Figure S2: The number of reads aligning to the *PsApxI* mRNA sequence and the alignment between *PsApxI* mRNA and its best hit to the pea bud transcriptome, comp92406_c0_seq1

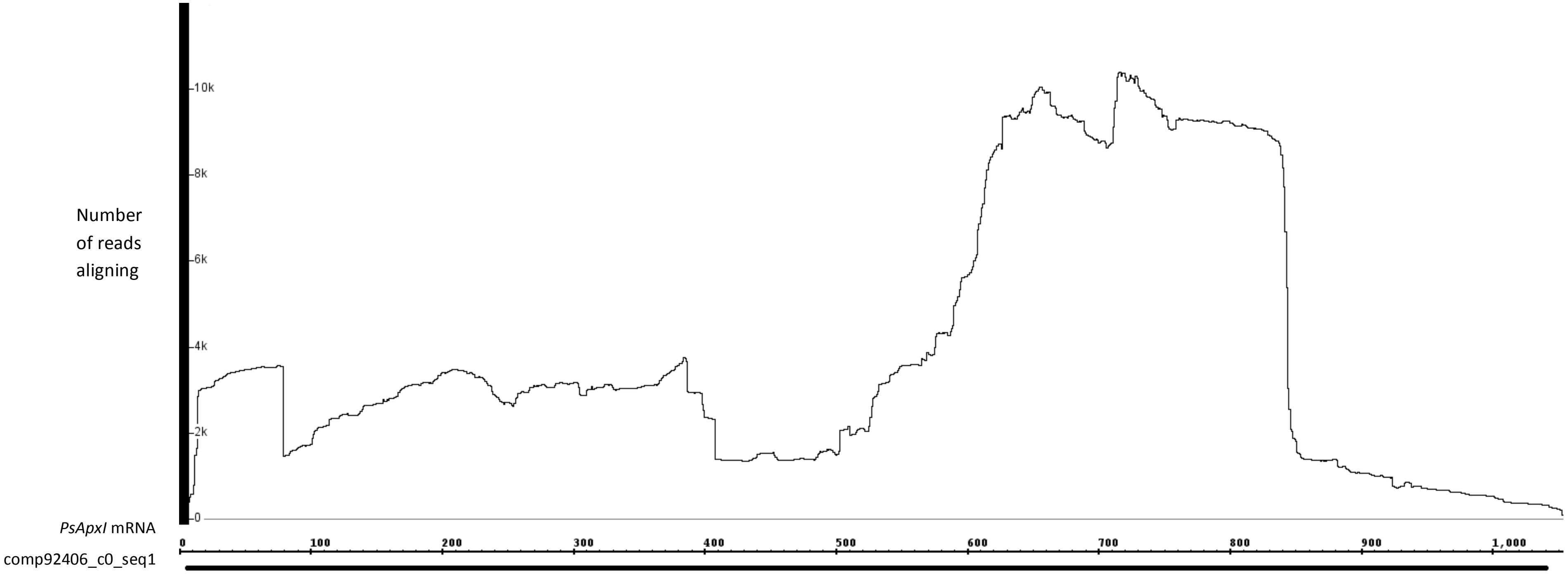

Figure S3: The number of reads aligning to the *PsBRC1* CDS and the alignment between *PsBRC1* CDS and its best hit to the pea bud transcriptome, comp78442_c0_seq1

