

Supplementary Materials: Estrogen Repression of MicroRNAs is Associated with High Guanine Content in the Terminal Loop Sequences of Their Precursors

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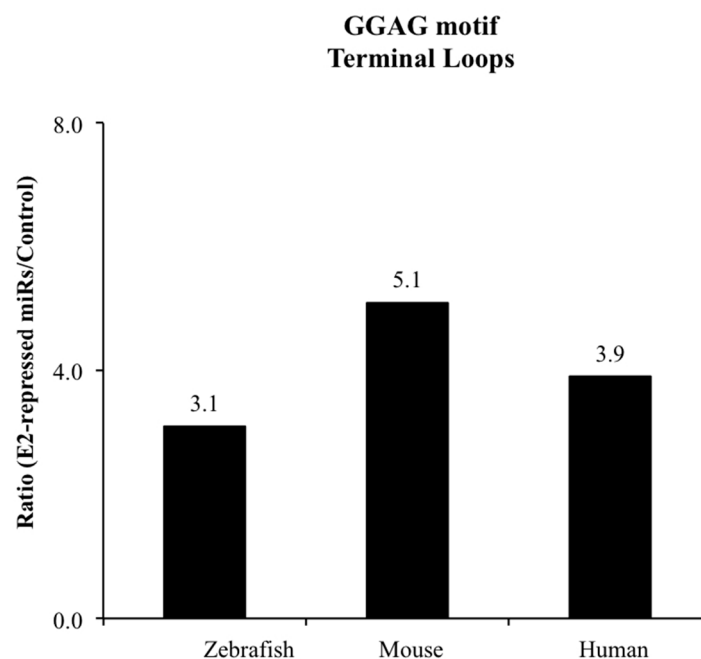


Figure S1. Relative enrichment of GGAG motif in terminal loops of the precursors of E2-repressed zebrafish, mouse and human miRNAs. The relative enrichment is represented as miRNA families.

Table S1. Lists of E2-repressed miRNAs in zebrafish liver, mouse uterus and human breast cancer MCF-7 cells and the overlap between them.

	Species			Common to			Only in			
	Zebrafish	Mouse	Human	Zebrafish-Mouse-Human	Zebrafish-Mouse	Zebrafish-Human	Mouse- Human	Zebrafish	Mouse	Human
microRNA	107a MI0001963	let-7d MI0000405	let-7a-1 MI0000060	miR-26a	let-7d	miR-26b	let-7g	miR-101b	miR-133a	miR-181a
	let-7d-1 MI0001868	26a-1 MI0000573	let-7a-2 MI0000061		miR-199		let-7f	miR-107a	miR-16	miR-181b
	let-7d-2 MI0001870	26a-2 MI0000706	let-7a-3 MI0000062		miR-143		let-7c	miR-338	miR-100	miR-181d
	143-1 MI0002007	125b-1 MI0000725	let-7c MI0000064		miR-126a		let-7a		miR-184	miR-193a
	143-2 MI0002008	125b-2 MI0000152	let-7f-1 MI0000067		miR-125b		miR-27b		miR-191	miR-193b
	125a-1 MI0001972	126a MI0000153	let-7f-2 MI0000068		miR-125a		miR-27a		miR-194	miR-203a
	125a-2 MI0001973	143 MI0000257	let-7g MI0000433		miR-145		miR-24		miR-195a	miR-203b
	125b-1 MI0001975	145a MI0000169	21 MI0000077				miR-23b		miR-214	miR-499a
	125b-2 MI0001976	199a-1 MI0000241	23a MI0000079				miR-23a		miR-29a	miR-499b
	125b-3 MI0001977	199a-2 MI0000713	23b MI0000439				miR-21		miR-30a	miR-520d*
	145 MI0002010	let-7a-1 MI0000556	24-1 MI0000080				miR-200c		miR-30c	
	126a MI0001979	let-7a-2 MI0000557	24-2 MI0000081						miR-30d	
	26a-1 MI0001923	let-7b MI0000558	26a-1 MI0000083						miR-30e	
	26a-2 MI0001925	let-7c-1 MI0000559	26a-2 MI0000750						miR-320	
	26a-3 MI0001926	let-7c-2 MI0000560	26b MI0000084						miR-497	
	26b MI0001927	let-7e MI0000561	27a MI0000085						miR-99a	
	199-1 MI0001373	let-7f-1 MI0000562	27b MI0000440						miR-99b	
	199-2 MI0001374	let-7f-2 MI0000563	98 MI0000100						let-7b	
	199-3 MI0001375	let-7g MI0000137	181a-1 MI0000289						let-7e	

101b MI0001961	let-7i MI0000138	181a-2 MI0000269
338-1	16-1 MI0000565	181b-1 MI0000270
MI0002063	16-2 MI0000566	181b-2 MI0000683
338-2	21a MI0000569	181d MI0003139
MI0002064	23a MI0000571	193a MI0000487
	23b MI0000141	193b MI0003137
	24-1 MI0000231	200a MI0000737
	24-2 MI0000572	200c MI0000650
	27a MI0000578	203a MI0000283
	27b MI0000142	203b MI0017343
	29a MI0000576	499a MI0003183
	30a MI0000144	499b MI0017396
	30c-1 MI0000547	520d* MI0003164
	30c-2 MI0000548	
	30d MI0000549	
	30e MI0000259	
	99a MI0000146	
	99b MI0000147	
	100 MI0000692	
	125a MI0000151	
	133a-1 MI0000159	
	133a-2 MI0000820	
	184 MI0000226	
	191 MI0000233	
	194-1 MI0000236	
	194-2 MI0000733	
	195a MI0000237	
	200c MI0000694	
	214 MI0000698	
	320 MI0000704	

let-7i

497a MI0004636

E2: 17beta-estradiol; miRNA: microRNA; MCF-7: Michigan Cancer Foundation-7.

Table S2. Sequences of stem-loops and terminal loops of E2-repressed and control miRNAs in zebrafish liver, mouse uterus and human breast cancer MCF-7 cells. The motif AGGGU is underlined in terminal loop sequences.

microRNA	Stem-Loop	Terminal loop
<i>Zebrafish-Estrogen regulated miRNAs (Cohen and Smith, 2014)</i>		
>dre-mir-107a MI0001963	UCUGUGUGCUCUGAGCUUCUUUACAGUGUUGUCUUGUGGCAUGGAGAUCAAGCAGCAUUGUACAGGGCUA UCACAGCACACUGAACAGC	UGGCAUGGAGAUCA
>dre-let-7d-1 MI0001868	UGUGCGUUGCGGUGUGAGGUAGUUGGUUGUAUGGUUUUGCAUAAUAAACAGCCCGGAGUUAACUGUACA ACCUUCUAGCUUCCCCUGCGGCUGCACG	UUGCAUAAUAAACAGCC CGGAGUUA
>dre-let-7d-2 MI0001870	CGCUGCAGGCUGAGGUAGUUGGUUGUAUGGUUUUGCAUAAUAAUCAGCCUGGAGUUAACUGUACAACCUU CUAGCUUCCCCUGCGGUG	UUGCAUCAUAAUCAGCC UGGAGUUA
>dre-mir-143- 1 MI0002007	GAUCUACAGUCGUCUGGCCCCGCGGUGCAGUGCUGCAUCUCUGGUCAACUGGGAGUCUGAGAUGAAGCACU GUAGCUCGGGAGGACAACACUGUCAGCUC	GGUCAACUGGGAGUC
>dre-mir-143- 2 MI0002008	GAUCUACAGUCGUCUGGCCCCGCGGUGCAGUGCUGCAUCUCUGGUCAACUGGGAGUCUGAGAUGAAGCACU GUAGCUCGGGAGGACAACACUGUCAGCUC	GGUCAACUGGGAGUC
>dre-mir- 125a-1 MI0001972	GUAUGUCUCUUUGUCCCCUGAGACCCUUAACCUUGUGAGGUCAAACUAGGUCACAGGUGAGGUCCUCAGGAA CAGGGCUGCAUGC	AGGUCAAACUAGGUCAC AGGU
>dre-mir- 125a-2 MI0001973	GAUCAGUCCAAAUCGAUGUAUGUCUGUGUCCCUGAGACCCUUAACCUUGUGAUGUCUCCAAGGUCACAGG UGAGGUCCUUGGGAACACGGCUGUAUAUGAUGACGUC	AUGUCUCCAAGGU
>dre-mir- 125b-1 MI0001975	UUCUGUUGCAGGUUGGCGGUUGGUCUGCAAAUGUGCCUCUCACAAUCCCUGAGACCCUAAACUUGUGACGU UUUCCUGUUAUGUGCACGGGUUAGGUUCUUGGGAGCUGAGAGGGGUGCUCUGUCAUCAGCCCGCCGGCGU CGGA	CGUUUCCUGUUAUGUG C
>dre-mir- 125b-2 MI0001976	GUGCCCCUCUCCUCCCCUGAGACCCUAAACUUGUGACGUUCUGCUUCGAUGUCCACGGGUUGGGUUCUCGGG AGCUGUGAGAGGCAC	CGUUCUGCUUCGAUGUC CA
>dre-mir- 125b-3 MI0001977	CCCGUGCGGCCACCGCUGCACUCCUCCUGGUCCCUGAGACCCUAAACUUGUGAGCUUUGUGUGCUAAAAAUC ACAGGUUAAGCUCUUGGGACCUGGGCAGAGGGCAAAAGCACUGG	GCUUUGUGUGCUAAAAA UC
>dre-mir-145 MI0002010	UCAGUCUUAUCAUUUCCUCAUCCCCGGGGUCCAGUUUUCCCAGGAAUCCCUUGGGCAAUCGAAAGGGGG AUUCCUGGAAAUACUGUUCUUGGGGUUGGGGGUGGACUACUGA	UUGGGCAAUCGAAAGGG

