

## **Supplementary Appendix materials for**

### **Breast cancer detection accuracy of AI in an entire screening population: a retrospective, multicentre study**

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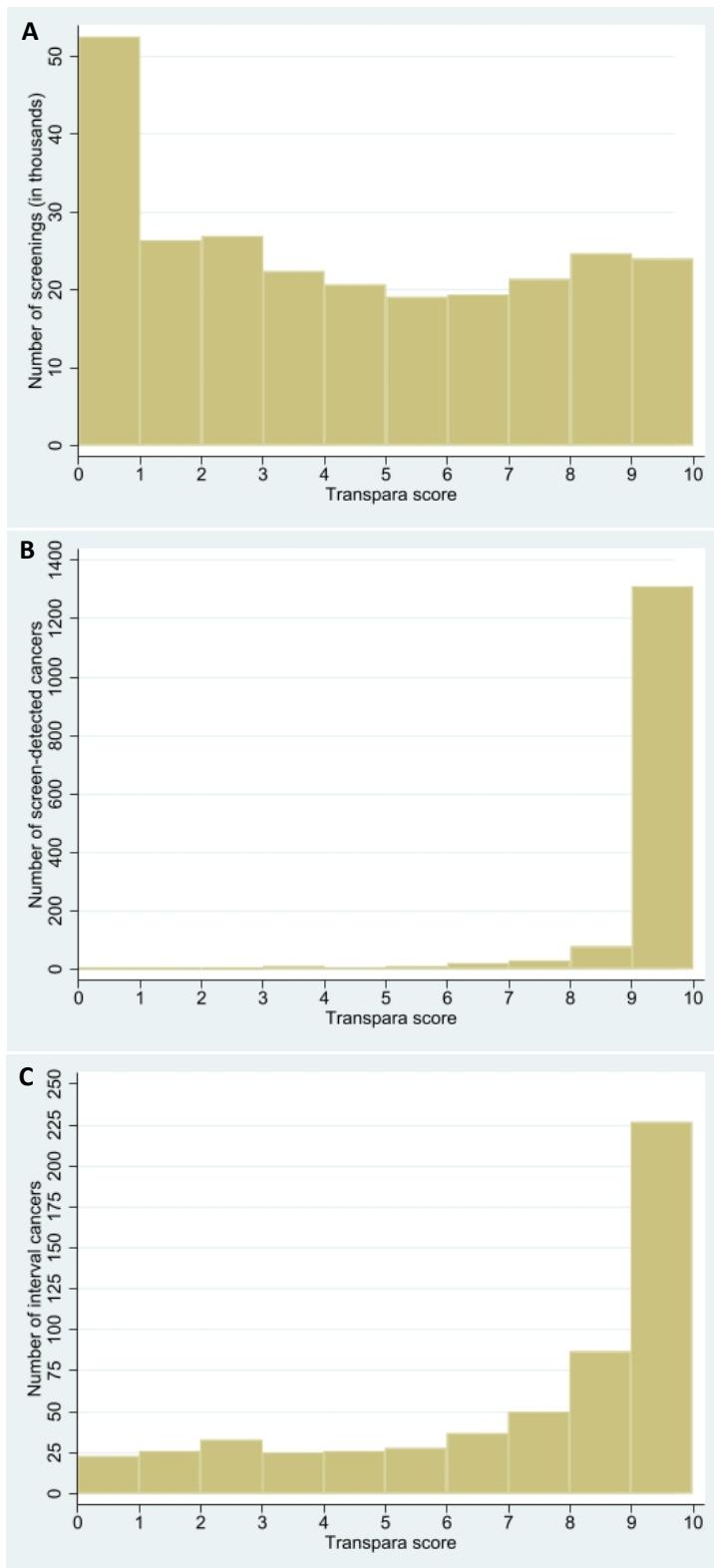
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## Supplementary eMethod 1: Standard for Reporting of Diagnostic Accuracy Studies (STARD) checklist

