Research Article

BEYOND EMBRYO QUALITY: ENDOMETRIAL FACTORS IN 66 CRYOPRESERVED EMBRYO TRANSFERS

***NANI TATISHVILI**, MD;* [1] ***NINO MUSERIDZE**, MD, PhD;* [1]
***ARMINE G. HARUTYUNYAN**, MD, PhD* [1,2]

[1] *Georgian German Reproduction Center, Tbilisi, Georgia*
[2] *BEGLARYAN Medical Center, Yerevan, Armenia*

ABSTRACT

Background: Cryopreserved embryo transfer now accounts for the majority of transfers in many programs, and embryo selection using preimplantation genetic testing for aneuploidy (PGT-A) has reduced, but not eliminated, implantation failure. 1,4 When implantation fails despite the transfer of euploid embryos, attention turns to the endometrium – its receptivity timing, assessed by Endometrial Receptivity Analysis (ERA), 2,3,5 and its microbial composition, assessed by endometrial microbiome metagenomic analysis (EMMA).6,8 Both tests are offered routinely in this program, but their yield and their relationship to each other have not previously been audited.

Methods: Retrospective single-center cohort study of 66 cryo ET cycles performed in 35 patients between February 2024 and August 2026, using the clinic cycle register together with data from 40 ERA and 36 EMMA reports (Igenomix, processed at Avrupa Laboratories). Donor status was assigned per transfer by matching each transfer to its originating oocyte pick-up cycle by cryopreservation date rather than by patient-level flag. Pregnancy outcome was classified as clinical, biochemical, negative, or pending. ERA recommendations were recorded as hours of progesterone administration and compared with the biopsy protocol. EMMA reports were parsed for all panel organisms. The association between ERA timing and EMMA status was tested using point-biserial correlation, Mann-Whitney U, and Fisher exact tests, with sensitivity analyses for outliers and a Bonferroni correction.

Results: Of 58 transfers with a recorded outcome, 23 resulted in a positive pregnancy test (39.7%), comprising 14 clinical (24.1%) and 9 biochemical pregnancies; thus, biochemical losses accounted for 39.1% of all positive tests. Donor oocytes were used in 37 of 66 transfers (56.1%), and 53 transfers (80.3%) used PGT-A euploid embryos. Among 40 ERAs, the modal recommended duration was 127 hours of progesterone (9/31, 29.0%); however, in all 25 receptive reports that carried a numeric hour, the recommendation reproduced the biopsy protocol

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exactly, so the modal value reflects clinic practice rather than a biological optimum. Of the 35 women with an interpretable result, 8 (22.9%) had a displaced window of implantation. Five of 40 reports (12.5%) were technical failures. Among 36 EMMA reports, Gardnerella vaginalis was the most common pathogenic organism (10/36, 27.8%); Bifidobacterium spp was detected more often (33.3%) but is not classed as pathogenic. In the 29 women with both tests, no association was found between ERA timing and EMMA findings (all $p \geq 0.38$ after sensitivity analysis and correction for multiple testing).

Conclusion: In a programme dominated by euploid embryos and donor oocytes, the clinical pregnancy rate per transfer was 24.1%, and 39.1% of positive tests were biochemical – a proportion high enough to warrant investigation and consistent with reports that biochemical loss is not explained by embryo chromosomal status.9,10 Endometrial receptivity testing identified a displaced window in roughly one woman in five, which is its clinically useful yield, but the modal hour must not be read as an optimal transfer time. ERA and EMMA showed no relationship to one another and should be interpreted as independent sources of information. Sample size, pending outcomes, and the absence of linkage between test results and transfer outcomes limit the analysis.

Patients are identified throughout by sequential codes (P01-P35) and oocyte donors by pseudonymous codes (D01-D21). No names, record numbers or original donor identifiers appear in this document.

Keywords: biochemical pregnancy; embryo implantation; endometrial microbiome; endometrial receptivity; euploid embryo transfer; preimplantation genetic testing for aneuploidy (PGT-A)

Transfer volume

Sixty-six cryo ET cycles were performed across 35 individual patients, a mean of 1.9 transfers per patient. Roughly two-thirds of patients underwent more than one transfer within the review window:

Table 1. Distribution of transfers per patient. No patient in the cohort underwent more than three transfers.

