Table S1. Clinicopathologic information of 2 datasets in discovery and *in silico* validation phase

Characteristics	**Discovery cohort (n=108)**	**Validation cohort (n=141)**
Accession No.	GSE15081	GSE62254
Technology	Microarray	Microarray
Median age in years (range)	N/A	63 (30-84)
Sex		
Male	N/A	95 (67.4%)
Female	N/A	46 (32.6%)
TNM stage		
2	N/A	72 (51.1%)
3	N/A	69 (48.9%)
Adjuvant treatment		
Yes	N/A	55 (39.0%)
No	N/A	85 (60.9%)
Unknown	N/A	1 (0.1%)
Peritoneal recurrence		
Yes	33 (30.6)	28 (19.9%)
No	75 (69.4)	113 (80.1%)

Table S2. Clinicopathologic characteristics of 3 clinical cohorts

	Peritoneal recurrence			Peritoneal metastasis
	Tissue samples, n (%)			Tissue samples, n (%)
Variables	**Training cohort (n=216)**	**Validation cohort (n=111)**	**Variables**	**Peritoneal metastasis evaluation cohort (n=210)**
Median age at operation, years (range)	63 (18-83)	59 (32-88)	Median age at operation, years (range)	60 (28-88)
Age distribution			Age distribution	
≤60	96 (44.4)	59 (53.2)	≤60	99 (47.1)
>60	120 (55.6)	52 (46.8)	>60	111 (52.9)
Sex			Sex	
Male	138 (63.9)	75 (67.6)	Male	150 (71.4)
Female	78 (36.1)	36 (32.4)	Female	60 (28.6)
Tumor differentiation			Tumor differentiation	
Differentiated	62 (28.7)	31 (27.9)	Differentiated	69 (32.9)
Undifferentiated	154 (71.3)	80 (72.1)	Undifferentiated	141 (67.1)

Median tumor size, cm (range)	6.0 (2.5 – 19.0)	5.2 (2.3 – 17.0)
Tumor morphology		
Borrmann type 3 & 4	116 (53.7)	70 (63.1)
Others	100 (46.3)	41 (36.9)
TNM stage*		
1	37 (17.2)	19 (17.1)
2	86 (39.8)	34 (30.6)
3	93 (43.0)	58 (52.3)
Adjuvant chemotherapy		
Yes	158 (73.1)	96 (86.5)
No	58 (26.9)	15 (13.5)
Peritoneal recurrence		
Yes	38 (17.6)	18 (16.2)
No	178 (82.4)	93 (83.8)

Median tumor size, cm (range)	5.5 (1.5 -18.0)
Tumor morphology	
Borrmann type 3 & 4	125 (59.5)
Others	85 (40.5)
TNM stage*	
1 and 2	85 (40.5)
3	94 (44.8)
4 (peritoneal metastasis)	31 (14.7)
Peritoneal metastasis	
P0/Cy1[#]	16 (51.6)
Gross metastasis	15 (48.4)

*TNM stage was based on the American Joint Committee on Cancer 7th edition

[#] P0/Cy1 refers to cases with cytology positive gastric cancer without gross metastatic tumor in peritoneal cavity

