Table II.1 DNA content in higher eukaryotes (Shapiro and Sternberg 2005)				
Species	**Genome size[1]**	**% repetitive DNA**	**% coding sequences**	**Reference**
Animals				
Caenorhabditis elegans	100 MB	16.5	14	(Stein, Bao et al. 2003)
Caenorhabditis briggsae	104 MB	22.4	13	(Stein, Bao et al. 2003)
Drosophila melanogaster	175 MB	33.7 (female) ~57 (male)[2]	<10	(Celniker, Wheeler et al. 2002; Bennett, Leitch et al. 2003)
Ciona intestinalis	157MB	35	9.5	(Dehal, Satou et al. 2002)
Fugu rubripes	365MB	15	9.5	(Aparicio, Chapman et al. 2002)
Canis domesticus	2.4GB	31	1.45	(Kirkness, Bafna et al. 2003)
Mus musculus	2.5GB	40	1.4	(Waterston, Lindblad-Toh et al. 2002)
Homo sapiens	2.9 GB	$\geq$50	1.2	(Lander, Linton et al. 2001)
Plants				
Arabidopsis thaliana	125-157 MB	13-14	21	(Initiative 2000; Bennett, Leitch et al. 2003)
Oryza sativa (indica)	466 MB	42	11.8	(Yu, Hu et al. 2002)
Oryza sativa (Japonica)	420 MB	45	11.9	(Goff, Ricke et al. 2002)
Zea mays	2.5 GB	77	1	(Meyers, Tingey et al. 2001)

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Table II.2 Different classes of annotated repetitive genome components (amplified from (Shapiro and Sternberg 2005))

Structural class	Structural or functional characteristics
Oligonucleotide motif	4 – 50 bp; protein binding or recognition sites
Homopolymeric tract	Repeats of a single nucleotide $(N)_n$
Variable nucleotide tandem repeats (VNTR)	Repeats of dinucleotides and longer sequences <100 bp that may vary in number in the tandem array: $(NN…N)_n$ (Csink and Henikoff 1998; Lindstedt 2005)
Composite elements	Composed of two or more oligonucleotide motifs, sometimes with non-specific spacer sequences; examples include palindromic operators, promoters, enhancers and silencers, replication origins, site-specific recombination sequences.
Tandem array microsatellites or simple sequence repeats (SSR)	Head-to-tail repeats of small sequence elements from 2-6 nucleotides in length; subject to frequent changes in repeat number and length; in genetic loci, expression levels tend to go down with increased microsatellite length. (Bagshaw, Pitt et al. 2008; Subirana and Messeguer 2008; Usdin 2008)
Tandem array satellites	Repeats of larger elements, typically 100-200 bp in length; satellite arrays typically contain thousands of copies; often found at centromeres. (Sharma and Raina 2005; Palomeque and Lorite 2008; Plohl, Luchetti et al. 2008; Tomilin 2008; Adega, Guedes-Pinto et al. 2009; Despons, Baret et al. 2010; Wang, Zhang et al. 2010)
Terminal inverted repeat (TIR) DNA transposons	DNA-based mobile genetic elements flanked by inverted terminal repeat sequences of ≤50 bp; may encode proteins needed for transposition; vary in length from several hundred to several thousand base pairs (Bergman and Quesneville 2007; Kapitonov and Jurka 2008; Moschetti, Chlamydas et al. 2008; Roberts, Chandler et al. 2008; Pritham 2009)
Foldback (FB) DNA transposons	DNA transposons with extensive (many kb) inverted repeats at each end (Casals, Caceres et al. 2005; Marzo, Puig et al. 2008)
Rolling circle DNA transposons (helitrons)	DNA transposons that insert from a circular intermediate by rolling circle replication; can generate tandem arrays (Zhou, Froschauer et al. 2006; Hollister and Gaut 2007; Kapitonov and Jurka 2007; Rousseau, Loot et al. 2007; Rousseau, Loot et al. 2008; Du, Fefelova et al. 2009; Yang and Bennetzen 2009)
Long terminal repeat (LTR) retrotransposons	Retroviruses and non-viral mobile elements flanked by direct terminal repeats of several hundred base pairs; insert at new locations following reverse transcription from an RNA copy into duplex DNA (Rho, Choi et al. 2007; Novikova 2009)
Long interspersed nucleotide element (LINE) retrotransposons	Mobile elements several kb in length with no terminal repeats; encode proteins involved in retrotransposition from a PolII-transcribed RNA copy by target-primed reverse transcription (Dewannieux and Heidmann 2005; Ohshima and Okada 2005; Ding, Lin et al. 2006)
Short interspersed nucleotide element (SINE) retrotransposons	Mobile elements, a few hundred base pairs in length with no terminal repeats; do not encode proteins (mobilised by LINE products from a PolIII-transcribed RNA copy) (Dewannieux and Heidmann 2005; Jurka, Kohany et al. 2005; Ohshima and Okada 2005; Wallace, Wagstaff et al. 2008)

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Table II.5 Control of bacterial protein synthesis (phase variation) and modification of protein structure (antigenic variation) by natural genetic engineering (expanded from (Wisniewski-Dye and Vial 2008))	
Phase variation by site-specific recombination	
Escherichia coli (Gammaproteobacteria intestinal flora), type I pili	(Abraham, Freitag et al. 1985; Klemm 1986)
Moraxella bovis (Gammaproteobacteria bovine pathogen), type I pili	(Marrs, Ruehl et al. 1988; Heinrich and Glasgow 1997)
Moraxella lacunata (Gammaproteobacteria human pathogen), type I pili	(Heinrich and Glasgow 1997)
Mycoplasma pulmonis (Mollicute mouse pathogen), DNA restriction and modification	(Dybvig and Yu 1994)
Pseudomonas fluorescens (Gammaproteobacteria plant pathogen), root colonization	(Dekkers, Phoelich et al. 1998; Sanchez-Contreras, Martin et al. 2002; Martinez-Granero, Capdevila et al. 2005)
Salmonella enterica serovar Typhimurium (Gammaproteobacteria mouse pathogen), flagella	(Silverman, Zieg et al. 1979; Heichman and Johnson 1990)
Clostridium difficile (Firmicute human intestinal pathogen), major cell wall protein	(Emerson, Reynolds et al. 2009)
Campylobacter fetus (Epsilonprotebacteria human pathogen), surface layer protein	(Tu, Ray et al. 2001)
Developmental activation of expression by site-specific excision from interrupted coding sequences in terminally differentiated cells	
Bacillus subtilis SigK expression in spore mother cell	(Stragier, Kunkel et al. 1989; Popham and Stragier 1992; Sato, Harada et al. 1996; Hilbert and Piggot 2004)
Anabaena (*Nostoc*) NifD and FdxN expression in nitrogen-fixing heterocysts	(Carrasco, Ramaswamy et al. 1994; Carrasco, Buettner et al. 1995; Carrasco and Golden 1995; Carrasco, Holliday et al. 2005); (Ramaswamy, Carrasco et al. 1997; Henson, Pennington et al. 2008)
Phase variation by transposon insertion and excision	
Acidithiobacillus ferrooxidans (Gammaproteobacteria soil bacteria), iron oxidation & swarming,	(Cabrejos, Zhao et al. 1999)
Pseudoalteromonas atlanticus (Gammaproteobacteria marine biofilm organism), extracellular polysaccharide synthesis (IS492 insertion & excision)	(Bartlett, Wright et al. 1988; Bartlett and Silverman 1989) (Perkins-Balding, Duval-Valentin et al. 1999; Higgins, Carpenter et al. 2007; Higgins, Popkowski et al. 2009)
Citrobacter freundii (Gammaproteobacteria opportunistic human pathogen), capsule synthesis	(Ou, Baron et al. 1988)
Legionella pneumophila (Gammaproteobacteria human respiratory pathogen), lipopolysaccharides	(Luneberg, Zahringer et al. 1998; Luneberg, Mayer et al. 2001)

