

Strategies For Effective CRISPR-Mediated Gene Modification

October 17, 2018

Presenter:

Ed Davis, Ph.D. Senior Application Scientist GeneCopoeia, Inc.

Goals of this presentation

- Help guide you though basic considerations, steps, and potential problems for using CRISPR to modify genes in cell lines
- Present CRISPR-based tools from GeneCopoeia for modifying genes in cell lines
- * Q&A



GeneCopoeia Products and Services

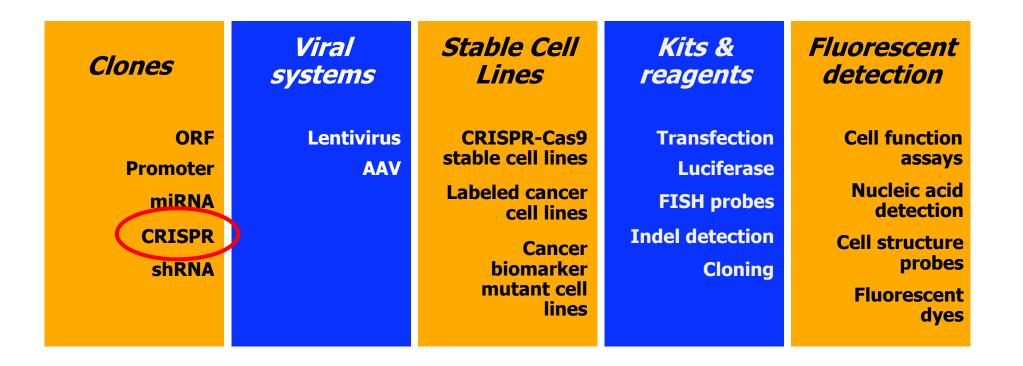
Functional Genomics & Cell Biology

Clones	Viral	Stable Cell	Kits &	Fluorescent
	systems	Lines	reagents	detection
ORF Promoter miRNA CRISPR shRNA	Lentivirus AAV	CRISPR-Cas9 stable cell lines Labeled cancer cell lines Cancer biomarker mutant cell lines	Transfection Luciferase FISH probes Indel detection Cloning	Cell function assays Nucleic acid detection Cell structure probes Fluorescent dyes



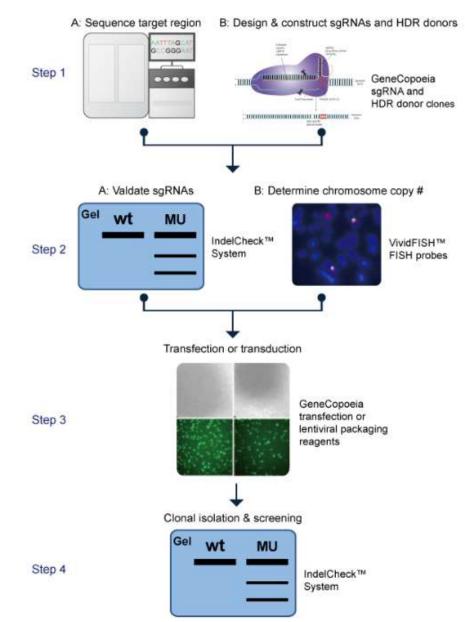
GeneCopoeia Products and Services

Functional Genomics & Cell Biology





GeneCopoeia CRISPR products for cell lines





Outline

- CRISPR technologies & applications
- Strategy considerations
- Delivery methods
- Preparation
- Screening
- Things to look out for



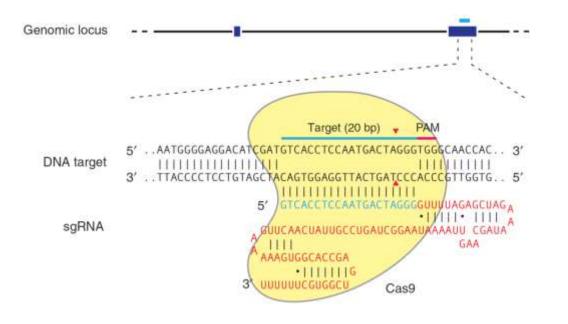
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CRISPR-Cas9: RNA-guided endonuclease

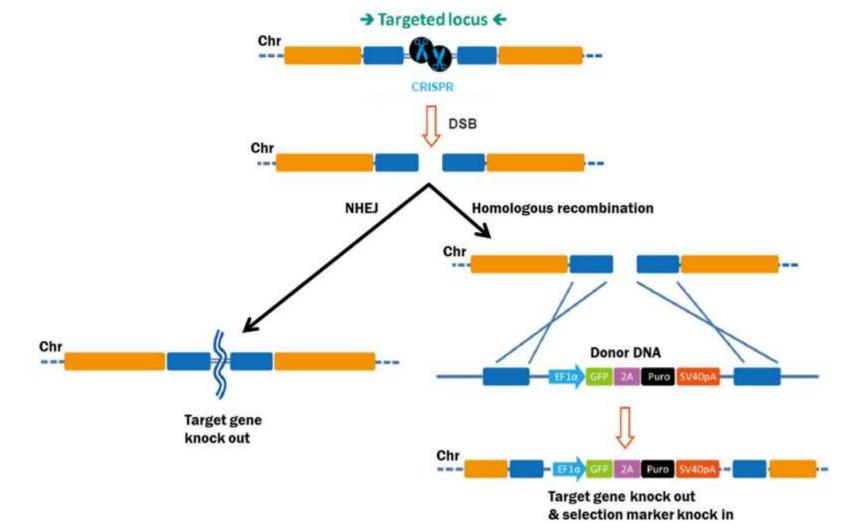


Ran, et al. (2013). Nature Protocols 8, 2281

- 17-20 nt single guide RNA (sgRNA) guides Cas9 nuclease to target site.
- Requires NGG "PAM" site immediately downstream of sgRNA target sequence.
- Cas9-sgRNA complex makes DSB 3 nt upstream of PAM.



