Supplementary

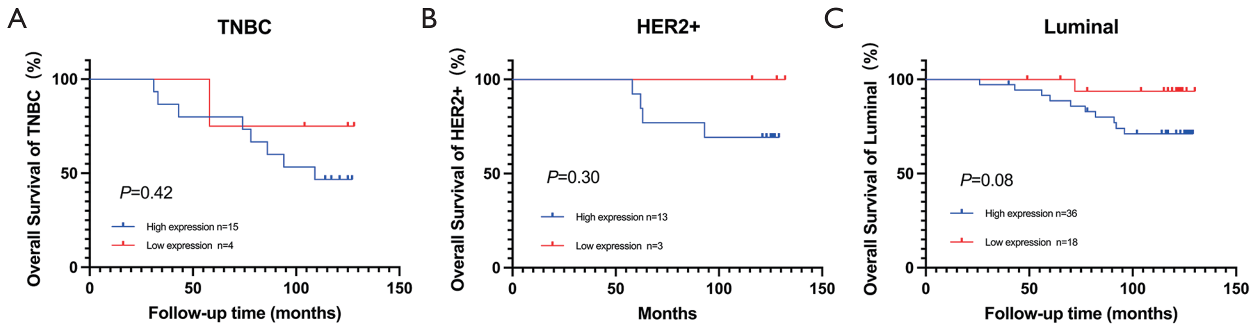

Figure S1 Stratified analysis across molecular subtypes. (A) TNBC patients with higher hsa_circ_0006522 expression did not have a significantly shorter overall survival than patients with low expression (P=0.42); (B) HER2-positive patients with higher hsa_circ_0006522 expression did not have a significantly shorter overall survival than patients with low expression (P=0.30); (C) Luminal patients with higher hsa_circ_0006522 expression did not have a significantly shorter overall survival than patients with low expression (P=0.08).

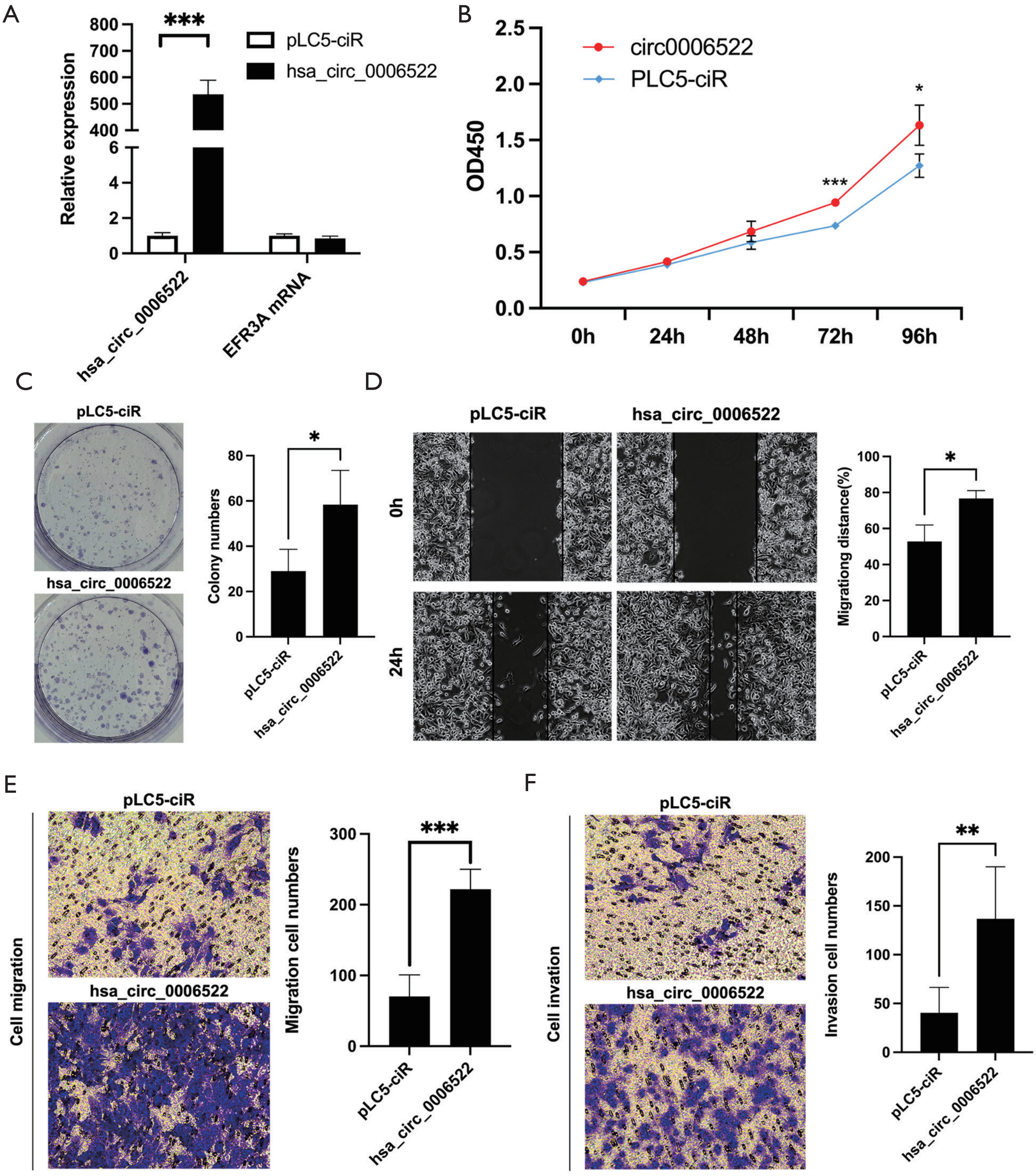

Figure S2 The overexpression of hsa_circ_0006522 promotes the proliferation, migration, and invasion of BT-549breast cancer