Transfers per patient	Patients	Transfers contributed	% of all transfers
1 transfer	11	11	16.7%
2 transfers	17	34	51.5%
3 transfers	7	21	31.8%
Total	35	66	100%

The repeat-transfer pattern matters when interpreting the headline rate: because 24 of 35 patients contributed two or three cycles each, the per-transfer rate reported below is not equivalent to a per-patient cumulative success rate, which would be higher.

Pregnancy outcomes

Outcomes were recorded for 58 of the 66 transfers. The remaining 8 have no result entered – these are almost entirely transfers dated late July and early August 2026, for which results were still pending at the time of extraction. All rates below therefore use 58 as the denominator.

Table 2. Outcome distribution across all 66 transfers.

Outcome	n	% of 58 with a result	% of all 66
Clinical pregnancy	14	24.1%	21.2%
Biochemical pregnancy	9	15.5%	13.6%
Negative	35	60.3%	53.0%
Result pending	8	-	12.1%
Total	66	100%	100%

Headline rates

- Positive pregnancy test per transfer (clinical + biochemical): 23 / 58 = 39.7%
- Clinical pregnancy per transfer: 14 / 58 = 24.1%
- Negative per transfer: 35 / 58 = 60.3%

The gap between the two headline figures is substantial and deserves emphasis. Of the 23 positive tests, 9 (39.1%) were biochemical – that is, a positive hCG that did not progress to a clinical pregnancy. Quoting the 39.7% figure without that qualifier materially overstates the outcome that patients care about. Early pregnancy loss at this rate is a finding worth monitoring in its own right, particularly given that the great majority of these transfers used euploid, PGT-A-screened embryos. Published series likewise report that biochemical loss is largely independent of embryonic developmental stage and chromosomal constitution,10 and a large cohort combining PGT-A, ERA, and donor oocytes found biochemical loss attributable to neither the embryo nor the endometrium.[9]

Donor oocyte use

Donor oocytes were used in 37 of the 66 transfers (56.1%); 25 transfers (37.9%) used the patient's own oocytes; and 4 transfers (6.1%) could not be confidently assigned. At the patient level, 19 of 35 patients (54.3%) had at least one donor-oocyte cycle. Twenty-one distinct donors are represented; one donor (D01) contributed to cycles in two different patients.

Table 3. Oocyte source at transfer level.

Oocyte source	Transfers	% of 66
Donor oocyte	37	56.1%
Patient's own oocyte	25	37.9%
Undetermined	4	6.1%

Assigning donor status is the least straightforward part of this dataset. Several patients underwent multiple oocyte pick-up (OPU) cycles, of which only one carries a donor code in the source register. Each transfer was therefore matched to its originating OPU cycle by cryopreservation date rather than by taking the patient-level donor flag at face value. This affects five patients: P01, P17, P25, P27 and P28. Taking the patient-level flag uncritically would have classified 40 transfers as donor and 26 as own – a three-transfer overstatement of donor use.

PGT-A status

The cohort is overwhelmingly PGT-A. Fifty-three transfers (80.3%) used embryos with a PGT-A result recorded as euploid. A further 6 transfers were mixed – a euploid-tested embryo was transferred alongside an untested embryo. Only 4 transfers were explicitly untested, and 3 transfers carry no PGT-A entry at all.

Table 4. PGT-A status at transfer level. The 6 mixed transfers are also counted within the 53 in the source register's own summary; they are separated here to avoid double-counting.

PGT-A status	Transfers	% of 66
Tested, euploid	53	80.3%
Mixed (1 tested + 1 untested)	6	9.1%
Not tested	4	6.1%
No entry recorded	3	4.5%

Because only 4 transfers were unambiguously untested, this dataset cannot support any comparison of tested versus untested outcomes. Four cycles is far too small a group to yield a meaningful rate, and any apparent difference would be noise. The practical reading is that the 39.7% positive-test and 24.1% clinical rate reported above are, in effect, the rates for a euploid-embryo transfer program. Randomized data indicate that PGT-A improves outcomes primarily in older patients, not universally.4

Endometrial receptivity (ERA)

Endometrial Receptivity Analysis (ERA) is a transcriptomic assay that dates the endometrium using expression profiles of a panel of receptivity genes and reports the timing of progesterone exposure at which the implantation window opens.[1] Reports were available for 40 women – the 35 patients in the transfer cohort plus 5 women (X36-X40) who were tested but have no transfer recorded in the cycle register. ERA determines whether the endometrium is receptive after a defined duration of progesterone exposure, and expresses its recommendation as the number of hours of progesterone administration at which blastocyst transfer should be performed.

