

Taxonomic lineage: Brachycera > Muscomorpha > Ephydroidea > Drosophilidae > Drosophila > Drosophila subgenus Drosophila > virilis group
Assembly: GCA_035045885.1_ASM3504588v1_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 7nt PSE: 0.94

GGGCGGCTTCTGCATCTTGCACATGACCAACGGGTTGGACATCCCGTTAAGCCCCACATCTGTAAATTTGTCCCTG1866T1867T1868T1869T1870T1871T1872T1873T1874T1875T1876T1877T1878T1879T1880T1881T1882T1883T1884T1885T1886T1887T1888T1889T1890T1891T1892T1893T1894T1895T1896T1897T1898T1899T1900T1901T1902T1903T1904T1905T1906T1907T1908T1909T1910T1911T1912T1913T1914T1915T1916T1917T1918T1919T1920T1921T1922T1923T1924T1925T1926T1927T1928T1929T1930T1931T1932T1933T1934T1935T1936T1937T1938T1939T1940T1941T1942T1943T1944T1945T1946T1947T1948T1949T1950T1951T1952T1953T1954T1955T1956T1957T1958T1959T1960T1961T1962T1963T1964T1965T1966T1967T1968T1969T1970T1971T1972T1973T1974T1975T1976T1977T1978T1979T1980T1981T1982T1983T1984T1985T1986T1987T1988T1989T1990T1991T1992T1993T1994T1995T1996T1997T1998T1999T2000T2001T2002T2003T2004T2005T2006T2007T2008T2009T2010T2011T2012T2013T2014T2015T2016T2017T2018T2019T2020T2021T2022T2023T2024T2025T2026T2027T2028T2029T2030T2031T2032T2033T2034T2035T2036T2037T2038T2039T2040T2041T2042T2043T2044T2045T2046T2047T2048T2049T2050T2051T2052T2053T2054T2055T2056T2057T2058T2059T2060T2061T2062T2063T2064T2065T2066T2067T2068T2069T2070T2071T2072T2073T2074T2075T2076T2077T2078T2079T2080T2081T2082T2083T2084T2085T2086T2087T2088T2089T2090T2091T2092T2093T2094T2095T2096T2097T2098T2099T2100T2101T2102T2103T2104T2105T2106T2107T2108T2109T2110T2111T2112T2113T2114T2115T2116T2117T2118T2119T2120T2121T2122T2123T2124T2125T2126T2127T2128T2129T2130T2131T2132T2133T2134T2135T2136T2137T2138T2139T2140T2141T2142T2143T2144T2145T2146T2147T2148T2149T2150T2151T2152T2153T2154T2155T2156T2157T2158T2159T2160T2161T2162T2163T2164T2165T2166T2167T2168T2169T2170T2171T2172T2173T2174T2175T2176T2177T2178T2179T2180T2181T2182T2183T2184T2185T2186T2187T2188T2189T2190T2191T2192T2193T2194T2195T2196T2197T2198T2199T2200T2201T2202T2203T2204T2205T2206T2207T2208T2209T2210T2211T2212T2213T2214T2215T2216T2217T2218T2219T2220T2221T2222T2223T2224T2225T2226T2227T2228T2229T2230T2231T2232T2233T2234T2235T2236T2237T2238T2239T2240T2241T2242T2243T2244T2245T2246T2247T2248T2249T2250T2251T2252T2253T2254T2255T2256T2257T2258T2259T2260T2261T2262T2263T2264T2265T2266T2267T2268T2269T2270T2271T2272T2273T2274T2275T2276T2277T2278T2279T2280T2281T2282T2283T2284T2285T2286T2287T2288T2289T2290T2291T2292T2293T2294T2295T2296T2297T2298T2299T2300T2301T2302T2303T2304T2305T2306T2307T2308T2309T2310T2311T2312T2313T2314T2315T2316T2317T2318T2319T2320T2321T2322T2323T2324T2325T2326T2327T2328T2329T2330T2331T2332T2333T2334T2335T2336T2337T2338T2339T2340T2341T2342T2343T2344T2345T2346T2347T2348T2349T2350T2351T2352T2353T2354T2355T2356T2357T2358T2359T2360T2361T2362T2363T2364T2365T2366T2367T2368T2369T2370T2371T2372T2373T2374T2375T2376T2377T2378T2379T2380T2381T2382T2383T2384T2385T2386T2387T2388T2389T2390T2391T2392T2393T2394T2395T2396T2397T2398T2399T2400T2401T2402T2403T2404T2405T2406T2407T2408T2409T2410T2411T2412T2413T2414T2415T2416T2417T2418T2419T2420T2421T2422T2423T2424T2425T2426T2427T2428T2429T2430T2431T2432T2433T2434T2435T2436T2437T2438T2439T2440T2441T2442T2443T2444T2445T2446T2447T2448T2449T2450T2451T2452T2453T2454T2455T2456T2457T2458T2459T2460T2461T2462T2463T2464T2465T2466T2467T2468T2469T2470T2471T2472T2473T2474T2475T2476T2477T2478T2479T2480T2481T2482T2483T2484T2485T2486T2487T2488T2489T2490T2491T2492T2493T2494T2495T2496T2497T2498T2499T2500T2501T2502T2503T2504T2505T2506T2507T2508T2509T2510T2511T2512T2513T2514T2515T2516T2517T2518T2519T2520T2521T2522T2523T2524T2525T2526T2527T2528T2529T2530T2531T2532T2533T2534T2535T2536T2537T2538T2539T2540T2541T2542T2543T2544T2545T2546T2547T2548T2549T2550T2551T2552T2553T2554T2555T2556T2557T2558T2559T2560T2561T2562T2563T2564T2565T2566T2567T2568T2569T2570T2571T2572T2573T2574T2575T2576T2577T2578T2579T2580T2581T2582T2583T2584T2585T2586T2587T2588T2589T2590T2591T2592T2593T2594T2595T2596T2597T2598T2599T2600T2601T2602T2603T2604T2605T2606T2607T2608T2609T2610T2611T2612T2613T2614T2615T2616T2617T2618T2619T2620T2621T2622T2623T2624T2625T2626T2627T2628T2629T2630T2631T2632T2633T2634T2635T2636T2637T2638T2639T2640T2641T2642T2643T2644T2645T2646T2647T2648T2649T2650T2651T2652T2653T2654T2655T2656T2657T2658T2659T2660T2661T2662T2663T2664T2665T2666T2667T2668T2669T2670T2671T2672T2673T2674T2675T

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 5nt Trailing-T: 5nt PSE: 0.92

[illegible]

	Dro_bore1	Dro_bore2
Dro_bore1	-	40
Dro_bore2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

Dro_bore1
 Dro_bore2
 Arthropod_7SK
 RNase_MRP
 U6
 U6
 U6atc
 tRNAsec
 snoRNAme18S1896
 U1
 U1
 U1
 U1
 U2
 U2
 U2
 U3
 U3
 U4
 U4
 U4atc
 U5
 U5
 U5
 U11
 U11
 OrC01

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNAME18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.