Section & Topic	No	Item	Reported on page # (submitted version)
<b>TITLE OR ABSTRACT</b>	<b>1</b>	Identification as a study of diagnostic accuracy using at least one measure of accuracy (such as sensitivity, specificity, predictive values, or AUC)	1-2
<b>ABSTRACT</b>	<b>2</b>	Structured summary of study design, methods, results, and conclusions (for specific guidance, see STARD for Abstracts)	2
<b>INTRODUCTION</b>	<b>3</b>	Scientific and clinical background, including the intended use and clinical role of the index test	3
	<b>4</b>	Study objectives and hypotheses	3
<b>METHODS</b>			
<i>Study design</i>	<b>5</b>	Whether data collection was planned before the index test and reference standard were performed (prospective study) or after (retrospective study)	4
<i>Participants</i>	<b>6</b>	Eligibility criteria	4
	<b>7</b>	On what basis potentially eligible participants were identified (such as symptoms, results from previous tests, inclusion in registry)	4
	<b>8</b>	Where and when potentially eligible participants were identified (setting, location and dates)	4
	<b>9</b>	Whether participants formed a consecutive, random or convenience series	4
<i>Test methods</i>	<b>10a</b>	Index test, in sufficient detail to allow replication	5-6
	<b>10b</b>	Reference standard, in sufficient detail to allow replication	5-6
	<b>11</b>	Rationale for choosing the reference standard (if alternatives exist)	5-6
	<b>12a</b>	Definition of and rationale for test positivity cut-offs or result categories of the index test, distinguishing pre-specified from exploratory	5-6
	<b>12b</b>	Definition of and rationale for test positivity cut-offs or result categories of the reference standard, distinguishing pre-specified from exploratory	4-6
	<b>13a</b>	Whether clinical information and reference standard results were available to the performers/readers of the index test	-
	<b>13b</b>	Whether clinical information and index test results were available to the assessors of the reference standard	-
<i>Analysis</i>	<b>14</b>	Methods for estimating or comparing measures of diagnostic accuracy	6-7
	<b>15</b>	How indeterminate index test or reference standard results were handled	4
	<b>16</b>	How missing data on the index test and reference standard were handled	4
	<b>17</b>	Any analyses of variability in diagnostic accuracy, distinguishing pre-specified from exploratory	6-7
	<b>18</b>	Intended sample size and how it was determined	-
<b>RESULTS</b>			
<i>Participants</i>	<b>19</b>	Flow of participants, using a diagram	8, Figure 2
	<b>20</b>	Baseline demographic and clinical characteristics of participants	8, Table 1
	<b>21a</b>	Distribution of severity of disease in those with the target condition	8, Tables 1,3,4
	<b>21b</b>	Distribution of alternative diagnoses in those without the target condition	-
	<b>22</b>	Time interval and any clinical interventions between index test and reference standard	-
<i>Test results</i>	<b>23</b>	Cross tabulation of the index test results (or their distribution) by the results of the reference standard	9, eTable 4
	<b>24</b>	Estimates of diagnostic accuracy and their precision (such as 95% confidence intervals)	9, Table 2, eTable 5
	<b>25</b>	Any adverse events from performing the index test or the reference standard	-
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**Supplementary eFigure 1: Distribution of Transpara exam scores across the study sample**



(A) The Transpara exam score distributed across (A) all screening mammograms, (B) screen-detected cancers, and (C) interval cancers in the study sample. The Transpara exam score was precalibrated in such a way that the number of screening mammograms in each category should be almost equal, i.e., 10% of the mammograms would fall into each category of scores. When matching the AI score thresholds in the study to the mean sensitivity and mean specificity of the first reader,  $AI_{sens}$  and  $AI_{spec}$  used a Transpara exam score of 9.56858 and 9.70159, respectively.