Distribution of test verdicts

Table 5. ERA verdicts across all 40 reports. Five reports (12.5%) failed technically – non-informative, invalid or insufficient RNA – against a manufacturer-quoted combined failure rate of roughly 2.7%.

ERA verdict	n	% of 40	Interpretation
Receptive	27	67.5%	Window of implantation in the expected place
Late receptive	5	12.5%	Transfer 12 h earlier than the biopsy protocol
Pre-receptive	3	7.5%	Window displaced later; 2 of 3 needed a repeat biopsy
Non-informative	2	5.0%	Profile matched no control; repeat biopsy advised
Invalid RNA	2	5.0%	Poor-quality genetic material; repeat biopsy
Insufficient RNA	1	2.5%	Too little genetic material; repeat biopsy

Recommended hour of transfer

A numeric hour could be extracted from 31 of the 40 reports. The remaining 9 comprised the 5 technical failures, 2 pre-receptive results issued without a recommendation pending a second biopsy, and 2 receptive results expressed only as cycle days (P+5 and P+6), with no hour stated.

Table 6. Distribution of ERA-recommended hours of progesterone administration (n = 31). The modal value is highlighted.

Recommended hour	Patients	Share of 31
113 h	1	3.2%
114 h	1	3.2%
115 h	2	6.5%
120 h	4	12.9%
121 h	1	3.2%
122 h	1	3.2%
125 h	2	6.5%
126 h	8	25.8%
127 h	9	29.0%
128 h	1	3.2%
152 h	1	3.2%

Verdict – the most frequently recommended hour is 127 hours of progesterone administration, in 9 of 31 patients (29.0%). Together, 126 h and 127 h account for 17 of 31 (54.8%). Median 126 h; range 113-152 h.

What the modal hour does and does not mean

This figure needs an important qualification, and it is the single most consequential point in this section. For a receptive result, ERA does not compute a new time – it endorses the protocol that was already used. We verified this directly: in all 25 receptive reports carrying a numeric hour, the recommended hour was identical to the hours of progesterone administration recorded for the biopsy cycle itself, with no exceptions.

The modal value of 127 hours therefore reflects the clinic's standard biopsy protocol, not a biological property observed in these patients. Reading it as "the optimal hour for embryo transfer in this population" would invert cause and effect. The tight 120-128 h cluster reflects consistency of clinic practice; the spread within it corresponds to when each patient actually started progesterone relative to the biopsy.

Randomized evidence on whether acting on displaced results improves live birth is conflicting: a multicentre trial reported higher cumulative rates with receptivity-guided transfer,2 whereas a double-blind randomized trial found no difference in live birth and a subsequent analysis argued the test may reduce success by misidentifying the window.3,5 The informative results here are the 8 displaced cases. Five late-receptive patients (P03, P04, P08, P28, P31) were moved 12 hours earlier, to 113-125 h. Three pre-receptive patients were moved later or required a repeat biopsy, including P27 at 152 hours – a full day beyond the standard protocol and the widest displacement in the series. In these data, 8 of 35 women with an interpretable

result (22.9%) had a window of implantation that did not align with the standard protocol assumption, which is the clinically useful yield of the test.

Endometrial microbiome (EMMA / ALICE)

Endometrial Microbiome Metagenomic Analysis (EMMA) quantifies bacterial DNA in endometrial tissue; a Lactobacillus-dominated profile has been associated with higher implantation and pregnancy rates, whereas non-Lactobacillus-dominated profiles have been associated with poorer outcomes.6,8 Reports were available for 36 women. Each covers three panels: Lactobacillus species; a chronic endometritis pathogen panel (the ALICE panel);7 and a broader reproductive tract bacteria panel. Lactobacillus spp was detected in 30 of 36 women (83.3%).