Neisseria meningitides (Betaproteobacteria human pathogen), capsule synthesis	(Hammerschmidt, Muller et al. 1996)
Shigella flexneri (Gammaproteobacterial human dysentery pathogen), cell surface markers	(Mills, Venkatesan et al. 1992)
Staphylococcus aureus (Firmicute human pathogen), extracellular polysaccharide & biofilm formation	(Kiem, Oh et al. 2004; Valle, Vergara-Irigaray et al. 2007)
Staphylococcus epidermidis (Firmicute human pathogen), extracellular polysaccharide & biofilm formation	(Ziebuhr, Krimmer et al. 1999; Conlon, Humphreys et al. 2004),
Xanthomonas oryzae (Gammaproteobacteria plant pathogen), extracellular polysaccharide & virulence	(Rajeshwari and Sonti 2000)
Phase variation by cassette-based recombination	
Geobacillus stearothermophilus (Firmicute soil bacterium), S-Layer proteins	(Scholz, Riedmann et al. 2001)
Antigenic variation by cassette-based recombination	
Borrelia burgdorferi (lyme disease Spirochaete), surface lipoproteins	(Zhang and Norris 1998)
Borrelia hermsi (relapsing fever Spirochaete)), surface lipoproteins	(Plasterk, Simon et al. 1985; Restrepo, Carter et al. 1994)
Helicobacter pylori (Epsilonproteobacteria gastric pathogen), outer membra proteins	(Pride and Blaser 2002; Solnick, Hansen et al. 2004)
Mycoplasma genitalium (Mollicute human pathogen), surface lipoproteins	(Iverson-Cabral, Astete et al. 2007)
Mycoplasma synoviae (Mollicute avian pathogen), surface lipoproteins	(Noormohammadi, Markham et al. 2000)
Neisseria gonorrhoea (Betaproteobacteria human pathogen), opacity protein (Opa)	(Stern, Brown et al. 1986)
Neisseria gonorrhoea (Betaproteobacteria human pathogen), type IV pili	(Howell-Adams and Seifert 2000)
Treponema pallidum (syphilis Spirochaete), major surface antigen	(Centurion-Lara, LaFond et al. 2004)
Anaplasma marginale (intracellular Rickettsial pathogen), immunodominan outer membrane protein	(Barbet, Lundgren et al. 2000; Brayton, Palmer et al. 2002)
Antigenic variation by site-specific recombination	
Bacteroides fragilis (intestinal microflora), polysaccharides	(Krinos, Coyne et al. 2001; Cerdeno-Tarraga, Patrick et al. 2005)
Campylobacter fetus (Epsilonprotebacteria opportunistic human pathogen), surface proteins	(Dworkin and Blaser 1996)
Dichelobacter nodosus (Gammaproteobacteria sheep pathogen), outer membrane proteins	(Moses, Good et al. 1995)
Mycoplasma bovis (Mollicute cattle pathogen), surface lipoproteins	(Lysnyansky, Rosengarten et al. 1996; Lysnyansky, Ron et al. 2001)
Mycoplasma penetrans (Mollicute opportunistic human pathogen), surface lipoproteins	(Horino, Sasaki et al. 2003; Horino, Kenri et al. 2009)

Mycoplasma pulmonis (Mollicute mouse pathogen), surface lipoproteins	(Bhugra, Voelker et al. 1995)
Bacteriophage Mu G tail protein	(Grundy and Howe 1984; Mertens, Klippel et al. 1988)
Plasmid R64 conjugative pilus shufflon	(Komano, Kim et al. 1994)
Other shufflons in genome sequences	(Komano 1999; Tam, Hackett et al. 2004; Tam, Hackett et al. 2005)
Antigenic variation by diversity-generating retroelements (DGRs)	
Bordetella bronchiseptica bacteriophage tail fiber	(Liu, Deora et al. 2002; Liu, Gingery et al. 2004; Guo, Tse et al. 2008)
Other DGRs in the genomes of a marine *Vibrio* virus and also in the chromosomes of a commensal "probiotic" *Bifidobacterium*, the dental spirochete *Treponema denticola*, and five different cyanobacteria.	(Doulatov, Hodes et al. 2004; Medhekar and Miller 2007)

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Table II.6. Applications of site-specific recombination to different functions in bacterial cells (Hallet and Sherratt 1997)
Integrate infecting viral genomes, which can later be excised by site-specific recombination (Groth and Calos 2004; Smith, Brown et al. 2010).
Integrate horizontally transferred DNA segments (genomic islands) (Manson and Gilmore 2006; Wilde, Mazel et al. 2008; Juhas, van der Meer et al. 2009).
Integrate and excise single-protein coding cassettes for antibiotic resistance and other cell properties into expression structures called "integrons" or (in the case of very large structures encoding diverse proteins) "super-integrons" (Hall and Collis 1995; Rowe-Magnus, Guérout et al. 1999; Rowe-Magnus, Guerout et al. 2002; Rowe-Magnus and Mazel 2002).
Separating intermediate structures in the movement of DNA transposons (Derbyshire and Grindley 1986; Brown and Evans 1991; Olorunniji and Stark 2010).
Resolve tandemly repeated chromosomes and smaller replicons into two separate molecules for proper distribution to daughter cells (Barre, Soballe et al. 2001; Sherratt, Soballe et al. 2004).
Resolve replicated telomeres on prokaryotic linear chromosomes (Kobryn and Chaconas 2001; Tourand, Lee et al. 2007; Chaconas and Kobryn 2010).
Invert DNA segments to regulate transcription (see Table II.5).
Invert DNA segments to alter protein coding sequences (see Table II.5).
Excise "DNA introns" to permit the expression of specialized functions in terminally differentiated bacterial cells (see Table II.5).

