building towards
cIQc
canadian Immunohistochemistry Quality control

Assessors' report for cIQc Run 5: Breast module (ER, PR and HER2)

All participating laboratories received a single slide for each test. The results obtained on benign tissue only were not included for calculations of the laboratory success. Minimum concordance of 90% for both positive and negative results is suggested as "satisfactory". Minimum concordance of 95% is suggested as "optimal". The calculations for ER and PR were done using each laboratory result and following reference values:

1) *Consensus Results*: These are the results that majority of laboratories agreed upon. If the tissue core was missing for majority of laboratories, such tissue cores were excluded from calculations.

2) *Reference Laboratory*: The results of the reference laboratory for breast carcinoma markers in the United States.

3) *Reference Method*: The results obtained by the FDA approved kit for ER and PR immunohistochemistry. For HER2, the results of FISH were used instead. Kappa values were also calculated and summarized in Table 1 at the end of this document.

RUN5 was made possible due to the contribution of the Jewish General Hospital (JGH) in Montreal, Quebec. The RUN5 tissue microarray (TMA) comprising 44 different breast cancer cases from recent material from the JGH laboratory was constructed by Naciba Benlimame, PhD at the Research Pathology Facility, Segal Cancer Centre JGH under close supervision of Dr. Dragana Pilavdzic, staff pathologist at JGH and assistant professor at McGill University who is a cIQc assessor for type II immunohistochemistry (IHC).

