**Table S3:** Bioinformatic analysis of segmental duplicated in *P. tricornutum*.

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| ## Alignment 0: score=250.0 e\_value=1.8e-06 N=5 11&8 plus | | | |
| 0-0: | Phatr3\_EG00819.p1 | Phatr3\_EG00972.p1 | 9.00E-72 |
| 0-1: | Phatr3\_EG00830.p1 | Phatr3\_EG01002.p1 | 5.00E-97 |
| 0-2: | Phatr3\_EG00814.p1 | Phatr3\_EG00988.p1 | 5.00E-66 |
| 0-3: | Phatr3\_EG00832.p1 | Phatr3\_EG00982.p1 | 4.00E-96 |
| 0-4: | Phatr3\_J37030.p1 | Phatr3\_EG00984.p1 | 0 |
| ## Alignment 1: score=496.0 e\_value=1.4e-18 N=10 13&7 plus | | | |
| 1-0: | Phatr3\_EG02301.p1 | Phatr3\_J54465.p1 | 3.00E-111 |
| 1-1: | Phatr3\_J37393.p1 | Phatr3\_J35472.p1 | 2.00E-171 |
| 1-2: | Phatr3\_J47242.p1 | Phatr3\_J35473.p1 | 0 |
| 1-3: | Phatr3\_J47243.p1 | Phatr3\_J45710.p1 | 0 |
| 1-4: | Phatr3\_EG00921.p1 | Phatr3\_J45711.p1 | 0 |
| 1-5: | Phatr3\_J47245.p1 | Phatr3\_J45712.p1 | 0 |
| 1-6: | Phatr3\_J47246.p1 | Phatr3\_J45713.p1 | 0 |
| 1-7: | Phatr3\_J37399.p1 | Phatr3\_J35478.p1 | 3.00E-107 |
| 1-8: | Phatr3\_EG00895.p1 | Phatr3\_EG01007.p1 | 3.00E-146 |
| 1-9: | Phatr3\_EG00891.p1 | Phatr3\_EG01031.p1 | 6.00E-102 |
| ## Alignment 2: score=749.0 e\_value=4.9e-34 N=15 15&24 plus | | | |
| 2-0: | Phatr3\_J38389.p1 | Phatr3\_J40592.p1 | 7.00E-84 |
| 2-1: | Phatr3\_J38390.p1 | Phatr3\_J40593.p1 | 0 |
| 2-2: | Phatr3\_J48036.p1 | Phatr3\_J40594.p1 | 0 |
| 2-3: | Phatr3\_J48037.p1 | Phatr3\_J49807.p1 | 0 |
| 2-4: | Phatr3\_EG02497.p1 | Phatr3\_J49808.p1 | 0 |
| 2-5: | Phatr3\_EG02496.p1 | Phatr3\_J5780.p1 | 4.00E-165 |
| 2-6: | Phatr3\_J4049.p1 | Phatr3\_J4048.p1 | 0 |
| 2-7: | Phatr3\_J48040.p1 | Phatr3\_J49810.p1 | 0 |
| 2-8: | Phatr3\_J48041.p1 | Phatr3\_J49811.p1 | 0 |
| 2-9: | Phatr3\_J48042.p1 | Phatr3\_J49812.p1 | 6.00E-65 |
| 2-10: | Phatr3\_J51110.p1 | Phatr3\_J42322.p1 | 0 |
| 2-11: | Phatr3\_J48044.p1 | Phatr3\_EG00250.p1 | 0 |
| 2-12: | Phatr3\_J29266.p1 | Phatr3\_J30643.p1 | 1.00E-132 |
| 2-13: | Phatr3\_J38402.p1 | Phatr3\_J40605.p1 | 8.00E-133 |
| 2-14: | Phatr3\_J38403.p1 | Phatr3\_J40606.p1 | 2.00E-95 |
| ## Alignment 3: score=350.0 e\_value=4.8e-10 N=7 16&16 plus | | | |
| 3-0: | Phatr3\_J22319.p1 | Phatr3\_J5467.p1 | 4.00E-112 |
| 3-1: | Phatr3\_J51128.p1 | Phatr3\_J29456.p1 | 0 |
| 3-2: | Phatr3\_J38694.p1 | Phatr3\_J38702.p1 | 0 |
| 3-3: | Phatr3\_J48278.p1 | Phatr3\_J48286.p1 | 0 |
