PXO Set of Recombinant Inbred Strains of the Rat: a New Strain Distribution Pattern Containing 448 Markers

(recombinant inbred strains of the laboratory rat / gene markers / strain distribution patterns)

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Abstract. A new PXO set of RIS represents a fixed F2 population derived from polydactylous (P) congenic strain SHR.*Lx* and oligodactylous (O) RI strain BXH2. The PXO strains were derived as a complementary set to current RIS (HXB, BXH) of the laboratory rat. All PXO strains are homozygous in the *Lx* allele and express different morphological phenotypes of the polydactyly-luxate syndrome (PLS) due to variable combinations of *Lx* modifying genes of either SHR or BN origin. The SDP is being built up by genotyping polymorphic microsatellite markers and several gene polymorphisms. The markers were ordered according to data from public mapping resources such as the Rat Genome Database (rgd.mcw.edu) and current SDP of the other RI strain sets (HXB, BXH). The resulting map corresponding to the common SDP of HXB, BXH RIS sets consists of 448 markers, from which 261 were proven to be polymorphic in the PXO set. The SDP of PXO strains with polymorphic markers arranged in approximately 5 cM intervals is ready for the association analysis and interval mapping in interconnection with the SDP of HXB/BXH strains.

The laboratory rat has been used in biomedical research for a long time (Gill et al., 1989). It has become a preferred model organism in the realm of complex genetics of such disorders as hypertension, non-insulin dependent diabetes mellitus, renal insufficiency, autoimmune diseases and behavioral impairments (Jacob, 1999). The role of the laboratory rat has recently been stressed in physiological genomics and pharmacogenetics (Jacob and Kwitek, 2002). The laboratory rat has been included to the group of best genetically described species within the human genome project. Moreover, the sequencing of the laboratory rat genome has been almost completed and the results are publicly available through the web-site http://hgsc.bcm.tmc.edu/projects/rat/.

The largest sets of recombinant inbred strains (RIS) of the laboratory rat (HXB/BXH) were designed for the analysis of complex trait genetics and serve as animal models of cardiovascular diseases (Pravenec et al., 1989, 1995), dyslipidemia (Bottger et al., 1996), stress-induced response (Dumas et al., 2000), and limb malformation (Křen et al., 1996). The SDP of these RIS is being continuously improved by adding new microsatellites (Pravenec et al., 1999; Jirout et al., 2003, in press) and amplified fragment length polymorphism (AFLP) markers (Bonné et al., 2003). The utility and exploitation of RIS in a wide spectrum of approaches in biomedical research has been recently reviewed by Printz et al. (2003).

The new PXO set of rat RIS was developed mainly for the purpose of morphogenetic and teratologic studies (Křen et al., 2000). PXO strains expand RI strain sets HXB and BXH by adding new combinations of Brown Norway rat (BN) and spontaneously hypertensive rat (SHR) genetic backgrounds.

The strain distribution pattern (SDP) of newly developed PXO rat RIS was constructed, in order to enable a genome-wide search for genome regions which at a given probability level contain genetic determinants for mendelian traits or quantitative trait loci (Knapp, 1991).

Material and Methods

Animals

The characteristics of the PXO set of RI strains and their progenitor BXH2 and SHR.*Lx* strains is given in Table 1.

The PXO set consists of 10 strains, 4 substrains of PXO3, PXO5, PXO7 and PXO8; 14 strains in total. All individual strains have been bred for 31–37 generations of inbreeding. The variability of phenotypic manifestation of the polydactyly-luxate syndrome is due to specific com-

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Abbreviations: BN – Brown Norway rat, PLS – polydactyly-luxate syndrome, RGD – Rat Genome Database, RIS – recombinant inbred strains, RNO – rat chromosome, SHR – spontaneously hypertensive rat, SDP – strain distribution pattern.

Table 1. Characteristics of the PXO RI strains and their progenitors: coat colour, limb phenotypes and generation of inbreeding

Strain	Coat colour	PLS phenotype			F
		FFD	HFT	HZEUG	
BXH2	Black	5T	4T	SLUX	>60
SHR.*Lx*	Albino	ND	6T-7r	NORM	>40
PXO1	Albino	5T-6r	6T	SLUX	32
PXO2	Black	ND	5T-6T	SLUX	31
PXO3a	Black	5T-6r	5T	MLUX	33
PXO3b	Albino	5T-6r	5T	MLUX	34
PXO4	Black	5T	5T	SLUX	37
PXO5a	Black	ND	5T	SLUX	34
PXO5b	Black	ND	(4)5T	SLUX	32
PXO6	Black	5T-6r	4T-5r	SLUX	30
PXO7a	Albino	5T	4T	SLUX	34
PXO7b	Albino	5T	5T	SLUX	33
PXO8a	Albino	ND	5T-6T	MLUX	33
PXO8b	Albino	ND	5T-6T	MLUX	32
PXO9	Black	5T-6r	5T	SLUX	35
PXO10	Black Hooded	5T-7r	5T-7r	NORM	35

PLS – polydactyly luxate syndrome, FFD – front feet digits, HFT – hind feet toes, HZEUG – hind zeugopod, 6T, 5T, 4T – 6, 5, 4, triphalangeal fingers, 5r, 6r, 7r – 5th, 6th, 7th rudimentarily developed finger, ND – normodactylous front feet with 4 triphalangeal digits and diphalangeal rudimentarily developed pollex, SLUX – severe zeugopod affliction, MLUX – mild zeugopod affliction, NORM – normal zeugopod, F – generation of inbreeding

binations of modifying genes of BN and SHR origin in particular RI strains. There is a continuous distribution of morphometric parameters among PXO RIS as shown on an example of tibia length in Printz et al. (2003).

Animals are kept in standardized cages, given standard diet and water ad libitum, with 12 hour light-darkness cycle. All the experimental protocols were approved by the local animal care commitee.

Genotyping

DNA from at least two animals (one male and one female) from each PXO strain and from one BXH2 and one SHR.*Lx* progenitor strain as controls was used.

Genotyping was performed by PCR in 0.2 microliter microtubes in a Techne Genius thermocycler with heated lits according to manufacturers' protocols.

Isolation of DNA and amplification conditions for individual primers were performed as described previously (Pravenec et al., 1996). PCR products were separated on 6–10% polyacrylamide gel (PAGE), detected after ethidium-bromide staining, visualized in UV light and recorded by the Insta DocTM Gel Documentation System (Biorad Laboratories, Hercules, CA). Primers for amplification of DNA anonymous microsatellite sequences were purchased from Research Genetics, Huntsville, AL, and primers for detection of the intragenic polymorphisms were synthesized on demand according to the given sequences from databases.

