

Online Resource 1

Cell-resolved virus-host programs across cancers associated with five human oncoviruses: a systematic review

Journal: Virus Genes

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Supplementary Table S1. Included-report evidence map

Ref./PMID	Virus / malignancy	Cohort and design	Principal cell-resolved finding	Confidence	Data provenance	Eligibility source
8 PMID 31924475	HPV; HNSCC	26 HPV-positive/negative patients; 131,224 intratumoral/peripheral immune cells	HPV-associated divergence concentrated in helper CD4 and B cells; Tfh-like program associated with longer progression-free survival	Higher	Primary clinical cohort	Full article
9 PMID 34921143	HPV; HNSCC	6 HPV-positive and 12 HPV-negative tumors with matched blood; 134,606 cells	HPV-associated inflammatory and fibroblast states; macrophages dominated checkpoint-ligand production	Moderate	Extension/reanalysis of the Cillo HNSCC cohort; not treated as an independent cohort.	Full article
10 PMID 36967539	HPV; cervical progression	2 HPV-negative normal, 2 HPV-positive normal, 2 HSIL, 3 cancers; scRNA plus spatial	HPV-related epithelial clusters and transition from antiviral activation to exhaustion/suppression	Higher	Primary clinical cohort	Full article
11 PMID 37012457	HPV; OPSCC	HPV-positive and HPV-negative tumors; single-cell plus genomic/viral-state analysis	Loss or repression of HPV expression marked invasive, treatment-resistant malignant states	Higher	Primary clinical cohort	Full article
12 PMID 37287196	HPV; cervical SCC versus adenocarcinoma	3 SCC and 3 adenocarcinoma tumors; 61,723 cells	SCC: EMT/hypoxia/cytotoxic infiltration; adenocarcinoma: cell cycle, Tregs, immunomodulatory macrophages/CAFs	Moderate	Primary clinical cohort	Full article
13 PMID 38235919	HPV; primary/metastatic HNSCC	8 scRNA and 6 spatial samples, matched primary/nodal sites	Lymphoid-rich HPV-positive ecosystem; PKM2 stemness and EPHA2 angiogenesis emphasized in HPV-negative metastasis	Moderate	Primary clinical cohort	Full article
14 PMID 38670879	HPV; penile SCC	16 tumors stratified by HPV/TP53 plus 6 controls; 83,682 cells; validation cohort	HPV-positive/TP53-wild-type tumors retained maturation/innate activity; TP53 loss produced immune exclusion and invasion	Higher	Primary clinical cohort	Full article
15 PMID 39105803	HPV; OPSCC	3 HPV-positive, 3 HPV-negative tumors and 1 normal tonsil	HPV-positive malignant MHC-II/interferon state communicated with CXCL13-positive CD4 cells and predicted favorable survival	Moderate	Virus-stratified HNSCC analysis with orthogonal/outcome validation; cohort overlap considered in the synthesis.	Full article
16 PMID 40936798	HPV; penile SCC	11 treatment-naïve patients; 52,980 cells	HPV-positive tumors had fewer proliferative macrophages and less exhausted CD8 cells; TIGIT network enriched in HPV-negative disease	Moderate	Primary clinical cohort	Full article
17 PMID 41381565	HPV; penile SCC	23 scRNA patients; validation in 85 patients plus functional models	B-cell/plasma-cell/TLS enrichment and IgA-PIGR epithelial axis supported antitumor immunity and survival	Higher	Primary clinical cohort	Full article
18 PMID 41913707	HPV; OPSCC	5 HPV-associated, 2 non-HPV-associated tumors, 3 normal tonsils; scRNA plus spatial	FBLN1-positive fibroreticular cells and tumor antigen presentation supported an immunogenic ecosystem	Moderate	Primary clinical cohort	Full article