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Table II.7 Various stimuli documented to activate natural genetic engineering			
Signal or condition	**Natural genetic engineering function**	**Organism(s)**	**Reference**
Quorum pheromones	DNA release and competence for DNA uptake	Multiple bacteria	(Miller and Bassler 2001; Sturme, Kleerebezem et al. 2002; Spoering and Gilmore 2006)
Chitin	Competence for DNA uptake	*Vibrio cholerae*	(Meibom, Blokesch et al. 2005)
Various stress conditions	Competence for DNA uptake	Gram-positive bacteria	(Claverys, Prudhomme et al. 2006)
DNA damage	Recombination and mutator polymerases (SOS response)	*Escherichia coli, Bacillus subtilis* and other bacteria	(Sutton, Smith et al. 2000; Au, Kuester-Schoeck et al. 2005)
DNA damage	Prophage excision	*E. coli, B. subtilis* and other bacteria	(Goranov, Kuester-Schoeck et al. 2006; Rokney, Kobiler et al. 2008).
DNA damage	Horizontal transfer of integrated conjugative (ICE) elements	Multiple bacteria	(Beaber, Hochhut et al. 2004; Auchtung, Lee et al. 2005).
DNA damage	ISDra2 transposition	*Deinococcus radiodurans*	(Pasternak, Ton-Hoang et al. 2010)
DNA damage	Genetic exchange	*Helicobacter pylori*	(Dorer, Fero et al. 2010)
UV irradiation	Tn10 transposition	*E. coli*	(Eichenbaum and Livneh 1998)
Oxidative stress	SOS responses, prophage induction	Multiple bacteria	(Giuliodori, Gualerzi et al. 2007; Selva, Viana et al. 2009)
Chemical damage	SOS response	*E. coli, Salmonella typhimurium*	(Mersch-Sundermann, Mochayedi et al. 1993; Mersch-Sundermann, Rosenkranz et al. 1994; Mersch-Sundermann, Schneider et al. 1994)
Antibiotic	SOS response	*E. coli*	(Phillips, Culebras et al. 1987; Miller, Thomsen et al. 2004)
Antibiotic	Competence for DNA uptake	*Staphylococcus aureus*	(Prudhomme, Attaiech et al. 2006)
Antibiotic	Prophage excision	*Staphylococcus aureus*	(Goerke, Köller et al. 2006)
Antibiotic (beta lactam)	SOS response and horizontal DNA transfer	*Staphylococcus aureus*	(Maiques, Ubeda et al. 2006)
Antibiotic	Mutator polymerase	*E. coli*	(Pérez-Capilla, Baquero et al. 2005)

Tetracycline	CTnDOT excision and conjugal transfer	*Bacteroides sp.*	(Moon, Shoemaker et al. 2005)
Quorum pheromones, plant metabolites (opines)	Conjugal transfer	*Agrobacterium tumefaciens*	(Fuqua and Winans 1994)
Plant phenolics	T-DNA transfer to plant cell	*A. tumefaciens*	(Gelvin 2006)
Magnetic fields	Tn5 transposition	*E. coli*	(Chow and Tung 2000)
Magnetic fields	Tn10 transposition	*E. coli*	(Del Re, Garoia et al. 2003; Del Re, Bersani et al. 2004)
Heat shock	F plasmid transfer	*E. coli*	(Zahrl, Wagner et al. 2007)
Growth phase	F plasmid transfer	*E. coli*	(Will, Lu et al. 2004)
Genome reduction	Stress-induced IS elements	*E. coli*	(Posfai, Plunkett et al. 2006)
Conjugation	ISPst9 transposition	*P. stutzeri*	(Christie-Oleza, Lanfranconi et al. 2009)
Sex pheromones	Conjugation agglutinins	*Enterobacter fecaelis*	(Kozlowicz, Dworkin et al. 2006; Kozlowicz, Shi et al. 2006; Clewell 2007; Dunny 2007)
Nucleic acid precursors	Reduce competence	*Haemophilus influenzae*	(MacFadyen, Chen et al. 2001)
Aerobic starvation	Mu prophage activation	*E. coli*	(Maenhaut-Michel and Shapiro 1994) (Lamrani, Ranquet et al. 1999)
Stringent response (starvation-induced ppGpp synthesis)	Activation of IS element transcription and IS3 transposition	*Culobcter crescentus*	(Boutte and Crosson 2011)
Aerobic starvation	Tn4652 activation	*Pseudomonas putida*	(Horak, Ilves et al. 2004; Ilves, Horak et al. 2004)
Aerobic starvation	Base substitutions	*E. coli*	(Bjedov, Tenaillon et al. 2003)
Aerobic starvation	Tandem duplications and amplifications	*Salmonella enterica*	(Kugelberg, Kofoid et al. 2006)
Aerobic starvation	Plasmid transfer and replication	*E. coli*	(Peters and Benson 1995; Peters, Bartoszyk et al. 1996)
Elevated temperature	IS element activation	*Burkholderia sp.*	(Taghavi, Mergeay et al. 1997; Ohtsubo, Genka et al. 2005)

Elevated temperature and high culture density	IS4Bsu1 element	*B. subtilis*	(Takahashi, Sekine et al. 2007)
Adenine starvation	Ty1 retrotransposon activation	*Saccharomyces cerevisiaea*	(Todeschini, Morillon et al. 2005) (Servant, Pennetier et al. 2008)
DNA damage (radiation or carcinogen)	Ty1 retrotransposon activation	*S. cerevisiaea*	(Bradshaw and McEntee 1989; Sacerdot, Mercier et al. 2005; Stoycheva, Massardo et al. 2007)
Telomere erosion	Ty1 retrotransposon activation	*S. cerevisiaea*	(Scholes, Kenny et al. 2003)
MAPK cascade activation during filamentous growth	Ty1 retrotransposon activation	*S. cerevisiaea*	(Conte and Curcio 2000; Morillon, Springer et al. 2000)
Oxidative conditions (H_2O_2) mediated by SREBP trancription factor	Tf2 retrotransposon activation	*Schizosaccharomyces pombe*	(Sehgal, Lee et al. 2007)
Mating pheromone	Ty3 retrotransposon activation	*S. cerevisiaea*	(Kinsey and Sandmeyer 1995)
Mating pheromone	Ty5 retrotransposon activity and transcription	*S. cerevisiaea*	(Ke, Irwin et al. 1997)
Prion formation	Genome instability	*S. cerevisaea*	(True and Lindquist 2000)
Improper cryopreservation	Ty1 retrotransposition	*S. cerevisaea*	(Stamenova, Dimitrov et al. 2008)
Nitrogen starvation	LTR retrotransposon transcription	Diatom (*P. tricornutum*)	(Maumus, Allen et al. 2009)
Aldehyde (decadienal) treatment	LTR retrotransposon transcription	Diatom (*P. tricornutum*)	(Maumus, Allen et al. 2009)
DNA damage (Mitomycin C)	Transposon and retrotransposon activation	*Drosophila melanogaster*	(Georgiev, Korochkina et al. 1990)
DNA damage	Alu retransposition	*Homo sapiens*	(Hagan, Sheffield et al. 2003)
Gamma irradiation	LINE-1 retrtransposition	*Homo sapiens* (human osteosarcoma cells)	(Farkash, Kao et al. 2006)
Benzpyrene	LINE-1 retrotransposition	*Homo sapiens* (HeLa cells)	(Stribinskis and Ramos 2006)