For SDP construction, anonymous simple sequence length polymorphism (SSLP) microsatellites differing in two to six nucleotides long CA-rich repetitions were selected from commercially available sets (Rat, Mit, Mgh series) and several intragenic polymorphisms were also included. SDP markers used were selected according to SDP of the BXH and HXB (Pravenec et al., 1999; Jirout et al., 2003) set of RIS or from mapping resources published both for high-resolution linkage maps and radiation hybrid maps (Steen et al., 1999; Watanabe et al., 1999). As data resources on microsatellite markers and their polymorphisms, databases provided by the Rat Genome Database (RGD) project (rgd.mcv.edu), The Jackson Laboratory (www.informatics.jax.org) and Ratmap (ratmap.gen.gu.se) via World Wide Web free access were mostly used.

Statistical procedures and SDP maintenance was performed using MapManager QTX v14 software (Manley and Olson, 1999).

Results and Discussion

The complete SDP of the PXO set together with the progenitor strain BXH2 is listed in Table 2. In all PXO strains, a total number of 448 microsatellite markers was mapped: 261 markers were found to be polymorphic, while 187 were of SHR origin in both progenitors and thus in all PXO strains. In chromosomes 2 and 13 only markers of SHR origin were detected in both progenitors and consequently in all PXO strains.

In the BXH2 progenitor strain and consequently in the PXO strains 1, 4, 7, 8, 9 and 10 a mutation of the D19Rat19 microsatellite was found with the PCR product of 142 bp, which is by 2 bp smaller than that of the SHR 144 bp (Bonné – personal communication).

A new mutation in a microsatellite marker D3Rat53 was found in the PXO6 strain, its PCR product being 178 bp long, which is by 4 bp smaller when compared to the B allele of the BXH2 progenitor strain (182 bp). This mutation must have arisen during the development of the PXO6 strain, more likely by a 4 bp deletion of the BN allele, the SHR allele being 156 bp long.

New mutations of microsatellite markers are also being found in mouse RIS and according to Williams et al. (2001) can be responsible for some residual heterozygosity of RIS.

Table 3 summarizes the distribution and number of markers used for the construction of the SDP on individual chromosomes. The theoretical ratio of genotypes of SHR origin is 75%, but based on actual results it yields 68%. The actual degree of heterozygosity is 4.2‰ (a fraction of total heterozygous loci and all segregating polymorphic genotypes), which means a significant improvement as compared to previous findings (Křen et al., 2000). This is in accord with the higher

Table 2. SDP of the PXO set of recombinant inbred strains

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO X	DXMit2[d)]	B	B	B	H	H	H	B	B	B	H	H	H	H	B	H	U	
RNO X	Ar	B	H	B	H	H	H	H	H	H	H	H	H	H	H	H	U	
RNO X	DXRat82	B	B	B	H	H	H	B	B	B	H	H	H	H	B	H	F	4.62
RNO X	DXMit5	B	H	B	H	H	H	H	H	H	H	H	H	H	B	B	P	14.89
RNO X	DXRat18	B	H	B	H	H	H	H	H	H	B	B	H	H	H	H	P	23.99
RNO X	DXRat19	B	B	B	B	B	H	H	H	H	B	B	B	B	H	H	F	30.90
RNO X	DXRat101	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	36.48
RNO 1	D1Rat327	B	H	H	H	H	H	H	H	B	B	B	H	H	B	B	F	6.98
RNO 1	D1Rat3	B	H	F	H	H	H	H	H	B	H	H	H	H	B	B	F	9.21
RNO 1	D1Rat186	B	H	H	H	H	H	H	H	B	H	H	H	H	B	B	F	11.45
RNO 1	D1Mgh2	B	H	H	H	H	H	H	H	B	B	B	H	H	B	B	P	15.98
RNO 1	D1Rat252	B	H	H	H	H	H	H	H	B	B	B	B	B	B	B	F	16.00
RNO 1	D1Rat14	B	B	H	H	H	H	H	H	H	B	B	H	H	B	H	P	18.27
RNO 1	D1Rat15	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	F	20.45
RNO 1	D1Rat253	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	P	20.49
RNO 1	D1Mit9	B	B	H	H	H	B	B	B	B	B	B	B	B	B	H	P	23.80
RNO 1	D1Rat18	B	B	H	H	H	B	B	B	B	B	B	B	B	B	H	P	23.88
RNO 1	D1Rat20	B	H	H	H	H	B	B	B	B	B	B	B	B	B	H	P	27.20
RNO 1	D1Rat256	B	B	H	H	H	B	B	H	B	B	B	B	B	B	H	F	28.34
RNO 1	D1Rat24	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	40.07
RNO 1	D1Rat212	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	43.41
RNO 1	D1Rat27	B	B	H	H	H	B	H	H	B	B	B	H	H	B	H	P	44.53
RNO 1	D1Rat266	B	H	H	H	H	B	H	H	B	B	B	H	H	B	H	F	46.80
RNO 1	D1Rat30	B	H	H	H	H	B	H	H	H	B	B	H	H	B	H	P	51.42
RNO 1	D1Rat268	B	B	H	H	B	B	H	H	B	H	H	H	H	B	H	F	53.79
RNO 1	D1Rat31	B	H	H	H	B	B	H	H	B	B	B	H	H	B	H	P	53.80
RNO 1	D1Arb11	B	B	B	H	H	B	H	H	B	H	H	H	H	B	H	U	
RNO 1	D1Rat35	B	B	B	B	H	B	H	H	B	H	H	H	H	B	H	P	59.42
RNO 1	D1Rat348	B	B	B	H	H	B	B	B	B	H	H	H	H	B	B	F	62.07
RNO 1	D1Rat270	B	B	B	B	H	B	B	B	B	H	H	H	H	B	B	P	65.43
RNO 1	D1Rat42	B	H	B	H	H	B	B	B	B	H	H	H	H	B	B	P	68.84
RNO 1	D1Rat273	B	H	B	B	H	B	B	B	B	H	H	H	H	B	B	F	71.12
RNO 1	C-c - albino	B	H	B	B	H	B	B	B	B	H	H	H	H	B	B	U	
RNO 1	D1Rat46	B	H	B	B	H	B	B	B	B	H	H	H	H	H	B	F	74.52
RNO 1	D1Rat47	B	B	B	H	H	B	B	B	H	H	H	H	H	H	B	F	77.90
RNO 1	D1Rat277	B	B	B	H	H	B	B	B	H	H	H	H	H	H	B	P	81.26
RNO 1	D1Rat55	B	B	B	H	H	B	B	B	H	H	H	H	H	B	B	F	83.52
RNO 1	D1Rat356	B	B	B	H	H	B	B	B	H	H	H	H	H	B	B	F	85.76
RNO 1	D1Rat155	B	B	B	H	H	B	B	B	B	H	H	H	H	B	B	P	89.12
RNO 1	Lsn	B	B	B	H	H	B	B	B	B	H	H	B	B	B	H	U	
RNO 1	D1Mit13	B	B	B	H	H	B	B	B	B	H	H	H	H	B	B	P	93.69
RNO 1	D1Rat287	B	B	B	H	H	B	B	B	B	H	H	H	H	B	B	F	94.80
RNO 1	D1Rat208	B	B	B	H	H	B	B	B	B	H	H	H	H	H	B	F	99.28
RNO 1	D1Rat69	B	B	B	H	H	B	B	B	B	H	H	H	H	H	H	F	101.51
RNO 1	D1Rat292	B	B	B	B	B	B	B	B	B	H	H	B	H	H	H	P	104.96
RNO 1	Igf2	B	B	B	B	B	B	B	B	B	H	H	B	H	H	H	P	104.96
RNO 1	D1Mit27	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	104.96
RNO 1	D1Rat293	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	106.05
RNO 1	D1Rat71	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	108.27
RNO 1	D1Rat296	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	115.40
RNO 1	D1Rat74	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	117.55
RNO 1	D1Mit34	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	125.45
RNO 1	D1Rat77	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	127.73
RNO 1	D1Rat304	B	B	B	H	H	B	H	H	B	B	B	H	H	B	H	P	130.21
RNO 1	D1Rat194	B	B	B	H	H	B	H	H	B	B	B	H	H	B	H	F	134.55
RNO 1	D1Rat235	B	B	H	H	H	B	H	H	B	B	B	H	H	B	H	P	134.59
RNO 1	D1Rat81	B	B	H	H	H	B	H	H	B	B	B	H	H	B	H	F	139.11
RNO 1	D1Rat225	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	143.59
RNO 2	D2Rat189	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	1.12
RNO 2	D2Rat124	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	7.21
RNO 2	D2Rat94	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	10.50
RNO 2	D2Rat116	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	12.75
RNO 2	D2Rat10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	15.05
RNO 2	D2Rat11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	15.05