Organisms detected

Table 7. All organisms detected across 36 EMMA reports. Chlamydia trachomatis, Neisseria gonorrhoeae, Mycobacterium tuberculosis, Treponema pallidum, Staphylococcus aureus, Enterococcus faecalis, Mycoplasma genitalium and the remaining panel members were not detected in any patient.

Organism	Patients	% of 36	Panel
Bifidobacterium spp	12	33.3%	Reproductive tract
Gardnerella vaginalis	10	27.8%	Reproductive tract
Ureaplasma urealyticum	5	13.9%	ALICE – chronic endometritis
Atopobium vaginae	3	8.3%	Reproductive tract
Sneathia spp	2	5.6%	Reproductive tract
Streptococcus agalactiae (GBS)	2	5.6%	ALICE – chronic endometritis
Mycoplasma hominis	1	2.8%	ALICE – chronic endometritis
Escherichia coli	1	2.8%	ALICE – chronic endometritis
Klebsiella pneumoniae	1	2.8%	ALICE – chronic endometritis
Mobiluncus spp	1	2.8%	Reproductive tract
Fusobacterium nucleatum	1	2.8%	Reproductive tract
Prevotella bivia	1	2.8%	Reproductive tract
Prevotella disiens	1	2.8%	Reproductive tract

Seventeen of 36 women (47.2%) had at least one organism detected. Excluding Bifidobacterium, 15 of 36 (41.7%) did. Seven of 36 (19.4%) carried at least one organism from the ALICE chronic-endometritis panel.

Which organism counts as “the most common infection”

The answer depends on what is meant by infection, and the distinction matters clinically.

- Bifidobacterium spp is the most frequently detected organism overall (12/36, 33.3%) – but it is not a pathogen. The reports explicitly state that Bifidobacterium, when detected alone, can often be displaced from its niche by probiotics. Counting it as an infection would overstate the burden by roughly a third.

- Gardnerella vaginalis is the most common clinically relevant pathogenic organism (10/36, 27.8%). It is the organism most commonly associated with bacterial vaginosis and endometrial dysbiosis6,8, and its detection prompted the metronidazole-plus-probiotic recommendation in these reports.
- Ureaplasma urealyticum is the most common organism on the ALICE chronic-endometritis panel specifically (5/36, 13.9%).

Verdict – Gardnerella vaginalis is the most common infectious organism, found in 10 of 36 patients (27.8%). Bifidobacterium spp is detected more often (33.3%) but is not classed as pathogenic. Within the chronic endometritis panel alone, Ureaplasma urealyticum leads with 13.9%.

Detected organisms clustered rather than appearing in isolation. P34 carried six organisms simultaneously (Atopobium, Bifidobacterium, Fusobacterium nucleatum, Gardnerella, Prevotella bivia and Prevotella disiens) at values up to 7.79 against a reference ceiling of 4.22 – a marked polymicrobial dysbiosis. P26 carried five. Nine of the ten Gardnerella-positive women had at least one additional organism, consistent with the mixed anaerobic pattern typical of bacterial vaginosis rather than single-organism infection.6,8 Chronic endometritis is common in women with repeated implantation failure, and reproductive outcomes improve after antibiotic treatment, which is the rationale for screening.7,11

Relationship between ERA timing and EMMA findings

Twenty-nine women had both an interpretable ERA hour and an EMMA report, allowing the two to be compared directly. Four pre-specified comparisons were conducted to test whether the recommended transfer hour differed by microbiological status.

Table 7. Point-biserial correlation between EMMA status and ERA-recommended hour (n = 29). Rank-based Mann-Whitney tests yielded p-values of 0.45, 0.67, 0.90, and 0.115, respectively.

