

LAP2 isoform profile in heart ageing and in cardiac cell proliferation and differentiation: input from CRISPR-Cas9-mediated LAP2a knockdown in H9C2

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Supplementary Data S1

**Results of *TMPO* DNA sequencing
for CRISPR-Cas9 KO LAP2a clones (H9C2 cells)**

Clone 22G2.....LAP2a +/-

YOUR UPLOAD

LABEL	GUIDE SEQUENCE(S)	CONTROL FILE	EXPERIMENT FILE
22G2 245R 200622_Premixed-TS03500300-copie	GGAATAAATAAGCTCCGTCC	CTRL H9C2 PCR2 245R_Premixed-TS03500304-copie.ab1	22G2 245R 200622_Premixed-TS03500300-copie.ab1

Analysis of 22G2 245R 200622_Premixed-TS03500300-copie

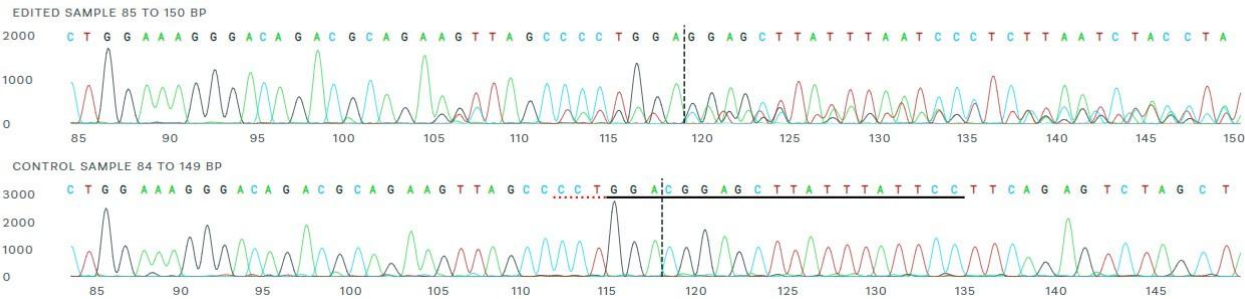
Contributions	Indel Distribution	Traces
Status [?] Succeeded	Guide Target [?] GGAATAAATAAGCTCCGTCC	PAM Sequence [?] AGG
	Indel % [?] 72	Model Fit (R²) [?] 0.96
		Knockout-Score [?] 72

RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

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INDEL	CONTRIBUTION	SEQUENCE
-1	48%	ACAGACGCAGAAAGTTAGCCCTGGAGGAGCTTATTTATTCCTTCAGAGTCTAGCTATGATAGATGTGTAGAGAA
-37	24%	ACAGACGC-----AGAGTCTAGCTATGATAGATGTGTAGAGAA
0	24%	ACAGACGCAGAAAGTTAGCCCTGGACGGAGCTTATTTATTCCTTCAGAGTCTAGCTATGATAGATGTGTAGAGAA

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Clone 22G3.....LAP2a +/-

YOUR UPLOAD

LABEL	GUIDE SEQUENCE(S)	CONTROL FILE	EXPERIMENT FILE
22G3 245R 140223_Premixed-TS03935050	GGAATAAATAAGCTCCGTCC	H9C2 22A11 245R 270622_Premixed-TS03543468.ab1	22G3 245R 140223_Premixed-TS03935050.ab1

Analysis of 22G3 245R 140223_Premixed-TS03935050

Contributions

Indel Distribution

Traces

Status	Guide Target	PAM Sequence	Indel %	Model Fit (R ²)	Knockout-Score
✓ Succeeded	GGAATAAATAAGCTCCGTCC	AGG	71	0.97	71

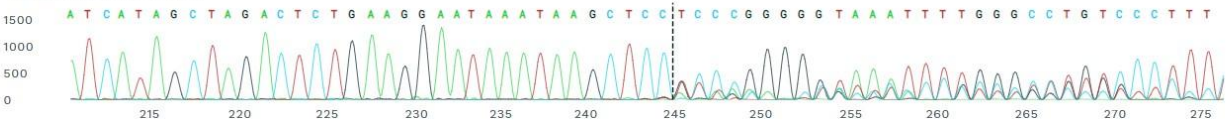
RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

