

Additional File: Table S1. Summary of Illumina sequencing. The numbers of reads before and after quality trimming are given. The percentage of reads mapped to the ferret genome is denoted.

	SRA accession number	Raw reads	Reads after trimming	Mapped reads %
Hooded seal visual cortex	SRR3001184	37,108,070	12,473,522	52.45
Ferret visual cortex	SRR3000035	45,683,734	45,351,462	54.23