Steroid hormones	Mouse mammary tumor virus (MMTV) activation	*Mus musculus*	(Truss, Chalepakis et al. 1992)
Plant alarm chemicals	Retrotransposon activation	*Nicotiana tabacum*	(Beguiristain, Grandbastien et al. 2001)
Free radical-generating agents, UVC or rose Bengal (RB)	Increased homologous recombination, systemically transmitted	Tobacco	(Filkowski, Yeoman et al. 2004)
Hydrostatic pressure	MITE DNA transposons	rice	(Lin, Long et al. 2006)
Cutting/wounding	Retrotransposon activation	*N. tabacum*	(Sugimoto, Takeda et al. 2000)
Protoplasting & growth in tissue culture	Transposon and retrotransposon activation	various plants	(Hirochika 1993; Huang, Zhang et al. 2009)
Protoplasting & growth in tissue culture	Tos17 retrotransposon activation	rice	(Hirochika, Sugimoto et al. 1996)
Growth in tissue culture	mPing transposition	rice	(Ngezahayo, Xu et al. 2009)
Cell culture growth	1731 LTR retrotransposon	*D. melanogaster*	(Maisonhaute, Ogereau et al. 2007)
Cell culture growth	LINE-1 element retrotransposition	Mouse cell line	(Moran, Holmes et al. 1996)
Fungal metabolites	TnT1 retrotransposon	*Nicotiana tabacum*	(Melayah, Bonnivard et al. 2001)
Chlorine ions (not sodium)	DNA strand breaks and recombination	*Arabidopsis thaliana*	(Boyko, Hudson et al. 2006; Boyko, Golubov et al. 2010)
Nickel, Cadmium and other heavy metals	LINE-1 retrotransposition	*Homo sapiens* tissue culture cells	(El-Sawy, Kale et al. 2005; Kale, Moore et al. 2005; Kale, Carmichael et al. 2006)
Temperature and day length	Homologou recombination	*Arabidopsis thaliana*	(Boyko, Filkowski et al. 2005)
Helicobacter pylori infection	Adenocarcinoma with microsatellite instability	human gastric mucosa	(Tahara 2004) (Li, Shi et al. 2005) (Moriichi, Watari et al. 2009)
Fungal or virus infection	(CT)n microsatellite contraction	wheat	(Schmidt and Mitter 2004) (Kovalchuk, Tryndyak et al. 2007)
Barley stripe mosaic virus (*Peronospora*	Increased somatic recombination and	*Arabidopsis*, maize	(Kovalchuk, Kovalchuk et al. 2003)

parasitica) infection	transposon activation; transmissible systemic response in tobacco	and tobacco	
Tobacco mosaic virus and oilseed rape mosaic virus infection	Increased somatic recombination (transmissible systemic response)	Tobacco, *Arabidopsis thaliana*	(Dong 2004; Boyko, Kathiria et al. 2007)
Temperature	Amplification/reduction in repetitive elements	*Festuca arundinacea* (Tall Fescue)	(Ceccarelli, Esposto et al. 2002)
Elevation and moisture	BARE-1 retrotransposition	*Hordeum spontaneum* (wild barley)	(Kalendar, Tanskanen et al. 2000)
Heat shock, toxic chemicals	SINE transcription	*Bombyx morii*	(Kimura, Choudary et al. 1999; Kimura, Choudary et al. 2001)
Various stress conditions	SINE transcription	*H. sapiens*	(Li and Schmid 2001)
Heat shock	B1 SINE transcription	*M. musculus*	(Li, Spearow et al. 1999)
Industrial air pollution	Microsatellite expansion	*M. musculus*	(Somers, Yauk et al. 2002)
Particulate air pollution	Germ-line mutations	Mouse	(Yauk, Polyzos et al. 2008)
Chemical mutagens and etoposide	Microsatellite expansion	*M. musculus*	(Vilarino-Guell, Smith et al. 2003)
Diet (extra folic acid, vitamin B12 choline, and betaine)	IAP retrotransposon at *Agouti* locus (*Avy* allele)	*M. musculus*	(Waterland and Jirtle 2003)
Lymphocyte differentiation and antigen activation	Activation of VDJ joining, somatic hypermutation and heavy chain class switching	*M. musculus* and *H. sapiens*	(Gellert 1997; Honjo, Kinoshita et al. 2002; Alt 2007)
Neuronal differentiation and exercise	LINE-1 retrotransposition	*M. musculus*	(Muotri, Chu et al. 2005; Muotri, Zhao et al. 2009); (Coufal, Garcia-Perez et al. 2009)
Hybrid dysgenesis	P factor transposon	*D. melanogaster*	(Kidwell 1985; Kidwell, Kimura et al. 1988) (Kocur, Drier et al. 1986)
Hybrid dysgenesis	I factor non-LTR	*D. melanogaster*	(Fawcett, Lister et al. 1986; Bucheton 1990; Busseau,

	retrotransposon		Chaboissier et al. 1994; Sezutsu, Nitasaka et al. 1995; de La Roche Saint Andre and Bregliano 1998; Gauthier, Tatout et al. 2000)
Hybrid dysgenesis	Hobo transposon	*D. melanogaster*	(Yannopoulos, Stamatis et al. 1987) (Simmons 1992) (Galindo, Ladeveze et al. 1995; Bazin, Denis et al. 1999; Bazin, Dejonghe et al. 2004)
Hybrid dysgenesis	Penelope retrotransposon and other transposable elements	*D. virilis*	(Scheinker, Lozovskaya et al. 1990; Zelentsova, Poluectova et al. 1999; Evgen'ev, Zelentsova et al. 2000; Lyozin, Makarova et al. 2001; Pyatkov, Shostak et al. 2002; Blumenstiel and Hartl 2005; Evgen'ev and Arkhipova 2005)
Hybrid dysgenesis	Mariner/Tc1, hAT transposons and gypsy/Ty3 LTR retrotransposons	Medfly (*Ceratitis capitata*)	(Torti, Gomulski et al. 1997; Gomulski, Torti et al. 2004)

