a Full genome

b Chr8

c Chr9

Supplementary Figure 1. Bayesian trees for haplotypes covering the two largest regions of introgression. Coloration is based on the three different pig groups: Asian domesticated pigs (orange), European wild boars (green) and European domesticated pigs (blue). All individuals that are included in the pairwise comparisons as described in the methods section are included. S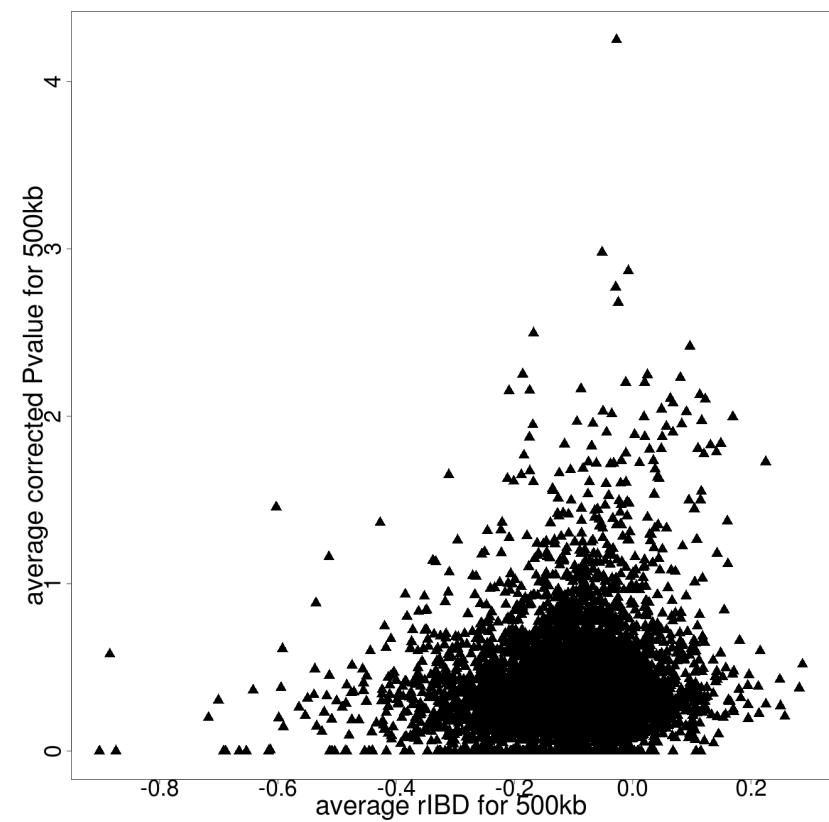1a. Phylogenetic tree based on all markers in the dataset. S1b. Tree based on the introgression region on chromosome 8 (rIBD>0). Each individual has two haplotypes in the tree. S1c. Tree based on the introgression region on chromosome 9 (rIBD>0). Each individual has two haplotypes in the tree.

