

A) kDNA Vertical transfer to chicken germ line 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	Locus	<i>G. gallus</i> repeats
1	HG53159 1	1-93	76-291	ACCAACCCCAATC GAACC	4e ⁻³¹	96%	6e ⁻¹⁰¹	98%	1	NW_001471534.2 (Dystrophin)	---
1	HG53159 2	1-263	246-461	ACCAACCCCAATC GAACC	9e ⁻¹¹	100%	3e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
1	HG53159 3	415-742	1-435	TATAATGTACGGGT GAGATGC	3e ⁻²⁰	77%	0.0	98%	5	NW_003763785.1 (Transcription Factor <i>SOX-6</i>)	---
1	HG53159 4	185-470	1-197	GACGCCCCCTCCC	2e ⁻¹⁴⁰	100%	2e ⁻⁸⁴	95%	2	NW_003763668.1 (Protein <i>PTHBI</i>)	CR1 (Non LTR)
1	HG53159 5	189-468	1-197	CCCCCTCCC	9e ⁻⁰⁹	81%	2e ⁻⁷⁷	92%	2	NW_003763668.1 (Protein <i>PTHBI</i>)	CR1 (Non LTR)
1	HG53159 6	173-459	1-185	GACGCCCCCTCCC	3e ⁻¹³⁹	100%	2e ⁻⁸⁴	98%	3	NW_001471668.2 (Probable Palmitoyl transferase <i>ZDHHC14</i> isoforms 1 or 2)	CR1 (Non LTR)
1	HG53159 7	76-130	1-104	ACCAATTTACATC ACAACCCAAACCC AT	7e ⁻¹⁹	100%	3e ⁻³¹	91%	4	NW_003763735.1 (Not determinante)	CR1 (Non LTR)
1	HG53159 8	53-346	1-63	AAGACCGCCCC	3e ⁻¹³⁷	98%	9e ⁻²⁴	100%	5	NW_003763785.1 (Not determined)	---
1	HG53159 9	1-719	698-1204	TACACCAACCCCA ATCGAACC	0.0	89%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---

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1	HG53160 0	1-477	456-963	ATACACCAACCCC AATCGAACC	0.0	96%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
1	HG53160 1	1-309	292-793	ACCAACCCCAATC GAACC	1e ⁻¹²⁸	37%	0.0	97%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
2	HG53160 2	1-250	233-393	ACCAACCCCAATC GAACC	3e ⁻⁶⁷	83%	6e-71	98%	3	NW_001471673.2 (Not determined)	Hitchcock (LTR)
2	HG53160 3	1-192	178-260	GTACGGGTGAGAT GC	9e ⁻⁷⁹	95%	5e ⁻²⁵	92%	1	NW_003763482.1 (Not determined)	---
2	HG53160 4	1-328	292-794	ACCAACCCCAATC GAACC	7e ⁻¹³¹	95%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
2	HG53160 5	1-265	244-749	ATACACCAACCCC AATCGAACC	4e ⁻¹⁰²	92%	0.0	97%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
3	HG53160 6	1-773	755-970	ACCAACCCCAATC GAACC	0.0	97%	1e ⁻⁹⁶	97%	1	NW_001471534.2 (Dystrophin)	---
3	HG53160 7	898- 1241	1-914	GAACCCCTCCCA AAA	3e ⁻⁷⁵	96%	0.0	97%	Not determined	NW_003780056.1 (Not determined)	---

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3	HG53160 8	108-810	1-121	CCCTTCCCAAACC	1e ⁻⁸⁶	94%	3e ⁻⁴⁰	98%	14	NW_001471454.1 Gga_WGA202_2 (Similar to KIAA1691 protein)	---
3	HG53160 9	1-79	58-167	ATACACCAACCCC AATCGAACC	7e ⁻¹⁴	92%	4e ⁻³⁷	92%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
3	HG53161 0	1-83	63-583	ACCAACCCCAATC GAACCCCA	1e ⁻²³	92%	0.0	99%	3	NW_001471673.2 (Not determined)	Hitchcock (LTR)
3	HG53161 1	1-83	55-125	ACCATAACACCAA CCCCAATCGAACCC CA	3e ⁻²⁴	92%	3e ⁻⁰⁶	92%	28	NW_003764302.1 (Not determined)	---
3	HG53161 2	1-141	107-293	AATATAACTCTAAT TACACCAACCCCA ATCGAACC	2e ⁻⁴²	95%	4e ⁻⁹⁰	97%	2	AB556723.1 (Centromere 2 repeat sequence)	---
3	HG53161 3	1-263	244-747	ACACCAACCCCAA TCGAACC	1e ⁻¹²⁰	97%	0.0	97%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
4	HG53161 4	1-62	53-317	CAATCGAACC	5e ⁻²⁰	98%	2e ⁻¹²⁵	98%	1	NW_003763650.1 (Teneurin-4)	CR1 (Non LTR)
4	HG53161 5	1-73	53-153	TACACCAACCCCA ATCGAACC	2e ⁻²⁰	96%	2e ⁻³³	96%	1	NW_003763650.1 (<i>NADP</i> -dependent Malic enzyme, mitochondrial)	---