>dre-mir-126a MI0001979	GAGCCAUUUUAAACUGCUUCACAGUCCAUAUUACUUUUUGGUACGCGCUAGGCCAGACUCAAAACUCGUACC GUGAGUAAUAAUGCACUGUGGCAGUGGGUUU	CUAGGCCAGACUCAAAAC
>dre-mir-26a- 1 MI0001923	UUUGGCCUGGUUCAAGUAAUCCAGGAUAGGCUUGUGAUGUCCGGAAGCCUAUUCGGGAUGACUUGGUUC AGGAUAUGA	UGUGAUGUCCGGAAG
>dre-mir-26a- 2 MI0001925	GUGUGGACUUGAGUGCUGGAAGUGGUUGUUCUUUGUUAAGUAAUCCAGGAUAGGCUGUCUGUCCUGGA GGCCUAUUAUGAUUACUUGCACUAGGUGGCAGCCGUUGCCCUUCAUGGAACUCAUGC	GUCUGUCCUGGAGG
>dre-mir-26a- 3 MI0001926	CUAAGCUGAUACUGAGUCAGUGUGUGGCUGCAACCUGGUUCAAGUAAUCCAGGAUAGGCUUUGUGGACUA GGGUUGGCCUGUUCUUGGUUACUUGCACUUGGUUGCAGCUACUAAACAACUAAGAAGAUCAGAAGAG	UUGUGGACU <u>AGGGUU</u>
>dre-mir-26b MI0001927	GCAUUUGGCCUUUGCCUGGUUCAAGUAAUCCAGGAUAGGUUAGUUCCACUAGUACGGCCUAUUCUUGGU UACUUGUUUCAGGAGGAGGCUACGAGC	AGUUCCACU
>dre-mir-199- 1 MI0001373	UCCUGCUCGCUCAUCCCAGUGUUCAGACUACCUGUUCAGGAUCAUACUGGUGUACAGUAGUCUGCACAUAU GGUUAGACUGUGCAUGG	AGGAUCAUACUGGUG
>dre-mir-199- 2 MI0001374	GGAGUUUUUGUGGACGCCCUGCCCUGCCCAGUGUUCAGACUACCUGUUCAGGAUUAGUGUUUGUAC AGUAGUCUGCACAUUGGUUAGGCUGG	AGGAAUUAGUGUUUG
>dre-mir-199- 3 MI0001375	CCUCCCCCUCGCCUGCCCAGUGUUCAGACUACCUGUUCAUCAUGCUGCAGCUGAACAGUAGUCCGCACAUAU GGUUAGGCUGGGCUGGGACACACACAC	AUCAUGCUGCAGCUGA
>dre-mir- 101b MI0001961	GCUCCUCCGCUAUGAAUUGUCCAUAUUUCAGUUAUCAUGGUACCGGUGCUGUGGCCUGUCAAGUACAGUA CUAUGAUAAACUGAAGAUUGACGGUGCCAAACAUCAGUGGAGU	GUGUGCCUGUCAAG
>dre-mir-338- 1 MI0002063	GGUUUCUCCCUGCAACAAUCUCCUGAUGCUGCCUGAGUGUUUUUCUCCACUCCAGCAUCAGUGAUUUUG UUGCCGGAGGUCACC	GUGUUUUUCUCCAC
>dre-mir-338- 2 MI0002064	GUGUGUGUGUGUGUUUCUGGUGCCUGCUGAGAACAAUAUCCUGAUGCUGAAUGAGUGUGUUGAAGGAAA CUCCAGCAUCAGUGAUUUUGUUGCCAGAGGAGCACUUUGGGCAUCCUGUGUAUAU	GUGUGUUGAAGGAAAC
<i>Zebrafish-Control miRNAs</i>		
>dre-mir-10a MI0001363	UGUCUGUCAUCUAUAUAUACCCUGUAGAUCGAAUUUGUGUGAAUAUACAGUCGCAAAUUCGUGUCUUGG GGAAUAUGUAGUUGACAUAAACACAACGC	GUGAAUAUACAGUCG
>dre-mir-9-1 MI0001880	GGGGUUGGCUGUUAUCUUUGGUUAUCUAGCUGUAUGAGUGUUUAUUAUUCUUAUAAAGCUAGAUAAACC GAAAGUAACAAGAAUCCC	GUGUUUAUUAUUCUUA
>dre-mir-24-1 MI0001921	ACCUGAGCUCGCGGUGCCUUCUGAGCUGAUUAUCAGUUGUAGUAAAUCACUGGCUCAGUUCAGCAGGAACAG GAGUGUGGCC	GUUGUAGUAAAUCAC
>dre-mir-27a MI0001928	UCUGGAUAUGAUGUCUGCUGAAGUUUCGUGAGGUGCAGGACUUAGCUCACUCUGUGAACAGAUUCUGGAU AUCCUAUGUUCACAGUGGCUAAGUCCGCUCCUCUGAGGCCACACUCGAAUUCAGCCAGG	GAUCUCGGAUAUCCUAU G
>dre-mir-34b MI0003690	GGGGUUGGUCUGUAGGCAGUGUUGUAGCUGAUUGUUUCAUAUGAACUAUAAUCACUAACCAUACUGCCA ACACAACAACCUACA	UUUCAUAUGAACUA
>dre-mir-92a- 1 MI0001951	UGGUCCCUUUCUGCGCAGGUUGGAUUGGUAGCAAUGCUGUGUGUUUGAAGGUUUGCACUUGUCCCGG CCUGUAAAGGAUUGU	GUGUGUUUGAAGG

dre-mir-365-2 MI0002069	AGGCAGCAAGAAAAAUGAGGGACUUUUAGGGGCAGCUGUGUUUUUAUUAACCCAGUCAUAAUGCCCCUAAA AAUCCUUAUUGCUCUUGCAAUUUUCAGC	GCUGUGUUUUUAUUAACC CAGUCA
>dre-mir-430a-7 MI0002116	GUCACUAUCGGUACCCUCACAAAGGCACUGACUUGGAUGCUGUAAUUGGUAAGUGCUAUUUGUUGGGGUA GUUUCAAGUGAC	UGGAUGCUGUAAUUGG
>dre-mir-181c MI0002024	GGGUCCUGAUUCACAUUCAUUGCUGUCGGUGGGUUUUUAUCUCUUCGACUCGCCGGACAAUGAAUGAGAAC UACGGCUC	UUUUUAUCUCUUCGA
>dre-mir-187-1 MI0001370	UGACCUGUGGCUGGGCCAGGGGCUGCAACACAGGACAUGGGAGCUGUCUCACUCCCGCUCGUGUCUUG UGUUGCAGCCAGUGGAACG	GGGAGCUGUCUCUCACU CCCGCU
>dre-mir-19c MI0001905	UGGAAAAGCCCUGUUAUCUGGGGUGAGUUUUGCAGGAUUGCAUCCGGCUUUUAUACAACAUGCUGUGCAA AUCCAUGCAAAACUCGCUGCGCCAGGGACAAACCA	CUUUAAUACAACAUGC
>dre-mir-23a-1 MI0001913	GCUGUGGCGGGGAGGGUUCUGGCACCGUGAUUUGGUGGAUAAACAGAAAUGAAAAUCACAUUGCCAGGG AUUUCACUCCUGCACGGU	UUGGUGGAUAAACAGAA AUGAAA
>dre-mir-153a MI0002021	GGUUGCCAGUGUCAUUUUUGUGAUGUUGCAGCUAGUUUAUAGAGCCCAGUUGCAUAGUCACAAAAGUGA UCAUUGGAAACU	AGUUUAUAGAGCCCAG
>dre-mir-7147 MI0023606	GAGUGCCCAGUGCUGUACCAUGCUGGUAGCCAGUAUGAAAUAGGGCUUGCUGGUAACCAGCGUUGUGCCC CACUGGUUGCUC	AUGAAAUAGGGCUU
>dre-mir-2197 MI0010857	AGUGUAAAAGGAAAACGUUGUGAUGAUUCGACUCAUUGGUGCUAUGCAGUAAUAGAGGGCUGGAAGCA UUUUGCUUGAGGAGAGUCUAAUCACUAGCAGGUACACAUUG	CUAUGCAGUAAUAGAGG GCUGGAAG
>dre-mir-124-6 MI0001971	GGGUGGUGACACAGGCCCGCCACUCUGCGUGUUCACGGCGGACCUUGAUUUUAUUAUCCAUAACAAUUAAGG CACGCGGUGAAUGCCAAGAGAGGGGUCUUAACGACAAACCC	UUAUAUCCAUAACAAU
>dre-mir-219-2 MI0001385	UGAUUGUCCAAACGCAAUUCUUGUGAAAUGUCGAGCGAUCAGUCGAGAAUUGUGCCUGGACAUCUGUUGC UGGAGGCUC	GUGAAAUGUCGAGCGAU CAGUC
>dre-mir-2198 MI0010847	CGGCGAGCAAUACUCAUAAACUCCCAAGCGCCUGCGAACGCAAGCUCUCCUUAACCCCGGUGCAGAUGGAGCU CGUGUCCCAAGGCGCCUCCAGGCCUAAACCCGGGCCUC	CUCCUUAACCCGGUGCA GAUGG
>dre-mir-202 MI0002040	CUGUCCUUUUUCCUUAUGCAUUAUACCUCUUUGACAUGCUGCUUUAAGAGGCAUAGGGCAUGGGAAAAUG GGGCGG	ACAUGCUGCUUUA
>dre-mir-216a MI0001382	GCUGAUUUUUGGCAUAAUCUCAGCUGGCAACUGUGAGUAGUGUUUUAUCCCUUCACAGGCGCUGCUGG GGUUCUGUCACACACAGCA	GUAGUGUUUUAUCCCU C
>dre-mir-301b MI0002061	AAGGUCUGUUGCUUUGACGAUGUUGCACUACUGAACCAUCUAAUCAAGCAGUGCAAUAGUAUUGUCAUUG CAUUCGGCUUU	UGAACCAUCUAAUCAAG
>dre-mir-1306 MI0023609	UCCACCACCUCUUUGCUGCAAACGUCCAGUGACGCAGAGGAAAUGGACGUUAGCUCUGGUGGUGAUGGACA	GUGACGCAGAGGAAA
>dre-mir-217 MI0001383	AUGAGAACUUUCUGAUGUUGGUGAUACUGCAUCAGGAACUGAUUGGAUGAUUAUUCAGGAGCCAUCAGUU CCUGAUGCACUCCCAUCAGCAUCGAAAGA	AUGAUUAUUCAGGAG
>dre-mir-20b MI0001899	GAGUUUGUCCUGGCAGUUCCAAAGUGCUCACAGUGCAGGUAGUGCCAGUGGAUCUACUGCAAUGUCUGCA CUUCAAGUAUUGCCGGACGCCUUC	UGCCAGUGGAUCU

>dre-mir-29b-2 MI0001934	UCUUCCUCCAGAUGCUGGUUUACAUUGGUGGUUUAGAUGUGUUCUACCAAAGUCUAGCACCAUUUGAAAUCAGUGUUCUUGGGGAGGG	GAUGUGUUCUACCAAAGUC
>dre-mir-93 MI0001954	GUGUGUGUUAAAAGUGCUGUUUGUGCAGGUAGUGUGUUCCUCUACUGUAGGAGCAGCACUUCACAACACACAC	GUGUGUUUCCUC
>dre-mir-190a MI0002027	UCUGGAGGUGAGGUAGACCUGGAAGCCUUUCUGCAGGCCUCUGUUUGAUUAUGUUUGAUUAUUAGGUUGUUAUUCUGUCCAACUUAUAUCAAACAUAUCCUACAGUGUCCUGCUCUGUCUCCAG	UGUUAUUCUGUCCA
>dre-mir-196a-1 MI0001372	CGCGCGGCUGGUGCGUGGUUUAGGUAGUUUCAUGUUGUUGGGAUUUGGCUUCCUGGCUCGACAACAAGAAACUGCCUUGAUUACGUCAGUUCGUCUUAUCAAGGGC	AUUGGCUUCCUGG
>dre-mir-375-1 MI0002072	UGCACUUGCUIUACGUUGAGCCACACGCACAAUACAUGUGGAUUCAGUUUUGUUCGUUCGGCUCGCGUUAAGCAAGUGCA	ACAUGUGGAUUCAGU
>dre-mir-222a MI0001388	GCCGGUGGCUUGUUCGGGUGCUCAUGAGAUGCUCAGUAGUCAGUGUAGAUCUGUGUCACAAUCAGCAGCUACAUCUGGCUACUGGGUCUCUGAUGGCAUUUUCUGCU	UGUGUCACAAUCA
>dre-mir-499 MI0004766	ACUGAGAGGGAGGCAGUUAAGACUUGCAGUGAUGUUUAGAGAAUGUCACAUGAACAUCACUUUAAGUCUGUGCUGGCUCUGUUCUGAGU	GAGAAAUGUCACAUG
>dre-mir-205 MI0001378	AAACUACUGUGCAUUCUAUCCUUAUUCACCGGAGUCUGUGUAGUUGUUCAAUCAGAUUUCAGUGGUGUGAAGUGUAGGAAACACGGA	UGUAGUUGUCAAUCA
>dre-mir-140 MI0002003	GUGUUUGUCUCCUGUGUCCCGUCAGUGGUUUUACCCUAUGGUAGGUUACGUCAUGCUGUUCUACCACAGGUGAGAACCACGGACGGGAUGUCUGGAGGUGUCUGC	GUUACGUCAUGCUGUUC
>dre-mir-1788 MI0010838	UCAACCACUGUCUUGUAUCCGAGGCUUGUUUUAAAGUUGCCUGCGAUCUCUAAUAGACUCAGGCAGCUAAAGCAAGUCUGGGAGGCCAGAGACAACACGACA	AUCUCUUAUGACU
>dre-mir-363 MI0002067	UAAAUUGCAAAUAAUUGUCUUGCUGUUUUCGGGUGGAUGACUCUGCAAUUUUAAUAGUGAUGGAAAAACUUCAAUAAAAUUGCACGGUAUCCAUCUGUAAUCCGCUGGAUCCAUAUACCUGCGUUUG	AUUAGUGAUGGAAAAACUCAAUAAA
>dre-mir-182 MI0001368	GUUUUUGGCAAUGGUAGAACUCACACUGGUGAGGUAGUCAGAUCGGUGGUUCUAGACUUGCCAACUAGGUGGUGGUGGUGUUGGUUGGUGUCAAUUGUAUUGUCAAAAGUGCUUACAGUGCAGGUAGUAUUUUGGAAUAUCUACUGCAGUGGAGGCACUUCUAGCAAUACACUUGACCAUUUUUAAACCUUCCUCCAGGCAUCC	CUGGUGAGGUAGUCAGAUCCGG
>dre-mir-17a-1 MI0001897	GGACUUUCUUGAGUGGACUUGGUUGGUGUCAAUUGUAUUGUCAAAAGUGCUUACAGUGCAGGUAGUAUUUUGGAAUAUCUACUGCAGUGGAGGCACUUCUAGCAAUACACUUGACCAUUUUUAAACCUUCCUCCAGGCAUCC	GUUUUAUGGAAUAUCU
>dre-mir-727 MI0004771	CUGUAUGUCAUUUUCAGUCUUAUUCUCCUCCAGCCCGUACCCAUCGAAACUGUGAGUUGAGGCGAGUUGAAGACUUAAGUGCUGUACAG	CCGUACCAUCGAAACUGUGA
>dre-mir-2188 MI0010850	GGACAAUAUCAGCAAUGUGAGAAAGGUCCAACCUCACAUGUCCUGUGAGGCUGAAGGAAGGCUGUGUGAGGUUAGACCUAUCCCACACGGCCCGUAUUCUUCCC	UGUGAGGCUGAAGGAAGG
>dre-mir-204-2 MI0002042	GUGUUGCUCUAGUGACCAGUUUGUGACCUCUGGGUUUCCCUUUGUCAUCCUAUGCCUGCAGUUCUGAUUGAGGCUGGGACAGCAAAGGGAGGUUCAGAUUGUCGACCUGUACUACAGUCAAUAC	GCAGUCCUGAUGAG
>dre-mir-206-1 MI0002045	GAAUGUUGCCUCUUGUGAAGACAUGCUUCCUUAUAUGCCCAUAUUAUUGCUCAAGUUAUGGAAUGUAAGGAAGUGUGUGGUUUCAGGGGGAAAUUUGUC	UUAAUGCUCAAGUUA
>dre-mir-193a-1 MI0002029	GACAUUAAUGUGUUAGAGGUUGGGUCUUUGCGGGCAAGGUGAGUAGUUAUUUACUCUCAACUGGCCUACAAAGUCCCAGUUUCUGGCUCAUGUUAUC	GUAGUAAAAUUUACUCUC