a

b iHS LW22 vs reference panel
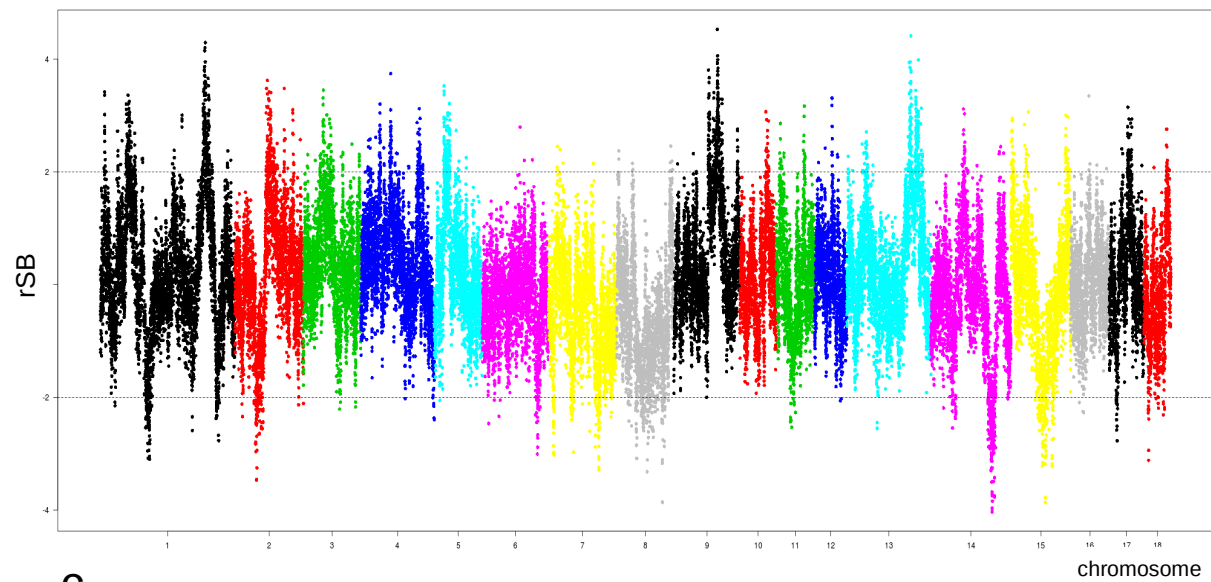
c
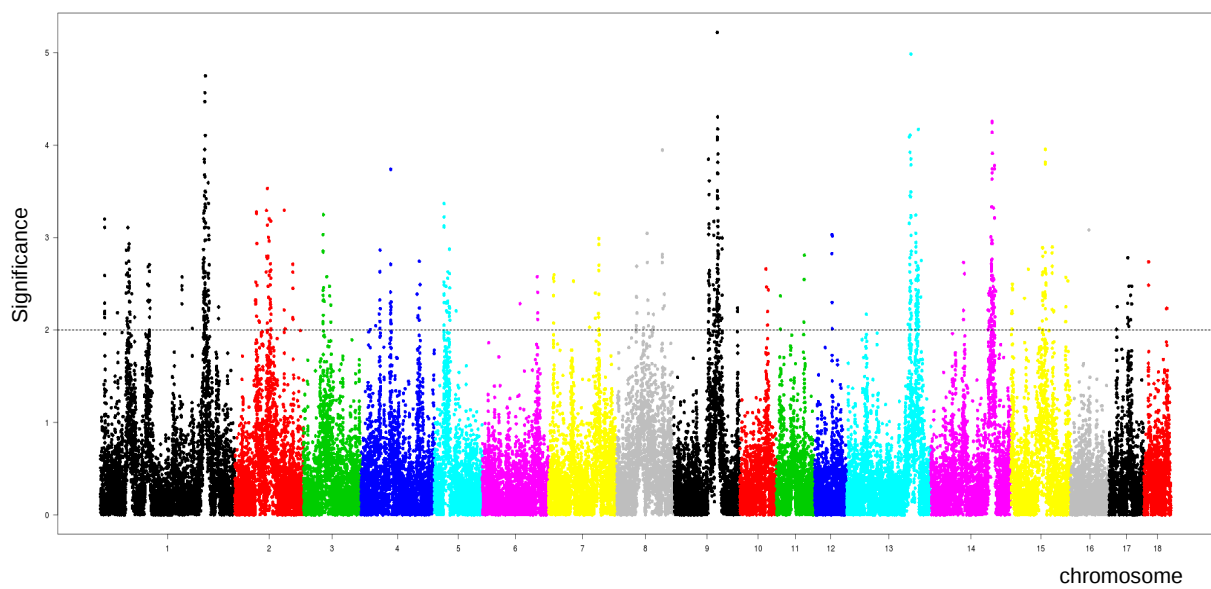
Supplementary Figure 2. Signatures of selection based on EHH in Large White. Regions of extended haplotype homozygosity within 56 LW individuals are identified for each chromosome. S2a. Correlation between iHS significance signals (y-axis) and rIBD signals (x-axis) in LW, averaged over 500kb. S2b. The iHS signals in LW are polarized with iHS signals in a reference panel of 4 other European breeds, resulting in rSB (standardized ratio of iES). S2c. Significance of the rSB signals in LW for each chromosome.
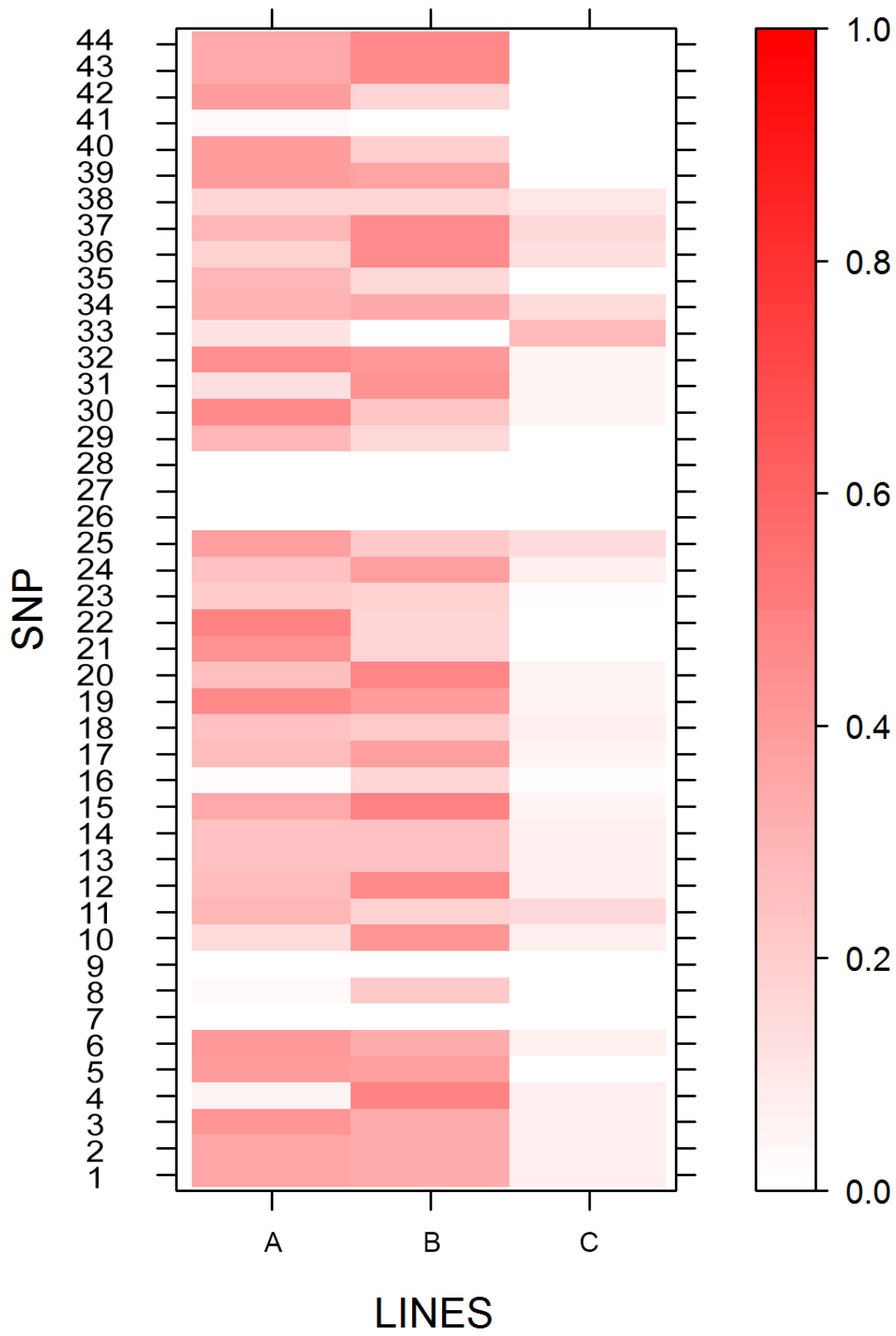
Supplementary Figure 3. Allele frequencies for markers surrounding the introgression region on chromosome 8. Allele frequencies are displayed for each 60K marker (44 total) that lies within the longest introgression region on chromosome 8. Frequencies are calculate for two reproduction-associated lines (line A, N=1053 and Line B, N=568) and one growth-associated line (Line C, N=965).