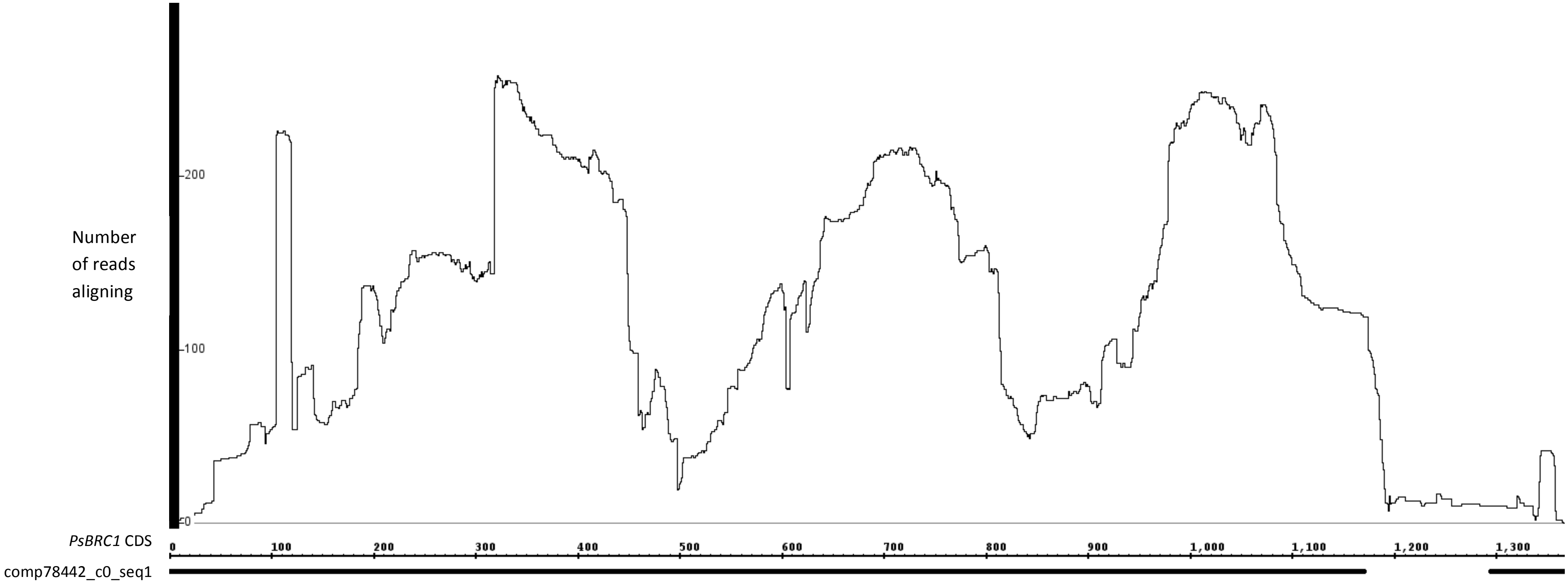

Figure S4: The number of reads aligning to the *PsEXGT1* mRNA and the alignment between *PsEXGT1* mRNA and its best hits to the pea bud transcriptome, comp88216_c0_seq1, 5, 7, 8, 11, 13, 14

