

Variety	Reads number	Total length	Min read length	Mean read length	Max read length	% of reads participating in the assembly of the plastom	Coverage
12-22-134	18,388	202,618,009	5,000	11,019.0	50,000	16.7	188.1
14-4-1	15,023	182,354,649	6,000	12,138.4	63,818	17.3	177.6
14-6-3	17,703	226,960,808	6,000	12,820.5	59,141	20.1	223.5
15-22-4	39,37	456,121,872	6,000	11,585.5	78,43	9.0	225.3
15-27-1	19,674	231,981,845	6,000	11,791.3	70,020	10.4	125.5
16-1-2	14,135	162,257,237	6,000	11,479.1	53,403	9.7	96.4
16-4-3	17,064	200,411,004	6,000	11,744.7	72,118	13.7	157.0
16-35-5	10,600	121,452,458	6,000	11,457.8	61,096	10.7	78.4
Alaska*	33,938	495,961,272	6,073	14,613.7	82,890	86.2	2,583.6
Amur	11,889	152,931,501	6,001	12,863.3	54,214	15.7	138
Argo*	51,708	698,952,197	6,000	13,517.3	66,362	86.4	3,648.8
Bagira	13,329	153,107,596	6,000	11,486.8	80,491	13.5	120.5
Bankir	12,544	150,064,855	6,000	11,963.1	55,963	15.6	136.8
Baron	19,191	221,274,095	6,000	11,530.1	62,333	14.4	193.2
Bravo	11,449	125,451,560	6,000	10,957.4	53,922	10.3	76.5
Gornyak	8,659	103,545,890	6,002	11,958.2	56,627	13.3	78.6
Irbitskiy	12,442	154,961,274	6,000	12,454.7	52,290	14.8	136.5
Iskra	21,603	259,703,281	6,000	12,021.6	60,904	15.8	236
Kamenskiy	45,675	455,124,157	5,000	9,964.4	63,213	14.4	354.2
Legenda*	27,166	324,604,429	6000	10,425.2	72,354	94.2	1,972.7
Luks	28,553	343,674,010	5,000	12,036.4	66,639	16	295.5
Mishka	23,000	265,499,292	6,000	11,543.4	52,333	18.4	275.2

Otrada	9,253	99,146,651	5,000	10,715.1	105,317	8.8	50.2
Shah*	42,672	606,574,939	6,889	14,214.8	96,525	92.8	3,544.8
Start	11,015	136,505,068	6,000	12,392.7	69,710	17.1	134.5
Terra	24,448	303,942,278	6,000	12,432.2	64,741	22.0	386.8
Utro ranneye	15,394	172,784,486	6,000	11,224.1	77,501	14.0	144.2
Zdraven	12,659	143,341,590	6,002	11,323.3	60,946	11.4	94.4

Sequencing and filtering results obtained using Oxford Nanopore Technologies whole genome sequencing of 28 potato varieties developed at Ural Research Institute of Agriculture. \* – marked samples sequenced individually, other samples were simultaneously sequenced in multiplex using a single flowcell.