POWERED BY SYNTHEGO ICE

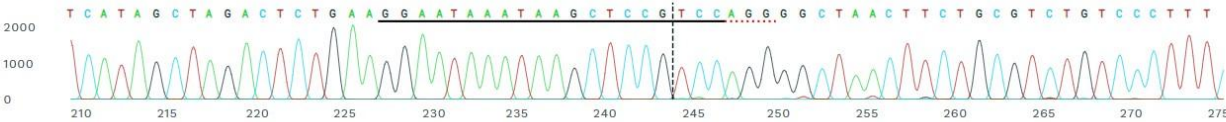
INDEL	CONTRIBUTION	SEQUENCE
-1	38%	ACTCTGAAGGAATAAATAAGCTCC- TCCAGGGGCTAACTTCTGCGTCTGTCCCTTTCCAGGCAAGGCTGTATCAG
0	26%	ACTCTGAAGGAATAAATAAGCTCCG TCCAGGGGCTAACTTCTGCGTCTGTCCCTTTCCAGGCAAGGCTGTATCAG
+1	16%	ACTCTGAAGGAATAAATAAGCTCCG NTCCAGGGGCTAACTTCTGCGTCTGTCCCTTTCCAGGCAAGGCTGTATCA
-2	9%	ACTCTGAAGGAATAAATAAGCTCCG --CAGGGGCTAACTTCTGCGTCTGTCCCTTTCCAGGCAAGGCTGTATCAG
-2	7%	ACTCTGAAGGAATAAATAAGCTCC- -CCAGGGGCTAACTTCTGCGTCTGTCCCTTTCCAGGCAAGGCTGTATCAG
-2	1%	ACTCTGAAGGAATAAATAAGCTC-- TCCAGGGGCTAACTTCTGCGTCTGTCCCTTTCCAGGCAAGGCTGTATCAG

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EDITED SAMPLE 211 TO 276 BP



CONTROL SAMPLE 210 TO 275 BP



Clone 22B3..... LAP2a -/-

Analysis of 22B3 245FNP 070323_Premixed-TS03935074

Contributions

Status

✓ Succeeded

Guide Target

GGAATAAATAAGCTCCGTCC

Indel Distribution

PAM Sequence

AGG

Indel %

100

Model Fit (R^2)

1

Traces

Knockout-Score

100

RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

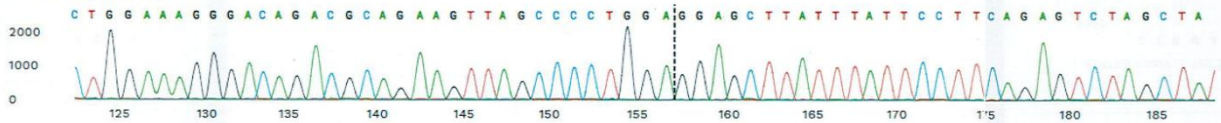
POWERED BY SYNTHGO ICE

INDF1 CONTRIBUTION

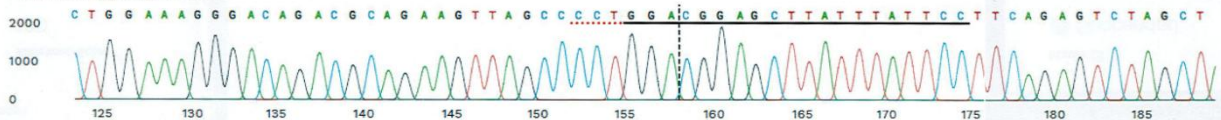
-1 100%

CTGGAAAGGGACAGACGCAGAACTTAGCCCTTGGAGGAGCTTATTATTTCCTTCAGAGTCTAGCTA

EDITED SAMPLE 123 TO 188 BP



CONTROL SAMPLE 124 TO 189 BP



This is the Sanger sequence view showing edited and wild-type (control) sequences in the region around the guide sequence. This shows sequence base calls from both the control and the experimental sample .ab1 files, which will contain mixed base calls. The horizontal black

