Supplementary Materials

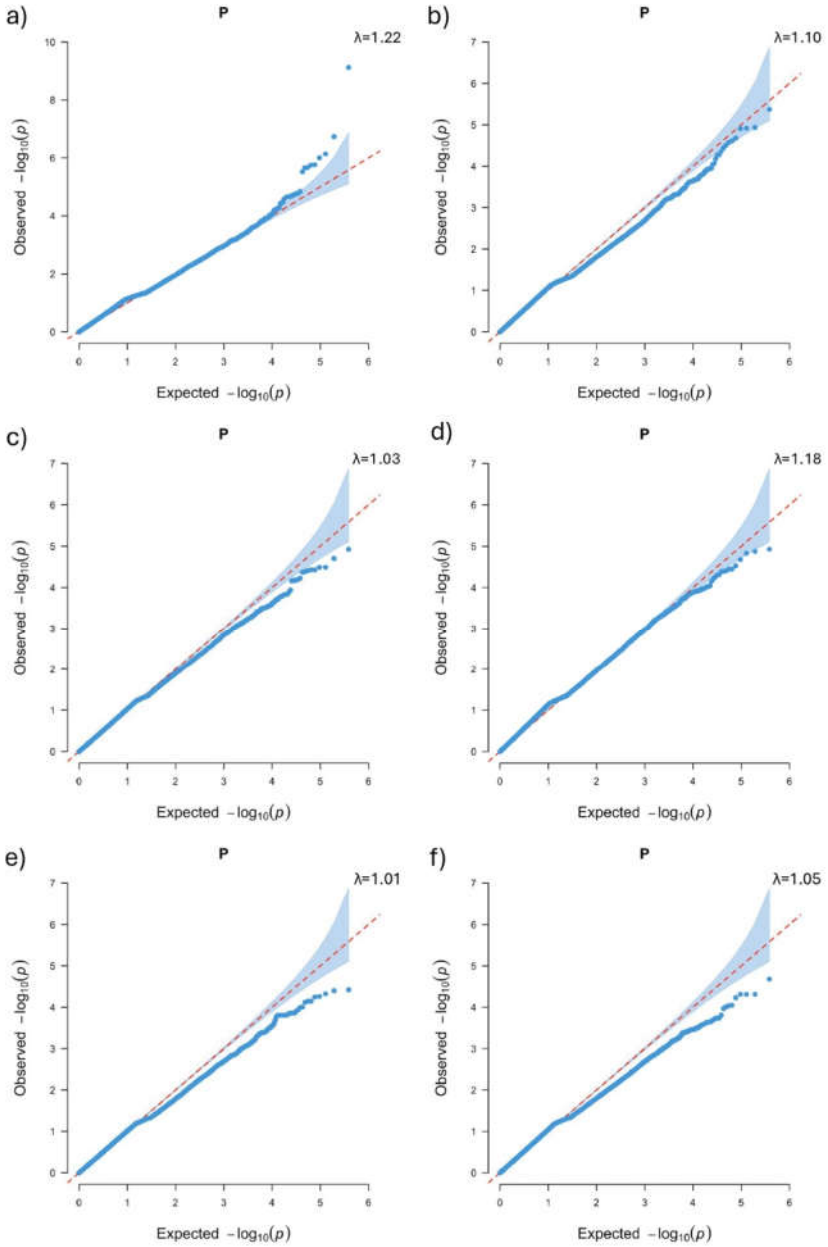


Figure S1. QQ-plots from the morphological defects a) feet and legs malformation; b) chamfer; c) hump; d) loin; e) jaw, and f) navel.

