



ACCELERATING PROGRESS IS IN OUR GENES

NGS PUBLICATIONS LIST Agricultural Biology Research

SureSelect Custom Plant

1. Stull GW, Moore MJ, Mandala VS, Douglas NA, Kates HR, Qi X, Brockington SF, Soltis PS, Soltis DE, Gitzendanner MA. **A targeted enrichment strategy for massively parallel sequencing of angiosperm plastid genomes.** *Applications in Plant Sciences*. (2013) 1(2): 1200497
2. Duvaux L, Geissmann O, Gharbi K, Zhou JJ, Ferrari J, Smadja GM, Butlin RK. **Dynamics of Copy Number Variation in Host Races of the Pea Aphid.** *Mol Biol Evol*. (2014): doi: 10.1093/molbev/msu266
3. Pont C, Muat F, Guizard S, Flores R, Foucrier S, Bidet Y, Quraishi UM, Alaux M, Doležel J, Fahima T, Budak H, Keller B, Salvi S, Maccaferri M, Steinbach D, Feuillet C, Quesneville H, Salse J. **Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleo- and neoduplicated subgenomes.** *The Plant Journal*. (2013) 76: 1030-1044
4. Neves LG, Davis JM, Barbazuk WB, Kirst M. **A high-density gene map of loblolly pine (Pinus taeda L.) based on exome sequence capture genotyping.** *G3-Genes, Genomes, Genetics*. (2013) doi:10.1534/g3.113.008714
5. Campoli C, Pankin A, Drosse B, Casao CM, Davis SJ, von Korff M. **HvLUX1 is a candidate gene underlying the early maturity 10 locus in barley: phylogeny, diversity, and interactions with the circadian clock and photoperiodic pathways.** *New Phytologist*. (2013) 199: 1045-1059
6. Sun L, Zhang Q, Xu Z, Yang W, Guo Y, Lu J, Pan H, Cheng T, Cai M. **Genome-wide DNA polymorphisms in two cultivars of mei (Prunus mume sieb. Et zucc.)** *BMC Genomics*. (2013) 14: 98
7. Neves LG, Davis JM, Barbazuk WB, Kirst M. **Whole-exome targeted sequencing of the uncharacterized pine genome.** *The Plant Journal*. (2013) 75: 146-156
8. Andolfo G, Jupe F, Witek K, Etherington GJ, Ercolano MR, Jones JDG. **Defining the full tomato NB-LRR resistance gene repertoire using genomic and cDNA RenSeq.** *BMC Plant Biology*. (2014) 14: 120
9. Jupe F, Witek K, Verweij W, Sliwka J, Pritchard L, Etherington GJ, Maclean D, Cock PJ, Leggett RM, Bryan GJ, Cardle L, Hein I, Jones JDG. **Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations.** *The Plant Journal*. (2013) 76: 530-544
10. Uitdewilligen JGAML, Wolters AMA, D'hoop BB, Borm TJA, Visser RGF, van Eck HJ. **A Next-Generation Sequencing Method for Genotyping-by-Sequencing of Highly Heterozygous Autotetraploid Potato.** *PLOS One*. (2013) 8(5): e62355



SureSelect Bovine All Exon

1. Charlier C, Li W, Harland C, Littlejohn M, Creagh F, Keehan M, Druet T, Coppieters W, Spelman R, Georges M. **NGS-based Reverse Genetic Scree Reveals Loss-of-function Variants Compromising Fertility in Cattle.** *Proceedings, 10th World Congress of genetics Applied to Livestock Production* (2014)

SureSelect Custom Animal

1. Pyron RA, Hendry CR, Chou VM, Lemmon EM, Lemmon AR, Burbrink FT. **Effectiveness of phylogenomic data and coalescent species-tree methods for resolving difficult nodes in the phylogeny of advanced snakes (Serpentes: Caenophidia).** *Molecular Phylogenetics and Evolution.* (2014) 81: 221-231
2. Muñoz-Fuentes V, Marcet-Ortega M, Alkorta-Aranburu G, Forsberg CL, Morrell JM, Manzano-Piedras E, Söderberg A, Daniel K, Villalba A, Toth A, Di Rienzo A, Roig I, Vilà C. **Strong artificial selection in domestic mammals did not result in an increased recombination rate.** *Mol Biol Evol.* (2014): doi: 10.1093/molbev/msu322
3. Chevalier FD, Valentim CLL, LoVerde PT, Anderson TJC. **Efficient linkage mapping using exome capture and extreme QTL in schistosome parasites.** *BMC Genomics.* (2014) 15:617
4. Runcie DE, Wiedmann RT, Archie EA, Altmann J, Wary GA, Alberts SC, Tung J. **Social environment influences the relationship between genotype and gene expression in wild baboons.** *Philosophical Transactions of the Royal Society B.* (2013) DOI: 10.1098/rstb.2012.0345
5. Stamps BW, Corsetti FA, Spear JR, Stevenson BS. **Draft genome of a novel Chlorobi member assembled by tetranucleotide binning of a hot spring metagenome.** *Genome Announcements.* (2014) 2(5): e00897-14

SureSelect Library Preparation Kit, Animal

1. Williams RC, Dawsn DA, Horsburgh GJ, Sinclair W. **Isolation and characterization of microsatellite loci for the ancient cephalopod, *Nautilus pompilius*.** *Conservation Genet Resour.* (2014): DOI 10.1007/s12686-014-0304-7
2. Morteaga KG, Horsburgh GJ, Illera JC, Dawson DA. **Characterization of microsatellite markers for *Saxicola* species.** *Conservation Genet Resour.* (2014): DOI 10.1007/s12686-014-0355-9

Request more information or buy online: www.agilent.com/genomics/ngs



Find an Agilent customer center in your country:

www.genomics.agilent.com/contactUs.jsp

U.S. and Canada: 1-800-227-9770 | cag_sales-na@agilent.com

For Research Use Only. Not for use in diagnostic procedures.

© Agilent Technologies, Inc. 2015, 2016

Printed in USA, April 2016

5992-5546EN

PR7000-0412

