

# Index

## A

Activin receptor-like kinase (ALK), preeclampsia dysfunction, 129  
*AF. See Amniotic fluid*  
*ALK. See Activin receptor-like kinase*  
Amniotic fluid (AF)  
    cell-free fetal RNA, 342–343  
    overview, 341–342  
    transcriptomics  
        cell-free versus cellular RNA comparison, 353–355  
        Down syndrome, 348–349  
        Edwards syndrome, 348–350  
        fetal therapy applications, 352–355  
        maternal obesity, 352  
        placenta-specific gene expression, 347  
        prospects, 355  
    RNA extraction, 343, 345  
    second trimester euploid fetus studies, 347–350  
    table of studies, 344–345  
    tissue-specific gene expression, 354  
    Turner syndrome, 350–361  
    twin–twin transfusion syndrome, 343, 345–346, 349, 351–352  
*AMPK*, salivary transcriptomics in neonates, 395  
Angiotensin, preeclampsia role, 258  
Argonaute  
    knockout effects on ovarian development, 3, 6  
    microRNA processing, 2  
ART. *See Assisted reproductive technology*  
Assisted reproductive technology (ART)  
    epigenetics  
        differences in children by type of conception, 84–85  
    DNA methylation, 81–84  
    environmental influences, 79–80  
    placenta studies, 84–86  
    plasticity, 81  
    prospects for study, 85–88  
    microRNA utilization, 14–15  
    overview of in vitro fertilization, 77–79  
    recurrent pregnancy loss and genetic testing  
        preimplantation genetic diagnosis, 225–226  
        preimplantation genetic screening, 225–226  
        biopsy

blastomere, 227–228  
overview, 226–227  
polar body, 227  
trophoectoderm, 228–229

## B

Bacterial vaginosis (BV), vaginal microbiome, 163, 167  
*Birth. See Parturition*  
*Bisphenol A (BPA)*, HOX gene expression response, 58–59  
*Blood group. See Fetal blood group*  
*BPA. See Bisphenol A*  
*BRCA*, newborn screening for mutations, 363  
*BV. See Bacterial vaginosis*

## C

Cell-free fetal DNA (cffDNA)  
    fetal blood group typing. *See Fetal blood group*  
    fetal single-gene disorder detection. *See Whole exome sequencing; Whole genome sequencing*  
    noninvasive prenatal testing. *See Noninvasive prenatal testing*  
    parturition timing role, 201  
*cffDNA. See Cell-free fetal DNA*  
*CHARGE syndrome*, 331  
*Chromosomal microarray analysis (CMA)*, prenatal genetic diagnosis, 325–326  
*CL. See Corpus luteum*  
*CMA. See Chromosomal microarray analysis*  
*Corin*  
    amniotic fluid, 341–342  
    placentation defects in preeclampsia, 259  
*Corpus luteum (CL)*  
    microRNA expression and function, 10–11  
    progesterone synthesis, 237–239  
*COX-2. See Cyclooxygenase-2*  
*Cyclooxygenase-2 (COX-2)*  
    late gestational changes, 190  
    progesterone effects, 184

## D

*DC. See Dendritic cell*  
*Dendritic cell (DC)*, uterus and immune tolerance, 95–96

