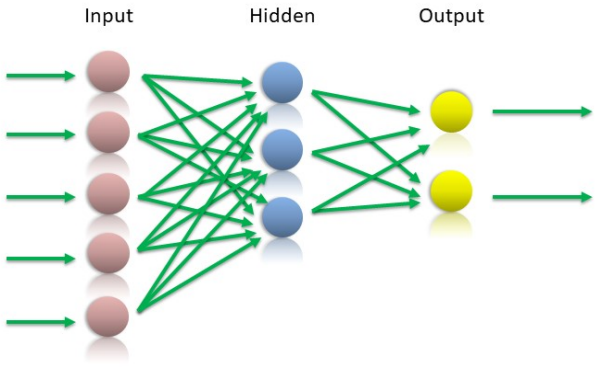

Figure S1. Layer architecture for analysis of human breast cancer. Deep learning algorithm has analogy of quantum computation algorithm because their algorithm steps contain coherence of layer architecture. METS analysis was inferred with the layer algorithm as shown. Input; therapeutic agents, Hidden; alteration of miRNAs, Output; drug resistance

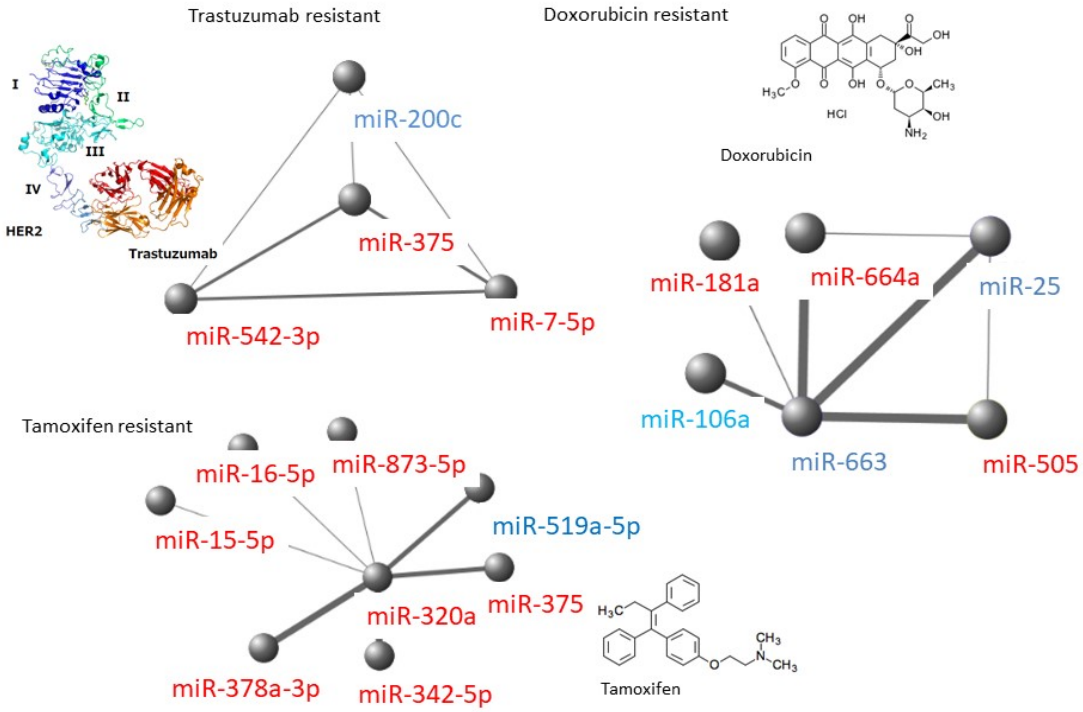

Figure S2. Drug resistance-related miRNAs in human breast cancer. miRNAs were illustrated by Cytoscape in trastuzumab, doxorubicin and tamoxifen resistance. Upregulation and downregulation were depicted in red and blue, respectively

		miR-320a	miR-15a-5p	miR-16-5p	miR-378a-3p	miR-342-5p	miR-873-5p	miR-375	miR-519a-	miR-301a-5p
	SNS	10	6	6	8	8	6	6	7	3
miR-320a	10									
miR-15-5p	6	60								
miR-16-5p	6	60	36							
miR-378a-3p	8	80	48	48						
miR-342-5p	8	80	48	48	64					
miR-873-5p	6	60	36	36	48	48				
miR-375	7	70	42	42	56	56	42			
miR-519a-5p	7	70	42	42	56	56	42	42		
miR-301a-5p	3	30	18	18	24	24	18	18	21	

Figure S3. Matrix analysis of tamoxifen resistance in human breast cancer. To construct layer architecture with tamoxifen resistant DNS, SNSs of 9 miRNAs, miR-320, miR-15-5p, miR-16-5p, miR-378a-3p, miR-342-5p, miR-873-5p, miR-375, miR-519a-5p and miR-301a-5p were applied for DNS matrix and the matrix of tamoxifen resistance was shown as an example of drug resistance

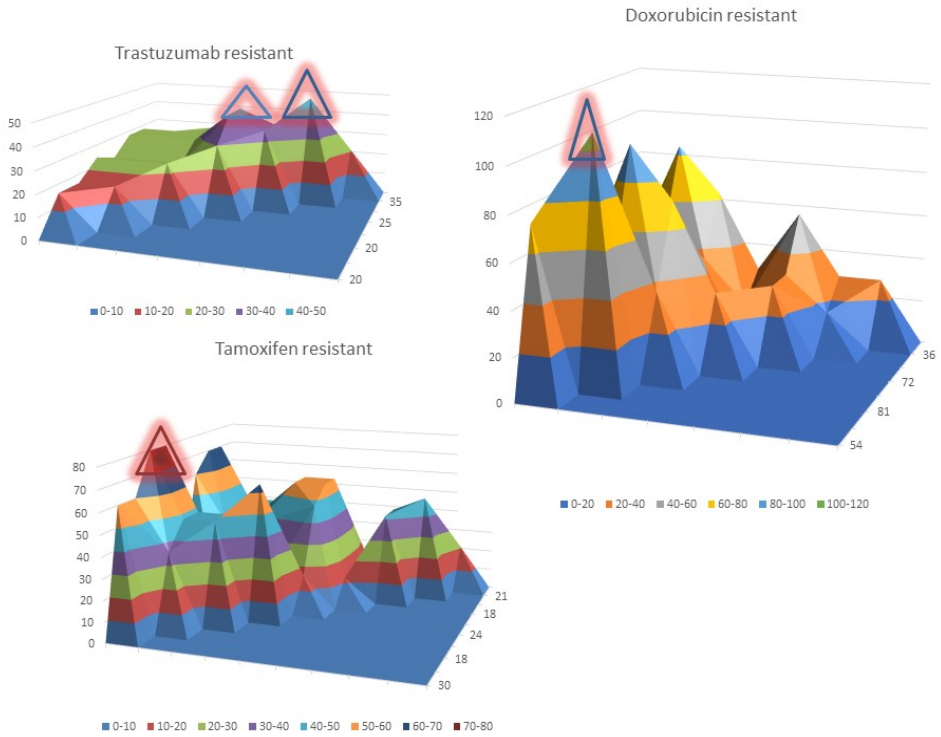

Figure S4. Quantum energy level diagram of drug resistance in breast cancer. Matrixes of three drug resistances were presented as colored contours of DNS layer architecture. Quantum energy levels of top layer (quantum code rage; QCR) were 40-50, 90-100 and 70-80 in trastuzumab, doxorubicin and tamoxifen resistances (triangles), respectively