>dre-mir-137-2 MI0002001	GUUCUGUUGUUUCCCCUCUAUAAAGGACUCUCUUCGGUGACGGGUAUUCUUGGGUGGAUAAUACGGCUCUC GUUGUUAUUGCUIAAGAAUACGCGUAGUCGAGGAGAGUCAUGUCGGCGGCGAGAGAGC	CGGCUCUCGUUG
>dre-mir-135b MI0003364	CUCUUUGCCCCGUAUGGCUUUUUUUAUCCUAUCUGAGAAUUGCUCAGGACUCAUAUAGGGAUGGAAGCCAU GCAGGGCUGGGG	AGAAUUGCUCAGGACUC
>dre-mir-132-1 MI0001989	GUCUCCAUGGCGACCGUGGCAUUAAGAUUGUUAACUGUAGGAACAGAAUUUUUGGUAACAGUCUACAGCCAU GGUCGCUAGUGGGCA	GUAGGAACAGAAUUUUU GG
>dre-mir-133a-1 MI0001993	CAUCAAACCACAAUGCUUUGCUAAAGCUGGUA AAAAUGGAACCAAUACACCUCUCAAUGGAUUUGGUCCC CUUCAACCAGCUGUAGCUAUGCUUUGAUG	CACCUCUCAAUGGA
>dre-mir-203a MI0001376	GUGUUUGGGUCUCUUCUGGUCCCUCUGGUGCAGUGGUUCUUAACAGUUAACAGUUCUAUCUAAAAUUG UGAAUUGUUUAGGACCACUUGACCAG	UCUAUCUAAAAU
>dre-mir-723 MI0004767	UGCGUAGAGAUAAAGACAGUUUUAAAUGAUGUUACUUUUUUCAAUUGGAGAAAGACAUCAAUAAAUC UGUGCUUAUCUCUACAAGCA	UUUUCAAAUGGAGA
>dre-mir-221 MI0001387	GUCGUGAACCUGGCAUACAAUGUAGAUUUCUGUGUGGUACUACUACAGCUACAUUGUCUGCUGGGUUUC AGGCCAGCAGAAUAAUUCUGCUC	GUGGUACUAUCUAC
>dre-mir-138 MI0002002	UGUGUGCUGCAGCUGGUGUUGUGAAUCAGGCCGAUGUCACACGUCAGCGAUAAACCCGGCUAUUUCACAAC ACCAGGGUGGCACCACA	GAUGUCACACGUCAGCG AUAACCCG
<i>Mouse-Estrogen regulated miRNAs (Yamagata et al. 2009)</i>		
>mmu-let-7d MI0000405	AAUGGGUUCUAGGAAGAGGUAGUAGGUUGCAUAGUUUUAGGGCAGAGAUUUUGCCCACAAGGAGUUAA CUAUACGACCUGCUGCCUUCUUAAGGGCCUUAU	UUAGGGCAGAGAUUUUG CCCACAAGGAGUUAA
>mmu-mir-26a-1 MI0000573	AAGGCCGUGGCCUCGUUCAAGUAAUCCAGGAUAGGCUGUGCAGGUCCCAAGGGGCCUAUUCUUGGUUACU UGCACGGGGACGCGGGCCUG	GUGCAGGUCCCAAGGGG
>mmu-mir-26a-2 MI0000706	GGCUGCGGCUGGAUUAAGUAAUCCAGGAUAGGCUGUGUCCGUCCAUGAGGCCUGUUCUUGAUUACUUGU UUCUGGAGGCAGCG	GUGUCCGUCCAUGAGG
>mmu-mir-125b-1 MI0000725	UGCUCUCCCCUCAGUCCUGAGACCCUAAUUGUGAUGUUUACCGUUUAAAUCCACGGGUUAGGCUCUUG GGAGCUG	UGUUUACCGUUUAAAUC C
>mmu-mir-125b-2 MI0000152	GCCUAGUCCCUGAGACCCUAAUUGUGAGGUUUUUAGUAACAUCACAAGUCAGGUUCUUGGGACCUAGG C	GGUAUUUUAGUAACAUC
>mmu-mir-126a MI0000153	UGACAGCACAUUAUUACUUUUGGUACGCGCUGUGACACUUCAAACUCGUACCGUGAGUAAUAAUGCGCGG UCA	CUGUGACACUCAAAC

>mmu-mir-143 MI0000257	CCUGAGGUGCAGUGCUGCAUCUCUGGUCAGUUGGGAGUCUGAGAUGAAGCACUGUAGCUCAGG	UCAGUUGGGAGUC
>mmu-mir-145a MI0000169	CUCACGGUCCAGUUUUCCCCAGGAAUCCCUUGGAUGCUAAGAUGGGGAUUCCUGGAAAUACUGUUCUUGAG	UGGAUGCUAAGAUGGGG
>mmu-mir-199a-1 MI0000241	GCCAUCCCAGUGUUCAGACUACCUGUUCAGGAGGCUGGGACAUGUACAGUAGUCUGCACAUUGGUUAGGC	AGGAGGCUGGGACAUGU
>mmu-mir-199a-2 MI0000713	UGGAAGCUUCAGGAGAUCCUGCUCCGUCGCCCCAGUGUUCAGACUACCUGUUCAGGACAAUGCCGUUGUA CAGUAGUCUGCACAUUGGUUAGACUGGGCAAGGGCCAGCA	AGGACAAUGCCGUUGU
>mmu-let-7a-1 MI0000556	UUCACUGUGGGAUGAGGUAGUAGGUUGUAUAGUUUAGGGUCACACCCACCACUGGGAGAUAAACUUAACA AUCUACUGUCUUUCCUAAGGUGAU	UUAGGGUCACACCCACC ACUGGGAGAUAA
>mmu-let-7a-2 MI0000557	CUGCAUGUUCCCAGGUUGAGGUAGUAGGUUGUAUAGUUUAGAGUUACAUAAGGGAGAUAAACUGUACAG CCUCCUAGCUUUCUUGGGACUUGCAC	UAGAGUUACAUAAGGG AGAUAA
>mmu-let-7b MI0000558	GCAGGGUGAGGUAGUAGGUUGUGUGGUUUCAGGGCAGUGAUGUUGCCCCUCCGAAGAUAAACUUAACAACC UACUGCCUUCUCCUGA	UCAGGGCAGUGAUGUUG CCCCUCCGAAGAUAA
>mmu-let-7c-1 MI0000559	UGUGUGCAUCCGGGUUGAGGUAGUAGGUUGUAUAGGUUAGAGUUACACCCUGGGAGUUAACUGUACAACC UUCUAGCUUUCUUGGAGCACACU	UAGAGUUACACCCUGGG AGUUA
>mmu-let-7c-2 MI0000560	ACGGCCUUUGGGGUGAGGUAGUAGGUUGUAUAGGUUUGGGCUCUGCCCCGCUCUGCGGUAACUUAACA CUACUGUCUUUCCUGAAGUGGCCGC	UUUGGGCUCUGCCCCGCU CUGCGGUAA
>mmu-let-7e MI0000561	CGCGCCCCCGGGCUGAGGUAGGAGGUUGUAUAGUUGAGGAAGACACCCGAGGAGAUACUUAACGGCCU CCUAGCUUUCUCCAGGCUGCGCC	GAGGAAGACACCCGAGG AGAUCA
>mmu-let-7f-1 MI0000562	AUCAGAGUGAGGUAGUAGAUUGUAUAGUUGUGGGGUAGUGAUUUUACCCUGUUUAGGAGAUAAACUUAAC AAUCUAUUGCCUUCUCCUGAG	GUGGGGUAGUGAUUUUA CCCUGUUUAGGAGAUAA
>mmu-let-7f-2 MI0000563	UGUGGGAUGAGGUAGUAGAUUGUAUAGUUUAGGGUCAUACCCCAUCUUGGAGAUAAACUUAACAGUCUA CUGUCUUUCCACG	UUAGGGUCAUACCCCAU CUUGGAGAUAA
>mmu-let-7g MI0000137	CCAGGCUGAGGUAGUAGUUUGUACAGUUUGAGGGUCUAUGAUACACCCGGUACAGGAGAUAAACUGUACA GGCCACUGCCUUGCCAGG	UGAGGGUCUAUGAUACC ACCCGGUACAGGAGAUAA
>mmu-let-7i MI0000138	CUGGCUGAGGUAGUAGUUUGUCUGUUGGUCGGGUUGUGACAUUGCCCGCUGUGGAGAUAAACUGCGCAAG CUACUGCCUUGCUAG	GGUCGGGUUGUGACAUU GCCCCGUGUGGAGAUAA
>mmu-mir-16-1 MI0000565	AUGUCAGCGGUGCCUAGCAGCACGUAAAUAUUGGCGUUAAGAUUCUGAAAUAUACCUCAGUAUUGACUG UGCUGCUGAAGUAAGGUUGGCAA	UUAAGAUUCUGAAAUA CCU
>mmu-mir-16-2 MI0000566	CAUGCUUGUCCACUCUAGCAGCACGUAAAUAUUGGCGUAGUGAAAUAUAAACACCAAUAUUAU GUGCUGCUUAGUGUGACAGGGAUA	UAGUGAAAUAUAAUA AAC