Jewish General Hospital, Montreal, Quebec, Canada

Figure 1. ER garrattogram

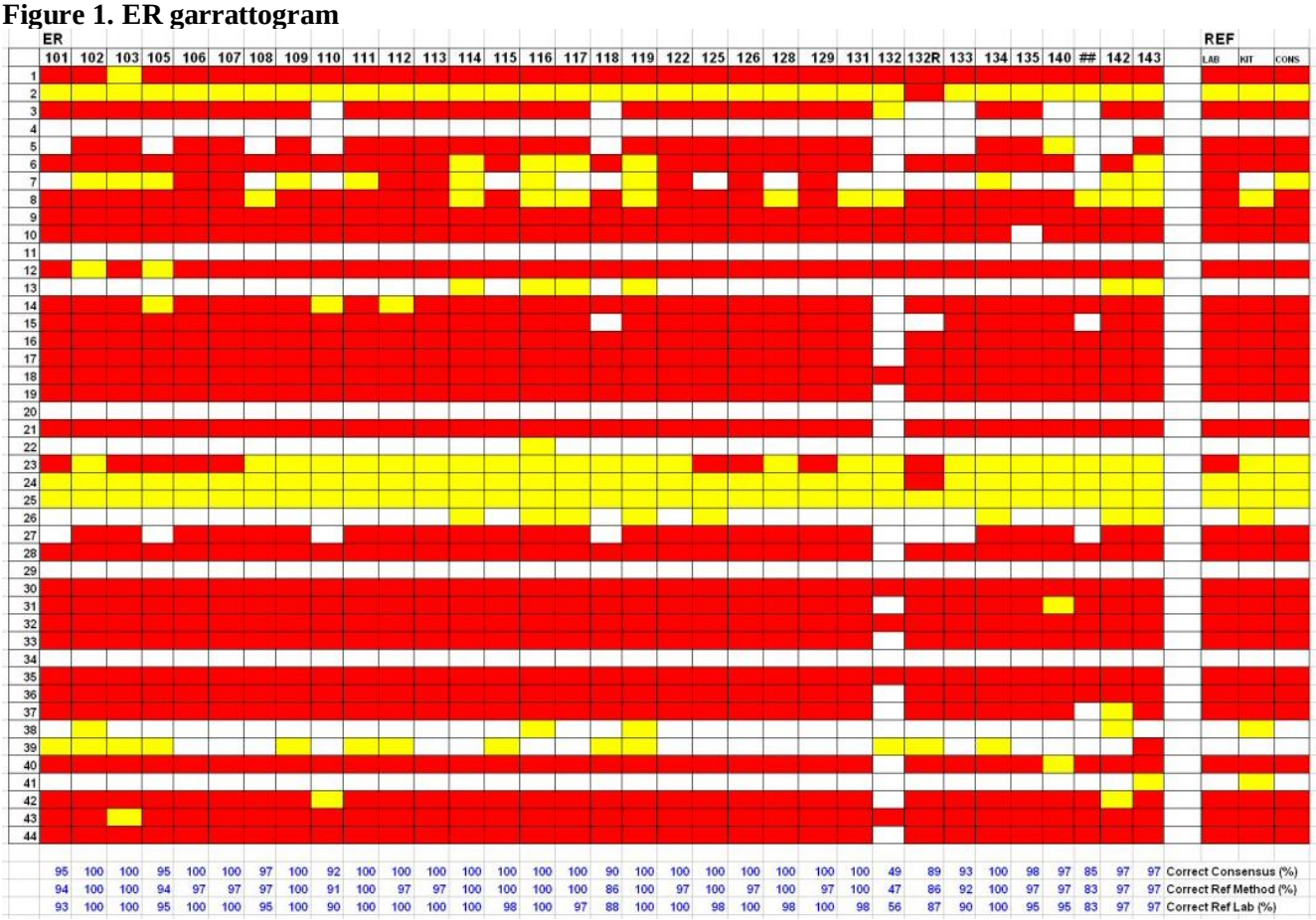

Figure 2. PR garrattogram

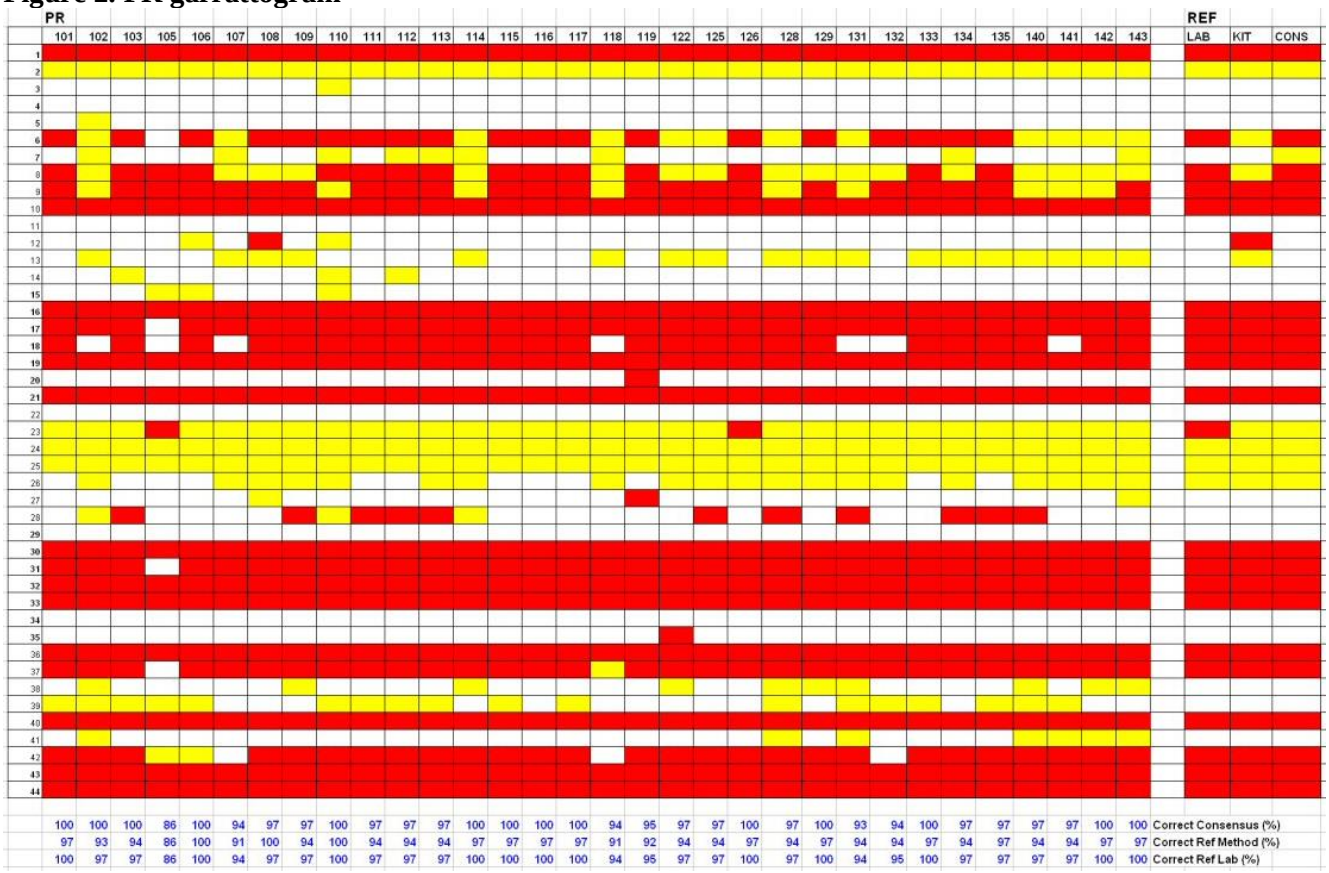

Figure 3. HER2 garrattogram

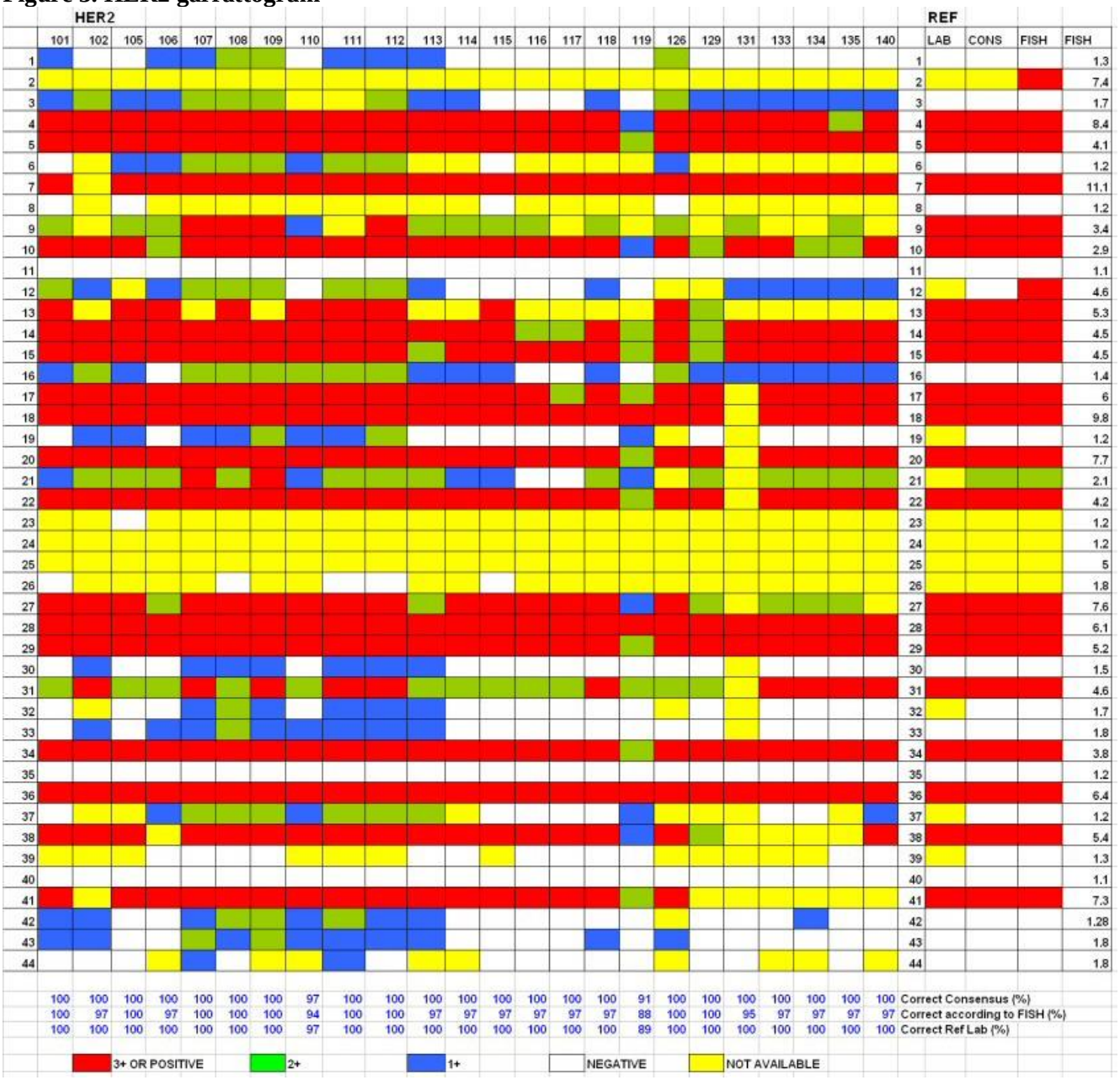

Table 1. Run 5 descriptive statistics

	CORRECT RESULTS/CONCORDANCE (%)									KAPPA-VALUE								
LAB	Consensus		Ref Laboratory		Ref Method		Consensus	Ref Laboratory	FISH	Consensus		Ref Laboratory		Ref Method		Consensus	FISH	LAB
	ER	PR	ER	PR	ER	PR	HER2	HER2	HER2	ER	PR	101	PR	ER	PR	HER2	HER2	
101	95	100	93	100	94	97	100	100	100	0.880	1.000	102	1.000	0.836	0.943	1.000	0.947	**101**
102	100	100	100	97	100	93	100	100	97	1.000	0.933	103	0.933	1.000	0.865	1.000	0.930	**102**
103	100	100	100	97	100	94	NA	NA	NA	1.000	0.943	105	0.945	1.000	0.881	NA	NA	**103**
105	95	86	95	86	94	86	100	100	100	0.870	0.719	106	0.734	0.815	0.703	1.000	1.000	**105**
106	100	100	100	100	97	100	100	100	97	0.939	1.000	107	1.000	0.820	1.000	1.000	0.942	**106**
107	100	94	100	94	97	91	100	100	100	0.939	0.886	108	0.886	0.820	0.830	1.000	0.944	**107**
108	97	97	95	97	97	100	100	100	100	0.941	0.942	109	0.994	0.837	1.000	1.000	0.947	**108**
