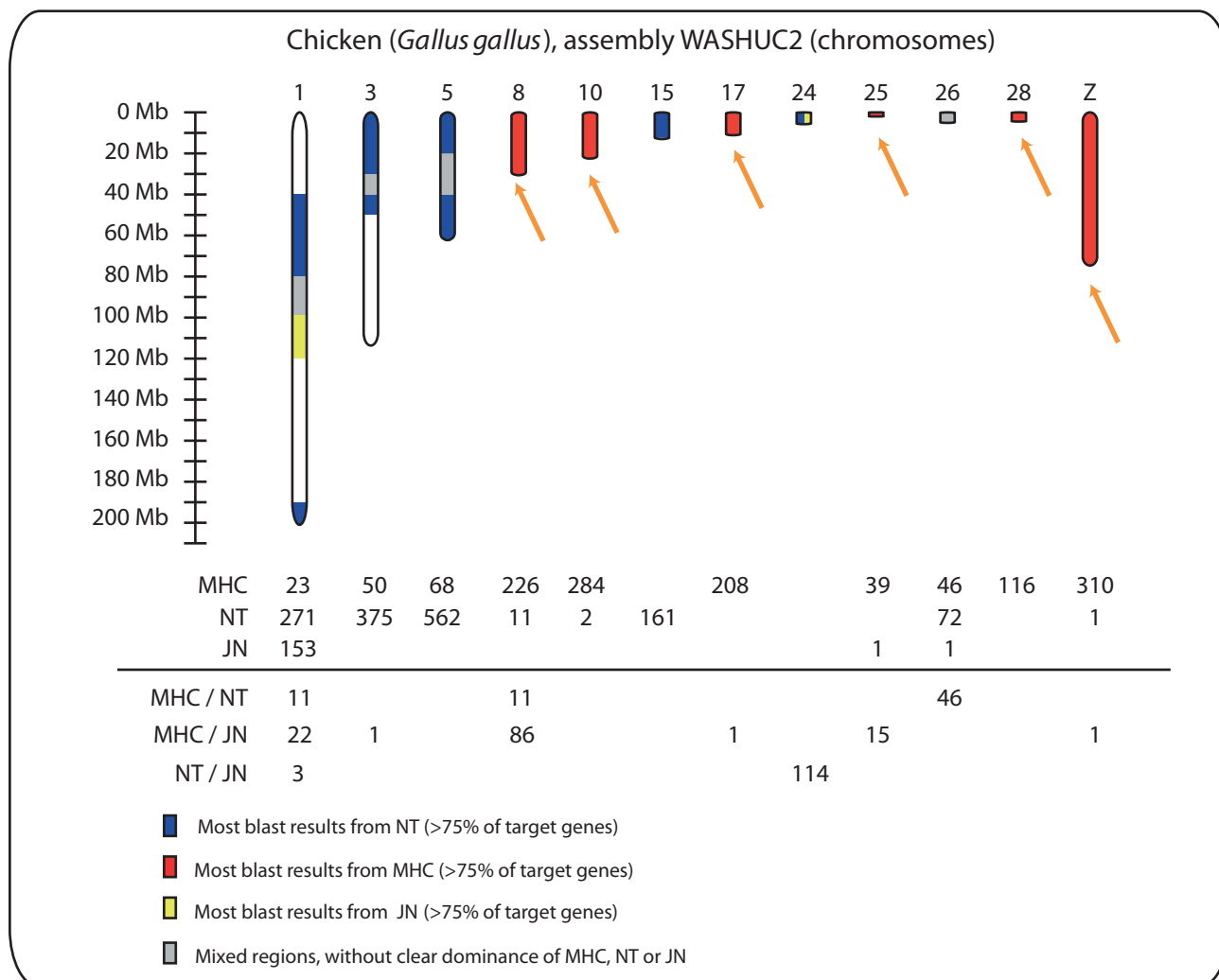


Supplemental Figure 1



Supplemental Figure 1. *Gallus gallus* RBBH distribution on genomic scaffolds identifies putative counterparts of MHC and MHC-related human paralogs. Scaffolds containing RBBH genes are divided in 10 Mb blocks. Blocks where >15 % of the genes were RBBH are colored. Orange arrows indicate Chromosomes where known MHC-related markers have been mapped previously.