>mmu-mir-21a MI0000569	UGUACCACCUUGUCGGAUAGCUUAUCAGACUGAUGUUGACUGUUGAAUCUCAUGGCAACAGCAGUCGAUG GGCUGUCUGACAUUUUGGUAUC	CUGUUGAAUCUCAUGG
>mmu-mir-23a MI0000571	CGGACGGCUGGGGUUCCUGGGGAUGGGAAUUUGAUGCCAGUCACAAAUCACAUUGCCAGGGAAUUCCAACU GACCC	GAUGCCAGUCACAA
>mmu-mir-23b MI0000141	GGCUGCUUGGGUUCCUGGCAUGCUGAUUUUGUGACUUGAGAUUAAAAUCACAUUGCCAGGGAAUACCACGC AACC	GUGACUUGAGAUUAAA
>mmu-mir-24-1 MI0000231	CUCCGGUGCCUACUGAGCUGAU AUCAGUUCUCAUUUCACACACUGGCUCAGUUCAGCAGGAACAGGAG	UCUCAUUUCACACAC
>mmu-mir-24-2 MI0000572	GCCUCUCUCCGGGCUCCGCCUCCCGUGCCUACUGAGCUGAAACAGUUGAUUCCAGUGCACUGGCUCAGUUC AGCAGGAACAGGAGUCCAGCCCCUAGGAGCUGGCA	UGAUUCCAGUGCAC
>mmu-mir-27a MI0000578	UGGCCUGAGGAGCAGGGCUUAGCUGCUUGUGAGCAAGGUCCACAGCAAAGUCGUGUUCACAGUGGCUAAG UUCCGCCCCCUGGACCC	AGGUCCACAGCAAAGUC GUG
>mmu-mir-27b MI0000142	AGGUGCAGAGCUUAGCUGAUUGGUGAACAGUGAUUGGUUUCGCUUUGUUCACAGUGGCUAAGUUCUGCA CCU	AGUGAUUGGUUUCGCU UUG
>mmu-mir-29a MI0000576	ACCCCUUAGAGGAUGACUGAUUUUCUUUUGGUGUUCAGAGUCAAUAGAAUUUUCUAGCACCAUCUGAAAUC GGUUAUAAUGAUUGGGGA	AGUCAAUAGAAUUUUC
>mmu-mir-30a MI0000144	GCGACUGUAAACAUCUCCUGACUGGAAGCUGUGAAGCCACAAAUGGGCUUUCAGUCGGAUGUUUGCAGCUG C	CUGUGAAGCCACAAAUG GG
>mmu-mir-30c-1 MI0000547	ACCAUGUUGUAGUGUGUGUAAACAUCUACACUCUCAGCUGUGAGCUCAAGGUGGCUGGGAGAGGGUUGU UUACUCCUUCUGCCAUGGA	UGUGAGCUCAAGGUGG
>mmu-mir-30c-2 MI0000548	GAGUGACAGAU AUUGUAAACAUCUACACUCUCAGCUGUGAAAAGUAAGAAAGCUGGGAGAAGGCUGUU UACUCUCUCUGCCUU	UGUGAAAAGUAAGAAAG
>mmu-mir-30d MI0000549	AAGUCUGUGUCUGUAAACAUCGCGACUGGAAGCUGUAAGCCACAGCCAAGCUUUCAGUCAGAUGUUUGC UGCUACUGGCUC	CUGUAAGCCACAGCCAA G

>mmu-mir-30e MI0000259	GGGCAGUCUUUGCUACUGUAAACAUCCUUGACUGGAAGCUGUAAGGUGUUGAGAGGAGCUUUCAGUCGGA UGUUUACAGCGGCAGGCUGCCA	CUGUAAGGUGUUGAGAG GAG
>mmu-mir-99a MI0000146	CAUAAACCCGUAGAUCCGAUCUUGUGGUGAAGUGGACCGCGCAAGCUCGUUUCUAUGGGUCUGUG	GUGAAGUGGACCGCG
>mmu-mir-99b MI0000147	GGCACCCACCCGUAGAACCGACCUUGCGGGGCCUUCGCCGCACACAAGCUCGUGUCUGUGGGUCCGUGUC	GGGCCUUCGCCGCACA
>mmu-mir-100 MI0000692	CCUGUUGCCACAAACCCGUAGAUCCGAACUUGUGCUGAUUUCUGCACACAAGCUUGUGUCUAUAGGUAUGU GUCUGUUAGG	CUGAUUCUGCACAC
>mmu-mir-125a MI0000151	CUGGGUCCCUGAGACCCUUUAACCUUGUGAGGACGUCCAGGGUCACAGGUGAGGUUCUUGGGAGCCUGG	GGACGUCCAGGGUC
>mmu-mir-133a-1 MI0000159	GCUAAAGCUGGUAAAAUGGAACCAAAUCGCCUCUUCAAUGGAUUUGGUCCCCUUAACCAGCUGUAGC	CGCCUCUUCAAUGGA
>mmu-mir-133a-2 MI0000820	AGAAGCCAAAUGCUUUGCUGAAGCUGGUAAAAUGGAACCAAAUCAGCUGUUGGAUGGAUUUGGUCCCCU CAACCAGCUGUAGCUGCGCAUUGAUCACGCCGCA	CAGCUGUUGGAUGGA
>mmu-mir-184 MI0000226	CCUUUCCUUAUCACUUUCCAGCCAGCUUUGUGACUCUAAGUGUUGGACGGAGAACUGAUAAGGGUAGG	UUUGUGACUCUAAGUGU
>mmu-mir-191 MI0000233	AGCGGGCAACGGAAUCCCAAAAGCAGCUGUUGUCUCCAGAGCAUUCAGCUGCACUUGGAUUUCGUUCCC UGCU	UUGUCUCCAGAGCAUUC CA
>mmu-mir-194-1 MI0000236	AUCGGGUGUAAACAGCAACUCCAUGUGGACUGUGCUCGGAUUCAGUGGAGCUGCUGUACUUCUGAU	CUGUGCUCGGAUU
>mmu-mir-194-2 MI0000733	GUGGCUCCCACCCUCUGUAACAGCAACUCCAUGUGGAAGUGCCCACUGGUUCCAGUGGGGCUGCUGUUAU CUGGGGUGGCGGCUAG	AGUGCCCACUGGUU
>mmu-mir-195a MI0000237	ACACCCAACUCUCCUGGCUCUAGCAGCACAGAAAUAUUGGCAUGGGGAAGUGAGUCUGCCAAUAUUGGCU GUGCUGCUCCAGGCAGGGUGGUGA	AUGGGGAAGUGAGUCUG

>mmu-mir-200c MI0000694	CCCUCGUCUUACCCAGCAGUGUUUGGGUGCUGGUUGGGAGUCUCUAAUACUGCCGGGUAAGAUGGAGG	GUGCUGGUUGGGAGUCU C
>mmu-mir-214 MI0000698	GGCCUGGCUGGACAGAGUUGUCAUGUGUCUGCCUGUCUACACUUGCUGUGCAGAACAUCCGCUCACCUGU ACAGCAGGCACAGACAGGCAGUCACAUGACAACCCAGCCU	AGAACAUCCGCUCACCU GU
>mmu-mir-320 MI0000704	GCCUCGCCGCCCUCCGCCUUCUCUUCGCCGGUUCUUCGCCGAGUCGGGAAAAGCUGGGUUGAGAGGGCGAAA AAGGAUGUGGG	CGGAGUCGGG
>mmu-mir-497a MI0004636	CCUGCCCCCGCCCCAGCAGCACACUGUGGUUUGUACGGCACUGUGGCCACGUCCAAACCACACUGUGGUGU UAGAGCGAGGGUA	CGGCACUGUGGCCACGU C

Mouse-Control miRNAs

>mmu-mir-10a MI0000685	GACCUGUCUGUCUUCUGUAUAUACCCUGUAGAUAUCCGAAUUUGUGUAAGGAAUUUUGUGGUCACAAAUUCG UAUCUAGGGGAUAUGUAGUUGACAUA AACACUCCGCUA	UAAGGAAUUUUGUGGUC A
>mmu-mir-9-1 MI0000720	CGGGGUUGGUUGUUAUCUUUGGUUAUCUAGCUGUAUGAGUGGUGUGGAGUCUUCAUAAAGCUAGAUAA CGAAAGUAAAAUAACCCCA	GUGGUGUGGAGUCUUC
>mmu-mir-34b MI0000404	GUGCUCGGUUUGUAGGCAGUGUAAUAGCUGAUUGUAGUGCGGUGCUGACAAUCACU AACUCCACUGCCA UCAAAACAAGGCAC	AGUGCGGUGCUGAC
>mmu-mir-92a-1 MI0000719	CUUUCUACACAGGUUGGGAUUUGUCGCAAUGCUGUGUUUCUCUGUAUGGU AUUGCACUUGUCCCGGCCUG UUGAGUUUGG	GUGUUUCUCUGUAUGG
>mmu-mir-365-2 MI0001645	AGAGUGAUCAAGGACAGCAAGAAAAAUGAGGGACUUUCAGGGGCAGCUGUGUUUCCUGACUCAGUCAUAA UGCCCCUAAAAAUCCUUAUUGUUCUUGCAGUGUGCAUCGGAG	UUUCCUGACUCAGUCA
>mmu-mir-431 MI0001524	CGUCCUGCGAGGUGUCUUGCAGGCCGUAUGCAGGCCACACUGACGGUAACGUUGCAGGUCGUCUUGCAG GGCUUCUCGCAAGACGACAUC	GGCCACACUGACGGUAA CGUUG
>mmu-mir-25 MI0000689	GGCCAGUGUUGAGAGGCGGAGACUUGGGCAAUUGCUGGACGCUGCCCUGGGCAUUGCACUUGUCUCGGUC UGACAGUGCCGGCC	UGGACGCUGCCCUGGG
>mmu-mir-28a MI0000690	GGUCCCUACCUUCAAGGAGCUCACAGUCUAUUGAGUUGCCUUCUGAUUUCUCCACUAGAUUGUGAGCUG CUGGAGGGCAGGCACU	UUGCCUUCUGAUUCUC C

>mmu-mir-181c MI0000724	GCCAAGGGUUUGGGGGAACAUUCAACCUGUCGGUGAGUUUGGGCAGCUCAGACAAACCAUCGACCGUUGA GUGGACCCCCGAGGCCUGGA	UUGGGCAGCUCAGACAA
>mmu-mir-187 MI0000229	UCAGGCUACAACACAGGACCCGGGCGCUGCUCUGACCCCUCGUGUCUUGUGUUGCAGCCGG	CGCUGCUCUGACCCC
>mmu-mir-19b-1 MI0000718	CACUGGUCUAUGGUUAGUUUUGCAGGUUUGCAUCCAGCUGUAUAAUUAUUCUGCUGUGCAAAUCCAUGCAA AACUGACUGUGGUGGUG	UGUAUAAUUAUUCUGC
>mmu-mir-22 MI0000570	ACCUGGCUGAGCCGCAGUAGUUCUUCAGUGGCAAGCUUUAUGUCCUGACCCAGCUAAAGCUGCCAGUUGA AGAACUGUUGCCCUCUGCCCCUGGC	UGUCCUGACCCAGCUA
>mmu-mir-153 MI0000175	CGGUGUCAUUUUUGUGACGUUGCAGCUAGUAAUAUGAGCCCAGUUGCAUAGUCACAAAAGUGAUCAUUG	AGUAAUAUGAGCCCAG
>mmu-mir-124-1 MI0000716	AGGCCUCUCUCUCCGUGUUCACAGCGGACCUUGAUUUAAAUGUCCAUACAAUUAAGGCACGCGGUGAAUG CCAAGAAUGGGGCUG	UUAAAUGUCCAUACAAU
>mmu-mir-219a-2 MI0000741	ACUCAGGGGCUUCGCCACUGAUUGUCCAAACGCAAUUCUUGUACGAGUCUGCGGCCAACCGAGAAUUGUG GCUGGACAUCUGUGGUUGAGCUCCGGG	UGUACGAGUCUGCGGCC AACCG
>mmu-mir-202 MI0000245	GUUCCUUUUUCCUAUGCAUAUACUUCUUGUGGAUCUGGUCUAAAGAGGUUAAGCGCAUGGGAAGAUGG AGC	GUGGAUCUGGUCUAA
>mmu-mir-216a MI0000699	UUGGUUUAAUCUCAGCUGGCAACUGUGAGAUGUCCCUAUCAUUCCUCACAGUGGUCUCUGGGAUUAUGCU AA	GAUGUCCCUAUCAUUCC U
>mmu-mir-301b MI0004122	UUUCCUGCUGGCUGCGGGUGCUCUGACUAGGUUGCACUACUGUGCUGUGAGAAGCAGUGCAAUGGUAAUUG UCAAGCAUCUGGGACCAGCCUCGAAG	GUGCUGUGAGAAG
>mmu-mir-1306 MI0009935	CAGUCUCCACCACCUCUCCUGCAAACGUCCAGUGAUGCAGAGGUAAUGGACGUUGGCUCUGGUGGUGAUG GACAGUCCG	AGUGAUGCAGAGGUAAU GG
>mmu-mir-217 MI0000731	AAACAUAGUCAUUAACAGUUUUUGAUGUUGCAGAUACUGCAUCAGGAACUGACUGGAUAAGACUUAUCC CAUCAGUUCCUAAUGCAUUGCCUUCAGCAUCUAAACAA	UAAGACUUAUCC
>mmu-mir-20b MI0003536	CCUAGUAGUGCCAAAGUGCUCUAGUGCAGGUAGUUUUUAUACCACUCUACUGCAGUGUGAGCACUUCUA GUACUCCUGG	UUUUUAUACCACUCU