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5	HG53161 6	1-94	77-292	ACCAACCCCAATC GAACC	4e ⁻³⁴	99%	2e ⁻⁹⁹	98%	1	NW_001471534.2 (Dystrophin)	---
5	HG53161 7	1-466	249-664	ACCAACCCCAATC GAACC	4e ⁻¹⁴⁶	97%	1e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
5	HG53161 8	1-170	133-368	ACCAACCCCAATC GAACTACACCAAC CCCAATCGAACC	5e ⁻²⁷	87%	6e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---
5	HG53161 9	1-264	246-461	ACCAACCCCAATC GAACC	1e ⁻¹²⁵	98%	8e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---
5	HG53162 0	117-185	1-127	TACACCAACCC	7e ⁻¹⁶	96%	2e ⁻⁴¹	91%	Not determined	NW_003771790.1 (Not determined)	---
5	HG53162 1	1-245	222-514	GTCGAACGCCCTC CCAAAACCAA	4e ⁻¹⁴⁴	99%	3e ⁻¹²¹	99%	15	NW_003763985.1 (Not determined)	---
5	HG53162 2	1-250	229-735	ATACACCAACCCC AATCGAACC	1e ⁻¹⁰²	94%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
5	HG53162 3	1-247	239-744	ATACACCAACCCC AATCGAACC	6e ⁻⁹³	92%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
11	HG53162 4	1-93	76-291	ACCAACCCCAATC GAACC	5e ⁻³²	98%	1e ⁻⁹⁶	99%	1	NW_001471534.2 (Dystrophin)	---
11	HG53162 5	263-556	1-286	CTGAACCCCTCC CAAAACCGCA	5e ⁻¹⁴³	99%	3e ⁻¹²⁰	94%	2	NW_003763673.1 (Not determined)	---

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11	HG53162 6	153-444	1-162	GAACGCCCT	1e ⁻¹⁴³	99%	9e ⁻⁷⁶	99%	6	NW_003763812.1 (Similar to attractin 1, isoform 2)	---
11	HG53162 7	58-350	1-73	TGAAAGCCCCCTCC CAA	5e ⁻¹⁴⁷	100%	5e ⁻²¹	90%	1	NW_003763464.1 (Not determined)	---
11	HG53162 8	1-39	39-330	G	7e ⁻¹⁴⁵	99%	2e ⁻¹²	94%	4	NW_003763735.1 (Not determined)	---
11	HG53162 9	299-600	1-321	CAGGAACGATGAA GCCCCCTCCC	8e ⁻¹⁴⁷	100%	3e ⁻¹⁵²	98%	6	NW_003763812.1 (Not determined)	CR1 (Non LTR)
11	HG53163 0	1-231	269-716	ATACACCAACCCC AATCGAACC	1e ⁻¹⁰²	98%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
11	HG53163 1	1-187	183-685	ACCAACCCCAATC GAACC	3e ⁻⁷²	95%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
11	HG53163 2	1-154	134-639	TACACCAACCCCA ATCGAACC	2e ⁻²³	80%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
13	HG53163 3	1-167	150-365	ACCAACCCCAATC GAACC	4e ⁻⁴⁷	91%	3e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
13	HG53163 4	1-75	51-274	GGAGATGCACAAC CCCAATCGAACC	2e ⁻¹⁹	94%	4e ⁻¹⁰²	99%	1	NW_001471534.2 (Dystrophin)	---

