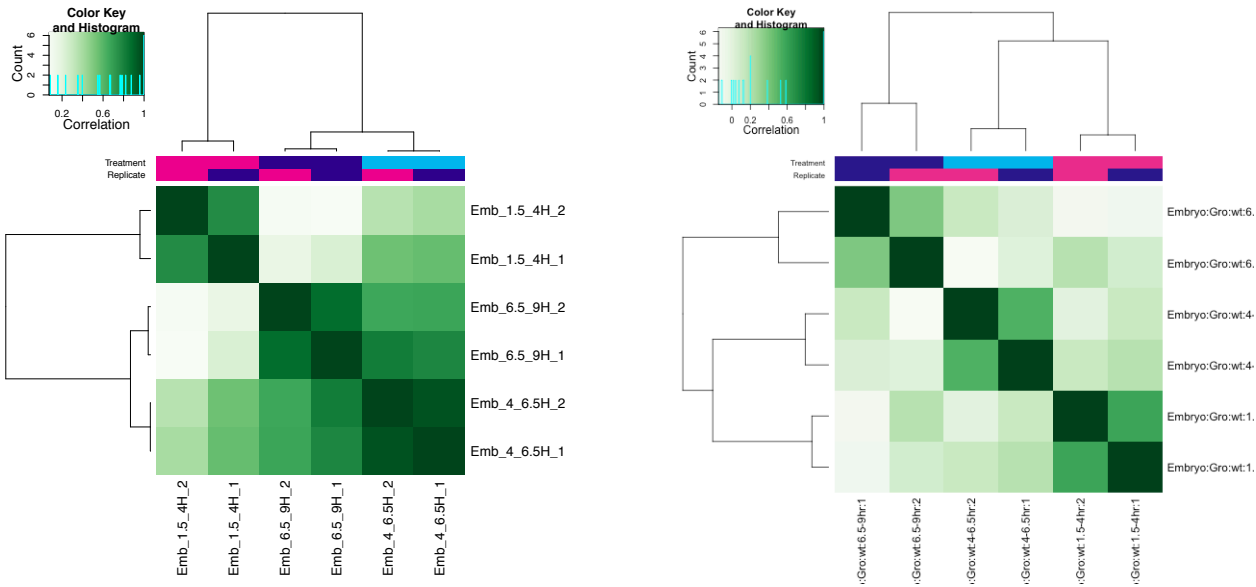


Fig. 2-a

A

Timepoint	Replicate	Total Reads	Uniquely Aligned	Multiply Aligned	Total Aligned	Overall Alignment Rate
Input	A	26,804,524	19,349,084	4,859,241	24,208,325	90%
Input	B	22,770,618	16,367,817	4,175,412	20,543,229	90%
1.5 - 4 hr	A	22,276,144	8,242,625	2,487,432	10,730,057	48%
1.5 - 4 hr	B	23,743,733	5,992,455	1,974,028	7,966,483	34%
4 - 6.5 hr	A	19,973,255	7,925,951	2,463,045	10,388,996	52%
4 - 6.5 hr	B	17,755,470	8,440,270	2,461,968	10,902,238	61%
6.5 - 9 hr	A	18,066,141	7,979,752	2,324,797	10,304,549	57%
6.5 - 9 hr	B	22,367,998	8,179,454	2,740,544	10,919,998	49%

