

Tail loss: investigating the Molgula

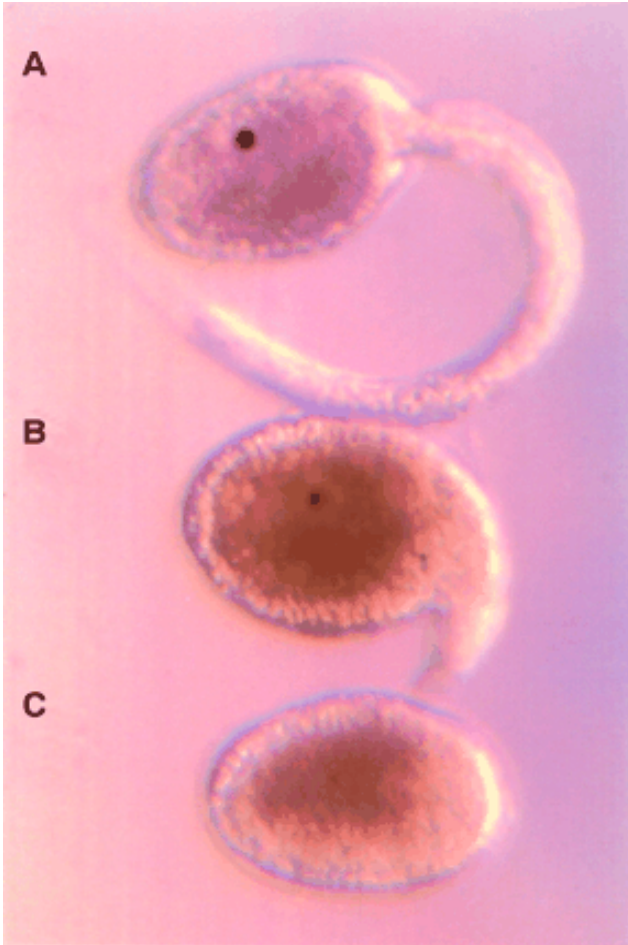
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Acknowledgements

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Two Species of Closely Related Ascidians and a Hybrid Larva

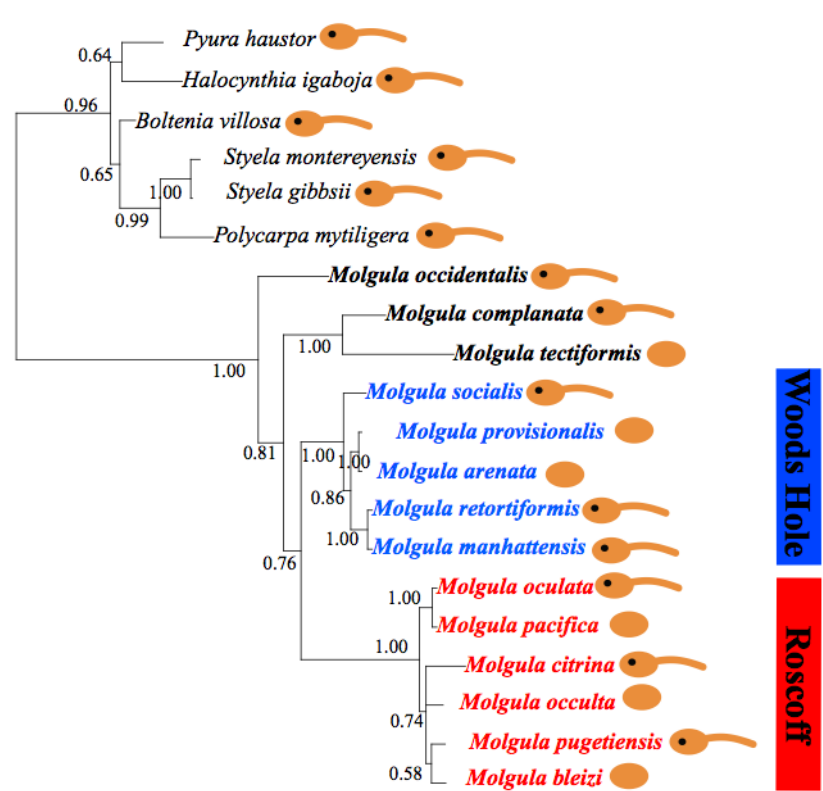


Molgula oculata has a head, tail, and otolith - chordate embryo.

M. occulta egg X *M. oculata* sperm has a head, short tail, and otolith.

Molgula occulta lacks chordate features - head, tail, and otolith.

