

CHROMOSOME MAPPING CHECKLIST

Building your complete chromosome map, segment by segment

Before you begin — quick glossary:

Chromosome map — a visual record assigning specific stretches of your 22 autosomes plus X chromosome to the ancestors who contributed them.

Autosome — any of your 22 non-sex chromosome pairs (as opposed to the X/Y sex chromosomes) — each carries DNA from both parents.

Orphan segment — a confirmed DNA segment with no ancestor assigned to it yet — usually because you don't yet have enough matches on that stretch to triangulate it.

A chromosome map assigns segments of your DNA to specific ancestors, building a visual record of exactly which ancestor contributed which piece of your genome.

Step 1 — Set up your map

- ☐ Choose a mapping tool — DNA Painter (free, at dnapainter.com — the most widely used option), a spreadsheet, or the Genetic Voyage chromosome mapping template
- ☐ Create a profile for yourself and enter your 22 autosomes plus the X chromosome — in DNA Painter: "Create a new profile" → choose the correct chromosome set for your sex (males have one X, females two)
- ☐ Decide on a colour-coding system before you add a single segment — the standard approach: one colour family per grandparent (e.g. blues for paternal grandfather, greens for paternal grandmother, etc.)
- ☐ Remember your total genome is roughly 6,800 cM (about 3,400 cM from each parent) — this is your target — you are working toward accounting for as much of that 6,800 cM total as your matches allow

Step 2 — Add confirmed segments

- ☐ For each triangulated segment, record chromosome, start, end, and cM — take this directly from your completed DNA Triangulation Checklist entries
- ☐ Assign the segment to the correct ancestor or ancestral couple
- ☐ Colour-code the segment according to your system — in DNA Painter: "Add match" → paste in the segment data → assign a group/colour
- ☐ Note the match(es) whose data confirmed the segment — keep this link so you can revisit the source evidence later

Step 3 — Work outward from your closest relatives first

- ☐ Map segments shared with parents or grandparents first, if they've tested — ★ known relatives anchor everything else — a parent's test alone tells you which half of every one of your segments is maternal vs. paternal
- ☐ Use full and half-sibling matches to divide maternal vs. paternal segments — a full sibling shares roughly 2,300–3,400 cM with you, spread across all 22 autosomes — comparing your shared segments to theirs helps assign sides quickly
- ☐ Progressively add segments from more distant confirmed matches — work from closest to most distant relationship, not in the order matches happen to appear

Step 4 — Track your progress

- ☐ Calculate percentage of genome mapped per grandparent line — DNA Painter's profile view shows this automatically as you add segments
- ☐ Identify chromosomes or regions still unmapped — check each of the 22 autosomes individually — some chromosomes are harder to fill in than others simply due to which matches you happen to have
- ☐ Flag "orphan" segments with no assigned ancestor yet — these are segments you know are inherited (matched to a real person) but haven't triangulated to a specific line yet

- ☐ Revisit orphan segments every few months as new matches appear — *set a recurring calendar reminder — new testers regularly fill in previously orphaned regions*

Step 5 — Use the map actively

- ☐ Cross-check new matches against your map to predict which line they belong to — *if a new match's segment falls inside a region you've already assigned to a specific ancestor, you can often place them immediately*
- ☐ Use overlapping segments to spot potential triangulation groups automatically — *DNA Painter flags overlapping segments visually as you add them*
- ☐ Export or back up your map periodically — *download a CSV/export of your profile data at least every few months in case of account issues*

Pro tip: Map from the inside out: confirmed close relatives first, then work toward more distant and less certain matches. A map built the other way around tends to accumulate unverified assumptions that are hard to unwind later.

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