GeneBench-Pro Case Study: DRX1 Carrier-Screening Residual Risk

GeneBench-Pro

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1 Overview

This case study asks whether an analyst can convert compact carrier-screening assay evidence into residual reproductive risk for an autosomal recessive DRX1 condition. Carrier screening is routinely interpreted through prevalence, assay detection rate, and residual risk after a negative result, but those quantities become harder to estimate when the screened alleles include sequence variants, copy-number alleles near paralogous sequence, and haplotypes that are only indirectly tagged by phased markers [1,2]. The released target is not an observed positive-call rate. It is an assay-calibrated, roster-standardized probability-scale answer with five fields: AFR and EUR screening-roster carrier frequencies, AFR residual carrier risk after a negative screen, full-partner-roster carrier frequency, and the resulting affected-conceptus risk after applying the prompt-defined autosomal-recessive 1/4 inheritance factor.

The analysis is a three-stage cascade. Stage 1 converts target-level assay rows into sample-level reportable carrier classes, excluding segmental-duplication copy-number mimics and collapsing two founder-marker rows into one phased haplotype. Stage 2 uses calibration controls to estimate ancestry-, assay-batch-, and allele-class-specific sensitivity and false-positive rates; in particular, the AFR exon-deletion sensitivity is much lower than the EUR deletion sensitivity, and deletion false positives remain nonzero even after quality control. Stage 3 assembles the clinical estimand by computing the AFR screen-negative posterior and standardizing partner carrier frequency to all rows in `partner_roster.tsv.gz` over ancestry, family-history tier, intake site, and collection wave. Naive analyses fail because they treat row-level positives as carriers, average away allele-class detection differences, condition on the tested partner subset instead of the full partner roster, or collapse visible selection strata that change the answer.

2 Released Prompt and Files

Prompt

```
Using cohort_roster.tsv.gz, partner_roster.tsv.gz, calibration_controls.tsv.gz, target_metadata.tsv
    .gz, and assay_observations.tsv.gz, estimate residual reproductive risk for an autosomal
    recessive DRX1 condition. Report all quantities on the probability scale, not as percentages:
    carrier_frequency_afr and carrier_frequency_eur among screening-roster adults;
    residual_carrier_risk_afr_negative for an AFR screening-roster adult with a negative DRX1
    screen; partner_carrier_frequency_full_roster for a uniformly sampled partner_roster.tsv.gz row
    ; and couple_reproductive_risk for an affected conceptus when the index person is AFR and
    screen-negative and the partner is drawn from partner_roster.tsv.gz. Assume autosomal recessive
     inheritance with a 1/4 affected-conceptus risk conditional on both biological parents being
    carriers.
These data came from a real experiment; you will be graded not just on numerical correctness but
    the quality of analytical reasoning you exhibit; do not attempt to take any shortcuts.
Return your final answer as exactly one JSON object.
Do not wrap the JSON in markdown.
Do not add prose before or after the JSON.
Do not omit any keys shown in the example.
Return the JSON object in your final answer:
{
  "answer": {
    "carrier_frequency_afr": <float>,
    "carrier_frequency_eur": <float>,
    "residual_carrier_risk_afr_negative": <float>,
    "partner_carrier_frequency_full_roster": <float>,
    "couple_reproductive_risk": <float>
  },
  "reasoning": "<description of method and QC>"
}
```

Released data files

File	Format	Contents
cohort_roster.tsv.gz	.tsv.gz	Screening adults: sample identifier, ancestry, and family-history tier.
partner_roster.tsv.gz	.tsv.gz	Full partner roster: ancestry, family-history tier, intake site, collection wave, and testing status.
calibration_controls.tsv.gz	.tsv.gz	Independently characterized controls with reference class and assay batch.
target_metadata.tsv.gz	.tsv.gz	Target labels, grouping labels, and metadata for four DRX1 targets.
assay_observations.tsv.gz	.tsv.gz	Target-level depth, allele fraction, copy-ratio, split-read, mapping, paralog, segmental-duplication, and phase evidence.

The released files contain 800 screening adults, 500 partner rows, 2,320 calibration controls, 4 target-metadata rows, and 13,196 target-level assay observations. The task is recoverable from these staged inputs together with the public answer contract.

3 Answer Fields and Tolerances

The public answer contract contains five probability-scale fields. The realized target values below are the finite released-data estimator values encoded in `eval_config.json`.

