Electronic Supplementary Material (ESI) for Molecular BioSystems.

Additional information concerning the design of the primers used for anti-ESR1 ChIPs:

The candidate approach mentioned in the manuscript combines the results of the Assay Design Center from Roche (https://www.roche-applied-science.com/sis/rtpcr/upl/index.jsp?id=UP030000) and the results indicated in Table S2.
(i) the Roche interface was used to scan the 10kb upstream the first pre-miRNA of each miRNA cluster. This procedure provides a list of potential qPCR primers.
(ii) this list was then confronted to the results indicated in Table S2.
(iii) the selected sets of primers corresponded to those that were predicted by the Roche interface and that were located at the vicinity of ESR1 binding sites.
(iv) when ESR1 binding sites were found scattered across the miRNA promoter, we favored the binding sites close to the pre-miRNA, assuming that this region contains the TSS.

For instance, in the case of the miR-17/92, the primers recognize the region located at positions -1444/-1403 from the pre-miR-17 and Table S2 indicates a potential ESR1 binding site at -903. In the case of miR-424/450b, ESR1 binding sites were predicted at positions -3426, -3518, -8033, -8063, -9741 (TableS2). We favored the binding sites close to the pre-miR-424 and selected set of primers amplifying the region -3501/-3457. In the case of miR-23a/24-2 and miR-210, a similar strategy was applied but we preferentially used sets of primers already available and experimentally validated by our laboratory (Saumet et al, Blood 2009).

Primer sequences are indicated in Table S1.