

Table 5. Short nonautonomous copies of *Galileo* characterized in the genomes of six *Drosophila* species

Species	Contig	Beginning	Total length	TIRa/TIRb length	TSD	Observations
<i>D. ananassae</i>	16072	49428	1145	317/317	ATAGTAG	—
	16215	13660	1226	329/329	GTAATAC	—
	16457	13174	1220	329/329	GTTATAT	—
	16780	48830	1194	331/331	CATCAAC	—
	16799	18339	1194	331/331	GTAGCAG	—
	17082	56734	1228	318/320	GTTTCGT	—
	18115	31181	1233	329/329	ATTATAG	—
	18348	28163	1225	329/329	CTACGAG	—
	18752	112063	1236	329/329	GTATAAT	—
	18811	266133	1244	329/328	GATGAAC	—
	18844	8374	1254	329/340	CTTTTAT	—
	18855	7980	1245	329/329	GTATTAT	—
	19356	469604	1219	329/329	ACTGTAC	—
	19465	81512	1158	329/317	GTATAGT	—
	19598	190010	1236	329/329	CTTGTAC	—
	19813	40154	1236	329/329	GTTCAAC	—
	19892	26883	1236	329/329	GTATAAC	—
	20116	42794	1227	331/330	ACCAAAC	—
20508	21472	1194	331/330	CTGCAAC	—	

Species	Contig	Beginning	Total length	TIRa/TIRb length	TSD	Observations
<i>D. pseudoobscura</i>	20509	13568	1208	329/304	GTGCAAG	—
	1082	770	2899	462/464	GTTCAAC	—
	3611	65029	4538	545/541	GTAATAT/GTTCTAT	—
	3949	17417	1095	515/417	ATAAATG	—
	4181	261898	2106	664/630	GTTCTAT	Worf insertion (263302-264678)
	4197	39495	2439	629/630	GTAGTAC	—
	4227	206109	1982	552/552	CTTCTGC	—
	4314	60436	4458	543/545	GTTCTAT	—
	4350	119298	1975	514/514	ATTCGAC	—
	4355	300467	4085	528/493	CTTTCAC/GTGAGAC	—
	4360	196165	2036	630/629	ATAAGAC	—
	4568	59125	2036	630/629	GCTAAAG	—
	4925	27994	2024	623/623	GTATACT	—
	5286	303008	2059	778/778	GTTTAAC	Insertion in TIRb (304447-304982)
	5301	784883	2059	630/658	CTACTAT	—
	5346	39465	1954	561/624	GTAATAT	—
	5574	101925	3481	662/630	ATAGCAT	—
5598	108632	2032	630/629	GTAATAT	—	
5611	88815	1610	536/535	GTTGAGG	—	
<i>D. persimilis</i>	43	22757	1892	555/565	GTTGAAT	—

Species	Contig	Beginning	Total length	TIRa/TIRb length	TSD	Observations
	497	41905	1893	558/549	ATTATAC	—
	661	13659	2012	737/733	GTTGTAC	—
	1311	29484	2087	550/555	ATAGCAC	—
	1330	56295	1957	515/515	ATTGTAC	—
	1462	9134	1908	559/559	ATAAAAC	—
	1531	30035	1949	725/719	TTGATGG	—
	2315	58360	1901	558/557	ATATGAC	—
	2841	31815	2005	555/553	GTACAAC	—
	3304	10212	1961	613/562	GCAAGTC	—
	4090	14313	1758	541/541	ACCAACC	—
	4609	1009	1902	559/569	GTAATAC	—
	5516	10726	2097	557/557	GTTTTCG	—
	6330	22364	1865	573/556	GTAGTAG	—
	9153	14702	1935	566/566	CCGCAAA	—
	9474	6659	1992	543/552	CTTTCAT	—
	10757	7184	2022	737/743	GTATATA	—
	11506	169	1946	727/725	GTTGTGC	—
<i>D. willistoni</i>	191	7706	1133	483/475	ATATTAG	—
	4171	163	1140	475/475	GTATAAC	—
	6280	219672	1126	517/517	TGCAAAG	—

