

An ultra-high density bin-map for rapid QTL mapping f large F2 maize population

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genetic basis of maize kernel starch content revealed by high-density single nucleotide polymorphism markers in a recombinant inbred line population. <i>BMC Plant Biology</i> , 2015, 15, 288.	1.6	31
2	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea (<i>Cicer</i>) Tj ETQq1 1,0,784314, rGBT / Ome	1.6	131
3	An ultra-high-density map as a community resource for discerning the genetic basis of quantitative traits in maize. <i>BMC Genomics</i> , 2015, 16, 1078.	1.2	55
4	Construction of a dense genetic linkage map and mapping quantitative trait loci for economic traits of a doubled haploid population of <i>Pyropia haitanensis</i> (Bangiales, Rhodophyta). <i>BMC Plant Biology</i> , 2015, 15, 228.	1.6	51
5	Quantitative trait locus analysis for kernel width using maize recombinant inbred lines. <i>Genetics and Molecular Research</i> , 2015, 14, 14496-14502.	0.3	1
6	The Identification of Two Head Smut Resistance-Related QTL in Maize by the Joint Approach of Linkage Mapping and Association Analysis. <i>PLoS ONE</i> , 2015, 10, e0145549.	1.1	12
7	Genome Assembly Improvement and Mapping Convergent Evolved Skeletal Traits in Sticklebacks with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1463-1472.	0.8	112
8	Introgression browser: high-throughput whole-genome SNP visualization. <i>Plant Journal</i> , 2015, 82, 174-182.	2.8	17
9	Genotyping-by-sequencing (GBS) identified SNP tightly linked to QTL for pre-harvest sprouting resistance. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1385-1395.	1.8	66
10	Characterizing Two Inter-specific Bin Maps for the Exploration of the QTLs/Genes that Confer Three Soybean Evolutionary Traits. <i>Frontiers in Plant Science</i> , 2016, 7, 1248.	1.7	18
11	QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 2110-2119.	4.1	177
12	Genome-wide association study (GWAS) reveals the genetic architecture of four husk traits in maize. <i>BMC Genomics</i> , 2016, 17, 946.	1.2	59
13	Genetic architecture of the maize kernel row number revealed by combining QTL mapping using a high-density genetic map and bulked segregant RNA sequencing. <i>BMC Genomics</i> , 2016, 17, 915.	1.2	63
14	Genotype-by-sequencing facilitates genetic mapping of a stem rust resistance locus in <i>Aegilops umbellulata</i> , a wild relative of cultivated wheat. <i>BMC Genomics</i> , 2016, 17, 1039.	1.2	39
15	Identification of quantitative trait loci controlling soybean seed weight in recombinant inbred lines derived from PI 483463 (<i>Glycine soja</i>) × Hutcherson TM (<i>G. max</i>). <i>Plant Breeding</i> , 2016, 135, 614-620.	1.0	17
16	High-resolution QTL mapping for grain appearance traits and co-localization of chalkiness-associated differentially expressed candidate genes in rice. <i>Rice</i> , 2016, 9, 48.	1.7	56
17	Genetic dissection of maize seedling root system architecture traits using an ultra-high density bin map and a recombinant inbred line population. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 266-279.	4.1	48
18	Genetic analysis of shoot fresh weight in a cross of wild (<i>G. soja</i>) and cultivated (<i>G. max</i>) soybean. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	16

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19	Quantitative trait loci mapping of yield and related traits using a high-density genetic map of maize. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	22
20	Genomic structure analysis of a set of <i>Oryza nivara</i> introgression lines and identification of yield-associated QTLs using whole-genome resequencing. <i>Scientific Reports</i> , 2016, 6, 27425.	1.6	45
21	Molecular Dissection of Seedling Salinity Tolerance in Rice (<i>Oryza sativa</i> L.) Using a High-Density GBS-Based SNP Linkage Map. <i>Rice</i> , 2016, 9, 52.	1.7	125
