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Identification of a Novel *FGFRL1* MicroRNA Target Site Polymorphism for Bone Mineral Density in Meta-Analyses of Genome-Wide Association Studies

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ABSTRACT

MicroRNAs (miRNAs) are critical post-transcriptional regulators. Based on a previous genome-wide association (GWA) scan, we conducted a polymorphism in microRNAs' Target Sites (poly-miRTS)-*centric* multistage meta-analysis for lumbar spine (LS)-, total hip (HIP)-, and femoral neck (FN)-bone mineral density (BMD). In stage I, 41,102 poly-miRTSs were meta-analyzed in 7 cohorts with a genome-wide significance (GWS) $\alpha = 0.05/41{,}102 = 1.22\times10^{-6}$. By applying $\alpha = 5\times10^{-5}$ (suggestive significance), 11 poly-miRTSs were selected, with *FGFRL1* rs4647940 and *PRR5* rs3213550 as top signals for FN-BMD (P-value = 7.67×10^{-6} and 1.58×10^{-5}) in gender-combined sample. In stage II *in silico* replication (two cohorts), *FGFRL1* rs4647940 was the only signal marginally replicated for FN-BMD (P-value = 5.08×10^{-3}) at $\alpha = 0.10/11 = 9.09\times10^{-3}$. *PRR5* rs3213550 was also selected based on biological significance. In stage III *de novo* genotyping replication (two cohorts), *FGFRL1* rs4647940 was the only signal significantly replicated for FN-BMD (P-value = 7.55×10^{-6}) at $\alpha = 0.05/2 = 0.025$ in gender-combined sample. Aggregating three stages, *FGFRL1* rs4647940 was the *single* stage I-discovered and stages II- and III-replicated signal attaining GWS for FN-BMD (P-value = 8.87×10^{-12}). Dual-luciferase reporter assays demonstrated that *FGFRL1* 3' untranslated region harboring rs4647940 appears to be hsa-miR-140-5p's target site. In a zebrafish microinjection experiment, dre-miR-140-5p is shown to exert a dramatic impact on craniofacial skeleton formation. Taken together, we provided functional evidence for a novel *FGFRL1* poly-miRTS rs4647940 in a previously known 4p16.3 locus, and experimental and clinical genetics studies have shown both *FGFRL1* and hsa-miR-140-5p are important for bone formation.

INTRODUCTION

Osteoporosis, a common skeletal disease characterized by low bone mineral density (BMD) and deterioration in bone microarchitecture, impaired bone strength and leads to an increased risk of fragility fractures (1). Twin and family studies of BMD have shown that 60-90% of BMD variation can be attributed to genetic factors (2-6).

MicroRNAs (miRNAs) are evolutionarily conserved, endogenous, single-stranded, noncoding RNAs of 18—24 nucleotides in length that regulate gene expression, typically by binding to their complementary sequences located at 3' untranslated regions (UTRs) of target mRNAs by mediating target mRNA degradation and/or protein synthesis repression (7, 8). There are 2,578 mature human miRNA sequences currently listed in miRBase (9, 10). Further, more than 45,000 conserved miRNA target sites within human 3' UTRs have been identified, and more than 60% of human protein-coding genes are under selective pressure to maintain pairing to miRNAs (11). Each miRNA can modulate about 200 target mRNAs (12, 13).

Canonical miRNA targeting is mediated by a perfect Watson-Crick pairing of miRNA's 5' seed region, typically comprising nucleotides 2–7 at 5'-end of an miRNA (12), which determines both target site specificity (14-16) and most of energy change involved in miRNA-mRNA binding (17, 18). Some 6-mer seeds also match to positions 1–6 (19, 20). The miRNA-mRNA binding is determined not only by the thermodynamic property of miRNA, but also by characteristic secondary structure of the target mRNA's 3' UTR containing the miRNA binding site (21), which can be affected by single nucleotide polymorphisms (SNPs)

either inside or outside the miRNA target site that alter miRNA accessibility (13, 22).

Disruptions of miRNA binding sites by SNPs present in 3' UTRs of mammalian genes known as polymorphisms in microRNAs Target Sites (poly-miRTSs), have been clearly documented [e.g., (23-25)]. By *abolishing*/*modifying/creating* miRNA target sites, such SNPs may affect target mRNA/protein expressions, which could modulate diseases risks (23, 26-28).

Although genome-wide association (GWA) studies have been successful in identifying new genes with common variants that exert modest effects on complex traits (e.g., BMD), conventional "hypothesis-free" GWA approach commonly performs 1 million independent association tests, and therefore has strict requirements for controlling occurrences of false positives in such an "unbiased" approach [typically, a genome-wide significance (GWS) threshold of $\alpha = 5\times10^{-8}$ is applied], resulting in severe multiple testing corrections. True positive associations could be missed, particularly in the presence of limited replication resources (29). More than 90% of SNPs collected in the National Human Genome Research Institute (NHGRI) Genome-wide Association Study catalog (30) are located within non-coding regions (31). However, many such non-coding SNPs are simply neglected due to a lack of functional annotations. Therefore, revisiting GWA scans from the perspective of biological knowledge (e.g., miRNA target sites, promoter methylation regions) could discover new genetic variants that are *experimentally testable*. Because the human genome harbors a large number of poly-miRTSs that are potentially important (32, 33), screening exclusively those poly-miRTSs could discover novel regulatory SNPs affecting gene expressions thanks

to a less number of statistical tests based on biological meaning. Because such a functional candidate genomic region association approach may increase type I error rate (i.e., α), to minimize false positives, a multi-stage approach was applied, such that those stage I-selected poly-miRTSs based on a moderate threshold ($\alpha = 5\times10^{-5}$) are subject to stringent stage II and stage III independent replications based on their respective Bonferroni-corrected significance thresholds.

RESULTS

Basic genotype information and phenotype characteristics for the three stages of GWA meta-analysis focusing on poly-miRTSs were presented in Table 1.

Stage I (GWA Discovery)

As shown in Fig. 1, seven cohorts (i.e., OOS, KCOS, COS, FHS, IFS, WHI-AA, and WHI-HIS) were included in this GWA discovery stage. Through genotype imputation using 1KG reference panels, 5,842,825 SNPs (genotyped + imputed) were imputed (34). Because the current study only focused on 41,102 poly-miRTSs of 5,842,825 SNPs, quantile-quantile (Q-Q) plots were generated exclusively for these 41,102 poly-miRTSs for gender-combined (i.e., male and female) sample and female-specific sample, respectively (Supplementary Material, Fig. S1). SNP ranks, names, and P-values for five top signals of 11 stage I-selected poly-miRTS for FN-BMD in gender-combined sample (i.e., rs4647940, rs3213550, rs523200, rs11581122, and rs10739677) and in female-specific sample (i.e., rs4647940, rs1599795, rs10739677, rs3213550, and rs523200) were indicated. After adjusting BMD phenotypes by

five principal components, genomic control (GC) inflation factor (λ_{GC}) was computed for each of lumbar spine (LS)-, total hip (HIP)-, and femoral neck (FN)-BMD traits for stage I 41,102 poly-miRTSs in gender-combined and female-specific samples, respectively, and these λ_{GC}'s were compared with those of 5,842,825 SNPs of the traditional GWA study of Zhang et al. (2014) (34). Overall, because these 41,102 poly-miRTSs were not random SNPs, but rather SNPs with biologically higher prior probabilities, λ_{GC}'s were slightly increased from the range of 1.03–1.04 to the range of 1.033–1.121 (Supplementary Material, Table S1). To protect against an increase in type I error rate (i.e., α), we applied a multi-stage approach such that those stage I-selected poly-miRTSs based on a moderate threshold ($\alpha = 5\times10^{-5}$) are subject to stage II and stage III independent replications based on their respective Bonferroni-corrected significance thresholds. Three poly-miRTSs of two genes attained GWS (i.e., $\alpha = 0.05/41{,}102 = 1.22\times10^{-6}$): *OSBPL2* rs6089342 (P-value = 2.70×10^{-7}) and rs6121978 (P-value = 3.65×10^{-7}) located on chromosome 20q13.33 for LS-BMD in gender-combined sample, and *TMEM135* rs550773 (P-value = 5.93×10^{-7}) located on chromosome 11q14.2 for FN-BMD in gender-combined sample. Another 37 poly-miRTSs had P-values in the range of 1.22×10^{-6} to 5×10^{-5}. Of these 40 top-ranking poly-miRTSs at $\alpha = 5\times10^{-5}$ (suggestive significance), 11 (i.e., *SLC22A2* rs3127592 and rs3127593, *FGFRL1* rs4647940, *CD80* rs1599795, *C6orf97-ESR1* rs9479085, *PRR5* rs3213550, *PTH2R* rs1057392, *FAM125B* rs10739677, *AMAC1* rs17547201, *FAM46C* rs11581122, and *SF1* rs523200, located in 10 gene regions) were selected based on SNP selection criteria: (i) statistical significance threshold (P-value < 5×10^{-5}), (ii) allelic association direction (if ≥ 2 traits are available, same directions for ≥ 6 of 7 cohorts for each trait; if only 1 trait is available, same directions for all 7 cohorts), and (iii) biological

significance [i.e., being an miRNA target site disease-associated SNP (miRTSdSNP) according to Bruno et al. (35)].

Stage II (*in silico* Replication)

At stage II, these above 11 stage I-selected poly-miRTSs were further subject to *in silico* replication in two independent cohorts: (i) RS (*N*=4,904, 57.0% women), and (ii) AOGC (*N*=1,955, 100.0% women). The following SNP selection criteria were applied for stage II SNP selection: (i) statistical significance threshold (Bonferroni-corrected marginal significance, i.e. P-value < 0.1/11 = 9.09×10^{-3}), and (ii) biological significance. Only one poly-miRTS met statistical significance threshold — *FGFRL1* rs4647940, with a P-value = 5.078×10^{-3} for FN-BMD in gender-combined sample (Table 2). At stage I, *FGFRL1* rs4647940 is top signal among these stage I-selected 11 poly-miRTSs for FN-BMD in gender-combined sample. As shown in Supplementary Material, Fig. S1A, for this trait, there was a bigger gap of $-\log_{10}$(P-value) between rs3213550 and rs523200 [Δ-$\log_{10}$(P-value) = $-\log_{10}(1.58\times10^{-5})+\log_{10}(4.76\times10^{-5}) = 0.4789$] than between rs523200 and rs11581122 [Δ-$\log_{10}$(P-value)=$-\log_{10}(4.76\times10^{-5})+\log_{10}(6.66\times10^{-5}) = 0.1459$], and between rs11581122 and rs10739677 [Δ-$\log_{10}$(P-value) = $-\log_{10}(6.66\times10^{-5})+\log_{10}(1.267\times10^{-4}) = 0.2793$]. In addition, as shown in Supplementary Material, Fig. S1B, second top signal for FN-BMD trait in female-specific sample, i.e., rs1599795, had a less significant P-value (i.e., 8.32×10^{-5}) than the P-value of second top signal (i.e., 1.58×10^{-5}) for the same trait in gender-combined sample, i.e. rs3213550. Further, besides rs4647940 (P-value =7.67×10^{-6}), which attained an $\alpha = 5\times10^{-5}$ threshold in gender-combined and female-specific samples, rs3213550 (P-value =1.58×10^{-5})

is the only other poly-miRTS that attained an $\alpha = 5\times10^{-5}$ threshold in gender-combined sample, and an $\alpha = 5.5\times10^{-4}$ (a more relaxed threshold compared to $\alpha = 5\times10^{-5}$) in female-specific sample, respectively. Taken together, at stage II, *PRR5* poly-miRTS rs3213550 exhibited a relatively robust association for FN-BMD at stage I. Although this SNP did not reach stage II marginal significance threshold (P-value = 0.3138 > 9.09×10^{-3}), it is notable that at stage I, it had consistent significant associations for FN-BMD in gender-combined and female-specific samples. PRR5 is a recently identified component of mammalian target of rapamycin complex 2 (mTORC2), which also contains four other components, i.e. mTOR, Rictor, mSin1, mLST8/GL and plays a critical role in bone development and homeostasis (36-38). PRR5 interacts with Rictor in regulating skeletal growth (39). Further, prior biological evidence suggests that rs3213550, which is located in 3' UTR of *PRR5* gene, is a disease-associated miRTSdSNP (35). Therefore, at stage II, based on biological significance of PRR5 and mTORC2 for bone growth and stage I statistical significance for FN-BMD (i.e., a runner up following rs4647940), *PRR5* poly-miRTS rs3213550 was also selected for stage III *de novo* replication.

