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Genome-wide association study between copy number variation regions and carcass and meat quality traits in Nellore cattle

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Table S1. Description of significant (P value<0.05) CNVRs associated with beef tenderness (BT) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR
CNVR_gain_3	1	Gain	1374155	3404571	2030417	27	45	0.026	0.36
CNVR_gain_644	2	Gain	81291862	83154452	1862591	32	15	0.015	0.40
CNVR_loss_936	5	Loss	22514133	22563988	49856	233	204	0.031	0.36
CNVR_loss_1571	8	Loss	10248664	15908996	5660333	88	114	0.041	0.37
CNVR_loss_1804	9	Loss	27779045	35400778	7621734	84	111	0.032	0.39
CNVR_loss_2268	11	Loss	105371400	106123357	751958	22	10	0.023	0.36
CNVR_loss_2269	11	Loss	106158972	106995276	836305	31	17	0.024	0.36
CNVR_loss_2314	12	Loss	32054331	32232492	178162	53	36	0.050	0.36
CNVR_loss_3436	20	Loss	70875830	71992748	1116919	32	19	0.043	0.36
CNVR_loss_4214	29	Loss	11791851	12281860	490010	69	48	0.031	0.36
CNVR_loss_3745	23	Loss	28828468	28861534	33067	26	42	0.040	0.36

	Genes
CNVR_gain_3	*IFNGR2, IFNAR1, LOC104970778, IL10RB, IFNAR2, LOC526226, OLIG1, LOC100848368, OLIG2, LOC100848215, C1H21orf62, PAXBP1, SYNJ1, C1H21orf59, EVA1C, LOC104970779, LOC104970780, URB1, MRAP, MIS18A, LOC101904359, HUNK, LOC104970781, SCAF4, SOD1*
CNVR_gain_644	*LOC785710*
CNVR_loss_936	*LOC784883*
CNVR_loss_1571	*PNOC, TRNAG-GCC, ELP3, NUGGC, SCARA5, PBK, ESCO2, CCDC2, SCARA3, CLU, TMEM215, NDUFB6, MIR2469, TOPORS, DDX58, ACO1, TRNAC-ACA, MIR2285M-5, LINGO2, MIR876, MIR873, LOC104969264, LOC104969267, LOC104968521, LOC104969273, LOC104969276, LOC104969274, LOC104969277, LOC104969278*
CNVR_loss_1804	*TRDN, CLVS2, SMPDL3A, FABP7, PKIB, SERINC1, HSF2, GJA1, TBC1D32, MAN1A1, FAM184A, ASF1A, CEP85L, MCM9, PLN, SLC35F1, NUS1, NEPN, GOPC, DCBLD1, FAM162B, KPNA5, ZUFSP, RWDD1, TRAPPC3L, DSE, FRK, COL10A1, NT5DC1*
CNVR_loss_2268	*CACNA1B, EHMT1, ARRDC1, ZMYND19, MRPL41, PNPLA7, NSMF, ENTPD8, NOXA1, EXD3, NRARP, TOR4A, NELFB, C11H9orf173, FAM166A, TUBB4B, SLC34A3, RNF224, CYSRT1, RNF208, NDOR1, TMEM203, TPRN, SSNA1, ANAPC2, TMEM210, LRRC26, GRIN1, RXRA*

CNVR_loss_2269	*UAP1L1, SAPCD2, ENTPD2, NPDC1, FUT7, ABCA2, CLIC3, LCNL1, PTGDS, LCN12, C8G, FBXW5, TRAF2, EDF1, MAMDC4, PHPT1, C11H9orf172, RABL6, CCDC183, TMEM141, LOC100295548, LCN6, LOC511158, MRPS2, C11H9orf116, PPP1R26, OLFM1, FCN1, COL5A1*
CNVR_loss_2314	*LOC10084733, LOC101902112*
CNVR_loss_3436	*IRX4, LPCAT1, SLC12A7, CEP72, LOC529500, NDUFS6, CLPTM1L, BRD9, LOC617224, EXOC3, CCDC127, LOC101907943, NKD2, SLC9A3, SLC6A3, TRIP13, LOC101903965, MRPL36, TERT, LOC104975297, LOC107131585, LOC104975299, LOC101903732, SLC6A19, LOC107131586, SLC6A18, TPPP*
CNVR_loss_4214	*LOC786987, LOC104975671*
CNVR_loss_3745	*LOC505383, LOC101906698, LOC104976224, LOC104976223, LOC104976227*

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.