cells. (A) The expression of hsa_circ_0006522 and linear EFR3A mRNA in BT-549 cells after transfection with hsa_circ_0006522 or pLC5-ciR empty vector were detected by qRT-PCR. (B,C) Proliferative capacity and colony formation ability of BT-549 cells transfected with either hsa_circ_0006522 or empty pLC5-ciR vector were quantified via CCK-8 and colony formation assays respectively. (D-F) Cell motility and invasive potential under identical transfection conditions were assessed using wound healing assays (×40), transwell migration chambers (crystal violet staining, ×100) and Matrigel-based invasion assays (crystal violet staining, ×100). *, P<0.05; **, P<0.01; ***, P<0.001.

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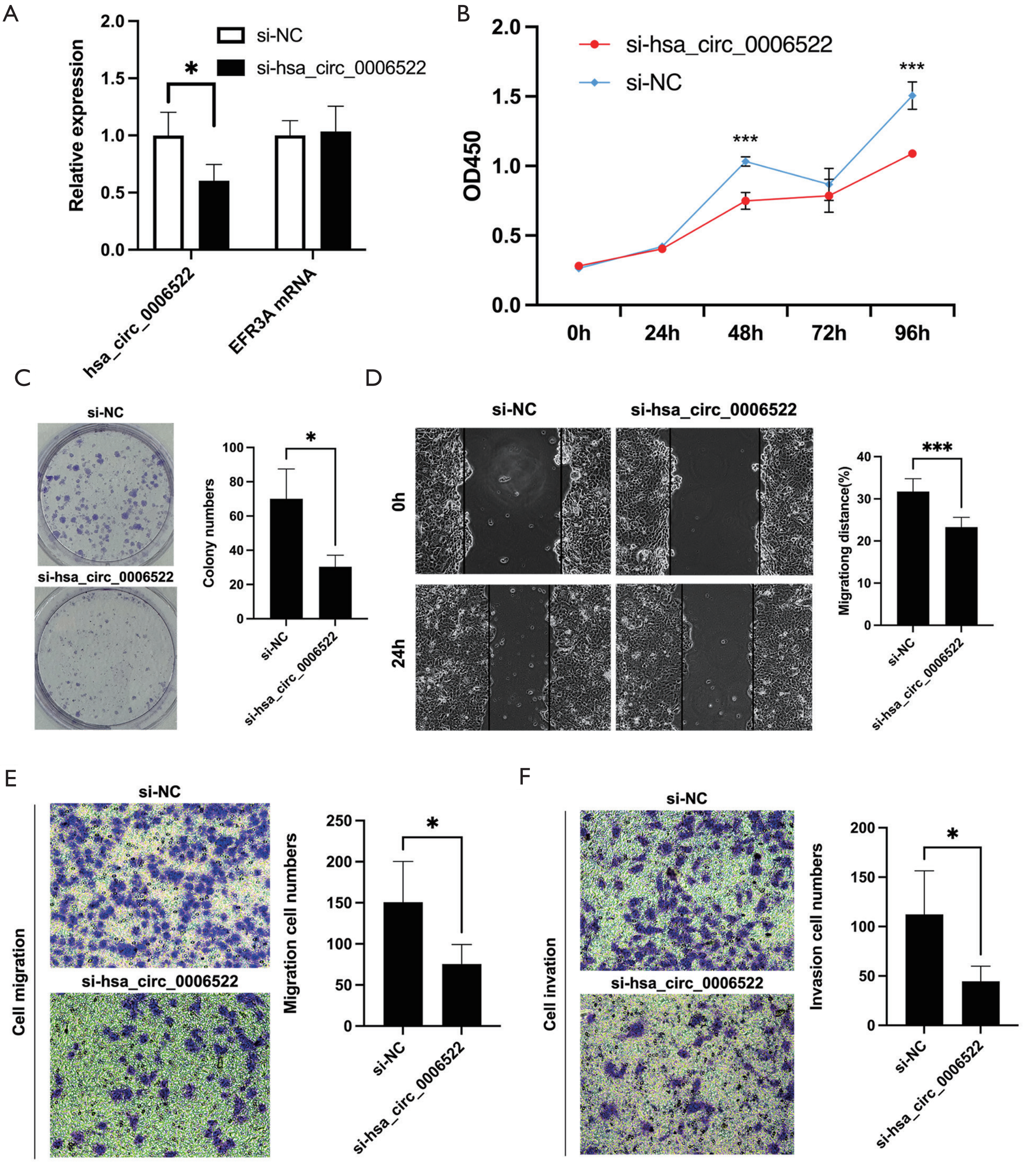

Figure S3 The knockdown of hsa_circ_0006522 suppresses the proliferation, migration, and invasion of MCF-7 breast cancer cells. (A) qRT-PCR analysis quantified the knockdown efficiency of hsa_circ_0006522-targeting siRNA in MCF-7 cells. (B,C) Proliferative capacity and colony formation ability of MCF-7 cells transfected with either hsa_circ_0006522 siRNA or NC siRNA were quantified via CCK-8 and colony formation assays respectively. (D-F) Cell motility and invasive potential under identical transfection conditions were assessed using wound healing assays (×40), transwell migration chambers (crystal violet staining, ×100) and Matrigel-based invasion assays (crystal violet staining, ×100). *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$.