Ref./PMID	Virus / malignancy	Cohort and design	Principal cell-resolved finding	Confidence	Data provenance	Eligibility source
19 PMID 32901110	EBV; NPC	19 EBV-positive NPC and 7 nonmalignant biopsies; about 104,000 cells	Global interferon response; epithelial-immune malignant state linked to CD8 inhibition and poor prognosis	Higher	Primary clinical cohort	Full article
20 PMID 33531485	EBV; NPC	10 tumor-blood pairs; 176,447 cells plus TCR sequencing	Exhausted CD8, TNFRSF4-positive Tregs, and LAMP3 dendritic cells formed an inhibitory network	Higher	Primary clinical cohort	Full article
21 PMID 37370788	EBV; gastric cancer	Integrated EBV-positive/negative gastric bulk and single-cell datasets	Proliferating T/B and follicular-helper-like states enriched in EBV-associated tumors	Exploratory	Bulk/single-cell integration with only one EBV-positive gastric single-cell case; exploratory report.	Full article
22 PMID 37735150	EBV; gastric cancer	Longitudinal scRNA plus TCR/BCR during immunochemotherapy	ISG15-positive CD8 transitional exhaustion predicted response; CXCL13 effectors emerged in responders; LAG3 persisted in nonresponders	Higher	Primary clinical cohort	Full article
23 PMID 37949673	EBV; extranodal NK/T-cell lymphoma	Patient tumor scRNA with in vitro/in vivo validation	LMP1-positive malignant NK cells secreted DPP4, impaired immune chemotaxis, and suppressed T cells	Higher	Primary clinical cohort	Full article
24 PMID 40492497	EBV; early NK/T lymphoma	Clinical trials n=192; scRNA-seq n=10 and bulk RNA-seq n=65	High baseline tumor glycolysis associated with inflammatory dendritic-cell infiltration and worse long-term outcome.	Higher	Primary clinical treatment cohort	Full article
25 PMID 42456326	EBV; primary/metastatic NPC	Primary and liver-metastatic NPC single-cell atlas	Metastasis associated with Treg stem-like features, MIF signaling, CXCL13-positive CD4 cells, and loss of IGHM-positive B cells	Moderate	Secondary analysis of public primary and metastatic NPC scRNA-seq datasets with bulk/outcome validation; overlaps a represented NPC cohort.	Publisher record and indexed abstract
26 PMID 34140495	HBV; HCC	HBV-associated HCC patient cohort	Macrophage-mediated T-cell exclusion and TIGIT-NECTIN2 signaling defined an immunosuppressive landscape	Moderate	Primary clinical cohort	Full article
27 PMID 34290079	HBV; HCC	Patient-derived HCC profiled with complementary single-cell protocols	Cell-level HBV reads correlated with differentiation, E2F/MYC targets, adipogenesis, and integration-derived fusions	Exploratory	Primary clinical cohort	Full article
28 PMID 36596711	HBV; recurrent HCC	34 samples from 20 patients; paired primary/recurrence plus validation	True and de novo recurrence had distinct CD8, dendritic, myeloid, and checkpoint-response ecosystems	Higher	Primary clinical cohort	Full article
29 PMID 38116005	HBV disease continuum/HCC	6 healthy, 4 chronic HBV, 5 cirrhosis, 3 HCC; 118,455 immune cells	Sequential CD9 macrophage states; HCC gained Tregs/LAG3-positive exhausted CD8 and lost TNF-positive effectors	Moderate	Primary clinical cohort	Full article
30 PMID 38159218	HBV; HCC	11 treatment-naïve patients; 64,581 tumor/adjacent cells plus cohort and functional validation	CK19-positive stem cells occupied an SPP1-positive macrophage niche driven by VEGFA-MMP9	Higher	Primary clinical cohort	Full article
31 PMID 38169544	HBV; HCC	9 patients; 31,664 cells plus functional and animal validation	CD24/CD47/ICAM1-high stem-like cells used S100A11-dependent bidirectional crosstalk with M2-like macrophages	Higher	Primary clinical cohort	Full article
32 PMID 38251896	HBV-positive versus HBV-negative HCC	Integrated discovery cohorts plus independent immunotherapy cohort	HBV-positive HCC enriched Tregs, exhausted CD8, MMP9-positive macrophages, checkpoints, and reduced MHC-II	Moderate	Integrated public HCC discovery data with an independent immunotherapy validation cohort.	Full article
33 PMID 40634523	HBV-positive versus non-HBV HCC	70,056 cells; viral-read mapping	HBV detected in hepatocytes, myeloid and lymphoid cells; dysfunctional CTLA4/MDK CD8 and MT1G-high macrophages	Higher	Primary clinical cohort	Full article

