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Development and implementation of high-throughput SNP genotyping in barley

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544	SNP Analysis with Duplicated Fish Genomes: Differentiation of SNPs, Paralogous Sequence Variants, and Multisite Variants. 2010 , 133-150		2
543	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. 2010 , 50, 556-566		88
542	From genetics to genomics in plants and animals. 2010 , 42, 177-194		1
541	Marker Genotype Imputation in a Low-Marker-Density Panel with a High-Marker-Density Reference Panel: Accuracy Evaluation in Barley Breeding Lines. 2010 , 50, 1269-1278		19
540	The genetics of barley low-tillering mutants: low number of tillers-1 (lnt1). 2010 , 121, 705-15		36
539	Construction of a high-density composite map and comparative mapping of segregation distortion regions in barley. 2010 , 284, 319-31		48
538	Features of SNP and SSR diversity in a set of ICARDA barley germplasm collection. 2010 , 26, 229-242		29
537	Association mapping of spot blotch resistance in wild barley. 2010 , 26, 243-256		121
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535	Physical mapping of a large plant genome using global high-information-content-fingerprinting: the distal region of the wheat ancestor <i>Aegilops tauschii</i> chromosome 3DS. <i>BMC Genomics</i> , 2010 , 11, 382	4.5	10
534	Highly-multiplexed SNP genotyping for genetic mapping and germplasm diversity studies in pea. <i>BMC Genomics</i> , 2010 , 11, 468	4.5	115
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