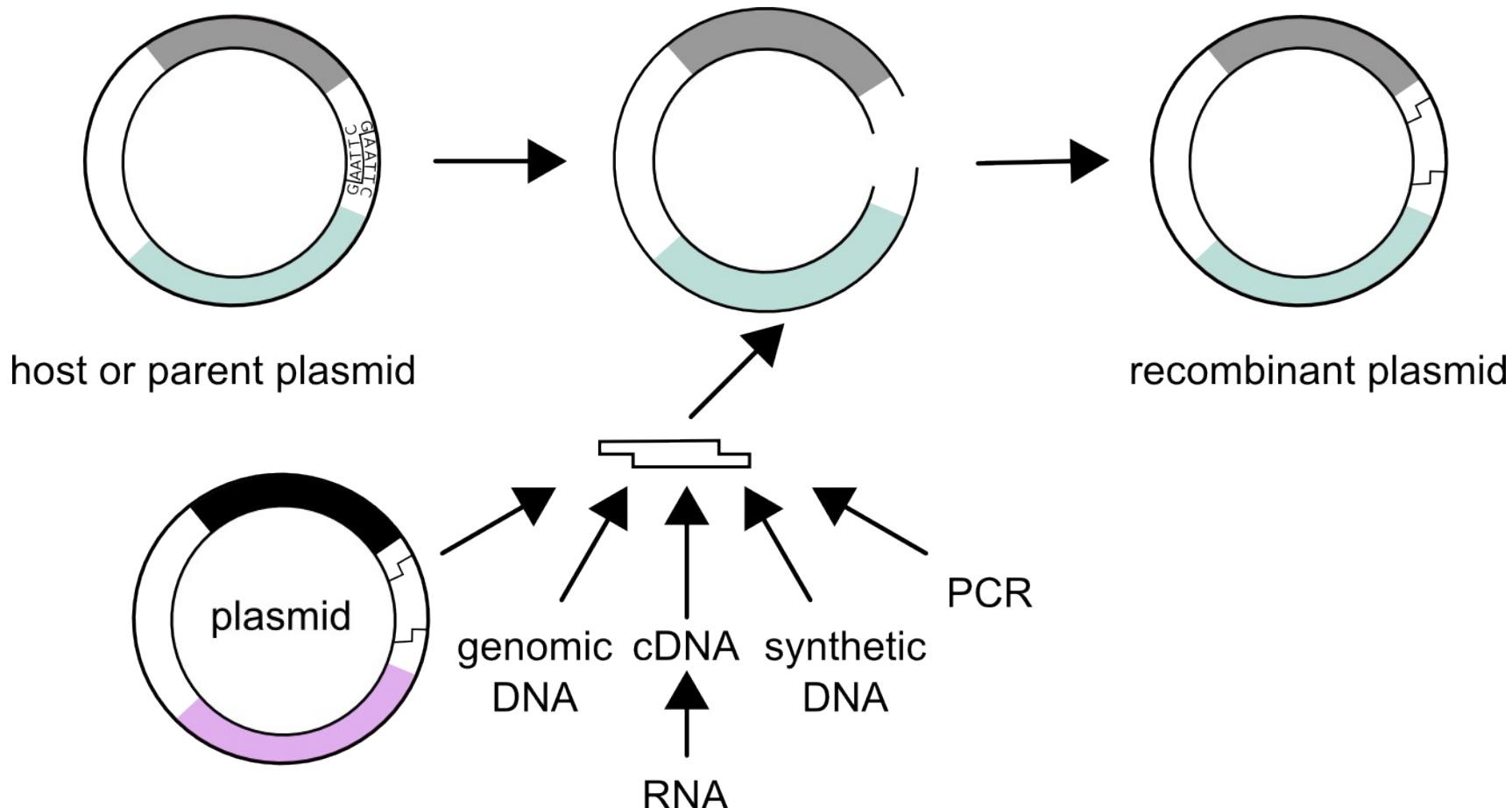


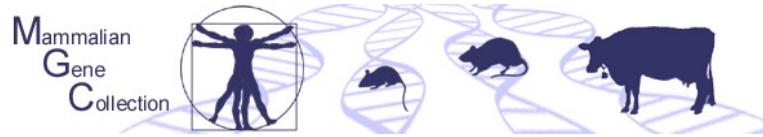


Sources of Sequences





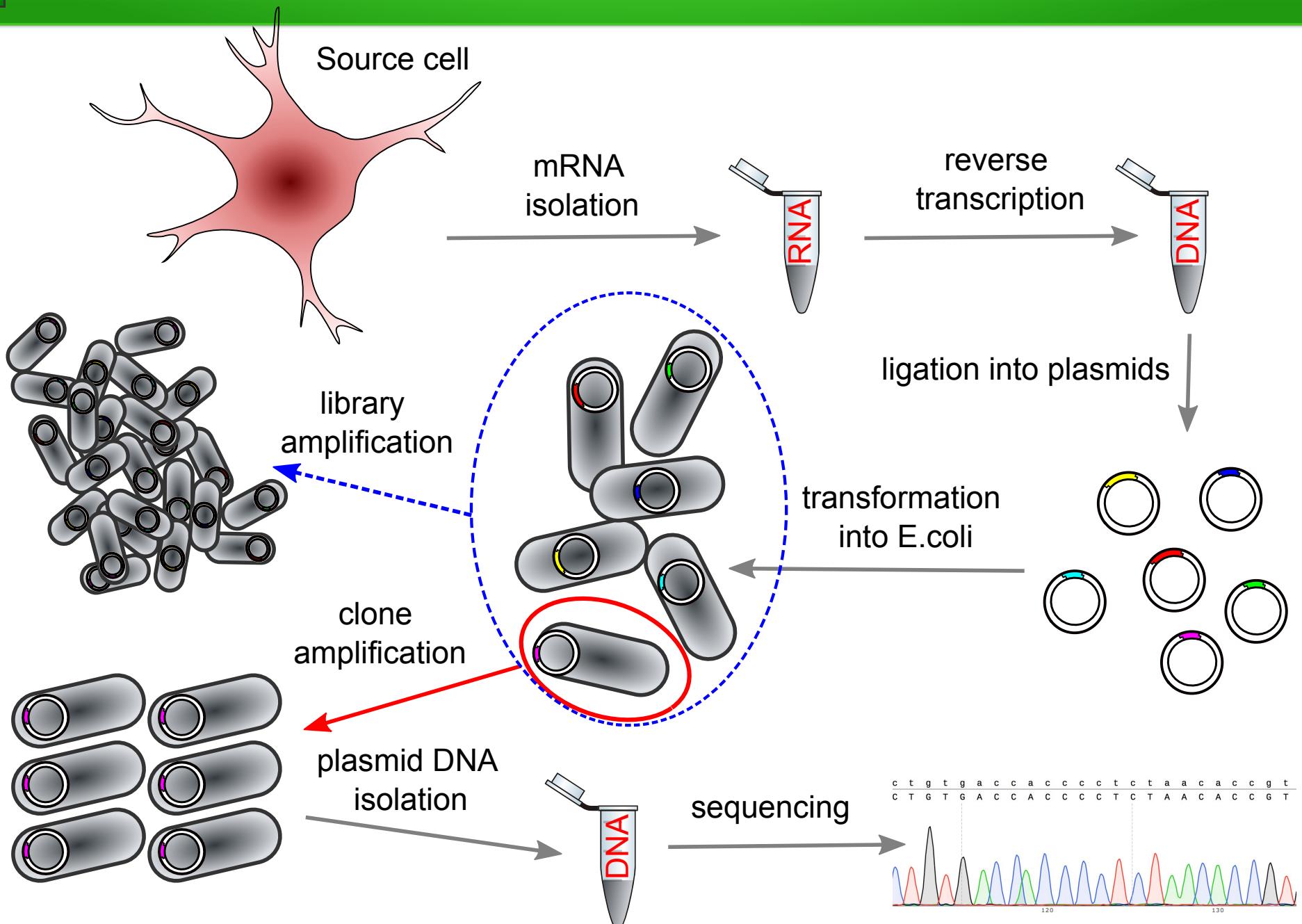
Gene Collections



- MGC (Mammalian Gene Collection = human, mouse, rat, bovine):
<http://mgc.nci.nih.gov/> (most of these clones are available for a nominal fee from <http://www.biocenter.helsinki.fi/bi/gbu/orf/>)
A guide for finding and evaluating MGC clones:
http://mgc.nci.nih.gov/files/GuideToFindingEvaluating_MGC_Clones.pdf
- Zebrafish gene collection: <http://zgc.nci.nih.gov/>
- Xenopus gene collection: <http://xgc.nci.nih.gov/>
- MGC, honey bee, chicken, fugu, Drosophila, C. elegans:
<http://www.lifesciences.sourcebioscience.com/>
- RIKEN (<http://dna.brc.riken.jp/en/resource150en.html>)
- Long cDNAs (~4.5kb):
Kazusa (<http://www.kazusa.or.jp/huge/>, KIAA designation)
NEDO (<http://www.kazusa.or.jp/NEDO>, FLJ designation)

