

**S3 Table. MiSeq read information**

		<b>Sample ID</b>		
		<b>AW (dog, Italy)</b>	<b>S8 (human, Croatia)</b>	<b>S6 (human, India)</b>
<b>Raw Reads</b>	Number	2,842,040	2,290,512	5,751,974
	Nucleotides	467,156,581	257,472,454	810,753,057
	Phred Score >=30	78.72%	93.44%	94.27%
	Average length	164	112	141
<b>Mapped Reads</b>	Number	27,678	20,441	307,416
	Nucleotides	3,059,234	2,035,914	48,487,366
	average length	110	100	158
	Coverage	224	147	3545