

Figure S2

Sequences of the 249 distinct previously-known mature miRNAs used in this study to seed searches for genomic regions that met expression- and secondary structure-based requirements for MIR loci. The set of 249 consists of 189 HC miRNAs and 60 non-HC *Hordeum vulgare* miRNAs.

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>osa-miR156bcfghj-5p_zma-miR156defgil-5p_aly-miR156abcd-5p
UGACAGAAGAGAGUGAGCAC
>osa-miR156b-3p
GCUCACUCUCUAUCUGUCAGC
>osa-miR156cg-3p
GCUCACUUCUCUCUCUGUCAGC
>osa-miR156fhl-3p_zma-miR156dfg-3p
GCUCACUUCUCUUUCUGUCAGC
>osa-miR156j-3p
GCUCGCUCCUCUUUCUGUCAGC
>osa-miR160abc-5p_zma-miR160bg-5p_atr-miR160
UGCCUGGCUCCUGUAUGCCA
>osa-miR160ab-3p_zma-miR160bg-3p
GCGUGCAAGGAGCCAAGCAUG
>osa-miR160c-3p
GCGUGCACGGAGCCAAGCAUA
>osa-miR166a-5p_zma-miR166bd-5p
GGAAUGUUGUCUGGUUCAAGG
>hvu-miR166abc_osa-miR166abcd-3p_zma-miR166a-3p_vvi-miR166d_atr-
miR166cd
UCGGACCAGGCUUCAUUCCCC
>osa-miR166b-5p_zma-miR166a-5p
GGAAUGUUGUCUGGCUCGGGG
>osa-miR166c-5p
GGAAUGUUGUCUGGUCCGAG
>osa-miR166d-5p
GGAAUGUUGUCUGGCUCGAGG
>osa-miR167a-5p_zma-miR167c-5p_aly-miR167a-5p
UGAAGCUGCCAGCAUGAUCUA
>osa-miR167a-3p
AUCAUGCAUGACAGCCUCAUUU
>osa-miR396c-5p_zma-miR396ef-5p_aly-miR396b-5p
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>osa-miR396c-3p_zma-miR396f-3p
GGUCAAGAAAGCUGUGGAAG
>osa-miR156l-5p
CGACAGAAGAGAGUGAGCAUA
>osa-miR166k-5p
GGUUUGUUGUCUGGCUCGAGG
>osa-miR166kl-3p_zma-miR166jkn-3p
UCGGACCAGGCUUCAUCCCU
>osa-miR166l-5p
GGAUUGUUGUCUGGUUCAAGG
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>osa-miR167egi-5p_zma-miR167ehij-5p
UGAAGCUGCCAGCAUGAUCUG
>osa-miR167ei-3p
AGAUCAUGUUGCAGCUUCACU
>hvu-miR168-5p_osa-miR168a-5p_zma-miR168b-5p
UCGCUUGGUGCAGAUCCGGAC
>hvu-miR168-3p_osa-miR168a-3p
GAUCCCGCCUUGCACCAAGUGAAU
>osa-miR169i-5p.2
UGGUGAUAAAGGUGUAGCUCUG
>osa-miR169i-5p.1_zma-miR169j-5p
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>osa-miR169i-3p
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>osa-miR171c-5p
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>hvu-miR171-3p_osa-miR171cde-3p_zma-miR171de-3p_tae-miR171a
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>osa-miR171d-5p
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>osa-miR166h-5p_zma-miR166m-5p
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>osa-miR171i-3p_zma-miR171l-3p
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>zma-miR156i-3p
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>osa-miR444a-3p.2
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>atr-miR8610.2
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>tae-miR5050
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>hvu-miR156ab
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>hvu-miR169
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>hvu-miR171-5p
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>hvu-miR397a

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>hvu-miR444b
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>hvu-miR6187
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>hvu-miR5049d
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>hvu-miR6189
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>hvu-miR6190
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>hvu-miR6191
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>hvu-miR6193
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>hvu-miR5049e
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>hvu-miR6200
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>hvu-miR6201
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>hvu-miR5049f
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>hvu-miR6210
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>hvu-miR6211
CAGAUCAAGACGCUCCGGCA
>hvu-miR6212
AUACAGUUUACAAUGCACGAU
>hvu-miR6213
ACAGAUUGCUACAGACUGGUC
>hvu-miR6214
CGACGACGACGAGCACGACA
>hvu-miR397b-3p
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Figure S3

Sequences of the -5p and -3p miRNA from the 33 MIR loci putative hairpin structures.