a

b

c

d

EHH plot

e

AHR locus on chr9: Ancestral Allele

f

AHR locus on chr9: Derived Allele
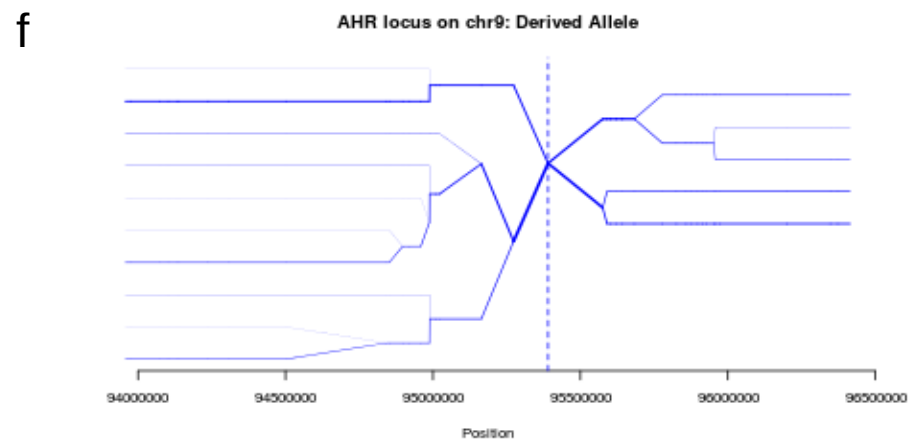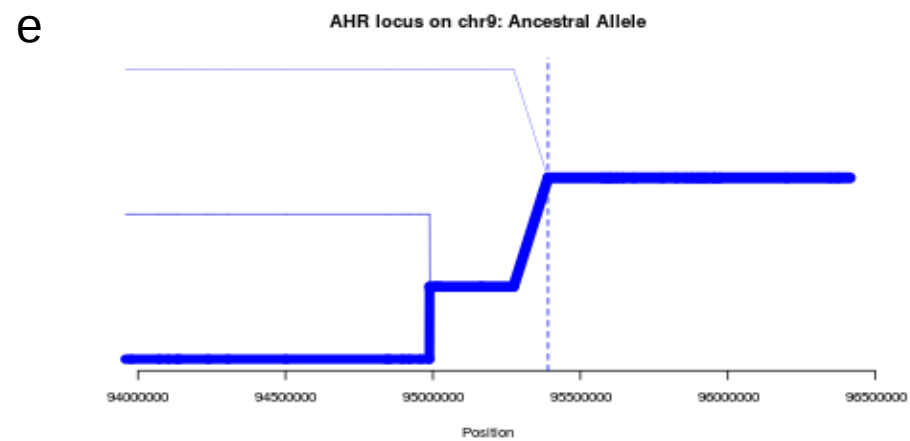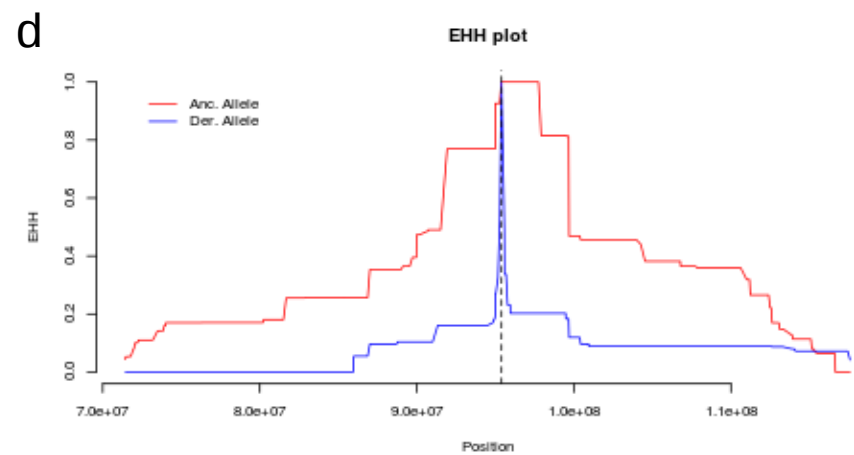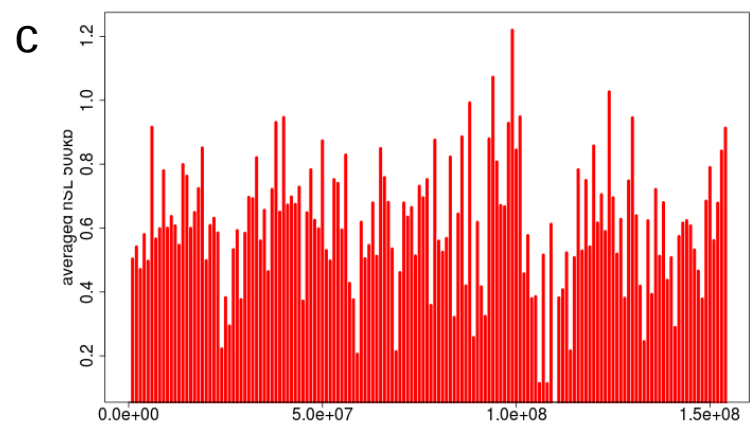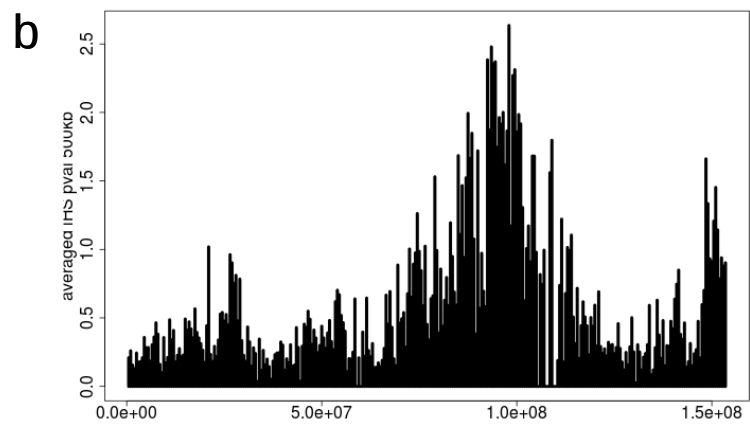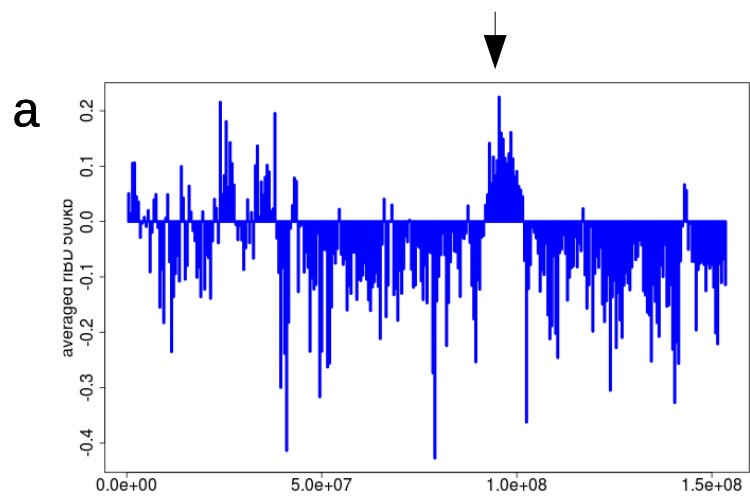
Supplementary Figure 4. Extended haplotype homozygosity in Large White at the *AHR* locus. Regions of extended haplotype homozygosity within 56 Large White individuals are identified for chromosome 9. S4a. The distribution of rIBD in LW over the full length of chromosome 9. The AHR locus is indicated with an arrow, resulting in the highest peak of rIBD. S4b. Significance of the iHS signals in LW for chromosome 9, averaged over 500kb. S4c. Significance of the nSL signals in LW for chromosome 9, averaged over 500kb. S4d. Extended haplotype homozygosity of the ancestral allele in LW at the *AHR* locus. S4e-f. Bifurcation diagrams of the breakdown of LD at increasing distance from the AHR locus.