Targeted DNA editing by DSB induction

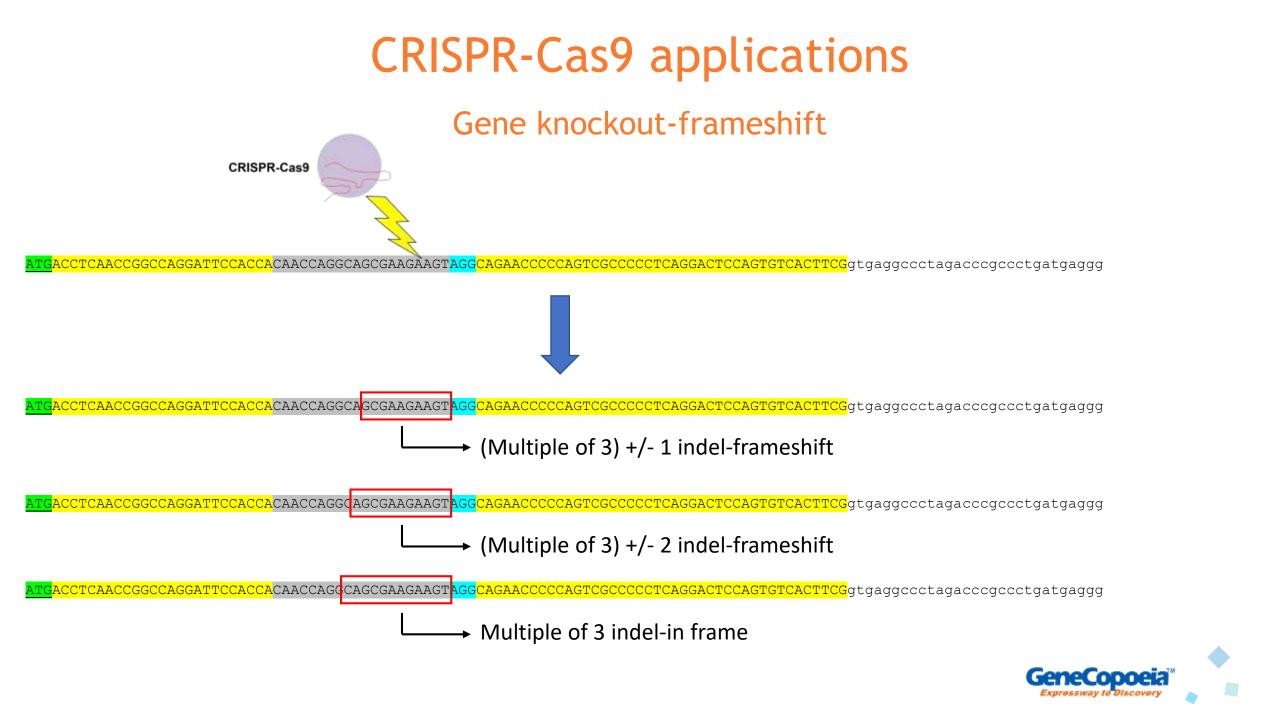




Technological variants

Technology	Description	PAM	Applications
SpCas9	Unmodified Cas9 from Streptococcus pyogenes	NGG	Gene knockout, knock-in, tagging, mutagenesis
SpCas9-NG	Mutagenized SpCas9 with relaxed (NG) PAM requirement	NG	Gene knockout, knock-in, tagging, mutagenesis
Cas9-HF, eSpCas9	Mutagenized, high-fidelity SpCas9 for reduced off-targeting	NGG	Gene knockout, knock-in, tagging, mutagenesis
HiFi Cas9	Mutagenized, high-fidelity SpCas9 for reduced off-targeting	NGG	Gene knockout, knock-in, tagging, mutagenesis
Cpf1 (Cas12a)	Nucleases from <i>Acidaminococcus sp. BV3L6</i> or <i>Lachnospiraceae bacterium ND2006</i> . Smaller than SpCas9, no requirement for tracrRNA, staggered DSB, lower off-targeting.	T/CTTN (5')	Gene knockout, knock-in, tagging, mutagenesis
SaCas9	Cas9 from <i>Staphylococcus aureus</i> . Smaller than SpCas9, usually used with adenoassociated virus (AAV)	NNGRRT	Gene knockout, knock-in, tagging, mutagenesis
dCas9	Nuclease-dead Cas9 for tethering to effectors	NGG	Gene mutagenesis, chromatin modification, transcriptional activation/repression
Cas13	Nuclease from Leptotrichia wadei. Targets RNA. 20-28 nt spacer	None	RNA knockdown or mutagenesis



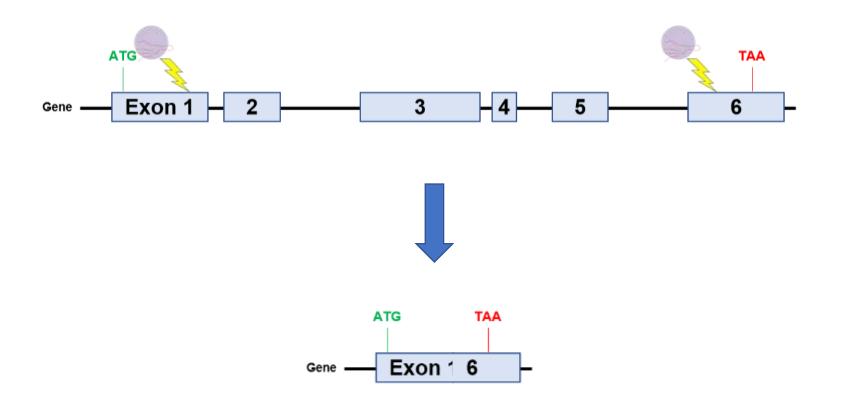


Gene knockout-frameshift

- NHEJ-mediated indels occur stochastically, with unpredictable lengths
- ✤ In general, 2/3 of indels will cause a frameshift. In most cases this will knock the gene out.
- In general, 1/3 of indels will be in-frame. This may or may not knock the gene out. It could also lead to the production of a protein with a new or altered function.
- Typically, each chromosome will contain a different indel (or no indel). So, only 4/9 of diploid cells with 2 indels will contain 2 frameshift indels.

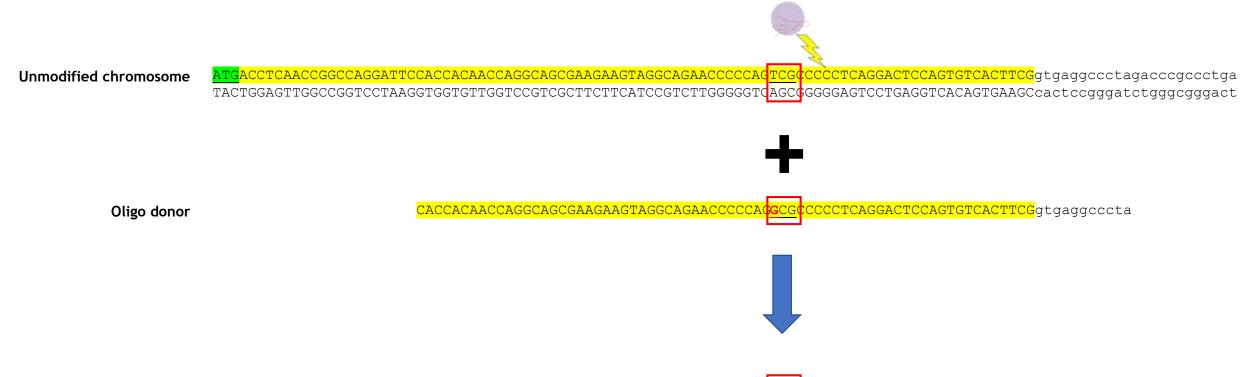


Gene knockout-large deletion





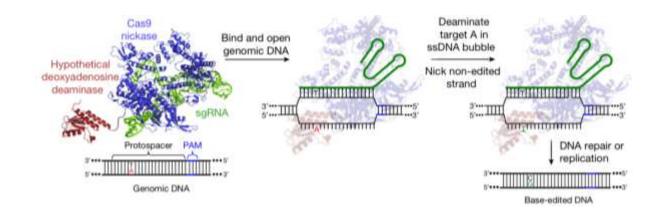
Gene mutagenesis-HDR



Modified chromosome



Gene mutagenesis-Base editors



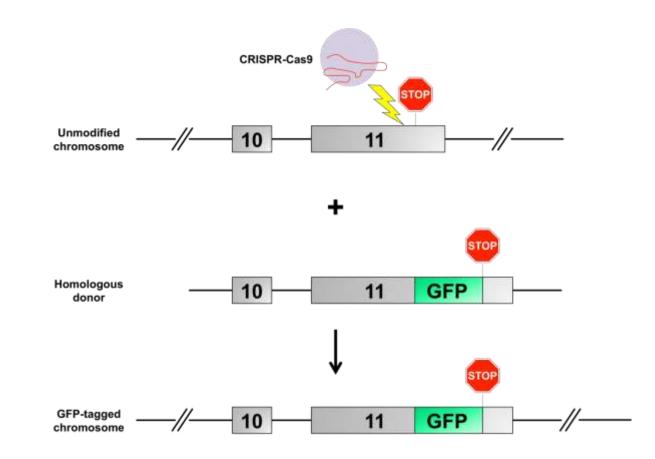
Gaudelli, et al. (2017). Nature 551, 464

 Cas9 nickase fused to cytidine and adenine deminases

- Permit changing of bases without DSBs
- Can change C to T, G to A, A to G, and T to C