## Index

- Dicer  
knockout effects on ovarian development, 3, 6, 11  
microRNA processing, 2
- DNA methylation. *See* Epigenetics; Placenta
- Down syndrome (DS), amniotic fluid transcriptomics, 348–349
- DREAM assay, 83
- Drosha, microRNA processing, 2
- DS. *See* Down syndrome
- E**
- Edwards syndrome, amniotic fluid transcriptomics, 348–350
- EGF. *See* Epidermal growth factor
- EMX2, 56, 60
- Endoglin, preeclampsia role, 253, 257, 260
- Endometriosis, HOX genes in pathogenesis, 59–61
- Endometrium  
fibroids. *See* Leiomyoma  
immunological priming, 202, 204  
transcriptomics  
clinical applicability, 71–72  
next-generation sequencing, 72  
overview, 69–70  
prospects for study, 72–73  
receptivity studies, 69, 71  
window of implantation, 67–69, 71–73
- Endoplasmic reticulum stress, preeclampsia role, 260
- Endothelial cell, placental extracellular vesicle  
interactions, 118–119
- Epidermal growth factor (EGF), extravillous trophoblast cell invasion regulation, 99
- Epigenetics  
assisted reproductive technology studies  
differences in children by type of conception, 84–85  
DNA methylation, 81–84  
environmental influences, 79–80  
placenta studies, 84–86  
plasticity, 81  
prospects for study, 86–88
- cell-free fetal DNA, 300
- cystine methylation, 40–41
- maternal obesity  
DNA methylation, 275–276, 282  
histone code variations, 276  
microRNA variations, 276–277, 283  
overview, 275
- molecular carriers, 40
- overview, 39–40
- placental methylome. *See* Placenta
- preterm birth studies, 208
- sperm intergenerational transfer  
environmental effects, 47–48  
model systems, 45
- nutrition effects, 45–46  
odorant training, 46–47  
stress effects, 46  
toxin effects, 46
- Estrogen, HOX gene expression regulation, 58–59
- Extravillous trophoblast cell. *See* Trophoblast
- F**
- Factor V Leiden (FVL), recurrent pregnancy loss gene defects, 224
- FAS-L, recurrent pregnancy loss gene defects, 223
- Fetal blood group  
hemolytic disease of the fetus and newborn, 315–316
- typing  
cell-free fetal DNA, 316  
next-generation sequencing  
polymerase chain reaction primers, 320–321  
principles, 316–317  
prospects, 321–322  
reporting, 320–321  
statistical analysis, 318–321  
technical aspects, 317–318  
overview, 316
- Fetal growth restriction (FGR)  
placental methylome findings, 149–150  
placental microRNA findings, 129–130
- FGR. *See* Fetal growth restriction
- Fibroid. *See* Leiomyoma
- Fibronectin, placental extracellular vesicle cargo, 115
- FIGLA, microRNA regulation, 13
- FLT. *See* Fms-like tyrosine kinase
- Fms-like tyrosine kinase (FLT), preeclampsia  
biomarker utilization, 260–263  
role, 253–255, 257, 260, 264
- Follicle-stimulating hormone (FSH), receptor variants  
in preterm birth, 245–246
- FSH. *See* Follicle-stimulating hormone
- FVL. *See* Factor V Leiden
- G**
- Gut microbiome. *See* Microbiome
- H**
- hCG. *See* Human chorionic gonadotropin
- HELLP syndrome, 264
- HELP assay, 83
- Heme oxygenase-1 (HO-1), preeclampsia  
role, 259  
therapeutic targeting, 263–264
- Hemolytic disease of the fetus and newborn. *See* Fetal blood group
- HLA-G, recurrent pregnancy loss gene defects, 223

HMP. *See* Human Microbiome Project

HO-1. *See* Heme oxygenase-1

HOX genes

*Drosophila* development role, 54

female reproductive tract

development role, 55–56

estrogen and progesterone in expression

regulation, 58–59

infertility pathogenesis

endometriosis, 59–61

hydrosalpinx, 82–63

leiomyoma, 62

polycystic ovarian syndrome, 61–62

reproductive function, 56–57

functional overview, 53

HOXD sperm chromatin cluster, 26–27

vertebrate axial development role, 54–55

Human chorionic gonadotropin (hCG), extravillous trophoblast cell invasion regulation, 99

Human Microbiome Project (HMP), 157–158

Hydrosalpinx, HOX genes in pathogenesis, 82–63

## I

IDO. *See* Indoleamine 2,3-dioxygenase

IGF-1. *See* Insulin-like growth factor-1

Immune tolerance, pregnancy and uterine cells

dendritic cells, 95–96

macrophages, 94–95

natural killer cells, 93–94

T cells, 95

Indoleamine 2,3-dioxygenase (IDO), fetal immune response prevention, 205

Insulin-like growth factor-1 (IGF-1), receptor as susceptibility gene for preterm birth, 247