Supplementary table 1

Origin	Groups	Individual	average coverage	usage
Euro breed	Duroc	DU23M01	10.885	Phasing
Euro breed	Duroc	DU23M02	11.776	Phasing
Euro breed	Duroc	DU23M03	6.206	Phasing
Euro breed	Duroc	DU23M04	7.759	Phasing
Euro breed	Hampshire	HA20U01	11.646	Phasing
Euro breed	Hampshire	HA20U02	10.299	Phasing
Euro breed	Landrace1	LR21M03	9.548	Phasing
Euro breed	Landrace2	LR24F01	13.917	Phasing
Euro breed	Landrace2	LR24F08	9.213	Phasing
Euro breed	Landrace3	LR30F02	7.604	Phasing
Euro breed	Landrace3	LR30F03	7.782	Phasing
Euro breed	Large White 1	LW22M04	9.771	Phasing + analysis
Euro breed	Large White 1	LW22M07	10.642	Phasing + analysis
Euro breed	Large White 1	LW22F01	5.888	Phasing + analysis
Euro breed	Large White 1	LW22F02	10.318	Phasing + analysis
Euro breed	Large White 1	LW22F03	10.316	Phasing + analysis
Euro breed	Large White 1	LW22F04	10.338	Phasing + analysis
Euro breed	Large White 1	LW22F06	9.547	Phasing + analysis
Euro breed	Large White 1	LW22F07	11.790	Phasing + analysis
Euro breed	Large White 2	LW36F01	10.070	Phasing + analysis
Euro breed	Large White 2	LW36F02	8.633	Phasing + analysis
Euro breed	Large White 2	LW36F03	9.004	Phasing + analysis
Euro breed	Large White 2	LW36F04	9.576	Phasing + analysis
Euro breed	Large White 2	LW36F05	8.737	Phasing + analysis
Euro breed	Large White 2	LW36F06	8.820	Phasing + analysis
Euro breed	Pietrain	PI21F02	10.760	Phasing
Euro breed	Pietrain	PI21F06	10.783	Phasing
Euro breed	Pietrain	PI21M17	8.671	Phasing
Euro breed	Pietrain	PI21M20	5.931	Phasing
Euro breed	Pietrain	PI21M21	11.435	Phasing
Asia breed	Jianquhai	JQ01U02	10.746	Phasing + analysis
Asia breed	Meishan1	MS20M03	10.331	Phasing
Asia breed	Meishan1	MS20M05	10.457	Phasing
Asia breed	Meishan1	MS20U10	9.410	Phasing
Asia breed	Meishan1	MS20U11	9.398	Phasing + analysis
Asia breed	Meishan1	MS20U13	7.782	Phasing
Asia breed	Meishan2	MS21M01	8.653	Phasing
Asia breed	Meishan2	MS21M05	10.610	Phasing
Asia breed	Meishan2	MS21M07	8.995	Phasing + analysis
Asia breed	Meishan2	MS21M08	9.013	Phasing
Asia breed	Meishan2	MS21M14	10.429	Phasing + analysis
Asia breed	Xiang	XI01U03	9.247	Phasing + analysis
Asia breed	Xiang	XI01U04	9.082	Phasing + analysis
Euro wild	Dutch wild1	WB21F03	10.559	Phasing