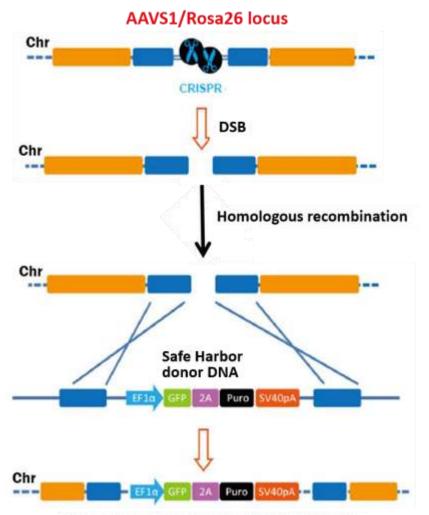


Gene tagging





Gene knock-in (transgenesis)



Features

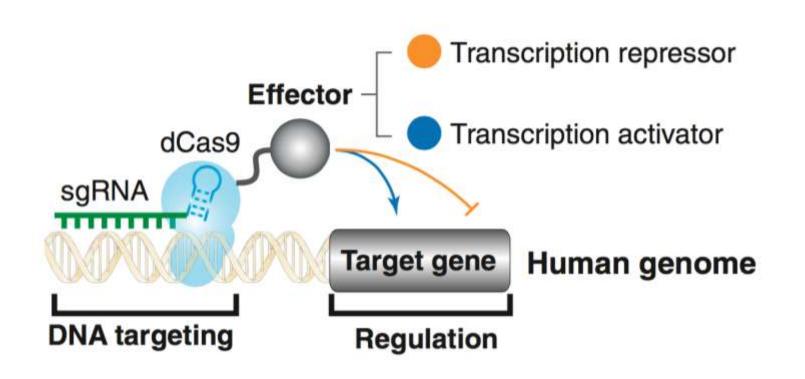
 Human AAVS1 & mouse Rosa26 sites ensure transcription-competency of the transgenes & present no known adverse effects on cells

 Safe Harbor integration provides low copy number of transgene & close to physiologicallevel expression.



Transgene and marker cassette knocked in

Gene activation or repression



Gilbert, et al. (2013). Cell 154, 442



Outline

CRISPR technologies & applications

- Strategy considerations
- Delivery methods
- Preparation
- Screening
- Things to look out for



Considerations before you start

- What type of application are you doing (gene knockout, mutagenesis, etc.)? This decision can effect the efficiency and the degree of difficulty screening for the modification.
- What type of cell line are you using (primary, immortalized)?
- Can the cell line be transfected? If it does not transfect well, or not at all, then you
 might need to use lentivirus for delivery. However, lentivirus cannot be used for HDR
 applications.
- Other cell line considerations: Growth rate, growth characteristics (adherent vs. suspension growth), target gene copy number.



Outline

CRISPR technologies & applications

Strategy considerations

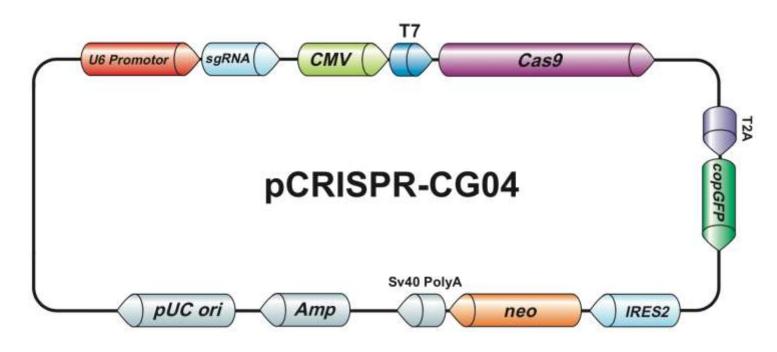
- Delivery methods
- Preparation

Screening

Things to look out for



Delivery method 1: Cas9/sgRNA plasmid DNA



- GeneCopoeia Cas9 + sgRNA "Allin-one" plasmid
- Fluorescent reporter allows for sorting
- Selection marker can be used for stable integration
- Cas9 needs to be transcribed and translated



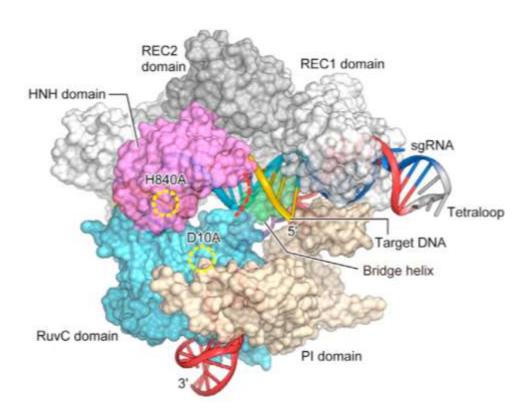
Delivery method 2: Cas9 mRNA + sgRNA

- Co-transfect in vitro transcribed Cas9 mRNA with sgRNA
- ✤ sgRNA can either be encoded on plasmid, *in vitro* transcribed, or synthetic

- Advantage: Plasmid-free, so cannot integrate
- Cas9 still needs to be translated



Delivery method 3: Cas9 ribonucleoprotein (RNP)

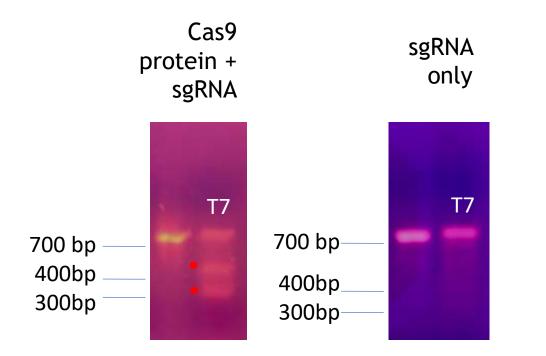


Nishimasu, et al. (2014). Cell 156, 935

- Pre-form complex of Cas9 protein and sgRNA in vitro to form RNP
- sgRNA can be either chemically synthesized or *in* vitro transcribed
- Transfect cells with RNP complex using either lipid transfection reagent or electroporation
- Efficiency of indel formation is generally similar to that of plasmid transfection (Kim, et al., 2014. Genome Research)
- Lower off-targeting compared with plasmid transfection (Kim, et al., 2014. Genome Research)
- ✤ Does not integrate, unlike plasmids



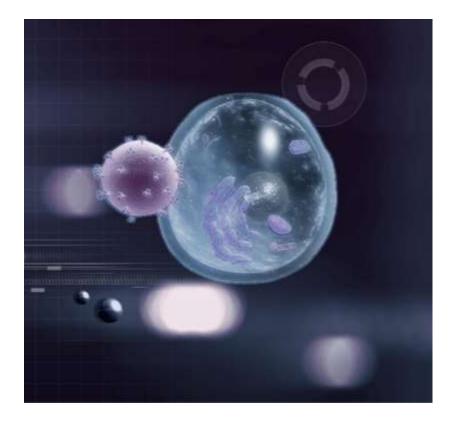
Coming soon! GeneHero[™] Cas9 nuclease



 Transfection of HEK293 cells using EndoFectin[™] Max



Delivery method 4: Lentivirus

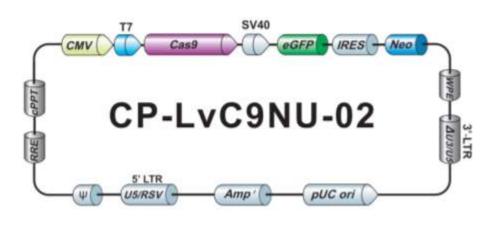


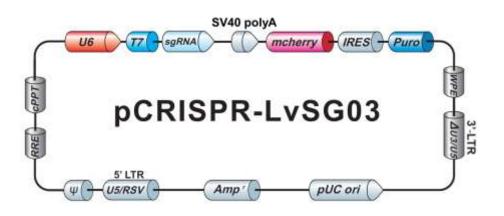
Why lentivirus?