Stage III (*de novo* Genotyping Replication)

At stage III, the above two stage II-selected poly-miRTSs located in two respective gene regions — *FGFRL1* and *PRR5*, were further subject to replication by *de novo* genotyping in two independent cohorts: (i) KCOSR (*N*=3,923, 57.6% women), and (ii) COSR (*N*=2,740, 57.7% women). In this stage, SNP selection criterion is solely based on Bonferroni-corrected statistical significance threshold (P-value < 0.05/2=0.025) for FN-BMD trait in gender-

combined sample. Only *FGFRL1* rs4647940 met this criterion for FN-BMD (P-value = 7.55×10^{-6}), in gender-combined sample (Table 2).

Stage I+II+III Meta-analysis

Meta-analysis results pooling all available data across stages I, II, and III for two poly-miRTSs — *FGFRL1* rs4647940 and *PRR5* rs3213550 for FN-BMD in gender-combined sample revealed that *FGFRL1* rs4647940 (P-value = 8.87×10^{-12}) was the only poly-miRTS that attained both the current study's GWS (i.e., P-value < 1.22×10^{-6}) and conventional GWS (i.e., P-value < 5×10^{-8}) (Table 2). Stage I's second top signal for FN-BMD of 11 stage I-selected poly-miRTSs — *PRR5* rs3213550 (P-value = 1.17×10^{-5}) did not attain the current study's reduced GWS. Taken together, the current study has identified and robustly replicated *FGFRL1* rs4647940 as the only signal associated with FN-BMD in gender-combined sample. As shown in forest plot of stage I+II+III meta-analysis of poly-miRTS, *FGFRL1* rs4647940 for FN-BMD in gender-combined sample (Fig. 2), not only the overall meta-analysis across these 11 cohorts attained conventional GWS (i.e., P-value < 5×10^{-8}), but also all replication cohorts of stage II (AOGC and RS) and stage III (COSR and KCOSR) have same directions of allelic associations as ≥ 6 out of 7 stage I cohorts.

Regional Association Plots and Linkage Disequilibrium (LD) r^2 Plots

A regional association plot of traditional GWA meta-analysis results for FN-BMD trait of *FGFRL1* poly-miRTS rs4647940 and those stage I SNPs in the ±100-kb flanking regions, particularly intergenic rs6827815 (currently considered as located within *IDUA* gene region;

http://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?rs=6827815) of Zhang et al. (34) and *IDUA* rs3755955 of Estrada et al. (40), were shown in Fig. 3A, with a zoom-in view of the middle part (i.e., ±27-kb flanking regions) spanning these three SNPs shown in Fig. 3B. In order to delineate a high-resolution LD structure for 4p16.3 locus encompassing these three SNPs, an LD r^2 plot for 58 SNPs (from rs11731377 to rs13114658 spanning 80.744-kb) was generated for OOS (Fig. 4A) and KCOS (Fig. 4B) cohorts, respectively, both of which are of Caucasian ancestry. This entire region is partitioned into left and right haplotype blocks: block 1 (left) extends from rs11731377 to rs4647940 (30 SNPs), and block 2 (right) extends from rs13137819 and rs13114658 (28 SNPs) in each cohort. All these three SNPs (i.e., rs3755955, rs6827815, and rs4647940) are located within block 1 in both cohorts, such that rs4647940 is in a *moderately high* LD with both rs3755955 [r^2 = 0.649 and 0.842 for OOS (N=987) and KCOS (N=2,250), respectively] and rs6827815 (r^2 = 0.702 and 0.857 in OOS and KCOS, respectively).

Conditional Meta-analysis

In rs3755955-rs6827815-rs4647940 region, because rs6827815 (distance: 20.946 kb) is physically closer to rs4647940 than rs3755955 (distance: 25.977 kb), two conditional analyses were performed: (i) rs4647940 conditional on rs6827815: under a fixed-effects model, P-value = 1.35×10^{-3} for FN-BMD in stage I gender-combined sample, which remains to be significant at $\alpha = 5.00\times10^{-3}$, suggesting rs4647940 and rs6827815 represent distinct signals at this chromosomal locus, and (ii) rs4647940 conditional on both rs3755955 and rs6827815: under a fixed-effects model, P-value = 1.33×10^{-3} for FN-BMD in stage I gender-

combined sample.

Predicted RNA Secondary Structures of *FGFRL1* 3' UTR Harboring rs4647940

The secondary structure of a 121-bp (i.e., rs4647940 with ±60-bp flanking regions) *FGFRL1* 3' UTR segment carrying either wild-type (WT) (i.e., "C") or mutant (MUT) (i.e., "G") allele of rs4647940 was predicted by RNAfold. Difference of minimum free energies (MFEs) between folding patterns for MUT and WT alleles is $\Delta MFE = MFE_{MUT} - MFE_{WT}$ = (-34.30) - (-34.10) = -0.20 kcal/mol. Therefore, the secondary structure of WT allele such that the SNP is located in a stem connected to a terminal loop and an internal loop (Fig. 5A) is less stable than that of MUT allele such that the SNP is located in a stem connected to two internal loops (Fig. 5B). Therefore, this SNP causes a change of RNA secondary structure of *FGFRL1* 3' UTR, potentially affecting miRNA target site accessibility.

Evolutionary Conservation of *FGFRL1* 3' UTR Harboring rs4647940

Multiple sequence alignment of orthologous sequences of *FGFRL1* 3' UTR segment encompassing rs4647940 from human, chimpanzee, gorilla, gibbon, orangutan, and rhesus macaque species showed that this SNP corresponds to a highly conserved nucleotide (Fig. 6), which could be under high selective pressures during evolution, and therefore is likely functional.

Predicted miRNAs that Potentially Bind to *FGFRL1* rs4647940

Based on predictions of four *in silico* tools (i.e., MicroSNiPer, MirSNP, RegRNA 2.0, and

TargetScan), 13 miRNAs could target *FGFRL1* rs4647940 (Table 3).

Differential Expressions of Mouse miRNA Orthologs in Bone during Skeletal Development

Based on miRNA-seq study of a mouse model for age-related osteoporosis (41), i.e., mmu-miR-140-5p, mmu-miR-143-5p, mmu-miR-34c-5p, mmu-miR-106b-3p, mmu-miR-30c-2-3p, mmu-miR-92a-2-5p, and mmu-miR-17-3p, were differentially expressed between 25-m versus 2-m, 8-m versus 2-m, and 25-m versus 8-m time points in bone (Table 4), with their corresponding human orthologs highlighted in Table 3. Two of them, i.e., mmu-miR-34c-5p and mmu-miR-140-5p, not only were significantly differentially expressed across all three comparisons, but also had same directions of fold changes (FCs) (i.e., consistently down-regulated from 2, to 8 and to 25 months). Most prominently, mmu-miR-140-5p had greatest FCs (5.88-, 4-, and 1.47-folds of down-regulation) among these 7 miRNAs, which attained highest statistical significance levels for 25-m versus 2-m (P-value = 9.15×10^{-91}) and 8-m versus 2-m (P-value = 9.63×10^{-82}) comparisons. Because hsa-miR-140-5p is highly conserved during evolution across a wide spectrum of species (Supplementary Material, Fig. S2), such that both mmu-miR-140-5p and dre-miR-140-5p have same sequences as hsa-miR-140-5p, only hsa-miR-140-5p was chosen for experimental validation.

***In vitro* Dual Luciferase Reporter Assay Results**

Human *FGFRL1* gene, which resides in chromosome 4p16.3, consists of six exons. Exon 1 contains 5’ UTR followed by a coding sequence for signal peptide (SP). Exons 2, 4, and 5

encode immunoglobulin (Ig)-like C2-type 1, Ig-like C2-type 2, and Ig-like C2-type 3 domains respectively. Exon 6 encodes transmembrane (TM) domain, cytoplasmic tail, and 3' UTR. Exon-intron structure of *FGFRL1* is highly conserved based on previous phylogenetic analysis (42), and rs4647940 is located in the 3' UTR, which is a part of exon 6 (Fig. 7). *FGFRL1* rs4647940 WT allele (i.e., "C") is complementary with the third position (underlined) of hsa-miR-140-5p 5' seed region (i.e., 5'-CAGUGG-3'), whereas MUT allele (i.e., "G") causes a mismatch. In dual luciferase reporter assay, a negative control (NC) miRNA mimic was co-transfected with an empty vector, or a vector carrying *FGFRL1* 3' UTR WT insert, or a vector carrying *FGFRL1* 3' UTR MUT insert. In human embryonic kidney (HEK) 293 cells, for NC miRNA co-transfection, compared with an empty vector as baseline, a vector carrying either *FGFRL1* 3' UTR WT insert (-12.15±4.83%, P-value = 0.031) or *FGFRL1* 3' UTR MUT insert (-18.33±5.66%, P-value = 8.88×10^{-3}) demonstrated significant inhibitions of respective relative luciferase activities, but no statistically significant difference was observed between 3' UTR WT and MUT inserts (P-value = 0.20) (Fig. 8). For hsa-miR-140-5p co-transfection, compared with an empty vector, a vector carrying either *FGFRL1* 3' UTR WT insert (-45.07±3.90%, P-value = 4.19×10^{-7}) or *FGFRL1* 3' UTR MUT insert (-48.20±5.95%, P-value = 1.06×10^{-5}) exhibited significant inhibitions of relative luciferase activities. No statistically significant difference was detected between 3' UTR WT and MUT inserts (P-value = 0.58). Nonetheless, relative luciferase activities differed significantly between NC miRNA and hsa-miR-140-5p for both 3' UTR WT insert (P-value = 1.33×10^{-5}) and 3' UTR MUT insert (P-value = 0.0051), indicating that the *FGFRL1* 3' UTR insert bearing rs4647940 is a potential target site for hsa-miR-140-5p.

In vivo Zebrafish Microinjection Experiment Results

Three independent miRNA microinjection experiments were performed, with similar morphological phenotype results obtained. Data from a representative experiment of them were shown in Fig. 9. *N*=11, 14 and 14 zebrafish embryos were respectively included in none-injection control (left panel), NC miRNA-injected (middle panel), and dre-miR-140-5p-injected (right panel) groups. Morphological phenotypes were obtained at two time points — 5 days post-fertilization (dpf) and 7 dpf, respectively. Fig. 9a-f compared zebrafish skeletal morphologies across none-injection control, NC miRNA-injected, and dre-miR-140-5p-injected groups at 5 dpf, whereas Fig. 9g-o compared skeletal morphologies across them at 7 dpf, respectively. At 5 dpf, the body length of dre-miR-140-5p-injected larva appeared shorter (in example shown, 22.61%) compared to either none-injection control, or NC miRNA-injected larva, which had same lengths (Fig. 9a-c). A similar pattern of body length comparisons was observed at 7 dpf (Fig. 9g-i). Further, compared to none-injection control and NC miRNA-injected larvae at 5 dpf (Fig. 9d and j) and 7 dpf (Fig. 9e and k), dre-miR-140-5p-injected larvae at 5 dpf (Fig. 9f**)** and 7 dpf (Fig. 9l) showed *somewhat reduced* Meckel's cartilage (denoted by "m") and *almost absent* ceratobranchial cartilages (denoted by "cb1-5"). Significant skeletal morphological differences were detected between none-injection control/NC miRNA-injected and dre-miR-140-5p-injected larvae at 7 dpf (Fig. 9m-o). Florescent images demonstrated that notochord (denoted by "nc") and parasphenoid (denoted by "ps") were present in none-injection control and NC miRNA-injected groups (Fig. 9m and n), but were absent in dre-miR-140-5p-injected group (Fig. 9o). Overall, skeletal

malformations were observed in 0/14 (0.00%), 2/14 (14.29%), and 5/11 (45.45%) for none-injection control, NC miRNA-injected, and dre-miR-140-5p-injected groups, respectively. Although the percentage of dre-miR-140-5p-injected group (45.45%) was not statistically different from that of NC miRNA-injected group (14.29%) [P-value (two-sided) = 0.18], the percentage of none-injection group (0.00%) was significantly different from that of dre-miR-140-5p-injected group (45.45%) with a P-value (two-sided) = 0.0087. Further, none-injection control + NC miRNA-injected groups compared with dre-miR-140-5p-injected group gives a significant P-value (two-sided) = 0.012.