Table S2. Description of significant (P value < 0.05) CNVRs associated with marbling index (MB) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR
CNVR_loss_82	1	Loss	36764094	37254059	489966	22	9	0.03	0.35
CNVR_loss_188	1	Loss	102146418	104368918	2222501	46	29	0.04	0.40
CNVR_loss_668	3	Loss	50819261	51600304	781044	24	10	0.02	0.36
CNVR_loss_827	4	Loss	24824291	24959800	135510	35	56	0.02	0.37
CNVR_loss_1016	4	Loss	118884897	118891222	6326	50	33	0.04	0.40
CNVR_gain_1822	5	Gain	115342811	118109413	2766603	55	77	0.03	0.35
CNVR_loss_1218	5	Loss	102375978	102896856	520879	91	116	0.05	0.35
CNVR_loss_1456	7	Loss	10826539	11486814	660276	66	99	0.006	0.36
CNVR_loss_1540	7	Loss	41223948	41241356	17409	30	15	0.02	0.35
CNVR_loss_2088	10	Loss	7498529	10676872	3178344	23	9	0.02	0.37
CNVR_gain_3467	11	Gain	20031	124362	104332	34	20	0.03	0.36

	Genes
CNVR_loss_82	EPHA3 LOC101904733
CNVR_loss_188	*BCHE LOC104970978 LOC100139653 SLITRK3 LOC782206 LOC782179 SI LOC104970979 LOC781603*

CNVR_loss_668	*EVI5 TRNAC-ACA GFI1 RPAP2 GLMN C3H1orf146 TRNAE-UUC BRDT EPHX4 BTBD8 LOC785783 LOC530756 LOC104971636*
CNVR_loss_827	*ISPD SOSTDC1*
CNVR_loss_1016	*RNF32*
CNVR_gain_1822	*EFCAB6 PARVB PARVG KIAA1644 LDOC1L PRR5 PHF21B NUP50 MIR1249 KIAA0930 UPK3A FAM118A SMC1B RIBC2 FBLN1 ATXN10 MIRLET7A-3 MIR2443 MIRLET7B MIR3596 PPARA CDPF1 PKDREJ TTC38 GTSE1 TRMU CELSR1 GRAMD4 CERK TBC1D22A*
CNVR_loss_1218	*LOC104972550 WC-7 LOC751788 LOC104972549 LOC751789 WC1-12 LOC100335428 LOC100336766*
CNVR_loss_1456	*LOC100337213 LOC100141148 LOC617305 LOC788068 LOC788080 LOC512296 LOC100296891 OR7A17 LOC100296808 LOC788246 LOC100847301 LOC100296694 LOC100138521 LOC789512 LOC789504 LOC789533 LOC786149 LOC100296166 LOC100296199 LOC786202 LOC100298599 LOC100298645 LOC512956 LOC104972799 LOC100298773 LOC100298811 LOC100301104 LOC100298850 LOC104972801*
CNVR_loss_1540	*LOC100336163*
CNVR_loss_2088	*SV2C IQGAP2 F2RL2 F2R F2RL1 S100Z CRHBP AGGF1 ZBED3 PDE8B WDR41 OTP TBCA MIR2285V MIR2284Z-1 AP3B1 SCAMP1 LHFPL2 ARSB DMGDH BHMT2 BHMT TRNAC-GCA CMYA5 HOMER1 PAPD4 JMY LOC781720 LOC104973029*
CNVR_gain_3467	*ZC3H6*

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.