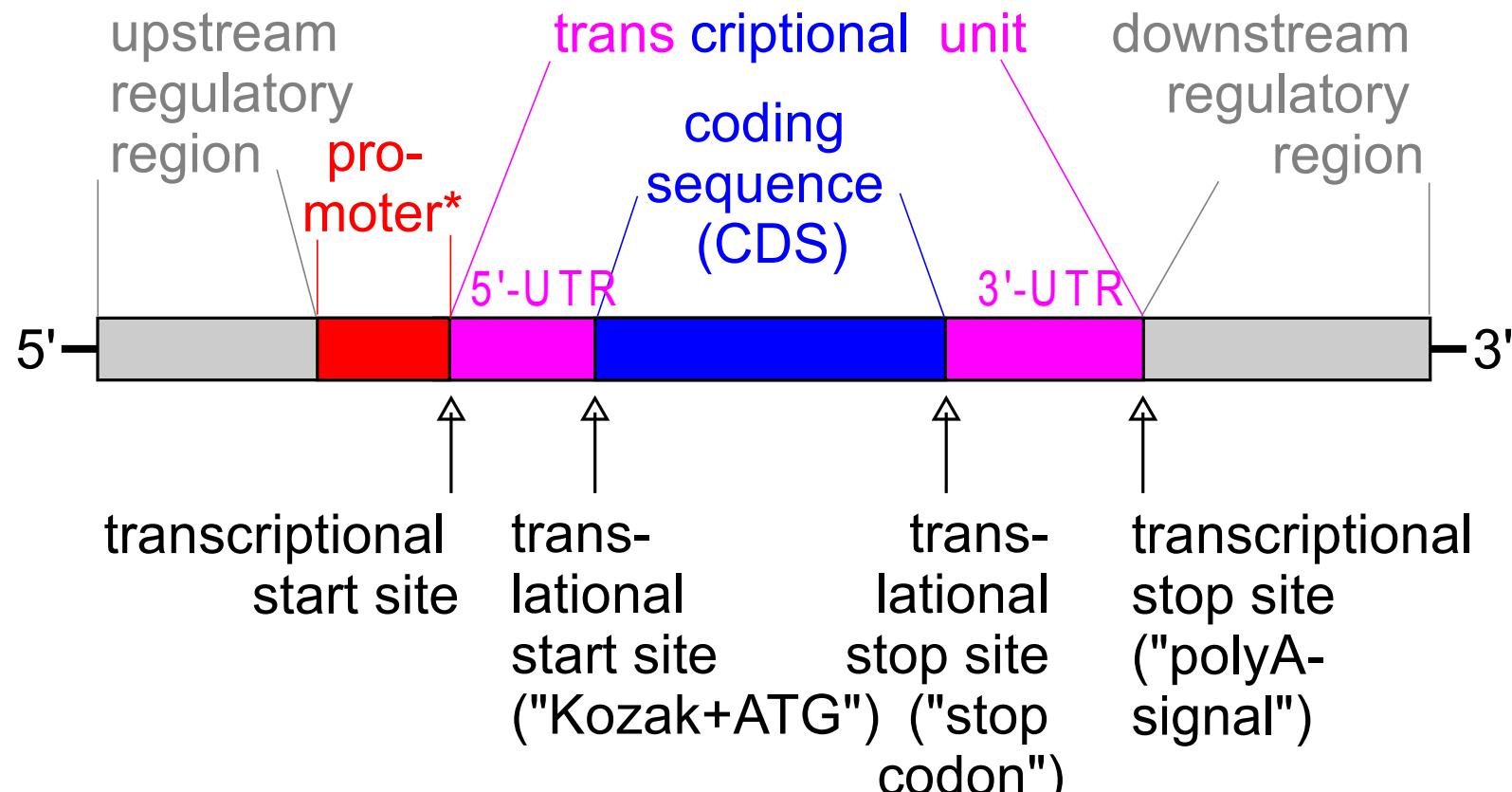


How to make a cDNA library





Reverse transcription into cDNA



* = RNA polymerase binding site

- House keeping genes and small ORFs are overrepresented in cDNA libraries
- Priming: "random hexamers", "oligo(dT)-primer", gene-specific primers
- cDNA library vs. cDNA expression library
- ORF clones (no 5'- & 3'-UTRs), with sequence-specific primers
- cDNA libraries → cDNA collections
- Reverse transcriptase (error rate: 1:17,000-1:30,000, max. length ~15kb)



Gateway site-specific recombination cloning system

Based on λ phage integration system:

$attB1 \times attP1 \rightarrow attL1$
 $attB2 \times attP2 \rightarrow attL2$

$attL1 \times attR1 \rightarrow attB1$
 $attL2 \times attR2 \rightarrow attB2$

+/- stop codon

8 aa between GOI and tag (from att site)

ccdB containing plasmids must be propagated in a *gyrA462+* strain!