B



C

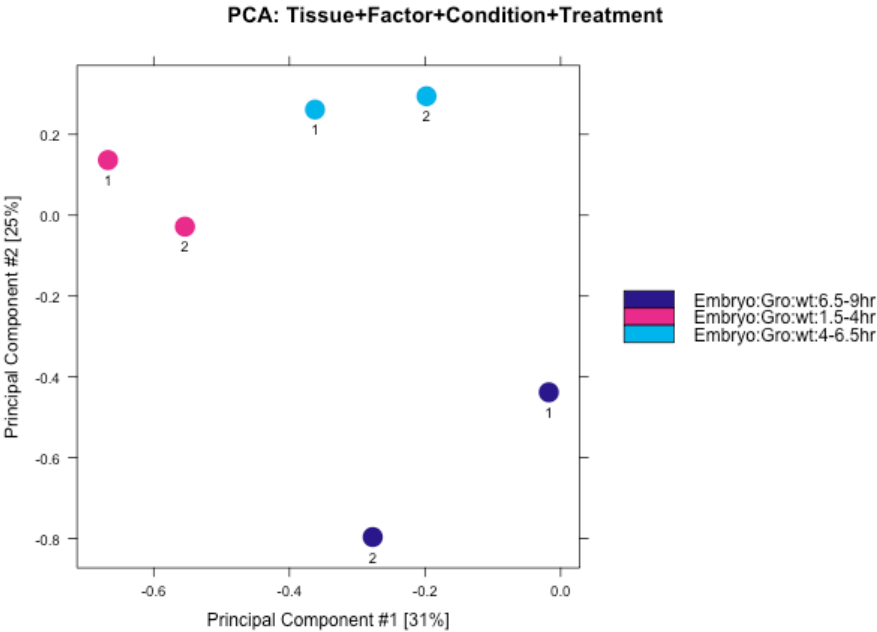


Fig. 2-b

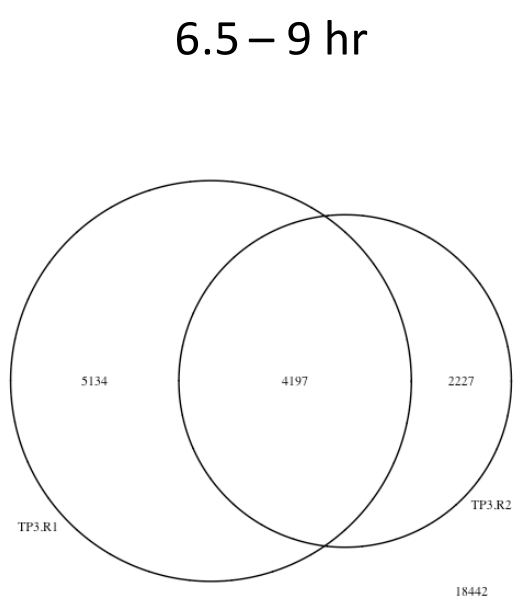
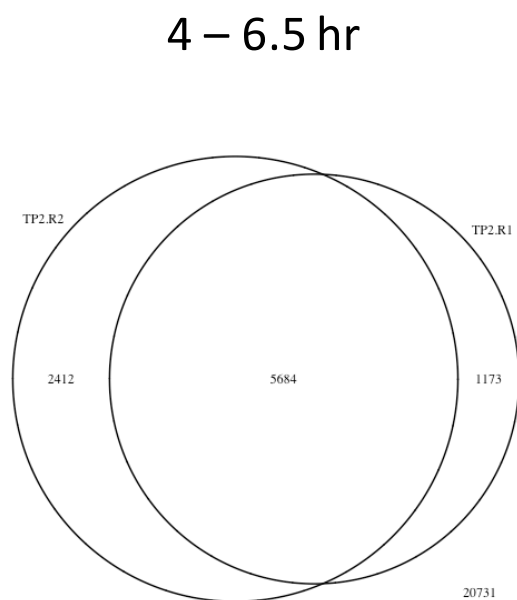