- DNA transfection not always possible or practical. Some cell lines difficult or impossible to transfect.
- Most mammalian cells support infection by engineered lentivirus



Delivery method 4: Lentivirus





Features

- 2-component system: 1) Cas9 lentivirus + sgRNA lentivirus
- Cannot be used for HDR
- ✤ Leads to stable selection
- GeneCopoeia provides either plasmids for doit-yourself packaging or ready-to-use particles
- Recommend that you first establish or obtain Cas9-stable cell line



GeneHero[™] Cas9 stable cell lines

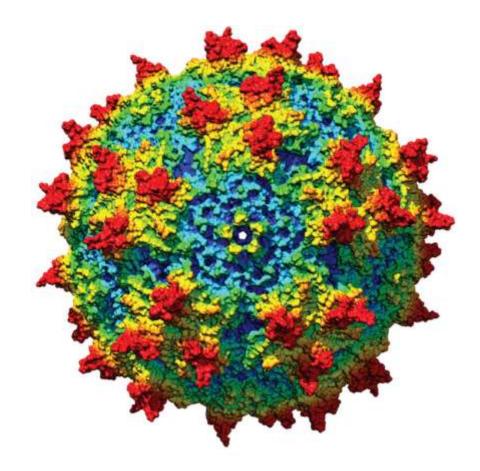


Features

- Cell lines with Cas9 stably integrated in the genome
- ✤ >70 pre-made cell lines available in human, mouse, and rat cell lines
- Functionally validated for Cas9 activity
- Ideal for lentiviral CRISPR applications



Delivery method 5: Adenoassociated virus (AAV)



- Identified as co-isolate of adenovirus (Ad)
- ✤ Single stranded DNA genome of 4.7 kb
- Limited genome size favors use of smaller Cas9 (e.g. SaCas9)
- Engineered AAV does not integrate into genomic DNA
- Infects dividing & non-dividing cells
- ✤ More frequently used in vivo



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Preparation

Screening

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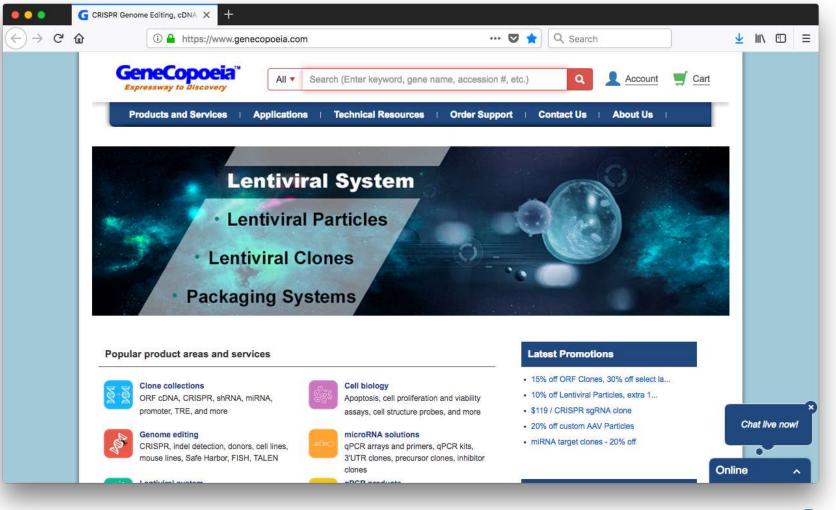
Workflow: Preparation

 Step 1: Choose your application (gene knockout, mutagenesis, etc.) This decision can affect the efficiency and the degree of difficulty in screening for modification.

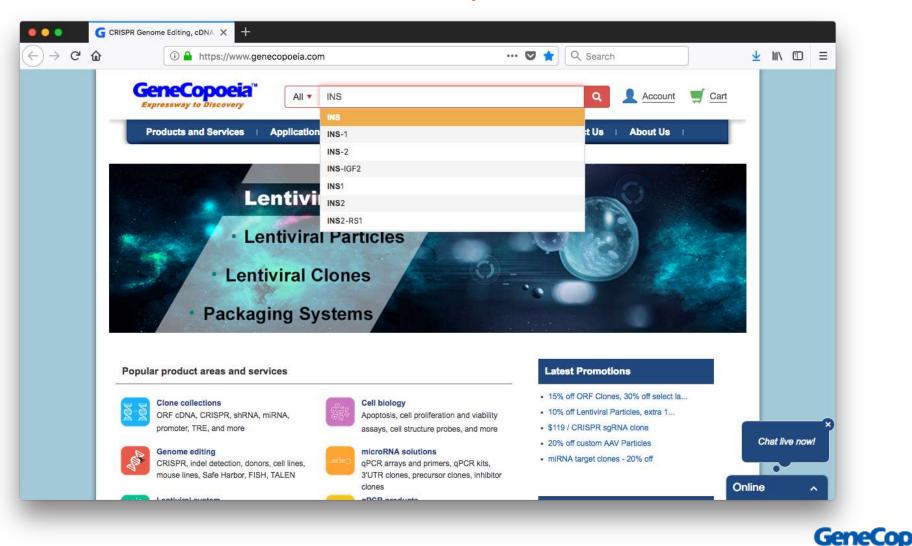
 Use GeneCopoeia's website to choose targets for knockout, or contact us for custom sgRNA design and donor design, if applicable