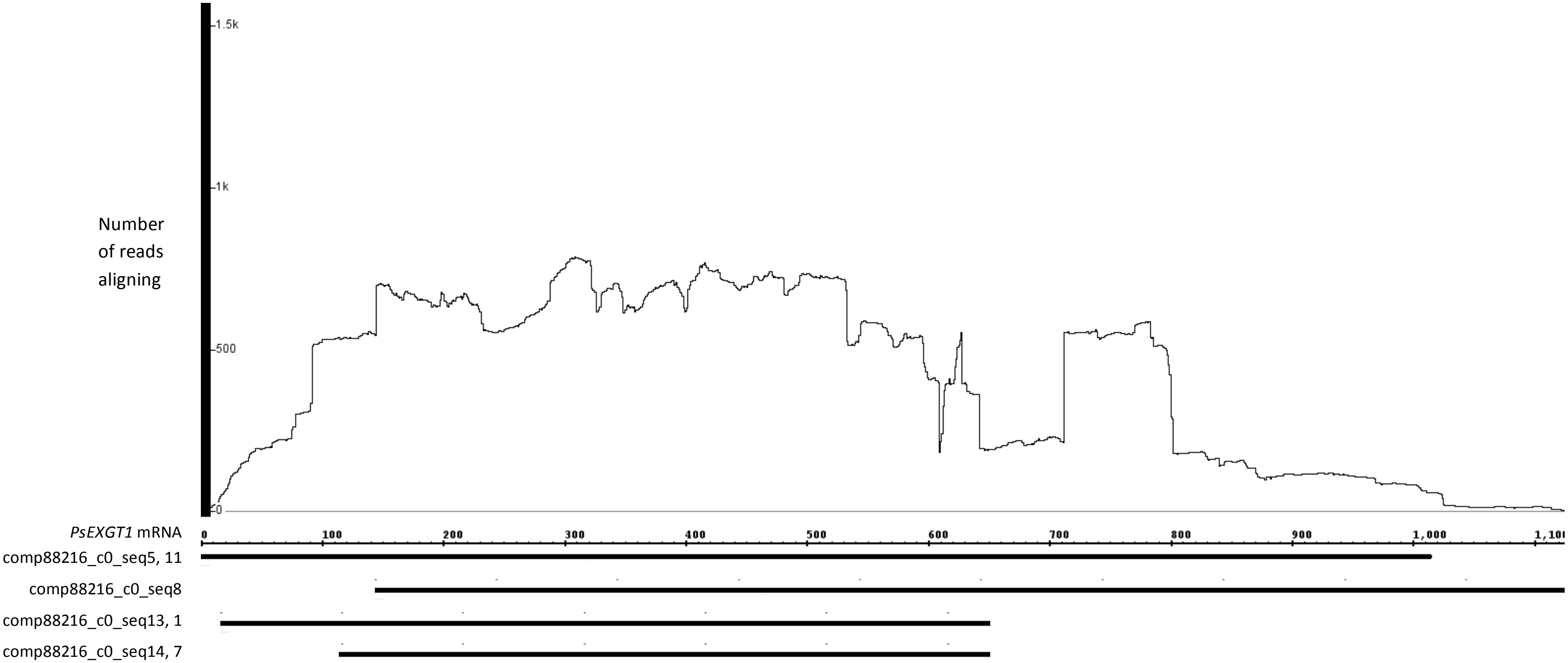

Figure S5: The number of reads aligning to the *PsFed-1* CDS and the alignment between *PsFed-1* CDS and its best hits to the pea bud transcriptome, comp55599_c1_seq1 and comp351273_c0_seq1

