

S2Table. Mapping of the sites of integration of *Trypanosoma cruzi* kDNA minicircle sequence into the avian chromosomes.

A) Lateral transfer to somatic cells

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	<i>Locus</i>	<i>G. gallus</i> repeats
1	HG531391	1-285	284-460	CC	1e ⁻¹³⁶	99%	1e ⁻²⁹	78%	Not determined	NW_001479132.1 (Not determined)	---
1	HG531392	427-682	1-447	TATAATGTAC GGGGGAGATG C	1e ⁻¹¹⁹	98%	0.0	98%	5	NW_003763785.1 (Transcription factor SOX-6)	---
1	HG531393	321-611	1-328	GACCGCCC	6e ⁻¹³⁶	98%	2e ⁻¹⁵⁶	98%	2	NW_003763668.1 (Not determined)	---
2	HG531394	1-310	293-508	ACCAACCCCA ATGGAACC	1e ⁻⁰⁴	79%	5e ⁻⁹⁹	98%	1	NW_001471534.2 (Dystrophin)	---
2	HG531395	1-266	249-464	ACCAACCCCA ATGGAACC	2e ⁻¹²⁸	99%	3e ⁻⁹⁵	96%	1	NW_001471534.2 (Dystrophin)	---
2	HG531396	1-231	214-429	ACCAACCCCA ATGGAACC	2e ⁻¹⁰⁸	98%	2e ⁻⁹⁷	97%	1	NW_001471534.2 (Dystrophin)	---
2	HG531397	102-182	1-101	-	6e ⁻²⁸	97%	5e ⁻⁴²	98%	14	NW_003763931.1 (Not determined)	---
2	HG531398	166-453	1-98 / 99-174	GACCGCCCC	5e ⁻²²	87%	1e ⁻³⁵ / 6e ⁻²⁷	95% / 97%	14 / 5	NW_003763931.1 (Not determined) / NW_003763785.1 (Not determined)	---
3	HG531399	1-263 / 459-600 / 740-835	246-461 / 597-742	ACCAACCCCA ATGGAACC / GAA / GAGA / TAC	1e ⁻¹²⁶ / 5e ⁻⁵⁹ / 4e ⁻²⁰	99% / 97% / 85%	8e ⁻⁹⁹ / 3e ⁻⁶⁶	98% / 99%	1 / Not determined	NW_001471534.2 (Dystrophin) / NW_001471746.1 (Not determined)	---
3	HG531400	1-149	140-305 / 288-503	GGGAGATGCA	4e ⁻⁴⁸	89%	2e ⁻⁷² / 2e ⁻⁹⁶	98% / 97%	Not determined / 1	NW_001471746.1 (Not determined) / NW_001471534.2 (Dystrophin)	---
3	HG531401	1-137	128-599	CAATCGAACC	4e ⁻⁰⁶	76%	0.0	96%	20	NW_003764128.1 (Not determined)	---

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3	HG531402	173-441	1-185	GACCCCCCT CCC	2e ⁻⁰⁶	81%	4e ⁻⁸⁷	99%	3	NW_001471668.2 (palmitoyl transferase ZDHHC14 isoform 1 and 2)	CR1 (Non LTR)
3	HG531403	236-317	1-247	GAACCCCCCT CC	6e ⁻¹⁰	97%	7e ⁻¹¹³	96%	2	NW_001471639.1 (Not determined)	---
3	HG531404	102-244	1-125	GAAGCCCCCT CCCAAACCA TAAT	4e ⁻²³	92%	2e ⁻⁴²	91%	8	NW_001471740.1 (Not determined)	---
3	HG531405	523-647	1-538	AAATAATGTA CGGGGG	4e ⁻²²	94%	0.0	95%	8	NW_001471740.1 (Not determined)	---
3	HG531406	148-290	1-155	GACCGCCC	1e ⁻⁵⁶	98%	2e ⁻⁶⁸	97%	1	NW_001471551.1 (Similar to protocadherin-9 isoform 1 and 2)	CR1 (Non LTR)
4	HG531407	487-741	1-502	ATAATGTACG GGTGGG	5e ⁻¹¹⁹	98%	0.0	99%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
4	HG531408	1-148	142-251	GAGATGC	5e ⁻⁵³	94%	6e ⁻⁴³	97%	5	NW_001471698.1 (Dickkopf homolog 3)	---
4	HG531409	1-94	77-869	ACCAACCCCA ATGGAACC	1e ⁻³²	95%	0.0	99%	3	NW_001471673.1 (Not determined)	Hitchcock (LTR)
4	HG531410	1-94	80-534	AACCCCAATG GAACC	5e ⁻³²	93%	0.0	93%	17	NW_001471503.1 (Not determined)	Hitchcock (LTR)
4	HG531411	1-100	79-217	CAACCCCAAT GGAACCAGAC CT	1e ⁻³²	94%	7e ⁻⁶¹	98%	17	NW_001471503.1 (Protein-O-mannosyl transferase 1)	---
4	HG531412	301-395	1-319	TGAACGCCCC TCCAAAAC	2e ⁻³²	95%	1e ⁻¹⁴³	96%	3	NW_001471673.1 (Not determined)	Hitchcock (LTR)
4	HG531413	194-329	1-202	ATAATGTAC	2e ⁻⁵⁶	97%	2e ⁻⁹⁶	99%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---

