*medical sciences*

MDPI

*Supplementary Materials*

# Chronic Venous Disease and Systemic Vascular Dysfunction: Mechanistic Links and Cardiovascular Associations—A Systematic Review

**María Lourdes del Río-Solá, Iván Alejandro Díaz Rengifo and Emilio Vargas Castrillón**

## Annex S3A Retained prompts and criteria

This annex accompanies File S3. It reproduces the 12 retained task prompts and criteria verbatim, using their original S3.1–S3.12 identifiers. File paths and output instructions belong to the historical working environment. These prompts document assisted tasks; the final eligibility rules and human verification are summarized in File S3 and detailed in Files S2 and S4. The exact search-strategy prompt was not retained; final search strings appear in File S1.

## S3.1. Title screening — task prompt

```
You are screening records for a systematic review. Read the criteria in /home/claude/scr/ts/CRITERIA.md carefully. Then screen ALL lines of /home/claude/scr/ts/batch5.tsv and /home/claude/scr/ts/batch6.tsv by reading the titles yourself (use the Read tool in chunks of ~400 lines; do NOT use keyword scripts to decide — you must judge each title). Write decisions to /home/claude/scr/ts/out5.tsv and /home/claude/scr/ts/out6.tsv (one line per input line: cid<TAB>M|R|X). Write incrementally (append per chunk) so progress is not lost. When done, verify with a script that every cid in each batch has exactly one decision, and report counts. Be inclusive: when unsure, M.
```

## S3.2. Title screening — criteria file

```
# Title screening criteria — systematic review "Chronic venous disease (CVeD) and systemic vascular dysfunction / cardiovascular associations"

Each line of your batch file: cid <TAB> year <TAB> publication type <TAB> title.

Decide for EVERY line one of:
- M (maybe/retain): could be a PRIMARY study (human or animal) in chronic venous disease (varicose veins, chronic venous insufficiency, CEAP C1–C6, venous leg ulcer, venous reflux, venous hypertension models) that measures ANY of:
  1. local venous pathobiology (vein wall/valve/tissue/endothelium: inflammation, oxidative stress, MMPs, remodeling, microcirculation, leukocytes, shear stress, gene/miRNA expression) — including animal models of venous hypertension;
  2. circulating/blood biomarkers (CRP, cytokines, ILs, TNF, vWF, D-dimer, fibrinogen, adhesion molecules, NO, oxidative markers, MMPs in blood) in CVeD patients;
  3. systemic/arterial vascular function or structure (FMD, pulse wave velocity, arterial stiffness, IMT, ABI, coronary calcium, endothelial function outside the leg veins);
  4. association of CVeD with cardiovascular disease/risk factors/comorbidity (CAD, MI, stroke, heart failure, AF, PAD, hypertension, diabetes, atherosclerosis), incl. cross-sectional;
  5. incident cardiovascular outcomes, thromboembolism or mortality in people with CVeD (cohorts, registries);
  6. cardiovascular risk prediction including CVeD;
  7. Mendelian randomization / genetic causal inference involving varicose veins/CVI.
  When in doubt, choose M.
- R (review/secondary): systematic/narrative review, meta-analysis, guideline, consensus, editorial ON the topics above (keep for context).
- X (exclude): clearly not relevant, e.g.: treatment/technique efficacy only (ablation, sclerotherapy, surgery, stockings, venoactive drugs, wound dressings, compression) without vascular/biomarker/CV outcome evident from title; quality of life/symptoms only; acute DVT/PE/VTE management without CVeD focus; esophageal/gastric varices, varicocele, hemorrhoids, portal hypertension, intracranial/retinal venous issues, dialysis access; diabetic/arterial ulcers; case reports; imaging technique; anatomy; anesthesia; cosmetic; unrelated disease.

Note: titles about "inflammation/biomarkers/MMP/endothelium in varicose veins" → M. Titles about mortality/complications after varicose vein SURGERY (perioperative safety) → X unless long-term mortality/CV outcomes of CVeD as exposure. Trials of venoactive drugs measuring inflammatory/endothelial markers → M (they may report biomarkers).
```

Output: write a TSV file with exactly one line per input line: cid <TAB> decision (M/R/X). No header. Do not skip lines. Then report counts of M, R, X.