>mmu-mir-93 MI0000581	AGUCAUGGGGGCUCCAAAGUGCUGUUCGUGCAGGUAGUGUAAUUACCUGACCUACUGCUGAGCUAGCACU UCCCGAGCCCCCAGGACA	UGUAAUUACCUGACCU
>mmu-mir-190a MI0000232	CUGUGUGAU AUGUU GAUAUAUUAGGUUGUUAUUUAAUCCAACUAUAUAUCAAGCAUAUUCCUACAG	UGUUAUUUAAUCCA
>mmu-mir-196a-1 MI0000552	UGAGCCGGGACUGUUGAGUGAAGUAGGUAGUUUCAUGUUGUUGGGCCUGGCUUUCUGAACACAACGACAU CAAACCACCUGAUUCAUGGCAGUUACUGCUUC	CCUGGCUUUCUGAACA
>mmu-mir-375 MI0000792	CCCCGCGACGAGCCCCUCGCACAAACCGGACCUGAGCGUUUUGUUCGUUCGGCUCGCGUGAGGC	CGGACCUGAGCGU
>mmu-mir-222 MI0000710	CCCUCAGUGGCUCAGUAGCCAGUGUAGAUAUCCUGUCUUUGGUAUUCAGCAGCUACAUCUGGCUACUGGGUC UCUGGUGGC	GUCUUUGGUAUUCAGC
>mmu-mir-671 MI0004133	UGGCAGGCCAGGAAGAGGAGGAAGCCCUGGAGGGGCUGGAGGUGAUGGAUGUUUCCUCCGGUUCUCAGG GCUCCACCUCUUUCGAGCCGUAGAGCCA	GUGAUGGAUGUUUCC
>mmu-mir-1a-1 MI0000139	GCUUGGGACACAUACUUCUUUAUAUGCCCAUAUGAACCUGCUAAGCUAUGGAAUGUAAAGAAGUAUGUA UUUCAGGC	UGAACCUGCUAAGCUA
>mmu-mir-205 MI0000248	CUCUUGUCCUUAUUAUCCACCGGAGUCUGUCUUAUGCCAACCAGAUUUCAGUGGAGUGAAGCUCAGGAG	UCUUAUGCCAACCA
>mmu-mir-300 MI0000400	GCUACUUGAAGAGAGGUUAUCCUUUGUGUGUUUGCUUUACGCGAAAUGAAUAUGCAAGGGCAAGCUCUCU UCGAGGAGC	GUGUUUGCUUUACGCGA AAUGAA
>mmu-mir-32 MI0000691	GGAGAU AUUGCACAUUACUAAGUUGCAUGUUGUCACGGCCUCAAUGCAAUUUAGUGUGUGUGAU AUUUU C	UGUUGUCACGGCCUCAA UG
>mmu-mir-127 MI0000154	CCAGCCUGCUGAAGCUCAGAGGGCUCUGAUUCAGAAAGAUCAUCGGAUCCGUCUGAGCUUGGCUGGUCGG	UCAGAAAGAUCA
>mmu-mir-134 MI0000160	AGGGUGUGUGACUGGUUGACCAGAGGGGCGUGCACUCUGUUCACCCUGUGGGCCACCUAGUCACCAACCC U	CGUGCACUCUGUUCACC
>mmu-mir-136 MI0000162	GAGGACUCCAUUUGUUUGAUGAUGGAUUCUUAAGCUCCAUCAUCGUCUCAA AUGAGUCUUC	AUUCUUAAGCUCC

>mmu-mir-140 MI0000165	CCUGCCAGUGGUUUUACCCUAUGGUAGGUUACGUCAUGCUGUUCUACCACAGGGUAGAACCACGGACAGG	GUUACGUCAUGCUGUUC
>mmu-mir-150 MI0000172	CCCUGUCUCCCAACCCUUGUACCAGUGCUGUGCCUCAGACCCUGGUACAGGCCUGGGGGAUAGGG	CUGUGCCUCAGACC
>mmu-mir-411 MI0001163	UGGUACUUGGAGAGAUAGUAGACCGUAUAGCGUACGCUUUAUCUGUGACGUAUGUAACACGGUCCACUAA CCCUCAGUAUCA	CUUUAUCUGUGACG
>mmu-mir-3090 MI0014083	UUCCUGUCCCAGUGGUCUGGGUGGGGCCUGAGAUCUGAAUUCUAAUGAGCUGCCAGGUGACACCCUGA CUCACUGUGCCAGAGGA	CUGAAUUCUAAUGAGC
>mmu-mir-5627 MI0019198	AGAGGGUGCGCCGGGCCUGCGUCCCCGCCCUAGAGGACAGGGCUCUCCGGCGCCCCUCGU	UCCCCGCCCUAGAGG
>mmu-mir-1981 MI0009992	GUAAAGGCUGGGCUUAGACGUGGCCUUUGGGUGUGGAAUGCACUUCGCUUUGUAACCGCCAUCUAACCCU GGCCUUGACAG	CUUUGGGUGUGGAAUGC ACUCCGUUUGUAACCG C
>mmu-mir-875 MI0005551	UCUGUGGUACUAUACCUCAGUUUUAUCAGGUGUUCAUUAAAAUACCCUGAAAAUACUGAGGCUAUGUUUC ACUGAGCA	UUCAUAAAAUCA
>mmu-mir-675 MI0004123	UGCGGCCACAGGACUGGUGCGGAAAGGGCCCACAGUGGACUUGGUACACUGUAUGCCCUAACCGCUCAGU CCCUGGGUCUGGCA	GGACUUGGUACA
>mmu-mir-466d MI0005546	CAUGUGUGUUUGUGUGUGCGUACAUGUACAUGUGUGUAUAUGAAUUAACAUACACACGCACACAU AGAUACGCACGCACACACACACAGG	UGUGUGUAUAUGAAUUA ACA
>mmu-mir-351 MI0000643	CAUGGCACCUCCGUUCCCCUGAGGAGCCCUUUGAGCCUGGAGUGAAAAAACAAGAGGCGC CUGGGAACUGGAGAAGAGUGUAAACUUC	GAGUGAAAAAACA A
>mmu-mir-330 MI0000607	GACCCUUUGGCGAUCUCUGCCUCUCUGGGCCUGUGUCUUAAGGCUCUUAAGAUAACGAGCAAAGCACA GGGCCUGCAGAGAGGUAGCGCUCUGCUC	UCUUAAGAUAACGA
>mmu-mir-292a MI0000390	CAGCCUGUGAUACUCAAACUGGGGGCUCUUUUGGAUUUUAUCGGAAGAAAAGUGCCGCCAGGUUUUGAG UGUCACCGGUUG	GAUUUUAUCGGAAGA

>mmu-mir-155 MI0000177	CUGUUA AUGCUAAUUGUGAUAGGGGUUUUGGCCUCUGACUGACUCCUACCUGUUAGCAUUAACAG	UUUGGCCUCUGA
>mmu-mir-182 MI0000224	ACCAUUUUUGGCAAUGGUAGAACUCACACCGGUAAGGUA AUGGGACCCGGUGGUUCUAGACUUGCCAACU AUGGU	GUAAGGUA AUGGGACCC G
>mmu-mir-17 MI0000687	GUCAGAAUAAUGUCAAGUGCUUACAGUGCAGGUAGUGAUGUGGCAUCUACUGCAGUGAGGGCACUUGU AGCAUUAUGCUGAC	UGAUGUGUGCAUCU
>mmu-mir-450a-1 MI0001653	GAGAGAUACUGAGCUGUUUUUGCGAUGUGUCCUAAUAUGUGCUAAUAAUUAUUGGGAACA UUUUGCA UAAAUAGCUUUGUGUCAAUACA	GUGCUAUAAUUAU
<i>Human MCF-7 cells-Estrogen regulated miRNAs (Maillot et al. 2009)</i>		
>hsa-let-7a-1 MI0000060	UGGGAUGAGGUAGUAGGUUGUAUAGUUUUAGGGUCACACCCACCACUGGGAGAUAA CUAUACAAUCUAC UGUCUUUCCUA	UU <u>AGGGU</u> CACACCCACCA CUGGGAGAUAA
>hsa-let-7a-2 MI0000061	AGGUUGAGGUAGUAGGUUGUAUAGUUUAGAAUUA CAUCAAGGGAGAUAA CUGUACAGCCUCCUAGCUUU CCU	UAGAAUUA CAUCAAGGGA GAUAA
>hsa-let-7a-3 MI0000062	GGGUGAGGUAGUAGGUUGUAUAGUUUUGGGGCUCUGCCCUGCUAUGGGAUAA CUAUACAAUCUACUGUCU UUCCU	UGGGGCUCUGCCCUGCUA UGGGAUAA
>hsa-let-7c MI0000064	GCAUCCGGGUUGAGGUAGUAGGUUGUAUGGUUUAGAGUUACACCCUGGGAGUUA ACUGUACAACCUUCU AGCUUUCCUUGGAGC	UAGAGUUACACCCUGGGA GUAA
>hsa-let-7f-1 MI0000067	UCAGAGUGAGGUAGUAGAUUGUAUAGUUGUGGGGUAGUGAUUUUACCCUGUUCAGGAGAUAA CUAUAC AAUCUAUUGCCUUCCCUGA	GUGGGGUAGUGAUUUUAC CCUGUUCAGGAGAUAA
>hsa-let-7f-2 MI0000068	UGUGGGAUGAGGUAGUAGAUUGUAUAGUUUAGGGUCAUACCCCAUCUUGGAGAUAA CUAUACAGUCUA CUGUCUUUCCACG	UU <u>AGGGU</u> CAUACCCCAUC UUGGAGAUAA
>hsa-let-7g MI0000433	AGGCUGAGGUAGUAGUUUGUACAGUUUGAGGGUCUAUGAUACCACCCGGUACAGGAGAUAA CUGUACAG GCCACUGCCUUGCCA	UG <u>AGGGU</u> CUAUGAUACCA CCCGGUACAGGAGAUAA
>hsa-mir-21 MI0000077	UGUCGGGUAGCUUAUCAGACUGAUGUUGACUGUUGAAUCUCAUGGCAACACCAGUCGAUGGGCUGUCUG ACA	CUGUUGAAUCUCAUGG
>hsa-mir-23a MI0000079	GGCCGGCUGGGGUUCCUGGGGAUGGGAUUUGCUUCCUGUCACAAAUCACAUUGCCAGGGAUUUCCAACC GACC	GCUUCCUGUCACAA
>hsa-mir-23b MI0000439	CUCAGGUGCUCUGGCUGCUUGGGUUCCUGGCAUGCUGAUUUGUGACUUAAGAUUAAAAUCACAUUGCCA GGGAUUACCACGCAACCACGACCUUGGC	GUGACUUAAGAUUAAA
>hsa-mir-24-1 MI0000080	CUCCGGUGCCUACUGAGCUGAU AUCAGUUCUUAUUUACACACUGGCUCAGUUCAGCAGGAACAGGAG	UCUCAUUUUACACAC
>hsa-mir-24-2 MI0000081	CUCUGCCUCCCGUGCCUACUGAGCUGAAACACAGUUGGUUUGUGUACACUGGCUCAGUUCAGCAGGAAC AGGG	UUGGU