Answer field	Ground truth	Tolerance / matching rule	Interpretation
`carrier_frequency_afr`	0.100298331312	Absolute error ≤ 0.002; range [0,1]	Detection-corrected probability that an AFR screening-roster adult carries any reportable DRX1 class.
`carrier_frequency_eur`	0.077298413255	Absolute error ≤ 0.002; range [0,1]	Detection-corrected probability that a EUR screening-roster adult carries any reportable DRX1 class.
`residual_carrier_risk_afr_negative`	0.039644286232	Absolute error ≤ 0.0005; range [0,1]	Posterior carrier probability for an AFR screening-roster adult after a negative DRX1 screen.
`partner_carrier_frequency_full_roster`	0.279249390064	Absolute error ≤ 0.003; range [0,1]	Carrier probability for a uniformly sampled row from the full partner roster.
`couple_reproductive_risk`	0.002767660687	Absolute error ≤ 0.0001; range [0,1]	Affected-conceptus probability for an AFR screen-negative index person and a full-roster partner.

4 Structure Diagram

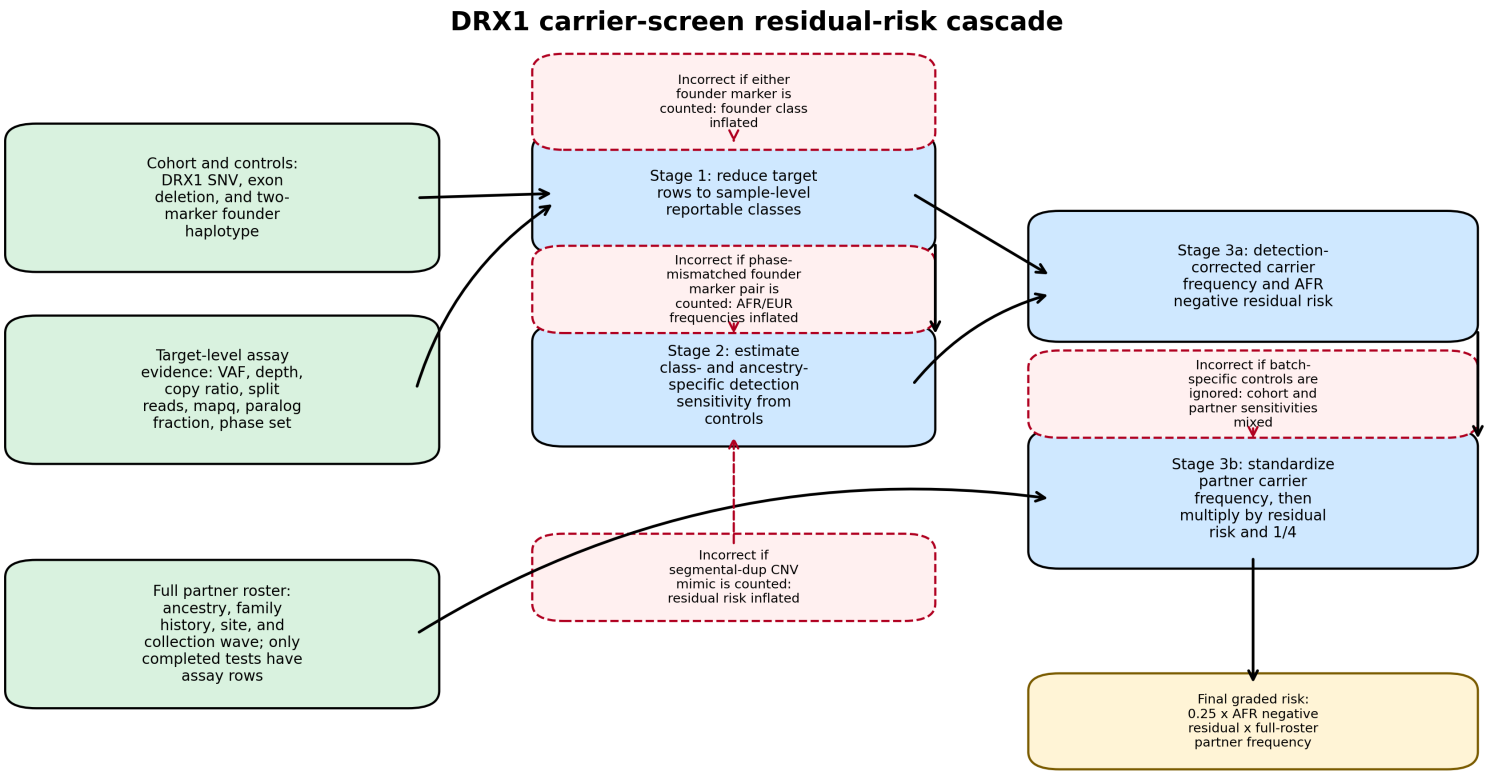

Figure 1: Pipeline view of the DRX1 residual-risk analysis. Green boxes are released input files, blue boxes and solid arrows show the intended workflow, red callouts show representative incomplete analyses, and the yellow box shows the final released risk. The structure is important because each stage changes the target of inference: sample-level reportable calls feed sensitivity and false-positive calibration, calibration feeds both the AFR residual-risk posterior and partner carrier-rate estimation, and the partner estimator must then be standardized to the full roster before the prompt-defined 1/4 inheritance factor is applied.

