

Table EV1

	Total uniquely mapped reads	Duplicated reads (% of mapped)	Reads in genes (% of total)
WT GROseq replicate 1	89896885	63753050 (70.92%)	68696367 (76.42%)
Spt5 ^{dep} GROseq replicate 1	102390490	79318592 (77.46 %)	78948489 (77.11%)
WT GROseq replicate 2	18985113	7128662 (37.55 %)	13802882 (72.70%)
Spt5 ^{dep} GROseq replicate 2	15883820	5637059 (35.49 %)	11707359 (73.71%)
WT total Pol II ChIPseq replicate 1	34254590	3555338 (10.38 %)	22312265 (65.14%)
Spt5 ^{dep} total Pol II ChIPseq replicate 1	35577930	2423266 (06.81 %)	22299605 (62.68%)
WT total Pol II ChIPseq replicate 2	45029421	6801516 (15.10 %)	30046035 (66.73%)
Spt5 ^{dep} total Pol II ChIPseq replicate 2	39537028	3241876 (08.20 %)	25226357 (63.80%)
WT Ser2P-Pol II ChIPseq replicate 1	42664581	4500611 (10.55 %)	27458814 (64.36%)
Spt5 ^{dep} Ser2P-Pol II ChIPseq replicate 1	44132040	3161695 (07.16 %)	27362949 (62.00%)
WT Ser2P-Pol II ChIPseq replicate 2	49160826	3222351 (06.55 %)	29845667 (60.71%)
Spt5 ^{dep} Ser2P-Pol II ChIPseq replicate 2	52476532	4640850 (08.84 %)	32936179 (62.76%)
WT Ser5P-Pol II ChIPseq replicate 1	39829885	2123150 (05.33 %)	23927307 (60.07%)
Spt5 ^{dep} Ser5P-Pol II ChIPseq replicate 1	34297409	1675519 (04.89 %)	20489372 (59.74%)
WT Ser5P-Pol II ChIPseq replicate 2	47145197	5937842 (12.60 %)	30794466 (65.32%)
Spt5 ^{dep} Ser5P-Pol II ChIPseq replicate 2	42161104	2446793 (05.80 %)	25439635 (60.34%)
WT NELF ChIPseq	29500979	2997434 (10.16 %)	15677563 (53.14%)
Spt5 ^{dep} NELF ChIPseq	32237185	2518311 (07.81 %)	15749669 (48.86%)

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The table summarizes the results from deep-sequencing for each replicate dataset used in this study. For each replicate, the total number of uniquely aligned reads, the number of duplicated reads and the number of unique reads mapping within genes are indicated. Percentages of duplicated and genic reads are indicated in parentheses.