Intrauterine growth restriction. *See* Fetal growth restriction

In vitro fertilization. *See* Assisted reproductive technology

## K

KEL, fetal blood group typing, 317, 319–323

## L

Leiomyoma, HOX genes in pathogenesis, 62

Leukemia inhibitory factor (LIF), recurrent pregnancy loss gene defects, 223

LH. *See* Luteinizing hormone

LIF. *See* Leukemia inhibitory factor

Lipopolysaccharide (LPS), preterm birth induction, 208–209

LPS. *See* Lipopolysaccharide

Luteinizing hormone (LH), microRNA expression effects in antral follicles, 8–10

## M

Macrophage

placental extracellular vesicle interactions, 117–118

uterus and immune tolerance, 94–95

Massively parallel sequencing. *See* Next-generation sequencing

Maternal obesity. *See* Obesity

Matrix metalloproteinases (MMPs), extravillous trophoblast cell invasion, 97–98

MED1, microRNA regulation of expression, 131

MER, repetitive elements and invasive placenta, 244

Metagenomics. *See* Microbiome

Methoxychlor (MXC), HOX gene expression response, 58

Microbiome

clinical significance in reproduction, 173

gut microbiome in pregnancy, 168

Human Microbiome Project, 157–158

infant colonization

cesarean versus vaginal delivery, 169

first microbial species, 170

probiotic studies, 169

maternal obesity studies, 278

metagenomics

omics data integration, 162

perinatal health studies, 159–160

16S-based metagenomics, 160–161

whole genome shotgun-based metagenomics, 161–162

placental microbiome, 171–173

vaginal microbiome

community state types, 163–164, 167–168

next-generation sequencing, 163–164

pregnancy, 164–168

MicroRNA

biogenesis, 1–2, 125–126

corpus luteum expression and function, 10–11

maternal obesity and epigenetic variations, 276–277, 283

myometrial quiescence maintenance in pregnancy

overview, 185–186

miR-200 family and targets, 186–188

downregulation of cyclooxygenase-2 regulators, 190–191

nomenclature, 2

oocyte expression and function, 11–13

ovarian development

antral follicles, 8–10

follicular development, 5–7

overview, 2–5

tissue expression, 8

ovarian disease studies

assisted reproductive technology utilization,

14–15

early reproductive senescence, 13–14

## Index

- MicroRNA (*Continued*)  
ovarian cancer, 13  
polycystic ovarian syndrome, 14  
sperm, 30, 32, 44–45
- Miscarriage, placental methylome findings, 149–150
- MKP-1, progesterone effects, 184
- MMPs. *See* Matrix metalloproteinases
- mTORC1, premature decidual senescence in mice, 208
- Müllerian duct, *HOX* genes in development, 55
- MXC. *See* Methoxychlor
- N**
- Natural killer (NK) cell  
spiral artery remodeling in pregnancy, 100–101, 257–259  
uterus and immune tolerance, 93–94
- NBS. *See* Newborn screening
- Neutrophil, placental extracellular vesicle interactions, 118
- Newborn screening (NBS)  
historical perspective, 359, 361  
next-generation sequencing challenges for incorporation in routine practice, 361–362  
ethics, 368–371  
gene selection, 360–361  
hearing loss, 363–364  
miscellaneous disease screening, 364–368  
monogenetic diseases in critically ill neonates.  
*See* Whole genome sequencing  
overview, 359–360  
phenylketonuria, 363  
prospects, 371  
secondary findings, 362–363
- Next-generation sequencing. *See* Fetal blood group; Microbiome; Newborn screening; Noninvasive prenatal testing; Whole exome sequencing; Whole genome sequencing
- NF-κB. *See* Nuclear factor-κB
- NIPT. *See* Noninvasive prenatal testing
- NK cell. *See* Natural killer cell
- Noninvasive prenatal testing (NIPT)  
cell-free fetal DNA historical perspective, 296–299  
overview, 295–296  
massively parallel sequencing of maternal plasma aneuploidy testing costs, 306–307  
failed test implications, 307  
false-positives, 304–306  
intellectual property issues, 308  
overview, 301, 304  
public health care implementation, 306–308  
stakeholder opinions and education, 307–308
- epigenetics, 300  
monogenetic disease detection overview, 301–303  
public health care implementation, 308–309
- overview, 299  
sizing of fetal DNA, 299–300  
transcriptomics, 300
- NPH4*, salivary transcriptomics in neonates, 395
- NPY2R*, salivary transcriptomics in neonates, 395
- Nuclear factor-κB (NF-κB), progesterone inhibition of activation, 184
- O**
- Obesity  
epidemiology, 273  
maternal obesity definitions, 274–275  
epigenetic modifications DNA methylation, 275–276, 282  
histone code variations, 276  
microRNA variations, 276–277, 283  
overview, 275  
gut microbiome studies, 278
- mechanistic studies animal models, 278–279  
humans, 279–280
- metabolic programming animal models, 280–282  
epidemiological studies, 280  
human studies, 281–283
- neurodevelopment studies in offspring animal models, 283–285  
epidemiological studies, 283  
human studies, 285
- prospects for study, 286–287
- sex-specific effects cardiometabolic programming, 285–286  
neurodevelopmental programming, 286  
transcriptomics and RNA sequencing, 277–278, 352
- metabolic imprinting, 274
- Oocyte  
microRNA expression and function, 11–13  
sperm penetration effects, 30–34
- Ovary, microRNA studies  
development antral follicles, 8–10  
follicular development, 5–7  
overview, 2–5  
tissue expression, 8
- disease studies assisted reproductive technology utilization, 14–15  
early reproductive senescence, 13–14  
ovarian cancer, 13  
polycystic ovarian syndrome, 14

