Supplementary Information

Subspecific origin and haplotype diversity in the laboratory mouse

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Supplementary Tables

Supplementary Table 2. Heterozygosity in strains from the Jackson Laboratory. Strains known to be maintained segregating for specific loci were used to validate our results.

Strain	Chromosome	Size	Gene
NZL/LtJ	4	2,098,542	
129X1/SvJ	7	2,168,841	Tyroxinase
SSL/LeJ	14	5,066,720	Piebald lethal (*Ednrb*$^{s\text{-}l}$)
DLS/LeJ	9	2,573,922	Dilute lethal (*Myo5a*$^{d\text{-}1}$)
STX/Le	18	5,930,531	*Twiler & extra-toes*
ZRDCT Rax+/ChUmdJ	1,4,15	10,442,495	
RBB/DnJ	2,18	16,066,083	
TKDU/DnJ	9	21,304,291	Tk and ducky (*Cacna2d2*^{du})
CALB/RkJ	2,3,7	22,841,024	
POHN/Dh	2,7,8,11,18	27,284,945	
PN/nBSWUmaDJ	2,5	54,028,495	
MOR/RkJ	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19	1,296,933,687	

Supplementary Table 3. Summary of large deletions. The table provides the name, chromosome, start and end of the deletion.

Strain	chr	Start	End
129T2/SvEmsJ	7	26789546	26983059
22MO	16	58785367	59162675
22MO	17	92003261	92194164
A/J	16	3498121	3663403
A/WySnJ	16	3498121	3663403
AEJ/GnLeJ	10	31337689	31828662
ALR/LtJ	16	3498121	3663403
ALS/LtJ	5	5976170	6110511
BAG102	6	133567929	133716909
BAG102	17	19096681	19565308
BAG68	5	109513961	109622470
BAG94	17	19097109	19533548

BAG99	17	19097109	19565308
BAG99	19	9442678	9738804
BALB/cJ	12	90846986	90935079
BIK/g	3	14316026	14495353
BIK/g	7	112977147	113584719
BIK/g	7	112975393	113403102
BIK/g	19	13443934	13527543
BUB/BnJ	5	5976170	6109939
BULS	17	18829316	18947496
BUSNA	1	5324073	5500583
BUSNA	5	109824615	109979078
BUSNA	17	19109122	19510071
BZO	7	112977147	113584719
C3HeB/FeJ	3	155954099	156073218
C3HeB/FeJ	4	21067022	21256183
C3HeB/FeJ	8	62320953	62553663
C57BL/10J	4	36413198	36531554
C57BL/10ScNJ	4	66476208	66541144
C57BLKS/J	14	39874746	40018597
C57L/J	14	39874746	40018597
CALB/RkJ	3	14316099	14495353
CALB/RkJ	17	38954486	39143608
CBA/CaJ	15	16116242	16295795
CE/J	7	113045282	113388699
CE/J	16	3498121	3663403
CKS	17	38954486	39212402
CZECHI/EiJ	17	19096681	19533548
CZECHI/EiJ	17	38319087	38791623
CZECHII/EiJ	17	18738050	18947496
CZECHII/EiJ	17	19096681	19533548
DBA/1J	9	27279421	27390452
DCA	7	112975393	113469612
DCP	4	121156931	121352149
DCP	8	40278435	40331732
DCP	8	40463107	40610661
DCP	17	39024941	39508178
DDO	17	39604477	39961048
DDY/JclSidSeyFrkJ	12	63967814	64288042
DEB	7	112975393	113469612
DEB	17	39024941	39508178
DGA	1	104967032	105785077
DGA	6	69712532	69877897
DIK	7	112975393	113388699
DJO	17	39024941	39375698
DMZ	6	133253073	133361109
DMZ	17	39024941	39508178
DOT	2	54628242	54733214

IHOT2	15	17558592	17705803
IN13	6	60178147	60353731
IN13	6	133526024	133604193
IN13	14	46798201	49126218
IN13	17	38780263	39160050
IN17	17	38515252	38906192
IN17	17	38954486	39160050
IN25	17	38680079	39160050
IN34	6	133481479	133604193
IN40	1	141498416	141761325
IN40	17	38954486	39159773
IN47	17	38954486	39160050
IN54	17	38954486	39160050
IN59	17	38954486	39160050
IN60	17	38954486	39160050
IS/CamRkJ	7	112977147	113584093
IS/CamRkJ	11	13875124	14924150
JF1/Ms	17	19097109	19565308
KCT222	17	39604477	40017129
LEWES/EiJ	6	79531120	79621729
LEWES/EiJ	7	101371747	101504333
LEWES/EiJ	11	17875185	17942535
MBK	3	91003481	91264911
MBK	17	18736416	18947496
MBK	17	19096681	19533548
MBK	19	9442678	9738804
MBS	17	18736416	18947496
MBS	17	19096681	19533548
MBS	19	9442678	9738804
MCZ	17	18736416	18947496
MCZ	17	19096681	19533548
MDH	5	109513961	109622470
MDH	12	116517871	117101462
MGA	17	18829316	18947496
MH	3	91003481	91264911
MH	17	19203820	19533548
MPB	5	109513961	109622470
MPB	17	18736416	18947496
MPB	17	19096681	19533548
MSM/Ms	5	88533676	88729981
MSM/Ms	17	19097109	19565308
MWN1030	3	14316099	14495353
MWN1214	5	57198805	57340535
MWN1214	17	38344285	39235510
MWN1287	7	130363157	137641892
NOD/ShiLtJ	5	5976170	6110511
NOD/ShiLtJ	5	46647683	46774817

NON/ShiLtJ	12	35187221	35277533
NONcNZO10/LtJ	12	35187534	35248304
NOR/LtJ	5	5976170	6110511
NOR/LtJ	5	46660847	46774817
NU/J	8	16720269	16809203
NZB/BlNJ	1	115024591	115117350
NZL/LtJ	6	132282499	132333345
NZO/HlLtJ	6	132282499	132333345
PERC/EiJ	6	124056934	124147282
PERC/EiJ	7	113045282	113388699
PERC/EiJ	17	38993969	39159350
PWD/PhJ	17	19096681	19533548
PWK/PhJ	17	19096681	19533548
RBF/DnJ	6	133236873	133396417
RBF/DnJ	14	85377044	85452559
RBF/DnJ	17	39604477	40047429
RDS10105	17	18829722	18947496
RDS13554	17	18736416	18947496
RDS13554	17	19096681	19533548
RDS13554	17	38319087	38715993
RHJ/LeJ	8	77896113	77998982
RIIIS/J	6	41077894	41156362
RIIIS/J	17	19815399	19994147
SF/CamEiJ	17	11075251	11170687
SF/CamEiJ	19	39578103	39818227
SJL/Bm	7	81318066	82154023
SKIVE/EiJ	5	109513961	109622470
SKIVE/EiJ	12	116517871	117101462
SKIVE/EiJ	14	90734253	96127574
SKIVE/EiJ	17	19194273	19533548
SOD1/EiJ	2	151012515	151252085
SOD1/EiJ	6	60178147	60353731
SOD1/EiJ	6	133253073	133381208
STLT	6	68413276	68431196
STLT	6	130735889	130776369
STLT	17	38319087	38629680
STRA	6	41077894	41155975
STRA	6	60178147	60353731
STRA	6	68413276	68431196
STRA	6	130735889	130776369
STRA	17	38319087	38704702
STRB	6	41077894	41155975
STRB	6	60178147	60353731
STRB	6	68413276	68431196
STRB	6	133236873	133396417
STRB	17	38319087	38620190
STUF	17	19203708	19533548

STUP	3	91003481	91264911
STUP	5	109824615	109979078
STUP	10	128482322	128787461
STUP	17	19203708	19448999
STUP	17	38319087	38704702
STUS	17	18736416	18947496
STUS	17	19096681	19533548
TIRANO/EiJ	17	39604477	39961048
RDS12763	6	69103765	69310728
WLA	6	41077894	41155975
WLA	6	130735889	130776369
WLA	10	78310446	78447275
YBR/EiJ	3	14316099	14523993
YBR/EiJ	6	133236873	133361109
Yu2095m	17	19096681	19533548
Yu2097m	2	86384203	86482107
Yu2097m	17	19096681	19533548
Yu2099f	17	19096681	19533548
Yu2113m	17	19096681	19533548
Yu2115m	19	9442678	9738804
Yu2116m	3	91003481	91271991
Yu2116m	19	9442678	9738804
Yu2120f	17	19096681	19533548
ZALENDE/EiJ	6	60178147	60353731
ZALENDE/EiJ	6	133236873	133396417
ZALENDE/EiJ	17	39604514	40047429

Supplementary Table 4. Targeted resequencing of VINOs. The table provides the probes, strains and primer sequences

JAX SNP ID	Chromosome	RS Number	SNP Type	SNP Position
JAX00241414	1	rs49515493	C->G	8256154
JAX00258870	1	rs38011870	A->G	92712832
JAX00518420	3	rs37921678	T->C	30594534
JAX00567838	4	rs27620154	G->A	135478894
JAX00149491	7	rs38180668	T->C	27149947
JAX00156936	7	rs33198758	T->C	135288535

JAX00642397	7	rs33119893	C->A	75763924
JAX00649359	7	rs51088408	A->G	109702805
JAX00300473	10	rs47495555	A->C	120184726
JAX00031437	11	rs27048205	A->G	106181677
JAX00303026	11	rs26931498	G->A	5701725
JAX00376696	14	rs46005263	G->A	32912805
JAX00434064	17	rs33779364	T->C	25185359
JAX00442587	17	rs47100906	A->G	57648914
JAX00470882	19	rs38205121	C->T	12662282

JAX SNP ID	+ Probe Seq.	- Probe Seq	+ Primer Seq	- Primer Seq
JAX00241414	ACAAAGGTACCAAAGACTATCAGAT	GTACCAAAGACTATCAGATAACCAT	GCAAGGTTTGACCCATGAGTTAGG	ATTACTTGTCTGACCACCAGGACC
JAX00258870	AGAGGTTGTTTCGAACAAAGTCCAG	GTTGTTTCGAACAAAGTCCAGAGAA	AATGAAGACCAGGGAGGAGTCGAA	CCATCCAACTTCAATGCCATCCGA
JAX00518420	TTCAGGTCCATTTCTAAGTCAAGAG	GGTCCATTTCTAAGTCAAGAGGCAT	GGGAGACCTTAGTGTAGGTCATTG	TAGGGTGCGGTATCTGAACACTTG
JAX00567838	AGGTACGTCGTCCTGACCACAAAGC	GTACGTCGTCCTGACCACAAAGCAT	TCCAGTGCCTCCATCCATTCTTGA	TTCAAAGTCTGGGAGTCCATCTGC
JAX00149491	CCTCTTTTTGAGTTCATCTTCAACC	CGAACCCCCCTCTTTTTGAGTTCAT	GGGTGGAACAATGTGGAAGAACAG	AAGAAGAGGGAGGATAGATTCCCAG
JAX00156936	CTTCCAGTAAAATATGCGGTGTACA	TCCAGTAAAATATGCGGTGTACACC	TCTAAGAGCCAGAGTGGGAAGGTA	TCCTGTGGATTTGCAAGCCTTCTG
JAX00642397	CTGGTATCGTGATTATCATTTTTGG	CTGGTATCGTGATTATCATTTTTGG	TCTACTGCTTTGGCTTCTGGAGCA	TCAGCTTCATCCTTGCAGCAACTC
JAX00649359	TGGGTATGGCACCTTTTAACTACAC	GGTATGGCACCTTTTAACTACACAG	AATGATTAGGGAAGCCTAGGGCAG	GGAGGCTGCGTTCTGCAATGATTA
JAX00300473	TTGTAAATACATAGTTGCAAATCCA	CAGATTGTAAATACATAGTTGCAAA	AATTTGGGAAGCAGAGCCAGGTTG	TGCTTGGACTCAGTGGTCCTTTCT
JAX00031437	CATCTCGAAGTCATCCTCACAGAGG	CATCTCGAAGTCATCCTCACAGAGG	AGCTGCCATGAACTTCTCCTCCAT	AATATCAAGGGTGACTGCGGCAAC
JAX00303026	CATGGCCTTCCGAACCGTCTCTTCG	TCCGAACCGTCTCTTCGTCTCCCAG	ACATGGTGGCTTGGGATAGCTGTA	GCTATTCATGGAGGGTGTTCTCGT
JAX00376696	ACCAGCGAGCTCCTGTTTAAGGTAA	ACCAGCGAGCTCCTGTTTAAGGTAA	CCCTCGAAACCTCATCTTGATTGC	TACATCAGGCACTTCGGCCATACT
JAX00434064	CAACAACAGTCCTGATTCCAAAATC	AACAGTCCTGATTCCAAAATCTACA	AGTCAGGTCCAAGTCATCCAATGC	AGTAGGCACATGCTGTTCTCACCA
JAX00442587	TTATTGGCTTTCACAATCGGAGTTT	ATTGGCTTTCACAATCGGAGTTTCA	GTGATGTGGCCACGTTCATTGTGT	ACTCACTGCATCCCTAAAGCTGTG
JAX00470882	TGGTCAAACATCTTTCGAGGGTCAG	TGGTCAAACATCTTTCGAGGGTCAG	AGGTTGCAGCTGAGCTACCAAAGA	TGCCCACTCACTTGAATCTATGCC

Supplementary Table 5. Regions with low SNP density in the Mouse Diversity array.

The table provides chromosome, start, end and size of these regions.

Chr	St	End	Size
1	85038401	87557133	2518732
1	111607486	111711660	104174
1	119559242	119744063	184821
1	157953868	158106086	152218
1	184903124	185342097	438973
2	90136993	90239598	102605
2	100291153	100618204	327051
2	113708202	113826761	118559
2	172416868	172531498	114630
2	174769062	177833120	3064058
3	15318017	15673164	355147
3	64221856	64374779	152923
3	93569016	93817560	248544
3	98255367	98379481	124114
3	113038097	113236252	198155
4	3013031	3270810	257779
4	31381321	31659784	278463
4	41600463	42789171	1188708
4	60004031	61354910	1350879
4	111700710	112074888	374178
4	112576250	113820165	1243915
4	121308985	122241517	932532
4	130021854	130185532	163678
4	145000943	146709730	1708787
5	10807083	11885511	1078428
5	14907823	15184941	277118
5	25421340	26468179	1046839
5	93800488	96262456	2461968
5	143204048	143509964	305916
6	3001778	3130317	128539
6	47599746	47730360	130614
6	59521665	59914848	393183
6	69467728	69601696	133968
6	70306625	70447524	140899
6	114438359	114588610	150251
6	123334737	123584342	249605
7	3005336	3796246	790910
7	7200974	10593801	3392827
7	11418742	12041428	622686
7	15240532	16173489	932957
7	17840762	18181257	340495

7	20658198	24074680	3416482
7	32329412	33973476	1644064
7	39102616	46555960	7453344
7	48768732	48994136	225404
7	50355668	50516611	160943
7	54844281	54976185	131904
7	66600125	67512311	912186
7	113103675	113378939	275264
8	53855	3083611	3029756
8	19705589	22566216	2860627
8	56192661	57917198	1724537
8	71976282	72107430	131148
9	80253144	80357752	104608
9	88499227	89068676	569449
10	21801884	22192453	390569
10	57560116	57670381	110265
10	81222936	81484838	261902
11	60374062	60506308	132246
12	17833851	18095965	262114
12	18463233	25052669	6589436
12	36427764	36597458	169694
12	42288898	42689946	401048
12	56190168	56355696	165528
12	84558819	84715185	156366
12	88960202	89267122	306920
12	90935079	91059705	124626
13	10987222	11175635	188413
13	12702166	13451347	749181
13	17985845	18164307	178462
13	22967465	23100721	133256
13	33419209	33527486	108277
13	61557678	61795283	237605
13	65406976	68567157	3160181
13	92136900	92796094	659194
14	3262706	8514187	5251481
14	20238815	20348997	110182
14	26694506	27115802	421296
14	42004463	45349671	3345208
14	52267986	52375663	107677
14	53761534	53961634	200100
14	119185827	119398904	213077
16	3158668	3426673	268005
16	68222339	68347499	125160
16	94119461	94366944	247483
17	6257979	6909183	651204
17	13434369	13649185	214816
17	15084369	15193544	109175