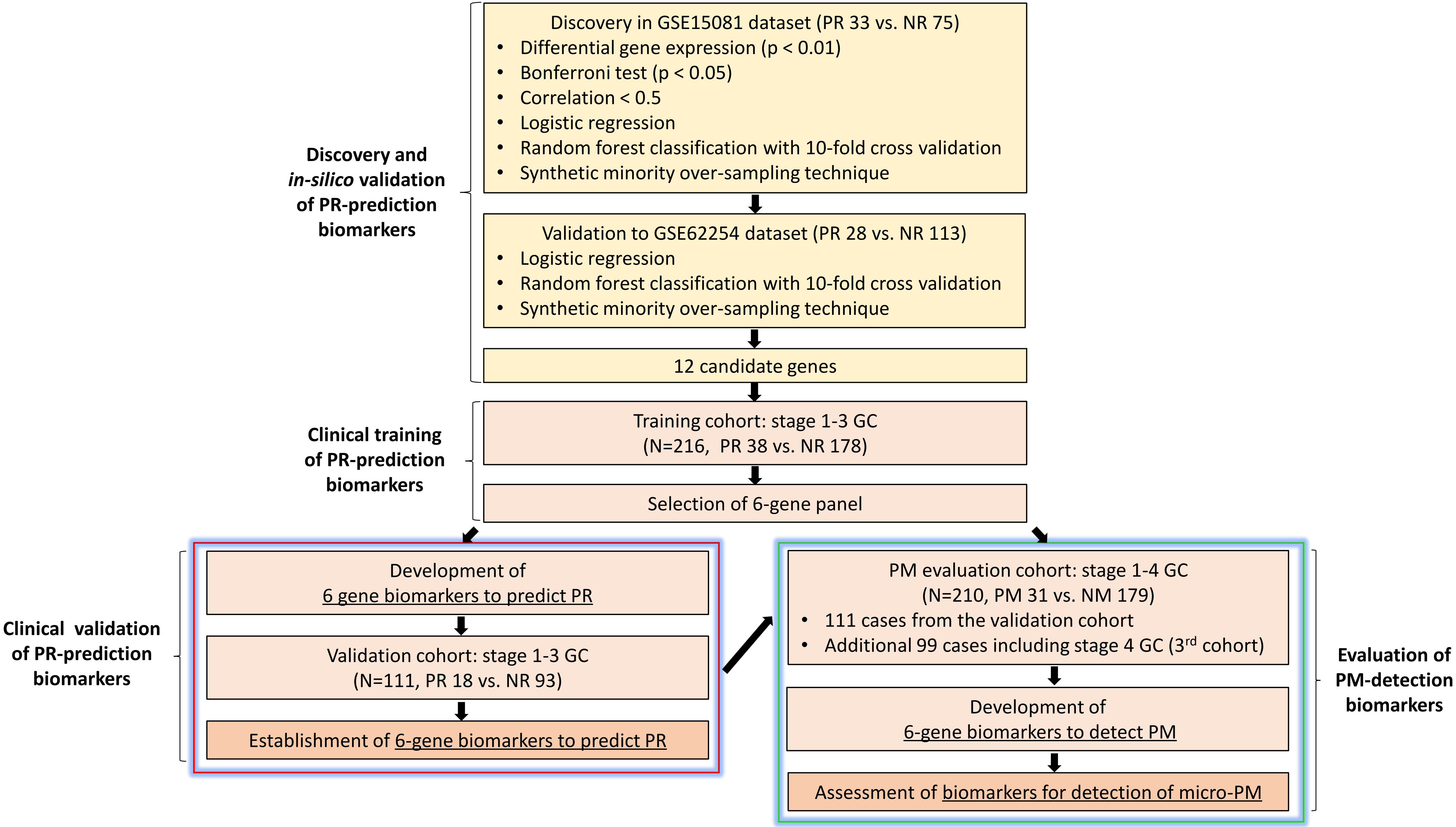
Table S3. Sequence of primers for 12 genes

No	Gene	Forward primer	Reverse primer	Product length
1	*ZBTB1*	CCCCCTAACAACAGCAGTCC	ATGACAGGTCCTCCTCGGTT	91
2	*CHCHD3*	TCTCAGCGGTATTCTGGTGC	TTCTTGGCTTGCTCCAATGC	95
3	*KLHL41*	TGCTACCTTACTGCACTGGC	TGCTGGGTAACAATGCTGGA	62
4	*POPDC2*	AGCAGGTCTTAACTCTGGCC	CTCACCCTCCACAGCATAGG	50
5	*LTBP3*	CAGTGTCGGGACAGTTGTCA	CTCTCCGATGAGCGTCATGT	51
6	*CAVIN2*	ATTTGCCCCACGATGAGGAG	TCTTCCACCTTTTCCTCGGC	55
7	*STT3B*	GGAGTGATGGTGCGACTGAT	GCAGACAGCATACACACGAC	56
8	*TXNDC16*	GTCCATCTCCAACTGGGCTT	AAGACGCCAAGCAACCCATT	99
9	*PHYHD1*	AAATTTCCTGGTCCCTCCGG	ATGCTCTTGAAGACGGGGTC	81
10	*KCNJ6*	CTCCATGGATCAGGACGTCG	TGTGTCTTGGCAGGTCATCC	86
11	*SLITRK6*	CCACCATCACGACCTTTCCA	GTGTGAAGCATCGTCAAGCC	59
12	*LMBR1*	AGATGCCATCGTCAACAGGA	GCGAGAGTGAACGTGCTCAA	51

