

Supplemental information

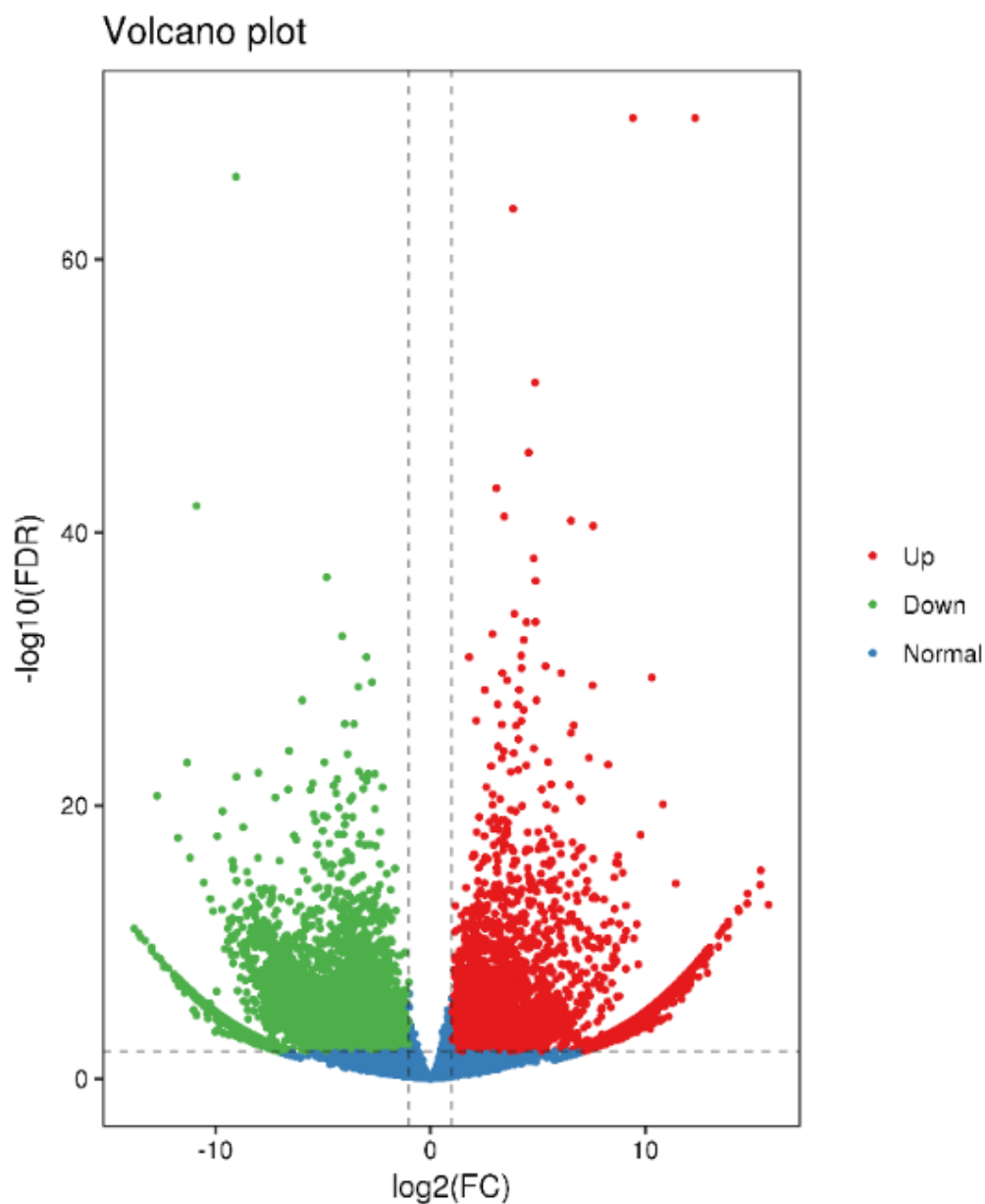


Figure S1 Analysis of differentially expressed genes (DEGs) between resistant (R) and susceptible (S) *Alopecurus japonicus* populations. Volcano plots showing the DEGs between R and S. A value of $q < 0.05$ was used as the threshold for the significance of DEGs. Red dots represent upregulated genes, green dots show downregulated genes, and blue dots indicate genes with no significant differences.