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Table II.8 Genomic responses to changes in ploidy and interspecific hybridization in plants and animals	
Plant Taxon	**Genomic response**
Asteraceae (Compositae)	Genome expansion and retrotransposon proliferation in sunflower hybrids (Ungerer, Strakosh et al. 2009)
	Chromosomal repatterning and the evolution of sterility barriers in hybrid sunflower species (Lai, Nakazato et al. 2005)
	Rapid chromosome evolution in polyploids (Lim, Soltis et al. 2008)
Grasses	Altered methylation patterns and chromosome restructuring in hybrids (Salmon, Ainouche et al. 2005)
Potato	Genome instability in hybrids (Marfil, Masuelli et al. 2006)
Nicotiana spp. (tobacco)	Elimination of repeated DNA in a synthetic allotetraploid (Skalicka, Lim et al. 2005)
Rice	Extensive genomic variability induced by introgression from wild rice (Wang, Dong et al. 2005)
	LTR retrotransposon movements in rice lines introgressed by wild rice (Shen, Lin et al. 2005)
	Retrotransposon activation following introgression (Liu and Wendel 2000)
	Incompatible crosspollination leading to transgenerational mobilization of multiple transposable elements (Wang, Chai et al. 2009)
	Transpositional activation of mPing in an asymmetric nuclear somatic cell hybrid of rice and *Zizania latifolia* accompanied by massive element loss. (Shan, Ou et al. 2009)
Brassica	Rapid genome change in synthetic polyploids (Song, Lu et al. 1995)
	Large scale chromosome restructuring (Kantama, Sharbel et al. 2007)
Wheat (Feldman and Levy 2005)	Sequence loss and cytosine methylation following hybridization and allopolyploidy (Shaked, Kashkush et al. 2001)
	Rapid genome evolution following allopolyploidy (Ozkan, Levy et al. 2001)

	Parental repeat elimination in newly synthesized allopolyploids (Han, Fedak et al. 2005)
	Rapid genomic changes in interspecific and intergeneric hybrids and allopolyploids (Han, Fedak et al. 2003)
Arabidopsis	Chromosome rearrangements after allotetraploid formation (Pontes, Neves et al. 2004)
	Aneuploidy and genetic variation in the *Arabidopsis thaliana* triploid response. (Henry, Dilkes et al. 2005)
	Genomic changes in synthetic polyploids (Madlung, Tyagi et al. 2005)
Animal Taxon	**Genomic Response**
Drosophila spp.	Increased retrotransposition in interspecific hybrid (Labrador, Farre et al. 1999)
Macropus marsupials	Centromere instability in interspecific hybrids (Metcalfe, Bulazel et al. 2007)
Wallabies	Chromosome remodeling in interspecific hybrids (O'Neill, O'Neill et al. 1998)
Mouse	Amplification and double minutes in a hybrid (Brown, Strbuncelj et al. 2002)
Rice fish (*medaka*)	Chromosome elimination in an interspecific hybrid (Sakai, Konno et al. 2007)
Odontophrynus americanus (amphibian)	Chromosome instabilities and centromere dysfunction in tetraploids (Becak and Becak 1998; Becak and Kobashi 2004)

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Table II.9 RNA-based defense against viruses and plasmids in bacteria, archaea, fungi and plants	
Organism	**Reference**
Multiple bacteria and archaea CRISPRs (= Clustered Regularly Interspaced Short Palindromic Repeats)	(Horvath and Barrangou 2010; Karginov and Hannon 2010; Sorokin, Gelfand et al. 2010)
Archaea	
Crenarchael thermophiles (archaea)	(Vestergaard, Shah et al. 2008; Shah, Hansen et al. 2009)
Pyrococcus furiosus (archaea)	(Carte, Wang et al. 2008; Hale, Kleppe et al. 2008; Hale, Zhao et al. 2009)
Sulfolobus islandicus (archaea)	(Held and Whitaker 2009)
Sulfolobus solfataricus (archaea)	(Han, Lehmann et al. 2009)
Bacteria	
C. diptheriae	(Mokrousov, Limeschenko et al. 2007)
E. coli	(Diez-Villasenor, Almendros et al. 2010)
Lactic acid bacteria	(Horvath, Coute-Monvoisin et al. 2009)
Leptospirillum group II bacteria	(Tyson and Banfield 2008)
Pseudomonas aeruginosa	(Zegans, Wagner et al. 2009)
Streptococcus thermophilus	(Deveau, Barrangou et al. 2008; Horvath, Romero et al. 2008; Mojica, Diez-Villasenor et al. 2009)
Streptococcus mutans	(van der Ploeg 2009)
Staphylococcus epidermidis	(Marraffini and Sontheimer 2008; Marraffini and Sontheimer 2010; Marraffini and Sontheimer 2010)
Thermus thermophilus	(Agari, Sakamoto et al. 2010)
Vibrio cholerae	(Chakraborty, Waise et al. 2009)
viridans streptococci	(Moore, Mason et al. 2008)
Xanthomonas oryzae	(Semenova, Nagornykh et al. 2009)
Yersinia pestis	(Cui, Li et al. 2008)
Yeast & Fungi	(Buhler 2009)
Saccharomyces cerevisiae (budding yeast)	(Drinnenberg, Weinberg et al. 2009)
Schizosaccharomyces pombe (fission yeast)	(Sugiyama, Cam et al. 2005; Zofall and Grewal 2006; Buker, Iida et al. 2007; Colmenares, Buker et al. 2007; White and Allshire 2008)
Neurospora crassa (fungus, bread mold)	(Cogoni and Macino 1999; Fulci and Macino 2007)
Aspergillus nidulans (fungus)	(Hammond and Keller 2005)
Plants	(Matzke and Birchler 2005; Jorgensen, Doetsch et al. 2006; Xie and Qi 2008)
Zea mays (maize) - monocot	(Hale, Erhard et al. 2009; Jia, Lisch et al. 2009; Pikaard and Tucker 2009; Sidorenko, Dorweiler et al. 2009)
Arabidopsis thaliana - dicot	(Lippman and Martienssen 2004; Martienssen, Kloc et al. 2008; Douet, Tutois et al. 2009; Grant-Downton, Le Trionnaire et al. 2009; Ha, Lu et al. 2009; Slotkin, Vaughn et al. 2009)
Tomato - dicot	(Denti, Boutla et al. 2004)
Rice - monocot	(Sunkar, Girke et al. 2005; Neumann, Yan et al. 2007); (Miki and Shimamoto 2008)
Tobacco - dicot	(Shimamura, Oka et al. 2007)
Grapevine - dicot	(Navarro, Pantaleo et al. 2009)
Conifers - gymnosperms	(Dolgosheina, Morin et al. 2008; Morin, Aksay et al. 2008)
Craterostigma plantagineum (blue gem, resurrection plant) - dicot	(Hilbricht, Varotto et al. 2008)