## S3.3. Abstract screening — task prompt

Systematic review abstract screening. Read the criteria /home/claude/scr/as/CRITERIA_ABS.md. Then screen EVERY record in /home/claude/scr/as/abs3.txt and /home/claude/scr/as/abs4.txt by reading title+abstract yourself (Read in chunks; never decide by keyword scripts). Write decisions to /home/claude/scr/as/dec3.tsv and dec4.tsv (append per chunk): cid<TAB>F|X<TAB>code<TAB>justification. Verify with a script that every cid (lines starting '### cid=') has exactly one decision. Report counts of F and X by code.

## S3.4. Abstract screening — criteria file

# Title/abstract screening — eligibility (systematic review: chronic venous disease and systemic vascular dysfunction / cardiovascular associations)

INCLUDE for full-text assessment (decision F) only if ALL apply:
A. Primary study (human observational/interventional, or experimental animal study). NOT reviews, meta-analyses, guidelines, editorials, letters without data, case reports, case series <10, conference abstracts without full paper (a conference abstract → decision X, reason "conference abstract").
B. Population: adults with chronic venous disease (varicose veins, CVI, CEAP C1–C6, venous leg ulcer, primary venous reflux) or, for animals, an experimental model of venous hypertension / venous wall or valve injury relevant to CVeD.
C. The study directly evaluates at least one of these domains, with CVeD as the exposure or the population of interest:
  1. Local venous pathobiology: vein wall/valve/endothelium/tissue/local venous blood measurements (inflammation, oxidative stress, MMPs, remodelling, adhesion molecules, leukocytes, shear-stress signalling, microcirculation) — must compare with a reference (non-varicose vein, control, severity strata, or experimental condition); purely descriptive histology of one group without comparator → F anyway if mechanistic.
  2. Circulating (systemic) biomarkers in CVeD patients (CRP, cytokines, ILs, TNF, vWF, D-dimer, fibrinogen, adhesion molecules, oxidative stress markers, MMPs, endothelial microparticles, etc.) — vs controls, vs severity, or longitudinal.
  3. Directly measured systemic/arterial vascular function or structure (FMD, PWV, arterial stiffness, IMT, ABI, coronary calcium, microvascular function outside the leg veins) in CVeD.
  4. Cardiovascular comorbidity / cardiovascular risk factors associated with CVeD (prevalence, cross-sectional, case-control) — includes atherosclerosis, CAD, MI, stroke, PAD, heart failure, AF, hypertension, diabetes, metabolic syndrome as associated conditions.
  5. Incident cardiovascular outcomes, venous thromboembolism, or mortality in people with CVeD vs without (or by severity) — cohorts, registries, claims databases.
  6. Cardiovascular risk prediction incorporating CVeD.
  7. Mendelian randomization / genetic causal inference linking CVeD with cardiovascular traits or inflammatory mediators.
D. Interventional studies (drugs, surgery, ablation, compression) qualify ONLY if they report one of the domain 1–3 measurements (e.g., biomarkers or FMD before/after) — otherwise X (reason: treatment/QoL only).

EXCLUDE (X) with ONE reason code:
- REV (secondary publication: review/meta-analysis/guideline/editorial/commentary)
- CONF (conference abstract / no full paper)
- CASE (case report or series <10)
- POP (population not CVeD, e.g., DVT/PTS only, other varices, diabetic/arterial ulcers, non-venous)
- OUT (no eligible domain: treatment efficacy, technique, QoL, symptoms, wound healing, imaging/diagnostics, genetics of CVeD susceptibility without cardiovascular/inflammatory link, epidemiology of CVeD risk factors without cardiovascular link)
- PERIOP (perioperative complications/mortality after venous procedures)
- OTHER (state briefly)

Note: "risk factors for CVeD" studies that analyse cardiovascular risk factors (hypertension, diabetes, dyslipidaemia, smoking, obesity) as correlates of CVeD → F (domain 4). Studies of VTE risk in varicose veins → F (domain 5). Wound-healing biomarker studies in venous ulcers measuring local wound fluid only → F only if they compare inflammatory/MMP markers (domain 1); otherwise X OUT.

Output: one line per record: cid<TAB>F|X<TAB>reason code (for X) or domain number(s) for F<TAB>very short justification (<15 words).

## S3.5. Domain classification — task prompt

Read /home/claude/scr/as/CRITERIA_S2.md. Classify EVERY record in /home/claude/scr/as/s2_3.txt by reading title+abstract yourself (Read in chunks; no keyword scripts). Write /home/claude/scr/as/s2out_3.tsv (cid<TAB>category<TAB>justification), appending per chunk. Verify all cids covered once. Report counts per category.