5 Variables and Assumptions

Symbol	Type/domain	Meaning and assumption
i	person index	Screening adult, calibration control, or partner row. Cohort adults and partner rows are different target populations.
A_i	$\{\text{AFR}, \text{EUR}\}$	Ancestry stratum used for cohort carrier-frequency estimation and control calibration.
H_i	$\{0, 1\}$	Family-history tier used in partner-roster standardization.
U_i, W_i	site and wave	Intake site and collection wave. Testing completion and carrier-rate estimates vary across these visible strata.
K	three carrier classes	Reportable allele classes: SNV_A, DEL_E10E11, and FOUNDER_H1.
O_{it}	target-row vector	Visible assay measurements for target t: depth, alternate reads, allele fraction, log2 copy ratio, split reads, mapping quality, paralog fraction, segmental-duplication score, and phase set.
Y_{ik}	$\{0, 1\}$	Detected reportable class after target-scope filtering, sequence/CNV quality control, and founder-haplotype collapse.
s_{abk}	probability	Sensitivity for ancestry a, assay batch b, and reportable class k.
f_{abk}	probability	False-positive rate for ancestry a, assay batch b, and reportable class k. In the realized call set, deletion false positives are the relevant nonzero component.
g	stratum tuple	Partner-standardization cell $g = (A, H, U, W)$.

The estimator treats the calibration controls as independent reference information for assay performance. Partner testing is assumed conditionally transportable within the visible (A, H, U, W) cells: completed tests identify the cell-specific calibrated carrier rates, and the full roster supplies the target-population weights. The public target is the recoverable released-data estimator, not a hidden latent population parameter.

6 Data-Generating Process

The simulation fixes finite roster and control counts first, then emits target-level observations with wide separation in the quality-control dimensions that matter for carrier-state recovery.

Rosters. The screening cohort has equal ancestry denominators,

$$n_{\text{AFR}} = 400, \qquad n_{\text{EUR}} = 400. \tag{1}$$

The partner roster has 500 rows over ancestry, family-history tier, intake site, and collection wave. Testing is selected rather than uniform. For example, AFR/FH0/site A/wave 1 has 130 partner rows but only 6 completed tests, while most site B cells are fully tested.

Latent classes and intended detections. The cohort latent reportable counts are

	SNV_A	DEL_E10E11	FOUNDER_H1
AFR	11	24	5
EUR	9	7	16

(2)

and the intended true-positive detected counts are

	SNV_A	DEL_E10E11	FOUNDER_H1
AFR	10	13	3
EUR	8	6	13.

(3)

Additional none-carrier rows are generated with deletion-like evidence: 18 AFR and 8 EUR rows can appear deletion-positive unless the analyst uses segmental-duplication evidence and then carries the remaining false-positive rate into the specificity correction.

Calibration controls. For each ancestry and assay batch, controls include 130 SNV, 150 deletion, 120 founder, and 180 none-reference rows. Cohort samples use batch lot_A17; tested partner rows use batch lot_C42. The cohort-batch sensitivity and false-positive rates recovered by the reference call set are

	$s_{\text{lot\_A17}}$			$f_{\text{lot\_A17}}$		
	SNV	DEL	FOUNDER	SNV	DEL	FOUNDER
AFR	0.907692	0.520000	0.733333	0	0.050000	0
EUR	0.938462	0.853333	0.833333	0	0.022222	0.

(4)

This is why the problem is not solved by dividing observed positives by a single detection rate.

Target observations. Reportable sequence positives have high depth, allele fractions near heterozygous dosage, high mapping quality, and low paralog fraction. Deletion positives have log2 ratios below -0.35, split-read support of at least 3, and low segmental-duplication scores; deletion mimics can share the log2 and split-read pattern but have high segmental-duplication scores. Founder carriers require both T03 and T04 to pass sequence rules on the same phase set; dropout controls present only one high marker, and phase decoys present high markers on different phase sets. Gene/pseudogene and structural-variant examples motivate this multi-evidence framing rather than a single readout [3–5].

Partner strata. Partner rows are generated over 16 (A, H, U, W) cells. Site and wave are both answer-changing because completion and carrier-rate estimates differ within otherwise similar cells. For example, EUR/FH0/site A/wave 1 contributes 0.084783 to the full-roster partner frequency, while EUR/FH0/site A/wave 2 contributes only 0.000193.