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4	HG531414	150-244	1-165	TGAACGCCCC TCCCAA	2e ⁻³²	95%	3e ⁻⁵³	93%	11	NW_001471432.1 (WD repeat domain 59)	CR1 (Non LTR)
4	HG531415	240-334	1-253	TGAACGCCCC TCCC	7e ⁻³²	95%	1e ⁻¹⁰⁹	95%	3	NW_001471673.1 (Not determined)	---
4	HG531416	341-738	1-349	GAACCCCCC	1e ⁻¹¹⁰	94%	1e ⁻¹⁶⁶	98%	13	NW_001471449.1 (Not determined)	---
4	HG531417	125-647	1-127	GAC	4e ⁻¹⁵¹	98%	1e ⁻⁵⁰	96%	8	NW_001471740.2 (Not determined)	---
4	HG531418	139-484	1-163	ATTCTCACTC CTCCCTCCCA AAA	3e ⁻¹¹¹	95%	2e ⁻⁵³	95%	1	NW_001471513.1 (Not determined)	---
4	HG531419	302-589	1-319	GACCCCCCT CCCAAAC	3e ⁻¹⁴⁰	99%	2e ⁻¹⁴²	95%	3	NW_001471673.2 (Not determined)	Hitchcock (LTR)
4	HG531420	301-540	1-319	GAACGCCCT CCCAAACC	8e ⁻¹¹⁷	99%	6e ⁻¹⁴²	96%	3	NW_001471673.2 (Not determined)	Hitchcock (LTR)
4	HG531421	265-358	1-284	GAACGCCCT CCCAAACCA	2e ⁻³³	95%	5e ⁻¹²²	95%	2	NW_003763673.1 (Not determined)	---
5	HG531422	102-316	1-110	GAACCCCCC	3e ⁻⁴⁶	90%	1e ⁻²⁵	86%	9	XM_419045.2 (Chromosome 9 open reading frame 4)	CR1 (Non LTR)
5	HG531423	86-361	1-103	GAACCCCCCT CCCAAAC	1e ⁻⁶⁴	89%	7e ⁻³²	92%	Not determined	NW_001477517.1 (Not determined)	CR1 (Non LTR)
5	HG531424	89-414	1-98	TGAACGCCCC	3e ⁻⁹⁹	92%	9e ⁻³¹	92%	8	NW_001471740.1 (Similar to protein tyrosine phosphatase, receptor type, F – PTPRF)	---
5	HG531425	55-261	1-70 / 253-379	GAACGCCCT CCCAA A / AACCATTAT	2e ⁻⁹⁵	99%	1e ⁻¹⁵ / 1e ⁻¹⁶	89% / 76%	1 / Not determined	NW_001471556.1 (Not determined) / NW_001479132.1 (Not determined)	---

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5	HG531426	192-457	1-199	TTTGAACG	1e ⁻¹³⁰	99%	4e ⁻⁹³	99%	1	NW_001471512.1 (Tetraspanin-12)	---
5	HG531427	152-485	1-166	ATAA TGTACGGGTG A	4e ⁻¹¹¹	97%	8e ⁻⁷¹	96%	13	NW_001471446.1 (Not determined)	---
5	HG531428	197-468	1-208	CCCTTCCCAA AA	5e ⁻⁹⁰	98%	3e ⁻⁷⁶	94%	Not determined	NW_001475305.1 (Similar to FLJ20433 protein)	---
5	HG531429	265-590	1-281	GACGGCCCT CCCAAAA	2e ⁻¹¹⁵	92%	3e ⁻¹³³	98%	2	NW_001471633.1 (Not determined)	---
5	HG531430	91-233	1-108	GAACCCCT CCCAAAAC	1e ⁻⁵⁵	99%	4e ⁻³²	95%	2	NW_001471633.1 (Similar to retina-derived POU-domain factor-1)	CR1 (Non LTR)
5	HG531431	407-549	1-408	GA	7e ⁻⁵⁸	97%	0.0	99%	1	NW_001471519.1 (hypothetical protein)	CR1 (Non LTR)
6	HG531432	71-391	1-93	ATAATGTACG GGTGA GATGCATG	3e ⁻²¹	88%	3e ⁻³¹	93%	15	NW_001471461.1 (Not determined)	---
6	HG531433	223-513	1-234	GACGGCCCT CC	2e ⁻⁰⁶	71%	8e ⁻¹⁰⁰	93%	Z	AC193222.4 (Not determined)	---
7	HG531434	1-68	51-393	TCGAACCATC TATCCCAA	3e ⁻⁰⁹	91%	7e ⁻¹⁶⁵	97%	16	NW_001471464.1/ AB268588.1 (MHC region - tenascin X B)	---
7	HG531435	61-133	1-76	GATAATGTAC GGGTGA	2e ⁻¹⁷	90%	3e ⁻²⁴	93%	11	NW_001471434.1 (Matrix Metalloproteinase 2 - MMP2)	---
7	HG531436	194-353	1-202	ATAATGTAC	1e ⁻²⁰	90%	2e ⁻⁹⁵	98%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---