**Supplementary eTable 1: Detection accuracy analysis across radiologist position**

	Sensitivity (95% CI); p value*	Specificity (95% CI); p value*	PPV (95% CI); p value†	NPV (95% CI); p value†	Recall rate (95% CI); p value†
First reader	63.7 (61.6-65.8); ref.	97.8 (97.7-97.8); ref.	18.7 (17.8-19.6); ref.	99.7 (99.7-99.7); ref.	2.7 (2.6-2.8); ref.
Second reader	68.3 (66.2-70.3); <0.0001	98.0 (98.0-98.1); <0.0001	21.7 (20.7-22.7); <0.0001	99.7 (99.7-99.8); 0.004	2.5 (2.4-2.6); <0.0001
Arbitrator	90.8 (87.5-93.5); <0.0001	53.0 (51.8-54.1); <0.0001	9.7 (8.7-10.7); <0.0001	99.0 (98.7-99.7); <0.0001	49.3 (48.2-50.5); <0.0001
Combined reading	73.9 (72.0-75.8); <0.0001	97.9 (97.9-98.0); <0.0001	22.0 (21.0-23.0); <0.0001	99.8 (99.8-99.8); <0.0001	2.7 (2.6-2.7); 0.18

Data are % (95% CI); p value. PPV=positive predictive value. NPV=negative predictive value. \*p values were calculated using McNemar's test. †p values were calculated using exact binomial test.