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13	HG53163 5	1-284	272-684	CCCCAATCGAACC	2e ⁻⁰⁴	79%	0.0	98%	17	NW_003764074.1 (Adenylate kinase 8)	---
13	HG53163 6	1-169	153-348	CCAACCCCAATCG AACC	6e ⁻⁵⁷	96%	1e ⁻⁹¹	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
13	HG53163 7	1-276	267-391	CAATCGAACC	2e ⁻⁷⁰	91%	9e ⁻⁵⁶	99%	5	NW_003763785.1 (Tetraspanin 18)	---
13	HG53163 8	1-226	205-709	ATACACCAACCCC AATCGAACC	2e ⁻¹⁰⁰	97%	0.0	97%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
13	HG53163 9	1-104	94-600	ATACACCAACCCC AATCGAACC	9e ⁻²⁷	94%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
14	HG53164 0	1-151	134-349	ACCAACCCCAATC GAACC	8e ⁻⁵⁰	94%	1e ⁻⁹⁸	97%	1	NW_001471534.2 (Dystrophin)	---
14	HG53164 1	1-265	248-463	ACCAACCCCAATC GAACC	1e ⁻⁹⁹	92%	3e ⁻¹⁰⁰	98%	1	NW_001471534.2 (Dystrophin)	---
14	HG53164 2	1-169	152-367	ACCAACCCCAATC GAACC	1e ⁻⁴⁸	92%	5e ⁻⁹⁷	97%	1	NW_001471534.2 (Dystrophin)	---
14	HG53164 3	115-400	1-124	GAACCCCT	2e ⁻¹⁴⁰	99%	1e ⁻⁴⁰	91%	13	NW_003763912.1 (Not determined)	---
14	HG53164 4	132-417	1-140	GACCCCT	2e ⁻¹⁴⁰	99%	6e ⁻³⁹	86%	Not determined	BX640540.3 (Not determined)	CR1 (Non LTR)

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14	HG53164 5	399-688	1-420	GAACGCCCCCTCCA AAACCAA	6e ⁻¹³⁷	100%	0.0	97%	25	NW_003764242.1 (Not determined)	---
17	HG53164 6	1-486	467-683	ACACCAACCCCAA TCGAACC	2e ⁻²⁷	80%	6e ⁻⁹⁹	98%	1	NW_001471534.2 (Dystrophin)	---
17	HG53164 7	1-317	300-515	ACCAACCCCAATC GAACC	7e ⁻⁵⁷	98%	5e ⁻⁹⁹	98%	1	NW_001471534.2 (Dystrophin)	---
17	HG53164 8	78-177	1-95	GAAGGCCCTCCC AAAAC	5e ⁻²⁹	89%	1e ⁻³¹	93%	14	NW_003763931.1 (xylosyltransferase 1)	---
17	HG53164 9	204-284	1-210	CATAATG	4e ⁻²⁷	96%	1e ⁻¹⁰³	100%	2	NW_003763661.1 (Not determined)	---
17	HG53165 0	1-601	582-1086	TACACCAACCCCA ATCGAACC	0.0	97%	0.0	98%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
18	HG53165 1	1-201	91-300	TACACCAACCCCA ATCGAACC	---	---	3e ⁻⁵⁵	91%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
18	HG53165 2	1-258	238-337	TACACCAACCCCA ATCGAACC	---	---	1e ⁻³⁵	94%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
18	HG53165 3	1-278	267-433	CCCAATCGAACC	9e ⁻¹²⁶	96%	1e ⁻⁷⁴	98%	2	NW_003763680.1 (Receptor-type tyrosine-protein)	---

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										phosphatase mu- like)	
18	HG53165 4	39-326	1-49	GACGGCCCCTC	1e ⁻¹⁴⁰	99%	2e ⁻¹²	94%	4	NW_003763735.1 (Not determined)	---
18	HG53165 5	264-551	1-277	GAACGCCCTCCCA	2e ⁻¹⁴¹	99%	2e ⁻¹³⁵	99%	12	NW_003763892.1 (Not determined)	---
18	HG53165 6	30-317	1-37	GAAGGCC	1e ⁻¹⁴¹	99%	2e ⁻⁰⁷	97%	5	NW_003763748.1 (Not determined)	---
18	HG53165 7	1-288	268-772	TACACCAACCCCA ATCGAACC	1e ⁻¹³⁴	99%	0.0	97%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
19	HG53165 8	1-209	192-406	ACCAACCCCAATC GAACC	7e ⁻⁴⁹	88%	4e ⁻⁹⁹	98%	1	NW_001471534.2 (Dystrophin)	---
19	HG53165 9	1-607	588-637	ACACCAACCCCAA ACGAACC	0.0	84%	5e ⁻⁰⁵	86%	1	NW_003763496.1 (Not determined)	---
19	HG53166 0	1-150	146-798	ATGCA	8e ⁻⁵⁴	94%	0.0	98%	3	NW_001471673.2 (Peptidyl-prolyl cis- trans isomerase <i>FKBP1B</i>)	CR1 (Non LTR)
19	HG53166 1	1-265	237-666	GATACACATACAC CAACCCCAATCGA ACC	7e ⁻¹⁰⁴	93%	0.0	96%	17	NW_003764074.1 (Adenylate kinase 8)	---