Table S1. Positional candidate genes identified for feet and legs malformation

Gene	Chromosome	Genomic Region (Start-End)		gene_id	gene_biotype
LCK	2	121262594	121283528	ENSBTAG00000012695	protein_coding
FAM167B	2	121285365	121288233	ENSBTAG00000002027	protein_coding
MTMR9L	2	121291097	121298198	ENSBTAG00000014390	protein_coding
EIF3I	2	121295602	121306440	ENSBTAG00000014388	protein_coding
TMEM234	2	121305656	121311475	ENSBTAG00000009163	protein_coding
DCDC2B	2	121311608	121316391	ENSBTAG00000026696	protein_coding
IQCC	2	121316668	121319689	ENSBTAG00000015103	protein_coding
CCDC28B	2	121319787	121324157	ENSBTAG00000015104	protein_coding
CLDN12	2	121377323	121416305	ENSBTAG00000019486	protein_coding
SHOX	2	121446978	121458374	ENSBTAG00000026788	protein_coding
U6	2	121351995	121352100	ENSBTAG00000046605	snRNA
TMPRSS5	15	24246030	24258672	ENSBTAG00000063291	protein_coding
ZW10	15	24284268	24319385	ENSBTAG00000020066	protein_coding
USP28	15	24336893	24400181	ENSBTAG00000002323	protein_coding
CLDN25	15	24328165	24328857	ENSBTAG00000039149	protein_coding
SLIT3	20	447017	1163732	ENSBTAG00000017746	protein_coding
IQSEC1	22	58592571	58878769	ENSBTAG00000003237	protein_coding
ACAD9	22	58892389	58940024	ENSBTAG00000003242	protein_coding
ALS2CL	22	52793614	52815789	ENSBTAG00000017812	protein_coding
FAM240A	22	52836432	52841404	ENSBTAG00000062614	protein_coding
CRIPTO	22	52867448	52872061	ENSBTAG00000021119	protein_coding
LRRC2	22	52883832	52926453	ENSBTAG00000008013	protein_coding
RTP3	22	52926963	52930809	ENSBTAG00000018767	protein_coding
LTF	22	52934900	52990568	ENSBTAG00000001292	protein_coding
CCR1	22	53199437	53237483	ENSBTAG00000019428	protein_coding
	22	52991916	53222543	ENSBTAG00000031355	protein_coding
CCRL2	22	52998319	53000315	ENSBTAG00000006155	protein_coding
CCR5	22	53024929	53032609	ENSBTAG00000067584	protein_coding
CCR2	22	53041056	53057320	ENSBTAG00000056962	protein_coding
CCR3	22	53134643	53166540	ENSBTAG00000001338	protein_coding
	22	52815938	52820885	ENSBTAG00000071496	lncRNA
	22	52815954	52820898	ENSBTAG00000074759	lncRNA
	22	52931000	52932045	ENSBTAG00000069054	lncRNA
LONRF1	27	24235745	24281816	ENSBTAG00000020084	protein_coding
	27	24222336	24223499	ENSBTAG00000059365	lncRNA
	27	24282931	24286512	ENSBTAG00000066045	lncRNA
	27	24292661	24293782	ENSBTAG00000066043	lncRNA
	27	24330725	24335267	ENSBTAG00000071517	lncRNA
	27	24375165	24383572	ENSBTAG00000069102	lncRNA
	27	24136711	24232205	ENSBTAG00000065743	lncRNA

	27	24295100	24305729	ENSBTAG00000063691	lncRNA
	27	24295972	24384717	ENSBTAG00000065714	lncRNA
CD6	29	37311550	37357284	ENSBTAG00000018367	protein_coding
CD5	29	37422886	37444466	ENSBTAG00000013730	protein_coding
VPS37C	29	37451425	37481097	ENSBTAG00000008064	protein_coding
	29	50930288	51001621	ENSBTAG00000019015	protein_coding
	29	50933710	50983567	ENSBTAG00000048470	protein_coding
	29	51003746	51006379	ENSBTAG00000019017	protein_coding
	29	51049730	51063351	ENSBTAG00000020242	protein_coding

Table S2. Positional candidate genes identified for chamfer defect trait

Gene	**Chromossome**	**Genomic Region (Start-End)**		**gene_id**	**gene_biotype**
GRAMD1B	15	33964574	34225319	ENSBTAG00000001410	protein_coding
CLMP	15	33689099	33794265	ENSBTAG00000020046	protein_coding
	15	33942972	33951828	ENSBTAG00000062583	lncRNA
	15	33949760	33955975	ENSBTAG00000058139	lncRNA

Table S3. Positional candidate genes identified for hump defect trait

Gene	**Chromosome**	**Genomic Region (Start-End)**		**gene_id**	**gene_biotype**
IQSEC1	22	58592571	58878769	ENSBTAG00000003237	protein_coding
ACAD9	22	58892389	58940024	ENSBTAG00000003242	protein_coding
ATXN1	23	40688296	40830587	ENSBTAG00000019675	protein_coding
GMPR	23	40838557	40899426	ENSBTAG00000015743	protein_coding
	23	40831987	40833465	ENSBTAG00000073862	protein_coding

Table S4. Positional candidate genes identified for the loin defect trait

Gene	**Chromosome**	**Genomic Region (Start – End)**		**gene_id**	**gene_biotype**
MARF1	25	14044148	14083629	ENSBTAG00000020387	protein_coding
NDE1	25	14084964	14144211	ENSBTAG00000015986	protein_coding
MYH11	25	14124964	14277425	ENSBTAG00000015988	protein_coding
BMERB1	25	13881271	14026628	ENSBTAG00000011692	protein_coding
bta-mir-484	25	14083795	14083857	ENSBTAG00000029976	miRNA
bta-mir-10161	25	13990737	13990828	ENSBTAG00000052331	miRNA

Table S5. Significant Gene Ontology (GO) terms (FDR-adjusted p-values < 0.05) identified from candidate genes associated with feet and legs malformation in Nellore cattle.

