

Supporting Information

Table S1. The oligonucleotide sequences

Criteria	Gene	Sequence (5'-3')
siRNA	siBRCA1 target	GGAACCUGUCUCCACAAAG
qRT-PCR	BRCA1	Forward: GGAACTAACCAAACGGAGCA
		Reverse: TAGGTTTCTGCTGTGCCTGA
	β -actin	Forward: TCACCCACACTGTGCCCATCTACGA
		Reverse: CAGCGGAACCGCTCATTGCCAATGG
	pri-miR-143	Forward: TCCCCTCTAACACCCCTTCTC
		Reverse: CACTCCTCCTGCCCAAGA
	pre-miR-143	Forward: TGAGGTGCAGTGCTGCATC
		Reverse: GCTACAGTGCTTCATCTCAGACTC
	pri-miR-145	Forward: TGGATTGCCTCCTTCCCA
		Reverse: TTGAACCCTCATCCTGTGAGCC

	pre-miR-145	Forward: CTTGTCCTCACGGTCCAGTT
		Reverse: ATTTCCAGGAATCCCCATCT
	hRNU6-1b	Forward: CTCGCTTCGGCAGCACA
		Reverse: AACGCTTCACGAATTTGCGT
pmirGLO	miR-143	Forward: GCGAATTCGCGGAGCAGCGCAGCGCCCT
		Reverse: GCGTCGACTGGCTGCAGAACAACCTTCTCT
	miR-145	Forward: GCGAATTCGGCGGCCTTGGCGCTGAAGGCCAC
		Reverse: GCGTCGACTGGGGTGGGAAGGAGGCAAATCCA