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO 2	D2Rat197	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	17.28
RNO 2	D2Mgh14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	18.45
RNO 2	D2Rat201	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	19.57
RNO 2	D2Rat202	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	22.95
RNO 2	D2Rat320	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	27.52
RNO 2	D2Mit6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	29.45
RNO 2	D2Rat21	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	29.45
RNO 2	D2Mit5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	29.77
RNO 2	D2Rat75	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	30.90
RNO 2	D2Rat95	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	33.14
RNO 2	Cpb	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	36.52
RNO 2	D2Rat24	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	36.55
RNO 2	D2Mit17	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	37.67
RNO 2	D2Mit7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	43.38
RNO 2	D2Rat115	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	51.53
RNO 2	D2Rat147	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	54.90
RNO 2	D2Rat34	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	57.18
RNO 2	D2Mit8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	58.26
RNO 2	D2Rat222	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	58.26
RNO 2	D2Rat221	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	58.29
RNO 2	D2Rat38	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	60.52
RNO 2	D2Rat152	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	63.91
RNO 2	D2Rat42	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	70.02
RNO 2	D2Rat228	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	70.05
RNO 2	Pklr	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	71.28
RNO 2	Atp1a1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	72.76
RNO 2	D2Mgh11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	72.76
RNO 2	D2Rat234	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	72.77
RNO 2	D2Mit14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	72.93
RNO 2	D2Rat236	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	75.12
RNO 2	D2Rat54	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	78.50
RNO 2	D2Rat157	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	80.73
RNO 2	D2Rat57	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	83.01
RNO 2	D2Rat61	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	88.65
RNO 2	D2Rat62	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	90.87
RNO 2	D2Rat63	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	94.32
RNO 2	D2Rat247	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	97.65
RNO 2	D2Rat66	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	99.94
RNO 2	D2Rat67	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	102.21
RNO 2	D2Rat69	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	106.75
RNO 2	D2Rat70	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	112.48
RNO 3	D3Mit7	B	B	H	H	H	B	H	H	H	B	B	H	H	H	H	U	
RNO 3	D3Rat194	B	B	H	B	B	B	B	B	B	B	B	B	B	B	B	F	3.53
RNO 3	D3Rat53[a)]	B	H	H	B	B	H	B	B	M	B	B	B	B	B	B	P	4.62
RNO 3	D3Rat82	B	H	H	B	B	B	H	H	H	B	B	B	B	H	H	F	15.11
RNO 3	D3Rat185	B	H	H	B	B	B	B	B	B	B	B	B	B	H	H	F	32.79
RNO 3	D3Rat183	B	H	B	B	B	B	B	B	B	B	B	B	B	B	H	F	36.13
RNO 3	D3Rat180	B	H	H	B	B	B	B	B	B	B	B	H	H	B	H	F	38.38
RNO 3	D3Rat37	B	H	H	B	B	B	B	B	H	B	B	H	H	B	H	F	40.57
RNO 3	D3Rat35	B	B	H	B	B	B	B	B	H	B	B	H	H	B	H	F	42.83
RNO 3	D3Rat29	B	B	H	H	H	B	H	H	H	B	B	H	H	H	H	F	44.51
RNO 3	D3Rat173	B	B	H	H	H	B	H	H	H	B	B	H	H	H	H	F	46.19
RNO 3	D3Rat170	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	F	47.30
RNO 3	D3Mit6	B	B	H	B	B	B	H	H	B	B	B	H	H	H	H	P	48.37
RNO 3	D3Mit15	B	B	H	H	H	B	H	H	B	B	B	H	H	H	H	P	48.45
RNO 3	D3Rat166	B	B	H	H	B	B	H	H	B	B	B	B	B	H	H	F	50.66
RNO 3	D3Rat20	B	B	H	H	B	B	H	H	B	B	B	B	B	B	H	F	52.91
RNO 3	D3Mit13	B	B	B	H	B	B	B	B	B	B	B	B	B	B	B	P	54.03
RNO 3	D3Rat257	B	B	B	H	B	B	B	B	B	B	B	B	B	B	B	F	55.15
RNO 3	D3Mit14	B	B	H	H	B	B	B	B	B	B	B	B	B	B	B	P	56.27
RNO 3	D3Rat159	B	B	H	H	B	B	B	B	B	B	B	B	B	B	B	F	58.55
RNO 3	D3Rat157	B	B	B	H	B	B	B	B	B	B	B	B	B	B	B	F	60.79
RNO 3	D3Mit2	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	U	
RNO 3	D3Mit3	B	B	H	H	H	B	B	B	B	B	B	B	B	B	H	P	64.15
RNO 3	D3Rat213	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	P	67.61
RNO 3	D3Rat6	B	B	H	H	H	B	B	B	F	B	B	B	B	B	H	F	71.00