Ref./PMID	Virus / malignancy	Cohort and design	Principal cell-resolved finding	Confidence	Data provenance	Eligibility source
34 PMID 41113120	HBV; HCC	8-patient multi-omics cohort; 106-patient validation	Exhaustion tracked with HBV integration, viral reservoir, TP53/proliferative subtype, and clonal expansion	Moderate	Primary clinical cohort	Full article
35 PMID 42254977	HBV-positive HCC	528 immunotherapy-treated patients with single-cell/spatial validation and mouse testing	PD-1-positive/CXCR6-positive exhausted-cytotoxic CD8 cells interacted with CXCL16-positive macrophages and predicted ICB benefit	Higher	Primary clinical cohort	Full article
36 PMID 42462708	HBV; recurrent HCC	Perioperative PD-1 trial with dynamic single-cell multi-omics	HBV-core-reactive, affinity-matured TLS B cells activated complement and contributed to antitumor response	Higher	Primary clinical cohort	Full article
37 PMID 34376672	HTLV-1; ATLL	Chronological pre-onset/ATLL specimens; genome plus scRNA integration	TCR/STAT3/NOTCH mutations drove clone-specific transcription and stepwise malignant expansion	Moderate	Primary clinical cohort	Full article
38 PMID 34907908	HTLV-1; carrier-to-ATLL	12 infected and 3 uninfected individuals; 87,742 PBMCs	Activation-to-ATLL continuum; Treg acquisition; Tax-induced HLA-II enabled tolerogenic presentation and anergy	Higher	Primary clinical cohort	Full article
39 PMID 35464471	HTLV-1; skin ATLL	Archived frozen skin tissue; scRNA plus TCR clonality	EGR1/EGR2-rich fibroblasts supported malignant and cytotoxic-cell expansion through FGF/PDGF/EGFR networks	Exploratory	Primary clinical cohort	Full article
40 PMID 40355804	HTLV-1; ATLL	Primary ATLL cells across clinical aggressiveness with functional validation	CCR4-positive/CD48-negative aggressive population; YY1/EZH2-MLH1 axis implicated therapeutically	Moderate	Primary clinical cohort	Full article
41 PMID 36719743	MCPyV; MCC	44 bulk tumor biopsies and 9 scRNA tumors plus cell models	Neuroendocrine-high versus YAP1/WWTR1-high axis crossed viral status; YAP1/WWTR1 repressed MCPyV T antigen	Moderate	Primary clinical cohort	Full article
42 PMID 39401968	MCPyV; refractory MCC	One longitudinal MCPyV-positive treated case plus STING survey of 88 tumors	Virus-specific exhausted CD8 cells; stromal/immune STING; treatment restored HLA-I and expanded CD8 cells	Exploratory	Primary clinical cohort	Full article
43 PMID 40026481	MCPyV; MCC/viral skin disease	Viral-read detection pipeline applied to human skin biopsies	Demonstrated cell-level MCPyV localization and host perturbation detection; limited replicated cancer-specific inference	Exploratory	Methodological viral-read analysis of existing human skin biopsy datasets; not an independent cancer cohort.	Full article
44 PMID 33208941	HPV; HNSCC	HPV-positive head-and-neck tumors; antigen-specific B/ASC profiling, scRNA-seq and monoclonal-antibody generation	Intratumoral activated/germinal-center B cells and ASCs produced somatically mutated HPV-specific antibodies, especially against E2.	Higher	Primary antigen-specific clinical study	Full article
45 PMID 34471285	HPV; HNSCC	Tetramer-sorted HPV-specific CD8 TILs; scRNA-seq, TCR clonotypes and peptide-stimulation assays	Stem-like TCF7-positive, transitory and terminal HPV-specific CD8 states formed a differentiation continuum; only the stem-like compartment retained proliferative capacity.	Higher	Primary antigen-specific clinical study	Full article
46 PMID 35039463	HPV16; OPSCC	Patient cohorts including therapeutic vaccination; HPV-specific CD4 TILs/clones and single-cell transcriptomics	CD161-positive effector-memory CD4 cells rapidly responded to limiting antigen; SOX4 and dynamic KLRB1 regulation linked the state to favorable survival.	Higher	Primary clinical/functional study	Full article
47 PMID 35812401	HPV-related cervical progression	Normal cervix, intraepithelial neoplasia, primary tumor and metastatic node; 59,913 cells	Premalignancy showed recently activated resident/cytotoxic immunity, invasive cancer was suppressive, and metastatic nodes showed a distinct activated composition.	Moderate	Primary progression cohort	Full article
48 PMID 36000446	HPV; cervical adenosquamous carcinoma	Two tumors; 18,046 cells with TCGA outcome association	Epithelial metabolic/proliferative heterogeneity coexisted with FGFBP2-positive cytotoxic T/NK subsets associated with survival.	Exploratory	Small primary cohort	Full article
49 PMID 36609919	HPV; cervical adenocarcinoma	Three tumors; 19,229 sorted epithelial cells	Six epithelial states differed in hypoxia, cell cycle, DNA repair, metabolism and patient-specific signaling.	Exploratory	Small primary cohort	Full article