Table S4. Random forest importance measures (10 times) in the discovery dataset (GSE15081)

Gene	1	2	3	4	5	6	7	8	9	10	Mean
ZBTB1	34.913	96.934	75.844	100.000	100.000	100.000	44.722	31.879	30.536	52.947	66.778
CHCHD3	24.556	90.138	18.197	23.921	57.163	25.258	0.000	19.217	16.493	0.000	27.494
KLHL41	56.639	59.688	100.000	57.295	64.784	66.590	62.510	26.064	100.000	21.133	61.470
POPDC2	59.591	51.052	55.865	44.144	46.647	70.768	87.110	53.114	14.382	100.000	58.267
LTBP3	100.000	0.000	0.000	5.536	23.168	30.870	50.694	13.193	15.813	26.036	26.531
CAVIN2	64.559	63.449	4.298	39.151	15.280	23.372	73.616	0.000	42.331	36.087	36.214
STT3B	32.460	7.197	21.347	10.641	34.799	17.132	39.715	17.705	0.000	41.439	22.243
TXNDC16	42.760	96.339	60.868	63.185	27.268	39.965	50.361	96.399	9.650	47.677	53.447
PHYHD1	54.510	74.704	15.025	11.784	32.599	0.000	57.617	7.228	25.625	34.781	31.387
KCNJ6	73.640	48.231	42.670	78.229	66.151	90.244	100.000	100.000	32.296	67.807	69.927
SLITRK6	47.635	100.000	20.769	14.456	0.000	7.420	68.337	38.516	8.562	40.407	34.610
LMBR1	34.457	20.391	70.471	0.000	23.476	31.840	77.062	32.634	75.637	33.569	39.954

FigureS1



Discovery and *in-silico* validation of PR-prediction biomarkers

Discovery in GSE15081 dataset (PR 33 vs. NR 75)

- Differential gene expression ($p < 0.01$)
- Bonferroni test ($p < 0.05$)
- Correlation < 0.5
- Logistic regression
- Random forest classification with 10-fold cross validation
- Synthetic minority over-sampling technique

Validation to GSE62254 dataset (PR 28 vs. NR 113)

- Logistic regression
- Random forest classification with 10-fold cross validation
- Synthetic minority over-sampling technique

12 candidate genes

Clinical training of PR-prediction biomarkers

Training cohort: stage 1-3 GC
(N=216, PR 38 vs. NR 178)

Selection of 6-gene panel

Clinical validation of PR-prediction biomarkers

Development of
<u>6 gene biomarkers to predict PR</u>

Validation cohort: stage 1-3 GC
(N=111, PR 18 vs. NR 93)