Supplemental Table I. MHC markers are significantly clustered in the *T. adhaerens* proto-MHC.

Total Nb of genes in the relevant scaffolds of the *T. adhaerens* genome (reference): 6721

Total Nb of genes in the proto-MHC regions in the *T. adhaerens* genome (as defined in Figure 2 and in Table I): 1198

Excluding genes that may belong either to MHC, neurotrophin or JAM-NECTIN set of paralogs in human:

Number of *T. adhaerens* counterparts of MHC paralogon markers, located within the “proto-MHC” = 282

Total number of *T. adhaerens* counterparts of MHC paralogon markers, located within the relevant scaffolds = 528

Number of *T. adhaerens* counterparts (single or multiple) of MHC paralogon markers, located within the relevant scaffolds:

- 491 single counterparts
- 14 pairs of co-orthologs (14 multigene families of size 2)
- 3 triples of co-orthologs (3 multigene families of size 3).

Number of *T. adhaerens* counterparts (single or multiple) of MHC paralogon markers, located within the “proto-MHC”:

- 261 single counterparts among the 491.
- Among the 14 multigene families of size 2:
6 families have only one of the two genes in this region;
5 families have both genes present in this region.
- Among the 3 multigene families of size 3:
1 family has one gene and 2 families have two genes present in this region.

As explained in the Experimental procedures, the weight of the “proto-MHC” region is computed as:

$$261 + 6 \times 1/2 + 5 \times 2 \times 1/2 + 1/3 + 2 \times 2/3 = 270 + 2/3.$$

Including genes that may belong either to MHC, neurotrophin or JAM-NECTIN set of paralogs in human (ie “with ambiguous markers”):

Number of *T. adhaerens* counterparts of MHC paralogon markers, located within the “proto-MHC” = 307

Total number of *T. adhaerens* counterparts of MHC paralogon markers, located within the relevant scaffolds = 579

Number of *T. adhaerens* counterparts (single or multiple) of MHC paralogon markers, located within the relevant scaffolds:

- 537 single counterparts
- 15 pairs of co-orthologs (15 multigene families of size 2)
- 4 triples of co-orthologs (4 multigene families of size 3).

Number of *T. adhaerens* counterparts (single or multiple) of MHC paralogon markers, located within the “proto-MHC”:

- 284 single counterparts among the 537.
- Among the 15 multigene families of size 2:
6 families have only one of the two genes in this region;
5 families have both genes present in this region.
- Among the 4 multigene families of size 3:
1 family has one gene and 3 families have two genes present in this region.

As explained in the Experimental procedures, the weight of the “proto-MHC” region is computed as:

$$284 + 6 \times 1/2 + 5 \times 2 \times 1/2 + 1/3 + 3 \times 2/3 = 294 + 1/3.$$

In both cases, the statistical test described in (52) gives a p-value which is extremely low (less than 10^{-50}), hence the clustering of MHC markers in *T. adhaerens* proto-MHC region is extremely significant.

