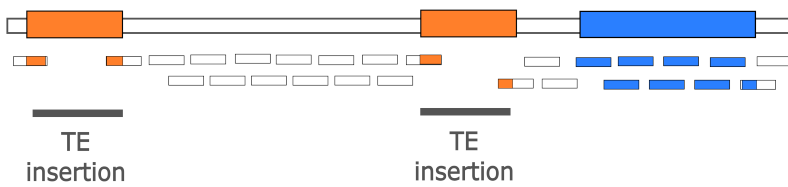


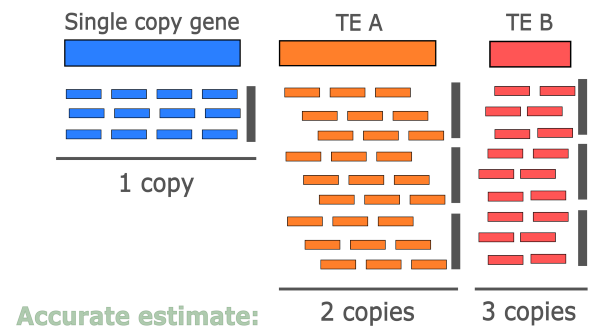
Standard approach: Reference genome



**Wrong estimate
due to reference genome bias:**

	TE A	TE B
TE count:	2 copies	0 copies

Our approach: Reference library



Accurate estimate:

	TE A	TE B
TE count:	2 copies	3 copies