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO 3	D3Rat5	B	B	H	H	H	B	B	B	F	B	B	B	B	B	H	F	73.26
RNO 3	D3Rat143	B	B	B	H	H	B	H	B	F	B	B	B	B	B	H	F	78.86
RNO 3	D3Mgh3	B	B	B	H	H	B	B	B	H	B	B	B	B	H	H	P	80.17
RNO 3	D3Rat132	B	B	B	H	H	B	B	B	B	B	B	B	B	B	H	F	91.49
RNO 4	Il6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	0.00
RNO 4	D4Rat4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	0.04
RNO 4	D4Rat148	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	3.42
RNO 4	D4Rat7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	5.64
RNO 4	D4Rat9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	10.28
RNO 4	D4Rat10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	11.35
RNO 4	D4Rat151	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	17.08
RNO 4	D4Rat252	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	18.16
RNO 4	D4Mgh14	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	21.52
RNO 4	D4Mgh2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	21.52
RNO 4	D4Rat152	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	24.95
RNO 4	D4Rat153	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	27.20
RNO 4	D4Rat16	B	H	B	B	B	B	H	H	B	B	B	B	B	H	H	P	29.41
RNO 4	D4Rat156	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	29.45
RNO 4	D4Mgh4	B	H	B	B	B	H	B	B	H	B	B	B	B	H	H	P	37.38
RNO 4	D4Rat168	B	H	B	B	B	H	B	B	F	B	B	B	B	H	H	F	37.41
RNO 4	D4Mit5	B	H	B	B	B	H	B	B	H	B	B	B	B	H	H	U	
RNO 4	D4Mit2	B	H	B	B	B	H	H	H	B	B	B	B	B	H	H	U	
RNO 4	Hoxa11	B	H	B	B	B	H	B	B	H	B	B	B	B	H	H	U	
RNO 4	D4Rat169	B	H	B	B	B	H	B	B	F	B	B	B	B	H	H	F	40.81
RNO 4	D4Rat33	B	H	B	B	B	H	B	B	F	B	B	B	B	H	H	P	40.85
RNO 4	D4Rat35	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	44.21
RNO 4	D4Rat37	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	46.45
RNO 4	D4Rat176	B	H	H	B	B	H	H	H	B	B	B	B	B	H	H	F	49.87
RNO 4	D4Rat44	B	H	H	B	B	H	H	H	B	B	B	H	H	H	H	F	52.12
RNO 4	D4Rat235	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	57.78
RNO 4	D4Mit22	B	H	H	B	B	B	H	H	H	B	B	H	H	B	H	U	
RNO 4	D4Mit19	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	U	
RNO 4	D4Rat58	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	60.61
RNO 4	D4Rat240	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	67.93
RNO 4	D4Rat198	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	72.51
RNO 4	D4Rat137	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	75.91
RNO 4	D4Rat202	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	79.31
RNO 4	D4Rat66	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	82.71
RNO 4	D4Rat140	B	H	H	H	H	B	H	H	H	B	B	H	H	B	H	F	98.81
RNO 4	D4Rat72	B	H	H	H	H	B	H	H	H	B	B	H	H	B	H	P	102.24
RNO 5	D5Mgh1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	0.00
RNO 5	D5Mgh17	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	5.82
RNO 5	D5Rat188	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	9.18
RNO 5	D5Rat218	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	13.28
RNO 5	D5Rat126	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	15.99
RNO 5	D5Rat133	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	31.75
RNO 5	D5Rat6	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	33.98
RNO 5	D5Mit1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	36.26
RNO 5	D5Mit10	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	36.26
RNO 5	D5Rat228	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	41.22
RNO 5	D5Rat147	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	48.01
RNO 5	D5Rat149	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	53.63
RNO 5	D5Mit5	B	B	B	H	B	B	H	H	B	H	H	H	H	H	H	P	58.16
RNO 5	D5Rat196	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	58.16
RNO 5	D5Rat158	B	H	B	H	H	B	H	H	F	H	H	H	H	H	H	F	63.81
RNO 5	D5Rat169	B	H	H	B	B	H	H	H	H	H	H	H	H	H	H	F	71.77
RNO 5	D5Rat34	B	H	H	B	B	H	H	H	H	H	H	H	H	B	H	F	74.00
RNO 5	D5Rat63	B	H	H	B	B	H	H	H	H	H	H	H	H	B	H	F	78.57
RNO 5	D5Rat38	B	H	B	B	B	H	B	B	H	H	H	H	H	H	H	F	80.81
RNO 5	D5Rat174	B	H	B	B	B	H	B	B	B	H	H	B	B	H	H	F	81.92
RNO 5	D5Rat39	B	H	B	B	B	H	B	B	B	H	H	B	B	H	H	F	83.03
RNO 5	D5Rat93	B	H	B	B	B	H	B	B	B	H	H	B	B	H	H	F	85.27
RNO 5	D5Rat45	B	H	B	B	B	H	B	B	B	H	H	B	B	H	B	F	89.83
RNO 5	D5Rat245	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	99.40
RNO 5	D5Rat49	B	H	B	B	B	H	B	B	B	H	H	B	B	H	B	P	105.66
RNO 6	D6Rat46	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	1.15

