

**Table S1.** Characteristics of the participants for discovery and validation cohort.

<i>Discovery cohort</i>				
Characteristics <sup>a</sup>	HC (n = 7)	Non-BCRL (n = 7)	BCRL (n = 7)	P-value
Age, years	49.00 ± 7.25	48.71 ± 7.22	45.86 ± 7.98	0.692
BMI, kg/m <sup>2</sup>	26.39 ± 5.04	30.19 ± 6.66	27.58 ± 6.15	0.494
Fat percentage, %	35.80 ± 5.81	37.55 ± 5.29	32.00 ± 6.63	0.229
Waist circumference, cm	92.65 ± 14.06	92.70 ± 10.19	87.37 ± 8.57	0.600
Waist-to-hip ratio	0.92 ± 0.05	0.90 ± 0.04	0.88 ± 0.04	0.445
Waist-to-height ratio	0.58 ± 0.09	0.59 ± 0.06	0.57 ± 0.07	0.758
Systolic blood pressure, mm/Hg	136.00 ± 18.56	128.14 ± 14.18	122.85 ± 23.93	0.456
Diastolic blood pressure, mm/Hg	80.14 ± 9.02	81.57 ± 15.59	79.85 ± 12.69	0.964
Heart rate, bpm	73.42 ± 9.01	78.28 ± 4.75	88.71 ± 16.67	0.059
<i>Validation cohort</i>				
Characteristics	BCRL (n = 16)	Non-BCRL (n = 83)	OR [95% C.I.]	P-value
Age, years <sup>b</sup>	55.31 ± 5.70	51.86 ± 8.61		0.052
Years after diagnosis <sup>c</sup>	3.50 (4.00)	4.00 (5.00)		0.430
BMI, kg/m <sup>2</sup> <sup>c</sup>	30.03 (6.04)	26.67 (7.83)		0.013*
Fat percentage, % <sup>c</sup>	39.30 (9.70)	37.20 (6.90)		0.790
Waist circumference, cm <sup>c</sup>	102.15 (15.85)	89.40 (17.30)		0.004 <sup>†</sup>
Waist-to-hip ratio <sup>b</sup>	0.92 ± 0.07	0.88 ± 0.07		0.029*
Waist-to-height ratio <sup>c</sup>	0.67 (0.09)	0.57 (0.10)		0.007 <sup>†</sup>
Systolic blood pressure, mm/Hg <sup>c</sup> , n = 96	133.00 (26.00)	126.00 (22.00)		0.051
Diastolic blood pressure, mm/Hg <sup>c</sup> , n = 96	81.00 (18.00)	79.00 (13.50)		0.467
Heart rate, bpm <sup>b</sup>	83.13 ± 14.97	81.31 ± 12.10		0.607
Arm disability scores (DASH) <sup>c</sup>	40.83 (33.41)	17.50 (21.67)		<0.001 <sup>φ</sup>
QoL scores (FACT-B) <sup>b</sup>	107.87 ± 21.3	115.37 ± 17.0		0.125
<b>Comorbidities</b>				
Hypertension <sup>d</sup>	9 (56.25%)	13 (15.12%)	6.92 [2.19-21.89]	<0.001 <sup>φ</sup>
Diabetes mellitus <sup>d</sup>	7 (43.75%)	7 (8.14%)	8.44 [2.41-29.62]	<0.001 <sup>φ</sup>

