Genomic data provides new insights on the demographic history and the extent of recent material transfers in Norway spruce

Supporting Information

Parameters	Point estimation
N _{OMORIKA}	40
NOBOVATA	17,749
N _{HYBRID}	200
N _{ALPINE}	2,991
N _{CARPATHIAN}	4,022
NFENNOSCANDIAN	3,770
$T_{OMO_OBO_ABIES}$	22,875,400
$T_{OBO-ABIES}$	17,600,050
<i>Т</i> _{ОВО-НУВ}	17,597,625
T _{FAC}	15,274,375
T _{AC}	15,272,700
ТАDM_ово-нув	103,150
TADM_OBO-ABIES	1,600
TBOT_ABIES	12,850
TBOT_OMORIKA	2,775

Table S1: Demographic parameter estimates rescaled by a generation time of 50 years for *P. omorika (омо)*, *P. obovata (ово)*, *P. abies* main domains and *P. abies* – *P. obovata* hybrids (*нув*).

^a Fennoscandian split from Alpine and Carpathian

^b Alpine – Carpathian split



Figure S1: Cross-validation error regarding number of cluster for unsupervised population clustering.



Figure S2: TreeMix graph with 8 migration events. Text colors showed the same genetic clusters in (Figure 2a and b). Russian-Baltic: Russia (RU), Belarus (BY), Estonia (EE), Latvia (LV), Lithuania (LT); Alpine: Germany (DE), Switzerland (CH), Denmark (DK), Sweden (SE); Central Europe: Slovakia (SK), Cze-republic (CZ), Southern Poland (SPL); Northern Poland (NPL); Romania (RO); Central Sweden (CSE); Fennoscandia: Finland (FI), Sweden (SE).



Figure S3: Likelihood ratio G-statistics distribution. The likelihood ratio G-statistics ($CLR = \log_{10}(CL_0/CL_E)$, where CL_0 and CL_E are the observed and estimated maximum composite likelihood, respectively) was computed to evaluate model goodness-of-fit. A non-significant *p*-value of this test indicates that the observed SFS is well explained by the model. The red dotted line is the CLR of our divergence model.



Figure. S4 Variant quality scores reported for final SNP dataset after VQSR using GATK toolkit. Density distributions of six quality scores (QD, MQ, SOR, FS, MQRankSum, and BaseQRankSum) were plotted to compare with generic recommendations (QD<2; MQ<40; FS>60; SOR > 3; MQRankSum < -12.5) for hard-filtering provided by Broad Institute.