Functional terms	Source	p_value	Description of function	Genes
GO:0070098	GO:BP	3,89E-06	chemokine-mediated signaling pathway	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:1990869	GO:BP	3,89E-06	cellular response to chemokine	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:1990868	GO:BP	3,89E-06	response to chemokine	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:0019221	GO:BP	4,49E-05	cytokine-mediated signaling pathway	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000019015,ENSBTAG00000048470
GO:0090026	GO:BP	1,21E-04	positive regulation of monocyte chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0090025	GO:BP	1,87E-04	regulation of monocyte chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0002548	GO:BP	5,39E-04	monocyte chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0071345	GO:BP	6,47E-04	cellular response to cytokine stimulus	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000019015,ENSBTAG00000048470
GO:0045071	GO:BP	6,63E-04	negative regulation of viral genome replication	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0009605	GO:BP	6,87E-04	response to external stimulus	ENSBTAG00000017746,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0034097	GO:BP	7,29E-04	response to cytokine	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000019015,ENSBTAG00000048470

GO:1901652	GO:BP	7,29E-04	response to peptide	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000019015,ENSBTAG00000048470
GO:0019722	GO:BP	1,29E-03	calcium-mediated signaling	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000001338
GO:0042330	GO:BP	1,74E-03	taxis	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:0007204	GO:BP	1,74E-03	positive regulation of cytosolic calcium ion concentration	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000001338
GO:0006935	GO:BP	1,74E-03	chemotaxis	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:0006952	GO:BP	1,82E-03	defense response	ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0045069	GO:BP	1,82E-03	regulation of viral genome replication	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0007165	GO:BP	1,82E-03	signal transduction	ENSBTAG00000002323,ENSBTAG00000017746,ENSBTAG00000003237,ENSBTAG00000008013,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000013730,ENSBTAG00000019015,ENSBTAG00000048470
GO:0048525	GO:BP	1,82E-03	negative regulation of viral process	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0006955	GO:BP	1,93E-03	immune response	ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0002690	GO:BP	2,74E-03	positive regulation of leukocyte chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962

GO:0071677	GO:BP	2,74E-03	positive regulation of mononuclear cell migration	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0035455	GO:BP	3,02E-03	response to interferon-alpha	ENSBTAG00000019015,ENSBTAG00000048470
GO:0023052	GO:BP	3,97E-03	signaling	ENSBTAG00000002323,ENSBTAG00000017746,ENSBTAG00000003237,ENSBTAG00000008013,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000013730,ENSBTAG00000019015,ENSBTAG00000048470
GO:0051851	GO:BP	3,97E-03	host-mediated perturbation of symbiont process	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0007154	GO:BP	4,08E-03	cell communication	ENSBTAG00000002323,ENSBTAG00000017746,ENSBTAG00000003237,ENSBTAG00000008013,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000013730,ENSBTAG00000019015,ENSBTAG00000048470
GO:0019079	GO:BP	4,25E-03	viral genome replication	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:1903900	GO:BP	4,26E-03	regulation of viral life cycle	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0035821	GO:BP	4,31E-03	modulation of process of another organism	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0070887	GO:BP	4,31E-03	cellular response to chemical stimulus	ENSBTAG00000017746,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367
GO:0060326	GO:BP	4,31E-03	cell chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:0002376	GO:BP	4,36E-03	immune system process	ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,

				ENSBTAG00000013730,ENSBTAG0 0000019015,ENSBTAG00000048470
GO:0002688	GO:BP	4,36E-03	regulation of leukocyte chemotaxis	ENSBTAG00000019428,ENSBTAG0 0000031355,ENSBTAG00000056962
GO:0046597	GO:BP	4,51E-03	host-mediated suppression of symbiont invasion	ENSBTAG00000019015,ENSBTAG0 0000048470
GO:0006954	GO:BP	5,50E-03	inflammatory response	ENSBTAG00000019428,ENSBTAG0 0000031355,ENSBTAG00000056962, ENSBTAG00000001338,ENSBTAG0 0000018367
GO:0002684	GO:BP	5,50E-03	positive regulation of immune system process	ENSBTAG00000001292,ENSBTAG0 0000019428,ENSBTAG00000031355, ENSBTAG00000056962,ENSBTAG0 0000018367,ENSBTAG00000013730
GO:0071675	GO:BP	5,50E-03	regulation of mononuclear cell migration	ENSBTAG00000019428,ENSBTAG0 0000031355,ENSBTAG00000056962
GO:0035456	GO:BP	5,50E-03	response to interferon-beta	ENSBTAG00000019015,ENSBTAG0 0000048470
GO:0002687	GO:BP	5,50E-03	positive regulation of leukocyte migration	ENSBTAG00000019428,ENSBTAG0 0000031355,ENSBTAG00000056962
GO:0050921	GO:BP	5,70E-03	positive regulation of chemotaxis	ENSBTAG00000019428,ENSBTAG0 0000031355,ENSBTAG00000056962
GO:0050792	GO:BP	5,73E-03	regulation of viral process	ENSBTAG00000001292,ENSBTAG0 0000019015,ENSBTAG00000048470
GO:0007166	GO:BP	5,97E-03	cell surface receptor signaling pathway	ENSBTAG00000017746,ENSBTAG0 0000001292,ENSBTAG00000019428, ENSBTAG00000031355,ENSBTAG0 0000056962,ENSBTAG00000001338, ENSBTAG00000018367,ENSBTAG0 0000019015,ENSBTAG00000048470
GO:0071222	GO:BP	5,97E-03	cellular response to lipopolysaccharide	ENSBTAG00000001292,ENSBTAG0 0000067584,ENSBTAG00000018367
GO:0007186	GO:BP	6,77E-03	G protein-coupled receptor signaling pathway	ENSBTAG00000017746,ENSBTAG0 0000019428,ENSBTAG00000031355, ENSBTAG00000067584,ENSBTAG0 0000056962,ENSBTAG00000001338
GO:0071219	GO:BP	6,94E-03	cellular response to molecule of bacterial origin	ENSBTAG00000001292,ENSBTAG0 0000067584,ENSBTAG00000018367
GO:0042221	GO:BP	7,33E-03	response to chemical	ENSBTAG00000017746,ENSBTAG0 0000001292,ENSBTAG00000019428, ENSBTAG00000031355,ENSBTAG0 0000067584,ENSBTAG00000056962, ENSBTAG00000001338,ENSBTAG0 0000018367,ENSBTAG00000019015, ENSBTAG00000048470