DISCUSSION

A traditional GWA meta-analysis approach has been widely applied for discovering novel genetic loci for common human diseases. To date, such an approach has identified a large number of genetic loci underlying disease susceptibilities (43-45). However, in traditional GWA studies, the significantly associated variants are seldom those that play functional roles in phenotypic determination, but are instead in high LD with a causal variant. Consequently, the identification of causal variants is important in understanding molecular mechanisms underlying disease pathogenesis, such that additional well-focused intensive studies (e.g., fine mapping) are required to complement traditional GWA studies to identify disease-causing alleles. Because a functional candidate genomic region association approach focusing exclusively on SNPs with higher prior probabilities for biological functions may increase the type I error rate (i.e., α), the best strategy to differentiate true positives from false positives is to perform replication studies in independent samples. Therefore, focusing exclusively on

those poly-miRTSs, a multi-stage approach, which typically includes a GWA discovery stage followed by *in silico* and *de novo* genotyping replication stages, is a conservative strategy to identify novel functional SNPs located in non-coding 3' UTRs potentially undetected by previous traditional GWA meta-analysis studies due to an overly strict statistical significance threshold. Such a "*hybrid*" approach combines *strengths* of both a *multi-stage GWA meta-analysis approach* and a *hypothesis-driven approach*. Johnson et al. (29) employed a similar multi-stage strategy of the current study for blood pressure and hypertension traits focusing exclusively on 6,683 SNPs located within 60-kb of each of 30 candidate gene regions encoding known anti-hypertensive drug targets in stage I. Two novel SNPs, i.e., *ADRB1* rs1801253 [for systolic blood pressure (SBP) and diastolic blood pressure (DBP)], and *AGT* rs2004776 (for DBP) were identified and replicated, which were missed by their previous traditional GWA scan (i.e., CHARGE Consortium) (46). Another study by Xu et al. (2014) (47) also applied a functional candidate gene association approach for coronary artery disease (CAD) that revealed two novel regulatory SNPs (rs7842 and rs4400266) located respectively in *C3AR1* and *C6* genes to be associated with CAD, which were missed by previous traditional GWA scans.

By interrogating exclusively 41,102 poly-miRTSs collected from PolymiRTS database (48, 49), the probability of detecting functional poly-miRTSs causally linked with BMD traits has significantly increased. A total of 11 stage I-selected poly-miRTSs (corresponding to 10 chromosomal loci) were selected based on (i) statistical significance threshold, (ii) allelic association direction, and (iii) biological significance. In stage II *in silico* replication,

FGFRL1 rs4647940 (P-value = 5.078×10^{-3}) met a relatively stringent statistical significance threshold (i.e., P-value < 9.09×10^{-3}) for FN-BMD in gender-combined sample. Because *FGFRL1* rs4647940 is top signal among these stage I-selected 11 poly-miRTSs for FN-BMD in gender-combined sample, in order to avoid missing potentially functional poly-miRTSs for FN-BMD trait, among these 11 stage I-selected poly-miRTSs, we also included stage I's second top signal for FN-BMD in gender-combined sample, i.e., *PRR5* poly-miRTS rs3213550 (P-value: 1.58×10^{-5}), which is a disease-associated miRTSdSNP, although this SNP did not reach stage II significance threshold. In stage III, based on Bonferroni-corrected statistical significance threshold (P-value < 0.05/2=0.025) for FN-BMD trait in gender-combined sample, only *FGFRL1* rs4647940 attained statistical significance (Fig. 1). In Zhang et al. (34), 33 stage 1-selected SNPs [i.e., 10 SNPs reaching GWS (i.e., $\alpha = 5.00\times10^{-8}$) and 23 SNPs reaching borderline significance (i.e., $\alpha = 1.00\times10^{-6}$)] corresponding to 33 chromosomal loci were selected and subjected to stage 2 *in silico* analysis. None of the current study's 11 stage I-selected poly-miRTSs overlap with these 33 stage 1-selected SNPs of previous traditional study. Four chromosomal loci [i.e., 2q33 (*PTH2R*), 4p16.3 [*intergenic* (currently *IDUA*)], 6q25.1 (*C6orf67–ESR1*) and 20q13.33 (*OSBPL2*)] were shared in common, but were represented by totally different SNPs. Of these 33 stage 1-selected chromosomal loci, 13 previously reported and 2 novel loci reached conventional GWS (34). Of them, only chromosome 4p16.3 [*intergenic* (currently *IDUA*)] was commonly shared with the current study, but was represented by a totally different gene, i.e., *FGFRL1*. Estrada et al. (40) performed a traditional multi-stage GWA scan that studied ~ 2.5 million autosomal + chromosome X SNPs in 17 cohorts (*N*=32,961) in stage 1 (GWA discovery). Based on SNP

selection criteria: (i) P-value < 5×10^{-6} (both unconditional and conditional analysis) for autosomal SNPs and (ii) P-value < 5×10^{-5} for Chromosome X SNPs, 96 SNPs (87 autosomal SNPs and 9 chromosome X SNPs) corresponding to 83 chromosomal loci were subject to stage 2 *de novo+in silico* replication in 34 cohorts (*N*=50,933). None of the current study's 11 stage I-selected poly-miRTSs overlap with these 96 stage 1-selected SNPs of Estrada et al. (40), but three chromosomal loci [4p16.3 (*IDUA*), 6q25.1 (*C6orf67–ESR1*) and 11q13.1 (*SCYL1*)] were shared in common, which were represented by totally different SNPs, and at 4p16.3 and 11q13.1, were represented by totally different genes. At stage 2 of Estrada et al. (40), 64 [54 chromosomal loci containing 56 gene loci (40)] of these 96 stage 1-selected SNPs attained conventional GWS (i.e., $P < 5\times10^{-8}$, stages 1+2-only), 16 (14 chromosomal loci) of which were further replicated in stage 3 for association with fractures ($P < 5\times10^{-4}$, stage 3-only) in 50 fracture cohorts (*N*=133,460). Of these 54 BMD-associated chromosomal loci that attained conventional GWS, only 4p16.3 (*IDUA*) was commonly shared with the current study, but was represented by a totally different gene, i.e., *FGFRL1*. None of those 16 BMD- and fracture-associated loci were shared with the current study. Taken together, *FGFRL1* rs4647940 is a novel poly-miRTS for FN-BMD that has been discovered in stage I and subsequently replicated in stages II and III of the current study, respectively. If *not focusing exclusively* on poly-miRTSs in stage I, this *FGFRL1* rs4647940 (P-value = 7.67×10^{-6} for FN-BMD at stage I) would *not have been discovered at all* — e.g., this potentially functional SNP *did not reach stage 1's borderline significance threshold* $\alpha = 1.0\times10^{-6}$ in Zhang et al. (34), and therefore did not survive to be further validated in stages 2 and 3. Therefore, by using a more relaxed statistical significance threshold (i.e., 5×10^{-5}, because only

41,102 poly-miRTSs were examined), this SNP was detected in stage I of the current study, and upon replications in subsequent stages II and III, reached GWS (P-value = 8.87×10^{-12}) in stage I+II+III (*N*=24,662). A meta-analysis of rs4647940 conditional on rs3755955 remained suggestively significant (P-value = 1.35×10^{-3}) for FN-BMD in stage I gender-combined sample at $\alpha = 5.00\times10^{-3}$, whereas a meta-analysis of rs4647940 conditional on both rs3755955 and rs6827815: was also significant (P-value = 1.33×10^{-3}) for FN-BMD in stage 1 gender-combined sample.

For *FGFRL1* rs4647940, based on predictions by four *in silico* programs, 13 human miRNAs could potentially bind to this poly-miRTS site (Table 3). Of them, according to miRNA-seq data (41), mouse orthologs of hsa-miR-17-3p, hsa-miR-30c-2-3p, hsa-miR-34c-5p, hsa-miR-92a-2-5p, hsa-miR-106b-3p, hsa-miR-140-5p and hsa-miR-143-5p appear to be *differentially expressed* at different time points during development in a mouse model of age-related osteoporosis (Table 4). Of them, hsa-miR-140-5p appeared to exhibit *greatest magnitudes* of *differential expressions* among comparisons of three time points (i.e., 2-m, 8im, and 25-m), and *highest levels of statistical significance* for 25-m versus 2-m and 8-m versus 2-m comparisons (Table 4). To experimentally test the potential biological role of *FGFRL1* poly-miRTS rs4647940, both *in vitro* and *in vivo* functional studies were conducted. First, luciferase activity assay results showed that, when co-transfected with hsa-miR-140-5p, reporter construct containing either *FGFRL1* 3' UTR WT insert or *FGFRL1* 3' UTR MUT insert repressed luciferase activity to similar extents (Fig. 8). These experimental findings are concordant with a regulatory role of hsa-miR-140-5p in modulating *FGFRL1* expression by

binding to this 3' UTR segment harboring rs4647940, causing a pronounced inhibition of luciferase activity. As indicated in both Fig. 7 and Supplementary Material, Fig. S2, hsa-miR-140-5p contains a 6-mer 5' seed region (predicted by MicroSNiPer) that is complementary to *FGFRL1* rs4647940 SNP site. Because miRNAs with 6-mer seed regions typically modestly down-regulate their respective mRNA targets (50), these luciferase activity assay results are in agreement with the notion that *FGFRL1* poly-miRTS rs4647940 is located in 5' seed region binding site of has-miR-140-5p. Because an miRNA's 5' seed sequence plays an important role in target recognition and binding, a 3' UTR polymorphism located in an miRNA's 5' seed region binding site, e.g. *FGFRL1* rs4647940, may have a higher probability of functional importance, compared with a 3' UTR polymorphism located in that miRNA's 3' mismatch tolerant region (MTR) binding site.(51) We further tested whether hsa-miR-140-5p plays a significant role in skeletal formation *in vivo*. Nakamura et al. (52) demonstrated that *Mir140*$^{-/-}$ mice had shortened endochondral bones. In another *Mir140*$^{-/-}$ mouse model, a mild skeletal phenotype was observed postnatally, with reduced stature and lower body weight, as well as craniofacial deformities characterized by shorter snout and domed skull (53). In a previous zebrafish model, *mir140* is found expressed in cartilage of pharyngeal arches and in head skeleton (54). Further, Eberhart et al. (2008) (55) observed that dre-miR-140-5p-injected zebrafish exhibited craniofacial skeletal defects. The current study's *in vivo* zebrafish miRNA microinjection experiments gave rise to similar results, demonstrating that dre-miR-140-5p-injected group had a significantly higher percentage of abnormal craniofacial skeletal formation compared with none-injected control + NC miRNA-injected groups.

Fibroblast growth factor (FGF) signaling pathway is pivotal in a variety of developmental processes, including cartilage formation (56) and bone growth (57). *FGFRL1* is *FGFR* gene family's fifth member, and mutations of *FGFR1- FGFR4* cause skeletal disorders (e.g., craniosynostosis syndromes and chondrodysplasias) (58). Interestingly, *FGFRL1* orthologous genes in species ranging from cnidarians to bilaterians are linked with other FGF signaling pathway members within a physical distance < 10 Mb (42). For instance, in sea urchin, *Fgfrl1* is closely linked to *Fgfr1*. Human *FGFRL1* is located in close proximity to *FGFR3* (42). The fact that *FGFRL1* is physically linked to other FGF signaling pathway genes throughout evolution is suggestive of *FGFRL1*'s functional importance in this biological pathway, and likely, also in bone formation: (i) *FGFRL1* is expressed in skeletal tissues shown by Northern blotting and *in situ* hybridization (59); (ii) a depletion of zebrafish *fgfrl1a* and *fgfrl1b* results in a craniofacial phenotype (60); (iii) $Fgfrl1^{-/-}$ mice exhibited hypoplasia of all skeletal elements, including shortened axial and appendicular skeletons, malformed vertebrae, small pelvic girdle and small rib cage (61); and (iv) in humans, as in zebrafish and mice, *FGFRL1* could be implicated in craniofacial formation during embryogenesis, such that *FGFRL1* deletions or frameshift mutation result in craniofacial malformations (62-64).

The current study's *in vitro* and *in vivo* experimental validation results, combined with findings of previous functional studies of *FGFRL1* and hsa-miR-140-5p as well as clinical genetic studies of *FGFRL1* gene mutations, provided *strong evidence* that *FGFRL1* and hsa-miR-140-5p, which are evolutionarily conserved, play significant biological roles during skeletogenesis. *FGFRL1* rs4647940, attaining conventional GWS for FN-BMD in the current

study, could change hsa-miR-140-5p's 5' seed region binding site located in *FGFRL1*'s 3' UTR, which could then modulate *FGFRL1*'s mRNA expression level that can affect bone formation.

Our study has several limitations. First, the luciferase activity assay's results demonstrated that *FGFRL1* 3' UTR WT and MUT inserts could both bind to hsa-miR-140-5p rather than NC miRNA, but MUT allele did not appear to significantly de-repress luciferase activity in comparison with WT allele. However, rs4647940 may only have a relatively moderate effect on *FGFRL*1 mRNA-has-miR-140-5p binding, because 5' seed region of has-miR-140-5p is a 6-mer. Further, multiple factors could affect results of luciferase activity assay, such as insert length, cell line, and transfection conditions. Besides hsa-miR-140-5p, *FGFRL1* rs4647940 could affect other bone metabolism-related miRNAs' binding sites, e.g., hsa-miR-17-3p and hsa-miR-92a-2-5p (Table 3) predicted by RNAfold. Second, *in vivo* experiment in zebrafish model showed that dre-miR-140-5p microinjection results in a dramatic effect on bone development (Fig. 9), but whether such an effect was mediated by its binding with a target site located on 3' UTR of either *fgfrl1a* or *fgfrl1b* in zebrafish remains to be elucidated. Nevertheless, results of mouse miRNA-seq (Table 4) and zebrafish microinjection (Fig. 9) experiments unequivocally demonstrated a critical role of miR-140-5p in bone growth. Given that *FGFRL1* rs4647940 is possibly located in a 5' seed region binding site of miR-140-5p based on *in vitro* luciferase activity assay results (Fig. 7), *FGFRL1* rs4647940 is likely a regulatory variant causally linked with BMD.