Workflow: Preparation

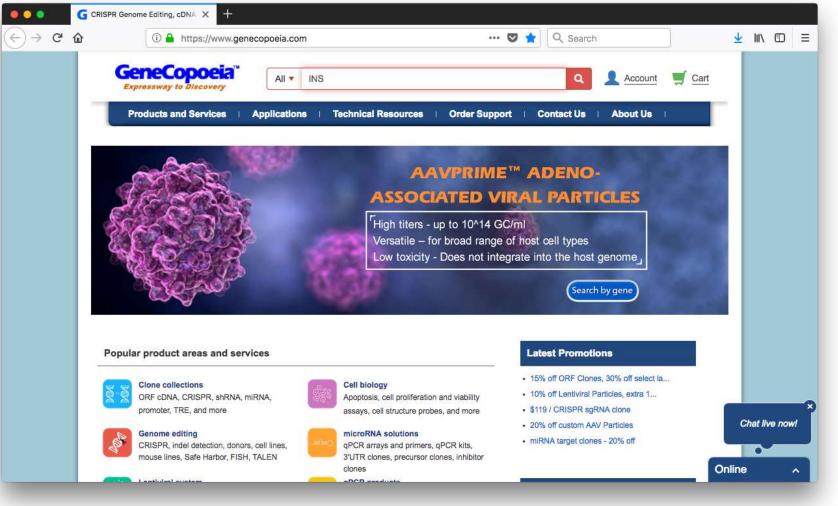


Workflow: Preparation



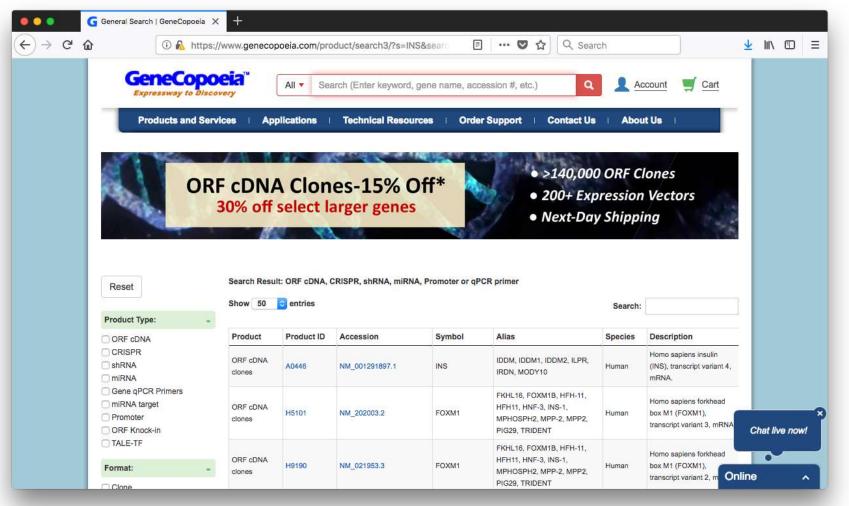
Expressway to Discovery

Workflow: Preparation



GeneCopoeia

Workflow: Preparation



GeneCopoeia Expressway to Discovery

Workflow: Preparation

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	Product Type:						oearcn.		
	ORF cDNA	Product	Product ID	Accession	Symbol	Alias	Species	Description	
	CRISPR shRNA miRNA	ORF cDNA clones	A0446	NM_001291897.1	INS	IDDM, IDDM1, IDDM2, ILPR, IRDN, MODY10	Human	Homo sapiens insulin (INS), transcript variant 4, mRNA.	
	Gene qPCR Primers MiRNA target Promoter ORF Knock-in	ORF cDNA clones	H5101	NM_202003.2	FOXM1	FKHL16, FOXM1B, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TRIDENT	Human	Homo sapiens forkhead box M1 (FOXM1), transcript variant 3, mRNA.	
	TALE-TF Format: Clone	ORF cDNA clones	H9190	NM_021953.3	FOXM1	FKHL16, FOXM1B, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TRIDENT	Human	Homo sapiens forkhead box M1 (FOXM1), transcript variant 2, mRNA.	
	C Lentiviral Particle AAV Particle Species:	ORF cDNA clones	10607	NM_001243088.1	FOXM1	FKHL16, FOXM1B, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TRIDENT	Human	Homo sapiens forkhead box M1 (FOXM1), transcript variant 4, mRNA.	
	☐ Human ☐ Mouse ☐ Rat	ORF cDNA clones	10608	NM_001243089.1	FOXM1	FKHL16, FOXM1B, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TRIDENT	Human	Homo sapiens forkhead box M1 (FOXM1), transcript variant 5, mRNA.	
	Reset	ORF cDNA clones	T8218	BC006192.2	FOXM1	FKHL16, FOXM1B, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TGT3, TRIDENT	Human	Homo sapiens forkhead box M1, mRNA (cDNA clone MGC:10704 IMAGE:3833837).	
		ORF cDNA clones	U1376	U83113.1	FOXM1	FKHL16, FOXM1B, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TGT3, TRIDENT	Human	Human INS-1 winged-helb homolog mRNA.	Chat live nov

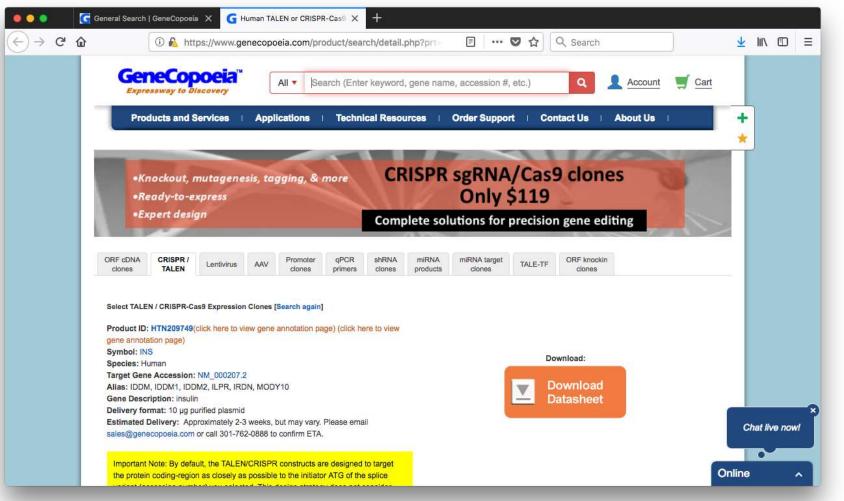


Workflow: Preparation

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	ORF cDNA	Product	Product ID	Accession	Symbol	Allas	Species	Description					
	CRISPR	CRISPR clones	HTN209749	NM_000207.2	INS	IDDM, IDDM1, IDDM2, ILPR, IRDN, MODY10	Human	insulin					
	MiRNA Gene qPCR Primers MiRNA target Promoter ORF Knock-in	CRISPR clones	HTN255592	NM_202002.2	FOXM1	FKHL16, FOXM1A, FOXM1B, FOXM1C, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TRIDENT	Human	forkhead box M1					
	TALE-TF	CRISPR clones	HTN257953	NM_001185097.1	INS	IDDM, IDDM1, IDDM2, ILPR, IRDN, MODY10	Human	insulin					
	Format:	CRISPR	HTN257954	NM_001185098.1	INS	IDDM, IDDM1, IDDM2, ILPR, IRDN, MODY10	Human	insulin	-				
	Lentiviral Particle AAV Particle Species:	CRISPR	HTN266992	NM_001243089.1	FOXM1	FKHL16, FOXM1A, FOXM1B, FOXM1C, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, NNPD 3, NNPD 3,	Human	forkhead box M1					
	V Human					MPP-2, MPP2, PIG29, TRIDENT							
	Mouse Rat	CRISPR	HTN266993	NM_001243088.1	FOXM1	FKHL16, FOXM1A, FOXM1B, FOXM1C, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29,	Human	forkhead box M1					
						TRIDENT							
		CRISPR clones	HTN270786	NM_001291897.1	INS	IDDM, IDDM1, IDDM2, ILPR, IRDN, MODY10	Human	insulin					
		CRISPR clones	HTN296566	NM_021953.3	FOXM1	FKHL16, FOXM1A, FOXM1B, FOXM1C, HFH-11, HFH11, HNF-3, INS-1, MPHOSPH2, MPP-2, MPP2, PIG29, TRIDENT	Human	forkhead box M1	Chat live nov				



Workflow: Preparation





Workflow: Preparation

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		Che	ck out our Cas9 Stable (Cell Lines!					_					
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		Buy	Catalog#	Description	sites	marker	gene	Vector						
		Non-viral clones												
			CP-C9NU-01	Cas9 nuclease expression clone	1	Neo	mCherry	CP-C9NU-01						
		0	HCP209749-SG01-1	1 × sgRNA expression clone targeting INS (NM_000207.2)	1	Hygro	N/A	pCRISPR-SG01						
		0	HCP209749-SG01-3	3 × sgRNA expression clones targeting INS (NM_000207.2)	3	Hygro	N/A	pCRISPR-SG01						
		Lentiviral clones (packaged particles can be found under Lentiviral particle tab)												
		0	CP-LvC9NU-01	Cas9 nuclease lentiviral expression clone (-CMV promoter)	1	Neo	N/A	CP-LvC9NU-01						
		0	CP-LvC9NU-02	Cas9 nuclease lentiviral expression clone (-CMV promoter)	1	Neo	eGFP	CP-LvC9NU-02						
			CP-LvC9NU-08	Cas9 nuclease lentiviral expression clone (-EF1a promoter)	1	Puro	N/A	CP-LvC9NU-08						
			CP-LvC9NU-09	Cas9 nuclease lentiviral expression clone (-EF1a promoter)	1	Neo	eGFP	CP-LvC9NU-09						
		0	CP-LvC9NU-10	Cas9 nuclease lentiviral expression clone (-EF1a promoter)	1	Hygro	eGFP	CP-LvC9NU-10						
		0	HCP209749-LvSG03-1	1×sgRNA lentiviral expression clone targeting INS (NM_000207.2)	1	Puro	mCherry	pCRISPR- LvSG03						
			HCP209749-LvSG03-3	3×sgRNA lentiviral expression clone targeting INS (NM_000207.2)	3	Puro	mCherry	pCRISPR- LvSG03	G	hat live n	ow!			
		All-in	n-one clones											
			HCP209749-CG02-1	1 × sgRNA/Cas9 all-in-one expression clone targeting INS (NM_000207.2)	1	N/A	N/A	pCRISPR-CG02		•				
		James	HCD200740 CC02 3	3 × sgRNA/Cas9 all-in-one expression clone targeting INS	9	N/A	NZA		Online		^			