GO:0051716	GO:BP	1,06E-02	cellular response to stimulus	ENSBTAG00000002323,ENSBTAG00000017746,ENSBTAG00000003237,ENSBTAG00000008013,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000013730,ENSBTAG00000019015,ENSBTAG00000048470
GO:0031663	GO:BP	1,08E-02	lipopolysaccharide-mediated signaling pathway	ENSBTAG00000001292,ENSBTAG00000018367
GO:0071216	GO:BP	1,09E-02	cellular response to biotic stimulus	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367
GO:0097529	GO:BP	1,14E-02	myeloid leukocyte migration	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0071674	GO:BP	1,30E-02	mononuclear cell migration	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0030595	GO:BP	1,30E-02	leukocyte chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0050870	GO:BP	1,33E-02	positive regulation of T cell activation	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0050920	GO:BP	1,36E-02	regulation of chemotaxis	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0002685	GO:BP	1,39E-02	regulation of leukocyte migration	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0019058	GO:BP	1,59E-02	viral life cycle	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0032496	GO:BP	1,59E-02	response to lipopolysaccharide	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367
GO:1903039	GO:BP	1,59E-02	positive regulation of leukocyte cell-cell adhesion	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:2000464	GO:BP	1,59E-02	positive regulation of astrocyte chemotaxis	ENSBTAG00000056962
GO:0043310	GO:BP	1,59E-02	negative regulation of eosinophil degranulation	ENSBTAG00000056962
GO:0035705	GO:BP	1,59E-02	T-helper 17 cell chemotaxis	ENSBTAG00000056962
GO:2000412	GO:BP	1,59E-02	positive regulation of thymocyte migration	ENSBTAG00000056962
GO:0002237	GO:BP	1,87E-02	response to molecule of bacterial origin	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367
GO:0090264	GO:BP	2,09E-02	regulation of immune complex clearance by	ENSBTAG00000056962

			monocytes and macrophages	
GO:0051251	GO:BP	2,09E-02	positive regulation of lymphocyte activation	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:1900191	GO:BP	2,09E-02	negative regulation of single-species biofilm formation	ENSBTAG00000001292
GO:0002436	GO:BP	2,09E-02	immune complex clearance by monocytes and macrophages	ENSBTAG00000056962
GO:0098630	GO:BP	2,09E-02	aggregation of unicellular organisms	ENSBTAG00000001292
GO:0060337	GO:BP	2,09E-02	type I interferon-mediated signaling pathway	ENSBTAG00000019015,ENSBTAG00000048470
GO:0061364	GO:BP	2,09E-02	apoptotic process involved in luteolysis	ENSBTAG00000017746
GO:1900190	GO:BP	2,09E-02	regulation of single-species biofilm formation	ENSBTAG00000001292
GO:0090265	GO:BP	2,09E-02	positive regulation of immune complex clearance by monocytes and macrophages	ENSBTAG00000056962
GO:0071357	GO:BP	2,09E-02	cellular response to type I interferon	ENSBTAG00000019015,ENSBTAG00000048470
GO:0044407	GO:BP	2,09E-02	single-species biofilm formation in or on host organism	ENSBTAG00000001292
GO:0002434	GO:BP	2,09E-02	immune complex clearance	ENSBTAG00000056962
GO:0022409	GO:BP	2,09E-02	positive regulation of cell-cell adhesion	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0032103	GO:BP	2,09E-02	positive regulation of response to external stimulus	ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:2000473	GO:BP	2,09E-02	positive regulation of hematopoietic stem cell migration	ENSBTAG00000056962
GO:2000471	GO:BP	2,09E-02	regulation of hematopoietic stem cell migration	ENSBTAG00000056962
GO:0033993	GO:BP	2,09E-02	response to lipid	ENSBTAG00000017746,ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367
GO:0034340	GO:BP	2,09E-02	response to type I interferon	ENSBTAG00000019015,ENSBTAG00000048470
GO:2000458	GO:BP	2,09E-02	regulation of astrocyte chemotaxis	ENSBTAG00000056962