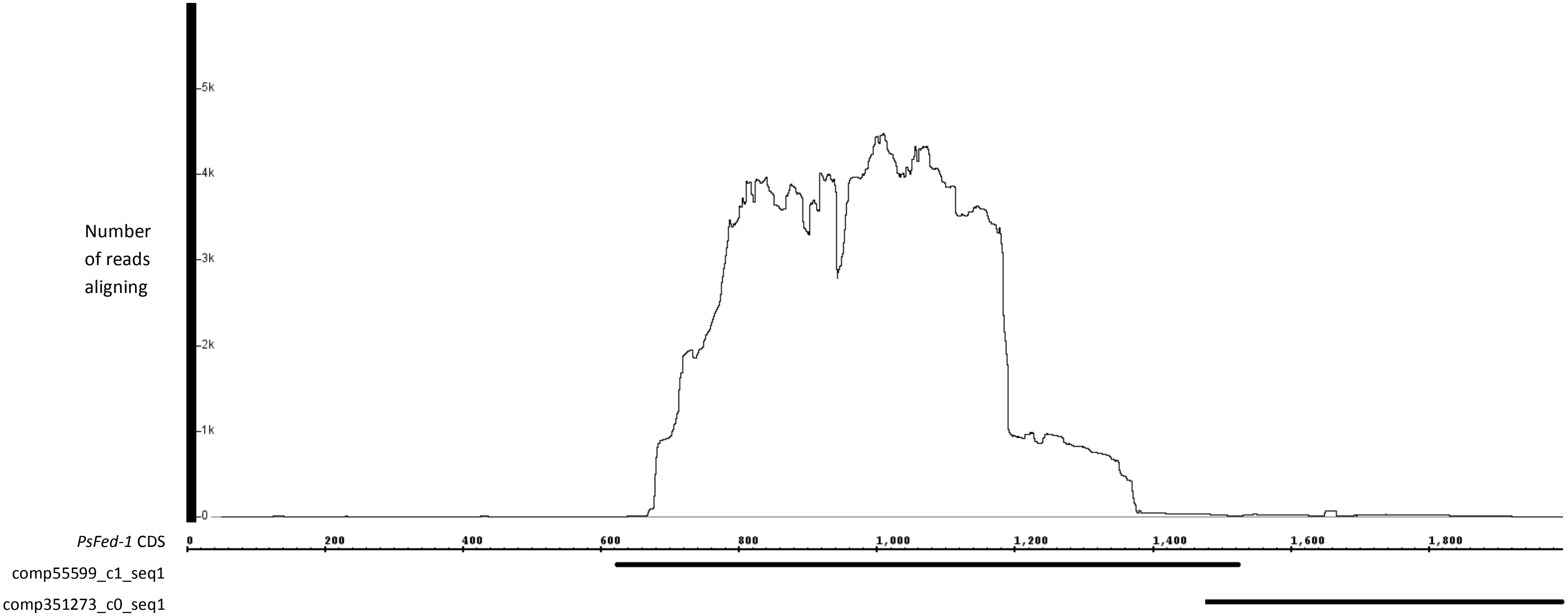

Figure S6: The number of reads aligning to the *PsHMG-1* mRNA and the alignment between *PsHMG-1* mRNA and its best hit to the pea bud transcriptome, comp81333_c0_seq1

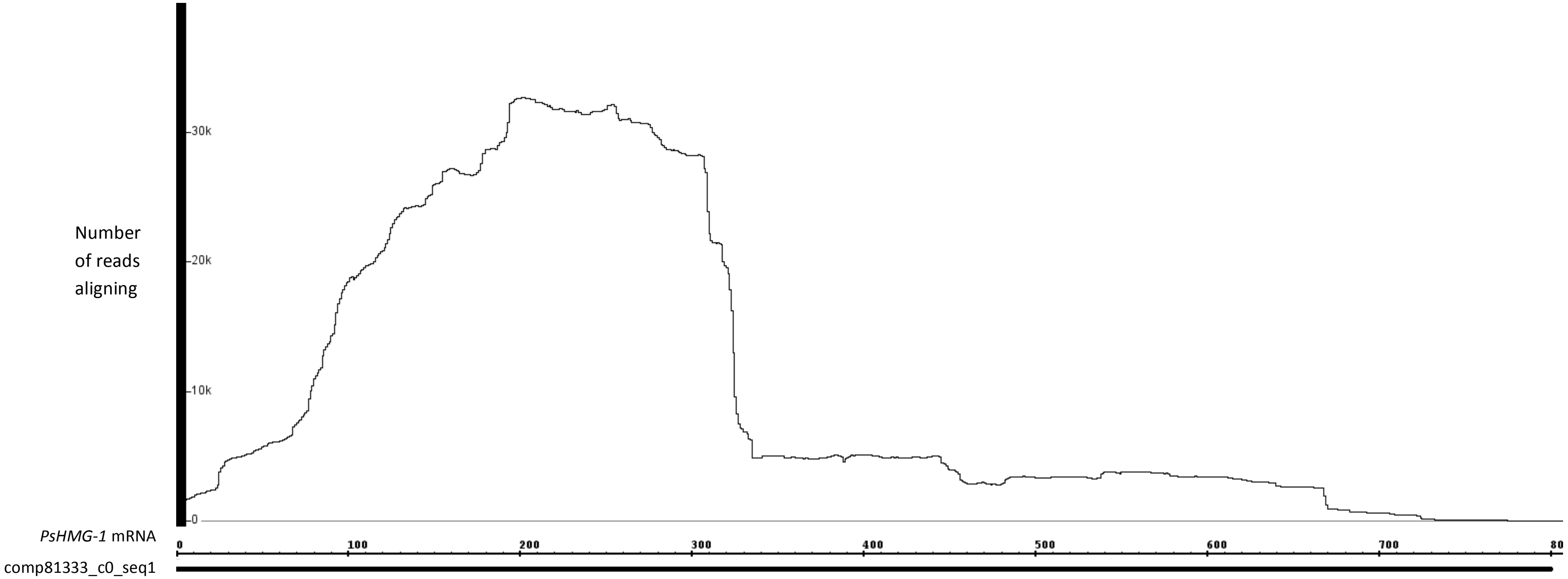

Figure S7: The number of reads aligning to the *PsKO1* mRNA and the alignment between *PsKO1* mRNA and its best hits to the pea bud transcriptome, comp71699_c1_seq1, 2, 3, 4