<sup>a</sup>P-value of differences between means were calculated using one-way ANOVA which data are expressed as mean ± standard deviation (SD). <sup>b</sup>P value of differences between means were calculated using independent Student's t-test and data are presented as mean ± SD. <sup>c</sup>P-value of differences between groups were calculated from Mann–Whitney U test, with data presented as median (interquartile range, IQR). <sup>d</sup>Test of association using the Pearson's chi-squared test, expressed as number of subjects for each case and percentage. \*p value < 0.05, <sup>†</sup>p value < 0.01, and <sup>φ</sup>p value < 0.001. Bpm beats per minute; C.I. confidence interval; DASH Disabilities of the Arm, Shoulder, and Hand; FACT-B Functional Assessment of Cancer Therapy – Breast; OR odd ratio; QoL – quality of Life

Table S2 Target gene prediction analysis

Gene	MiRNA	Integrated score
SERPINE2	hsa-miR-199a-3p	0.8774
MAP3K4	hsa-miR-199a-3p	0.8741
CELSR2	hsa-miR-199a-3p	0.8508
CDK17	hsa-miR-199a-3p	0.8397
QKI	hsa-miR-199a-3p	0.8338
ITGB8	hsa-miR-199a-3p	0.8233
ADAMTSL3	hsa-miR-199a-3p	0.8140
NAA25	hsa-miR-199a-3p	0.8132
VAMP3	hsa-miR-199a-3p	0.8119
KATNBL1	hsa-miR-199a-3p	0.8108
KLHL3	hsa-miR-199a-3p	0.8096
GNA12	hsa-miR-199a-3p	0.8052
ERBB4	hsa-miR-199a-3p	0.8047
NOVA1	hsa-miR-199a-3p	0.8021
CD2AP	hsa-miR-199a-3p	0.7972
CISD2	hsa-miR-199a-3p	0.7964
BCAR3	hsa-miR-199a-3p	0.7938
ADAMTS3	hsa-miR-199a-3p	0.7936
ZHX1	hsa-miR-199a-3p	0.7936
FXR1	hsa-miR-151a-3p	0.7921
ACVR2A	hsa-miR-199a-3p	0.7913
G3BP2	hsa-miR-199a-3p	0.7911
PFN2	hsa-miR-151a-3p	0.7906
FAM199X	hsa-miR-199a-3p	0.7905
CLASP2	hsa-miR-151a-3p	0.7857
DEPDC1B	hsa-miR-199a-3p	0.7850
PAWR	hsa-miR-199a-3p	0.7835
SCD	hsa-miR-199a-3p	0.7795
ZBTB18	hsa-miR-199a-3p	0.7775
NID2	hsa-miR-199a-3p	0.7769
CLK1	hsa-miR-151a-3p	0.7695
AK4	hsa-miR-199a-3p	0.7688
KTN1	hsa-miR-199a-3p	0.7676
ITPK1	hsa-miR-199a-3p	0.7667
PLEKHA3	hsa-miR-199a-3p	0.7661
ETNK1	hsa-miR-199a-3p	0.7660
PON2	hsa-miR-199a-3p	0.7645
NEDD4	hsa-miR-199a-3p	0.7630
VLDLR	hsa-miR-199a-3p	0.7614
KDM6A	hsa-miR-199a-3p	0.7601
CFL2	hsa-miR-199a-3p	0.7579
HIF1A	hsa-miR-151a-3p	0.7527
MEIS2	hsa-miR-199a-3p	0.7520
SLC20A2	hsa-miR-199a-3p	0.7504
ARL15	hsa-miR-199a-3p	0.7495
MTOR	hsa-miR-199a-3p	0.7495
SINHCAF	hsa-miR-199a-3p	0.7483
ZNF217	hsa-miR-199a-3p	0.7452
RB1	hsa-miR-199a-3p	0.7420
FXR1	hsa-miR-199a-3p	0.7413
AEBP2	hsa-miR-199a-3p	0.7398
TRA2B	hsa-miR-151a-3p	0.7396
ARHGEF3	hsa-miR-199a-3p	0.7393
MAP3K5	hsa-miR-199a-3p	0.7384