Table S1 Hsa_circ_0006522-related miRNAs

CircRNA Mirbase ID	CircRNA (Top) - miRNA (Bottom) pairing	Site type	context+ score percentile
hsa_circ_0006522 (5' ... 3')	AAUUAGAGGUAUUCAAGGUGUGG	7mer-m8	96
	|||||||		
hsa-miR-1228 (3' ... 5')	CCCCCCGCUCCGUCCACACU		
hsa_circ_0006522 (5' ... 3')	UCUGCAACUGACAAA--GAAGAGAA	7mer-1a	80
	||||| ||||||		
hsa-miR-1236 (3' ... 5')	GACCUCUCUGUUCCCCUUCUCC		
hsa_circ_0006522 (5' ... 3')	GAGGCACUGGACCAACUUCUCAU	7mer-1a	84
	||| ||||||		
hsa-miR-1253 (3' ... 5')	ACGUCCGACUAGAA-GAAGAGA		
hsa_circ_0006522 (5' ... 3')	CGCAUAGGCCCUCCUUCUUCUCC	7mer-m8	93
	|||| |||||||		
hsa-miR-1253 (3' ... 5')	ACGUCCGACUAGAAGAAGAGA		
hsa_circ_0006522 (5' ... 3')	UUGAAGAAGACACACCAUCCUAU	7mer-1a	83
	||||||		
hsa-miR-1265 (3' ... 5')	UUGUUGUGAACUGGUGUAGGAC		
hsa_circ_0006522 (5' ... 3')	AAUCGGGGGAACCAAAGCUUCAA	8mer-1a	98
	|||||||		
hsa-miR-127-5p (3' ... 5')	UAGUCUCGGGAGACUCGAAGUC		
hsa_circ_0006522 (5' ... 3')	CGAGCAACUUUUGGGAAUAUGAA	7mer-1a	87
	||||||		
hsa-miR-1279 (3' ... 5')	UCUUUCUUCGUUAUACU		
hsa_circ_0006522 (5' ... 3')	CAAAGCAUUAAGCCAUUUGUAGA	8mer-1a	98
	||||| |||||||		
hsa-miR-1283 (3' ... 5')	UCUUUCGCGAAAGG--AAACAUCU		
hsa_circ_0006522 (5' ... 3')	UUCCUGUCAUAGUGAUCCAGAAA	7mer-1a	79
	||||||		
hsa-miR-1299 (3' ... 5')	AGGGAGUGUGUCUUAAGGUCUU		
hsa_circ_0006522 (5' ... 3')	CUUGUGAAAACUGAUAUGGAGAA	7mer-1a	91
	||||| ||||||		
hsa-miR-136 (3' ... 5')	AGGUAGUAGUUUUGUU--UACCUCA		
hsa_circ_0006522 (5' ... 3')	UAUCUGCUCCAGAGAAACUGGAU	7mer-m8	91
	|||||||		
hsa-miR-145 (3' ... 5')	UCCCUAAGGACCCUUUUGACCUG		
hsa_circ_0006522 (5' ... 3')	GCUUGCCAUUCUCAAAGCAUUAA	8mer-1a	98
	|||||||		
hsa-miR-155 (3' ... 5')	UGGGGAUAGUGCUAAUCGUAAUU		
hsa_circ_0006522 (5' ... 3')	UUGAUUGCUAUGGAGGCACUGGA	8mer-1a	97
	|||||||		
hsa-miR-1825 (3' ... 5')	CCUCUCCUCCCGUGACCU		
hsa_circ_0006522 (5' ... 3')	UUGUGUCUCGAUUCAGUGCCAUG	7mer-m8	92
	|||||||		
hsa-miR-183 (3' ... 5')	UCACUUAAGAUGGUCACGGUAU		
hsa_circ_0006522 (5' ... 3')	UCGAUUCAGUGCCAUGUGCCAUU	7mer-m8	94
	|||| |||||||		
hsa-miR-183 (3' ... 5')	UCACUUAAGAUGGU---CACGGUAU		
hsa_circ_0006522 (5' ... 3')	AAGUUCUUGGAACAAAUUCUUUU	7mer-m8	97
	|||||||		
hsa-miR-186 (3' ... 5')	UCGGGUUUUCCUCUUAAGAAAC		
