

Map page	Chrom. Band (human)	Genes/features	Human	Mouse	Dog	Opossum	Platypus	Chicken
1	1p36.32	TP73	chr1:3,558,944-3,642,625 (I)	chr4:152,902,082-152,984,008 (I)	chr5:61,199,527-61,241,393	chr4:389,858,020-389,945,132	Ultra178:1,123,945-1,143,179	chr21:912,435-939,684
NA	1p31	ARHI/DIRAS3	chr1:68,283,023-68,290,278 (I)	NO	NO	NO	NO	NO
2	2p15	COMMD1 (U2af1-rs1)	chr2:61,986,292-62,216,698 (NI) NO'	chr11:22,799,728-22,882,284 (I) chr11:22,873,215-22,876,498 (I)	chr10:65,037,469-65,210,770 NO	chr1:630,290,345-630,540,770 NO	Ultra56:4,473,791-4,620,115 NO	chr3:8,903,451-8,969,942 NO
NA	4q13	(Mkrr1-ps1)	NO'	In the interval chr5:89,857,838-90,009,9311 (I)	NA	NA	NA	NA
3	4q22	NAP1L5	chr4:89,837,380-89,837,928 (NR)	chr6:58,836,075-58,836,545 (I)	chr32:14,918,042-14,918,578	NO	NO	NO
4	6q24	PLAGL1 HYMAI	chr6:144,303,130-144,371,246 (I) I	chr10:12,780,986-12,819,853 (I)	chr1:38,462,172-38,467,955	chr2:422,110,909-422,129,064	chr2:17,204,472-17,210,716	chr3:54,201,457-54,202,728
5	6q25	IGF2R cluster	chr6:160,310,121-160,796,004	chr17:12,263,330-12,613,022	chr1:52,221,869-52,539,630	chr2:442,406,287-442,973,871	Fragmented & most genes not in WGS assembly	chr3:47,288,282-47,411,223
		IGF2R	NI	I	O	O	Chr 2 - centric* Fragment on Ultra61	O
		(Air)	NO'	I	NA	NA	NA	NA
		SLC22A2	NR	I	O	O	Missing from WGS assembly	O
		SLC22A3	NR	I	O	O	Contig2038	O
6	7p12	GRB10	chr7:50,625,260-50,828,652 (I)	chr11:11,830,511-11,937,390 (I)	chr18:4,878,320-4,905,682	chr6:267,072,104-267,174,894	chr4:9,189,613-9,284,939 (chr 4p*)	chr2:83,096,709-83,234,014
7	7q21	PEG10 cluster	chr7:92,891,735-96,492,079	chr6:3,637,395-6,874,963	chr14:21,872,312-25,033,706	chrUn:10,910,032-84,197,983 Some are clustered to contigs.	The cluster is fragmented and most genes are not present in the WGS assembly.	chr2:22,860,906-24,415,562
		CALCR	PD	I	O	NO	NO	NO
		SGCE	I	I	O	O	O (Contig1947)	O
		PEG10	I	I	NO	NO	NO	NO
		PPP1R9A	I	I	O	NO	NO	NO
		PON1	PD	NI	O	O	Not present	
		PON3	NR	PD	O	O	Not present	A single PON family member is present
		PON2	NR	PD	O	O	Not present	
		ASB4	NR	I	O	O	Not present	O
		DLX5	I	NI	O	O	Not present	O
8	7q32	MEST cluster	chr7:129,720,229-130,004,138	chr6:30,518,386-30,827,142	chr14:9,304,266-9,594,583	chr8:190,305,230-190,512,697	chr10:4,897,302-5,045,606	chr1:818,869-873,265
		CPA4	I	NR	O	O	O	P
		MEST	I	I	O	O	O	O
		MESTIT1	I	NO'	NA	NA	NA	NA
		COPG2IT1	I	I	NA	NA	NA	NA
		COPG2	CD	I	O	O	O	NO
NA	mouse 15qD3	(Peg13)	NO'	chr15:72,632,860-72,637,580 (I)	NA	NA	NA	NA
9	10q22	CTNNA3	chr10:67,349,725-69,125,933 (PD)	chr10:62,899,394-64,398,190 (NR)	chr4:20,577,292-20,755,158 chr4:22,057,498-22,195,110	chr1:29,149,665-29,267,868	chr3:54,029,573-54,043,119	chr6:7,775,606-8,203,040
NA	10q25	Ins1	NO'	chr19:52,317,765-52,318,343 (CD)	NO	NO	NO	NO
10	11p15	IGF2 cluster	chr11:1,972,984-3,143,116	chr7:142,244,367-143,587,755	chr18:49,099,550-50,068,310	The cluster is fragmented and several genes are not present in the WGS. TH is on chr8:82,441,041-82,502,283	None of the eutherian-imprinted genes are present in the annotation. Cluster is split across multiple contigs. TH is on Ultra443.	chr5:14,090,506-14,883,396 Key orthologues are present & clustered.
		H19	I	I	NA	NA	NA	NA
		IGF2	I	I	O	NA	NA (Chr 2 centric*)	O
		IGF2AS	I	I	NA	NA	NA	NA
		INS	I	I	O	NA	NA	O
		ASCL2	CD	I	NO	NO	NO	NO
		PHEMX	NI	I	O	NO	NO	NO
		CD81	NI	I	O	NO	NO	NO
		TSSC4	NI	I	O	O (chrUn:76,673,683-76,674,915)	NO	O
		TRPM5	PD	NI	I	NO	NO	O
		KCNQ1	I	I	O	O (chrUn:76,673,683-76,674,915)	NO	O
		KCNQ1OT1	I	I	NA	NA	NA	NA
		KCNQ1DN	I	NO	NO	NO	NO	NO
		CDKN1C	I	I	NO	NO	NO	NO
		SLC22A1L5	PD	NO	NO	NO	NO	NO
		(Msuit1)	NO	I	NA	NA	NA	NA
		SLC22A18	I	I	O	NO	NO	O
		PHLDA2	I	I	NO	NO	O (Contig17670)	NO
		NAP1L4	NR	I	O	O (chr5:301647943-301923441)	NO	O

