|  |  |  |
| --- | --- | --- |
| Variable |  |  |
| nct\_id |  |  |
| Results\_first\_submitted\_date |  |  |
| Is\_fda\_regulated\_drug |  |  |
| Is\_fda\_regulated\_device |  |  |
| Overall\_status | In (‘Completed’, ‘Terminated’) |  |
| Primary\_completion\_date |  |  |
| Completion\_date |  |  |
| Completion\_Date\_type |  |  |
| Study\_type |  |  |
| Verification\_date |  |  |
| Phase |  |  |
| Plan\_to\_share\_ipd |  |  |
| Plan\_to\_share\_ipd\_description |  |  |
| Has\_dmc |  |  |
| Disposition\_first\_submitted\_date |  |  |
| Is\_us\_export |  |  |
| First\_results\_pending | Min(event\_date) |  |
| dthaeYN | Adverse\_event\_term in (‘Total, all-cause mortality’, ‘Death’, ‘death’) |  |
| AEasYN | Reported\_Events.default\_assessment != ‘’ |  |
| AEtfYN | Reported\_Events.time\_frame != ‘’ |  |
| outcomeYN | Has **Outcomes** |  |
| oPOPYN | Outcomes.population != ‘’ |  |
| oPOPcount | Count(DISTINCT population) [group by nct\_id] |  |
| aeYN | Has **Reported\_Events** |  |
| analysisYN | Has **Outcome\_Analyses** |  |
| POcount | Outcomes.outcome\_type = ‘Primary’ |  |
| SOcount | Outcomes.outcome\_type = ‘Secondary’ |  |
| baseYN | Has **Baseline\_Measurements** |  |
| Basecount | Count(distinct title) from baseline\_measurements |  |
| raceYN | Baseline\_Measurements.title in (‘Race/Ethnicity’, ‘Customized’, ‘Ethnicity (NIH/OMB)’, ‘Race (NIH/OMB)’ |  |
| ACT | Us\_site = 1  Study\_type = “Interventional”  riskyIntervention = 1  phase NOT IN (‘Early Phase 1’, ‘Phase 1’, ‘N/A’)  primary purpose != ‘Device Feasibility’ |  |
| Countries | In (‘United States’, ‘American Samoa’, ‘Guam’, ‘Northern Mariana Islands’, ‘Puerto Rico, ‘U.S. Virgin Islands’)  And removed is NULL |  |
| Designs |  |  |
| Risky\_intervention | Intervention\_type in (‘Drug’, ‘Diagnostic Test’, ‘Device’, ‘Biological’, ‘Combination Product’, ‘Genetic’, ‘Radiation’) |  |
| Funding | When Sponsors.agency\_class = ‘NIH’ or b.NIHcol=1  Where Sponsors.agency\_class = |  |