

Supplementary Information

Electronic Supplementary Material 2 (ESM_2)

Article title: Generative Molecular Design for Senescence-Associated Secretory Phenotype (SASP) Reversal: A REINVENT4 Pipeline Trained on Real LINCSeq L1000 Transcriptomic Data

Journal: Molecular Diversity

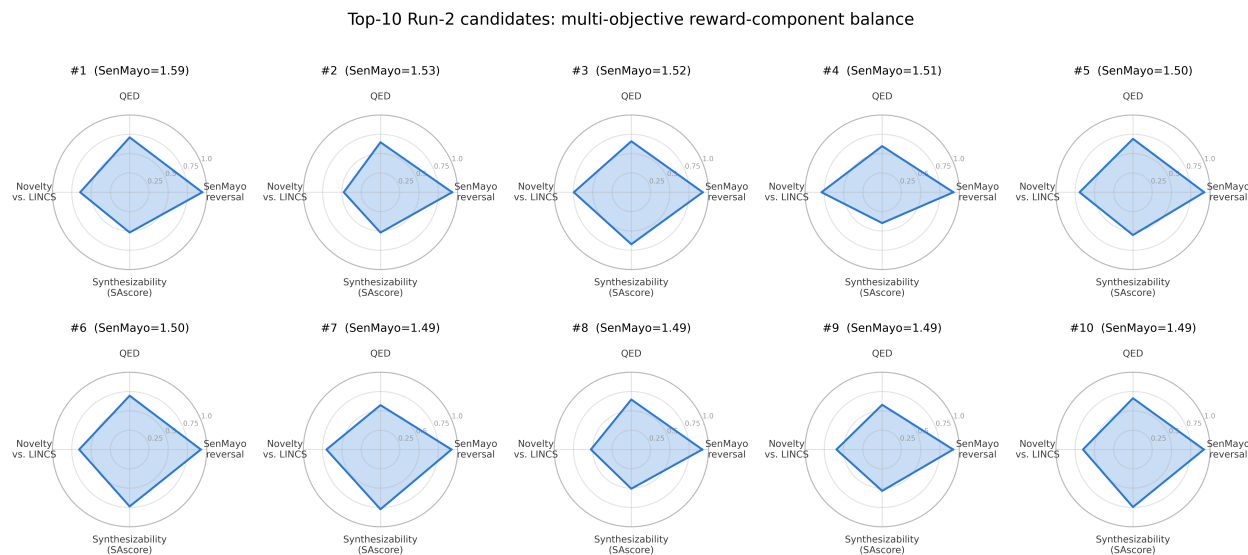
Author: Selahattin Alperen Uysal, MD, PhD (ORCID 0000-0003-3777-6411)

Affiliation: Department of Medical Biology and Genetics, School of Medicine, Ege University, Bornova, 35050 İzmir, Türkiye

Corresponding author e-mail: dralperenuysal@gmail.com

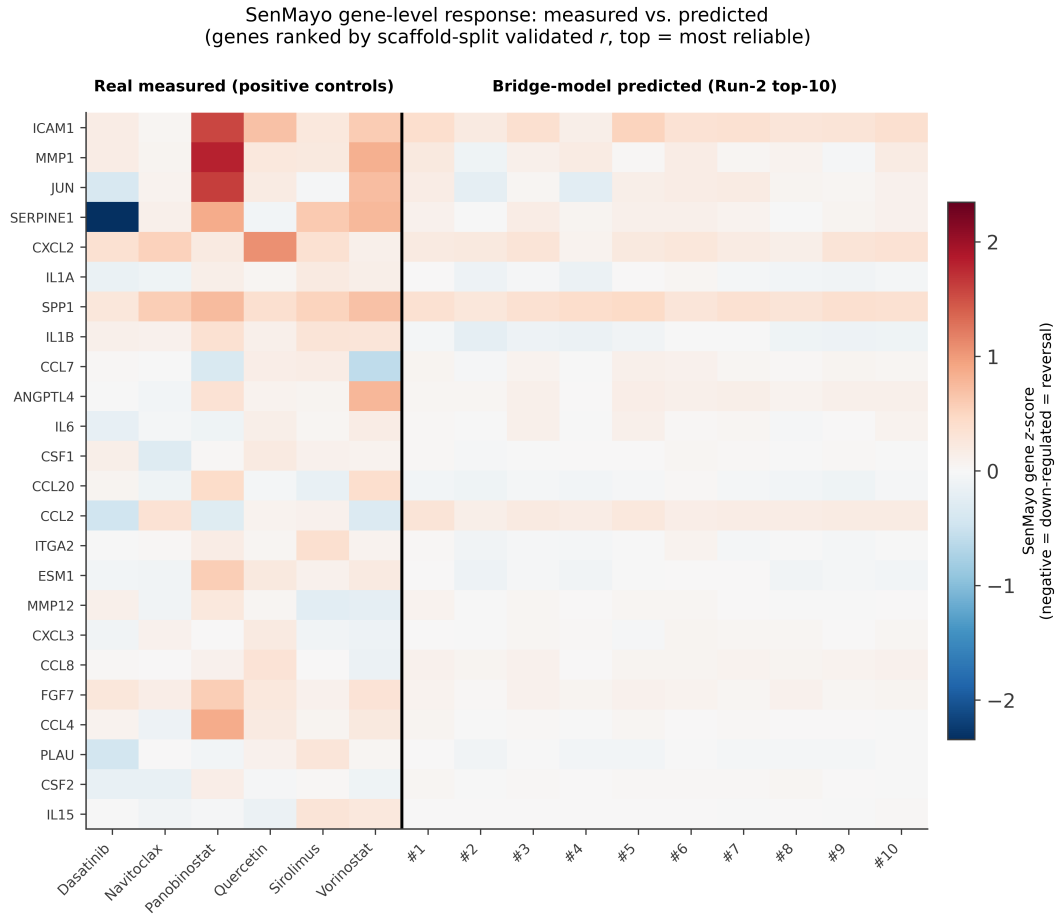
Note: All compounds discussed in this supplementary material are computationally generated virtual candidates; no chemical synthesis was performed and no analytical data are applicable.

Fig. S1. Multi-objective reward-component balance for the top-10 Run-2 candidates



Each panel is one candidate (ranked as in the top-10 candidates figure of the main text), plotting the four transformed (0–1) reward components actually optimized during reinforcement learning: SenMayo reversal, QED, novelty versus LINCSeq, and synthesizability (SAscore-derived).

Fig. S2. SenMayo gene-level response



Real measured response (six positive controls, left) versus structure-based predicted response (top-10 Run-2 candidates, right), for the 24 SenMayo genes most correlated with the aggregate reversal score. Genes are ranked top-to-bottom by their own scaffold-split validated Pearson r . Red = up-regulated (SASP induction); blue = down-regulated (SASP reversal).