TGIF2	hsa-miR-199a-3p	0.7384
CELF2	hsa-miR-199a-3p	0.7379
RYBP	hsa-miR-151a-3p	0.7360
RBM47	hsa-miR-199a-3p	0.7357
SLC39A10	hsa-miR-199a-3p	0.7355
LCOR	hsa-miR-199a-3p	0.7336
PPP2R5E	hsa-miR-199a-3p	0.7331
PAK4	hsa-miR-199a-3p	0.7310
DDHD1	hsa-miR-199a-3p	0.7308
PRKCE	hsa-miR-199a-3p	0.7301
LRRC1	hsa-miR-199a-3p	0.7293
CPEB4	hsa-miR-199a-3p	0.7280
APLP2	hsa-miR-199a-3p	0.7273
TAB2	hsa-miR-199a-3p	0.7253
MCFD2	hsa-miR-199a-3p	0.7230

Gene	MiRNA	Integrated score
LRP2	hsa-miR-199a-3p	0.7229
LPAR4	hsa-miR-199a-3p	0.7221
GRK3	hsa-miR-199a-3p	0.7220
ZFPM2	hsa-miR-151a-3p	0.7217
YTHDF3	hsa-miR-151a-3p	0.7205
TACC2	hsa-miR-199a-3p	0.7179
C9orf40	hsa-miR-199a-3p	0.7175
TSPAN3	hsa-miR-199a-3p	0.7172
FUBP1	hsa-miR-199a-3p	0.7139
YWHAE	hsa-miR-199a-3p	0.7137
CCDC88A	hsa-miR-199a-3p	0.7137
FOXQ1	hsa-miR-199a-3p	0.7132
DNMT3A	hsa-miR-199a-3p	0.7110
DCBLD2	hsa-miR-199a-3p	0.7109
GREM1	hsa-miR-199a-3p	0.7108
CSRP2	hsa-miR-199a-3p	0.7073
KCTD16	hsa-miR-199a-3p	0.7064
RNGTT	hsa-miR-199a-3p	0.7064
KIAA0319L	hsa-miR-199a-3p	0.7060
RAP2A	hsa-miR-199a-3p	0.7053
CEP85L	hsa-miR-199a-3p	0.7046
FGF7	hsa-miR-199a-3p	0.7046
FBXW11	hsa-miR-199a-3p	0.7035
PNRC1	hsa-miR-199a-3p	0.7032
IL13RA1	hsa-miR-199a-3p	0.7027
ATAD1	hsa-miR-199a-3p	0.7023
DDIT4	hsa-miR-199a-3p	0.7017
RUNX1	hsa-miR-199a-3p	0.7013
PTPN3	hsa-miR-199a-3p	0.7004
CNEP1R1	hsa-miR-199a-3p	0.6994
CYB5R4	hsa-miR-199a-3p	0.6986
SLC6A5	hsa-miR-199a-3p	0.6985
PPP2R2A	hsa-miR-199a-3p	0.6971
TAOK1	hsa-miR-199a-3p	0.6962
IREB2	hsa-miR-199a-3p	0.6956
UPP2	hsa-miR-151a-3p	0.6954
PURB	hsa-miR-151a-3p	0.6944
SOCS5	hsa-miR-151a-3p	0.6941
PIGB	hsa-miR-199a-3p	0.6928
SDC2	hsa-miR-199a-3p	0.6926
WDR47	hsa-miR-199a-3p	0.6920
DLC1	hsa-miR-151a-3p	0.6901
MKRN1	hsa-miR-199a-3p	0.6898
FN1	hsa-miR-199a-3p	0.6894
IFFO2	hsa-miR-199a-3p	0.6885
UBE2W	hsa-miR-199a-3p	0.6884
PLEKHH1	hsa-miR-199a-3p	0.6876
ZHX2	hsa-miR-199a-3p	0.6864
RNF216	hsa-miR-199a-3p	0.6833
MBNL1	hsa-miR-199a-3p	0.6829
RABGAP1	hsa-miR-199a-3p	0.6822
CRK	hsa-miR-151a-3p	0.6819
MDGA2	hsa-miR-199a-3p	0.6811
DUSP5	hsa-miR-199a-3p	0.6804
ATRX	hsa-miR-199a-3p	0.6801
ITGA3	hsa-miR-199a-3p	0.6787
RORB	hsa-miR-199a-3p	0.6780
GOLGA4	hsa-miR-199a-3p	0.6779
NLK	hsa-miR-199a-3p	0.6777
NACC2	hsa-miR-199a-3p	0.6772