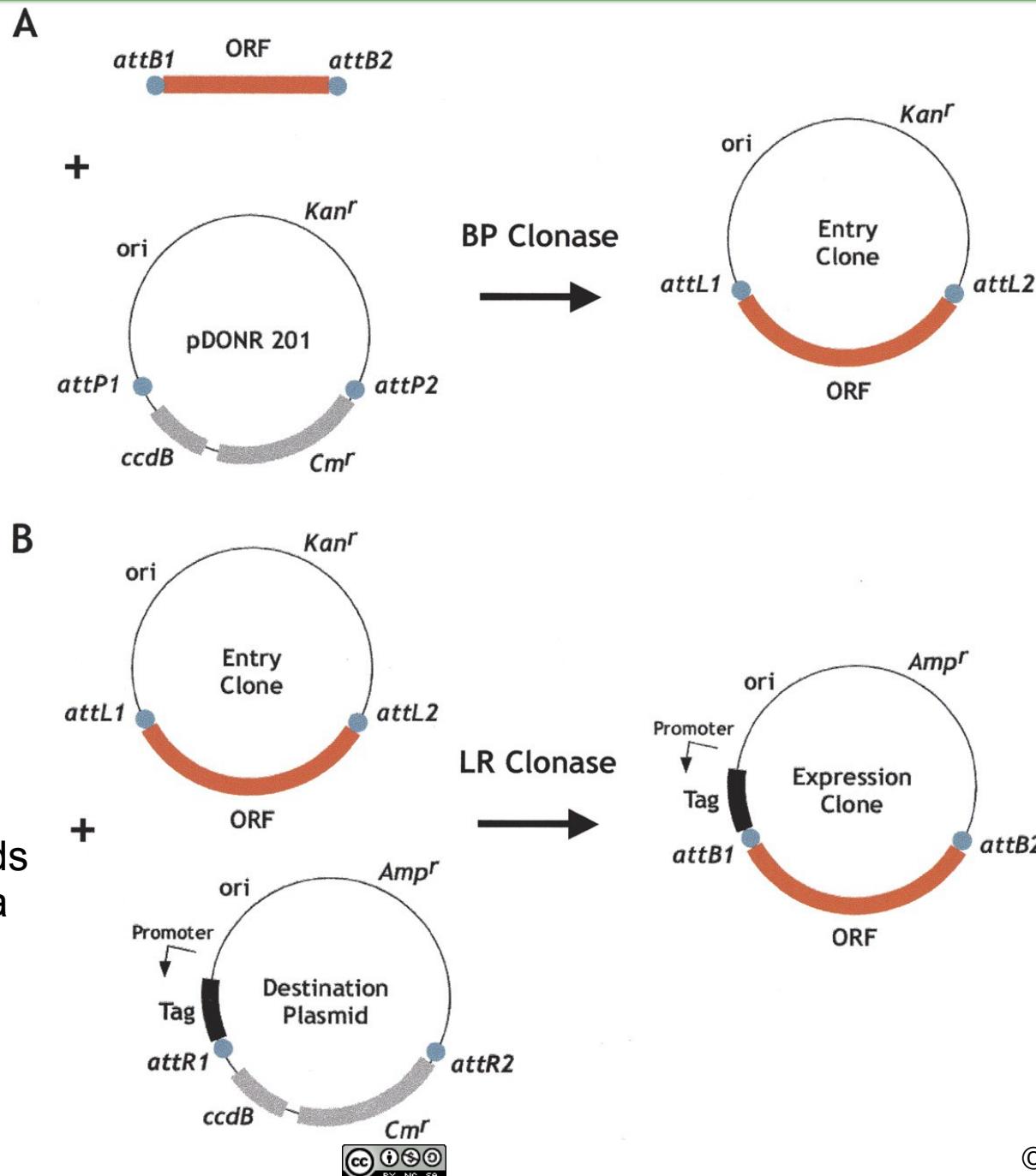


Figure from:
[Marsischky G & LaBaer J Genome Res. 2004; 14: 2020-2028](#)