## S3.6. Domain classification — criteria file

# Second-pass (refined) eligibility — focus on SYSTEMIC evidence

For each record decide ONE category (first matching), using title+abstract:

- S3 = directly measured vascular function/structure OUTSIDE the affected leg veins (FMD, PWV, arterial stiffness, IMT, ABI, coronary calcium, systemic microvascular function e.g. forearm/skin away from legs, retinal) in CVeD patients, any design (observational or before/after treatment).
- S2 = circulating (peripheral/systemic blood) biomarkers in CVeD patients compared with participants WITHOUT venous disease (healthy/non-CVeD controls) — observational. (Severity-only comparisons without non-CVeD controls → S2b.)
- S2b = circulating biomarkers in CVeD without a non-CVeD control group (severity strata, local vs systemic blood, pre/post treatment, ulcer cohorts).
- S4 = association between CVeD and cardiovascular DISEASE or atherosclerosis (CAD, MI, angina, stroke, PAD, heart failure, AF, hypertension as disease, CV risk scores, carotid plaque) — cross-sectional/case-control/cohort.
- S4rf = only traditional risk factors (obesity, diabetes, dyslipidaemia, smoking, metabolic syndrome) as correlates of CVeD, no CV disease outcome.
- S5 = incident cardiovascular events, venous thromboembolism, or mortality in CVeD vs no CVeD (or by severity) — longitudinal.
- S7 = Mendelian randomization / genetic causal inference linking CVeD with cardiovascular traits, risk factors, or inflammatory mediators.
- L = actually local only (vein wall/tissue/wound fluid/local venous blood or leg skin microcirculation) — misclassified.
- N = not eligible after closer reading (give reason in justification).

Output: cid<TAB>category<TAB>justification (<15 words). One line per record.

## S3.7. Full-text assessment — task prompt

Systematic review full-text assessment. Read /home/claude/ft/PROTOCOL_FT.md and follow it exactly. Records: /home/claude/ft/cand1.json. For each record retrieve the full text (WebSearch/WebFetch; PMC, publisher open access, doi.org). If WebFetch is blocked for a site, you may use the Claude in Chrome browser tools (load via ToolSearch"select:mcp__claude-in-chrome__tabs_context_mcp,mcp__claude-in-chrome__tabs_create_mcp,mcp__claude-in-chrome__navigate,mcp__claude-in-chrome__get_page_text,mcp__claude-in-chrome__tabs_close_mcp"); ALWAYS create your own new tab, only read pages (no form submission, no downloads), and close your tab when done. The user's Chrome has institutional access via Biblioteca Sanitaria de Castilla y León. Assess eligibility and extract data; append one JSON object per line to /home/claude/ft/out1.jsonl as you go (so progress is saved). Never invent numbers; use source locations. At the end verify every cid has exactly one line and report counts of include/exclude by reason and how many were abstract_only.

## S3.8. Full-text assessment and extraction — protocol file

# Full-text assessment and data extraction — protocol for assessors

Review: chronic venous disease (CVeD) and systemic vascular dysfunction / cardiovascular associations (systematic component: domains 2–7).

## Eligibility at full text (ALL required)
1. Primary study in humans (observational or interventional) with full peer-reviewed report (not conference abstract, not review, not letter without data, not case report/series <10).
2. Participants with chronic venous disease (varicose veins, CVI, CEAP C1–C6, venous leg ulcer, primary venous reflux).
3. Reports at least one of:
   - D2: circulating (peripheral, systemic blood — antecubital/arm or unspecified peripheral venous blood) biomarkers of inflammation, endothelial activation, oxidative stress, coagulation/prothrombotic state, MMPs, compared between CVeD and a comparator WITHOUT venous disease (observational). (Studies of leg/varicose-vein blood only, or without non-CVeD controls → exclude reason "no non-CVeD comparator / local blood only"; they go to the evidence map.)
   - D3: directly measured vascular function/structure outside the affected venous territory (FMD, PWV, augmentation index, arterial stiffness, carotid IMT/plaque, ABI, coronary calcium, systemic microvascular function), CVeD vs comparator or within CVeD severity or before/after treatment.
   - D4: association between CVeD and cardiovascular disease (CAD, MI, angina, stroke, PAD, heart failure, AF, hypertension, atherosclerosis, CV risk score), cross-sectional/case-control/cohort, with a comparator (non-CVeD or severity strata).
   - D5: incident cardiovascular events, VTE, or mortality in CVeD vs no CVeD (or by severity), longitudinal.
   - D6: incremental CV risk prediction including CVeD.
   - D7: Mendelian randomization or genetic causal inference linking CVeD (as exposure or outcome) with CV diseases, CV risk factors, or inflammatory mediators.
Exclusion reasons (use exactly one): NOT_PRIMARY; CONF_ABSTRACT; CASE; POP_NOT_CVeD; NO_ELIGIBLE_OUTCOME; NO_COMPARATOR_OR_LOCAL_ONLY; DUPLICATE_OR_OVERLAP (state of which); NO_FULL_TEXT (only if neither full text nor sufficient abstract data can be obtained); RETRACTED; OTHER (state).