Supplemental Table II. Microsytney region between human chromosome 9 and *T. adhaerens* scaffold 2

human gene name	human gene ID	human gene location	human gene start (bp)	human gene end (bp)	T.adhaerens gene ID	T.adhaerens scaffold	T.adhaerens gene start (bp)	T.adhaerens gene end (bp)	human => T.adhaerens blast e value	T.adhaerens => human blast e value	human coding gene rank on chromosome	T. adhaerens coding gene rank on scaffold
FKBP15	ENSG00000119321	9q32	115,923,286	115,983,641	TriadG53397	scaffold_2	4,350,281	4,357,979	1.27E-42	2.33E-73	499	530
SLC31A1	ENSG00000136868	9q32	115,983,842	116,029,217	TriadG53435	scaffold_2	4,632,127	4,632,826	7.78E-26	9.50E-17	500	568
PRPF4	ENSG00000136875	9q32	116,037,623	116,055,466	TriadG21736	scaffold_2	2,216,277	2,219,409	2.19E-130	1.25E-127	502	242
ATP6V1G1	ENSG00000136888	9q32	117,350,026	117,360,653	TriadG63629	scaffold_2	2,379,312	2,381,212	4.97E-18	1.55E-12	519	271
PAPPA	ENSG00000182752	9q33.1	118,916,083	119,164,601	TriadG53495	scaffold_2	5,131,410	5,136,712	0.00E+00	0.00E+00	525	623
PSMD5	ENSG00000095261	9q33.2	123,577,774	123,605,229	TriadG53315	scaffold_2	3,769,913	3,772,292	9.21E-64	1.26E-131	535	452
TTLL11	ENSG00000175764	9q33.2	124,584,207	124,855,885	TriadG53460	scaffold_2	4,838,778	4,842,428	5.19E-91	2.89E-79	545	590
MORN5	ENSG00000185681	9q33.2	124,922,190	124,962,367	TriadG53356	scaffold_2	4,055,945	4,057,042	4.85E-56	2.59E-65	547	492
RC3H2	ENSG00000056586	9q33.2	125,606,835	125,667,562	TriadG53314	scaffold_2	3,762,831	3,767,132	2.32E-61	4.00E-49	569	451
RABGAP1	ENSG00000011454	9q33.2	125,703,112	125,867,145	TriadG21193	scaffold_2	2,779,273	2,783,927	2.03E-153	2.15E-169	572	330
PSMB7	ENSG00000136930	9q33.3	127,115,745	127,177,723	TriadG21588	scaffold_2	3,540,945	3,542,771	3.90E-88	8.74E-86	579	434
RPL35	ENSG00000136942	9q33.3	127,620,159	127,624,260	TriadG35487	scaffold_2	4,164,693	4,166,285	6.69E-27	2.13E-22	585	507
HSPA5	ENSG00000044574	9q33.3	127,997,132	128,003,609	TriadG63625	scaffold_2	2,306,968	2,309,757	0.00E+00	0.00E+00	591	258
GAPVD1	ENSG00000165219	9q33.3	128,024,073	128,129,486	TriadG20735	scaffold_2	2,737,466	2,739,193	1.63E-103	3.54E-94	592	323
PBX3	ENSG00000167081	9q33.3	128,509,624	128,729,656	TriadG21171	scaffold_2	4,562,738	4,564,320	5.50E-119	6.04E-111	594	558
FAM125B	ENSG00000196814	9q33.3	129,089,128	129,269,320	TriadG53300	scaffold_2	3,582,753	3,588,285	6.09E-19	1.47E-50	595	440
GARNL3	ENSG00000136895	9q33.3	129,986,544	130,155,939	TriadG53303	scaffold_2	3,626,882	3,635,282	8.67E-152	7.32E-168	601	443
LRSAM1	ENSG00000148356	9q33.3	130,213,765	130,265,780	TriadG53391	scaffold_2	4,306,726	4,314,157	6.66E-49	6.86E-36	605	525