22	Updated sesame genome assembly and fine mapping of plant height and seed coat color QTLs using a new high-density genetic map. <i>BMC Genomics</i> , 2016, 17, 31.	1.2	84
23	An ultra-high-density bin map facilitates high-throughput QTL mapping of horticultural traits in pepper (<i>Capsicum annuum</i>). <i>DNA Research</i> , 2016, 23, 81-91.	1.5	111
24	Quantitative trait loci mapping for <i>Gibberella</i> ear rot resistance and associated agronomic traits using genotyping-by-sequencing in maize. <i>Theoretical and Applied Genetics</i> , 2016, 129, 17-29.	1.8	40
25	Genetic dissection of maize plant architecture with an ultra-high density bin map based on recombinant inbred lines. <i>BMC Genomics</i> , 2016, 17, 178.	1.2	104
26	Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. <i>Plant Biotechnology Journal</i> , 2016, 14, 1551-1562.	4.1	121
27	Mapping of QTL conferring resistance to northern corn leaf blight using high-density SNPs in maize. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	33
28	Analysis of the genetic architecture of maize ear and grain morphological traits by combined linkage and association mapping. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1011-1029.	1.8	66
29	Construction of genotyping-by-sequencing based high-density genetic maps and QTL mapping for fusarium wilt resistance in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1911.	1.6	55
30	Genotyping-by-sequencing of three mapping populations for identification of candidate genomic regions for resistance to sterility mosaic disease in pigeonpea. <i>Scientific Reports</i> , 2017, 7, 1813.	1.6	48
31	Development and Evaluation of Near-Isogenic Lines with Different Blast Resistance Alleles at the <i>Piz</i> Locus in <i>japonica</i> Rice from the Lower Region of the Yangtze River, China. <i>Plant Disease</i> , 2017, 101, 1283-1291.	0.7	11
32	Inheritance, fine-mapping, and candidate gene analyses of resistance to soybean mosaic virus strain SC5 in soybean. <i>Molecular Genetics and Genomics</i> , 2017, 292, 811-822.	1.0	35
33	Construction of a high-density genetic map using genotyping by sequencing (GBS) for quantitative trait loci (QTL) analysis of three plant morphological traits in upland cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2017, 213, 1.	0.6	37
34	QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2017, 15, 927-941.	4.1	198
35	QTL mapping of general combining abilities of four traits in maize using a high-density genetic map. <i>Journal of Integrative Agriculture</i> , 2017, 16, 1700-1707.	1.7	5
36	Identification and molecular genetic mapping of Chili veinal mottle virus (ChiVMV) resistance genes in pepper (<i>Capsicum annuum</i>). <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	41

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37	Dissection of the genetic architecture for tassel branch number by QTL analysis in two related populations in maize. <i>Journal of Integrative Agriculture</i> , 2017, 16, 1432-1442.	1.7	14
38	Genetic Determinants of Crop Timing and Quality Traits in Two Interspecific <i>Petunia</i> Recombinant Inbred Line Populations. <i>Scientific Reports</i> , 2017, 7, 3200.	1.6	8
39	Mapping QTLs and meta-QTLs for two inflorescence architecture traits in multiple maize populations under different watering environments. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	14
40	Genotyping-by-Sequencing Derived High-Density Linkage Map and its Application to QTL Mapping of Flag Leaf Traits in Bread Wheat. <i>Scientific Reports</i> , 2017, 7, 16394.	1.6	103
41	Genetic dissection of carotenoids in maize kernels using high-density single nucleotide polymorphism markers in a recombinant inbred line population. <i>Crop Journal</i> , 2017, 5, 63-72.	2.3	13
