

Resource Summary Report

Generated by [RRID](#) on Aug 19, 2026

hSTARR-seq_ORI vector

RRID:Addgene_99296

Type: Plasmid

Proper Citation

RRID:Addgene_99296

Plasmid Information

URL: <http://www.addgene.org/99296>

Proper Citation: RRID:Addgene_99296

Bacterial Resistance: Chloramphenicol and Ampicillin

Defining Citation: [PMID:29256496](#)

Vector Backbone Description: Backbone Marker:Promega; Backbone Size:2537; Vector Backbone:hSTARR-seq_ORI vector; Vector Types:Mammalian Expression, hSTARR-seq screening vector; Bacterial Resistance:Chloramphenicol and Ampicillin

Comments: This screening vector can screen a DNA library which can be inserted via the AgeI and SalI restriction sites using subsequent In-Fusion reaction (Clontech). In this vector the origin of replication (ORI) substitutes a core promoter . Please see bioRxiv for preprint article. Posted 17 July 2017. DOI: 10.1101/164590

Plasmid Name: hSTARR-seq_ORI vector

Record Creation Time: 20220422T222633+0000

Record Last Update: 20260815T082246+0000

Ratings and Alerts

No rating or validation information has been found for hSTARR-seq_ORI vector.

No alerts have been found for hSTARR-seq_ORI vector.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Tardaguila M, et al. (2026) Integrating natural and engineered genetic variations to decode regulatory influence on blood traits. *Cell reports*, 45(2), 116937.

Weaver S, et al. (2026) Segmentally Duplicated Regulatory Elements Undergo Human-Specific Rewiring. *Molecular biology and evolution*, 43(7).

Wang SK, et al. (2026) Single-cell multiome and enhancer connectome of human retinal pigment epithelium and choroid nominate causal variants in macular degeneration. *Cell reports*, 45(1), 116814.

Siklenka K, et al. (2026) Enhancer hubs govern chromatin topology and Th17 cell identity. *bioRxiv : the preprint server for biology*.

Dong SS, et al. (2025) Systematic functional characterization of non-coding regulatory SNPs associated with central obesity. *American journal of human genetics*, 112(1), 116.

Weaver S, et al. (2025) Segmentally duplicated regulatory elements undergo human-specific rewiring. *bioRxiv : the preprint server for biology*.

Gao C, et al. (2025) Analysis of biased allelic enhancer activity of schizophrenia-linked common variants. *Communications biology*, 8(1), 1034.

Hansen TJ, et al. (2024) Human gene regulatory evolution is driven by the divergence of regulatory element function in both cis and trans. *Cell genomics*, 4(4), 100536.

McCann AA, et al. (2024) Context dependent activity of p63-bound gene regulatory elements. *bioRxiv : the preprint server for biology*.

Chang TY, et al. (2024) HDI-STARR-seq: Condition-specific enhancer discovery in mouse liver in vivo. *BMC genomics*, 25(1), 1240.

Chang TY, et al. (2024) HDI-STARR-seq: Condition-specific enhancer discovery in mouse liver in vivo. *bioRxiv : the preprint server for biology*.

Gaynor-Gillett SC, et al. (2024) Validation of Enhancer Regions in Primary Human Neural Progenitor Cells using Capture STARR-seq. *bioRxiv : the preprint server for biology*.

Chang TY, et al. (2024) HDI-STARR-seq: Condition-specific enhancer discovery in mouse liver in vivo. *Research square*.

Wang C, et al. (2024) Constructing eRNA-mediated gene regulatory networks to explore the genetic basis of muscle and fat-relevant traits in pigs. *Genetics, selection, evolution : GSE*, 56(1), 28.

Chen XF, et al. (2024) Integrative high-throughput enhancer surveying and functional verification divulges a YY2-condensed regulatory axis conferring risk for osteoporosis. *Cell*

genomics, 4(3), 100501.

Hansen T, et al. (2023) Human gene regulatory evolution is driven by the divergence of regulatory element function in both cis and trans. *bioRxiv : the preprint server for biology*.

Ahmed I, et al. (2023) eRNA profiling uncovers the enhancer landscape of oesophageal adenocarcinoma and reveals new deregulated pathways. *eLife*, 12.

Gallego Romero I, et al. (2023) Leveraging massively parallel reporter assays for evolutionary questions. *Genome biology*, 24(1), 26.

Baniulyte G, et al. (2023) Shared gene regulatory strategies for the p53 and ATF4-dependent transcriptional networks. *bioRxiv : the preprint server for biology*.

Duan YY, et al. (2023) High-throughput functional dissection of noncoding SNPs with biased allelic enhancer activity for insulin resistance-relevant phenotypes. *American journal of human genetics*, 110(8), 1266.