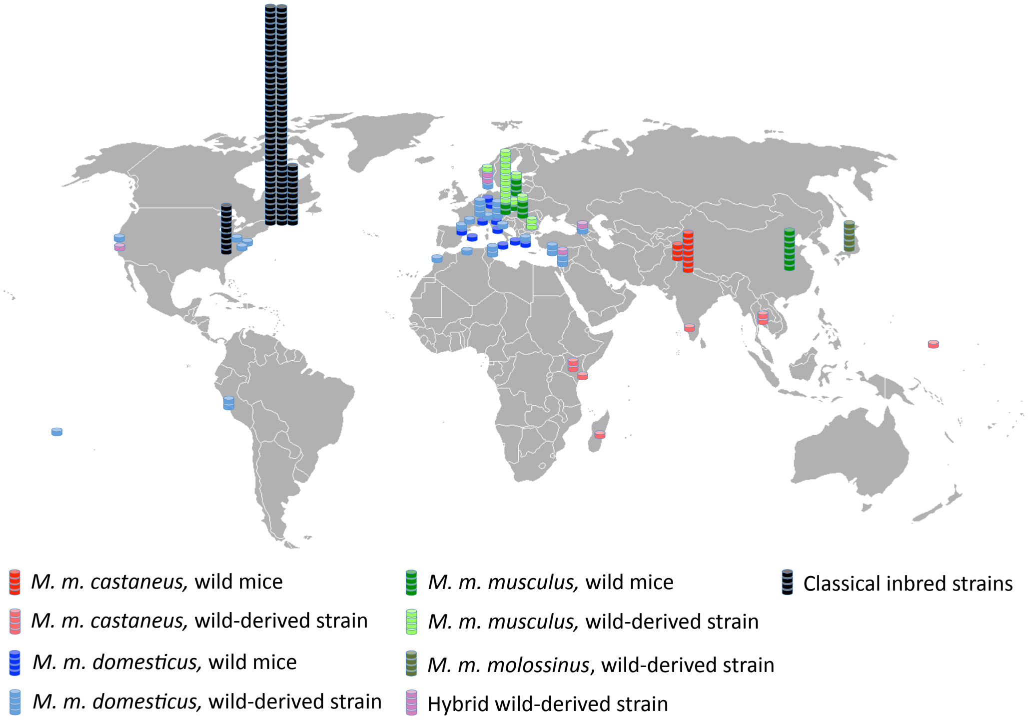
17	17154611	17328797	174186
17	33274181	33377052	102871
17	35476061	35581130	105069
17	40047429	40289604	242175
17	62216801	62328562	111761
17	93303421	93533499	230078
18	3013018	3149782	136764
18	76627770	76770221	142451
19	6677985	6889166	211181
19	9237903	9378038	140135
19	39181023	39284915	103892
20	3054629	4894504	1839875
20	22815010	33248619	10433609
20	34701743	34983849	282106
20	51313749	53061669	1747920
20	71854875	71966052	111177
20	120024406	122716250	2691844
20	124350225	124500860	150635
20	131871707	132106216	234509
20	144104004	146550583	2446579
20	150500887	150602567	101680

Supplementary Table 6. Putative structural variation. The table provides the strain, chromosome, start and end.

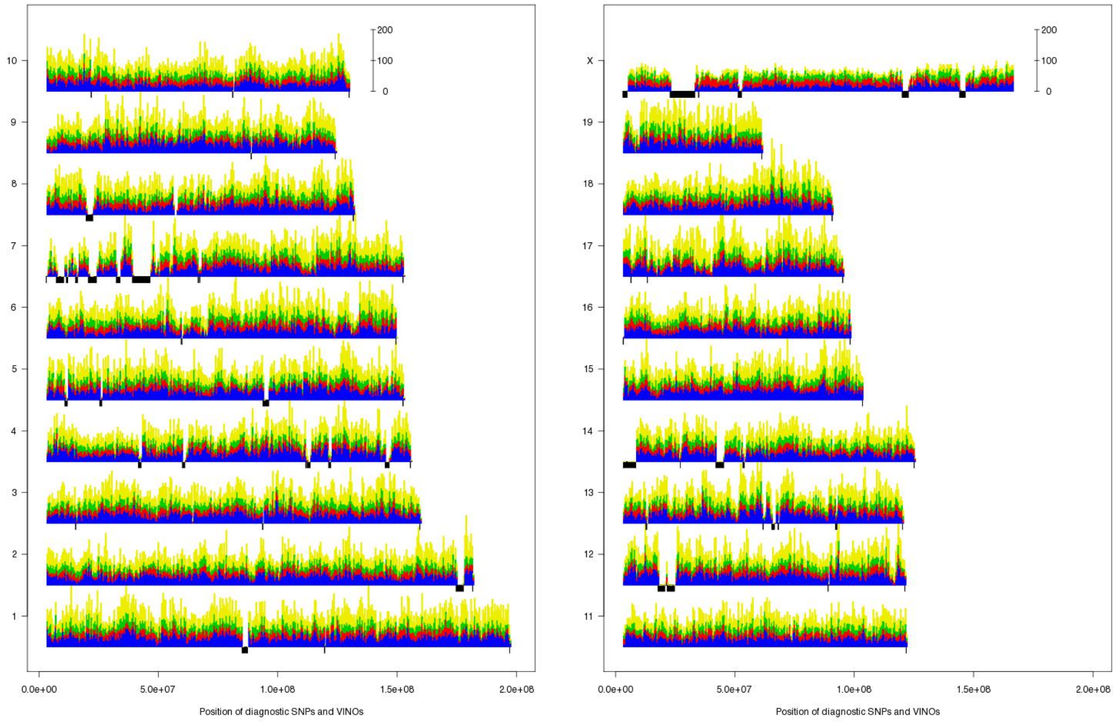
strain	Chromosome	Start	Position
KK/HIJ	10	122132584	122289929
MOLD/RkJ	10	122132584	122289929
MOLG/DnJ	10	122132584	122289929
DDK	10	122133030	122289929

Supplementary Figures

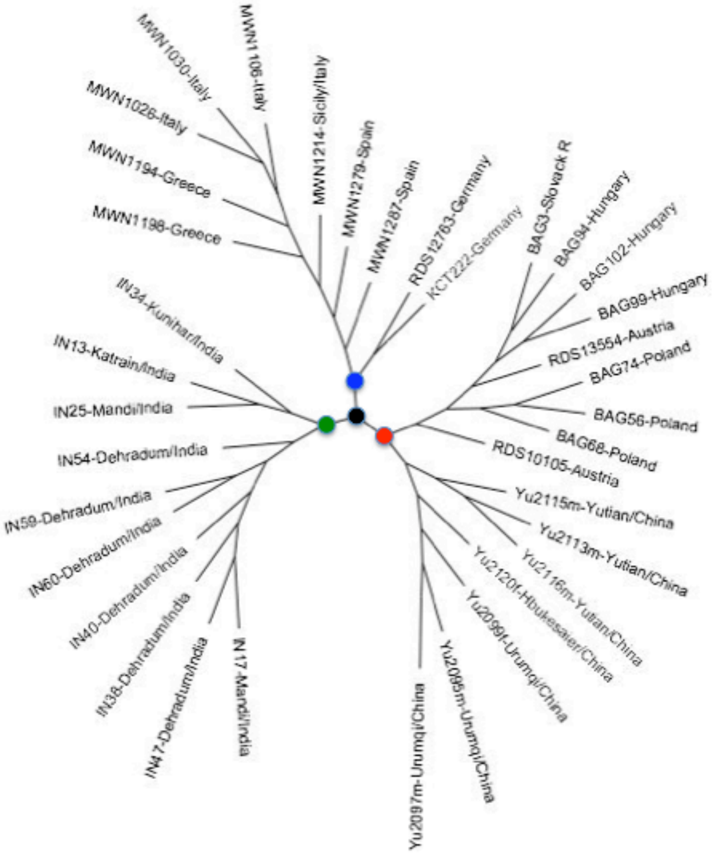
Supplementary Figure 1. Geographical origin of the samples. For classical inbred strains we indicate the provider.



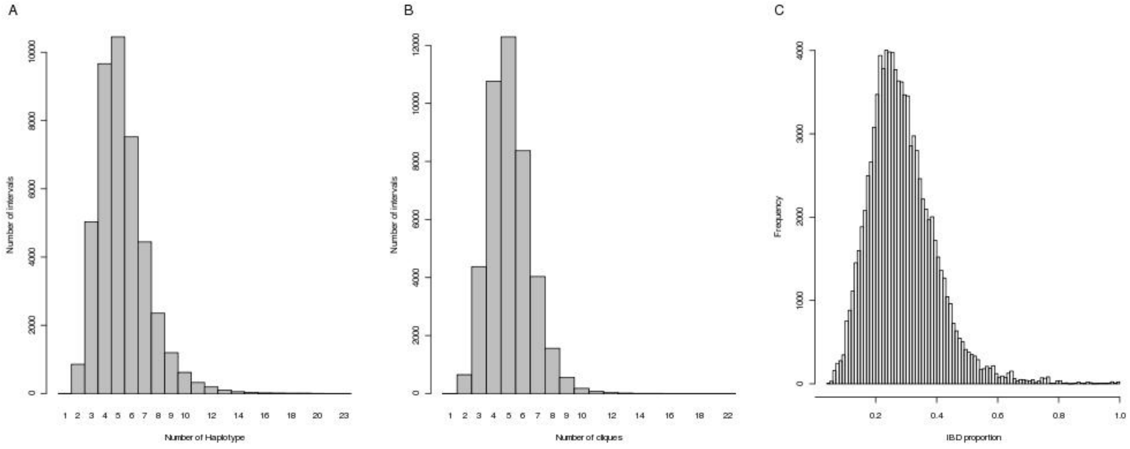
Supplementary Figure 2. Spatial distribution of SNPs and VINOs with informative alleles. Each vertical bar represent the number of informative SNPs and VINOs in 500kb windows for the *M. m. domesticus* (blue), *M. m. musculus* (red) and *M. m. castaneus* (green) subspecies. The black thick horizontal lines represent regions of the genome without SNP markers. Yellow bars represent the number of non-informative SNPs and VINOs.



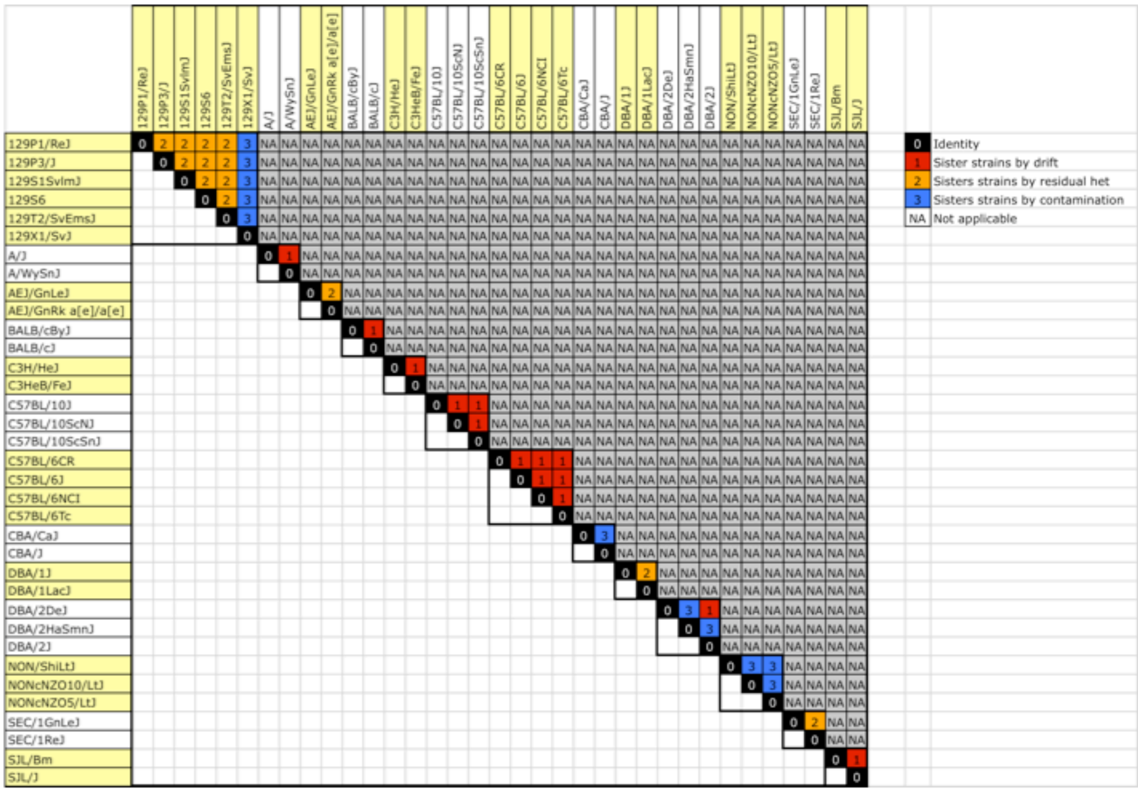
Supplementary Figure 3. Phylogenetic tree for wild caught samples based on VINOs. The red, green and blue circles represent the basal node for the *M. m. musculus, M. m. castaneus* and *M. m. domesticus* subspecies, respectively.



Supplementary Figure 4. Haplotype diversity and IBD in classical inbred strains. A) Number of haplotypes per compatible interval. B) Number of cliques per compatible interval. C) Proportion of the genome that is IBD in pairwise comparisons between classical strains.



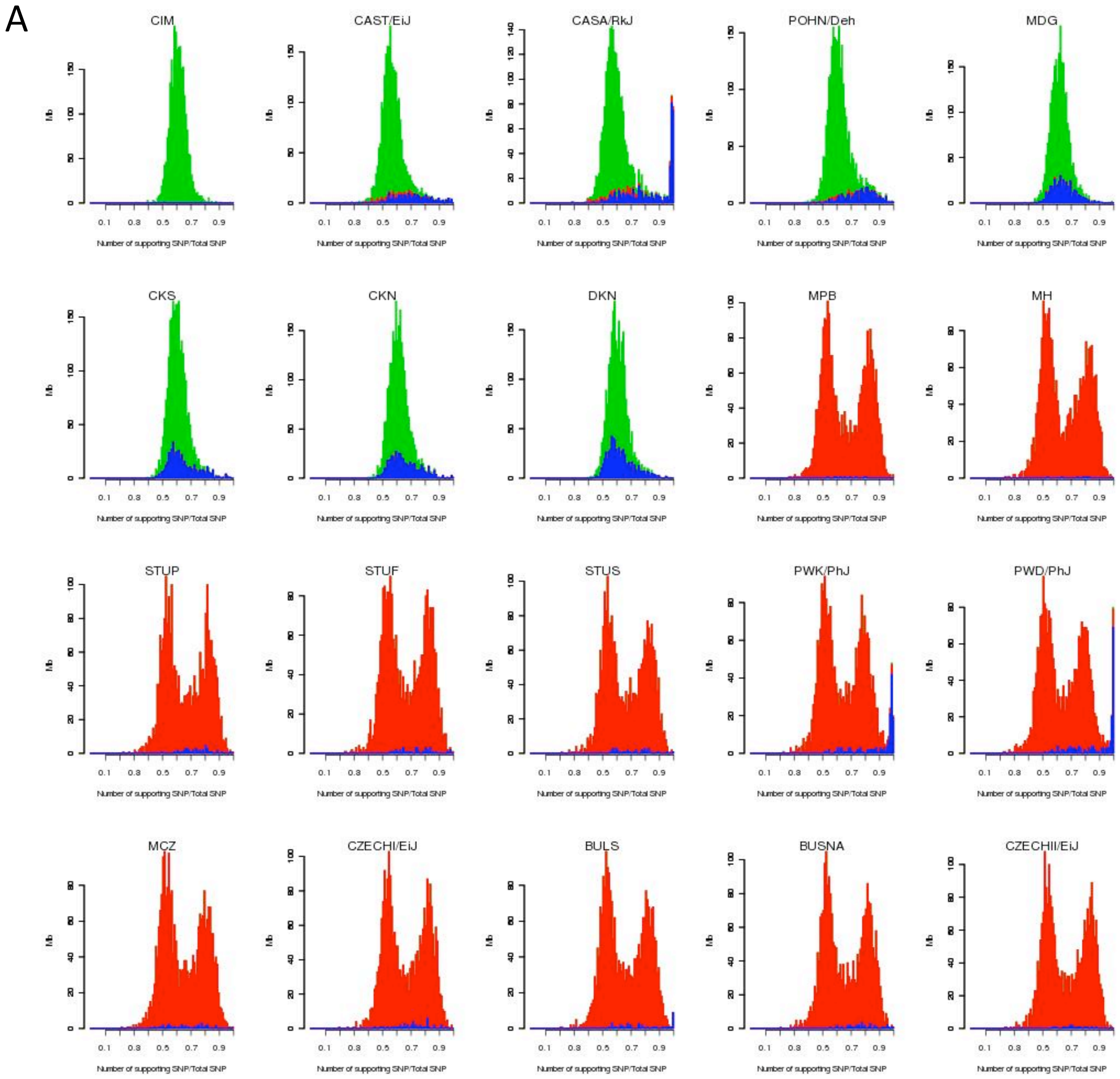
Supplementary Figure 5. IBD in sister strains. The figure classifies 13 sets of sister strains into three classes depending on the likely origin of the genetic diversity observed in each pair.