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO 6	D6Rat80	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	18.40
RNO 6	D6Rat171	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	25.15
RNO 6	D6Rat84	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	28.52
RNO 6	D6Mit9	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	28.56
RNO 6	D6Rat37	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	29.63
RNO 6	D6Rat29	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	33.03
RNO 6	D6Rat28	B	B	H	B	B	B	H	H	H	H	H	H	H	H	B	F	33.05
RNO 6	D6Rat132	B	B	H	B	B	B	H	H	B	B	B	H	H	H	B	F	39.81
RNO 6	D6Rat24	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	43.13
RNO 6	D6Mit2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	52.23
RNO 6	D6Rat167	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	52.26
RNO 6	D6Rat165	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	54.50
RNO 6	D6Mit8	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	55.62
RNO 6	D6Rat87	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	56.75
RNO 6	D6Rat88	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	57.86
RNO 6	D6Rat15	B	B	B	B	B	H	B	B	B	B	B	B	B	H	B	F	58.97
RNO 6	D6Rat117	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	64.62
RNO 6	D6Rat11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	66.86
RNO 6	D6Rat184	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	70.26
RNO 6	D6Rat160	B	B	B	H	H	B	H	B	B	H	H	B	B	B	B	F	76.03
RNO 6	D6Rat111	B	H	B	H	H	H	H	H	B	H	H	B	B	B	B	P	77.27
RNO 6	D6Rat101	B	H	B	B	B	H	B	B	H	H	H	B	B	B	B	F	81.77
RNO 7	D7Mit12	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	U	
RNO 7	D7Rat35	B	B	B	B	B	H	B	B	H	B	B	B	B	B	B	F	6.83
RNO 7	D7Rat32	B	B	B	B	B	F	B	B	H	B	B	B	B	B	H	F	11.42
RNO 7	D7Rat152	B	B	H	B	B	H	B	B	H	B	B	B	B	B	H	F	17.91
RNO 7	D7Rat181	B	B	H	H	H	B	B	B	H	B	B	B	B	B	B	F	23.17
RNO 7	D7Rat103	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	F	25.40
RNO 7	D7Rat107	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	F	28.10
RNO 7	D7Rat51	B	B	H	H	H	B	B	B	H	B	B	B	B	B	H	P	31.05
RNO 7	D7Mit6	B	H	H	H	H	H	B	B	H	B	B	B	B	B	H	U	
RNO 7	D7Rat25	B	H	H	H	H	H	B	B	H	B	B	B	B	B	H	F	36.71
RNO 7	D7Rat110	B	B	B	H	H	H	B	B	H	B	B	B	B	H	H	F	44.42
RNO 7	D7Mit5	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	F	47.81
RNO 7	D7Rat20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	52.31
RNO 7	D7Rat19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	54.56
RNO 7	D7Rat17	B	H	H	H	H	H	B	B	B	B	B	B	B	H	H	F	57.96
RNO 7	D7Mit3	B	H	H	H	H	H	B	B	B	B	B	B	B	H	H	P	58.00
RNO 7	HCaRG[b)]	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	U	59.70
RNO 7	D7Rat133	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	F	60.18
RNO 7	D7Mit14	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	P	62.40
RNO 7	D7Rat131	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	F	62.43
RNO 7	D7Mit11	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	P	64.27
RNO 7	D7Rat129	B	H	H	H	H	H	B	B	H	B	B	B	B	H	H	F	64.65
RNO 7	D7Rat6	B	B	H	H	H	B	H	H	H	B	B	H	H	H	H	F	72.56
RNO 7	D7Rat196	B	B	B	H	H	B	H	H	H	B	B	H	H	H	H	F	75.99
RNO 7	D7Rat119	B	B	B	H	H	B	H	H	H	B	B	H	H	H	H	F	78.24
RNO 7	D7Rat4	B	B	B	H	H	B	H	H	H	B	B	H	H	H	H	F	80.48
RNO 7	D7Rat2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	86.21
RNO 7	Prph	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	86.21
RNO 7	D7Rat3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	86.23
RNO 8	D8Rat68	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	12.90
RNO 8	D8Rat219	B	H	H	F	B	H	H	H	B	B	B	H	H	B	H	F	27.78
RNO 8	D8Rat213	B	B	B	B	B	B	B	B	B	B	B	B	B	B	B	F	42.53
RNO 8	D8Rat135	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	50.48
RNO 8	D8Rat131	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	52.71
RNO 8	D8Rat130	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	57.27
RNO 8	Rbp2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	59.54
RNO 8	D8Rat123	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	66.27
RNO 8	D8Rat202	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	71.86
RNO 9	D9Rat88	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	5.90
RNO 9	D9Rat131	B	B	B	B	B	B	B	B	B	H	H	B	B	B	B	F	15.14
RNO 9	D9Rat159	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	F	17.63
RNO 9	D9Rat128	B	B	B	B	B	B	B	B	B	H	H	B	B	B	B	P	22.58
RNO 9	D9Rat124	B	H	B	H	H	H	H	H	B	B	B	B	B	H	B	F	37.72
RNO 9	D9Rat23	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	39.95

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO 9	D9Rat60	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	41.07
RNO 9	D9Rat156	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	43.31
RNO 9	D9Rat15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	44.42
RNO 9	D9Rat12	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	46.67
RNO 9	D9Rat171	B	B	H	H	H	B	H	H	B	H	H	H	H	H	H	F	50.08
RNO 9	D9Rat4	B	B	H	H	H	H	H	H	H	B	B	H	H	H	B	F	60.27
RNO 9	D9Mit1	B	B	H	H	H	B	H	H	H	H	H	H	H	H	B	U	
RNO 9	D9Rat153	B	H	H	H	H	B	H	H	H	B	B	H	H	H	B	F	70.47
RNO 9	D9Rat108	B	H	H	H	H	B	H	H	H	B	B	H	H	H	B	F	73.85
RNO 9	D9Rat1	B	B	H	H	H	B	H	H	H	B	H	H	H	H	B	F	79.52
RNO 10	D10Wox12	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	U	
RNO 10	Ppy	B	H	H	B	B	B	B	B	B	H	H	B	B	H	H	U	
RNO 10	D10Rat95	B	B	H	B	B	B	H	B	H	B	B	B	B	H	B	F	0.04
RNO 10	D10Rat218	B	B	H	B	B	B	H	H	H	B	B	B	B	H	B	F	4.60
RNO 10	D10Mit6	B	B	H	B	B	F	B	B	H	B	B	B	B	H	B	U	
RNO 10	D10Rat121	B	B	H	B	B	B	H	H	B	B	B	B	B	H	B	F	9.18
RNO 10	D10Rat182	B	B	H	B	B	B	H	H	B	H	H	B	B	H	B	F	17.15
RNO 10	D10Rat45	B	B	H	B	B	B	B	B	B	H	H	B	B	H	B	F	21.60
RNO 10	D10Mit5	B	H	H	H	H	H	B	B	B	B	B	B	B	B	B	U	
RNO 10	D10Rat71	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	29.52
RNO 10	D10Rat72	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	31.76
RNO 10	D10Mit4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	31.80
RNO 10	D10Rat215	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	34.00
RNO 10	D10Rat34	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	34.04
RNO 10	D10Rat33	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	35.12
RNO 10	D10Rat166	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	38.58
RNO 10	D10Rat73	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	40.82
RNO 10	D10Rat31	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	44.19
RNO 10	D10Rat32	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	44.19
RNO 10	Myh3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	44.19
RNO 10	D10Rat116	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	P	45.38
RNO 10	D10Mgh6	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	45.54
RNO 10	D10Rat30	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	46.00
RNO 10	D10Rat77	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	P	46.18
RNO 10	D10Rat161	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	46.56
RNO 10	D10Mgh7	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	U	
RNO 10	D10Wox13	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	U	
RNO 10	D10Wox4	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	U	
RNO 10	D10Rat133	B	H	B	H	H	H	B	B	B	H	H	B	B	B	H	P	46.57
RNO 10	D10Rat80	B	H	B	H	B	B	B	B	B	B	B	B	B	B	H	P	46.58
RNO 10	D10Rat69	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	46.59
RNO 10	D10Mit2	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	46.60
RNO 10	D10Rat29	B	H	B	H	H	H	B	B	B	H	H	B	B	B	H	P	46.61
RNO 10	D10Mit8	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	P	46.62
RNO 10	D10Rat59	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	U	
RNO 10	D10Rat160	B	H	B	H	H	B	B	B	B	B	B	B	B	B	H	P	46.63
RNO 10	D10Rat211	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	46.64
RNO 10	D10Rat240	B	H	B	H	B	H	B	B	B	H	H	B	B	B	H	P	46.64
RNO 10	D10Rat242	B	H	B	H	B	H	B	B	B	B	B	B	B	B	H	P	46.64
RNO 10	D10Rat28	B	H	B	H	B	H	B	B	B	H	H	B	B	B	H	P	47.61
RNO 10	D10Rat70	B	H	B	F	H	H	B	B	B	H	H	B	B	B	H	P	47.64
RNO 10	D10Rat155	B	H	B	H	H	H	B	B	B	H	H	B	B	B	H	F	47.64
RNO 10	D10Rat26	B	H	B	H	H	H	B	B	B	H	H	B	B	B	H	F	51.03
RNO 10	D10Rat24	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	52.27
RNO 10	D10Rat151	B	H	B	H	H	H	B	B	B	H	H	B	B	B	H	P	53.00
RNO 10	D10Rat93	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	57.43
RNO 10	D10Rat20	B	H	H	B	B	H	H	H	B	H	H	B	B	B	H	P	58.54
RNO 10	D10Rat145	B	H	H	B	B	H	H	H	B	H	H	B	B	B	H	P	58.54
RNO 10	D10Rat86	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	58.54
RNO 10	D10Mit7	B	H	H	B	B	B	B	B	B	H	H	B	B	H	H	P	66.50
RNO 10	D10Mit1	B	H	H	B	B	B	B	B	B	H	H	B	B	B	H	P	68.71
RNO 10	Dcp1	B	H	H	B	B	B	B	B	B	H	H	B	B	B	H	P	68.71
RNO 10	D10Rat267	B	H	H	B	B	B	B	B	B	H	H	B	B	B	H	F	78.99
RNO 10	D10Rat228	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	84.78
RNO 10	D10Rat7	B	H	B	B	B	B	B	B	B	H	H	B	B	B	H	F	87.00
RNO 10	D10Rat6	B	H	B	B	B	B	B	B	B	H	H	B	B	B	H	P	88.11