In-Fusion/Creator Cloning System

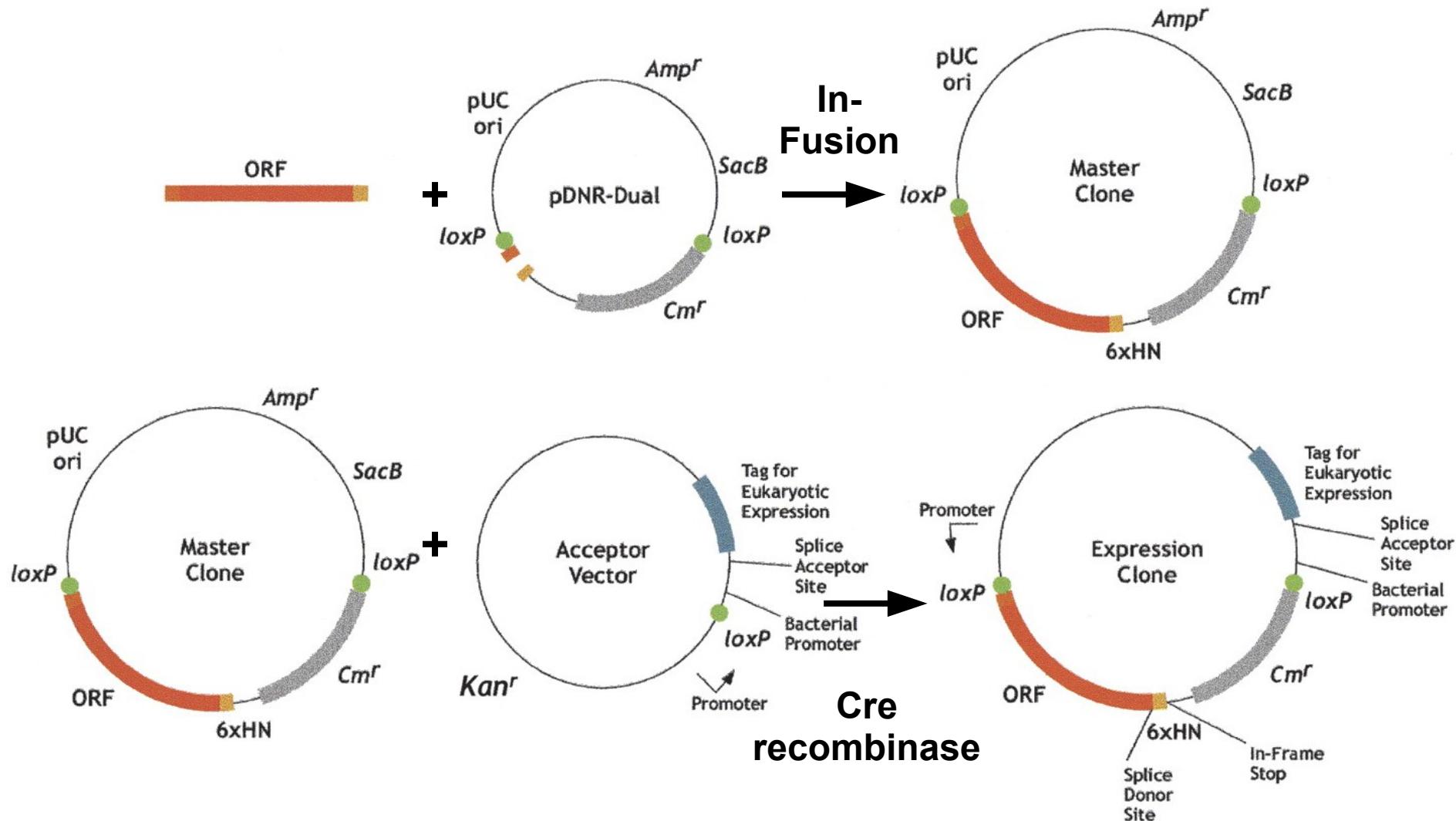


Figure from: Marsischky G & LaBaer J Genome Res. 2004; 14: 2020-2028



Univector site-specific recombination cloning system

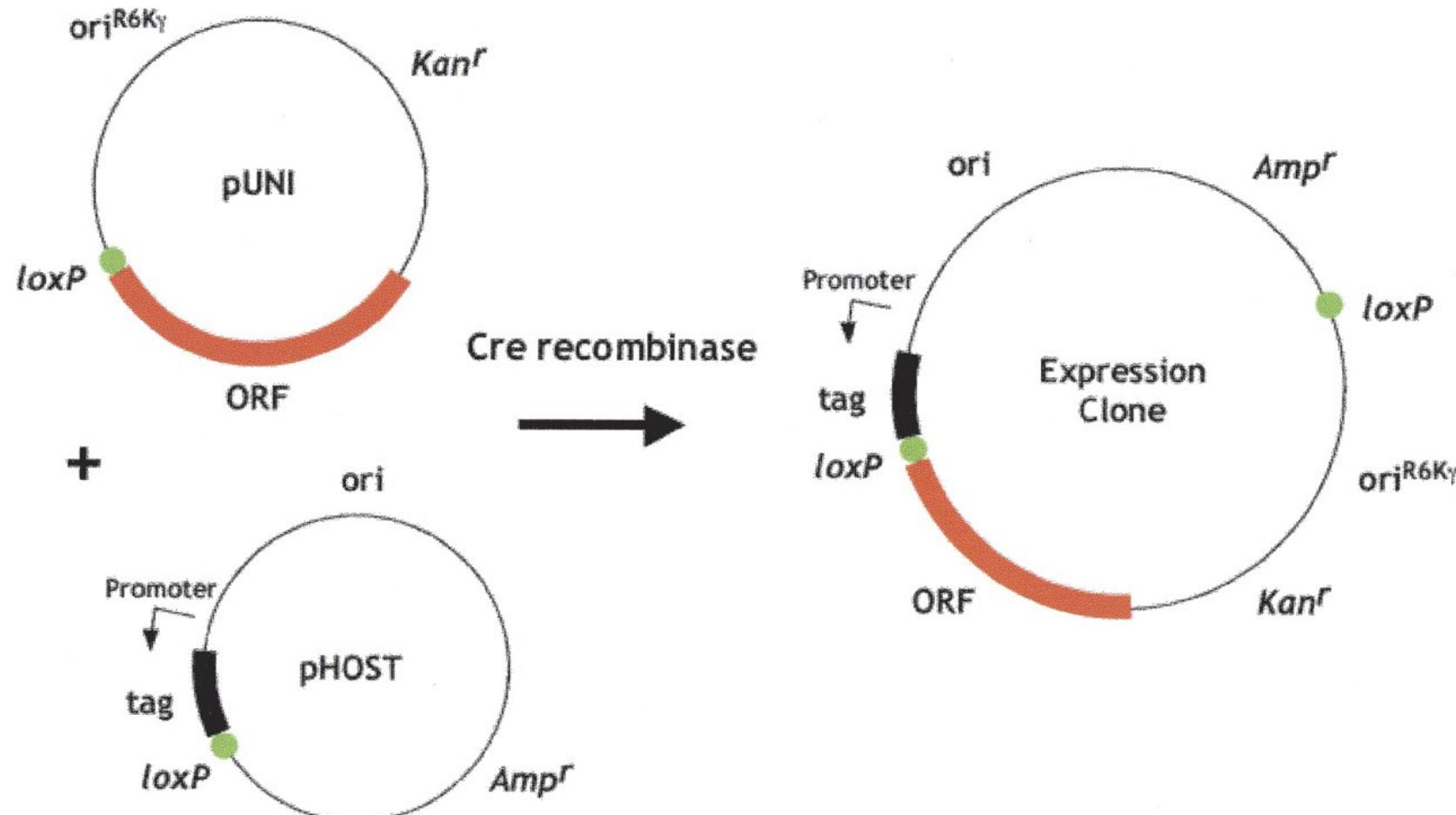
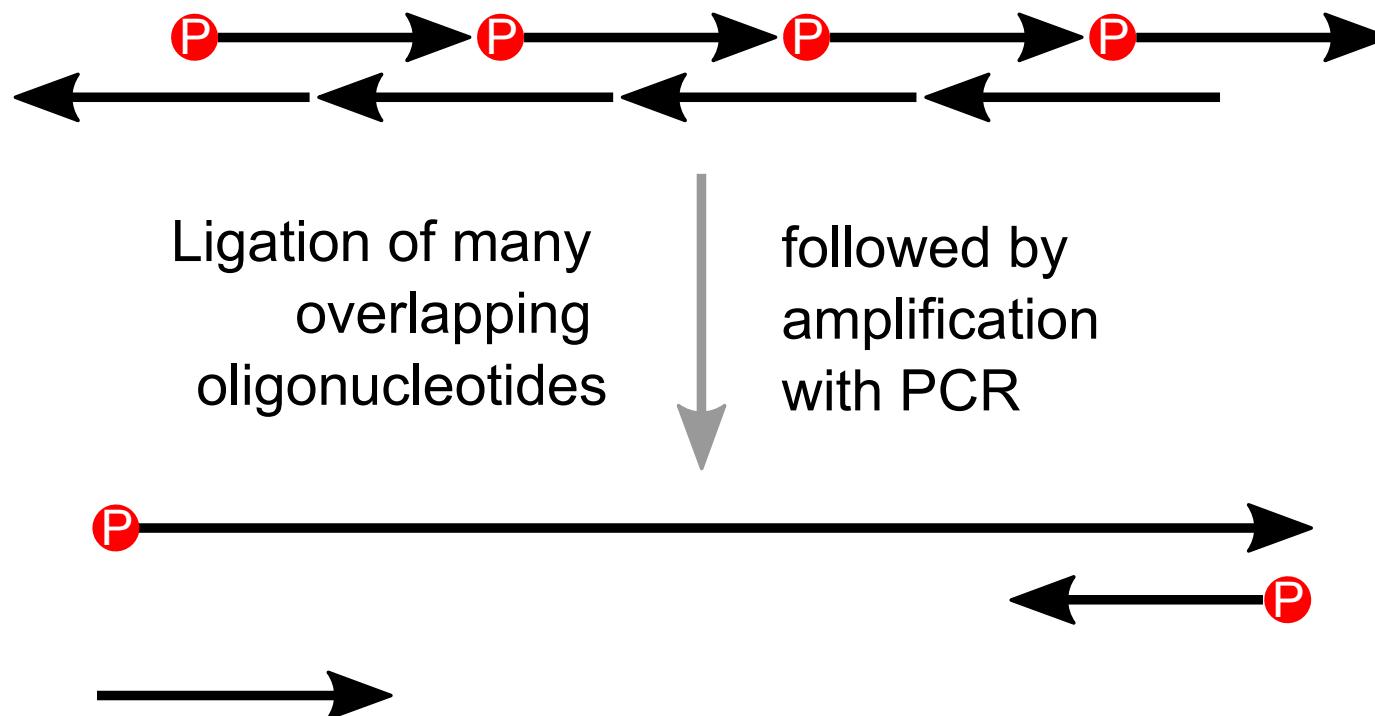


Figure from:
Marsischky G & LaBaer J Genome Res. 2004; 14: 2020-2028



Artificial/De-novo gene synthesis

- No template needed
- Chemical synthesis, max. length 200 bp
- Further assembly by different methods, e.g.



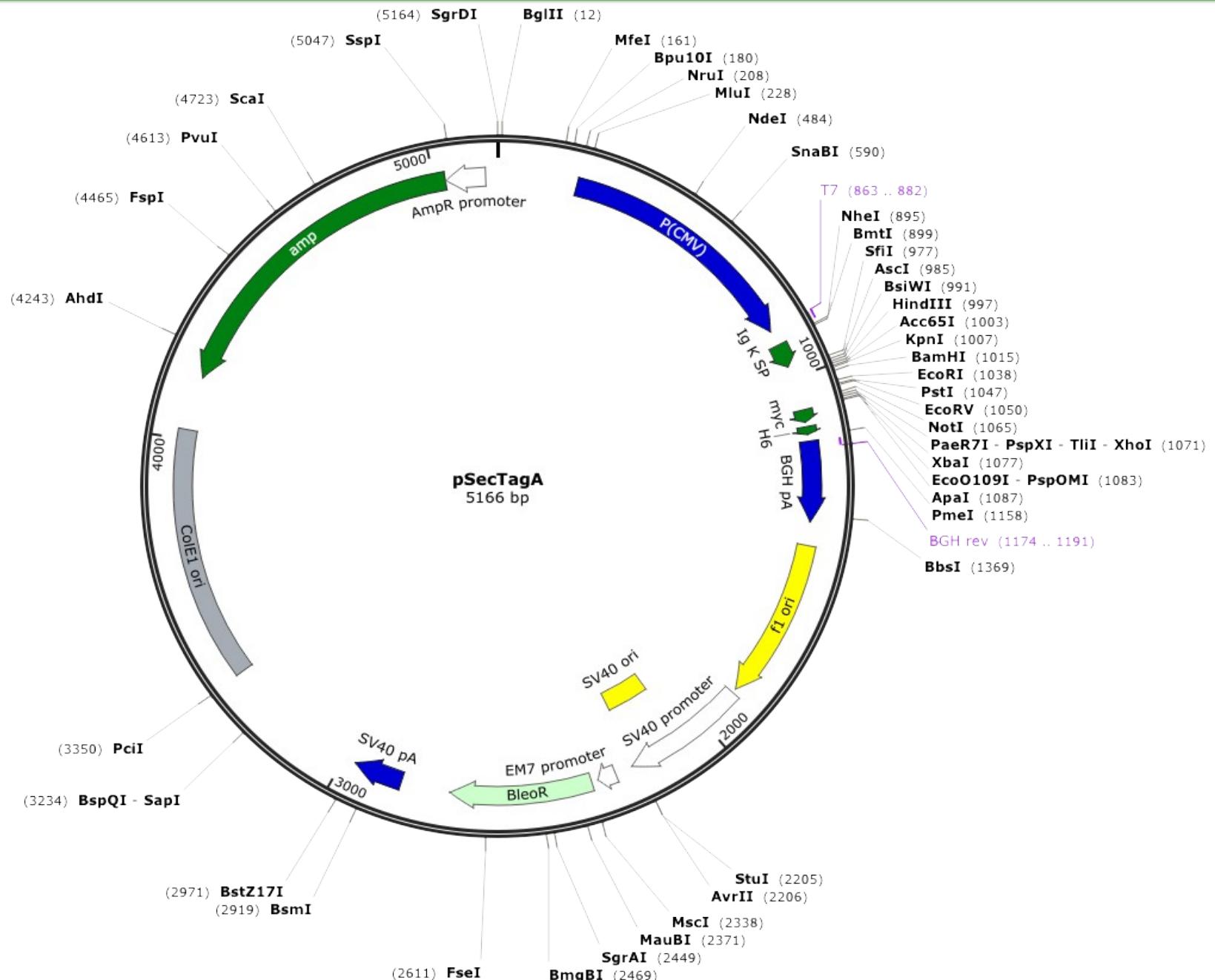
- Sequence verification!
- atm ~0.22€/bp (LifeTechnologies/GeneArt)



