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A Sequence-Anchored Integrated Genetic Linkage Map For Apple, *Malus X domestica* Borkh

[Michela Troggio](#)¹, [Andrey Zharkikh](#)², [Massimo Pindo](#)¹, [Paolo Baldi](#)¹, [Fabrizio Costa](#)¹, [David Chagné](#)³, [Diego Micheletti](#)¹, [Giuseppina Coppola](#)¹, [Alessandro Cestaro](#)¹, [Pauline Lasserre](#)⁴, [Ross N. Crowhurst](#)⁵, [Vincent Bus](#)⁶, [Pierluigi Magnago](#)¹, [Matteo Komjanc](#)¹, [Yves Lespinasse](#)⁴, [Silvio Salvi](#)^{1,7}, [Charles-Eric Durel](#)⁴, [Susan E. Gardiner](#)³, [Riccardo Velasco](#)¹

¹ IASMA Research and Innovation Centre, Foundation Edmund Mach, via E. Mach 1, San Michele all'Adige, Trento, 38010, Italy

² Myriad Genetics Inc, 320 Wakara Way, Salt Lake City, UT 84108, USA

³ The New Zealand Institute for Plant and Food Research Limited, Palmerston North Research Centre, Private Bag 11600, Palmerston North 4442, New Zealand

⁴ INRA Angers-Nantes, UMR1259 Genetics and Horticulture, IFR149 QUASAV, 42 rue G. Morel, Beaucouze Cedex, 49071, France

⁵ The New Zealand Institute for Plant and Food Research Limited, Mt Albert Research Centre, Private Bag 92169, Auckland 1142, New Zealand

⁶ The New Zealand Institute for Plant and Food Research Limited, Hawke's Bay Research Centre, PO Box 8285, Havelock North 4157, New Zealand

⁷ Department of Agroenvironmental Sciences and Technologies, University of Bologna viale Fanin 44, Bologna, 40127, Italy

Genome resources for apple (*Malus x domestica* Borkh), the main fruit crop of temperate regions, have built up over the past five years, culminating in the sequencing of the apple cultivar 'Golden Delicious' (GD) genome. In spite of the availability of a high-quality genome sequence, a large collection of expressed sequence tags, and a physical map, high-resolution genetic maps remain crucial resources for molecular breeding programs as well as for fine-mapping quantitative trait loci. We describe here the construction of an apple dense integrated genetic map derived from six F1 populations and, for the first time, its physical anchor to the sequenced genome of GD. Polymorphisms discovered by assembling the two haplotypes of the GD genome were used to develop markers for each metacontig to correlate them with linkage groups. The map included 1,730 polymorphic markers, 196 SSRs, 1,500 genomic-derived SNPs and 34 EST-derived SNPs. In total, 17 linkage groups were identified based on SSR markers mapping to existing apple linkage maps. All sequenced markers, well positioned on the genetic map, were used to order and to orient metacontigs along the appropriate linkage groups. In addition, marker information was used to avoid building chimerical metacontigs from different linkage groups. Many genes related to disease resistance, fruit quality, plant development, and reaction to environment have been identified and mapped to chromosomes. Region-dependent estimations of physical and recombinational distance, and correlation of recombination with specific sequence parameters are also presented.