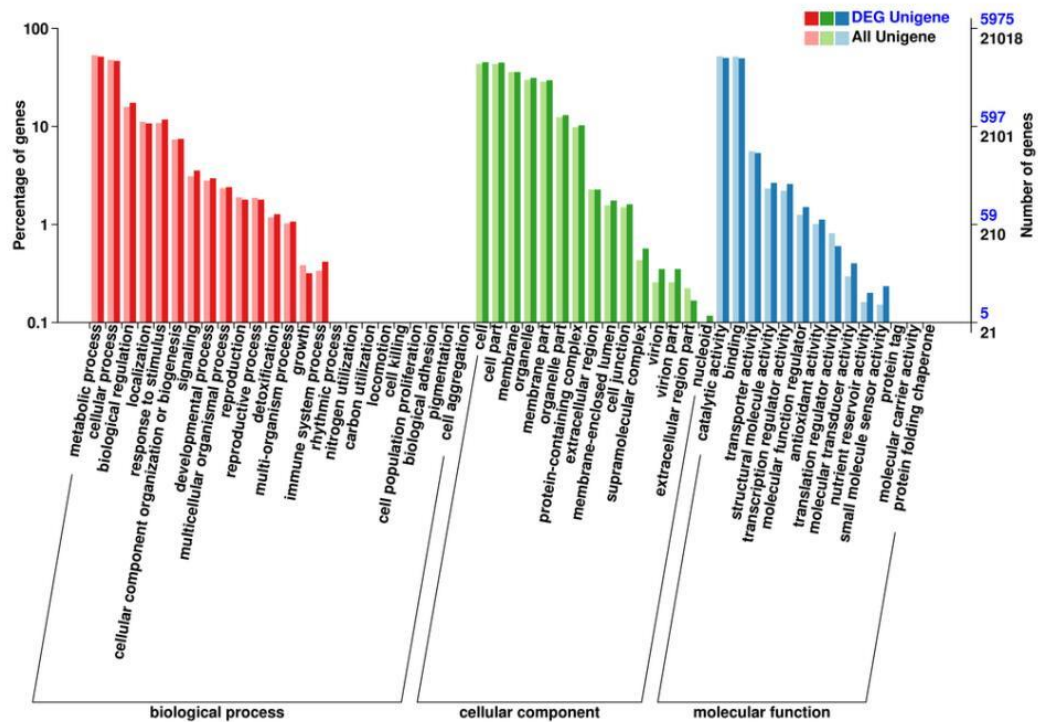


Figure S2 Gene ontology (GO) classifications of *Alopecurus japonicus* all and DEGs according to their involvement in biological process, cellular component, and molecular function.

Table S1 Herbicides and their doses used in dose–response experiments for resistant (R) and susceptible (S) populations in *Alopecurus japonicus*.

Group	Herbicides	Formulation*	Doses (g ai. ha ⁻¹)	
			S	R
APP	Fenoxaprop-P-ethyl	69 g L ⁻¹ EW	0, 7.7625, 15.525, 31.05, 62.1, 124.2	0, 124.2, 248.4, 496.8, 993.6, 1987.2
	Haloxypop-R-methyl	108 g L ⁻¹ EC	0, 32, 64	0, 32, 64
	Quizalofop-p-ethyl	10% EC	0, 52.5, 105	0, 52.5, 105
	Clodinafop-propargyl	15% ME	0, 45, 90	0, 45, 90
CHD	Clethodim	240 g L ⁻¹ EC	0, 48.6, 97.2	0, 48.6, 97.2
	Sethoxydim	12.5% EC	0, 156, 312	0, 156, 312
DEN	Pinoxaden	5% EC	0, 45, 90	0, 45, 90

*EW, emulsion in water; EC, emulsifiable concentrate; ME, micro-emulsion

Table S2 Primers used in ACCase sequence and RT-qPCR analysis in *Alopecurus japonicus*.

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')
ACCase	TTTTCGAAGCTGTAACCA	CTGACCTGAACTTGATCT
UBQ	ACCAGCAGCGTCTCATCTT	GGCTTGGTGTAGGTCTTCTTCT
GT-71C	TATTACTCCACCCGCCAAAG	TGGACTCTGCCATTCTGATG
GT-73C	ACCGAGACAGCAACACAATG	TGACAAAGATTACTGAGCCTGG
GT-75C	AGAGCAGAATCGCCAATCAT	TTTGACGCGGGGAATAGTAG
GT-80B	GTAAACTTGCCTCCCATTTGC	TCCCACGACATCCACTAGAG
GT-83A	TTTCTGTGCTGGCCCTACTT	CACGCCTTATCCTTCCACAT
GT-86A	CCTCTGACGGACCTCTCTTG	GCGATAGCGACGGATTACAT
GT-88B	AGCAGTGGATGAACAAGGTG	ACGCTCCCTTACTCCATTTG
GT-89B	TTTATTACACCCCAGCTCC	CCAAACTCCAATGCCACAAG
GT-91A	TATGGGAGGGAAATGTGCGAG	AGGGACGGAGCCAAGATTTA
GT-92	ATAGCCCAGTGAACCATTAC	TCAACAGCATCGACTCCAAG
ABC-B11	CGGACGTCACCAAGAAAAAT	CCCTCTGAGTGGCTCAAGTC
ABC-B13	TGATTCTCGTTCGCAATCTG	CAGGAGGTTCTGATCCAAA
ABC-B28	GCGCGGTACTATGAGCCTAC	CATGAGCATTGGCAGCTTTA
ABC-C2	CCCCTTTCTCCAATCTCTGTG	TGGATCTTCAATGCTACCGTC
ABC-C10	TTGACGAAGCAACAGAATGC	TGCCCCGAAAAGATAAACAG
ABC-D1	GGCTTTTCCCTTGTACCACA	AGCTTCGTAGCCTTTGGTGA
ABC-E2	GAGGTACTGCGGGAGAACAC	TAGCCCAGTGGACAGCTCTT
ABC-G53	GAAGTCAGCAACGCCTTTTC	TGCTACAACCTGCACCAGAG

Table S3 Sequence annotation of *Alopecurus japonicus* transcriptome.

Public database	Number of genes	Percentage (%)
Annotated in COG	10824	12.03
Annotated in GO	21017	23.36
Annotated in KEGG	20473	22.76
Annotated in KOG	15874	17.65
Annotated in Pfam	19418	21.59
Annotated in Swissprot	22930	25.49
Annotated in nr	35108	39.03
Annotated in at least one database	37723	41.94
Total genes	89951	100.00