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Table II.10 Life history events that alter the epigenome (DNA methylation and chromatin formatting)		
Event (Organism)	**Results**	**Reference(s)**
Polyploidy (plants)	Histone acetylation changes	(Chen and Tian 2007)
Allopolyploidy (plants)	Changes in methylation patterns of mobile elements	(Dong, Liu et al. 2005)
Synthetic allotetraploids (*Arabidopsis*)	Remodeling of DNA methylation, phenotypic and transcriptional changes	(Madlung, Masuelli et al. 2002; Ha, Lu et al. 2009)
Interspecific hybrids (plants)	Altered DNA methylation patterns; Phenotypic and epigenetic variability	(Salmon, Ainouche et al. 2005; Marfil, Camadro et al. 2009)
Introgression from *Zizania latifolia* into rice	Extensive alterations in DNA methylation	(Liu, Wang et al. 2004)
Incompatible cross-pollination (rice)	Transgenerational epigenetic instability.	(Wang, Chai et al. 2009)
Tissue culture growth	Altered mPing transposon cytosine methylation	(Ngezahayo, Xu et al. 2009)
Tobacco tissue culture	Gradual and frequent epigenetic reprogramming of invertedly repeated transgene epialleles	(Krizova, Fojtova et al. 2009)
Immortalized *Arabidopsis* cell suspension culture	Euchromatin DNA hypermethylation and DNA hypomethylation of specific transposable elements	(Tanurdzic, Vaughn et al. 2008)
Antibiotics and tissue culture (tobacco)	Genome-wide hypermethylation	(Schmitt, Oakeley et al. 1997)
Rice plants subjected to space flight	Heritable hypermethylation of TEs and other sequences	(Ou, Long et al. 2009)
Interspecific hybrids (mouse)	Placental DNA methylation changes	(Schutt, Florl et al. 2003)
Interspecific hybrid (mouse)	Methylation perturbations in retroelements	(Brown, Golden et al. 2008)
Interspecific hybrids (*Peromyscus* mice)	Genomic imprinting disrupted	(Vrana, Guan et al. 1998)
Interspecific hybrids (Wallabies)	Loss of retroelement methylation	(O'Neill, O'Neill et al. 1998)
X irradiation	Transgenerational cancers and modifications in DNA methylation	(Koturbash, Baker et al. 2006)
Particulate air pollution (Mouse)	DNA global hypermethylation	(Yauk, Polyzos et al. 2008)
Nutrition (mouse)	Retrotransposon methylation in response to dietary methionine	(Waterland and Jirtle 2003)

Wolbachia endosymbiosis in *Drosophila* males	Sperm chromatin remodeling; cytoplasmic incompatibility	(Harris and Braig 2003)
Wolbachia endosymbiosis in leafhopper (*Zyginidia pullula*) males	Feminization, sterility, female-specific DNA methylation patterns	(Negri, Franchini et al. 2009)
Bacterial infection (human)	Histone modifications and chromatin remodeling (particularly immune cells)	(Arbibe 2008; Hamon and Cossa 2008)
Bacterial infection (mice)	DNA hypermethylation	(Bobetsis, Barros et al. 2007)
Fungal infection (tobacco)	Transgenerational instability	(Boyko, Kathiria et al. 2007)
Helicobacter infection (human)	LINE-1 hypomethylation	(Yamamoto, Toyota et al. 2008)
Helicobacter infection (human)	Aberrant or hypermethylation of CpG islands	(Maekita, Nakazawa et al. 2006; Nardone, Compare et al. 2007; Nardone and Compare 2008; Moriichi, Watari et al. 2009; Nakajima, Yamashita et al. 2009; Hong, Oh et al. 2010; Yoshida, Yamashita et al. 2011)
Campylobacter rectus infection of the placenta (human)	DNA methylation and histone modification changes	(Minarovits 2009)

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Table II.11 Examples of targeted natural genetic engineering		
Example	**Observed specificity (mechanism)**	**References**
DNA import and export	Special DNA uptake signals; *oriT* sites for initiating conjugal transfer replication	DNA uptake signals in bacterial transformation (Smith, Gwinn et al. 1999; Wang, Goodman et al. 2002; Findlay and Redfield 2009; Maughan, Wilson et al. 2010), *oriT* signals in conjugative plasmids and elements (Adams, Lyras et al. 2002; Grohmann, Muth et al. 2003; Parker, Becker et al. 2005; Garcillan-Barcia, Francia et al. 2009)
Homologous recombination	Special sequences stimulating DS breaks and other biochemical events in homologous exchange	(Cromie, Hyppa et al. 2007; Bagshaw, Pitt et al. 2008; Pryce and McFarlane 2009; Steiner, Steiner et al. 2009) – *Chi*-like sequences (Smith 1994; Sourice, Biaudet et al. 1998; El Karoui, Biaudet et al. 1999; El Karoui, Schaeffer et al. 2000; Halpern, Chiapello et al. 2007; Dillingham and Kowalczykowski 2008); Spo11 targets and hotspots in *S. cerevisiae* (Fukuda, Kugou et al. 2008; Nicolas 2009; Tsai, Burt et al. 2010); M26 and other recombination hotspots in *S. pombe* (Smith 1994; Cromie, Hyppa et al. 2007; Pryce and McFarlane 2009; Steiner, Steiner et al. 2009); repeats in plant and animal genomes (Mezard 2006; Buard and de Massy 2007; Coop and Myers 2007; McVean 2010)
Transposon insertions at special DNA structures	Insertion at REP palindromes (transposase specificity), DNA replication forks (interaction with processivity factor)	(Tobes and Pareja 2006); (Jomantiene, Zhao et al. 2007);(Wolkow, DeBoy et al. 1996; Nunvar, Huckova et al.) (Peters and Craig 2000; Peters and Craig 2001) (Parks, Li et al. 2009)
IS200/IS605 family target site selection	DNA sequence homology	(Barabas, Ronning et al. 2008; Guynet, Achard et al. 2009)
IS911 target site selection	InsAB transposase binding to specific DNA sequences; regulated by synthesis of InsA transposase without specificity	(Rousseau, Loot et al. 2007)
Cassette replacement/conversion in antigenic variation	DNA sequence homology at cassette boundaries	(Barbour and Restrepo 2000; Brayton, Palmer et al. 2002; Palmer, Futse et al. 2006; Palmer and Brayton 2007; Palmer, Bankhead et al. 2009)
Site-specific recombination (phase variation, antigenic variation, insertions and excisions)	Protein recognition of DNA sequence; protein-protein interaction	(Nash 1981), (Silverman, Zieg et al. 1979; Komano, Kim et al. 1994; Komano 1999)
Diversity-generating retroelements	Localized mutagenesis at duplicated segment of coding region; reverse transcription, RNA-DNA sequence homology	(Medhekar and Miller 2007; Guo, Tse et al. 2008)
Mating type cassette switching (*S. cerevisiae, S. pombe, Kluyveromyces lactis*)	Protein recognition of DNA sequence (endonuclease or transposase cleavage at unique site), DNA sequence homology at cassette boundaries	(Haber 1998; Klar, Ivanova et al. 1998; Dalgaard and Klar 1999; Haber 2006; Klar 2007; Barsoum, Martinez et al. 2010); (Rusche and Rine 2010)
Hermes transposon in	Preferential insertion in nucleosome-free	(Gangadharan, Mularoni et al. 2010)