Comparison	Detected (n, mean h)	Not detected (n, mean h)	r	p
Any organism	15 – 125.7 h	14 – 123.4 h	+0.17	0.383
Excluding Bifidobacterium	13 – 125.6 h	16 – 123.8 h	+0.13	0.498
Gardnerella vaginalis	9 – 123.1 h	20 – 125.3 h	−0.15	0.444
ALICE-panel organism	6 – 129.8 h	23 – 123.3 h	+0.39	0.037

The one nominally significant result is an artefact

Three of the four comparisons are unambiguously null. The fourth – ALICE-panel organisms – returned p = 0.037, which would conventionally be called significant. It should not be reported as a finding, for three independent reasons:

- A single patient drives it. P27 combined the series' most extreme ERA result (152 h, pre-receptive) with a Streptococcus agalactiae detection. Removing her alone collapses the association from r = +0.39, p = 0.037 to r = +0.18, p = 0.360.
- It does not survive correction for multiple testing. Four comparisons were made; the Bonferroni-corrected p is 0.037 × 4 = 0.148.
- The rank-based test never agreed. Mann-Whitney yielded p = 0.115 for the same data, indicating that the parametric result depends on the outlier's magnitude rather than on a consistent shift between groups.

Two further checks were also null: the number of organisms detected did not correlate with the recommended hour (Spearman rho = +0.14, p = 0.459), and a displaced window of implantation was no more likely in women with an organism detected than in those without (odds ratio 1.05, Fisher exact p = 1.00).

Verdict – no association was found between endometrial receptivity timing and endometrial microbiome findings. Every comparison that survives basic robustness checks is null.

How to read a null result here

This is a negative finding, not evidence of absence. With 29 paired cases and only 6 to 15 women in each exposed group, the analysis could only have detected a very large effect – a shift of roughly 5 to 6 hours or more between groups. A real but modest relationship, of the size that would plausibly matter in practice, would be invisible at this sample size. The honest conclusion is that these data neither support nor exclude a link.

It is also worth noting that no strong mechanistic reason to expect one has been established. ERA measures the transcriptomic timing of endometrial receptivity; EMMA measures bacterial DNA present in the same tissue. Both have been separately associated with implantation failure1,6, but that does not imply they are associated with each other; a large cohort applying PGT-A, ERA, and endometrial assessment together likewise failed to attribute early loss to either compartment.9 The practical implication is that these two tests appear to capture independent information, and a normal result on one gives no reassurance about the other – which is an argument for interpreting them separately rather than as a combined score.

Limitations

- Pending results. Eight transfers have no recorded outcome. If those cycles ultimately differ from the cohort average, the reported rates will shift; they should be recomputed once results are entered.
- Unconfirmed donor status. P17's 10.07.2025 transfer came from embryos frozen on 10.03.2025, and no matching OPU row exists in the source register for that cycle. Her only listed OPU (27.01.2026) is a donor cycle, so the donor status for this transfer is inferred rather than confirmed.
- No stratified rates. Donor status is reliably known at patient level but only partially reconstructed at transfer level, and the untested group is too small for comparison. Outcomes are therefore not broken down by oocyte source or PGT-A status; doing so with this data would produce figures that look more precise than the underlying records justify.
- Per-transfer, not cumulative. All rates are per transfer. A cumulative per-patient live birth rate cannot be derived here – the register records pregnancy test outcomes, not deliveries.
- Register inconsistencies. Three transfers have no PGT-A entry, four have indeterminate donor status, and one patient (P35) has a second, empty transfer row. These gaps are small in number but should be closed at source.
- ERA hours are protocol-dependent. For a receptive result, the recommended hour reproduces the biopsy protocol exactly, so the modal 127 h describes clinic practice, not patient biology. Only the 8 displaced results carry independent information.

- ERA technical failure rate. Five of 40 reports (12.5%) were non-informative, invalid, or had insufficient RNA, exceeding the manufacturer's quoted rate. This warrants review of biopsy and sample-handling technique.
- EMMA detects bacterial DNA, not viable infection. A positive result indicates DNA above a reference threshold; it does not establish active infection or causation, and no histological or hysteroscopic confirmation of chronic endometritis was available.6,8
- Timing of tests relative to transfer was not recorded. Whether each ERA/EMMA result preceded or followed a given transfer, and whether detected organisms were treated before transfer, cannot be determined from the records supplied. Outcomes are therefore not linked to test results anywhere in this report.
- No control or comparison group. This is a descriptive single-cohort audit, not a controlled comparison. No causal inference should be drawn from any figure in it.

Conclusions

Across 66 cryopreserved embryo transfers in 35 patients, 39.7% of transfers with a recorded outcome resulted in a positive pregnancy test, and 24.1% resulted in a clinical pregnancy. The programme is predominantly a donor-oocyte and PGT-A-screened one: 56% of transfers used donor oocytes and 80% used embryos reported euploid.