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10	HG531437	1-308	291-506	ACCAACCCCA ATCGAACC	3e ⁻⁹⁵	88%	4e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
15	HG531438	1-283	263-506	TACACCAACC CCAATCGA ACC	1e ⁻¹³⁴	98%	5e ⁻¹¹¹	96%	1	NW_001471554.1 (Similar to spinal cord-derived growth factor-B - SCDGFB)	---
15	HG531439	1-286	270-465	CCAACCCCAA TCGAACC	2e ⁻¹³⁴	98%	9e ⁻⁸⁹	97%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
15	HG531440	1-286	276-400	CCAATCGAAC C	6e ⁻⁰⁵	84%	1e ⁻⁵⁴	98%	5	NW_003763785.1 (Tetraspanin-18)	---
18	HG531441	1-81	61-169	TACACCAACC CCAATCGAAC C	0.002	85%	6e ⁻³⁵	90%	1	NW_001471554.1 (Not determined)	---
18	HG531442	1-279	262-457	CCAACCCCAA TCGAACCC	4e ⁻¹⁴	68%	2e ⁻⁹¹	98%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
18	HG531443	1-284	262-457	CCAACCCCAA TCGAACCCAC CAT	1e ⁻¹³³	97%	2e ⁻⁹⁰	97%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
18	HG531444	1-276	261-449	CCAACCCCAA TCGAAC	3e ⁻²¹	73%	1e ⁻⁸⁶	97%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
18	HG531445	1-291	275-496	CCAACCCCAA TCGAACC	2e ⁻¹⁴⁴	99%	4e ⁻¹⁰⁰	96%	3	NW_001471679.1 (Not determined)	CR1 (Non LTR) / ERV3
18	HG531446	184-468	1-197	GGACGCCCC TCCC	8e ⁻⁰⁸	79%	3e ⁻⁸⁸	96%	2	NW_001471633.1 (Similar to parathyroid hormone-responsive B1 - PTHB1)	CR1 (Non LTR)
19	HG531447	1-94	86-536	AATCGAACC	0.002	84%	0.0	99%	10	NW_001471429.1 (Not determined)	---
19	HG531448	1-281	263-315	CACCAACCC AATCGAACC	2e ⁻⁰⁴	88%	3e ⁻¹¹	90%	1	NW_001471548.1 (Hypothetical protein)	---
20	HG531449	51-315	1-59	TGAACGCC	2e ⁻¹⁰⁵	94%	5e ⁻²⁰	99%	5	NW_001471710.1 (Not determined)	---

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20	HG531450	64-327	1-80	GAACGCCCT CCCAAAA	2e ⁻¹⁰⁶	94%	1e ⁻²⁷	97%	21	NW_001471571.1 (Hypothetical protein)	---
20	HG531451	49-338	1-63	GAAGCCCCCT CCCAA	2e ⁻⁹⁹	92%	2e ⁻¹⁸	94%	22	NW_001471585.1 (Not determined)	---
21	HG531452	1-153	136-351	ACCAACCCCA ATCGAACC	4e ⁻⁰⁴	84%	6e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---
21	HG531453	306-391	1-324	GACCGCCCT CCCAAAACC	5e ⁻¹⁰	81%	2e ⁻¹⁴⁵	96%	3	NW_001471668.2 (Not determined)	---
22	HG531454	1-152	140-461	GGGAGATGCG TGA	2e ⁻⁵³	94%	2e ⁻¹⁵³	98%	2	NW_001471654.1 (Similar to RIM2-5B)	---
22	HG531455	1-149	127-262	ATATAATGTA CGGGTGAGAT GCA	1e ⁻⁵⁴	95%	3e ⁻⁵⁵	96%	1	NW_001471554.1 (Similar to spinal cord-derived growth factor-B- SCDGFB)	---
22	HG531456	268-489	1-288	AATTTTGAAG GCCCTCCCA A	8e ⁻⁶⁶	83%	2e ⁻¹⁴¹	99%	2	NW_001471637.1 (Similar to CDK5 regulatory subunit associated protein 1-like 1)	CR1 (Non LTR)
22	HG531457	185-381	1-195	ATAATGTACG G	7e ⁻⁵⁴	82%	6e ⁻⁹⁰	98%	14	NW_001471454.1 (Similar to mitotic checkpoint protein)	---
22	HG531458	86-362	1-103	GAACCCCCCT CCCAAAAC	6e ⁻⁹³	86%	7e ⁻³²	92%	Not determined	NW_001476599.1 (Not determined)	CR1 (Non LTR)
22	HG531459	269-485	1-272	TGAA	5e ⁻⁶²	83%	2e ⁻¹²¹	95%	10	NW_001471426.1 (Protogenin)	---
22	HG531460	125-560	1-137	GACCCCCCT CCC	6e ⁻¹¹⁶	92%	2e ⁻⁵²	94%	8	NW_001471740.2 (Not determined)	---
22	HG531461	71-165	1-79	TGAAGCCCC	1e ⁻²⁹	93%	6e ⁻²⁸	95%	1	NW_001471534.1 (Not determined)	---