S. cerevisiae	regions	
Immune system V(D)J joining	Cleavage at specific recombination signal sequences (recognition of RSSs by RAG1+2 transposase); flexible joining by non-homologous end joining (NHEJ) functions	(Bassing, Swat et al. 2002; Gellert 2002)
Immune system somatic hypermutation	5' exons of immunoglobulin sequences (transcriptional specificity determinants), DIVAC element to suppress repair	(Kinoshita and Honjo 2001; Inlay, Gao et al. 2006; Yang, Fugmann et al. 2006; Xiang and Garrard 2008; Blagodatski, Batrak et al. 2009)
Immune system class switching	Lymphokine-controlled choice of switch region transcription (promoter activation)	(Kinoshita and Honjo 2001; Honjo, Kinoshita et al. 2002)
Budding yeast (*S. cerevisaea*) retroviral-like elements Ty1-Ty4	Strong preference for insertion upstream of RNA polymerase III initiation sites (protein-protein interaction of integrase with RNA polymerase III factors TFIIIB and TFIIIC).	(Kirchner, Connolly et al. 1995; Kim, Vanguri et al. 1998; Bushman 2003; Bachman, Gelbart et al. 2005; Mou, Kenny et al. 2006)
Budding yeast retroviral-like element Ty1	Preference for insertion upstream of RNA polymerase II initiation sites rather than exons.	(Eibel and Philippsen 1984)
Budding yeast retroviral-like element Ty5	Strong preference for insertion in transcriptionally silenced regions of the yeast genome (protein-protein interaction of integrase targeting domain (TD) with Sir4 silencing protein). Regulated in response to stress by modulation of integrase TD protein phosphorylation.	(Zou, Ke et al. 1996; Gai and Voytas 1998; Zhu, Zou et al. 1998; Xie, Gai et al. 2001; Bushman 2003; Zhu, Dai et al. 2003; Brady, Schmidt et al. 2008); (Dai, Xie et al. 2007)
Fission yeast (*S. pombe*) retroviral-like elements Tf1 & Tf2	Insertion almost exclusively in intergenic regions (>98% for Tf1); biased towards PolII promoter-proximal sites, 100 – 400 bp upstream of the translation start by protein-protein interaction with transcription activators; prefers chromosome 3.	(Behrens, Hayles et al. 2000; Singleton and Levin 2002; Bowen, Jordan et al. 2003); (Bushman 2003; Kordis 2005; Leem, Ripmaster et al. 2008); (Chatterjee, Leem et al. 2009) (Novikova 2009) (Guo and Levin 2010)
MAGGY (fungal Ty3/gypsy family) retrotransposon	Targeting to heterochromatin by chromodomain in integrase protein	(Gao, Hou et al. 2008)
Dictyostelium discoideum non-LTR retrotransposon TRE5-A	Insertion upstream of tRNA sequences by protein-protein interactions with RNA Pol III transcription factors	(Siol, Boutliliss et al. 2006; Chung, Siol et al. 2007)
Rapidly expanding *mPing* transposons in rice	Insertion upstream of coding sequences	(Naito, Zhang et al. 2009)
Drosophila ZAM LTR retrotransposons	Site-specific insertions by protein-DNA recognition	(Faye, Arnaud et al. 2008)
Murine Leukemia	Preference for insertion upstream of	(Bushman 2003; Wu, Li et al. 2003; Mitchell,

Virus (MLV)	transcription start sites in human genome; role for IN (integrase) and GAG proteins	Beitzel et al. 2004); (Dunbar 2005; Lewinski, Yamashita et al. 2006)
HIV, SIV	Preference for insertion into actively transcribed regions of human genome; role for IN (integrase) and GAG proteins; HIV integrase interaction with LEDGF/p75 transcription factor	(Mitchell, Beitzel et al. 2004; Ciuffi, Llano et al. 2005; Dunbar 2005; Ciuffi and Bushman 2006; Ciuffi, Diamond et al. 2006; Lewinski, Yamashita et al. 2006; Llano, Saenz et al. 2006; Botbol, Raghavendra et al. 2008; Ciuffi 2008); (Engelman and Cherepanov 2008; Desfarges and Ciuffi 2010; Levin, Rosenbluh et al. 2010)
Gammaretroviral (but not lentiviral) vectors	Insertion at transcription factor binding sites; 21% recurrence rate at hotspots	(Cattoglio, Facchini et al. 2007; Deichmann, Hacein-Bey-Abina et al. 2007; Felice, Cattoglio et al. 2009)
Drosophila gypsy retrovirus	Site-specific insertion into *Ovo* locus regulatory region guided by Ovo protein binding sites	(Labrador and Corces 2001; Labrador, Sha et al. 2008)
Drosophila P-factors	Preference for insertion into the 5' end of transcripts	(Spradling, Stern et al. 1995)
Drosophila P-factors	Targeting ("homing") to regions of transcription factor function by incorporation of cognate binding site; region-specific	(Kassis, Noll et al. 1992; Taillebourg and Dura 1999; Bender and Hudson 2000) (Fauvarque and Dura 1983; Hama, Ali et al. 1990; Kassis 2002)
HeT-A and TART retrotransposons	Insertion at Drosophila telomeres	(Casacuberta and Pardue 2002; Casacuberta and Pardue 2003; Casacuberta and Pardue 2003; Pardue and DeBaryshe 2003)
R1 and R2 LINE element retrotransposons	Insertion in arthropod ribosomal 28S coding sequences (sequence-specific homing endonuclease)	(Xiong, Burke et al. 1988; Xiong and Eickbush 1988; Xiong and Eickbush 1988; Burke, Malik et al. 1989)
Group I homing introns (DNA based)	Site-specific insertion into coding sequences in bacteria and eukaryotes (sequence-specific endonuclease)	(Belfort and Perlman 1995)
Group II homing introns (RNA based)	Site-specific insertion into coding sequences in bacteria and eukaryotes (RNA recognition of DNA sequence motifs, reverse transcription)	(Mohr, Smith et al. 2000; Karberg, Guo et al. 2001)
Group II intron retroelements	Insertion after intrinsic transcriptional terminators.	(Robart, Seo et al. 2007)