hsa_circ_0006522 (5' ... 3')	UAGAUCAUCACAAACUGUGGGAU	7mer-m8	92
	|||||||		
hsa-miR-188-3p (3' ... 5')	ACGUUUGGGACGUACACCCUC		
hsa_circ_0006522 (5' ... 3')	AGAAAUUGACAUUUUAUGCAGUA	8mer-1a	99
	|||||||		
hsa-miR-217 (3' ... 5')	AGGUUAGUCAAGGACUACGUCAU		
hsa_circ_0006522 (5' ... 3')	UUCUUCUCCUUCUGCAACUGACA	8mer-1a	97
	|||||||		
hsa-miR-223 (3' ... 5')	ACCCCAUAAACUGUUUGACUGU		
hsa_circ_0006522 (5' ... 3')	ACCAACUUCUCAUGGCUUGCCAU	7mer-1a	84
	||||||		
hsa-miR-31 (3' ... 5')	UCGAUACGGUCGUAGAACGGA		
hsa_circ_0006522 (5' ... 3')	ACUGCUUUAAAAUUAUAAUGUAU	7mer-1a	94
	||||||		
hsa-miR-323-3p (3' ... 5')	UCUCCAGCUGGCACAUUACAC		
hsa_circ_0006522 (5' ... 3')	UAUGCAGUAUCUGCUCCAGAGAA	7mer-1a	83
	||||||		
hsa-miR-326 (3' ... 5')	GACCUCCUUCCCGGGUCUCC		
hsa_circ_0006522 (5' ... 3')	UAUGCAGUAUCUGCUCCAGAGAA	7mer-1a	82
	||||||		
hsa-miR-330-5p (3' ... 5')	CGGAUUCUGUGUCCGGGUCUCU		
hsa_circ_0006522 (5' ... 3')	AUAUGGUGGCAAAGCUGCUGGAA	7mer-1a	79
	||||||		
hsa-miR-338-3p (3' ... 5')	GUUGUUUUAGUGACUACGACCU		
hsa_circ_0006522 (5' ... 3')	AACAGAGAUACGAAUUGCUGGAA	7mer-1a	87
	||||||		
hsa-miR-338-3p (3' ... 5')	GUUGUUUUAGUGACUACGACCU		
hsa_circ_0006522 (5' ... 3')	AGCUUCAAGUUCUUGGAACAAAU	7mer-1a	91
	||||||		
hsa-miR-375 (3' ... 5')	AGUGCGCUCGGCUUGCUUGUUU		
hsa_circ_0006522 (5' ... 3')	CAUCACAAACUGUGGGAUCCCAA	8mer-1a	98
	|||||||		
hsa-miR-450b-3p (3' ... 5')	AUACCUACGUUUUACUAGGGUU		
hsa_circ_0006522 (5' ... 3')	CAUCACAAACUGUGGGAUCCCAA	8mer-1a	99
	|||||||		
hsa-miR-769-3p (3' ... 5')	UUGGUUCUGGGGCCUCUAGGGUC		
hsa_circ_0006522 (5' ... 3')	GUGCUGGCUGAAAACUGUUUCAG	7mer-1a	86
	||||||		
hsa-miR-494 (3' ... 5')	CUCCAAAGGGCACAUACAAAGU		
hsa_circ_0006522 (5' ... 3')	CCCUCCUGUUUAACAUGCAAAAG	7mer-1a	84
	|||| ||||||		
hsa-miR-507 (3' ... 5')	AAGUGAGGUUUUCC---ACGUUUU		
hsa_circ_0006522 (5' ... 3')	CCCUCCUGUUUAACAUGCAAAAG	7mer-1a	82
	||||||		
hsa-miR-557 (3' ... 5')	UCUGUUCCGGGUGGGCACGUUUG		
hsa_circ_0006522 (5' ... 3')	UUUUGAUUGCUAUGGAGGCACUG	7mer-m8	78
	|||||||		
hsa-miR-515-3p (3' ... 5')	UUGCGAGGUUUUCUUCCGUGAG		
hsa_circ_0006522 (5' ... 3')	UUUUGAUUGCUAUGG--AGGCACUG	7mer-m8	88
	||| |||||||		
hsa-miR-519e (3' ... 5')	UUGUGAGAUUUUCCUCCGUGAA		