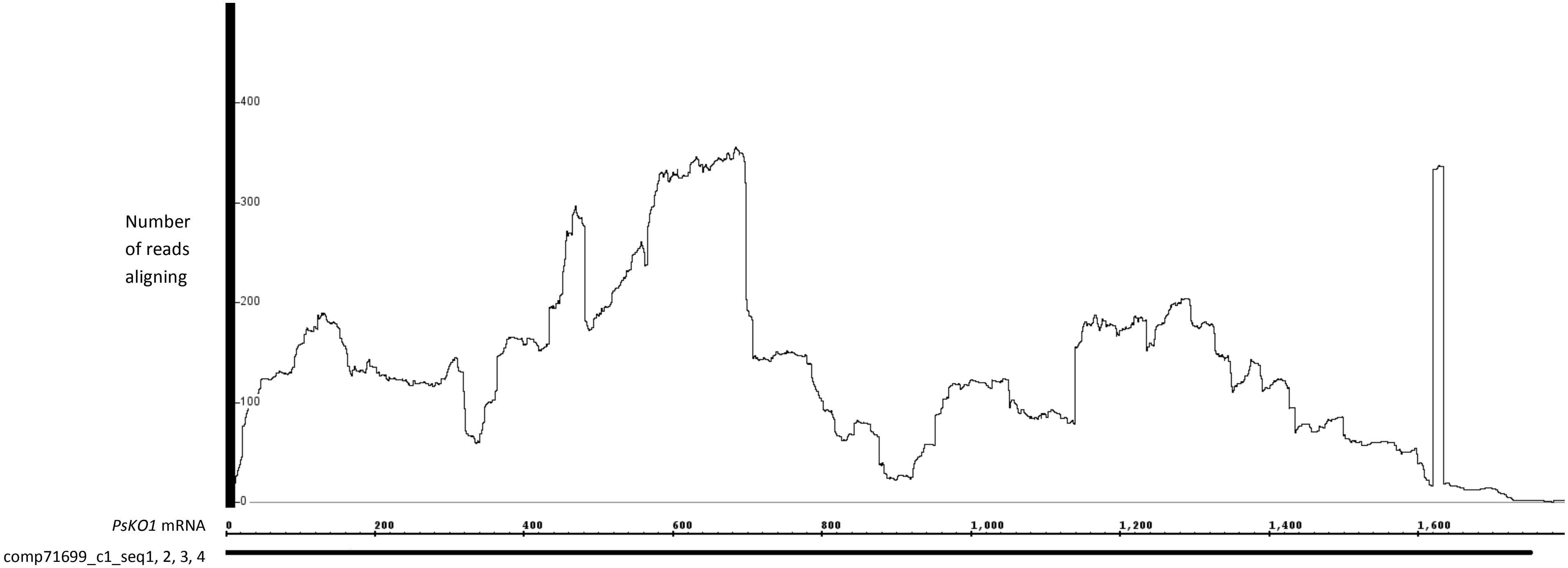

Figure S8: The number of reads aligning to the *PsPCNA* mRNA and the alignment between *PsPCNA* mRNA and its best hit to the pea bud transcriptome, comp93178_c0_seq1