>hsa-mir-26a-1 MI0000083	GUGGCCUCGUUCAAGUAAUCCAGGAUAGGCUGUGCAGGUCCCAAUGGGCCU AUUCUUGGUUACUUGCAC GGGGACGC	GUGCAGGUCCCAAUGGG
>hsa-mir-26a-2 MI0000750	GGCUGUGGCUGGAUUCAAGUAAUCCAGGAUAGGCUGUUUCCAUCUGUGAGGCCU AUUCUUGAUUACUUG UUUCUGGAGGCAGCU	GUUUCCAUCUGUGAGG
>hsa-mir-26b MI0000084	CCGGGACCCAGUUCAAGUAAUUCAGGAUAGGUUGUGUGCUGUCCAGCCUGUUCUCCAUAUACUUGGCUCG GGGACCGG	UGUGUGCUGUCCAG
>hsa-mir-27a MI0000085	CUGAGGAGCAGGGCUUAGCUGCUUUGUGAGCAGGGUCCACACCAAGUCGUGUUCACAGUGGCUAAGUUCC GCCCCCAG	GGGUCCACACCAAGUCGU G
>hsa-mir-27b MI0000440	ACCUCUCUAACAAGGUGCAGAGCUUAGCUGAUUGGUGAACAGUGAUUGGUUUCCGCUUUGUUCACAGUG GCUAAGUUCUGCACCUGAAGAGAAGGUG	AGUGAUUGGUUCCGCUU UG
>hsa-mir-98 MI0000100	AGGAUUCUGCUCAUGCCAGGGUGAGGUAGUAAGUUGUAUUGUUGUGGGGUAGGGAU AUUAGGCCCCAAU UAGAAGAUAAACUAUACAACUUAUACUUAUCCUGGUGUGGGCAUAUUA	GUGGGGUAGGGAU AUUAG GCCCAAUUAAGAAGAUAA
>hsa-mir-181a-1 MI0000289	UGAGUUUUGAGGUUGCUUCAGUGAACAUAUCAAACGCUGUCGGUGAGUUUGGAAUUA AAAAUCAAAACCAUC GACCGUUGAUUGUACCCUAUGGCUAACCAUCAUCUACUCCA	UUGGAAUUA AAAAUCAAA
>hsa-mir-181a-2 MI0000269	AGAAGGGCUAUCAGGCCAGCCUUCAGAGGACUCCAAGGAACAUAACGCUGUCGGUGAGUUUGGGAUU UGAAAAAACACUGACCGUUGACUGUACCUUGGGGUCCUUA	UUGGGAUUUGAAAAA
>hsa-mir-181b-1 MI0000270	CCUGUGCAGAGAUUAUUUUUUA AAAAGGUCACAAUCAACAUAUUGCUGUCGGUGGGUUGAACUGUGUG GACAAGCUCACUGAACA AUGAACUGUGGGCCCCGCUU	UGAACUGUGUGGACAAG
>hsa-mir-181b-2 MI0000683	CUGAUGGCUGCACUCAACAUAUUAUUGCUGUCGGUGGGUUUGAGUCUGAAUCAACUCACUGAUCAAUGAA UGCAAACUGCGGACCAAACA	UUGAGUCUGAAUCA
>hsa-mir-181d MI0003139	GUCCCCUCCCCUAGGCCACAGCCGAGGUCACAAUCAACAUAUUGUUGUCGGUGGGUUGUGAGGACUG AGGCCAGACCCACCGGGGAUGAAUGUCACUGUGGCUGGGCCAGACACGGCUUAAGGGGAUUGGGGAC	UGUGAGGACUGAGGCCAG AC
>hsa-mir-193a MI0000487	CGAGGAUGGGAGCUGAGGGCUGGGUCUUUGCGGGCGAGAUGAGGGUGUCGGAUCAACUGGCCUACAAAG UCCCAGUUCUCGGCCCCCG	GGGUGUCGGAUC
>hsa-mir-193b MI0003137	GUGGUCUCAGAAUCGGGGUUUUGAGGGCGAGAUGAGUUUAUGUUUUUAUCCAACUGGCCCUC AAAGUCCC GCUUUUGGGGUCAU	GUUUUAUGUUUAUCC
>hsa-mir-200a MI0000737	CCGGGCCCCUGUGAGCAUCUUAACGGACAGUGCUGGAUUUCCAGCUUGACUCUAACACUGUCUGGUAAC GAUGUUCAAGGUGACCCGC	UUUCCAGCUUGACUC
>hsa-mir-200c MI0000650	CCCUCGUCUUAACCCAGCAGUGUUUGGGUGCGGUUGGGAGUCUCUAAUACUGCCGGGUAAUGAUGGAGG	GUGCGGUUGGGAGUCUC

>hsa-mir-203a MI0000283	GUGUUGGGGACUCGCGCGCUGGGUCCAGUGGUUCUUAACAGUUCAACAGUUCUGUAGCGCAAUUGUGAA AUGUUUAGGACCACUAGACCCGGCGGGCGCGGACAGCGA	CUGUAGCGCAAUU
>hsa-mir-203b MI0017343	GCGCCCCCGGGUCUAGUGGUCCUAAACAUUUCACAAUUGCGCUACAGAACUGUUGAACUGUUAAGAAC CACUGGACCCAGCGCGC	AUUGCGCUACAGAACUG
>hsa-mir-499a MI0003183	CCCCUGUCCCCUGUGCCUUGGGCGGGCGGCUGUUAAGACUUGCAGUGAUGUUUAACUCCUCUCCACGUGA ACAUCACAGCAAGUCUGUGCGCUUCCCGUCCCUACGCUGCCUGGGCAGGGU	AACUCCUCUCCACGUG
>hsa-mir-499b MI0017396	GGAAGCAGCACAGACUUGCUGUGAUGUUCACGUGGAGAGGAGUUAAACAUCACUGCAAGUCUUAACAGC CGCC	CGUGGAGAGGAGUUA
>hsa-mir-520d* MI0003164	UCUCAAGCUGUGAGUCUACAAAGGGAAGCCCUUUCUGUUGUCUAAAAGAAAAGAAAGUGCUUCUCUUUG GUGGGUUACGGUUUGAGA	UGUUGUCUAAAAG
<i>Human-Control miRNAs</i>		
>hsa-mir-10a MI0000266	GAUCUGUCUGUCUUCUGUAUUAUACCCUGUAGAUCCGAAUUGUGUAAGGAAUUUUGUGGUCACAAAUUC GUAUCUAGGGGAAUAUGUAGUUGACAUA AACACUCCGCUCU	UAAGGAAUUUUGUGGUCA
>hsa-mir-9-1 MI0000466	CGGGGUUGGUUGUUAUCUUUGGUUAUCUAGCUGUAUGAGUGGUGUGGAGUCUUCAUAAAGCUAGAUAA CCGAAAGUAAAAUAACCCCA	GUGGUGUGGAGUCUUC
>hsa-mir-34b MI0000742	GUGCUCGGUUUGUAGGCAGUGUCAUUAAGCUGAUUGUACUGUGGUGGUUACAAUCACUAACUCCACUGCC AUCAAAACAAGGCAC	UACUGUGGUGGUUA
>hsa-mir-92a-1 MI0000093	CUUUCUACACAGGUUGGGAUCGGUUGCAAUGCUGUGUUUCUGUAUGGUAUUGCACUUGUCCCGGCCUGU UGAGUUUGG	GUGUUUCUGUAUGG
>hsa-mir-365b MI0000769	AGAGUGUUCAAGGACAGCAAGAAAAAUGAGGGACUUCAGGGGCAGCUGUGUUUUCUGACUCAGUCAUA AUGCCCCUAAAAAUCCUUAUUGUUCUUGCAGUGUGCAUCGGG	GUUUUCUGACUCAGUCA
>hsa-mir-431 MI0001721	UCCUGCUUGUCCUGCGAGGUGUCUUGCAGGCCGUGAUGCAGGCCACACUGACGGUAACGUUGCAGGUCGU CUUGCAGGGCUUCUCGCAAGACGACAUCUCAUACCAACGACG	GGCCACACUGACGGUAAC GUUG
>hsa-mir-25 MI0000082	GGCCAGUGUUGAGAGGCGGAGACUUGGGCAAUUGCUGGACGCUGCCCUGGGCAUUGCACUUGUCUCGGU CUGACAGUGCCGGCC	CUGGACGCUGCCCUGGG
>hsa-mir-28 MI0000086	GGUCCUUGCCCUCAAGGAGCUCACAGUCUUAUUGAGUUAACUUCUGACUUUCCACUAGAUUGUGAGCU CCUGGAGGGCAGGCACU	UUACCUUUCUGACUUUCC

>hsa-mir-187 MI0000274	GGUCGGGCUCACCAUGACACAGUGUGAGACCUCGGGCUACAACACAGGACCCGGGCGCUGCUCUGACCCC UCGUGUCUUGUGUUGCAGCCGGAGGGACGCAGGUCCGCA	GCUGCUCUGACCCC
>hsa-mir-19b- 1 MI0000074	CACUGUUCUAUGGUUAGUUUUGCAGGUUUGCAUCCAGCUGUGUGAUUUCUGCUGUGCAAAUCCAUGCA AAACUGACUGUGGUAGUG	UGUGUGAUUUCUGC
>hsa-mir-22 MI0000078	GGCUGAGCCGCAGUAGUUCUUCAGUGGCAAGCUUUAUGUCCUGACCCAGCUAAAGCUGCCAGUUGAAGA ACUGUUGCCCUCUGCC	UGUCCUGACCCAGCUA
>hsa-mir-153- 2 MI0000464	AGCGGUGGCCAGUGUCAUUUUUGUGAUGUUGCAGCUAGUAAUUGAGCCCAGUUGCAUAGUCACAAAAG UGAUCAUUGGAAACUGUG	AGUAAUUGAGCCCAG
>hsa-mir-124- 1 MI0000443	AGGCCUCUCUCUCCGUGUUCACAGCGGACCUUGAUUUAAAUGUCCAUAACAAUUAAGGCACGCGGUGAAU GCCAAGAAUGGGGCUG	UUAAAUGUCCAUAACAAU
>hsa-mir- 219a-1 MI0000296	CCGCCCCGGGCGCGGCUCUGAUUGUCCAAACGCAAUUCUCGAGUCUAUGGCUCCGGCCGAGAGUUGAG UCUGGACGUCCCGAGCCGCCGCCCCCAAACCUCGAGCGGG	CGAGUCUAUGGCUCCGGC CG
>hsa-mir-202 MI0003130	CGCCUCAGAGCCGCCCGCCGUUCCUUUUCCUAUGCAUAUACUUCUUGAGGAUCUGGCCUAAAGAGGUA UAGGGCAUGGGAAAACGGGGCGGUCGGGUCCUCCCCAGCG	AGGAUCUGGCCUAA
>hsa-mir-216a MI0000292	GAUGGCUGUGAGUUGGCUAAUUCUCAGCUGGCAACUGUGAGAUGUUCAUACAAUCCUCACAGUGGUCU CUGGGAUUAUGCUAAACAGAGCAAUUCUAGCCCUCACGA	GAUGUUCAUACAAUCCC
>hsa-mir- 301b MI0005568	GCCGCAGGUGCUCUGACGAGGUUGCACUACUGUGCUCUGAGAAGCAGUGCAAUGAUUUGUCAAAAGCAU CUGGGACCA	GUGCUCUGAGAAG
>hsa-mir-1306 MI0006443	GUGAGCAGUCUCCACCACCUCCCCUGCAAACGUCCAGUGGUGCAGAGGUAAUGGACGUUGGCUCUGGUGG UGAUGGACAGUCCGA	GUGGUGCAGAGGUAAUGG
>hsa-mir-20b MI0001519	AGUACCAAAGUGCUCAUAGUGCAGGUAGUUUUGGCAUGACUCUACUGUAGUAUGGGCACUCCAGUACU	UUUUGGCAUGACUCU
>hsa-mir-93 MI0000095	CUGGGGGCUCCAAAGUGCUGUUCGUGCAGGUAGUGUGAUUACCCAACCUACUGCUGAGCUAGCACUCC CGAGCCCCCGG	UGUGAUUACCCAACCU
>hsa-mir-190a MI0000486	UGCAGGCCUCUGUGUGAUUUGUUUGAUUUAUUUAGGUUGUUAUUUAAUCCAACUAUAUAUCAAACAUU UCCUACAGUGUCUUGCC	UGUUUUUAAUCCAA
>hsa-mir- 196a-2 MI0000279	UGCUCGCUCAGCUGAUCUGUGGCUUAGGUAGUUUCAUGUUGUUGGGAUUGAGUUUUGAACUCGGCAACA AGAAACUGCCUGAGUUACAUCAGUCGGUUUUCGUCGAGGGC	AUUGAGUUUUGAACU
>hsa-mir-222 MI0000299	GCUGCUGGAAGGUGUAGGUACCCUCAUUGGCUCAGUAGCCAGUGUAGAUCUGUCUUUCGUAAUCAGCA GCUACAUCUGGCUACUGGGUCUCUGAUGGCAUCUUCUAGCU	GUCUUUCGUAAUCAGC