Molgulids have many anural embryos - why??
(Ascidians generally: ~1% of 3,000 are tailless)

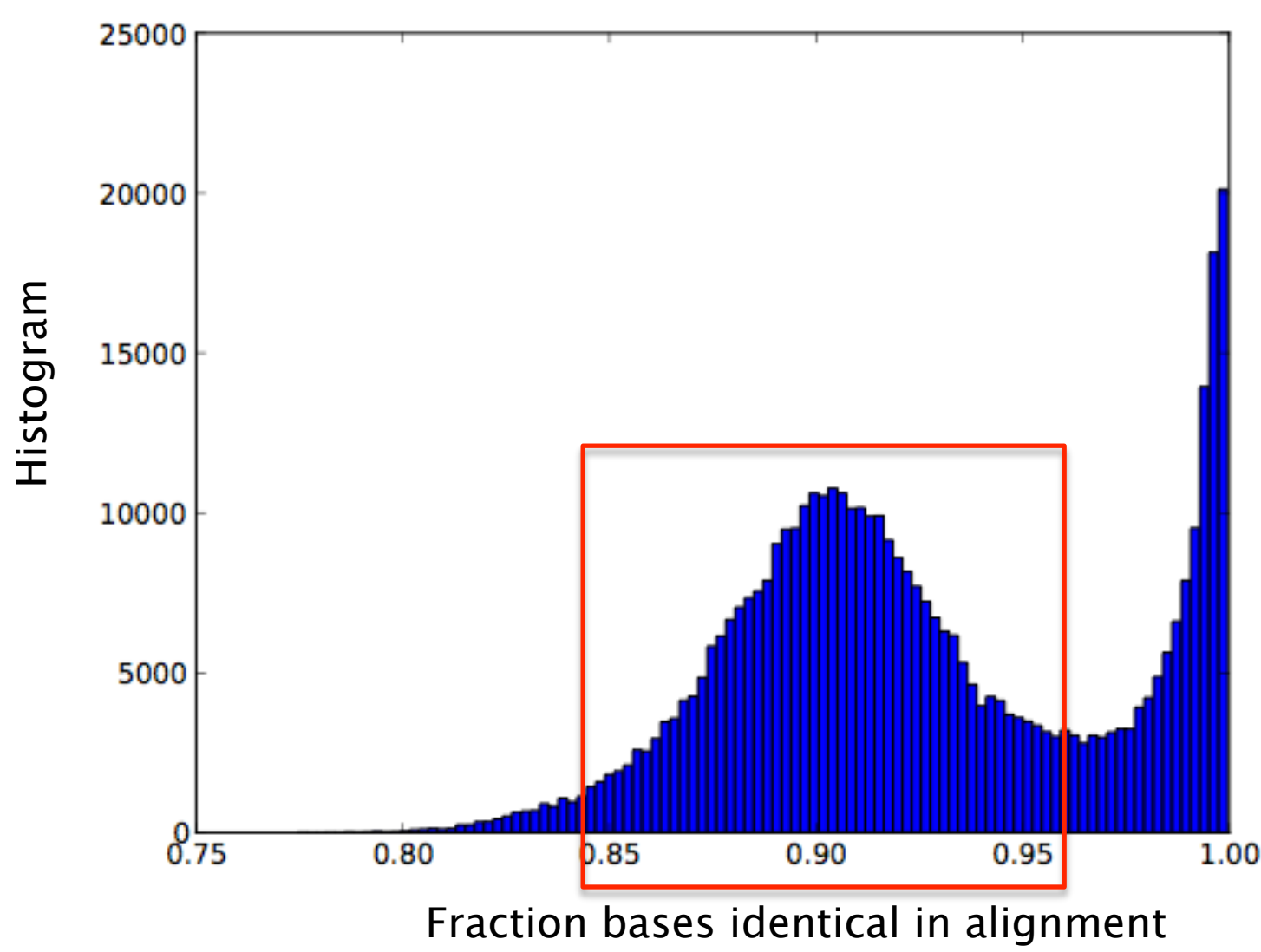


Is the transcriptome assembly any good?

