

**Supplementary Table 1. Summary of *Pinus pinaster* sequencing data trimming, number of mapped reads**

<b>Genotype</b>	<b>Oria 6/R1S</b>			<b>Gal 1056/R1S</b>			<b>Gal 1056/R18T</b>			<b>Oria 6/R18T</b>		
<b>Library Number</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>	<b>9</b>	<b>10</b>	<b>11</b>	<b>12</b>
<b>Raw reads (Mb)</b>	13.23215	12.65581	13.00199	15.99188	14.89687	16.95577	22.64033	12.65853	16.14964	16.05427	26.35359	28.38755
<b>Average Length</b>	75.51	75.52	75.54	75.52	75.52	75.53	75.52	75.56	75.55	75.53	75.52	75.53
<b>Average Quality</b>	33.89	34.45	34.40	34.27	34.52	34.45	34.45	34.33	34.31	34.36	34.42	34.45
<b>Reads after reformat.sh and Sortmerna processing (Mb)</b>	11.77858	11.62967	7.17227	12.50118	13.12024	10.90749	19.52082	4.90925	7.62297	11.48367	24.15501	22.23719
<b>Average Length after processing</b>	73	73	73	73	73	73	73	73	73	73	73	73
<b>Number of mapped reads (Mb)</b>	10.92487	10.68927	6.512493	11.37022	12.34044	10.11667	17.87468	4.19261	6.83618	10.56037	22.596	20.49219