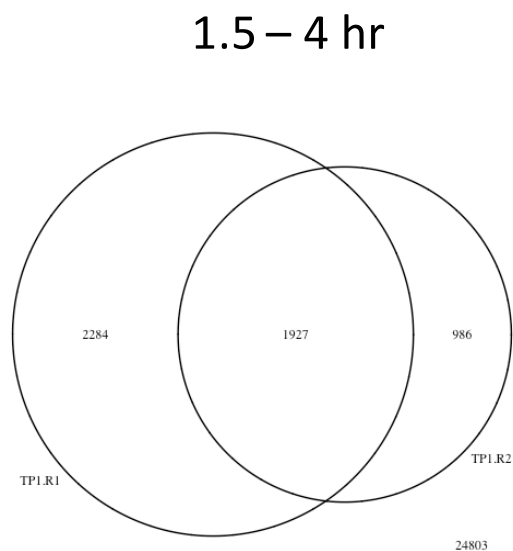
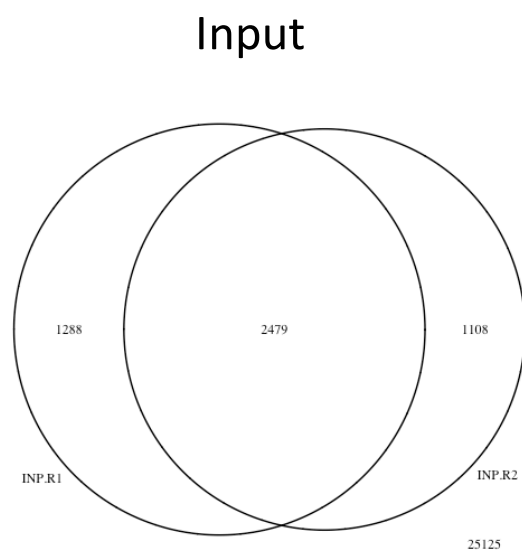
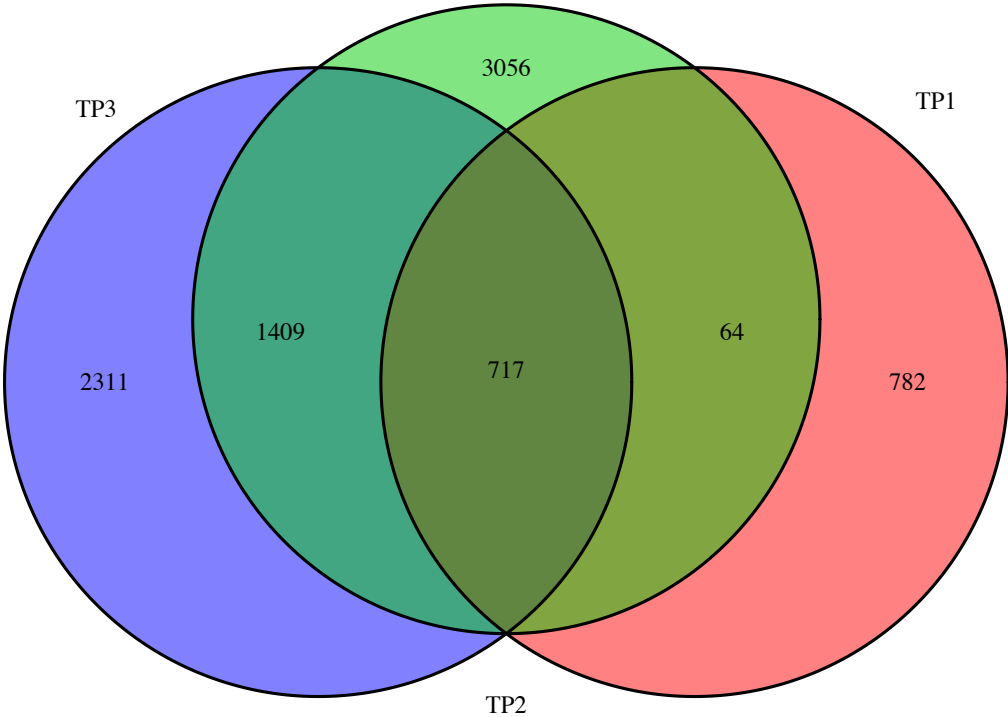


