Part A: One-Pager

Section 1: Problem & User

- **Target Users:** Oncologists, NSCLC researchers, patients, and pharmaceutical developers - pioneers in the fight against the world's deadliest cancer. Each year, 2.2 million people face NSCLC (85% of lung cancers), a disease fueled by genetic mutations (e.g., EGFR, ALK, KRAS) and tangled molecular networks (oncogenic signaling, tumor-immune interactions).
- **Pain Points:** Current NSCLC care struggles with three critical gaps:
    1. Blind spots: Many patients lack known druggable mutations, leaving chemo or immunotherapy as last resorts - often ineffective.
    2. Resistance: Tumors evolve, hijacking pathways (e.g., EGFR C797S mutations) to outsmart inhibitors like osimertinib.
    3. Toxicity risks: Off-target effects (e.g., PD-1 inhibitors harming T-cell signaling) complicate polytherapy, endangering patients.
    4. Lack of a particular effective treatment.

Today's tools analyze single genes or pathways, missing the dynamic interplay of mutations, inhibitors, and tumor biology that truly drive outcomes. Moreover, we face the generalization of healthcare, lacking a personalized approach for each patient.

- **Importance/Urgency:** NSCLC claims 1.8 million lives annually, with advanced disease survival rates stagnant. By 2030, cases could surge 30%, amplifying the need for precision. Stakeholders can't afford trial-and-error; patients demand therapies tailored to their unique networks, not just one-size-fits-all. Time is critical: every delay in personalized care costs lives.

Section 2: What You'll Build

- **Core Offering:** K2 Think is a scalable theragnostic AI-powered oncology engine that transforms patient molecular data into personalized therapy. It integrates four core data collections - patients, samples, molecular_profiles, and k2think_analysis - to decode each tumor's molecular landscape and predict the most effective treatment strategy. From a lung tumor sample, K2 Think analyzes mutations, gene expression, and copy number variations (CNVs) to build a molecular profile. The AI then identifies driver genes (e.g., EGFR, KRAS), simulates inhibitor interactions, and predicts drug response, resistance risks, and optimal therapy combinations.
- **User Flow:** (https://k2vynce.lutherbanze.com/workflow-data.html)
    I. Input: Include NGS genomic profile (driver/resistance mutations) and current/planned medications (cancer inhibitors + supportive drugs).
    II. Process: K2 Think cross-references NSCLC databases (COSMIC, TCGA) and drug libraries (DrugBank, ChEMBL) to model tumor's unique network, identifying disruptions and interactions.
    III. Output: The app displays insights, such as primary targets, drug efficiency, risks of resistance, and suggested combinations.

- **Tech Stack:** Native iOS/Android app powered by Firestore (NoSQL) and Firebase Authentication, with Node.js and Objective-C Cloud Functions managing AI automation.
- **Key Highlight:** All outputs persist in Firestore, enabling clinicians to review analyses, monitor responses, and provide feedback, creating a continuously improving AI model and expanding drug findings with personalized healthcare.

Section 3: Why K2 Think

K2 Think's ultra-fast reasoning (≈2,000 tokens/sec) enables real-time genomic interpretation and interactive molecular modeling. Its superior mathematical and analytical precision empowers the system to decode complex oncogenic networks, simulate molecular interactions, and recommend optimal drug strategies - capabilities essential for advancing personalized NSCLC treatment beyond current computational limits.

Section 4: Demo (MVP)

In 48 hours we will build a native application for iOS and Android connected to Firestore (NoSQL) through Node.js Cloud Functions, including the K2 Think API to analyze patient molecular profiles, simulate drug responses, predict resistance and generate actionable therapeutic recommendations in real time.

Part B: Team Info

- **All member CVs:**
    1. Luther: Luther Banze CV.pdf
    2. Aibarly: Aibarly Tleuberdi CV.pdf
    3. Zhasmin: Zhasmin Abdilda CV.pdf
    4. Axel: Axel Ortega CV.pdf

- **Main contact number:**

    Tleuberdi Aibarly: +7 778 099 88 64 (or 8 778 099 88 64)

- **Roles in the team:**
  - Zhasmin: Clinical and Pharmacology Research Lead
  - Aibarly: K2 Logic and Verification Engineer, Researcher, and Team Leader
  - Luther: Project Manager, Developer, Data Integration & Backend Engineer
  - Axel: UI/UX Designer, and Demo Engineer

- **3 relevant links:**
    1. **Wireframe Design:** **K2 Vynce DFD.jpg**
    2. **Demo Website:** https://k2vynce.lutherbanze.com/
    3. **Data Portal:** https://portal.gdc.cancer.gov/

Appendix: Key Resources (Verified & Authoritative):

A. COSMIC Database: Global catalog of somatic cancer mutations (https://cancer.sanger.ac.uk/cosmic).
B. TCGA: Compendium of genomic, clinical, and molecular cancer data (https://portal.gdc.cancer.gov).
C. OncoKB: Clinically validated oncology knowledge base (https://www.oncokb.org).
D. ChEMBL: Drug bioactivity and chemical structure database (https://www.chembl.org).
E. Cytosapce: Open-source software platform for visualizing complex networks and integrating data (https://cytoscape.org/).