Taken together, through a combination of a three-stage, poly-miRTS-centric GWA meta-analysis and functional experiments, *FGFRL1* poly-miRTS rs4647940 is significantly associated with FN-BMD trait, attaining conventional GWS. Based on abundant data accumulated from *in vitro* and *in vivo* experimental and clinical genetics studies, *FGFRL1* rs4647940 is likely to play an important role in modulating expressions of *FGFRL1* during skeletogenesis, and further functional characterizations of this SNP in bone metabolism is deserved.

MATERIALS AND METHODS

A flow chart outlining steps of the current study is depicted in Fig. 1. Detailed information on study participants, phenotype measurement and modeling, DNA genotyping, quality control (QC), and genotype imputation for the three-stage GWA meta-analysis is provided in Supplementary Materials and Methods.

Association Analysis

In the current study, only at stage I (7 GWA cohorts), gender-specific (i.e., male- and female-specific) and gender-combined (i.e., male and female) analyses were performed. Nonetheless, only 4 stage I's GWA cohorts (i.e., OOS, KCOS, COS, and FHS) contain males (Table 1), such that male-specific sample size was much smaller than female-specific sample size, giving rise to less statistical power. Therefore, same as in the traditional GWA scan (34), Q-Q plot was generated only for female-specific and gender-combined samples, respectively. At stages II and III, because there were two cohorts at each stage, only gender-combined analyses were performed. Association

tests at each stage are elaborated as follows. In stage I, associations of 41,102 directly-typed or imputed poly-miRTSs with LS-, HIP-, and FN-BMD traits were tested under an additive genetic model for each GWA cohort. Specifically, for five *population-based* samples — OOS, KCOS, COS, WHI-AA, and WHI-HIS, associations were examined by fitting a linear regression model by MACH2QTL (http://www.sph.umich.edu/csg/abecasis/MACH/download/), in which an allele dosage was used as a predictor of phenotype. For two family-based samples — FHS and IFS, a mixed linear model was applied that took into consideration the effect of genetic relatedness within each pedigree (65). In stage II, association analyses in RS sample were performed by MACH2QTL implemented by GRIMP (66). Imputation and association analyses in KoGES were performed by IMPUTE v2 (67) and PLINK (68). Detailed statistical methods for association analyses of HIP-, LS-, and FN-BMD traits in AOGC sample were presented previously by Duncan et al. (2011). Briefly, for HIP-BMD, association analysis for imputed SNPs was performed using an additive genetic model including four EIGENSTRAT eigenvectors by MACH2DAT (69), accounting for uncertainties in imputed genotype data by weighting genotypes by their posterior probabilities. For LS- and FN-BMD, Z-transformed residual BMD scores (in g/cm^2) were generated for the entire AOGC cohort after adjusting for age, age^2, weight, and center of BMD measurement. An association test developed by Kung et al. (2010) (70) was applied to account for selections of extreme samples. In stage III, association tests were carried out using PLINK (68) for each study.

Meta-analysis

As described by Zhang et al. (2014) (34), a p-value based meta-analysis was used in METAL

(http://www.sph.umich.edu/csg/abecasis/metal/) (71), weighted by square root of sample size. *Cochran*'s Q statistic and I^2 were computed as measures of between-study heterogeneity. Random-effect meta-analyses were performed for those poly-miRTSs with Q statistic P-value < 0.05 or I^2 value > 50% by applying the "rmeta" package (http://cran.r-project.org/web/packages/rmeta/index.html). In stage 1, meta-analysis of a given SNP conditional on one or two other SNPs in LD was also performed by GCTA version 1.20 (http://www.complextraitgenomics.com/software/gcta/massoc.html) (72).

Regional Association Plot and Linkage Disequilibrium (LD) r^2 Plot

Regional association plots were generated by applying LocusZoom (http://csg.sph.umich.edu/locuszoom/) (73). LD r^2 Plots were generated by Haploview (74, 75) for 58 SNPs at chromosome 4p16.3 for OOS and KCOS cohorts, respectively.

Poly-miRTSs in miRNA Target Sites

The poly-miRTS-*centric* GWA meta-analysis focuses exclusively on 41,102 poly-miRTSs in stage I, in contrast to 5,842,825 SNPs in stage 1 of previous traditional GWA scan (34). Detailed information on poly-miRTS selection is presented in Supplementary Material, Text S1.

Computational Predictions of RNA Secondary Structures

The miRNA-mRNA hybridization is a two-step process such that an miRNA first binds to a short accessible region of its target mRNA, and then, the target mRNA's secondary structure

unfolds as the miRNA completes its binding to target site (76). The secondary structure of an mRNA can influence its accessibility to miRNA (77). In order to assess potential impacts of WT and MUT alleles on the secondary structure of the 3' UTR of *FGFRL1*, a 121-bp *FGFRL1* 3' UTR segment carrying either WT or MUT allele of rs4647940 were predicted by RNAfold from the Vienna RNA package (http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi) (78, 79) based on MFE algorithm with default parameters.

Multiple Sequence Alignment and Sequence Logo

Polymorphisms located at evolutionarily conserved nucleotides are likely to be of greater functional significance than those located at evolutionarily divergent nucleotides. To further bioinformatically assess functional significance for *FGFRL1* rs4647940, cross-species comparisons of orthologous sequences of *FGFRL1* 3' UTR segment encompassing rs4647940 from six species, i.e., human, chimpanzee, gorilla, gibbon, orangutan, and rhesus macaque, was performed by ClustalX version 1.81 (80) with default parameters. A Sequence Logo corresponding to a middle 15-bp DNA segment was generated using WebLogo online program (81).

***In Silico* Predictions of miRNAs that Bind to a Poly-miRTS**

Human miRNAs that could bind to *FGFRL1* rs4647940 were predicted by four online tools: (i) MicroSNiPer (http://cbdb.nimh.nih.gov/microsniper) (82), (ii) MirSNP (http://cmbi.bjmu.edu.cn/mirsnp) (83), (iii) RegRNA 2.0 (http://regrna2.mbc.nctu.edu.tw/) (84, 85), and (iv) TargetScan (http://www.targetscan.org/) 6.2 (11, 16, 86).

In Vitro Dual Luciferase Reporter Assays

To assess whether *FGFRL1* 3' UTR segment containing either WT or MUT allele of rs4647940 could bind to hsa-miR-140-5p *in vitro*, a pmirGLO dual-luciferase miRNA target expression vector harboring *FGFRL1* 3' UTR WT or MUT inset was constructed, which was subsequently transfected into HEK 293 cells. Details about cloning and transfection, as well as luciferase activity assays are presented in Supplementary Material, Text S1.

In vivo Zebrafish Microinjection Experiments

To assess an *in vivo* role of hsa-miR-140-5p in bone formation, zebrafish microinjection experiments were performed, with each experiment consisting of three groups: (1) a none-injection control group, (2) an NC miRNA microinjection group, and (3) a dre-miR-140-5p microinjection group, respectively. Detailed experimental procedures were described in Supplementary Material, Text S1. These procedures were repeated three times, and microscope image data of morphological phenotypes from a representative experiment at 5 dpf and 7 dpf were obtained from each respective group.

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SUPPLEMENTARY MATERIAL

Supplementary Material is available at *HMG* online.

Conflict of interest Statement. None declared.

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FIGURE LEGENDS

Figure 1. A flow chart of the poly-miRTS-*centric* three-stage GWA meta-analysis and experimental validation. Abbreviations: GWA, genome-wide association; SNP, single nucleotide polymorphism; DB, database; poly-miRTSs, polymorphisms in microRNAs Target Sites; study name abbreviations are shown in footnote of Table 1

Figure 2. A forest plot of *FGFRL1* rs4647940 for FN-BMD trait for stage I+II+III for gender-combined (i.e., Male and Female) Cohort. Abbreviations: BMD, bone mineral density; FN, Femoral Neck

Figure 3. Regional association plots for chromosome 4p16.3 loci *FGFRL1* rs4647940, *IDUA* rs6827815 and *IDUA* rs3755955 for FN-BMD trait (based on hg19/1000 Genomes Mar 2012 EUR). (A) The region encompassing rs4647940 with ±100-kb flanking regions, and (B) a zoom-in view of the center region [i.e., the dashed rectangle in (A)], encompassing rs4647940 with ±27-kb regions. Abbreviations: BMD, bone mineral density; EUR, European; FN, Femoral Neck

Figure 4. The physical locations and linkage disequilibrium pairwise r^2 plot generated by Haploview (74, 75) for the 80.744-kb human *FGFRL1* region (total 58 SNPs) encompassing *FGFRL1* rs4647940 (current study), rs6827815 (Zhang et al. (34)) and rs3755955 (Estrada et al. (40)) for (A) OOS and (B) KCOS, respectively. Haplotype blocks 1 and 2 are shown by dashed lines. Abbreviations: OOS, Omaha Osteoporosis Study; KCOS, Kansas-City Osteoporosis Study; SNP, single nucleotide polymorphism

Figure 5. Predicted secondary structure of *FGFRL1* 3' UTR 121-bp mRNA sequence carrying either (A) rs4647940-C allele or (B) rs4647940-G allele by RNAfold. Abbreviations:

MFE, minimum free energy; UTR, untranslated region

Figure 6. Cross-species comparison of DNA sequences of *FGFRL1* 3' UTR encompassing rs4647940 in human (GenBank accession number NM_001004356.2), chimpanzee (GenBank accession number AC194569.3), gibbon (GenBank accession number NW_003501383.2), gorilla (GenBank accession number NW_004002168.1), orangutan (GenBank accession number NW_002878038.1), and rhesus macaque (GenBank accession number NW_001111081.1). A 15-bp consensus motif surrounding *FGFRL1* rs4647940 is represented by a WebLogo. The box (a 6-bp sequence) denotes a 5' seed region binding site for hsa-miR-140-5p, which includes *FGFRL1* rs4647940 (i.e., at fourth position). Multiple DNA sequence alignment was performed by ClustalX version 1.81. The asterisks denote nucleotides conserved across all the species that were compared

Figure 7. *FGFRL1* gene structure, rs4647940 physical location, and the potential binding of *FGFRL1* mRNA with hsa-miR-140-5p. Abbreviations: aa, amino acid; bp, base pair; Acc #, Accession Number; Ig, immunoglobulin; SP, signal peptide; TM, transmembrane; UTR, untranslated region; WT, wild-type; MUT, mutant. "|" denotes perfect match; ":" denotes G:U wobble

Figure 8. Dual luciferase report assay results for *FGFRL1* rs4647940. The relative luciferase activities for six different conditions (3 reporter constructs: Empty/WT/MUT vectors, 2 miRNA types: NC miRNA/hsa-miR-140-5p miRNA). On the y-axis, relative luciferase activity (in percentage), was computed as the ratio of firefly luciferase activity to Renilla luciferase activity is given. On the x-axis, different transfection groups are shown. Data are presented as mean ± SEM from six independent replicates. Abbreviations: miRNA,

microRNA; MUT, mutant; NC, negative control; SEM, standard error of the mean

Figure 9. Craniofacial and overall morphological phenotypes of zebrafish larvae in microRNA microinjection experiments. Left, middle and right panels depict images corresponding to None-injection Control, NC miRNA-injected, and dre-miR-140-5p-injected groups at 5 dpf and 7 dpf larval stages, respectively. The RNA sequence of dre-miR-140-5p is exactly the same as that of hsa-miR-140-5p, indicating cross-species conservation (Supplementary Fig. S1). Three independent experiments comparing None-injection Control, NC miRNA-injected, and dre-miR-140-5p-injected groups were performed, and consistent morphological phenotypes were obtained for each of these three groups across these experiments. Images presented are from one representative experiment. Abbreviations: NC, Negative Control; dpf, days post-fertilization

Table 1. Basic Genotype Information and Phenotype Characteristics of the Study Cohorts at Stages I, II and III*