hsa_circ_0006522 (5' ... 3')	UUGUGAAAACUGAUAUGGAGAAA	7mer-1a	91
	||||||		
hsa-miR-515-5p (3' ... 5')	GUCUUUCACGAAAGAAAACCUCUU		
hsa_circ_0006522 (5' ... 3')	UUUAUGCAGUAUCUGCUCCAGAG	7mer-m8	92
	|||||||		
hsa-miR-516b (3' ... 5')	UUUCACGAAGAAUGGAGGUCUA		
hsa_circ_0006522 (5' ... 3')	UUCCUGUCAUAGUGAUCCAGAAA	7mer-1a	77
	||||||		
hsa-miR-516b (3' ... 5')	UUUCACGAAGAAUGGAGGUCUA		
hsa_circ_0006522 (5' ... 3')	AAUUCUUUUGUCAAAUUUGCAAA	7mer-1a	86
	||||||		
hsa-miR-518a-5p (3' ... 5')	CUUUCCCGAAGGGAAACGUC		
hsa_circ_0006522 (5' ... 3')	AAUUCUUUUGUCAAAUUUGCAAA	7mer-1a	86
	||||||		
hsa-miR-527 (3' ... 5')	CUUUCCCGAAGGGAAACGUC		
hsa_circ_0006522 (5' ... 3')	AAACUGGAUCGAAUUGGUUCUUA	8mer-1a	99
	|||||||		
hsa-miR-548b-3p (3' ... 5')	UGUUUUCGUUGACUCCAAGAAC		
hsa_circ_0006522 (5' ... 3')	AGGUUGAGCAGGGAUGUUGUCAG	7mer-1a	80
	||||||		
hsa-miR-549 (3' ... 5')	UCUCGAGUAGGUAUCAACAGU		
hsa_circ_0006522 (5' ... 3')	UUCUCAUGGCUUGCCAUUCUCAA	8mer-1a	96
	|||||||		
hsa-miR-580 (3' ... 5')	GGAUUACUAAGUAGUAAGAGUU		
hsa_circ_0006522 (5' ... 3')	GAAUAAUGCUGUUAGACCAGUUU	7mer-m8	95
	|||| |||||||		
hsa-miR-582-3p (3' ... 5')	CCAAGUCAACAAGUUGGUCAAU		
hsa_circ_0006522 (5' ... 3')	CAUCACAAACUGUGGGAUCCCAA	7mer-1a	96
	||||||		
hsa-miR-638 (3' ... 5')	UCCGGCGGUGGGCGGGCGCUAGGGA		
hsa_circ_0006522 (5' ... 3')	UUCAUAUGGUGGCAAAGCUGCUG	7mer-m8	84
	|||||||		
hsa-miR-646 (3' ... 5')	CGGAGUCUCCGUCGACGAA		
hsa_circ_0006522 (5' ... 3')	GAGCAGGGAUGUUGU-CAGACAUC	7mer-m8	93
	|||| |||||||		
hsa-miR-654-3p (3' ... 5')	UUCCACUACCAGUCGUCUGUAU		
hsa_circ_0006522 (5' ... 3')	CUGCUGGAAUCGGGGGAACCAAA	8mer-1a	93
	|||||||		
hsa-miR-659 (3' ... 5')	ACCCCUGGGAGGGACUUGGUUC		
hsa_circ_0006522 (5' ... 3')	UCAACGAUGAACUUCGGGCCACC	7mer-m8	92
	|||||||		
hsa-miR-663b (3' ... 5')	GGAGUCCGUGCCGGCCCGGUGG		
hsa_circ_0006522 (5' ... 3')	UGCGCAUUUAGAUCAUCACAAAC	7mer-1a	84
	||||||		
hsa-miR-758 (3' ... 5')	CCAAUCACCUGGUCCAGUGUUU		
hsa_circ_0006522 (5' ... 3')	ACCUGGCAGAAAGGUUGAGCAGG	7mer-m8	89
	|||||||		
hsa-miR-767-3p (3' ... 5')	UCUUUGGUACCCCAUACUCGUCU		
hsa_circ_0006522 (5' ... 3')	GAAUUGCUGGAAUUAGAGGUAUU	7mer-m8	96
	|||||||		
hsa-miR-875-5p (3' ... 5')	GUGGACUAUUUUGACUCCAUAU		