**Supplementary eTable 2: Detection agreements and discrepancies across cancer subgroups in the Standalone AI scenario**

	Detected by both First reader and		Detected by First reader, missed by		Missed by First reader, detected by		Missed by both First reader and	
	Standalone AI <sub>sens</sub>	Standalone AI <sub>spec</sub>	Standalone AI <sub>sens</sub>	Standalone AI <sub>spec</sub>	Standalone AI <sub>sens</sub>	Standalone AI <sub>spec</sub>	Standalone AI <sub>sens</sub>	Standalone AI <sub>spec</sub>
<b>All cancers (n=2041)</b>	1043 (51.1)	981 (48.1)	258 (12.6)	320 (15.7)	258 (12.6)	216 (10.6)	482 (23.6)	254 (25.7)
<b>Screen-detected cancers (n=1479)</b>	1018 (68.8)	961 (65.0)	244 (16.5)	301 (20.4)	144 (9.7)	127 (8.6)	73 (4.9)	90 (6.1)
<b>Interval cancers (n=562)</b>	25 (4.4)	20 (3.6)	14 (2.5)	19 (3.4)	114 (20.3)	89 (15.8)	409 (72.8)	434 (77.2)
<12 months after screening (n=170)	7 (4.1)	6 (3.5)	6 (3.5)	7 (4.1)	36 (21.2)	30 (17.6)	121 (71.2)	127 (74.7)
≥12 months after screening (n=392)	18 (4.6)	14 (3.6)	8 (2.0)	12 (3.1)	78 (19.9)	59 (15.1)	288 (73.5)	307 (78.3)
<b>Histological subtype</b>								
Invasive ductal (n=1393)	733 (52.6)	689 (49.5)	172 (12.3)	216 (15.5)	174 (12.5)	144 (10.3)	314 (22.5)	344 (24.7)
Invasive lobular (n=222)	93 (41.9)	87 (39.2)	24 (10.8)	30 (13.5)	35 (15.8)	27 (12.2)	70 (31.5)	78 (35.1)
Other invasive (n=215)	65 (30.2)	60 (27.9)	38 (17.7)	43 (20.0)	22 (10.2)	19 (8.8)	90 (41.9)	93 (43.3)
Ductal carcinoma in situ (n=211)	152 (72.0)	145 (68.7)	24 (11.4)	31 (14.7)	27 (12.8)	26 (12.3)	8 (3.8)	9 (4.3)
<b>Tumour size*</b>								
0-10 mm (n=577)	302 (52.3)	277 (48.0)	97 (16.8)	122 (21.1)	77 (13.3)	65 (11.3)	101 (17.5)	113 (19.6)
11-20 mm (n=790)	431 (54.6)	409 (51.8)	90 (11.4)	112 (14.2)	82 (10.4)	66 (8.4)	187 (23.7)	203 (25.7)
21-50 mm (n=380)	136 (35.8)	129 (33.9)	38 (10.0)	45 (11.8)	58 (15.3)	48 (12.6)	148 (38.9)	158 (41.6)
51+ mm (n=49)	15 (30.6)	15 (30.6)	2 (4.1)	2 (4.1)	11 (22.4)	8 (16.3)	21 (42.9)	24 (49.0)
Unknown (n=34)	7 (20.6)	6 (17.6)	7 (20.6)	8 (23.5)	3 (8.8)	3 (8.8)	17 (50.0)	17 (50.0)
<b>Malignancy grade*</b>								
Grade 1 (n=507)	283 (55.8)	263 (51.9)	48 (9.5)	68 (13.4)	76 (15.0)	61 (12.0)	100 (19.7)	115 (22.7)
Grade 2 (n=815)	417 (51.2)	395 (48.5)	103 (12.6)	125 (15.3)	109 (13.4)	92 (11.3)	186 (22.8)	203 (24.9)
Grade 3 (n=358)	141 (39.4)	131 (36.6)	52 (14.5)	62 (17.3)	33 (9.2)	26 (7.3)	132 (36.9)	139 (38.8)
Unknown (n=150)	50 (33.3)	47 (31.3)	31 (20.7)	34 (22.7)	13 (8.7)	11 (7.3)	56 (37.3)	58 (38.7)
<b>TNM stage*</b>								
Local (I + II) (n=1761)	876 (49.7)	822 (46.7)	229 (13.0)	283 (16.1)	224 (12.7)	184 (10.4)	432 (24.5)	472 (26.8)
Locally advanced (III) (n=44)	10 (22.7)	10 (22.7)	5 (11.4)	5 (11.4)	4 (9.1)	3 (6.8)	25 (56.8)	26 (59.1)
Distant metastasis (IV) (n=20)	4 (20.0)	3 (15.0)	0 (0.0)	1 (5.0)	3 (15.0)	3 (15.0)	13 (65.0)	13 (65.0)
Unknown (n=5)	1 (20.0)	1 (20.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	4 (80.0)	4 (80.0)
<b>Lymph node positivity*</b>								
No (n=1340)	665 (49.6)	624 (46.6)	175 (13.1)	216 (16.1)	161 (12.0)	135 (10.1)	339 (25.3)	365 (27.2)
Yes (n=490)	226 (46.1)	212 (43.3)	59 (12.0)	73 (14.9)	70 (14.3)	55 (11.2)	135 (27.6)	150 (30.6)
<b>ER positivity*</b>								
0% (n=207)	62 (30.0)	57 (27.5)	34 (16.4)	39 (18.8)	13 (6.3)	10 (4.8)	98 (47.3)	101 (48.8)
1-9% (n=98)	26 (26.5)	22 (22.4)	20 (20.4)	24 (24.5)	12 (12.2)	11 (11.2)	40 (40.8)	41 (41.8)
10-100% (n=1514)	799 (52.8)	753 (49.7)	178 (11.8)	224 (14.8)	204 (13.5)	167 (11.0)	333 (22.0)	370 (24.4)
Unknown (n=11)	4 (36.4)	4 (35.4)	2 (18.2)	2 (18.2)	2 (18.2)	2 (18.2)	3 (27.3)	3 (27.3)
<b>HER2 status*</b>								
Negative (n=1581)	782 (49.5)	733 (46.4)	210 (13.3)	259 (16.4)	204 (12.9)	169 (10.7)	385 (24.4)	420 (26.6)
Positive (n=225)	103 (45.8)	97 (43.1)	20 (8.9)	26 (11.6)	25 (11.1)	19 (8.4)	77 (34.2)	83 (36.9)
Unknown (n=24)	6 (25.0)	5 (25.0)	4 (16.7)	4 (16.7)	2 (8.3)	2 (8.3)	12 (50.0)	12 (50.0)