	129P1/ReJ	129P3/J	129S1SvImJ	129S6	129T2/SvEmsJ	129X1/SvJ	A/J	A/WySnJ	AEJ/GnLeJ	AEJ/GnRk a[e]/a[e]	BALB/cByJ	BALB/cJ	C3H/HeJ	C3HeB/FeJ	C57BL/10J	C57BL/10ScNJ	C57BL/10ScSnJ	C57BL/6CR	C57BL/6J	C57BL/6NCI	C57BL/6Tc	CBA/CaJ	CBA/J	DBA/1J	DBA/1LacJ	DBA/2DeJ	DBA/2HaSmnJ	DBA/2J	NON/ShiLtJ	NONcNZO10/LtJ	NONcNZO5/LtJ	SEC/1GnLeJ	SEC/1ReJ	SJL/Bm	SJL/J
129P1/ReJ	0	2	2	2	2	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
129P3/J		0	2	2	2	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
129S1SvImJ			0	2	2	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
129S6				0	2	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
129T2/SvEmsJ					0	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
129X1/SvJ						0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A/J							0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
A/WySnJ								0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AEJ/GnLeJ									0	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AEJ/GnRk a[e]/a[e]										0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BALB/cByJ											0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BALB/cJ												0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C3H/HeJ													0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C3HeB/FeJ														0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/10J															0	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/10ScNJ																0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/10ScSnJ																	0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/6CR																		0	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/6J																			0	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/6NCI																				0	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C57BL/6Tc																					0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CBA/CaJ																						0	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CBA/J																							0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DBA/1J																								0	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DBA/1LacJ																									0	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DBA/2DeJ																										0	3	1	NA	NA	NA	NA	NA	NA	NA
DBA/2HaSmnJ																											0	3	NA	NA	NA	NA	NA	NA	NA
DBA/2J																												0	NA	NA	NA	NA	NA	NA	NA
NON/ShiLtJ																													0	3	3	NA	NA	NA	NA
NONcNZO10/LtJ																														0	3	NA	NA	NA	NA
NONcNZO5/LtJ																															0	NA	NA	NA	NA
SEC/1GnLeJ																																0	2	NA	NA
SEC/1ReJ																																	0	NA	NA
SJL/Bm																																		0	1
SJL/J																																			0

0	Identity
1	Sister strains by drift
2	Sisters strains by residual het
3	Sisters strains by contamination
NA	Not applicable

Supplementary Figure 6. A) Genotype identity between wild-derived and classical inbred strains. For each wild-derived strain we determined the maximum genotype identity to any of our 100 classical inbred strains in 1Mb intervals. Colored bars in the histograms denote the subspecific origin of the interval in the wild-derived strain, green *M. m. castaneus*, red *M. m. musculus* and blue *M. m. domesticus*. B) Pairwise comparison of genotype identity between wild-derived strains. Genotype identity was calculated on 1Mb intervals. Blue histograms denote comparisons between pairs of wild-derived strains from *M. m. domesticus* origin. Red histograms denote comparisons between pairs of wild-derived strains from *M. m. musculus* origin. Green histograms denote comparisons between pairs of wild-derived strains from *M. m. castaneus* origin. Purple histograms denote comparisons between pairs of wild-derived strains from *M. m. molossinus* origin. Finally, black histograms denote comparisons between selected pairs of wild-derived strains from different subspecific origin.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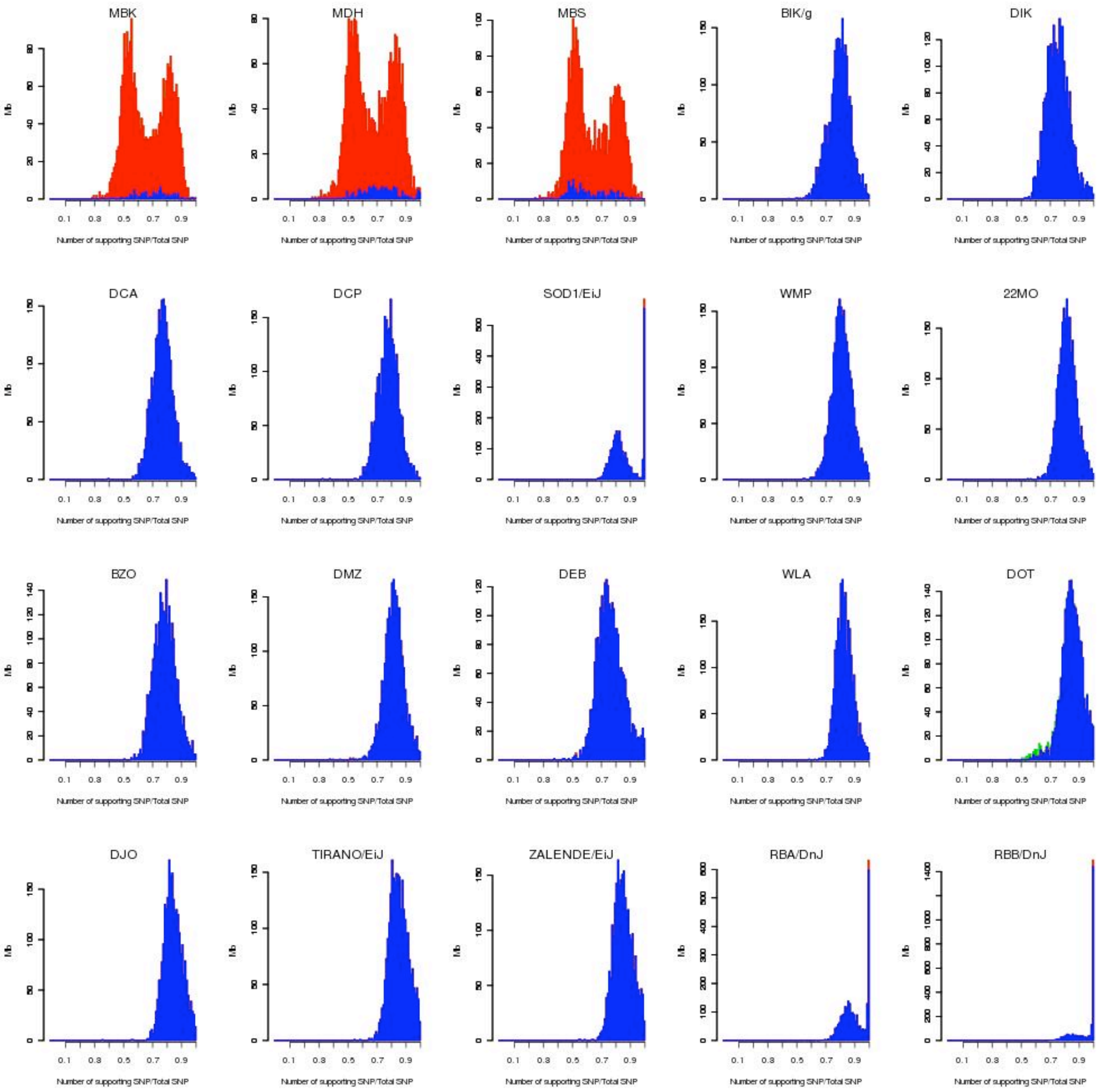
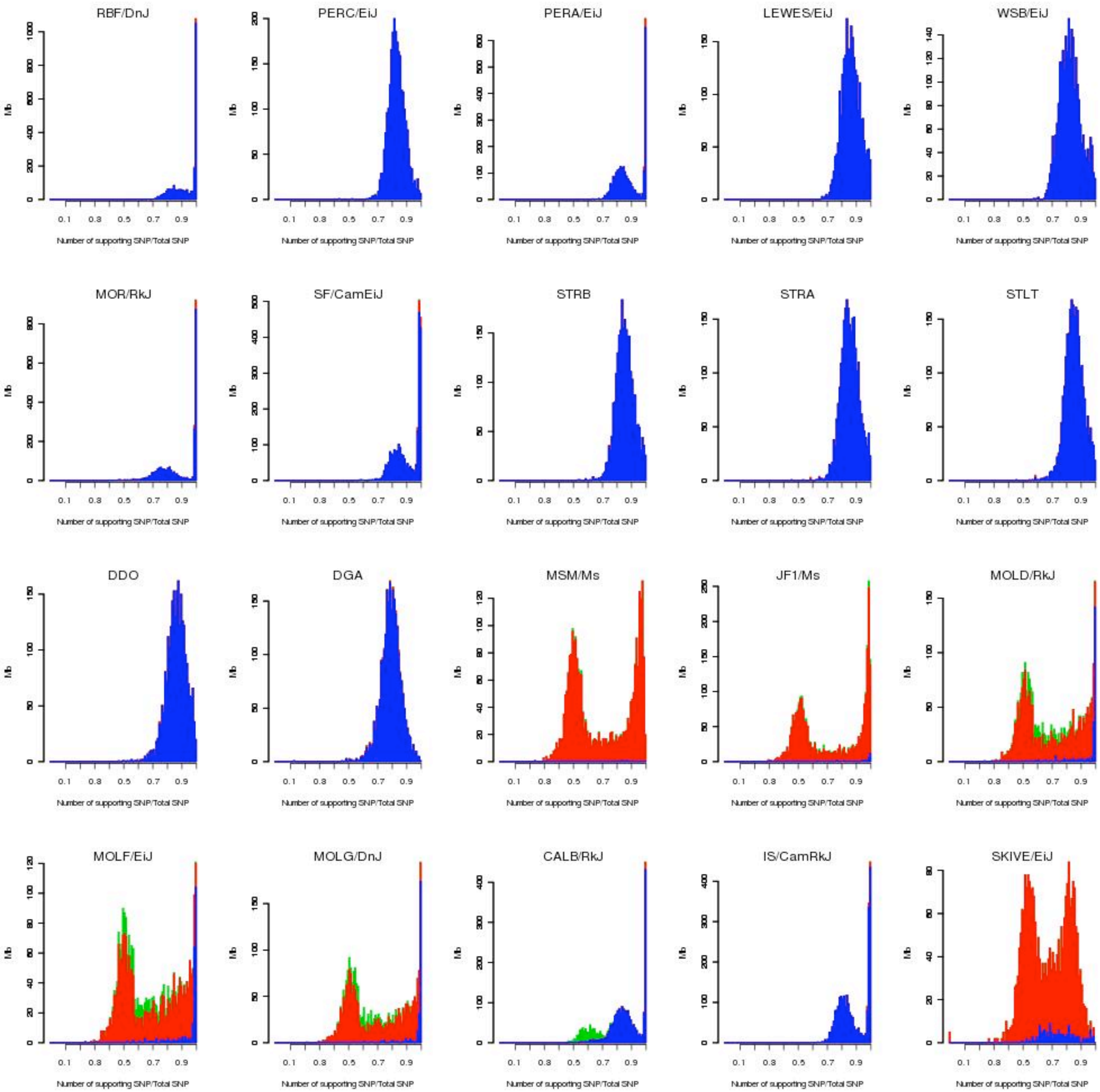
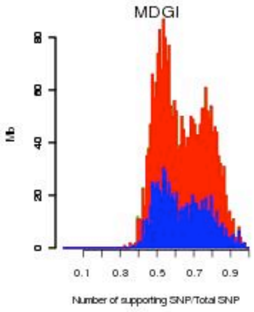
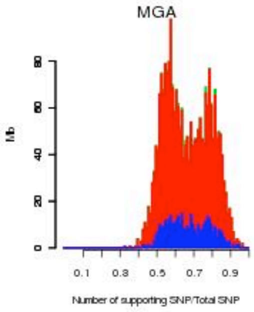
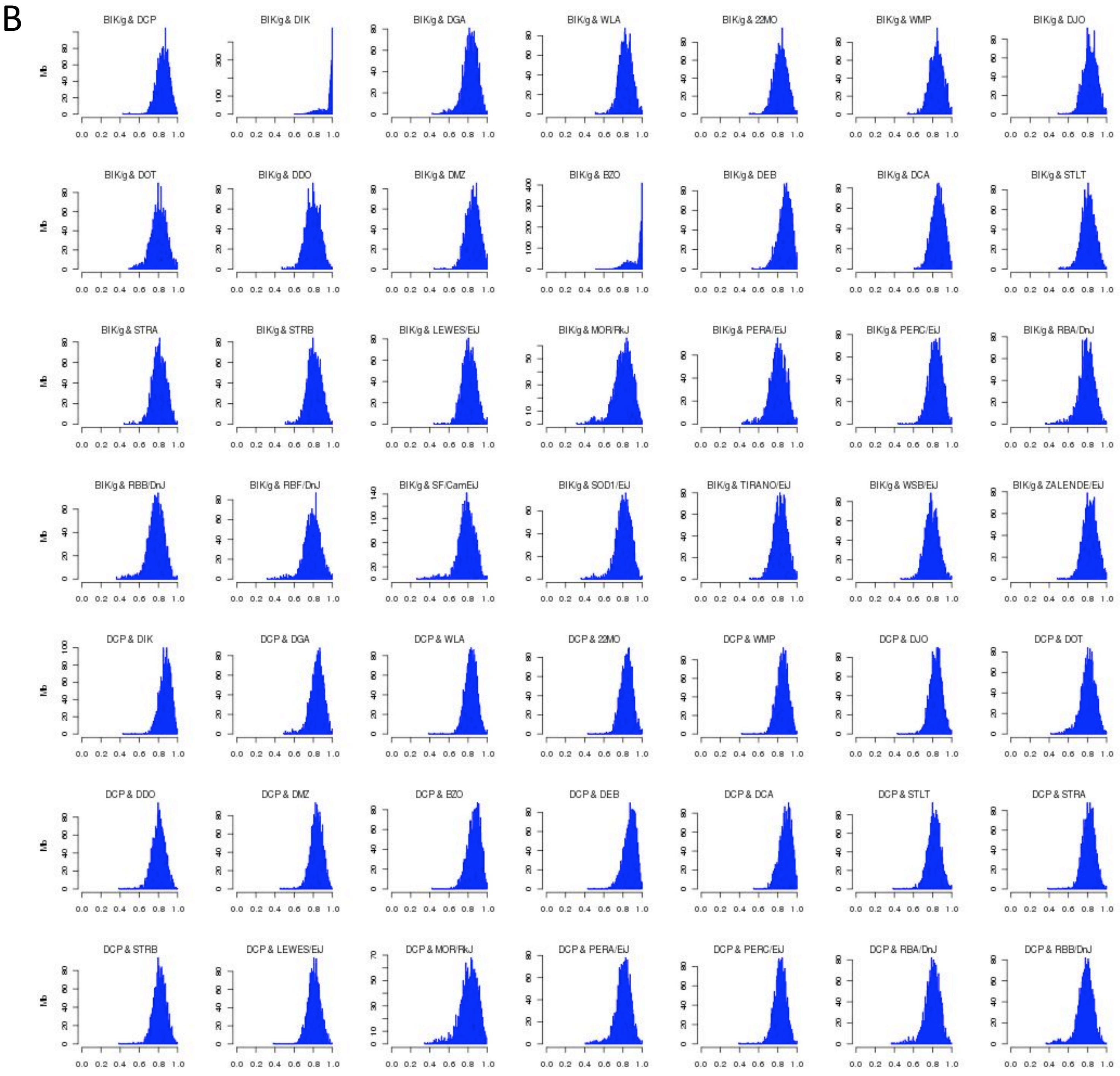
CIM
CAST/EiJ
CASA/RkJ
POHN/Deh
MDG
CKS
CKN
DKN
MPB
MH
STUP
STUF
STUS
PWK/PhJ
PWD/PhJ
MCZ
CZECHI/EiJ
BULS
BUSNA
CZECHII/EiJ
Mb
0.1
0.3
0.5
0.7
0.9
Number of supporting SNP/Total SNP


