

AFTER RECEIVING YOUR RESULTS

The complete first-week checklist — orient yourself, set up your tools, and work through your matches methodically

Before you begin — quick glossary:

Ethnicity estimate — a statistical estimate of your geographic origins, based on comparing your DNA to reference populations. It shifts over time as reference panels improve — treat it as a rough guide, not a precise record.

Raw DNA data — the underlying file of your genetic data, downloadable from your account settings, which you can upload (usually free) to other sites to widen your match pool.

cM (centimorgan) — the unit for measuring shared DNA between you and a match — see the reference chart below.

Your results just came in. Work through this in order over your first week — it turns an overwhelming new match list into a manageable, organized starting point.

Phase 1 — First look: orient yourself, don't conclude anything yet

- ☐ Read your ethnicity estimate for what it is, not more — *a statistical estimate that will shift as the company's reference data improves — expect it to change over the coming years, sometimes significantly*
- ☐ Locate your match list and sort it by shared cM, descending — *on Ancestry: "DNA Matches"; MyHeritage: "DNA Matches"; FTDNA: "Matches"; 23andMe: "DNA Relatives"*
- ☐ Identify your single closest match and note their name, relationship estimate, and shared cM
- ☐ Resist making any big conclusions in your first sitting — ★ *spend this first session only orienting yourself — decisions and messages can wait until Phase 3*

Phase 2 — Set up your tools

- ☐ Download your raw DNA data file — *usually found in Account Settings under "DNA Data", "Download Raw Data", or similar — save it somewhere safe outside the testing company's platform*
- ☐ Upload your raw data (free) to GEDmatch, MyHeritage, and FamilyTreeDNA if you tested elsewhere — *this widens your match pool at no extra cost — 23andMe is the one major exception that doesn't accept uploads*
- ☐ Create a DNA Painter profile for your future chromosome map — *free at dnainter.com — see the Chromosome Mapping Checklist for the full process*
- ☐ Set up your master match spreadsheet — *see the DNA Match Research Checklist for the exact columns to use*

Phase 3 — Work through your closest matches first

Quick reference — shared cM to likely relationship

Shared cM	Most likely relationship(s)
3,330–3,720 cM	Parent / child, identical twin
2,300–3,400 cM	Full sibling
1,300–2,300 cM	Grandparent/grandchild, aunt/uncle, half-sibling, niece/nephew
575–1,330 cM	1st cousin, great-grandparent, great-aunt/uncle, half-aunt/uncle
200–850 cM	1st cousin once removed, half-1st cousin
90–450 cM	2nd cousin, 1st cousin twice removed
25–200 cM	2nd cousin once removed, 3rd cousin
0–50 cM	3rd cousin once removed, 4th cousin, or more distant

Ranges overlap significantly between relationship types — always cross-check with shared matches, ages, and tree research rather than the cM figure alone.

- ☐ Apply the chart above to your top 10–20 matches for a first-pass relationship estimate on each
- ☐ Run the full DNA Match Research Checklist on any match closer than 2nd cousin — *roughly 200+ cM — these are the matches most likely to meaningfully advance your research*
- ☐ Message your closest 2–3 unexplained matches early — *the people you most need to hear from may not check their account often, so an early message gives the longest possible runway for a reply*

Phase 4 — Handle anything unexpected calmly

- ☐ If a match's relationship estimate contradicts what you expected, don't panic or conclude immediately — *e.g. an unexpected "half-sibling" result*
- ☐ Follow the NPE Research Checklist step by step if a genuine surprise appears — *it's built specifically for this situation*
- ☐ Give yourself time before reacting to any single data point — *one surprising match is a clue, not proof — see Step 1 of the NPE checklist for how to confirm a finding properly*

Phase 5 — Build your foundation for ongoing research

- ☐ Compare your ethnicity estimate against your documented tree — *note anywhere they don't align as a flag for further research, not as a definitive answer on its own*
- ☐ Begin the Leeds Method or run an AutoCluster tool once you have 20–30 matches in the 40–400 cM range — *see the Leeds Method Checklist for the full process*
- ☐ Set a recurring reminder (weekly or bi-weekly) to check for new matches going forward — *your match list will keep growing for years as more people test*

Phase 6 — Longer-term habits

- ☐ Back up your match spreadsheet and raw data file somewhere outside the testing company's platform — *a local folder or cloud drive you control, not just the company's website*
- ☐ Revisit your DNA Painter chromosome map periodically as more segments get triangulated
- ☐ Consider testing additional close relatives if your budget allows — *each parent, sibling, or aunt/uncle who tests meaningfully expands what your existing matches can tell you, and helps sort matches to the correct side of your tree*

Pro tip: Your matches don't just sit still — your list keeps growing every week as more people test, so a match list that looks thin today can look completely different in six months. Revisit it on a schedule (Phase 5) rather than assuming today's picture is final.