Sample	N	Population	# Genotyped SNPs	# Imputed SNPs	Female (%)	Age (yrs)	LS-BMD (g/cm^2)	HIP-BMD (g/cm^2)	FN-BMD (g/cm^2)	Bone densitometer
Stage I**	(GWA meta-analysis)									
OOS	987	Caucasian	407,634	6,427,198	49.6	50.3(18.3)	1.03(0.16)	0.97(0.16)	0.81(0.14)	Hologic QDR 4500W
KCOS	2,250	Caucasian	743,768	7,085,256	75.9	51.4(13.8)	1.02(0.16)	0.97(0.17)	0.80(0.15)	Hologic QDR 4500W
COS	1,547	Han Chinese	725,883	5,823,600	50.7	34.8(13.4)	0.95(0.13)	0.92(0.13)	0.81(0.13)	Hologic QDR 4500W
FHS	3,747	Caucasian	405,948	6,456,277	57.3	60.3(10.7)	1.22(0.23)	0.95(0.17)	0.89(0.16)	Lunar DPX-L
IFS	1,488	Caucasian	543,932	7,202,569	100.0	32.7(7.2)	---	---	---	Lunar DPX-L
WHI-AA	712	African American	799,328	11,862,114	100.0	60.9(6.9)	1.05(0.17)	0.95(0.15)	0.83(0.14)	Hologic QDR-2000
WHI-HIS	409	Hispanic	647,362	6,916,926	100.0	60.7(7.2)	0.97(0.16)	0.86(0.13)	0.73(0.12)	Hologic QDR-2000
Total	11,140									
Stage II***	(*in silico* replication)									
RS	4,904	Caucasian	512,349	6,986,425	57.0	69.4(9.0)	1.09(0.18)	NA	0.86(0.13)	Lunar DPX-L
AOGC	1,955	Caucasian	Region-wise	Region-wise	100.0	69.6(8.6)	1.08(0.26)	0.89(0.25)	0.79(0.21)	Multiple§
Total	6,859									
Stage III	(*de novo* genotyping replication)									
KCOSR	3,923	Caucasian	3	0	57.6	46.8(14.5)	1.03(0.15)	0.96(0.15)	0.80(0.14)	Hologic QDR
COSR	2,740	Han Chinese	3	0	57.7	32.3(14.4)	0.93(0.12)	0.91(0.13)	0.80(0.13)	Hologic QDR 4500W
Total	6,663									

*Adapted from Supplementary Table 1 of Zhang et al. (2014) (34). Although KoGES was included in stage 2 (*in silico* replication) of Zhang et al. (2014) (34), because none of the Korean Genome Epidemiology Study (KoGES) results were included in the *in silico* replication of stage I-selected poly-miRTSs, the stage II (*in silico* replication) of the current study only included RS and AOGC, but not KoGES. Data were presented as mean (SD). N denotes sample size for each study cohort. Abbreviations: OOS, Omaha Osteoporosis Study; KCOS, Kansas-City Osteoporosis Study; COS, China Osteoporosis Study; FHS, Framingham Heart Study; IFS, Indiana Fragility Study; WHI-AA, Women's Health Initiative African American sample; WHI-HIS, Women's Health Initiative Hispanic sample. RS, Rotterdam Study; AOGC, Australian Osteoporosis Genetics Consortium; KCOSR, KCOS Replication; COSR, COS Replication. SNP, single nucleotide polymorphism; poly-miRTS, polymorphism in microRNAs Target Sites; BMD, bone-mineral density; LS, lumbar spine; HIP, total hip; FN, femoral neck. "---", not available. λ_{GC} ranges from 0.99 to 1.06 (34).

**As indicated in Zhang et al. (34), 5842,825 common SNPs (either genotyped or imputed) were shared across the seven stage I Genome Wide-Association studies and only those 41,102 poly-miRTSs were included in stage I.

***As indicated in Zhang et al. (34), for AOGC study, genotype imputations were only performed for specific regions, and only 11 stage I-selected poly-miRTSs were included in stage II of the current study.

§Either Hologic QDR or Lunar DPX-L series was used to measure BMD.

Table 2. GWA Meta-analysis Results for *FGFRL1* and *PRR5* Poly-miRTSs*

Poly-miRTS			Stage I			Stage II			Stage III			Stage I+II+III
dbSNP ID	**Locus**	**Gene**	**Phenotype**	**Analysis**	**P-value**	**Phenotype**	**Analysis**	**P-value**	**Phenotype**	**Analysis**	**P-value**	**P-value**
rs3127592	6q25.3	*SLC22A2*	HIP-BMD	Combined	3.24×10^{-6}	FN-BMD	Combined	0.5034	---	---	---	---
rs3127593	6q25.3	*SLC22A2*	HIP-BMD	Combined	6.59×10^{-6}	FN-BMD	Combined	0.4638	---	---	---	---
rs4647940	**4p16.3**	***FGFRL1***	**FN-BMD**	**Combined**	**7.67×10^{-6}**	**FN-BMD****	**Combined**	**5.078×10^{-3}**	**FN-BMD****	**Combined**	**7.55×10^{-6}**	**8.87×10^{-12}**
rs1599795	3q13.33	*CD80*	HIP-BMD	Combined	1.32×10^{-5}	FN-BMD	Combined	0.3689	---	---	---	---
rs9479085	6q25.1	*C6orf97*	LS-BMD	Combined	1.47×10^{-5}	LS-BMD**	Combined	9.202×10^{-3}	---	---	---	---
rs3213550	22q13.31	*PRR5*	FN-BMD	Combined	1.58×10^{-5}	FN-BMD**	Combined	0.3138	FN-BMD	Combined	0.08208	1.17×10^{-5}
rs1057392	2q34	*PTH2R*	HIP-BMD	Combined	2.60×10^{-5}	FN-BMD	Combined	0.3167	---	---	---	---
rs10739677	9q33.3	*FAM125B*	HIP-BMD	Female	2.67×10^{-5}	FN-BMD	Combined	0.4262	---	---	---	---
rs17547201	17q12	*AMAC1*	HIP-BMD	Female	2.79×10^{-5}	FN-BMD	Combined	0.4009	---	---	---	---
rs11581122	1p12	*FAM46C*	HIP-BMD	Combined	4.47×10^{-5}	FN-BMD	Combined	0.6717	---	---	---	---
rs523200	11q13.1	*SF1*	FN-BMD	Combined	4.76×10^{-5}	FN-BMD**	Combined	0.1879	---	---	---	---

*Abbreviations: BMD, bone mineral density; FN, femoral neck; HIP, total hip; LS, lumbar spine; poly-miRTS, polymorphism in microRNAs Target Sites, SNP, single nucleotide polymorphism. Combined refers to male and female. Genome-wide significance (GWS) is defined as $\alpha = 5.00\times10^{-8}$ in the previous traditional study **(34)** and 5.21×10^{-6} in the current study, respectively. P-values attaining the GWS level are highlighted in bold font. Shaded regions were matched regions between these two studies, although different SNPs were identified. The SNP reaching GWS for stage I+II+III (i.e., P-value < 5.21×10^{-6}) was highlighted in bold font.

**Data were available for two cohorts in each respective stage of stages II and III. Otherwise, data were available for only one cohort in each respective stage of stages II and III.

Table 3. Putative Human miRNAs that Bind to *FGFRL1* Poly-miRTS rs4647940

miR-Name	# Programs	MicroSNiPer	MirSNP Score	RegRNA2.0 Score	TargetScan Context Score Percentile
hsa-miR-17-3p	*1*	*Seed length: 7 (Yes)*	*--- (No)*	*<150 (No)*	*--- (No)*
hsa-miR-30c-2-3p	*1*	*Seed length: 7 (Yes)*	*--- (No)*	*<150 (No)*	*--- (No)*
hsa-miR-34c-5p	*1*	*Seed length: 6 (Yes)*	*--- (No)*	*<150 (No)*	*--- (No)*
hsa-miR-92a-2-5p	*1*	*Seed length: 8 (Yes)*	*--- (No)*	*<150 (No)*	*--- (No)*
hsa-miR-106b-3p	*1*	*Seed length: 6 (Yes)*	*--- (No)*	*<150 (No)*	*--- (No)*
hsa-miR-140-5p	***1***	***Seed length: 6 (Yes)***	***--- (No)***	***<150 (No)***	***--- (No)***
hsa-miR-143-5p	*1*	*Seed length: 6 (Yes)*	*--- (No)*	*<150 (No)*	*--- (No)*
hsa-miR-4667-5p	2	Seed length: 8 (Yes)	144.00 (Yes)	<150 (No)	--- (No)
hsa-miR-4700-5p	2	Seed length: 11 (Yes)	161.00 (Yes)	<150 (No)	--- (No)
hsa-miR-4723-5p	2	Seed length: --- (No)	144.00 (Yes)	<150 (No)	77 (Yes)
hsa-miR-5698	2	Seed length: --- (No)	162.00 (Yes)	≥150 (Yes)	--- (No)
hsa-miR-3175	3	Seed length: --- (No)	159.00 (Yes)	≥150 (Yes)	86 (Yes)
hsa-miR-491-5p	4	Seed length: 8 (Yes)	148.00 (Yes)	≥150 (Yes)	76 (Yes)

*Abbreviations: GWA, genome-wide association; poly-miRTS, polymorphism in microRNAs Target Sites; "# Programs", total number of programs that gave the prediction, denoted by "Yes" in parentheses (otherwise, "No" is shown in parentheses); "---", not available. Seven human miRNAs that correspond to mouse miRNAs significantly differentially expressed in bone between different time points (He et al., 2013(41)) were *in italic font*, which includes has-miR-140-5p (in bold font). The miRNAs were first sorted by the "# Programs" (lowest to highest), and then sorted by miR number (smallest to largest).

Table 4. Mouse miRNAs that Show Differential Expressions in Bone Among Three Time Points Determined by miRNA-Seq

	25-m vs. 2-m		8-m vs. 2-m		25-m vs. 8-m	
miR-Name	**FC**	**P-value**	**FC**	**P-value**	**FC**	**P-value**
mmu-miR-140-5p	***0.17***	***9.15×10^{-91}***	***0.25***	***9.63×10^{-82}***	***0.68***	***1.79×10^{-3}***
mmu-miR-143-5p	*0.45*	*1.91×10^{-27}*	*0.34*	*1.22×10^{-51}*	*1.34*	*1.90×10^{-3}*
mmu-miR-34c-5p	*0.47*	*7.33×10^{-24}*	*0.72*	*8.95×10^{-8}*	*0.66*	*1.85×10^{-7}*
mmu-miR-106b-3p	1.34	1.10×10^{-4}	1.00	0.96	1.33	1.43×10^{-4}
mmu-miR-30c-2-3p	0.91	0.048	0.88	2.80×10^{-3}	1.04	0.44
mmu-miR-92a-2-5p	0.66	0.1134	1.45	0.061	0.45	1.11×10^{-3}
mmu-miR-17-3p	0.91	0.17	1.90	2.90×10^{-32}	0.47	1.20×10^{-33}

*Abbreviations: 2-m, 2-month; 8-m, 8-month; 25-m, 25-month; FC, fold change. Data were obtained from He et al., 2013 (41). Three mouse miRNAs with significant differences (i.e., P-value < 0.05/3 = 0.0167) of their expressions across three time points (i.e., 2-m, 8-m, and 25-m) were shown *in italic font*, which includes -miR-140-5p (in bold font). The miRNAs were sorted by their levels of statistical significance for 25-m vs. 2-m comparison (highest to lowest).