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19	HG53166 2	1-433	417-624	CCAACCCCAATCG AACC	3e ⁻¹⁷¹	92%	4e ⁻⁹⁴	97%	5	NW_003763785.1 (Inositol-triphosphate 3-kinase A)	---
19	HG53166 3	141-405	1-159	GACCCCCCTCCCA AAACC	1e ⁻¹⁰⁵	94%	1e ⁻⁶⁷	96%	1	NW_001471534.2 ([Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial)	CR1 (Non LTR)
19	HG53166 4	151-757	1-169	GACGCCCCCTCCCA AAACC	0.0	84%	1e ⁻⁵¹	88%	Not determined	NW_003776158.1 (Not determined)	CR1 (Non LTR)
20	HG53166 5	1-98	79-272	CAACCCCAATCGA ACCCACC	1e ⁻³³	95%	1e ⁻⁸⁹	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
20	HG53166 6	1-39	16-105	AACCATAATGTAC GGGTGAGATGC	9e ⁻¹⁰	100%	2e ⁻²⁵	92%	1	NW_003763482.1 (Not determined)	---
20	HG53166 7	1-241	224-419	CCAACCCCAATCG AACC	6e ⁻⁷¹	98%	2e ⁻⁹⁰	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
22	HG53166 8	31-308	1-38	CCCCTCCC	2e ⁻¹³³	99%	8e ⁻⁰⁵	89%	4	NW_003763740.1 (Not determined)	---
22	HG53167 3	303-585	1-315	GACGCCCCCTCCC	1e ⁻¹³⁸	96%	2e ⁻¹⁴³	96%	1	NW_003763493.1 (Not determined)	CR1 (Non LTR)
22	HG53166 9	36-318	1-43	GACGGCCC	2e ⁻⁰⁵	89%	2e ⁻¹¹	98%	27	NW_003764296.1 (Amiloride- sensitive cation channel 1, neuronal)	---

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22	HG53167 0	74-346	1-82	GAACGCCCTCCCA AAACC	3e ⁻¹³⁷	99%	1e ⁻²⁷	96%	21	NW_003764143.1 (Cytidine deaminase)	---
22	HG53167 1	278-533 / 835-927	1-277 / 522-846	GAACGCCCTCCCA/ GGGAGAAGAGTT/ GACGCCCTCCC	3e ⁻⁹⁷ / 1e ⁻³²	93% / 98%	7e ⁻¹³² / 1e ⁻¹⁵⁴	98% / 98%	12 / 6	NW_003763892.1 (Not determined) / NW_003763812.1 (Not determined)	--- / CR1 (Non LTR)
22	HG53167 2	43-318	1-45	TCC	7e ⁻⁶²	78%	0.012	83%	5	NW_003763748.1 (Not determined)	---
24	HG53167 4	1-130	120-219	TACACCAACCCCA ATCGAACC	6e ⁻⁵³	97%	2e ⁻³⁶	92%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
24	HG53167 5	1-201	195-296	ATACACCAACCCC AATCGAACC	1e ⁻⁷¹	91%	2e ⁻³⁶	94%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
24	HG53167 6	1-130	120-295	CCATCGAACC	3e ⁻⁵³	97%	3e ⁻⁷³	97%	2	NW_003763680.1 (Receptor-type tyrosine-protein phosphatase mu- like)	---
24	HG53167 7	1-150	134-683	CCAACCCCAATCG AACC	9e ⁻⁴⁶	90%	0.0	99%	5	NW_003763785.1 (Not determined)	---
24	HG53167 8	1-264	242-437	CCAACCCCAATCG AACCCACCAT	4e ⁻⁷⁹	86%	2e ⁻⁹¹	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)