109	100	97	100	97	100	94	100	100	100	1.000	0.942	110	0.994	1.000	0.885	1.000	0.942	**109**
110	92	100	90	100	91	100	97	97	94	0.829	1.000	111	1.000	0.697	1.000	0.940	0.879	**110**
111	100	97	100	97	100	94	100	100	100	1.000	0.945	112	0.947	1.000	0.885	1.000	0.942	**111**
112	100	97	100	97	97	94	100	100	100	0.934	0.943	113	0.943	0.904	0.876	1.000	0.945	**112**
113	100	97	100	97	97	94	100	100	97	0.939	0.945	114	0.945	0.820	0.881	1.000	0.940	**113**
114	100	100	100	100	100	97	100	100	97	1.000	1.000	115	1.000	0.904	0.937	1.000	0.937	**114**
115	100	100	98	100	100	97	100	100	97	1.000	1.000	116	1.000	1.000	0.943	1.000	0.947	**115**
116	100	100	100	100	100	97	100	100	97	1.000	1.000	117	1.000	0.890	0.944	1.000	0.942	**116**
117	100	100	97	100	100	97	100	100	97	1.000	1.000	118	1.000	0.915	0.943	1.000	0.941	**117**
118	90	94	88	94	86	91	100	100	97	0.772	0.878	119	0.878	0.700	0.819	1.000	0.942	**118**
119	100	95	100	95	100	92	91	89	88	1.000	0.894	122	0.897	1.000	0.832	0.767	0.719	**119**
122	100	97	100	97	97	94	NA	NA	NA	0.939	0.941	125	0.943	0.820	0.885	NA	NA	**122**
