

Table 1 Distribution test of genes among chromosomes of *Populus* by Poisson calculator

Chromosome	A,T,G,C readings (bp)	No. of Gene	Expect No. of Gene	Distribution test (p value)	Significance $P(m_{ij} < \lambda_{ij})$ or $P(m_{ij} > \lambda_{ij})$	A,T,G,C readings of transcripts (bp)	Genes with EST Proof
LG_I	31073085	3168	3298	0.012	*-	3714996	514
LG_II	23365393	2681	2480	0.000	**+	3169289	476
LG_III	17446680	1849	1852	0.482		2241785	312
LG_IV	15079815	1433	1600	0.000	**-	1624733	236
LG_V	16635682	1701	1766	0.063		1957848	295
LG_VI	17657228	1966	1874	0.017	*+	2402959	326
LG_VII	11904284	1286	1263	0.257		1462110	210
LG_VIII	15448287	1979	1640	0.000	**+	2344995	351
LG_IX	12408518	1627	1317	0.000	**+	1879011	318
LG_X	19213814	2337	2039	0.000	**+	2732426	480
LG_XI	13171956	1275	1398	0.000	**-	1465093	165
LG_XII	13024900	1274	1382	0.002	**-	1464484	164
LG_XIII	11495653	1155	1220	0.032	*-	1358065	153
LG_XIV	13682591	1422	1452	0.219		1635836	248
LG_XV	10190784	1208	1082	0.000	**+	1318402	189
LG_XVI	12122487	1297	1287	0.378		1490746	202
LG_XVII	5444010	454	578	0.000	**-	513598	55
LG_XVIII	12437986	889	1320	0.000	**-	1385337	197
LG_XIX	10250695	933	1088	0.000	**-	1042867	124
Genome wide	282053848	29934	29934			35204580	5015

Note: * Significant at $\alpha=0.05$; ** significant at $\alpha=0.01$; “-” following the “*” indicates less than expected number at corresponding significant level; “+” following the “*” indicates more abundant than expected number at corresponding significant level