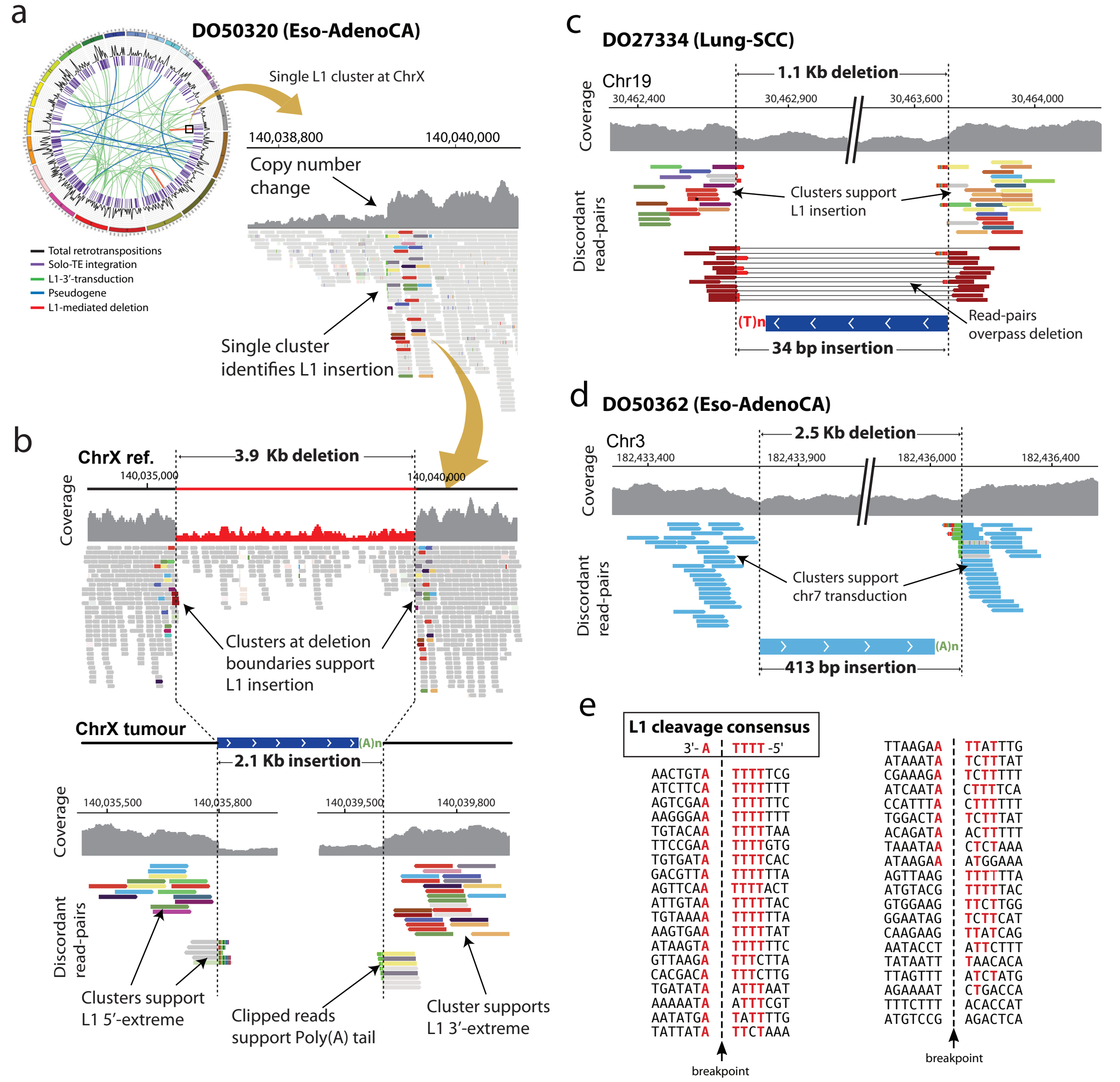
a
DO50320 (Eso-AdenoCA)
Single L1 cluster at ChrX
140,038,800
140,040,000
Copy number change
Total retrotranspositions
Solo-TE integration
L1-3'-transduction
Pseudogene
L1-mediated deletion
Single cluster identifies L1 insertion
b
ChrX ref.
3.9 Kb deletion
140,035,000
140,040,000
Coverage
Clusters at deletion boundaries support L1 insertion
ChrX tumour
(A)n
2.1 Kb insertion
140,035,500
140,035,800
140,039,500
140,039,800
Discordant read-pairs
Clusters support L1 5'-extreme
Clipped reads support Poly(A) tail
Cluster supports L1 3'-extreme
c
DO27334 (Lung-SCC)
Chr19
1.1 Kb deletion
30,462,400
30,462,900
30,463,600
30,464,000
Clusters support L1 insertion
(T)n
Read-pairs overpass deletion
34 bp insertion
d
DO50362 (Eso-AdenoCA)
Chr3
2.5 Kb deletion
182,433,400
182,433,900
182,436,000
182,436,400
Clusters support chr7 transduction
(A)n
413 bp insertion
e
L1 cleavage consensus
3'- A TTTT -5'
AACTGTA TTTTTCG
ATCTTCA TTTTTTT
AGTCGAA TTTTTTC
AAGGGAA TTTTTTT
TGTACAA TTTTTAA
TTCCGAA TTTTGTG
TGTGATA TTTTCAC
GACGTTA TTTTTTA
AGTTCAA TTTTACT
ATTGTAA TTTTTAC
TGTAAAA TTTTTTA
AAGTGAA TTTTTAT
ATAAGTA TTTTTTC
GTTAAGA TTTCTTA
CACGACA TTTCTTG
TGATATA ATTTAAT
AAAAATA ATTTCGT
AATATGA TATTTTG
TATTATA TTCTAAA
breakpoint
TTAAGAA TTATTTG
ATAAATA TCTTTAT
CGAAAGA TCTTTTT
ATCAATA CTTTTCA
CCATTTA CTTTTTT
TGGACTA TCTTTAT
ACAGATA ACTTTTT
TAAATAA CTCTAAA
ATAAGAA ATGGAAA
AGTTAAG TTTTTTA
ATGTACG TTTTTAC
GTGGAAG TTCTTGG
GGAATAG TCTTCAT
CAAGAAG TTATCAG
AATACCT ATTCTTT
TATAATT TAACACA
TTAGTTT ATCTATG
AGAAAAT CTGACCA
TTTCTTT ACACCAT
ATGTCCG AGACTCA
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