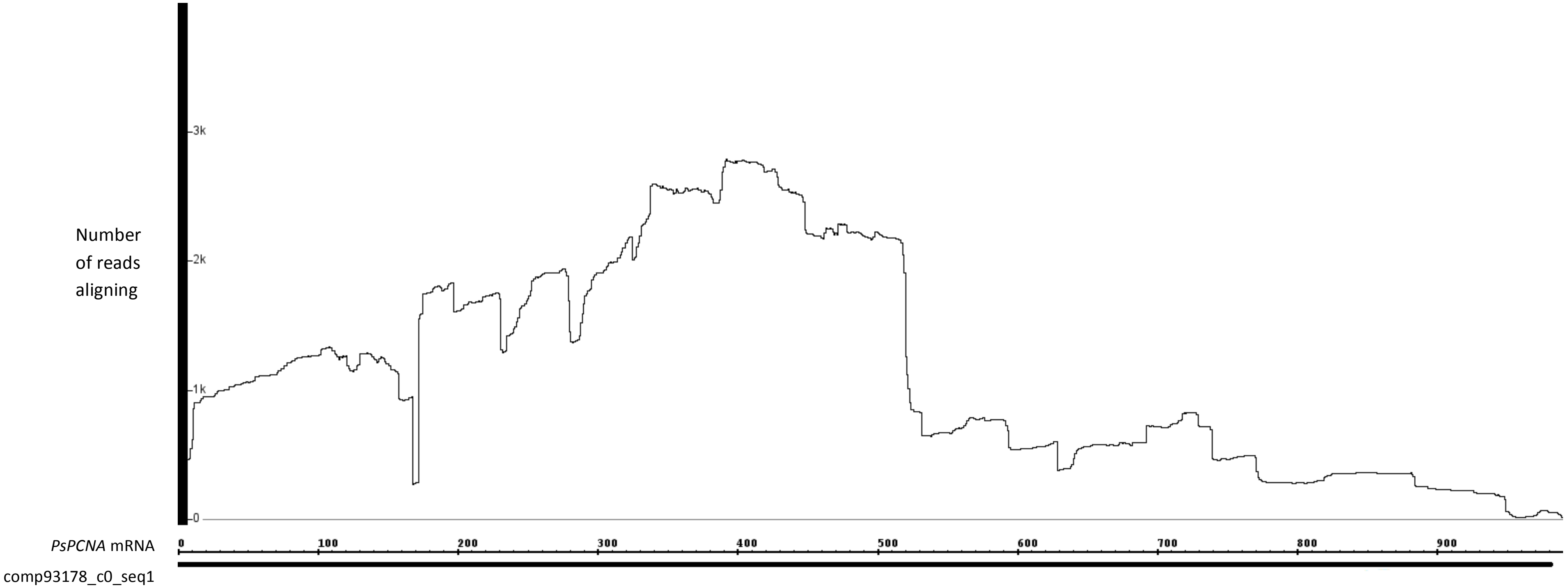

Figure S9: The number of reads aligning to the *PsPETE* gene and the alignment between *PsPETE* gene and its best hit to the pea bud transcriptome, comp92360_c0_seq1