GO:2000451	GO:BP	2,09E-02	positive regulation of CD8-positive, alpha-beta T cell extravasation	ENSBTAG00000056962
GO:0001554	GO:BP	2,09E-02	luteolysis	ENSBTAG00000017746
GO:2000449	GO:BP	2,09E-02	regulation of CD8-positive, alpha-beta T cell extravasation	ENSBTAG00000056962
GO:0035697	GO:BP	2,09E-02	CD8-positive, alpha-beta T cell extravasation	ENSBTAG00000056962
GO:0035700	GO:BP	2,09E-02	astrocyte chemotaxis	ENSBTAG00000056962
GO:2000437	GO:BP	2,09E-02	regulation of monocyte extravasation	ENSBTAG00000056962
GO:0002682	GO:BP	2,09E-02	regulation of immune system process	ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:2000410	GO:BP	2,09E-02	regulation of thymocyte migration	ENSBTAG00000056962
GO:1900229	GO:BP	2,09E-02	negative regulation of single-species biofilm formation in or on host organism	ENSBTAG00000001292
GO:1900228	GO:BP	2,09E-02	regulation of single-species biofilm formation in or on host organism	ENSBTAG00000001292
GO:0044010	GO:BP	2,09E-02	single-species biofilm formation	ENSBTAG00000001292
GO:2000439	GO:BP	2,09E-02	positive regulation of monocyte extravasation	ENSBTAG00000056962
GO:0042710	GO:BP	2,09E-02	biofilm formation	ENSBTAG00000001292
GO:0006950	GO:BP	2,21E-02	response to stress	ENSBTAG00000002323,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0140888	GO:BP	2,21E-02	interferon-mediated signaling pathway	ENSBTAG00000019015,ENSBTAG00000048470
GO:0002696	GO:BP	2,25E-02	positive regulation of leukocyte activation	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0016032	GO:BP	2,32E-02	viral process	ENSBTAG00000001292,ENSBTAG00000019015,ENSBTAG00000048470
GO:0042102	GO:BP	2,37E-02	positive regulation of T cell proliferation	ENSBTAG00000056962,ENSBTAG00000018367
GO:0050867	GO:BP	2,55E-02	positive regulation of cell activation	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730

GO:0141124	GO:BP	2,55E-02	intracellular signaling cassette	ENSBTAG00000003237,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000001338
GO:1903037	GO:BP	2,56E-02	regulation of leukocyte cell-cell adhesion	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0050863	GO:BP	2,73E-02	regulation of T cell activation	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0051414	GO:BP	2,76E-02	response to cortisol	ENSBTAG00000017746
GO:0072679	GO:BP	2,76E-02	thymocyte migration	ENSBTAG00000056962
GO:0006968	GO:BP	2,76E-02	cellular defense response	ENSBTAG00000056962
GO:0043309	GO:BP	2,76E-02	regulation of eosinophil degranulation	ENSBTAG00000056962
GO:0050900	GO:BP	3,00E-02	leukocyte migration	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0040011	GO:BP	3,25E-02	locomotion	ENSBTAG00000017746,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962,ENSBTAG00000001338
GO:0007159	GO:BP	3,33E-02	leukocyte cell-cell adhesion	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0019732	GO:BP	3,40E-02	antifungal humoral response	ENSBTAG00000001292
GO:0035696	GO:BP	3,40E-02	monocyte extravasation	ENSBTAG00000056962
GO:0070100	GO:BP	3,40E-02	negative regulation of chemokine-mediated signaling pathway	ENSBTAG00000017746
GO:0034341	GO:BP	3,40E-02	response to type II interferon	ENSBTAG00000019015,ENSBTAG00000048470
GO:0097350	GO:BP	3,40E-02	neutrophil clearance	ENSBTAG00000056962
GO:2000409	GO:BP	3,40E-02	positive regulation of T cell extravasation	ENSBTAG00000056962
GO:0050896	GO:BP	3,68E-02	response to stimulus	ENSBTAG00000002323,ENSBTAG00000017746,ENSBTAG00000003237,ENSBTAG00000008013,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367,ENSBTAG00000013730,ENSBTAG00000019015,ENSBTAG00000048470
GO:0050671	GO:BP	3,69E-02	positive regulation of lymphocyte proliferation	ENSBTAG00000056962,ENSBTAG00000018367