Table S3. Description of significant (P value <0.05) CNVRs associated with lightness (L*) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR
CNVR_gain_890	2	Gain	132410699	136335277	3924579	44	64	0.04	0.58
CNVR_gain_2304	7	Gain	42241178	43182417	941240	25	45	0.02	0.86
CNVR_loss_1452	7	Loss	44143560	44449912	306353	185	214	0.04	0.58
CNVR_loss_1920	9	Loss	92776813	92786911	10099	90	47	$6x10^{-5}$	0.01
CNVR_loss_1982	10	Loss	21938238	22038109	99872	20	4	0.003	0.35
CNVR_loss_2028	10	Loss	42436483	42467266	30784	32	18	0.05	0.56
CNVR_gain_3544	11	Gain	5713292	5828686	115395	94	123	0.02	0.56
CNVR_gain_3900	12	Gain	41017103	42372438	1355336	20	35	0.04	0.58
CNVR_loss_2560	13	Loss	53932232	53985223	52992	52	35	0.05	0.58
CNVR_loss_2848	15	Loss	47480277	49693685	2213409	38	62	0.01	0.56
CNVR_loss_2998	16	Loss	39379458	39665952	286495	58	83	0.02	0.56
CNVR_loss_4442	29	Loss	27612781	28009673	396893	58	39	0.05	0.58
CNVR_loss_3879	23	Loss	25315725	25465450	149726	138	165	0.05	0.58

Genes

CNVR_gain_890	*EIF4G3, SH2D5, KIF17, DDOST, CDA, UBXN10, PLA2G2F, PLA2G2D4, PLA2G2D1, PLA2G5, PLA2G2A, OTUD3, RNF186, CAPZB, UBR4, ALDH4A1, PAX7, TAS1R2, KLHDC7A, ACTL8, ARHGEF10L, PADI6, PADI1, PADI2, SDHB, MFAP2, CROCC, SZRD1, SPATA21, NECAP2*
CNVR_gain_2304	*GCSAML, OR2G2, LOC508626, LOC100335194, OR2G3, LOC524985, LOC787559, LOC532075, OR6F1, LOC101904415, OR6T1, OR11L1, LOC518816, TRIM58, OR2W3, LOC526765, LOC787758, LOC787816, LOC614090, LOC787898, OR2T33, LOC787932, LOC787946, LOC787963, LOC104969163, LOC104969162, LOC788055, LOC616716, LOC788079, OR2L13*
CNVR_loss_1452	*LOC614592, LOC100848897*
CNVR_loss_1920	-
CNVR_loss_1982	*LOC104973083, LOC10497308, LOC615040, LOC101907557, LOC785963, LOC100337505, LOC100337215, LOC785995*
CNVR_loss_2028	*LOC104973136*
CNVR_gain_3544	*SLC10A6, PTPN13*
CNVR_gain_3900	*LOC104973593, LOC101902172, LOC788820*
CNVR_loss_2560	*SIRPB1*
CNVR_loss_2848	*FAM160A2, OR52B2, OR52L1, OR56A1, OR56A3, OR56A4, OR52E8, OR52E6, OR52N2, OR52N5, OR56B4, LOC616948, TRIM34, TRIM6, OR52B6, OR52H1, UBQLN3, OR52D1, OR51I2, OR51I1, OR51Q1, OR51M1, HBE1, HBE4, HBB, HBE2, OR51S1, HBG, OR51F2, OR51V1*
CNVR_loss_2998	*FMO1, FMO2, LOC517828, FMO3, TRNAE-UUC, MROH9, LOC104974426, LOC104974425*
CNVR_loss_3879	*BOLA-DQA2, BOLA-DQB, BOLA-DQA5, LOC100848815, LOC100851058*
CNVR_loss_4442	*LOC781277, LOC509323, LOC100139052, OR8D2, LOC782375, TRNAV-CAC, LOC516940, LOC782297, LOC782257, LOC782221, LOC782191, LOC787625, LOC100141288, LOC510984, LOC787694, LOC514864, LOC101903186, LOC513062, LOC782009, LOC526276, LOC616755, OR8G5, LOC781842, LOC100301297, LOC788544, LOC788554, LOC788620, LOC788590, LOC788607, LOC788573*

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.