Figure 1

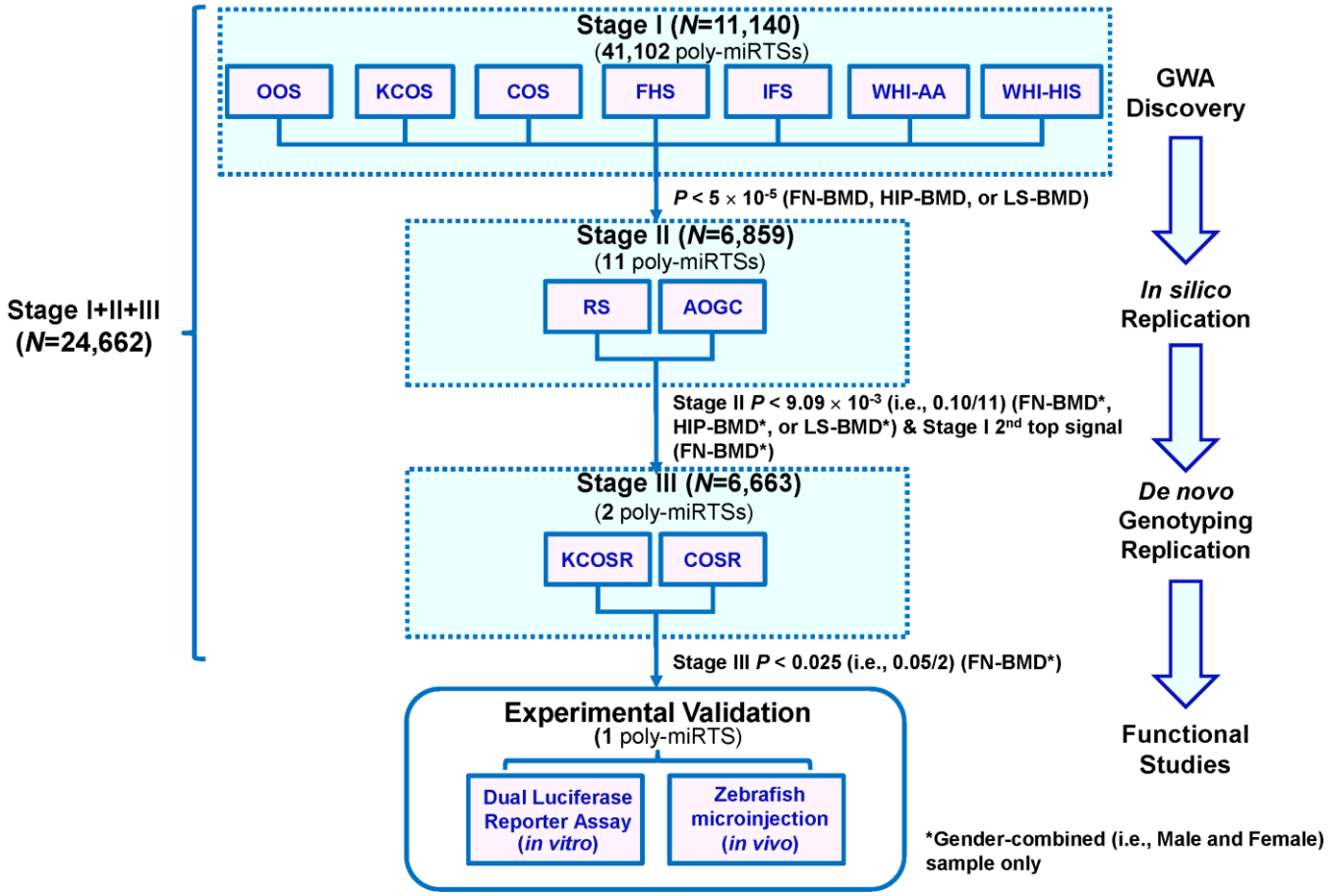

Stage I (N=11,140)
(41,102 poly-miRTSs)
OOS
KCOS
COS
FHS
IFS
WHI-AA
WHI-HIS
GWA Discovery
P < 5 × 10-5 (FN-BMD, HIP-BMD, or LS-BMD)
Stage II (N=6,859)
(11 poly-miRTSs)
RS
AOGC
In silico Replication
Stage II P < 9.09 × 10-3 (i.e., 0.10/11) (FN-BMD*, HIP-BMD*, or LS-BMD*) & Stage I 2nd top signal (FN-BMD*)
Stage III (N=6,663)
(2 poly-miRTSs)
KCOSR
COSR
De novo Genotyping Replication
Stage III P < 0.025 (i.e., 0.05/2) (FN-BMD*)
Experimental Validation
(1 poly-miRTS)
Dual Luciferase Reporter Assay (in vitro)
Zebrafish microinjection (in vivo)
Functional Studies
Stage I+II+III (N=24,662)
*Gender-combined (i.e., Male and Female) sample only

Figure 2

Forest Plot of *FGFRL1* rs4647940 for FN-BMD

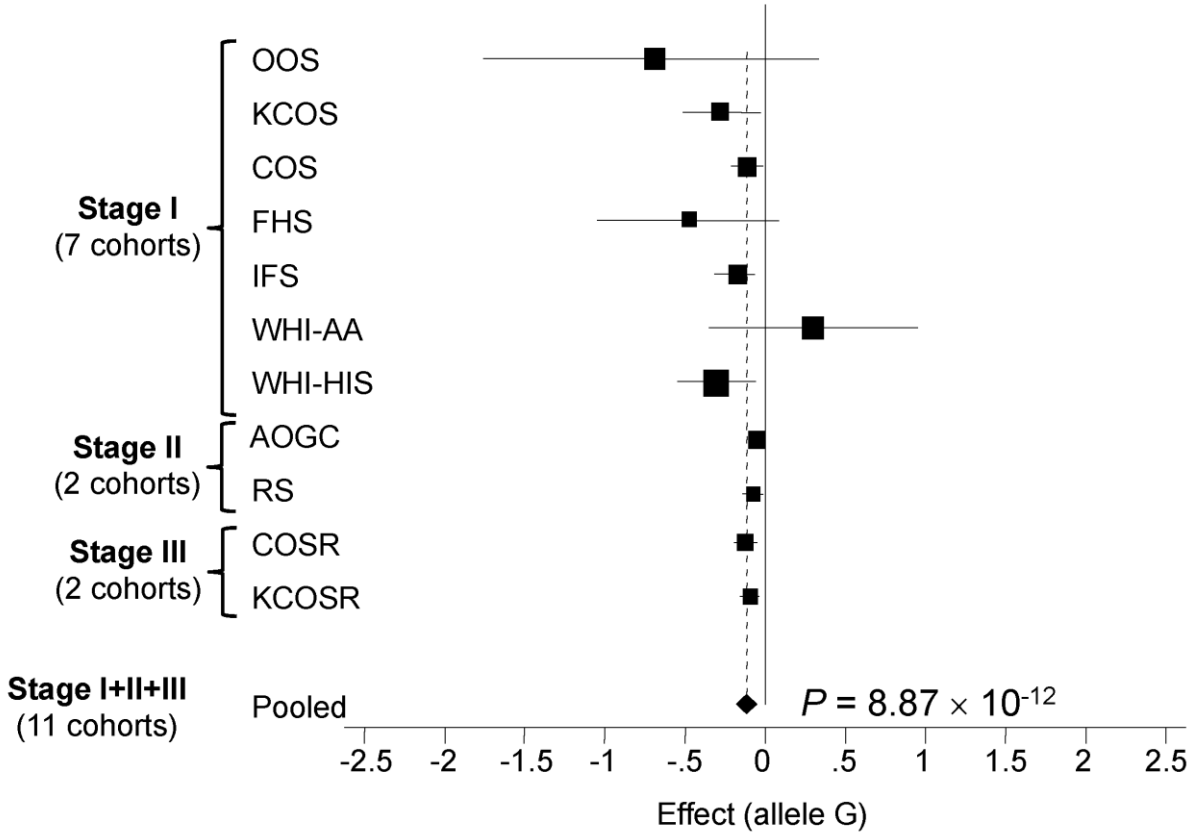
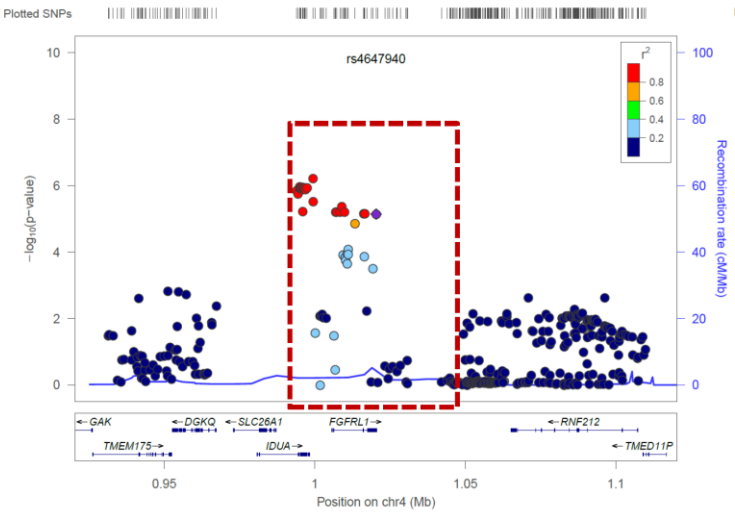


Figure 3

(A)

Chromosome 4p16.3



(B)

Chromosome 4p16.3
(Zoom-in View)

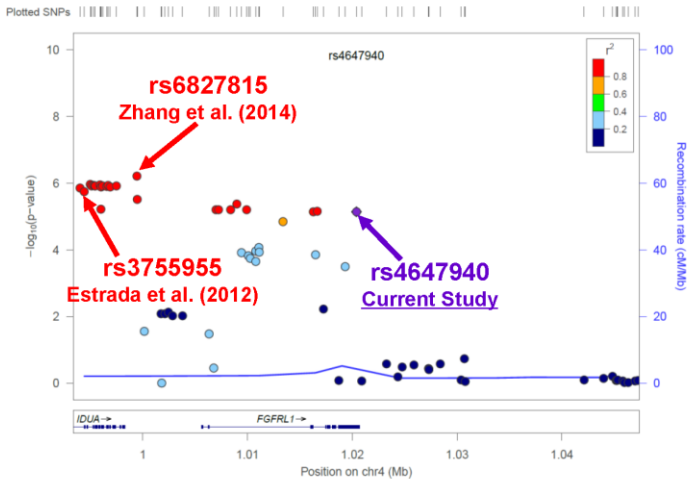


Figure 4

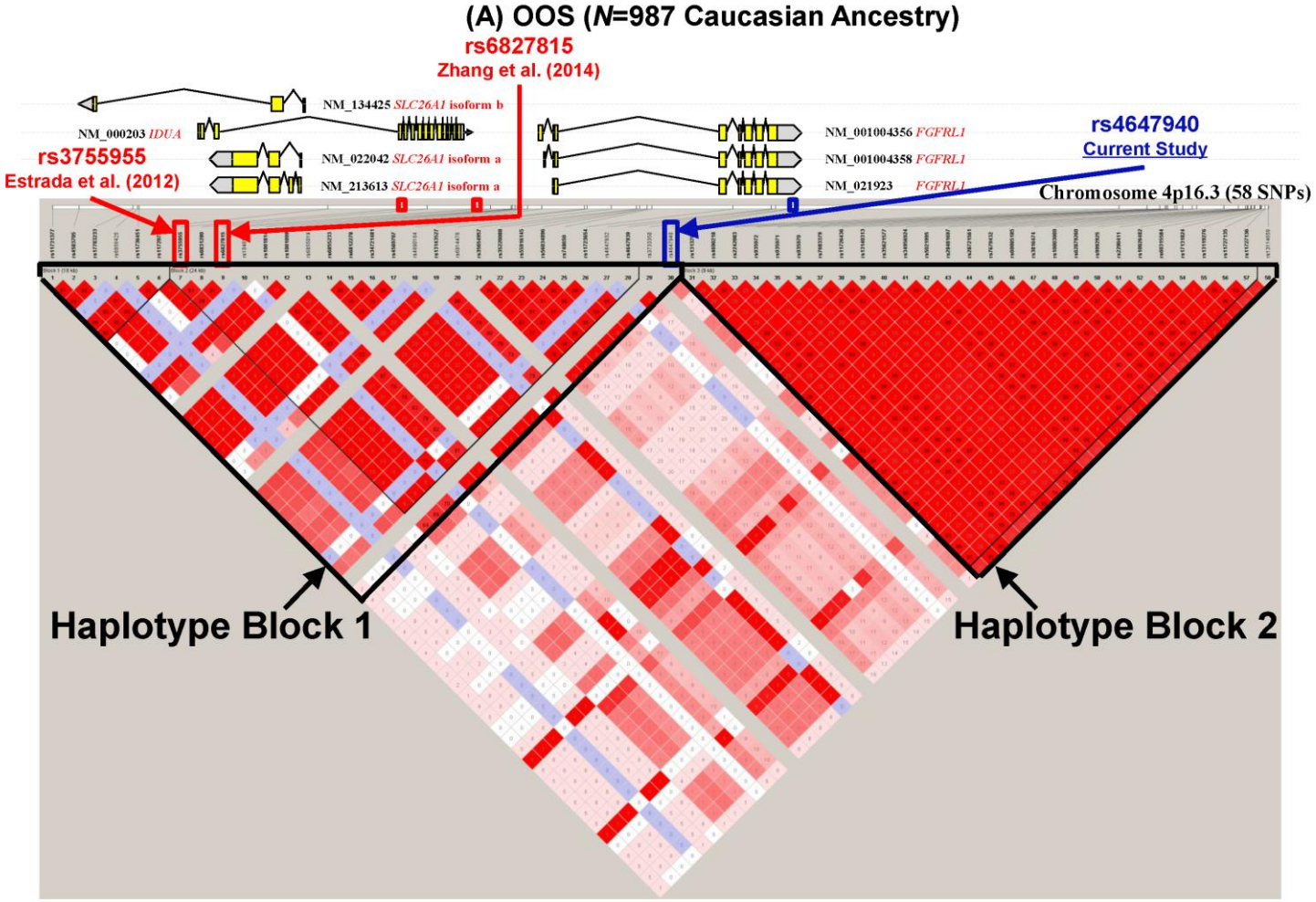

(A) OOS (N=987 Caucasian Ancestry)
rs6827815
Zhang et al. (2014)
NM_134425 SLC26A1 isoform b
NM_000203 IDUA
NM_022042 SLC26A1 isoform a
NM_213613 SLC26A1 isoform a
rs3755955
Estrada et al. (2012)
NM_001004356 FGFRL1
NM_001004358 FGFRL1
NM_021923 FGFRL1
rs4647940
Current Study
Chromosome 4p16.3 (58 SNPs)
Haplotype Block 1
Haplotype Block 2

