

Genomics

Genetic maps in humans

The trouble with humans...

- ◆ Markers
- ◆ Crosses

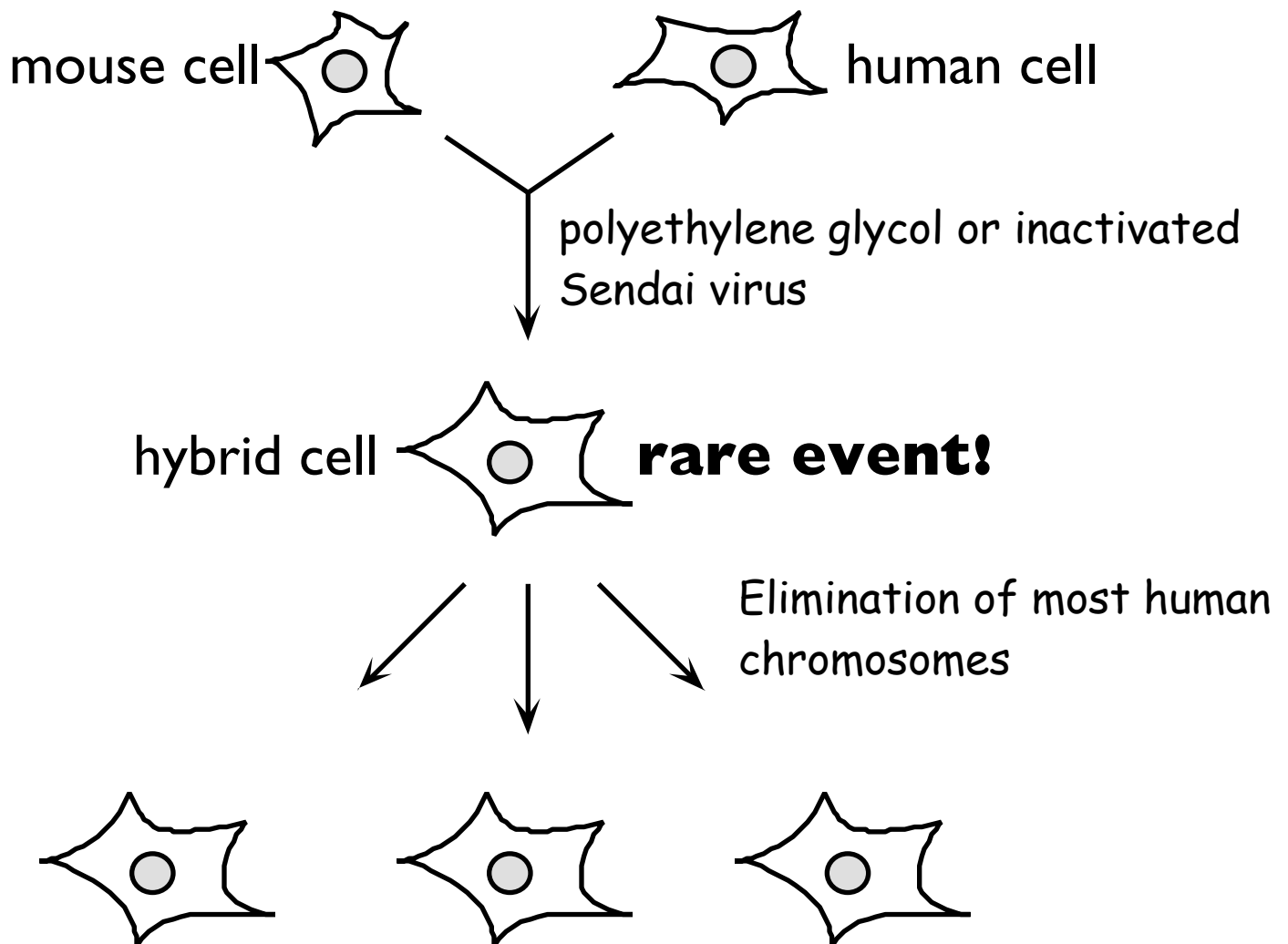
Establishing linkage: which chromosome?