MBK
MDH
MBS
BIK/g
DIK
DCA
DCP
SOD1/EiJ
WMP
22MO
BZO
DMZ
DEB
WLA
DOT
DJO
TIRANO/EiJ
ZALENDE/EiJ
RBA/DnJ
RBB/DnJ
Mb
0.1
0.3
0.5
0.7
0.9
Number of supporting SNP/Total SNP


RBF/DnJ
PERC/EiJ
PERA/EiJ
LEWES/EiJ
WSB/EiJ
MOR/RkJ
SF/CamEiJ
STRB
STRA
STLT
DDO
DGA
MSM/Ms
JF1/Ms
MOLD/RkJ
MOLF/EiJ
MOLG/DnJ
CALB/RkJ
IS/CamRkJ
SKIVE/EiJ
Mb
0.1
0.3
0.5
0.7
0.9
Number of supporting SNP/Total SNP


MDGI
Mb
0
20
40
60
80
0.1
0.3
0.5
0.7
0.9
Number of supporting SNP/Total SNP


MGA
Mb
0
20
40
60
80
0.1
0.3
0.5
0.7
0.9
Number of supporting SNP/Total SNP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BIK/g & DCP
BIK/g & DIK
BIK/g & DGA
BIK/g & WLA
BIK/g & 22MO
BIK/g & WMP
BIK/g & DJO
BIK/g & DOT
BIK/g & DDO
BIK/g & DMZ
BIK/g & BZO
BIK/g & DEB
BIK/g & DCA
BIK/g & STLT
BIK/g & STRA
BIK/g & STRB
BIK/g & LEWES/EiJ
BIK/g & MOR/RkJ
BIK/g & PERA/EiJ
BIK/g & PERC/EiJ
BIK/g & RBA/DnJ
BIK/g & RBB/DnJ
BIK/g & RBF/DnJ
BIK/g & SF/CamEiJ
BIK/g & SOD1/EiJ
BIK/g & TIRANO/EiJ
BIK/g & WSB/EiJ
BIK/g & ZALENDE/EiJ
DCP & DIK
DCP & DGA
DCP & WLA
DCP & 22MO
DCP & WMP
DCP & DJO
DCP & DOT
DCP & DDO
DCP & DMZ
DCP & BZO
DCP & DEB
DCP & DCA
DCP & STLT
DCP & STRA
DCP & STRB
DCP & LEWES/EiJ
DCP & MOR/RkJ
DCP & PERA/EiJ
DCP & PERC/EiJ
DCP & RBA/DnJ
DCP & RBB/DnJ
Mb
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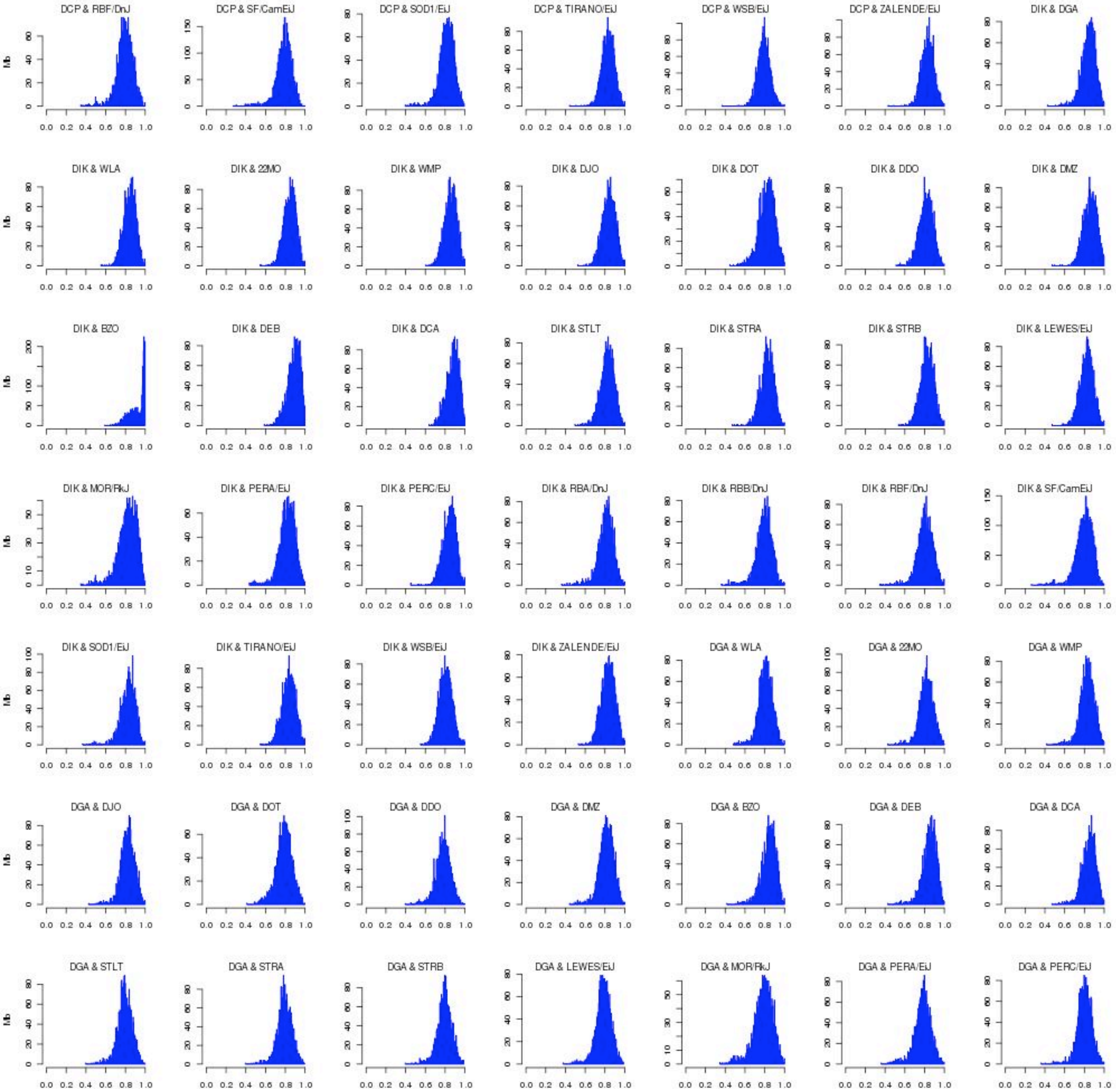
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DCP & SF/CamEiJ
DCP & SOD1/EiJ
DCP & TIRANO/EiJ
DCP & WSB/EiJ
DCP & ZALENDE/EiJ
DIK & DGA
DIK & WLA
DIK & 22MO
DIK & WMP
DIK & DJO
DIK & DOT
DIK & DDO
DIK & DMZ
DIK & BZO
DIK & DEB
DIK & DCA
DIK & STLT
DIK & STRA
DIK & STRB
DIK & LEWES/EiJ
DIK & MOR/RkJ
DIK & PERA/EiJ
DIK & PERC/EiJ
DIK & RBA/DnJ
DIK & RBB/DnJ
DIK & RBF/DnJ
DIK & SF/CamEiJ
DIK & SOD1/EiJ
DIK & TIRANO/EiJ
DIK & WSB/EiJ
DIK & ZALENDE/EiJ
DGA & WLA
DGA & 22MO
DGA & WMP
DGA & DJO
DGA & DOT
DGA & DDO
DGA & DMZ
DGA & BZO
DGA & DEB
DGA & DCA
DGA & STLT
DGA & STRA
DGA & STRB
DGA & LEWES/EiJ
DGA & MOR/RkJ
DGA & PERA/EiJ
DGA & PERC/EiJ
Mb
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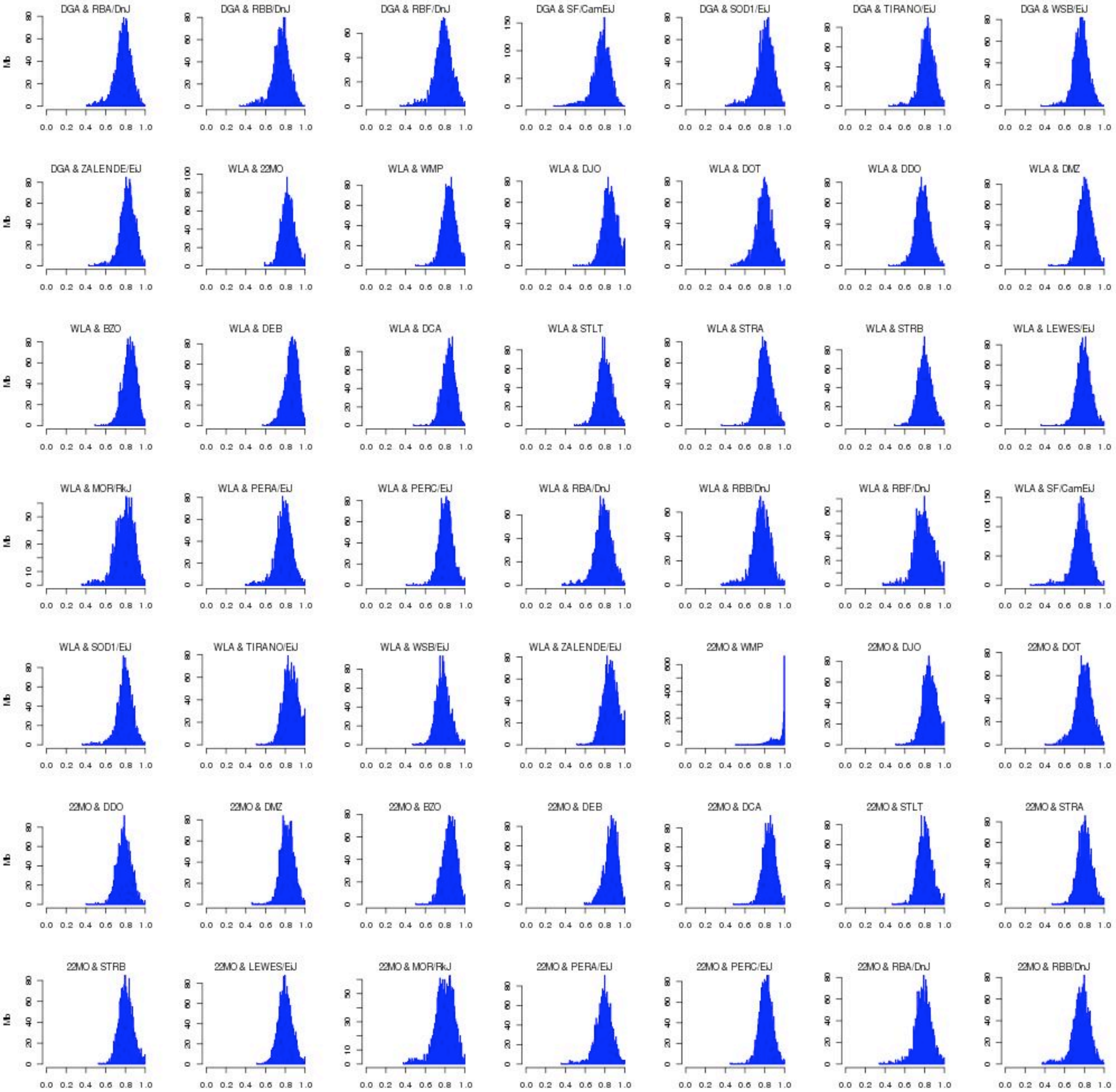
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DGA & RBB/DnJ
DGA & RBF/DnJ
DGA & SF/CamEiJ
DGA & SOD1/EiJ
DGA & TIRANO/EiJ
DGA & WSB/EiJ
DGA & ZALENDE/EiJ
WLA & 22MO
WLA & WMP
WLA & DJO
WLA & DOT
WLA & DDO
WLA & DMZ
WLA & BZO
WLA & DEB
WLA & DCA
WLA & STLT
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WLA & STRB
WLA & LEWES/EiJ
WLA & MOR/RkJ
WLA & PERA/EiJ
WLA & PERC/EiJ
WLA & RBA/DnJ
WLA & RBB/DnJ
WLA & RBF/DnJ
WLA & SF/CamEiJ
WLA & SOD1/EiJ
WLA & TIRANO/EiJ
WLA & WSB/EiJ
WLA & ZALENDE/EiJ
22MO & WMP
22MO & DJO
22MO & DOT
22MO & DDO
22MO & DMZ
22MO & BZO
22MO & DEB
22MO & DCA
22MO & STLT
22MO & STRA
22MO & STRB
22MO & LEWES/EiJ
22MO & MOR/RkJ
22MO & PERA/EiJ
22MO & PERC/EiJ
22MO & RBA/DnJ
22MO & RBB/DnJ
Mb
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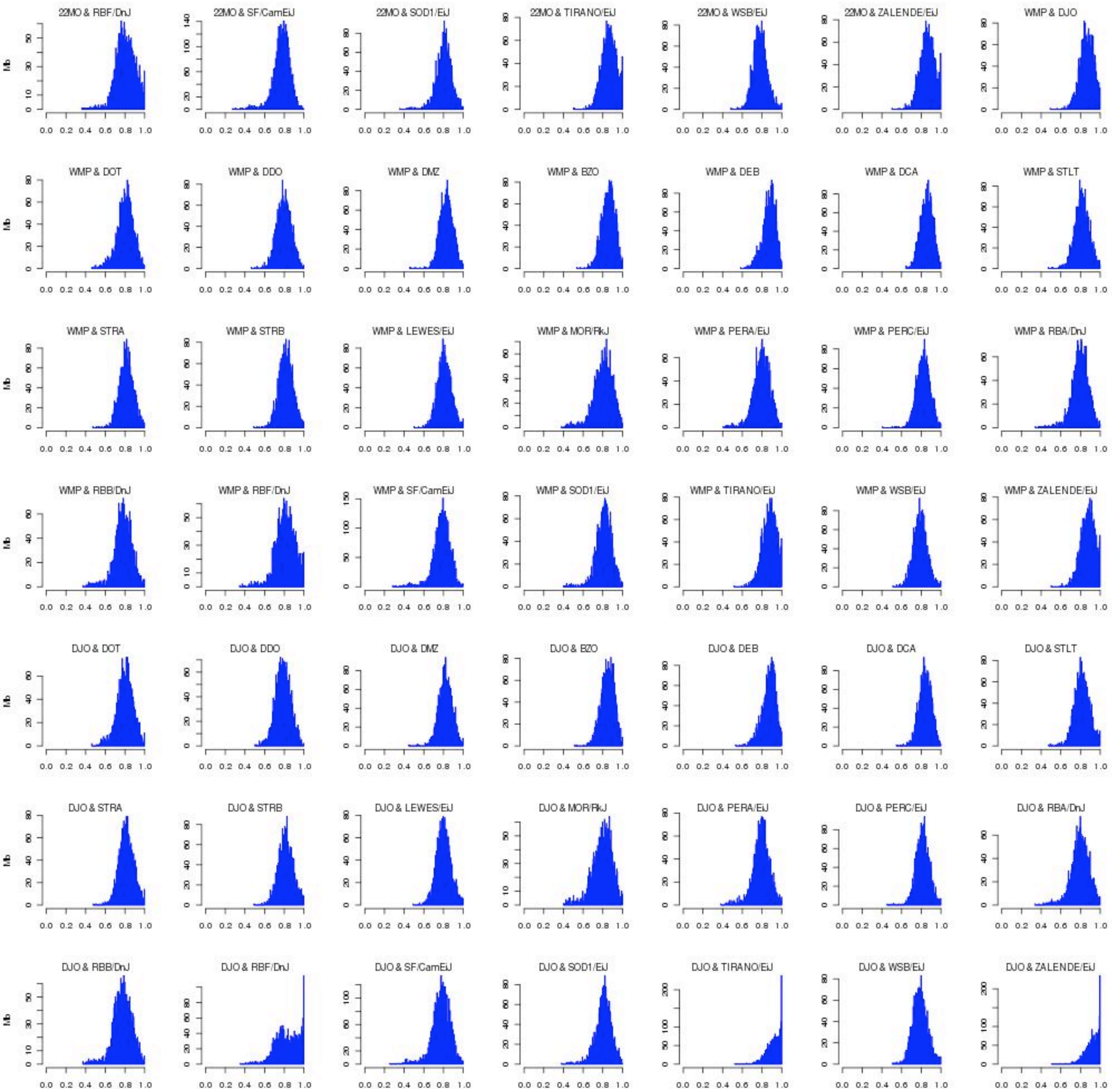
0 50 100 150
0 200 400 600
0 10 30 50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22MO & SF/CamEiJ
22MO & SOD1/EiJ
22MO & TIRANO/EiJ
22MO & WSB/EiJ
22MO & ZALENDE/EiJ
WMP & DJO
WMP & DOT
WMP & DDO
WMP & DMZ
WMP & BZO
WMP & DEB
WMP & DCA
WMP & STLT