Workflow: Preparation

Step 2: Determine the DNA sequence of the sgRNA target site in your cell line

Necessary to ensure highest possible nucleotide match. Might need to do custom sgRNA synthesis



Smart-Join[™] Blunt-end PCR Cloning Kit

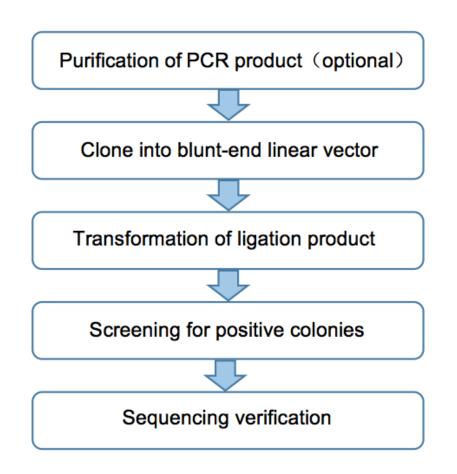
Features

- Convenient method for high efficiency cloning of blunt-end PCR products
- Higher positive ligation rate and true positive colonies by the elimination of self-ligating products
- Cloning of blunt-end PCR products without additional sequences or restriction sites
- Ideal for sequencing regions of genomic DNA



Smart-Join[™] Blunt-end PCR Cloning Kit

<u>Workflow</u>





Workflow: Preparation

Step 3: Validate sgRNA function in your cell line

 Not all sgRNAs are created equal. It is the best practice to try multiple target sites and pre-validate the best one



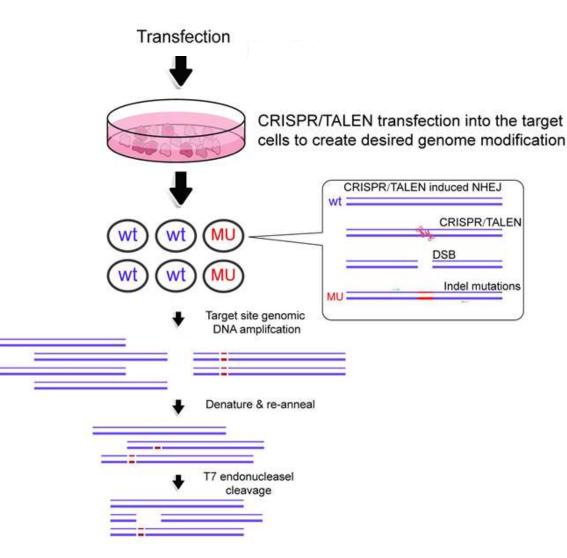
IndelCheck[™] CRISPR indel detection system

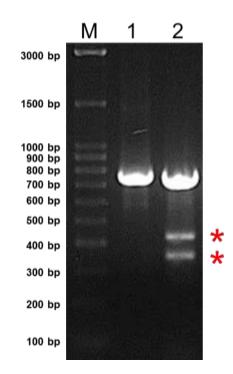
Features

- Useful for 1) CRISPR sgRNA functional validation; 2) Screening for positive clones
- 3-component system: 1) Target site PCR kit; 2) T7 Endonuclease I kit; 3) Blunt-end PCR cloning kit
- No genomic DNA isolation is required



IndelCheck[™] CRISPR indel detection system







Workflow: Preparation

Step 4: Copy number determination

- ✤ For complete knockouts or mutagenesis, might need to modify <u>all</u> alleles
- Not all cell lines are diploid. Some lines, like HeLa, have 3, 4, or more genomes
- Would expect multi-allele modification to be more difficult to achieve than single allele
- However, double allele occurs more frequently than single allele (Gonzalez, et al., 2014. Cell Stem Cell 15, 1)



CRISPR-Cas9 genome editing technology Application: Using FISH with a CRISPR knockout

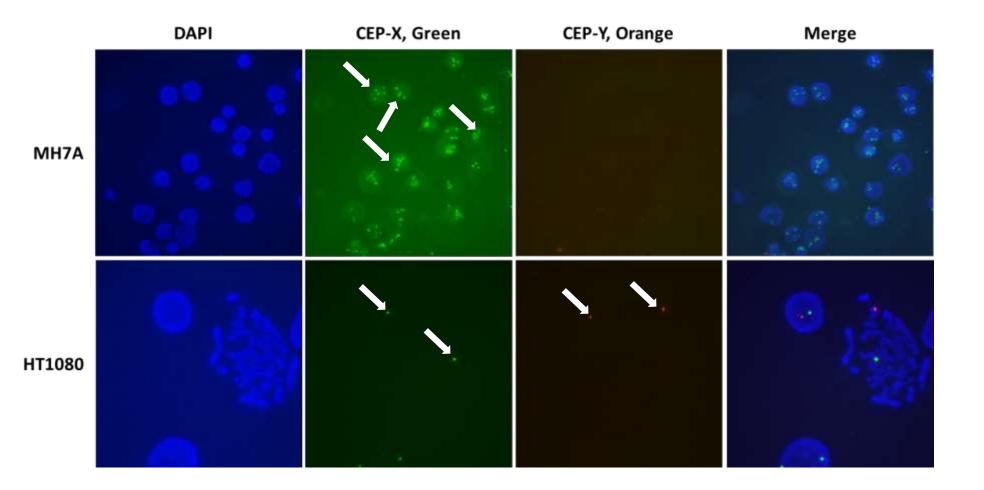
Project: Knock out HDAC6 gene in human MH7A cells

HDAC6 (NCBI geneID:10013): Located on X chromosome (Xp11.23)

- ✤ MH7A cells: Human immortalized synovial fibroblast line
- HDAC6 copy number: Unknown



CRISPR-Cas9 genome editing technology Application: Using FISH with a CRISPR knockout