Figure 4

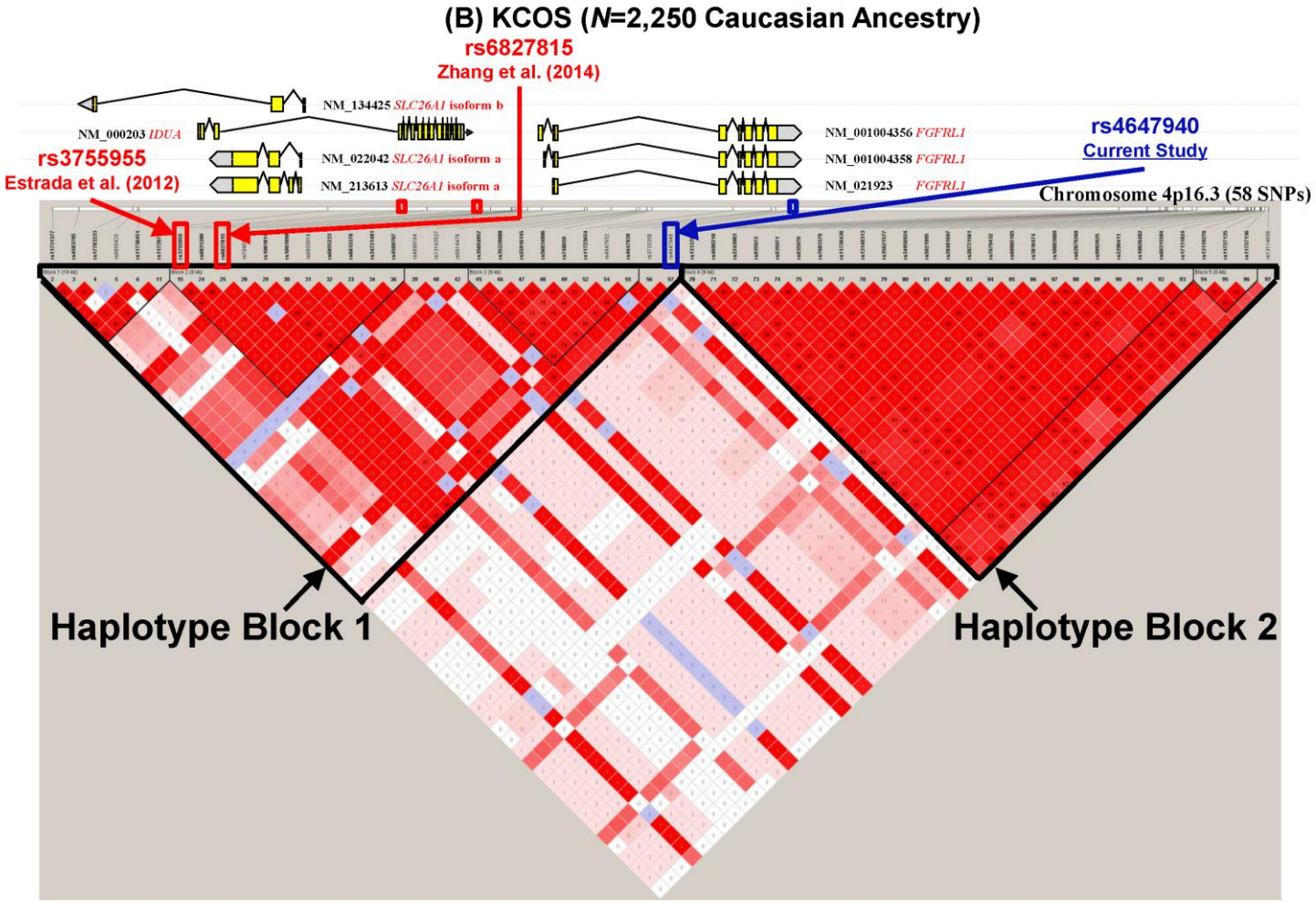

(B) KCOS (N=2,250 Caucasian Ancestry)
rs6827815
Zhang et al. (2014)
NM_134425 SLC26A1 isoform b
NM_000203 IDUA
NM_022042 SLC26A1 isoform a
NM_213613 SLC26A1 isoform a
NM_001004356 FGFRL1
NM_001004358 FGFRL1
NM_021923 FGFRL1
rs4647940
Current Study
rs3755955
Estrada et al. (2012)
Chromosome 4p16.3 (58 SNPs)
Haplotype Block 1
Haplotype Block 2

Figure 5

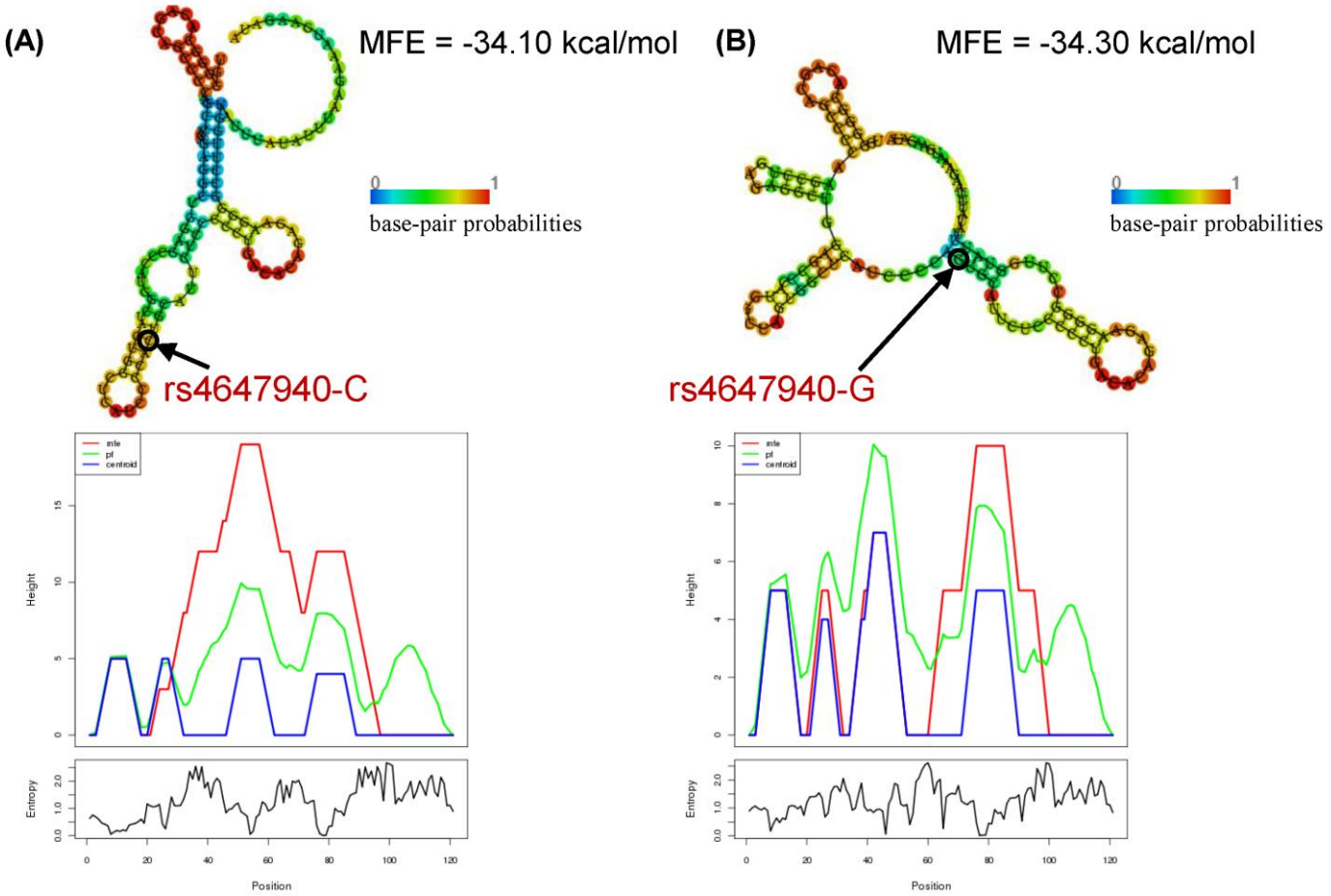

(A)
MFE = -34.10 kcal/mol
0
1
base-pair probabilities
rs4647940-C
(B)
MFE = -34.30 kcal/mol
0
1
base-pair probabilities
rs4647940-G
mfe
pf
centroid
Height
Entropy
Position

Figure 6

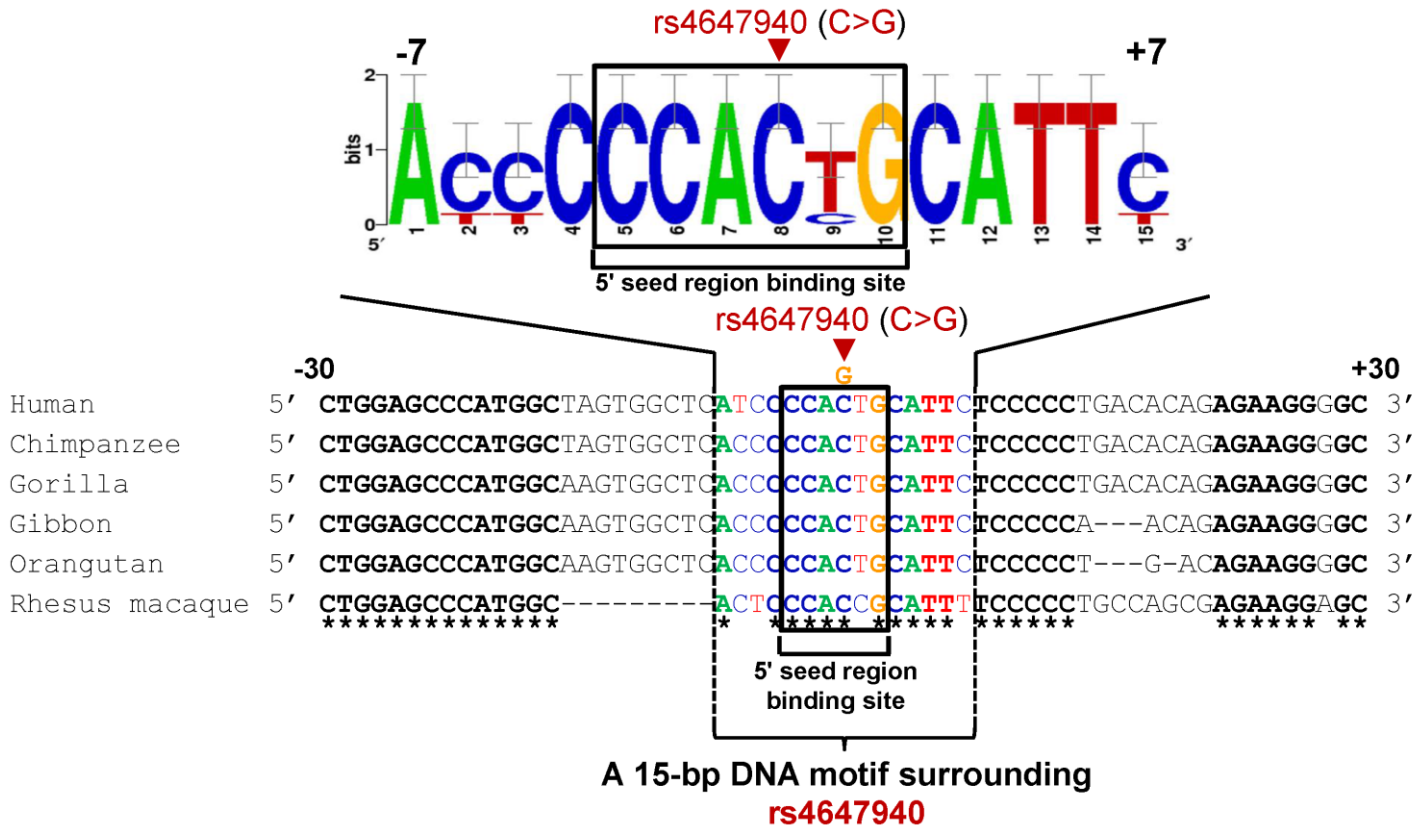

rs4647940 (C>G)
-7
+7
bits
5′
3′
5' seed region binding site
rs4647940 (C>G)
-30
+30
Human 5′ CTGGAGCCCATGGCTAGTGGCTGATCCCCACTGCATTCTCCCCCTGACACAGAGAAGGGGC 3′
Chimpanzee 5′ CTGGAGCCCATGGCTAGTGGCTGACCCCCACTGCATTCTCCCCCTGACACAGAGAAGGGGC 3′
Gorilla 5′ CTGGAGCCCATGGCAAGTGGCTGACCCCCACTGCATTCTCCCCCTGACACAGAGAAGGGGC 3′
Gibbon 5′ CTGGAGCCCATGGCAAGTGGCTGACCCCCACTGCATTCTCCCCCA---ACAGAGAAGGGGC 3′
Orangutan 5′ CTGGAGCCCATGGCAAGTGGCTGACCCCCACTGCATTCTCCCCCT---G-ACAGAAGGGGC 3′
Rhesus macaque 5′ CTGGAGCCCATGGC---------ACTCCCACCGCATTTTCCCCCTGCCAGCGAGAAGGAGC 3′
5' seed region binding site
A 15-bp DNA motif surrounding
rs4647940