Fig. 2-c

A



B

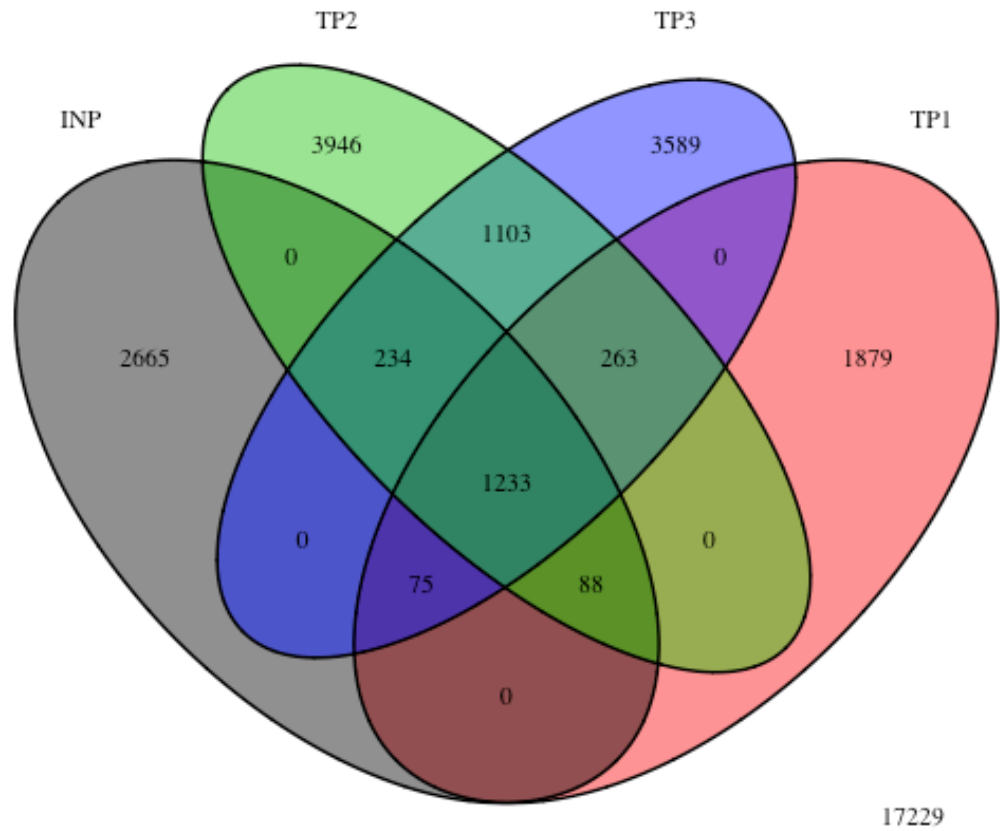


Fig. 2-d