Two findings warrant further investigation. First, the proportion of positive tests that were biochemical – 9 of 23, or 39% – is high for a euploid-embryo cohort and is the single most useful signal in this dataset. Second, the data-capture gaps described in Section 8, while individually minor, systematically undermine any attempt at stratified analysis. Recording donor status and PGT-A result against the transfer rather than the patient would allow the next review to report outcomes by oocyte source and testing status, which is where the clinically actionable comparisons lie.

The ERA and EMMA data add two further points. Approximately one in five women had a displaced window of implantation, which is the real yield of receptivity testing; this should be weighed against randomized evidence that routine receptivity-guided timing does not improve live birth rates.3,5 Gardnerella vaginalis was present in more than a quarter of women tested and rarely alone, indicating that endometrial dysbiosis in this population is typically polymicrobial and consistent with the non-Lactobacillus-dominated profiles associated with poorer reproductive outcome.6,8 The two tests showed no relationship to each other and should be interpreted as independent sources of information rather than combined into a single assessment.

Declarations

Ethics and data statement: This retrospective audit used routinely collected clinical data. All patient identifiers were removed prior to analysis; patients are reported by sequential codes and oocyte donors by pseudonymous codes, and the re-identification key is held separately by the clinic.

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Conflict of Interest: The authors declare no competing interests. ERA and EMMA/ALICE are proprietary assays performed by Igenomix.

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Appendix A – Per-patient detail

All 66 transfers by patient, in source-register order. Format: date · PGT-A status / pregnancy outcome.

Table A1. Transfer-level detail for all 35 patients. “Mixed” denotes one PGT-A-tested and one untested embryo transferred together. Codes P01-P35 and D01-D21 are pseudonyms assigned for this document; the re-identification key is held separately.

Patient	n	Transfers (date · PGT-A / outcome)	Oocyte donor
P01	1	15.06.26 Normal / Yes	Yes (D01)
P02	1	06.04.26 Normal / No	No
P03	1	22.04.26 Normal / Yes	No
P04	1	02.03.26 Normal / Yes	Yes (D02)
P05	2	04.12.25 No PGT / No; 24.04.26 No PGT / No	Yes (D03)
P06	1	13.03.26 Normal / Biochemical	No
P07	3	08.10.25 Normal / No; 24.06.26 Normal / Biochem; 28.07.26 No PGT / pending	No
P08	2	17.03.26 Normal / Biochem; 15.06.26 Normal / Yes	No
P09	2	07.11.25 Normal / No; 17.02.26 Normal / Yes	Yes (D04)
P10	2	18.07.24 Normal / No; 02.03.26 Normal / Yes	No
P11	1	20.10.25 Normal / No result	No
P12	2	25.11.25 Normal / No; 25.03.26 Normal / Yes	Yes (D01)
P13	1	24.11.25 Normal / No	No
P14	2	05.08.25 Normal / No; 05.11.25 Normal / No	Yes (D05)
P15	2	13.01.26 Normal / no result; 29.05.26 Normal / No	Yes (D06)
P16	2	15.05.26 Normal / No; 05.08.26 pending (no AH/AI)	No
P17	3	10.07.25 Normal / No; 23.03.26 pending; 20.04.26 Normal / Yes	Yes (D07, OPU 27.01.26)
P18	3	27.09.24 mixed / No; 04.11.24 mixed / No; 06.08.26 pending	Yes (D08)
P19	1	23.04.26 mixed (1 PGT + 1 no PGT) / Biochem	Yes (D09)
P20	2	30.01.26 Normal / Biochem; 22.06.26 Normal / Yes	Yes (D10)
P21	2	31.12.25 Normal / No; 15.04.26 Normal / Yes	Yes (D11)
P22	2	21.01.26 Normal / No; 14.04.26 Normal / Yes	Yes (D12)
P23	2	24.06.26 Normal / No; 27.07.26 Normal / pending	No
P24	3	17.10.24, 06.01.26, 01.06.26 – all Normal / all No	Yes (D13, D14)
P25	3	16.01.26 Normal / No; 23.03.26 mixed / No; 14.07.26 Normal / Yes	Yes (D15)
P26	3	27.01.26 Normal / Biochem; 02.03.26 Normal / No; 15.06.26 Normal / No	No
P27	2	21.03.26 Normal / No; 17.07.26 Normal / Biochem	Yes (D16)
P28	2	08.12.25 Normal / Biochem; 05.03.26 No PGT / No	Yes (D17)
P29	1	28.07.26 Normal / pending	No