P

p53

recurrent pregnancy loss gene defects, 223  
uterine knockout and preterm birth in mice, 208,  
240

Parturition. *See also* Preterm birth

inflammatory response, 182  
progesterone functional decline at term, 191  
placental clock  
cell-free fetal DNA role, 201  
decidual prostaglandin synthesis suppression in  
pregnancy, 205–206  
models for nine-month clock, 198–201  
overview, 198  
prospects for study, 211  
supporting evidence for decidual clock, 201–203  
T cells, 202, 204–205  
selective pressures and adaptive evolution in human  
pregnancy and parturition, 245–246

PBMC. *See* Peripheral blood mononuclear cell

PBX2, 57

PCOS. *See* Polycystic ovarian syndrome

PDGF. *See* Platelet-derived growth factor

Peripheral blood mononuclear cell (PBMC), placental  
extracellular vesicle interactions, 116–117

Peroxisome proliferator-activated receptor- $\gamma$  (PPAR- $\gamma$ ),  
metabolic programming in maternal  
obesity, 282

PGC. *See* Primordial germ cell

PGD. *See* Preimplantation genetic diagnosis

PGS. *See* Preimplantation genetic screening

Phenylketonuria (PKU), newborn screening, 359,  
363, 369

PKU. *See* Phenylketonuria

PLA2G4C, preterm birth variants, 246

PLAC4, noninvasive prenatal testing, 296

Placenta. *See also* Trophoblast

DNA methylation

characteristics

gene promoter hypomethylation, 145  
global hypomethylation, 143  
monoallelic methylation and genomic  
imprinting, 145–146  
overview, 142–143  
partially methylated domains, 144  
retrotransposable element hypomethylation,  
144

X-chromosome promoter hypomethylation  
in females, 144–145

environmental exposure effects, 150–151

gestational age and changes, 147–149

overview, 141–142

pregnancy complication studies, 148–149

villous tree structure and distribution, 146–147

epigenetic studies of assisted reproductive

technology effects, 84–86

extracellular vesicles

cargo

immune regulatory proteins, 114

lipids, 116

nucleic acids, 115–116

overview, 113

vascular-reactive proteins, 115

endothelial cell interactions, 118–119

immune cell interactions

monocytes/macrophages, 117–118

neutrophils, 118

peripheral blood mononuclear cells, 116–117

T cells, 116

nanovesicles, 112–113

overview of types, 108

preeclampsia effects, 113

prospects for study, 119

purification, 108–111

syncytial nuclear aggregates, 108, 111–112

trophoblast deportation, 113

microbiome, 171–173

microRNA

circulating levels in pregnancy and biomarker  
use, 131–135

expression, 126–129

fetal growth restriction findings, 129–130

preeclampsia dysfunction, 129

prospects for study, 134

viral infection studies, 130–131

structure, 107–108

timing of birth. *See* Parturition

Placental growth factor (PIGF)

placental extracellular vesicle cargo, 115

preeclampsia

biomarker utilization, 260–263

role, 253–255

Platelet-derived growth factor (PDGF), spiral artery  
remodeling in pregnancy, 100

PIGF. *See* Placental growth factor

PLXNA1, salivary transcriptomics in neonates, 395

Polycystic ovarian syndrome (PCOS)

