

Index

- Acrosome – impaired acrosome reaction, 205
 Adaptation in horse breeds (genetic underpinning), 318
 Albinism, 163
 Alopecia (Linear/Areata), 166
 Arabian fading syndrome (AFS), 164–165
- Banding techniques, 2–4
 C-banding, 3
 G-banding, 3, 50
 NOR-banding, 3, 51
 Q-banding, 3, 50
 R-banding, 3, 50
 T-banding, 3, 50
- Cerebellar abiotrophy, 220–221
 Chromosome aberrations, 4
 Autosome, 4
 Gametes and embryos, 201–202
 Mosaics/chimeras, 4–5
 Numerical, 4
 Structural, 4
 X chromosome, 4
 Y chromosome, 74, 83–84
- Cervical vertebral malformation and malarticulation, 224–225
 Chromosome number - horse, 1, 50
 Chromosome size, 51–52
 Chromosome/cytogenetic analysis (services), 248–250
 Chromosomes and fertility, 200–201
 Circadian clock – mammalian, 286–288
 Circadian desynchrony, 299–301
 Circadian-immune interaction, 297–299
 Clock genes – peripheral, 290–292
 Coat color genetics, 143–151
 Base colors (Black, Chestnut, Bay, Seal Brown), 143–144
 Dilutions (Cream, Pearl, Champagne, Dun and Lavender Foal), 144–146, 164
- White spotting and depigmentation (Frame, Tobiano, Sabino, Dominant
 White, Leopard Complex, Gray, Roan and White face & legs), 146–151, 163
 Comparative map/genomics, 62, 64, 106–107
 Cryptorchidism, 204–205
 Curly coat syndrome, 165–166
 Cytogenetic map, 54–56
 Cytogenetic resources, 251
- Degenerative myeloencephalopathy, 221–223
 Dermal hypersensitivity – insect bite, 159–160
 Dermatitis – pastern chronic, 160–162
 Domestication of equids (mitochondrial basis), 315–317
- Equine breeds – genomic attributes, 108–109
 Equine genome sequence, 103–111
 functional elements, 126–127
 genes and numbers, 108
 genome assembly features, 105
 repetitive elements, 106
 special centromeres, 107
- Equine SNP genotyping array (Beadchip)
 first generation, 113–115
 second generation, 122
 Use among *Perrisodactyls*, 120–122
 Use for genomewide mapping, 115–116
 Use for mapping across breeds, 118–119
 Use for mapping complex traits, 117–118
 Use for mapping simple traits within breeds, 116–117
 Use for population genetic analysis, 119–120
- Evolution of *Equidae* – genetic basis (mitochondria), 312
- Flowsorted and microdissected chromosomes, 56
 Fluorescence in situ hybridization, 54–58
 Forensic analysis, 243–244

- Functional genomics, 125
 Biological understanding, 135–137
 Gene networks, 134
- Genetic linkage maps, 12–46
 ECA1-ECAX maps, 17–44
 IEGMW map, 16
 IHRFP map, 14
 Newmarket map, 14
 Uppsala map, 14
- Genetic testing
 diseases, 244–246
 phenotypic traits, 246–248
- Glycogen branching enzyme deficiency (GBED),
 173–174
- Horse breeds history delineation (underlying genetics),
 317
- Hyperkalemic Periodic Paralysis (HYPP), 172
- Hypotrichosis (follicular dysplasia), 165
- Idiogram, 2
- Immunodeficiency syndrome (foal), 165
- Junctional epidermolysis bullosa, 157–159
- Juvenile idiopathic epilepsy, 228–229
- Karyotype, 2, 51, 53
- Keratosis – linear, 162
- Laminitis 255–262
 Functional genomics, 255–260
 Therapy trends, 261–262
 Transcriptional profiling, 260–261
- Laryngeal neuropathy – recurrent, 233
- Lavender foal syndrome, 164, 219–220
- Major Histocompatibility Complex (MHC), 93–94
- Malignant hyperthermia (MH), 172–173
- Melanoma – Gray coat color, 163
- Mitochondrial genome, 5, 311–319
- Molecular map of equine MHC, 94–95
- Monogenic trait mapping using linkage map, 45
- mtDNA and diversity, 6
- mtDNA and phylogenetics, 6
- Myoclonus – inherited, 227–228
- Narcolepsy, 231–223
- Navicular disease, 194
- Nuclear genome, 1
- Occipitoatlantoaxial malformation, 229–231
- Optimum racing distance – GWAS (in Thoroughbreds),
 275
- Osteochondrosis (OC), 187–188
 Gene expression and candidate genes, 192–194
 Heritability and genetic correlation, 188–191
 Quantative trait loci for OC, 191–192
- Parentage analysis, 241–243
- Performance – athletic, 265–278
 Circadian regulation of, 292–297
 Functional genomics and proteomics, 276
 Genetic variation impacting (in Thoroughbreds),
 271–273
 Genomic regions under selection (in Thoroughbreds),
 269–271
 Global gene expression variation, 277
 Heritability of, 266
 Mitochondrial genes impacting (in Thoroughbreds),
 267–269
 Nuclear genes impacting, 267
- Photic headshaking, 233–234
- Physical maps, 49
- Polymorphic genetic markers, 12–13
- Polysaccharide storage myopathy – type I (PSSM),
 174–178
- Polysaccharide storage myopathy – type II (PSSM),
 178–179
- Proteome, 133–134
- Pseudoautosomal region (PAR), 82–83
- Radiation hybrid (RH) mapping, 58–62
- Recurrent exertional rhabdomyolysis, 179–181
- Regional dermal asthenia (HERDA), 156–157
- Reproduction and fertility, 199
- Sensory deafness (American Paint horse), 226–227
- Sex reversal, 5, 84–85, 201
- Shivers, 223–224
- SNP map, 108
- “Speed” gene, 273–275
- Stallion fertility – genetics of, 202–205
- Synten mapping, 58
- Transcriptome, 128
 mRNA transcriptome, 128–133
 non-coding RNA transcriptome, 133
 sperm transcriptome, 207–210
 testis transcriptome, 206–207
- White foal syndrome – lethal, 164, 217–218
- Y chromosome (ECAY), 73–101
 Y chromosome gene catalog, 77–80
 Y chromosome map, 78, 80–82
- Zoo-FISH map, 62, 63