7 Analyst Walkthrough

Step 1: orient the target populations. A careful analyst first separates the screening roster, the partner roster, and the calibration controls. The screening denominators are 400 AFR and 400 EUR adults. The partner denominator is all 500 partner rows, not the 179 rows with completed testing, because the prompt asks for a uniformly sampled row from `partner_roster.tsv.gz`. The control file supplies 2,320 reference rows for assay calibration. These three denominators are enough to disqualify the two most tempting shortcuts before any model is fit: treating observed cohort positives as carrier frequencies, and estimating partner frequency only among completed tests.

Step 2: reduce target rows to reportable carrier classes. Sequence targets must satisfy depth, allele-fraction, mapping-quality, paralog, and report-scope checks before they become reportable calls. Copy-number evidence must satisfy both a deletion signal and a segmental-duplication quality check. Founder evidence must be collapsed from two marker rows into one phased haplotype, because accepting either marker or counting both markers estimates a different biological class. Figure 2 shows the relevant separations: deletion-like none controls are distinguishable by segmental-duplication score, high founder-marker pairs only define the haplotype when the phase set agrees, and partner testing is visibly selected by site and wave.

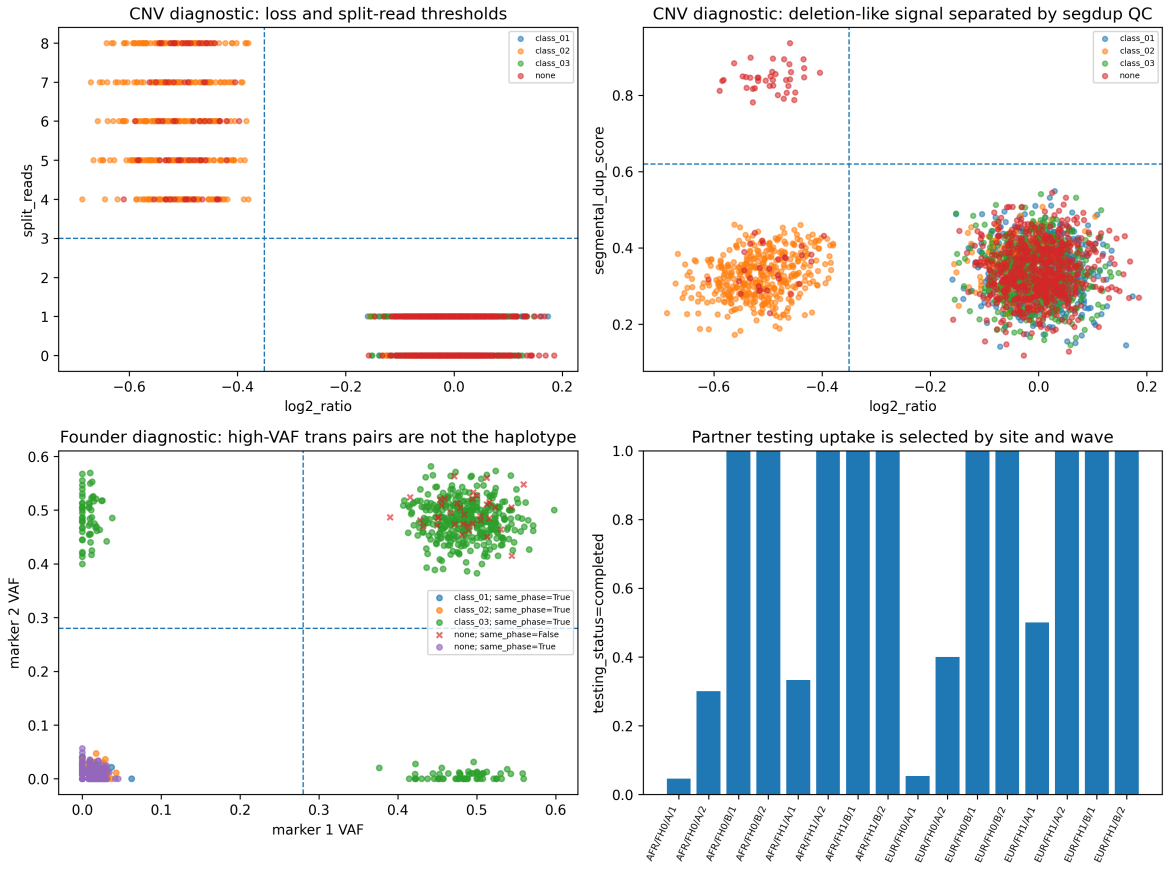

Figure 2: Stage-1 and selection diagnostics. The copy-number panels show that log2 ratio and split reads identify deletion-like evidence, but segmental-duplication score separates reportable deletion calls from deletion mimics. The founder panel shows why both marker rows and same-phase evidence are needed for one haplotype call. The partner panel shows that completed testing varies across visible ancestry, family-history, site, and wave cells.

