Table S4| Shotgun sequencing versus hybridization capture enrichment for mtDNA flanking target region

Sample	Sequencing	Total reads	% reads matching bait flank	% reads not related to mtDNA flanking targeted region*	Flank fold coverage
Rattus exulans					
R4824	capture	739801	16,20%	83.8%	432
R4824	shotgun	10755900	1.3%	98,70%	1016

* Mapping of sequences was to the *R. exulans* mtDNA genome exluding the bait region (control region) to specifically examine enrichement of bait flanking sequences in the shotgun sequences compered to those obtained by hybridization capture