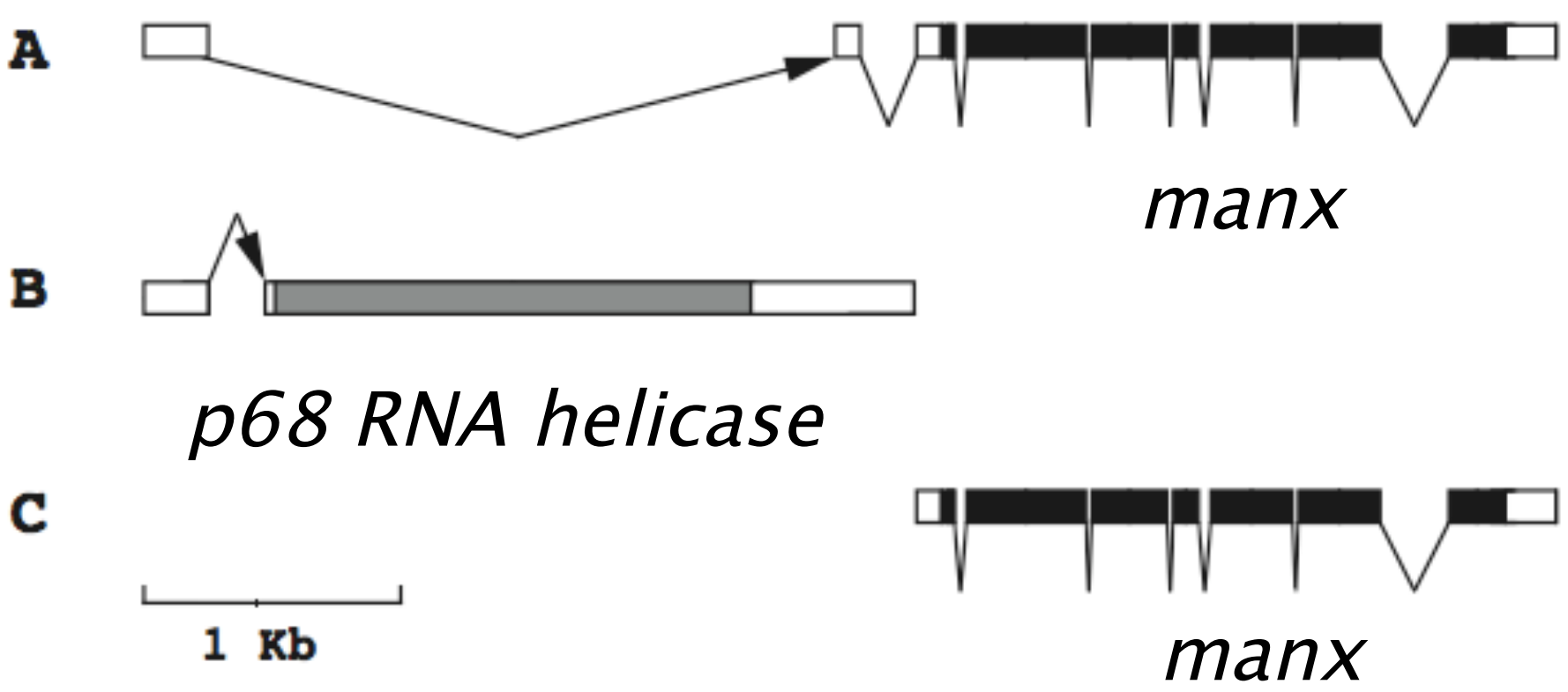
- ▶ No reference genome! ...
- ▶ 96/98 Sanger-sequenced Molgulid genes found in assembly of individual lanes.
- ▶ Can we distinguish & count parent transcripts in the hybrid?

Query: 1 MDSSNRSHPNHLQYHTDYNYPFRVMLAAVKEGLYHPRLPSLRMDMDTATHKLPDEH 60
MDSSNRSHPNHLQYHTDYNYPFR+VMLAAVKEGLYHPRLPSLRMDMDTATHKLPDEH
Sbjct: 60 MDSSNRSHPNHLQYHTDYNYPFRKVMLAAVKEGLYHPRLPSLRMDMDTATHKLPDEH 229

