normal epithelial</i>	<i>Non-epithelial</i>
<i>MSLN</i>	0.20 (20%)	1.13 (73%)	0.47 (37%)	0.02 (1%)
<i>TROP-2</i>	2.55 (94%)	0.86 (65%)	1.41 (80%)	0.11 (8%)
<i>LIV-1</i>	0.21 (36%)	0.19 (26%)	0.24 (37%)	0.09 (9%)
<i>EpCAM</i>	0.73 (61%)	1.69 (88%)	0.82 (61%)	0.04 (3%)

Table S7. Single-cell expression by subtype and per patient (GSE197461). Mean expression (percent positive) of each target in tumour epithelium by subtype (upper panel) and per patient (lower panel). Cervical scRNA-seq (5 adenocarcinoma, 3 squamous patients; 10x Genomics), Seurat v5.

<i>Target</i>	<i>SCC epi (n=1340)</i>	<i>Adeno epi (n=3367)</i>	<i>Non-epithelial</i>
<i>MSLN</i>	0.28 (23%)	0.88 (66%)	0.00 (0%)
<i>TROP-2</i>	1.65 (75%)	1.28 (75%)	0.04 (3%)
<i>LIV-1</i>	0.21 (35%)	0.12 (20%)	0.16 (16%)
<i>EpCAM</i>	0.61 (51%)	1.83 (87%)	0.02 (2%)

<i>Target</i>	<i>Adeno_1 (n=1166)</i>	<i>Adeno_2 (n=370)</i>	<i>Adeno_3 (n=1346)</i>	<i>Adeno_4 (n=185)</i>	<i>Adeno_5 (n=300)</i>	<i>SCC_1 (n=538)</i>	<i>SCC_2 (n=105)</i>	<i>SCC_3 (n=697)</i>
<i>MSLN</i>	0.61 (58%)	0.42 (31%)	1.27 (80%)	0.72 (76%)	0.81 (66%)	0.02 (4%)	0.72 (73%)	0.41 (30%)
<i>TROP-2</i>	1.62 (88%)	1.08 (67%)	1.06 (64%)	1.25 (82%)	1.26 (76%)	1.02 (72%)	2.50 (93%)	2.00 (74%)
<i>LIV-1</i>	0.10 (18%)	0.40 (46%)	0.06 (10%)	0.26 (59%)	0.10 (23%)	0.29 (54%)	0.29 (46%)	0.14 (19%)
<i>EpCAM</i>	2.11 (92%)	1.58 (79%)	1.83 (86%)	1.05 (83%)	1.47 (82%)	0.31 (51%)	0.82 (77%)	0.80 (47%)

Table S8. Independent cohort validation (GSE63514). Cancer-versus-normal comparison in an independent cohort (24 normal cervix, 28 cervical cancer; Affymetrix U133 Plus 2.0, log₂ RMA; laser-captured epithelium). One-sided Wilcoxon, Benjamini–Hochberg FDR. Non-validated candidates shown by anonymised identifier.