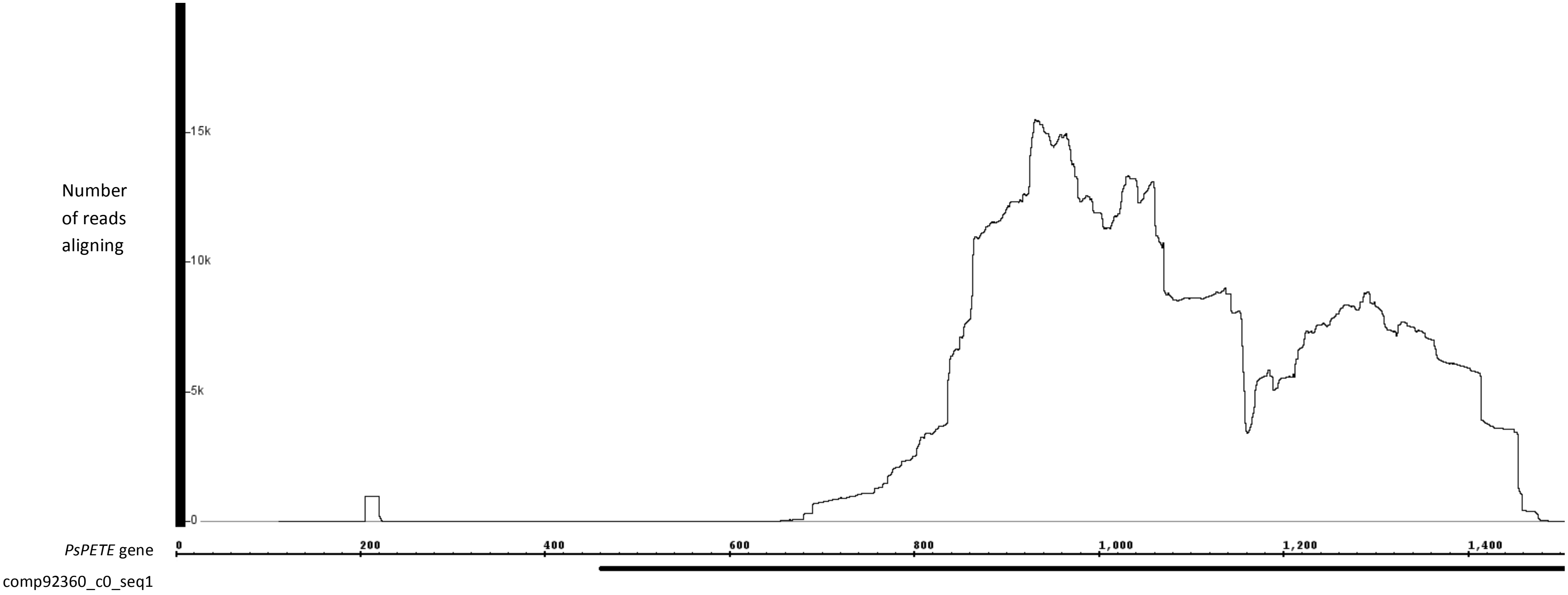

Figure S10: The number of reads aligning to the *PsRMS4* CDS and the alignment between *PsRMS4* CDS and its best hit to the pea bud transcriptome, comp97254_c0_seq1

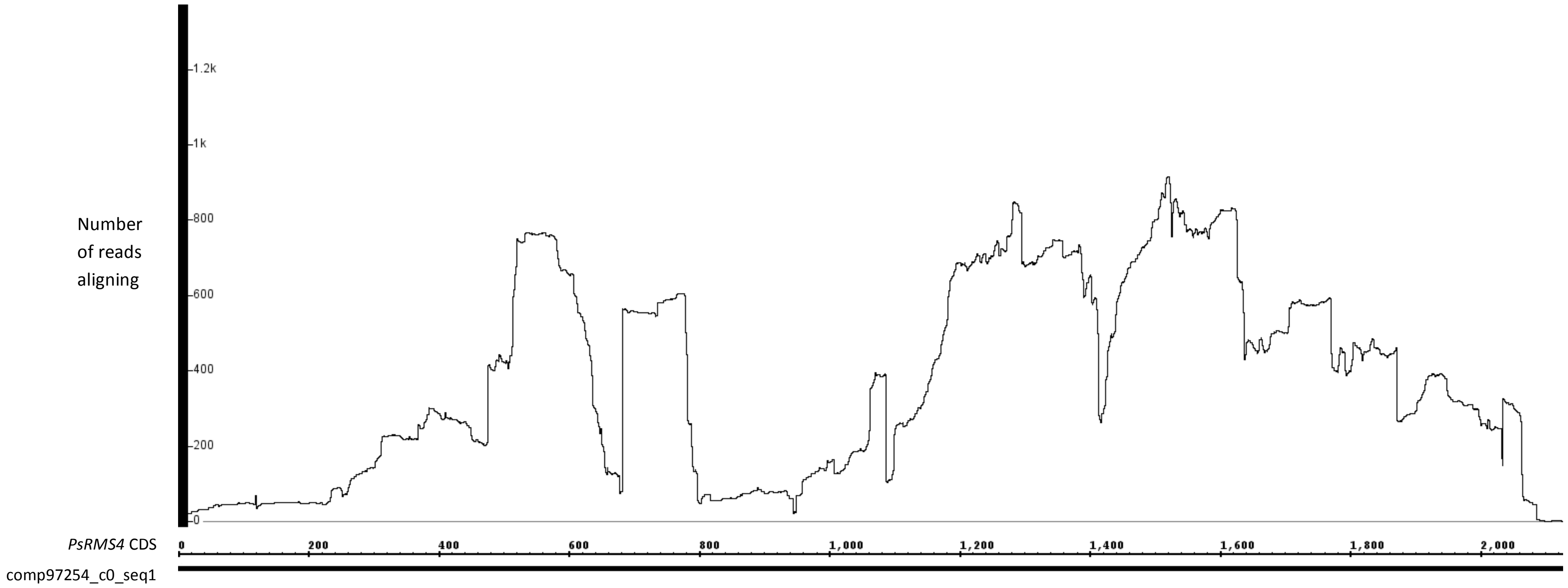

Figure S11: The number of reads aligning to the *PsRMS5* CDS and the alignment between *PsRMS5* CDS and its best hits to the pea bud transcriptome, comp74555_c0_seq1 and comp27382_c0_seq1