Table S4. Description of significant (P value <0.05) CNVRs associated with redness (a*) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR
CNVR_loss_1356	5	Loss	99519486	100191241	671756	124	73	3.5 x 10^{-05}	0.35
CNVR_loss_2677	11	Loss	105382384	107100431	1718048	31	13	0.006	0.35
CNVR_loss_1362	5	Loss	102343832	102794601	450770	80	112	0.007	0.35
CNVR_loss_1011	4	Loss	64879673	65070486	190814	76	49	0.01	0.35
CNVR_loss_858	3	Loss	120123602	121408443	1284842	36	18	0.01	0.35
CNVR_loss_1284	5	Loss	59421039	59999377	578339	238	202	0.01	0.35
CNVR_gain_1314	6	Gain	79120452	81712012	2591561	26	11	0.01	0.35
CNVR_loss_2741	12	Loss	32054331	32232492	178162	36	57	0.02	0.35
CNVR_gain_1098	5	Gain	73614554	78618081	5003528	23	10	0.02	0.35
CNVR_loss_2573	11	Loss	57708025	59291525	1583501	50	31	0.02	0.35
CNVR_gain_3496	21	Gain	18893292	22569077	3675786	36	20	0.03	0.35
CNVR_gain_572	2	Gain	132500252	136908437	4408186	76	53	0.03	0.009
CNVR_loss_1210	5	Loss	22514133	22563988	49856	228	197	0.03	0.35
CNVR_loss_2005	8	Loss	61609739	61877938	268200	23	11	0.03	0.35
CNVR_loss_3555	17	Loss	73151207	75148791	1997585	35	20	0.03	0.35
CNVR_loss_3948	20	Loss	70875830	71992748	1116919	29	16	0.04	0.35

	Genes
CNVR_loss_1356	*LOC513869, LOC788694, LOC100140174, LOC101904048, KLRC1, LOC101904370, LOC101904370, LOC788558, LOC101905165, LOC100336869, LOC101904903, LOC104970137, LOC104970137, LOC100847738 , LOC101904774, KLRJ1, TRNAC-GCA, LOC100296778, CD94, LOC101905403, NKG2A, NKG2C, , LOC100847813, LOC100847813, KLRK1, LOC100335509, KLRD1, LOC618565, LOC100848575*
CNVR_loss_2677	*CACNA1B, EHMT1, ARRDC1, ZMYND19, NSMF, ENTPD8, NOXA1, FAM166A, SLC34A3, NDOR1, TPRN, SSNA1, GRIN1, MAN1B1, UAP1L1, ENTPD2, NPDC1, FUT7, ABCA2, PTGDS, LCN12, FBXW5, EDF1, C11H9orf172, CCDC183, LCN6, MRPS2, C11H9orf116, PPP1R26, COL5A1*
CNVR_loss_1362	*LOC751811, LOC104972550, LOC104972550, WC-7, LOC751788 LOC104972549, LOC104972549, LOC751789, WC1-12, DV10, LOC100335428*
CNVR_loss_1011	*PDE1C*

