

**Table S6.** Phenotypic variance explained (PVE) by identified SNPs by multi-locus methods associated with hereditary AA-amyloidosis in mixed Siamese/Oriental cats.

Method	SNP ID	PVE SNP	Total PVE of all detected SNPS
mrMLM	<b>CHRA1.33307498</b>	26.61	93.55
	<b>CHRA1.87876182</b>	12.22	
	CHRB1.204283203	7.55	
	<b>CHRD1.112359805</b>	11.86	
	CHRD2.3894331	11.55	
	<b>CHRA1.170535359</b>	5.39	
	CHRE2.26012148	10.75	
	CHRF1.2996541	7.62	
FASTmrMLM	<b>CHRA1.33307498</b>	28.50	65.05
	<b>CHRA1.87876182</b>	4.21	
	<b>CHRUN5.1424878</b>	15.65	
	<b>CHRD1.112359805</b>	1.96	
	<b>CHRD2.113529492</b>	14.73	
FASTmrEMMA	<b>CHRA1.33307498</b>	16.75	40.58
	<b>CHRA1.87876182</b>	3.74	
	CHRA1.169994536	6.05	
	<b>CHRD1.83154354</b>	3.23	
	<b>CHRD2.113529492</b>	10.81	
pLARmEB	<b>CHRA1.35096216</b>	17.36	87.74
	CHRA1.168026137	7.98	
	CHRA1.223820842	7.01	
	CHRA2.179873843	9.23	
	<b>CHRD1.83154354</b>	8.47	
	CHRD1.104974246	16.12	
	<b>CHRD1.112359805</b>	5.01	
	<b>CHRD2.113529492</b>	16.56	
ISIS EM-BLASSO	<b>CHRA1.35096216</b>	18.54	83.91
	CHRC2.4289851	5.71	
	<b>CHRUN5.1424878</b>	15.35	
	<b>CHRD2.113529492</b>	27.57	
	<b>CHRA1.170535359</b>	10.35	
	CHRX.13778263	6.39	

SNPs in bold have been detected by at least two methods simultaneously, PVE SNP: Percentage of phenotypic variance explained of each SNP identified by method, Total PVE: Percentage of phenotypic variance explained of all SNPs identified by method.