Data are n (%). The cancer detection rate is reported as the number of detected cancers out of the number of true cancers for the subgroup in the same row. TNM=tumour, node, metastasis. ER=estrogen receptor. HER2=human epidermal growth factor receptor 2. AI<sub>sens</sub>=artificial intelligence score cut-off point matched at mean first reader sensitivity. AI<sub>spec</sub>=artificial intelligence score cut-off point matched at mean first reader specificity. \*Reported for invasive cancers only.

**Supplementary eTable 3: Detection agreements and discrepancies across cancer subgroups in the AI-integrated screening scenario**

	Detected by both Combined reading and		Detected by Combined reading, missed by		Missed by Combined reading, detected by		Missed by both Combined reading and	
	Integrated AI <sub>sens</sub>	Integrated AI <sub>spec</sub>	Integrated AI <sub>sens</sub>	Integrated AI <sub>spec</sub>	Integrated AI <sub>sens</sub>	Integrated AI <sub>spec</sub>	Integrated AI <sub>sens</sub>	Integrated AI <sub>spec</sub>
<b>All cancers (n=2041)</b>	1450 (71.0)	1439 (70.5)	59 (2.9)	70 (3.4)	105 (5.1)	83 (4.1)	427 (20.9)	449 (22.0)
<b>Screen-detected cancers (n=1479)</b>	1425 (96.3)	1413 (95.5)	54 (3.7)	66 (4.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<b>Interval cancers (n=562)</b>	27 (4.8)	27 (4.8)	3 (0.5)	3 (0.5)	103 (18.3)	82 (14.6)	429 (76.3)	450 (80.1)
<12 months after screening (n=170)	13 (7.6)	13 (7.6)	1 (0.6)	1 (0.6)	34 (20.0)	28 (16.5)	122 (71.8)	128 (75.3)
≥12 months after screening (n=392)	14 (3.6)	14 (3.6)	2 (0.5)	2 (0.5)	69 (17.6)	54 (13.8)	307 (78.3)	322 (82.1)
<b>Histological subtype</b>								
Invasive ductal (n=1393)	996 (71.5)	990 (71.1)	38 (2.7)	44 (3.2)	76 (5.5)	63 (4.5)	283 (20.3)	296 (21.2)
Invasive lobular (n=222)	137 (61.7)	134 (60.4)	6 (2.7)	9 (4.1)	17 (7.7)	11 (5.0)	62 (27.9)	68 (30.6)
Other invasive (n=215)	110 (51.2)	113 (52.6)	11 (5.1)	8 (3.7)	12 (5.6)	9 (4.2)	82 (38.1)	85 (39.5)
Ductal carcinoma in situ (n=211)	207 (98.1)	202 (95.7)	4 (1.9)	9 (4.3)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)
<b>Tumour size*</b>								
0-10 mm (n=577)	468 (81.1)	469 (81.3)	28 (4.9)	27 (4.7)	16 (2.8)	13 (2.3)	65 (11.3)	68 (11.8)
11-20 mm (n=790)	560 (70.9)	554 (70.1)	21 (2.7)	27 (3.4)	38 (4.8)	29 (3.7)	171 (21.6)	180 (22.8)
21-50 mm (n=380)	185 (48.7)	183 (48.2)	4 (1.1)	6 (1.6)	41 (10.8)	33 (8.7)	150 (39.5)	158 (41.6)
