

S.No.	Clone ID/ Length in bp/Accessi on No.	Database Searched	E- value	Query cover age	Identity (%)	Nucleotide position of the query sequence	Accession no. / length (bp) of homologues in bp	Nucleotide position of uncovered sequence	Description
1	pDp1/1331/ <u>AY940196.1</u>	Btau_4.0 (mega blast)	0.0	45%	95	730-1331	<u>NW_001494496.2</u> <u>Bt29_WGA2180.4</u> / 1798093	980194- 980797	<i>Bos taurus</i> chromosome 29 genomic contig, reference assembly (based on Btau_4.0) Features flanking this part of subject sequence: 241560 bp at 5' side: polycomb protein EED 13727 bp at 3' side: phosphatidylinosit ol-binding clathrin assembly protein
Sequence present on multiple chromosomes									
		Nucleotide collection (nr/nt)	0.0	45%	94	730-1331	<u>AY944236.1</u> / 207929	90253-90856 45229-45830 51286-51889 13678-13078 99923-100396 10283-10752 182753-183342 103392-102813 138913-138355 52505-52311	<i>Bos taurus</i> prion preproprotein (PRNP) and prion- like protein doppel preproprotein (PRND) genes, complete cds; and RASSF2 gene, complete sequence
			0.0	45%	94	730-1331	<u>AJ871176</u> / 171712	73112- 72510 59325- 59932 171411- 170808 38560- 37959 113334- 113906 122107- 122702 112853- 112458 116659- 116949 49549- 49264 4709- 4621	<i>Bos taurus</i> ABCG2 gene, PKD2 gene and SPP1 gene, clone RPCI42_5K14
			0.0	45%	95	730-1331	<u>AY644517.5</u> / 243699	82863- 83466 190820- 191423 150408- 149813	<i>Bos taurus</i> T cell receptor gamma cluster 1 (TCRG1)

							102622- 102152 183784- 184376 111170- 111029 152660- 152726	gene, complete sequence	
			0.0	45%	93	730-1331	AF060172/1139	338-942	<i>Bos taurus</i> repeat region
			0.0	45%	92	729-1331	AC147842.3/ 139569	43134- 42530	<i>Ovis aries</i> clone CH243-255B6, complete sequence
	Reference mRNA sequences (refseq_rna)		0.0	45%	90	730-1331	NM_001103275.1/ 2628	2532- 1926	<i>Bos taurus</i> acyl- CoA thioesterase 11 (<i>ACOT11</i>), mRNA
			2e- 127	26%	91	257-604	ref NM_174654.2/ 3504	2900-3249	<i>Bos taurus</i> solute carrier organic anion transporter family, member 1A2 (<i>SLCO1A2</i>), mRNA
2.	pDp2/ 651/ AY873795.1	Btau_4.0 (mega blast)	0.0	99%	97	2-651	NW_001495040.2/ Bt5_WGA568_4/ 2175351	1545534- 1544884	<i>Bos taurus</i> chromosome 5 genomic contig, reference assembly (based on Btau_4.0). Features in this part of subject sequence: protein phosphatase 1H (PP2C domain containing) isoform 2
Sequence present on multiple chromosomes									
	Nucleotide collection (nr/nt)		6e-69	68%	78	36-484	AC099791.2/ 239704	169998- 170458	<i>Homo sapiens</i> chromosome 1 clone RP11- 430G17, complete sequence
			1e-61	67%	77	39-477	AC188548.5/ 190240	106992- 106547	<i>Canis Familiaris</i> chromosome 12,

								clone XX-511E22, complete sequence
			6e-21	45%	69	117-413	AF136741.1/ 530	214- 515 <i>Bos taurus</i> L1MC1-like repeat region, complete sequence
			3e-37	52%	71	141-483	FN432136.1/ 127420	66562-97170 <i>Ovis aries</i> pitx3 gene for paired- like homeodomain 3, BAC clone CH243-315I22
	Reference mRNA sequences (refseq_rna)		1e-37	43%	77	109-394	XM_0011384271/ 3182	3133- 2848 PREDICTED: <i>Pan</i> <i>trogodytes</i> vacuolar protein sorting 24, transcript variant 3 (VPS24), mRNA
			1e-37	43%	77	109-394	NM_016079.2/ 3174	3123-2838 <i>Homo sapiens</i> vacuolar protein sorting 24 homolog (<i>S.cerevisiae</i>) (VPS24), transcript variant 1, mRNA
3.	pDp3/603/ DQ020282.1	Btau_4.0 (mega blast)	0.0	99%	98	2-603	NW_001504011.1/ BtUn_WGA36024/ 44357	35042-35643 <i>Bos taurus</i> genomic contig, reference assembly (based on Btau_4.0 ChrUn.004.1271)
			0.0	99%	86	7-593	NW_001508692.2/ BtX_WGA2236_4/ 391646	230121-229522 <i>Bos taurus</i> chromosome X genomic contig, reference assembly (based on Btau_4.0) Features flanking this part of subject sequence: 36076 bp at 5' side: hypothetical protein LOC100302527

[illegible]

Nucleotide collection (nr/nt)	1e-76	87%	97	1-170	<u>AC149783.4/</u> 205084	110423- 110253 138412- 138245	<i>Bos taurus</i> BAC CH240-3K17 (Children's Hospital Oakland Research Institute Bovine BAC Library complete sequence.
	7e-69	59%	94	1-170	<u>AC148245.3/</u> 153498	126277- 126107 152716- 152546 77825- 77995 122902- 123072 2611- 2783 45960- 45791 10704- 10862 106525- 106621 105959- 106040 86492- 86524 6368- 6339 34943- 34911 6515- 6479 21672- 21636 86345- 86381 129399- 129435 24358- 24329 134277- 134248 26-94 95746- 95718 133200- 133236	<i>Ovis aries</i> clone CH243-293L12, complete sequence
Reference mRNA sequences (refseq_rna)	1e-25	23%	93	90-170	<u>NM_174654.2/</u> 3504	2761-2841	<i>Bos taurus</i> solute carrier organic anion transporter family, member 1A2 (<i>SLCO1A2</i>), mRNA

The "Percentage", "E-value", "Accession no." and "Description" are taken from the highest relevant hit obtained from the BLAST query at NCBI database collection. The databases consulted are mRNA, genomic nucleotide or Btau_4.0 references.

Additional File 1