Figure 7

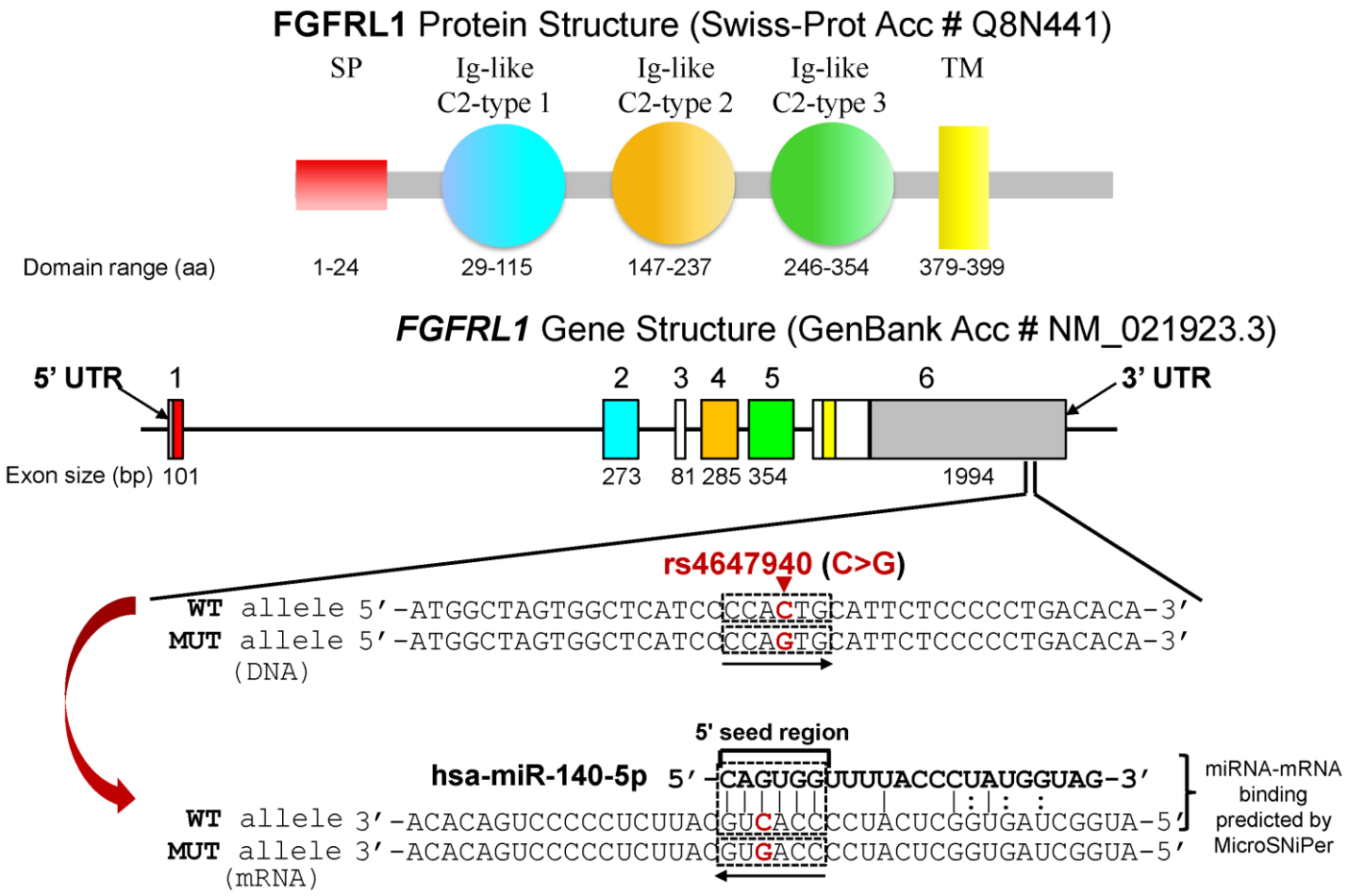

FGFRL1 Protein Structure (Swiss-Prot Acc # Q8N441)
SP
Ig-like C2-type 1
Ig-like C2-type 2
Ig-like C2-type 3
TM
Domain range (aa)
1-24
29-115
147-237
246-354
379-399
FGFRL1 Gene Structure (GenBank Acc # NM_021923.3)
5' UTR
1
2
3
4
5
6
3' UTR
Exon size (bp) 101
273
81 285 354
1994
rs4647940 (C>G)
WT allele 5'-ATGGCTAGTGGCTCATCCCCACTGCATTCTCCCCCTGACACA-3'
MUT allele 5'-ATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACA-3'
(DNA)
5' seed region
hsa-miR-140-5p 5'-CAGUGGUUUUACCCUAUGGUAG-3'
WT allele 3'-ACACAGUCCCCCUCUUACGUCACCCCUACUCGGUGAUCGGUA-5'
MUT allele 3'-ACACAGUCCCCCUCUUACGUGACCCCUACUCGGUGAUCGGUA-5'
(mRNA)
miRNA-mRNA binding predicted by MicroSNiPer

Figure 8

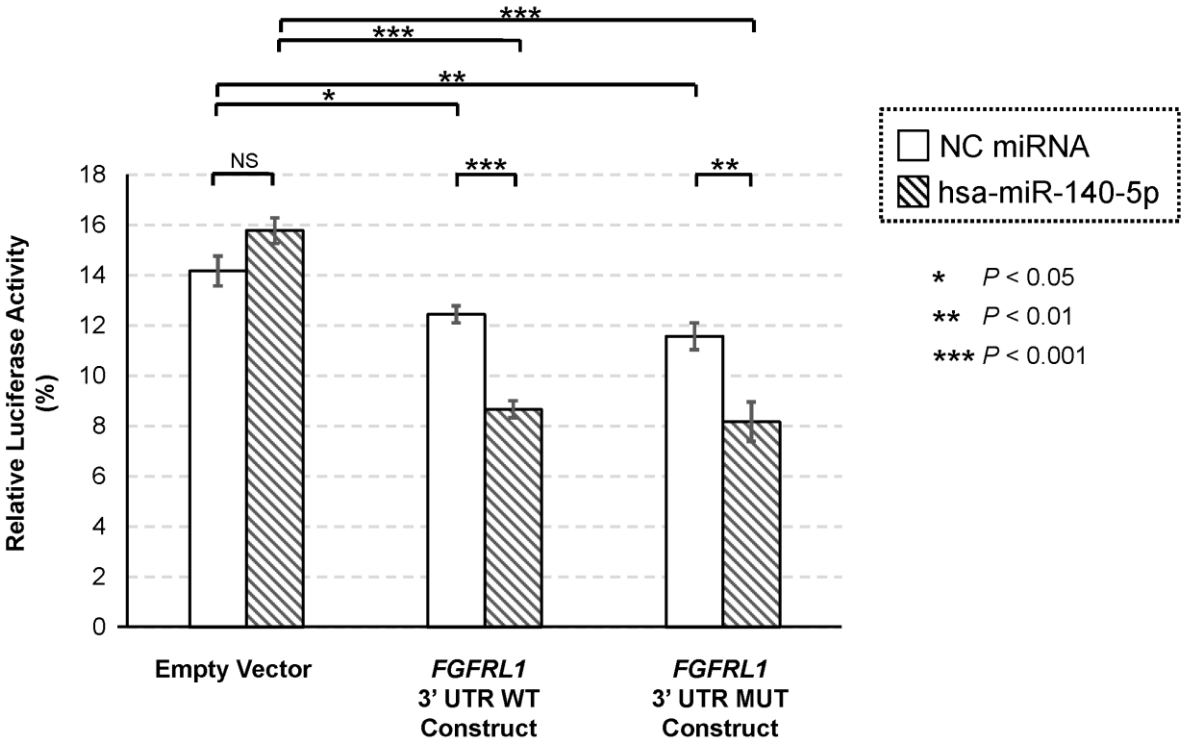
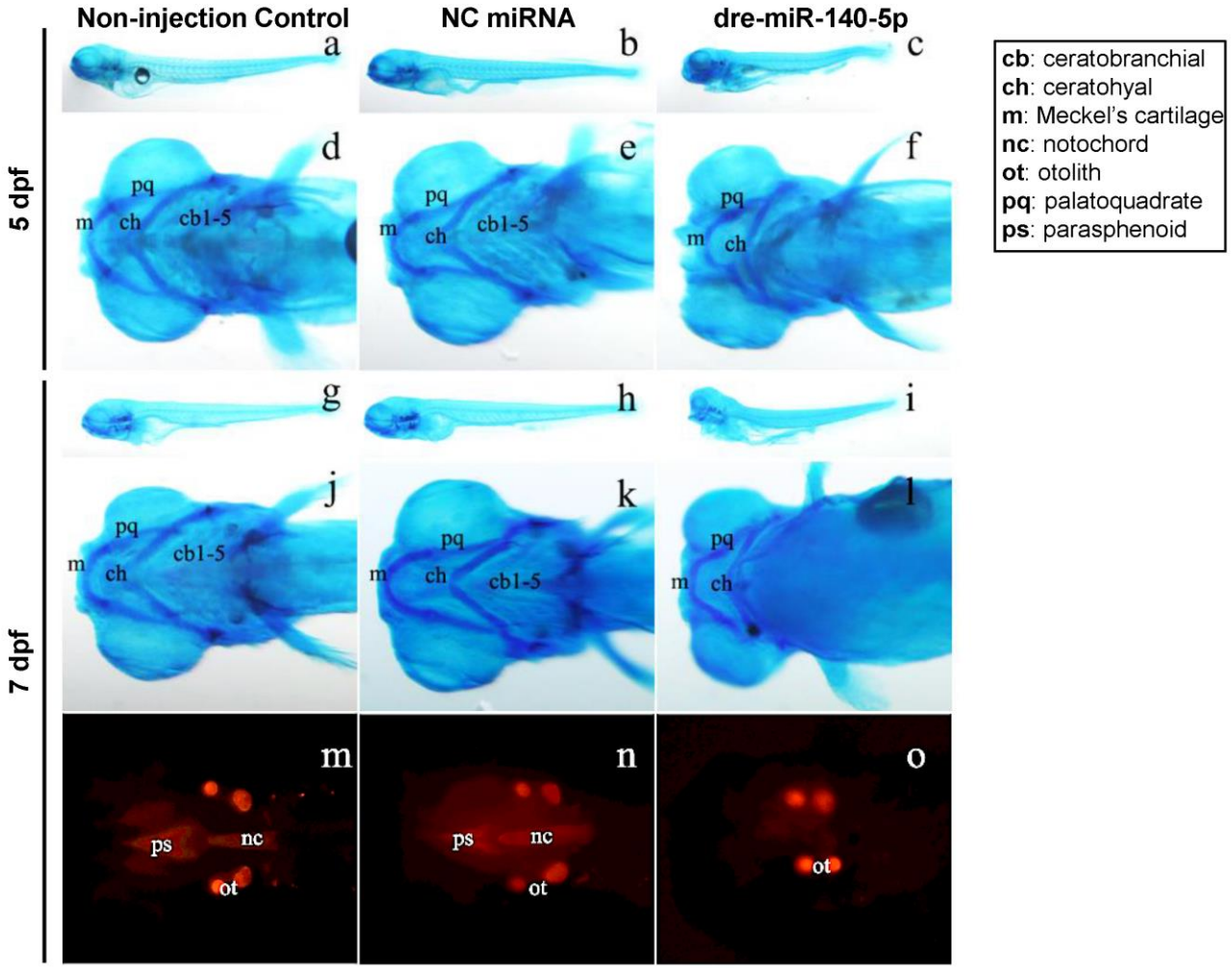

***
***
**
*
NS
***
**
18
16
14
12
10
8
6
4
2
0
Relative Luciferase Activity (%)
Empty Vector
FGFRL1 3' UTR WT Construct
FGFRL1 3' UTR MUT Construct
NC miRNA
hsa-miR-140-5p
* P < 0.05
** P < 0.01
*** P < 0.001

Figure 9


Non-injection Control
NC miRNA
dre-miR-140-5p
5 dpf
7 dpf
a
b
c
d
e
f
g
h
i
j
k
l
m
n
o
pq
m
ch
cb1-5
ps
nc
ot
cb: ceratobranchial
ch: ceratohyal
m: Meckel's cartilage
nc: notochord
ot: otolith
pq: palatoquadrate
ps: parasphenoid