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24	HG53167 9	1-216	200-395	CCAACCCCAATCG AACC	1e ⁻⁷²	91%	1e ⁻⁹¹	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
24	HG53168 0	1-283	269-351	GTACGGGTGAGAT GC	5e ⁻¹⁰⁹	92%	7e ⁻²⁵	92%	1	NW_003763482.1 (Not determined)	---
26	HG53168 1	1-158	141-250	TACACCAACCCCA ATCGA	---	---	1e ⁻³³	90%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
26	HG53168 2	1-265	249-444	CCAACCCCAATCG AACC	1e ⁻⁴¹	94%	2e ⁻⁹⁰	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
28	HG53168 3	101-392	1-112	GAAGGCCCTCC	8e ⁻¹⁴⁵	99%	1e ⁻⁴⁷	98%	1	NW_003763482.1 (Not determined)	---
28	HG53168 4	98-387	1-104	GACCGCC	1e ⁻¹⁴¹	99%	2e ⁻⁴⁴	99%	5	NW_001471710.2 (<i>RAC</i> -alpha serine/threonine- protein kinase)	---
28	HG53168 5	264-555	1-277	GAACGCCCTCCCA	1e ⁻¹⁴³	99%	3e ⁻¹³⁴	99%	12	NW_003763892.1 (Not determined)	---
28	HG53168 6	265-556	1-286	GAAGGCCCTCCCA AAACCACA	1e ⁻¹⁴⁴	99%	8e ⁻¹²⁸	96%	2	NW_003763673.1 (Not determined)	---
28	HG53168 7	62-353	1-74	GAAGGCCCTCCC	9e ⁻¹⁴⁴	99%	2e ⁻²⁵	96%	9	NW_001471743.2 (Uncharacterized)	---

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										protein LOC769332)	
28	HG53168 8	362-653	1-369	GAAGCCCC	4e ⁻¹⁴⁵	99%	0.0	99%	4	NW_003763739.1 (Not determined)	---
28	HG53168 9	52-343	1-59	GAAGGCC	2e ⁻¹³⁸	98%	3e ⁻¹⁷	93%	5	NW_003763785.1 (Not determined)	---
28	HG53169 0	175-463	1-180	GAACCC	9e ⁻¹³⁹	99%	4e ⁻⁸⁷	100%	12	NW_003763892.1 (Not determined)	---
36	HG53169 1	68-417	1-91	CACATAATGTACG GGGGAGATGCA	5e ⁻¹⁰⁹	95%	2e ⁻³³	97%	15	NW_001471461.2 (Not determined)	---
36	HG53169 2	235-526	1-253	GAACGCCCTCCCA AAACC	1e ⁻¹⁴⁴	99%	1e ⁻¹¹⁹	98%	15	NW_003763985.1 (Not determined)	---
36	HG53169 3	382-673	1-397	GAAGGCCCTCCCA AAA	1e ⁻¹⁴⁴	99%	0.0	97%	Z	NW_003764323.1 (Not determined)	Z-Rep (Sat)
36	HG53169 4	394-690	1-414	TTTGCGAAGGCCCC TCCAAA	2e ⁻¹⁴³	99%	0.0	98%	11	NW_003763865.1 (Not determined)	Z-Rep (Sat)/ CR1 (Non LTR)
36	HG53169 5	268-559	1-285	GACCCCCCTCCCA AAAC	1e ⁻¹⁴³	99%	6e ⁻¹³⁶	98%	2	NW_003763664.1 (Not determined)	---
36	HG53169 6	382-673	1-397	GAAGGCCCTCCCA AAA	3e ⁻¹⁴⁰	99%	0.0	96%	Z	NW_003764324.1 (Not determined)	Z-Rep (Sat)
36	HG53169 7	620-911	1-638	GAAGGCCCTCCCA AAAAC	3e ⁻¹⁴³	99%	0.0	96%	2	NW_003763668.1 (E3 ubiquitin- protein ligase HECW1)	---