GO:0032946	GO:BP	3,74E-02	positive regulation of mononuclear cell proliferation	ENSBTAG00000056962,ENSBTAG00000018367
GO:2000407	GO:BP	3,88E-02	regulation of T cell extravasation	ENSBTAG00000056962
GO:0043308	GO:BP	3,88E-02	eosinophil degranulation	ENSBTAG00000056962
GO:0002887	GO:BP	3,88E-02	negative regulation of myeloid leukocyte mediated immunity	ENSBTAG00000056962
GO:0043307	GO:BP	3,88E-02	eosinophil activation	ENSBTAG00000056962
GO:0043301	GO:BP	3,88E-02	negative regulation of leukocyte degranulation	ENSBTAG00000056962
GO:0035385	GO:BP	3,88E-02	Roundabout signaling pathway	ENSBTAG00000017746
GO:1903977	GO:BP	3,88E-02	positive regulation of glial cell migration	ENSBTAG00000056962
GO:0002278	GO:BP	3,88E-02	eosinophil activation involved in immune response	ENSBTAG00000056962
GO:0097305	GO:BP	3,89E-02	response to alcohol	ENSBTAG00000017746,ENSBTAG00000067584
GO:0043207	GO:BP	4,24E-02	response to external biotic stimulus	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0051707	GO:BP	4,24E-02	response to other organism	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0070665	GO:BP	4,30E-02	positive regulation of leukocyte proliferation	ENSBTAG00000056962,ENSBTAG00000018367
GO:0022407	GO:BP	4,30E-02	regulation of cell-cell adhesion	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:1903238	GO:BP	4,32E-02	positive regulation of leukocyte tethering or rolling	ENSBTAG00000056962
GO:0051968	GO:BP	4,32E-02	positive regulation of synaptic transmission, glutamatergic	ENSBTAG00000056962
GO:0043615	GO:BP	4,32E-02	astrocyte cell migration	ENSBTAG00000056962
GO:0045785	GO:BP	4,32E-02	positive regulation of cell adhesion	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0002447	GO:BP	4,32E-02	eosinophil mediated immunity	ENSBTAG00000056962

GO:0008284	GO:BP	4,34E-02	positive regulation of cell population proliferation	ENSBTAG00000001292,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000018367
GO:0071396	GO:BP	4,43E-02	cellular response to lipid	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367
GO:0051249	GO:BP	4,43E-02	regulation of lymphocyte activation	ENSBTAG00000056962,ENSBTAG00000018367,ENSBTAG00000013730
GO:0009607	GO:BP	4,43E-02	response to biotic stimulus	ENSBTAG00000001292,ENSBTAG00000067584,ENSBTAG00000018367,ENSBTAG00000019015,ENSBTAG00000048470
GO:0032680	GO:BP	4,43E-02	regulation of tumor necrosis factor production	ENSBTAG00000001292,ENSBTAG00000056962
GO:0032640	GO:BP	4,43E-02	tumor necrosis factor production	ENSBTAG00000001292,ENSBTAG00000056962
GO:1903555	GO:BP	4,53E-02	regulation of tumor necrosis factor superfamily cytokine production	ENSBTAG00000001292,ENSBTAG00000056962
GO:0071706	GO:BP	4,53E-02	tumor necrosis factor superfamily cytokine production	ENSBTAG00000001292,ENSBTAG00000056962
GO:0035556	GO:BP	4,55E-02	intracellular signal transduction	ENSBTAG00000002323,ENSBTAG00000003237,ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000001338
GO:0035701	GO:BP	4,64E-02	hematopoietic stem cell migration	ENSBTAG00000056962
GO:0031665	GO:BP	4,64E-02	negative regulation of lipopolysaccharide-mediated signaling pathway	ENSBTAG00000001292
GO:0070099	GO:BP	4,64E-02	regulation of chemokine-mediated signaling pathway	ENSBTAG00000017746
GO:0042129	GO:BP	4,96E-02	regulation of T cell proliferation	ENSBTAG00000056962,ENSBTAG00000018367
GO:0009897	GO:CC	2,67E-05	external side of plasma membrane	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000013730
GO:0098552	GO:CC	1,42E-04	side of membrane	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000013730

GO:0009986	GO:CC	1,42E-04	cell surface	ENSBTAG00000001292,ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000013730
GO:0016493	GO:MF	5,10E-10	C-C chemokine receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0019957	GO:MF	5,10E-10	C-C chemokine binding	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0001637	GO:MF	1,95E-09	G protein-coupled chemoattractant receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0004950	GO:MF	1,95E-09	chemokine receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0019956	GO:MF	3,05E-09	chemokine binding	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0071791	GO:MF	3,15E-08	chemokine (C-C motif) ligand 5 binding	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584
GO:0035717	GO:MF	3,15E-08	chemokine (C-C motif) ligand 7 binding	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000056962
GO:0004896	GO:MF	4,49E-07	cytokine receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0140375	GO:MF	1,20E-06	immune receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0019955	GO:MF	1,57E-06	cytokine binding	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0004930	GO:MF	3,93E-03	G protein-coupled receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0001530	GO:MF	4,33E-03	lipopolysaccharide binding	ENSBTAG00000001292,ENSBTAG00000018367