Ref./PMID	Virus / malignancy	Cohort and design	Principal cell-resolved finding	Confidence	Data provenance	Eligibility source
50 PMID 36725337	HPV; cervical SCC and adenocarcinoma	scRNA/TCR-seq comparing SCC, HPV-associated and non-HPV-associated adenocarcinoma; organoid/animal validation	Histology and HPV association defined distinct malignant, stromal and immune reaction patterns and differential checkpoint vulnerabilities.	Higher	Primary comparative/validated cohort	Full article
51 PMID 36777180	HPV; cervical cancer	Clinical, genomic, transcriptomic, proteomic, phosphoproteomic and single-cell integration	Productive, rather than silent, integration increased with progression and associated with E6/E7 abundance, aggressiveness and immune evasion.	Higher	Primary multi-omics study	Full article
52 PMID 37638381	HPV16; cervical cancer	HPV-positive tumor with cell-level E1/E6/E7 and epithelial-layer analysis	HPV-positive fractions and viral-gene expression varied across epithelial states and associated with extracellular-matrix, adhesion, proliferation and apoptosis programs.	Exploratory	Small direct viral-read study	Full article
53 PMID 38857913	HPV; OPSCC immunotherapy	Pretreatment scRNA-seq n=20 and TCR-seq n=10; immunofluorescence and external validation	CD161-high resident-memory CD8 cells and reduced CLEC2D-positive B-cell support were associated with weaker immunotherapy response in HPV-positive disease.	Higher	Primary treatment cohort	Full article
54 PMID 39757146	HPV; HNSCC	HPV-positive/negative single-cell and spatial comparison with in-vitro and pan-cancer validation	FRC-like fibroblasts were enriched in HPV-positive immune-hot tumors and TLSs, whereas IL11-positive inflammatory CAFs occupied monocyte-rich niches.	Higher	Primary spatial/functional study	Full article
55 PMID 39831355	HPV; cervical small-cell neuroendocrine carcinoma	Two tumors and adjacent tissue; scRNA-seq plus whole-exome sequencing	HPV-infected and SOX2-high epithelial distributions supported a squamous origin and HPV/SOX2 contribution to neuroendocrine evolution.	Exploratory	Small rare-tumor cohort	Full article
56 PMID 40044748	HPV; penile SCC	Ten tumors across primary, nodal and distant sites; four matched primary-node pairs	Advanced disease accumulated terminally exhausted CD8 cells, M2-like macrophages and hypoxia; HPV-positive and negative tumors differed in immune infiltration and dysfunction.	Moderate	Primary stage/viral-status cohort	Full article
57 PMID 40151001	HPV; cervical progression	Normal, HSIL, microinvasive and invasive tissues; cell-level integration detection from scRNA-seq	HPV integration was enriched in squamous cells and increased with progression, with recurrent patient- and cell-level integration targets.	Exploratory	Direct viral-read/integration analysis	Full article
58 PMID 40621740	HPV; HNSCC	TCGA/pathology plus single-cell/spatial analyses; mIHC, flow, ELISA and neoadjuvant treatment validation	Mature TLSs were enriched in HPV-positive tumors and after chemoimmunotherapy and contained germinal-center B, T _{fh} and resident-memory CD8 cells.	Higher	Integrated single-cell/spatial analysis with independent pathology, flow, serology, and treatment validation.	Full article
59 PMID 41035636	HPV; cervical cancer	Collected HPV-positive/negative tumors; scRNA-seq, spatial transcriptomics and multiplex immunofluorescence	HPV status reorganized epithelial-to-myeloid/T-cell communication and spatial immune composition; MDK-LRP1 emerged as a suppressive circuit.	Moderate	Primary multi-omics cohort	Full article
60 PMID 41088355	HPV; OPSCC metastasis	Matched primary and cervical-node metastases; scRNA-seq, spatial and in-situ platforms	Metastatic clones showed translational adaptation, immunoproteasome dysfunction, reduced interferon responses and immune evasion.	Higher	Primary matched-site cohort	Full article
61 PMID 41286405	HPV; multiphenotypic sinonasal carcinoma	One HMSC tumor with public ACC/OPSCC comparisons and HPV-on/off cell analysis	HPV-expressing malignant cells showed greater MYB and MYB-target expression, suggesting an HPV-MYB association.	Exploratory	Single rare-tumor exploratory study	Full article
62 PMID 41462011	HPV; HNSCC	IHC n=59 plus integrated scRNA/spatial/bulk data, cytology, multiplex IF and mouse models	HPV-associated KRT15-high malignant cells secreted CCL20, promoted TLS formation and enhanced anti-PD-1 activity.	Higher	Integrated public single-cell/spatial discovery with independent tissue and functional validation.	Full article
63 PMID 41827778	HPV; HNSCC	Reanalysis of 28 published tumors with independent IHC n=10 and TCGA outcomes	A cytotoxic CX3CR1-positive/KLRB1-dim NK state enriched in HPV-positive tumors contrasted with a suppressive CLEC2-KLRB1 axis in HPV-negative disease.	Moderate	Published HNSCC scRNA-seq reanalysis with an independent FFPE-IHC validation cohort.	Full article
64 PMID 41964419	HPV; cervical SCC	Paired tumor core/edge; scRNA-seq n=13, TCR-seq n=9, bulk n=41 and immunofluorescence	Tumor cores contained more inhibitory/cytotoxic programs, stress-associated exhausted CD8 cells and clonal expansion than edges.	Higher	Primary spatially paired cohort	Full article