HOX genes in pathogenesis, 61–62

microRNA role, 14

prenatal androgen exposure, 5

PPAR- $\gamma$ . *See* Peroxisome proliferator-activated receptor- $\gamma$

Preeclampsia

angiogenic factors

biomarker utilization, 260–263

pathogenesis, 253–257

therapeutic targeting, 263–264

epidemiology, 253

long term complications, 264–265

placental extracellular vesicle effects, 113

placental microRNA dysfunction, 129

placentation defect mechanisms, 257–260

prospects for study, 265–266

## Index

- Pregnancy loss. *See* Recurrent pregnancy loss
- Preimplantation genetic diagnosis (PGD), recurrent pregnancy loss and genetic testing
- biopsy
    - blastomere, 227–228
    - overview, 226–227
    - polar body, 227
    - trophoectoderm, 228–229
  - overview, 225–226
- Preimplantation genetic screening (PGS), recurrent pregnancy loss and genetic testing
- biopsy
    - blastomere, 227–228
    - overview, 226–227
    - polar body, 227
    - trophoectoderm, 228–229
  - overview, 225–226
- Preterm birth
- animal models
    - clinical relevance, 239–240
    - fetal membrane rupture comparative genomics, 243–244
    - overview, 236–237
  - progesterone
    - function evolution, 237
    - levels across different species, 240–241
    - luteal production, 237–239
    - repetitive elements and invasive placenta, 244
  - biological continuum, 210
  - definition, 235
  - epidemiology, 181–182
  - epigenetics, 208
  - follicle-stimulating hormone receptor variants, 245–246
  - genome-wide analysis, 246–247
  - heritability, 206–208
  - insulin-like growth factor-1 receptor as susceptibility gene, 247
  - myometrial quiescence maintenance in pregnancy.  
*See* MicroRNA

Primordial germ cell (PGC), ovarian development, 2–4

### Progesterone

- PLA2G4C* variants, 246
- progesterone evolutionary genomics
  - receptor
    - evolution, 240–241
    - genetic variation and function, 243
    - withdrawal mechanisms, 242–243
  - prostaglandin roles, 237, 240, 248
  - selective pressures and adaptive evolution in human pregnancy and parturition, 245–246
  - two-hit hypothesis and decidual dysregulation, 208–211

### Progesterone

- evolution of function, 237

- levels across different species, 240–241
- HOX* gene expression regulation, 58–59
- myometrial quiescence maintenance in pregnancy
  - anti-inflammatory mechanisms, 183–184
  - functional decline in parturition, 190
  - overview, 182
  - prospects for study, 191–192
  - signaling, 183
  - ZEB1* induction, 184
- Prolactin, decidual expression, 244–245
- Prostaglandins
  - preterm birth role, 237, 240, 248
  - decidual prostaglandin synthesis suppression in pregnancy, 205–206
- Protein C, recurrent pregnancy loss gene defects, 224

## R

- Recurrent pregnancy loss (RPL)
- assisted reproductive technology genetic testing
    - biopsy
      - blastomere, 227–228
      - overview, 226–227
      - polar body, 227
      - trophoectoderm, 228–229
    - preimplantation genetic diagnosis, 225–226
    - preimplantation genetic screening, 225–226
  - clinical evaluation of etiology, 217–218
  - definition, 217
  - fetal aneuploidy
    - overview, 218–220
    - product of conception genetic testing, 220–222, 229
  - parental genetic testing
    - immunologic gene defects, 223–224
    - musculoskeletal gene defects, 223
    - peripheral blood karyotyping, 221, 223, 228
    - thrombophilic gene defects, 224–225
  - prospects for study, 229–230

*RET*, newborn screening for mutations, 368

*RHCE*, fetal blood group typing, 316, 321

*RHD*, fetal blood group typing, 316

RPL. *See* Recurrent pregnancy loss

## S

### Saliva

- biomarkers, 391–392
- composition, 392
- transcriptomics in neonates
  - applications, 394–395
  - collection, storage, and processing, 392–394
  - Normal Core Salivary Transcriptome, 394
  - prospects, 396–397
- SERPINB5, noninvasive prenatal testing, 296

SMGT. *See* Sperm-mediated gene transfer  
SMRGT. *See* Sperm-mediated reverse gene transfer  
Sperm  
  DNA packaging, 21–27, 41–43  
  epigenetic intergenerational transfer  
    environmental effects, 47–48  
  model systems, 45  
  nutrition effects, 45–46  
  odorant training, 46–47  
  stress effects, 46  
  toxin effects, 46  
microRNA, 30, 32, 44–45  
oocyte penetration effects, 30–34  
RNA features and functions, 27–30, 43–45  
Sperm-mediated gene transfer (SMGT), 31  
Sperm-mediated reverse gene transfer (SMRGT), 31–32  
Spiral artery  
  placental defects in preeclampsia, 257–259  
  remodeling in pregnancy, 100–101, 257–259  
Spontaneous abortion. *See* Recurrent pregnancy loss  
STAT5b, progesterone effects, 189  
Syncytial nuclear aggregate. *See* Placenta