125	100	97	98	97	100	94	NA	NA	NA	1.000	0.943	126	0.944	0.915	0.889	NA	NA	**125**
126	100	100	100	100	97	97	100	100	100	0.939	1.000	128	1.000	0.820	0.944	1.000	1.000	**126**
128	100	97	98	97	100	94	NA	NA	NA	1.000	0.934	129	0.937	0.915	0.873	NA	NA	**128**
129	100	100	100	100	97	97	100	100	100	0.939	1.000	131	1.000	0.820	0.943	1.000	1.000	**129**
131	100	93	98	94	100	94	100	100	95	1.000	0.870	132	0.875	0.915	0.811	1.000	0.904	**131**
132	49	94	56	95	47	97	NA	NA	NA	0.239	0.889	132R	0.829	0.197	0.830	NA	NA	**132**
132R	89	NA	87	NA	86	NA	NA	NA	NA	0.759	NA	133	NA	0.673	NA	NA	NA	**132R**
133	93	100	90	100	92	97	100	100	97	0.833	1.000	134	1.000	0.703	0.943	1.000	0.933	**133**
134	100	97	100	97	100	94	100	100	97	1.000	0.944	135	0.944	1.000	0.885	1.000	0.933	**134**
135	98	97	95	97	97	97	100	100	97	0.942	0.943	140	0.945	0.837	0.885	1.000	0.937	**135**
140	97	97	95	97	97	94	100	100	97	0.940	0.870	141	0.875	0.832	0.811	1.000	0.935	**140**
141	85	97	83	97	83	94	NA	NA	NA	0.683	1.000	142	1.000	0.590	0.939	NA	NA	**141**
142	97	100	97	100	97	97	NA	NA	NA	0.921	1.000	143	1.000	0.817	0.939	NA	NA	**142**
143	97	100	97	100	97	97	NA	NA	NA	0.915	1.000	0.915	1.000	1.000	0.939	NA	NA	**143**