Blunt-end cloning according to Katri

Preparation of vector

- Check completeness of digestion by agarose gelelectrophoresis

Blunting with Klenow

- also 3'-overhangs can be blunted with Klenow
- final conc. (dNTPs) 50 mM
- same buffer as digestion
- Klenow 1U/pmol DNA-ends
- 15 min RT
- Inactivation 10 min 75°C

Dephosphorylation with CIP

- 1U/pmol DNA-ends
- 1h 37°C (5'-overhangs) or 50°C (3'-overhangs and blunt-ends)
- Inactivation: EDTA to final conc. 5 mM & 10 min 75°C
- Phenol/Chloroform/Isoamylalcohol-extraction 2x
- Chloroform-extraction 2x
- Adjust volume with HPLC-grade H₂O to 2 ml
- Desalt with Centricon C-100 and concentrate to ~100 ng/μl

Preparation of insert

Blunting with Klenow like vector

Isolation from agarose with Qiaex

Ligation

200 ng vector approx. 2x equimolar amount of insert 1 μl 50% PEG-4000 1 μl ATP 5 mM 1 μl blunt-end-ligation buffer H₂O to a final volume of 9 μl 1 μl undiluted T4 DNA ligase

Transformation

- Ligation mix (between 1 and 5 μl)
- Ligation mix without insert (background control)
- no DNA (contamination control)
- 1-10 ng of supercoiled plasmid (transformation control)

Partial digests are easy!

- Select an enzyme combination that allows isolation of your desired fragment.
- Only do partial digests of linearized plasmids.
- Calculate the exact amount of enzyme needed to completely digest 20-100 µg of plasmid in 2h.
- Start digest and take aliquots at t = 0,1,2,4,8,15,30,60 and 120 min
- Stop reaction adding proteinase K and incubating at 50°C for 10 min
- Heat inactivation works for some enzymes, especially if you want to blunt your fragment thereafter, be aware of the time lag!

How do I calculate the exact amount of enzyme needed for complete digestion?

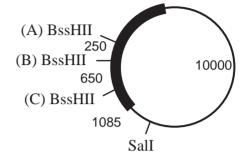
1 unit of a restriction enzyme cuts 1 µg of assay DNA in 1 hour

How many µl of BssHII did I add to 80 µg of the plasmid shown above?

conc. (BssHII) = 20,000 units/ml

assayed on λ (~48 kb) BssHII cuts λ 6 times

enz. survival: 0.5 units required for digestion of 1 µg assay DNA in 16 h



BssHII cuts resulting fragment sizes

nowhere	11985
only at A	10000, 1985
only at B	10250, 1735
only at C	10900, 1085
at A+B	10000, 1735, 250
at A+C	10000, 1085, 900
at B+C	10250, 1085, 650
all sites	10000, 1085, 650, 250