## T

T cell  
  endometrium, 202, 204, 209  
  placental extracellular vesicle interactions, 116  
  uterus and immune tolerance, 95  
TGF- $\beta$ . *See* Transforming growth factor- $\beta$   
Thyrotropin (TSH), preeclampsia levels, 264–265  
TLRs. *See* Toll-like receptors  
Toll-like receptors (TLRs), lipopolysaccharide-induced  
  preterm birth role, 208–209, 211  
Transcriptomics. *See* Amniotic fluid; Endometrium;  
  Obesity; Saliva  
Transforming growth factor- $\beta$  (TGF- $\beta$ )  
  extravillous trophoblast cell invasion regulation, 99  
  preeclampsia role, 253, 356–357  
Trophoblast  
  cell types, 96  
  extravillous trophoblast cell invasion  
    overview, 96–97  
    regulators  
      cytokines, 99–100  
      decidual cells, 97–99  
      growth factors, 100  
      hormones, 99  
      signaling, 100  
  placental extracellular vesicle deportation, 113  
  placentation defects in preeclampsia, 257  
TS. *See* Turner syndrome  
TSH. *See* Thyrotropin  
TTTS. *See* Twin–twin transfusion syndrome  
Turner syndrome (TS), amniotic fluid transcriptomics,  
  350–361

Twin–twin transfusion syndrome (TTTS), amniotic  
fluid transcriptomics, 343, 345–346, 349,  
351–352

## U

Uterus. *See* Endometrium; Placenta; Spiral artery;  
Trophoblast

## V

Vaginal microbiome. *See* Microbiome  
Vascular endothelial growth factor (VEGF)  
  extravillous trophoblast cell invasion regulation, 99  
  placental extracellular vesicle cargo, 115  
  preeclampsia  
    role, 253–257  
    therapeutic targeting, 263–264  
  recurrent pregnancy loss gene defects, 223  
  spiral artery remodeling in pregnancy, 100  
VEGF. *See* Vascular endothelial growth factor

## W

WES. *See* Whole exome sequencing  
WGS. *See* Whole genome sequencing  
Whole exome sequencing (WES)  
  fetal single-gene disorder detection  
    costs, 334  
    data reanalysis and reclassification, 336–337  
    examples, 331–332  
    expectations, 334  
    gene panels and targeted sequences, 328,  
      330–331  
    genetic counseling availability, 334  
    incidental finding management, 334–335  
    informed consent, 334  
    inherited disease considerations for extended  
      family, 336  
    next-generation sequencing strategies,  
      326–328  
    noninvasive testing, 333  
    parental samples, 336  
    privacy and confidentiality, 336  
    prospects, 337  
    technical issues and challenges, 332–333  
    variants of uncertain significance, 335–336  
Mendelian disease gene discovery and diagnosis,  
  328–330  
Whole genome sequencing (WGS)  
  fetal single-gene disorder detection  
    costs, 334  
    data reanalysis and reclassification, 336–337  
    expectations, 334  
    gene panels and targeted sequences, 328,  
      330–331

## Index

- Whole genome sequencing (WGS) (*Continued*)  
genetic counseling availability, 334  
incidental finding management, 334–335  
informed consent, 334  
inherited disease considerations for extended family, 336  
next-generation sequencing strategies, 326–328  
noninvasive testing, 333  
parental samples, 336  
privacy and confidentiality, 336  
prospects, 337  
variants of uncertain significance, 335–336  
Mendelian disease gene discovery and diagnosis, 328–330  
monogenetic disease screening in critically ill neonates  
application, 383
- benefits, 378  
diseases  
    impact and incidence, 377–378  
    types, 376–377  
overview, 375–376  
prospects, 382–386  
technique, 379–382  
variant classification scheme, 382  
Window of implantation. *See* Endometrium  
WNT3, salivary transcriptomics in neonates, 395

## Z

- ZEB1  
    miR-200 family effects, 188–190  
    progesterone induction, 184