42	High Density Linkage Map Construction and Mapping of Yield Trait QTLs in Maize (<i>Zea mays</i>) Using the Genotyping-by-Sequencing (GBS) Technology. <i>Frontiers in Plant Science</i> , 2017, 8, 706.	1.7	78
43	Quantitative Trait Locus Analysis for Deep-Sowing Germination Ability in the Maize IBM Syn10 DH Population. <i>Frontiers in Plant Science</i> , 2017, 8, 813.	1.7	44
44	Mapping QTL for Seed Germinability under Low Temperature Using a New High-Density Genetic Map of Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1223.	1.7	79
45	Effect of Co-segregating Markers on High-Density Genetic Maps and Prediction of Map Expansion Using Machine Learning Algorithms. <i>Frontiers in Plant Science</i> , 2017, 8, 1434.	1.7	9
46	Dissection of Recombination Attributes for Multiple Maize Populations Using a Common SNP Assay. <i>Frontiers in Plant Science</i> , 2017, 8, 2063.	1.7	6
47	qNCLB7.02, a novel QTL for resistance to northern corn leaf blight in maize. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	13
48	Deciphering genetic factors that determine melon fruit quality traits using RNA-seq-based high-resolution QTL and eQTL mapping. <i>Plant Journal</i> , 2018, 94, 169-191.	2.8	133
49	Genetic and Molecular Mechanisms of Quantitative Trait Loci Controlling Maize Inflorescence Architecture. <i>Plant and Cell Physiology</i> , 2018, 59, 448-457.	1.5	37
50	Comparative mapping of quantitative trait loci for tassel-related traits of maize in $F_2:3$ and RIL populations. <i>Journal of Genetics</i> , 2018, 97, 253-266.	0.4	9
51	A retrotransposon in an HKT1 family sodium transporter causes variation of leaf Na^+ exclusion and salt tolerance in maize. <i>New Phytologist</i> , 2018, 217, 1161-1176.	3.5	229
52	Combining Three Mapping Strategies to Reveal Quantitative Trait Loci and Candidate Genes for Maize Ear Length. <i>Plant Genome</i> , 2018, 11, 170107.	1.6	6
53	Discovery of Anthocyanin Acyltransferase1 (AAT1) in Maize Using Genotyping-by-Sequencing (GBS). <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3669-3678.	0.8	22
54	Whole Genome Resequencing from Bulk Populations as a Rapid QTL and Gene Identification Method in Rice. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4000.	1.8	23

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55	Quantitative Trait Loci Mapping for Theobromine and Caffeine Contents in Tea Plant (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.4	26
56	High-density genetic map construction and mapping of the homologous transformation sterility gene (hts) in wheat using GBS markers. BMC Plant Biology, 2018, 18, 301.	1.6	12
57	Identification and Fine-Mapping of a Major Maize Leaf Width QTL in a Re-sequenced Large Recombinant Inbred Lines Population. Frontiers in Plant Science, 2018, 9, 101.	1.7	21
58	Construction of a SNP-Based High-Density Genetic Map Using Genotyping by Sequencing (GBS) and QTL Analysis of Nut Traits in Chinese Chestnut (<i>Castanea mollissima</i> Blume). Frontiers in Plant Science, 2018, 9, 816.	1.7	26
59	Linkage mapping combined with association analysis reveals QTL and candidate genes for three husk traits in maize. Theoretical and Applied Genetics, 2018, 131, 2131-2144.	1.8	19
60	Genetic dissection and fine mapping of a novel dt gene associated with determinate growth habit in sesame. BMC Genetics, 2018, 19, 38.	2.7	16
61	Identification of minor effect QTLs for plant architecture related traits using super high density genotyping and large recombinant inbred population in maize (<i>Zea mays</i>). BMC Plant Biology, 2018, 18, 17.	1.6	33
62	Combined bulked segregant sequencing and traditional linkage analysis for identification of candidate gene for purple leaf sheath in maize. PLoS ONE, 2018, 13, e0190670.	1.1	8
63	Construction of a high-density genetic map of tree peony (<i>Paeonia suffruticosa</i> Andr. Moutan) using restriction site associated DNA sequencing (RADseq) approach. Tree Genetics and Genomes, 2019, 15, 1.	0.6	7