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>novel-5p.Cluster_68
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>novel-3p.Cluster_68
GAGGGCGGCGAUAAACAUUUUC
>miR166-3p.Cluster_426.Cluster_3396
UCGGACCAGGCUUCAUUC CCC
>miR166-5p.Cluster_426
GGAAUGUUGUCUGGUUCAAGG
>miR171-5p.Cluster_456
UAUUGGCUCGGCUCACUCAGG
>miR171-3p.Cluster_456
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>novel-5p.Cluster_1155
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>novel-3p.Cluster_1155
ACCUCACAUGCGUCAUUGUUA
>miR827-5p.Cluster_1545
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>miR827-3p.Cluster_1545
UUAGAUGACCAUCAGCAAACA
>miR156-5p.Cluster_1557.Cluster_1973.Cluster_4963
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>miR156-3p.Cluster_1557
GCUCACUGCUCUAUCUGUCACC
>novel-5p.Cluster_1580
ACCCACACCGGUGAUCCCGGCC
>novel-3p.Cluster_1580
CCGGGCGUCAUGGCGGGGAG
>miR171-5p.Cluster_1682
CGGUAAUUGGUGCGGUUCAUC
>miR171-3p.Cluster_1682
UUGAGCCGUGCCAAUAUCACG
>novel-3p.Cluster_1777
UAAGCAGAAACGCCACGGACU
>novel-5p.Cluster_1777
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>miR396-5p.Cluster_1803
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>miR396-3p.Cluster_1803
GUUCAAGAAAGCCCAUGGAAA
>miR393-5p.Cluster_1822
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>miR393-3p.Cluster_1822
CAGUGCGAUCCCUCUGGAAUU
>miR159-3p.Cluster_1875
UUUGGAUUGAAGGGAGCUCUG
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>miR159-5p.Cluster_1875
GAGCUCCUAUCAUCCAAUGA
>miR156-3p.Cluster_1973
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>miR319-5p.Cluster_2046
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>miR319-3p.Cluster_2046
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>novel-3p.Cluster_2558
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>miR5051-3p.Cluster_3388
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CCAGUUUCAAGGUUCAAAGC
>miR167-5p.Cluster_3392.Cluster_3623
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>miR167-3p.Cluster_3392
AGGUCAUGUGGCAGCUUCAUU
>miR166-5p.Cluster_3396
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>miR171-3p.Cluster_3461
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>miR167-3p.Cluster_3623
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>miR167-3p.Cluster_4244
AUCGUGCUGUGACAGUUUCACU
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>novel-3p.Cluster_4290
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>miR156-3p.Cluster_4963
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>miR9660-3p.Cluster_5234
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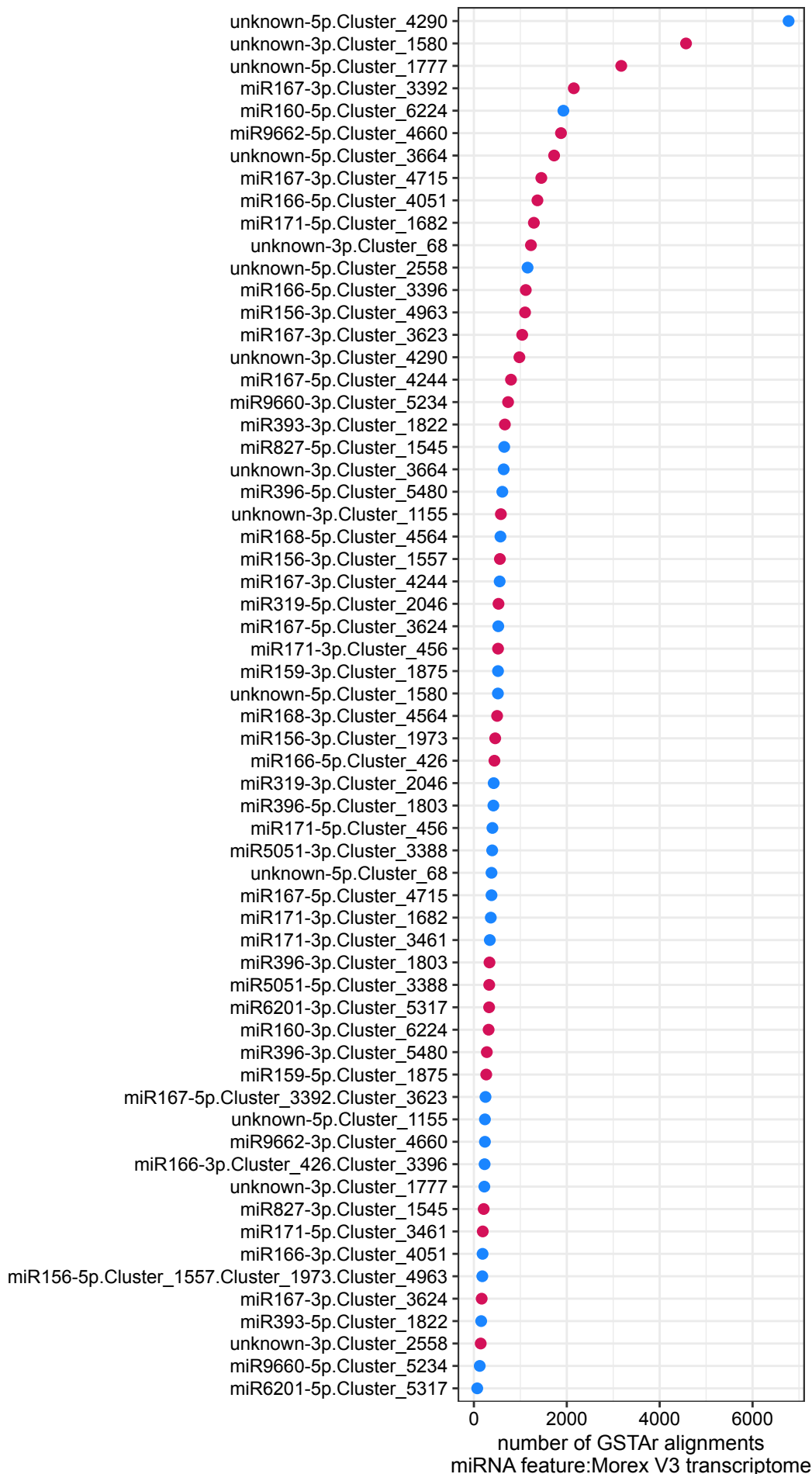


Figure S4
 Dotplot of the number of GSTAr alignments between the 62 distinct miRNA feature sequences and the reverse complement strand of the *Hordeum vulgare* Morex V3 transcriptome. These alignments are used by CleaveLand4 to generate a list of potential target sites for miRNA-directed slicing. Color corresponds to whether the miRNA is the more (major arm) or less (minor arm) abundant feature expressed from the MIR hairpin during malting.

hairpin arm
 ● major arm
 ● minor arm