Step 3: use controls to estimate assay performance. After reportable-call construction, the cohort detected counts are

	SNV_A	DEL_E10E11	FOUNDER_H1
AFR	10	31	3
EUR	8	14	13.

(5)

These are detected-call counts, not carrier-frequency estimates. The correct estimator uses controls to estimate s_{abk} and f_{abk}, then solves the specificity-adjusted detected-call equation. Figure 3 shows

the most important pattern: AFR deletion sensitivity is much lower than EUR deletion sensitivity in the cohort batch, and class contributions differ by ancestry after calibration. Ignoring assay specificity reports `carrier_frequency_afr` = 0.186808 and `residual_carrier_risk_afr_negative` = 0.086301, both far outside tolerance.

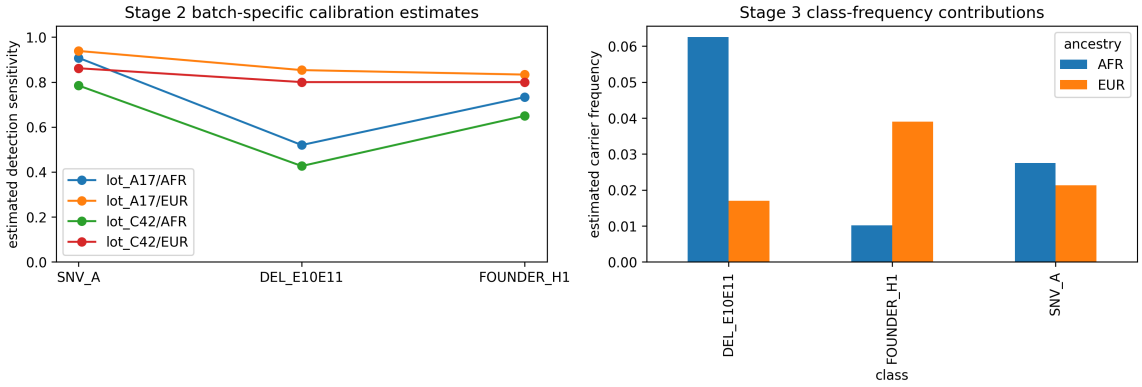

Figure 3: Control-calibrated sensitivity and cohort class-frequency estimates. The left panel shows batch-, ancestry-, and class-specific sensitivity, including the low AFR deletion sensitivity in lot_A17. The right panel shows the detection-corrected carrier-frequency contributions that sum to the two released ancestry-specific carrier frequencies.

Step 4: compute carrier frequencies and the AFR negative-screen posterior. Solving the specificity equations gives the class-frequency ledger

	SNV_A	DEL_E10E11	FOUNDER_H1	sum
AFR	0.027542	0.062529	0.010227	0.100298
EUR	0.021311	0.016987	0.039000	0.077298.

(6)

Residual risk after a negative screen is then a class-specific missed-carrier posterior, not total carrier frequency multiplied by one minus an average sensitivity [2]. The numerator for AFR is

$$0.027542(1 - 0.907692) + 0.062529(1 - 0.520000) + 0.010227(1 - 0.733333) = 0.035283, \tag{7}$$

and the denominator is the probability of a negative reportable screen after accounting for deletion false positives. Because the observed positive probability is 0.110000,

$$\texttt{residual\_carrier\_risk\_afr\_negative} = 0.035283/(1 - 0.110000) = 0.0396442862. \tag{8}$$

Step 5: standardize partner carrier frequency to the full roster. The partner estimator uses the same reportable-call and lot C42 calibration logic, but the target population is different. The completed partner tests estimate carrier rates within visible cells; all 500 partner rows define the weights. Figure 4 shows why this is necessary. Some large full-roster cells are sparsely tested, carrier-rate estimates change sharply by wave inside the same family-history and site cell, and limited standardizations miss the released full (A, H, U, W) estimand.