51+ mm (n=49)	17 (34.7)	17 (34.7)	1 (2.0)	1 (2.0)	7 (14.3)	5 (10.2)	24 (49.0)	26 (53.1)
Unknown (n=34)	13 (38.2)	14 (41.2)	1 (2.9)	0 (0.0)	3 (8.8)	3 (8.8)	17 (50.0)	17 (50.0)
<b>Malignancy grade*</b>								
Grade 1 (n=507)	91 (60.7)	94 (62.7)	8 (5.3)	5 (3.3)	5 (3.3)	3 (2.0)	46 (30.7)	48 (32.0)
Grade 2 (n=815)	397 (78.3)	391 (77.1)	13 (2.6)	19 (3.7)	21 (4.1)	19 (3.7)	76 (15.0)	78 (15.4)
Grade 3 (n=358)	561 (68.8)	560 (68.7)	26 (3.2)	27 (3.3)	56 (6.9)	45 (5.5)	172 (21.1)	183 (22.5)
Unknown (n=150)	194 (54.2)	192 (53.6)	8 (2.2)	10 (2.8)	23 (6.4)	16 (4.5)	133 (37.2)	140 (39.1)
<b>TNM stage*</b>								
Local (I + II) (n=1761)	1226 (69.6)	1219 (69.2)	54 (3.1)	61 (3.5)	98 (5.6)	77 (4.4)	383 (21.7)	404 (22.9)
Locally advanced (III) (n=44)	12 (27.3)	13 (29.5)	1 (2.3)	0 (0.0)	4 (9.1)	3 (6.8)	27 (61.4)	28 (63.6)
Distant metastasis (IV) (n=20)	4 (20.0)	4 (20.0)	0 (0.0)	0 (0.0)	3 (15.0)	3 (15.0)	13 (65.0)	13 (65.0)
Unknown (n=5)	1 (20.0)	1 (20.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	4 (80.0)	4 (80.0)
<b>Lymph node positivity*</b>								
No (n=1340)	942 (70.3)	941 (70.2)	42 (3.1)	43 (3.2)	63 (4.7)	51 (3.8)	293 (21.9)	305 (22.8)
Yes (n=490)	301 (61.4)	296 (60.4)	13 (2.7)	18 (3.7)	42 (8.6)	32 (6.5)	134 (27.3)	144 (29.4)
<b>ER positivity*</b>								
0% (n=207)	91 (44.0)	94 (45.4)	11 (5.3)	8 (3.9)	9 (4.3)	7 (3.4)	96 (46.4)	98 (47.3)
1-9% (n=98)	48 (49.0)	45 (45.9)	1 (1.0)	4 (4.1)	9 (9.2)	6 (6.1)	40 (40.8)	43 (43.9)
10-100% (n=1514)	1097 (72.5)	1091 (72.1)	43 (2.8)	49 (3.2)	86 (5.7)	69 (4.6)	288 (19.0)	305 (20.1)
Unknown (n=11)	7 (63.6)	7 (63.6)	0 (0.0)	0 (0.0)	1 (9.1)	1 (9.1)	3 (27.3)	3 (27.3)
<b>HER2 status*</b>								
Negative (n=1581)	1105 (69.9)	1097 (69.4)	46 (2.9)	54 (3.4)	89 (5.6)	71 (4.5)	341 (21.6)	359 (22.7)
Positive (n=225)	127 (56.4)	129 (57.3)	8 (3.6)	6 (2.7)	15 (6.7)	11 (4.9)	75 (33.3)	79 (35.1)
Unknown (n=24)	11 (45.8)	11 (45.8)	1 (4.2)	1 (4.2)	1 (4.2)	1 (4.2)	11 (45.8)	11 (45.8)

Data are n (%). The cancer detection rate is reported as the number of detected cancers out of the number of true cancers for the subgroup in the same row. TNM=tumour, node, metastasis. ER=estrogen receptor. HER2=human epidermal growth factor receptor 2. AI<sub>sens</sub>=artificial intelligence score cut-off point matched at mean first reader sensitivity. AI<sub>spec</sub>=artificial intelligence score cut-off point matched at mean first reader specificity. \*Reported for invasive cancers only.