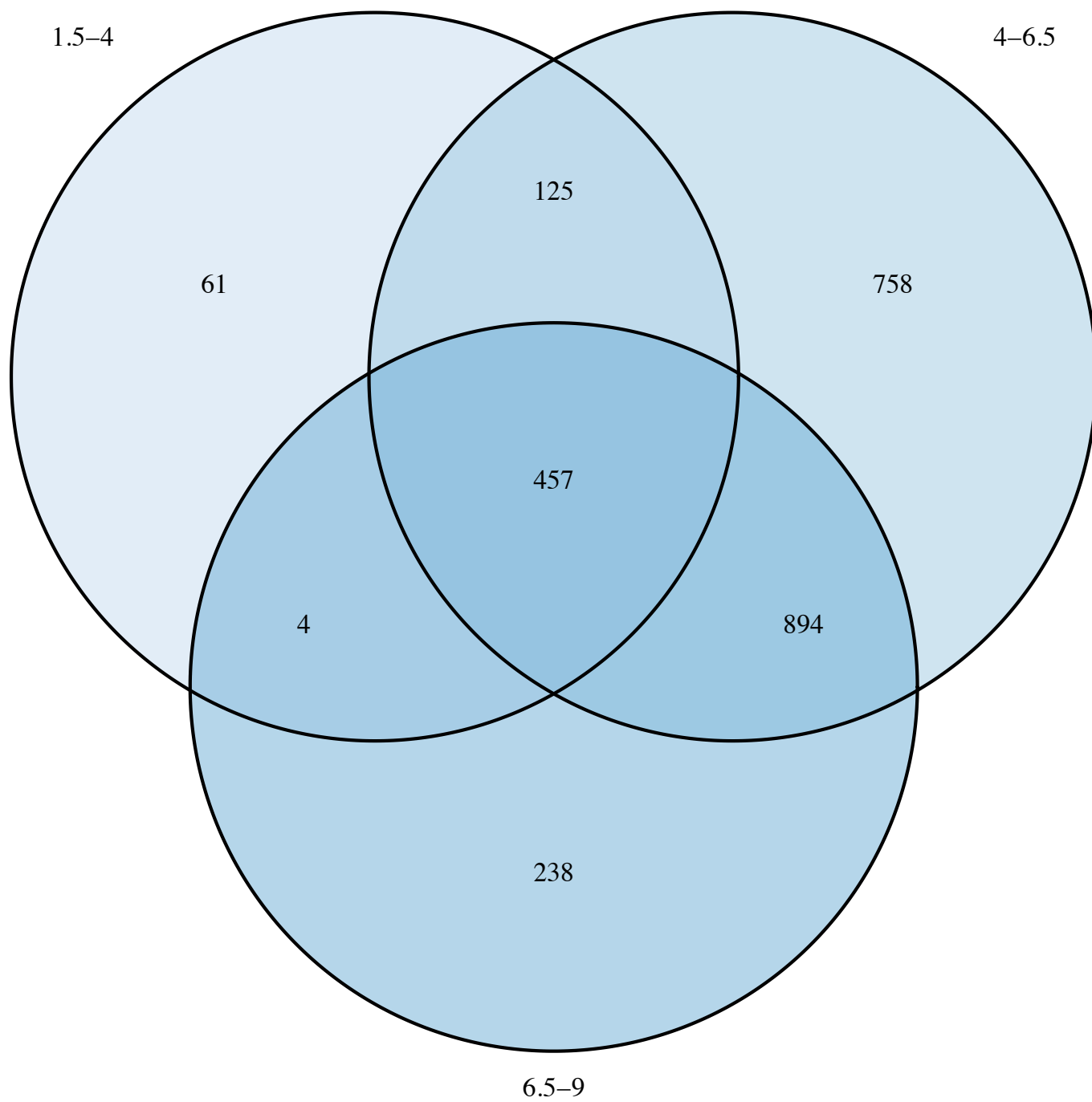
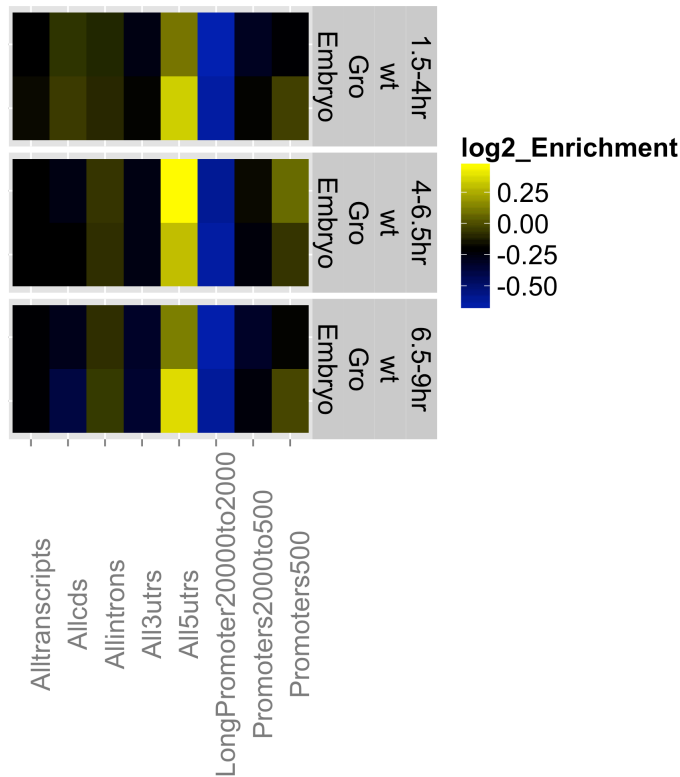