RT-PCR/PCR

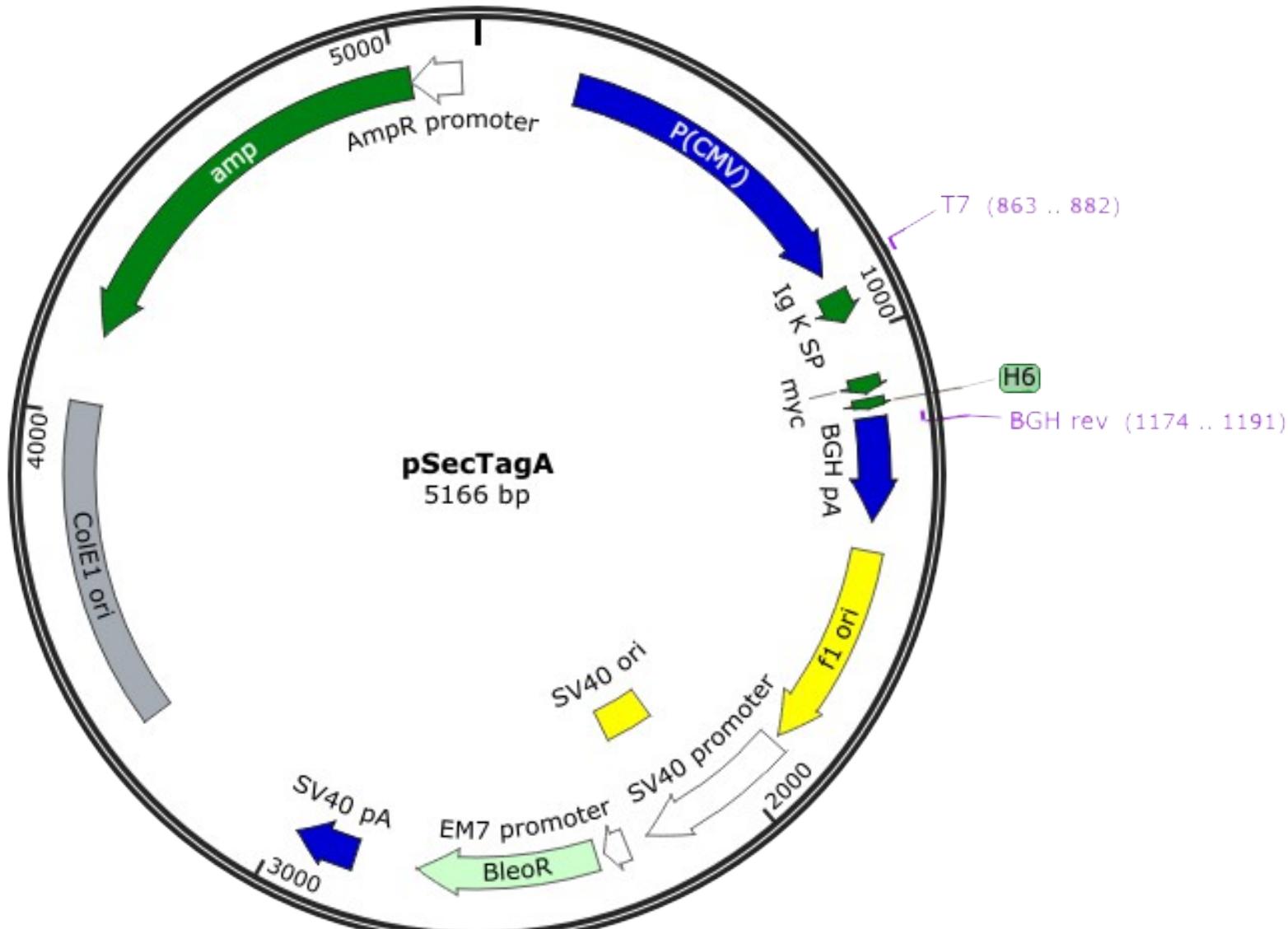
- PCR: see lecture 1, slides 18 & 19
- RT-PCR: full-length cDNA as a goal; really needed? About 900 intronless genes in the human genome (notably histones and G-protein coupled receptors)
- Non-CDS introns in 3'- and 5'-UTR
- Genes with few exons (e.g. Prox-1: 5 exons (4 CDS, 575 of 737 aa encoded by exon 2)
- Average: 8-9 exons per gene
- Mega-Genes: Titin 35991 aa (363 exons)
- Guide to the human genome:
http://www.cshlp.org/ghg5_all/section/gene.shtml