Species	Contig	Beginning	Total length	TIRa/TIRb length	TSD	Observations
	6423.1	286322	1452	624/620	GTATTAG	—
	6423.2	472923	1120	476/476	ATTATAT	—
	6463.1	759004	1141	475/483	GTATTAG	—
	6463.2	269200	1142	485/487	ATCGTTT/ATCGTAT	38-bp repeat at end of TIRb
	6463.3	165185	1132	492/484	ATATTAG	—
	6661	512446	1269	522/528	CTAAAAC	—
	6834	123142	1105	517/521	ATTCTGC	—
	6840	36681	1130	519/519	CTTGAAG	—
	6847	108816	1114	518/517	GTATTGA	—
	6851	324389	1124	517/517	CCTTAC	—
	7963	399697	1196	557/557	CTACTGC	—
	8445	45999	1140	518/518	ATAGAAC	—
	8628	277645	1133	475/483	ATATTAC	—
	9000	395296	1133	483/475	GTCAAAG	—
	9436	199308	1109	482/490	CTTCTAC	—
	9906	5225	1422	482/483	GTATTAG	—
	10422	27432	1402	476/475	ATAACAG/CTCTAAC	—
	13546	3646	1991	852/990	GTAATAC	Insertion within TIRa (3665-4506)
	13964	226944	1602	709/696	ACTGAAC/GCGATAG	—
	14705	256157	1339	584/400	ATATTAT	—

Species	Contig	Beginning	Total length	TIRa/TIRb length	TSD	Observations
<i>D. mojavensis</i>	15758	236804	2232	785/785	CTTAAAC	—
	16069	102584	1480	608/614	ACTTAAC	—
	16071	203037	2343	1051/1003	GTAACAG	—
	16072	413871	1774	795/839	GTATAAT/-	5 terminal bp and TSD missing from TIRb
	16403	21843	1635	725/730	ATCGAGC/ATGCTGC	—
	17557	39646	1882	824/832	-/ATTACCA	12 terminal bp and TSD missing from TIRa
	17577	4833	1247	305/307	GTAATAG	—
	17588	42042	1616	699/687	CAAGCAA	GTG is repeated between end of TIR and TSD
	17658	62428	1947	710/723	GTGATAC/CCATAAG	—
	18052	6453	1597	698/722	GTATTAC	—
	8189	12012	2382	894/894	GTGCAGC	124-bp internal direct repeats
	8783	2229	2162	1039/990	CTATAAC	Insertion in TIRa (2503-4931)
	9647	4614	1903	578/578	ATTGAA	—
	9832	28557	1600	577/565	GTGATAT/AATACAC	—
	10246	221912	2826	1116/1116	GTATTTT	Two 220-bp repeats in each TIR; 127-bp internal direct repeats
	10309	10744	2426	1147/1153	GTACCGC	Two 220-bp repeats in each TIR
	10727.1	44829	2206	1028/1030	TCATTAC	—
10727.2	104767	3214	1260/1214	GTATTAT	—	

Species	Contig	Beginning	Total length	TIRa/TIRb length	TSD	Observations
	10741	55570	3363	1216/987	ATATGTA/CTAATTG	TIRa has three copies of 220-bp repeat. TIRb has only two. Immediately upstream of this copy there is another TIR 813 bp long with two copies of 220-bp repeat flanked by 7-bp sequence CTATAAC.
<i>D. mojavensis</i>	10751	25070	2195	1021/1026	TGTATAC	—
	10758.2	55001	1660	486/508	GTTATGC	119-bp end duplication in TIRb
	10764	29199	2369	715/715	TTTATAT	Insertion in TIRb (35259-35358); ISBu insertion (30625-34928)
	10770.2	92188	3199	1107/1107	ATAGTAG/CTACTAT	—
	10790.1	49101	1967	556/494	ATACTAC	—
	10790.2	84962	2199	1022/1028	TCGAAAC	—
	10940	39859	1547	458/458	ATTGGGG	—
	10945	2811	2179	1033/997	GATACAC	Insertion in TIRb (4741-5878)
	11229	48344	1736	769/766	TTAATGC	—
	11267	12789	2355	627/616	GTATCAA	—
	11679	95650	2174	1012/1014	TTATGAG	ISBu insertion in TIRb (97089-97880)

TIRa is the first TIR that appears in the contig and TIRb is the other one. When both TSD are exactly the same, only one sequence is given. Total length is given in bp.