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
36	HG53169 8	404-695	1-421	GAACGCCCTCCCA AAAC	2e ⁻¹⁴³	99%	0.0	95%	1	NW_003763449.1 (Not determined)	---
36	HG53169 9	156-447	1-164	GACGGCCCC	9e ⁻¹⁴⁵	99%	4e ⁻⁷⁴	98%	1	NW_003763484.1 (Not determined)	---
36	HG53170 0	264-555	1-277	GAAGGCCCTCCCA A	3e ⁻¹³⁹	98%	2e ⁻¹³⁵	99%	12	NW_003763892.1 (Not determined)	---
38	HG53170 1	1-276	255-365	CTACACCAACCCCA ATCGAACC	5e ⁻⁴⁶	77%	3e ⁻³⁶	92%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
38	HG53170 2	1-133	117-667	CCAACCCCAATCG AACC	5e ⁻⁴⁹	99%	0.0	99%	5	NW_003763785.1 (Not determined)	---
39	HG53170 3	1-109	76-281	CACCAACCCCAATC GAACCGTTTCTCC CCTAAA	7e ⁻³⁰	89%	2e ⁻⁹³	97%	Not determined	NW_003779328.1 (Not determined)	GGXOI (Simple Sat)
39	HG53170 4	1-111	99-515	CCCCAATCGAACC	2e ⁻²¹	97%	0.0	97%	17	NW_003764074.1 (Adenylate kinase 8)	---
39	HG53170 5	1-197	194-599	ACCA	5e ⁻⁴⁹	83%	0.0	98%	17	NW_003764074.1 (Adenylate kinase 8)	---
39	HG53170 6	629-827	1-641	GAAGCCCCCTCCCA	4e ⁻⁷⁷	97%	0.0	97%	13	NW_003763913.1 (Solute carrier Family 25 member 48)	---

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
39	HG53170 7	427-675	1-533	ATAATG	3e ⁻³⁹	87%	0.0	99%	9	NW_001471743.2 (Not determined)	---
39	HG53170 8	160-308	1-163	CATA	2e ⁻³⁸	92%	8e ⁻⁶⁸	96%	1	NW_001471534.2 ([Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial)	CR1 (Non LTR)
39	HG53170 9	1-42	33-276	GAGATGCATA	3e ⁻⁰⁹	98%	1e ⁻¹¹⁶	98%	2	NW_003763661.1 (Not determined)	---
40	HG53171 0	1-149	129-238	TACACCAACCCCA ATCGAACC	---	---	2e ⁻³⁵	91%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
40	HG53171 1	1-130	110-219	TACACCAACCCCA ATCGAACC	2e ⁻⁵⁴	98%	2e ⁻³⁶	92%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
40	HG53171 2	1-100	85-704	GTACGGGGGAGAT GCA	5e ⁻³⁰	91%	0.0	98%	12	NW_003763903.1 (forkhead box protein P1)	---
40	HG53171 3	68-250	1-93	CACATAATGTACG GGTGAGATGCATG	2e ⁻⁸⁰	97%	1e ⁻³³	96%	15	NW_001471461.2 (Not determined)	---
40	HG53171 4	256-465	1-289	TAGCACAATCCGA CCCCCCTCCCAAA AC	4e ⁻⁸⁰	98%	9e ⁻¹³³	98%	2	NW_003763664.1 (Not determined)	---