WMP & STRA
WMP & STRB
WMP & LEWES/EiJ
WMP & MOR/RkJ
WMP & PERA/EiJ
WMP & PERC/EiJ
WMP & RBA/DnJ
WMP & RBB/DnJ
WMP & RBF/DnJ
WMP & SF/CamEiJ
WMP & SOD1/EiJ
WMP & TIRANO/EiJ
WMP & WSB/EiJ
WMP & ZALENDE/EiJ
DJO & DOT
DJO & DDO
DJO & DMZ
DJO & BZO
DJO & DEB
DJO & DCA
DJO & STLT
DJO & STRA
DJO & STRB
DJO & LEWES/EiJ
DJO & MOR/RkJ
DJO & PERA/EiJ
DJO & PERC/EiJ
DJO & RBA/DnJ
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DJO & SF/CamEiJ
DJO & SOD1/EiJ
DJO & TIRANO/EiJ
DJO & WSB/EiJ
DJO & ZALENDE/EiJ
Mb
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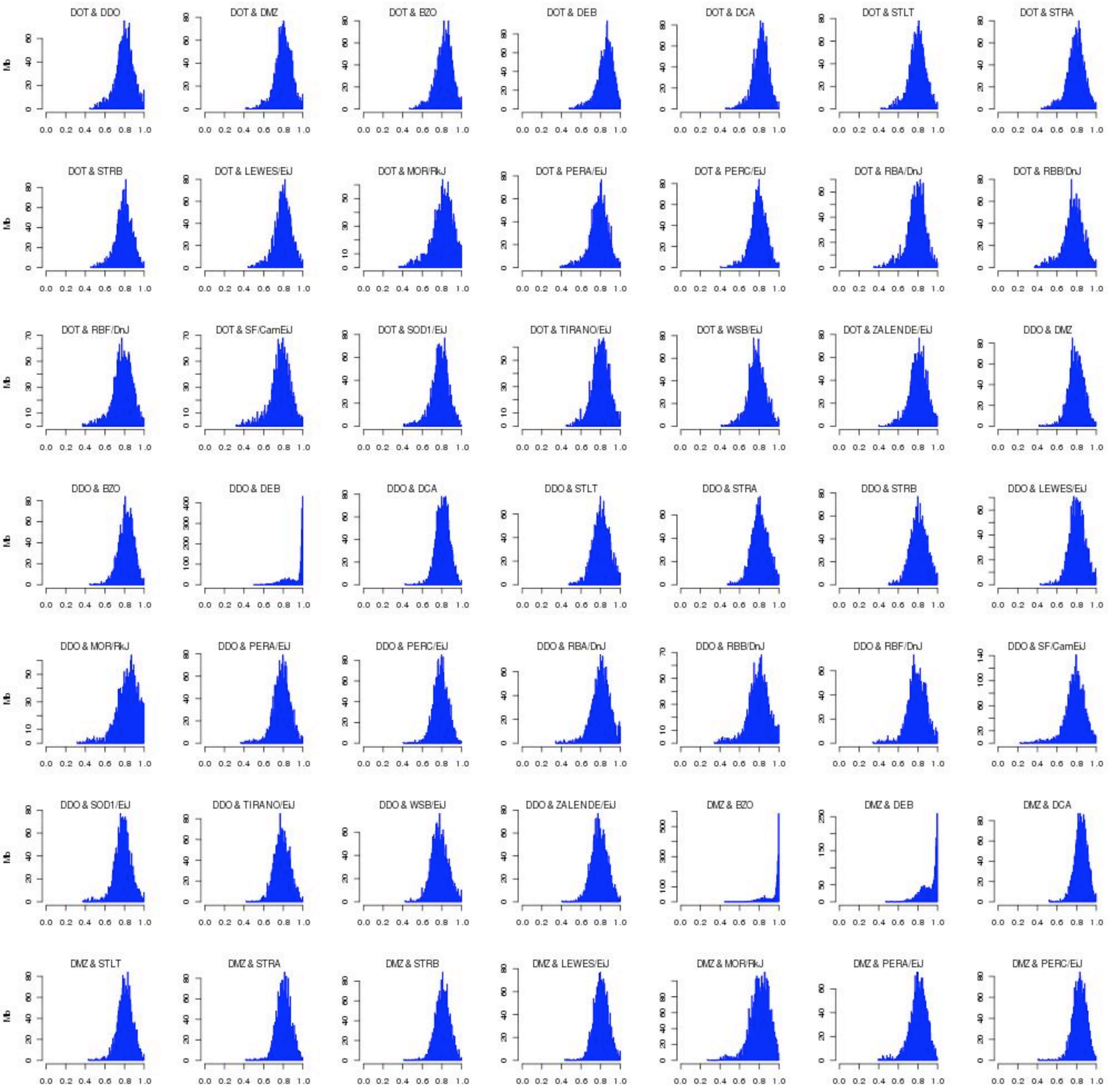
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DOT & BZO
DOT & DEB
DOT & DCA
DOT & STLT
DOT & STRA
DOT & STRB
DOT & LEWES/EiJ
DOT & MOR/RkJ
DOT & PERA/EiJ
DOT & PERC/EiJ
DOT & RBA/DnJ
DOT & RBB/DnJ
DOT & RBF/DnJ
DOT & SF/CamEiJ
DOT & SOD1/EiJ
DOT & TIRANO/EiJ
DOT & WSB/EiJ
DOT & ZALENDE/EiJ
DDO & DMZ
DDO & BZO
DDO & DEB
DDO & DCA
DDO & STLT
DDO & STRA
DDO & STRB
DDO & LEWES/EiJ
DDO & MOR/RkJ
DDO & PERA/EiJ
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DDO & RBA/DnJ
DDO & RBB/DnJ
DDO & RBF/DnJ
DDO & SF/CamEiJ
DDO & SOD1/EiJ
DDO & TIRANO/EiJ
DDO & WSB/EiJ
DDO & ZALENDE/EiJ
DMZ & BZO
DMZ & DEB
DMZ & DCA
DMZ & STLT
DMZ & STRA
DMZ & STRB
DMZ & LEWES/EiJ
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DMZ & PERC/EiJ
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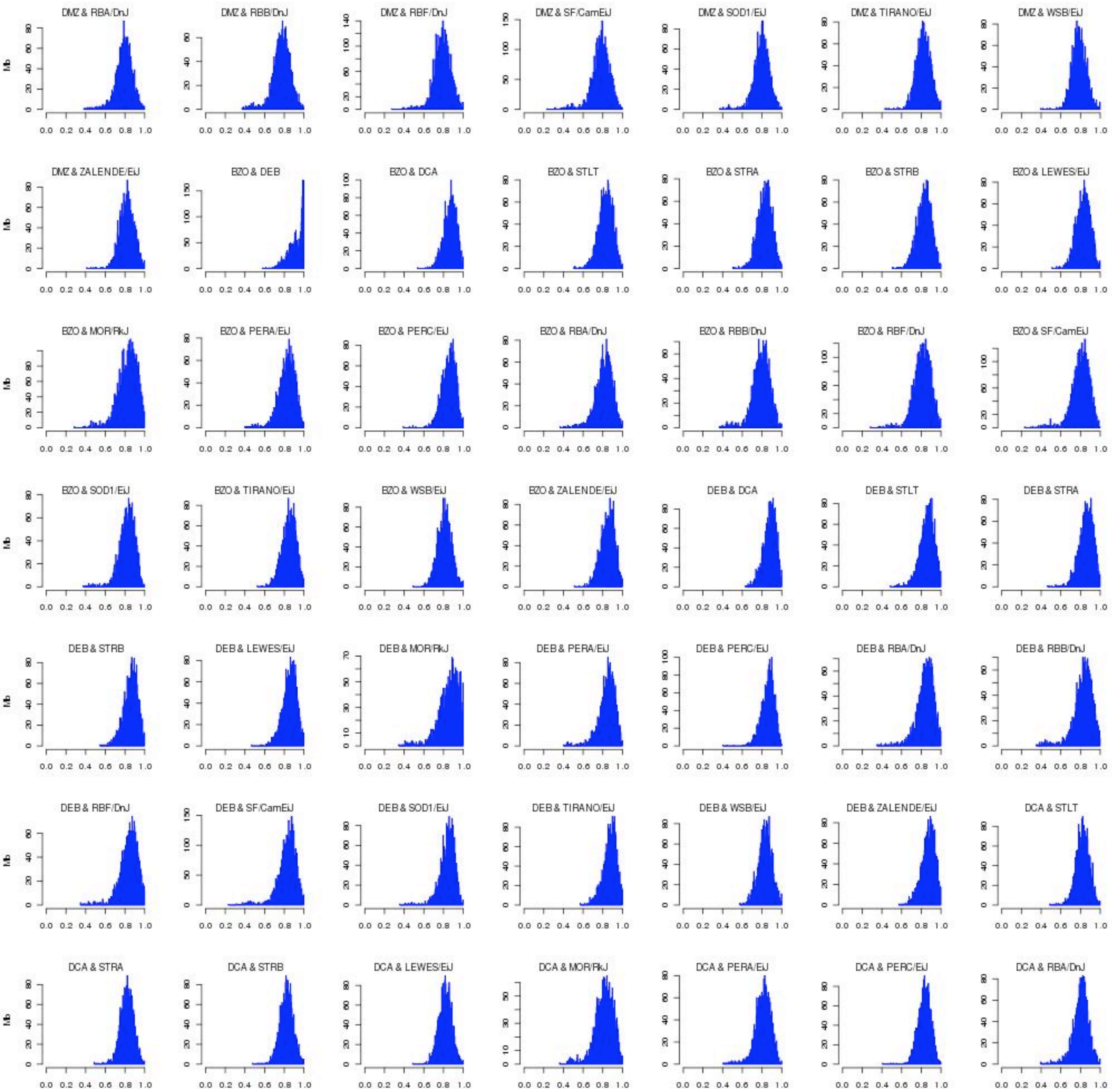
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DMZ & RBB/DnJ
DMZ & RBF/DnJ
DMZ & SF/CamEiJ
DMZ & SOD1/EiJ
DMZ & TIRANO/EiJ
DMZ & WSB/EiJ
DMZ & ZALENDE/EiJ
BZO & DEB
BZO & DCA
BZO & STLT
BZO & STRA
BZO & STRB
BZO & LEWES/EiJ
BZO & MOR/RkJ
BZO & PERA/EiJ
BZO & PERC/EiJ
BZO & RBA/DnJ
BZO & RBB/DnJ
BZO & RBF/DnJ
BZO & SF/CamEiJ
BZO & SOD1/EiJ
BZO & TIRANO/EiJ
BZO & WSB/EiJ
BZO & ZALENDE/EiJ
DEB & DCA
DEB & STLT
DEB & STRA
DEB & STRB
DEB & LEWES/EiJ
DEB & MOR/RkJ
DEB & PERA/EiJ
DEB & PERC/EiJ
DEB & RBA/DnJ
DEB & RBB/DnJ
DEB & RBF/DnJ
DEB & SF/CamEiJ
DEB & SOD1/EiJ
DEB & TIRANO/EiJ
DEB & WSB/EiJ
DEB & ZALENDE/EiJ
DCA & STLT
DCA & STRA
DCA & STRB
DCA & LEWES/EiJ
DCA & MOR/RkJ
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Mb
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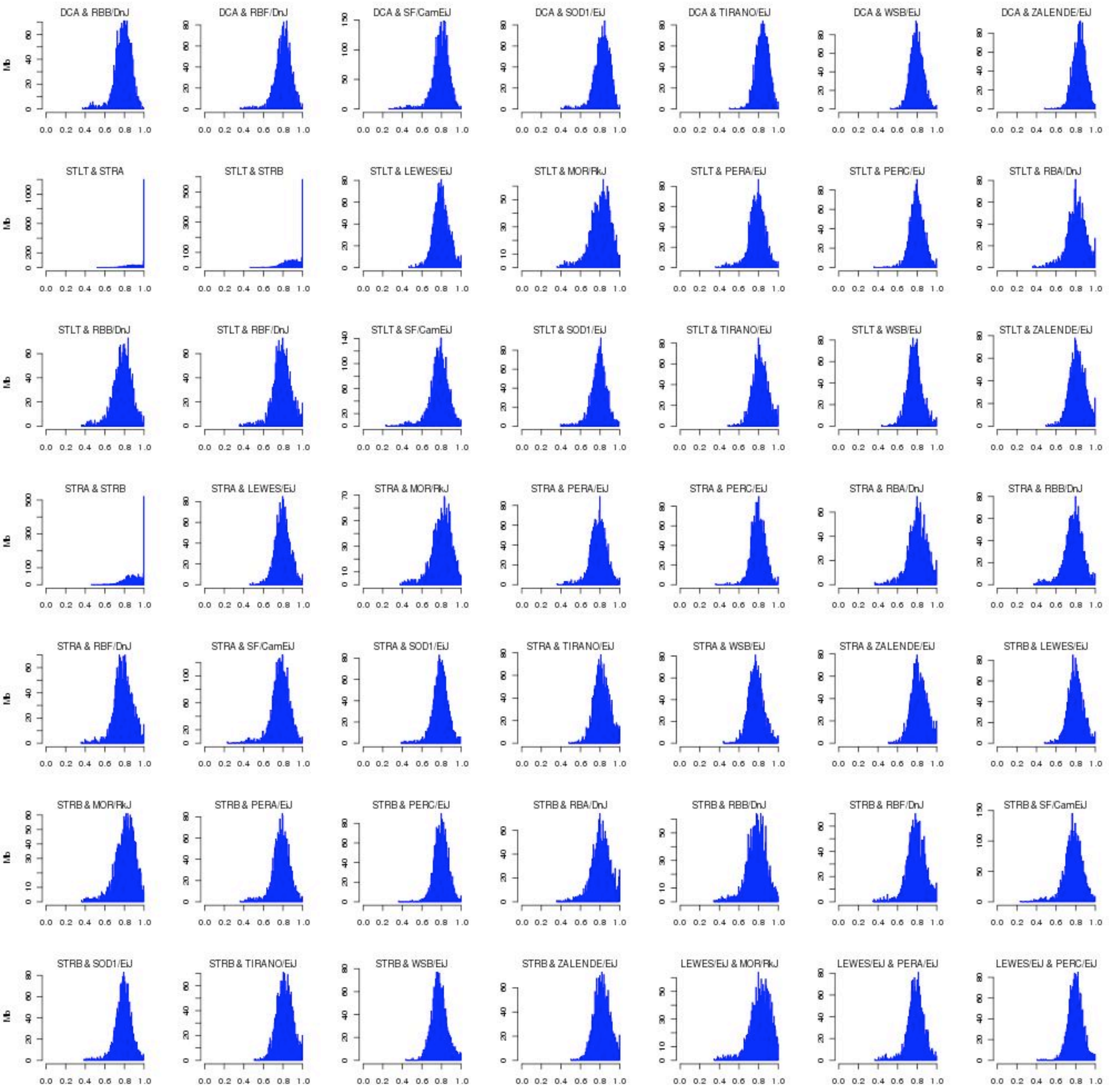
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DCA & RBF/DnJ
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DCA & SOD1/EiJ
DCA & TIRANO/EiJ
DCA & WSB/EiJ
DCA & ZALENDE/EiJ
STLT & STRA
STLT & STRB
STLT & LEWES/EiJ
STLT & MOR/RkJ
STLT & PERA/EiJ
STLT & PERC/EiJ
STLT & RBA/DnJ
STLT & RBB/DnJ
STLT & RBF/DnJ
STLT & SF/CamEiJ
STLT & SOD1/EiJ
STLT & TIRANO/EiJ
STLT & WSB/EiJ
STLT & ZALENDE/EiJ
STRA & STRB
STRA & LEWES/EiJ
STRA & MOR/RkJ
STRA & PERA/EiJ
STRA & PERC/EiJ
STRA & RBA/DnJ
STRA & RBB/DnJ
STRA & RBF/DnJ
STRA & SF/CamEiJ
STRA & SOD1/EiJ
STRA & TIRANO/EiJ
STRA & WSB/EiJ
STRA & ZALENDE/EiJ
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STRB & MOR/RkJ
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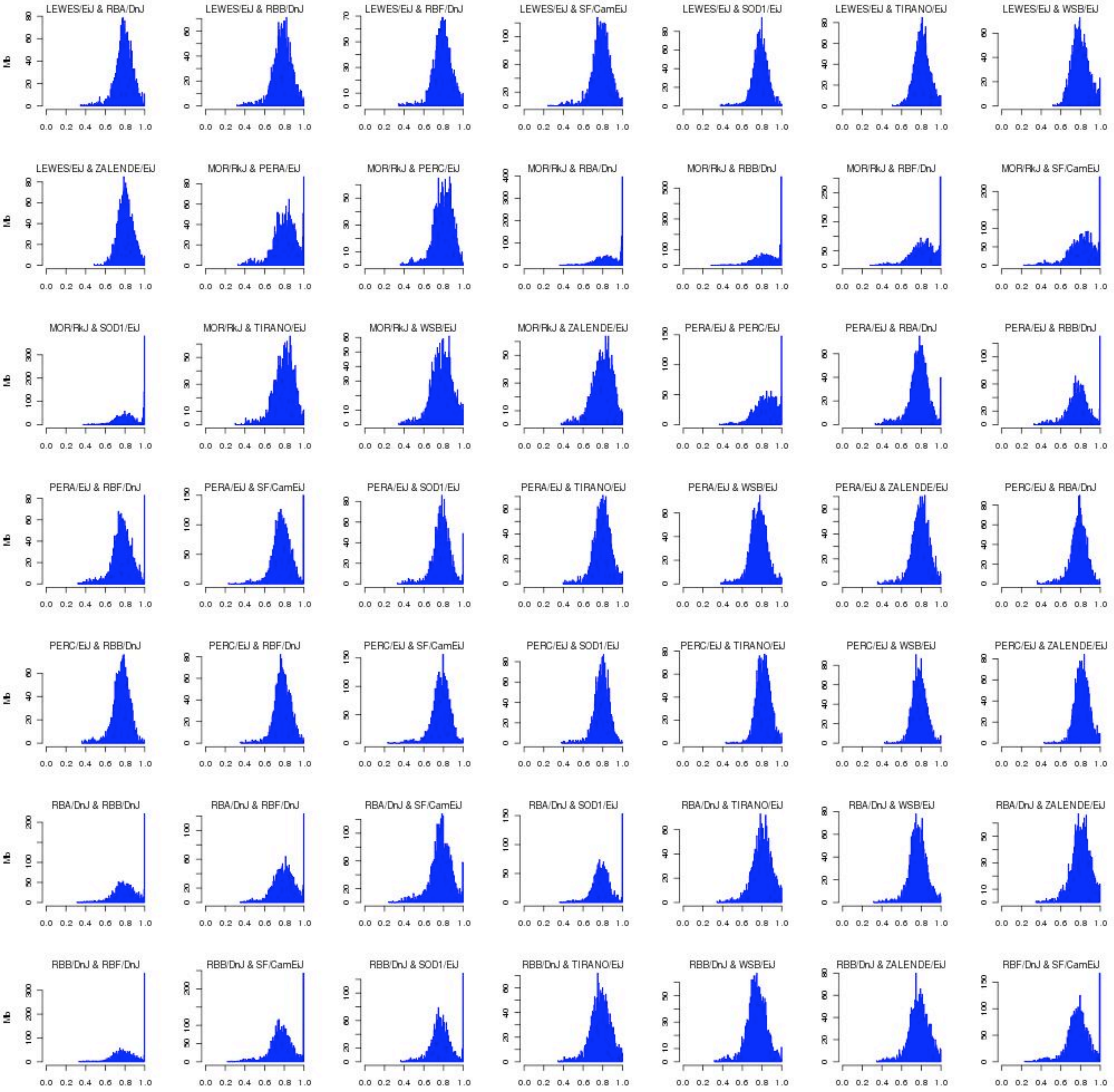
STRB & WSB/EiJ
STRB & ZALENDE/EiJ
LEWES/EiJ & MOR/RkJ
LEWES/EiJ & PERA/EiJ
LEWES/EiJ & PERC/EiJ
Mb
0.0 0.2 0.4 0.6 0.8 1.0


