manufacturer recommendations, followed by CL via transvaginal ultrasound. Caregivers were blinded to PAMG-1 and phIGFBP-1 test results. Subjects who delivered within 14 days of testing following either induction or C-section were excluded from the final analysis as endpoint was prediction of imminent spontaneous PTD. Standard performance statistics with 95% confidence intervals were calculated and compared based on pairwise estimates from a generalized model.

RESULTS: Of 341 pts enrolled, 196 were from Finland, 95 from Macedonia, 50 from Russia. 13 (4%) were excluded (6 delivered within 14 days non-spontaneously, 4 were < 18 y/o, 2 were tested twice, and 1 had no test result for either biomarker test), leaving 328 evaluable subjects. Median GA and CL at presentation were 31 wks and 27 mm, respectively. 25 (8%) women delivered ≤7 days from testing. PAMG-1 was positive in 30 (9%) women, whereas phIGFBP-1 was positive in 99 (30%). Tables 1 and 2 show performance for each test in all patients and those with CL 15-30 mm, respectively.

CONCLUSION: In PTL symptomatic pts overall, PAMG-1 is significantly more specific than phIGFBP-1 for the prediction of spontaneous PTD within 7 days ($p<.0001$), whereas both tests have comparable sensitivity. In PTL symptomatic pts with CL 15-30 mm, PAMG-1 has a significantly higher PPV and specificity compared to phIGFBP-1 for the prediction of spontaneous PTD within 7 days ($p<.01$), whereas both tests have comparable sensitivity and NPV. In conclusion, PAMG-1 is the most accurate biomarker for the prediction of imminent spontaneous PTD in PTL symptomatic women when compared to phIGFBP-1 or CL alone. In patients with non-obvious CL between 15 and 30 mm, the PAMG-1 test is significantly superior to phIGFBP-1 at identifying patients who deliver spontaneously within 7 days of testing.

Tables 1 & 2. Prediction of spontaneous PTD within 7 days of testing

Table 1. Prediction of spontaneous PTD within 7 days of testing in all pts (n=328)

	PAMG-1	phIGFBP-1	CL <25 mm
Statistic	% (Prop.) [95% CI]	% (Prop.) [95% CI]	% (Prop.) [95% CI]
SN	72 (18/25)[51, 88]	84 (21/25)[64, 95]	68 (17/25)[47, 85]
SP	96 (291/303)[93, 98]	74 (225/303)[69, 79]	63 (191/303)[57, 68]
PPV	60 (18/30)[41, 77]	21 (21/99)[14, 31]	13 (17/129)[8, 20]
NPV	98 (291/298)[95, 99]	98 (225/229)[96, 100]	96 (191/199)[92, 98]

Table 2. Prediction of spontaneous PTD within 7 days of testing in pts with CL 15-30 mm (n=177)

	PAMG-1	phIGFBP-1
Statistic	% (Prop.) [95% CI]	% (Prop.) [95% CI]
SN	74(14/19)[49, 91]	84 (16/19) [60, 97]
SP	94 (149/158)[89, 97]	77 (122/158)[70, 84]
PPV	61 (14/23)[39, 80]	31 (16/52)[19, 45]
NPV	97 (149/154)[93, 99]	98 (122/125)[93, 100]

17 Assessing the potential impact of extending antenatal corticosteroid use

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OBJECTIVE: In 2016 ACOG/SMFM issued guidance extending antenatal steroid use for *selected* late preterm singleton pregnancies based on new evidence for improved neonatal respiratory outcomes. Our objective was to assess antenatal steroid use and the potential impact of these guidelines.

STUDY DESIGN: This cohort study used chart-abstracted data from singleton deliveries at 12 centers participating in the Obstetric Clinical Outcomes Program (OB COAP), a quality initiative in Washington State. Centers contributing data for all or part of the study period (January 1, 2012-March 31, 2016) were included. Pregnancies with missing gestation at delivery, fetal anomalies, or antepartum demise were excluded. Newborn respiratory complications were calculated for pregnancies considered eligible and ineligible for late preterm steroids based on the 2016 guidelines.

RESULTS: The analytic sample included 60243 singleton deliveries at 24^{+0}-42^{+6} weeks. Of the 3949 preterm (24^{+0}-36^{+6} weeks) deliveries, 74.5% (n=2942) were late preterm. Eighty percent (n=2363) of late preterm deliveries were potentially steroid eligible and 60% of these (n=1411) delivered at 36 weeks. Steroid eligible late preterm deliveries represented 4.0% (2363/59236) of all deliveries at ≥34 weeks. Approximately 80% (248/312) of late preterm newborns with respiratory complications were in the steroid eligible group and of those 69% (171/248) occurred in deliveries at 34-35 weeks. The rate of newborn respiratory complications was highest in those *ineligible* for steroids due to pre-pregnancy diabetes or chorioamnioninitis regardless of gestational age at delivery.(Table 1) For deliveries at 36 weeks, those *eligible* for steroids or *ineligible* due to prior steroids had similar rates of respiratory complications (5.5% vs 4.9%).

CONCLUSIONS: In our study up to 4% of singleton deliveries at ≥34 weeks could be considered targets for late preterm steroids based on new guidelines. Nearly 3/4 of newborn respiratory complications in this group were in those delivering at 34-35 weeks.

	Rate of Newborn Respiratory Complications Based on Potential Eligibility for Late Preterm Steroids		
Gestational Week on Delivery	*Eligible* % (n=2363)	*Ineligible* - earlier steroids % (n=480)	*Ineligible* – chorioamnionitis or pre-pregnancy diabetes % (n=99)
34	24.1 (76/315)	13.9 (26/187)	35.0 (7/20)
35	14.9 (95/637)	7.4 (11/149)	15.4 (4/26)
36	5.5 (77/1411)	4.9 (7/144)	17.0 (9/53)
Total	10.5 (248/2363)	9.2 (44/480)	20.2 (20/99)

18 Maternal gene variants in human telomerase reverse transcriptase are associated with preterm labor and preterm premature rupture of membranes

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OBJECTIVE: Telomere shortening is associated with in utero feto-placental aging and parturition; however, various pregnancy associated risk factors can accelerate this process. Premature aging and short telomere lengths of fetal tissues are associated with adverse pregnancy outcomes like spontaneous preterm birth (PTB) and preterm premature rupture of membranes (pPROM). Maintenance of telomere length and protection of chromosome integrity is performed by the enzyme telomerase. Human telomerase reverse transcriptase (hTERT) is a subunit of telomerase, and its dysfunction can affect telomere length. This study determined if maternal or fetal genetic variations (single nucleotide polymorphisms [SNPs]) in the hTERT gene are associated with PTB or pPROM.

STUDY DESIGN: A case (PTB or pPROM) control (term birth) genetic association study was conducted in 546 non-Hispanic white mothers (390 term, 125 PTB, 31 pPROM) and 389 non-Hispanic white infants (281 term, 79 PTB, 29 pPROM). Maternal and infant DNA samples were genotyped for 23 SNPs within the hTERT gene. Single locus allele frequencies were compared between cases and controls. Logistic regression was performed on mother and infant data independently, stratified by the type of case (PTB or pPROM). The