Fig. 2-e

A



B

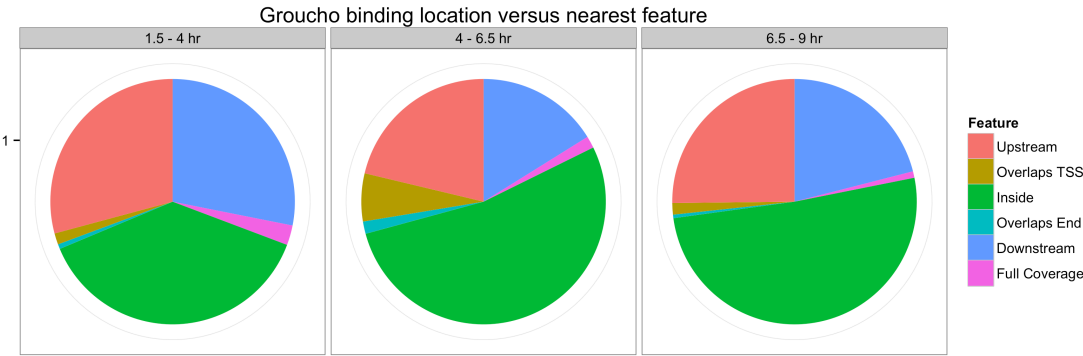


Fig. 2-f

Groucho binding location versus nearest feature

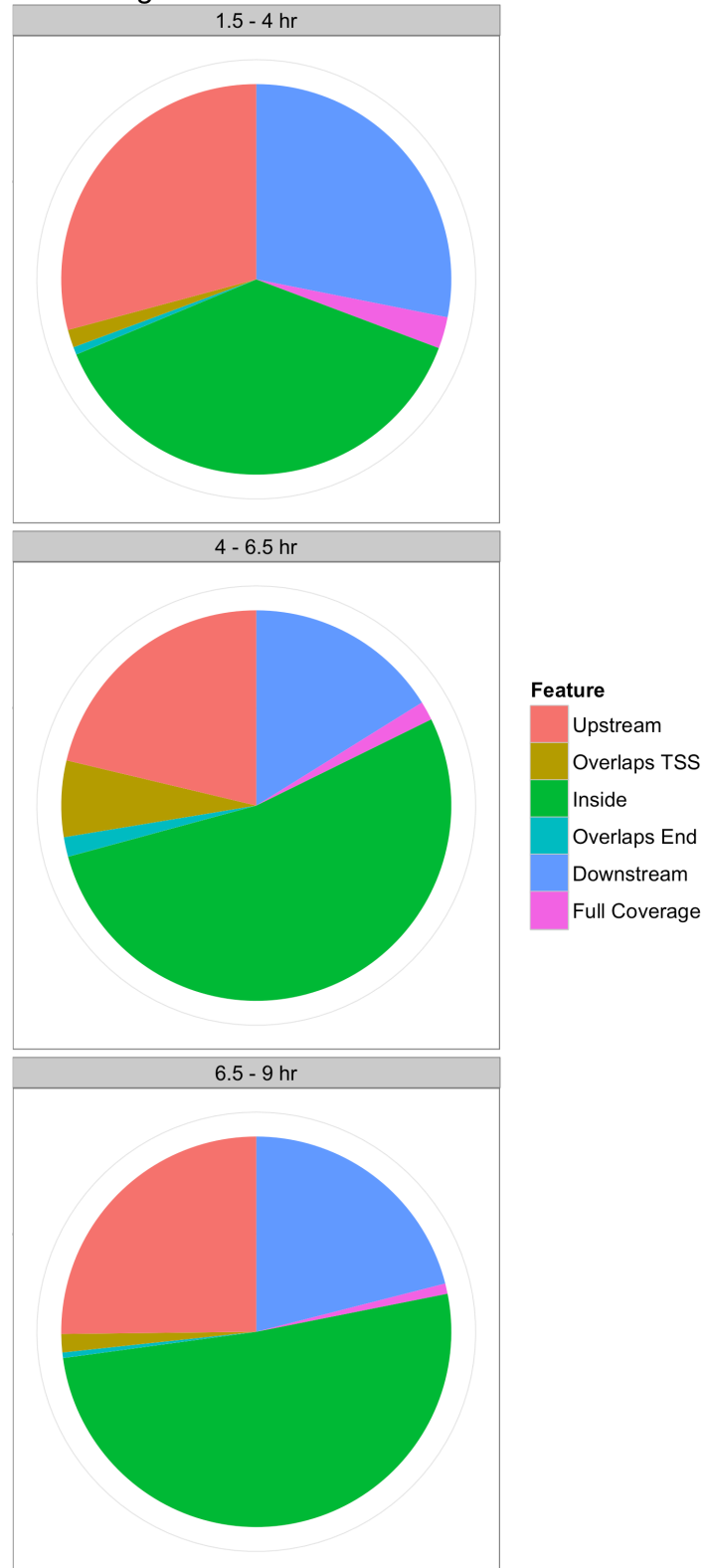
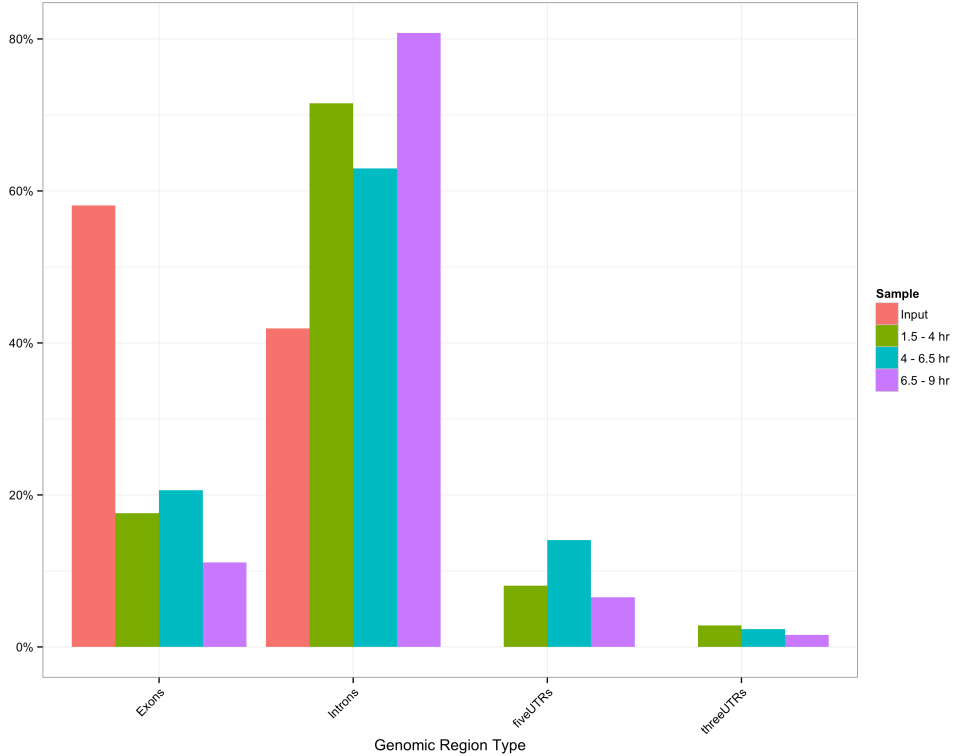