The Anatomy of an Expression Vector



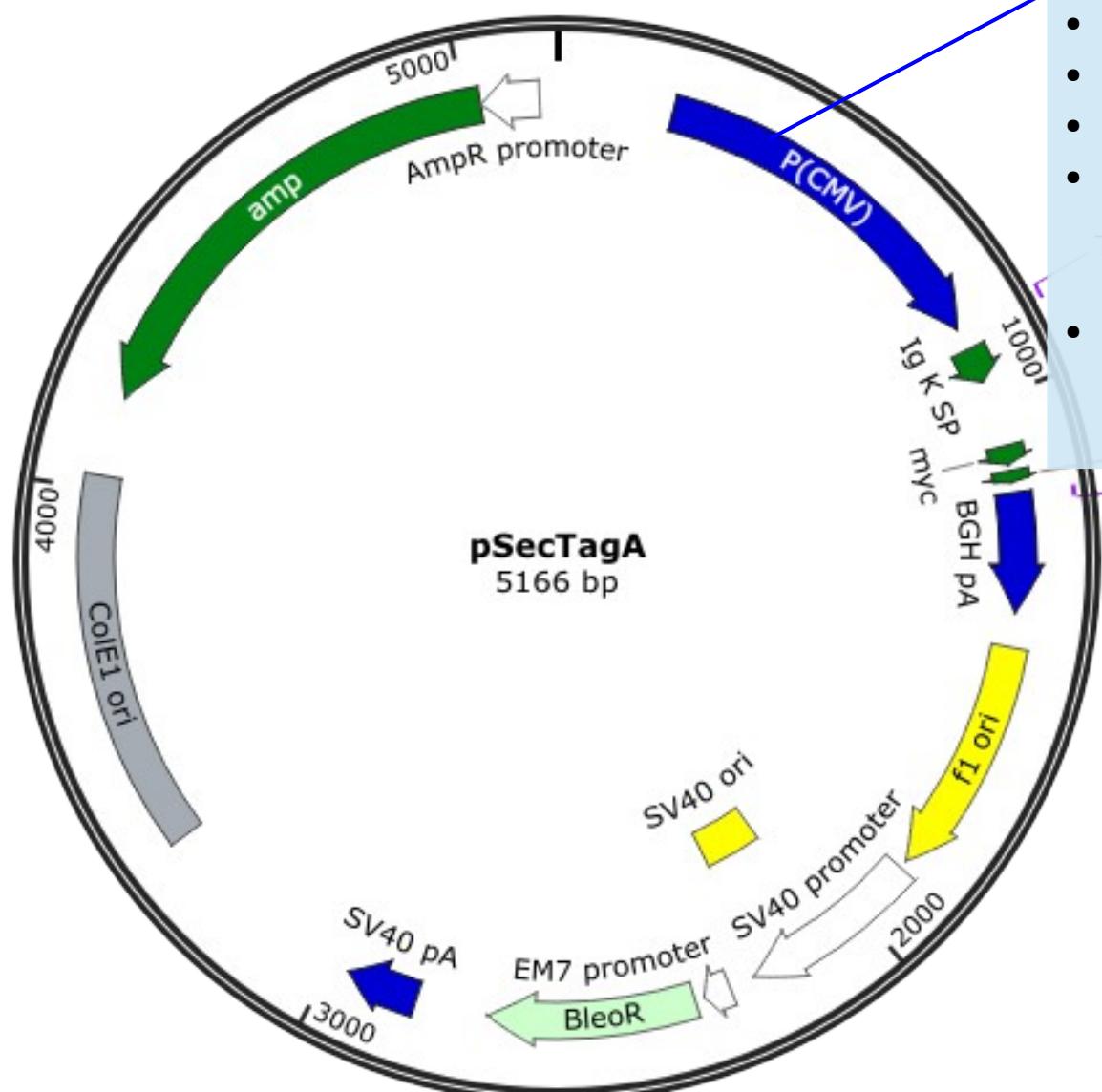


The Anatomy of an Expression Vector





The Anatomy of an Expression Vector

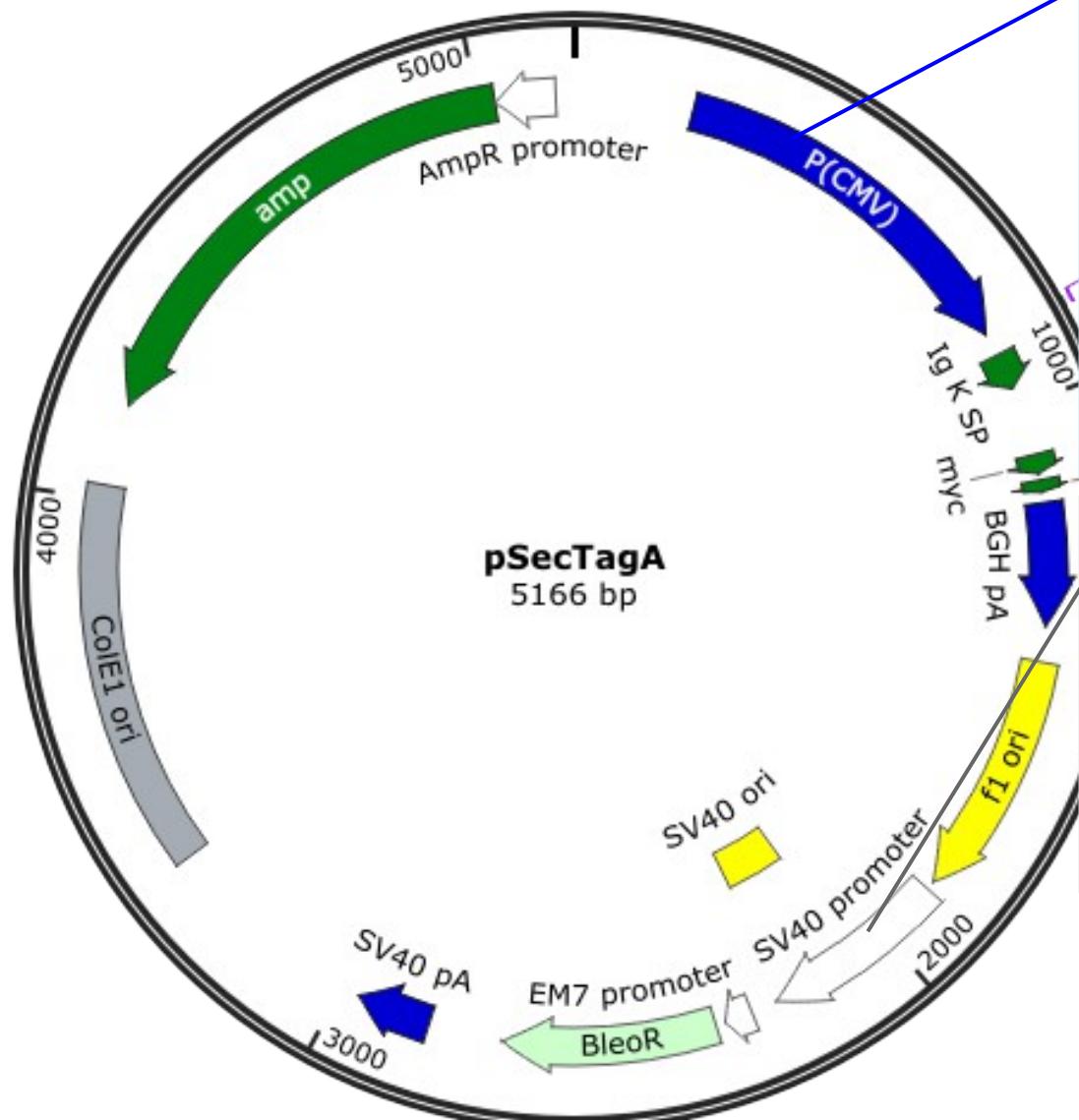


Promoter & polyA for the GOI

- general (mostly viral) promoters
- cell line specific promoters
- Choice important for expression levels
- Sometimes you want low expression levels (better alternative: titrating the amount of DNA used for transfection)
- Constitutive vs. inducible by heat, steroid hormones, heavy metals, hypoxia, interferons, etc.



The Anatomy of an Expression Vector



Promoter & polyA for the GOI

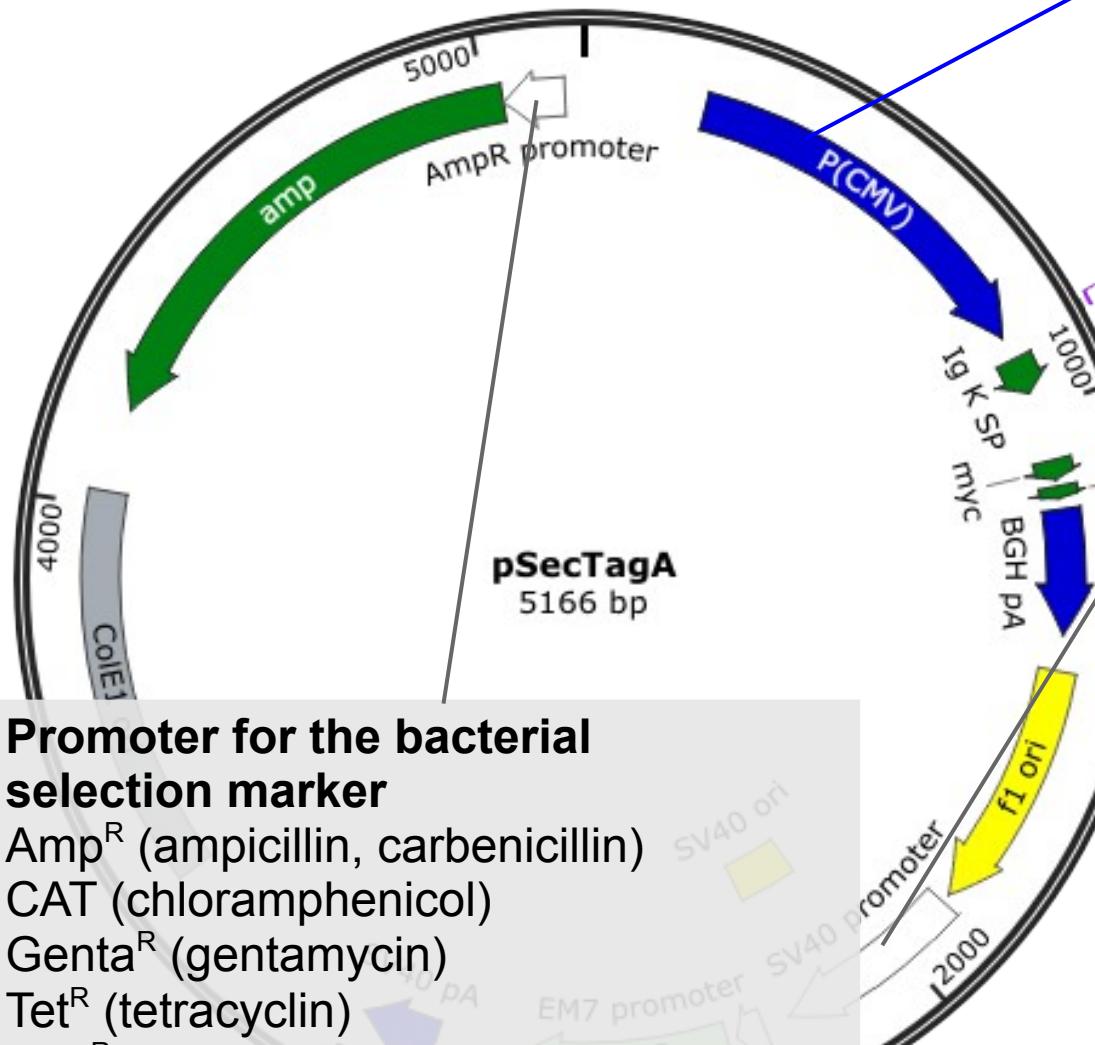
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Promoter & polyA for the mammalian selection marker