| 3-4: | Phatr3\_J48279.p1 | Phatr3\_J48287.p1 | 0 |
| 3-5: | Phatr3\_J48280.p1 | Phatr3\_J38705.p1 | 0 |
| 3-6: | Phatr3\_J22325.p1 | Phatr3\_J22332.p1 | 0 |
| ## Alignment 4: score=600.0 e\_value=4.5e-25 N=12 22&28 plus | | | |
| 4-0: | Phatr3\_J49350.p1 | Phatr3\_J50339.p1 | 0 |
| 4-1: | Phatr3\_J49351.p1 | Phatr3\_J50340.p1 | 1.00E-174 |
| 4-2: | Phatr3\_J49352.p1 | Phatr3\_J16669.p1 | 0 |
| 4-3: | Phatr3\_J49353.p1 | Phatr3\_EG02589.p1 | 0 |
| 4-4: | Phatr3\_J40043.p1 | Phatr3\_J41277.p1 | 4.00E-180 |
| 4-5: | Phatr3\_J40044.p1 | Phatr3\_J50343.p1 | 1.00E-110 |
| 4-6: | Phatr3\_EG02555.p1 | Phatr3\_J50344.p1 | 0 |
| 4-7: | Phatr3\_J49355.p1 | Phatr3\_J50345.p1 | 0 |
| 4-8: | Phatr3\_J4593.p1 | Phatr3\_J16719.p1 | 0 |
| 4-9: | Phatr3\_J40048.p1 | Phatr3\_J41282.p1 | 4.00E-164 |
| 4-10: | Phatr3\_J49357.p1 | Phatr3\_J50346.p1 | 0 |
| 4-11: | Phatr3\_J49358.p1 | Phatr3\_J50347.p1 | 0 |
| ## Alignment 5: score=397.0 e\_value=1.4e-14 N=8 24&29 plus | | | |
| 5-0: | Phatr3\_J40625.p1 | Phatr3\_J41286.p1 | 5.00E-63 |
| 5-1: | Phatr3\_J40626.p1 | Phatr3\_J41287.p1 | 2.00E-99 |
| 5-2: | Phatr3\_EG00240.p1 | Phatr3\_EG00090.p1 | 2.00E-65 |
| 5-3: | Phatr3\_J49826.p1 | Phatr3\_J50348.p1 | 0 |
| 5-4: | Phatr3\_J49827.p1 | Phatr3\_J50349.p1 | 0 |
| 5-5: | Phatr3\_J7293.p1 | Phatr3\_J7294.p1 | 0 |
| 5-6: | Phatr3\_J40630.p1 | Phatr3\_J41291.p1 | 0 |
| 5-7: | Phatr3\_J16195.p1 | Phatr3\_J6435.p1 | 2.00E-136 |
| ## Alignment 6: score=648.0 e\_value=3e-28 N=13 28&7 minus | | | |
| 6-0: | Phatr3\_J41117.p1 | Phatr3\_J35181.p1 | 0 |
| 6-1: | Phatr3\_J50214.p1 | Phatr3\_J45465.p1 | 0 |
| 6-2: | Phatr3\_J50216.p1 | Phatr3\_J45464.p1 | 0 |
| 6-3: | Phatr3\_J50217.p1 | Phatr3\_J35176.p1 | 0 |
| 6-4: | Phatr3\_J50218.p1 | Phatr3\_J45463.p1 | 0 |
| 6-5: | Phatr3\_EG00162.p1 | Phatr3\_EG01019.p1 | 0 |
| 6-6: | Phatr3\_J41125.p1 | Phatr3\_J45461.p1 | 1.00E-81 |
| 6-7: | Phatr3\_EG00150.p1 | Phatr3\_EG01038.p1 | 3.00E-156 |
| 6-8: | Phatr3\_J50220.p1 | Phatr3\_J45460.p1 | 0 |
| 6-9: | Phatr3\_J50221.p1 | Phatr3\_J35171.p1 | 0 |
| 6-10: | Phatr3\_J8044.p1 | Phatr3\_J8045.p1 | 3.00E-120 |
| 6-11: | Phatr3\_J52684.p1 | Phatr3\_J54412.p1 | 0 |
| 6-12: | Phatr3\_J41129.p1 | Phatr3\_J45457.p1 | 0 |

Note: 140 pairs of segmental-duplicated gene pairs were identified, but none of them were PtHSF gene pair.