Supplementary table 1

Euro wild	Dutch wild1	WB21F04	12.613	Phasing
Euro wild	Dutch wild1	WB21F05	9.406	Phasing + analysis
Euro wild	Dutch wild1	WB21M03	11.663	Phasing
Euro wild	Dutch wild1	WB21M05	15.245	Phasing + analysis
Euro wild	Dutch wild2	WB22F01	5.725	Phasing
Euro wild	Dutch wild2	WB22F02	8.167	Phasing + analysis
Euro wild	Dutch wild2	WB22F03	9.429	Phasing
Euro wild	Dutch wild2	WB22F04	9.022	Phasing
Euro wild	Dutch wild2	WB22M03	11.907	Phasing
Euro wild	French wild	WB25U11	9.622	Phasing + analysis
Euro wild	Swiss wild	WB26M09	14.618	Phasing + analysis
Euro wild	Samos wild	WB33U04	11.524	Phasing + analysis
Euro wild	Samos wild	WB33U05	10.318	Phasing + analysis
Euro wild	Italian wild	WB42U06	12.674	Phasing
Euro wild	Italian wild	WB44U06	12.158	Phasing + analysis
Euro wild	Italian wild	WB44U07	10.721	Phasing
Asia wild	Japanese wild	WB20U02	11.315	Phasing
Asia wild	Chinese wild1	WB29U04	5.492	Phasing
Asia wild	Chinese wild1	WB29U12	10.385	Phasing
Asia wild	Chinese wild1	WB29U14	9.035	Phasing
Asia wild	Chinese wild1	WB29U16	12.772	Phasing
Asia wild	Chinese wild2	WB30U01	5.405	Phasing
Asia wild	Chinese wild2	WB30U08	10.092	Phasing
Asia wild	Chinese wild2	WB30U09	11.846	Phasing
Outgroup	Sumatra wild	INDO22	11.494	Phasing + outgroup
Outgroup	Sumatra wild	INDO33	11.155	Phasing

Supplementary Table 1. Overview of re-sequenced individuals that are used in the experiment. The origin of each sample is shown in the column "Origin" and the breed name or geographical region of the population is found in the column "Groups". The usage of each individual in the experiment is explained in the column "Usage" where "phasing" represents individuals that are used only for phasing the data, and "analysis" means that they were also used for pairwise IBD comparisons.

Supplementary table 2

Chromosome	start	stop	Length (ZrIBD>2)	genes		
Ssc10_2_1	4090000	4100000	10000			
Ssc10_2_1	6840000	6860000	20000			
Ssc10_2_1	7550000	7640000	90000			
Ssc10_2_1	7710000	7720000	10000			
Ssc10_2_1	27170000	27190000	20000			
Ssc10_2_1	28540000	28700000	160000	REPS1	C6ORF115	
Ssc10_2_1	29650000	29660000	10000			
Ssc10_2_1	29670000	29700000	30000			
Ssc10_2_1	30780000	30800000	20000			
Ssc10_2_1	30810000	30860000	50000			
Ssc10_2_1	30880000	30970000	90000			
Ssc10_2_1	31090000	31130000	40000			
Ssc10_2_1	31190000	31200000	10000			
Ssc10_2_1	31790000	31840000	50000			
Ssc10_2_1	32020000	32310000	290000	MYB	AHI1	
Ssc10_2_1	32410000	32440000	30000			
Ssc10_2_1	32620000	32630000	10000			
Ssc10_2_1	52110000	52280000	170000	EYS		
Ssc10_2_1	53390000	53760000	370000			
Ssc10_2_1	54040000	54080000	40000			
Ssc10_2_1	56830000	57020000	190000	C6orf57	FAM135A	
Ssc10_2_1	71440000	71470000	30000			
Ssc10_2_1	71480000	71510000	30000			
Ssc10_2_1	71530000	71540000	10000			
Ssc10_2_1	71610000	71640000	30000			
Ssc10_2_1	74270000	74390000	120000	POU3F2		
Ssc10_2_1	77060000	77160000	100000	GRIK2		
Ssc10_2_1	77170000	77210000	40000			
Ssc10_2_1	81970000	82020000	50000	AIM1		
Ssc10_2_1	83100000	83110000	10000	SCML4		
Ssc10_2_1	84510000	84520000	10000			
Ssc10_2_1	84550000	84600000	50000	CEP57L1		
Ssc10_2_1	84870000	84890000	20000	AKD1		
Ssc10_2_1	84970000	84990000	20000	AKD1		
Ssc10_2_1	85040000	85060000	20000			
Ssc10_2_1	85520000	85640000	120000	WASF1		
Ssc10_2_1	86090000	86120000	30000			
Ssc10_2_1	86140000	86910000	770000	GTF3C6	CDK19	RPF2
				AMD1	REV3L	KIAA1919
				SLC16A10		
Ssc10_2_1	87040000	87060000	20000	TRAF3IP2		
Ssc10_2_1	87400000	87530000	130000			
Ssc10_2_1	87540000	87570000	30000			
Ssc10_2_1	90300000	90340000	40000			