- Neo^R (G418)
- Bleo^R (zeocin)
- Puro^R (puromycin)
- Hygro^R (hygromycin)
- Bla^R (blasticidin)



The Anatomy of an Expression Vector



Promoter for the bacterial selection marker

- Amp^R (ampicillin, carbenicillin)
- CAT (chloramphenicol)
- Genta^R (gentamycin)
- Tet^R (tetracycline)
- Kan^R (kanamycin, neomycin, G418)
- Bleo^R (zeocin)
- Bla^R (blasticidin)

Promoter & polyA for the GOI

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- cell line specific promoters
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Promoter & polyA for the mammalian selection marker

- Neo^R (G418)
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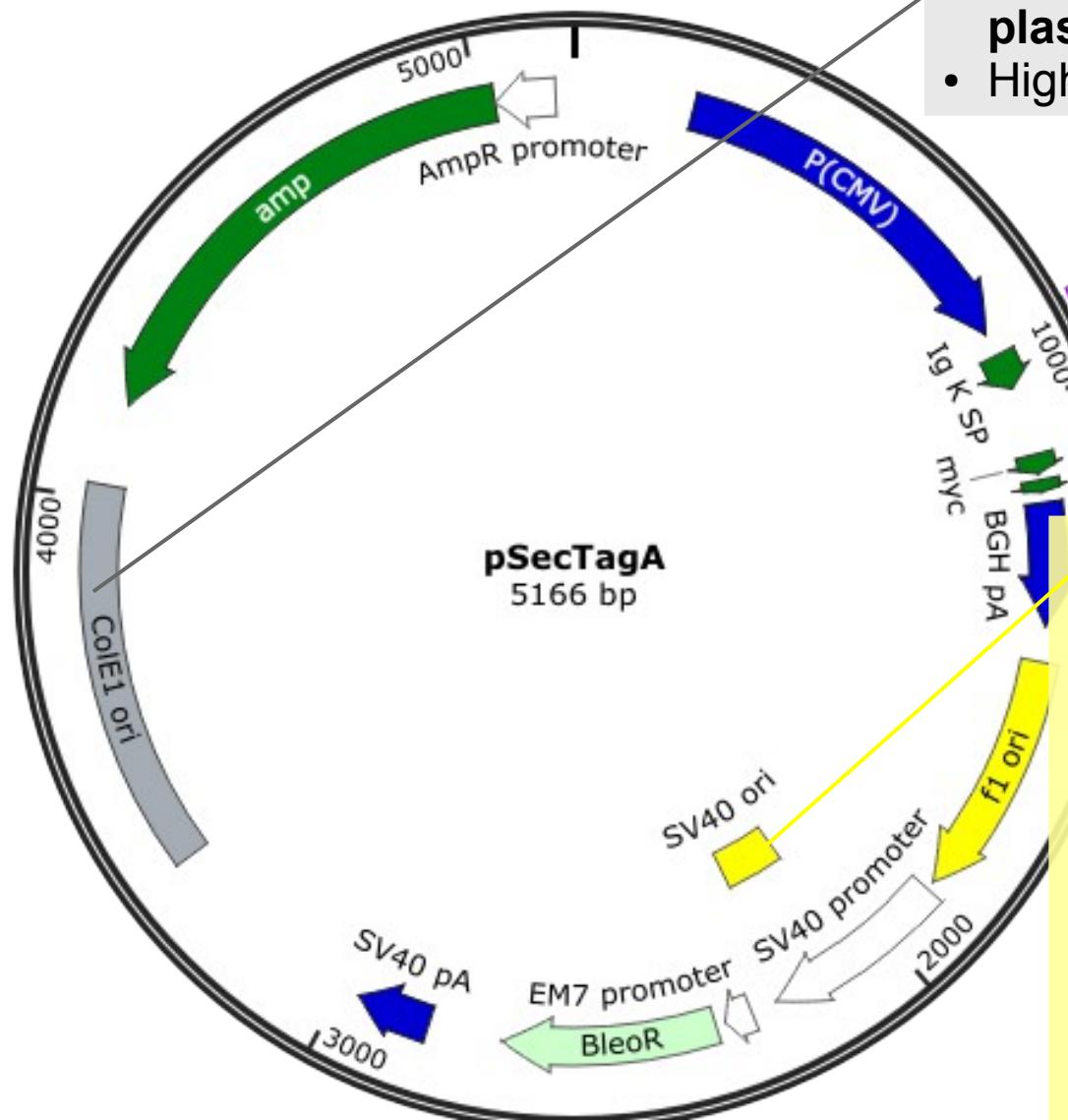


Aminoglycoside antibiotics

antibiotic	Primary target	typical effective concentration for bacteria	typical effective concentration for mammalian cells	~Price (€/25g)	used as a human drug
G418 (geneticin)	Prokaryotic & eukaryotic ribosome	5 µg/ml	100-1500 µg/ml	2330	no
neomycin	Prokaryotic ribosome	150 µg/ml	-	45	yes
kanamycin	Prokaryotic ribosome	25 µg/ml	-	412	yes
paromomycin	Prokaryotic & eukaryotic ribosome	?	?	?	yes

- KanR and NeoR are the same thing!
- There are several different KanR/NeoR resistance genes (from different origins), but they all code for aminoglycoside phosphotransferases and all inactivate G418/neomycin/kanamycin/paromomycin
- The difference is the promoter (mammalian promoter → neo^R, bacterial promoter → kana^R)
- One kana/neo or zeo resistance gene can be used with dual (bacterial/mammalian) promoters to confer resistance in both E.coli and mammalian cells (smaller plasmid size for “shuttle vectors”)
- No G418 in 293T cells (293T cells have been stably transfected with a large T antigen-expressing vector, which carries neoR)