CDK9	ENSG00000136807	9q34.11	130,547,958	130,553,066	TriadG20854	scaffold_2	3,031,618	3,035,153	2.73E-133	6.28E-122	613	364
PFGS	ENSG00000136877	9q34.11	130,556,876	130,576,606	TriadG53217	scaffold_2	3,009,000	3,013,836	2.74E-126	3.35E-148	614	362
DPM2	ENSG00000136908	9q34.11	130,697,378	130,700,763	TriadG21546	scaffold_2	3,440,253	3,441,035	3.76E-21	4.53E-10	620	421
PTGSE2	ENSG00000148334	9q34.11	130,882,972	130,890,741	TriadG63654	scaffold_2	4,517,811	4,519,901	5.08E-71	4.33E-55	624	552
DNM1	ENSG00000106976	9q34.11	130,965,658	131,017,527	TriadG53484	scaffold_2	5,050,177	5,055,303	0.00E+00	0.00E+00	629	612
SWI5	ENSG00000175854	9q34.11	131,037,658	131,051,269	TriadG53400	scaffold_2	4,382,364	4,383,821	7.94E-14	2.53E-13	631	533
COQ4	ENSG00000167113	9q34.11	131,084,815	131,096,351	TriadG20604	scaffold_2	2,721,513	2,723,324	1.17E-107	1.06E-107	634	320
SLC27A4	ENSG00000167114	9q34.11	131,102,925	131,123,502	TriadG21641	scaffold_2	3,556,998	3,560,672	0.00E+00	0.00E+00	635	437
URM1	ENSG00000167118	9q34.11	131,133,598	131,153,015	TriadG53360	scaffold_2	4,066,365	4,068,560	5.87E-22	1.42E-35	637	496
CERCAM	ENSG00000167123	9q34.11	131,174,030	131,199,626	TriadG21834	scaffold_2	3,471,863	3,480,314	4.95E-138	1.65E-98	638	425
ZER1	ENSG00000160445	9q34.11	131,492,065	131,534,693	TriadG53463	scaffold_2	4,889,365	4,894,133	5.08E-59	1.26E-60	646	592
TBC1D13	ENSG00000107021	9q34.11	131,549,483	131,572,711	TriadG53506	scaffold_2	5,214,731	5,218,574	9.35E-85	6.13E-81	647	633
C9orf114	ENSG00000198917	9q34.11	131,581,930	131,592,100	TriadG53475	scaffold_2	4,976,837	4,980,209	1.73E-110	3.08E-121	649	603
CCBL1	ENSG00000171097	9q34.11	131,595,221	131,644,773	TriadG20976	scaffold_2	2,626,568	2,629,964	6.36E-130	8.26E-133	650	302
DOLPP1	ENSG00000167130	9q34.11	131,843,379	131,852,717	TriadG53442	scaffold_2	4,679,479	4,682,665	1.69E-27	3.26E-33	658	575
CRAT	ENSG00000095321	9q34.11	131,857,089	131,873,468	TriadG20587	scaffold_2	4,684,648	4,688,140	0.00E+00	0.00E+00	659	576
PPP2R4	ENSG00000119383	9q34.11	131,873,229	131,911,225	TriadG53478	scaffold_2	4,988,266	4,991,549	8.82E-147	2.81E-174	660	606
NC51	ENSG00000107130	9q34.11	132,934,857	132,999,583	TriadG35468	scaffold_2	2,537,306	2,541,466	8.22E-65	5.63E-56	674	292
ASS1	ENSG00000130707	9q34.11	133,320,094	133,376,661	TriadG21771	scaffold_2	2,361,821	2,367,439	0.00E+00	0.00E+00	677	267
PRDM12	ENSG00000130711	9q34.12	133,539,981	133,558,368	TriadG14897	scaffold_2	4,668,543	4,670,264	7.24E-51	7.06E-52	679	574
EXOSC2	ENSG00000130713	9q34.12	133,569,108	133,580,248	TriadG21452	scaffold_2	4,003,090	4,004,790	4.82E-77	5.54E-64	680	482