GO:0048020	GO:MF	5,46E-03	CCR chemokine receptor binding	ENSBTAG00000006155,ENSBTAG00000056962
GO:0035716	GO:MF	1,04E-02	chemokine (C-C motif) ligand 12 binding	ENSBTAG00000056962
GO:0035715	GO:MF	1,04E-02	chemokine (C-C motif) ligand 2 binding	ENSBTAG00000056962
GO:0042379	GO:MF	1,25E-02	chemokine receptor binding	ENSBTAG00000006155,ENSBTAG00000056962
GO:0031727	GO:MF	1,74E-02	CCR2 chemokine receptor binding	ENSBTAG00000056962
GO:0140912	GO:MF	1,74E-02	membrane destabilizing activity	ENSBTAG00000001292
GO:0004888	GO:MF	1,86E-02	transmembrane signaling receptor activity	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
GO:0070891	GO:MF	2,23E-02	lipoteichoic acid binding	ENSBTAG00000018367
GO:0070991	GO:MF	2,23E-02	medium-chain fatty acyl-CoA dehydrogenase activity	ENSBTAG00000003242
GO:0004466	GO:MF	2,84E-02	long-chain fatty acyl-CoA dehydrogenase activity	ENSBTAG00000003242
GO:0048495	GO:MF	4,06E-02	Roundabout binding	ENSBTAG00000017746
GO:0052890	GO:MF	4,98E-02	oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	ENSBTAG00000003242
GO:0003995	GO:MF	4,98E-02	acyl-CoA dehydrogenase activity	ENSBTAG00000003242
KEGG:04061	KEGG	6,28E-06	Viral protein interaction with cytokine and cytokine receptor	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
KEGG:04060	KEGG	5,62E-05	Cytokine-cytokine receptor interaction	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338,ENSBTAG00000020242
KEGG:04062	KEGG	8,13E-05	Chemokine signaling pathway	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000056962,ENSBTAG00000001338
KEGG:05167	KEGG	1,64E-03	Kaposi sarcoma-associated herpesvirus infection	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000001338
KEGG:05163	KEGG	2,28E-03	Human cytomegalovirus infection	ENSBTAG00000019428,ENSBTAG00000031355,ENSBTAG00000067584,ENSBTAG00000001338

KEGG:04514	KEGG	8,39E-03	Cell adhesion molecules	ENSBTAG00000019486,ENSBTAG00000039149,ENSBTAG00000018367
KEGG:03260	KEGG	2,40E-02	Virion - Human immunodeficiency virus	ENSBTAG00000067584
KEGG:04144	KEGG	2,40E-02	Endocytosis	ENSBTAG00000003237,ENSBTAG00000067584,ENSBTAG00000008064
KEGG:04670	KEGG	4,69E-02	Leukocyte transendothelial migration	ENSBTAG00000019486,ENSBTAG00000039149

Abbreviations: GO:BP, Gene Ontology Biological Process; GO:MF, Gene Ontology Molecular Function; KEGG, Kyoto Encyclopedia of Genes and Genomes pathway.

Table S6. Significant Gene Ontology (GO) terms (FDR-adjusted p-values < 0.05) identified from candidate genes associated with chamfer defect in Nellore cattle.

Functional terms	Source	p_value	Description of function	Genes
GO:0099170	GO:BP	0,024	postsynaptic modulation of chemical synaptic transmission	ENSBTAG00000020046
GO:0036315	GO:BP	0,024	cellular response to sterol	ENSBTAG00000001410
GO:0070723	GO:BP	0,024	response to cholesterol	ENSBTAG00000001410
GO:0036314	GO:BP	0,024	response to sterol	ENSBTAG00000001410
GO:0071397	GO:BP	0,024	cellular response to cholesterol	ENSBTAG00000001410
GO:0097306	GO:BP	0,046	cellular response to alcohol	ENSBTAG00000001410
GO:0055092	GO:BP	0,046	sterol homeostasis	ENSBTAG00000001410
GO:0042632	GO:BP	0,046	cholesterol homeostasis	ENSBTAG00000001410
GO:0140268	GO:CC	0,045	endoplasmic reticulum-plasma membrane contact site	ENSBTAG00000001410
GO:0001786	GO:MF	0,009	phosphatidylserine binding	ENSBTAG00000001410
GO:0120020	GO:MF	0,009	cholesterol transfer activity	ENSBTAG00000001410
GO:0120015	GO:MF	0,009	sterol transfer activity	ENSBTAG00000001410
GO:0120013	GO:MF	0,009	lipid transfer activity	ENSBTAG00000001410
GO:0070300	GO:MF	0,009	phosphatidic acid binding	ENSBTAG00000001410
GO:0043178	GO:MF	0,009	alcohol binding	ENSBTAG00000001410
GO:0072341	GO:MF	0,009	modified amino acid binding	ENSBTAG00000001410
GO:0015485	GO:MF	0,009	cholesterol binding	ENSBTAG00000001410
GO:0032934	GO:MF	0,009	sterol binding	ENSBTAG00000001410
GO:0005496	GO:MF	0,010	steroid binding	ENSBTAG00000001410
GO:0005319	GO:MF	0,015	lipid transporter activity	ENSBTAG00000001410
GO:0005543	GO:MF	0,036	phospholipid binding	ENSBTAG00000001410

Abbreviations: GO:BP, Gene Ontology Biological Process; GO:MF, Gene Ontology Molecular Function; KEGG, Kyoto Encyclopedia of Genes and Genomes pathway.