TMEM62	hsa-miR-199a-3p	0.6769
SLC49A4	hsa-miR-199a-3p	0.6768
RNF14	hsa-miR-199a-3p	0.6767
PLAG1	hsa-miR-199a-3p	0.6767
PHF6	hsa-miR-199a-3p	0.6753
PDE4B	hsa-miR-199a-3p	0.6753
LIN28B	hsa-miR-199a-3p	0.6726
EDEM3	hsa-miR-199a-3p	0.6721
TXLNG	hsa-miR-199a-3p	0.6720
AGO2	hsa-miR-151a-3p	0.6717
PLCB1	hsa-miR-199a-3p	0.6714

<i>Gene</i>	<i>MiRNA</i>	<i>Integrated score</i>
<i>KLF12</i>	hsa-miR-151a-3p	0.6714
<i>GPBP1L1</i>	hsa-miR-199a-3p	0.6710
<i>COPS2</i>	hsa-miR-199a-3p	0.6706
<i>ZFAND5</i>	hsa-miR-151a-3p	0.6697
<i>TEAD1</i>	hsa-miR-199a-3p	0.6696
<i>SEMA3A</i>	hsa-miR-199a-3p	0.6680
<i>KDM3A</i>	hsa-miR-199a-3p	0.6673
<i>ADD3</i>	hsa-miR-199a-3p	0.6673
<i>ACOX1</i>	hsa-miR-199a-3p	0.6662
<i>CITED2</i>	hsa-miR-199a-3p	0.6645
<i>SOWAHC</i>	hsa-miR-199a-3p	0.6631
<i>SNN</i>	hsa-miR-199a-3p	0.6631
<i>ILRUN</i>	hsa-miR-151a-3p	0.6630
<i>TWIST1</i>	hsa-miR-151a-3p	0.6623
<i>ARID4B</i>	hsa-miR-199a-3p	0.6616
<i>CRIM1</i>	hsa-miR-199a-3p	0.6611
<i>UCK2</i>	hsa-miR-199a-3p	0.6602
<i>YAP1</i>	hsa-miR-199a-3p	0.6599
<i>ABCA1</i>	hsa-miR-199a-3p	0.6597
<i>ALX4</i>	hsa-miR-199a-3p	0.6595
<i>CREBRF</i>	hsa-miR-199a-3p	0.6594
<i>ADRB1</i>	hsa-miR-199a-3p	0.6590
<i>WAPL</i>	hsa-miR-199a-3p	0.6589
<i>STIM2</i>	hsa-miR-199a-3p	0.6583
<i>ACVR2B</i>	hsa-miR-199a-3p	0.6582
<i>ENOX2</i>	hsa-miR-199a-3p	0.6581
<i>NACC1</i>	hsa-miR-199a-3p	0.6580
<i>ESRP1</i>	hsa-miR-199a-3p	0.6578
<i>DIO2</i>	hsa-miR-199a-3p	0.6574
<i>PTPRZ1</i>	hsa-miR-199a-3p	0.6563
<i>RAPGEF4</i>	hsa-miR-199a-3p	0.6561
<i>UXS1</i>	hsa-miR-199a-3p	0.6560
<i>TANC1</i>	hsa-miR-199a-3p	0.6531
<i>AREL1</i>	hsa-miR-199a-3p	0.6526
<i>SECISBP2L</i>	hsa-miR-199a-3p	0.6524
<i>CHAD</i>	hsa-miR-199a-3p	0.6519
<i>AKT3</i>	hsa-miR-151a-3p	0.6505
<i>FBXO28</i>	hsa-miR-199a-3p	0.6499
<i>SIX1</i>	hsa-miR-151a-3p	0.6494
<i>SEC16B</i>	hsa-miR-199a-3p	0.6493
<i>NFIA</i>	hsa-miR-199a-3p	0.6492
<i>CNOT7</i>	hsa-miR-199a-3p	0.6483
<i>FAM104A</i>	hsa-miR-151a-3p	0.6429
<i>ATP2A2</i>	hsa-miR-151a-3p	0.6358
<i>PANK2</i>	hsa-miR-151a-3p	0.6281
<i>CASD1</i>	hsa-miR-151a-3p	0.6276
<i>NPAS3</i>	hsa-miR-151a-3p	0.6194
<i>MEX3C</i>	hsa-miR-151a-3p	0.6179
<i>EIF4G2</i>	hsa-miR-151a-3p	0.6165
<i>POU4F1</i>	hsa-miR-151a-3p	0.6162
<i>CHL1</i>	hsa-miR-151a-3p	0.6131