Establishment of <u>6-gene biomarkers to predict PR</u>

Evaluation of PM-detection biomarkers

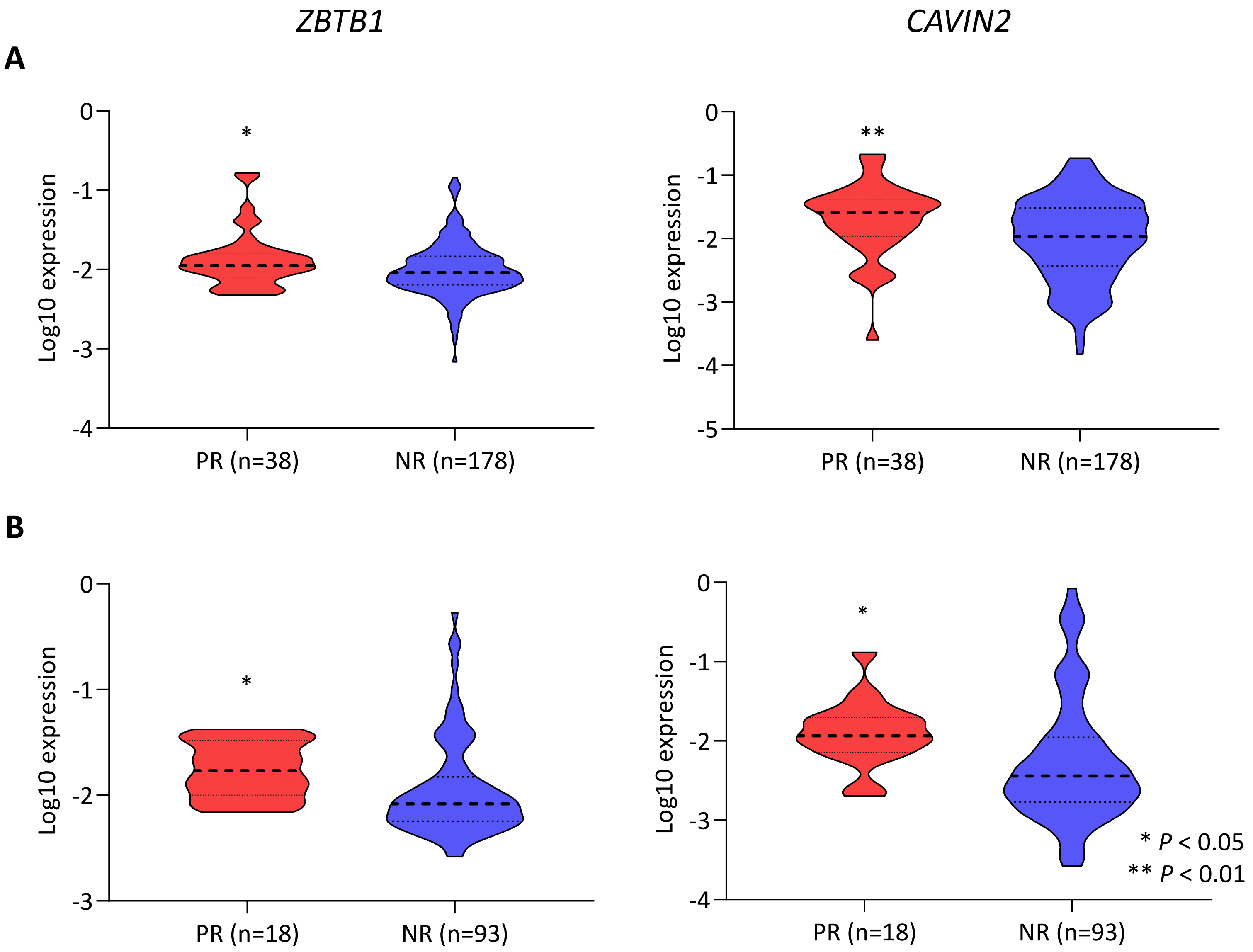
PM evaluation cohort: stage 1-4 GC
(N=210, PM 31 vs. NM 179)

- 111 cases from the validation cohort
- Additional 99 cases including stage 4 GC (3rd cohort)