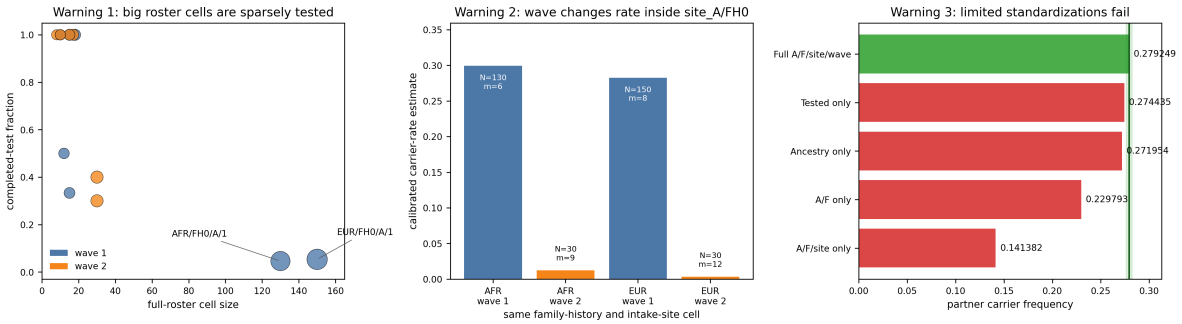

Figure 4: Partner-standardization diagnostics. The left panel shows that large target-roster cells can have very low completed-test fractions. The middle panel shows that collection wave changes calibrated carrier-rate estimates inside the same family-history and site context. The right panel compares limited standardizations against the full ancestry/family-history/site/wave estimator; the green band marks the released tolerance around the correct partner frequency.

The full-roster standardization is

$$\widehat{f}_{\text{partner}} = \sum_{g} \frac{N_g}{500} \widehat{p}_g, \qquad g = (A, H, U, W), \tag{9}$$

where N_g is the number of rows in the full partner-roster cell and $\widehat{p}_g$ is the calibrated carrier-rate estimate from completed tests in that cell. This is the same reweighting logic used to recover target-population quantities from selected observations when selection is explainable by observed strata [7]. The 16 cell contributions sum to `partner_carrier_frequency_full_roster` = 0.2792493901. Tested-only standardization is close but still wrong at 0.274435; omitting collection wave is much worse at 0.141382.

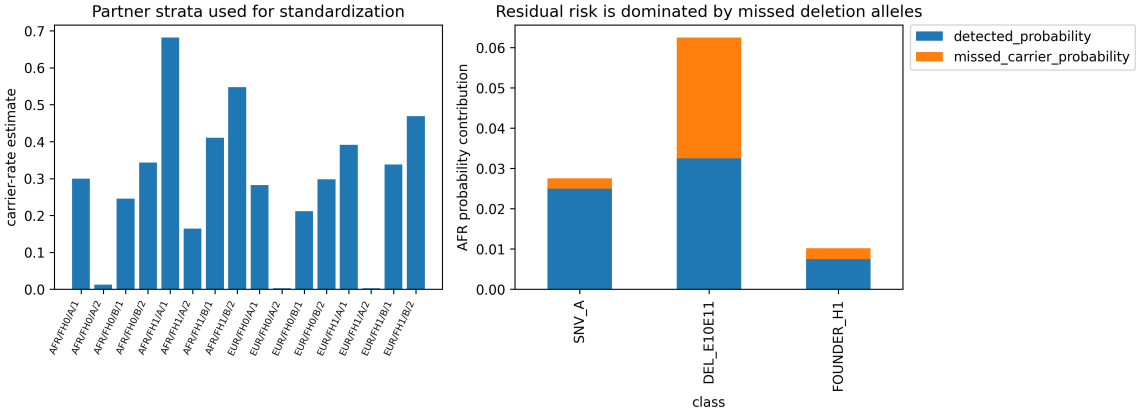

Figure 5: Final accounting diagnostics. The partner panel shows the per-cell carrier-rate estimates used by the full-roster standardization. The residual-risk panel decomposes AFR detected and missed probability by allele class, showing why missed deletion alleles dominate the negative-screen numerator.

Step 6: assemble the affected-conceptus probability. Once the two parental probabilities are on the correct target-population scale, the final multiplication is direct:

$$\texttt{couple\_reproductive\_risk} = 0.25 \times 0.0396442862 \times 0.2792493901 = 0.0027676607. \tag{10}$$

8 Estimand

Let $K = \{\text{SNV\_A}, \text{DEL\_E10E11}, \text{FOUNDER\_H1}\}$. For screening ancestry a, the released carrier frequency is

$$\widehat{f}_a = \sum_{k \in K} \widehat{p}_{ak}, \tag{11}$$

where $\widehat{p}_{ak}$ is the specificity-deconvolved reportable carrier probability among screening adults.