<i>PITPNA</i>	hsa-miR-151a-3p	0.6118
<i>PKN2</i>	hsa-miR-151a-3p	0.6063
<i>MAP1B</i>	hsa-miR-151a-3p	0.5979
<i>CALCR</i>	hsa-miR-151a-3p	0.5783
<i>CALD1</i>	hsa-miR-151a-3p	0.5739
<i>UBE2N</i>	hsa-miR-151a-3p	0.5687
<i>PAPOLG</i>	hsa-miR-151a-3p	0.5673
<i>TMX1</i>	hsa-miR-151a-3p	0.5620
<i>QKI</i>	hsa-miR-151a-3p	0.5563
<i>DEUP1</i>	hsa-miR-151a-3p	0.5553
<i>RANBP17</i>	hsa-miR-151a-3p	0.5533
<i>SMARCAD1</i>	hsa-miR-151a-3p	0.5532
<i>SEPTIN7</i>	hsa-miR-151a-3p	0.5515
<i>NAV3</i>	hsa-miR-151a-3p	0.5496
<i>NIPAL2</i>	hsa-miR-151a-3p	0.5430
<i>ZMAT1</i>	hsa-miR-151a-3p	0.5421
<i>RBM5</i>	hsa-miR-151a-3p	0.5418
<i>INSR</i>	hsa-miR-151a-3p	0.5410
<i>MAF</i>	hsa-miR-151a-3p	0.5237
<i>AGO3</i>	hsa-miR-151a-3p	0.5237

<i>Gene</i>	<i>MiRNA</i>	<i>Integrated score</i>
<i>RC3H1</i>	hsa-miR-151a-3p	0.5156
<i>CYLD</i>	hsa-miR-151a-3p	0.5141
<i>KBTBD2</i>	hsa-miR-151a-3p	0.5140
<i>CEP41</i>	hsa-miR-151a-3p	0.5130
<i>NAPEPLD</i>	hsa-miR-151a-3p	0.5122
<i>HK2</i>	hsa-miR-151a-3p	0.5096
<i>LAMTOR3</i>	hsa-miR-151a-3p	0.5095
<i>TANC2</i>	hsa-miR-151a-3p	0.5090
<i>NPL</i>	hsa-miR-151a-3p	0.5087
<i>GHR</i>	hsa-miR-151a-3p	0.5071
<i>LPIN2</i>	hsa-miR-151a-3p	0.5063
<i>TNIK</i>	hsa-miR-151a-3p	0.5055
<i>FBXL3</i>	hsa-miR-151a-3p	0.5049
<i>ZNF292</i>	hsa-miR-151a-3p	0.5017
<i>BRINP3</i>	hsa-miR-151a-3p	0.5015
<i>NUFIP2</i>	hsa-miR-151a-3p	0.4991
<i>CYP7B1</i>	hsa-miR-151a-3p	0.4987
<i>TMEM98</i>	hsa-miR-151a-3p	0.4986
<i>SLC4A7</i>	hsa-miR-151a-3p	0.4981
<i>CREBRF</i>	hsa-miR-151a-3p	0.4948
<i>TSC1</i>	hsa-miR-151a-3p	0.4915
<i>HMGA2</i>	hsa-miR-151a-3p	0.4910
<i>VAMP1</i>	hsa-miR-151a-3p	0.4909
<i>TNPO1</i>	hsa-miR-151a-3p	0.4897
<i>PCBP2</i>	hsa-miR-151a-3p	0.4850
<i>RPS6KA5</i>	hsa-miR-151a-3p	0.4775
<i>STRN3</i>	hsa-miR-151a-3p	0.4753
<i>SLC35F5</i>	hsa-miR-151a-3p	0.4685
<i>SEC63</i>	hsa-miR-151a-3p	0.4679
<i>CSNK1G1</i>	hsa-miR-151a-3p	0.4673
<i>PSME3</i>	hsa-miR-151a-3p	0.4646
<i>CHD9</i>	hsa-miR-151a-3p	0.4645
<i>RPRD2</i>	hsa-miR-151a-3p	0.4627
<i>MIER3</i>	hsa-miR-151a-3p	0.4626
<i>API5</i>	hsa-miR-151a-3p	0.4570
<i>PTGER3</i>	hsa-miR-151a-3p	0.4540
<i>BRWD1</i>	hsa-miR-151a-3p	0.4535
<i>PTPN12</i>	hsa-miR-151a-3p	0.4496
<i>FIGN</i>	hsa-miR-151a-3p	0.4493
<i>RPS6KA3</i>	hsa-miR-151a-3p	0.4493
<i>GLS</i>	hsa-miR-151a-3p	0.4490
