Step	Denovo tool		Classification	Variant Reduction in child
0	**Load most recent VCF/HCDIFF files for child, father, mother**			
1	**Remove parental variants**		PV MV, PV, MV	~ 120.000 -> 20.000
2	**Prefilter variants using prefilter file**			~ 20.000 -> 500 ~ 1.500
3	**For all remaining variants**	**Values**	**Classification**	**Related Variables**
	If the Pileups failed			
	Mark variant as		UNKNOWN - NO PILEUP RESULTS	
	If the **GATK** variant quality is below	300		gatk_low_quality_cutoff
	Mark variant as		LOW QUALITY	
	If the coverage in one of the parents **is lower** then	10		parental_coverage_threshold
	check for alternative reads			
	NO alternative reads			
	Mark variant as		SHARED,PATERNAL,MATERNAL - LOW COVERAGE	
	Alternative reads in one of the two parents Between 0 and	2		inheritance_cutoff_value
	Mark variant as		SHARED,PATERNAL,MATERNAL	
	if the coverage **is equal or higher** in both parens than	10		parental_coverage_threshold
	If there are **NO** alternative reads in the parents:			
	Mark variant as		POSSIBLE DE NOVO	
	If the number of alternative reads in one of the two parents Between 0 and	3		parental_variant_reads_threshold
	The percentage variation reads in both parents **is below**	15%		parental_percentage_variantion_low
	Mark variant as		POSSIBLE DE NOVO	
	The percentage variation reads in both parents **is equal or larger** than	15%		parental_percentage_variantion_low
	Mark variant as		SHARED,PATERNAL,MATERNAL	
	If the number of alternative reads in one of the two parents larger than	3		parental_variant_reads_threshold
	If the variant in the **child** has an allele frequency **between**	30% - 70%		child_percentage_variantion_threshhold - child_percentage_variantion_cutoff
	AND variant in the **child** has a GATK score of at least	500		gatk_high_quality_threshold
	AND If the variation percentage in the parent is lower then	25%		parental_percentage_variantion_high
	AND the variant meets the minimal coverage in the parent of	40		parental_mosaic_coverage_threshold
	Mark variant as		POSSIBLE MOSIAC (Paternal / Maternal)	
	ELSE			
	Mark variant as		SHARED,PATERNAL,MATERNAL	
	ELSE			
	Mark variant as		UNDETERMINED	
4	**Add classification supplements**			
	IF Variant is **MATERNAL** and on the **X** chromosome		MATERNAL - X-Linked	
	IF Variant is **POSSIBLE DE NOVO** and basecount(=x) of the child > 2		POSSIBLE DE NOVO - x - CALLS	
5	**Write results to hcdiffs.denovo file**			