

Table 4

	V SERIES					BV SERIES					B SERIES					ANY CASE TYPE					
	Cases	Controls	n, uniq Controls	OR (95% CI)	p	Cases	Controls	n, uniq Controls	OR (95% CI)	p	Cases	Controls	n, uniq Controls	OR (95% CI)	p	Cases	Controls	n, uniq Controls	OR (95% CI)	p	
Extracted RNA																					
ER IHC	ER-	99	76	72	Ref.	96	74	71	Ref.	50	68	64	Ref.	245	218	184	Ref.				
	ER+	147	170	160	0.67 (0.46-0.97)	0.04	162	184	174	0.69 (0.47-1.0)	0.05	188	170	158	1.5 (1.0-2.3)	0.05	497	524	436	0.86 (0.68-1.1)	0.2
Total		246	246	232		258	258	245		238	238	222		742	742	620					
IHC subtypes	ER+HER2-	68	70	67	Ref.	78	74	72	Ref.	86	84	80	Ref.	232	228	196	Ref.				
	ER+HER2+	23	25	23	0.99 (0.50-1.9)	1.0	25	17	17	1.4 (0.68-2.8)	0.4	22	15	14	1.5 (0.71-3.1)	0.3	70	57	43	1.4 (0.90-2.1)	0.1
	ER-HER2+	35	12	12	2.9 (1.4-6.2)	0.005	30	13	13	2.1 (1.0-4.5)	0.04	13	11	9	1.3 (0.55-3.4)	0.5	78	36	31	2.1 (1.4-3.4)	0.001
	TNBC	36	31	30	1.2 (0.66-2.1)	0.6	33	25	23	1.3 (0.71-2.5)	0.4	14	23	23	0.57 (0.27-1.2)	0.1	83	79	68	1.0 (0.71-1.5)	0.9
	Total	162	138	132		166	129	125		135	133	126		463	400	338					
Not assigned (missing IHC data)		84	108	100		92	129	120		103	105	96		279	342	282					
Total (extracted RNA)		246	246	232		258	258	245		238	238	222		742	742	620					
GWDb																					
PAM50	Luminal A	21	34	33	Ref.	33	45	42	Ref.	32	45	42	Ref.	86	124	109	Ref.				
	Luminal B	17	9	9	3.0 (1.1-8.2)	0.03	26	13	12	2.7 (1.2-6.4)	0.02	28	16	15	2.5 (1.1-5.4)	0.02	71	38	35	2.6 (1.6-4.2)	0.0002
	Basal	28	17	15	2.9 (1.3-6.9)	0.01	21	13	13	2.1 (0.9-4.8)	0.09	9	17	16	0.74 (0.28-1.9)	0.5	58	47	40	1.8 (1.1-3.0)	0.02
	HER2	30	15	14	3.4 (1.5-8.0)	0.005	20	12	12	2.1 (0.92-5.1)	0.08	18	12	10	2.4 (0.98-6.0)	0.06	68	39	33	2.6 (1.6-4.4)	<1e-4
	Normal	9	11	11	1.3 (0.45-3.6)	0.6	6	7	7	1.1 (0.32-3.6)	0.9	11	8	7	2.1 (0.7-6.2)	0.2	26	26	23	1.4 (0.76-2.7)	0.3
	Total	105	86	82		106	90	86		98	98	90		309	274	240					
Not assigned (not in GWDb)		141	160	150		152	168	159		140	140	132		433	468	380					
Total (extracted RNA)		246	246	232		258	258	245		238	238	222		742	742	620					
IntClust, grouped 3		9	21	20	Ref.	14	25	25	Ref.	19	25	23	Ref.	42	71	66	Ref.				
	1,6,9	20	8	8	5.6 (1.8-18)	0.003	26	13	12	3.9 (1.5-10)	0.01	18	17	15	1.5 (0.45-1.5)	0.4	64	38	35	2.9 (1.6-5.1)	0.0003
	2,4	24	18	17	3.1 (1.2-8.9)	0.03	14	18	17	1.5 (0.6-3.9)	0.4	26	14	13	2.4 (1.0-6.1)	0.05	64	50	42	2.4 (1.4-4.2)	0.002
	5	20	6	5	8.9 (2.7-34)	0.001	17	3	3	10 (2.8-49)	0.001	7	5	4	2.1 (0.55-9.1)	0.3	44	14	11	6.3 (3.0-14)	<1e-4
	7,8	12	22	21	1.3 (0.44-3.7)	0.7	22	23	21	1.9 (0.78-4.6)	0.2	24	27	26	1.1 (0.49-2.6)	0.8	58	72	59	1.5 (0.91-2.6)	0.1
	10	20	11	11	4.0 (1.4-12)	0.01	13	8	8	2.9 (0.99-9.0)	0.06	4	10	9	0.54 (0.13-1.9)	0.4	37	29	27	2.2 (1.2-4.1)	0.02
	Total	105	86	82		106	90	86		98	98	90		309	274	240					
Not assigned (not in GWDb)		141	160	150		152	168	159		140	140	132		433	468	380					
Total (extracted RNA)		246	246	232		258	258	245		238	238	222		742	742	620					

Footnotes: Logistic regression model.

stats::glm, Case_Control ~ x, family="binomial"

Note: This is an unpaired test. A small number of patients were duplicated within a control series by design; here, patients were de-duplicated within each control series ("n, uniq"). There are no duplicates within each case series by design. Duplicates were permitted between cases and controls. Entries with missing values in the independent variable were excluded.