Patient	n	Transfers (date · PGT-A / outcome)	Oocyte donor
P30	2	16.01.26 Normal / No; 30.06.26 Normal / Yes	No
P31	2	23.01.26 Normal / No; 14.05.26 Normal / Yes	No
P32	3	30.07.24 mixed / No; 21.11.24 mixed / No; 31.10.25 Normal / No	Yes (D18, D19, D20)
P33	1	26.02.24 Normal / No	No
P34	2	21.07.25 Normal / Biochem; 23.01.26 Normal / No	Yes (D21)
P35	1	04.05.26 Normal / No (second row exists but is empty)	No

Appendix B – ERA and EMMA results by patient

Codes P01-P35 match the transfer cohort in Appendix A. Codes X36-X40 are women with ERA/EMMA results but no transfer recorded in the cycle register.

Table B1. Combined ERA and EMMA results, 40 ERA reports and 36 EMMA reports. "-" indicates no numeric hour was issued. P04, P09, P18 and X36 have an ERA report but no EMMA report.

Patient	ERA verdict	Hour	Organisms detected (EMMA)
P01	Receptive	127 h	Atopobium vaginae, Bifidobacterium spp, Gardnerella vaginalis, Sneathia spp
P02	Receptive	127 h	None detected
P03	Late receptive	115 h	Bifidobacterium spp, Gardnerella vaginalis
P04	Late receptive	125 h	No EMMA report
P05	Non-informative	-	None detected
P06	Receptive	120 h	None detected
P07	Receptive	127 h	Bifidobacterium spp, Gardnerella vaginalis, Ureaplasma urealyticum
P08	Late receptive	115 h	None detected
P09	Receptive	P+6	No EMMA report
P10	Receptive	127 h	None detected
P11	Receptive	125 h	None detected
P12	Receptive	120 h	Bifidobacterium spp, Escherichia coli, Klebsiella pneumoniae, Streptococcus agalactiae
P13	Receptive	126 h	Gardnerella vaginalis
P14	Receptive	127 h	Ureaplasma urealyticum
P15	Insufficient RNA	-	None detected
P16	Receptive	127 h	None detected
P17	Invalid RNA	-	Bifidobacterium spp, Gardnerella vaginalis
P18	Receptive	P+5	No EMMA report
P19	Receptive	127 h	Bifidobacterium spp
P20	Receptive	127 h	Bifidobacterium spp, Gardnerella vaginalis

Patient	ERA verdict	Hour	Organisms detected (EMMA)
P21	Pre-receptive	-	None detected
P22	Receptive	126 h	Bifidobacterium spp
P23	Receptive	126 h	None detected
P24	Receptive	126 h	Ureaplasma urealyticum
P25	Receptive	126 h	None detected
P26	Receptive	127 h	Bifidobacterium spp, Gardnerella vaginalis, Mobiluncus spp, Mycoplasma hominis, Sneathia spp, Ureaplasma urealyticum
P27	Pre-receptive	152 h	Bifidobacterium spp, Streptococcus agalactiae
P28	Late receptive	113 h	Gardnerella vaginalis
P29	Pre-receptive	-	None detected
P30	Receptive	126 h	None detected
P31	Late receptive	114 h	None detected
P32	Non-informative	-	Ureaplasma urealyticum
P33	Receptive	128 h	None detected
P34	Receptive	120 h	Atopobium vaginae, Bifidobacterium spp, Fusobacterium nucleatum, Gardnerella vaginalis, Prevotella bivia, Prevotella disiens
P35	Receptive	121 h	None detected
X36	Receptive	122 h	No EMMA report
X37	Receptive	126 h	Atopobium vaginae, Bifidobacterium spp, Gardnerella vaginalis
X38	Receptive	120 h	None detected
X39	Receptive	126 h	None detected
X40	Invalid RNA	-	None detected