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Author	Patrik Eriksson	
Title (English)	Development of software tools for the design and evaluation of MLGA assays	
Title (Swedish)		
Abstract	<p>Multiplex ligation dependent genome amplification (MLGA) is a novel method for the multiplex targeted measurement and validation of genetic copy-number variations (CNVs). A design software for MLGA assays and a simple analyse software have been developed. Three design sets were created during the development of the software for evaluation purposes.</p>	
Keywords	MLGA, In silico digestion, GC content, Folding energy, polymorphism	
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