CNVR_loss_858	*COPS9, OTOS, ANKMY1, LOC511497, CAPN10, GPR35, GPC1, MIR149, AQP12B, KIF1A, AGXT, C3H2orf54, CROCC2, MTERF4, PASK, PPP1R7, HDLBP, SEPT2, FARP2, STK25, BOK, THAP4, ATG4B, DTYMK, ING5, D2HGDH, GAL3ST2, NEU4, PDCD1, RTP5*
CNVR_loss_1284	*LOC788242, LOC788258, LOC100140889, LOC100139544, LOC788285, LOC788298, LOC788322, LOC100138400, LOC788357, LOC788372, OR10A7, LOC788396, LOC788413, LOC788428, LOC788438, LOC788512, LOC100139733, LOC788502, LOC788490, LOC788524, LOC104972492, LOC100140668, LOC788535, LOC104972457, LOC788540, LOC788552, LOC100137966, LOC788569, LOC788583, LOC100139543*
CNVR_gain_1314	*ADGRL3, LOC104968895, LOC100140587, LOC101904414, LOC785233, LOC104968896, LOC104968896, LOC782855, LOC101904777, TECRL*
CNVR_loss_2741	*LOC100847339, LOC101902112*
CNVR_gain_1098	*TOM1, HMOX1, MCM5, RASD2, MB, RBFOX2, MYH9, TXN2, FOXRED2, EIF3D, CACNG2, PVALB, NCF4, CSF2RB, TST, KCTD17, TMPRSS6, RAC2, CYTH4, ELFN2, MFNG, CARD10, USP18, ALG10, SYT10, PKP2, YARS2, DNM1L, KIAA1551, AMN1*
CNVR_loss_2573	*LOC100847903, LOC101907748, LOC784779, LRRTM4*
CNVR_gain_3496	*NTRK3, MRPL46, MRPS11, DET1, ACAN, HAPLN3, MFGE8, ABHD2, RLBP1, FANCI, POLG, RHCG, TICRR, KIF7, PLIN1, ANPEP, AP3S2, ZNF710, IDH2, GDPGP1, VPS33B, PRC1, RCCD1, UNC45A, MAN2A2, FES, FURIN, BLM, CRTC3, IQGAP1*
CNVR_gain_572	*SH2D5, KIF17, DDOST, CDA, PLA2G2F, PLA2G2D4, PLA2G2D1, PLA2G5, PLA2G2A, OTUD3, CAPZB, UBR4, ALDH4A1, TAS1R2, LOC536229, ACTL8, ARHGEF10L, PADI6, PADI1, PADI2, SDHB, MFAP2, CROCC, NECAP2, SZRD1, FBXO42, ARHGEF19, EPHA2, FAM131C, CLCNKA*
CNVR_loss_1210	*LOC784883*
CNVR_loss_2005	*ZCCHC7*
CNVR_loss_3555	*IGLL1, VPREB3, SMARCB1, MIF, SUSD2, GGT5, ADORA2A, VPREB1, TOP3B, PPM1F, MAPK1, CCDC116, UBE2L3, TMEM191C, SERPIND1, PI4KA, P2RX6, CCDC74B, MED15, KLHL22, DGCR2, SLC25A1, CDC45, CLDN5, TXNRD2, COMT, TANGO2, TRMT2A, RTN4R*
CNVR_loss_3948	*IRX4, LOC104975301, NDUFS6, MRPL36, LOC104975297, LOC101907943, LPCAT1, SLC6A3, CLPTM1L, TERT, SLC6A18, SLC6A19, SLC12A7, LOC104975298, NKD2, TRIP13, BRD9, LOC101910077, TPPP, LOC104975299, LOC617224, CEP72, SLC9A3, EXOC3, LOC529500, IGCGAMMA, PDCD6, SDHA, CCDC127, LRRC14B*

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.

Table S5. Description of significant (P value <0.05) CNVRs associated with yellowness (b*) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR

CNVR_gain_876	2	Gain	132500252	136908437	4408186	74	53	0.05	0.24
CNVR_gain_972	3	Gain	41212982	41743300	530319	45	26	0.02	0.25
CNVR_loss_835	4	Loss	106642849	106871918	229070	37	19	0.01	0.24
CNVR_loss_751	4	Loss	64879673	65070486	190814	77	54	0.03	0.33
CNVR_loss_1084	5	Loss	99519486	100191241	671756	123	82	0.001	0.22
CNVR_loss_954	5	Loss	22514133	22563988	49856	231	200	0.02	0.24
CNVR_loss_1292	6	Loss	114526782	115180727	653946	36	20	0.03	0.24
CNVR_loss_1233	6	Loss	75333800	79074711	3740912	25	42	0.05	0.24
CNVR_loss_1322	7	Loss	6708218	6718398	10181	49	31	0.04	0.24
CNVR_loss_2646	15	Loss	3219275	3419690	200416	21	46	0.002	0.22
CNVR_gain_4868	17	Gain	24619850	25828235	1208386	20	9	0.05	0.24
CNVR_loss_3214	19	Loss	5972577	6837130	864554	23	10	0.03	0.24
CNVR_loss_4242	29	Loss	26773871	28082218	1308348	38	57	0.05	0.24