## Retrieval
Try in order: PMC full text (search PMC by PMID or DOI), publisher page via DOI (open access), WebFetch of doi.org link. If the full text is not accessible, use the abstract and set "source":"abstract_only" (allowed for eligibility if the abstract clearly settles it; extraction marked incomplete). Do not fabricate. Every number must be traceable to the source with a location (section/table/abstract).

```
## Output (one JSON object per record, JSON Lines file)
{
 "cid":..., "title":..., "first_author":..., "year":..., "doi":..., "source":"full_text|abstract_only",
 "decision":"include|exclude", "exclusion_reason":null|"...", "domains":["D3",...],
 "country":..., "setting":..., "design":..., "period":..., "data_source":...,
 "population":"CVeD definition, CEAP", "n_cved":..., "n_comparator":..., "comparator":...,
 "exposure_definition":..., "outcome_or_measure":..., "followup":...,
 "events_or_values":"group values / events / rates as reported",
 "effect_estimate":"e.g. HR 1.46 (95% CI 1.19–1.79), adjusted",
 "adjustment":"variables or 'unadjusted'",
 "direction":"positive|null|inverse|mixed",
 "key_limitations":..., "funding_coi":...,
 "rob_tool":"NOS-cohort|NOS-case-control|JBI-ACS|JBI-cohort|JBI-QE|MR-framework",
 "rob_items":{"item":"Y/P/U/N/NA — reason (location)"},
 "rob_summary":{"selection":"L/S/H/U","confounding":"L/S/H/U","measurement":"L/S/H/U","other":"L/S/H/U"},
 "locations":"where key data were found",
 "notes":...
}
RoB item lists:
- NOS cohort: S1 representativeness, S2 selection non-exposed, S3 ascertainment exposure, S4 outcome absent at start, C1 main confounder, C2 additional, O1 outcome assessment, O2 follow-up length, O3 follow-up adequacy. Map S1–S4→selection, C→confounding, O1→measurement, O2–O3→other.
- NOS case-control: S1 case definition, S2 representativeness, S3 control selection, S4 control definition, C1, C2, E1 exposure ascertainment, E2 same method, E3 non-response. Map S→selection, C→confounding, E1–E2→measurement, E3→other.
- JBI analytical cross-sectional (8): Q1 inclusion criteria, Q2 subjects/setting, Q3 exposure valid, Q4 objective criteria condition, Q5 confounders identified, Q6 strategies confounding, Q7 outcome valid, Q8 statistics. Map Q1–Q2→selection (also judge appropriateness of comparison group), Q5–Q6→confounding, Q3,Q4,Q7→measurement, Q8→other.
- JBI cohort (11) and JBI quasi-experimental (9) as standard.
- MR framework: instrument threshold/strength (F), independence/confounder screening, population structure (ancestry), phenotype definition, sample overlap, pleiotropy tests, heterogeneity, sensitivity/direction (Steiger, reverse MR), MVMR, multiple-testing. Map relevance→selection, independence/structure→confounding, phenotype/overlap→measurement, pleiotropy/sensitivity→other.
Column rule: H if any mapped item N; S if any U/P and none N; L if all Y; U only if all U.
```