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO 10	D10Rat226	B	H	B	B	B	B	B	B	B	H	H	B	B	B	H	F	92.77
RNO 11	D11Rat28	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	2.55
RNO 11	D11Rat20	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	4.25
RNO 11	D11Rat19	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	5.95
RNO 11	D11Rat16	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	8.19
RNO 11	D11Mit1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	11.56
RNO 11	D11Rat11	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	11.59
RNO 11	D11Rat69	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	13.81
RNO 11	D11Rat7	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	19.57
RNO 11	D11Rat94	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	29.86
RNO 11	Sst	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	35.70
RNO 11	D11Rat1	B	H	H	B	B	H	B	H	B	B	B	B	B	H	H	F	38.23
RNO 11	D11Rat43	B	H	H	B	B	H	H	H	B	B	B	B	B	H	H	F	41.63
RNO 12	D12Mit8 [d)]	B	H	H	B	H	H	H	H	B	H	H	H	H	B	H	U	
RNO 12	D12Rat61	B	B	H	B	B	B	B	B	B	B	B	H	H	B	H	F	12.56
RNO 12	D12Rat10	B	H	H	B	B	H	B	B	B	H	H	B	B	H	H	F	27.27
RNO 12	D12Mit3[d)]	B	H	H	B	B	H	B	B	B	H	H	B	B	H	H	U	
RNO 12	D12Rat42	B	B	H	B	B	H	B	B	B	H	H	B	B	H	H	P	28.38
RNO 12	D12Rat14	B	H	H	H	H	H	B	B	B	H	H	B	B	H	H	F	33.03
RNO 12	D12Rat53	B	H	B	H	H	H	B	B	B	H	H	B	B	H	H	F	51.79
RNO 13	D13Rat113	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	4.57
RNO 13	D13Rat88	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	10.21
RNO 13	Ren	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	14.75
RNO 13	D13Rat126	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	19.34
RNO 13	D13Mit2	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	22.65
RNO 13	D13Mit1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	22.65
RNO 13	D13Rat62	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	22.69
RNO 13	D13Rat58	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	26.04
RNO 13	D13Mit5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	29.50
RNO 13	D13Rat32	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	30.60
RNO 13	D13Rat131	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	33.98
RNO 13	D13Mit4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	40.75
RNO 13	D13Rat152	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	40.78
RNO 14	D14Mit7[d)]	B	B	B	H	H	B	B	B	B	H	H	B	B	H	H	U	
RNO 14	D14Rat77	B	B	B	H	H	B	B	B	B	H	H	B	B	H	H	F	6.92
RNO 14	D14Rat7	B	B	B	H	H	B	B	B	B	H	H	B	B	H	H	P	14.58
RNO 14	D14Rat8	B	B	B	B	B	B	B	B	B	H	H	B	B	B	B	F	18.18
RNO 14	D14Rat13	B	B	B	B	B	B	B	B	B	H	H	B	B	B	H	F	23.82
RNO 14	D14Rat52	B	B	B	B	B	B	B	B	B	H	H	B	B	B	H	F	26.06
RNO 14	D14Mit4[d)]	B	B	B	B	B	B	B	B	B	H	H	B	B	B	H	U	
RNO 14	D14Rat64	B	B	B	B	B	B	B	B	H	H	H	B	B	B	H	F	30.53
RNO 14	D14Rat89	B	B	B	B	B	B	B	B	B	H	H	B	B	B	H	P	34.63
RNO 14	D14Rat90	B	B	B	B	B	B	B	B	B	H	H	B	B	B	H	F	34.67
RNO 14	D14Rat37	B	B	B	B	B	H	F	F	B	H	H	B	B	H	B	F	41.75
RNO 14	D14Rat38	B	H	B	H	H	B	H	B	B	H	H	B	B	H	H	F	63.96
RNO 15	D15Rat1	B	H	H	B	B	H	H	H	B	B	B	B	B	B	B	F	1.63
RNO 15	D15Mit3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	15.34
RNO 15	D15Rat6	B	B	H	H	H	H	H	H	H	H	B	H	H	H	H	F	25.62
RNO 15	D15Rat123	B	B	H	H	H	H	B	B	B	H	H	B	B	H	H	F	35.75
RNO 15	D15Rat68	B	B	H	H	H	B	B	B	H	H	B	B	B	B	H	F	39.15
RNO 15	D15Rat21	B	B	H	H	H	H	H	H	B	B	B	B	B	B	B	F	41.39
RNO 15	D15Rat98	B	B	H	H	H	H	H	H	B	H	H	B	B	B	B	F	43.62
RNO 15	D15Rat101	B	B	B	H	H	H	H	H	B	B	B	B	B	B	H	F	53.95
RNO 15	D15Rat107	B	H	H	H	H	B	B	B	B	H	H	B	B	B	H	F	65.40
RNO 16	D16Mit2[d)]	B	H	H	B	B	B	H	H	B	H	H	H	H	B	B	P	1.16
RNO 16	D16Rat41	B	H	H	B	B	B	B	B	B	H	H	H	H	B	B	P	3.40
RNO 16	D16Rat30	B	H	H	B	B	B	B	B	B	H	H	H	H	B	B	F	5.67
RNO 16	D16Mit5[d)]	B	H	H	B	B	B	B	B	B	H	H	H	H	B	B	P	5.71
RNO 16	D16Mit3[d)]	B	H	H	B	B	B	B	B	H	H	H	H	H	B	H	P	12.35
RNO 16	D16Rat3	B	H	H	B	B	B	B	B	H	H	H	H	H	B	H	P	12.35
RNO 16	D16Rat46	B	H	H	B	B	B	B	B	H	H	H	H	H	B	H	P	12.35
RNO 16	D16Rat28	B	H	B	B	B	H	B	B	H	H	H	H	H	B	B	F	22.69
RNO 16	D16Rat42	B	H	B	B	B	H	B	B	B	B	B	H	H	B	B	P	33.94
RNO 16	D16Rat37	B	H	B	B	B	H	B	B	B	B	B	H	H	B	B	P	38.52
RNO 16	D16Rat14	B	H	B	B	B	H	B	B	B	B	B	H	H	B	B	P	38.59
RNO 16	D16Rat15	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	45.50