>hsa-mir-671 MI0003760	GCAGGUGAACUGGCAGGCCAGGAAGAGGAGGAAGCCCUGGAGGGGCUGGAGGUGAUGGAUGUUUCCUC CGGUUCUCAGGGCUCCACCUCUUUCGGGCCGUAGAGCCAGGGCUGGUGC	GUGAUGGAUGUUUCC
>hsa-mir-1-1 MI0000651	UGGGAACAUAUUCUUUAUAUGCCCAUAUGGACCUGCUAAGCUAUGGAAUGUAAAGAAGUAUGUAUCU CA	AUGGACCUGCUA
>hsa-mir-205 MI0000285	AAAGAUCUCAGACAAUCCAUGUGCUUCUCUUGUCCUUCAUUCCACCGGAGUCUGUCUCAUACCCAACCA GAUUUCAGUGGAGUGAAGUUCAGGAGGCAUGGAGCUGACA	UCUCAUACCCAACCA
>hsa-mir-32 MI0000090	GGAGAUAUUGCACAUUACUAAGUUGCAUGUUGUCACGGCCUCAUGCAAUUUAGUGUGUGUGAUUUUU C	UGUUGUCACGGCCUCAU G
>hsa-mir-127 MI0000472	UGUGAUCACUGUCUCCAGCCUGCUGAAGCUCAGAGGGCUCUGAUUCAGAAAGAUAUCGGAUCCGUCUG AGCUUGGCUGGUCGGAAGUCUCAUCAUC	UCAGAAAGAUA
>hsa-mir-134 MI0000474	CAGGGUGUGUGACUGGUUGACCAGAGGGGCAUGCACUGUGUACCCUGUGGGCCACCUAGUCACCAACC CUC	CAUGCACUGUGUUCAC
>hsa-mir-136 MI0000475	UGAGCCCUCGGAGGACUCCAUUUGUUUGAUGAUGGAUUCUUAUGCUCCAUAUCGUCUCAAUGAGUC UUCAGAGGGUUCU	UUCUUAUGCUC
>hsa-mir-140 MI0000456	UGUGUCUCUCUCUGUGUCCUGCCAGUGGUUUUACCCUAUGGUAGGUUACGUCAUGCUGUUCUACCACAG GGUAGAACCACGGACAGGAUACCGGGGCACC	GUUACGUCAUGCUGUUC
>hsa-mir-150 MI0000479	CUCCCCAUGGCCCUGUCUCCCAACCCUUGUACCAGUGCUGGGCUCAGACCCUGGUACAGGCCUGGGGGAC AGGGACCUGGGGAC	CUGGGCUCAGACC
>hsa-mir-411 MI0003675	UGGUACUUGGAGAGAUAGUAGACCGUAUAGCGUACGCUUUAUCUGUGACGUAUGUAACACGGUCCACUA ACCCUCAGUAUCAAAUCCAUCCCCGAG	CUUUAUCUGUGACG
>hsa-mir-3074 MI0014181	GCUCGACUCCUGUCCUGCUGAACUGAGCCAGUGUGUAAAAUGAGAACUGAUUAUCAGCUCAGUAGGCAC CGGAGGGCGGGU	UGUGUAAAAUGAGAACU
>hsa-mir-5591 MI0019151	UGGGAGCUAAGCUAUGGGUAUACUGAGCUUAUGUAUGCAUCUGCAUACCCAUAAGCUUAGCUCCCA	ACUGAGCUUAUGUAUGCA UCUGC
>hsa-mir-1914 MI0008335	CGUGUGAGCCCGCCCUGUGCCCGGCCACUUCUGCUUCCUCUUAGCGCAGGAGGGGUCCCGCACUGGGAG GGGCCUCAC	CUUCCUCUAGCGCA
>hsa-mir-875 MI0005541	UUAGUGGUACUAUACCUCAGUUUAUCAGGUGUUCUAAAAUCACCUGGAAACACUGAGGUUGUGUCUC ACUGAAC	UUCUAAAAUCA
>hsa-mir-675 MI0005416	CCCAGGGUCUGGUGCGGAGAGGGCCACAGUGGACUUGGUGACGCUGUAUGCCCUCACCGCUCAGCCCCU GGG	GACUUGGUGACG

>hsa-mir-483 MI0002467	GAGGGGGAAGACGGGAGGAAAGAAGGGAGUGGUUCCAUCACGCCUCCUCACUCCUCUCCUCCCGUCUUCU CCUCUC	UGGUUCCAUCACGCCUCC
>hsa-mir-361 MI0000760	GGAGCUUAUCAGAAUCUCCAGGGGUACUUUAUAAUUUCAAAGUCCCCCAGGUGUGAUUCUGAUUUUGC UUC	UUUAUAAUUUCAAAG
>hsa-mir-330 MI0000803	CUUUGGCGAUCACUGCCUCUCUGGGCCUGUGUCUUAGGCUCUGCAAGAUAACCGAGCAAAGCACACGGC CUGCAGAGAGGCAGCGCUCUGCCC	UCUGCAAGAUAACCGA
>hsa-mir-296 MI0000747	AGGACCCUUCAGAGGGCCCCCCCCUCAAUCCUGUUGUGCCUAAUUCAGAGGGUUGGGUGGAGGCUCUCCU GAAGGGCUCU	UGUGCCUAAUUA
>hsa-mir-155 MI0000681	CUGUAAUAGCUAAUCGUGAUAGGGGUUUUUGCCUCCAACUGACUCCUACAUAUAGCAUUAACAG	UUUUGCCUCCAACUGA
>hsa-mir-182 MI0000272	GAGCUGCUUGCCUCCCCCGUUUUGGCAAUGGUAGAACUCACACUGGUGAGGUAAACAGGAUCCGGUGG UUCUAGACUUGCCAACUAUGGGGCGAGGACUCAGCCGGCAC	GGUGAGGUAAACAGGAUCC GG
>hsa-mir-17 MI0000071	GUCAGAAUAAUGUCAAGUGCUUACAGUGCAGGUAGUGAUUUGUGCAUCUACUGCAGUGAAGGCACUUG UAGCAUUAUGGUGAC	UGAUUUGUGCAUCU
>hsa-mir-450a-1 MI0001652	AAACGAUACUAAACUGUUUUUGCGAUGUGUCCUAAUAUGCACUAUAAAUAUUAUUGGGAACAUUUUGC AUGUAUAGUUUUGUAUCAAUAUA	GCACUAUAAAUAU
>hsa-mir-454 MI0003820	UCUGUUUAUCACCAGAUCCUAGAACCCUAUCAAUUUGUCUCUGCUGUGUAAAUAUUCUGAGUAGUGC AAUAUUGCUUAUAGGGUUUUGGUGUUUGGAAAGAACAUGGGCAGG	UGUGUAAAUAUUCUGAG
>hsa-mir-508 MI0003195	CCACCUUCAGCUGAGUGUAGUGCCUACUCCAGAGGGCGUCACUAUGUAAACUAAAACAUGAUUGUAG CCUUUUGGAGUAGAGUAAUACACAUCACGUAACGCAUAUUUGGUGG	UAAACUAAAACA
>hsa-mir-532 MI0003205	CGACUUGC UUUCUCUCCUCCAUGCCUUGAGUGUAGGACCGUUGGCAUCUUAAUUACCCUCCACACCCAA GGCUUGCAGAAGAGCGAGCCU	UGGCAUCUUAAUUAC
>hsa-mir-766 MI0003836	GCAUCCUCAGGACCUGGGCUUGGGUGGUAGGAGGAAUUGGUGCUGGUCUUCAUUUUGGAUUUGACUCC AGCCCCACAGCCUCAGCCACCCCAGCCAAUUGUCAUAGGAGC	UCAUUUUGGAUUUG

Table S3. Lists of common differentially expressed genes to E2-treated zebrafish and breast cancer. Presented are fold ratios results of gene expression microarrays of zebrafish livers after treatment with E2 for 12, 24 and 48 hrs, and of breast cancer vs. normal breast.

Gene	Zebrafish-E2 treatment (12 vs. 4 hrs)	Human breast (cancer vs. Normal)	Gene	Zebrafish-E2 treatment (24 vs. 4 hrs)	Human breast (cancer vs. Normal)	Gene	Zebrafish-E2 treatment (48 vs. 4 hrs)	Human breast (cancer vs. Normal)
foxo1	-3.81543	-3.286984681	cebpd	-4.39698	-3.715873006	krt15	-2.61975	-9.799437967

