**Table S12 Functional categories of amplicons and signatures of selection. These are the raw data used in Figure 4 to which loess smoothing was applied. Values for the Direction of Selection statistic (DoS) and Tajima's *D* are weighted averages where the weights are the sample size.**

| Functional category | Assoc | Unassoc | Total | DoS | *D* (NS) | *D* (SY) |
|---|---|---|---|---|---|---|
| zinc.finger.proteins | 4 | 10 | 29 | -0.189 | -0.524 | -0.838 |
| isomerase.activity.topoisomerase.epimerase.isomerases. | 3 | 6 | 19 | -0.134 | -0.931 | -0.587 |
| ATPases | 4 | 6 | 18 | -0.125 | -0.495 | 0.009 |
| vitamin.binding.Vitamin.B6.anthocyanidin.flavin.dependent.beta.carotene. | 5 | 13 | 34 | -0.109 | -0.366 | -0.509 |
| calmodulin.binding.proteins.Calmodulin. | 6 | 8 | 34 | -0.101 | -0.063 | 0.037 |
| ion.channel.glutamate.gated.ion.channel.KAB.potassium.channels.CLC. | 2 | 8 | 15 | -0.094 | -0.417 | -0.981 |
| vesicle.mediated.transport.VAMP.VPS.exosomes.coatomer.NECAP.exocysts. | 2 | 12 | 26 | -0.082 | -0.708 | -1.032 |
| Glycosidase.chitinase.glycosylase.glycosidase.glucanase. | 7 | 16 | 50 | -0.079 | -0.634 | -0.394 |
| signal.transducers.tranducins.protein.kinases. | 4 | 17 | 38 | -0.071 | -0.697 | -0.362 |
| pigment.binding.light.receptors.chlorophyll. | 0 | 9 | 14 | -0.045 | -0.508 | -1.183 |
| structural.constituent.of.ribosome.ribosomal.subunits. | 5 | 23 | 43 | -0.029 | -0.363 | -0.499 |
| structural.constituent.of.cell.wall.actin.tubulin.extensin.expansin. arabinogalactans. | 5 | 24 | 56 | -0.017 | -0.384 | -0.191 |
| stress.response.USP. | 3 | 11 | 26 | -0.015 | -0.339 | -0.495 |
| hormone.binding.auxin.receptors.ethylene.receptors.brassinosteroid.receptors. | 11 | 24 | 72 | -0.004 | -0.341 | -0.228 |
| Protease.Peptidase.serine.threonine.kinases.endopeptidases.aspartyl.metalloproteases.TMK.cysteine.proteases. | 18 | 65 | 152 | -0.003 | -0.602 | -0.701 |
| peroxidases.cationic.peroxidase.Haem.peroxidase. | 10 | 14 | 38 | 0.004 | -0.456 | -0.626 |
| ubiquitin.ligase.PUB.f.box.ubiquitin.protein.ligase. | 5 | 25 | 65 | 0.008 | -0.647 | -0.647 |
| hydrolases.HAD.hydrolases. | 19 | 28 | 90 | 0.010 | -0.450 | -0.551 |
| transporters.ABC.transporter.OPT.POT.nodulin.amino.acid.transporter.MATE.MDR.hexose.transporter.permease. | 22 | 51 | 136 | 0.012 | -0.269 | -0.455 |
| pectin.esterases.pectinesterase. | 1 | 10 | 17 | 0.014 | -0.690 | -0.817 |
| oxidoreductases.cytochrome.P450.cytochrome.c.catalases.dehydrogenases. reductases. | 27 | 70 | 219 | 0.027 | -0.509 | -0.291 |
| disease.resistance.NBS. | 3 | 19 | 45 | 0.027 | -0.214 | -0.464 |
| GTPase.GTP.binding.RAB.GTPase.RAS.GTPase.RAN.GTPase. | 3 | 11 | 35 | 0.033 | -0.315 | -0.236 |

| | | | | | | |
|---|---|---|---|---|---|---|
| transcription.factors.Myb.Myc.GRAS.WRKY.bZIP.ARR. | 19 | 52 | 132 | 0.041 | -0.536 | -0.324 |
| chromatin.binding.RCC1.chromosome.condensation.complex.chromatin. remodeling.histone.proteins. | 5 | 17 | 35 | 0.043 | -0.317 | 0.519 |
| RNA.polymerase.RDR.RNA.polymerase. | 2 | 9 | 14 | 0.043 | 0.027 | 0.037 |
| lyase.activity.dehydratase.pectate.lyase.carbon.sulfer.lyase. | 8 | 25 | 70 | 0.043 | -0.388 | -0.583 |
| transferases.PFK.glucuronosyltransferases.SEC. | 22 | 80 | 219 | 0.045 | -0.410 | -0.300 |
| nucleic.acid.nucleotide.binding.Anth.retinoblastoma.argonaute.BLHL. VARICOSE.SWAP.DNA.Polymerase. | 16 | 48 | 135 | 0.060 | -0.378 | -0.084 |
| lipid.binding.lipase.phospholipase.EXL.clathrin.associated.complex. | 6 | 17 | 50 | 0.062 | -0.616 | -0.370 |
| translation.Initiation.elongation.Factors.EIFG.elongation.factors. | 3 | 6 | 19 | 0.063 | -0.512 | -0.416 |
| water.channel.aquaporins.MIP.TIP.HOS. | 0 | 7 | 9 | 0.081 | -0.412 | 0.125 |
| electron.transporter.photosystems.cytochrome.b6.photo.assimilate. | 6 | 6 | 16 | 0.104 | -0.350 | -1.164 |
| heat.shock.HSP.DnaJ. | 7 | 33 | 71 | 0.112 | -0.574 | -0.357 |
| carbohydrate.binding.sucrase.glyoxyl.oxidase.VTC.INT.lectin.protein.kinase. carbohydrate.protein.kinase. | 5 | 16 | 32 | 0.140 | -0.665 | -0.831 |
| phosphatase.regulator.activity.phosphatase.2.pho1.phosphatases.NIF. | 2 | 9 | 15 | 0.140 | -0.986 | -1.019 |
| ligase.activity.synthetases.ligases. | 0 | 5 | 20 | 0.212 | -0.566 | 0.084 |
| metal.cluster.binding.embryo.defective.proteins.germins.Rieske.ALS. ferredoxins. | 5 | 25 | 50 | 0.230 | -0.623 | -0.258 |
| microtubule.motor.proteins.kinesin.microtubule. | 3 | 6 | 12 | 0.374 | -0.790 | -0.713 |

***Abbreviations:*** Assoc, associated to at least one phenotype; *D*, Tajima's *D*; DoS, Direction of Selection statistic (Stoletzki and Eyre-Walker 2011); NS, nonsynonymous; SY, synonymous; Unassoc, unassociated to at least one phenotype.

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