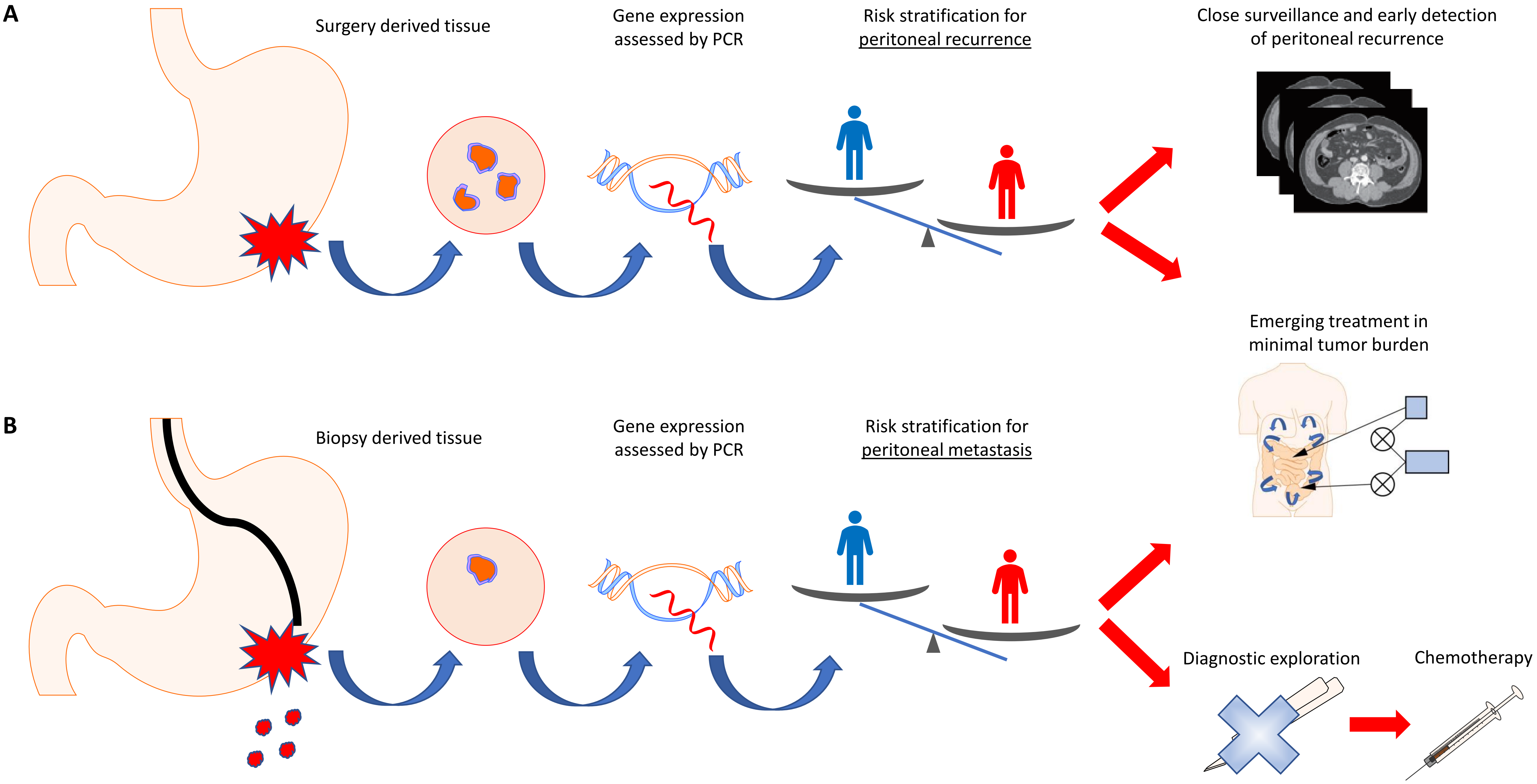
Development of
<u>6-gene biomarkers to detect PM</u>

Assessment of <u>biomarkers for detection of micro-PM</u>

FigureS2


ZBTB1
CAVIN2
A
0
-1
-2
-3
-4
Log10 expression
*
PR (n=38)
NR (n=178)
0
-1
-2
-3
-4
-5
Log10 expression
**
PR (n=38)
NR (n=178)
B
0
-1
-2
-3
Log10 expression
*
PR (n=18)
NR (n=93)
0
-1
-2
-3
-4
Log10 expression
*
PR (n=18)
NR (n=93)
* P < 0.05
** P < 0.01

FigureS3


A
Surgery derived tissue
Gene expression assessed by PCR
Risk stratification for peritoneal recurrence
Close surveillance and early detection of peritoneal recurrence
Emerging treatment in minimal tumor burden
B
Biopsy derived tissue
Gene expression assessed by PCR
Risk stratification for peritoneal metastasis
Diagnostic exploration
Chemotherapy