

Discovery of Novel CARs for Solid Tumors Using Senti REVEAL™

A High Throughput Technology
Platform Comprising Pooled Screening,
Machine Learning, and Lab Automation

Nick Frankel, PhD
Associate Director, Gene Circuit Discovery
Senti Biosciences, Inc.

American Society for Gene and Cell Therapy, 2024



Disclosures



Employee of Senti Biosciences, and receive salary and benefits from the company

Senti Bio's Internal Programs Focus on Oncology, Partnering to Support Non-Oncology Indications



Program	Target/Disease Candidate	Preclinical	Early Stage Clinical	Late Stage Clinical	Collaborator
SENTI-202	AML, MDS and other blood cancers		https://www.c	Trial ID NCT063257 linicaltrials.gov/study/NCT0632 clinical data by YE 2024	5748
SENTI-301A	HCC and other solid tumors		Enroll first	t patient in 1H 2024	CELEST 晟临生物
Multiple Gene Therapy Programs	Eye, CNS and liver diseases				Spark. Roche
Multiple iPSC Cell Therapy Programs	Regenerative medicine				BlueRock BAYER R

Senti's Gene Circuit Platform to Enable Next-Gen Cell and Gene Therapies

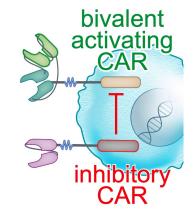


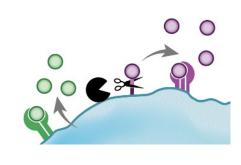


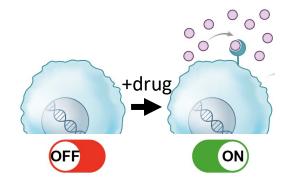


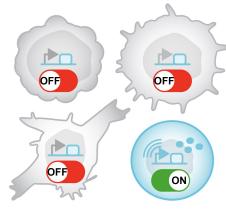


Example Implementation









Components and Variants

Multivalent CARs for heterogeneous targets

Inhibitory CARs for reducing off-target

Potent CAR signaling domains

Calibrated Release (cr) system

Potent immuneactivating payloads

Multi-payload combinations

Payload expression induced by FDA approved drugs at physiological levels

High sensitivity safety/kill switches

Tissue and cell type specific promoters

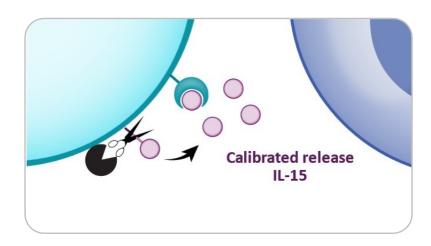
Cell activation inducible promoters

Potent constitutive promoters

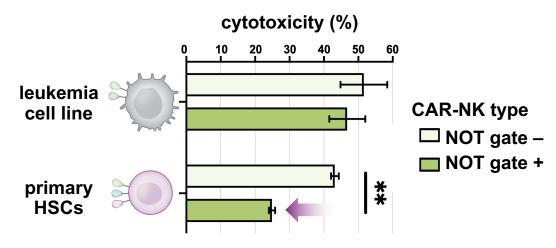
SENTI-202: Logic-Gating and Multi-Arming to Address Clinical Needs in AML



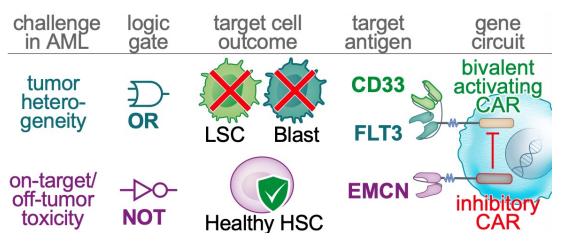
Calibrated release of IL-15 for persistence



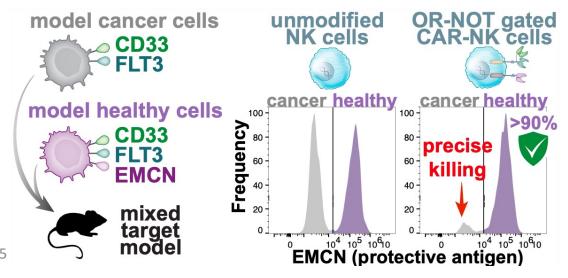
Protecting HSCs without compromising efficacy



Logic gating for efficacy and safety



Precision killing in vivo



Senti's Discovery and Optimization Engine for Novel Protein and DNA Assets



Senti REVEALTM

Research Engine for Validation of Engineered Asset Libraries

Project Design Specs



Bioinformatics Platform



Library Design



Statistical Insigh

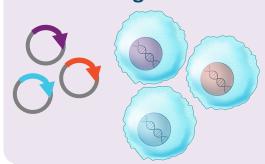


ML Hit Prediction

Pooled Libraries

10⁴-10⁵ elements

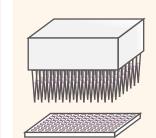
High Throughput Screening Platform



Clonal Libraries

10²-10³ elements

Automated Clonal Validation Platform









Validated Candidates











NGS Datasets

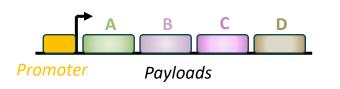
Individual Profiling Data

REVEAL can be used to discover and optimize novel sequences of **both nucleic and amino acids** and is cell type agnostic.