Ref./PMID	Virus / malignancy	Cohort and design	Principal cell-resolved finding	Confidence	Data provenance	Eligibility source
65 PMID 42415251	HPV; cervical cancer	Integrated 31 samples/141,785 cells with IHC, IF and Mendelian-randomization validation	HPV-positive tissues expanded terminal CXCL8-positive neutrophils with suppressive T-cell communication and adverse clinical associations.	Moderate	Integrated cervical single-cell data with independent spatial protein and causal-inference validation.	Full article
66 PMID 42503644	HPV; OPSCC	Bulk n=56; scRNA/TCR n=4 including a longitudinal primary-metastasis pair; functional TCR validation	High-avidity HPV-specific KLRB1-positive CD8 clones persisted in metastasis, whereas stem-like TCF7-associated cells decreased.	Higher	Small single-cell cohort with functional validation	Full article
67 PMID 32532891	EBV; gastric adenocarcinoma	Nine tumors and three non-tumor samples; 27,677 cells with histological/bulk validation	One immune-related malignant subgroup carried EBV and expressed MHC-II, illustrating an EBV-specific state within a broader gastric atlas.	Exploratory	One EBV-positive single-cell case	Full article
68 PMID 36860875	EBV; NPC	Ten NPC tumors and one non-tumor tissue; 28,423 cells; EBV-DNA seropositive versus seronegative	Seropositivity associated with less differentiated/stem-like malignant cells, early cytotoxic activation and global interferon programs.	Higher	Primary direct serostatus cohort	Full article
69 PMID 37024479	EBV; NPC	Public multicenter cohort: 357,206 cells/50 patients; organoids, humanized mice and ATAC-seq	EBV-dependent epigenetic upregulation of tumor CD70 promoted CD27-mediated Treg development; CD70 blockade restored CD8 activity.	Higher	Secondary discovery with strong functional validation	Full article
70 PMID 37098551	EBV; nonkeratinizing NPC	Public scRNA: 10 NPC/3 hyperplasia; new proteomics 3/3 and IHC	ZNF683-positive tissue-resident NK exhaustion and an active-to-latent EBV-associated malignant trajectory were identified.	Moderate	Secondary single-cell analysis with independent validation	Full article
71 PMID 37138889	EBV; CAEBV-derived NK/T lymphoma	One patient before/after PD-1 inhibitor; single-cell transcriptomics	PD-1 therapy preceded hyperinflammation and marked lymphocyte/NK expansion and activation.	Exploratory	Single-patient exploratory report	Full article
72 PMID 39231979	EBV; NPC	343,829 cells from 77 biopsy/blood samples plus spatial profiles from 15 tumors	CXCL13-positive fibroblasts organized TLSs, plasma-cell maturation and EBV-related malignant-cell apoptosis linked to immunotherapy response.	Higher	Large primary single-cell/spatial cohort	Full article
73 PMID 41142990	EBV; NK/T lymphoma	Patient single-cell and spatial transcriptomics with in-vitro/in-vivo testing	MYC-high/FABP5-dependent malignant programs and macrophage interactions supported growth and T-cell suppression.	Higher	Primary spatial/functional study	Full article
74 PMID 37522289	HBV; liver cancer	Bulk and single-cell multi-omics with multiple independent patient cohorts	HBV infection/integration altered androgen-receptor, complement and immune-cell programs with sex-linked regulatory effects.	Higher	Primary multi-omics/validated study	Full article
75 PMID 40464412	HBV; HCC	Public scRNA: 160 samples/124 patients; independent multiplex-IF/TMA n=198	HLA-DR-positive malignant cells were distinctive in HBV-HCC and associated with checkpoint activity, stem-like/exhausted CD8 trajectories and poor survival.	Higher	Public HCC scRNA-seq integration with independent multiplex-IHC/tissue-microarray validation.	Full article
76 PMID 40636452	HBV; HCC	HBV-positive versus negative HCC scRNA-seq	HBV positivity associated with SLC4A10-positive CD8 cells, IFITM3-positive macrophages, SLC35F1 expression and deeper T-cell suppression/exhaustion.	Moderate	Primary direct etiologic cohort	Full article
77 PMID 40898206	HBV; HCC	Public single-cell/external transcriptomic discovery with clinical IHC and cell-line validation	SLC16A3 marked suppressive Kupffer-cell programs, was enriched in HBV-positive HCC and associated with poor prognosis.	Moderate	Public single-cell discovery with independent clinical and functional validation.	Full article
78 PMID 41205757	HBV/MASLD; HCC	Paired tumor/adjacent tissue from 12 patients; IHC n=224, external cohorts and functional models	Etiology altered CD8/macrophage composition; HBV-positive tumors showed stronger tumor-reactive T-cell scores, while FABP4 mediated MASLD-associated vascular normalization.	Higher	Primary etiology-stratified/validated cohort	Full article
79 PMID 41491521	HBV/Clonorchis; HCC	Clinical cohort n=269; primary scRNA/spatial dual-infection samples plus public HBV comparator and validation	Dual infection enriched SPP1 macrophages, exhausted CD8 cells and COL1A1 fibroblasts and produced the most aggressive malignant program.	Higher	Mixed primary/secondary infection-comparative study	Full article
80 PMID 41673425	HBV; HCC	ILCs from 50 HBV and nonviral HCC patients; scRNA, bulk RNA and CyTOF	HBV-HCC ILC1 states were more exhausted, whereas nonviral HCC showed activated/cytotoxic ILC1 and profibrotic ILC2 programs.	Moderate	Primary direct etiology cohort	Full article