	Genes
CNVR_gain_876	*SH2D5, KIF17, DDOST, CDA, PLA2G2F, PLA2G2D4, PLA2G5, PLA2G2D1, PLA2G2A, OTUD3, RNF186, CAPZB, UBR4, ALDH4A1, TAS1R2, PAX7, ACTL8, ARHGEF10L, PADI6, PADI1, PADI2, SDHB, MFAP2, CLCNKA, NECAP2, SPATA21, SZRD1, ARHGEF19, FAM131C, CROCC*
CNVR_gain_972	*OLFM3, LOC522984*
CNVR_loss_835	*LOC101904045, LOC101903865, LOC101903933, LOC101909872, LOC104972267, LOC101903672, LOC101903590, LOC101903755, LOC101904075, LOC509513, LOC101904148, LOC101902874, LOC101902921, LOC101902797, LOC101902717, LOC101904200, LOC100300510, LOC101902515, LOC101902455, LOC786254*
CNVR_loss_751	*PDE1C*
CNVR_loss_1084	*LOC513869, LOC788694, LOC100140174, LOC101904048, LOC100139049, LOC101904370, LOC788558, LOC101905165, LOC100336869, LOC101904903, LOC104970137, LOC100847738, LOC101904774, KLRJ1, TRNAC-GCA, LOC100296778, LOC101905403, KLRC1, NKG2C, LOC100847813, KLRK1, LOC100335509, KLRD1, LOC618565, LOC100848575*
CNVR_loss_954	*LOC784883*
CNVR_loss_1292	*LOC104968943, CPEB2*
CNVR_loss_1233	*LOC100141023, LOC101903089, LOC101902242, TRNAC-GCA, ADGRL3*
CNVR_loss_1322	*LOC101905208*
CNVR_loss_2646	-
CNVR_gain_4868	*PCDH10, PRAME, TRNAC-GCA, LOC786811, LOC101908157, LOC100138665, LOC101902151, LOC100336402*

CNVR_loss_3214	*PCTP, TMEM100, LOC528282, LOC781415, LOC616574, LOC100138217, LOC104974983, LOC781298, LOC513767, LOC100298860, LOC100298821, LOC100139255*
CNVR_loss_4242	*OR8D4, OR4D5, OR10S1, VWA5A, OR8G2, TMEM225, OR8D2, OR8G5, LOC787455, LOC100299320, LOC100299628, LOC100301071, LOC782288, LOC782366, LOC782329, LOC100301320, LOC100300342, LOC100301231, LOC781828, LOC781509, LOC531816, LOC782297, LOC788607, LOC782191, LOC787625, LOC787694, LOC782009, LOC788554, LOC788573, LOC782221*

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.

Table S6. Description of significant (P value < 0.05) CNVRs associated with Rib eye area (REA) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR
CNVR_loss_65	1	Loss	27782968	28111487	328520	22	9	0.02	0.61
CNVR_loss_26	1	Loss	11769851	14989060	3219210	59	39	0.03	0.61
CNVR_loss_172	1	Loss	93730576	93819471	88896	222	193	0.04	0.65
CNVR_loss_91	1	Loss	46754269	49508661	2754393	33	19	0.05	0.69
CNVR_loss_79	1	Loss	36764094	37962776	1198683	25	13	0.05	0.69
CNVR_loss_985	4	Loss	90360104	91486921	1126818	57	83	0.02	0.65
CNVR_gain_1435	4	Gain	83370720	83480472	109753	83	60	0.03	0.65
CNVR_loss_1171	5	Loss	59421039	60167240	746202	242	212	0.03	0.61
CNVR_gain_2220	7	Gain	9873696	10182428	308733	92	57	0.001	0.26
CNVR_loss_1647	7	Loss	78032478	79823123	1790646	28	14	0.03	0.61
CNVR_loss_1727	8	Loss	12695628	13901047	1205420	29	14	0.02	0.61
CNVR_gain_2651	8	Gain	32516387	34000737	1484351	42	26	0.04	0.61
CNVR_loss_2614	12	Loss	75462926	75946247	483322	105	144	0.003	0.28
CNVR_loss_2518	12	Loss	5559123	9441294	3882172	54	30	0.007	0.46
CNVR_gain_4540	15	Gain	45470174	45562968	92795	92	68	0.03	0.61
CNVR_loss_2893	15	Loss	12016909	13476961	1460053	29	15	0.04	0.61
CNVR_loss_3046	16	Loss	16691955	18431191	1739237	29	15	0.04	0.61
CNVR_loss_3217	17	Loss	23678088	24942099	1264012	22	8	0.01	0.61
CNVR_loss_4416	28	Loss	28447018	29050764	603747	30	14	0.02	0.61