High-Throughput Engineering of Enhanced Constitutive Promoters to Drive Multi-Payload Constructs for Next-Gen Cell Therapies



Challenge: driving expression of 4 therapeutic payloads from a single promoter in NK cells



- A. Secreted cytokine
- B. Calibrated release cytokine
- C. activating CAR
- D. inhibitory CAR

Senti REVEAL with three iterative design cycles and tens of thousands of promoters.

Start-to-finish under 9 months

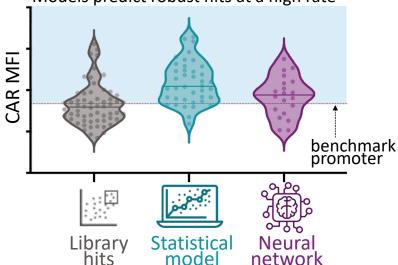






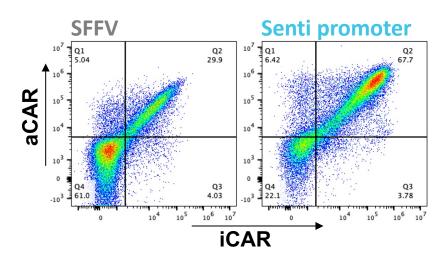
Automated clonal validation

100s of candidates validated in parallel Models predict robust hits at a high rate



Enhanced multi-payload expression

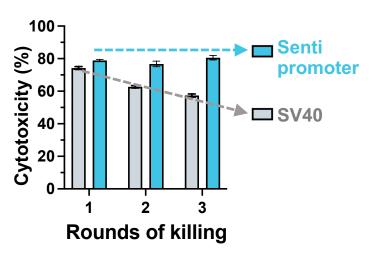
Showing payloads 3 and 4. Payloads 1 and 2 also higher. 2-4x higher expression than SFFV or SV40



*2-4x depending on metric. Not due to copy number differences

Expression drives performance

Persistence in serial re-challenge in vitro killing assay (solid tumor cell line)



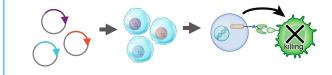
Discovery of Novel CAR Signaling Domains for Tackling Solid Tumors by Screening Libraries of Tens of Thousands of CAR Signaling Domains

CAR Library Design binder hinge TM Collection of 87 sequences from different signaling pathways Variable intracellular domain

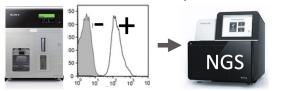
- ✓ Intracellular domains are combinatorial assemblies containing from 1 to 5 subdomains
- ✓ Subdomains sizes range from isolated motifs <10 AA to full-size domains >300 AA
- ✓ Increased diversity by building multiple sub-libraries with different design principles and assembly methods
- ✓ Over 50,000 CARs in total, works with T or NK cells