A large subset of transcripts have variation ~10% (at DNA level)



manx and p68/bobcat - probable isoform variation



Swalla et al. (1999) *Development* 126:1643-1653

Preliminary round of sequencing

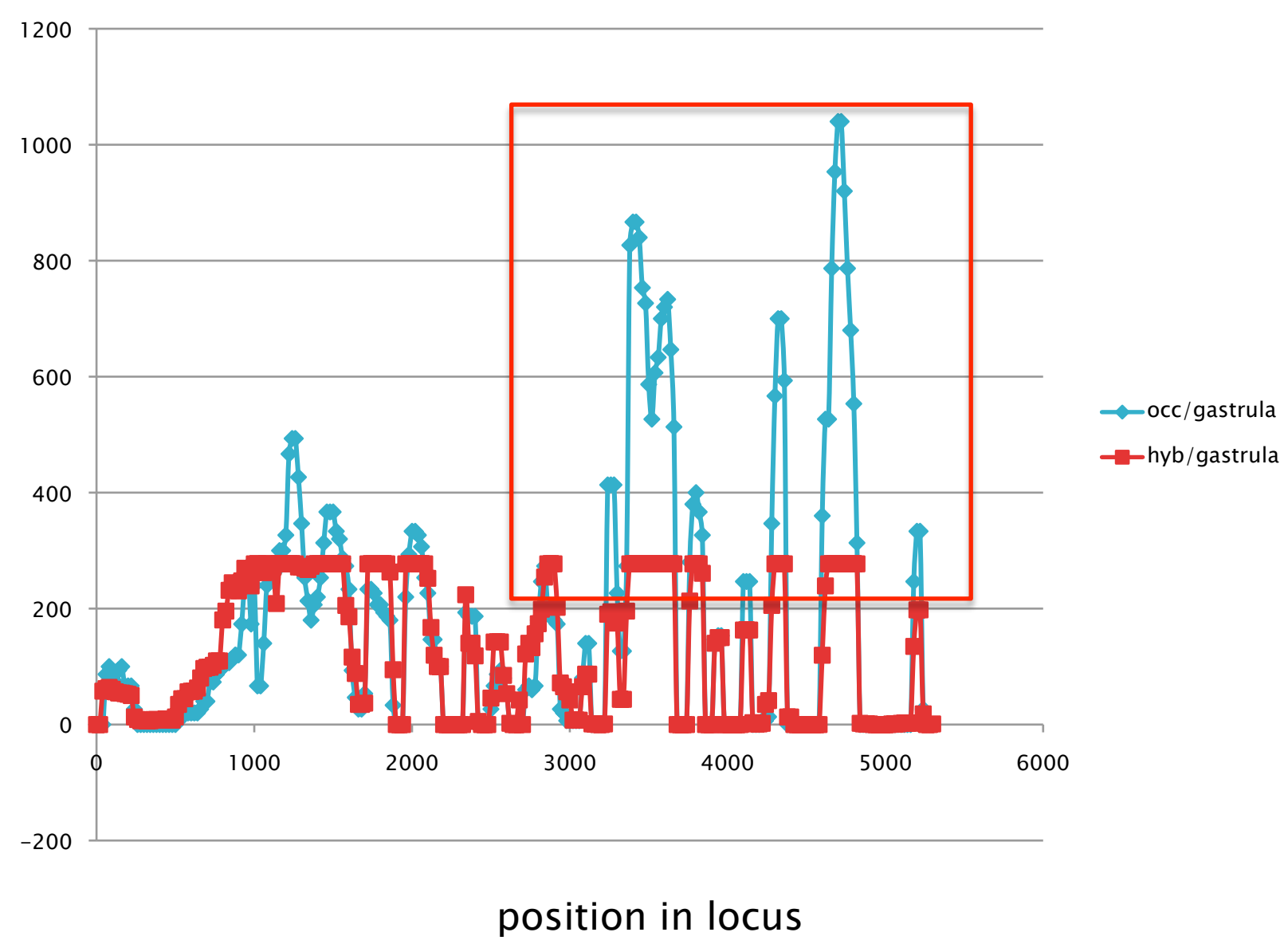
M. occulta and *M. oculata* genes assemble together as splice variants

Sample Name	Total reads after trim+filter	Loci (total genes, > 500)	Total incl splice variants (> 500)
M. oculata (gastrula)	35,252,607	13,172	16,269
Hybrid (gastrula)	38,690,601	14,148	24,209
M. occulta (gastrula)	22,548,831	8,046	10,802
M. oculata (neurula)	38,030,938	10,365	11,043
Hybrid (neurula)	38,699,913	14,400	29,189
M. oculata (tailbud)	38,073,640	14,204	17,835
Hybrid (tailbud)	34,307,907	15,399	26,594

Hybrids express *only* M. oculata (tailless) versions??