CNVR_loss_4539	29	Loss	49670579	50361506	690928	21	4	0.002	0.26

	Genes
CNVR_loss_65	-
CNVR_loss_26	*LOC100847925, NCAM2*
CNVR_loss_172	*LOC100294973, LOC100847574*
CNVR_loss_91	*LOC785485, LOC781452, LOC100299050, ZPLD1, TRNAF-AAA, LOC104970829*
CNVR_loss_79	*EPHA3, LOC101904733, LOC101904787, LOC104970810, PROS1, ARL13B, STX19, LOC104970089, NSUN3*
CNVR_loss_985	*LOC782604, TRNAR-ACG, GRM8*
CNVR_gain_1435	*LOC104972168, LOC100295719, TRGC3, LOC104972166, TRGC4*
CNVR_loss_1171	*LOC788242, LOC788258, LOC100140889, LOC100139544, LOC788285, LOC788298, LOC788322, LOC788357, LOC788372, OR10A7, LOC788396, LOC788413, LOC788428, LOC788438, LOC788512, LOC100139733, LOC788524, LOC104972492, LOC100140668, LOC788535, LOC104972457, LOC788540, LOC788552, LOC788583, LOC100139543, OR9K2, LOC512340, LOC511753, LOC527216, LOC788998*
CNVR_gain_2220	*LOC787882, LOC100295693, LOC100295734, LOC516132, LOC512689, LOC788031, LOC100295806, LOC100301138, LOC100301179, LOC100295735, LOC785898, LOC789459, LOC78684, LOC512488, LOC100848268, LOC513101*
CNVR_loss_1647	*LOC104968962, LOC104968963, LOC785099, LOC104968967*
CNVR_loss_1727	*LOC104969269, LOC104969271, LOC104969270, MIR2285M-5, LOC786692, LOC10014078, LOC104969273, LOC104969276*
CNVR_gain_2651	*LOC104969318, LOC782926*
CNVR_loss_2614	*LOC522174, LOC100296113, LOC104973640, LOC523126, LOC104969731, LOC10190681, LOC523126, LOC100847548*
CNVR_loss_2518	*LOC100141157, LOC104968471, LOC101903582, LOC101905933, LOC100141168, LOC100138474*
CNVR_gain_4540	*LOC782645, LOC782678, LOC782718, LOC516263, LOC782791, LOC523139*
CNVR_loss_2893	*LOC529492, LOC104974177*
CNVR_loss_3046	*LOC529930, LOC101907125, LOC100140427*
CNVR_loss_3217	*PABPC4L, LOC784179, LOC104974592*
CNVR_loss_4416	*ASCC1, ANAPC16, DDIT4, MCU, TRNAG-CCC, MIR2891, MICU1, DNAJB12, LOC104969715, LOC104969716*
CNVR_loss_4539	*KCNQ1, TRPM5, TSSC4, CD81, CTSD, TSPAN32, ASCL2, TH, INS, IGF2, MIR483, H19, MRPL23, TNNT3, PRR33, LSP1, TNNI2, SYT8, LOC101902361, LOC101902537, LOC104976310, LOC101902793, LOC104976309*

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.

Table S7. Description of significant (P value < 0.05) CNVRs associated with the back fat thickness (BFT) and candidate genes within the CNVRs.