LEWES/EiJ & RBA/DnJ
LEWES/EiJ & RBB/DnJ
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LEWES/EiJ & SOD1/EiJ
LEWES/EiJ & TIRANO/EiJ
LEWES/EiJ & WSB/EiJ
LEWES/EiJ & ZALENDE/EiJ
MOR/RkJ & PERA/EiJ
MOR/RkJ & PERC/EiJ
MOR/RkJ & RBA/DnJ
MOR/RkJ & RBB/DnJ
MOR/RkJ & RBF/DnJ
MOR/RkJ & SF/CamEiJ
MOR/RkJ & SOD1/EiJ
MOR/RkJ & TIRANO/EiJ
MOR/RkJ & WSB/EiJ
MOR/RkJ & ZALENDE/EiJ
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PERA/EiJ & RBF/DnJ
PERA/EiJ & SF/CamEiJ
PERA/EiJ & SOD1/EiJ
PERA/EiJ & TIRANO/EiJ
PERA/EiJ & WSB/EiJ
PERA/EiJ & ZALENDE/EiJ
PERC/EiJ & RBA/DnJ
PERC/EiJ & RBB/DnJ
PERC/EiJ & RBF/DnJ
PERC/EiJ & SF/CamEiJ
PERC/EiJ & SOD1/EiJ
PERC/EiJ & TIRANO/EiJ
PERC/EiJ & WSB/EiJ
PERC/EiJ & ZALENDE/EiJ
RBA/DnJ & RBB/DnJ
RBA/DnJ & RBF/DnJ
RBA/DnJ & SF/CamEiJ
RBA/DnJ & SOD1/EiJ
RBA/DnJ & TIRANO/EiJ
RBA/DnJ & WSB/EiJ
RBA/DnJ & ZALENDE/EiJ
RBB/DnJ & RBF/DnJ
RBB/DnJ & SF/CamEiJ
RBB/DnJ & SOD1/EiJ
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RBB/DnJ & WSB/EiJ
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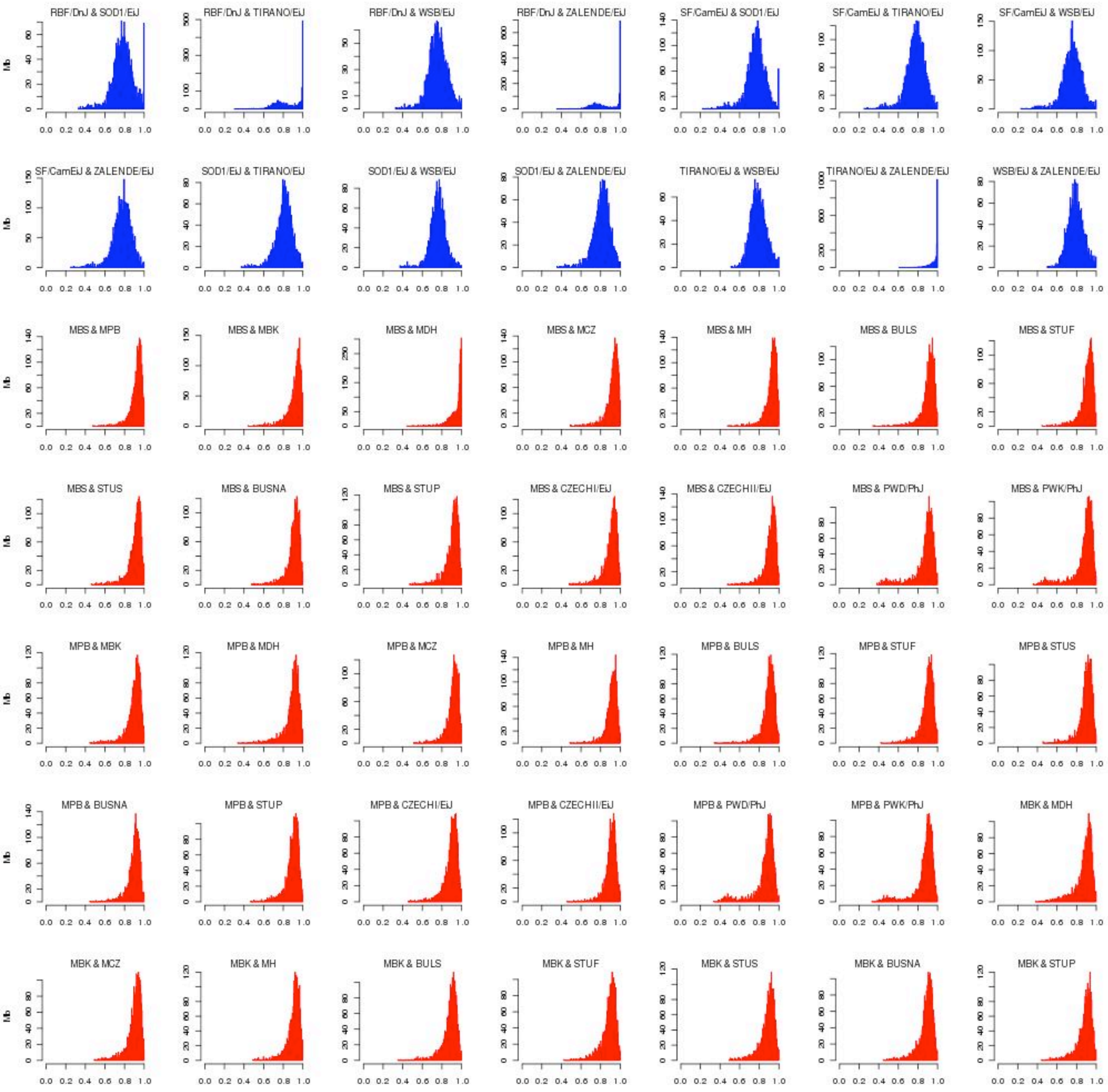
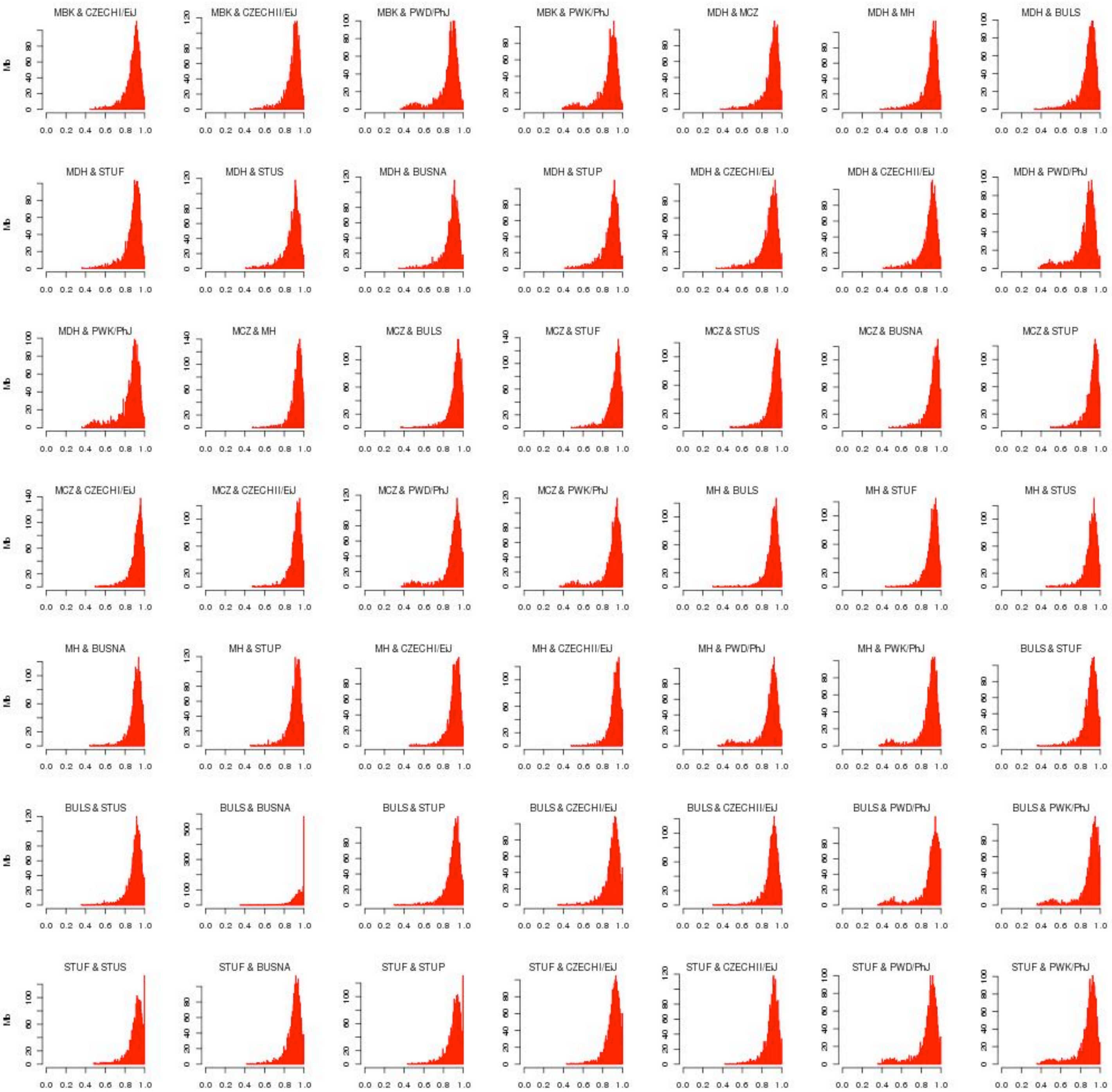

RBF/DnJ & SOD1/EiJ
RBF/DnJ & TIRANO/EiJ
RBF/DnJ & WSB/EiJ
RBF/DnJ & ZALENDE/EiJ
SF/CamEiJ & SOD1/EiJ
SF/CamEiJ & TIRANO/EiJ
SF/CamEiJ & WSB/EiJ
SF/CamEiJ & ZALENDE/EiJ
SOD1/EiJ & TIRANO/EiJ
SOD1/EiJ & WSB/EiJ
SOD1/EiJ & ZALENDE/EiJ
TIRANO/EiJ & WSB/EiJ
TIRANO/EiJ & ZALENDE/EiJ
WSB/EiJ & ZALENDE/EiJ
MBS & MPB
MBS & MBK
MBS & MDH
MBS & MCZ
MBS & MH
MBS & BULS
MBS & STUF
MBS & STUS
MBS & BUSNA
MBS & STUP
MBS & CZECHI/EiJ
MBS & CZECHII/EiJ
MBS & PWD/PhJ
MBS & PWK/PhJ
MPB & MBK
MPB & MDH
MPB & MCZ
MPB & MH
MPB & BULS
MPB & STUF
MPB & STUS
MPB & BUSNA
MPB & STUP
MPB & CZECHI/EiJ
MPB & CZECHII/EiJ
MPB & PWD/PhJ
MPB & PWK/PhJ
MBK & MDH
MBK & MCZ
MBK & MH
MBK & BULS
MBK & STUF
MBK & STUS
MBK & BUSNA
MBK & STUP
Mb
0.0 0.2 0.4 0.6 0.8 1.0