Chromosome	Marker	BXH2	PXO1	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10	Type	Position in RGD (cM)
RNO 17	Drd1a	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	8.30
RNO 17	D17Rat144	B	H	H	B	B	B	B	B	B	H	H	B	B	B	B	F	25.57
RNO 17	D17Mit2[d)]	B	H	H	B	B	B	B	B	B	B	B	B	B	B	B	P	25.62
RNO 17	D17Rat17	B	H	H	B	B	B	B	B	B	B	B	B	B	B	B	F	28.16
RNO 17	Chrm3	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	32.62
RNO 17	D17Rat151	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	32.66
RNO 17	D17Rat39	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	36.04
RNO 17	D17Rat62	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	42.35
RNO 17	D17Rat50	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	47.56
RNO 18	D18Rat112	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	2.48
RNO 18	D18Mit1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	3.61
RNO 18	Ttr	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	3.61
RNO 18	D18Rat29	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	5.88
RNO 18	D18Rat47	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	9.29
RNO 18	D18Rat103	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	11.54
RNO 18	D18Rat97	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	16.04
RNO 18	Grl	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	G	17.16
RNO 18	D18Rat57	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	21.67
RNO 18	D18Rat55	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	22.79
RNO 18	D18Rat41	B	H	H	B	B	H	H	H	H	B	B	H	H	H	H	F	25.02
RNO 18	D18Mit10[d)]	B	H	H	H	H	H	B	B	B	B	B	H	H	H	H	U	
RNO 18	D18Mit8[d)]	B	H	H	H	H	H	B	B	B	B	B	H	H	H	H	P	32.17
RNO 18	D18Rat86	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	38.75
RNO 18	D18Rat12	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	P	43.25
RNO 19	D19Rat21	B	H	B	B	B	H	B	B	H	B	B	B	B	B	B	U	
RNO 19	D19Rat88	B	H	B	H	H	B	B	B	H	B	B	B	B	B	B	U	
RNO 19	D19Rat34	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	0.00
RNO 19	D19Rat19[c)]	M	M	H	H	nt	M	H	nt	H	M	nt	M	nt	M	M	P	2.20
RNO 19	D19Rat28	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	2.20
RNO 19	D19Rat84	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	4.52
RNO 19	D19Rat32	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	P	5.28
RNO 19	D19Rat82	B	B	H	H	H	B	B	B	B	H	H	B	B	B	B	P	6.75
RNO 19	D19Rat56	B	B	H	H	H	B	B	B	B	B	B	B	B	B	B	F	6.78
RNO 19	D19Mit2	B	B	H	H	H	B	B	B	B	H	H	B	B	B	B	U	
RNO 19	D19Rat15	B	B	H	H	H	B	B	B	B	B	B	B	B	B	B	P	11.27
RNO 19	D19Rat52	B	B	H	H	H	B	B	B	B	B	B	B	B	B	B	P	11.27
RNO 19	D19Rat75	B	H	H	H	H	H	B	B	B	B	B	B	B	B	B	P	16.87
RNO 19	D19Rat14	B	H	B	H	H	H	B	B	B	B	B	B	B	B	B	F	16.91
RNO 19	D19Rat12	B	H	B	H	H	H	B	B	H	B	B	B	B	B	B	P	20.26
RNO 19	D19Rat48	B	H	B	H	H	H	B	B	B	B	B	B	B	B	B	F	20.30
RNO 19	D19Rat46	B	H	B	H	H	H	B	B	H	B	B	B	B	B	B	P	23.65
RNO 19	D19Rat71	B	H	B	H	H	H	B	B	H	B	B	B	B	B	B	F	27.87
RNO 19	D19Rat9	B	H	B	H	H	H	B	B	H	B	B	B	B	B	B	P	29.47
RNO 19	Tat[d)]	B	H	B	H	H	H	B	B	H	B	B	B	B	B	B	U	
RNO 19	Eta[d)]	B	H	B	H	H	H	B	B	H	B	B	B	B	B	B	U	
RNO 19	D19Rat64	B	H	B	H	H	H	B	B	H	H	H	B	B	B	B	F	38.05
RNO 19	D19Rat103	B	H	B	H	B	H	B	B	H	H	H	B	B	B	B	F	44.92
RNO 20	D20Mgh5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	8.03
RNO 20	D20Rat4	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	12.65
RNO 20	D20Rat5	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	F	16.66
RNO 20	D20Rat55	B	H	B	H	H	H	H	B	B	B	B	H	H	B	B	F	34.40
RNO 20	D20Rat19	B	H	B	H	H	H	B	B	B	B	B	B	B	B	H	F	37.79
RNO 20	D20Mgh1[d)]	B	H	B	H	H	H	B	B	B	B	B	H	H	B	H	U	
RNO 20	D20Mit1	B	H	H	H	H	H	H	B	B	B	B	B	B	B	H	P	44.63

SDP legend: B – allele of BN origin in the homozygous state, H – allele of SHR origin in the homozygous state, F – heterozygosity, M – mutation – a newly discovered allele

Type: U – unknown position in public databases, ordered according to linkage in BXH and HXB sets
F – framework, P – positional. G – genes

Notices:
a) D3Rat53 in PXO6 exhibits a 4 bp deletion from the B allele of the original BXH2 progenitor
b) D7HcaRG (Solban et al., 2002) was tested in HXB and BXH and also in PXO sets by Southern blot (Tremblay J., personal communication)
c) D19Mit19 mutation found in BXH2 with the PCR product being 142 bp, which is by 2 bp smaller than that of SHR (Bonné, A., personal communication)
d) Microsatellites tested by PCR by Vacík, T., Institute of Molecular Genetics, Academy of Sciences of the Czech Republic

Table 3. Distribution and number of markers used for the construction of the SDP of PXO RIS

Chromosome	Total[a)]	BXH2		PXO		
		B[b)]	H[c)]	B[d)]	H[e)]	F[f)]
RNO X	7	6	1	26	58	0
RNO 1	51	41	10	283	430	1
RNO 2	47	0	47	0	658	0
RNO 3	29	29	0	263	139	3
RNO 4	36	20	16	125	376	3
RNO 5	25	11	14	62	287	1
RNO 6	23	6	17	49	273	0
RNO 7	29	23	6	171	234	1
RNO 8	9	2	7	19	106	1
RNO 9	17	11	6	71	167	0
RNO 10	57	42	15	373	423	2
RNO 11	12	2	10	15	153	0
RNO 12	7	7	0	46	52	0
RNO 13	13	0	13	0	182	0
RNO 14	12	12	0	115	51	2
RNO 15	9	8	1	54	72	0
RNO 16	12	11	1	85	83	0
RNO 17	9	3	6	34	92	0
RNO 18	15	5	10	32	178	0
RNO 19	22	18	4	169	139	0
RNO 20	7	4	3	30	68	0
Total	**448**	**261**	**187**	**2022**	**4221**	**14**