Ref./PMID	Virus / malignancy	Cohort and design	Principal cell-resolved finding	Confidence	Data provenance	Eligibility source
81 PMID 34661162	HTLV-1; infection and ATLL	Genome sequencing plus single-cell transcriptome/TCR/BCR/surface protein; conditional mouse validation	Premalignant regulatory differentiation, malignant clonal evolution and tumor-specific myeloid expansion were separated; T-cell PD-L1 transfer was functionally demonstrated.	Higher	Primary multimodal/validated cohort	Full article
82 PMID 38340723	MCPyV; MCC	Twenty-seven patients; viral peptide multimers, 26-color flow, single-cell transcriptomics/TCR and prospective PD-1 trial	Circulating MCPyV-specific CD8 frequency predicted recurrence-free survival and showed more stem/memory and less exhaustion than intratumoral cells.	Higher	Primary antigen-specific treatment cohort	Full article

Supplementary Table S2. Database strategies, coverage, and reporting notes

Database	Executed	Coverage / filters	Search strategy and reporting note	Records
PubMed/MEDLINE	2026-08-02	2020-01-01 to 2026-08-02; articles; reviews/meta-analyses excluded	Ten virus-specific searches were run: an exact-phrase formulation and a sensitivity formulation for each of the five prespecified viruses. Each combined its virus block with malignancy terms, the following technology block, the 2020-2026 date interval, and exclusion of review/meta-analysis publication types: <pre>("single-cell RNA sequencing"[Title/Abstract] OR "single cell RNA sequencing"[Title/Abstract] OR scRNA-seq[Title/Abstract] OR "single-cell RNA-seq"[Title/Abstract] OR "single cell RNA-seq"[Title/Abstract] OR "single-cell transcriptomic"[Title/Abstract] OR "single cell transcriptomic"[Title/Abstract] OR "single-cell transcriptome"[Title/Abstract] OR (("single-cell"[Title/Abstract] OR "single cell"[Title/Abstract] OR "single cells"[Title/Abstract]) AND (transcript*[Title/Abstract] OR "RNA sequencing"[Title/Abstract] OR RNA-seq[Title/Abstract] OR scRNA*[Title/Abstract])))</pre> The searches produced 537 query hits and 312 unique PubMed records after PMID, DOI, and normalized-title deduplication. The original set-level export files were not retained. TITLE-ABS-KEY(<pre>("single-cell RNA sequencing" OR "single cell RNA sequencing" OR "scRNA-seq" OR "single-cell RNA-seq" OR "single cell RNA-seq" OR "single-cell transcriptom*" OR "single cell transcriptom*" OR (("single-cell" OR "single cell" OR "single cells") W/3 (transcriptom* OR "RNA sequencing" OR "RNA-seq" OR scRNA*))) AND ("human papillomavirus" OR HPV OR "Epstein-Barr virus" OR EBV OR "hepatitis B virus" OR HBV OR "human T-cell leukemia virus type 1" OR "human T-cell leukaemia virus type 1" OR HTLV-1 OR HTLV1 OR "Merkel cell polyomavirus" OR MCPyV) AND (neoplasm* OR cancer* OR tumor* OR tumour* OR carcinoma* OR lymphoma* OR leukemia* OR leukaemia* OR malignan* OR oncogen* OR carcinogenesis)) AND PUBYEAR > 2019 AND PUBYEAR < 2027 AND DOCTYPE(ar)</pre>	537 raw query hits; 312 after query-level deduplication
Scopus	Date not recorded; completed before 2 August 2026	2020-2026; Article	<pre>("human papillomavirus" OR HPV OR "Epstein-Barr virus" OR EBV OR "hepatitis B virus" OR HBV OR "human T-cell leukemia virus type 1" OR "human T-cell leukaemia virus type 1" OR HTLV-1 OR HTLV1 OR "Merkel cell polyomavirus" OR MCPyV) AND (neoplasm* OR cancer* OR tumor* OR tumour* OR carcinoma* OR lymphoma* OR leukemia* OR leukaemia* OR malignan* OR oncogen* OR carcinogenesis)) AND PUBYEAR > 2019 AND PUBYEAR < 2027 AND DOCTYPE(ar)</pre>	Raw yield not retained; no additional eligible reports