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22	HG531462	134-393	1-145	CCCTTCCCAA AA	8e ⁻¹⁰⁰	93%	3e ⁻⁵⁰	96%	Not determined	NW_001475305.1 (Similar to FLJ20433 protein)	---
22	HG531463	67-203	1-88	AATAATGTAC GGGGGAGATG CA	4e ⁻⁴⁹	93%	2e ⁻²⁹	94%	6	NW_001471715.1 (Not determined)	---
22	HG531464	68-264	1-88	ATAATGTACG GGGGAGATGC A	1e ⁻⁵⁶	83%	2e ⁻²⁹	94%	6	NW_001471715.1 (Not determined)	---
22	HG531465	51-320	1-73	AACCTGAACC CCCCTCCCAA AAC	3e ⁻¹⁰³	93%	1e ⁻²¹	94%	4	NW_001471681.1 (Not determined)	CR1 (Non LTR)
23	HG531466	1-260	243-458	ACCAACCCCA ATCGAACC	-	-	3e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
23	HG531467	1-263	246-459	ACCAACCCCA ATCGAACC	5e ⁻¹²⁹	99%	9e ⁻¹⁰¹	99%	1	NW_001471534.2 (Dystrophin)	---
23	HG531468	418-480	1-437	ATAATGTACG GGGGAGATGC	6e ⁻¹²	100%	0.0	96%	5	NW_001471698.1 (Hypothetical protein)	---
23	HG531469	90-397	1-103	GAAGCCCCCT CCCA	1e ⁻⁹⁵	88%	4e ⁻⁴¹	97%	1	NW_001471513.1 (Similar to SH3- domain binding protein 1)	---
23	HG531470	109-396	1-120	CCCTTCCCAA AA	2e ⁻¹³³	97%	7e ⁻³⁹	88%	1	NW_001471526.1 (limbic system- associated membrane protein)	---
23	HG531471	143-433	1-143	A	2e ⁻¹³¹	96%	5e ⁻⁵³	92%	1	NW_001471534.1 (pyruvate dehydrogenase kinase, isoenzyme 3)	CR1 (Non LTR)
24	HG531472	1-281	264-464	ACCAACCCCA ATCGAACC	-	-	1e ⁻⁹³	99%	1	NW_001471534.2 (Dystrophin)	---
24	HG531473	1-129	113-327	ACCAACCCAA TCGAACC	1e ⁻⁴⁵	97%	8e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
24	HG531474	251-393	1-262	TGACGGCCCC TC	1e ⁻⁵⁴	96%	6e ⁻¹¹⁵	96%	3	NW_001471669.1	CR1 (Non LTR)

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										(Similar to phosphodiesterase 7B)	
24	HG531475	86-411	1-103	GAAGCCCCCT CCCAAAAC	6e ⁻¹³³	98%	8e ⁻³²	92%	Not determined	NW_001476599.1 (Not determined)	CR1 (Non LTR)
24	HG531476	335-497	1-339	GTGAC	2e ⁻⁷¹	98%	8e ⁻¹⁷²	99%	7	NW_001471733.1 (Not determined)	---
24	HG531477	181-384	1-193	GACGGCCCCCT CCC	2e ⁻⁸³	97%	7e ⁻⁸³	96%	1	NW_001471550.1 (Not determined)	CR1 (Non LTR)
24	HG531478	264-468	1-284	TGAAGCCCCC TCCCAAAACC A	2e ⁻⁸⁴	97%	2e ⁻¹¹⁵	97%	2	NW_001471638.1 (Similar to GDP-mannose 4, 6-dehydratase)	---
24	HG531479	301-429	1-319	TGAACCCCCC TCCCAAAAC	4e ⁻⁵⁵	99%	1e ⁻¹⁴³	96%	3	NW_001471673.1 (Not determined)	Hitchcock (LTR)
24	HG531480	122-325	1-134	GACCGCCCCCT CCC	8e ⁻⁸⁶	97%	2e ⁻⁴⁹	93%	8	NW_001471740.2 (Not determined)	---
24	HG531481	264-468	1-281	TGACCGCCCC TCCCAAAA	5e ⁻⁸⁶	97%	3e ⁻¹³³	98%	2	NW_001471633.1 (Not determined)	---
24	HG531482	152-350	1-163	CCCTTCCCAA AA	1e ⁻⁸²	97%	3e ⁻⁵⁵	96%	1	NW_001471513.1 (Not determined)	---
24	HG531483	1-277	265-365	GGAGGGGGCG TCA	2e ⁻¹²⁰	96%	7e ⁻³⁸	97%	18	NW_001471505.1 (Hypothetical protein)	---
24	HG531484	1-311	300-400	GGAGGGGGGT TC	3e ⁻⁹²	81%	4e ⁻³¹	90%	18	NW_001471505.1 (Hypothetical protein)	---
25	HG531485	424-559	1-443	ATAATGTACG GGGGAGATGC	1e ⁻⁴⁹	93%	0.0	98%	5	NW_003763785.1 (Transcription factor SOX-6)	---
25	HG531486	236-376	1-252	ATAATGTACG GGTGAGA	4e ⁻⁶¹	89%	3e ⁻¹¹⁹	98%	3	NW_001471673.2 (Disintegrin and Metalloproteinase domain-containing protein 17 precursor)	---

