

DNA TRIANGULATION CHECKLIST

Confirming a shared segment genuinely traces to a real common ancestor

Before you begin — quick glossary:

Identical by descent (IBD) — a shared DNA segment inherited from a real common ancestor — this is what you're trying to confirm.

Identical by state (IBS) — a shared DNA segment that matches by pure chance, with no common ancestor behind it — most common on small segments under 7 cM.

Chromosome browser — a visual tool showing exactly which chromosome positions you share with a match. Available on FTDNA and MyHeritage natively; Ancestry requires GEDmatch or DNA Painter for this.

Triangulation confirms that a shared DNA segment actually descends from a specific common ancestor — rather than being a coincidental match. Use it before adding any DNA-based conclusion to your tree.

Step 1 — Identify a candidate segment

- ☐ Choose a chromosome, start position, and end position to test — *positions are given in base-pair numbers, e.g. Chr 12: 45,000,000–62,000,000*
- ☐ Identify at least three matches who share this exact segment — ★ *three is the practical minimum — two matches sharing a segment could still be coincidence (see the glossary: IBS)*
- ☐ Confirm the segments genuinely overlap in range — *not just "all three overlap chromosome 12" — check that the start/end positions actually intersect using a chromosome browser or DNA Painter's "Chromosome Mapping" tool*
- ☐ Set a minimum segment size of 7 cM for anything you plan to rely on — *segments below 7 cM have a meaningfully higher chance of being identical by state (a coincidental match) rather than a real inherited segment*

Step 2 — Verify the matches also share DNA with each other

- ☐ Check that all candidate matches appear on each other's shared-match lists, not just on yours — ★ *this is the step people skip most often — three people can each match you on the same position without matching each other, which means it's NOT a valid triangulation group*
- ☐ Use a chromosome browser to visually confirm overlap — *GEDmatch: "One-to-many" then "One-to-one" comparison tool; DNA Painter: upload segment data and use the Chromosome Mapping tool; FTDNA: built-in Chromosome Browser under the match list*
- ☐ Rule out matches who overlap on position but don't match each other — *these form a false triangulation group — set them aside rather than including them*

Step 3 — Connect the segment to a genealogical line

- ☐ Identify the most recent common ancestor shared by all matches in the group — *cross-reference each match's tree; the ancestor should appear, directly or via descendants, in more than one of the group's trees*
- ☐ Confirm the paper-trail relationship for at least two of the matches — *birth, marriage, and census records connecting them to the shared ancestor*
- ☐ Record which ancestor (or ancestral couple) the segment is assigned to — *write the full name and approximate birth year, not just a surname*

Step 4 — Document the triangulated group

- ☐ Log the chromosome, start/end position, and cM size in your spreadsheet
- ☐ List all matches confirmed within the group, with links to their profiles
- ☐ Record the assigned ancestor and your confidence level — *use the same Confirmed / Probable / Speculative labels as your match spreadsheet*
- ☐ Add the segment to your chromosome map — *see the Chromosome Mapping Checklist for the full process*

Pro tip: Two people can share the same stretch of chromosome by chance (identical by state) without sharing an ancestor there (identical by descent), especially on small segments under 7 cM. Require at least three mutually-matching people before calling a segment triangulated.

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