Supplementary table 2

Ssc10_2_1	90640000	90730000	90000			
Ssc10_2_1	91830000	91880000	50000	NT5DC1		
Ssc10_2_1	92080000	92240000	160000			
Ssc10_2_1	92460000	92540000	80000	SULT2B1		
Ssc10_2_1	92840000	92890000	50000			
Ssc10_2_1	92900000	93420000	520000	RWDD2A	PRSS35	ME1
				PGM3	DOPEY1	
Ssc10_2_1	93450000	93540000	90000	UBE3D	TSPAN13	
Ssc10_2_1	94010000	94270000	260000			
Ssc10_2_1	97970000	97990000	20000			
Ssc10_2_1	98040000	98090000	50000	IRAK1BP1		
Ssc10_2_1	103820000	103930000	110000			
Ssc10_2_1	104740000	104870000	130000			
Ssc10_2_1	107740000	107880000	140000			
Ssc10_2_1	107910000	107920000	10000			
Ssc10_2_1	108000000	108020000	20000			
Ssc10_2_1	177280000	177340000	60000	CDH20		
Ssc10_2_1	178680000	178690000	10000			
Ssc10_2_1	178700000	178730000	30000			
Ssc10_2_1	230010000	230030000	20000			
Ssc10_2_1	281820000	281830000	10000			
Ssc10_2_1	284430000	284510000	80000	SAL1		
Ssc10_2_1	312000000	312010000	10000			
Ssc10_2_10	410000	420000	10000			
Ssc10_2_10	440000	450000	10000			
Ssc10_2_10	460000	480000	20000			
Ssc10_2_10	2290000	2310000	20000	B3GALT2		
Ssc10_2_10	2320000	2330000	10000			
Ssc10_2_10	4200000	4210000	10000			
Ssc10_2_10	4360000	4400000	40000			
Ssc10_2_10	4410000	4420000	10000			
Ssc10_2_10	4430000	4440000	10000			
Ssc10_2_10	4480000	4780000	300000			
Ssc10_2_10	23740000	23750000	10000			
Ssc10_2_10	47760000	47770000	10000			
Ssc10_2_10	48260000	48310000	50000			
Ssc10_2_10	48370000	48420000	50000			
Ssc10_2_10	48550000	48630000	80000	PTPLA		
Ssc10_2_10	50420000	50440000	20000			
Ssc10_2_10	50530000	50550000	20000			
Ssc10_2_11	8620000	8650000	30000	FRY		
Ssc10_2_11	8700000	8720000	20000	N4BP2L2		
Ssc10_2_11	25780000	25800000	20000			
Ssc10_2_11	25900000	25930000	30000			
Ssc10_2_12	680000	720000	40000			

Supplementary table 2

Ssc10_2_12	990000	1020000	30000			
Ssc10_2_12	1030000	1180000	150000	NPLOC4	FASN	C17orf70
				FSCN2	BETA-ACTIN	
Ssc10_2_12	1230000	1380000	150000	SLC38A10		
Ssc10_2_12	1400000	1410000	10000			
Ssc10_2_12	1420000	1500000	80000	AATK	C12H17orf56	AZI1
Ssc10_2_12	1520000	1650000	130000	CHMP6	RPTOR	
Ssc10_2_12	1660000	1720000	60000			
Ssc10_2_12	21660000	21670000	10000	KRTAP1-3		
Ssc10_2_12	21680000	21740000	60000	KRT39	KRTAP3-1	
Ssc10_2_12	25130000	25220000	90000	IGF2BP1		
Ssc10_2_12	25300000	25350000	50000			
Ssc10_2_12	26800000	26820000	20000	ACSF2		
Ssc10_2_12	28440000	28460000	20000			
Ssc10_2_12	41520000	41550000	30000	NLE1		
Ssc10_2_12	46340000	46380000	40000			
Ssc10_2_12	53520000	53530000	10000			
Ssc10_2_13	14220000	14290000	70000	NGLY1		
Ssc10_2_13	15470000	15520000	50000	SLC4A7		
Ssc10_2_13	16170000	16290000	120000			
Ssc10_2_13	16670000	16720000	50000			
Ssc10_2_13	29740000	29750000	10000			
Ssc10_2_13	29800000	29810000	10000			
Ssc10_2_13	45170000	45200000	30000			
Ssc10_2_13	45210000	45240000	30000			
Ssc10_2_13	53960000	54000000	40000			
Ssc10_2_13	54030000	54050000	20000			
Ssc10_2_13	61610000	61660000	50000			
Ssc10_2_13	158690000	158700000	10000			
Ssc10_2_13	170850000	170860000	10000			
Ssc10_2_14	130000	150000	20000	CDK20		
Ssc10_2_14	180000	220000	40000			
Ssc10_2_14	240000	250000	10000			
Ssc10_2_14	9450000	9470000	20000			
Ssc10_2_14	9510000	9520000	10000			
Ssc10_2_14	11830000	11840000	10000			
Ssc10_2_14	13330000	13380000	50000	RPLP1		
Ssc10_2_14	19320000	19340000	20000			
Ssc10_2_14	25070000	25090000	20000			
Ssc10_2_14	90970000	91000000	30000			
Ssc10_2_15	7130000	7220000	90000			
Ssc10_2_15	7690000	7750000	60000			
Ssc10_2_15	9330000	9500000	170000			
Ssc10_2_15	30010000	30230000	220000			
Ssc10_2_15	33360000	33380000	20000			