MBK & CZECHI/EiJ
MBK & CZECHII/EiJ
MBK & PWD/PhJ
MBK & PWK/PhJ
MDH & MCZ
MDH & MH
MDH & BULS
MDH & STUF
MDH & STUS
MDH & BUSNA
MDH & STUP
MDH & CZECHI/EiJ
MDH & CZECHII/EiJ
MDH & PWD/PhJ
MDH & PWK/PhJ
MCZ & MH
MCZ & BULS
MCZ & STUF
MCZ & STUS
MCZ & BUSNA
MCZ & STUP
MCZ & CZECHI/EiJ
MCZ & CZECHII/EiJ
MCZ & PWD/PhJ
MCZ & PWK/PhJ
MH & BULS
MH & STUF
MH & STUS
MH & BUSNA
MH & STUP
MH & CZECHI/EiJ
MH & CZECHII/EiJ
MH & PWD/PhJ
MH & PWK/PhJ
BULS & STUF
BULS & STUS
BULS & BUSNA
BULS & STUP
BULS & CZECHI/EiJ
BULS & CZECHII/EiJ
BULS & PWD/PhJ
BULS & PWK/PhJ
STUF & STUS
STUF & BUSNA
STUF & STUP
STUF & CZECHI/EiJ
STUF & CZECHII/EiJ
STUF & PWD/PhJ
STUF & PWK/PhJ
Mb
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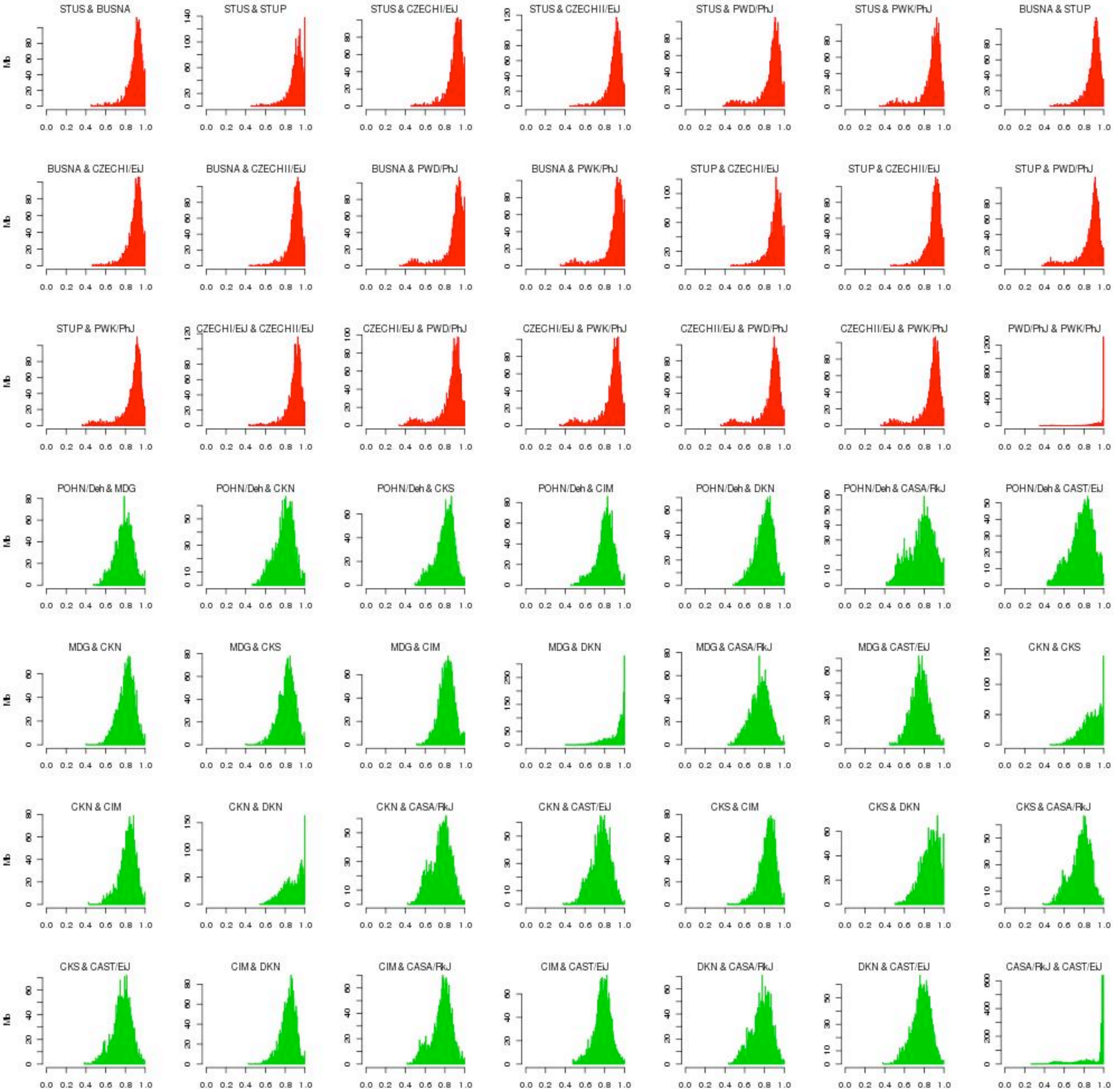
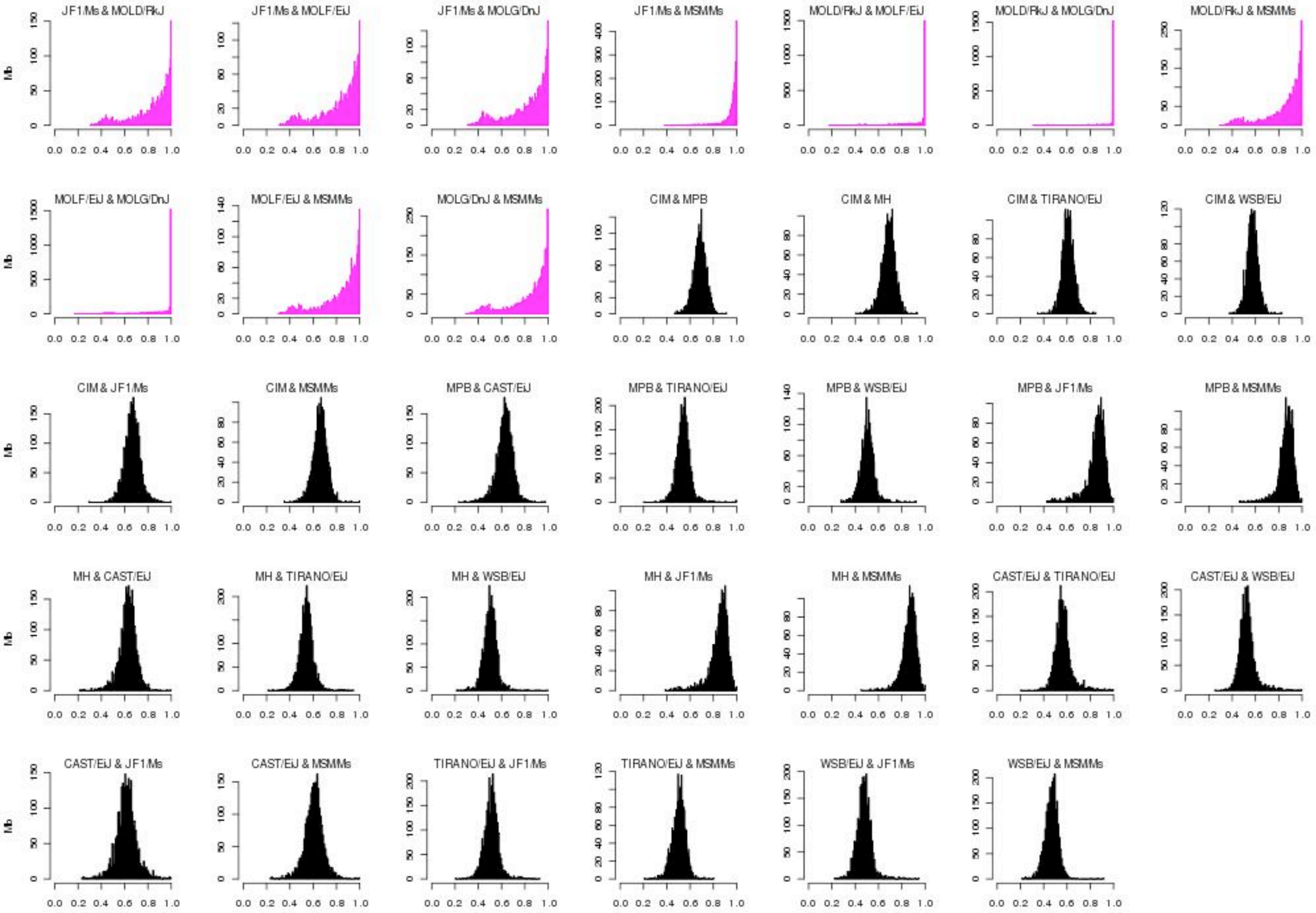
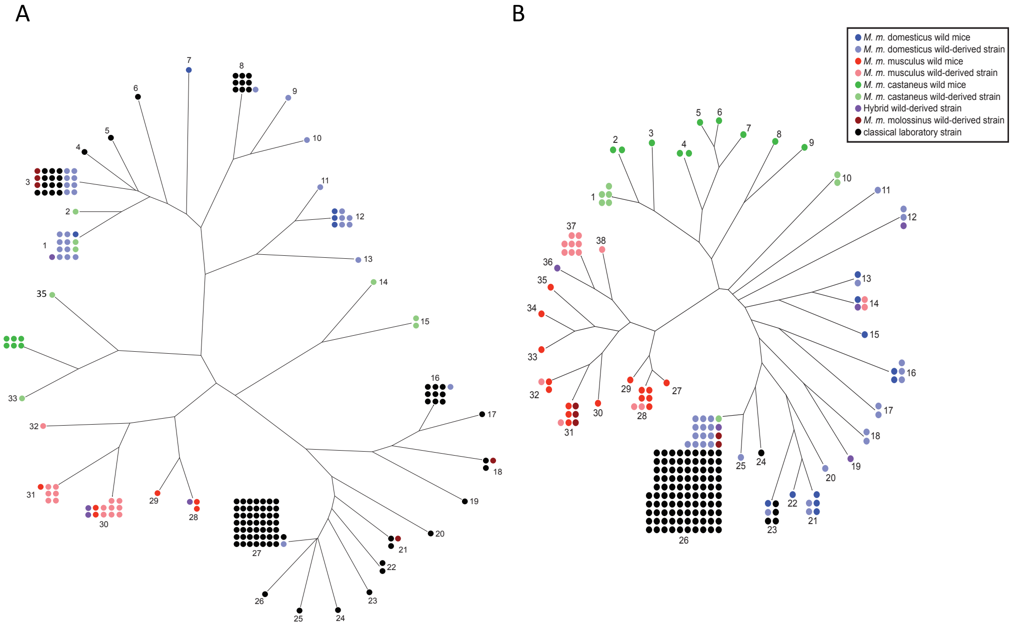

STUS & BUSNA
STUS & STUP
STUS & CZECHI/EiJ
STUS & CZECHII/EiJ
STUS & PWD/PhJ
STUS & PWK/PhJ
BUSNA & STUP
BUSNA & CZECHI/EiJ
BUSNA & CZECHII/EiJ
BUSNA & PWD/PhJ
BUSNA & PWK/PhJ
STUP & CZECHI/EiJ
STUP & CZECHII/EiJ
STUP & PWD/PhJ
STUP & PWK/PhJ
CZECHI/EiJ & CZECHII/EiJ
CZECHI/EiJ & PWD/PhJ
CZECHI/EiJ & PWK/PhJ
CZECHII/EiJ & PWD/PhJ
CZECHII/EiJ & PWK/PhJ
PWD/PhJ & PWK/PhJ
POHN/Deh & MDG
POHN/Deh & CKN
POHN/Deh & CKS
POHN/Deh & CIM
POHN/Deh & DKN
POHN/Deh & CASA/RkJ
POHN/Deh & CAST/EiJ
MDG & CKN
MDG & CKS
MDG & CIM
MDG & DKN
MDG & CASA/RkJ
MDG & CAST/EiJ
CKN & CKS
CKN & CIM
CKN & DKN
CKN & CASA/RkJ
CKN & CAST/EiJ
CKS & CIM
CKS & DKN
CKS & CASA/RkJ
CKS & CAST/EiJ
CIM & DKN
CIM & CASA/RkJ
CIM & CAST/EiJ
DKN & CASA/RkJ
DKN & CAST/EiJ
CASA/RkJ & CAST/EiJ
Mb
0.0 0.2 0.4 0.6 0.8 1.0

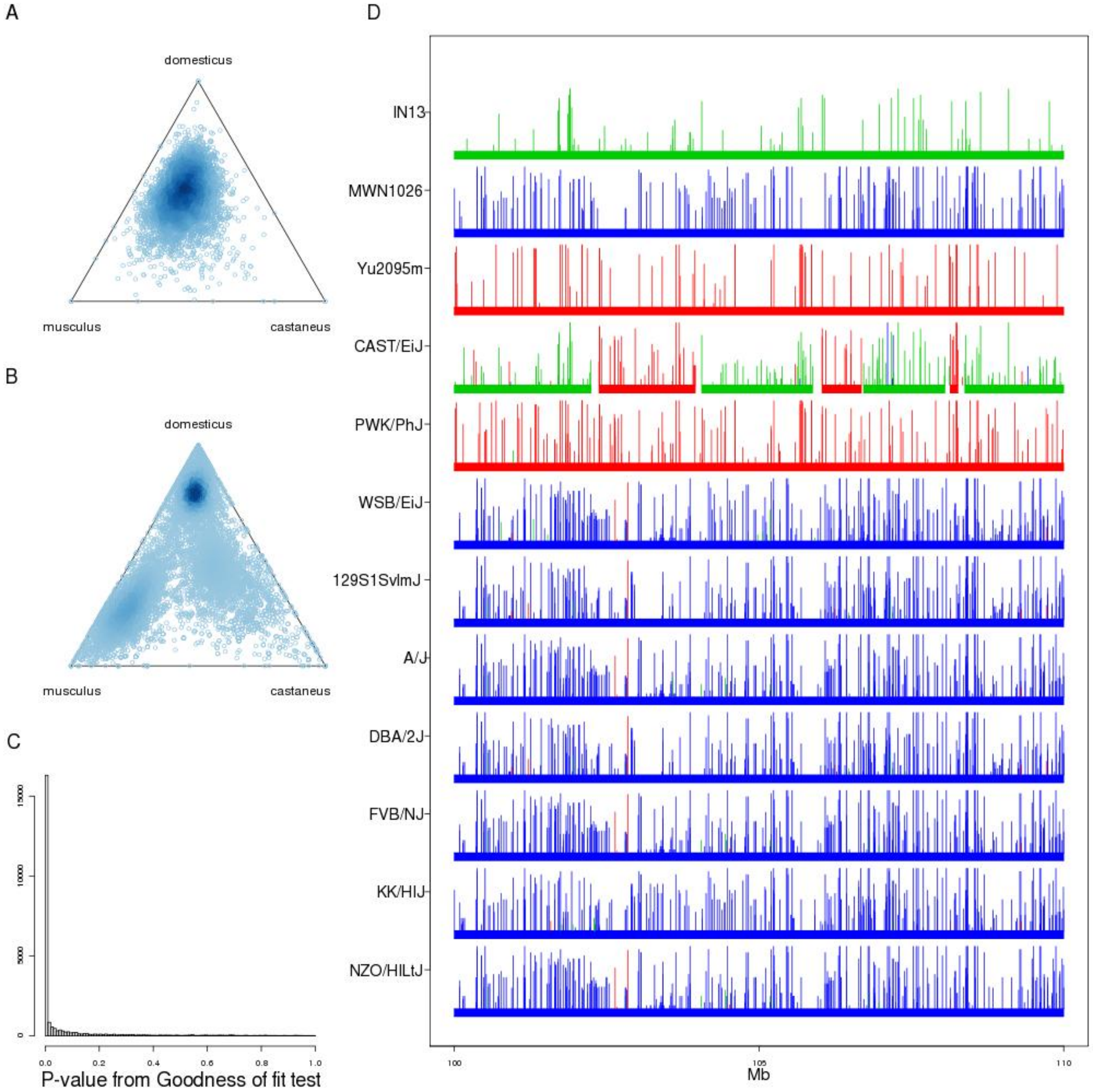

JF1/Ms & MOLD/RkJ
JF1/Ms & MOLF/EiJ
JF1/Ms & MOLG/DnJ
JF1/Ms & MSM/Ms
MOLD/RkJ & MOLF/EiJ
MOLD/RkJ & MOLG/DnJ
MOLD/RkJ & MSM/Ms
MOLF/EiJ & MOLG/DnJ
MOLF/EiJ & MSM/Ms
MOLG/DnJ & MSM/Ms
CIM & MPB
CIM & MH
CIM & TIRANO/EiJ
CIM & WSB/EiJ
CIM & JF1/Ms
CIM & MSM/Ms
MPB & CAST/EiJ
MPB & TIRANO/EiJ
MPB & WSB/EiJ
MPB & JF1/Ms
MPB & MSM/Ms
MH & CAST/EiJ
MH & TIRANO/EiJ
MH & WSB/EiJ
MH & JF1/Ms
MH & MSM/Ms
CAST/EiJ & TIRANO/EiJ
CAST/EiJ & WSB/EiJ
CAST/EiJ & JF1/Ms
CAST/EiJ & MSM/Ms
TIRANO/EiJ & JF1/Ms
TIRANO/EiJ & MSM/Ms
WSB/EiJ & JF1/Ms
WSB/EiJ & MSM/Ms
Mb
0.0 0.2 0.4 0.6 0.8 1.0