## S3.9. Full-text extraction from author-supplied PDFs — task prompt

```
Read these original article PDFs (use `pdftotext -layout` via Bash; do NOT use any browser or web tools) in /home/claude/in/bib/BIBLIOGRAFIA 02/ :
- nóbrega-et-al-2023-...pdf (Nobrega, Vascular 2024, FMD before/after varicose vein surgery)
- tomita-et-al-2025-...pdf (Tomita, Phlebology 2025, CVI and coronary calcium)
- 1-s2.0-S0914508725001327.pdf (Yu HR, J Cardiol 2025, reflux-sensitive microRNAs)
- 11010_2025_Article_5398.pdf (Ratiu, Mol Cell Biochem 2026, MAO in varicose veins)
- wound.2023.0028.pdf (Kim J, Adv Wound Care 2024, biofilm, CRP in CVLU)
- chervonski-et-al-2026-...pdf (Chervonski, Phlebology 2026, VLU and survival)
- 1-s2.0-S075333222600185X.pdf (Karthika, Biomed Pharmacother 2026, NRF2)

Report ONLY what the text states, with page/section/table location for every item; write "not reported" otherwise. Never infer.

For EACH paper extract: country, institution, recruitment/study period, sample size (enrolled/analysed per group), design, funding statement, conflicts of interest statement, any industry affiliation.
Specific items:
- Nobrega: exact FMD values pre and post (mean or median? SD/SE/IQR?), n enrolled, n analysed, reasons for losses, statistical test, whether paired, any paired mean difference/CI/SD of difference, blinding, control group, power calculation.
- Tomita: CACS values with dispersion type (SD?), recruitment period, how controls were selected, covariates in multivariable model.
- Yu: number of human specimens per group (reflux ~1 s, >2 s, normal saphenous), source of control veins, period.
- Ratiu: country/city, period, n, groups.
- Kim J 2024: what "BF" means (Bayes factor? BF10?), the exact BF value for biofilm–CRP, CRP units, sample size, parent study/grant IDs, recruitment period.
- Chervonski 2026: institution, period, total n, VLU n, reference group (C2–C4?), follow-up, number of deaths per group, HRs (crude/adjusted, CI), adjustment covariates, whether the 2025 JVS-VL abstract is mentioned as prior presentation.
- Karthika: number of VV and control veins, control source, authors' group, overlap of tissue samples with Sreelakshmi 2024 (Eur J Cell Biol) if mentioned.

Also, for risk-of-bias support, for each human study note: inclusion criteria clarity, setting description, confounders identified/handled, outcome measurement validity, statistical analysis, missing data/attrition — each with page/section location.

Return a concise structured report.
```

## S3.10. Evidence map — task prompt

Build an evidence map (descriptive, abstract-level) for a systematic review on chronic venous disease (CVeD).
Input: /home/claude/scr/as/map_input.txt (770 records; header line has cid, year, and 'refined' category: D1 = local venous pathobiology from first pass, L = local-only, S2b = circulating biomarkers without non-CVeD controls, S4rf = traditional CV risk factors as correlates of CVeD).
Read every record yourself (Read in chunks; no keyword-based deciding). For each record write a TSV line to /home/claude/scr/as/map_out.tsv (append per chunk):
cid<TAB>species (human|animal|both|in_vitro_human_tissue)<TAB>compartment (vein_wall_valve|venous_endothelium_cells|local_venous_blood|leg_skin_microcirculation|wound_fluid_ulcer_tissue|systemic_blood|whole_patient_clinical)<TAB>main_theme (one of: MMP_ECM_remodelling | oxidative_stress | inflammation_leukocytes_cytokines | endothelial_activation_adhesion_NO | shear_stress_mechanotransduction | hypoxia_HIF | smooth_muscle_cell_phenotype | gene_or_miRNA_expression | coagulation_prothrombotic | microcirculation_capillaries | risk_factors_obesity_metabolic | other)<TAB>comparator (non_CVeD_tissue_or_controls|severity_strata|pre_post_treatment|local_vs_systemic|none)<TAB>eligible_for_map (Y|N with reason if N, e.g. not CVeD, review, no data)
Verify each cid appears once. Then write /home/claude/scr/as/map_summary.md with counts by species, compartment, theme, comparator, and decade of publication (for Y only), plus a 6–8 line narrative summary of consistent findings (e.g., direction of MMP, oxidative stress findings) based only on the abstracts.