Application: Using FISH with a CRISPR knockout

Clone 1

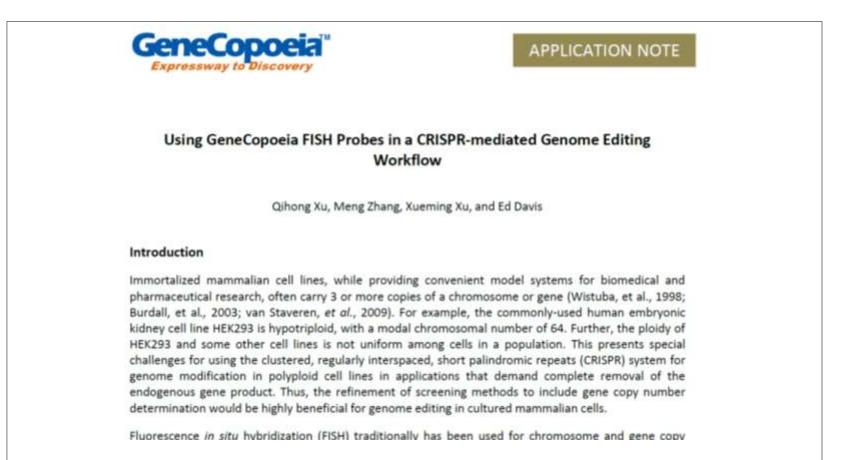
	(500)	500	510	520	530	540	550	560	570	580	590	600	610	620	635
HDAC6 Targeting region NC 018934	C2-4_PREMIX (471)	TTCACAGAA	GCGAAATAT	TAAAAAG	GAGCOSTICO	CONTRACC	TAL TAL	AGGCCTCCTCC	GAGOGGATGT	ACCCCGAGGA	CGGDGCOO	CAGSTAAAC	AAGAAAGGCAA	AATGAAGAAGC	TOGGECAA
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Allele b	C2-11_PREMIX (469)	TTCACAGAA	GCGAAATAT	TAAAAAG	GGAGCCGTTCC	<u></u>	********					AAAD	ARGANAGGCA	MATGAAGAAGC	TOGGCCAA
Allele c	C2-7_PREMIX (472)	TTCACAGAA	GCGAAATA1	TAAAAAG	GAGCCUTTCO	CONTRACC	CCRAT'				G	GAGGTAAAA	AAGAAAGGCAA	AATGAAGAAGE	TUGGOCAN
Allele c	2A-F_PREMIX (470)	TTCACINGAA	OCGAANTAT	TAAAAAG	GEAGCOGTTCO	COSCILCTATOS	CCANTO					GAGGTAAAO	AGAAAGGCAI	MATGAAGAAGC	TOGGOCAA
Allele d	C2-5_PREMIX (470)	TTCACAGAA	OCGAAATAT	TAAAAAG	SAGCOUTTOO	DIGCTOTATOO	CCAAD TAG	G		*********		Arritaral	AAGAAAGGEAJ	WATGAAGAAGE	TOGECCAR
Allele d	C2-8_PREMIX (474)	TTCMCWGAA	OCGARATAT	TAAAAAG	DEMOCOGTICO	COCTOWNTOO	COMPCEME	G	********		<mark>('6</mark>	GAGGTAAAG	AAGAAAGGCAA	ANTONIGANGO	TOGGOCAA
Allele d	2B-F_PREMIX (472)	TTCACAGAA	GCGAAATA 1	TRAAAAG	GGAGCOGTICO	DEGETETATOO	CCARTCYAG	G			<mark>ĽG</mark>	GAGGTAAAO	AAGAAAGGEAA	AATGAAGAAGC	TOGGOCAR
Allele d	2C-F_PREMIX (470)	TTCACAGAA	OCGAAATAT	TABAAAS	GEAGCOGTTOO	DESCRETATOO	CCAATCTAG	G			<mark>06</mark>	SAGGTAAAO	AAGAAAGGCAI	WATGAAGAAGC	TOSSOCAA
Allele e l	DAC6 Targeting Region NC_018934 (500)	TTCACAGAA	OCGNAATA7	TAAAAAG	GGAGOOGTICO	COSCILLATOO	CCAATCTAG	C			G	GAGGTAAAA	AAGAAAGGCAJ	WATGAAGAAGC	TOGGOCAR
Consensus	Consensus (500)	TICACAGAA	OCGAAATAT	TAAAAAG	GGAGCCGTTCC	COCTUTATOO	OCAATCTAG				CG	GAGGTAAAC	AAGAAAGGCAA	VAATGAAGAAGC	TOGGOCAA

Clone 2

	(553)	553	560	570	580	590	600	610	620	630	640	650	660	670	68	8
HDAC6 Targeting region NC 018934	C3-11_PREMIX (487)	TANA	GACCOST	O DE C	ATOCOCANT	CTAGAGGCCTC	CTCCGAG	OGGATGTACECOS	AGGACGGCGC	CCCGGAGGT	A GINGINA	GCAMAT	MGMOCTO	GOCHAGCAA	GGAAGAAG	Ā.
Allele f	C3-8_PREMIX (516)	GC <mark>ATTA</mark> A	T <mark>GA</mark> AT <mark>CO</mark> G	C <mark>C</mark> AA <mark>C (</mark> GCG	GGGAGAGGC	GGTTTG		OGTATTGGGCGCT	CTICCGCTIC	CTEGETCACT	GACTOSCIG	COCTOGET	GTTCG CTG	C <mark>GGGGAOC</mark> GG	ATCA CTCN TC	<u> </u>
Allele g	C3-6_PREMIX (487)	TAAAAAG	GACCET	1 <mark>0000</mark>	*******	*********			********		AND A GANA	GOCAMAT	SAAGAAN <mark></mark> O	GOCHATCAA	GGANGAAG <mark>AC</mark> UT	
	3C-F_PREMIX (487)		GAL COT	7 <mark>0 10</mark>	-						A <mark>A</mark> TAA <mark>G</mark> AAA	GSCAAAA	IANGANG <mark>CT</mark> O	OCCAROCAN	GEAAGAAG <mark>AC</mark> CT	
Allele h	C3-10_PREMIX (487)		GA COGT	r <mark>aca<mark>c</mark>ecter</mark>	ATCCGC					GGAGGT	A <mark>A</mark> GAA <mark>G</mark> AAA	G <mark>oc</mark> haaad	angang <mark>en</mark> o	Sectandera	GGAAGAAG <mark>ACCT</mark>	<u> </u>
Allele i	3A-F_PREMIX (487)		SA CG	grager						A	A <mark>A</mark> GAA <mark>G</mark> AAA	GCNRAAT	IAMIAAG <mark>CI</mark> O	o <mark>gocaadca</mark> a	ICCAN-ANNACCE	
Allele i	3B-F_PREMIX (492)	TAAAAA	GA COOT	toroper-						h	A <mark>M</mark> EAA <mark>G</mark> AAA	GOGANAA	IANGANG <mark>CT</mark> C	GCCAACCAA	IGGAAGAAGACET	4
Allele i	C3-4_PREMIX (488)	TAARAAG	ATTA CCCL	a dan							AAGAAGAAA	GSCAAAA	AAGAAG <mark>CT</mark> C	GECCAAGCAR	GGAAGAAGACCT	4
Allele i	C3-5_PREMIX (487)	TAAAAAG	CA CO	d date-							AAGAAGAAA	GOCANAAT	ANJAN CTO	IGCENAGEA A	GEAAGAGACET	
	C3-9_PREMIX (488)	TAAAAAG	GACCOT	0.00							AAGAAGAAA	GSCRAAM	HAAAA CLO	GCCCACAA	GGAAGAAGACUI	
Allele iHDAC6 Targeting Regi		TAPAN	EN CON		ATCCCCAAT	CTAG				CGGAGGT	MEMCAN	GOGAMAT	AN AN CIC	PRECAMPEAN	GERAGAGACCE	
Consensus	Consensus (553)	TAAAAAG	GGAGCCGT	TOCCOGCT						A	AAGAAGAAA	GGCAAAATV	ANGAAGCTO	GGCCAAGCAA	IGGAAGAAGACCT	<u>8</u>



GeneCopoeia Application Note: FISH with CRISPR



Download from:

http://www.genecopoeia.com/wp-content/uploads/2016/02/FISH-for-CRISPR.pdf



Outline

CRISPR technologies & applications

- Strategy considerations
- Preparation
- Delivery methods
- Screening
- Things to look out for





Isolate single clones post-transfection/transduction



 Minimizes potential effects of unwanted modifications resulting from random insertion, cell division or off-targeting





Isolate single clones post-transfection/transduction

IMPORTANT:

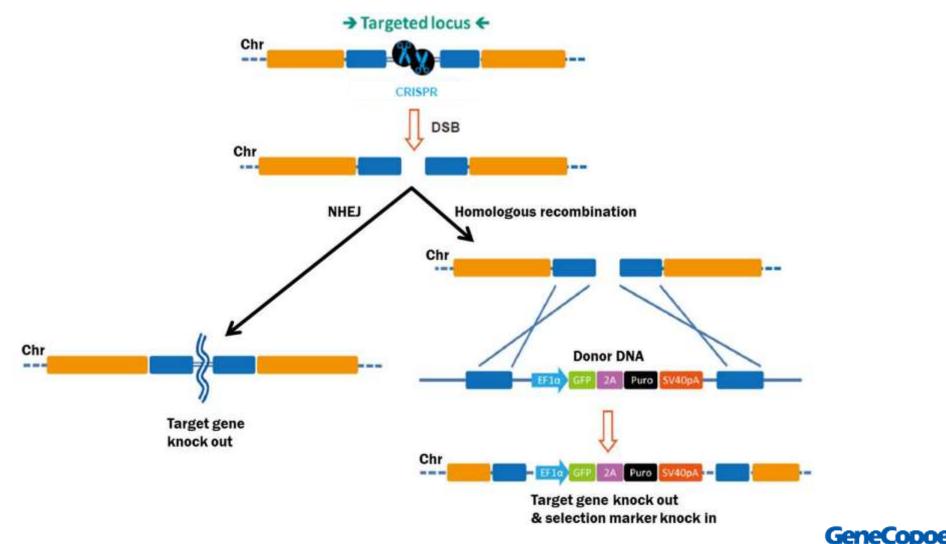
Connect genotype to phenotype!