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25	HG531487	834-920	1-851	ATGGTATGAA CCTCCCTC	2e ⁻¹²⁷	93%	0.0	96%	1	NW_003763584.1 (Not determined)	CR1 (Non LTR)
25	HG531488	229-418	1-244	GAACGCCCT CCCAA	4e ⁻⁸⁰	96%	2e ⁻¹⁰⁸	96%	15	NW_003763985.1 (Not determined)	---
25	HG531489	81-446	1-101	ATAATGTACG GGTGAGATGC A	2e ⁻¹⁷¹	97%	4e ⁻³⁶	94%	2	NW_003763673.1 (Not determined)	---
26	HG531490	231-524	1-236	GAAGCC	2e ⁻²⁸	73%	4e ⁻¹¹³	99%	7	NW_003763822.1 (zinc finger protein 804A)	---
26	HG531491	1-203	197-525	GAGATGC	1e ⁻⁹³	99%	6e ⁻¹⁶¹	98%	15	NW_003763985.1 (WSC domain-containing protein 2)	CR1 (Non LTR)
26	HG531492	1-455	433-1065	CATATAATGT ACGGGTGAGA TGC	0.0	95%	0.0	96%	1	NW_003763645.1 (Not determined)	---
26	HG531493	1-296	285-705	CCCAATCGAA CC	9e ⁻¹⁴¹	99%	0.0	97%	7	NW_003763823.1 (Collagen alpha-1(VI) chain precursor)	---
26	HG531494	161-555	1-160	-	2e ⁻¹¹⁸	84%	6e ⁻⁶³	94%	1	NW_001471534.2 (Pyruvate dehydrogenase kinase, isozyme 3)	CR1 (Non LTR)
26	HG531495	142-640	1-148	GAACGCC	1e ⁻¹³¹	91%	3e ⁻⁵³	92%	4	NW_001471685.2 (Amyloid beta A4 precursor protein-binding family B member 2)	CR1 (Non LTR)
26	HG531496	147-418	1-165	GACCCCCCT CCCAAACC	1e ⁻⁹²	93%	3e ⁻⁶²	94%	2	NW_003763668.1 (Eukaryotic translation initiation factor 1b)	CR1 (Non LTR)

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	Locus	<i>G. gallus</i> repeats
27	HG531497	1-302	282-525	TACACCAACC CCAATCGAAC C	2e ⁻⁰⁶	80%	2e ⁻¹⁰⁹	96%	1	NW_001471554.1 (Similar to spinal cord-derived growth factor-B- SCDGF-B)	---
27	HG531498	1-301	290-365	CCCAATCGAA CC	4e ⁻⁰⁶	71%	1e ⁻²³	93%	10	NW_001471428.1 (ST8 alpha-N-acetylneuraminide alpha-2,8 -sialyltransferase 2)	---
27	HG531499	1-308	288-531	TACACCAACC CCAATCGAAC C	7e ⁻¹³⁴	97%	2e ⁻¹¹⁰	96%	1	NW_001471554.1 (Similar to spinal cord-derived growth factor-B- SCDGF-B)	---
27	HG531500	1-291	274-324	ACCAACCCCA ATCGAACCC	5e ⁻⁰⁵	75%	4e ⁻⁰⁹	88%	Z	NW_001488823.1 (3-oxoacid CoA transferase 1)	---
27	HG531501	1-295	277-328	ACCAACCCCA ATCGAACCC	3e ⁻⁰⁸	68%	1e ⁻⁰⁸	87%	Z	NW_001488823.1 (3-oxoacid CoA transferase 1)	---
27	HG531502	1-263	252-505	CCCAATCGAA CC	0.001	88%	5e ⁻⁸⁶	91%	2	NW_001471651.1 (Similar to aminopeptidase)	---
27	HG531503	1-264	246-297	ACCAACCCCA ATCGAACCC	1e ⁻⁰⁴	68%	1e ⁻⁰⁹	88%	Z	NW_001488823.1 (3-oxoacid CoA transferase 1)	---
27	HG531504	1-263	244-279	ACACCAACCC CAATCGAACCC	0.002	91%	7e ⁻⁰⁵	91%	3	NW_001471673.1 (Suppressor of Ty 3 homolog)	---
27	HG531505	1-287	271-466	CCAACCCCAA TCGAACC	4e ⁻¹²⁴	95%	2e ⁻⁹⁰	97%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
27	HG531506	1-308	298-423	CCAATCGAAC C	6e ⁻¹⁵¹	99%	2e ⁻⁵²	98%	5	NW_003763785.1 (Tetraspanin-18)	---
27	HG531507	1-286	276-400	CCAATCGAAC C	5e ⁻⁰⁶	86%	1e ⁻⁵⁵	99%	5	NW_003763785.1 (Tetraspanin-18)	---

