

**TABLE S1**

**Power of GENECONV to detect simulated gene conversion events of various sizes between two sequences  
(1500 bp each) at varying levels of divergence in 1000 simulations**

		Divergence					
		0.01	0.02	0.05	0.075	0.1	0.18
Length of	501	37.1%	85.5%	99.9%	99.9%	99.9%	100.1%
conversion	402	27.0%	66.9%	100.1%	100.0%	100.0%	100.1%
tract (bp)	252	15.2%	27.9%	98.5%	100.5%	100.6%	101.0%
	150	9.6%	12.4%	40.8%	90.3%	101.3%	102.3%
	90	6.7%	7.2%	13.3%	22.7%	49.2%	103.7%
	45	5.3%	5.2%	7.5%	7.1%	7.5%	21.6%