Fig. 2-g

A



B

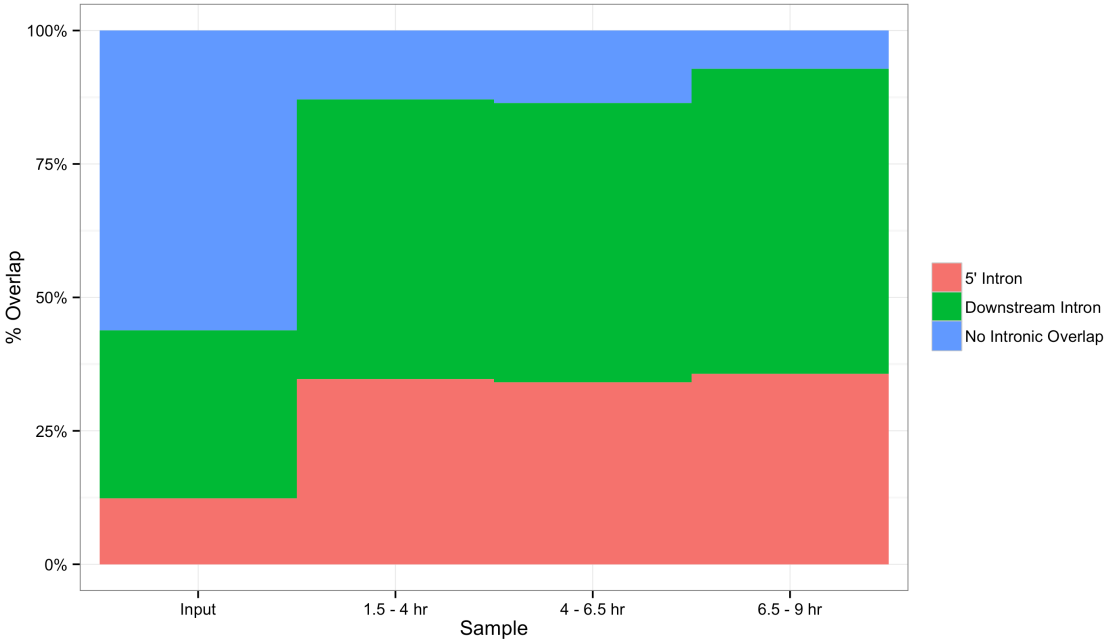


Fig. 2-h

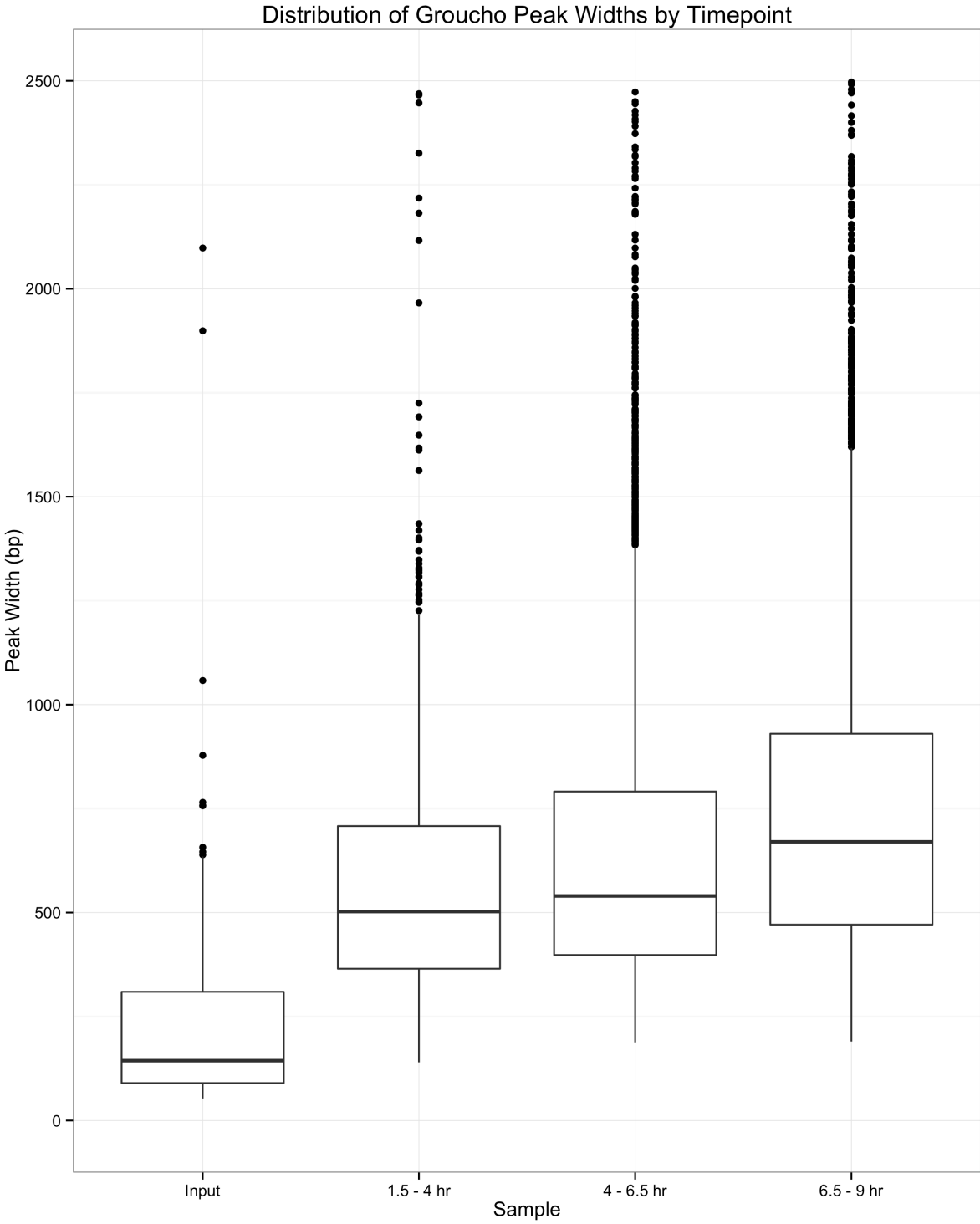




Fig. 2-i

		Percentage of genes with internal Grouch binding								
		Whole Gene			Exon			Intron		
		Down	No Change	Up	Down	No Change	Up	Down	No Change	Up
Gro LoF	1.5 - 4 hr	4%	2%	5%	2%	1%	2%	3%	2%	4%
	4 - 6.5 hr	11%	9%	14%	8%	6%	7%	8%	6%	12%