Recognizing chromosomes

- ◇ Size
- ◇ Staining pattern – bands



Somatic cell hybrids

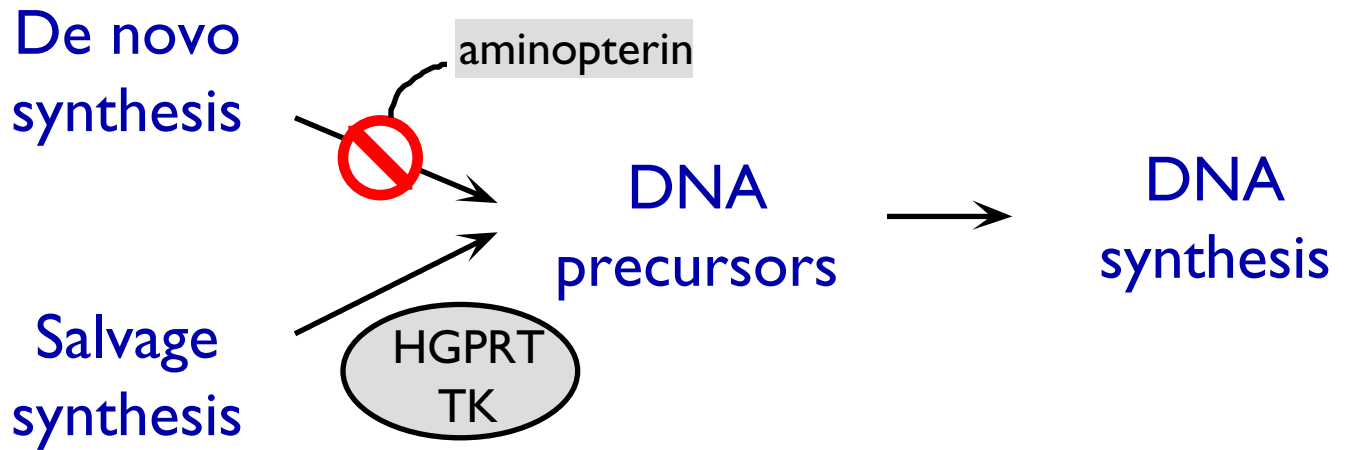


Hybrid cell lines: mostly mouse plus a few human chromosomes

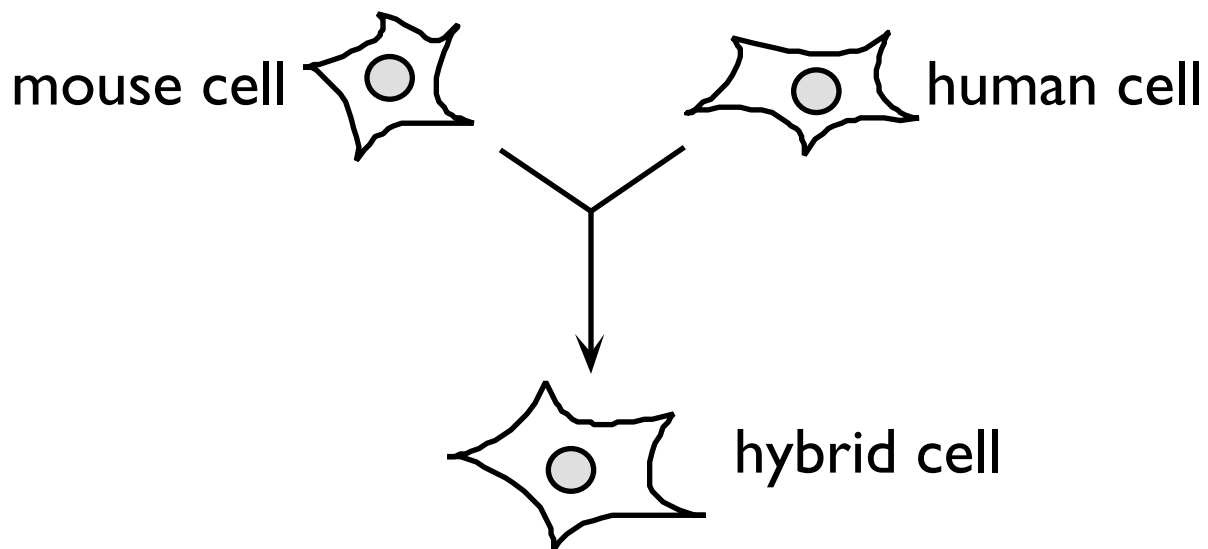
How to pick out those rare fusion events?

...**selection** based on DNA precursor synthesis

Two pathways of DNA precursor synthesis:

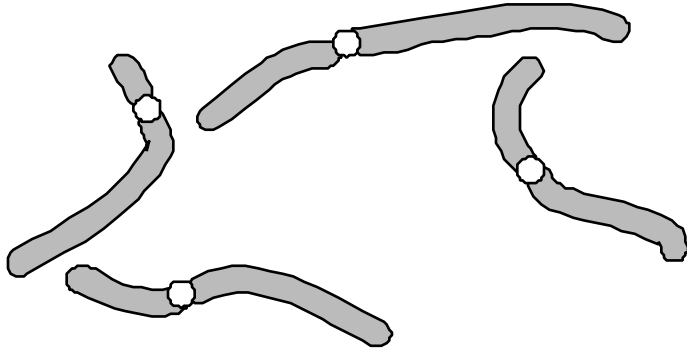


To select fusion product...



Fluorescent in situ hybridization (FISH)

Hybridize fluorescent-labeled probe to chromosome spread



...can be used in combination with somatic cell hybrids

Mapping by linkage

...linkage with respect to what?

The conventional approach – look at recombination frequency between the gene of interest and a neighboring marker gene

Conventional markers (alleles that result in overt phenotypes) are hard to come by...

But DNA sequence differences (polymorphisms) are plentiful

Therefore: construct a map of polymorphic sites

To map a gene: look at recombination frequency between the gene of interest and a neighboring polymorphic site

...so, we use DNA sequence polymorphism as just another pair of alleles – without an overt phenotype, but detectable

Useful polymorphisms

Originally – Restriction fragment length polymorphisms (RFLP)

These days – **Sequence repeat** polymorphisms

Repeated sequences constitute up to 35% of the human genome

- ◆ **Minisatellite repeats:** ~ 30 bp
- ◆ **Microsatellite repeats:** ~2–5 bp
 - ◇ Dispersed throughout the genome
 - ◇ Highly variable numbers of repeats at each location; individuals often heterozygous