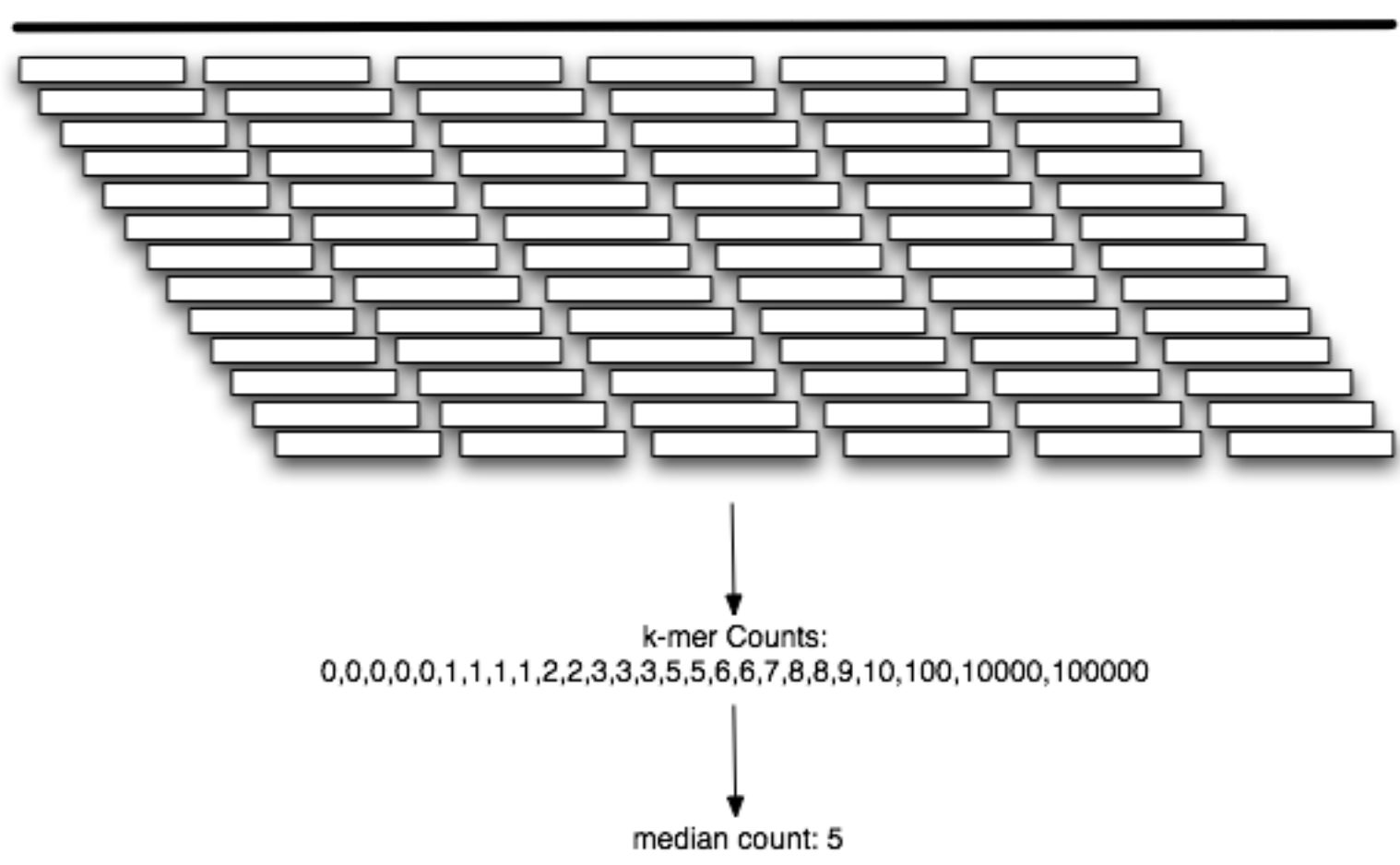
Sample Name	M. oculata manx	M. occulta manx	M. oculata bobcat	M. occulta bobcat
M. oculata (gastrula)	9	0	11	0
Hybrid (gastrula)	0	28	0	255
M. occulta (gastrula)	0	41	0	76
M. oculata (neurula)	5	0	4	1
Hybrid (neurula)	0	38	0	223
M. oculata (tailbud)	6	0	6	0
Hybrid (tailbud)	0	8	0	121

M. occulta (tailless) bobcat gene - differential expression by exon



Expression analysis - how?

Decompose sequence into k-mers (k ~ 32); count; take median



Allele specific expression

- ▶ Detect haplotype-specific changes in gene *expression* as indicator of functional cis-variation.