<i>Target</i>	<i>Normal log₂</i>	<i>Cancer log₂</i>	<i>Log₂FC</i>	<i>Wilcoxon p</i>	<i>FDR</i>	<i>Replicates</i>	<i>n probes</i>	<i>probe</i>
<i>CSR-559564</i>	5.48	8.51	3.03	2.5e-07	4.46e-06	YES (up, FDR<0.05)	3	210845_s_at
<i>CSR-DBF43D</i>	7.32	9.85	2.54	2.9e-07	4.46e-06	YES (up, FDR<0.05)	1	206247_at
<i>CSR-27F664</i>	10.45	12.15	1.69	1.3e-05	8.25e-05	YES (up, FDR<0.05)	2	217901_at
<i>EpCAM</i>	11.74	13.32	1.58	3.8e-03	0.013	YES (up, FDR<0.05)	1	201839_s_at
<i>CSR-606EBC</i>	9.21	10.47	1.26	2.5e-03	0.0112	YES (up, FDR<0.05)	2	223687_s_at
<i>CSR-7CBD2E</i>	9.72	10.95	1.23	3.6e-03	0.013	YES (up, FDR<0.05)	4	203510_at
<i>CSR-3FA3D7</i>	1.89	3.04	1.15	9.0e-06	6.98e-05	YES (up, FDR<0.05)	2	216950_s_at
<i>CSR-6C3866</i>	10.11	11.11	1.0	2.9e-02	0.0803	up (ns)	1	203256_at
<i>CSR-A22AA4</i>	4.7	5.58	0.88	1.9e-02	0.0592	up (ns)	2	204118_at
<i>LIV-1</i>	12.71	13.41	0.71	1.1e-03	0.00574	YES (up, FDR<0.05)	4	202088_at
<i>CSR-25666B</i>	8.24	8.83	0.59	4.6e-02	0.111	up (ns)	2	238542_at
<i>CSR-CA255C</i>	8.56	9.1	0.54	3.4e-02	0.0873	up (ns)	1	205831_at
<i>CSR-78F76F</i>	11.87	12.32	0.46	6.8e-02	0.15	up (ns)	4	203917_at
<i>CSR-A80B71</i>	2.57	2.96	0.39	5.5e-06	5.63e-05	YES (up, FDR<0.05)	2	207011_s_at
<i>CSR-4DD813</i>	10.9	11.2	0.3	1.7e-01	0.337	up (ns)	3	226545_at
<i>CSR-7E8AA6</i>	9.69	9.98	0.29	2.2e-01	0.377	up (ns)	2	218856_at
<i>CSR-8A7DB4</i>	2.83	2.9	0.07	8.1e-01	1	up (ns)	1	202711_at
<i>CSR-6A5781</i>	3.95	3.98	0.03	4.6e-01	0.751	up (ns)	4	210651_s_at
<i>CSR-AA62BC</i>	8.15	8.16	0.02	2.0e-01	0.37	up (ns)	5	204990_s_at
<i>CSR-613CFC</i>	3.68	3.67	-0.01	8.4e-01	1	not up	1	204116_at
<i>CSR-B9FBE2</i>	9.94	9.78	-0.16	8.1e-01	1	not up	3	41660_at
<i>CSR-D025D8</i>	10.44	10.26	-0.18	5.6e-01	0.87	not up	1	201195_s_at
<i>MSLN</i>	5.13	4.93	-0.2	1.2e-01	0.246	not up	1	204885_s_at
<i>TROP-2</i>	14.72	14.3	-0.42	9.9e-01	1	not up	4	202286_s_at
<i>CSR-2DBC31</i>	8.49	7.97	-0.52	9.5e-01	1	not up	3	227184_at
<i>CSR-2E068C</i>	14.04	13.5	-0.54	1.0e+00	1	not up	2	201131_s_at
<i>CSR-A661D0</i>	13.81	12.87	-0.95	9.9e-01	1	not up	4	226817_at
<i>CSR-FB97DA</i>	14.12	12.78	-1.34	1.0e+00	1	not up	4	217528_at
<i>CSR-0508C7</i>	9.71	8.19	-1.52	1.0e+00	1	not up	1	203499_at
<i>CSR-E3CEA0</i>	10.52	8.99	-1.53	9.9e-01	1	not up	3	203108_at
<i>CSR-6C64FC</i>	12.82	11.21	-1.61	1.0e+00	1	not up	5	1552797_s_at

Table S9. Target expression in an independent tumour cohort (GSE151666). Median TPM and percent of tumours expressing each target across 68 pre-treatment primary cervical tumours (bulk RNA-seq). Non-validated candidates shown by anonymised identifier.

<i>Target</i>	<i>Median TPM</i>	<i>% tumours expressed</i>
<i>TROP-2</i>	980.2	100
<i>CSR-AA62BC</i>	151.9	100
<i>CSR-6C64FC</i>	107.2	100
<i>CSR-6C3866</i>	89.0	100
<i>CSR-2E068C</i>	88.5	99
<i>CSR-D025D8</i>	75.2	100
<i>CSR-8A7DB4</i>	71.2	100
<i>CSR-FB97DA</i>	66.1	96
<i>CSR-0508C7</i>	64.1	100
<i>CSR-A80B71</i>	56.8	100
<i>CSR-7E8AA6</i>	50.2	100
<i>EpCAM</i>	40.4	100
<i>CSR-613CFC</i>	35.7	100
<i>CSR-E3CEA0</i>	35.5	100
<i>CSR-559564</i>	31.5	100
<i>CSR-B9FBE2</i>	30.9	100
<i>CSR-27F664</i>	30.1	99
<i>CSR-A661D0</i>	21.9	99
<i>MSLN</i>	21.7	91
<i>LIV-1</i>	20.8	100
<i>CSR-2DBC31</i>	19.5	100
<i>CSR-606EBC</i>	18.1	93
<i>CSR-CA255C</i>	15.3	100
<i>CSR-7CBD2E</i>	12.3	99
<i>CSR-25666B</i>	11.2	96
<i>CSR-4DD813</i>	9.7	96
<i>CSR-A22AA4</i>	9.0	99
<i>CSR-DBF43D</i>	8.9	99
<i>CSR-78F76F</i>	8.4	97
<i>CSR-6A5781</i>	4.8	93
<i>CSR-3FA3D7</i>	2.4	82