Database	Executed	Coverage / filters	Search strategy and reporting note	Records
Web of Science Core Collection	Date not recorded; completed before 2 August 2026	2020-2026; Article	TS=(("single-cell RNA sequencing" OR "single cell RNA sequencing" OR "scRNA-seq" OR "single-cell RNA-seq" OR "single cell RNA-seq" OR "single-cell transcriptom*" OR "single cell transcriptom*" OR (("single-cell" OR "single cell" OR "single cells") NEAR/3 (transcriptom* OR "RNA sequencing" OR "RNA-seq" OR scRNA*))) AND ("human papillomavirus" OR HPV OR "Epstein-Barr virus" OR EBV OR "hepatitis B virus" OR HBV OR "human T-cell leukemia virus type 1" OR "human T-cell leukaemia virus type 1" OR HTLV-1 OR HTLV1 OR "Merkel cell polyomavirus" OR MCPyV) AND (neoplasm* OR cancer* OR tumor* OR tumour* OR carcinoma* OR lymphoma* OR leukemia* OR leukaemia* OR malignan* OR oncogen* OR carcinogenesis)) AND PY=(2020-2026) AND DT=(Article)	Raw yield not retained; no additional eligible reports

Supplementary Table S3. Reports excluded after full-report assessment

PMID	Report	Exclusion category	Reason
32193227	B Cells Improve Overall Survival in HPV-Associated Squamous Cell Carcinomas and Are Activated by Radiation and PD-1 Blockade.	no eligible human tumor scRNA-seq cohort	Human outcomes were bulk RNA-seq; the single-cell experiment was murine.
33298893	Global immune characterization of HBV/HCV-related hepatocellular carcinoma identifies macrophage and T-cell subsets associated with disease progression.	viral etiologies not separable	HBV- and HCV-related HCC were pooled for the reported single-cell conclusions.
35025968	EBV+ tumors exploit tumor cell-intrinsic and -extrinsic mechanisms to produce regulatory T cell-recruiting chemokines CCL17 and CCL22.	no eligible human tumor scRNA-seq cohort	The single-cell experiment was performed in a mouse tumor model.
35433690	Multiscale Transcriptomic Integration Reveals B-Cell Depletion and T-Cell Mistrafficking in Nasopharyngeal Carcinoma Progression.	secondary/overlapping dataset without qualifying added evidence	Public NPC datasets were reanalysed without a new virus-resolved clinical cohort.
35933472	A single-cell atlas of the multicellular ecosystem of primary and metastatic hepatocellular carcinoma.	viral etiologies not separable	The HCC atlas did not isolate an HBV-specific host program from HBV/HCV-associated disease.
36157879	Single-Cell Transcriptome Analysis Reveals Different Immune Signatures in HPV- and HPV + Driven Human Head and Neck Squamous Cell Carcinoma.	secondary/overlapping dataset without qualifying added evidence	Reanalysis of an already represented HNSCC single-cell cohort.
36252564	Transcriptional and functional analyses of neoantigen-specific CD4 T cells during a profound response to anti-PD-L1 in metastatic Merkel cell carcinoma.	no eligible virus-associated comparator	The profiled Merkel cell carcinoma was MCPyV negative.
36389736	Single-cell RNA sequencing reveals TCR+ macrophages in HPV-related head and neck squamous cell carcinoma.	secondary/overlapping dataset without qualifying added evidence	Macrophage-focused reanalysis of an already represented HNSCC cohort.
37031202	Single-cell transcriptomic analysis of HPV16-infected epithelium identifies a keratinocyte subpopulation implicated in cancer.	no eligible human malignancy	HPV16-infected epithelial model without an eligible clinical malignant cohort.
37063858	Three-dimensional and single-cell sequencing of liver cancer reveals comprehensive host-virus interactions in HBV infection.	no eligible human tumor scRNA-seq cohort	Cell-line/3D-genome study with secondary public single-cell analysis.
37071208	The HDAC inhibitor domatinostat induces type I interferon α in Merkel cell carcinoma by HES1 repression.	no eligible human tumor scRNA-seq cohort	Cell-line experiment with secondary public single-cell analysis.
37645794	Identification of HPV oncogene and host cell differentiation associated cellular heterogeneity in cervical cancer via single-cell transcriptomic analysis.	non-peer-reviewed/duplicate report	Preprint duplicate of the peer-reviewed article PMID 37638381.
38032223	Single-cell atlas reveals characteristic changes in intrahepatic HBV-specific leukocytes.	wrong single-cell modality	The human and mouse experiments used mass cytometry, flow cytometry, and immunofluorescence; no eligible scRNA-seq cohort was reported.
38103888	Clonal Origin and Lineage Ambiguity in Mixed Neuroendocrine Carcinoma of the Uterine Cervix.	no eligible human tumor scRNA-seq cohort	Single-cell analysis was performed in patient-derived organoid/xenograft models.
38532566	Analyses of tertiary lymphoid structures observed in cases of Merkel cell carcinoma showing spontaneous regression.	wrong single-cell modality	Spatial proteomic imaging rather than scRNA-seq.
39346086	HPV-driven heterogeneity in cervical cancer: study on the role of epithelial cells and myofibroblasts in the tumor progression based on single-cell RNA sequencing analysis.	secondary/overlapping dataset without qualifying added evidence	Public cervical scRNA-seq reanalysis; validation did not establish an independent cell-state cohort.
39424708	Single-cell transcriptomics of pediatric Burkitt lymphoma reveals intra-tumor heterogeneity and markers of therapy resistance.	no eligible virus-associated comparator	Pediatric Burkitt lymphoma cohort lacked an eligible EBV-positive stratum.
39524999	Exploring a specific type of tissue-resident natural killer cell involved in the anti-tumor and immunotherapy response in human papillomavirus-positive head and neck squamous cell carcinoma using scRNA-seq.	secondary/overlapping dataset without qualifying added evidence	Public scRNA-seq reanalysis without independent cell-state validation.
39549431	Immune checkpoint expression on tumor-infiltrating lymphocytes (TIL) is dependent on HPV status in oropharyngeal carcinoma (OPSCC) - A single-cell RNA sequencing analysis.	secondary/overlapping dataset without qualifying added evidence	Original bulk profiling paired with an already represented public scRNA-seq cohort.
39764057	Same-Slide Spatial Multi-Omics Integration Reveals Tumor Virus-Linked Spatial Reorganization of the Tumor Microenvironment.	wrong single-cell modality	Spatial multi-omics study without an eligible scRNA-seq cohort.