The Anatomy of an Expression Vector



Bacterial origin of replication allows plasmid replication in E.coli

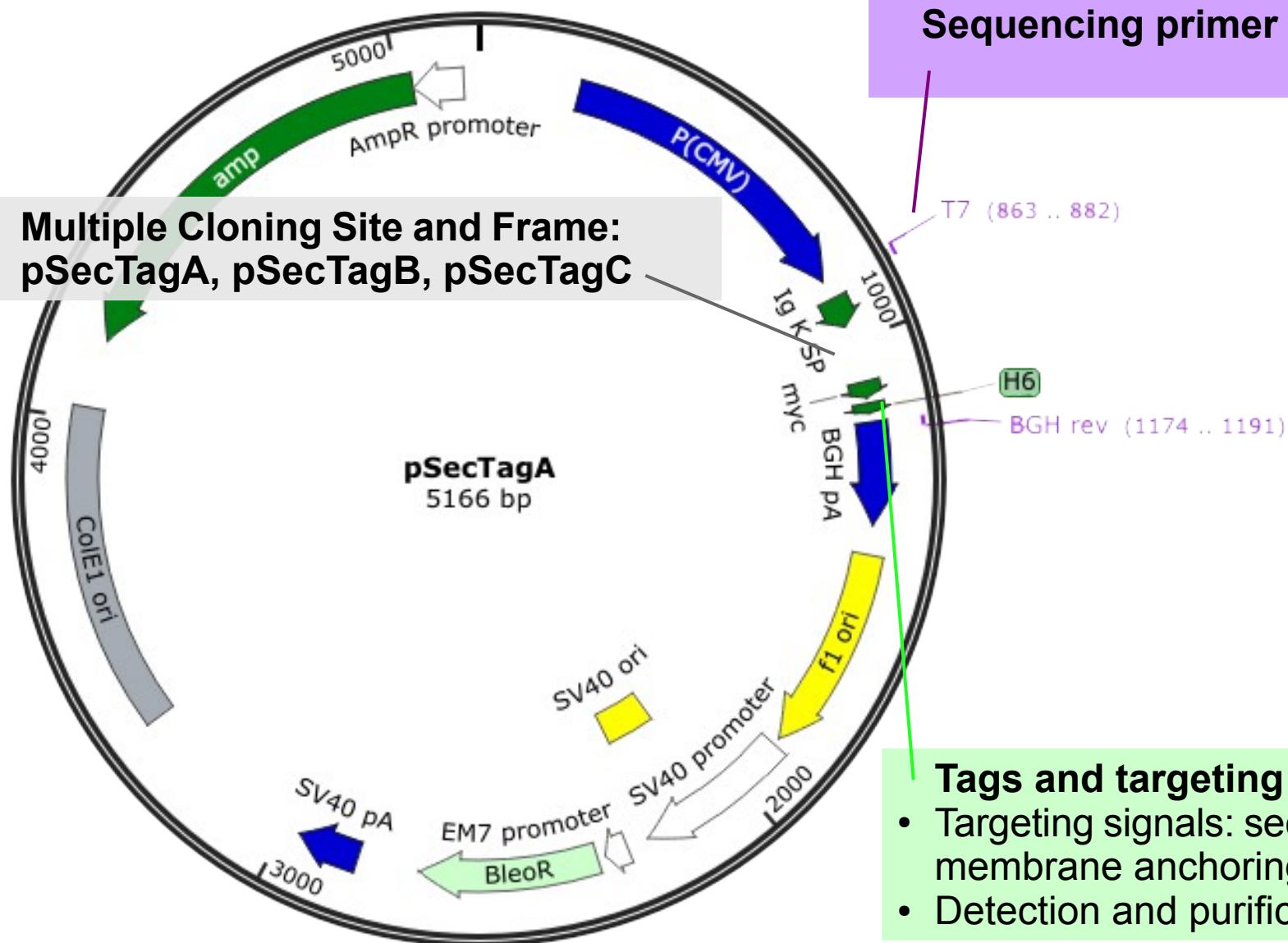
- High copy or low copy

Viral origin of replication enables plasmid to replicate in mammalian cells resulting in very high expression levels

- SV40 ori (works with cells that express the SV40 large T antigen: Cos-7, 293T)
- OriP (works with human cells that express EBNA-1: 293EBNA)
- No stable cell lines possible for these episomally maintained plasmids (primary cells can contain viruses!)

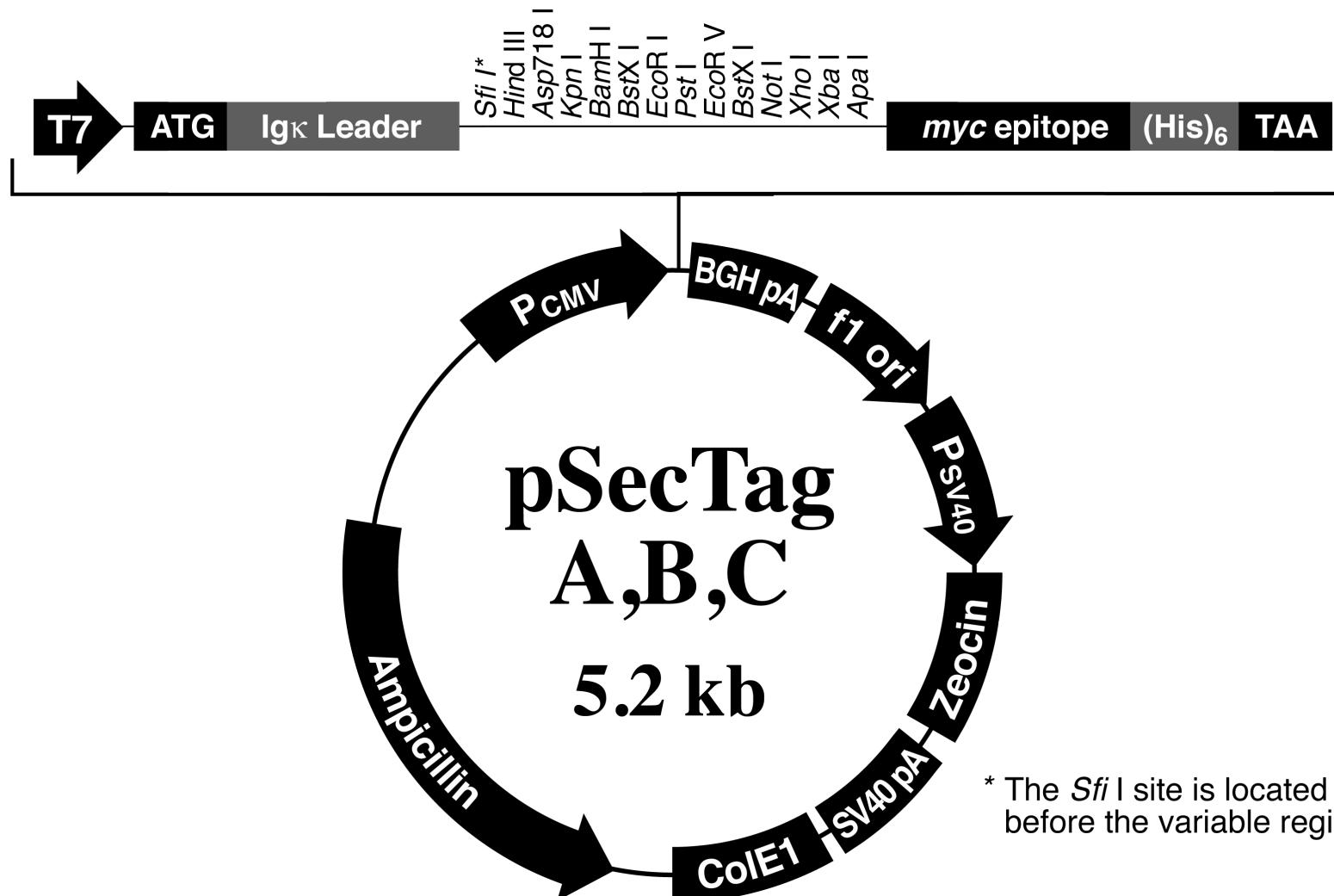


The Anatomy of an Expression Vector





Multiple Cloning Site & Frame





Multiple Cloning Site & Frame

The figure shows a sequence of DNA or RNA with various annotations:

- CAAT** and **TATA** boxes are indicated above the sequence.
- A blue arrow labeled **3' end of hCMV** points downwards from the sequence.
- A bracket labeled **putative transcriptional start** spans the sequence.
- A bracket labeled **T7 promoter primer binding site** covers the region from position 839 to approximately 900.
- A bracket labeled **Ig κ-chain leader sequence** covers the region from position 908 to approximately 1050.
- Restriction enzyme sites** are marked: *Sfi* I, *Hind* III, *Asp*718 I, *Kpn* I, *Bam* H I, *Bst* XI, *Eco* RI, *Pst* I, *Eco* R V, *Bst* XI, *Not* I, *Xho* I, *Xba* I, and *Apa* I.
- myc epitope** is located between positions 1030 and 1098.
- Polyhistidine tag** is located between positions 1098 and 1155.
- pcDNA3.1/BGH reverse priming site** is located between positions 1098 and 1155.
- Start codon** (**ATG**) and **Met** are indicated at position 839.
- Stop codon** (*******) is indicated at position 1155.

Different number of nucleotides in the yellow area for A/B/C version of the vector to enable in-frame cloning for each possible reading frame



Literature

- **Many Paths to Many Clones: A Comparative Look at High-Throughput Cloning Methods**
Gerald Marsischky and Joshua LaBaer *Genome Res.* 2004 14: 2020-2028
<http://genome.cshlp.org/content/14/10b/2020.long>
- **Mammalian Expression Vectors**
LifeTechnologies
http://tools.lifetechnologies.com/content/sfs/productnotes/F_071215_MammalianExpressionVectors.pdf