64	Combination of multi-locus genome-wide association study and QTL mapping reveals genetic basis of tassel architecture in maize. Molecular Genetics and Genomics, 2019, 294, 1421-1440.	1.0	12
65	Fine mapping and identification of ub4 as a candidate gene associated with tassel branch number in maize (<i>Zea mays</i> L.). Genetic Resources and Crop Evolution, 2019, 66, 1557-1571.	0.8	3
66	Identification of a major QTL for seed number per silique in cabbage (<i>Brassica oleracea</i> L. var. capitata) using genotyping by sequencing. Euphytica, 2019, 215, 1.	0.6	9
67	Construction of the first high-density genetic map and QTL mapping for photosynthetic traits in <i>Lycium barbarum</i> L.. Molecular Breeding, 2019, 39, 1.	1.0	8
68	Functional models in genome-wide selection. PLoS ONE, 2019, 14, e0222699.	1.1	3
69	Genotyping-by-sequencing based QTL mapping for rice grain yield under reproductive stage drought stress tolerance. Scientific Reports, 2019, 9, 14326.	1.6	46
70	Unraveling the genetic architecture of grain size in einkorn wheat through linkage and homology mapping and transcriptomic profiling. Journal of Experimental Botany, 2019, 70, 4671-4688.	2.4	19
71	A SNP-Based High-Density Genetic Map Reveals Reproducible QTLs for Tassel-Related Traits in Maize (<i>Zea</i>) Tj ETQq0 0 0 rgBT /Overlock 1	1.0	3
72	Genetic mapping of folate QTLs using a segregated population in maize. Journal of Integrative Plant Biology, 2019, 61, 675-690.	4.1	16

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73	A recombination bin-map identified a major QTL for resistance to Tomato Spotted Wilt Virus in peanut (<i>Arachis hypogaea</i>). <i>Scientific Reports</i> , 2019, 9, 18246.	1.6	25
74	High-density quantitative trait locus mapping revealed genetic architecture of leaf angle and tassel size in maize. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	10
75	A major QTL and candidate genes for capsaicinoid biosynthesis in the pericarp of <i>Capsicum chinense</i> revealed using QTL-seq and RNA-seq. <i>Theoretical and Applied Genetics</i> , 2019, 132, 515-529.	1.8	43
76	Genetic mapping of quantitative trait locus for the leaf morphological traits in a recombinant inbred line population by ultra-high density maps across multi-environments of maize (<i>Zea mays</i>). <i>Plant Breeding</i> , 2020, 139, 107-118.	1.0	6
77	Fine mapping and candidate gene analysis of a seed glucosinolate content QTL, qGSL-C2, in rapeseed (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 479-490.	1.8	20
78	Genome-wide association study (GWAS) reveals genetic basis of ear-related traits in maize. <i>Euphytica</i> , 2020, 216, 1.	0.6	9
79	Genetic Dissection of the General Combining Ability of Yield-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 2020, 11, 788.	1.7	4
80	A novel adult plant leaf rust resistance gene <i>Lr2K38</i> mapped on wheat chromosome 1AL. <i>Plant Genome</i> , 2020, 13, e20061.	1.6	5
81	Genetic basis of maize ear angle revealed by high-density single nucleotide polymorphism markers in four recombinant inbred line populations. <i>Euphytica</i> , 2020, 216, 1.	0.6	0
82	Mapping quantitative trait loci associated with stem-related traits in maize (<i>Zea mays</i> L.). <i>Plant Molecular Biology</i> , 2020, 104, 583-595.	2.0	9
83	All-in-one sequencing: an improved library preparation method for cost-effective and high-throughput next-generation sequencing. <i>Plant Methods</i> , 2020, 16, 74.	1.9	10
84	Fine mapping and candidate gene prediction of a major quantitative trait locus for tassel branch number in maize. <i>Gene</i> , 2020, 757, 144928.	1.0	1
85	Discovery and Fine Mapping of qSCR6.01, a Novel Major QTL Conferring Southern Rust Resistance in Maize. <i>Plant Disease</i> , 2020, 104, 1918-1924.	0.7	8