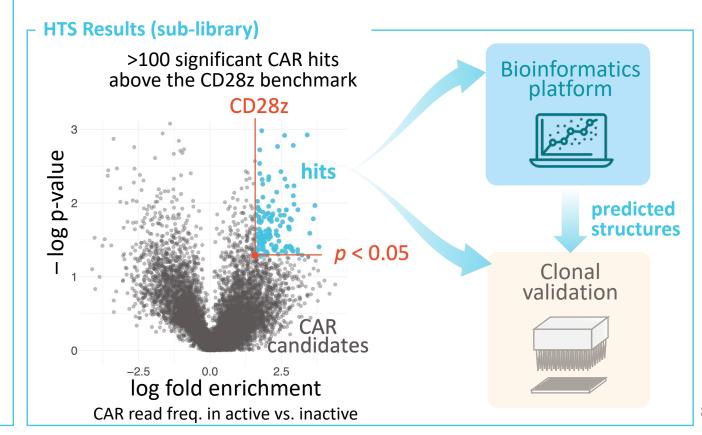
Sort-seq Workflow

Transduce CAR library into immune cells and challenge with target cells



Sort activated from non-activated immune cells and sequence CARs

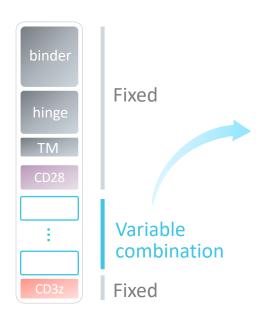


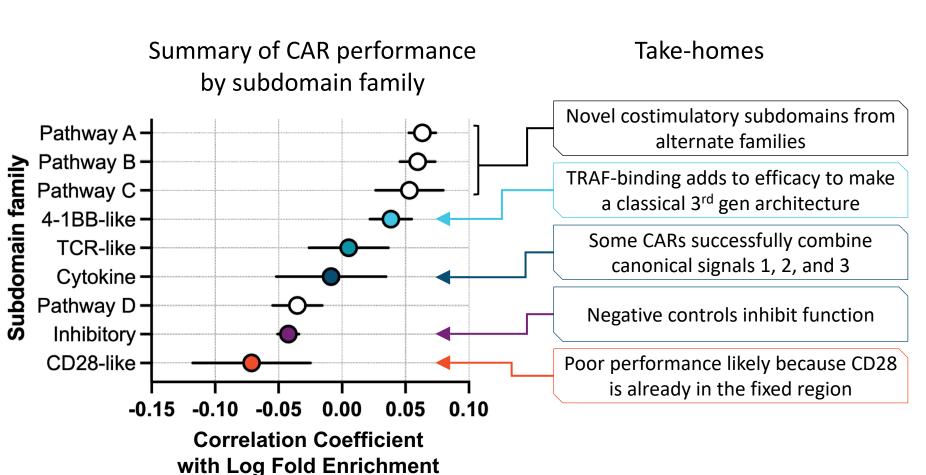


Certain Subdomain Families Are Enriched in High Performing CAR Intracellular Domains in the Context of a 3rd Generation CAR architecture

Trends at the sub-library level

Sub-library with fixed CD28 and CD3z plus variable domain (3rd gen)





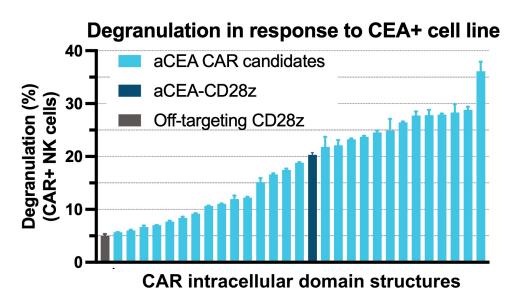
Mean +/- standard deviation across all sequences in family and across all positions. Correlation of each sequence in each position is calculated over all combinations in sub-library.

Clonal Validation Using Automated Liquid Handling



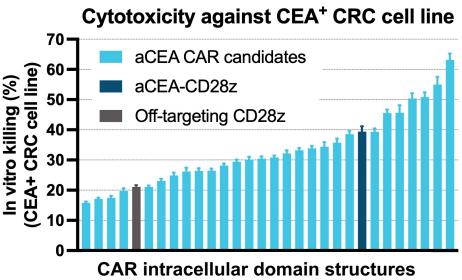
Individual hit validation

Degranulation (CD107a)



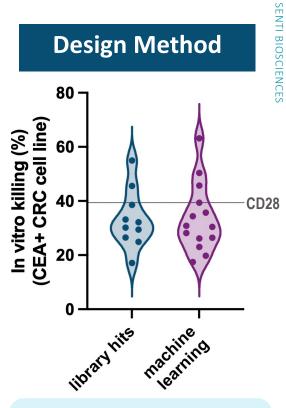
~50% hit validation rate using the same assay used as in the pooled screen sort-seg protocol.

Cytotoxicity (Solid tumor cell line)



Top CAR exhibits >50% higher cytotoxicity than CD28z in killing a solid tumor cell line

Design Method

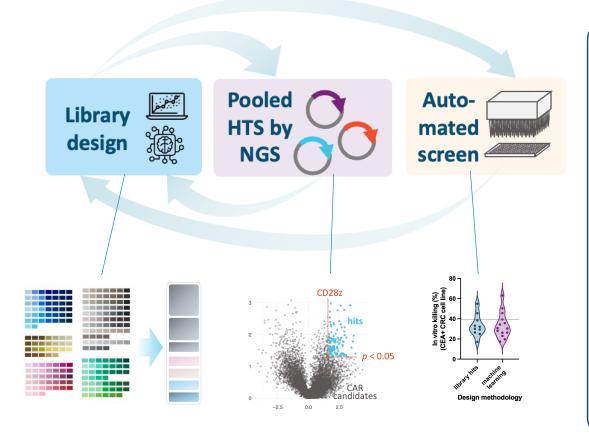


ML model trained on HTS data predicts potent CARs.

Conclusions and future directions



Discovery of novel potent CARs using Senti's REVEAL™ platform



- Senti's gene circuit platform includes potent and specific promoters, logic-gated CARs, calibrated release cytokines, and inducible systems.
- Our discovery engine, REVEAL, combines pooled screening, machine learning, and automated liquid handling
- We used REVEAL to discover CARs with greater degranulation, cytotoxicity, and cytokine release (not shown) than CD28z, but with novel structures.





Acknowledgements

Gene Circuit Discovery @ Senti

Researchers: Tony Hua, PhD, Marcus Gainer

Brian Garrison, PhD, VP of Research

Kanya Rajangam, MD, PhD, CMO and Head of Research and Development

Tim Lu, MD, PhD, CEO and Co-Founder