(or, check the chromosome first before doing functional assays for your target)



Screening

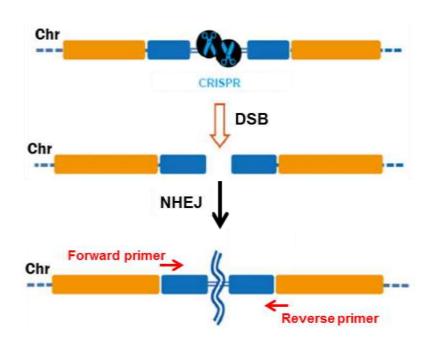
Isolate single clones post-transfection/transduction



Expressway to Discovery



NHEJ-mediated mutations (knockouts)

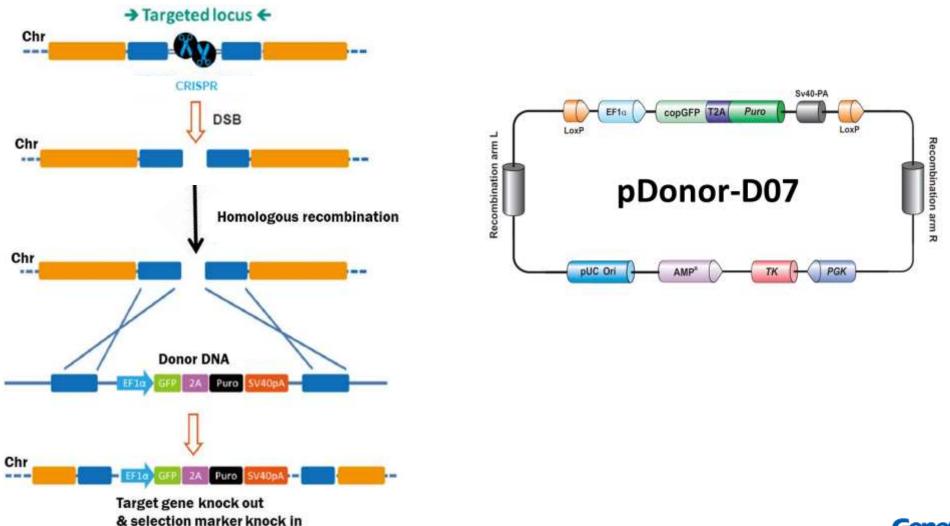


- Isolate clones without selection 2-3 days post transfection/transduction
- Generate PCR products using primers flanking the DSB site (can use same primers as used for validation)
- Screen PCR products by T7 Endonuclease I assay OR direct sequencing. Use GeneCopoeia's IndelCheck system
- Re-screen positive clones by direct sequencing





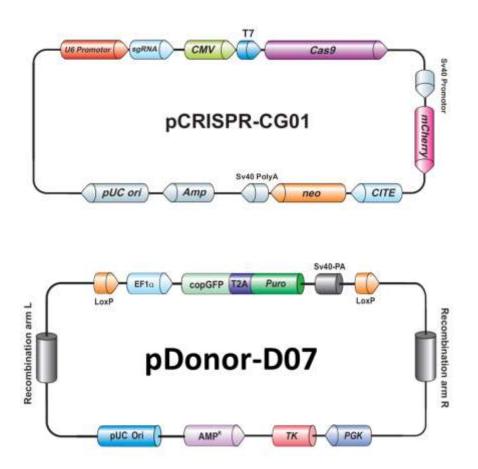
HDR-mediated applications using donor plasmids







HDR-mediated applications using donor plasmids

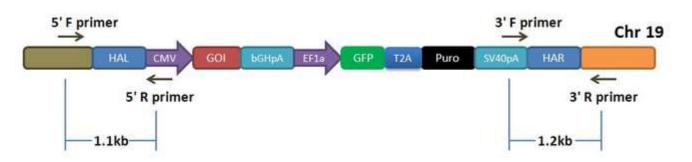


- Co-transfect Cas9, sgRNA, and donor plasmids
- 2-3 days post transfection, apply selection for donor selection cassette, or sort cells expressing fluorescent reporter
- Isolate single clones
- Screen single clones for correct integration by PCR

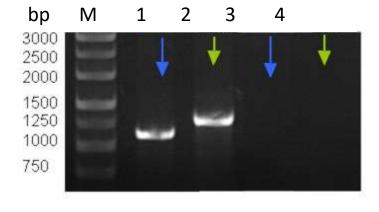




HDR-mediated applications using donor plasmids



Junction PCR



Will only get PCR products if donor has integrated at the correct site



Outline

- CRISPR technologies & applications
- Strategy considerations
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Gene copy number

- For complete knockouts or mutagenesis, might need to modify all alleles
- Not all cell lines are diploid. Some lines, like HeLa, have 3, 4, or more genomes!
- Would expect multi-allele modification to be more difficult to achieve than single allele
- However, one publication showed that double allele occurs more frequently than single allele (Gonzalez, et al., 2014. Cell Stem Cell 15, 1)



Cleavage efficiency

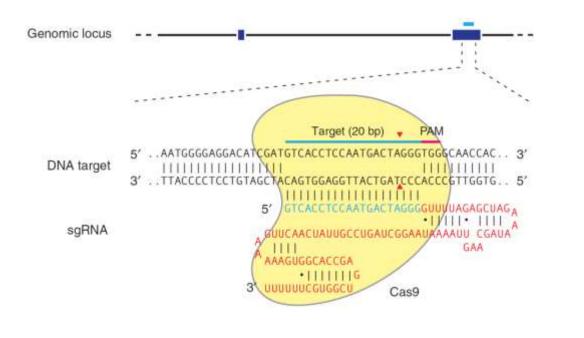
Efficiencies of indel formation by CRISPR usually 5%-70%

Expect to screen 2x as many clones for a CRISPR sgRNA with 40% cutting efficiency as you would for one with 80% cutting efficiency

Selection for modifications using a donor can help screening



Off-targeting



Ran, et al. (2013). Nature Protocols 8, 2281

- CRISPR sgRNAs can tolerate up to 5 mismatches with chromosomal target
- CRISPR sgRNAs can also recognize non-canonical NAG PAM
- Mismatch tolerance and noncanonical PAM recognition can lead to cleavage at other, non-target, or "off-target" sites
- Off-target modifications can have adverse consequences on research results or patient safety!



Off-targeting

- Off-targeting should be addressed. GeneCopoeia designs sgRNAs with the lowest possible predicted off-target potential. However, this is a prediction, not experimentally determined.
- Whole genome next-generation sequencing (NGS) is the most comprehensive, unbiased approach. However, this is expensive.
- Can also use targeted, NGS methods such as Digenome-seq and VIVO
- Alternatively, can sequence predicted off-target sites. This is an inexpensive method but is biased.



Summary

- The workflow for CRISPR genome editing experiments must be carefully considered, for aspects such as type of modification you are using, the delivery method, the cell line you are using, etc.
- Other considerations must be taken into account for successful genome editing experiments, such as transfection efficiency, copy number variation, and cleavage efficiency

 GeneCopoeia offers many products and services, including plasmid design & construction, functional validation, validation and screening kits, and transgenic mice, to meet your genome editing needs



Thank You!

If you have any additional questions, please call 1-866-360-9531 x227 Email: edavis@genecopoeia.com Or visit us on the web: www.genecopoeia.com

GeneCopoeia, Inc.

9260 Medical Center Drive Suite 101

Rockville, Maryland USA 20850

