

**Table S10**

BLAST results of the repeat sequences found in the A+T-rich region of Flatidae species.

Species	Repeat A			Repeat B			Repeat C		
	Description	Identity (Query Cover)	GenBank no.	Description	Identity (Query Cover)	GenBank no.	Description	Identity (Query Cover)	GenBank no.
<i>M. pruinosa</i>	<i>Pan troglodytes</i> BAC clone RP43-29J18 from chromosome 7 (Chimpanzee)	94.12% (29%)	AC146279	<i>Raphanus sativus</i> chromosome 8 (Radish)	100% (83%)	LR778317	<i>Spirometra</i> <i>erinaceieuropaei</i> , scaffold0147443 (Cestoda)	100% (100%)	LN165237
							<i>Sarcophilus harrisii</i> , chromosome X (Tasmanian devil)	100% (100%)	LR735560
<i>S. marginella</i>	<i>Rhodocytophaga</i> sp. 172606-1 chromosome, complete genome (Bacteria)	84.62% (54%)	CP048222	<i>Aquila chrysaetos</i> <i>chrysaetos</i> chromosome 18 (Golden eagle)	85.37% (62%)	LR606198	<i>Canis lupus familiaris</i> breed Labrador retriever chromosome 06a (Dog)	100% (100%)	CP050586
<i>G. distinctissima</i>	<i>Schistosoma mansoni</i> chromosome W (Trematoda)	96.00% (64%)	HE601631	<i>Frederiksenia canicola</i> complete genome (Bacteria)	93.55% (26%)	CP015029	<i>Crassostrea gigas</i> , chromosome 10 (Pacific oyster)	100% (100%)	CP048848
							<i>Culicoides sonorensis</i> , scaffold33 (Punkie)	100% (100%)	LN483383