86	Genetic Dissection of Germinability under Low Temperature by Building a Resequencing Linkage Map in japonica Rice. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1284.	1.8	20
87	Phenotypic Plasticity Contributes to Maize Adaptation and Heterosis. <i>Molecular Biology and Evolution</i> , 2021, 38, 1262-1275.	3.5	32
88	Genetic analysis of maize shank length by QTL mapping in three recombinant inbred line populations. <i>Plant Science</i> , 2021, 303, 110767.	1.7	4
89	<i>QDtbn1</i> , an <i>F-box</i> gene affecting maize tassel branch number by a dominant model. <i>Plant Biotechnology Journal</i> , 2021, 19, 1183-1194.	4.1	14
90	Identification and Validation of a Novel Locus Controlling Spikelet Number in Bread Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Ove	1.7	26

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91	Identifying Wild Versus Cultivated Gene-Alleles Conferring Seed Coat Color and Days to Flowering in Soybean. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1559.	1.8	6
92	Genetic analysis of ear-related traits under different pollination treatments in maize (<i>Zea mays</i>). <i>Plant Breeding</i> , 2021, 140, 211-222.	1.0	3
93	Identification and Fine-Mapping of a Novel QTL, <i>qMrdd2</i> , That Confers Resistance to Maize Rough Dwarf Disease. <i>Plant Disease</i> , 2022, 106, 65-72.	0.7	7
94	Construction of high density genetic map and QTL mapping in sorghum- <i>Ã—</i> - <i>Ã—</i> sudangrass. <i>Euphytica</i> , 2021, 217, 1.	0.6	7
95	Dissecting the Genetic Basis of Flowering Time and Height Related-Traits Using Two Doubled Haploid Populations in Maize. <i>Plants</i> , 2021, 10, 1585.	1.6	3
96	QTL Mapping and Validation for Kernel Area and Circumference in Common Wheat via High-Density SNP-Based Genotyping. <i>Frontiers in Plant Science</i> , 2021, 12, 713890.	1.7	6
97	Genetic architecture of maize yield traits dissected by QTL mapping and GWAS in maize. <i>Crop Journal</i> , 2022, 10, 436-446.	2.3	17
98	Mapping of QTL for agronomic traits using high-density SNPs with an RIL population in maize. <i>Genes and Genomics</i> , 2021, 43, 1403-1411.	0.5	7
99	Mapping causal genes and genetic interactions for agronomic traits using a large F2 population in rice. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	5
100	Fine mapping and gene cloning in the post-NGS era: advances and prospects. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1791-1810.	1.8	94
101	Whole-genome resequencing: Current status and future prospects in genomics-assisted crop improvement. , 2016, , 187-211.		2
102	Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. <i>PLoS ONE</i> , 2015, 10, e0121624.	1.1	69
103	Benchmarking sequencing methods and tools that facilitate the study of alternative polyadenylation. <i>Genome Biology</i> , 2021, 22, 291.	3.8	23
105	Molecular Breeding in Maize Improvement. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2020, 9, 722-729.	0.0	0
106	High-Resolution Bin Maps Provide Insights for QTL Mapping of Yield-Related Traits with Milyang23/Gihobyeo Recombinant Inbred Lines. <i>Plant Breeding and Biotechnology</i> , 2020, 8, 293-306.	0.3	1
107	QTL analysis of seed size by a high-density GBS genetic map in watermelon (<i>Citrullus lanatus</i> L.). <i>Acta Horticulturae</i> , 2020, , 121-126.	0.1	1
108	Fine-Mapping of a Major Quantitative Trait Locus <i>q2ID1</i> for Rice Stem Diameter. <i>Plant Breeding and Biotechnology</i> , 2021, 9, 298-309.	0.3	1
109	Genome resequencing-based high-density genetic map and QTL detection for yield and fiber quality traits in diploid Asiatic cotton (<i>Gossypium arboreum</i>). <i>Molecular Genetics and Genomics</i> , 2022, 297, 199-212.	1.0	2

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110	Germplasm Resources and Strategy for Genetic Breeding of Lycium Species: A Review. <i>Frontiers in Plant Science</i> , 2022, 13, 802936.	1.7	9