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
40	HG53171 5	1-100	93-342	GAGATGCT	1e ⁻³⁴	95%	3e ⁻¹¹⁹	98%	20	NW_003764128.1 (Not determined)	---
42	HG53171 6	185-475	1-197	GACGCCCCCTCCC	5e ⁻¹⁴²	99%	2e ⁻⁸⁹	97%	2	NW_003763668.1 (Protein <i>PTHBI</i>)	CR1 (Non LTR)
42	HG53171 7	50-396	1-97	GAACCTCCCCTGGC ACAACCTCAACCAT CACCTCTCCTTCTG TTGCTG	2e ⁻¹²²	99%	2e ⁻³²	93%	Z	NW_003764322.1 (Not determined)	CR1 (Non LTR)
42	HG53171 8	185-474	1-197	GACGCCCCCTCCC	1e ⁻¹⁴²	100%	1e ⁻⁸⁶	96%	2	NW_003763668.1 (Protein <i>PTHBI</i>)	CR1 (Non LTR)
44	HG53171 9	1-200	183-274	ACCAACCCCAATC GAACC	---	---	3e ⁻³⁴	96%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
44	HG53172 0	1-132	112-307	CCAACCCCAATCG AACCACC	3e ⁻³⁵	91%	1e ⁻⁹⁰	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
44	HG53172 1	1-150	139-373	GGGTGAGATGCA	4e ⁻⁶⁰	96%	2e ⁻¹¹⁴	99%	2	NW_003763693.1 (Protein tyrosine phosphatase type IVA 3 isoform 1)	---
49	HG53172 2	1-179	173-431	GAGATGC	9e ⁻⁵⁰	93%	4e ⁻¹³⁰	100%	5	NW_003763785.1 (Not determined)	---
49	HG53172 3	1-102	99-755	ATGC	1e ⁻²⁵	87%	0.0	98%	3	NW_001471673.2 (Peptidyl-prolyl cis- trans isomerase <i>FKBP1B</i>)	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	<i>Locus</i>	<i>G. gallus</i> repeats
49	HG53172 4	1-265	246-297	ACCAACCCCAATC GAACCC	5e ⁻¹²⁷	99%	1e ⁻⁰⁸	87%	Z	NW_001488830.2 (Succinyl-CoA: 3- ketoacid-coenzyme A transferase 1, mitochondrial)	---
49	HG53172 5	1-442	422-786	TATAATGTACGGG GGAGATGC	2e ⁻⁹⁸	83%	0.0	97%	5	NW_003763785.1 (Transcription Factor SOX-6)	---
50	HG53172 6	264-555	1-277	GAACCCCTCCCA	2e ⁻¹¹⁷	93%	3e ⁻¹³⁴	99%	12	NW_003763892.1 (Not determined)	---
50	HG53172 7	383-494	1-104	TATAATGTACGGGT GAGATGCA	7e ⁻³⁹	94%	0.0	98%	3	NW_001471673.2 (Mitochondrial peptide methionine sulfoxide reductase)	CR1 (Non LTR)
50	HG53172 8	1-76	58-172	GCAGATAATGTAC GGGTGA	3e ⁻⁴⁵	97%	1e ⁻²³	92%	11	NW_003763881.1 (72kDa type IV collagenase preproprotein)	---
51	HG53172 9	1-296	279-475	CCAACCCCAATCG AACCC	7e ⁻¹³⁴	98%	7e ⁻⁹⁰	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
51	HG53173 0	1-84 / 271-347	85-273	TCC	4e ⁻²⁴ / 3e ⁻²⁶	92% / 94%	1e ⁻¹²	72%	12	NW_003763903.1 (Uncharacterized protein LOC416093)	---
53	HG53173 1	185-314	1-197	GACGCCCTCCC	1e ⁻⁵¹	98%	2e ⁻⁸⁹	97%	2	NW_003763668.1 (Protein <i>PTHBI</i>)	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
53	HG53173 2	318-448	1-329	GAAGGCCCTC	5e ⁻⁵³	97%	1e ⁻¹⁵⁶	98%	20	NW_003764126.1 (Retinoblastoma- like protein 1)	CR1 (Non LTR)
53	HG53173 3	121-425	1-123	AAC	4e ⁻⁶⁷	83%	3e ⁻⁰⁶	71%	Z	NW_003764319.1 (Not determined)	---
55	HG53173 4	1-339	318-429	ATACACCAACCC AATCGAACC	2e ⁻⁹⁷	86%	1e ⁻³⁴	94%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
55	HG53173 5	1-285	265-374	TACACCAACCCCA ATCGAACC	5e ⁻¹⁴¹	99%	3e ⁻³⁶	92%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
60	HG53173 6	1-187	180-224	TGAGATGC	6e ⁻⁷⁴	95%	8e ⁻⁰⁹	91%	1	NW_003763650.1 (Not determined)	---
60	HG53173 7	1-279	262-480	CCAACCCCAATCG AACCA	2e ⁻¹⁰⁸	91%	7e ⁻⁹⁰	93%	2	NW_003763686.1 (Not determined)	CR1 (Non LTR)
60	HG53173 8	1-543	525-728	CACCAACCCCAATC GAACC	2e ⁻⁷⁵	96%	1e ⁻⁸³	94%	Not determined	NW_003779328.1 (Not determined)	---
67	HG53173 9	1-304	275-387	TACACCAACCCCA ATCGAACCTAAC ACC	1e ⁻¹¹⁷	93%	2e ⁻³²	89%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---
67	HG53174 0	1-167	146-258	ATACACCAACCC AATCGAACC	1e ⁻⁴⁴	90%	6e ⁻³⁷	92%	1	NW_003763650.1 (<i>NADP</i> -dependent malic enzyme, mitochondrial)	---