Ssc10_2_15	33390000	33450000	60000			
Ssc10_2_15	59950000	60170000	220000	NRG1		
Ssc10_2_15	60290000	60300000	10000			
Ssc10_2_15	97710000	97860000	150000	FRZB	DNAJC10	
Ssc10_2_15	97900000	98380000	480000	NUP35	NCKAP1	DUSP19
Ssc10_2_15	119770000	119780000	10000			
Ssc10_2_15	119790000	119800000	10000	VCL		
Ssc10_2_15	120330000	120510000	180000			
Ssc10_2_15	123770000	123880000	110000			
Ssc10_2_15	124040000	124200000	160000	MAP2		
Ssc10_2_15	136610000	136620000	10000			
Ssc10_2_15	140000000	140010000	10000			
Ssc10_2_15	140790000	140800000	10000			
Ssc10_2_16	3500000	3510000	10000			
Ssc10_2_16	6130000	6140000	10000			
Ssc10_2_16	23150000	23160000	10000			
Ssc10_2_16	23170000	23220000	50000			
Ssc10_2_16	24940000	25000000	60000			
Ssc10_2_17	35900000	36040000	140000	SMOX		
Ssc10_2_17	41500000	41530000	30000	BPIFB4		
Ssc10_2_17	58300000	58340000	40000			
Ssc10_2_17	66810000	66820000	10000			
Ssc10_2_18	40000	50000	10000			
Ssc10_2_18	17560000	17580000	20000			
Ssc10_2_18	18370000	18410000	40000			
Ssc10_2_18	23950000	24210000	260000			
Ssc10_2_18	24630000	24800000	170000	GPR37		
Ssc10_2_18	24920000	24940000	20000			
Ssc10_2_18	25070000	25100000	30000			
Ssc10_2_18	25130000	25140000	10000			
Ssc10_2_2	11330000	11370000	40000	OSBP		
Ssc10_2_2	11390000	11410000	20000			
Ssc10_2_2	11440000	11450000	10000	OR4D10		
Ssc10_2_2	11470000	11490000	20000	OR5A2		
Ssc10_2_2	12620000	12640000	20000	LDHB		
Ssc10_2_2	12990000	13140000	150000	OR4K15	OR4K1	OR4L1
Ssc10_2_2	13320000	13340000	20000	PRG3	PRG3	
Ssc10_2_2	24410000	24450000	40000			
Ssc10_2_2	24460000	24570000	110000			
Ssc10_2_2	33760000	33810000	50000			
Ssc10_2_2	33880000	33920000	40000			
Ssc10_2_2	33990000	34000000	10000			
Ssc10_2_2	34210000	34280000	70000			
Ssc10_2_2	34550000	34930000	380000	KIF18A	METT5D1	
Ssc10_2_2	35310000	35320000	10000			

Ssc10_2_2	36610000	36730000	120000			
Ssc10_2_2	40640000	40650000	10000			
Ssc10_2_2	42060000	42080000	20000	NAV2		
Ssc10_2_2	42110000	42120000	10000	DBX1		
Ssc10_2_2	42180000	42190000	10000			
Ssc10_2_2	50200000	50210000	10000			
Ssc10_2_2	67840000	67860000	20000			
Ssc10_2_2	68110000	68120000	10000			
Ssc10_2_2	68840000	68870000	30000	OR7D4	OR7D4	ZNF846
Ssc10_2_2	69110000	69360000	250000	P2RY11	COL5A3	RDH8
				C3	C19ORF66	ANGPTL6
				PPAN	EIF3G	DNMT1
Ssc10_2_2	69410000	69560000	150000	ZGLP1	ICAM1	ICAM5
				ICAM6	ZGLP1	FDX1L
				RAVER1	RAVER1	ICAM-3
				TYK2	CDC37	
Ssc10_2_2	69570000	69610000	40000	PDE4A		
Ssc10_2_2	70060000	70090000	30000	C19ORF52	YIPF2	
Ssc10_2_2	86740000	86760000	20000			
Ssc10_2_2	86850000	86870000	20000			
Ssc10_2_2	86880000	86900000	20000			
Ssc10_2_2	86910000	87010000	100000	IQGAP2		
Ssc10_2_2	88570000	88780000	210000	AP3B1		
Ssc10_2_2	88910000	88930000	20000			
Ssc10_2_2	89280000	89300000	20000			
Ssc10_2_2	89320000	89370000	50000	ARSB		
Ssc10_2_2	89500000	89530000	30000			
Ssc10_2_2	90480000	90490000	10000			
Ssc10_2_2	90500000	90520000	20000	THBS4		
Ssc10_2_2	90580000	90620000	40000			
Ssc10_2_2	90890000	91020000	130000	FAM151B	ZFYVE16	
Ssc10_2_2	93160000	93260000	100000			
Ssc10_2_2	94090000	94110000	20000			
Ssc10_2_2	97000000	97080000	80000			
Ssc10_2_2	101260000	101330000	70000			
Ssc10_2_2	101590000	101640000	50000			
Ssc10_2_2	106910000	106960000	50000	CAST		
Ssc10_2_2	107030000	107330000	300000	ERAP2	ERAP1	
Ssc10_2_2	107370000	107440000	70000	IRAP		
Ssc10_2_2	107450000	107480000	30000			
Ssc10_2_2	107490000	107560000	70000	LIX1		
Ssc10_2_2	107950000	107980000	30000			
Ssc10_2_2	108680000	108850000	170000			
Ssc10_2_2	110280000	110340000	60000			
Ssc10_2_2	110950000	111000000	50000			