<i>PLEKHA1</i>	hsa-miR-151a-3p	0.4452
<i>WDFY3</i>	hsa-miR-151a-3p	0.4451
<i>DBT</i>	hsa-miR-151a-3p	0.4444
<i>GRM3</i>	hsa-miR-151a-3p	0.4423
<i>TRIM33</i>	hsa-miR-151a-3p	0.4416
<i>SLC8A1</i>	hsa-miR-151a-3p	0.4413
<i>SP3</i>	hsa-miR-151a-3p	0.4404
<i>GOLM2</i>	hsa-miR-151a-3p	0.4346
<i>CALN1</i>	hsa-miR-151a-3p	0.4344
<i>MBTD1</i>	hsa-miR-151a-3p	0.4337
<i>MYLK4</i>	hsa-miR-151a-3p	0.4331
<i>PELI1</i>	hsa-miR-151a-3p	0.4287
<i>USP6NL</i>	hsa-miR-151a-3p	0.4284
<i>CUX1</i>	hsa-miR-151a-3p	0.4278
<i>KCNH8</i>	hsa-miR-151a-3p	0.4275
<i>ADNP</i>	hsa-miR-151a-3p	0.4263
<i>ANKRD44</i>	hsa-miR-151a-3p	0.4263
<i>NAA15</i>	hsa-miR-151a-3p	0.4250
<i>RAB22A</i>	hsa-miR-151a-3p	0.4236
<i>GABRB1</i>	hsa-miR-151a-3p	0.4224
<i>ASXL2</i>	hsa-miR-151a-3p	0.4222
<i>NIPBL</i>	hsa-miR-151a-3p	0.4211
<i>PTEN</i>	hsa-miR-151a-3p	0.4187
<i>ME1</i>	hsa-miR-151a-3p	0.4184
<i>NSD3</i>	hsa-miR-151a-3p	0.4138
<i>RFESD</i>	hsa-miR-151a-3p	0.4134
<i>ATAD2B</i>	hsa-miR-151a-3p	0.4115
<i>GAN</i>	hsa-miR-151a-3p	0.4111
<i>GLCCI1</i>	hsa-miR-151a-3p	0.4100
<i>KDM7A</i>	hsa-miR-151a-3p	0.4090

<i>Gene</i>	<i>MiRNA</i>	<i>Integrated score</i>
<i>SPAG9</i>	hsa-miR-151a-3p	0.4059
<i>PLCL2</i>	hsa-miR-151a-3p	0.4059
<i>PCDHAC1</i>	hsa-miR-151a-3p	0.4052
<i>MAN1A2</i>	hsa-miR-151a-3p	0.4043
<i>NEURL1B</i>	hsa-miR-151a-3p	0.4037
<i>RBM27</i>	hsa-miR-151a-3p	0.4030
<i>TAB3</i>	hsa-miR-151a-3p	0.4025
<i>HSPA4L</i>	hsa-miR-151a-3p	0.4010
<i>ALCAM</i>	hsa-miR-151a-3p	0.3993
<i>UHMK1</i>	hsa-miR-151a-3p	0.3992
<i>IDE</i>	hsa-miR-151a-3p	0.3987
<i>NFAT5</i>	hsa-miR-151a-3p	0.3974
<i>LRCH1</i>	hsa-miR-151a-3p	0.3973
<i>TP53</i>	hsa-miR-151a-3p	0.3951
<i>RNF20</i>	hsa-miR-151a-3p	0.3933
<i>GAREM1</i>	hsa-miR-151a-3p	0.3929
<i>FOXP1</i>	hsa-miR-151a-3p	0.3921
<i>OXR1</i>	hsa-miR-151a-3p	0.3915
<i>PGM3</i>	hsa-miR-151a-3p	0.3913
<i>MBNL2</i>	hsa-miR-151a-3p	0.3907
<i>GNA13</i>	hsa-miR-151a-3p	0.3900
<i>PLXNA4</i>	hsa-miR-151a-3p	0.3873
<i>SMAD2</i>	hsa-miR-151a-3p	0.3870
<i>SPATS2</i>	hsa-miR-151a-3p	0.3865
<i>WIPF2</i>	hsa-miR-151a-3p	0.3850
<i>LPGAT1</i>	hsa-miR-151a-3p	0.3818
<i>PPP1R16B</i>	hsa-miR-151a-3p	0.3814
<i>PTPRS</i>	hsa-miR-151a-3p	0.3805
<i>TIMP3</i>	hsa-miR-151a-3p	0.3790
<i>SAP30L</i>	hsa-miR-151a-3p	0.3780