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
67	HG53174 1	1-716	697-832	ATAATGTACGGGG GAGATGC	0.0	85%	4e ⁻⁵²	96%	1	NW_003763650.1 (Platelet-derived growth factor D)	---
70	HG53174 2	1-280	272-406	TGAGATGCA	9e ⁻⁷⁷	82%	2e ⁻⁴⁴	97%	1	NW_003763584.1 (Not determined)	---
70	HG53174 3	1-333	325-431	TGAGATGCA	3e ⁻⁷⁶	93%	1e ⁻⁴⁵	98%	1	NW_003763584.1 (Not determined)	---
70	HG53174 4	1-217	220-744		4e ⁻⁷⁰	90%	0.0	98%	5	NW_003763785.1 (Not determined)	---
70	HG53174 5	1-588	573-655	GTACGGGTGAGAT GC	6e ⁻¹²⁴	75%	2e ⁻²³	90%	1	NW_003763482.1 (Not determined)	---
70	HG53174 6	156-522	1-162	GAAGGCC	3e ⁻⁸³	80%	3e ⁻²⁰	92%	1	NW_003763484.1 (Not determined)	---
72	HG53174 7	1-150	142-248	TGAGATGC	8e ⁻⁵⁴	94%	4e ⁻⁴⁵	98%	1	NW_003763584.1 (Not determined)	---
72	HG53174 8	1-90	72-618	CCAACCCCAATCG AACCAA	2e ⁻²⁹	92%	0.0	93%	5	NW_003763785.1 (Not determined)	---
72	HG53174 9	98-155	1-106	TGCATCTCA	2e ⁻¹⁵	96%	4e ⁻⁴²	95%	1	NW_003763584.1 (Not determined)	---
72	HG53175 0	1-105	88-283	CCAACCCCAATCG AACCC	1e ⁻³⁹	96%	1e ⁻⁹¹	98%	9	NW_003763840.1 (Not determined)	CR1 (Non LTR)
72	HG53175 1	1-219 / 437-550	202-436 / 537-593	ACTCACTTCTCACT TCCTCCCTCCC / TCTCACTTCTCCC	3e ⁻⁷⁸ / 2e ⁻⁴⁷	96% / 90%	1e ⁻¹² / 6e ⁻⁰⁹	70% / 93%	12 / 15	NW_003763903.1 (Uncharacterized protein LOC416093)/	--- / ---

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
										NW_001471461.2 (cytospin-A)	
72	HG53175 2	1-80 / 164-379 / 495-564	81-170 / 380-501	CCCTCCC / CCCTCCC	$8e^{-27}$ / $1e^{-80}$	97% / 92%	0.26 / $1e^{-05}$	70% / 71%	Z / Z	NW_003764324.1 (Not determined) / NW_003764324.1 (Not determined)	--- / ---
73	HG53175 3	1-285	263-340	CCTACACCAACCCC AATCGAACC	$3e^{-137}$	99%	$7e^{-25}$	94%	20	NW_003764128.1 (Not determined)	---
73	HG53175 4	1-150	135-212	CAACCCCAATCGA ACC	$5e^{-43}$	88%	$5e^{-24}$	92%	20	NW_003764128.1 (Not determined)	---
73	HG53175 5	304-610	1-317	GAACGCCCTCCCA	$4e^{-06}$	67%	$5e^{-157}$	99%	20	NW_003764127.1 (Not determined)	---
73	HG53175 6	252-381	1-265	GAAGCCCCCTCCCA	$6e^{-47}$	97%	$2e^{-127}$	98%	12	NW_003763892.1 (Not determined)	---
73	HG53175 7	1-290	285-456	ATAATG	$3e^{-46}$	96%	$5e^{-142}$	99%	1	NW_003763650.1 (Not determined)	---
73	HG53175 8	1-160	142-373	GACCCCCCTCCCA AAACC	$9e^{-26}$	100%	$1e^{-67}$	96%	1	NW_001471534.2 ([Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial)	CR1 (Non LTR)
73	HG53175 9	142-324	1-152	GACGCCCTC	$7e^{-44}$	87%	$9e^{-49}$	87%	1	NW_001471534.2 ([Pyruvate dehydrogenase [lipoamide]] kinase)	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	<i>Locus</i>	<i>G. gallus</i> repeats
										isozyme 3, mitochondrial)	