mgp	2.80279	-2.390571296	ducp1	-2.23362	-3.658357673	aldh1a3	1.81365	-3.831731219
hnrnpa0	-2.12121	-1.69209092	per2	-5.61861	-3.289145222	cebpd	-6.55645	-3.715873006
prim1	10.037	1.417340798	foxo1	-7.21616	-3.286984681	per2	-6.77169	-3.289145222
ero1l	2.42642	1.432254841	zfp36l2	-3.64205	-2.990533927	foxo1	-5.26883	-3.286984681
rnaseh2a	3.00748	1.433627632	f10	-1.98831	-2.906108159	per1	3.93669	-3.197253939
asf1b	18.5255	1.454146297	slc27a6	-3.83008	-2.815101002	zfp36l2	-4.81279	-2.990533927
pola2	7.74327	1.459987281	igf1	-6.27184	-2.664885124	f10	-2.89311	-2.906108159
rrm1	6.08966	1.489958926	ducp6	-2.07292	-2.596607569	csrp1	-2.18495	-2.901962759
mthfd2	-3.38525	1.504245035	tspan7	-2.69697	-2.573601486	slc27a6	-8.64909	-2.815101002
ggps1	-1.89698	1.513723548	mcp	2.17853	-2.390571296	igf1	-9.73548	-2.664885124
rfc5	3.47921	1.514018734	cyrr1	3.26514	-2.043111289	txnlp	2.79376	-2.655372076
pold1	6.78738	1.548995908	ptgds	-3.02223	-1.863103863	epas1	-3.00885	-2.621489869
sec23b	-2.97717	1.648495345	cfl2	2.65817	-1.737153377	tftp12	-3.75159	-2.429668803
smc4	6.98819	1.70670637	hnrnpa0	-2.92791	-1.69209092	mcp	2.49668	-2.390571296
dtl	14.662	1.835357884	dcat2	-3.51216	-1.670901971	rnf128	-2.62835	-2.325877835
mybl2	23.8424	1.844821634	add3	-2.28626	-1.586622115	cugbp2	-3.20665	-2.287741676
smc2	10.9393	1.899810545	mpzl2	-1.95628	-1.58179144	wee1	2.36895	-2.268617377
wdsol1	1.95377	1.908540251	mylip	-3.3032	-1.522541776	aspa	4.34759	-2.164373857
orc6l	39.7162	1.996606079	rps4x	1.70553	-1.519380517	smarca2	-2.44616	-2.143116006
pcna	7.95076	2.024529832	fstl1	33.4639	-1.51051838	sgce	-2.06081	-2.113035139
cenpk	14.0709	2.049555097	cat	-3.2306	-1.509138661	cav2	-3.72884	-2.090702147
mcm4	17.6252	2.098250835	tead1	-2.03245	-1.501055976	serhl	6.37268	-2.009605721
rmi1	5.89567	2.324631182	eif1b	-1.70681	-1.471538723	st5	-2.25223	-1.928018968
tdo2	-8.56957	2.471779729	eef1b2	2.09271	-1.450967025	thra	-2.67027	-1.906318117
tyms	36.547	3.496174985	tfdp1	2.12983	1.414310599	ccnl1	-1.78391	-1.873146955
uhrf1	16.7852	4.555218501	ilf2	2.48423	1.414319174	ptgds	-4.05337	-1.863103863
pbk	12.9965	5.151937534	xrcc4	4.19725	1.415014875	tppp3	-3.25671	-1.823331217
			prim1	24.7691	1.417340798	POLR2A	-2.48781	-1.794616293
			pigf	2.15886	1.422719719	fbxo32	-5.59889	-1.790637489
			mapre1	2.28514	1.423686224	pik3r1	1.88741	-1.781297119
			slc37a2	-2.19438	1.428426492	zfp36l1	-7.93313	-1.754658906
			mrpl35	1.77788	1.428977723	bhlhb2	2.56887	-1.720101877
			fam136a	2.51099	1.431168332	il4r	-9.25584	-1.711371363

ero1l	11.0466	1.432254841	asph	2.54849	-1.707484483
rnaseh2a	3.64306	1.433627632	hnrnpa0	-3.01253	-1.69209092
nudt1	4.27212	1.435274704	dgat2	-3.35212	-1.670901971
pgd	2.35249	1.438710194	sf3a2	1.98431	-1.616915196
sub1	2.12331	1.442626183	add3	-1.98257	-1.586622115
txnrd1	1.72042	1.44284304	ypel5	-1.72095	-1.560853046
nras	3.44101	1.444631855	eef1g	1.9011	-1.546805605
psmd1	2.74486	1.445324247	fstl1	17.6834	-1.51051838
psmc6	2.79967	1.447146633	cat	-4.3411	-1.509138661
tbl2	3.0555	1.452537134	wtap	-1.92222	-1.502643969
asf1b	35.5925	1.454146297	dio2	-38.9144	-1.468795942
ppil1	2.37249	1.454969076	gnmt	-5.51585	-1.459169814
usp5	1.84483	1.458189181	flt1	-2.12765	-1.450368894
pmm2	5.87116	1.458738209	tfdp1	1.92668	1.414310599
alg6	2.02018	1.458773155	ilf2	3.23788	1.414319174
pola2	14.1718	1.459987281	xrcc4	3.0535	1.415014875
gapdh	-2.45543	1.463665172	ephx1	7.6625	1.41553214
timp2	-5.6871	1.467501867	prim1	19.6215	1.417340798
cse1l	2.17358	1.467578674	pigf	2.83157	1.422719719
edem1	1.76062	1.467959489	mapre1	2.14555	1.423686224
psmb2	1.74832	1.471121299	nup155	4.15803	1.427710528
cd2bp2	3.77782	1.482307111	slc37a2	-1.90142	1.428426492
Slbp	14.7099	1.48531021	mrpl35	1.96658	1.428977723
nutf2	8.85058	1.485689463	fam136a	1.78568	1.431168332
slc35b1	2.87696	1.486307377	ero1l	20.1057	1.432254841
mrpl14	2.38429	1.489483513	sdhc	1.74505	1.432624661
rrm1	11.1679	1.489958926	rnaseh2a	2.27723	1.433627632
dnmt1	9.11021	1.493170264	vangl1	-2.81137	1.43613676
EIF5	1.73516	1.494305035	tmed3	3.18595	1.438582331
kif11	11.6072	1.499763759	cd9	-2.31546	1.439563747
pgrmc2	2.78977	1.503000307	cant1	-2.89341	1.440125404
rfc5	10.5553	1.514018734	srpk1	-1.89795	1.441570681
hm13	2.03241	1.523191788	sub1	2.8413	1.442626183

rer1	1.80009	1.527240002	nme4	-3.76738	1.443574654
stam	1.72167	1.529470932	nrns	6.31616	1.444631855
stip1	2.15636	1.532837137	psmd1	3.38609	1.445324247
slc30a5	2.05287	1.54749931	psmc6	2.76992	1.447146633
pold1	21.7502	1.548995908	fkbp4	-1.76363	1.449729834
tmco1	2.71463	1.569276615	stk38l	-1.91245	1.45103741
sec61g	2.89537	1.574475761	mastl	12.5682	1.451540388
cct5	2.30011	1.582603358	tbl2	2.57236	1.452537134
snrpb	2.13288	1.586326443	asf1b	24.3983	1.454146297
ipo9	2.27617	1.587401052	ppil1	3.14452	1.454969076
iars	2.3444	1.589895408	usp5	2.26843	1.458189181
sgpl1	-2.12949	1.592093585	pmm2	7.9622	1.458738209
atm	1.80909	1.601355475	alg6	3.5197	1.458773155
tmem49	2.23668	1.608868085	pola2	9.25999	1.459987281
psmd2	2.13579	1.611279958	gapdh	-4.92895	1.463665172
copb2	2.03515	1.629230105	tmem33	-1.86198	1.464835732
uap1	2.47554	1.63150354	cse1l	2.77585	1.467578674
p4ha2	3.20901	1.646940773	edem1	1.91663	1.467959489
psma5	2.44957	1.664836263	psmb2	1.85704	1.471121299
cct3	2.7086	1.676586786	cd2bp2	4.97323	1.482307111
atic	3.87609	1.681138854	Slbp	9.25509	1.48531021
nlk	-2.42299	1.687963062	nutf2	9.77599	1.485689463
lsm4	1.97111	1.688191735	slc35b1	2.83404	1.486307377
smc4	10.6127	1.70670637	mrpl14	1.96133	1.489483513
npl	-5.86003	1.715350843	rrm1	10.4819	1.489958926
seh1l	2.21282	1.728509515	hmgb2	6.70188	1.490474444
usp14	3.28818	1.730855476	eno3	-3.80569	1.490797923
c20orf24	2.25082	1.743396856	hsh2d	-3.63634	1.49388592
psmd3	2.47586	1.743932795	pgm3	4.11477	1.496173805
nudt5	3.17445	1.758329369	kif11	125.151	1.499763759
psmc4	2.03406	1.761362944	pgrmc2	2.15459	1.503000307
idh2	1.80843	1.778205094	ppt1	-1.74453	1.507944984
arf1	-1.81248	1.790169538	rfc5	6.91719	1.514018734

adss	2.15049	1.801385325	ssx2ip	2.29336	1.519080616
lypla1	2.03039	1.808349836	hm13	4.39345	1.523191788
actn2	-1.84881	1.815948134	rer1	2.32976	1.527240002
dtl	61.2282	1.835357884	stam	3.28385	1.529470932
mybl2	66.5984	1.844821634	nnt	2.15113	1.531210069
plk4	7.01819	1.898742735	slc30a5	2.36581	1.54749931
smc2	16.3267	1.899810545	pold1	10.2219	1.548995908
wdsof1	2.10243	1.908540251	tmco1	3.38197	1.569276615
h2afx	19.437	1.92592813	sec61g	4.16278	1.574475761
tmpo	3.74855	1.978475073	cct5	2.26977	1.582603358
orc6l	113.132	1.996606079	ipo9	2.15049	1.587401052
ggh	-1.74194	2.013006708	iars	3.13612	1.589895408
pcna	15.2001	2.024529832	sgpl1	-1.80358	1.592093585
cenpk	30.1604	2.049555097	slc39a1	-2.14988	1.592672078
kpna2	15.4713	2.085126482	agt	-1.93794	1.595674299
mcm4	28.7386	2.098250835	pdia4	4.54807	1.606044615
wdr51a	8.7916	2.204609324	tmem49	1.87835	1.608868085
trip13	10.4199	2.299644226	psmd2	2.50824	1.611279958
rmi1	7.80228	2.324631182	copb2	2.20149	1.629230105
lmnb1	2.37698	2.400206245	uap1	2.61916	1.63150354
rad51	37.9369	2.53591429	bub3	4.01934	1.636390464
rad54l	20.0014	2.928812504	p4ha2	2.15144	1.646940773
ttk	26.6462	2.933502238	cdc20	119.51	1.651354897
rrm2	19.944	3.073668947	psma5	2.4536	1.664836263
cdkn3	4.12387	3.10330563	kifc1	129.498	1.670075473
tyms	107.449	3.496174985	cct3	2.01443	1.676586786
uhrf1	42.4609	4.555218501	atic	3.64924	1.681138854
fn1	-4.16217	5.072483097	smc4	26.1882	1.70670637
pbk	40.6059	5.151937534	npl	-2.47514	1.715350843
			comtd1	-3.88031	1.721312702
			rgs4	-2.55589	1.722760956
			rtcd1	-1.79768	1.726442502
			rad21	2.56552	1.727853373

seh1l	3.31866	1.728509515
usp14	3.36637	1.730855476
c20orf24	1.93973	1.743396856
psmd3	3.86722	1.743932795
nudt5	2.91624	1.758329369
psmc4	2.1999	1.761362944
idh2	1.79505	1.778205094
kif23	113.288	1.794612857
tnfrsf165	3.86243	1.798032339
lypla1	1.8892	1.808349836
ampd3	2.4186	1.812614615
actn2	-2.22765	1.815948134
derl1	3.83111	1.819959161
dtl	20.4795	1.835357884
mybl2	90.4897	1.844821634
plk4	16.5408	1.898742735
smc2	45.2633	1.899810545
wdsof1	1.79969	1.908540251
h2afx	43.1699	1.92592813
rab2a	1.76868	1.930261142
tmpo	7.58711	1.978475073
orc6l	70.8605	1.996606079
ggh	-2.11368	2.013006708
pcna	10.3336	2.024529832
cenpk	57.3806	2.049555097
gpsm2	4.78013	2.053051799
rnpep	2.09379	2.080784818
kpna2	78.449	2.085126482
shcbp1	18.8991	2.085423614
mcm4	13.9048	2.098250835
tacc3	22.7956	2.191710961
wdr51a	53.1455	2.204609324
trip13	23.3392	2.299644226

cfb	-6.52074	2.307960165
hmmr	8.90855	2.310369158
ccnb1	262.419	2.311043153
rmi1	6.92355	2.324631182
lmnb1	4.59828	2.400206245
rad51	34.4706	2.53591429
ccnb2	48.2483	2.637727172
tk1	7.48057	2.638434781
aspm	46.2409	2.750297633
top2a	94.565	2.917488708
rad54l	48.7024	2.928812504
racgap1	20.8442	2.929986682
ttk	206.479	2.933502238
rrm2	41.9177	3.073668947
cdkn3	12.2778	3.10330563
melk	59.6723	3.325744311
cdc2	182.604	3.336384246
tym	159.059	3.496174985
dlg7	95.5377	3.652341315
nek2	91.2569	3.926110638
uhf1	10.8183	4.555218501
fn1	-5.24084	5.072483097
pbk	220.286	5.151937534