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Table III.1 Examples of intercellular and interkingdom DNA transfer	
Horizontal transfer mode	**Documented transfers**
Uptake of environmental and liposomal DNA	***Bacteria – bacteria***: (Averhoff and Friedrich 2003; Claverys, Prudhomme et al. 2006; Averhoff 2009) ***Archaea-archaea***: (Bertani and Baresi 1987; Worrell, Nagle et al. 1988); (Cline, Schalkwyk et al. 1989; Patel, Nash et al. 1994; Metcalf, Zhang et al. 1997; Soppa 2006; Almeida, Leszczyniecka et al. 2008; Berkner and Lipps 2008; Soppa, Baumann et al. 2008) **Algal transfection:** (Walker, Purton et al. 2005). **Plant – bacteria:** (Kay, Vogel et al. 2002; de Vries, Herzfeld et al. 2004) **Plastid transfection:** (O'Neill, Horvath et al. 1993) **Mammalian cell transfection:** (Wolff and Budker 2005; Khalil, Kogure et al. 2006; Kim and Eberwine 2010) and **lipofection**: (Felgner 1987; Zuhorn, Kalicharan et al. 2002) **Plant protoplasts:** (Potrykus 1990; Davey, Anthony et al. 2005)
Conjugal transfer	***Bacteria – bacteria*****:** (Hayes 1968) ***Archaea – archaea*****:** (Prangishvili, Albers et al. 1998) ***Bacteria – archaea*****:** (Dodsworth, Li et al. 2010) **Bacteria – yeast**: (Heinemann and Sprague 1989; Heinemann and Sprague 1991) **Bacteria – plant**: (Winans 1992; Broothaerts, Mitchell et al. 2005)
Viral transduction and GTAs (gene transfer agents)	***Bacteria – bacteria*****:** (Stanton 2007; McDaniel, Young et al. 2010) ***Archaea -- archaea***: (Meile, Abendschein et al. 1990; Bertani 1999); (Zillig, Prangishvilli et al. 1996; Eiserling, Pushkin et al. 1999; Prangishvili 2003; Snyder, Stedman et al. 2003; Prangishvili and Garrett 2005; Prangishvili, Forterre et al. 2006; Prangishvili, Garrett et al. 2006) **Bacteria – plant:** (Chung, Vaidya et al. 2006) **Animal cell – animal cell:** (El-Aneed 2004)

	Animal cell – virus: (Filee, Pouget et al. 2008)
direct fusion of cells or protoplasts that lack a rigid outer covering.	***Bacteria -- bacteria*:** (Schaeffer, Cami et al. 1976; Hopwood, Wright et al. 1977; Patnaik, Louie et al. 2002; Dai, Ziesman et al. 2005) **Mammal -- mammal:** (Ramos, Bonenfant et al. 2002; Trontelj, Usaj et al. 2010; Yamanaka and Blau 2010) **Plant -- plant:** (Gamborg and Holl 1977; Binding, Krumbiegel-Schroeren et al. 1986; Nehls, Krumbiegel-Schroeren et al. 1986; Potrykus 1990; Fahleson and Glimelius 1999; Davey, Anthony et al. 2005; Poma, Limongi et al. 2006; Savitha, Sadhasivam et al. 2010)
Parasitic or endosymbiotic association	**Plant – fern:** (Davis, Anderson et al. 2005) **Plant – plant:** (Davis and Wurdack 2004) (Mower, Stefanovic et al. 2004) **Bacteria – invertebrate:** (Hotopp, Clark et al. 2007; Nikoh, Tanaka et al. 2008; Nikoh and Nakabachi 2009)
Undetermined mechanism	***Archaea – Bacteria***: (Woese, Olsen et al. 2000; Koonin, Makarova et al. 2001) **Bacteria – fungus:** (Belbahri, Calmin et al. 2008) **Bacteria – protist:** (Huang, Mullapudi et al. 2004; Stechmann, Baumgartner et al. 2006; Whitaker, McConkey et al. 2009) **Archaea – protist**: (Andersson, Sarchfield et al. 2005; Huang, Xu et al. 2005) **Protist – protist**: (Andersson 2005; Andersson, Sarchfield et al. 2005; Andersson, Hirt et al. 2006; Andersson, Sjogren et al. 2007; Andersson 2009; Andersson 2009)

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Table III.2 Natural genetic engineering documented in the evolution of sequenced genomes	
Rearrangement feature(s) noted	**Reference**
Pack-MULE transposons mediating coding sequence duplications and exon shuffling in rice	(Jiang, Bao et al. 2004; Hanada, Vallejo et al. 2009)
Exon shuffling by a CACTA transposon in beans (*glycine max*)	(Zabala and Vodkin 2007)
Exon shuffling and amplification by helitrons in maize	(Gupta, Gallavotti et al. 2005; Lai, Li et al. 2005; Morgante, Brunner et al. 2005; Xu and Messing 2006; Jameson, Georgelis et al. 2008)
Exon origination in coffee and Arabidopsis from transposable elements	(Lopes, Carazzolle et al. 2008)
The *Hobo* transposon involved in endemic inversions in natural *Drosophila* populations	(Lyttle and Haymer 1992)
Gross chromosome rearrangements mediated by transposable elements in *Drosophila melanogaster*; the data include natural populations	(Lim and Simmons 1994)
Generation of a widespread *Drosophila buzzatii* inversion by a transposable element; two natural hotspots and multiple other rearrangements in the *Drosophila buzzatii* genome induced by the *Gallileo* transposon	(Caceres, Ranz et al. 1999; Caceres, Puig et al. 2001; Delprat, Negre et al. 2009)
Penelope and *Ulysses* retroelements involved in *Drosophila virilis* chromosome rearrangements at natural breakpoints	(Evgen'ev, Zelentsova et al. 2000; Evgen'ev, Zelentsova et al. 2000)
Chromosome rearrangements involving two transposons	(Gray 2000)
Reviews role of hotspots in transposon-generated chromosome rearrangements	(Lonnig and Saedler 2002)
Abundance and recent occurrence of segmental duplications in the human genome	(Samonte and Eichler 2002)
Segmental duplications found at syntenic region breakpoints in human and mouse genomes	(Bailey, Baertsch et al. 2004)
Review role of transposable elements as chromosome rearrangement catalysts	(Bourque 2009; Zhao and Bourque 2009)
Richness of transposable elements in *Drosophila* pericentric heterochromatin	(Bergman, Quesneville et al. 2006)
Novel transposable element insertions found near loci encoding insecticide-metabolizing enzymes in *Drosophila*	(Chen and Li 2007)
Segmental duplication associated with a chromosome inversion in malaria mosquito vector	(Coulibaly, Lobo et al. 2007)
Dispersed LINE and SINE repeats in the human genome as substrates for ectopic homologous recombination	(Gu, Zhang et al. 2008)
Coincidence of primate syntenic breakpoints with presence of transposable elements	(Kehrer-Sawatzki and Cooper 2008)
LINE-1 elements associated with deletions in human genome variation	(Han, Lee et al. 2008)
DS breaks associated with repetitive DNA in yeast	(Argueso, Westmoreland et al. 2008)
Many inversions associated with L1 repeats	(Zhao and Bourque 2009)
Syntenic breakpoints between human and gibbon genomes showed new insertions of gibbon-specific repeats and mosaic structures involving segmental duplications, LINE, SINE, and LTR elements	(Girirajan, Chen et al. 2009)
Chromosome rearrangements by Ty element recombinations in a wild strain of yeast used for wine fermentation	(Rachidi, Barre et al. 1999)
Evolutionary breakpoints in Wallaby genome associated with SINEs, LINEs and endogenous retroviruses	(Longo, Carone et al. 2009)
P element insertions next to heat shock promoters in wild *Drosophila*	(Shilova, Garbuz et al. 2006; Haney and Feder 2009)

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