Clone 22A11..... LAP2a +/-

YOUR UPLOAD

LABEL	GUIDE SEQUENCE(S)	CONTROL FILE	EXPERIMENT FILE
H9C2 22A11 245R 270622_Premixed- TS03543468-copie	GGAATAAATAAGCTCCGTCC	CTRL2 245 090522_Premixed- TS03340827-copie.ab1	H9C2 22A11 245R 270622_Premixed-TS03543468- copie.ab1

Analysis of H9C2 22A11 245R 270622_Premixed-TS03543468-copie

Contributions

Status ⓘ ✔ Succeeded	Guide Target ⓘ GGAATAAATAAGCTCCGTCC	PAM Sequence ⓘ AGG	Indel % ⓘ 0	Model Fit (R ²) ⓘ 1
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Indel Distribution

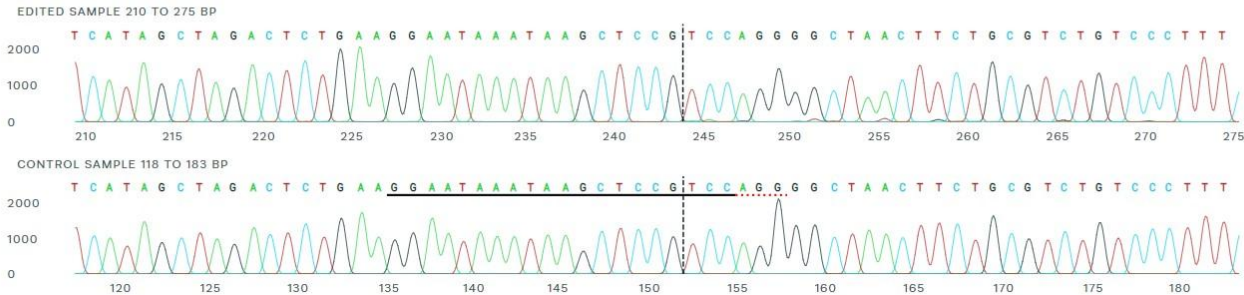
Traces

RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

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Clone 21E10..... LAP2a +/-

Analysis of 21E10

Contributions

Indel Distribution

Traces

Status ⓘ

✓ Succeeded

Guide Target ⓘ

TGAGGCTCCTCAGCACGCGA

PAM Sequence ⓘ

TGG

Indel % ⓘ

0

Model Fit (R^2) ⓘ

1

RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

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The contributions show the inferred sequences present in your edited population and their relative proportions (in contrast to the Indel plot (Indel Distribution tab) that does not specify sequence contributions). Cut sites are represented by black vertical dotted lines, and the wild-type sequence is marked by a "+" symbol on the far left.

Clone 21B1..... LAP2a +/-

Analysis of 21B1 446F 210223_Premixed-TS03935064

Contributions

Indel Distribution

Traces

Status ⓘ

✓ Succeeded

Guide Target ⓘ

TGAGGCTCCTCAGCACGCGA

PAM Sequence ⓘ

TGG

Indel % ⓘ

0

Model Fit (R^2) ⓘ

1

RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

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Clone 21H4..... LAP2a +/-

YOUR UPLOAD

LABEL	GUIDE SEQUENCE(S)	CONTROL FILE	EXPERIMENT FILE
21H4 446R 210622_Premixed-TS03500310-copie	TGAGGCTCCTCAGCACGCGA	10C4 446R 130622_Premixed-TS03500263-copie.ab1	21H4 446R 210622_Premixed-TS03500310-copie.ab1

Analysis of 21H4 446R 210622_Premixed-TS03500310-copie

Contributions	Indel Distribution	Traces
Status ⓘ ✓ Succeeded Last guide at position 208 of 287, consider repositioning primers around the cutsites, WARNING - Inf. window after cutsite, 45, is less than 3x indel_max_size of 20, inference on a short reading window. Possible large deletions or shorter than average readable sequence length.	Guide Target ⓘ TGAGGCTCCTCAGCACGCGA	PAM Sequence ⓘ TGG Indel % ⓘ 83 Model Fit (R²) ⓘ 0.99 Knockout-Score ⓘ 83

RELATIVE CONTRIBUTION OF EACH SEQUENCE (NORMALIZED)

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POWERED BY SYNTHEGO ICE