**Supplementary eTable 4: Comparison of screening outcome and results of the reference standard in both study scenarios with descriptive workload analysis.**

	Standalone AI			AI-integrated screening		
	First reader	Standalone AI <sub>sens</sub>	Standalone AI <sub>spec</sub>	Combined reading	Integrated AI <sub>sens</sub>	Integrated AI <sub>spec</sub>
<b>Number of episodes</b>						
True positive	1301 (ref.)	1301 (0.0)	1197 (-7.9)	1509 (ref.)	1555 (+3.0)	1522 (+0.9)
True negative	249959 (ref.)	246590 (-1.3)	249952 (<-0.1)	250278 (ref.)	248616 (-0.7)	250234 (<-0.1)
False positive	5671 (ref.)	9040 (+59.4)	5678 (+0.1)	5352 (ref.)	7014 (+31.1)	5396 (+0.8)
False negative	740 (ref.)	740 (0.0)	844 (+14.1)	532 (ref.)	486 (-8.6)	519 (-2.4)
<b>Workload</b>						
Recalls	6972 (ref.)	10341 (+48.3)	6875 (-1.4)	6861 (ref.)	8569 (+24.9)	6918 (+0.8)
Human readings	257671 (ref.)	0 (-100)	0 (-100)	522105 (ref.)	270936 (-48.1)	267946 (-48.7)
Arbitrations	NA	NA	NA	7434 (ref.)	13265 (+74.4)	10275 (+38.2)

Data are n ( $\Delta\%$ ). AI<sub>sens</sub>=artificial intelligence score cut-off point matched at mean first reader sensitivity. AI<sub>spec</sub>=artificial intelligence score cut-off point matched at mean first reader specificity.

**Supplementary eTable 5: Detection accuracy analysis with inclusion of next-round screen-detected cancers and long-term cancers in both study scenarios**

	Sensitivity (95% CI); p value <sup>*</sup>	Specificity (95% CI); p value <sup>*</sup>	PPV (95% CI); p value <sup>†</sup>	NPV (95% CI); p value <sup>†</sup>
<b>Standalone AI</b>				
First reader	30.5 (29.2-31.8); ref.	97.8 (97.7-97.9); ref.	20.2 (19.3-21.2); ref.	98.7 (98.7-98.8); ref.
Standalone AI <sub>sens</sub>	37.7 (36.2-39.2); <0.0001	96.6 (96.5-96.7); <0.0001	16.9 (16.1-17.7); <0.0001	98.8 (98.8-98.9); <0.0001
Standalone AI <sub>spec</sub>	33.3 (31.8-34.7); <0.0001	97.9 (97.8-98.0); 0.03	22.4 (21.3-23.4); <0.0001	98.8 (98.7-98.8); 0.02
<b>AI-integrated screening</b>				
Combined reading	34.5 (33.2-35.8); ref.	97.9 (97.9-98.0); ref.	23.2 (22.2-24.3); ref.	98.8 (98.7-98.8); ref.
Integrated AI <sub>sens</sub>	39.1 (37.7-40.6); <0.0001	97.3 (97.3-97.4); <0.0001	21.1 (20.2-22.0); <0.0001	98.9 (98.8-98.9); 0.0004
Integrated AI <sub>spec</sub>	37.3 (35.9-38.7); <0.0001	97.9 (97.9-98.0); 0.28	24.9 (23.9-26.0); 0.001	98.8 (98.8-98.9); 0.02

Data are % (95% CI); p value. Next-round screen-detected cancers (n=1232) and long-term cancers (n=2372) include ductal carcinoma in situ. Linear regression with the measure of performance was used to take the correlation between women and possible multiple cancers into account. PPV=positive predictive value. NPV=negative predictive value. AI<sub>sens</sub>=artificial intelligence score cut-off point matched at mean first reader sensitivity from the primary analysis presented in study table 2. AI<sub>spec</sub>=artificial intelligence score cut-off point matched at mean first reader specificity from the primary analysis presented in study table 2. \*p values were calculated using McNemar's test. †p values were calculated using exact binomial test.