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	Locus	<i>G. gallus</i> repeats
28	HG531508	270-546	1-288	GAAGCCCCCT CCCCAAAACC	1e ⁻¹²⁵	96%	6e ⁻¹³⁶	98%	1	NW_003763584.1 (gamma-aminobutyric acid receptor subunit gamma-3)	---
28	HG531509	707-985	1-713	GAACGCC	3e ⁻¹³⁶	99%	0.0	97%	6	NW_003763812.1 (Not determined)	---
36	HG531510	1-286	269-464	CCAACCCCAA TCGAACCC	3e ⁻⁰⁷	77%	1e ⁻⁸⁷	96%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
36	HG531511	71-403	1-90	ATAATATACG GGTGAGATGC	5e ⁻¹⁹	69%	1e ⁻²⁸	91%	15	NW_001471461.1 (Not determined)	---
37	HG531512	1-281	271-492	CCAATCGAAC C	4e ⁻⁵²	96%	4e ⁻⁸⁶	91%	1	NW_001471549.1 (Not determined)	Hitchcock (LTR)
37	HG531513	1-285	277-564	AATCGAACC	2e ⁻⁶²	99%	2e ⁻¹⁴⁰	98%	15	NW_001471461.1 (Not determined)	---
42	HG531514	1-270	247-462	ACCAACCCCA ATCGAACCAA GACC	-	-	8e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---
43	HG531515	1-93	70-285	ACCAACCCCA ATCGAACCAA GACC	-	-	5e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---
45	HG531516	1-336	319-534	ACCAACCCCA ATCGAACC	1e ⁻⁴⁹	76%	9e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---
45	HG531517	185-408	1-197	GACGCCCCCT CCC	6e ⁻¹⁰⁸	99%	2e ⁻⁸⁹	97%	2	NW_001471633.1 (Similar to parathyroid hormone-responsive B1)	CR1 (Non LTR)
45	HG531518	185-447	1-197	GAACCCCCCT CCC	3e ⁻¹²⁵	98%	6e ⁻⁸⁴	95%	2	NW_003763668.1 (parathyroid hormone-responsive B1)	CR1 (Non LTR)
47	HG531519	1-293	280-380	ACCCCAATCG AACC	2e ⁻⁰⁴	73%	5e ⁻⁴⁰	97%	3	NW_001471679.1 (Similar to Eml4 protein)	---
54	HG531520	1186-1479	1-1189	TTGA	3e ⁻¹⁴⁴	99%	0.0	99%	2	NW_001471639.1 (Not determined)	CR1 (Non LTR)

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	Locus	<i>G. gallus</i> repeats
54	HG531521	288-579	1-305	GAACGCCCT CCCAAAC	1e ⁻¹⁴³	99%	3e ⁻¹³⁴	94%	3	NW_001471673.1 (Not determined)	Hitchcock (LTR)
55	HG531522	1-433	416-631	ACCAACCCCA ATCGAACC	1e ⁻¹⁶⁹	97%	1e ⁻¹⁰¹	99%	1	NW_001471534.2 (Dystrophin)	---
55	HG531523	1-136 / 332-691	119-335 / 684-877	ACCAACCCCA ATCGAACC / GAAG / CCAAAACC	2e ⁻⁵⁶ / 2e ⁻¹⁶⁹	97% / 97%	4e ⁻¹⁰² / 2e ⁻⁹⁴	99% / 100%	1 / 1	NW_001471534.2 (Dystrophin)/ NW_001471534.2 (Dystrophin)	---
55	HG531524	1-111	94-308	ACCAACCCCA ATCGAACC	2e ⁻⁴³	96%	7e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
57	HG531525	487-622	1-495	ATAATGTAC	1e ⁻⁵⁰	94%	0.0	100%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
57	HG531526	47-311	1-60	GAACGCCCT CCCA	5e ⁻¹⁰¹	93%	8e ⁻¹⁸	95%	3	NW_001471667.1 (Similar to beige protein homolog)	---
57	HG531527	403-670	1-416	CTTGAACCCC CCTC	4e ⁻¹⁰⁰	92%	0.0	98%	4	NW_001471687.1 (Not determined)	---
57	HG531528	1218-1435	1-1222	GGTAG	3e ⁻⁷⁶	92%	0.0	96%	3	NW_001471668.1 (Not determined)	CR1 (Non LTR)
57	HG531529	75-344	1-88	AACCTGAACC CCCC	2e ⁻¹⁰⁰	92%	6e ⁻³²	96%	3	NW_001471671.1 (Not determined)	CR1 (Non LTR)
57	HG531530	481-615	1-488	ATAATGTA	6e ⁻⁴⁷	93%	0.0	99%	1	NW_001471545.1 (Hypothetical protein)	---
57	HG531531	406-845	1-416	GAAGCCCCCT C	4e ⁻¹¹⁴	91%	0.0	98%	4	NW_001471687.1 (Not determined)	---
57	HG531532	398-843	1-420	GAACGCCCT CCCAAACCA CAG	6e ⁻¹⁷⁵	98%	0.0	96%	25	NW_001471602.1 (Not determined)	---
58	HG531533	487-793	1-495	ATAATGTAC	3e ⁻¹⁰⁹	90%	0.0	99%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
58	HG531534	487-880	1-495	ATAATGTAC	7e ⁻¹¹²	91%	0.0	99%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	Locus	<i>G. gallus</i> repeats
58	HG531535	193-482	1-194	GA	9e ⁻⁰⁴	68%	3e ⁻⁵³	95%	2	NW_001471633.1 (Not determined)	---
58	HG531536	345-636	1-86 / 87-360	TTGAAGCCCC CTCCCA	3e ⁻⁰⁵	70%	3e ⁻³³ / 6e ⁻¹³¹	96% / 98%	15 / 2	NW_001471461.1 (Not determined)/ NW_001471646.1 (Not determined)	---
58	HG531537	267-558	1-268	GA	2e ⁻⁰⁵	71%	5e ⁻¹²⁵	99%	2	NW_001471633.1 (Not determined)	---
58	HG531538	43-333	1-58	GAACCCCCCT CCCAA	3e ⁻⁰⁷	70%	4e ⁻¹⁶	93%	4	NW_001471688.1 (Not determined)	---
58	HG531539	262-524	1-275	GAACGCCCT CCCA	2e ⁻⁰⁵	84%	8e ⁻⁵²	99%	12	NW_001471441.1 (Not determined)	---
58	HG531540	194-327	1-202	ATAATGTAC	2e ⁻²¹	100%	2e ⁻⁹⁵	98%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
58	HG531541	1-150	145-335	CATTAT	9e ⁻²¹	94%	2e ⁻⁶⁴	87%	2	NW_001471633.1 (Not determined)	---
58	HG531542	142-216	1-160	GACCCCCCT CCCAAACC	2e ⁻²⁸	98%	5e ⁻⁶⁸	96%	1	NW_001471534.2 (Pyruvate dehydrogenase kinase, isozyme 3)	CR1 (Non LTR)
58	HG531543	521-585	1-534	AAATAATGTA CGGG	6e ⁻¹³	100%	0.0	99%	8	NW_001471740.1 (Not determined)	---
59	HG531544	487-791	1-495	ATAATGTAC	2e ⁻¹⁴⁹	99%	0.0	100%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
59	HG531545	487-724	1-495	ATAATGTAC	9e ⁻⁴⁰	76%	0.0	100%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
59	HG531546	488-603	1-496	ATAATGTAC	7e ⁻³⁴	98%	0.0	99%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
59	HG531547	99-162	1-108	CATAATGTAC	4e ⁻²³	100%	6e ⁻⁴¹	96%	8	NW_001471740.2 (Not determined)	---
59	HG531548	362-424	1-377	ATAATGTACG GGGGAG	3e ⁻²⁰	97%	0.0	99%	4	NW_003763740.1	CR1 (Non LTR)