FAM78A	ENSG00000126882	9q34.13	134,133,463	134,151,934	TriadG16229	scaffold_3	1,757,243	1,757,887	5.82E-32	1.49E-26	687	212
C9orf171	ENSG00000188523	9q34.13	135,285,430	135,448,704	TriadG53154	scaffold_2	2,610,981	2,614,153	5.67E-48	8.67E-47	697	299
AK8	ENSG00000165695	9q34.13	135,600,965	135,754,164	TriadG53152	scaffold_2	2,581,928	2,585,581	3.82E-110	5.16E-108	701	297
TSC1	ENSG00000165699	9q34.13	135,766,735	135,820,020	TriadG53459	scaffold_2	4,832,576	4,838,314	5.42E-87	1.95E-49	703	589
GTF3C5	ENSG00000148308	9q34.2	135,906,076	135,933,888	TriadG53254	scaffold_2	3,291,947	3,294,989	3.53E-36	2.25E-51	705	397
MED22	ENSG00000148297	9q34.2	136,205,160	136,214,986	TriadG53358	scaffold_2	4,061,590	4,062,574	1.10E-21	1.38E-24	711	494
RPL7A	ENSG00000148303	9q34.2	136,215,069	136,218,281	TriadG37190	scaffold_2	4,058,253	4,060,388	9.99E-95	6.96E-90	712	493
SURF1	ENSG00000148290	9q34.2	136,218,610	136,223,552	TriadG63643	scaffold_2	4,063,403	4,064,984	1.53E-69	1.16E-68	713	495
SURF4	ENSG00000148248	9q34.2	136,228,325	136,242,970	TriadG20615	scaffold_2	5,183,765	5,187,932	7.91E-75	5.49E-66	715	629
CACFD1	ENSG00000160325	9q34.2	136,325,089	136,335,970	TriadG53141	scaffold_2	2,507,360	2,512,350	2.34E-31	1.90E-29	719	287
SARDH	ENSG00000123453	9q34.2	136,528,682	136,605,077	TriadG53512	scaffold_2	5,263,071	5,268,515	0.00E+00	0.00E+00	725	639
VAV2	ENSG00000160293	9q34.2	136,627,016	136,857,726	TriadG53249	scaffold_2	3,258,746	3,268,600	1.11E-71	1.19E-92	727	392
RXRA	ENSG00000186350	9q34.2	137,208,944	137,332,431	TriadG49897	scaffold_2	5,288,894	5,297,903	2.72E-126	1.10E-147	730	642
MRPS2	ENSG00000122140	9q34.3	138,391,830	138,396,519	TriadG21033	scaffold_2	2,890,195	2,891,237	3.69E-86	7.00E-73	739	343
INPP5E	ENSG00000148384	9q34.3	139,323,071	139,334,274	TriadG53207	scaffold_2	2,945,323	2,950,140	2.30E-62	5.98E-55	762	352
SEC16A	ENSG00000148396	9q34.3	139,334,549	139,372,141	TriadG53450	scaffold_2	4,775,821	4,783,131	7.44E-93	1.61E-115	763	582
EDF1	ENSG00000107223	9q34.3	139,756,571	139,760,738	TriadG63634	scaffold_2	2,710,456	2,713,799	2.16E-33	3.26E-19	780	317
NPDC1	ENSG00000107281	9q34.3	139,933,922	139,940,655	TriadG53106	scaffold_2	2,281,540	2,285,193	1.77E-18	9.46E-12	793	254
MAN1B1	ENSG00000177239	9q34.3	139,981,379	140,003,635	TriadG53127	scaffold_2	2,409,470	2,413,023	1.22E-179	0.00E+00	798	274
COBRA1	ENSG00000188986	9q34.3	140,149,625	140,167,998	TriadG13686	scaffold_2	2,633,511	2,635,449	4.89E-93	8.84E-86	815	304
NELF	ENSG00000165802	9q34.3	140,342,022	140,353,786	TriadG53430	scaffold_2	4,591,874	4,596,283	9.21E-34	5.33E-31	821	563
PNPLA7	ENSG00000130653	9q34.3	140,354,404	140,444,986	TriadG10294	scaffold_2	4,030,616	4,039,638	0.00E+00	0.00E+00	822	488