

Development and applicability of GBS approach for genomic studies in Japanese plum (*Prunus salicina* Lindl.)

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© 2018, © 2018 The Journal of Horticultural Science & Biotechnology Trust. Genotyping by sequencing (GBS) provides a large quantity of useful data suitable for the identification of single nucleotide polymorphisms (SNPs), facilitating accurate genomic studies in plant species. In this study, GBS-based SNPs were used to characterise 11 Japanese plum cultivars and to explore their natural allelic diversity in relation to the most important phenology events (flowering date, ripening date and fruit development period) and fruit quality traits (weight, shape, skin and flesh colour, over colour, skin and flesh chlorophyll index, flesh firmness and soluble solids concentration). GBS-based SNPs were shown to be a powerful tool for genetic diversity and other genomic studies where SNP markers were related to several traits, particularly for flowering date, ripening date, fruit development period, skin chlorophyll degradation, flesh chlorophyll degradation and flesh colour. These results represe