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	Locus	<i>G. gallus</i> repeats
										(mineralocorticoid receptor)	
59	HG531549	289-351	1-317	ATAATGTACG GGGGAGATGC ATGAATTTC	2e ⁻²⁰	97%	2e ⁻¹⁴⁷	97%	13	NW_003763912.1 (Not determined)	---
60	HG531550	102-399	1-107	AAAGTG	8e ⁻¹⁴⁵	99%	6e ⁻⁴⁶	99%	19	NW_003764121.1 (Putative polypeptide N-acetylgalactosa minyltransferase-like protein 3-like)	---
60	HG531551	296-558	1-308	GAACCCCCCT CCC	6e ⁻¹²⁹	99%	5e ⁻¹⁴³	97%	1	NW_003763493.1 (Not determined)	CR1 (Non LTR)
60	HG531552	304-593	1-313	GAACCCCCCT	5e ⁻¹⁴³	99%	3e ⁻¹⁴⁷	97%	3	NW_001471668.2 (Not determined)	---
60	HG531553	421-686	1-442	TTTGACCCCC CCTCCCAAAA CC	2e ⁻¹¹¹	93%	0.0	97%	2	NW_003763661.1 (integrin alpha-8 precursor)	---
60	HG531554	137-203	1-146	AAAATAATAA	7e ⁻²²	97%	1e ⁻⁶³	97%	3	NW_003763720.1 (Not determined)	---
60	HG531555	760-813	1-767	TATAGTGT	2e ⁻⁰⁴	80%	0.0	98%	Not determined	NW_003764339.1 (Not determined)	---
60	HG531556	204-328	1-210	CATAATG	1e ⁻⁴⁶	97%	1e ⁻¹⁰³	100%	2	NW_003763661.1 (Not determined)	---
61	HG531557	1-263	245-298	CACCAACCCC AATCGAACC	1e ⁻¹⁰⁸	94%	8e ⁻¹¹	90%	2	NW_001471639.1 (Similar to KIAA0222)	---
61	HG531558	1-263	247-332	CCAACCCCAA TCGAACC	1e ⁻⁰⁶	78%	9e ⁻³⁰	94%	5	NW_001471698.1 (UDP-N-acetyl- alpha-D- galactosamine:poly peptide N-acetyl galactosaminyltransf erase-like 4)	---
62	HG531559	1-286	270-465	CCAACCCCAA TYGAACC	1e ⁻⁰⁴	89%	3e ⁻⁷⁵	90%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)

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62	HG531560	1-290	274-469	CCAACCCCAA TCGAACC	3e ⁻¹³²	97%	2e ⁻⁹¹	98%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
62	HG531561	81-363	1-89	GACCGCCCC	2e ⁻⁰⁵	86%	3e ⁻³⁶	99%	1	NW_003763647.1 (Not determined)	CR1 (Non LTR)
62	HG531562	138-425	1-144	AAGCTGA	1e ⁻⁰⁵	94%	4e ⁻⁶¹	96%	3	NW_001471671.1 (Not determined)	CR1 (Non LTR)
62	HG531563	141-423	1-142	GA	4e ⁻⁰⁶	100%	2e ⁻⁵⁷	95%	Z	NW_001488823.1 (Not determined)	CR1 (Non LTR)
66	HG531564	1-297	279-352	CACCAACCCC AATCGAACC	6e ⁻⁰⁴	88%	6e ⁻²⁰	90%	Not determined	NW_001477862.1 (Not determined)	---
66	HG531565	1-286	270-465	CCAACCCCAA TCGAACC	8e ⁻¹³⁹	99%	9e ⁻⁸⁹	97%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
66	HG531566	1-308	292-487	CCAACCCCAA TCGAACC	2e ⁻¹²⁷	94%	2e ⁻⁹¹	98%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
66	HG531567	1-267	247-442	CCAACCCCAA TCGAACCCAC C	2e ⁻¹²⁸	99%	6e ⁻⁹¹	97%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
66	HG531568	1-283	263-373	TACACCAACC CCAATCGAAC C	4e ⁻⁰⁶	100%	6e ⁻³³	90%	1	NW_001471554.1 (Not determined)	---
66	HG531569	1-278	254-775	ACCAACCCCA ATCGAACCCC CAACT	3e ⁻⁰⁶	82%	0.0	89%	3	NW_001471673.1 (Not determined)	Hitchcock (LTR)
66	HG531570	1-271	253-306	CACCAACCCC AATCGAACC	2e ⁻⁰⁴	81%	8e ⁻¹¹	90%	2	NW_001471639.1 (Similar to KIAA0222)	---
66	HG531571	1-263	250-658	ACCCCAATCG AACC	1e ⁻⁰⁴	94%	0.0	97%	4	NW_001471687.1 (fibroblast growth factor receptor 3)	---
67	HG531572	1-394	373-496	ACACACCAAC CCCAATCGAA CC	5e ⁻¹⁶¹	93%	1e ⁻⁴⁹	96%	2	NW_003763686.1 (Not determined)	---