PMID	Report	Exclusion category	Reason
39865078	Intratumor heterogeneity of HPV integration in HPV-associated head and neck cancer.	scRNA-seq not a central eligible method	Single-cell data were used only to support a genomic integration study.
40284904	A Single-Cell Transcriptome Atlas of Epithelial Subpopulations in HPV-Positive and HPV-Negative Head and Neck Cancers.	secondary/overlapping dataset without qualifying added evidence	Published HNSCC datasets reanalysed without independent validation.
40335578	Spatial transcriptomics reveals tumor microenvironment heterogeneity in EBV positive diffuse large B cell lymphoma.	scRNA-seq not a central eligible method	The primary human experiment used 10x Visium spatial transcriptomics; a published DLBCL scRNA-seq atlas served only as the Cell2location reference for spot deconvolution.
40437003	Deciphering the cellular and molecular landscape of cervical cancer progression through single-cell and spatial transcriptomics.	secondary/overlapping dataset without qualifying added evidence	Progression atlas reused represented cervical single-cell data without a distinct clinical cohort.
40455063	Single-Cell Analysis of Posttranslational Modifications Identifies Immunosuppressive Macrophage Subtypes in the HBV-Positive Hepatocellular Carcinoma Microenvironment.	wrong single-cell modality	Single-cell post-translational-modification mass cytometry rather than scRNA-seq.
40470730	Single-Cell and Spatial Transcriptomic Profiling of Penile Squamous Cell Carcinoma Reveals Dynamics of Tumor Differentiation and Immune Microenvironment.	wrong single-cell modality	Single-nucleus RNA sequencing rather than scRNA-seq under the prespecified scope.
41029323	Single-cell analysis reveals the regulatory role of ECT2 in HPV-driven cervical carcinogenesis process.	scRNA-seq not a central eligible method	Public scRNA-seq served as an annotation layer for a bulk/gene-centric analysis.
41314067	Hpv-driven rewiring of the tumor immune microenvironment through single-cell profiling informs prognosis and therapy in HNSCC.	scRNA-seq not a central eligible method	Database-derived prognostic model; scRNA-seq was used as an annotation layer.
41855857	Spatial remodeling of the tumor immune microenvironment in hepatocellular carcinoma with cirrhosis driven by Treg-CD8 ⁺ T cell crosstalk via the SPP1-ITGA4 axis.	scRNA-seq not a central eligible method	Primary spatial cohort with public scRNA-seq used only for downstream annotation.
42039670	Not so cold after all: tumor infiltrating CD8 ⁺ T cells in EBV-positive Burkitt lymphoma are quiescent, not exhausted.	non-peer-reviewed/duplicate report	Preprint at the search cutoff.
42098219	Distinct single-cell cellular states and ecosystems linked to HPV status distinguish therapeutic vulnerability of head and neck squamous cell carcinoma.	secondary/overlapping dataset without qualifying added evidence	EcoTyper analysis of public HNSCC data without independent validation.
42181284	A unified single-cell atlas of HNSCC: Toward characterizing HPV- and sex-associated TME variability.	secondary/overlapping dataset without qualifying added evidence	Unified public HNSCC atlas without a new clinical cohort or qualifying validation.
42393223	Single-cell analyses of liver and blood reveal distinct immune cell signatures of HBV-related HCC patients.	wrong single-cell modality	CyTOF rather than scRNA-seq.
42465316	TAOK3 inhibition constrains invasion, potentiates paclitaxel, and reprograms the tumor microenvironment toward anti-tumor immunity in cervical cancer.	scRNA-seq not a central eligible method	Public scRNA-seq localized a target tested mainly in cell and xenograft models.