<i>CKAP5</i>	hsa-miR-151a-3p	0.3779
<i>PDHA1</i>	hsa-miR-151a-3p	0.3765
<i>KCNC1</i>	hsa-miR-151a-3p	0.3757
<i>THBS1</i>	hsa-miR-151a-3p	0.3754
<i>SLC39A10</i>	hsa-miR-151a-3p	0.3750
<i>NUDT4</i>	hsa-miR-151a-3p	0.3730
<i>MTPN</i>	hsa-miR-151a-3p	0.3726
<i>RAB8B</i>	hsa-miR-151a-3p	0.3708

**Table S3 Top 10 enriched biological processes, molecular functions, and cellular components of miR-199a-3p and miR-151a-3p associated genes in BCRL group**

	GO terms	Adjusted p-value
<b>Biological process</b>	regulation of gene expression (GO:0010468)	1.62E-08
	regulation of cellular macromolecule biosynthetic process (GO:2000112)	3.84E-05
	regulation of transcription, DNA-templated (GO:0006355)	6.07E-05
	regulation of nucleic acid-templated transcription (GO:1903506)	6.07E-05
	negative regulation of nucleic acid-templated transcription (GO:1903507)	1.95E-04
	negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	2.57E-04
	positive regulation of transcription, DNA-templated (GO:0045893)	2.57E-04
	positive regulation of macromolecule metabolic process (GO:0010604)	2.71E-04
	negative regulation of transcription by RNA polymerase II (GO:0000122)	4.06E-04
	negative regulation of transcription, DNA-templated (GO:0045892)	6.92E-04
<b>Molecular function</b>	mRNA binding (GO:0003729)	5.74E-07
	protein serine/threonine kinase activity (GO:0004674)	5.45E-04
	histone deacetylase binding (GO:0042826)	0.002277
	transcription cis-regulatory region binding (GO:0000976)	0.019429
	mRNA 3'-UTR binding (GO:0003730)	0.020853
	disordered domain specific binding (GO:0097718)	0.020853
	sequence-specific double-stranded DNA binding (GO:1990837)	0.020853
	RNA binding (GO:0003723)	0.020853
	PDZ domain binding (GO:0030165)	0.020853
	protein phosphorylated amino acid binding (GO:0045309)	0.020853
<b>Cellular component</b>	nucleus (GO:0005634)	8.87E-08
	intracellular membrane-bounded organelle (GO:0043231)	1.63E-06
	axon (GO:0030424)	0.001367
	neuron projection (GO:0043005)	0.063685
	cytoplasmic stress granule (GO:0010494)	0.109715
	dendrite (GO:0030425)	0.109715
	activin receptor complex (GO:0048179)	0.109715
	protein kinase complex (GO:1902911)	0.109715
	RISC-loading complex (GO:0070578)	0.12868
	focal adhesion (GO:0005925)	0.158116

