	10	20	30 5'TSD	40	50 Pol	60 A Box	70	80	90	100	110 Pol B I	120 Box
Consensus F.catus L.colocolo L.wiedii O.guigna L.pardalis L.jacobita L.tigrina O.geoffroyi	АААСТСТGGTTATAC	GTTT <mark>AAAATA</mark>	AAGATTTATTT	GGGGCGCC	TGGGTGGCGCA	AGTCGGTTA	AGCGTCCGAC	TTCAGCCAGG	TCACAATCT	CGCGGTCCGT	GAGTTCGAGC	CCCGCGTCGGGCTCTGGG
			•••••	•••••	•••••	••••		• • • • • • • • • • • •	•••••	• • • • • • • • • • • • •	•••••	
	140	150	160 >>>>>ст	170 Rich Reg	180	190 >>>>****	200	210 ****Polv A	220 T tail***	230	240 TSD	250
Consensus F.catus L.colocolo L.wiedii O.guigna L.pardalis L.jacobita	CTGATGGCTCAGAGC	CTGGAGCCTG	TTTCCGATTCT	GTGTCTCT	GTCTCTCTCTC	TCCCAAAAA	АТАААТАААС	TTTAAAAAAA	ААТАААТАА	ATAAC <mark>AAATA</mark>	AAGATTTATT	<mark>T</mark> TTAATCCAAGTTTTCAT
									••••••••			
L.tigrina O.geoffroyi				 		••••						

Figure S5. Alignment of Ocelot (Leopardus) lineage individuals at locus 133135 reveals, a Can-SINE insert in all 9 L. pardalis, 8 L.

tigrina, 8 O. geoffroyi and each O. guigna and L. jacobita individuals examined, yet absent from all 3 L. colocolo and 2 L. wiedii

individuals examined. Yellow-highlighted regions mark target site duplications and gray-shaded regions denote the A and B RNA

polymerase III recognition sequences.