Figure S1 The Bayesian network construction process

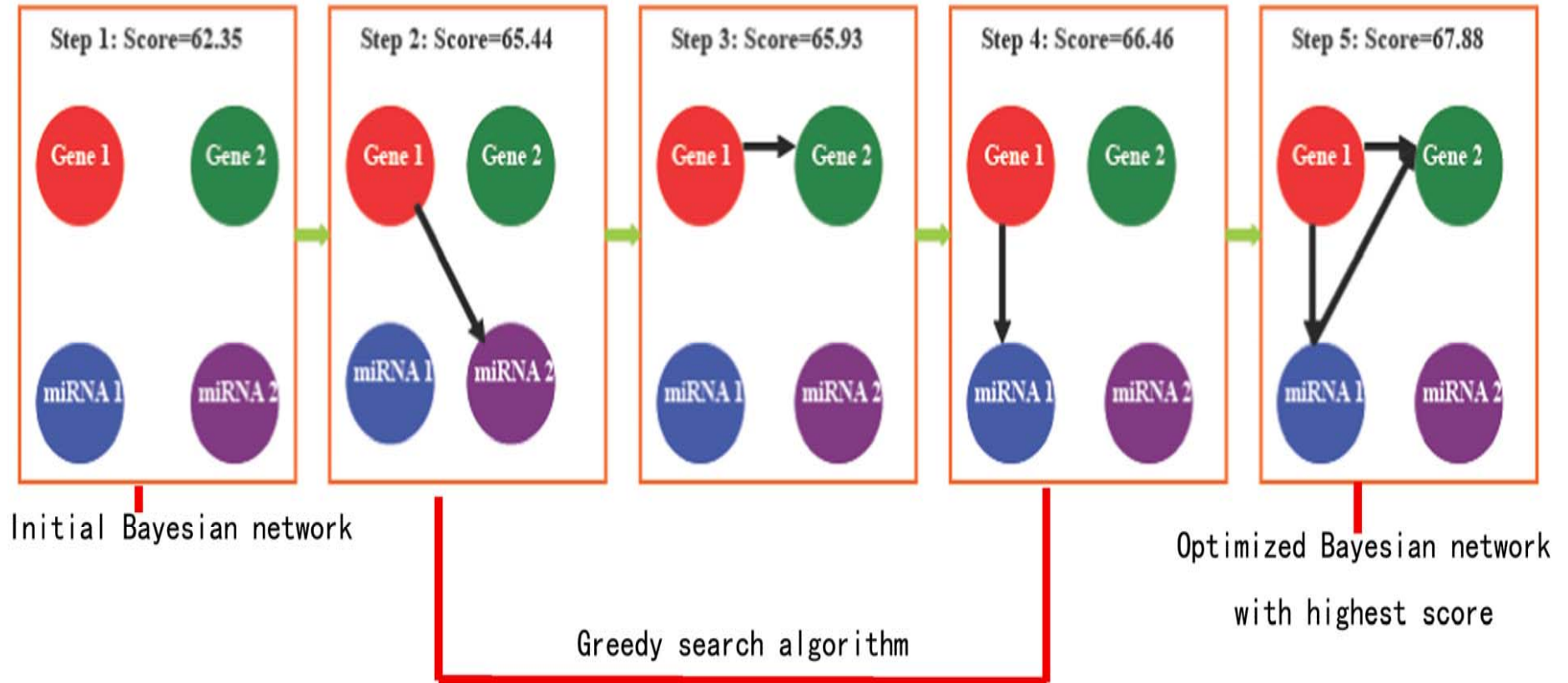
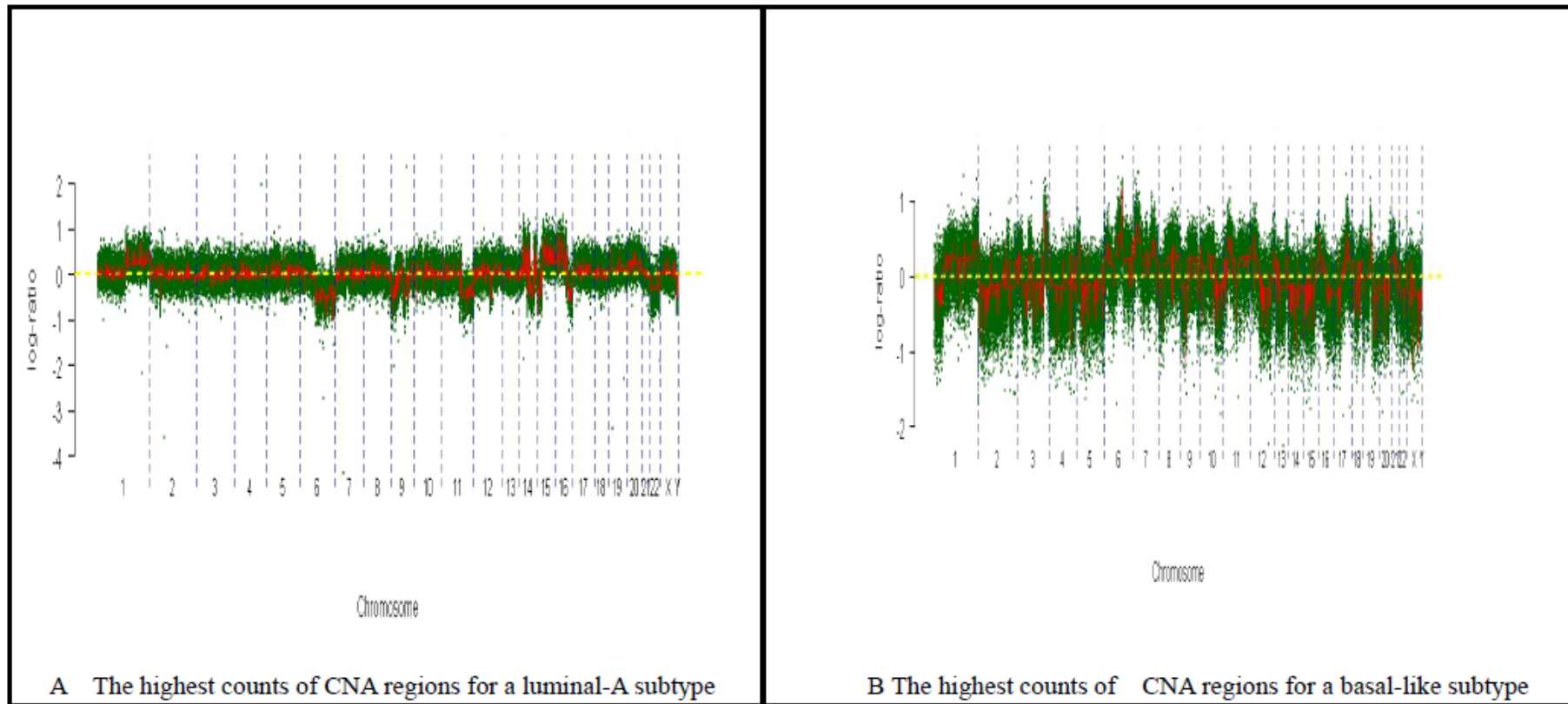
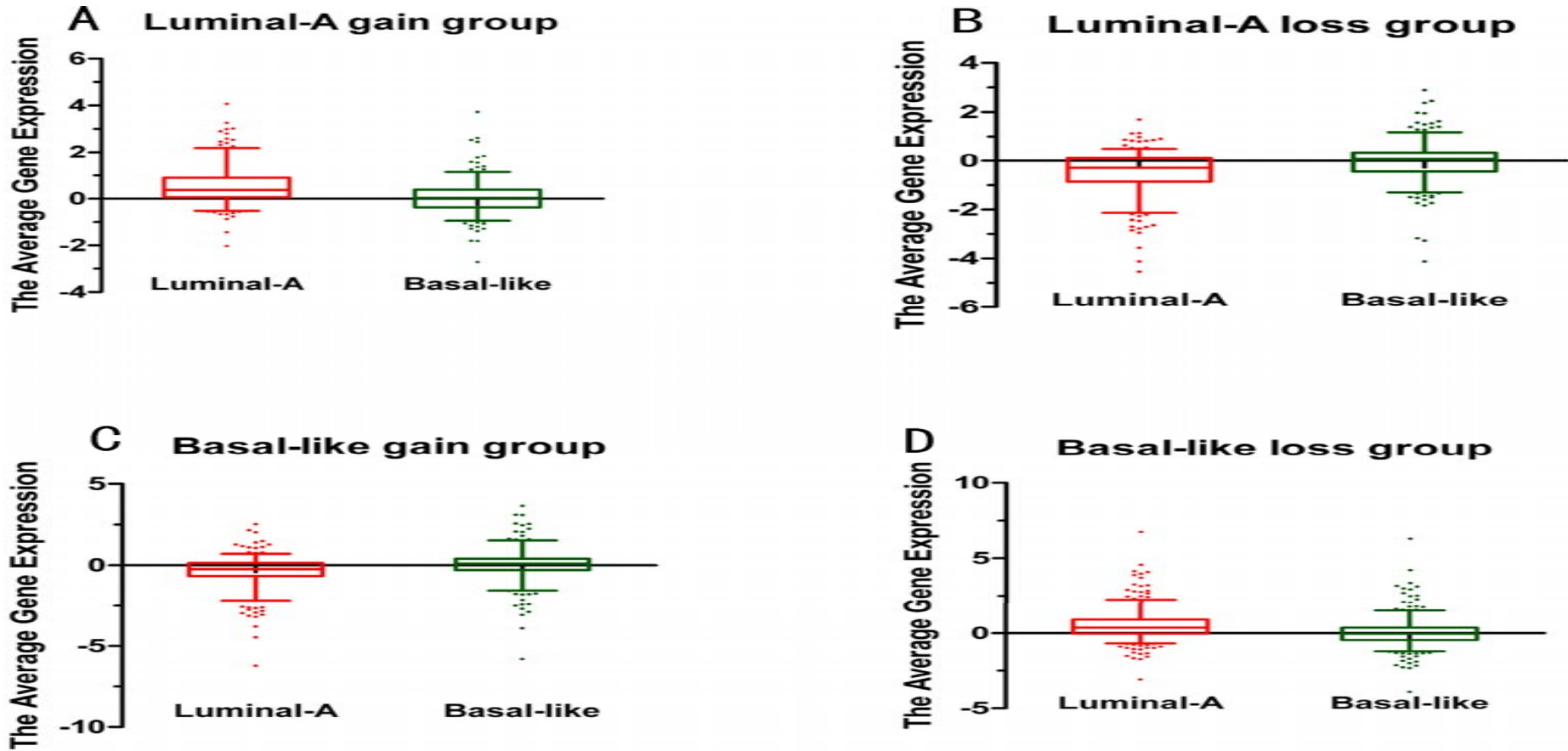


Figure S2 The highest counts of CNA regions for a luminal-A subtype and a basal-like subtype



(A) The highest counts of CNA regions for a luminal-A subtype (B) The highest counts of CNA regions for a basal-like subtype.

Figure S3 The average gene expression of four gene groups



Note: The Average Gene Expression indicates the average expression value of genes involved in the corresponding sample group.

Figure S4 Kaplan-Meier (KM) survival analysis for genes involved in the identified network motifs

