

Supplementary Table 1. Summary of FISH probes and mapping.

Clone name	Library	Orthologous position in the zebra finch genome*	GenBank accession or TI #	ZAL2	ZAL2M
297B14	TGMCBa	chr3:164,019-304,807	1874389138, 1877213243	centromere	centromere
140L08	TGMCBa	chr3:4,723,480-4,854,756	1874672486, 1874679763	p-arm	p-arm
77A01**	TG_Ba	chr3:8,937,745-	908596257	q-arm	q-arm
56A01**	TG_Ba	chr3:10,302,904-10,437,399	908596251, 908596265	q-arm	q-arm
173L23	TGMCBa	chr3:15,123,246-15,319,325	1876907291, 1876898114	q-arm	q-arm
94A01**	TG_Ba	chr3:20,584,215-20,727,192	908596146, 908596196	p-arm	p-arm
182O02	TGMCBa	chr3:23,927,627-24,060,240	1856371955, 1856378681	p-arm	p-arm
193N07	TGMCBa	chr3:24,060,284-24,191,449	1856375547, 1856377123	p-arm	p-arm
262K17	CHORI-264	chr3:24,125,887-24,291,118	FI596421, FI596420	p-arm	p-arm
123F24	CHORI-264	chr3:24,392,369-24,552,730	FI596292, FI596293	p-arm	p-arm
297H09	TGMCBa	chr3:26,679,287-26,793,490	1874382409, 1877202929	p-arm	p-arm
347B14	TGMCBa	chr3:27,396,201-27,551,570	1864211762, 1870125031	p-arm	p-arm
211J19	TGMCBa	chr3:27,699,459-27,845,517	1922679860, 1861446857	p-arm	p-arm
217G15	TGMCBa	chr3:27,899,827-28,044,970	1922682902, 1861445578	p-arm	p-arm
156C22**	TGMCBa	chr3:29,410,654-29,554,925	1290207524, 1290207824	p-arm	p-arm
250N04	CHORI-264	chr3:33,893,969-34,016,333	FI592812, FI592813	q-arm	q-arm
300O4**	TG_Ba	chr3:39,645,123-39,781,205	AC154073.2	q-arm	q-arm
13A01**	TG_Ba	chr3:47,291,914-47,411,978	908596236, 908596109	q-arm	q-arm
134P12	CHORI-264	chr3:56,089,082-56,238,448	FI593437, FI593436	q-arm	q-arm
21H11**	TGMCBa	chr3:61,388,963-61,558,045	1277186752, 1277186958	q-arm	q-arm
352K13**	TG_Ba	chr3:61,967,954-61,972,436	n.a.	q-arm	q-arm
91E01**	TGMCBa	chr3:65,952,224-66,079,504	1277187221, 1277187497	q-arm	q-arm
369N22	TGMCBa	chr3:67,786,009-67,923,160	1864209691, 1864208155	q-arm	q-arm
340K05	TGMCBa	chr3:69,512,595-69,652,410	1877211565, 1876900573	q-arm	q-arm
168I11	TGMCBa	chr3:69,609,668-69,765,827	1813135609, 1813139718	q-arm	q-arm
353A16	TGMCBa	chr3:69,699,319-69,846,404	1874384547, 1876895097	q-arm	q-arm
18P12	TGMCBa	chr3:69,853,733-69,986,803	1883516069, 1883518119	q-arm	q-arm
063M06***	CHORI-264	chr3:70,179,860-70,180,398, 108,264,948-108,265,660	FI594040, FI594041	q-arm	q-arm
060N14***	CHORI-264	chr3:70,281,419-70,282,341, 108,370,693-108,370,952	FI596204, FI596205	p-arm	p-arm
143F23	TGMCBa	chr3:70,6512,55-70,759,502	1916838414, 1813137015	p-arm	p-arm
120H07**	TGMCBa	chr3:70,773,591-70,924,763	1290206795, 1290207123	p-arm	p-arm
321F19	CHORI-264	chr3:71,294,142-71,443,061	FI593519, FI593520	p- and q-arm	p-arm
516O05	CHORI-264	chr3:71,321,392-71,468,248	FI593982, FI593983	p- and q-arm	p-arm
309M10	TGMCBa	chr3:71,389,158-71,525,060	1874388649, 1874681325	p- and q-arm	p-arm
393K07	CHORI-264	chr3:71,414,167-71,560,750	FI594164, FI594163	p- and q-arm	p-arm

345H01	CHORI-264	chr3:71,488,503-71,628,527	FI593721,FI593720	q-arm	p-arm
289F19	TGMCBa	chr3:72,972,181-73,116,346	1925270444, 1887701181	q-arm	p-arm
360K17	TGMCBa	chr3:75,547,309-75,663,917	1877202688, 1876896798	q-arm	p-arm
64A01**	TG_Ba	chr3:78,724,313-78,843,809	908596166, 908596247	q-arm	p-arm
71A01**	TG_Ba	chr3:81,966,117-82,080,690	908596264, 908596235	q-arm	p-arm
5K13**	TG_Ba	chr3:90,507,078-90,508,264	n.a.	q-arm	p-arm
57J12	TGMCBa	chr3:91,350,896-91,473,582	1874387425, 1876893840	q-arm	p-arm
83G17	TGMCBa	chr3:93,898,132-94,055,102	1887564249, 1887673423	q-arm	p-arm
71J02	TGMCBa	chr3:96,908,245-97,078,000	1889559939, 1887582378	q-arm	p-arm
328M16	TGMCBa	chr3:97,878,058-98,000,878	1864212479, 1864208517	q-arm	p-arm
63J19	TGMCBa	chr3:98,303,987-98,426,416	1864198974, 1864198412	q-arm	p-arm
303D07	TGMCBa	chr3:98,788,065-98,942,209	1874669373, 1874671030	q-arm	p-arm
159F19	CHORI-264	chr3:98,919,011-99,081,613	FI594700, FI594699	q-arm	p-arm
400C13	CHORI-264	chr3:99,187,133-99,340,937	FI596254, FI596255	q-arm	q-arm
106J15	TGMCBa	chr3:99,737,315-99,909,020	1712399927, 1712404705	q-arm	q-arm
55A01**	TG_Ba	chr3:101,686,984-101,826,796	908596203, 908596220	q-arm	q-arm
29M23	TGMCBa	chr3:104,000,510-104,158,215	1864198543, 1864199106	q-arm	q-arm
277O03	TGMCBa	chr3:105,977,598-106,123,295	1925267977, 1877711038	q-arm	q-arm
159B09	TGMCBa	chr3:106,949,395-107,079,764	1923803285, 1815752090	q-arm	q-arm
258I11**	TG_Ba	chr3:108,824,262-108,969,467	AC159936.2	p-arm	p-arm
232I20	TGMCBa	chr3:110,977,131-111,143,005	1889559183, 1883525914	p-arm	p-arm
193L22	TGMCBa	chr3:112,089,276-112,427,106	1815752926, 1813134367	p-arm	p-arm
24I15	TGMCBa	chr3_random:115,851-272,249	1856888724, 1856372879	p-arm	p-arm

*The orthologous positions of the zebra finch BAC clones in the chicken genome were based on alignments of zebra finch complete BAC, or BAC-end sequences to the chicken genome assembly (taeGut1). In the case of clones 352K13 and 5K13, the orthologous position was estimated based on the location of the hybridization probes used to identify those BACs.

**Previously published mapped BAC clones (Thomas et al, 2008).

***Previously published mapped BAC clones (Davis et al, 2010)

n.a. = not available.