	6.5 - 9 hr	11%	6%	6%	5%	3%	3%	10%	4%	5%
2x Overexpression	1.5 - 4 hr	15%	2%	2%	7%	1%	1%	11%	1%	1%
	4 - 6.5 hr	43%	9%	6%	30%	6%	2%	32%	6%	4%
	6.5 - 9 hr	23%	6%	5%	9%	3%	2%	21%	5%	4%
4x Overexpression	1.5 - 4 hr	14%	2%	2%	8%	1%	0%	10%	2%	2%
	4 - 6.5 hr	42%	9%	6%	30%	6%	3%	32%	6%	3%
	6.5 - 9 hr	22%	5%	5%	9%	3%	2%	20%	4%	4%

Fig. 2-j

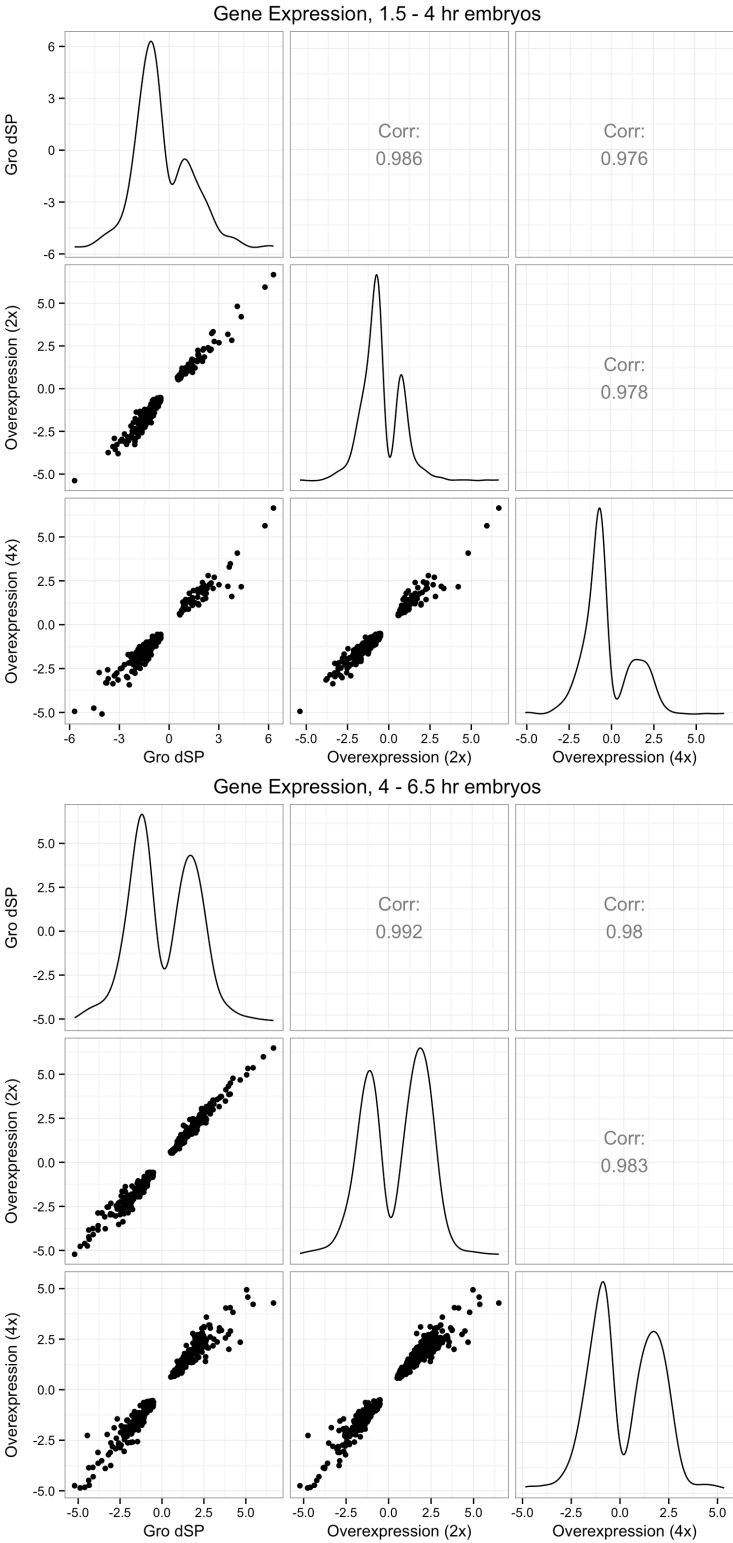


Fig. 2-j (continued)