Ssc10_2_2	111340000	111370000	30000	
Ssc10_2_2	111380000	111560000	180000	
Ssc10_2_2	115770000	115810000	40000	
Ssc10_2_2	115980000	115990000	10000	
Ssc10_2_2	123230000	123240000	10000	
Ssc10_2_2	125130000	125360000	230000	COMMD10
Ssc10_2_2	125390000	125470000	80000	SEMA6A
Ssc10_2_2	125550000	125560000	10000	
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Ssc10_2_3	12150000	12170000	20000	
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Ssc10_2_3	29750000	29760000	10000	
Ssc10_2_3	29830000	29840000	10000	
Ssc10_2_3	30940000	30960000	20000	
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Ssc10_2_4	132700000	132720000	20000			
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Ssc10_2_6	19010000	19030000	20000			
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Ssc10_2_6	21210000	21230000	20000			
Ssc10_2_6	22850000	23020000	170000			
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Ssc10_2_6	38340000	38430000	90000			
Ssc10_2_6	39160000	39300000	140000			
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Ssc10_2_6	46230000	46370000	140000	PLAUR	PHLDB3	LYPD3
Ssc10_2_6	52330000	52440000	110000	DPRX	SLC7A3	
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Ssc10_2_6	54270000	54290000	20000	SYT5	DNAAF3	
Ssc10_2_6	56310000	56400000	90000	OR5R1		
Ssc10_2_6	56410000	56430000	20000			
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Ssc10_2_6	112940000	112950000	10000			
Ssc10_2_6	119350000	119370000	20000			
Ssc10_2_6	156300000	156310000	10000			
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Ssc10_2_7	15640000	15660000	20000			
Ssc10_2_7	15690000	15700000	10000			
Ssc10_2_7	15840000	15850000	10000			
Ssc10_2_7	18890000	18900000	10000			
Ssc10_2_7	22950000	23000000	50000			
Ssc10_2_7	23010000	23060000	50000			
Ssc10_2_7	23660000	23710000	50000	OR1F1	OR2G6	
Ssc10_2_7	23870000	23990000	120000	ZNF167	ZNF192	ZNF389
				ZNF165	ZSCAN16	
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				ZNF397	ZKSCAN4	PGBD1
				ZSCAN12	OR2B11	GPX5
				GPX6		
Ssc10_2_7	24270000	24360000	90000	ZNF232		
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Ssc10_2_7	24760000	24780000	20000	AFP		
Ssc10_2_7	24810000	25230000	420000	RNF39	TRIM15	TRIM10
				TRIM40	TRIM31	PPP1R11
				ZNRD1	C7H6ORF12	KRAB
				MOG	RNF39	ZNRD1
				KRAB	GABBR1	
Ssc10_2_7	25320000	25350000	30000	UBD		
Ssc10_2_7	25360000	25390000	30000	OR2G6	OR2G3	OR6Q1
Ssc10_2_7	25450000	25700000	250000	OR14J1	OR12D2	OR12D2

				OR5V1	OR14J1	
Ssc10_2_7	25740000	25750000	10000	OR12D2		
Ssc10_2_7	25760000	25780000	20000	OR12D3	OR5V1	
Ssc10_2_7	26670000	26930000	260000	C7H6orf136	SLA-11	TRIM39
				RPP21	GNL1	PRR3
				ABCF1	PPP1R10	MRPS18B
				ATAT1	DHX16	
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Ssc10_2_7	132350000	132380000	30000			
Ssc10_2_7	132390000	132500000	110000			
Ssc10_2_7	132640000	132680000	40000	OR4F3	OR4F16	OR4F29
Ssc10_2_8	8850000	8870000	20000			
Ssc10_2_8	9770000	9790000	20000			
Ssc10_2_8	10340000	10350000	10000			
Ssc10_2_8	13890000	13900000	10000			
Ssc10_2_8	14070000	14080000	10000			
Ssc10_2_8	14200000	14250000	50000			
Ssc10_2_8	14620000	14630000	10000			
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Ssc10_2_8	98780000	98800000	20000			
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				MFSD8		
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Ssc10_2_8	107310000	107320000	10000			
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Ssc10_2_8	145870000	145900000	30000			
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Ssc10_2_8	146660000	146690000	30000	FGF5		
Ssc10_2_9	90000	110000	20000			

Ssc10_2_9	230000	290000	60000	TMEM41B		
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				OR10A6		
Ssc10_2_9	2360000	2370000	10000	OR5P3		
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Ssc10_2_9	5210000	5230000	20000			
Ssc10_2_9	5550000	5560000	10000	OR52A5		
Ssc10_2_9	5890000	5910000	20000	OR51H1P		
Ssc10_2_9	6560000	6570000	10000			
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Ssc10_2_9	25410000	25430000	20000			
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Ssc10_2_9	25560000	25570000	10000			
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Ssc10_2_9	32480000	32520000	40000			
Ssc10_2_9	32530000	32560000	30000			
Ssc10_2_9	32580000	32590000	10000			
Ssc10_2_9	32780000	32860000	80000			
Ssc10_2_9	33240000	33330000	90000	ENY2		
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Ssc10_2_9	35660000	35670000	10000			
Ssc10_2_9	35930000	35980000	50000			
Ssc10_2_9	35990000	36020000	30000			
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Ssc10_2_9	119600000	119610000	10000		
Ssc10_2_9	125520000	125530000	10000		
Ssc10_2_9	142330000	142350000	20000		
Ssc10_2_9	142680000	142690000	10000		
Ssc10_2_9	143230000	143260000	30000		

Supplementary Vable 2. Overview of introgressed regions in the Large white genome. Regions in the genome where Asian introgression is most pronounced (ZrIBD >2) and the genes within these regions are listed. "Start" represents the startbin of 10.000bp and length indicates how long the stetch within the region of inferred introgression is.