[a)]total number of markers on the chromosome

[b)]number of alleles of BN (B) origin in the BXH2 progenitor strain

[c)]number of alleles of SHR (H) origin in the BXH2 progenitor strain

[d)]number of genotypes of BN (B) origin in PXO strains

[e)]number of genotypes of SHR (H) origin in PXO strains

[f)]number of heterozygous (F) genotypes in PXO strains

Table 4. Percentage of common genotypes in all PXO strains compared with each other

	PXO2	PXO3a	PXO3b	PXO4	PXO5a	PXO5b	PXO6	PXO7a	PXO7b	PXO8a	PXO8b	PXO9	PXO10
PXO1	47.9	44.2	46.2	74	43.2	43.2	45.8	45	45.4	45.4	44.6	46.5	58.1
PXO2		46.3	45.6	45.1	65.1	66.7	59.1	39.8	39.4	57.9	57.1	56.4	53.3
PXO3a			91.9	47.3	46.3	44.7	46.6	37.2	36.8	45.3	44.6	37.6	54.7
PXO3b				48.4	47.1	45.6	49.4	41.9	41.5	50.8	50	40.4	52.7
PXO4					52.1	52.9	55.8	45.7	45.3	45.3	44.6	58.5	50.8
PXO5a						96.9	62.3	47.9	48.3	76.4	75.7	66.4	45.9
PXO5b							62.7	47.9	48.3	77.2	76.4	67.2	46.7
PXO6								42.3	41.9	63.2	62.5	64.8	46.2
PXO7a									98.8	58.1	58.8	52.3	41.5
PXO7b										58.5	59.2	52.7	40.4
PXO8a											99.2	58.8	42.7
PXO8b												59.6	43.5
PXO9													53.1

Table 5. Frequency of BN genotypes and recombinations within RIS polymorphic regions

Strain	Genotypes[a)]	% BN[b)]	Intervals[c)]	% Recomb.[d)]	Av. per chrom.[e)]
PXO 1	260	41.54	220	16.36	1.71
PXO 2	259	49.81	218	11.01	1.14
PXO 3a	258	39.53	217	12.44	1.29
PXO 3b	260	43.08	220	14.09	1.48
PXO 4	258	54.65	216	18.52	1.90
PXO 5a	259	67.95	218	14.68	1.52
PXO 5b	259	69.50	218	13.30	1.38
PXO 6	253	65.22	211	18.48	1.86
PXO 7a	260	61.15	220	16.36	1.71
PXO 7b	260	61.54	220	17.27	1.81
PXO 8a	260	64.62	220	10.00	1.05
PXO 8b	260	63.85	220	9.55	1.00
PXO 9	260	64.23	220	12.73	1.33
PXO 10	260	34.23	220	13.64	1.43

[a)]total number of genotypes in markers polymorphic within PXO strains without heterozygosity
[b)]percentage of informative markers of BN origin
[c)]informative intervals are pairs of neighbouring informative markers
[d)]percentage of informative intervals where recombination occured
[e)]average number of recombinations per chromosome

degree of inbreeding reached (F31-37). The number of markers analysed provides sufficient density of the SDP, so that linkage association analysis can be performed. However, for further research some intervals should be covered with more markers, eventually adding the real positions of genes involved in morphogenesis.

Table 4 characterizes the percentage of genotypes shared, displayed for each pair of strains. It was computed as a fraction of polymorphic markers in which the genotypes in the pair of compared strains were the same. Non-polymorphic markers were not calculated because these represent the shared constant SHR background common to all PXO RIS (68%). The percentage of shared genotypes in the PXO set ranges from 37.2 to 76.4%, on average 51.52%, with the exception of sublines. The closest relationship - 99.2% - was found in PXO8 sublines, which were found to be different in two markers on chromosome 1 in a short segment containing the *Igf-2* gene as was intended during production of these sublines. PXO5 sublines differ in markers on seven chromosomes, in PXO7 sublines differences were found on two chromosomes. PXO3 substrains are also highly genotypically related, with 91.2% of markers shared. The close relationship in sublines can facilitate future exclusion mapping based on phenotype differences between these substrains.

Individual strains in the PXO set were characterized by summarized information from the complete SDP in Table 5. The percentage of loci corresponding to the BN genetic background out of all segregating markers quantifies the content of the BN genetic background in each RI strain. The theoretical value is 50%. This parameter also describes the continuous distribution of genotypes within the set of RI strains. The number of informative intervals among adjacent markers had to be determined, while at the edges of chromosomes and non-segregating chromosome segments the crossover cannot be detected. The numbers of recombinations are expressed both relatively and absolutely. In mice the absolute value of 43.9 recombinations per RIS in SDP consisting of 1575 markers was reported (Williams et al., 2001), which is in accord with the Jirout et al. (2003) result (44 ± 7) in the HXB/BXH set. In our PXO set we observed 31 ± 6 recombinations per RIS, which is a significantly lower frequency as compared to the above mouse and rat RIS data. As a matter of fact, this discrepancy reflects that nearly 70% of PXO genotypes were of SHR origin and so crossovers within these segments cannot be detected.

In mice, RIS are considered as an important resource for mapping and analysing complex traits and over 100 murine RIS are currently available in the combined BXN set (Williams et al., 2001). In spite of this there has been a claim for the production of a new set of mouse RIS aimed specifically to complex trait analysis (Threadgill et al., 2002). The rationale of our PXO set derived from polydactylous, congenic strain SHR.*Lx* and oligodactylous strain BXH2 was to expand current RI strain sets HXB and BXH by adding new combinations of polydactyly-luxate syndrome-modifying genes of BN and SHR origin. The progenitors were chosen due to their extreme phenotypic display of the polydactyly-luxate syndrome (Křen et al., 1996) as well as a sharp difference in teratogen sensitivity (Bílá et al., 2000). Along with other RI strains from the HXB and BXH sets even phenotypic continuous distribution can be observed in many morphometric traits and sensitivity to teratogenic action of retinoic acid (Křen et al., 2000; Kemlink et al., unpublished results; Printz et al., 2003).

The newly constructed SDP of the PXO set will be used as the input for the association analysis in search for QTLs underlying variance in the polydactyly-luxate syndrome expression. Current SDP with markers arranged approximately in 5 cM intervals would enable an association analysis, linkage analysis and interval mapping of any polymorphic complex trait phenotype, even metabolic. A close relationship between morphogenetic and metabolic pathways has recently been strongly indicated (Gofflot et al., 2003). Triparanol-induced cholesterol deficiency in rats modified Sonic Hedgehog expression in limb buds and consequently led to limb defects. Continuous genotyping of PXO chromosomes in shorter intervals, together with mapping specific genes engaged in limb morphogenesis, is now underway.

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