## S3.11. Table-cell condensation — task prompt

You are condensing data-extraction records of a systematic review into short, publication-ready table cells.
Input: /home/claude/cond/in1.json (a JSON list of records). Output: write /home/claude/cond/out1.jsonl with exactly one JSON object per input record (same order), with these keys:
- "cid" (copy as-is)
- "design": design + country + data source/setting, ≤ 18 words (e.g., "Retrospective PS-matched cohort; Taiwan; NHI claims database")
- "followup": follow-up duration, ≤ 8 words, or "NR" if not reported / not applicable for cross-sectional ("—")
- "n": numbers as "CVeD n / comparator n" with a 2–6 word label of the comparator, ≤ 18 words (e.g., "4644 VV / 17,742 matched controls"). Use "NR" for unknown numbers.
- "exposure": exposure definition, ≤ 15 words
- "outcome": outcome(s) or measurement(s), ≤ 15 words
- "events": events, rates or group values, ≤ 25 words, or "NR"
- "estimate": the main effect estimate(s) with 95% CI and adjusted/unadjusted status, ≤ 35 words; keep the most important (adjusted, primary outcome) numbers; for multiple outcomes keep up to 3–4 key ones
- "adjustment": main adjustment/matching variables, ≤ 15 words, or "Unadjusted"/"NR"

STRICT RULES:
1. Use ONLY information present in the record. Never add, infer, or round numbers; copy numbers exactly (you may change "-" in CIs to "–").
2. Never end a cell with "…" or "..." and never cut a sentence mid-way: each cell must read as a complete phrase. Shorten by selecting the most important items and using standard abbreviations (HR, aHR, OR, aOR, CI, VV, CVI, CVeD, VTE, DVT, PE, HF, AF, PAD, CHD, MI, MACE, PS, FMD, PWV, CAVI, ABI, IMT, CRP, IL, MMP, vWF, BMI, SBP, MR, IVW, GWAS).
3. Remove source-location notes such as "(Abstract)", "(Table 2)", "(Methods)" and remarks like "not verifiable without full text".
4. English, no markdown. Write valid JSON lines with ensure_ascii=False. Use a Python script to write the file if convenient, but write the condensed text yourself — do not truncate programmatically.
When done, verify the line count equals the number of input records and that no value contains "…" or "...". Reply only "done N".

## S3.12. Pre-classification of disagreements for adjudication — task prompt

You are pre-classifying records for a systematic review adjudication. Input: /home/claude/r2/adj/in1.json (list of records with cid, year, title, abstract, pubtype, journal). A human screener wanted these to go to full-text review; an earlier automated pass had excluded them. Your job: mark each record EXCLUIR only when the title/abstract/publication type UNAMBIGUOUSLY shows it fails the criteria; otherwise mark DUDOSO (the human will decide). Be conservative: if a full text could plausibly contain eligible data, use DUDOSO.

Eligibility (all needed): primary study in humans (≥10 participants; not review, editorial, letter without data, conference abstract, case report); population with chronic venous disease of the LOWER LIMBS (varicose veins, chronic venous insufficiency, CEAP C1–C6, venous leg ulcer, primary venous reflux); AND reports at least one of: circulating blood biomarkers (inflammation, endothelial, oxidative, coagulation, MMP) compared with people WITHOUT venous disease; vascular function/structure measured outside the affected venous territory (FMD, PWV, arterial stiffness, IMT, ABI, coronary calcium, systemic microcirculation); association with cardiovascular disease (CAD, MI, stroke, PAD, heart failure, AF, hypertension, atherosclerosis); incident cardiovascular events, venous thromboembolism or mortality; cardiovascular risk prediction; Mendelian randomization/genetic causal inference with CV traits.
Separate category MAPA (evidence map) = primary studies of LOCAL venous pathobiology (vein wall/valve, local venous blood, leg skin microcirculation, ulcer tissue/fluid), animal models, or circulating markers without a non-venous-disease control group. If a record clearly belongs to MAPA, mark MAPA.
Clear EXCLUIR reasons (use exactly one Spanish label): "Revisión/no primario", "Congreso", "Carta/editorial", "Caso o serie <10", "Población no ECV MMII" (e.g., pelvic varices, esophageal varices, post-thrombotic syndrome only, acute DVT only, mixed/arterial ulcers without separate CVeD data, healthy populations), "Sin resultado

elegible" (e.g., only treatment efficacy, surgical technique, symptoms, quality of life, wound healing, recurrence, imaging technique, epidemiology of risk factors without CV outcome), "Retractado", "Otro".
Output: write /home/claude/r2/adj/out1.tsv with one line per input record: cid<TAB>DECISION(EXCLUIR|DUDOSO|MAPA)<TAB>reason label (empty if DUDOSO)<TAB>short justification in Spanish (≤20 words). Process every record (read the JSON in chunks if needed); write the file with a Python script containing your decisions. Verify line count equals number of records. Reply only "done N (EXCLUIR x, DUDOSO y, MAPA z)".