CNVR ID	BTA	Type*	Start (bp)	End (bp)	Size (bp)	Low**	High**	P value	FDR
CNVR_1110	6	mixed	77657589	77666699	9111	20	6	0.0076	0.78
CNVR_1025	5	mixed	99542086	99577125	35040	115	87	0.0196	0.78
CNVR_1669	9	mixed	17019870	17036083	16214	26	12	0.0221	0.78
CNVR_2704	15	mixed	64523465	64582415	58951	20	8	0.0249	0.78
CNVR_511	3	mixed	38503182	38827065	323884	25	12	0.0307	0.78
CNVR_1065	6	mixed	34465561	34486562	21002	23	11	0.0375	0.78
CNVR_3487	23	mixed	25747610	25881173	133564	92	69	0.0382	0.78
CNVR_775	4	mixed	90699813	90705987	6175	54	76	0.0385	0.78
CNVR_1234	7	mixed	35312206	35318219	6014	20	9	0.0395	0.78
CNVR_597	3	mixed	105711958	105720505	8548	24	40	0.0432	0.78
CNVR_1621	8	mixed	103917356	104025778	108423	26	42	0.0467	0.78
CNVR_517	3	mixed	41242544	41447611	205068	59	41	0.0509	0.78
CNVR_3729	26	mixed	2698467	2768799	70333	26	14	0.0525	0.78
CNVR_3058	19	mixed	1591038	1679507	88470	94	119	0.0538	0.78

	Genes
CNVR_1110_2	-
CNVR_1025_1	*BOTA-T2R10B, KLRA1, KLRC1, KLRJ1, LOC100296778, LOC100336869, LOC100847738, LOC101904370, LOC101904370, LOC101904903, LOC101905165, LOC101905403, LOC513869, LOC782957, MAGOHB, NKG2A, NKG2C, SMIM10L1, STYK1, T2R10C, T2R12, T2R43P, T2R45P, T2R65A, TAS2R10, TAS2R46, TAS2R7, TRNAC-GCA, YBX3*
CNVR_1669_2	*LOC104972965, HTR1B, TRNAA-UGC*
CNVR_2704_2	*CSTF3, HIPK3, TRNAC-ACA, TRNAE-UUC, LOC101907405, KIAA1549L*
CNVR_511_2	-
CNVR_1065_3	*LOC104972717, LOC526089, LOC104972718, CCSER1*
CNVR_3487_1	*BOLA-DQA2, BOLA-DQB, BOLA-DQA5, LOC100851058, LOC100848815, BOLA-DRB3, BOLA-DQA1, LOC786695, LA-DRB, BOLA-DRB2, LOC101902890, BOLA-DRA, BTNL2, LOC525599, LOC504295, LOC101903024, LOC101903077, LOC104969893, LOC101903155, LOC104975658, BLA-DQB, LOC783151, LOC101903211, BTNL2, LOC104972343, LOC100847163, LOC790332, LOC100847163*

CNVR_775_1	*LOC782604, TRNAR-ACG*
CNVR_1234_4	*LOC101907698, LOC101907651, LOC104969135, LOC101907740, LOC540403, LOC100295797, HSD17B4, LOC104970228, TNFAIP8*
CNVR_597_1	*HIVEP3, EDN2, LOC100847906, LOC101902150, SCMH1*
CNVR_1621_1	*PTBP3, LOC534155, HSDL2, KIAA1958, INIP, LOC101905894, SNX30, SLC46A2, LOC513329, LOC783399, LOC104969451, ZFP37, LOC104972947, LOC104969452, LOC104969448, SLC31A2, FKBP15, SLC31A1, CDC26, PRPF4, RNF183, LOC104969449, WDR31, BSPRY, HDHD3, LOC104969450, ALAD, POLE3, C8H9orf43, RGS3*
CNVR_517_2	*MIR2471, GLIS3, MIR2470, LOC104969708, LOC100335699, LOC101904171, RFX3, LOC101905621, LOC100847144, LOC100139044, LOC101905770, PUM3*
CNVR_3729_1	-
CNVR_3058_1	-

*type of copy variation (loss, gain or mixed); **number of CNVRs found in the Low and High groups.