Map page	Chrom. Band (human)	Genes/features	Human	Mouse	Dog	Opossum	Platypus	Chicken
		RASGRF1	NR	I	O	O	O	O
20	18q11	IMPACT	chr18:20,260,680-20,287,490 (NI)	chr18:13,115,421-13,136,117 (I)	chr7:66,986,620-66,996,951	chr3:259,995,454-260,031,256	Contig20839	chr2:106,529,413-106,547,483
21	18q21	TCEB3C	chr18:42,808,571-42,810,211 (I)	NO	NO	NO	NO	NO
22	19q13		chr19:61,977,742-62,422,337	chr7:6281009-6600000	chr1:104,184,489-104,196,263	No conserved synteny	No conserved synteny	No conserved synteny
		PEG3/ZIM2 (Zim1)	I	I	O	NO	NO	NO
		ZIM2	NO	I	NO	NO	NO	NO
		USP29	I	I	NO	NO	NO	NO
		ZIM3	NR	I	NO	NO	NO	NO
		ZNF264	NR	I	NO	NO	NO	NO
23	20q11	NNAT	chr20:35,583,021-35,585,502 (I)	chr2:157,251,551-157,253,958 (I)	chr24:29,090,140-29,091,946	NO	NO	NO
24	20q13	L3MBTL	chr20:41,575,558-41,603,949 (I)	chr2:162,638,630-162,665,966 (NR)	chr24:34,211,452-34,235,635	chr1:385,894,559-385,957,809	Ultra337:4,152,550-4,172,414	chr20:29,872-47,955
25	20q13	GNAS locus	chr20:56,848,168-56,919,642	chr2:173,927,270-173,989,683	chr24:46,583,771-46,639,038	chr1:483,863,859-484,051,250	Ultra516:8,105,240-8,223,121	chr20:10,870,284-10,950,671
		GNAS	I	I	O	O	O (Chr 8p*)	O
		SANG (Nespas)	I	I	NA	NA	NA	NA
NA	Xq13	XIST locus	chrX:72,957,211-72,989,313	chrX:99,663,092-99,670,276				
		XIST	NI	I	NA	NA	NA	NA
		TSIX	NI	I	NA	NA	NA	NA

Additional Data file 4: Conservation of imprinted gene orthologues and regions within the human, mouse, dog, opossum, platypus and chicken genomes. The location of orthologous sequences is listed for each species. Localisations denoted with * are derived from reference Edwards et al. 2007. O indicates the presence of a gene orthologue, NO indicates no orthologue found, NO' indicates no orthologue found, based on previous analyses (Morison et al. 2005), NA indicates orthologues were not in the assembly/annotation, I indicates imprinted genes, NI indicated non-imprinted genes, NR indicated no reports of imprinting status, CD indicated conflicting data with respect to imprint status and PD indicated provisional data based on previous analyses (Morison et al. 2005). With the exception of the SNRPN locus, the genes that are conserved across all species, form ancient syntenic clusters. Some clusters have arisen recently and appear to be specific to the eutherians. Further detailed analyses of repeat distribution were performed on nineteen genes or regions shown from this analysis (highlighted in yellow) to be conserved across all genomes examined.