**Table S4 Top 20 enriched KEGG pathway analysis of the associated genes in BCRL group**

Term	Adjusted <i>p</i> -value	Genes
PI3K-Akt signaling pathway	1.37E-05	YWHAE;ITGA3;INSR;ITGA1;FN1;PTEN;PPP2R2A;TSC1;LPAR4;FGF2;THBS1;MTOR;GHR;FGF7;PPP2R5E;ERBB4;AKT3;DDIT4;CHAD;ITGA8;ITGB8;PKN2;ITGA6;TP53
MAPK signaling pathway	2.78E-04	MAP3K2;DUSP5;INSR;NLK;FGF2;RPS6KA3;RPS6KA6;FGF7;RPS6KA5;ERBB4;TAOK1;AKT3;GNA12;TAB2;TP53;LAMTOR3;CRK;MAP3K4;MAP3K5
Regulation of actin cytoskeleton	2.78E-04	ITGA3;ITGA1;FN1;LPAR4;FGF2;MYLK4;GNA13;FGF7;CFL2;GNA12;ITGA8;ITGB8;ITGA6;CRK;PFN2;PAK4
Central carbon metabolism in cancer	0.002742	PDHA1;AKT3;PTEN;TP53;HIF1A;HK2;MTOR;GLS
Sphingolipid signaling pathway	0.0037	GNA13;PPP2R5E;PRKCE;AKT3;GNA12;PTEN;PPP2R2A;PLCB1;TP53;MAP3K5
Focal adhesion	0.004191	ITGA3;ITGA1;FN1;PTEN;THBS1;MYLK4;AKT3;CHAD;ITGA8;ITGB8;ITGA6;CRK;PAK4
Shigellosis	0.006548	FBXW11;PRKCE;SEPTIN7;HK2;MTOR;RPS6KA5;AKT3;UBE2N;TAB3;TAB2;PLCB1;TP53;CRK;PFN2
ECM-receptor interaction	0.006548	ITGA3;ITGA1;CHAD;ITGA8;FN1;ITGB8;ITGA6;THBS1
MicroRNAs in cancer	0.006548	PRKCE;DNMT3A;PTEN;HMGA2;THBS1;MTOR;GLS;FOXP1;RPS6KA5;MMP16;DDIT4;TIMP3;ZFPM2;TP53;CRK;PAK4
Dilated cardiomyopathy	0.00934	ITGA3;ITGA1;ITGA8;ATP2A2;ITGB8;ITGA6;ADRB1;SLC8A1
Phospholipase D signaling pathway	0.00934	GRM3;GNA13;INSR;AKT3;GNA12;TSC1;LPAR4;PLCB1;MTOR;RAPGEF4
Proteoglycans in cancer	0.00934	SMAD2;ERBB4;SDC2;AKT3;FN1;TWIST1;TIMP3;TP53;HIF1A;FGF2;THBS1;MTOR
Human papillomavirus infection	0.00934	RB1;ITGA3;ITGA1;FN1;PTEN;PPP2R2A;TSC1;THBS1;MTOR;PPP2R5E;AKT3;CHAD;ITGA8;ITGB8;ITGA6;TP53
Arrhythmogenic right ventricular cardiomyopathy	0.009775	ITGA3;ITGA1;ITGA8;ATP2A2;ITGB8;ITGA6;SLC8A1
mTOR signaling pathway	0.010036	RPS6KA3;RPS6KA6;INSR;AKT3;DDIT4;PTEN;TSC1;LAMTOR3;LIPIN2;MTOR
Insulin resistance	0.013881	RPS6KA3;RPS6KA6;PRKCE;INSR;AKT3;PTEN;PTPRF;MTOR
Pathways in cancer	0.014248	RB1;SMAD2;ITGA3;PTGER3;FN1;PTEN;LPAR4;HIF1A;FGF2;MTOR;RUNX1;GNA13;FGF7;RPS6KA5;AKT3;GNA12;ITGA6;PLCB1;TP53;CRK;IL13RA1
Apelin signaling pathway	0.014248	SMAD2;GNA13;PRKCE;AKT3;TFAM;PLCB1;SLC8A1;MTOR;MYLK4
cGMP-PKG signaling pathway	0.014763	GNA13;PRKCE;INSR;AKT3;GNA12;ATP2A2;ADRB1;PLCB1;SLC8A1;MYLK4
Hypertrophic cardiomyopathy	0.017311	ITGA3;ITGA1;ITGA8;ATP2A2;ITGB8;ITGA6;SLC8A1