For an AFR screening adult with a negative screen, the released residual-risk target is

$$\widehat{r}_{\text{AFR},-} = \frac{\sum_{k \in K} \widehat{p}_{\text{AFR},k}(1 - \widehat{s}_{\text{AFR,lot\_A17},k})}{1 - \sum_{k \in K} \left[\widehat{p}_{\text{AFR},k}\widehat{s}_{\text{AFR,lot\_A17},k} + (1 - \sum_{\ell \in K} \widehat{p}_{\text{AFR},\ell})\widehat{f}_{\text{AFR,lot\_A17},k}\right]}. \tag{12}$$

For partners, the released target is the full-roster standardized carrier probability

$$\widehat{p}_{\text{partner}} = \sum_{g} \frac{N_g}{500} \sum_{k \in K} \widehat{p}_{gk}, \qquad g = (A, H, U, W), \tag{13}$$

where $\widehat{p}_{gk}$ is estimated from completed tests in the same visible stratum using partner-batch controls. The released couple risk is

$$\widehat{q} = \frac{1}{4}\widehat{r}_{\text{AFR},-}\widehat{p}_{\text{partner}}. \tag{14}$$

9 Estimator

Stage 1 builds sample-by-class calls from target-level rows. The SNV call uses target scope plus depth, allele fraction, mapping-quality, and paralog filters. The deletion call uses copy-ratio, split-read, and segmental-duplication filters. The founder call requires both founder-marker rows on the same non-missing phase set:

$$Y_{i,\text{SNV}} = \mathbf{1}\{\text{T01 sequence pass},\ \text{scope}_{T01} = \text{reportable}\}, \tag{15}$$

$$Y_{i,\text{DEL}} = \mathbf{1}\{\ell_{i,T02} \le -0.35,\ r_{i,T02} \ge 3,\ \text{segdup}_{i,T02} \le 0.62\}, \tag{16}$$

$$Y_{i,\text{FOUNDER}} = \mathbf{1}\{\text{T03 pass},\ \text{T04 pass},\ \text{phase}_{T03} = \text{phase}_{T04} \neq .\}. \tag{17}$$

Phasing and cis/trans resolution are central to interpreting recessive allele configurations, which is why the founder-marker rows are not treated as independent alleles [6].

Stage 2 estimates assay performance in controls by ancestry, assay batch, and class:

$$\widehat{s}_{abk} = \Pr(Y_k = 1 \mid A = a, B = b, G = k), \tag{18}$$

$$\widehat{f}_{abk} = \Pr(Y_k = 1 \mid A = a, B = b, G = \text{none}). \tag{19}$$

Stage 3 solves the finite-sample class-frequency equation

$$\widehat{q}_{gk} = \widehat{p}_{gk}\widehat{s}_{abk} + \left(1 - \sum_{\ell \in K} \widehat{p}_{g\ell}\right)\widehat{f}_{abk}, \tag{20}$$

with a nonnegative active-set least-squares fit when finite observed rates fall below the control-derived false-positive rate. Cohort rows use $b = \text{lot\_A17}$, partner rows use $b = \text{lot\_C42}$, and the estimand equations above map the fitted class probabilities to the five released JSON fields.

10 Decision-Point and Ablation Walkthrough

Method	Pass	Output values (AFR, EUR, residual, partner, couple)	Decision point	Interpretation
`correct`	yes	0.100298, 0.077298, 0.039644, 0.279249, 0.002768	Reference	Reference estimator; all fields are within the public grader contract.
`cnv_no_segmental_dup_qc`	no	0.124143, 0.075672, 0.055963, 0.223263, 0.003124	Stage 1 CNV QC	Counts segmental-duplication deletion mimics as reportable deletions.
`founder_ignore_phase`	no	0.112561, 0.082373, 0.046334, 0.253756, 0.002939	Stage 1 founder phasing	Treats phase-mismatched marker pairs as the founder haplotype.
`founder_marker_rows`	no	0.112096, 0.082478, 0.023018, 0.262686, 0.001512	Stage 1 founder collapse	Counts the two founder markers as independent alleles.
`founder_either_marker`	no	0.111761, 0.082564, 0.039742, 0.245836, 0.002443	Stage 1 founder collapse	Calls the haplotype from either marker and absorbs dropout as carrier evidence.
`no_founder_sensitivity_correction`	no	0.097281, 0.070625, 0.036423, 0.257669, 0.002346	Stage 2 founder sensitivity	Uses phased calls but fails to correct for founder-marker dropout.
`ignore_assay_specificity`	no	0.186808, 0.101327, 0.086301, 0.325737, 0.007028	Stage 2 specificity	Treats all detected positives as true carriers despite deletion false positives.
`no_cnv_sensitivity_correction`	no	0.068705, 0.074750, 0.005921, 0.203146, 0.000301	Stage 2 deletion sensitivity	Misses the low AFR deletion sensitivity and severely understates residual risk.
`pooled_batch_sensitivity`	no	0.104242, 0.073215, 0.046650, 0.264003, 0.003079	Stage 2 batch matching	Pools cohort and partner assay batches even though control performance differs.
`pooled_detection_sensitivity`	no	0.102313, 0.064954, 0.027786, 0.263767, 0.001832	Stage 2 class calibration	Averages detection across classes and loses allele-specific missed-carrier accounting.
`nominal_95_percent_detection`	no	0.066667, 0.070359, 0.003745, 0.184519, 0.000173	Stage 2 calibration	Substitutes a nominal detection rate for the released control evidence.
`partner_ancestry_family_site_no_wave`	no	0.100298, 0.077298, 0.039644, 0.141382, 0.001401	Stage 3 partner target	Collapses collection wave, erasing a visible answer-changing selection stratum.
`partner_ancestry_family_standardization`	no	0.100298, 0.077298, 0.039644, 0.229793, 0.002277	Stage 3 partner target	Standardizes by ancestry and family history only, omitting site and wave.
`partner_tested_only_standardization`	no	0.100298, 0.077298, 0.039644, 0.274435, 0.002720	Stage 3 partner target	Estimates the tested subset rather than the uniformly sampled full partner roster.
`partner_raw_tested_only`	no	0.100298, 0.077298, 0.039644, 0.223464, 0.002215	Stage 3 partner target	Uses raw tested positives without calibration or target-population weighting.