Supplementary Figure 7. A) Phylogenetic tree of the Y chromosome. Numbers denote the following samples: **1**) 22MO, BIK/g, BZO, CALB/RkJ, CKN, DIK, DJO, DKN, MOR/RkJ, MWN1026, RBA/DnJ, WLA and WMP, **2**) CKS; **3**) DDO, DMZ, DEB, STLT, STRA, STRB, PERA/EiJ, PERC/EiJ, MOLD/RkJ, MOLF/EiJ, MOLG/DnJ, ALS/LtJ, BTBRT+tf/J, BUB/BnJ, DDY/JclSidSeyFrkJ, FVB/NJ, NOD/ShiLtJ, NON/ShiLtJ, NONcNZO10/LtJ, NONcNZO5/LtJ, SJL/Bm, ST/bJ, SWR/J and TALLYHO/JngJ; **4**) SJL/J; **5**) ALR/LtJ; **6**) NOR/LtJ; **7**) KCT222; **8**) DOT, AKR/J, BPN/3J, MRL/MpJ, PN/nBSwUmabJ, RF/J, IBWSR2, ICOLD2 and IHOT1; **9**) LEWES/EiJ; **10**) WSB/EiJ; **11**) DCP; **12**) MWN1194, MWN1198, MWN1279, DCA, DGA, RBF/DnJ, TIRANO/EiJ and ZALENDE/EiJ; **13**) SOD1/EiJ; **14**) POHN/Deh; **15**) CASA/RkJ and CAST/EiJ; **16**) SF/CamEiJ, BPH/2J, BXB/MpJ, C3HeB/FeJ, CBA/CaJ, CBA/J, DBA/1LacJ, DBA/2HaSmnJ, DBA/2J and RSV/LeJ; **17**) C3H/HeJ; **18**) JF1/Ms, SB/LeJ and STX/Le; **19**) DBA/1J; **20**) 129S6; **21**) MSM/Ms, ILS and ISS; **22**) C57BL/6CR and IHOT2; **23**) 129S1SvImJ; **24**) BALB/cJ; **25**) C57BL/10J; **26**) A/J; **27**) RBB/DnJ, 129P1/ReJ, 129P3, 129T2/SvEmsJ, 129X1/SvJ, A/WySnJ, AEJ/GnLeJ, AEJ/GnRk, BALB/cByJ, BDP/J, BPL/1J, C57BL/10ScNJ, C57BL/10ScSnJ, C57BL/6J, C57BL/6NCI, C57BL/6Tc, C57BLKS/J, C57BR/cdJ, C57L/J, C58/J, CE/J, CHMU/LeJ, DLS/LeJ, EL/SuzSeyFrkJ, HPG/BmJ, I/LnJ, JE/LeJ, KK/HlJ, LG/J, LP/J, LT/SvEiJ, NU/J, NZB/BlNJ, NZL/LtJ, NZM2410/J, NZO/HlLtJ, NZW/LacJ, P/J, RHJ/LeJ, RIIIS/J, SEA/GnJ, SEC/1GnLeJ, SEC/1ReJ, SH1/LeJ, SI/ColTyrp1Dnahc11/J, SM/J, SSL/LeJ, TKDU/DnJ, TSJ/LeJ, YBR/EiJ and ZRDCTRaxChUmdJ; **28**) MGA, Yu2115 and Yu2097; **29**) Yu2113; **30**)

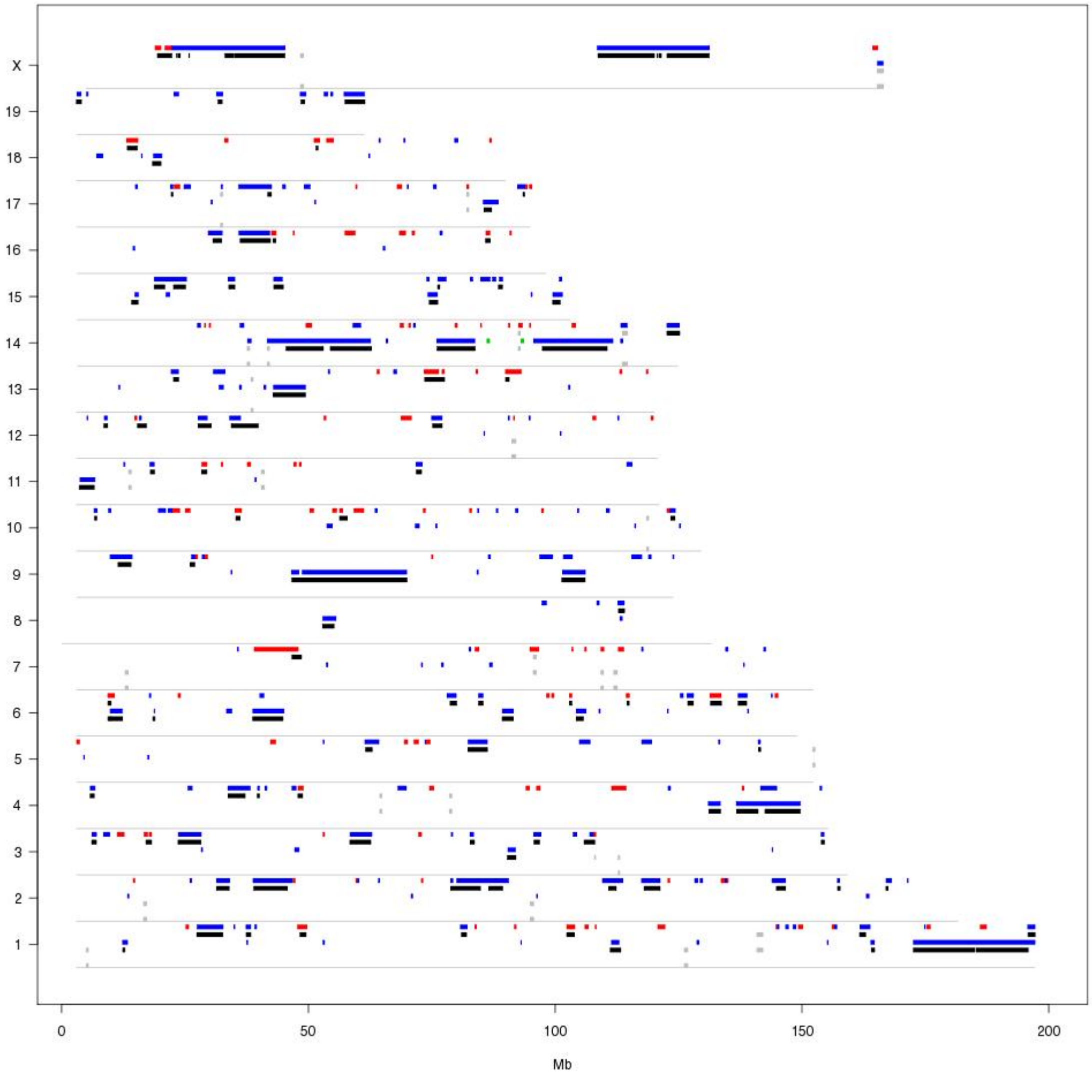
SKIVE/EiJ, BAG74, BAG56, STUP, STUS, STUF, MDGI, MCZ, MDH, MPB, MBK and MBS; **31**) PWK/PhJ, PWD/PhJ, CZECHI/EiJ, BAG99, BUSNA, BULS and MH; **32**) CZECHII/EiJ; **33**) MDG; **34**) IN13, IN17, IN25, IN34, IN47 and IN60; **35**) CIM. B) Phylogenetic tree of the mitochondrial genome. Numbers denote the following samples: **1**) CAST/EiJ, CIM, CKS, CKN and POHN/Deh; **2**) IN17 and IN47; **3**) IN60; **4**) IN25 and IN54; **5**) IN34; **6**) IN38; **7**) IN40; **8**) IN13; **9**) IN59; **10**) DKN and MDG; **11**) DGA; **12**) BIK/g, DIK and SKIVE/EiJ; **13**) MWN1106 and WMP; **14**) MWN1279, MBS, MDH and MDGI ; **15**) KCT222; **16**) MWN1194, MWN1214, 22MO, DCA and SF/Cam/EiJ; **17**) PERA/EiJ and PERC/EiJ; **18**) TIRANO/EiJ and ZALENDE/EiJ; **19**) IS/CamRkJ; **20**) DCP; **21**) RDS12763, MWN1030, MWN1198, DJO and WLA; **22**) MWN1026; **23**) MWN1287, RBB/DnJ, NZB/BINJ, NZL/LtJ, NZM2419/J and NZO/HiLtJ; **24**) C57BL/10ScSnJ; **25**) BZO; **26**) DOT, DDO, DMZ, DEB, STLT ,STRA, STRB, CASA/RkJ, LEWES/EiJ ,MOR/RkJ, RBA/DnJ, RBF/DnJ, SOD1/EiJ, WSB/EiJ, CALB/RkJ, MOLD/RkJ, MOLG/DnJ, 129P1/ReJ, 129P3/J, 129S6, 129S1SvImJ, 129T2/SvEmsJ, 129X1/SvJ, A/J, A/WySnJ, AEJ/GnLeJ, AEJ/GnRk, AKR/J, ALR/LtJ, ALS/LtJ, BALB/cByJ, BALB/cJ, BDP/J, BPH/2J, BPL/1J, BPN/3J, BTBRT+tf/J, BUB/BnJ, BXSB/MpJ, C3H/HeJ, C3HeB/FeJ, C57BL/10J, C57BL/10ScNJ, C57BL/6CR, C57BL/6J, C57BL/6NCI, C57BL/6Tc, C57BLKS/J, C57BR/cdJ, C57L/J, C58/J, CBA/CaJ, CBA/J, CE/J, CHMU/LeJ, DBA/1J, DBA/1LacJ, DBA/2DeJ, DBA/2HaSmnJ, DBA/2J, DDK/Pas, DDY/JclSidSeyFrkJ, DLS/LeJ, EL/SuzSeyFrkJ, FVB/NJ, HPG/BmJ, I/LnJ, JE/LeJ, KK/HlJ, LG/J, LP/J, LT/SvEiJ, MRL/MpJ, NOD/ShiLtJ, NON/ShiLtJ, NONcNZO10/LtJ, NONcNZO5/LtJ, NOR/LtJ, NU/J, NZW/LacJ, P/J, PL/J, PN/nBSwUmabJ, RF/J, RHJ/LeJ, RIIIS/J, RSV/LeJ, SB/LeJ, SEA/GnJ, SEC/1GnLeJ, SEC/1ReJ, SH1/LeJ, SI/ColTyrp1Dnahc11/J, SJL/Bm, SJL/J, SM/J, SSL/LeJ, ST/bJ, STX/Le, SWR/J, TALLYHO/JngJ, TKDU/DnJ, TSJ/LeJ, YBR/EiJ, ZRDCTRaxChUmdJ, IBWSP2, IBWSR2, ICOLD2, IHOT1, IHOT2, ILS and ISS; **27**) Yu2095; **28**) BAG3, BAG94, Yu2115, Yu2099 Yu2097, CZECHII/EiJ and MH,; **29**) BAG99; **30**) Yu2113; **31**) BAG102, RDS10105, Yu2116, JF1/Ms, MBK, MOLF/EiJ and MSM/Ms; **32**) RDS13554, MPB and Yu2120; **33)** BAG56; **34**) BAG68; **35**) BAG74; **36**) MGA, **37**) BULS, BUSNA, CZECHI/EiJ, PWK/PhJ, PWD/PhJ, STUP, STUS and STUF ; **38**, MCZ. Note the significant differences between the known subspecific origin of the strains and their mitochondrial and Y chromosome genomes. For example, CASA/RkJ is a *M. m. castaneus* strain with a *M. m. domesticus* mitochondria; MOLD/RkJ and MOLG/DnJ are *M. m. molossinus* strains with *M. m. domesticus* mitochondria and Y chromosomes; MOLF/EiJ is a *M. m. molossinus* strain with a *M. m. domesticus* Y chromosome; CKN, DKN and CKS are *M. m. castaneus* strains with *M. m. domesticus* Y chromosomes and, RBB/DnJ is *M. m. domesticus* strains with a *M. m. musculus* Y chromosome.


A
B
● M. m. domesticus wild mice
● M. m. domesticus wild-derived strain
● M. m. musculus wild mice
● M. m. musculus wild-derived strain
● M. m. castaneus wild mice
● M. m. castaneus wild-derived strain
● Hybrid wild-derived strain
● M. m. molossinus wild-derived strain
● classical laboratory strain

Supplementary Figure 8. Subspecific assignment. A, Proportion of diagnostic alleles in wild caught mice in every 500K window. The proportion simplex, and the center (0.47, 0.32, 0.21) matches the number of informative sets reported in the results. B, Proportion of diagnostic allele in laboratory strains. Subspecific assignment was performed based on HMM. The figure shows the diagnostic allele score from the corresponding assignment window. C, Frequency distribution of the p-value from goodness of fit test using laboratory strains. For each wild-derived and classical strain, we calculated the diagnostic allele score, and compared it to the center proportion (0.47, 0.32, 0.21). D, distribution of diagnostic alleles in 10Mb window of chromosome 1 for 12 samples. Each bar represents the presence of diagnostic allele in that sample. The height of each bar represents the diagnostic score for that allele while the color represent the subspecies (*M. m. domesticus* (blue), *M. m. musculus* (red) and *M. m. castaneus* (green)). Horizontal lines represent the subspecific assignments.


A
domesticus
musculus
castaneus
B
domesticus
musculus
castaneus
C
15000
10000
5000
0
0.0
0.2
0.4
0.6
0.8
1.0
P-value from Goodness of fit test
D
IN13
MWN1026
Yu2095m
CAST/EiJ
PWK/PhJ
WSB/EiJ
129S1SvImJ
A/J
DBA/2J
FVB/NJ
KK/HIJ
NZO/HILtJ
100
105
110
Mb

Supplementary Figure 9. Concordance between intersubspecific introgression in wild-derived strains identified in this and a previous study[5]. Black bars denote regions of introgression identified previously. Blue, red and green bars denote the subspecific origin of the corresponding region. In each chromosome CAST/EiJ, PWD/PhJ and WSB/EiJ data are depicted from bottom to top and within each strain current data are on top and prior results on the bottom.



Supplementary Figure 10. Spatial distribution of haplotype diversity in classical inbred strains. A) Average genotype identity among classical inbred strains. B) Total length of the distance tree. Both figures are based on distance trees constructed on the basis of the genotype identity among strains from different cliques on each compatible interval.