

long DNA molecule:  
ligated random fragments

nanopore  
sequencing

fragment  
junction

N	T	T	A	A	N
N	A	A	T	T	N

long read (~8 kb)

unrelated random  
restriction fragments  
(~150 nt)

fragments re-ligated  
at restriction cut sites

mapping identifies  
distinct fragments

SMURF-seq efficiency = read length / fragment length  
 $\approx$  mapped fragments / read

chr4

chr8

chr17