Method	Pass	Output values (AFR, EUR, residual, partner, couple)	Decision point	Interpretation
`partner_ancestry_only_standardization`	no	0.100298, 0.077298, 0.039644, 0.271954, 0.002695	Stage 3 partner target	Adjusts ancestry only and leaves family-history, site, and wave selection.
`residual_mean_detection_rate`	no	0.100298, 0.077298, 0.030234, 0.279249, 0.002111	Stage 3 residual risk	Uses an average detection rate instead of class-specific missed-carrier probability.
`strict_cnv_evidence_cutoff`	no	0.098630, 0.088742, 0.053206, 0.215074, 0.002861	Stage 1 CNV QC	Over-filters CNV evidence and changes both cohort and partner quantities.
`compound_founder_phase_no_cnv_qc`	no	0.140199, 0.081021, 0.066031, 0.195496, 0.003227	Compound Stage 1	Combines founder-phase and CNV-QC failures.
`compound_specificity_batch_pooled`	no	0.204121, 0.104357, 0.105754, 0.304841, 0.008060	Compound Stage 2	Combines false-positive neglect with pooled assay-batch calibration.
`compound_specificity_partner_no_wave`	no	0.186808, 0.101327, 0.086301, 0.214970, 0.004638	Compound Stages 2-3	Inflates cohort risk and omits wave in partner standardization.
`compound_specificity_partner_tested`	no	0.186808, 0.101327, 0.086301, 0.336982, 0.007270	Compound Stages 2-3	Inflates cohort risk and targets tested partners rather than the roster.
`compound_cnv_qc_batch_pooled`	no	0.125244, 0.071213, 0.062969, 0.212847, 0.003351	Compound Stages 1-2	Keeps CNV mimics and pools batch sensitivity.
`compound_batch_pooled_partner_no_wave`	no	0.104242, 0.073215, 0.046650, 0.138757, 0.001618	Compound Stages 2-3	Pools assay batches and omits collection wave.
`compound_batch_pooled_partner_tested`	no	0.104242, 0.073215, 0.046650, 0.261620, 0.003051	Compound Stages 2-3	Pools assay batches and uses the tested partner subset.
`compound_marker_rows_partner_tested`	no	0.112096, 0.082478, 0.023018, 0.215575, 0.001241	Compound Stages 1-3	Counts founder marker rows and changes the partner denominator.
`compound_no_founder_sens_partner_no_wave`	no	0.097281, 0.070625, 0.036423, 0.124556, 0.001134	Compound Stages 2-3	Skips founder sensitivity correction and wave standardization.
`shortcut_raw_target_rows`	no	0.215000, 0.195000, 0.000000, 0.245810, 0.000000	Shortcut	Thresholds raw target rows and skips reportability, calibration, residual posterior, and partner standardization.
`shortcut_report_rate_no_calibration`	no	0.110000, 0.087500, 0.000000, 0.223464, 0.000000	Shortcut	Uses observed report rates without assay calibration or residual-risk conditioning.
`shortcut_controls_only_prevalence`	no	0.689655, 0.689655, 0.068966, 0.689655, 0.011891	Shortcut	Uses the enriched control panel as a prevalence source, which is not the target population.

11 References

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