111	Quantitative Trait Loci Mapping for Earliness, Fruit, and Seed Related Traits Using High Density Genotyping-by-Sequencing-Based Genetic Map in Bitter Gourd (<i>Momordica charantia</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 799932.	1.7	7
112	Comparative mapping of quantitative trait loci for tassel-related traits of maize in F and RIL populations. <i>Journal of Genetics</i> , 2018, 97, 253-266.	0.4	3
113	Genetic Variation in ZmPAT7 Contributes to Tassel Branch Number in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2586.	1.8	5
114	Genotyping by sequencing-based linkage map construction and identification of quantitative trait loci for yield-related traits and oil content in <i>Jatropha</i> (<i>Jatropha curcas</i> L.). <i>Molecular Biology Reports</i> , 2022, 49, 4293-4306.	1.0	5
116	QTL analysis for plant height and fine mapping of two environmentally stable QTLs with major effects in soybean. <i>Journal of Integrative Agriculture</i> , 2022, 21, 933-946.	1.7	4
127	Genetic Structure and Molecular Mechanisms Underlying the Formation of Tassel, Anther, and Pollen in the Male Inflorescence of Maize (<i>Zea mays</i> L.). <i>Cells</i> , 2022, 11, 1753.	1.8	7
128	Identification of QTLs linked with watermelon fruit and seed traits using GBS-based high-resolution genetic mapping. <i>Scientia Horticulturae</i> , 2022, 303, 111237.	1.7	8
129	Construction of a high-density bin-map and identification of fruit quality-related quantitative trait loci and functional genes in pear. <i>Horticulture Research</i> , 2022, 9, .	2.9	6
130	Construction of Chromosome Segment Substitution Lines and Inheritance of Seed-Pod Characteristics in Wild Soybean. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	11
131	Molecular Approaches in Conservation and Restoration of Agrobiodiversity. , 2022, , 169-216.		1
132	Whole-genome resequencing identified QTLs, candidate genes and Kompetitive Allele-Specific PCR markers associated with the large fruit of Atlantic Giant (<i>Cucurbita maxima</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
133	QTL mapping and genomic selection for Fusarium ear rot resistance using two F2:3 populations in maize. <i>Euphytica</i> , 2022, 218, .	0.6	2
134	Genetic dissection of ear-related traits using immortalized F2 population in maize. <i>Journal of Integrative Agriculture</i> , 2022, 21, 2492-2507.	1.7	2
135	Teosinte confers specific alleles and yield potential to maize improvement. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3545-3562.	1.8	7
136	Genetic mapping revealed that the Pun2 gene in <i>Capsicum chacoense</i> encodes a putative aminotransferase. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
137	Identification of quantitative trait loci for related traits of stalk lodging resistance using genome-wide association studies in maize (<i>Zea mays</i> L.). <i>BMC Genomic Data</i> , 2022, 23, .	0.7	5
138	Drought stress tolerance in wheat: Recent QTL mapping advances. , 2023, , 149-161.		0

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139	Genetic basis of maize kernel protein content revealed by high-density bin mapping using recombinant inbred lines. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
140	High-resolution quantitative trait locus mapping for rice grain quality traits using genotyping by sequencing. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
141	QTL localisation of seed-related traits in Tibetan hulless barley based on a high-density single-nucleotide polymorphism genetic map. <i>Czech Journal of Genetics and Plant Breeding</i> , 2023, 59, 95-108.	0.4	0
142	Advances in deciphering salt tolerance mechanism in maize. <i>Crop Journal</i> , 2023, 11, 1001-1010.	2.3	7
143	QTL Mapping of Leaf-Related Traits Using a High-Density Bin Map in <i>Brassica rapa</i> . <i>Horticulturae</i> , 2023, 9, 433.	1.2	0