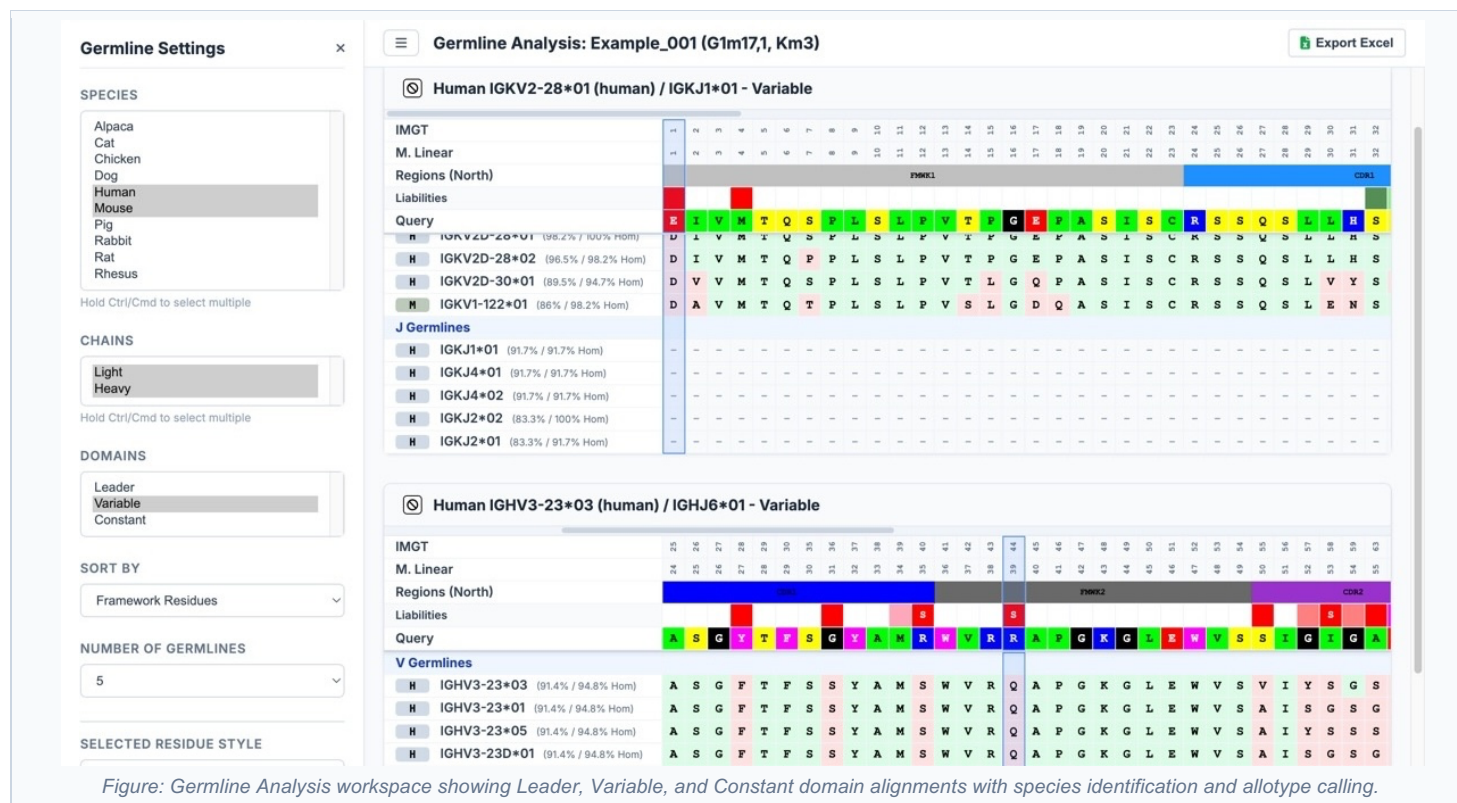


Multi-Species Origin Mapping, Framework Homology, and Automated Constant Allotyping

Deconstruct antibody sequences into Leader, Variable (V and J), and Constant domains aligned against reference databases. AbLead utilizes deterministic framework-first identity and ABHAND homology ranking to identify precise germline origins and automatically calls IgG allotypes and isotypes based on EU numbering.



- **Species Reference Database:** Curated germline repertoires for Human, Rhesus, Mouse, Rat, Rabbit, Alpaca, Dog, Cat, Chicken, and Pig.
- **Framework-First Deterministic Ranking:** Evaluates FR1–FR3 (V) and FR4 (J) identity and homology to prevent misclassification from affinity-matured CDRs.
- **Automated Constant Allotyping:** Calls IgG1, IgG2, IgG4 subclasses and human allotypes (G1m17,1, G1m3, Km3) based on EU-numbered constant markers.
- **Multi-Domain Alignment View:** Dissects sequences into Leader, V-domain, J-domain, and Constant domains (CH1, Hinge, CH2, CH3, CL) with aligned matches.

- **Species Verification and Lineage QC:** Rapidly verifies parental species identity in multi-species hybridoma and transgenic animal discovery campaigns.
- **Immunogenicity Baseline:** Quantifies somatic divergence from unmutated germline precursors to assess baseline immunogenicity risks.
- **Constant Domain Integrity:** Ensures proper constant region subclass assembly, hinge matching, and light chain isotype pairing (Kappa vs Lambda).
- **Integrated Developability Alerts:** Overlays sequence liability motifs and language model stability outliers directly above the query sequence.

The AbLead Advantage: Precision germline mapping and allotype calling establish the essential structural foundation required for reliable humanization, developability assessment, and patent characterization.

Accelerate Your Antibody Lead Optimization and De-Risk Development

Request a Live Demo: ablead@ketchemconsulting.com | Explore Platform: ablead.ketchemconsulting.com

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