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67	HG531573	1-624	608-801	CCAACCCCAA TCGAACC	0.0	94%	3e ⁻⁷³	92%	6	NW_003763812.1 (Not determined)	---
67	HG531574	1-214	208-332	GAGATGC	5e ⁻⁸³	93%	1e ⁻⁴⁷	94%	13	NW_003763912.1 (Kv channel- interacting protein 1 isoform 2)	---
67	HG531575	1-301	292-893	GGGAGATGCA	2e ⁻¹³⁰	95%	0.0	96%	4	NW_003763740.1 (Collagen alpha- 1(XXV) chain)	---
67	HG531576	1-316	310-573	GAGATGC	1e ⁻¹⁴⁵	98%	3e ⁻¹²⁷	99%	17	NW_003764072.1 (Not determined)	---
68	HG531577	1-290	279-445	CCCAATCGAA CC	2e ⁻⁰⁶	72%	2e ⁻⁷⁷	98%	2	NW_001471642.1 (Not determined)	---
68	HG531578	1-290	270-350	TACACCAACC CCAATCGAAC C	5e ⁻⁰⁵	70%	4e ⁻²⁸	95%	1	NW_003763650.1 (NADP-dependent malic enzyme, mitochondrial)	---
68	HG531579	1-290	270-381	TACACCAACC C CAATCGAACC	4e ⁻⁰⁷	72%	7e ⁻³²	89%	1	NW_003763650.1 (NADP-dependent malic enzyme, mitochondrial)	---
68	HG531580	1-288	271-476	ACCAACCCCA ATCGAACC	3e ⁻⁵⁴	98%	6e ⁻⁸⁸	96%	Z	AC200647.3 (Not determined)	---
68	HG531581	1-294	278-473	CCAACCCCAA TCGAACC	4e ⁻¹⁴³	99%	2e ⁻⁹¹	98%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
71	HG531582	1-70	71-239	—	2e ⁻⁰⁸	84%	1e ⁻⁷⁷	98%	9	NW_001471744.1 (Not determined)	CR1 (Non LTR)
72	HG531583	514-806	1-525	GTTGAACCCC CC	3e ⁻¹⁴¹	99%	0.0	99%	6	NW_003763812.1 (Metal transporter CNNM2 isoform 2)	---
73	HG531584	91-306	1-103	CCCCTCCCAA AAC	2e ⁻¹⁰⁰	99%	9e ⁻²⁹	90%	Z	AC216895.3 (Not determined)	CR1 (Non LTR)
74	HG531585	74-366	1-92	TGACCCCCC TCCAAAAC	7e ⁻¹⁴⁵	99%	3e ⁻²⁹	91%	12	NW_003763892.1	---

Ave	EMBL	kDNA	<i>G. gallus</i> DNA	Intermediate recombination site	kDNA <i>E-value</i>	kDNA Identity	<i>G. gallus</i> <i>E-value</i>	<i>G. gallus</i> Identity	<i>G. gallus</i> Chromosome	<i>Locus</i>	<i>G. gallus</i> repeats
										(Dedicator of cytokinesis protein 3)	
74	HG531586	376-668	1-389	TGAACCCCC TCCC	5e ⁻¹⁴⁴	99%	0.0	99%	18	NW_003764078.1 (Uncharacterized protein LOC100858297)	---
74	HG531587	181-475	1-200	TTTGAACCCC CCTCCCAAAA	2e ⁻¹⁴⁶	99%	4e ⁻⁸⁷	96%	10	NW_003763854.1 (Immunoglobulin superfamily DCC subclass member 4- like)	---
74	HG531588	388-679	1-395	GAAGCCCC	1e ⁻¹⁴⁴	99%	0.0	99%	14	NW_003763931.1 (Ubiquitin carboxyl- terminal hydrolase 22-A)	---
74	HG531589	527-818	1-534	GAACGCCC	4e ⁻¹⁴⁰	98%	0.0	96%	Z	AC231413.2 (Not determined)	Z-REP (Sat) / CR1 (Non LTR)
74	HG531590	382-673	1-389	GAAGACCC	1e ⁻¹⁴⁴	99%	0.0	96%	Z	NW_003764323.1 (Not determined)	Z-REP (Sat)