Table S7. Significant Gene Ontology (GO) terms (FDR-adjusted p-values < 0.05) identified from candidate genes associated with hump defect in Nellore cattle.

Functional terms	Source	p_value	Description of function	Genes
GO:0032011	GO:BP	0,049	ARF protein signal transduction	ENSBTAG00000003237
GO:0032012	GO:BP	0,049	regulation of ARF protein signal transduction	ENSBTAG00000003237
GO:0051791	GO:BP	0,049	medium-chain fatty acid metabolic process	ENSBTAG00000003242
GO:0042405	GO:CC	0,048	nuclear inclusion body	ENSBTAG00000019675
GO:0003920	GO:MF	0,014	GMP reductase activity	ENSBTAG00000015743
GO:0070991	GO:MF	0,014	medium-chain fatty acyl-CoA dehydrogenase activity	ENSBTAG00000003242
GO:0004466	GO:MF	0,014	long-chain fatty acyl-CoA dehydrogenase activity	ENSBTAG00000003242
GO:0046857	GO:MF	0,014	oxidoreductase activity, acting on other nitrogenous compounds as donors, with NAD or NADP as acceptor	ENSBTAG00000015743
GO:0034046	GO:MF	0,016	poly(G) binding	ENSBTAG00000019675
GO:0052890	GO:MF	0,016	oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	ENSBTAG00000003242
GO:0003995	GO:MF	0,016	acyl-CoA dehydrogenase activity	ENSBTAG00000003242
GO:0016661	GO:MF	0,022	oxidoreductase activity, acting on other nitrogenous compounds as donors	ENSBTAG00000015743
GO:0008266	GO:MF	0,024	poly(U) RNA binding	ENSBTAG00000019675
GO:0008187	GO:MF	0,024	poly-pyrimidine tract binding	ENSBTAG00000019675
GO:0070717	GO:MF	0,025	poly-purine tract binding	ENSBTAG00000019675
GO:0016491	GO:MF	0,035	oxidoreductase activity	ENSBTAG00000003242, ENSBTAG00000015743
GO:0016627	GO:MF	0,045	oxidoreductase activity, acting on the CH-CH group of donors	ENSBTAG00000003242

Abbreviations: GO:BP, Gene Ontology Biological Process; GO:MF, Gene Ontology Molecular Function; KEGG, Kyoto Encyclopedia of Genes and Genomes pathway.

Table S8. Significant Gene Ontology (GO) terms (FDR-adjusted p-values < 0.05) identified from candidate genes associated with loin defect in Nellore cattle

Functional terms	Source	p_value	Description of function	Genes
GO:0021822	GO:BP	0,018	negative regulation of cell motility involved in cerebral cortex radial glia guided migration	ENSBTAG00000011692
GO:0021987	GO:BP	0,018	cerebral cortex development	ENSBTAG00000015986,ENSBTAG00000011692

GO:0031109	GO:BP	0,018	microtubule polymerization or depolymerization	ENSBTAG00000015986,ENSBTAG00000011692
GO:0097435	GO:BP	0,018	supramolecular fiber organization	ENSBTAG00000015986,ENSBTAG00000015988,ENSBTAG00000011692
GO:0021543	GO:BP	0,024	pallium development	ENSBTAG00000015986,ENSBTAG00000011692
GO:0021537	GO:BP	0,043	telencephalon development	ENSBTAG00000015986,ENSBTAG00000011692
GO:1903976	GO:BP	0,043	negative regulation of glial cell migration	ENSBTAG00000011692
GO:0021814	GO:BP	0,044	cell motility involved in cerebral cortex radial glia guided migration	ENSBTAG00000011692
GO:0005871	GO:CC	0,040	kinesin complex	ENSBTAG00000015986
GO:0016460	GO:CC	0,040	myosin II complex	ENSBTAG00000015988
GO:0031616	GO:CC	0,040	spindle pole centrosome	ENSBTAG00000015986
GO:0032982	GO:CC	0,040	myosin filament	ENSBTAG00000015988
GO:0000146	GO:MF	0,030	microfilament motor activity	ENSBTAG00000015988
GO:0008092	GO:MF	0,030	cytoskeletal protein binding	ENSBTAG00000015986,ENSBTAG00000015988
GO:0008307	GO:MF	0,030	structural constituent of muscle	ENSBTAG00000015988
KEGG:04810	KEGG	0,033	Regulation of actin cytoskeleton	ENSBTAG00000015988
KEGG:04814	KEGG	0,033	Motor proteins	ENSBTAG00000015988
KEGG:04530	KEGG	0,033	Tight junction	ENSBTAG00000015988
KEGG:04270	KEGG	0,033	Vascular smooth muscle contraction	ENSBTAG00000015988

Abbreviations: GO:BP, Gene Ontology Biological Process; GO:MF, Gene Ontology Molecular Function; KEGG, Kyoto Encyclopedia of Genes and Genomes pathway.